CCSBT-OMMP/1609/07
(same as CCSBT-ESC/1609/BGD 06)

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Methods for data generation in projections

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CCSBT-OMMP/1609/7

Prepared for the Seventh Operating Model and Management Procedure Technical Meeting held in Kaohsiung, Taiwan 2th-4th of September 2016

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Contents

Abstract

The CCSBT ESC is about to begin a new round of MP development and testing. A number of new data sources are being collected for use in the OM. This paper details how they can be simulated in the OM projections and their potential information content for use in a new MP. We outline a flexible model for simulating the gene tagging data that can incorporate additional variance. For the parent-offspring close-kin data we detail a flexible simulation approach and also how to use the empirical data (numbers of comparisons and detections) as an indicator of spawning abundance. The simulation of the next generation of close-kin data, finding half-sibling pairs among juveniles, is outlined. We also show how these data, again in their empirical form, can be developed into very informative indices for both relative spawning abundance - independent of the POP data - and mean adult total mortality rate.

1 Background

The Extended Commission has requested the development of a new MP, by 2019, which will potentially use a new recruitment index and other sources of data. [1]. This paper focusses on the data generation of indices that can be considered for potential inclusion in any future candidate MPs. This will allow for simulation testing of new MPs using data generated in the OM projections. This paper should be read in conjunction with the paper focussing on required structural changes to the OM to incorporate new data sources [2]. To simulate the various data sets we employ an SBT-like Operating Model. We use a simplified OM with all the key life-history and fishery characteristics of SBT (growth, reproductive output, natural mortality, population selectivity across all fisheries) and with the same current spawner abundance. We explore the main population change drivers: three similar trends (in terms of logarithmic change) for both mean recruitment and overall fishing mortality in the future. This allows us to see the potential information content in the various data sources across a plausible range of overall abundance change scenarios, and given the two obvious drivers: mortality and recruitment.

Gene tagging has been recommended as an essential recruitment index for a new MP, following extensive work done both for and at last year's ESC which demonstrated the need for such an index [1]. The general design study for the pilot gene tagging program can be found in [3] and the successful release of 3,800 fish occurred in January of this year. In [2] we outlined the mathematical and statistical features of the gene tagging estimator, and the associated beta-binomial likelihood we suggest for the OM in conditioning mode. In this paper we propose to use the same generic likelihood in the OM in projection mode. We also explore the information content in the simulated gene tagging data, with respect to trends in mean recruitment under a variety of future scenarios.

In both the OM and the adopted MP, the major index of non-juvenile abundance is the long-line CPUE. Figure 1.1 shows that these data have a complex, non-linear relationship to the OM-estimates of spawner abundance. Only from 1969 to the mid-1980s (i.e. higher SSB levels) is the relationship close to being linear. From that point on to the present (where CPUE levels drop below 1 consistently), and even before factoring in the additional uncertainty in CPUE given the over-catch in the majority of this period, there is little strong correlation between CPUE and spawner abundance. The more recent long-line CPUE data are very clearly important indices relating to the sub-adult fish and, given the general move to target younger, smaller fish over the last two decades (although slightly different in 2015), are also more informative on recruitment than they once were. Future changes in targeting as the stock recovers might increase their information content with respect to mature animals, but presently they are not as informative. With only gene tagging and long-line CPUE we have no potential indices for inclusion in an MP that overlap significantly with the major reproductive age-classes (an issue we faced with the current MP also). The primary focus of any current candidate MP is, however, to drive the recovery of the spawning population to Commission agreed levels (in terms of both overall level and probability of attaining it).

The Commission has agreed to continue the collection and genotyping close-kin tissue samples [4]. Ef-

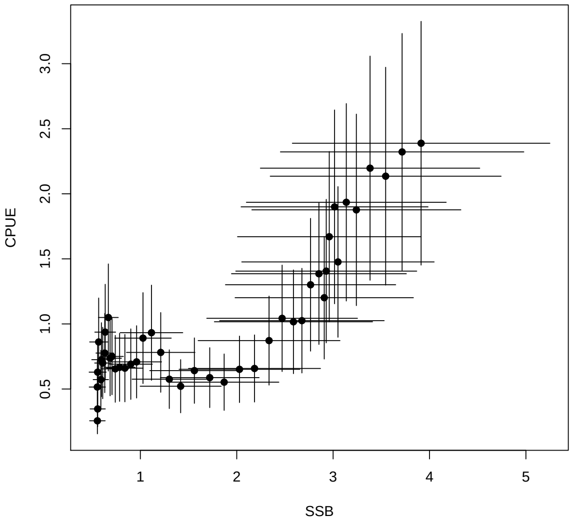

Figure 1.1: *CPUE observations (y-axis) versus current OM estimates of SSB (x-axis) in terms of median and 80%CI.*

forts are underway to process the historical backlog of samples using the next-generation sequencing technology that is both cheaper than the original microsatellite approach and will allow us to find both parent-offspring pairs and half-sibling pairs among the juvenile samples. The primary use of the POP data has been in the OM [5], where they have been very influential with respect to both current absolute and relative spawning abundance, but also adult mortality rates. The half-sibling pair (HSP) data have the potential to be very influential given they directly relate to spawner abundance, adult mortality, and relative reproductive output (RRO) *independently* of the POP data [6]. In this paper we also explore the potential information content in both the POP and HSP data in an empirical setting - methods to structure the data in such a way as to be informative on relative spawner abundance (POPs/HSPs) and mean adult mortality (HSPs only).

2 Material & Methods

The same simulation model is used for all data sources so we outline the specifics of that model first. It is an annual age-structured model, with the same key life-history and fishery characteristics as the CCSBT OM:

- The model has the same median M-vector, length-at-age distribution, recruitment variability (σ_r), and RRO (φ_a) as the SBT OM
- A single selectivity, constructed by normalising across current fleet-aggregated fishing mortality, is assumed
- Initial Fs are set so as to obtain an initial spawning abundance very close the median current spawning abundance predicted in the reference OM

We omit a stock-recruit relationship for simplicity, and we purposely explore trends in both mean recruitment and F. We are not testing the performance of candidate MPs or stock rebuilding times; we are exploring the generation and information content of data sources focussed on monitoring recruitment and spawner abundance. For both the mean recruitment and annual F multiplier we explored three simple scenarios: constant, and $\pm 1\%$ log-scale trends over time. We cross these scenarios with each other to obtain 9 scenarios in total, and each one is explored for all three data sources. This allows us to efficiently, but also simply, explore a number of scenarios for both fish entering the fishery for the first time (where gene-tagging is focussed), and for the spawning stock and where abundance trends can have differing and antagonistic/synergistic drivers (i.e. recruitment and/or mortality).

