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Updated design models informing the sampling strategy for a Close-kin mark-recapture application to South Pacific albacore

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Important disclaimer

1 Executive summary

Project 100c was established by SC 17 to assess the feasibility of applying close-kin mark-recapture in the Western and Central Pacific Commission, starting with south Pacific albacore as a trial population. Initial design studies based on the 2018 stock assessment for this population provided first estimates of the number of individuals that should be sampled in order to achieve an estimate of adult biomass (4 years and older) that would be useful for management (CV ¡ 15%). These numbers are updated here to account for the two most recent assessments for this stock and correct an issue with the initial data inputs.

The sampling design model used the same framework as that developed by Bravington et al. (2021) (SC17-SA-IP-14) but explored alternative population scenarios to account for the changes in assessment methodology and assumed stock structure since 2018. The impact of sampling program length and the proportion of juvenile to adult samples were also examined. Depending on the population scenario used, the sampling numbers required to achieve sufficient precision on adult biomass estimates from a CKMR model vary from 36,000 to 84,000 tissue samples collected over three years. This wide range reflects the variability in the numbers-at-age predicted by recent stock assessments for south Pacific albacore and uncertainty about stock structure and key life-history parameters. Genotyping the samples collected to date might provide further insights as to the most likely population scenario and reduce the range of samples needed according to the statistical design. Also, the numbers of samples to be collected annually could be reduced if the sampling program is extended to a fourth year.

Recommendations

SC 20 is invited to:

- consider these updated sampling numbers for the statistical sampling design for south Pacific albacore under Project 100c;
- consider supporting the genotyping of samples collected to date to narrow the range of population scenarios considered from the sampling design;
- consider supporting the investigation into the optimal allocation of ageing methods across ages to minimise ageing costs while improving overall ageing precision.

2 Introduction

Close-kin mark-recapture (CKMR) is a fisheries-independent approach that can provide an estimate of absolute abundance, total mortality, and other key population metrics (Bravington et al., 2016). It can also yield insights about spatial connectivity within a population. In short, CKMR treats observations of kin pairs (genetically related individuals, such as parents and offsprings) as tag recaptures (an offspring 'tags' its parents), and the likelihood of observing a set number of kin pairs given population size, age and sex structure is calculated. This likelihood can then be used on its own in a population dynamics model to estimate the parameter vector that maximizes the likelihood given observations, or used in an integrated stock assessment framework in combination with other data sources. To observe kin pairs, tissue samples of a pre-specified number of individuals are collected from the population of interest. The samples are then genotyped and examined for evidence of genetic relatedness.

When using CKMR, precise estimates of key parameters can only be produced if enough samples are collected from the population across suitable age groups. As such, before implementing CKMR, it is important to undertake a design phase to assess the number of samples needed and their age distribution given a target precision in parameter estimates (typically a CV $<$ 15%, but this can be modified depending on preference). In general, the larger the number of individuals collected, the better precision on the resulting model-derived estimates of population metrics. Apart from information on the biology and life-history of the species, the design phase requires that an assumption be made about the likely true population size. If the true population size is lower than the assumed size, then CKMR will provide abundance estimates with a precision that is greater than the target precision. If the true population size is larger than assumed, then the CKMR estimate of abundance will be less precise, but it will reveal that the stock is larger than what was assumed during the design study.

Project 100c was established by SC 17 to assess the feasibility of applying CKMR in the Western and Central Pacific Commission (WCPFC), starting with south Pacific albacore (*Thunnus alalunga*) as a trial population. Initial design studies (Bravington et al. 2020, followed by an update in Bravington et al. 2021) provided early estimates of the number of individuals that should be sampled in order to achieve an estimate of adult biomass (4 years and older) that would be useful for management (CV $<$ 15%)[1]. However, these studies used the 2018 stock assessment (Tremblay-Boyer et al., 2018) as a baseline for population dynamics, which means that sampling numbers were optimized for a population assumed to match the most recent period in the stock assessment (i.e., years 2014 to 2016). There have been two updates to the south Pacific albacore stock assessments since which have made changes to stock structure (most notably by extending the stock to include the Eastern Pacific ocean) and assumptions about life-history, both of which impact the best estimate of population dynamics in the recent period. As such, this Information Paper to SC 20 presents an updated sampling design for south Pacific albacore based on the most recent stock assessment for this population. Of note, the basic modelling framework developped under Bravington et al. (2021) was used here, including assumptions about the spatial structure of juveniles vs. adults. Issues regarding the treatment of some of the data inputs have also been corrected.

3 Methods

3.1 Overview

The statistical sampling design requires a population model that approximates ‘recent’ population dynamics for the stock, as that is what is effectively being targeted by the sampling program. Ideally, the most recent stock assessment for the population of interest would be used as a baseline. However, there were important changes in the methods and assumptions about stock structure in each of the three most recent stock assessments for south Pacific albacore, and these have impacted the scaling of predicted population numbers over similar time periods.

