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Updates to the SBT OM

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Contents

Abstract

The SBT operating models (OMs) are being reconditioned this year for MSE testing of candidate MPs. In addition to updating existing data, we also have gene tagging estimates of abundance of 2 year olds for 2016 and 2017 to include for the first time. This paper details the technical specifications of how the gene-tagging data are included in the SBT OM, and the relevant settings and fixed parameters required in the various OM configuration files. It also explores the fits to the data sources for the reconditioned OM. Finally, we explore the LL1 size data as used in the OM for evidence of the strength of the large estimated 2013 year-class.

1   Background

This year the OMMP and ESC have resumed the MSE work begun in 2018 to develop a new MP for the CCSBT. A reconditioning update of the OM is required in 2019. This update will include two gene tagging data points, one for for 2016 and for 2017, in the conditioning code. These data have already been included in projection code [1, 2] and the same assumptions about the generation of these data in the projections are mirrored in the conditioning part of the OM.

2   Gene tagging process & likelihood

The gene tagging data collection process is as follows:

1. In year y, T_y (assumed to be) 2 year old fish are tissue-sampled and re-released in the Great Australian Bight, South Australia **after** the surface fishery has caught all its TAC

2. In year $y + 1$, S_{y+1} (assumed to be) 3 year old fish are tissue-sampled in the processing facilities in Port Lincoln through-out the harvest period

3. In year $y + 2$, R_{y+2} recaptures are detected and data are available for inclusion in models

We don't go into specifics about the length distribution of tagging and resampling, here, save that we do this to ensure the maximum chance of tagging 2 year old and resampling 3 year old fish [3, 4] . In the MP work, we use the simple Petersen estimator for the age 2 abundance in year y, $\widehat{N}_{y,2}$:

$$\widehat{N}_{y,2} = \frac{T_y S_{y+1}}{R_{y+2}},$$

with the Poisson approximation to the variance where the CV in abundance is assumed to be approximated by $1/\sqrt{R_{y+2}}$. For the conditioning of the OM we assume a more flexible distribution: the beta-binomial distribution. The underlying probability of recapturing a biopsied fish is as follows:

$$\pi^r_{y+2} = \frac{T_y}{q^{\mathrm{gt}} N_{y,2}},$$

where q^{gt} represents the fraction of age 2 juveniles available to be tagged in the GAB (default is 1). The other key parameter for the gene tagging likelihood is the over-dispersion coefficient, φ^{gt}: the degree to which the variance in the recaptures exceeds that assumed in the vanilla binomial distribution (i.e $\varphi^{\mathrm{gt}} \geq 1$). With the binomial ($\varphi^{\mathrm{gt}} \equiv 1$), we have the following likelihood:

$$\Lambda^{\mathrm{gt}} \left(R_{y+2} \,|\, S_{y+1}, \pi^r_{y+2} \right) \propto \left(\pi^r_{y+2} \right)^{R_{y+2}} \left(1 - \pi^r_{y+2} \right)^{S_{y+1} - R_{y+2}}$$

For the over-dispersed case, $\varphi^{\mathrm{gt}} > 1$, the likelihood is as follows:

$$\alpha^{\mathrm{gt}} = \frac{\left(S_{y+1} - \varphi^{\mathrm{gt}}\right) \pi_{y+2}^r}{\left(1 - \pi_{y+2}^r\right) \left(\pi_{y+2}^r + \left(1 - \pi_{y+2}^r\right) \left(\varphi^{\mathrm{gt}} - 1\right)\right)}$$

$$\beta^{\mathrm{gt}} = \frac{\left(S_{y+1} - \varphi^{\mathrm{gt}}\right) \pi_{y+2}^r}{\pi_{y+2}^r + \left(1 - \pi_{y+2}^r\right) \left(\varphi^{\mathrm{gt}} - 1\right)}$$

$$\Lambda^{\mathrm{gt}}\left(R_{y+2} \,|\, S_{y+1}, \alpha^{\mathrm{gt}}, \beta^{\mathrm{gt}}\right) \propto \frac{\Gamma\left(R_{y+2} + \alpha^{\mathrm{gt}}\right) \Gamma\left(S_{y+1} - R_{y+2} + \beta^{\mathrm{gt}}\right) \Gamma\left(\alpha^{\mathrm{gt}} + \beta^{\mathrm{gt}}\right)}{\Gamma\left(S_y + \alpha^{\mathrm{gt}} + \beta^{\mathrm{gt}}\right) \Gamma\left(\alpha^{\mathrm{gt}}\right) \Gamma\left(\beta^{\mathrm{gt}}\right)}$$

and $\Gamma()$ is the gamma function.

