**Expected Improvements in Precision when Integrating Opportunistic Close-Kin Mark-Recapture Data into Fisheries Stock Assessments**

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Abstract

Close-Kin Mark-Recapture (CKMR) sampling, by providing information on abundance and survival rates (and potentially other quantities), offers a promising new data source for fisheries stock assessments. To date and to my knowledge, most applications have focused on fitting standalone CKMR models outside of stock assessment models. Fewer studies have directly integrated the CKMR data into the stock assessment model. Sample design in order to achieve a desired precision is somewhat straightforward in simple CKMR models however when integrated within a full stock assessment model with many other data sources, the value of the data (in terms of a reduction in uncertainty of model estimates) is less clear. Herein I demonstrate, using self-test simulations, the expected improvements in accuracy and precision of derived quantities and estimated parameters within statistical catch-at-age models when opportunistic CKMR sampling is conducted and the data integrated within the assessment. By opportunistic CKMR sampling I mean to describe the genetic sampling of individuals that comprise the age composition data, such that increases in CKMR sampling would also increase the age composition samples (and vice versa). I examine the expected improvements (conditional on model being correct representation of the system) across three life history types (cod-like, flatfish-like, and sardine-like) and different amounts of data available to the assessment, including the uncertainty and inclusion of an abundance index, and the sample size and time series length of CKMR and age composition samples. Results suggest CKMR data can provide considerable improvements in accuracy and precision of spawning stock biomass at the end of the time series and parameters defining natural mortality and scale of the population, provided an adequate annual sample size is collected relative to the spawning abundance of the stock during the period of CKMR inference. The time-series length and uncertainty or inclusion of an abundance index played a much more moderate role in how much improvement CKMR data provided over models fit without CKMR. This was likely a function of the model being privy to an effectively known catch time series and known steepness, allowing it to estimate stock scale and trend reasonably well without CKMR data given informative composition data. I recommend simulation analyses including stock assessments as estimation models be carried out for those considering routinely collecting and integrating CKMR data into fisheries stock assessments.

Introduction

Close-Kin Mark-Recapture (CKMR, Bravington et al. 2016) offers a promising new source of information to fisheries stock assessments, which largely form the basis of commercial fisheries management throughout the world (Dichmont et al., 2016; Mace et al., 2001). Traditionally, stock assessments have been developed using routinely collected data from fisheries monitoring programs on total removals, age/length composition of the removals, and catch rates (Maunder and Punt, 2013). CKMR, given it allows for lethal sampling (e.g., sampling of the removals), may provide another data source to be routinely collected from commercial fisheries, contributing additional information on abundance and survival levels within fisheries stock assessments.

The theory of CKMR dates back to the early 2000s (Nielsen et al., 2001; Skaug, 2001) and since the publication of Bravington et al. (2016) has greatly increased in application within fisheries (see Casas and Saborido-Rey (2023) for a suite of examples). The theory operates primarily by making inference on the number of parent-offspring and half-sibling pairs (POPs and HSPs) expected from a sample of a population. At its most basal level the theory posits that the expected number of POPs from a sample of a population is inversely related to the spawning abundance of that population. That is, the more POPs found in samples from a population, the smaller the population likely is, and vice versa. For HSPs, inference is based on an unobserved shared parent of the sibling pair, who must give birth to the older sibling and then survive to give birth to the younger sibling. Thus the expected number of HSPs in a sample is inversely related to both the adult mortality rates in the population and the spawning abundance in the year of each siblings birth. I avoid an in depth presentation of the theory as it is covered extensively in Bravington et al. (2016) and subsequent publications.

