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Running the Cape Town Procedure for 2025

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Contents

1 Background

This paper details the key data inputs to the Cape Town Procedure (CTP) [1], the TAC calculation given the agreed data, and the breakdown of the MP calculation. The full specification of the CTP, the data inputs and the associated meta-rules for implementation are provided in Attachment 2 of the report of ESC25 [2].

2 Data inputs

There are four data inputs in the CTP:

1. **Gene tagging**: the MP uses the abundance estimate and the number of matches associated with that estimate
2. **Japanese LL CPUE**: the agreed Japanese long-line CPUE series
3. **CKMR POPs**: the updated parent-offspring pairs
4. **CKMR HSPs**: the updated half-sibling pairs

2.1 Gene tagging

We now have seven years of gene tagging 2 year old abundance estimates for the years 2016–2023 (minus 2020 because of COVID-19) [3]. Table 2.1 details the estimates and the number of recaptures associated with the estimate as these are the inputs to the MP. The MP is designed to handle singular instances of missing data (the 2020 data point has a weight of 0). The most recent estimated (age 2 abundance in 2023) is the highest estimate of the series, but also the most uncertain (lowest number of matches).

Year	Estimate	Recaptures
2016	2.27e+6	20
2017	1.15e+6	67
2018	1.14e+6	66
2019	1.52e+6	31
2020	-	-
2021	1.67e+6	41
2022	1.97e+6	38
2023	2.62e+6	14

Table 2.1: *Gene tagging abundance estimates and associated recaptures, both used as inputs to the MP.*

2.2 Japanese long-line CPUE

The CPUE used in the CTP is now the revised GAM-based single CPUE series that has been developed. Figure 2.1 shows the CPUE index used as an input to the CTP, as well as the key MP-related values that drive the CPUE part of the HCR in the CTP. The series runs from 1969 to 2024 and the most recent point is the highest of the series.

2.3 CKMR POPs & HSPs

The juvenile cohorts covered by the CKMR POP and HSP data are now 2002–2020 - these are in effect the years for which we have direct information on the abundance, overall mortality and age-structure of the adult population. In terms of POPs there are now 119 POPs from 197

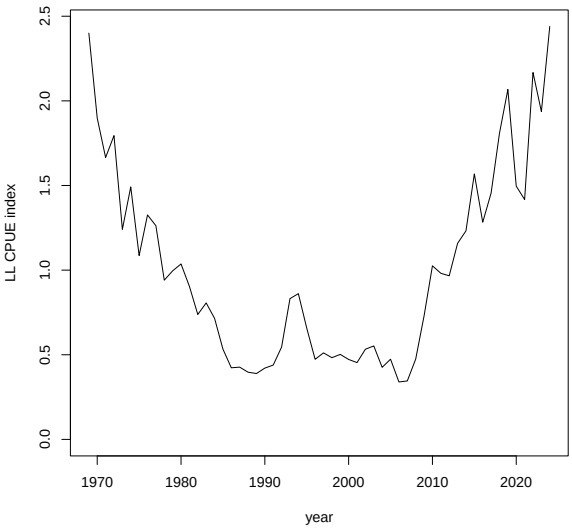

Figure 2.1: *CPUE index used as input to the 2025 MP.*

million comparisons. The overall detection rate has stabilised over the last few years. In terms of HSPs there are 157 true HSPs, from 130 million juvenile comparisons, above the false-positive threshold PLOD value, which currently implies a false-negative retention probability (key MP input) of 0.682.

3 Structure of the Cape Town Procedure

The Cape Town Procedure (CTP) has 3 components based on the data inputs from the following monitoring programs: Gene-tagging, CPUE and Close-Kin Mark Recapture (CKMR). Gene-Tagging provides an index of recruitment (abundance of 2 year-olds), CPUE provides an index of abundance for the age-classes exploited by the Japanese longline fishery and CKMR provides two indices of spawning biomass (one from Parent-Offspring-Pairs and one from Half-Sibling-Pairs) as well as information on the total mortality on the spawning component of the population.

For the gene-tagging component, the input is the most recent 5-year weighted average of the abundance estimates, where the weighting is proportional to the number of matches in each year. For the 2025 TAC decision only 4 estimates are available (2019–2023 minus 2020). The TAC change variable for the gene-tagging component will be less than one if the recent average is below the fixed lower bound, or will be greater than one if the recent average is above the fixed upper bound. If the recent average is between the upper and lower bounds, then the TAC multiplier is equal to one. Missing data points have a weight of 0 in the calculation of the weighted average.