3   Settings required in OM configuration files

The data are included as follows in the `sbtdata2018.dat` file as a table with the following columns: year of release, age of release, year of recapture, number of releases, number of resamples, number of matches. Table 4.1 shows the current data set.

Year of rel.	Age of rel.	Year of recap.	T	S	R
2016	2	2017	2,952	15,389	20
2017	2	2018	6,480	11,932	67

Table 3.1: *Summary of current gene tagging data.*

The remaining control parameters are located in the `sqrt.dat` file:

- `qgt` (q^{gt}): default is set to 1 (and assumed that $q^{\mathrm{gt}} \leq 1$)
- `gtOD` (φ^{gt}): default is set to 1 (and $\varphi^{\mathrm{gt}} \geq 1$)
- `gtsw`: 0/1 switch flag to turn GT data off/on (default set to 1)

4   Abundance fits given reconditioned reference set of OMs

The following updated and new sources of data have been included in the 2019 reconditioning:

- Catch biomass, composition and Japanese longline CPUE up to and including 2018
- CKMR POP and HSP data up to and including sampling year 2017, which would observe the adult population up to and including 2014
- The two gene tagging estimates of age 2 abundance in 2016 and 2017

A full diagnostic check of the fits for all updated data sets will be undertaken for the stock assessment scheduled for 2020. However, given this is the first time the gene tagging data have been included in the OM, we do summarise how the reconditioned OM fits to these data. The approach taken in the past few years [5] is to simulate a particular data set from its predictive distribution (simulate from the likelihood while integrating across the model ensemble included in the reference set). If the reference set of OMs was a true posterior, this would be the posterior predictive distribution; given we use the reference set as a proxy for the posterior we refer to it as the predictive distribution.
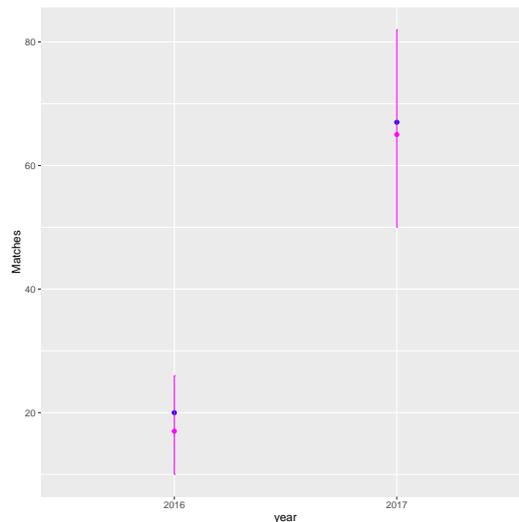
Figure 4.1: *Observed (blue) and predictive median and 95% credible interval (magenta) for the 2016 and 2017 gene tagging recaptures.*

Figure 5.1 shows the observed and predictive distribution of (in terms of median and 95% credible interval) matches in the 2016 and 2017 gene tagging data (year is denoted as year of release/year of abundance estimate). In both cases the median number of matches is slightly below the observed number, indicating a slight preference for lower age 2 abundance in the gene tagging data, but the credible interval easily encapsulates the data in both cases.

It might seem odd that these data are not fitted effectively perfectly, given no other data sets in the OMs observe these year-classes at the present time. There is, however, a reasonably informative prior on the year-class strength deviations in the OM, and with auto-correlation built in. The estimates of recruitment prior to 2016 were well above average (especially age 2 abundance in 2015), so built in to the recruitment deviation prior in 2016 and 2017 is a preference for above-average recruitment deviations. This is why the effect lis more apparent for 2016 (which follows the highest recruitment estimate for decades) than for 2017 (as the 2016 age 2 abundance was estimated closer to the expected level). In summary:

- The conditioning part of the OM has been modified to incorporate the gene tagging data using a flexible beta-binomial likelihood and is implemented in the same manner as the data are simulated in projection part of the OM

- The data from 2016 and 2017 are fitted well in the reconditioned OM, but suggest *slightly* lower 2016 and 2017 estimates of age 2 abundance than those coming from the previous OM and the recruitment deviation prior

- The 2017 gene tagging estimate is below the previous run of above-average recruitment.