The lower limit of the precision of an abundance estimate from a CKMR model can be relatively straightforward to compute for the simplest case. For example, the lower limit of the coefficient of variation (CV) of an abundance estimate for a POP model with a single sampling event can be expressed as (Bravington and Grewe, 2007)

where *n* denotes the total sample size of potential POPs examined (equally split among juveniles and adults), and the true abundance of adults in the population. Within an integrated fisheries assessment, the expected precision of estimates is less tractable and does not have a simple analytical solution, as it depends on a variety of different data sources and a complex, highly-parameterized non-linear model. However, the tool of self-test simulations can be employed to examine what might be expected in terms of precision of abundance estimates (and other desired quantities) when CKMR data are integrated into the assessment. According to CKMR theory, we expect that the information content of the CKMR data will depend on the size of the spawning abundance of the population and on the sample size collected. However, it is less clear how much specific additional information it will provide when combined with other data sources collected in fisheries assessments, such as age composition data. Given that CKMR data are ideally aged, age composition samples should increase commensurate with increases in opportunistic CKMR data collected from the catch. In addition, within a fisheries assessment one might expect that even for cases where the population is very large and the CKMR sample size relatively small, zeroes in data (no pair matches) may still provide some important information to the assessment in helping rule out probabilities of small population sizes, thereby potentially improving the precision of estimates.

In this study, I simulate a case where the age composition of the removals from populations are simultaneously observed for CKMR sampling. I refer to this as “opportunistic” CKMR as little additional sampling effort is required other than genetic sampling of the age composition data that is already collected. This also has the effect of increasing the amount of composition data when the sample size of CKMR is increased. I therefore explore what one might expect in terms of improvements in model performance if CKMR data is collected and integrated within the stock assessment compared to identical assessments without CKMR data. I examine this comparison across three fish life history types (Cod-like, Flatfish-like, Sardine-like), in addition to across different amounts and quality of data such as the uncertainty in or the inclusion of an abundance index, and the sample size of CKMR and age-composition data.

Methods

The structure of the study was to have identical assessment models that were fit with and without CKMR data, so as to ascertain its value to the assessment. In the following I describe the population simulation operating model and the sampling model, including a separate component for the CKMR section.

Population simulation operating model

The population model is an annual time-step, age structured model that only considers one combined sex. I chose to use similar population specifications and life-history scenarios to those used in Ono et al. (2015) and Hurtado-ferro et al. (2015) for simplicity and ease of comparison. The different life history scenarios include cod-like, flatfish-like, and sardine-like models. The main differences are that the cod-like life history simulates a very abundant stock of fish that is slow-growing, attains a large maximum size, has an old maximum age, a low natural mortality, and low recruitment variability, where the flatfish stock is much less abundant but has more recruitment variability, a greater steepness and growth rate. Finally the sardine-like model has the highest recruitment variability, a moderate abundance, rapid growth, high natural mortality, and low steepness. The parameter values and equations governing the model are given in Tables 1 and 2, respectively. The population model runs for 100 years, with a fishing time series beginning in year 26 (years 26-100 experience fishing). The fishing time series was simulated as a two way trip with a linear increase from 0 in year 25 to a fully selected fishing mortality that was >*F*msy () and achieved 85% of maximum sustainable yield (MSY) at equilibrium in year 85 of the time series, followed by a linear decrease to a fully selected fishing mortality that was <*F*msy () in year 100 and also achieved 85% of MSY at equilibrium.

One hundred simulation iterations were run for each population model specification (Table 3), with stochasticity included using log-normal draws for recruitment deviations in each year. A sampling model then sampled from the population and fishery exploitation model to simulate the data collection process.

Sampling model

Annual landings were simulated using a log-normal distribution with a standard deviation (SD) of 0.05. A fishery index was simulated using a lognormal distribution where the SD was specified as a treatment within the simulation design, taking values of 0.25 or 0.5 (Table 3). The catch age-composition available for select years throughout the time series was simulated using a multinomial distribution. Age composition data was simulated from years 26, 36, 46, 51, 56, 61, 66, 71, and annually from year 76 to 100. The number of samples prior to CKMR data collection began at *n*=30 in year 26 of the model (first year with fishing), increasing by 10 each decade until year 51, and then increasing by 10 every 5 years until year 76 where it was fixed at *n*=100 for the rest of the time series. This composition specification was similar to that used in Ono et al., (2015). Given CKMR data are aged samples, when CKMR data collection increased, as did the composition sample size, thus the composition sample size increased commensurate with CKMR data collection treatments (either 100, 1000, or 5000 sampled from the catch from the final 5, 10, or 20 years in the time series).