For the CPUE component, the TAC change variable is also calculated based on fixed upper and lower bounds. It uses the average of the 4 most recent years from the specified standardised CPUE time-series. If this average value is between the bounds, the contribution to the overall TAC change is zero. If this average is below the lower bound, then the TAC change variable is negative, and if above the upper bound, the TAC change variable is positive. When the rebuilding target of 30% of TRO_0 is approached (approximated in the Close-Kin component), the MP

is designed to become less reactive, i.e. the recommended TAC changes will be smaller, to minimise future fluctuations in TAC while maintaining the spawning stock close to the target level.

The Close-Kin Mark-Recapture (CKMR) Parent-Offspring-Pair and Half-Sibling-Pair data are used in a simple population dynamics model of abundance and total mortality of adults, which provides a trend in adult abundance. This trend is compared to a threshold growth rate required to rebuild the adult abundance to the target in 2035. If the trend in adult abundance is above the threshold growth rate then the TAC change variable will be positive, and if the trend is lower than the threshold growth rate, the TAC change variable will be negative. The threshold growth rate is not fixed in the CTP but is calculated in the population model. This TAC change variable also becomes less reactive as the target level of rebuilding of the stock is approached. These three components are combined to give a single multiplier of the current TAC (see Appendix 1). The final TAC recommendation is constrained to be within a maximum change of 3,000t and minimum change of 100t.

4 TAC calculation and breakdown

The Cape Town Procedure standalone ADMB code was run with the agreed 4 data inputs (gene tagging, Japanese LL CPUE, CKMR POPs and HSPs). For the given initial parameter vector the maximum likelihood estimate of the adult population model fitted to the CKMR data was attained (maximum gradient 5.23e-6) and showed essentially no sensitivity to close-by alternative initial parameter values. Given that the CKMR data were are than adequately explained by the adult model (see Appendix 2), we would suggest that there are no complications with the model-based part of the CTP. Table 4.1 details the influence breakdown (in terms of a TAC multiplier purely for that part of the HCR) for each of the three components of the CTP, as well as the current and suggested TAC when all components are combined together as per Eq. (6.1).

Variable	Value
Δ^{gt}	1
Δ^{cpue}	0.36132
Δ^{ck}	0.00841
$(1+\Delta^{\mathrm{cpue}}+\Delta^{\mathrm{ck}})\times\Delta^{\mathrm{gt}}$	1.36973
Current TAC	20,647t
Suggested TAC	23,647t

Table 4.1: *Breakdown by HCR component, and the current and suggested TACs.*

For the gene tagging, the (5 year) recapture-weighted average age 2 abundance is 1.83 million, so within the 1–2.6 million region where the TAC multiplier is 1. This equates to “no-change” in TAC from the gene tagging component of the HCR. The CKMR log-linear trend in the estimated TRO is above the minimum required level and suggests a small increase in TAC. In the case of the CPUE index, the 4 year mean (2021–2024) is 1.99, which is above the threshold value at which the CPUE part of the HCR wants to increase the TAC (1.42); hence, the CPUE part of the HCR recommends an increase in the TAC. The combined change in TAC is 7,634t (just above a 35% increase) which is above the 3,000t maximum change constraint of the CTP. Taking this into account, the suggested TAC change from the CTP is 3000t which would mean a TAC of 23,647t i.e for the 2027-2029 TAC block - **the maximum permitted increase**.

1. The MP is acting as expected when it was selected; an updated set of projections done in 2023 demonstrated. In particular the projected dynamics for the 2025 TAC decision were that there will almost certainly be a full increase in 2025. This is what has happened in reality so the current maximum permitted increase is not unexpected in terms of what we projected might happen back in 2019, 2022, and after the 2023 updating of the OM. Given the stability and precision the CKMR data have brought to OM estimates of SSB, and the overall slower nature of SBT dynamics relative to say tropical tuna, this consistency is perhaps to be expected.
2. The median of the relative TRO in 2035 was projected to be 0.3 based on the 2023 OM reconditioning done as part of the stock assessment. This is precisely the value the CTP was tuned to achieve in 2019, so the MP appears to still be on target. Additionally, the most recent OMMP did not see any reason to reject the recommended TAC, as originally tuned and adopted, with the most recent updated data.