The grid configuration agreed to in 2017 for MP testing is detailed in Table 3.1 and, in line with previous reconditionings, we sample 2,000 times from the current suite of 432 using the resampling scheme outlined in Table 3.1. We summarise the `base18UAM1` grid of operating models, given this is our current reference case for the MSE work. For the best fitting grid element, the fits to the abundance data (CPUE, aerial survey and gene-tagging) are shown in Figure 3.1. The fits to the conventional tagging data are provided in Figure 3.2; and the aggregated fits to the CKMR POP and HSP data (as per [5]) are detailed in Figure 3.3.
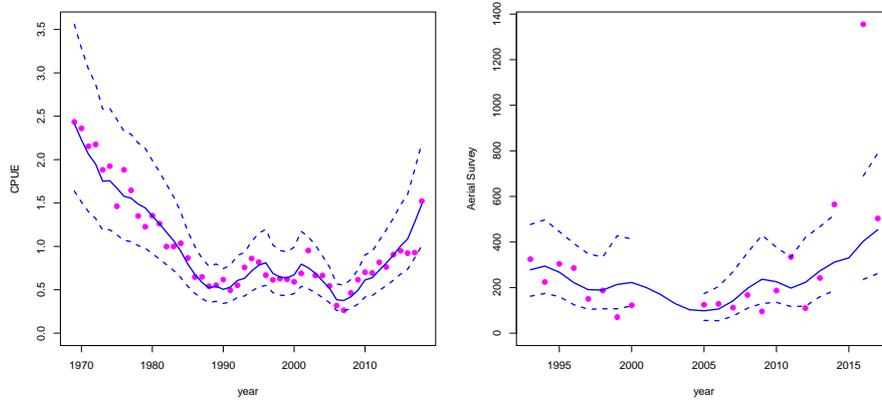
Figure 4.2: *Observed (magenta) and predicted median and 95% CI (blue) for the Japanese longline CPUE (left) and aerial survey (right) indices.*
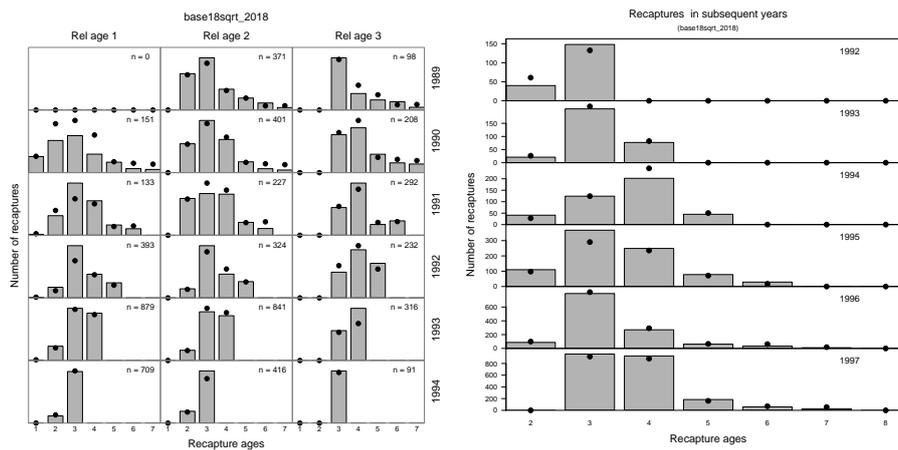