The 2018 stock assessment (Tremblay-Boyer et al. 2018; final prediction year 2016) was used for the most recent sampling design model (Bravington et al. 2021), and has guided sampling targets to date for the pilot sampling program under Project 100c. This assessment assumed the stock was fully contained within the southern WCPFC convention area. That assumption was

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[1] about 25,000 individuals over three years, evenly spread between adult and juveniles

modified in the 2021 stock assessment (Castillo Jordán et al. 2021; final prediction year 2019) with the extension of the stock to the eastern Pacific ocean. The most recent stock assessment (Teears et al. 2024; final prediction year 2022) also assumed a stock spanning the southern Pacific ocean, but modifications to assumptions about natural mortality resulted in much higher numbers-at-age across similar time periods compared to previous assessments. To account for this, the current close-kin sampling design was updated for each stock assessment separately with the assumption they represented different population 'scenarios', or states of nature.

All data inputs were derived directly from the assessments' diagnostic case input and output files made available by SPC in the public domain[2], including total catches by fleet, numbers-at-age, and maturity and weight-at-age ogives. As the 2024 stock assessment had not been published at the time of the analyses presented here, a draft version of the diagnostic case was provided by SPC (J. Hampton, *pers. comm*, July 2024).

There are several considerations in the close-kin design approach to allow for uncertainty with regards to the spatial structuring of the south Pacific albacore stock (see Bravington et al. 2021 for a discussion). The inclusion of a scaling parameter in the design population model to represent the proportion of the juvenile population accessible by the sampling program was retained here. In addition, while main sampling numbers are presented for a population assumed to span the WCPFC convention area (including the overlap area), alternative scenarios where the stock spans the southern Pacific ocean are also included for the 2021 and 2024 stock assessments.

3.2 Catch-at-age

Catch-at-age distributions were built for each fleet from the length observations. The growth curve from the assessment was used to simulate the probability of observing an age from a given length (based on the standard deviation of lengths-at-age). Length records for each fleet were aggregated by 1cm bin class, based on the last five years for which length records were available for the fleet. These were assumed to be representative of a recent catch-at-age distribution for this fleet. Records by length bin were spread across possible age bins, rounded to the nearest integer, and summed across age bins by fleet. The proportion-at-age was obtained as the ratio of predicted observations by age bins to the total length observations for the fleet. The catch-at-age distribution for the fleet was then the product of this proportion-at-age vector and the average catch for the fleet over the last three years.

Only fleets active in the last three years of the assessment were retained. For active fleets missing sufficient recent length samples to approximate a catch-at-age distribution, the proportional catch-at-age distribution of a similar fleet was used. 'Similar' fleets were chosen to prioritize those using the same gear in the same stock assessment region.

3.3 Numbers-at-age and life-history

To approximate recent population dynamics, 'target' numbers-at-age for the simplified design model were specified as the annual average for the most recent period spanned by each of the three stock assessments. For the 2018 and 2024 assessments, a 'recent' period of three years from the final assessment year was used (i.e., 2014 to 2016 for the 2018 stock assessment

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[2] `https://oceanfish.spc.int/en/publications/cat_view/116-ofp-publications-a-documents/131-stock-assessment-and-modelling/181-stock-assessments/229-input-and-result-files`

and 2020 to 2022 for the 2024 stock assessment). For the 2021 stock assessment, a 'recent' period of two years was used (i.e. 2018 and 2019) to avoid using population predictions adjacent to 2016, given concerns raised at previous WCPFC SC18 and SC19 with regards to the recruitment predictions made for that year (e.g., see Scott et al. 2023). For seasonal assessment models (2018 and 2021), annual numbers-at-age were first averaged over seasons. The resulting numbers-at-age vectors are shown in Figure 1 for both the recent period and an overlap period of 2014 to 2016 to showcase the difference in population scaling.

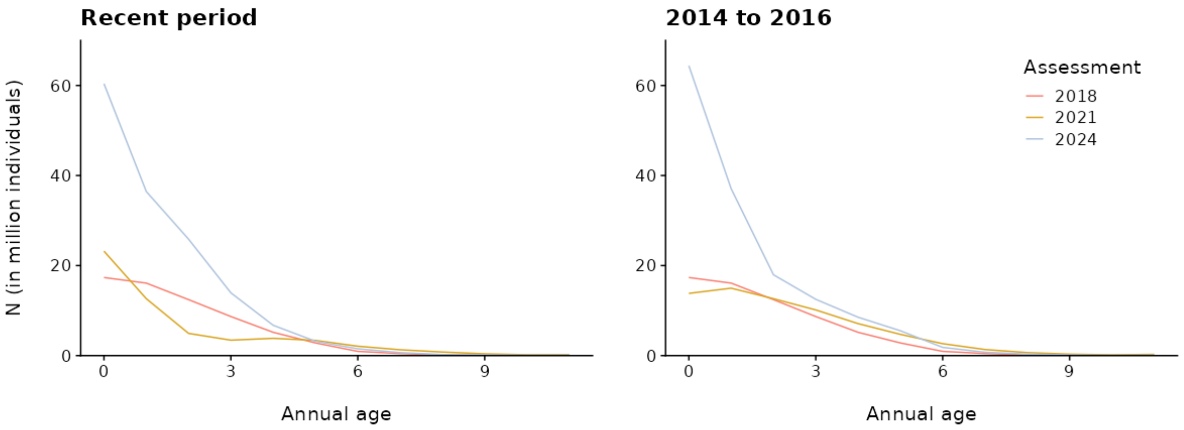


Figure 1: Numbers-at-age for the 'recent' (left panel) and an overlap (right panel) time period of each of the stock assessment scenarios (in colours) used in the statistical sampling design.