CKMR data

CKMR data were simulated from the terminal 5, 10, or 20 years of the time series (Table 3). Data were censused from the age composition for those years to make up the CKMR comparisons. That is, the age frequencies of the catch-at-age samples were those for which kinship comparisons were then made. Given the sampling year, the birth year of the older individual, and the birth year of the younger individual, the probability of being a POP or a HSP was calculated. The CKMR pair comparisons were aggregated to pairs with similar covariates (Table 4) and the number of POPs and HSPs for a given set of covariates was then simulated using a multinomial distribution. Note in the following that I do not distinguish “juveniles” and “adults” as the population is age structured with proportional maturity at age. Thus any individual whose age difference with another places them in a potentially mature age (at the year of birth of younger individual) has the potential to be a parent of the individual. I make comparisons between “younger” () and “older” () individuals in reference to both potential POPs and HSPs (rather than say, juveniles and adults). I limit comparisons to omit same-cohort siblings (i.e., age difference must be greater than 0).

CKMR Simulator/Estimator

*Parent-offspring pairs*

Given the birth year of an older individual (), the birth year of a younger individual (), and the year the older individual was sampled (), the probability of the older individual being a parent-offspring pair with the younger individual is calculated as

which describes the expected reproductive output of the potential parent in the year of younger individuals birth ( denotes age difference) divided by the total reproductive output in that year. A potential parent has to have been sampled after or on the year of younger individuals birth, because sampling is lethal in this case (as it is made up of the catch). Note that sex is not modeled and the total reproductive output is assumed to be made up of both males and females who contribute equally to spawning biomass. The 2 in the numerator reflects the fact that an individual has two parents. An alternative way of thinking about this probability, assuming a 50:50 sex ratio, is the probability that the older sampled individual is female is 0.5 and the probability that the female is a maternal-offspring pair with the younger individual is Thus, adding the probability of a maternal-offspring pair () and a paternal-offspring pair gives

*Half-sibling pairs*

For HSPs, given the parent is not directly observed, a sum is taken over the probabilities of all the potential parents of the pair alive at the year of *i*’s birth (hence ). The first term within the summation describes the expected reproductive output of a potential parent (age ) over the total reproductive output in the year of the *i*’s birth. The addition of is to account for the abundance alive at *i*’s birth, and assuming a 50:50 sex ratio, 0.5 in the numerator and denominator cancel out. The second term is the probability that a potential parent survives from the time of *i*’s (older individual) birth to the time of *j*’s (younger individual) birth (i.e., through the year prior to *j*’s birth), assuming that spawning happens at the very start of the year. So a potential parent has to survive the year of *i*’s birth up to the age difference of the potential pair. Once the survival of the potential parent is accounted for, the third term in the equation is the probability of a parent-offspring pair between that potential parent and the younger individual (), where the 4 in the numerator in this case accounts for the fact that the parent is unobserved and could be a mother or a father (, Hillary et al. 2018).

Treatment Overview

Table 3 depicts the levels of each treatment type, which were implemented in a full factorial design to examine all combinations of treatments. Treatments included the species life history type, the sample size of CKMR and composition data, the length of time CKMR or increased composition data was collected, and the inclusion or sampling variance of the abundance index.

Estimation Model

The estimation/assessment models were identical in structure to the population operating model. They began in year 26 of the time series (first year with data). The fixed-effect parameters estimated within the model included the unfished recruitment, the recruitment SD, a natural mortality parameter, two logistic selectivity parameters, catchability of the fishery index (if the index is included in assessment), and annual fully selected fishing mortality levels in each year (Table 1). Recruitment deviations in each year and those that make up the initial unfished abundance were treated as random effects. All other parameters were fixed at their true values from the operating model. The assessment models also fit the data using the same likelihoods used to generate data in the sampling model. In real-world situations, grandparent-grandchild pairs are difficult to distinguish genetically from HSPs (Bravington et al. 2016). In order to simulate a case where the chance of analyzing grandparent-grandchild pairs is minimal, HSP comparisons within the multinomial likelihood in the assessment were restricted to comparisons whose age difference was <2 times the age at 50% maturity for each life history (3.02, 4.8, and 3.4 for cod-like, flatfish-like, and sardine-like, respectively).