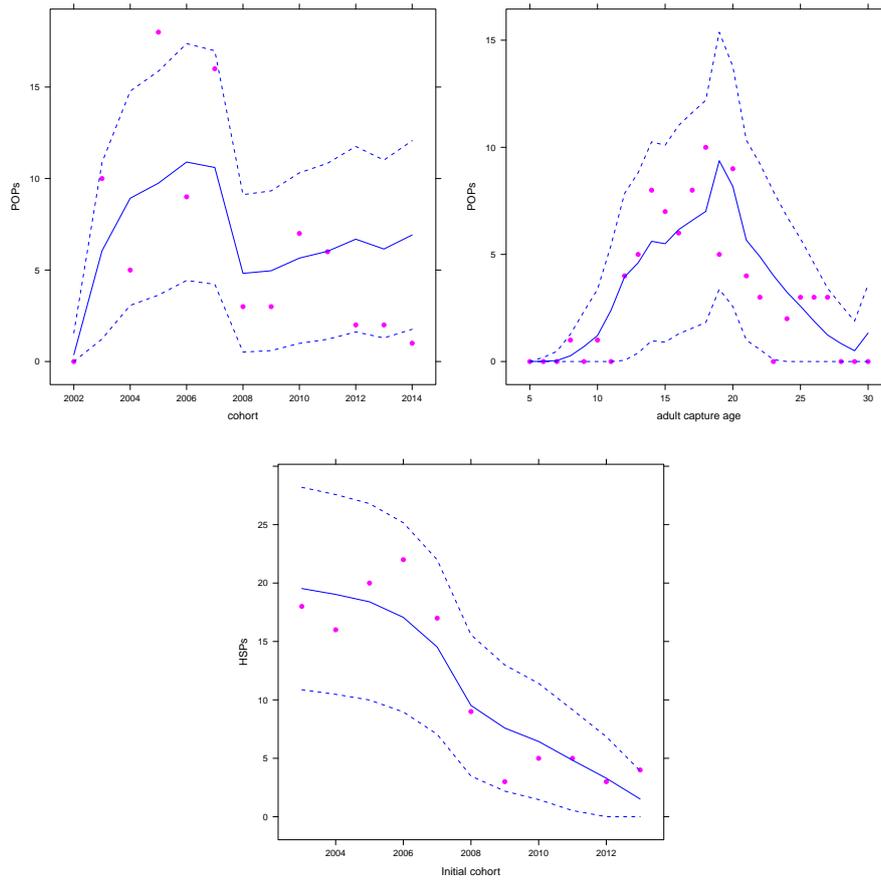Figure 4.3: *Disaggregated (left) and pooled (right) 1990s tagging data fitting summaries.*

Figure 4.4: *Observed (magenta) and predicted median and 95% CI (blue) for fits to the POP data aggregated to the cohort (top left) and adult capture age (top right) levels, and the HSP data aggregated to the initial comparison cohort level (bottom).*

Parameter	Values	Prior	Resampling	CumulN
Steepness	$\{0.6, 0.7, 0.8\}$	Uniform	Prior	3
M_0	$\{0.35, 0.4, 0.45, 0.5\}$	Uniform	Objf	12
M_{10}	$\{0.0.5, 0.085, 0.12\}$	Uniform	Objf	36
ω	$\{1\}$	Uniform	Prior	36
CPUE ind.	$\{2, 3\}$	Uniform	Prior	72
CPUE ages	$\{4, 18\}$ & $\{8, 12\}$	$\{0.67, 0.33\}$	Prior	144
ψ	$\{1.5, 1.75, 2\}$	$\{0.25, 0.5, 0.25\}$	Prior	432

Table 4.1: *Summary of the agreed grid configuration for the 2019 reconditioning*

The fits to the CPUE are similar to previous years, and the notable increase in CPUE in 2018 is fitted well (driven by the already large estimate of recruitment in 2013 driven by the 2016 aerial survey). The fits to the aerial survey haven't changed since the previous assessment [5] and the fit to conventional tagging data are also similar to previous years. The fits to the aggregated POP data are similar to previous years but there is a slight trend in number of POPs for the most recent juvenile birth years (2012–2014) being over-estimated. Apart from the last point which is just outside the bounds, there is no clear significant misfit, and the data for these cohorts will be not be static - in the coming years we will compare new adults to juveniles born in these years and so could detect more matches which will change this trend. The fits to the adult capture age lof the POPs is good as are the HSP fits when aggregated to the initial cohort level. It is also worth noting the sample sizes for the CKMR monitoring are based on previous OMs. Given the updated estimates of status and population dynamics since the original design study and the use of CKMR for stock assessment, monitoring the rebuilding plan and input to candidate MPs, a review of this monitoring program and associated sample sizes should be a priority to ensure appropriate samples sizes in the future.

