The Age-structured Production Modelling approach for assessment of the Rock Lobster Resources at the Tristan da Cunha group of islands

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The stock assessment approach for all four islands of the Tristan da Cunha group is to use an age-structured production model (ASPM) to fit to catch, longline standardised CPUE and catch-at-length (CAL) data. The models consider only catches from 1990, i.e. models are initiated in 1990. The method for setting up the initial population age structure in 1990 is given below.

1. The population model

The resource dynamics are modeled by the equations:

$$N^{m}_{y+1,0} = R_{y+1} \tag{1}$$

$$N^{f}_{y+1,0} = R_{y+1} \tag{2}$$

$$N^{m}_{y+1,a+1} = \sum_{l} [\vec{N}^{m}_{y,a,l} e^{-M^{m}/2} - \vec{C}^{m}_{y,a,l} - D^{m}_{y,a,l}] e^{-M^{m}/2} \tag{3}$$

$$N^{f}_{y+1,a+1} = \sum_{l} [\vec{N}^{f}_{y,a,l} e^{-M^{f}/2} - \vec{C}^{f}_{y,a,l} - D^{f}_{y,a,l}] e^{-M^{f}/2} \tag{4}$$

$$N^{m}_{y+1,p} = \sum_{l} [\vec{N}^{m}_{y,p-1,l} e^{-M^{m}/2} - \vec{C}^{m}_{y,p-1,l} - D^{m}_{y,p-1,l}] e^{-M^{m}/2} + \sum_{l} [\vec{N}^{m}_{y,p,l} e^{-M^{m}/2} - \vec{C}^{m}_{y,p,l} - D^{m}_{y,p,;}] e^{-M^{m}/2} \tag{5}$$

$$N^{f}_{y+1,p} = \sum_{l} [\vec{N}^{f}_{y,p-1,l} e^{-M^{f}/2} - \vec{C}^{f}_{y,p-1,l} - D^{f}_{y,p-1,l}] e^{-M^{f}/2} + \sum_{l} [\vec{N}^{f}_{y,p,l} e^{-M^{f}/2} - \vec{C}^{f}_{y,p,l} - D^{f}_{y,p,l}] e^{-M^{f}/2} \tag{6}$$

where

$N^{m/f}_{y,a}$	is the number of male or female (*m/f*) lobsters of age *a* at the start of year *y* ,
$\vec{N}^{m/f}_{y,a,l}$	is the number of male or female (*m/f*) lobsters of age *a* of length *l* at the start of year *y* (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 0.20 in this model.
$\vec{C}^{m/f}_{y,a,l}$	is the catch of male or female (*m/f*) lobsters of age *a* of length *l* in year *y* ,
$D^{m/f}_{y,a,l}$	is the number of male or female (*m/f*) lobsters of age *a* of length *l* in year *y* that die due to discard mortality, and
p	is the maximum age considered (taken to be a plus-group).

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:

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

where

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

ς_y reflects fluctuation about the expected (median) recruitment for year *y* (here we estimate stock-recruit residuals for the period 1992-2003) and

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

$$B_y^{sp} = \sum_{a=0}^{p} f_a w_a^f N_{y,a}^f \qquad (8)$$

where w_a^f is the begin-year mass of female lobsters at age *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 $B^{sp} = K^{sp}$):

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

and

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

where

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

The total catch by mass in year *y* is given by:

$$C_y = \sum_{m/f} \sum_{a} \sum_{l \geq \min} w_{a+\frac{1}{2}}^{m/f} \vec{C}_{y,a,l}^{m/f} \qquad (12)$$

where

$$\vec{C}_{y,a,l}^{m} = \vec{N}_{y,a,l}^{m} S_l^m F_y \qquad (13)$$

$$\vec{C}_{y,a,l}^{f} = \vec{N}_{y,a,l}^{f} S_l^f F_y \qquad (14)$$

where $w_{a+1/2}^{m/f}$ denotes the mid-year mass of a *m/f* lobster of age *a*, and where

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

F_y is the fully selected fishing proportion in year *y* for lobsters, and which is constrained to be ≤ 0.90,

min is the minimum legal carapace length in mm, and

$$\vec{N}^{m/f}_{y,a,l} = N^{m/f}_{y,a} Q^{m/f}_{a,l} \tag{15}$$

where $Q^{m/f}_{a,l}$ is the proportion of fish of age *a* that fall in the length group *l* for the sex and area concerned (thus $\sum_l Q^{m/f}_{a,l} = 1$ 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.:

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

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 modeled to be proportional to the expected length-at-age *a*, i.e.:

$$\theta_a = \beta^* l^{m/f}_\infty\left(1-e^{-\kappa(a-t_0)}\right) \tag{17}$$

with β^* a fixed parameter of the model, and set here to 0.20.