For consistency, maturity-at-age and weight-at-age ogives were set to the values used by Bravington et al. (2021) based on the 2018 stock assessment.

3.4 Population model

A simple age-structured population model was developed using the same framework as in Bravington et al. (2021). For each stock assessment scenario, the model was initialized using the target numbers-at-age vector described above (i.e., that from the corresponding stock assessment, converted to annual age bins where needed), and annual numbers-at-age were projected over a period of ten years. To avoid the need for a plus-group (which complicates the calculation of kin probabilities), the maximum age is set to 15 and the stock assessments' plus-group (at age 12) is distributed in the remaining age bins assuming a log-linear relationship between numbers and age. The population was then sampled by the sampling program over the last three years of that period, with samples allocated to juveniles (0 to 3 years) and adults (4 years and older). The model is sex-structured, assuming a sex ratio of 1:1. As dynamics are the same for males and females, the description below shows dynamics by time and age only. Recruitment to the first age class is assumed constant throughout. Model parameters are described in Table 1.

The initial population-at-age is set to that of the stock assessment. For subsequent years:

$$N_{t\,\in\,2:Y,\;a=1} = R_0 \cdot \sigma_{R_t}$$
$$N_{t\,\in\,2:Y,\;a+1} = N_{t,a} \cdot e^{-(F_a+M)}$$

where a is the age bin, R_0 (in numbers of fish) is calculated from B_0 using weight-at-age and

Table 1: Description of model parameters.

Symbol	Description
M	Natural mortality
α	Negative slope of the log-linear numbers-at-age relationship (i.e., Z, total mortality)
w_s	Scaling parameter by sex for the fecundity vs. weight relationship
B_0	Mean recruitment (by weight) in the first year
σ_R	Annual recruitment deviations
HS_P	Proportion of juvenile population targeted by sampling program

the theoretical numbers-at-age distribution given α, and F_a is solved for iteratively at each model step using assumed catch-at-ages and the Baranov equation.

Finally, to estimate the variance in the distribution of recruitment deviations (used when computing the model's covariance matrix, see below), a linear model of numbers as a function of age was first fitted assuming a quasi-poisson error distribution (with log-link) to the target numbers-at-age distribution. The variance of the model residuals was extracted and assumed equal to the variance of the log recruitment deviation.

3.5 Estimation of CVs for population metrics

The estimation of CVs for quantities computed within a CKMR population modelling framework consisted of three main steps:

Step 1: Population dynamics for south Pacific albacore were estimated as described above. For close-kin computations, three resulting quantities are especially important: numbers-at-age ($N_{t,a,s}$, abundance at time t, age a and sex s), survival-at-age (from natural and fishing mortality), and Total Reproductive Output (TRO) for the population at time t:

$$TRO_{t,s} = \sum_{a=0}^{A} N_{t,a,s}\varphi_{a,s}$$

where $\varphi_{a,s}$ is fecundity-at-age a and sex s, defined by a power relationship between weight-at-age W_a and the reproductive output by sex coefficient w_s, scaled by maturity-at-age m_a:

$$\varphi_{a,s} = m_a \cdot W_a^{w_s}$$

Step 2: Given population dynamics estimated in the first step, compute the probability of observing a Parent-offspring Pair (POP) or a Half-sibling Pair (HSP) for each pairwise combination of individual samples, as a function of the year they were sampled, their age at sampling and, for POPs only, the sex of the parent, for a given number of samples. The following assumptions are made:

- Age is known exactly for both adults and juveniles;
- Population dynamics (selectivity, maturity, fecundity, length) vary across age only, with no variability in individual length-at-age;

- POPs and HSPs are computed but grandparent-grand offspring pairs (GGPs) are not explicitly modelled.

The probability that an individual of age a_i captured in year t_i is the parent of an individual born in year c_j is defined as:

$$\mathbb{P}\left(POP \,|\, \{i,j\}\right) = \mathbb{I}(c_j < t_i < c_j + a_i) \times \frac{\varphi_{a_i-(t_i-c_j),s_i}}{TRO_{c_j,s_i}}$$

which is the ratio of the fecundity of a possible parent of that age in the year that the juvenile was born and the TRO of the population in that year. This probability is computed if the possible offspring was born before the possible parent was captured (given lethal sampling), and if the possible offspring was born after the possible parent was mature. Otherwise, it is set to zero.

