Specification of the population model and HCR used in the MP

Abstract

The Cape Town Procedure (MP) uses CPUE, gene tagging and CKMR (POP and HSP) data in three components of the Harvest Control Rule. For the CKMR component a simplified adult population model (abundance and total mortality) is fitted to the CKMR data. The log-linear trend in TRO is then used in the HCR. For the Gene-tagging and CPUE components of the HCR an upper and lower limit specifies a zone where no change is recommended to the TAC and above or below these limits there is a linearly increasing or decreasing change in TAC.

Adult population model

The adult population model is defined as follows:

$$
\begin{aligned}
N_{y_{\min},a_{\min}} &= \bar{R}\exp\left(\xi_{y_{\min}} - \sigma_R^2/2\right), \\
N_{y,a_{\min}} &= \bar{R}\exp\left(\epsilon_y - \sigma_R^2/2\right), \\
\epsilon_y &= \rho\epsilon_{y-1} + \sqrt{1-\rho^2}\xi_y, \\
\xi_y &\sim N(0,\sigma_R^2), \\
N_{y+1,a+1} &= N_{y,a}\exp\left(-Z_{y,a}\right) \qquad a \in (a_{\min}, a_{\max}), \\
N_{y+1,a_{\max}} &= N_{y,a_{\max}-1}\exp\left(-Z_{y,a_{\max}-1}\right) + N_{y,a_{\max}}\exp\left(-Z_{y,a_{\max}}\right), \\
Z_{y,a} &= Z_y \qquad a \le 25, \\
Z_{y,a} &= Z_y + \frac{a-25}{a_{\max}-25}\left(Z_{a_{\max}} - Z_y\right) \qquad a \in [26, a_{\max}], \\
Z_y &= \frac{Z_{\max}e^{\chi_y} + Z_{\min}}{1+e^{\chi_y}}, \\
\chi_{\text{init}} &\sim N(\mu_{\chi_{\text{init}}}, \sigma^2_{\chi_{\text{init}}}), \\
\chi_{y+1} &= \chi_y + \zeta_y, \\
\zeta_y &\sim N(0,\sigma_\chi^2), \\
TRO_y &= \sum_a N_{y,a}\varphi_a
\end{aligned}
$$

The fixed parameters and settings of this model are given by the following table:

Parameter	Value
$a_{\min}$	6
$a_{\max}$	30
σ_r	0.25
ρ	0.5
σ_χ	0.15
$Z_{\min}$	0.05
$Z_{\max}$	0.4
$Z_{a_{\max}}$	0.5
$\mu_{\chi_{\text{init}}}$	-1.38
$\sigma_{\chi_{\text{init}}}$	0.2
q_{hsp}	1

The estimated parameters of this model are:

1. The mean adult recruitment, $\bar{R}$
2. The adult recruitment deviations, ϵ_y
3. The initial value, χ_{init}, that "starts" the random walk for Z_y (with an associated normal prior mean and SD)
4. The random walk deviations ζ_y

The likelihood for the POP data is similar to that used in the OM. The total reproductive output is calculated as follows:

$$TRO_y = \sum_{a=a_{\text{amin}}}^{a_{\max}} N_{y,a}\varphi_a$$

and consider a juvenile-adult pair $\{i, j\}$, where $z_i = \{c\}$ is the juvenile covariate and c is it's cohort (year of birth) and $z_j = \{y, a\}$ is the adult covariate and y and a are the year and age at sampling, respectively. The probability of that pair being a POP is given by

$$\mathbb{P}\left(K_{ij} = POP \,|\, z_i, z_j\right) = \mathbb{I}\left(c < y < c + a\right) \frac{2\varphi_{a-(y-c)}}{TRO_c}$$

This probability is used to create the binomial likelihood for the POP data. For the HSP data the comparison is of a juvenile-juvenile pair i and i', where the key covariates are their respective years of birth - or cohorts - c. The probability of finding an HSP is defined as follows:

$$\mathbb{P}\left(K_{ii'} = HSP \,|\, z_i, z_{i'}\right) = \frac{4\pi^{\eta} q_{\text{hsp}}}{TRO_{c_{\max}}} \left(\sum_a \gamma_{c_{\min},a} \left(\prod_{k=0}^{\delta-1} \exp\left(-Z_{c_{\min}+k,a+k}\right) \right) \varphi_{a+\delta} \right),$$

$$\begin{aligned}
\gamma_{y,a} &= \frac{N_{y,a}\varphi_a}{TRO_y}, \\
\{z_i, z_{i'}\} &= \{c_i, c_{i'}\}, \\
c_{\min} &= \min\{c_i, c_{i'}\}, \\
c_{\max} &= \max\{c_i, c_{i'}\}
\end{aligned}$$

and this probability forms the basis of the binomial likelihood for the HSP data.