1.1 Initial conditions

For the first year (1990) considered in the model, the stock is assumed to be at a fraction (θ) of its pre-exploitation spawning biomass, i.e.:

$$B^{sp}_{1990} = \theta \cdot K^{sp} \tag{18}$$

with the starting age structure for the first year given by:

$$N^{m,f}_{1990,0} = \theta^* R \tag{19}$$

where *R* is the recruitment corresponding to the *K* (for unexploited population size). The numbers at age for the starting population size in 1990 are then calculated as follows:

$$N^{m/f}_{1990,a} = N^{m/f}_{1990,a-1} e^{-(M+\varphi)} \qquad \text{for } 1 \le a \le m \tag{20}$$

and

$$N^{m,f}_{1990,m} = N^{m,f}_{1990,m} / [1 - e^{-(M-\varphi)}] \qquad \text{for } a=m \tag{21}$$

where φ is the average fishing proportion over the years immediately preceding 1990.

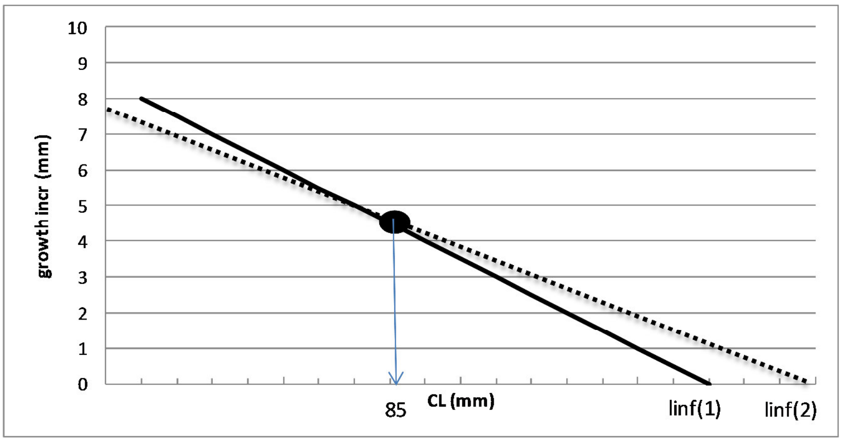
The value of φ is fixed at 0.01.

By adding a penalty to the likelihood, the value of fishing proportion in 2009, F_{1990}, can be set equal to any required level.

1.2 The von Bertalanffy Growth Function

Johnston (2011) reports the von Bertalanffy growth parameters for each island and sex as found in the literature. Note that the data for males were from Tristan and Nightingale only, and for females data from Tristan only. Johnston (2011) provides suggested von Bertalanffy parameters for each island and sex based on discussions with James Glass (pers. commn). The original growth parameter estimates were obtained from studies by Pollock and Roscoe (1977) and Pollock (1981). The tagging data centered around lobsters of carapace length 85mm. Original model fits using the von Bertalanffy parameters as reported in Johnston (2011) did not produce satisfactory fits to catch-at-length data. It was found that by changing the value slightly one could greatly improve model fits. The authors thus decided to follow the following method for setting the von Bertalnaffy growth parameters:

- Since most of the tagging data centered around carapace length 85mm, it would be assumed that the length increment for this length (i.e. 85mm CL) would remain fixed at the value reported in the literature.
- The value would be allowed to be increased or decreased in order to produce better fits to the CPUE and CAL data (this was done by fixing the values at different values and observing the resultant model fits)
- The κ value would be re-calculated for the new value, assuming a "pivot" through the growth increment line at 85mm, thus as the value changes, so does the κ value, but the growth increment at 85mm is not altered.



In the figure above, the solid line shows fit to the data as reported in the literature with linf(1) being the estimate produced. The dotted line shows how the authors modified this line by increasing the value in this case, but retaining the growth increment at the pivot CL of 85mm.

