



Summary of updated CKMR data and model performance in the Cape Town Procedure

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1 Background

In this paper we detail the key facets of the updated CKMR data, how they compare to the 2019 data, the fits to the data for the simplified CKMR model of adult abundance in the MP, and the resulting estimated population dynamic variables.

2 Adult population dynamics & CKMR likelihoods

For the CKMR part of the Cape Town Procedure (CTP) we used an adult-focused (ages 6 and above) age-structured population model, with auto-correlated “recruitment” deviations:

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

The estimate 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

This is similar to the number of parameters estimated in the Bali Procedure population model. There are not a large number of model parameters, and many of them are constrained deviation parameters. The rationale for the total mortality model is as follows: from the ages 6 to 25 we can approximate the cumulative effect of fishing and natural mortality using an age-independent random effect type approach; for ages 25 to 30 we attempt to represent the senescence term in OM by increasing the mortality to a pre-specified maximum value given estimates of M_{30} in the OM. The assumed settings for the CKMR MP population model are detailed in Table 2.1.

Parameter	Value
a_{\min}	6
a_{\max}	30
σ_R	0.25
ρ	0.5
σ_X	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

Table 2.1: Settings for CKMR MP population model

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

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

and consider a juvenile-adult pair $\{i, j\}$, where $z_i = \{c\}$ is the juvenile covariate and c is its 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

$$\mathbb{P}(K_{ij} = POP | z_i, z_j) = \mathbb{I}(c < y < c + a) \frac{2\varphi_{a-(y-c)}}{TRO_c} \quad (2.1)$$

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:

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

$$\gamma_{y,a} = \frac{N_{y,a} \varphi_a}{TRO_y},$$

$$\{z_i, z_{i'}\} = \{c_i, c_{i'}\},$$

$$c_{\min} = \min\{c_i, c_{i'}\},$$

$$c_{\max} = \max\{c_i, c_{i'}\}$$

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

3 Updated CKMR data

In 2019 there were around 101 million comparisons and 82 detected POPs; in the 2020 data that increases to around 112 million comparisons and 89 detected POPs. The “hit-rate” (ration of detected POPs to comparisons) *decreased* by 2.2% from 2019 to 2020 - this is qualitatively commensurate with a slightly more optimistic view of total reproductive output especially in the most recent years. Figure 3.1 compares the previously used POP-derived empirical abundance

index when using the 2019 and the 2020 data. The index itself is defined as the total number of comparisons done for a given juvenile birth-year/cohort divided by the total number of detected POPs for that particular cohort.

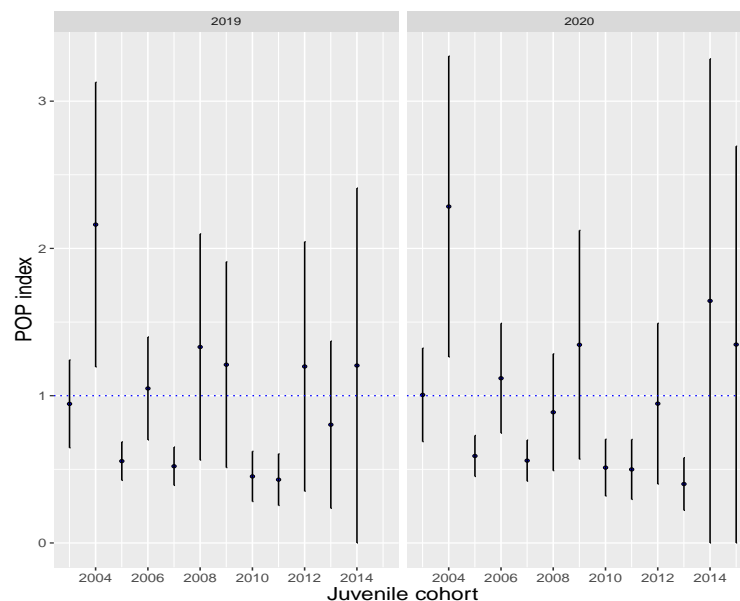


Figure 3.1: *Empirical POP index using 2019 (left) and updated 2020 (right) data.*

Comparing the data in 2019 to the updated 2020 data we do see some changes:

- There are little to no changes in the 2003–2007 index, which is a result of there being very few new comparisons for those juvenile cohorts for adults sampled recently
- The 2008 index comes down *slightly* as increased numbers of comparisons but a higher *per capita* number of POPs found
- The 2012 and 2013 indices comes down as we get more POPs for these juvenile cohorts
- The 2014 and 2015 indices are, as expected, highly variable given they are the most recent

Figure 3.2 shows the empirical cumulative distribution of the adult ages (back-calculated to the year of the juvenile in the comparison) for both POPs and unrelated pairs (UPs). There is no obvious difference between the 2019 and 2020 data, and as before shows a clearly peaked distribution in the POPs at around age 16, with very few young adults in the POPs and also not POPs greater than age 26, despite there being such animals in the UP comparisons.