2.1 Gene Tagging

For the gene tagging design study [3] a simple Petersen estimator was outlined, where we assumed we can target age 2 releases and age 3 recaptures perfectly. In [2] we detail the specifics of how the gene tagging estimator will work, where this idealised targeting of specific age classes will not be quite so clear cut. Figure 2.1(a) shows the probable length distribution of age 2, 3 and 4 in the GAB in summer and, given our OM assumptions, is also the same as that in our simulation model explorations.

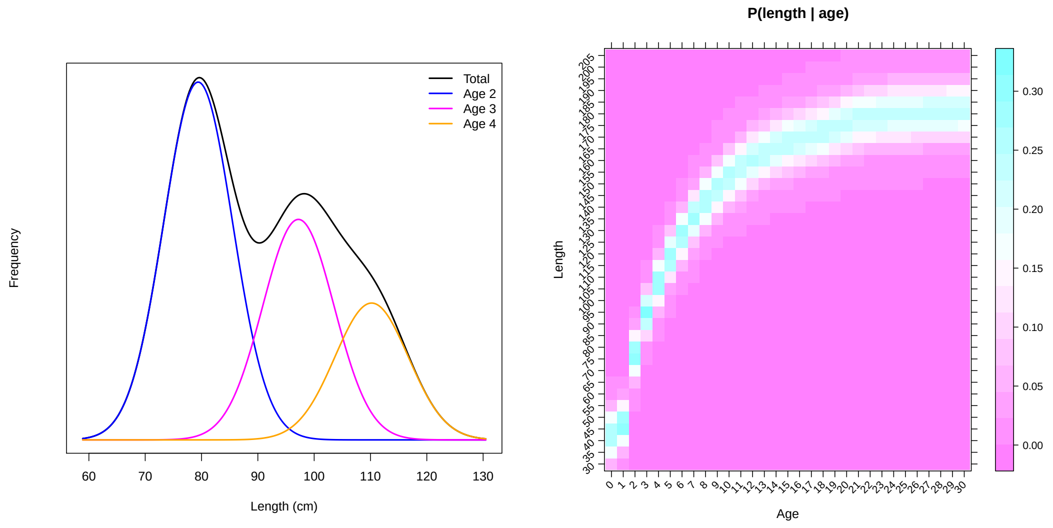

Figure 2.1: *(a, left) the probable length distribution of ages 2, 3 and 4 year old fish in the simulation model given current mortality rates; (b, right) the distribution of length-at-age assumed in the simulation model.*

The length partition used for the population is in 5cm bins, from 30cm to 210cm. The length-at-age distribution in the simulation model can be found in Figure 2.1(b). In terms of tag releases they are assumed to be uniformly released into the three length bins between 65 and 75cm (65-80cm). The subsequent recapture effort (1 year after the releases) focusses on the three length bins between 95 and 105cm (fish in sizes 95-110cm), so most likely to be age 3 fish, very very few age 2 fish, but with a higher chance of sampling age 4 fish as well.

The simple estimator we explore focusses only on *effective* numbers of recaptures of age 3 fish, tagged a year before at age 2. We say effective because we estimate the number of actual age 2 and 3 fish in the releases and recapture samples, respectively. Eqn. (2.2) in [2] outlines the distribution of age given length in the samples. We then estimate the (prior) age composition of the given length samples, for the length-at-age distribution (see Figure 2.1(b)), given the length distribution of both the release and scanned-for-recapture fish. This approach explicitly accounts for the potential information loss we are likely to get, in terms of not being able to target **only** age 2 releases and age 3 recaptures. As noted in [2] there will be additional information gained (via multi-year recaptures on the same cohort), but we focus on the MP-centric idea of getting an abundance index of age 2 fish. This information gain will feature more in an OM sense, but should not be ignored in the wider discussions of the merits or otherwise of these data.

The main potential bias identified in the gene-tagging design study can occur if some of the juvenile fish spawned on the spawning grounds never, or intermittently, spend the majority of their summers in the GAB between ages 2–4. The Global Spatial Dynamics project suggested the evidence for a significant part of the juvenile population behaving in this way was weak, but it is still an ongoing hypothesis. It was proposed in the Gene-Tagging design study that we could investigate this through a q factor for the proportion in the GAB. Alternatively, probably the simplest method is to impose a cap on the selectivity of the surface fishery. For a “fully mixed” population where all fish of the relevant ages visit the GAB at the time of the fishery, that selectivity will have a maximum of one, as is currently assumed in the SBT OM. We can explore scenarios where the maximum selectivity of the surface fishery is capped at some value $\zeta < 1$, and the true probability of finding a released tag in the GAB is then not proportional to $1/N$ but $1/\zeta N$. In this scenario $1-\zeta$ is the age-independent fraction of the juvenile population that never visits the GAB. Note none of the other mixing scenarios examined in the design study resulted in biased estimates of age 2 abundance - see [3] - but it is worth exploring results for this case detailed as scenario 2b in [3]. It is also testable in a non-spatial OM context (as described herein via capped selectivity).

For the purposes of data generation in the MP context we explore the information content in a simple moving average of relative recruitment, much as how the aerial survey is currently used. We explore the correlation of the gene-tagging derived estimates of (relative) age 2 abundance with their true simulation model counterparts, for all 9 recruitment and fishing mortality scenarios (below).

