

## AGE-STRUCTURED PRODUCTION MODEL SPECIFICATIONS, SEPTEMBER 1996

*Geromont, H.F.<sup>1</sup>*

### 1 Introduction

ASPM is an age-structured production model program, written by André Punt, which was used at the 1994 ICCAT SCRS meeting. The code has subsequently been revised and extended. A brief methodology and user's guide follow below.

### 2 The model

The resource dynamics are modelled by the equations:

$$N_{y+1,0} = R_{y+1} \quad (1)$$

$$N_{y+1,a} = N_{y,a} \exp^{-(M_a + S_{y,a} F_y)} = N_{y,a} \exp^{-Z_{y,a}} \quad \text{for } 1 \leq a < m \quad (2)$$

$$N_{y+1,m} = N_{y,m-1} \exp^{-(M_{m-1} + S_{y,m-1} F_y)} + N_{y,m} \exp^{-(M_m + S_{y,m} F_y)} \quad (3)$$

where

$N_{y,a}$  is the number of fish of age  $a$  at the start of year  $y$ ,

$M_a$  denotes the natural mortality rate on fish of age  $a$ ,

$S_{y,a}$  is the age-specific selectivity for year  $y$  (for all fleets and gears combined),

$F_y$  is the (asymptotic) fishing mortality in year  $y$ , and

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

The number of recruits at the start of year  $y$  is related deterministically to the spawner stock size by either the Beverton-Holt stock-recruit relationship:

$$R_y = \frac{\alpha B_y^{sp}}{\beta + B_y^{sp}} \quad (4)$$

or the Ricker stock-recruit relationship:

$$R_y = \alpha B_y^{sp} \exp^{-\beta B_y^{sp}} \quad (5)$$

where

$\alpha$  and  $\beta$  are spawner biomass-recruitment parameters, and

$B_y^{sp}$  is the spawner biomass at the start of year  $y$ ,

given by:

$$B_y^{sp} = \sum_{a=1}^m f_a w_a N_{y,a} \quad (6)$$

where

$w_a$  is the begin-year mass of a fish of age  $a$ , and

$f_a$  is the proportion of fish of age  $a$  that are mature.

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

$$C_y = \sum_{a=0}^m w_{a+\frac{1}{2}} N_{y,a} \frac{S_{y,a} F_y}{Z_{y,a}} (1 - \exp^{-Z_{y,a}}) \quad (7)$$

where  $w_{a+\frac{1}{2}}$  denotes the mid-year mass of a fish at age  $a$ .

The model estimate corresponding to an abundance index depends on whether the abundance series is an index of resource biomass:

$$\hat{I}_y^i = \sum_{a=0}^m w_a S_a^i N_{y,a} \quad \text{begin-year biomass} \quad (8)$$

$$\hat{I}_y^i = \sum_{a=0}^m w_{a+\frac{1}{2}} S_a^i N_{y,a} \exp^{-(Z_{y,a})/2} \quad \text{mid-year biomass} \quad (9)$$

or mid-year population numbers:

$$\hat{I}_y^i = \sum_{a=0}^m S_a^i N_{y,a} \exp^{-(Z_{y,a})/2} \quad (10)$$

where

$\hat{I}_y^i$  is the model estimate of abundance for year  $y$  and series  $i$ , and

$S_a^i$  is the selectivity function corresponding to the  $i$ th abundance series.

It is assumed that the resource is at the deterministic equilibrium that corresponds to an absence of harvesting at the start of the initial year ( $B_1 = K$ ). In order to reduce the number of parameters which need to be estimated from the data, selectivity at age ( $S_{y,a}$ ) is input.

#### 2.1 The likelihood function

The likelihood is calculated assuming that the observed abundance index is either normally distributed about its expected value:

$$I_y^i = q^i \hat{I}_y^i + \epsilon_y^i \quad \text{or} \quad \epsilon_y^i = I_y^i - q^i \hat{I}_y^i \quad (11)$$

or log-normally distributed:

$$I_y^i = q^i \hat{I}_y^i e^{\epsilon_y^i} \quad \text{or} \quad \epsilon_y^i = \ln(I_y^i) - \ln(q^i \hat{I}_y^i) \quad (12)$$

where

<sup>1</sup> Department of Mathematics and Applied Mathematics, University of Cape Town, Rondebosch 7700, South Africa.