Model Fitting

Models were fit in a mixed-effects maximum marginal likelihood context in Template Model Builder (TMB, Kristensen et al., 2016) with recruitment deviations specified as random effects and the remainder of the fixed effect parameters identified in Table 1. TMB calculates the marginal negative log-likelihood given the fixed effect parameters using the Laplace approximation to integrate over random effects. Fixed effect parameters are estimated via minimizing the marginal negative log-likelihood within the program R using the nlminb function. Random effects and derived quantities are then predicted using empirical Bayes (Kristensen et al., [2016](javascript:;)). Starting parameter values for each simulation iteration were chosen by sampling from a uniform distribution with the bounds specified as 50% below and 50% above the true parameter value. Standard errors of parameter estimates were extracted in addition to those of derived quantities using the generalized delta method built into TMB.

Comparison

I focused the comparison of assessment models with and without CKMR data on the accuracy achieved between simulations and on the precision achieved within and between simulations. In addition, although the models were correctly specified, I make note of the bias in relative error for a subset of assessment models. The accuracy of point estimates between simulations was assessed by examining the median absolute relative error over simulations, with absolute relative error defined as

Where denotes a point estimate from the assessment and the true value for that quantity in simulation iteration *s*. The precision within simulations was assessed by examining the estimated standard errors for quantities within an individual simulation iteration, summarized using the median of the distribution of standard errors over simulations. The precision between simulations was assessed by examining the interquartile range (IQR) of the distribution of relative error over simulations, with relative error calculated as

I chose to focus the comparison on spawning stock biomass over the time series (*SSBy*), unfished recruitment (*R0*), and natural mortality (*M*) as they are of general interest in fisheries assessment and CKMR data are thought to primarily inform abundance and survival (Eqs. 2-3). I summarize performance metric results by presenting the values obtained from assessment models fit with CKMR data divided by those obtained from the same assessment models fit without CKMR data (e.g., including CKMR data led to median AREs that were 80% of those from models without CKMR [20% improvement in accuracy]). I also note the scale of performance metrics regarding select CKMR models for context.

Results

*Bias*

Estimation models were effectively unbiased in *SSBy*, however were negatively biased in *R0* and *M* for each life history type. The level of bias increased from cod to flatfish to sardine. For example, in one of the more data-poor scenarios – max composition sample size 100, index SD=0.5, no CKMR data – the cod models had negligible bias levels with median relative errors of -0.01 and -0.02 for *R0* and *M*, respectively. This bias increased to -0.06 and -0.04 for flatfish and further to -0.13 and -0.08 for sardine (Supplemental Figure 6). This trend was present in all models and appeared to be due to the sparseness or lack of composition data at the beginning of the time series, as the models became unbiased when composition data was simulated in every year of the time series (with sample sizes n=100, Supplemental Figure 7).

*POPs and HSPs from operating and sampling models*

The number of pairs found differed greatly between the life-history types (Table 5). For each combination of life-history, sample size, and length of CKMR data collection, more HSPs were found than POPs. The cod-like model, largely due to the size of the spawning stock at the time of CKMR inference, resulted in very few POPs and HSPs found for most sampling models. For sample sizes less than 5,000, the mean (over simulations) number of pairs found was nearly always <1 (exception being HSPs at *n*=1000 for 20 years). The flatfish models resulted in the greatest number of pairs found, often in the thousands and tens of thousands. Even at the lowest sample sizes (100 collected for 5 years), the flatfish models produced >1 POP and >6 HSPs on average. The sardine models resulted in moderate numbers of pairs found, with few (<1 on average) found when sample sizes were 100 annually and hundreds found when samples sizes were 5,000 annually.

In terms of simply finding kin pairs, the sample size collected did appear more important than the length of data collection given 5,000 individuals sampled for 5 years resulted in considerably more pairs than the treatments that sampled 1,000 for 20 years in each scenario (and likewise for 1,000 sampled for 5 years compared to 100 sampled for 20 years). Although I note that the total sample sizes in these cases is not necessarily equivalent (e.g., 25,000 total fish vs 20,000), this result persisted when the sample sizes were equivalent in additional exploratory runs.