The probability that an individual i born in year c_i is the half-sibling of an individual i' born in year $c_{i'}$ is the probability that an unobserved individual of unknown age would have been the parent of offspring born in two different cohorts separated by the difference in birth years between the cohorts ($\delta_i = c_{i'} - c_i$):

$$\mathbb{P}\left(HSP \,|\, \{i,i',s\}\right) = \frac{1}{HS_P} \cdot \sum_a \left(\frac{N_{c_i,a,s}\varphi_{a,s}}{TRO_{c_i,s}} \times \left[\frac{N_{c_{i'},a+\delta_i,s}}{N_{c_i,a,s}} \right] \times \frac{\varphi_{a+\delta_i,s}}{TRO_{c_{i'},s}} \right)$$

The first term computes the probability that the unobserved parent was the parent of the older juvenile, the second term computes the probability that the unobserved parent survived from the birth year of the older juvenile to the birth year of the younger juvenile (given natural and fishing mortality), and the third term computes the probability that the unobserved parent was in fact the parent of the younger juvenile given its reproductive output in that birth year. This is integrated over all possible parent ages, as we do not know the actual age of the unobserved parent, and repeated for both potential parent sexes (shared parent sex will be known from mitochondrial DNA), and scaled by HS_P, the proportion of the juvenile population accessed by the sampling program.

For HSPs, same cohort comparisons (i.e. individuals born in the same year) are not performed to avoid possible bias from ‘good years’ that could result in an excess of HSPs born in the same year.

Finally, a false-negative probability of detecting a HSP of 15% is assumed.

Step 3: Once the probabilities of observing a POP and observing a HSP for each combination of sampled individuals has been predicted by the model, the expected covariance matrix of the input parameter vector is computed and used to approximate the variance for quantities of interest using the delta method. This process is equivalent to simulating a large number of input datasets, fitting the CKMR model to each one, and calculating the variance in the resulting estimated quantities (see Bravington et al. 2016 for a technical description). Steps 2 and 3 are updated for each sampling and assessment scenario.

3.6 Sampling scenarios

Three main population scenarios were developped for a south Pacific albacore population assumed to span the Western and Central Pacific Ocean (WCPO) based on each of the stock assessments (2018, 2021 and 2024). Annual sample sizes for juveniles and adults were trialled over three and four years sampling programs, varying total annual samples from 10,000 to 40,000. The default sampling program assumed even sampling of adults and juveniles, with alternative sampling scenarios varying the total proportion of juveniles in the sample from 0.1 to 0.9. Lastly, design numbers were updated for a population assumed to span both the WCPO and the Eastern Pacific Ocean (EPO) based on the scenarios using the 2021 and 2024 assessments, assuming even sampling of adults and juveniles.

4 Results

Annual samples required to achieve a CV of 15% or less for the recent adult biomass differed depending on the assumed population state as defined by the stock assessment scenario are shown for three and four year sampling programs (Figure 2). For the stock assessment which predicted the smallest population numbers (2021; Figure 1), 36,000 samples were required over three years (corresponding to 6,000 annual samples each of adults and juveniles). For the 2018 stock assessment scenario (predicting higher population numbers), the total annual samples over three years is 60,000 (corresponding to 10,000 annual samples each of adults and juveniles). For the 2024 stock assessment scenario, which predicts the highest population numbers overall, the total annual samples required would be 84,000. CVs on total mortality were high (above 15%) for most sampling scenarios considered (Figure 2, right-hand panel). When the sampling program is extended to four years, improved CVs are achieved for all scenarios under lower annual sampling regimes.

The trends in the number of kin pairs detected matched those in the predicted adult biomass CVs, that is, within each population scenario, a higher number of detected pairs resulted in a lower adult biomass CV (Figure 3), and more pairs are detected when the sampling programs are extented from three to four years. There was less relative improvement in the adult biomass CV achieved past approximately 100 pairs of each kin type.

The kin numbers shown in Figure 3 are expected (average) predictions for each scenario, but in practice the actual number might differ due to natural variability (Figure 4). Despite this, early genotyping of samples collected to date could provide some insights to differentiate between the most likely population scenarios, especially between the 2024 population scenario vs. the 2018 and 2021 population scenarios. This is because a much smaller number of kin pairs would be detected after two years under the population scenario corresponding to the 2024 stock assessment, even when accounting for natural variability. The 2018 and 2021 population scenarios would be harder to differentiate from each other after two years of sampling only.

CVs achieved for adult biomass are robust to some variation in the proportion of adults and juveniles in the annual samples (±10%, Figure 5). In general, increasing juvenile prevalence in the samples did not overtly impact the adult biomass CV.