For a new value, linf(2), a new kappa value, kappa(2) (the slope parameter) is calculated as follows:

(22)

1.3 Discard Mortality

The number of lobsters that die due to discard mortality is calculated as follows:

$$D^m_{y,a,l} = d(\vec{N}^m_{y,a,l} S^m_l F_y) \qquad (23)$$

$$D^f_{y,a,l} = d(\vec{N}^f_{y,a,l} S^f_l F_y) \qquad (24)$$

where $D^{m/f}_{y,a,l}$ is calculated for $l < \min$, and *d* is the value of discard mortality which is set equal to 0.1 here.

1.4 Biomass estimates

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

$$B_y = B^m_y + B^f_y \qquad (25)$$

where

$$B^f_y = \sum_a \sum_{l\geq \min} S^f_l [w^f_{a+\frac{1}{2}} \vec{N}^f_{y,a,l} e^{-M^f/2}] \qquad (26)$$

$$B^m_y = \sum_a \sum_{l\geq \min} S^m_l [w^m_{a+\frac{1}{2}} \vec{N}^m_{y,a,l} e^{-M^m/2}] \qquad (27)$$

and where

B_y is the total (male plus female) model estimate of mid-year exploitable biomass for year *y*.

1.5 Fishing proportion:

$$F_y = \frac{C^{obs}_y}{B_y} \qquad (28)$$

The model constrains the upper fishing proportion limit to be 0.90.

1.6 Catch-at-length proportions

$$\hat{p}^m_{y,l} = \frac{\sum_a \vec{C}^m_{y,a,l}}{\sum_l \sum_m \sum_a \vec{C}^m_{y,a,l} + \vec{C}^f_{y,a,l}} \qquad (29)$$

$$\hat{p}^f_{y,l} = \frac{\sum_a \vec{C}^f_{y,a,l}}{\sum_l \sum_f \sum_a \vec{C}^m_{y,a,l} + \vec{C}^f_{y,a,l}} \qquad (30)$$

where $\hat{p}^{m/f}_{y,l}$ is the estimated proportion of catch of *m/f* lobsters in length class *l* in year *y.*

1.7 Selectivity-at-length function

The selectivity function (which depends on length) is assumed constant over time. Male and female selectivities are estimated separately as follows:

$$S_l^m = \frac{e^{-\mu^m l}}{1+e^{-\delta^m (l-l_*^m)}} \tag{31}$$

$$S_l^f = P\frac{e^{-\mu^f l}}{1+e^{-\delta^f (l-l_*^f)}} \tag{32}$$

The estimable parameters are thus:

- $l_*^{m/f}$,
- $\mu^{m/f}$,
- $\delta^{m/f}$, and
- *P* (the female scaling parameter)

The selectivity functions for males are scaled so that the maximum selectivity value is 1.0, and the female selectivity function is scaled by the multiplicative parameter *P*.

2. The likelihood function

The model is fitted to CPUE and catch-at-length (male and female separately) data, 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:

$$CPUE_y = q\ B_y e^{\varepsilon_y} \text{ or } \varepsilon_y = \ln(CPUE_y) - \ln(q\ B_y) \tag{33}$$

where

$CPUE_y$ is the CPUE abundance index for year *y*,

B_y is the model estimate of mid-year exploitable biomass for year *y* in given by equation 25,

q is the constant of proportionality (catchability coefficient), and

ε_y from $N(0,(\sigma\ )^2)$.

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

$$-\ln L = \sum_y \left[(\varepsilon_y)^2 / 2(\sigma\ )^2 + \ln(\sigma\ )\right] \tag{34}$$

where

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

$$\hat{\sigma}\ = \sqrt{1/n\sum_y \left(\ln CPUE_y - \ln\hat{q}\ \hat{B}_y\right)^2} \tag{35}$$

where

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

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

$$\ln\hat{q} \ = 1/n\sum_{y}\left(\ln CPUE_{y} - \ln\hat{B}_{y}\right) \tag{36}$$