*General patterns*

As expected given the pair information, in terms of improvements in performance metrics, the CKMR data were most informative for the flatfish models followed by the sardine models and finally the cod models. For *SSBy* performance metrics, the improvements (if present) manifested in terms of reductions in metrics during the latter portion of the time series to a minimum (i.e., maximum improvement) that was often 5-8 years prior to the terminal year followed by an increase in metrics to the terminal year. There was a negligible effect regarding the length of collection on which year in the time series showed maximum improvement. In what follows I make reference the minimum level as the level for a specific year where a performance metric *SSBy* exhibited the maximum improvement compared to a model with no CKMR. At their most informative (no index, flatfish life history, 20yrs of CKMR at *n*=5,000), integrating CKMR data into the stock assessment improved accuracy, precision within, and precision between simulations to ~10% of the levels achieved from estimation models fit without CKMR data for *SSBy* (the minimum level achieved in the time series, Figures 1-3). For *M* and *R0*, the maximum improvement was realized in the same treatment scenario and was ~30 and ~60% of the levels from estimation models fit without CKMR data, respectively (Figure 4). A pattern evident across most models was that CKMR data appeared to improve performance metrics on *M* more so than on *R0.*

*Inclusion and uncertainty of abundance index*

Compared to other treatment options, there appeared to be a more minor effect regarding the inclusion or standard deviation of the abundance index data. The inclusion of CKMR data did provide greater improvements in performance metrics to the models that did not include an abundance index time series compared to those that were fit with an index and an index SD of 0.25 (Figures 1-4). As an example, for the flatfish model fit without an index, at CKMR sample sizes of 1,000 fish collected for 5 years, the median ARE of SSB was 22% and 46% the level of models without CKMR data at the minimum and terminal year in the time series, respectively (year 70 and 76). For the same scenario where the models included an index with a SD of 0.25, the median ARE of SSB was 38% and 63% the level of models fit without CKMR data at the minimum and terminal year in the time series. In the interest of brevity, I focus the remainder of the results on the moderate case where the abundance index SD=0.5.

*Performance metrics*

*Accuracy*

For each life history type and duration of data collection, the CKMR data collection scenarios that collected 100 fish per year did not appear to improve the accuracy of *SSBy* point estimates (Figure 1). Although in these scenarios, at least for the flatfish models, the accuracy of *M* and *R0* estimates did appear to improve to 85-90% of the levels from models fit without CKMR (Figure 4). For the cod models, even the largest CKMR sample sizes collected for 20 years did not appear to notably improve the accuracy of *SSBy*, *M*, or *R0* point estimates compared to models fit without CKMR.

For the sardine models, improvements in accuracy were evident for scenarios which sampled 1,000 fish for 20 years or 5,000 fish for 5, 10, or 20 years. Improvements manifested in terms of reductions in median AREs for *SSBy* in the second half of the time series, and in *M* and *R0*. At their most informative (*n*=5,000 for 20 years), inclusion of CKMR data led to median ARE for *SSBy* that was 32% at its minimum (year 69) and 87% in the terminal year compared to models fit without CKMR data. For context of scale, this resulted in median AREs that were 0.032 and 0.158, respectively. For the same CKMR treatment, the accuracy of point estimates of *M* and *R0* in improved to 24% and 69% of the median ARE for models fit without CKMR data (Figure 4).

For the flatfish models, across all treatments where *n*>100, the accuracy of point estimates markedly improved for *M*, *R0*, and *SSBy* near the end of the time series compared to models fit with no CKMR data. As an example of a moderate treatment where *n*=1,000 for 10 years, median ARE in *SSBy* improved to 27% at its minimum (year 70) and 55% in the terminal year compared to models with no CKMR and *M* and *R0* improved to 55% and 60%, respectively. For context of scaling regarding *SSBy* AREs, the referenced CKMR model resulted in median AREs that were 0.021 and 0.098 in year 70 and 76, respectively. There did appear to be an effect specific to the flatfish models where the accuracy in *SSBy* for the first half of the time series actually worsened compared to models fit with no CKMR, before markedly improving in the second half of the time series.