2.2 Parent-Offspring Pairs (POPs)

The original POP data have been officially included in the SBT OM since 2013 [5]. The current format for the data is as follows: we have juvenile sample, i, and an adult sample, j, each with either a direct estimate of age, or an expected age given its length. The probability of finding a POP will be the same for the same year of adult capture and age, and the juvenile birth-year (cohort), and the data are currently grouped in this manner. We use this (adult capture year and age, y and a, respectively; juvenile cohort, c) as the base disaggregation level for simulating the POPs. The probability of finding a POP for an juvenile-adult comparison $\{i,j\}$ is as follows:

$$p_{\text{pop}} = \mathbb{I}\left(c < y < c+a\right) \frac{2\varphi_{a-(y-c)}}{\sum\limits_{k} N_{c,k}\varphi_k}, \tag{2.1}$$

where $\mathbb{I}(\bullet)$ is the indicator function, and φ_a is the RRO at age a. There is a fairly obvious set of constraints about what kind of samples are legitimate, given Eqn. (2.1):

- If the distance between the birth year of the juvenile and the capture year of the adult exceeds the capture age of the adult - i.e. $(y-c) > a$ - that comparison cannot be made (the adult was not alive to potentially sire the juvenile).
- If the adult capture year was before the birth year of the juvenile - i.e. $c > y$ - then that comparison cannot be made (again the adult was not alive at the time of the juvenile’s birth given sampling is lethal).
- Comparisons between adults caught in the same year as the juvenile was born - i.e. $y = c$ - are also not made (the adult could have been caught prior to spawning)

So, even if we describe the sampling regime in terms of M_i juveniles and M_j adults per year, we will always have less than $M_i M_j$ total comparisons given these rules for fair comparisons. The base likelihood assumed in the current OM is binomial, and the evidence for over-dispersion is estimated to be very weak [5]. However, in the MP context it makes sense to use the more flexible beta-binomial likelihood to simulate these data just in case we wish to explore some over-dispersion scenarios in a robustness test.

$\{R, F\}$ scenario	corr($\bar{N}^{\text{true}}_{y,2}$, $\bar{N}^{\text{gt}}_{y,2}$)
$\{0, 0\}$	0.92 (0.83–0.95)
$\{0.01, 0\}$	0.9 (0.77–0.95)
$\{-0.01, 0\}$	0.96 (0.93–0.98)
$\{0, 0.01\}$	0.92 (0.83–0.96)
$\{0.01, 0.01\}$	0.9 (0.81–0.96)
$\{-0.01, 0.01\}$	0.97 (0.93–0.98)
$\{0, -0.01\}$	0.91 (0.82–0.96)
$\{0.01, -0.01\}$	0.91 (0.8–0.95)
$\{-0.01, -0.01\}$	0.97 (0.93–0.98)

Table 3.1: *Temporal correlation (median and 80%CI in brackets) for first 50 years of projection between the GT-derived 5 year moving average of age 2 abundance and its "true" model counterpart.*

2.3 Half-Sibling Pairs (HSPs)

The likelihood for the comparison of two juveniles i and i', assumed to come from different cohorts c_i and $c_{i'}$, is detailed in [2] and is given by the following:

$$p_{\text{hsp}} = \frac{4q_{\text{hsp}}}{S_{c_{\max}}} \left(\sum_a \left[\gamma_{c_{\min},a} \exp\left(- \sum_{y=c_{\min}}^{c_{\max}-1} Z_{y,a} \right) \varphi_{a+|c_i - c_{i'}|} \right] \right), \tag{2.2}$$

where $S_y = \sum_a N_{y,a}\phi_a$ is the spawning abundance, $c_{\max}$ is the most recent cohort, $c_{\min}$ is the earliest cohort, q_{hsp} (with default value of 1) is a "catchability" term explained in [2], and $\gamma_{y,a}$ is the age distribution of adults in year y:

$$\gamma_{y,a} = \frac{N_{y,a}\phi_a}{S_y}. \tag{2.3}$$

With the POP data there are certain combinations of juveniles and adults that are not fair comparisons, but this is not the case with the HSP data. The only stipulation we enforce is that all comparisons are *cross-cohort* - i.e. $c_i \neq c_{i'}$ - for the reasons explained in [2]. We have no empirical evidence either in favour or against over-dispersion in the HSP data, unlike the POP case. We therefore use the beta-binomial as the simulation distribution, as with the GT and POP data, with the reference case being no over-dispersion.

3 Results

For all three data sources we explored 3 scenarios - *status quo* and $\pm 1\%$ - for the (logarithmic) trend in mean recruitment and overall fishing mortality, so 9 in total when crossing them. In terms of notation, a scenario labelled as $\{0.01, -0.01\}$ would denote mean recruitment increasing by 1% and total fishing mortality decreasing by 1%, whereas $\{0, 0\}$ would imply no change in either over time. Figure 3.1 details the spawner abundance dynamics for each of these future recruitment and fishing mortality scenarios.

3.1 Gene Tagging

For the gene tagging data, we set the following sample sizes for releases, T, and the scanning of recaptures, S: $T = 4,000$ and $S = 8,000$. Note these are slightly lower than recommended for the actual SBT pilot study [3] because the corresponding age 2 abundances in this particular model are slightly lower than for SBT. The sample sizes here will still produce the same level of expected recaptures (around 16–25) and, hence, precision as in [3] for "current" model abundances. This will ensure that the simulated correlation between the GT-derived and "true" age 2 abundance trends are meaningful in the real-world SBT context.

We simulate the GT data for each of the 100 projection years, given the sample sizes outlined, and with year 99 the last year of an estimate (given it needs recaptures from year 100). The default assumption