In terms of an overall summary for the revised CKMR data:

- The POP and HSP “hit-rate” (per comparison number of matches) both decreased *slightly* which is consistent with a slowly increasing adult population
- The empirical POP index is broadly very similar to the 2019 index, albeit with some modifications as new POPs are found for the post-2007 juvenile birth years
- The adult age distribution in the POPs is essentially the same as 2019, with a clear peak in the POP adult ages of around age 16, very few adult POPs less than 8 and none above 26

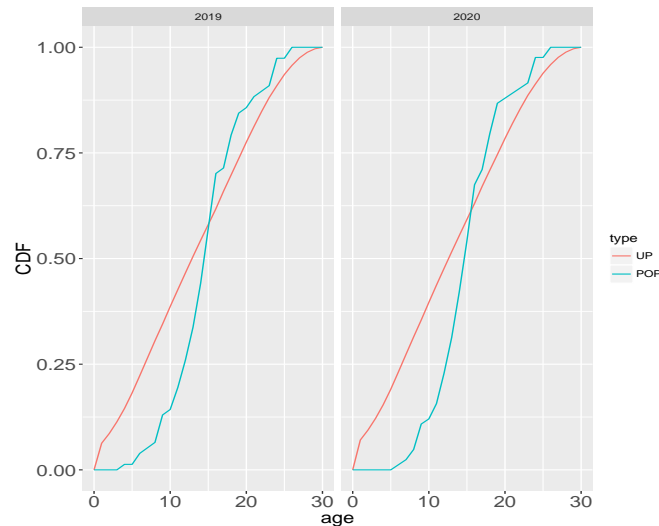


Figure 3.2: Empirical cumulative distribution function for the adult ages (back-dated to putative juvenile birth year in comparison) for the POPs (green) and the UPs (red) for both 2019 (L) and 2020 (R).

4 Fits and estimated population dynamics

As was done when running the Bali Procedure [3] we show how well the population model embedded within the CTP performs given the input data. This was to ensure that the model we have used in the MP can in fact fit to the available data and, hopefully, give us a useful representation of the adult dynamics for use in the MP.

For the CKMR data - especially the POP data - have tended to show the fits to the data at levels above the base data structure (i.e. adult capture year, capture age and juvenile birth year) given the sparsity therein. For the POPs we aggregate over adult capture age (to look for adult sampling year-effects), adult capture year and juvenile cohort (to see how well we are fitting the adult age distribution in the POPs), and adult capture year *and* age (to see if we are getting the total adult abundance about right). For the HSPs we have generally shown the fitting summary at two levels: (i) for a given initial cohort the number of HSPs found for each the following cohorts; (ii) for a given initial cohort *all* the HSPs found among the following cohorts

Figure 4.1(a) shows the fits to the POP data at the juvenile cohort and adult capture year level, Figures 4.1 (b) and (c) shows the fits to the POP data at the juvenile cohort level and the adult capture age level, respectively. The fits are generally good - no obvious consistent adult year effects, we seem to be getting the POP adult age distribution about right, and the cohort-level fits suggest we cannot be too far out on overall adult abundance. Figure 4.2(a) shows the fits to the full HSP data set, and 4.2(b) shows the fits when aggregated to the initial cohort level. Fits to the HSP data seem fine at both the disaggregated and initial cohort levels. This also suggests that both the POP and HSP data contain consistent information about adult abundance in particular, thus giving weight to the assumption that $q_{\text{hsp}} = 1$ in the HSP likelihood.