*Precision within simulations*

The precision within simulations showed similar results to those from the accuracy performance metric. One notable exception was for the cod life history, where for all data collection treatments accuracy did not appear to improve, for treatments where *n*=5,000 the precision within simulations instead did improve for *SSBy* at the end of the time series (~80-90% at minimum, Figure 2) and for *M* and *R0* (~90-95%, Figure 4) relative to models with no CKMR. For context of scale regarding median SEs of *SSBy*, they led to median CVs (SE/point estimate) of 0.094 at the maximal improvement over models with no CKMR and 0.18 in the terminal year for *n*=5,000 for 20 years.

For the sardine models, precision within simulations notably appeared to improve only in cases where *n*=5,000. For the case where *n*=5,000 for 20 years, integration of CKMR data into the assessment led to SEs that were 46% and 77% of those from models without CKMR for *M* and *R0*, respectively. For the same treatment, improvement in SEs of *SSBy* was 46% at its minimum (year 68) and 86% in the terminal year of the time series. In these years, the median CVs for *SSBy* of models fit with CKMR data was 0.041 and 0.185, respectively.

For the flatfish models, precision within simulations did improve for *n*=100 however this improvement was minimal (>95%, Figure 2). At *n*>100, precision within simulations improved markedly compared to models fit with no CKMR. For example, in a moderate case where *n*=1,000 collected for 10 years, the median SE of *SSBy* improved to 30% at its minimum (year 69) and 58% in the terminal year of the time series relative to models with no CKMR (Figure 2). In these years, the median CVs for *SSBy* were 0.03 and 0.134 for the models fit with CKMR, respectively. In the same treatment for *M* and *R0*, the median SEs for each improved to 55% and 60% of the levels for models fit without CKMR data, respectively.

*Precision between simulations*

No marked improvements in precision of estimates between simulations were observed in the cod models. For the sardine models, precision between simulations for estimates of *M* and *R0* improved for all treatments where *n*>100. Metrics regarding *SSBy* however only appeared to markedly improve upon the models without CKMR data when either *n*=1,000 for 20 years or when n=5,000 for 5, 10, or 20 years. For example, in the case where *n*=1,000 for 20 years, the IQR of *SSBy* improved to 66% of the IQR for models without CKMR at the minimum (year 68) and 94% in the terminal year of the time series. For context on scale, in these years the IQR for the models fit with CKMR was 0.079 and 0.378, respectively. In the same scenario for *M* and *R0*, IQR improved to 76% and 93% of the IQR for models with no CKMR, respectively.

For the flatfish models, precision between simulations improved for all scenarios where *n*>100. For example, in the case where *n*=1,000 for 20 years, IQR of *SSBy* improved to 24% of the IQR for models without CKMR at the minimum (year 69) and 48% in the terminal year of the time series. For context on scale, in these years the IQR for the models fit with CKMR was 0.031 and 0.195, respectively. In the same scenario for *M* and *R0*, IQR improved to 52% and 66% of the IQR for models with no CKMR, respectively. Similar to the accuracy results, there did appear to be an effect specific to the flatfish models where the IQR for *SSBy* for the first half of the time series actually worsened compared to models fit with no CKMR, before markedly improving in the second half of the time series when *n*=5,000.

Discussion

The integration of opportunistically collected CKMR data within fisheries stock assessments can, provided sufficient kin pairs are found, result in marked improvements in accuracy and precision of estimated quantities important to management beyond those observed from increased composition data alone. Pairs found needed to be approximately >100 to really provide assessments with much information above that provided by the increased composition data alone, as increases in non-pairs when CKMR sample size increased did not appear to provide much additional information to the assessments.