5 Discussion

This paper detailed the structure of the Cape Town Procedure, the four data sets used as inputs (gene tagging, Japanese long-line CPUE, CKMR POP and HSP data), and how they all link together within the adopted MP to give the suggested TAC for the 2027-2029 period.

6 Acknowledgements

This work was funded by CSIRO and the Australian Fisheries Management Authority.

References

[1] Anonymous (2019) Report of the 24th meeting of the Extended Scientific Committee. Cape Town, South Africa.

[2] Anonymous (2020) Report of the 25th meeting of the Extended Scientific Commitee (held online).

[3] Preece, A.L. *et al.*. (2025) Update on the gene-tagging program 2025. *CCSBT–ESC/2508/9*

Appendix 1

The general structure of the CTP is as follows:

- The MP uses CPUE, gene tagging and CKMR (POP and HSP) data
- For the CKMR part a simplified adult population model (abundance and total mortality) is fitted to the CKMR data. The log-linear trend in TRO, λ^{ck}, is then used in the HCR. Prior to the estimated recovery of the stock to the tuning a level TAC increases are permitted *only* for positive trends above a minimum positive level. As the stock reaches the target level this reverts to positive/negative trends increasing/decreasing the TAC.
- For both the CPUE and CKMR trend terms the gain parameter is density-dependent. For a given level of TRO rebuilding (relative to the recent estimates) the gain parameter is stronger prior to reaching the rebuilding then decreases as the TRO reaches the target level. This ensures reactivity when needed (in the rebuilding phase) but stability when rebuilding is achieved.
- For the gene tagging term a limit-type approach is used: (i) for values of the current 5 year average 2-year old abundance below the limit strong (supralinear) decreases in TAC are enacted; (ii) for values above the upper level weaker (sublinear) increases in TAC are permitted; (iii) for values between the two nothing is done to the TAC. A crucial difference for the GT part of the HCR is that there is *no* inertia: once the values appear outside the bounds of inaction the TAC is proportionally changed
- For the CPUE data the HCR is similar to that applied to the gene tagging data: there is a zone where no change is recommended and above and below this level of mean recent CPUE there is a linearly increasing or decreasing change in TAC

The Harvest Control Rule (HCR) is as defined follows:

$$TAC_{y+1} = TAC_y \left(1 + \Delta_y^{\mathrm{cpue}} + \Delta_y^{\mathrm{ck}}\right) \times \Delta_y^{\mathrm{gt}}, \tag{6.1}$$

where the inertial terms for the CPUE and CKMR parts of the HCR are additive, not multiplicative. This avoids the quadratic term in the multiplicative case where both trends are consistently positive consistently making the TAC increases larger than for the additive case, despite the trends being the same in both cases. 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
- $\eta = I_y^{\mathrm{ck}}/(\gamma\tilde{I}) - 1$: 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:

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

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 6.1 details the parameter values for the HCR in the adopted 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 6.1: *Fixed values of parameters of the HCR in the CTP.*

Appendix 2

Herein we provide the key data fitting summaries and adult population dynamic variables from the population model fitted to the CKMR POPs and HSPs in the CTP. Figure 6.1 details the POP fitting summaries; Figure 6.2 the HSP fitting summaries; and Figure 6.3 the TRO and mean adult total mortality summaries.