The key estimated population dynamic quantities, in terms of the MP, are the estimated total reproductive output (TRO; adult abundance) and the mean adult total mortality rate (Z ; weighted mean Z). The CKMR-derived estimates and approximate 95%iles can be found in Figure 4.3. The TRO is estimated to be mostly flat, albeit with a small increasing trend in the most recent

years. The mean adult Z has followed an increasing then decreasing trend over the time period, though also estimated to be fairly flat. An interesting observation is how the uncertainty in the key quantities trends over time, and how those trends are different for the two variables. For the TRO, the estimate is most accurate for the mid-to-late 2000s where we have the most POPs in terms of juvenile birth years; either side of this where POP numbers are the lower the uncertainty increases. For the HSPs it is very different: estimates of adult Z are most accurate in the early 2000s and gradually decrease in precision as we get to 2015. This is because we have the most HSPs when comparing the earliest years to the subsequent ones and a longer time-frame of information on Z . This demonstrates the complex manner in which information from the CKMR data flows into the key population dynamic variables.

5 Discussion

The updated CKMR data for 2020 were summarised and found to be very similar to those used in 2019. Both the POP and HSP data showed slight decreases in hit-rate (match-per-comparison) which would be qualitatively consistent with a slightly more optimistic outlook for the adult stock relative to 2019. The details of the adult-only population model and likelihoods for the POP and HSP data were outlined, along with the associated assumed parameters and priors. Fits to the data were generally quite good, with no obvious year or age effects in the POPs and no cohort-specific effects in the HSPs. Estimates of the adult abundance (TRO) were fairly flat with a very small recent increasing trend; estimates of mean adult Z were also fairly flat but with a recent decreasing trend. Both are consistent with a qualitatively positive trend in the adult abundance. Given the acceptable fits to the data, and estimates of the key population dynamics that are not inconsistent with previous stock assessment results we judge the CKMR part of the MP to be performing as expected and acceptable for use in the MP calculations for the TAC.

6 Acknowledgements

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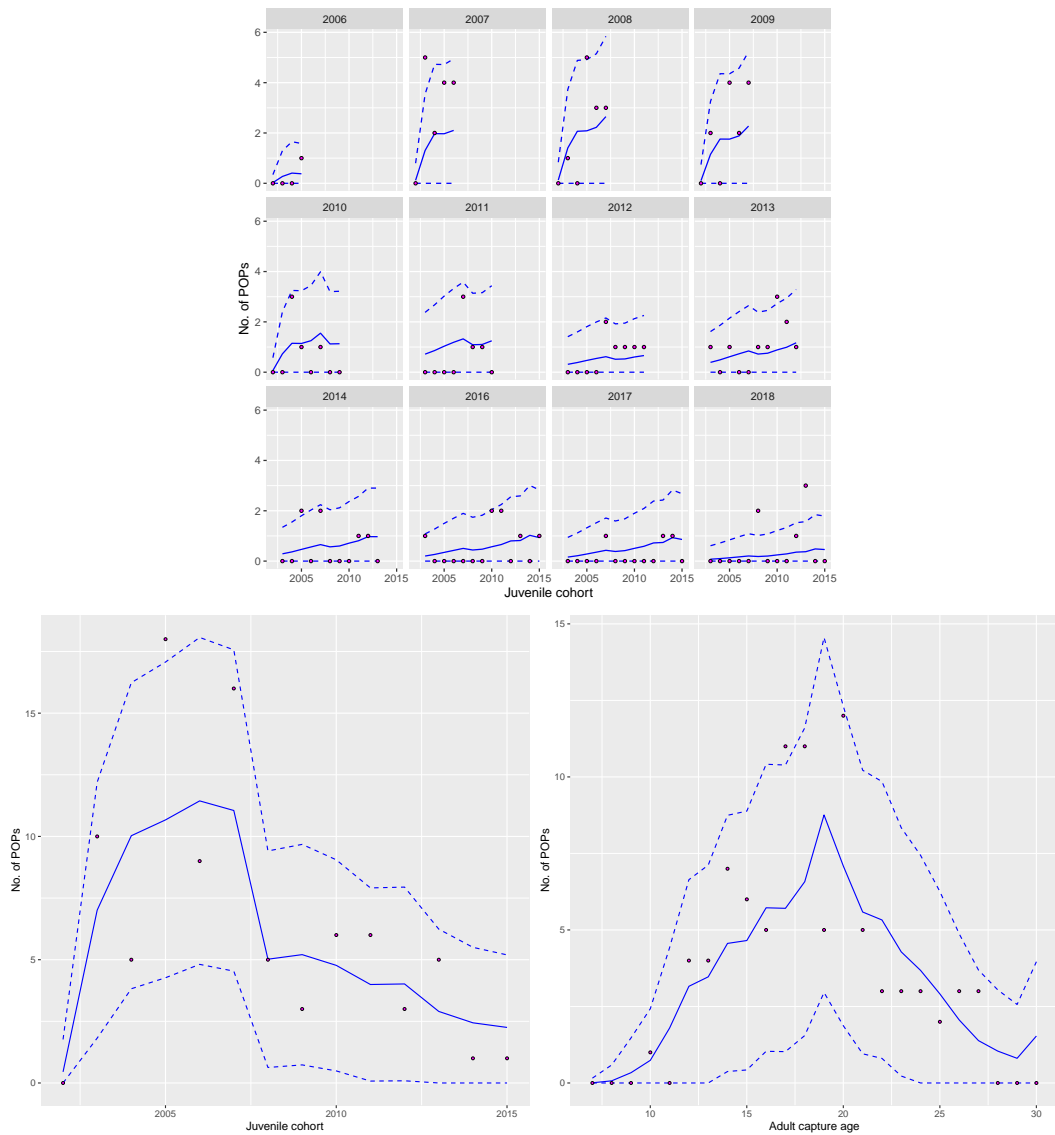