The main factor in finding sufficient kin pairs remained the spawning abundance of the stock coupled with the annual sample size, while the number of years the CKMR data were collected proved far less important (as did the natural mortality level). This was likely a function of the decreasing probability of finding kin pairs as the time lag increases and thus fewer annual samples collected over a longer time period may not find enough kin pairs to provide the assessment with much information. Although I do note that the simulation experiment was not designed tease apart the individual effect of every life history quality/population parameter, it appears unlikely these differences in the number of kin pairs found and thus information content would have been driven by another aspect of the simulations (and none outside of abundance were ordered for cod to sardine to flatfish). A critical aspect of the sampling design for CKMR involves the sample size level (Bruce et al., 2018; Maunder et al., 2021; Rodriguez-Ezpeleta et al. 2020), and in particular for the case of routine opportunistic CKMR sampling from a fishery, the annual sample size level. Bravington et al. (2016) notes that although the sample size requirements increase with the abundance of a population, they are lower in terms of the percentage of the population sampled. This is depicted in comparing the sardine and flatfish models. The spawning abundance levels around the time of CKMR data collection were approximately 2e8-2.5e8 for cod, 2.5e4-5e4 for flatfish, and 2e6-4.5e6 for the sardine population operating models (supplemental figure 4). For the sardine case with moderate abundance levels, the notable improvements were largely isolated to cases where 5,000 fish were sampled per year, approximately 0.1-0.25% of the spawning abundance. This percentage is actually less than that from the flatfish model at *n*=100 per year (~0.4-0.2% spawning abundance) while resulting in more pairs and improved assessment performance relative to those fit with no CKMR. Although some rules of thumb have been suggested, such as a sample size of 10 for a CV of ~15% in POP based studies (for or a single sampling event with equal mix of juveniles and adults, Bravington et al., 2016) or 50 HSPs to achieve a CV less than 20% (Rodriguez-Ezpeleta et al, 2020), these studies did not consider the routine collection and integration of the data into fisheries assessment nor a commensurate increase in composition data if opportunistically sampled from the fishery. In considering routine collection for integration into stock assessments, ideally simulation-estimation analysis closely resembling the individual case study would be carried out.

Although the length of data collection appeared to be of little importance in this study, continuous data collection over longer time periods could further help provide information on stock abundance trend (Bruce et al., 2018) as well as the absolute level in real-world cases, especially when there may not be any information or highly suspect information on catch and indices of abundance. Herein the inclusion or uncertainty in the abundance index did not greatly affect how much additional information CKMR data provided to the stock assessment (although it did have a minor effect). This was likely a function of the model being privy to an effectively known catch series and known steepness. Consequently, in a correctly specified model with informative catch and composition data, the model is able to estimate the trend and scale of the population with reasonable accuracy. In real-world cases, assessment models are much more crude approximations of reality, and can be importantly misspecified (Hordyk et al. 2019). Longer time series of CKMR data could prove more useful in the real-world provided the CKMR observation model is not grossly misspecified. A particular case that comes to mind is if the observation model of an index of abundance is misspecified by not being proportional to stock abundance in reality (often a worry among analysts), which has little to do with the observation model of the CKMR data.

CKMR is a retrospective inference, backdated to the year of birth of the younger individual for POPs and the years of birth for each sibling in HSPs. Hence the maximum improvements in performance metrics on *SSBy* will be observed some years prior to the terminal year of the time series. In the simulations tested, this maximum improvement was observed 5-8 years prior to the terminal year, however metrics were still improved for the terminal year of *SSBy* compared to the assessments without CKMR data. Although the life history type did not appear to affect when this maximum level of improvement was observed, it is conceivable that this level could be affected by the selectivity of a species (each life-history type simulated herein was selected at an early age, supplemental figure 5) and the maximum age (a function of *Z*). If individuals are not vulnerable to the fishery until later in life, backdating to the year of birth would result in inference on abundance and survival in earlier years, as would simply capturing and sampling older individuals (regardless of early-life selectivity). Partly for this reason, Bravington et al, (2016) note that CKMR may not be as useful for long-lived species that are selected later in life. Although for a fisheries stock assessment, it may still prove useful to provide information on stock scale and mortality, regardless of the length of backdating. Future simulations on long-lived species such as pacific rockfishes may prove useful in this regard.