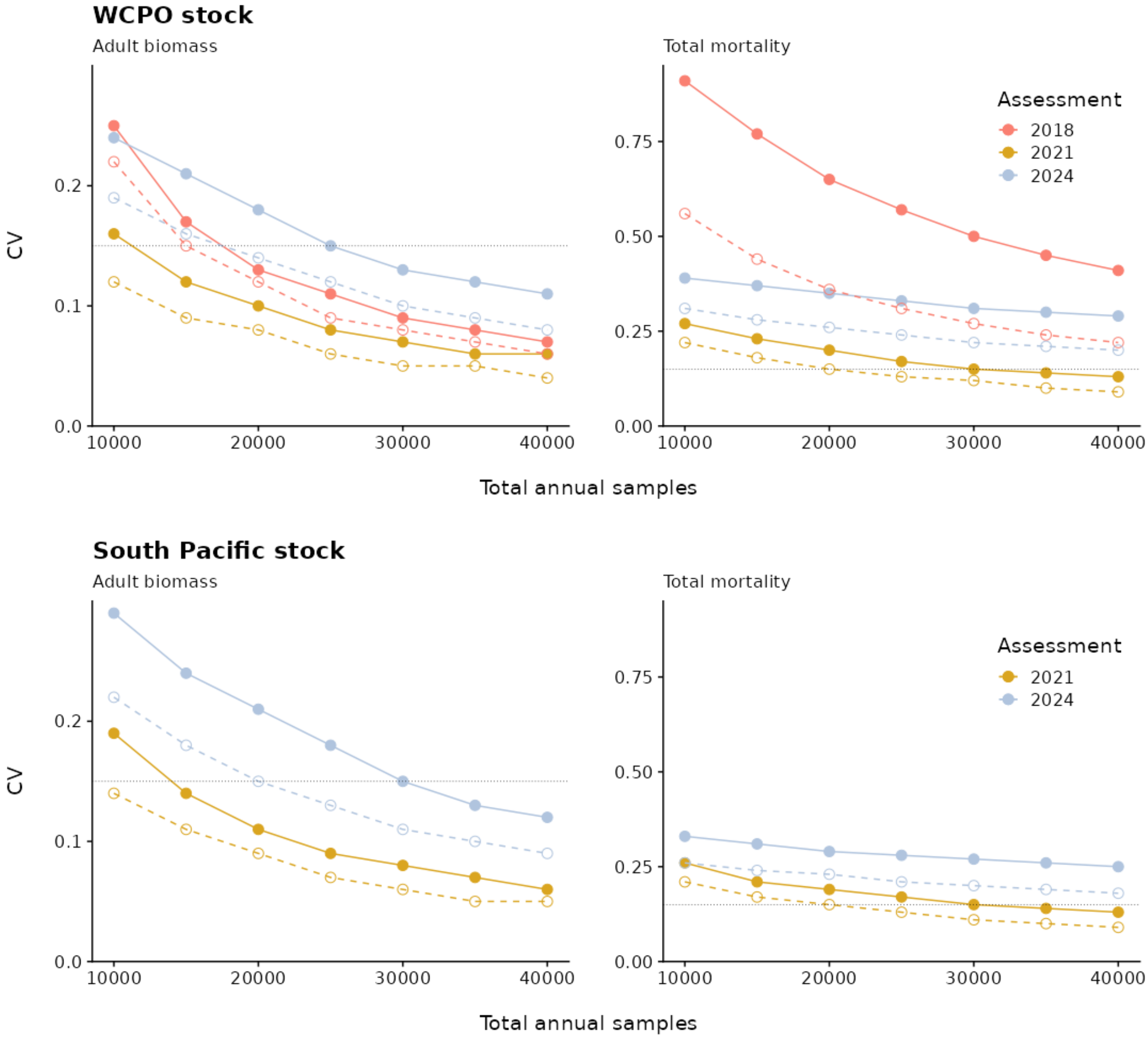


Figure 2: Estimated CVs for adult biomass (left; individuals four years and older) and total mortality (right) under sample sizes evenly spread over three (line) and four (dashed line) years, and by assessment scenario (colours). Note these assume equal numbers of adults and juvenile samples. The top row shows the sampling scenarios assuming a population contained in the WCPO; the bottom row shows the sampling scenarios assuming a population spanning the south Pacific. The dotted hortizontal line shows a potential target CV of 0.15 for reference.