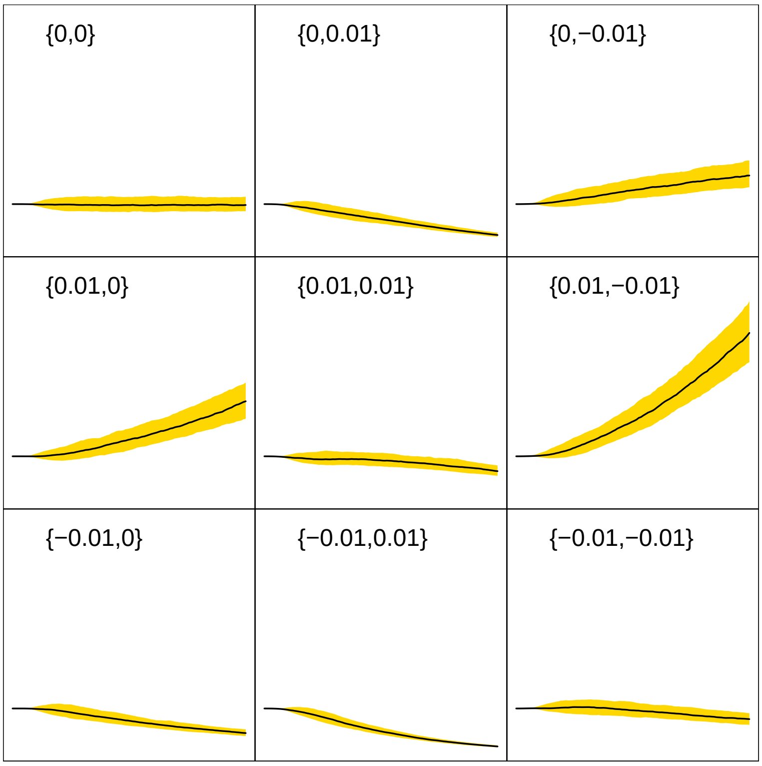

Figure 3.1: *The spawner abundance projections (100 years, median and 80%CI) for each of the 9 mean recruitment and total fishing mortality scenarios. Each simulation starts with the same spawner abundance (purposely set at the current SBT level) and the minimum level in the plot is zero. The first and second terms in brackets at the top of each panel denote the log-scale mean recruitment and total fishing mortality trends, respectively.*

was no over-dispersion and the actual index we focus on is a moving average of the GT age 2 estimates:

$$\bar{N}^{\mathrm{gt}}_{y,2} = \frac{1}{\tau} \sum_{i=y-\tau+1}^{y} \widehat{N}_{i,2}, \tag{3.1}$$

where $\widehat{N}_{y,2}$ are the GT estimates of true age 2 abundance. We choose a 5-year ($\tau = 5$) moving average time-scale, just as is done in the current MP with respect to the aerial survey part of the rule. Table 3.1 summarises the results, in terms of the temporal correlation between the trends in true (simulated) and GT-derived moving average age 2 abundance, across all the 9 scenarios.

Median correlations across all scenarios are 0.9 or higher, with the lower 10%ile never going below 0.75. If mean recruitment, and obviously age 2 abundance, experiences a downward trend the median correlation rises to above 95% (and almost always above the 0.9 level). This is driven by an increasing number of recaptures and, hence, a more accurate estimate of current true abundance. Even if mean recruitment increases (eventually by 50% at the end of the simulations), the median correlation still holds at 0.9, for these fixed sample sizes, there were and with very very few - less than 0.1% - years in the simulation where no recaptures were detected.

3.2 Parent-Offspring Pairs (POPs)

The GT data are easier to generate into a workable mean recruitment index, given we already have a simple, workable estimator in place. The close-kin data, in both the POP and HSP settings, require detailed population dynamic and statistical models to estimate actual abundance and mortality [6]. In the

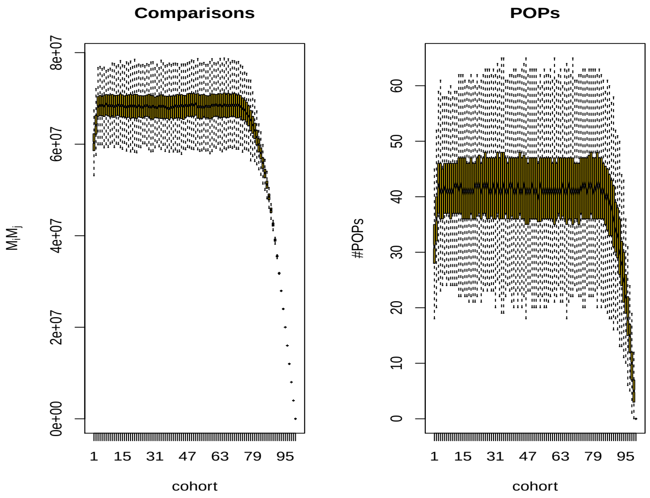

Figure 3.2: *Number of comparisons (left) and the number of POPs (right) for the full suite of 99 cohorts simulated for the* $\{0, 0\}$ *recruitment/fishing mortality scenario.*

following two sections we explore options for generating empirical indices from the close-kin data (of both types) that are (potentially) informative on relative spawner abundance and adult mortality.

For the POP data we define a simple, time-invariant sampling strategy: the number of juvenile (age 3) fish sampled is $M_i = 2,000$, and the number of adult samples taken is $M_j = 2,000$ also. The raw POP data are simulated for the 100 year projection period, and all 9 scenarios, using the beta-binomial likelihood with probability defined by Eq. (2.1), but with over-dispersion set to zero. Figure 3.2 shows the number of effective comparisons and resultant POPs across the future cohorts of interest in the projection model, for the full *status quo* $\{0, 0\}$ recruitment/fishing mortality scenario. Both the number of effective comparisons and POPs increase quite rapidly with increasing cohorts observed and equilibrate for many years, then rapidly decreasing as the number of observations (and, hence, POPs) of the very last cohorts goes to zero. The important feature for the purposes of this paper, is what happens to the ratio of effective comparisons to POPs - for this example it holds very steady over time, much as the spawner abundance does.

For the simple relative spawner abundance index we propose to basically use a modified version of the original "cartoon" estimator [6]:

$$\widehat{N} = \frac{2M_iM_j}{R}, \tag{3.2}$$

where R is the number of POPs and $\widehat{N}$ is the adult abundance. We use this fundamental idea, that the ratio of comparisons to POPs is informative about spawner abundance, when constructing the index. For each juvenile cohort, c, and year, y, and age, a, of adult capture we have a number of comparisons, $M_{c,y,a}$, and detected POPs, $R_{c,y,a}$. In a given year, the age distribution of samples is assumed to be multinomial with probability given by the adult age distribution, $\gamma_{y,a}$, and sample size M_j.