2.2 Catches-at-length (from Rademeyer 2003)

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

$$-\ell\text{n}\, L^{\text{length}} = w_{len}\sum_{y}\sum_{l}\sum_{m/f}\left[\ln\left(\sigma_{len}/\sqrt{p^{m/f}_{y,l}}\right)+p^{m/f}_{y,l}\left(\ln p^{m/f}_{y,l}-\ln\hat{p}^{m/f}_{y,l}\right)^{2}/2\left(\sigma_{len}\right)^{2}\right] \tag{37}$$

where

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

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

$$\hat{\sigma}_{len} = \sqrt{\sum_{m/f}\ \sum_{y}\sum_{l} p^{m/f}_{y,l}\left(\ln p^{m/f}_{y,l}-\ln\hat{p}^{m/f}_{y,l}\right)^{2}/\sum_{m/f}\ \sum_{y}\sum_{l}1} \tag{38}$$

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 $p^{m/f}_{y,l}$ to downweight contributions from observed small proportions which will correspond to small predicted sample sizes.

2.3 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:

$$-\ln L = -\ln L + \sum_{y=y1}^{y2}\left[\frac{\varepsilon_{y}-\rho\varepsilon_{y-1}}{\sqrt{1-\rho^{2}}}\right]^{2}/2\sigma_{R}^{2} \tag{39}$$

where

$\varsigma_{y} = \rho\tau_{y-1}+\sqrt{1-\rho^{2}}\,\varepsilon_{y}$ is the recruitment residual for year *y* (see equation 1),

$\varepsilon_{y} \sim N(0,\sigma_{R}^{2})$,

σ_{R} is the standard deviation of the log-residuals, which is input,

ρ is their auto-correlation coefficient, and

y1=1992 and *y2*=2003 here.

Note that here , ρ is set equal to zero, i.e. the recruitment residuals are assumed uncorrelated, and σ_{R} is set equal to 0.4. Recruitment residuals are estimated for years 1992 to 2003 only.

The following term is added to constrain the size of these terms (i.e. to fit to genuine difference rather than to noise) and to force the average of the residuals to equal zero:

$$-\ln L = \ln L + W\left[\sum_{1992}^{2003}\frac{\varepsilon_{y}}{\sigma_{R}}\right]^{2} \tag{40}$$

where the weighting factor *W* is set high to ensure that the sum above ends as zero. This is to ensure that when projecting, the stock-recruitment curve used more closely reflects the past patterns of recruitment and its variability.

Future recruitment: The model estimates residuals for 1992-2003. For 2004+ recruitment is set equal to its expected values given the fitted stock-recruit relationship. The relationship itself is $R_y = \frac{\alpha B_y^{sp}}{\beta + B_y^{sp}} e^{\varepsilon_y}$ where $\varepsilon_y \sim N(0, \sigma_R^2)$ and $\sigma_R = 0.4$. This means that the expected recruitment

$$E[R_y] = \frac{\alpha B_y^{sp}}{\beta + B_y^{sp}} e^{\frac{\sigma_R^2}{2}} = \frac{\alpha B_y^{sp}}{\beta + B_y^{sp}} e^{0.08} \tag{41}$$

The residuals for years 1990 and 1991 are set equal to zero.

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 0.20. Lower values result in higher rates of decrease of selectivity at larger lengths. The value of 0.20 was considered to be the highest realistic value, given an intent to reduce this decrease in selectivity as far as possible.

Age-at-maturity: The proportion of lobsters of age *a* that are mature is approximated by $f_a = 1$ for *a* > 5 years (i.e. $f_a = 0$ for *a* = 0, …,5).

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 $w_a^{m/f}$ of a *m/f* lobster at age *a* is given by:

$$w_a^{m/f} = \alpha^{m/f} \left[\hat{L}_\infty^{m/f} \left(1 - e^{-\hat{\kappa}^{m/f} \left(a - \hat{t}_0^{m/f} \right)} \right) \right]^{\beta^{m/f}} \tag{42}$$

where the values assumed for the observed growth parameters and length-weight are reported in Johnston (2010).

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 and catch-at-length, to provide posterior distribution for these parameters and other model quantities.

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

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.
$l_*^{m/f}$:	U[1, 180] mm
$\mu^{m/f}$	U[0, 1]
$\delta^{m/f}$	U[0, 1]
P	U[0,5]
θ	U[0,1]
ς_y	U[-5,5]

References

Johnston, S.J. 2011. Data available for input to an age-structured production model of the Tristan lobster fishery. MARAM/Tristan/2011/Feb/01. 13pp.

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