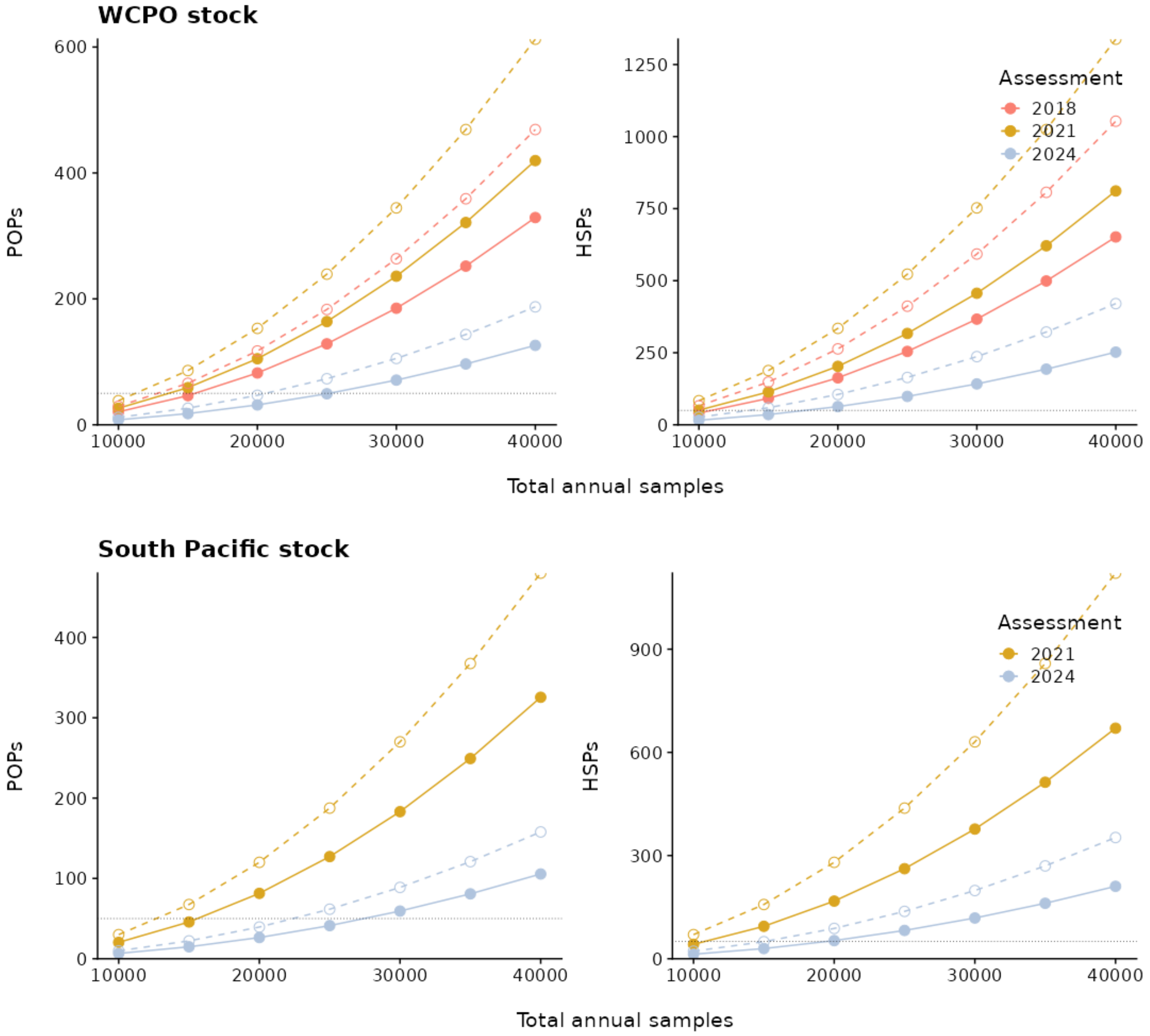


Figure 3: Estimated number of parent-offspring (left; POPs) and half-sibling (right; HSPs) pairs observed under sample sizes evenly spread over three (line) and four (dashed line) years, and by assessment scenario (colours). Note these assume equal numbers of adults and juvenile samples. The top row shows the sampling scenarios assuming a population contained in the WCPO; the bottom row shows the sampling scenarios assuming a population spanning the south Pacific. The dotted horizontal line shows the rule-of-thumb target of 50 for reference.