Variable	TRO depletion	B_{10+} depletion	F/F_{msy}	B/B_{msy}	B_{msy}/B_0
Summary	0.17 (0.15–0.21)	0.14 (0.12–0.17)	0.55 (0.41–0.74)	0.64 (0.47–0.91)	0.27 (0.22–0.32)

Table 4.2: *Population dynamic summaries (median and 90% CI) for the reconditioned OM.*

The main population dynamic summaries can be found in Table 3.2 (for the reference set which includes the UAM1 scenario). Current TRO depletion has a median (and 90% CI) of 0.17 (0.15–0.21) so higher than the 0.13 estimate of 2017 [5] but consistent with the projections done in both 2017 and 2018. Current estimates of F are just above half of F_{msy} with a very low probability of exceeding it. The ratio of the adult biomass at MSY relative to the unfished level is also consistent with previous estimates: 0.27 (0.22–0.32).

5 Effect of large 2013 recruitment on LL1 OM data

An issue that arose at the OMMP meeting was that the recent run of good recruitment - and in particular the 2013 year class - seemed consistent with the signals in both the aerial survey data and the Japanese long-line CPUE abundance index [6] but was seemingly not apparent in the LL1 size frequency or, specifically, the Japanese long-line data [7]. In this section we explore whether it is reasonable to *expect* the LL1 (or Japanese) size data to show consistent tracking of an individual strong year class, given the large variation in length at age for SBT.

It is true for almost all teleost fish that length tends to become a poor indicator of individual,

age as the overall growth of the fish slows down and the variability in individual length given age increases. In the case of SBT, after age 3 it becomes increasingly difficult to define a size range that would be expected to include *only* one age-class. So, either visually inspecting length data or cohort-slicing the length data to obtain estimates of the underlying age distribution will become increasingly uninformative as the size of the animals increases. Only by collecting direct age data can one get a sense of the actual age distribution within a given set of length data above around 100cm - which is where the vast majority of the LL1 data are reported to be.
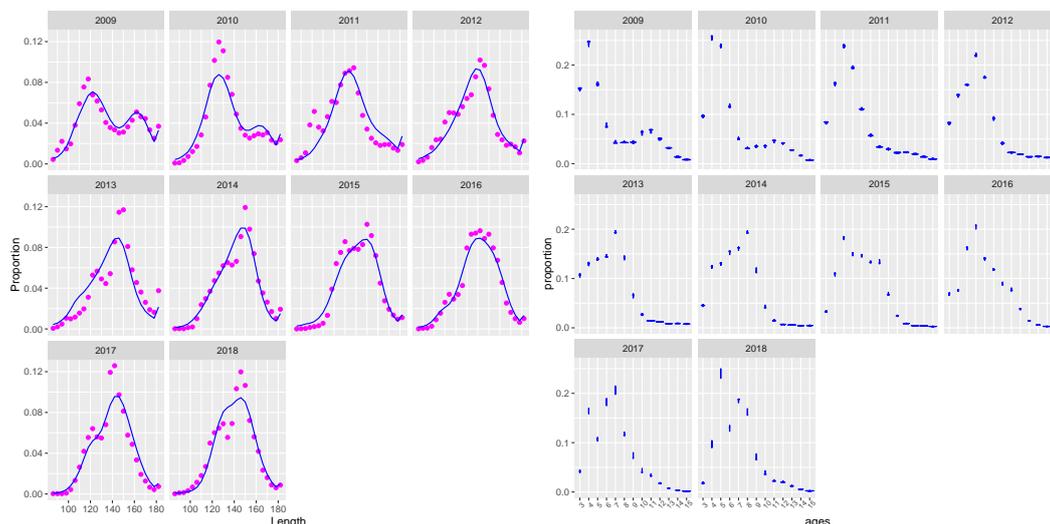