To construct the index we first sum over the adult capture ages:

$$M_{c,y} = \sum_a M_{c,y,a}, \tag{3.3}$$

$$R_{c,y} = \sum_a R_{c,y,a}, \tag{3.4}$$

$$I_{c,y} = \frac{M_{c,y}}{R_{c,y}}. \tag{3.5}$$

To finally obtain an index that focusses on the particular cohort, we use a weighted sum:

$$I_c = \sum_y I_{c,y} \omega_{c,y}, \tag{3.6}$$

where the weighting term $\omega_{c,y}$ is defined as follows:

$$\omega_{c,y} = \frac{R_{c,y}}{\sum\limits_y R_{c,y}}. \tag{3.7}$$

This makes the weighting effectively proportional to the inverse square of the CV of the cartoon estimate and, as such, a simple proxy for an inverse variance type weighting (more POPs, more weight effectively). As with the GT we focus on the first 50 cohorts, in terms of examining the relationship between the index (and statistics derived from it) and the spawner abundance, to avoid complications in the latest years when sampling and, hence, POPs reduces to zero.

The first analysis we did was to explore the evidence for the following relationship between the POP index, I_c, and the true spawner abundance, S_c, and looked at the following form: $\log S_c = \alpha \log I_c$. If the index is a “good” spawning index we would want it to approach zero as S does and be as close to linear in real space (i.e. $\alpha = 1$) as possible. For all 9 scenarios, and across all the random samples simulated, α was both highly significant and ranged from 0.96–0.99. We cannot explain why the relationship is very slightly sub-linear across all population scenarios explored, but what is clear is that the base index is **very** close to linearly related to spawner abundance.

To offset to some degree the sampling variability in the single-cohort index we explore to alternatives:

1. A moving average index, similar to the GT index:

   $$\bar{I}_y^{\text{pop}} = \frac{1}{\tau} \sum_{c=y-\tau+1}^{y} I_c, \tag{3.8}$$

   and here we explored $\tau = 7$, mostly because changes in spawner abundance will be on a slower time-scale than for age 2 abundance and so we can afford to average over a longer time-scale

2. Estimating the log-linear trend λ_y in the cohort-specific index, much as we do in the trend part of the MP with respect to CPUE:

   $$\lambda_y^{\text{pop}} = \frac{\sum\limits_{c=y-\tau+1}^{y} \left((I_c - \bar{I})(c - \bar{c})\right)}{\sum\limits_{c=y-\tau+1}^{y} \left((c - \bar{c})\right)^2} \tag{3.9}$$

   where $\bar{I}$ and $\bar{c}$ are the respective means of the index and cohort over the relevant time-frame, but we use a $\tau = 10$ time-scale here. The reason behind this is for the same reason as using a longer time-scale for the moving average index above: changes will be slower and we will, in principle, follow less noise by doing this

We look at the correlation between these derived indices and their true counterparts from the OM over the first 50 years in the simulation. For some perspective on what these correlations might imply, we also compare them to a hypothetical unbiased survey of the spawner abundance with a CV of 0.3. Obviously, we cannot achieve this kind of index in practice, but it will hopefully give an indication of what we can obtain by comparing it to a more familiar type of abundance index.

Table 3.2 details the correlations for both types of derived index (moving average and log-scale trend), for the POP-derived and hypothetical survey “raw” indices, relative to their “true” model counterparts.

$\{R, F\}$ scenario	corr($\bar{S}_y^{\text{true}}$, $\bar{I}_y^{\text{pop}}$)	corr($\bar{S}_y^{\text{true}}$, $\bar{S}_y^{\text{surv}}$)	corr(λ_y^{true},λ_y^{pop})	corr(λ_y^{true},λ_y^{surv})
$\{0, 0\}$	0.4 (-0.14–0.73)	0.52 (-0.01–0.73)	0.09 (-0.28–0.4)	0.26 (-0.08–0.56)
$\{0.01, 0\}$	0.68 (0.13–0.89)	0.73 (0.29–0.92)	0.1 (-0.24–0.42)	0.32 (-0.04–0.61)
$\{-0.01, 0\}$	0.73 (0.29–0.89)	0.74 (0.28–0.89)	0.09 (-0.25–0.45)	0.32 (-0.05–0.61)
$\{0, 0.01\}$	0.75 (0.29–0.92)	0.75 (0.39–0.91)	0.1 (-0.25–0.45)	0.29 (-0.07–0.6)
$\{0.01, 0.01\}$	0.42 (-0.14–0.74)	0.53 (-0.04–0.82)	0.08 (-0.27–0.41)	0.26 (-0.09–0.57)
$\{-0.01, 0.01\}$	0.91 (0.74–0.97)	0.88 (0.73–0.95)	0.13 (-0.3–0.5)	0.4 (-0.03–0.58)
$\{0, -0.01\}$	0.59 (0.04–0.84)	0.68 (0.16–0.89)	0.12 (-0.27–0.41)	0.31 (-0.09–0.57)
$\{0.01, -0.01\}$	0.84 (0.58–0.94)	0.87 (0.63–0.95)	0.12 (-0.24–0.45)	0.32 (-0.02–0.6)
$\{-0.01, -0.01\}$	0.44 (-0.13–0.78)	0.51 (-0.02–0.84)	0.08 (-0.3–0.43)	0.28 (-0.12–0.58)

Table 3.2: *Temporal correlation (median and 80%CI in brackets) for first 50 years of projection between both the 7 year moving average and the log-scale linear trend and their "true" model counterparts, for the POP-derived index and a hypothetical unbiased survey with a CV of 0.3.*

Focussing on the moving average trend first, the hypothetical survey index marginally outperforms the POP-derived index for scenarios where little to no change in spawner biomass occurs over time, with median correlation values for both types of index all at 40% or above in these cases. For scenarios where spawner biomass is changing over time, be it up or down, the POP-derived index is at least as good as, and sometimes better than (for pessimistic scenarios), the survey-based index. For the log-scale linear trend the survey consistently outperforms the POP-derived index across all scenarios, with median correlation levels 2.5–3 times that of the POP-derived index. What is very noticeable about the log-scale index trends, however, is the overall poor performance of either index - POP-derived or survey-based. Median correlations never exceed 0.4 for the most pessimistic scenario, with the lower 10%ile permanently sitting at between -0.3 to -0.05 for either index across all scenarios.