$I_y^i$  is the abundance index for year  $y$  and series  $i$ ,

$\hat{I}_y^i$  is the corresponding model estimate,

$q^i$  is the constant of proportionality for abundance series  $i$ , and

$\epsilon_y^i$  from  $N(0, (\sigma^i)^2)$ .

The quantity minimised to estimate the model parameters ( $\alpha$ ,  $\beta$  and the catchability coefficients  $q^i$ ) is the negative of the log-likelihood function (after removal of constants):

$$-\ln L = \sum_i \left[ \sum_y (\epsilon_y^i)^2 / 2(\sigma_y^i)^2 + \ln \sigma_y^i \right] \quad (13)$$

**Relative abundance:** In the case of relative abundance series,  $\sigma_y^i = \sigma^i$  is the residual standard deviation for abundance series  $i$ , estimated in the fitting procedure by:

$$\hat{\sigma}^i = \sqrt{1/n_i \sum_y (I_y^i - q^i \hat{I}_y^i)^2} \quad \text{normal distribution} \quad (14)$$

or:

$$\hat{\sigma}^i = \sqrt{1/n_i \sum_y (\ln I_y^i - \ln q^i \hat{I}_y^i)^2} \quad \text{log-normal distribution} \quad (15)$$

where

$n_i$  is the number of data points for abundance series  $i$ , and

$q^i$  is catchability coefficient for abundance series  $i$ , estimated by its maximum likelihood value:

$$\hat{q}^i = \frac{\sum_y I_y^i \hat{I}_y^i}{\sum_y \hat{I}_y^i \hat{I}_y^i} \quad \text{normal distribution} \quad (16)$$

or:

$$\ln \hat{q}^i = 1/n \sum_y (\ln I_y^i - \ln \hat{I}_y^i) \quad \text{log-normal distribution} \quad (17)$$

**Absolute abundance:** In the case of absolute abundance series,  $\sigma_y^i$  is the estimate of the standard error of the resource biomass estimate for year  $y$ , which is input.

The constant of proportionality (effectively the bias) for absolute abundance series  $i$  is estimated by its maximum likelihood value:

$$\ln \hat{q}^i = \frac{\sum_y 1/(\sigma_y^i)^2 (\ln I_y^i - \ln \hat{I}_y^i)}{\sum_y 1/(\sigma_y^i)^2} \quad (18)$$

## 2.2 Estimation of standard errors

The option to calculate standard errors is available only for the assumption of log-normally distributed errors, and is effected by a parametric bootstrap procedure. Bootstrap samples are generated from the predicted abundance series obtained by fitting the model to the data. Error is then added to the predicted abundance indices according to the formula:

$$I_y^{i,U} = \hat{q}^i \hat{I}_y^i e^{\epsilon_y^{i,U}} \quad \text{where } \epsilon_y^{i,U} \sim N(0, (\hat{\sigma}_y^i)^2) \quad (19)$$

where

$I_y^{i,U}$  is the abundance index for year  $y$  and series  $i$  in bootstrap data set  $U$ ,

$\hat{I}_y^i$  is the estimate of the abundance index for year  $y$  and series  $i$  obtained by fitting the model to the actual data, and

$\hat{\sigma}_y^i$  is the estimate of the standard deviation for relative abundance (see equations 14 and 15) or absolute abundance series  $i$ .

The population model is fitted to each bootstrap data set in turn. Statistical properties, including standard error estimates, are then derived from the resultant set of estimates for quantities of interest.

## 3 Data

Annual total catch-by-mass ( $C_y$ ), relative and absolute abundance indices ( $I_y^i$ ), along with the sampling standard errors of the latter ( $\sigma_y^i$ ), are required as input. The following biological parameters are also input:

$m$ , the maximum age considered,

$S_{y,a}$ , the selectivity-at-age for each year for all fleets and gears combined,

$S_a^i$ , the selectivity at age  $a$  corresponding to abundance index  $i$ ,

$w_{a+\frac{1}{2}}$ , the mid-year mass of a fish at age  $a$ ,

$w_a$ , the begin-year mass of a fish at age  $a$ ,

$M_a$ , the natural mortality rate on fish of age  $a$ ,

$f_a$ , the proportion of fish of age  $a$  that are mature.