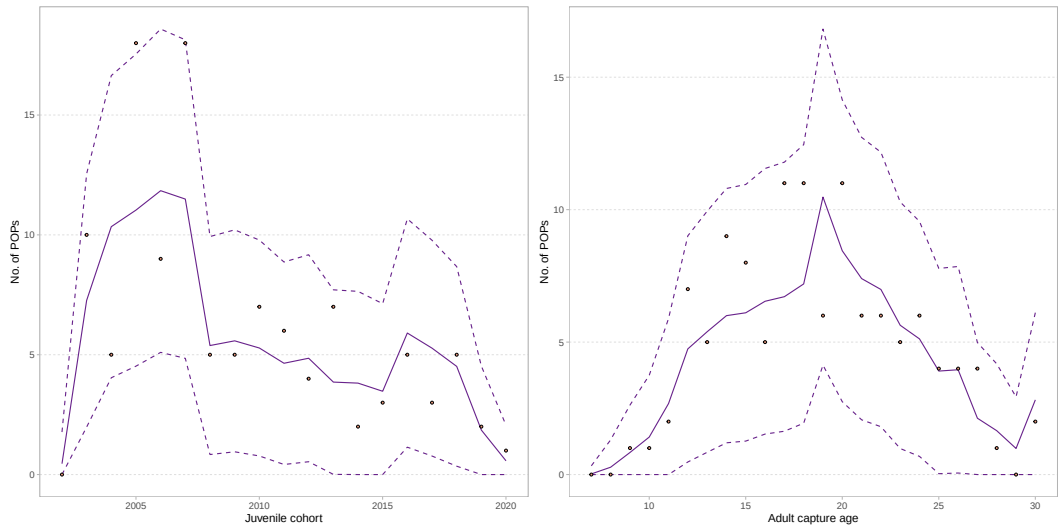

Figure 6.1: *Fits to the CKMR POP data at the juvenile cohort (left) and adult capture age (right) aggregation levels. Dot points are observations, median and approximate 95%iles are the full and dotted lines, respectively.*

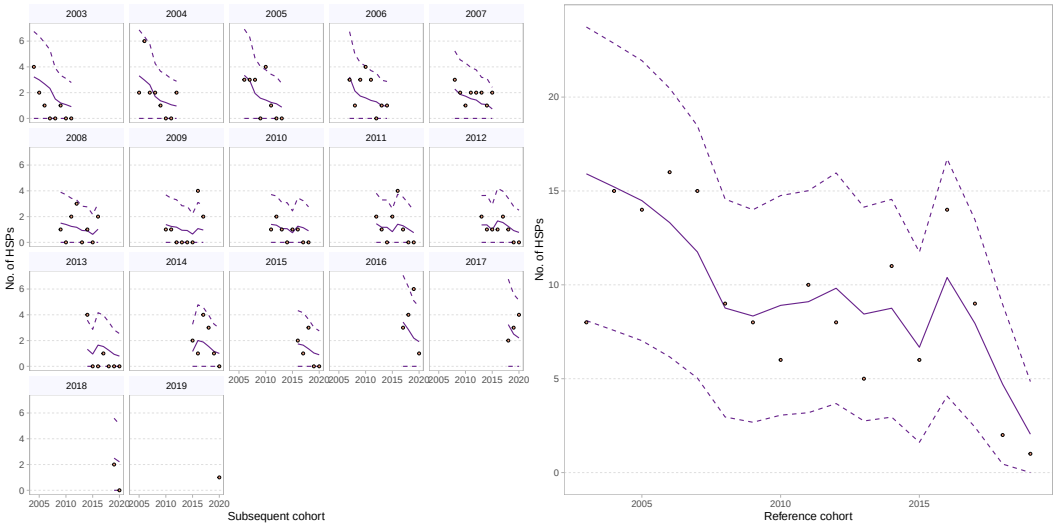

Figure 6.2: *Fits to the CKMR HSP data at the base (left) and initial cohort (right) aggregation levels. Dot points are observations, median and approximate 95%iles are the full and dotted lines, respectively.*

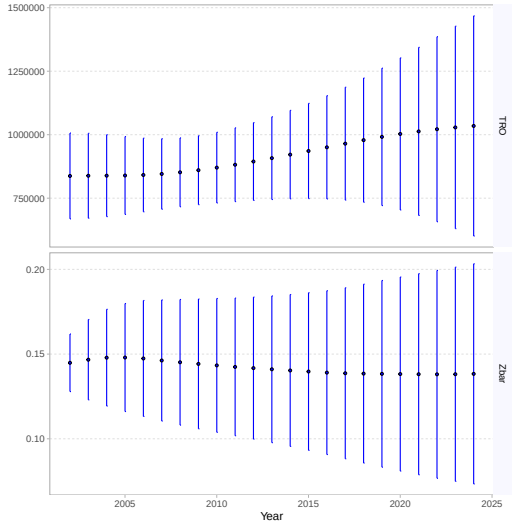

Figure 6.3: *Absolute TRO (top) and mean adult total mortality (bottom) median (dots) and approximate 95%ile (whiskers) for the CKMR-driven population model in the CTP.*

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