3.3 Half-Sibling Pairs (HSPs)

One very important point to make first is that the HSP data are **independent** of the POP data. Whatever we may derive from the HSP data, even though it is informative on the spawning population, it can be used alongside - and, potentially, in combination with - any POP indices we care to use. The HSP data present more of a challenge than the POP data, which really relate to spawner abundance in a given year. The HSP data, when considering the comparison of two juveniles i and i', informs us about spawner abundance in the most recent juvenile cohort *and* the cumulative mortality of the adult population in between the two cohorts. In conjunction with other data (catch biomass and composition, abundance data) it could also inform us on the RRO ogive as it is free from adult sampling effects (like selectivity) [6]. Given the likely information content of the HSP data, and the results of the POP-derived indices, we explore the following two possibilities as potential candidates as input series for candidate MPs:

- Derivation of a relative spawner abundance index, similar in concept to that derived from the POP data
- Derivation of an adult mortality index, which can only be attempted for the HSP data (and is not derivable from any hypothetical survey)

We simulate the sampling of $M_i = M_{i'} = 2,000$ juveniles per year, so the total number of comparisons between two cohorts is always $M_i M_{i'} = 4e+6$, and never compare two samples from the same cohort. Figure 3.3 outlines two plots of the simulated HSPs for the $\{0, 0\}$ full *status quo* recruitment and fishing mortality scenario: (i) the total number of HSPs relating to each of the first 96 cohorts of interest (recall the target is sampling age is 3, so we cannot have information for any cohorts after 96); and (ii) the number of HSPs found between the first cohort and all the subsequent ones.

A number of key points can be made using Figure 3.3:

- There will be, for the current proposed sample sizes and in general, more HSPs than POPs - they are a weaker (genetically) relationship than parent-offspring and, therefore, more common. In this

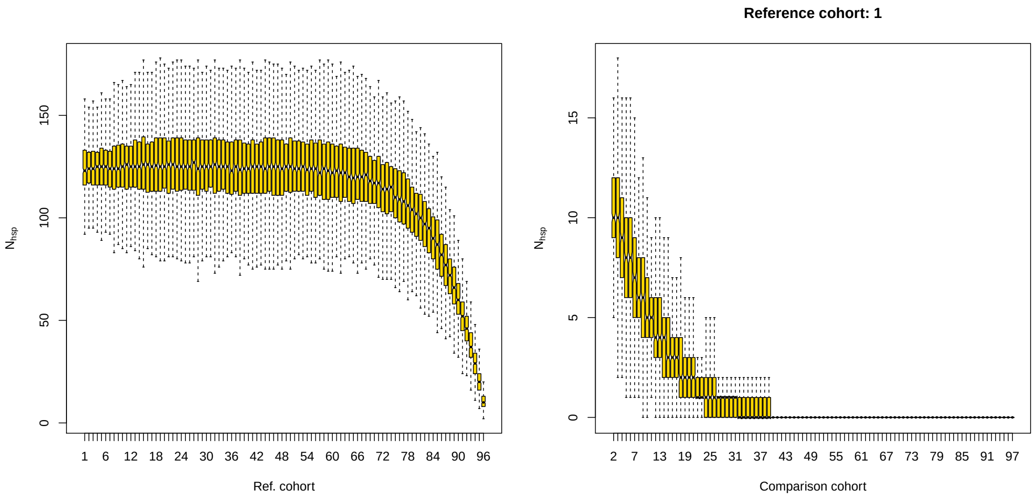

Figure 3.3: *Number of HSPs for each of the 96 cohorts (left) and between the first cohort and all the subsequent ones (right). In each case the number of total comparisons made between each cohort is 4e+6.*

example almost 3 times as common. In the cartoon it is 2 times as many *but* when accounting for lost comparisons in the POP framework, whereas none save intra-cohort comparisons are lost when comparing juvenile samples, we actually obtain more than 2 times the number of HSPs. This means any comparable HSP-derived indices are likely to be more informative than for the POP-derived ones based on sample sizes alone.

- Looking at the plot on the right of Figure 3.3 we see the adult mortality effect in the HSP data. As we compare progressively more distant cohorts, the number of HSPs found between them declines because the probability of an adult living that long (which it would have to for there to be any HSPs) becomes smaller and smaller. There is a sort-of-analogy with catch curves here, where catches often decrease down a cohort with total mortality. The **crucial** difference with the HSPs is that they are **not** biased by selectivity effects, which catch-curves are.
- The *status quo* scenario is the easiest with which to make this distinction between the abundance and mortality signals in the data. With changing abundance and/or adult mortality over time these two will inevitably alias for one another. The key is how do we derive the two indices to see if we can tease the signals apart? To make the most of the HSP data in an empirical sense we want to derive two indices that could reflect abundance and mortality effects as independently as possible.

The HSP spawner relative abundance index for a given cohort, c, is derived as follows:

$$I_{c,c'} = \frac{M_c M_{c'}}{R_{c,c'}}, \tag{3.10}$$

$$I_c = \sum_{i=c-\nu}^{c-1} I_{c,i} \varepsilon_{c,i}, \tag{3.11}$$

$$\tag{3.12}$$

where $c' < c$, ν is a back-averaging time-scale, and $\varepsilon_{c,c'}$ is a weighting proportional to the number of HSPs found between the two reference cohorts c and c'. The parameter ν is set at 3 - it should not be set too large so as to avoid including mortality trend effects in the abundance index. The actual abundance index, $\bar{I}_c^{\text{hsp}}$, is defined much as the POP index as a moving average of the "raw" index I_c (with the same time-frame of $\tau = 7$. The time-frames over which the HSP index actually works are somewhat different to