Figure 4.1: Fits (median and approximate 95% CI) to the POP data (magenta dots) at the (a) adult capture year and juvenile cohort (top), (b) juvenile cohort (bottom left), (c) and adult capture age (bottom right) levels, respectively.

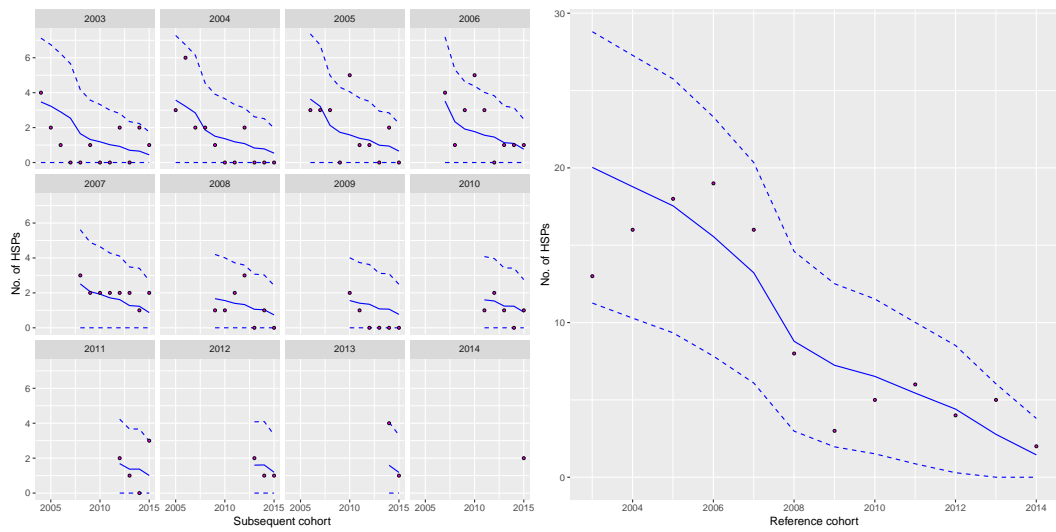


Figure 4.2: Fits (median and approximate 95% CI) to the HSP data (magenta dots) at the (a) full disaggregation (left), and (b) initial cohort (right) levels, respectively.

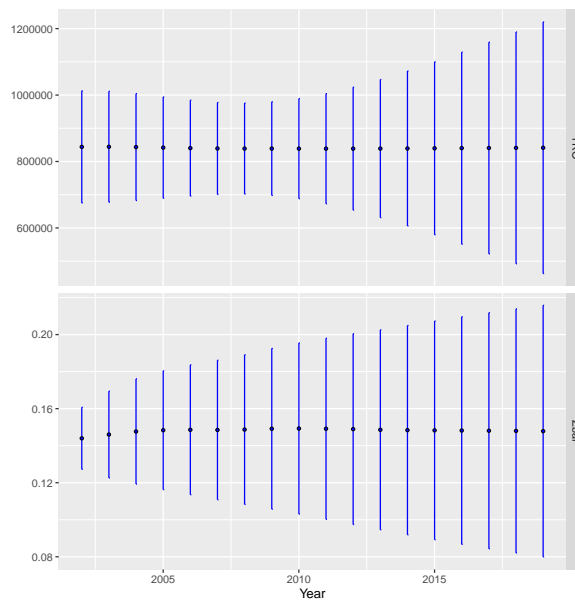


Figure 4.3: MLE (dots) and approximate 95%ile (bars) for the TRO (top) and mean adult Z (bottom).

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