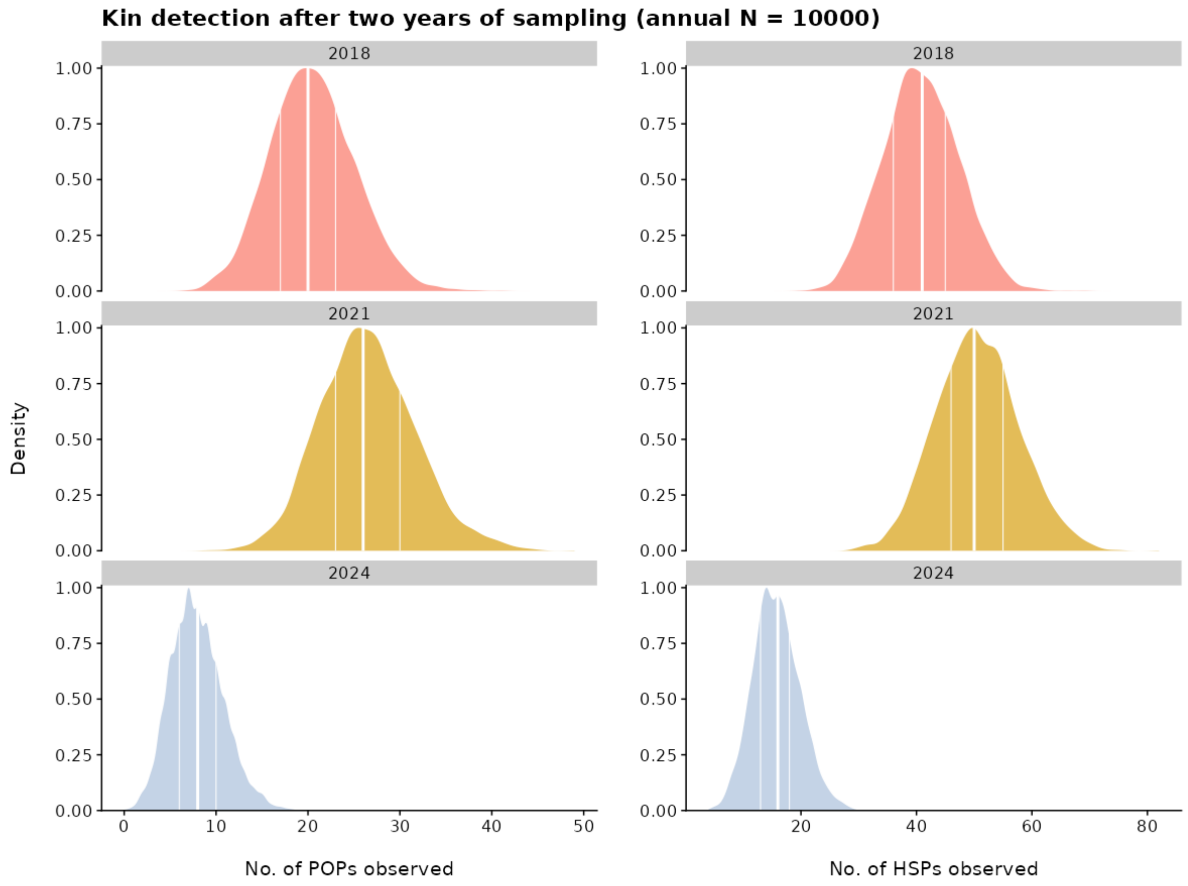
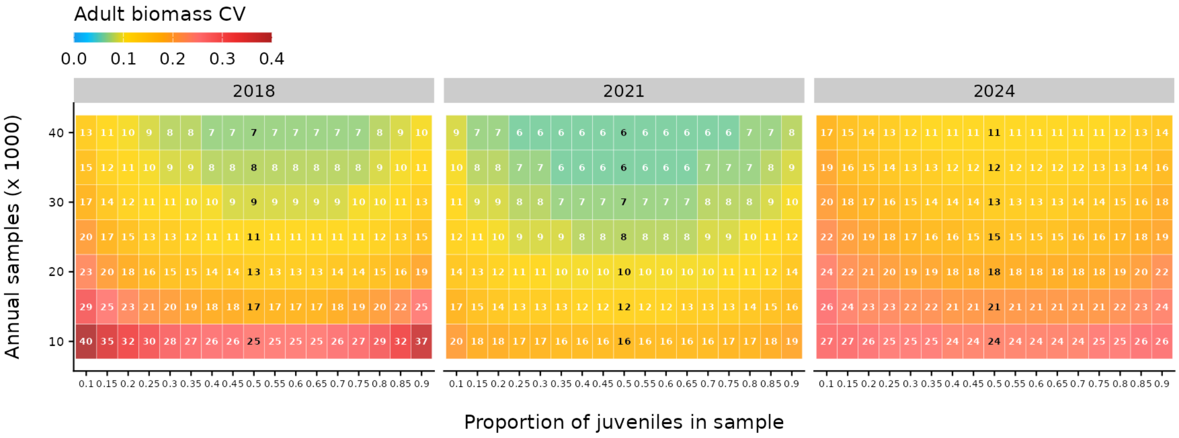


Figure 4: Example of the numbers of kin pairs that could be detected if early genotyping of the first two years of sampling was undertaken (left panel, POPs; right panel, HSPs), assuming 10,000 total annual samples distributed evenly across adults and juveniles and a WCPO-spanning stock. The distributions are shown for each population scenario (by colours). The vertical lines show the 25th, 50th and 75th quantiles of each distribution, corresponding to the probability of observing the associated number of kin pairs under that population scenario.



2018

	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7	0.75	0.8	0.85	0.9
40	13	11	10	9	8	8	7	7	**7**	7	7	7	7	7	8	9	10
	15	12	11	10	9	9	8	8	**8**	8	8	8	8	8	9	10	11
30	17	14	12	11	11	10	10	9	**9**	9	9	9	9	10	10	11	13
	20	17	15	13	13	12	11	11	**11**	11	11	11	11	11	12	13	15
20	23	20	18	16	15	15	14	14	**13**	13	13	13	14	14	15	16	19
	29	25	23	21	20	19	18	18	**17**	17	17	17	18	19	20	22	25
10	40	35	32	30	28	27	26	26	**25**	25	25	25	26	27	29	32	37

2021

	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7	0.75	0.8	0.85	0.9
40	9	7	7	6	6	6	6	6	**6**	6	6	6	6	6	7	7	8
	10	8	8	7	7	6	6	6	**6**	6	6	6	7	7	7	8	9
30	11	9	9	8	8	7	7	7	**7**	7	7	7	8	8	8	9	10
	12	11	10	9	9	9	8	8	**8**	8	8	8	9	9	10	11	12
20	14	13	12	11	11	10	10	10	**10**	10	10	10	10	11	11	12	14
	17	15	14	13	13	13	12	12	**12**	12	12	13	13	13	14	15	16
10	20	18	18	17	17	16	16	16	**16**	16	16	16	16	17	17	18	19