$\{R,F\}$ scenario	corr($\bar{S}_y^{\mathrm{true}}$, $\bar{I}_y^{\mathrm{hsp}}$)	corr($\bar{S}_y^{\mathrm{true}}$, $\bar{S}_y^{\mathrm{surv}}$)	corr(Z_y^{true},$\mathcal{Z}_y^{\mathrm{hsp}}$)
$\{0,0\}$	0.79 (0.48–0.91)	0.58 (0.07–0.85)	0.08 (-0.14–0.32)
$\{0.01,0\}$	0.89 (0.68–0.96)	0.79 (0.41–0.92)	0.05 (-0.2–0.3)
$\{-0.01,0\}$	0.92 (0.77–0.97)	0.77 (0.44–0.91)	0.1 (-0.13–0.32)
$\{0,0.01\}$	0.92 (0.77–0.97)	0.84 (0.59–0.93)	-0.38 (-0.58– -0.09)
$\{0.01,0.01\}$	0.77 (0.4–0.92)	0.59 (0.1–0.84)	-0.38 (-0.58– -0.08)
$\{-0.01,0.01\}$	0.97 (0.94–0.99)	0.93 (0.83–0.96)	-0.37 (-0.61– -0.09)
$\{0,-0.01\}$	0.85 (0.63–0.95)	0.75 (0.31–0.91)	-0.02 (-0.28–0.24)
$\{0.01,-0.01\}$	0.94 (0.86–0.98)	0.9 (0.78–0.96)	-0.03 (-0.29–0.25)
$\{-0.01,-0.01\}$	0.79 (0.5–0.93)	0.57 (0.03–0.81)	-0.04 (-0.3–0.22)

Table 3.3: *Temporal correlation (median and 80%CI in brackets) for first 50 years of projection between the 7 year moving average, and the "true" model counterparts, for the HSP-derived index and a hypothetical unbiased survey with a CV of 0.3. Also included is the correlation between the true weighted mean adult total mortality and the HSP-derived index.*

the POP index. For the raw index we are initially summing over cohorts that *precede* the reference cohort c, and we do not compare within a cohort, so $c = 4$ is the first year we can derive a raw index point for. For the moving average we than add $\tau = 7$ years to this so $c = 11$ is effectively the first year we get an HSP index for. For the POP data it is $c = 8$, given we do not compare juveniles and adults from the same year of capture (ruling out $c = y = 1$).

The adult mortality index is more subtle. For unrelated pairs (UPs) of juveniles i and i', the likely time between their respective birth years (cohorts), $\Delta_{i,i'} = |c_i - c_{i'}|$, is unaffected by adult abundance and mortality; for HSPs it is strongly affected - see Eq. (2.2). The expected value of $\Delta_{i,i'}$ is, for the example of no changes in adult abundance, always going to be smaller for HSPs than UPs because of the adult mortality effect (see also the r.h.s. of Figure 3.3 for this effect). To derive and adult mortality index using this idea we explore the following:

$$\mathcal{Z}_c^{\mathrm{hsp}} = \log\left(\frac{\mathbb{E}\left(\Delta_{i,i'}^{\mathrm{hsp}}\right)}{\mathbb{E}\left(\Delta_{i,i'}^{\mathrm{up}}\right)}\right), \tag{3.13}$$

where the expection in Eq. (3.13) is taken over the cohorts c to $c - \psi + 1$, and we chose a time-frame of $\psi = 10$ for this example (thus making $c = 11$ the first cohort with the index available). The mean adult total mortality rate, $\bar{Z}_y$, that we explore for correlation with $\mathcal{Z}^{\mathrm{hsp}}$ is calculated via

$$\bar{Z}_y = \sum_a \gamma_{y,a} Z_{y,a}, \tag{3.14}$$

where $\gamma_{y,a}$ is the relative age distribution of the adults in year y.

Table 3.3 summarises the correlations of the HSP (as well as the POP and hypothetical survey) derived abundance indices, and the adult mortality index, with their "true" model counterparts. Unlike the POP example, the HSP-derived abundance index outperforms an unbiased survey with a CV of 0.3 in all cases - not just for declining abundance scenarios. For the HSP index median correlation never goes below 0.77 and the lower 10%ile never less than 0.4; for the survey-derived index comparison the minimum median correlation is 0.58 and the minimum lower 10%ile is 0.03.

For the adult mortality index, where if there is a relationship the correlation should be negative, the situation is very case dependent. For scenarios where F (and, hence, Z) is time-independent we see no obvious linkage, as one would expect given the nature of the index and the level of sampling variability inherent in it. For decreasing Z we see a very very weak effect (marginally negative correlation). It is only for the case of increasing adult Z that we see a clear and consistent signal. This is to be expected given both the comparatively low levels of adult Z overall, and the signal in the HSP data. For increasing Z the distribution of the temporal distance between cohorts of the HSPs begins to increasingly contract over time, resulting in the relationship (negative correlation) we see in Table 3.3. From the originally fairly low level, if Z decreases the opposite widening effect in the cohort difference distribution of the HSPs is *much* weaker, resulting in the minimally negative correlations in Table 3.3 for these scenarios.

4 Discussion

This paper focusses on the statistical specifics of the generation of new data sources, specifically gene-tagging and both POP and HSP close-kin data. It also explores on their potential information content for use in an MP, exploring the derivation of empirical indices of relative spawner abundance and adult mortality. Given the impending cessation of the current MP, and the initialisation of a new round of MP and OM development to replace it, we decided that the SBT OM and constant catch projections was not the best way to explore the generation of new data sources and their potential information content. Instead, we employed an SBT-like OM with very similar life-history, overall fishery selectivity, and current spawner abundance properties as the SBT OM. This permitted us to efficiently explore a wide range of future abundance scenarios, as well as a wide range of potential indices given sampling regimes directly relevant to the current SBT situation. We explored three different mean recruitment and overall fishing mortality trends (*status quo*, ±1% log-scale) and crossed them for a total of nine scenarios to obtain a very wide variety of future dynamics for both the stock and fishery from which to generate the new data sources.

In relation to gene tagging, we employed a hypothetical sampling regime with the similar release and recapture properties (overall expected range of recapture numbers) as outlined in the design study [3]. The default assumption was a straight binomial distribution (no over-dispersion at this stage) for simulating the recaptures of age 2 releases, with the associated information loss likely to result from imperfect cohort identification included directly. In terms of indices for more MP related purposes, we explored the correlation of a 5-year moving average of relative age 2 abundance with its simulated counterpart. For all future recruitment and fishing mortality scenarios median correlation over the first 50 years were all at 0.9 levels or above, with the lower 10%iles all above 0.75. These correlations will hold true even if there is some fixed (or lightly varying mean) fraction of the overall recruits that never enter the GAB - absolute abundance may be biased in these extreme mixing scenarios but the relative trend is well represented in the actual empirical data. This suggests the gene tagging data have the potential to be a highly informative recruitment index for use in any candidate MPs.