Harvest Control Rule

The general structure of the revised MP is as follows:

$$TAC_{y+1} = TAC_y \left(1 + \Delta_y^{\text{cpue}} + \Delta_y^{\text{ck}}\right) \times \Delta_y^{\text{gt}}, \tag{1}$$

Before detailing the functional form of the HCR we recap some useful variables:

- I_y^{ck}: moving average (of length τ^{ck}) of the estimated TRO from the MP population model (projected forward to the current year using the model to project forward for 4 years to avoid too much intertia in the signal when you need it)
- $\tilde{I}$: average estimated TRO from 2003 to 2014 (reference period w.r.t. relative rebuilding criterion)
- γ: proportional amount of TRO rebuilding we wish to achieve
- $\eta = I_y^{\text{ck}}/(\gamma\tilde{I}) - 1$: the variable at which passing from negative to positive indicates the point at which the TRO rebuilding has been achieved and the transition in the reactivity of the MP occurs (i.e. it goes from reactive to passive w.r.t. CPUE and CKMR signals *only*)

For the CPUE part of the HCR we used a density-dependent gain parameter:

$$k^{\text{cpue}}(\eta) = w_1^{\text{cpue}} \left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right) + w_2^{\text{cpue}} \left(1 + e^{-2\kappa\eta}\right)^{-1}$$

This is using the logistic function approximation to the Heaviside step function $H[\eta]$ ($H[\eta < 0] = 0$, $H[\eta \geq 0] = 1$). We set $\kappa = 20$ so the transition between the two gain parameters, given η, happens within $\pm 5\%$ of $\delta = 1$. The CPUE multiplier is then just defined as follows:

$$\Delta_y^{\text{cpue}} = k^{\text{cpue}}(\eta)\left(\delta_y^{\text{cpue}} - 1\right)$$

and δ_y^{cpue} is actually very similar in form to the gene tagging part of the HCR

$$\begin{aligned}
\delta_y^{\text{cpue}} &= \left(\frac{\bar{I}_{\text{cpue}}}{I_{\text{low}}}\right)^{\alpha_1} && \forall \bar{I}_{\text{cpue}} \leq I_{\text{low}}, \\
\delta_y^{\text{cpue}} &= 1 && \forall \bar{I}_{\text{cpue}} \in (I_{\text{low}}, I_{\text{high}}), \\
\delta_y^{\text{cpue}} &= \left(\frac{\bar{I}_{\text{cpue}}}{I_{\text{low}}}\right)^{\beta_1} && \forall \bar{I}_{\text{cpue}} \geq I_{\text{high}},
\end{aligned}$$

where $\bar{I}_{\text{cpue}}$ is the (4 year) moving average LL1 CPUE, $\bar{I}_{\text{low}}$ and $\bar{I}_{\text{high}}$ are upper and lower threshold CPUE values, and α_1 and β_1 allow for an asymmetric response above or below the threshold zone.

For the CKMR part of the HCR we try to ensure a minimum rate of increase in the TRO *beneath* the target level, and once it is achieved we would like to maintain the TRO at that level. To include this kind of behaviour in the HCR we also include some density-dependence in the log-linear growth rate at which the HCR moves from a TAC increase to a TAC decrease:

$$\begin{aligned}
\Delta_y^{\text{ck}} &= k^{\text{ck}}(\eta)\left(\lambda^{\text{ck}} - \tilde{\lambda}(\eta)\right), \\
k^{\text{ck}}(\eta) &= k_1^{\text{ck}}\left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right) + k_2^{\text{ck}}\left(1 + e^{-2\kappa\eta}\right)^{-1}, \\
\tilde{\lambda}(\eta) &= \lambda_{\min}\left(1 - \left(1 + e^{-2\kappa\eta}\right)^{-1}\right)
\end{aligned}$$

The threshold level at which the log-linear trend, λ^{ck}, goes from supporting a TAC decrease to an increase essentially begins at $\lambda_{\min} > 0$ and, as the estimated TRO approaches the target level, rapidly decreases to zero (in a similar way to the CPUE trend term). This is to ensure that a minimum level of rebuilding is encouraged for **all** trajectories below the target, and where above the target the *status quo* is preferred.

To calculate the recent mean age 2 abundance from the gene tagging data consider a weighted moving average approach:

$$\bar{N}_{y,2} = \sum_{i=y-1-\tau^{\text{gt}}}^{y-2} \omega_i \widehat{N}_{i,2}$$

where ω_i is a weighting proportional to the number of matches used to produce the GT estimate $\widehat{N}_{i,2}$ (basically inverse variance weighting). The 2 year delay between having the estimate and what year it actually refers to is factored into the calculation. The multiplier for the GT part of the HCR is as follows:

$$\Delta_y^{\mathrm{gt}} = \left(\frac{\bar{N}_{y,2}}{N_{\mathrm{low}}}\right)^{\alpha} \quad \text{if} \quad \bar{N}_{y,2} \leq N_{\mathrm{low}},$$
$$\Delta_y^{\mathrm{gt}} = 1 \quad \text{if} \quad \bar{N}_{y,2} \in (N_{\mathrm{low}}, N_{\mathrm{high}}),$$
$$\Delta_y^{\mathrm{gt}} = \left(\frac{\bar{N}_{y,2}}{N_{\mathrm{high}}}\right)^{\beta} \quad \text{if} \quad \bar{N}_{y,2} \geq N_{\mathrm{high}}$$

with N_{low} the limit level and N_{high} the upper level at where TAC increases are permitted. Table 2 details the parameter values for the HCR in the adqpted MP.

Parameter	Value
τ^{cpue}	4
w_1^{cpue}	0.9
w_2^{cpue}	0.005
I_{low}	0.45
I_{high}	1.42
α_1	1
β_1	1
τ^{gt}	5
N_{low}	1e+6
N_{high}	2.6e+6
α	1.5
β	0.25
τ^{ck}	3
k_1^{ck}	1.25
k_2^{ck}	0.05
γ	1.5
λ_{min}	0.001
κ	20

Table 2: *Fixed values of parameters of the HCR in the CTP.*