Figure 5.1: *On the left the observed (magenta points) and predicted (blue lines) LL1 size frequency from 2009 to 2019. On the right violin plot summaries of the predicted age distribution in the long-line size data for the same years for ages 3–15.*

To make this point quantitatively, Figure 5.1 shows the observed and predicted LL1 data from 2009 to 2018. It also shows the predicted age distribution within the LL1 size data across all grid runs: the distribution-at-age derived from multiplying the true numbers-at-age in the population by the LL1 selectivity-at-age. The effect can be seen across several different years, but focussing on 2017 and 2018 when the 2013 age class would be 4 and 5 years old, respectively, and approaching full selectivity in the LL1 data. In the observed and - importantly - predicted length data there are no obvious peaks around 117cm and 127cm - the mean lengths at age 4 and 5, respectively. Looking at the predicted age distribution, however, it is apparent that the 2013 year class in 2017 makes up over 10% of the LL1 catch-at-age and in 2018 that increases to almost 25% of the LL1 catch-at-age.

The OM clearly estimates a large year-class for 2013 - with or without the 2016 aerial survey and the 2018 CPUE index. When both are included it is by far the largest estimate of recruitment seen over the last 4 decades. Yet, in the predicted length data there is no obvious peak centred around the mean length of this age-class - the argument essentially being made in [7] in terms of questioning why this year-class doesn't appear to be obvious in the observed size data. The point is really that we would not *expect* to see such a peak, given the variability in length-at-age for the ages likely being currently exploited by the LL1 fleet. Only by collecting direct age data representative (spatiotemporally) of the LL1 catch would we be able to make some kind of statement on the size of the 2013 recruitment using the LL1 size data. So, we don't think we can conclude that the LL1 size data do not appear to confirm the large estimated 2013 year-class. At

most, the data are compatible with the large estimate as there are no obvious issues with the fits to the 2017 and 2018 LL1 size data. The important point is that we would not expect these data to be informative for specific **individual** year-class strength. Where they have been informative, for example, was in the extreme case of the run of very low year-classes from 1999–2002, as they were quite clearly seen to be absent for a number of years in the left-hand side of the LL1 length frequency data.

6 Discussion

The CCSBT OM has been reconditioned for data up to and including 2018 as well as the first inclusion of the two gene tagging data points. The new likelihood function for the gene tagging data was described - with the current default being a binomial distribution. We have, however, programmed in the option for the more flexible beta-binomial distribution to allow for over-dispersion in these data, very similar to how this is done for the 1990s tagging data. It will take a number of years, however, before we can in-principle estimate of the potential over-dispersion factor as with only two data points the estimate would be highly uncertain. In any case the two data points are fitted very well, given little else in the data sets observes those year-classes currently, so it would be not just uncertain but effectively zero (i.e. reduced to a binomial anyway). The base grid agreed at the previous ESC (and subsequently confirmed at the 2019 OMMP) was used and the UAM1 unaccounted mortality scenario was used to create the reference set of OMs used in the MSE work. The data were generally fitted well - including the new gene tagging data - and there were no obvious issues with the resulting OM that would suggest it could not be used in the MP testing work this year.

One issue relating to the large estimated 2013 year-class, largely driven by first the 2016 aerial survey index and then the 2018 LL1 CPUE index, is why it does not appear to give a strong signal in the LL1 (and Japanese) length frequency data [7]. We demonstrated that even the model predicted size frequency data do not show obvious peaks centered around the mean length of this 2013 year class in both 2017 and 2018 (when it would be 4 and 5 years old, respectively) yet the year-class is the largest one estimated for over 4 decades. What *is* very apparent is that the model predicted age distribution in the LL1 data show this year class as fairly strong at age 4 (more than 10% of the total catch) and very strong at age 5 (almost a quarter of the total catch).The variability in size-at-age at the sizes caught in the LL1 and Japanese fleets means that length frequency data are essentially uninformative on **individual** year-class strength - clearly so even for very large estimated recruitments. So we do not think it is appropriate to say that the LL1 and Japanese size frequency data do not appear to confirm the presence of a large 2013 year-class. The data are consistent with the model estimated 2013 year-class - the data are fitted fine in both 2017 and 2018 - but could not be expected to be informative on a single year-class.

7 Acknowledgements

References

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