For the close-kin POP data we explored a variant on the original “cartoon” abundance estimator [6] to generate a relative spawner abundance index. The cohort-specific index, weighted over adult recapture years using the relative number of POPs linked to each year, was compared to a hypothetical survey of spawning abundance with a (non-autocorrelated) observation error CV of 0.3. Both were converted to moving averages with a 7 year time-frame to reduce sampling error effects. For scenarios where spawner abundance was not changing very much over time, the survey marginally outperformed the POP-derived index. For scenarios where spawner abundance was changing quite strongly over time (both up but especially down) the POP-derived index performed at least as well, and sometimes better than, the survey. Median correlations over the first 50 years of the simulation were never lower than 0.4 and sometimes as high as 0.9 for the POP index. An alternative index, focussed on the log-scale linear trend in the two indices over time, performed poorly. The survey performed better, in terms of relative magnitude of correlation, but never exceeded a median correlation of 0.4 - even for strong trends in spawner abundance. A likely reason the POP-derived trend index performed consistently worse than a hypothetical survey is the more temporally complex and compound sampling error (in terms of both adult age sampling and in relation to POPs, given the juvenile and adult samples). Another curiosity relating to the POP index in general is that it will experience a period of precision increase over time as the number of POPs relating to a particular cohort build up in the data set. The impact of this would be observed in a full MP testing context, but this initial work was focussed only on generating the data and their overall information content.

For the HSP data we explored both a relative abundance index (independent of, but complimentary to, the POP index) and a mean adult mortality index also. This is, in principle, made possible by the additional information content inherent to the HSP data. A similar weighted approach as that used for the POP-derived index was used to generate the HSP abundance index, and a 7 year moving average also used to compare to the hypothetical spawner survey. In this case the HSP abundance index universally outperformed the survey across all scenarios: median correlations with true spawner abundance never fell below 0.75 and the lower 10%ile never fell below 0.4. This improvement in performance, relative to the POP index, is driven by both a higher overall number of HSPs relative to POPs (and, therefore, lower variability) and no additional sampling variability arising from having to sample the adults across their age-range (as is the case in the POP framework). The HSP adult mortality index was derived using the relative difference in the distribution of times between birth years for both unrelated and half-sibling pairs. The HSP mortality index was shown to correlate fairly well with mean adult mortality *only* in cases where it was increasing over time. This is because of the asymmetric nature of what happens to the distribution of cohort differences across unrelated and half-sibling pairs when adult mortality changes over time for this particular example.

In terms of operational changes required in the projection component of the current OM to accommodate these new data sources, we will require additional routines in `sbtproj.tpl` to simulate and store in external files similar to the current `sbtOMdata` format. These changes are fairly straightforward, and certainly possible using the current `ADMB` software structure, but will need some care to ensure the temporal build up of data in the POP paradigm, as well as the combination of actual historical and simulated close-kin data (be it POP or HSP related), is correctly handled.

The results in this paper clearly demonstrates that the gene tagging data have the potential to be a very informative data source on relative recruitment levels and, therefore, for use as input data series to candidate MPs. Using them in a manner similar to that employed for aerial survey in the current MP, a 5-year moving average, results in indices that show strong correlation with the true average age-2 abundance over time. As seen clearly in Figure 1.1 the CPUE index exhibits a complicated and highly non-linear relationship with estimated spawner abundance over time. Over the last two decades, and for future spawner abundance levels we are likely to be able to rebuild to over the next two decades, the relationship between CPUE and spawner abundance is very far from being linear. Given the CCSBT has funded the collection and genotyping of future C-K samples, and plans are underway to process historical ones, it makes sense to explore if we can generate actual indices of spawning abundance from these data.

The close-kin POP data have clearly been informative with respect to absolute abundance and adult mortality in the SBT OM [5], and the new HSP data could be very informative also [6]. In this work we have also demonstrated their empirical potential, in relation to indices that can be derived from the raw data and considered as input series to candidate MPs. This would be in addition to their value in either the standalone models [6] or the SBT OM [5] in terms of estimating absolute adult abundance and mortality. From the POPs we can derive a relative spawner abundance index that performs close to, and sometimes better than, a high quality unbiased hypothetical survey with a CV of 0.3. From the HSP data we can derive a relative spawner abundance index that easily outperforms such a survey with a similar CV of 0.3. In combination - i.e. a combined POP and HSP index - we could obtain an index that correlates with true spawner abundance as well as a high quality survey with a CV of 0.2–0.25. In addition to this, using the HSP data we can derive an index that can detect if mean adult mortality is increasing over time, providing a basis to separate causes of decline in spawning abundance.

5 Acknowledgements

This work was funded by the Department of Agriculture & Water Resources, and CSIRO Oceans & Atmosphere.

References

[1] Report of the 20th Meeting of the Scientific Committee. CCSBT, Incheon, South Korea, September 2015.

[2] Hillary, R. M., Preece, A., and Davies, C. R. (2016) Reconsideration of OM structure and new data sources for 2017 reconditioning. *CCSBT-OMMP/1609/4*.

[3] Preece, A., Eveson, J. P., Davies, C. R., Grewe, P. G., Hillary, R. M., and Bravington, M .V. (2015) Report on gene-tagging design study. *CCSBT-ESC/1509/18*.

[4] Report of the 22nd Annual Meeting of the Commission. CCSBT, Yeosu, South Korea, October 2015.

[5] Hillary, R. M., Preece, A., and Davies, C. R. (2014) Assessment of stock status of southern bluefin tuna in 2014 with reconditioned operating model. *CCSBT-ESC/1409/21*.

[6] Bravington, M. V., Skaug, H. J., and Anderson, E. C. (2016) Close-kin mark-recapture. *Stat. Sci.* (in press).

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