2024

	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7	0.75	0.8	0.85	0.9
40	17	15	14	13	12	11	11	11	**11**	11	11	11	11	11	12	13	14
	19	16	15	14	13	13	12	12	**12**	12	12	12	12	13	13	14	16
30	20	18	17	16	15	14	14	14	**13**	13	13	13	14	14	15	16	18
	22	20	19	18	17	16	16	15	**15**	15	15	15	16	16	17	18	19
20	24	22	21	20	19	19	18	18	**18**	18	18	18	18	18	19	20	22
	26	24	23	23	22	22	21	21	**21**	21	21	21	21	21	22	23	24
10	27	27	26	25	25	25	24	24	**24**	24	24	24	24	25	25	26	26

Figure 5: Coefficients of variation (CVs) for adult biomass under two axes of sampling scenarios: increasing proportion of juveniles in the sample (X-axis) and annual number of samples (Y-axis). Numbers in bold highlight the scenarios with equal proportion of adults and juveniles, with the size of the CV depicted by the coloured gradient.

5 Discussion

The sampling design prescribes a range of optimal sample sizes over three years, from 36,000 to 84,000 depending on the population scenario used, and assuming a stock spanning the WCPO. This directly results from changes in some of the methods used in recent stock assessments of south Pacific albacore, which impacted assumptions of population numbers used to drive the sampling design. The increase in the overall sampling number also resulted from the correction to the data inputs used in the initial design estimates.

The wide range in sampling numbers might appear at first impractical for planning. However, the population scenario requiring the least samples is based on the 2021 stock assessment, and concerns were raised about unreasonably low estimates for its predicted recent recruitments (*sensu* the 2016 'big dip' in recruitment, see Scott et al. 2023). As such, it might be cautious to focus on the population scenarios stemming from the 2018 and 2024 stock assessments when planning sampling numbers.

In addition, early genotyping results based on samples collected to date by Project 100c should provide valuable insights as to which population scenario is most plausible, especially with regards to assessing the likelihood of the '2024' population scenario compared to the others.

The wide range of population scenarios estimated from the three most recent stock assessments highlights the appeal of the CKMR approach, which is that, unlike traditional stock assessments, it can provide a reliable estimate of total abundance. As such, the population scenarios used here should only be viewed as informative guidelines when planning the sampling. If more samples were to be collected than needed given the true state of the population (for instance, if 84,000 samples were collected when only 36,000 were needed for informative estimates), the resulting estimates of population metrics would be much more precise than initially aimed for and further improve the quality of the information provided to future integrated stock assessments.

The assumed population numbers driving the design is strongly impacted by assumptions about stock structure, with a wider span (e.g., including the EPO) implying a larger population (and thus more tissue samples to reliably estimate population size). In addition to other initiatives undertaken under Project 100c to improve our understanding of south Pacific albacore stock structure (e.g., MacDonald et al. 2024), the pattern of kin pair detection resulting from the CKMR sampling program will provide valuable insights as to the likely connectivity of this population across the south Pacific. One advantage of CKMR in that regard is that it provides a signal of connectivity over a single generation, unlike other tools (e.g., population genetics) which can be sensitive to small rates of exchange over longer time frames, and may be of lesser practical use for fisheries managers.

The population model used to inform the sampling design made a number of simplifying assumptions in order to approximate the population dynamics used in the SPA. As such, refinements to aspects of the population model could modify the optimal sampling design structure. However, as the statistical design currently only prescribes the overall scale of sampling required, useful information on south Pacific albacore population scaling and structure will still be gained from the CKMR sampling program even if the assumed population dynamics are wrong. One influential assumption is that the ages of all individuals is known exactly. In practice, age will be estimated from epigenetics, otoliths and/or individual length, which are all imprecise ageing methods with increasing degrees of error, also varying depending on age class. While this will introduce additional uncertainty in the estimated population metrics, allowing for uncertain age in future CKMR population models will increase the number of kin included during model fitting, as same-cohort half-sibling pairs can no longer be excluded (since their age is uncertain, i.e., they might not actually be from the same-cohort). In practice, this inclusion of more kin pairs can compensate to some degree for the added uncertainty from the ageing process. More precise ageing methods should be favoured, but cost by method and varying precision by age class can also be considered when determining the best ageing approach for an individual of a likely age class. For instance, relatively cheap length-based measurements could be favoured for juveniles as these will be a better indicator of age than for adults.

Finally, the sampling numbers produced by the statistical design model assume all samples are of suitable quality for genotyping. In practice, field conditions may result in the collection of degraded and/or contaminated samples. As such, the total number of samples effectively collected by the sampling program needs to account for the potential that some samples will have to be discarded (see SC20-SA-WP-09 for a discussion in the context of Project 100c). As there is some robustness of the sampling design to variability in the proportion of juveniles and adults, increasing samples (within reason) from locations with easier sampling logistics should not overtly impact CKMR modelling outcomes.

Recommendations

SC 20 is invited to:

- consider these updated sampling numbers for the statistical sampling design for south Pacific albacore under Project 100c;
- consider supporting the genotyping of samples collected to date to narrow the range of population scenarios considered from the sampling design;
- consider supporting the investigation into the optimal allocation of ageing methods across ages to minimise ageing costs while improving overall ageing precision.

6 Acknowledgements

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