For the sake of simplicity, I focused on how CKMR data affects the estimation of abundance and survival, however these data can inform other parameters in an integrated assessment as well (Casas and Saborido-Rey, 2023). Specifically, given Eq. 3 makes use of *Z*, HSPs could theoretically inform on fishery selectivity. The ability to model time-varying fishery selectivity is increasingly incorporated into fisheries stock assessment frameworks (e.g., stock synthesis, Xu et al., 2019; Woods Hole Assessment Model, Stock and Miller, 2021; state-space assessment model, Nielsen and Berg, 2014; Berg and Nielsen, 2016) and longer time series of CKMR data could theoretically aid in its estimation. A similar point could be made about time varying natural mortality, although CKMR data itself may not necessarily help distinguish between the two (given that it necessitates *Z* which itself is a function of *M* and *F*). I recommend further simulation analyses on each of the previously mentioned topics regarding CKMR integration in fisheries stock assessments.

I have presented a simple case with no pair assignment error, no ageing error, and no spatial dynamics, each of which should likely be expected in the real world and could negatively affect the expected improvements from opportunistic CKMR integration within fisheries assessments (Swenson et al. *in-review*; Conn et al. 2020; Trenkel et al. 2022). I also presented a case where composition data were randomly sampled from the catch at age and where CKMR data, conditional on covariates such as age, were random with respect to kin (a necessary assumption of CKMR, Casas and Saborido-Rey, 2023). It is often the case that in the real world composition data are overdispersed (Pennington and Volstad 1994; McAlister and Ianelli 1997, Francis 2014) and thus less informative to the assessment. The assumption that CKMR data are random with respect to kin is not necessarily violated when composition data that are genetically sampled are overdispersed with respect to age. If this is the case, the improvements in integrating CKMR data into fisheries assessments may be even greater than depicted herein despite increases in the nominal number of age composition samples. However, if samples are not random with respect to kin, regardless of overdispersion in composition data, CKMR inference can be severely biased (Davies et al. 2017; Conn et al, 2020).

In addition, often in commercial fishery and research survey sampling programs individual samples are able to be sexed, and many contemporary assessments are sex-specific. The ability to sex biological samples would further refine CKMR analysis and change Equations 2 and 3 to be sex-specific (Bravington et al. 2016). Such refinement could ideally lead to further improvements in estimating sex-specific mortality and abundance when integrating opportunistic CKMR data into stock assessments. For a more extensive suite of considerations which may affect CKMR inference, such as HSPs estimating effective population size rather than adult abundance, readers are referred to Casas and Saborido-Rey, (2023).

*Summary*

When deemed prudent, the routine collection of CKMR data as part of commercial fishery monitoring/sampling and their integration into modern statistical fisheries integrated stock assessments may markedly improve estimates from fisheries stock assessments. Prudence regarding their collection is best evaluated on a case-by-case basis and I do not make specific sampling recommendations herein. Rather I would instead recommend simulation analyses be carried out including assessments as estimation models. This simple exercise could theoretically be undertaken for any given assessment to evaluate whether collecting and integrating CKMR data would be of value, although it would be highly dependent on the scale of the operating model chosen being reasonably close to the real-world stock. Simulations could be carried out regarding a range of plausible operating models to determine the ideal annual sample size for a specific scenario depending on goals and budget. I also recommend the use of an age-structured pedigree simulator such as CKMRpop (Anderson, 2022) to add more realism to the CKMR simulation operating model.

Data accessibility

All code associated with analysis is available on *https://github.com/nickcfisch/CKMR\_Project*.

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References

Anderson, E. C. 2022. CKMRpop: forward-in-time simulation and tabulation of pairwise kin relationships in age-structured populations. Mol. Ecol. Resour. 22, 1190– 1199. doi: 10.1111/1755-0998.13513

Berg, C.W., Nielsen, A., 2016. Accounting for correlated observations in an age-based state-space stock assessment model. ICES Journal of Marine Science 73, 1788\_1797.

Bravington, M. V., and Grewe, J. P. 2007. A method for estimating the absolute spawning stock size of SBT, using close-kin genetics. CCSBT-ESC/0709/18. CSIRO, Hobart, Australia. 25pp. Available at: https://www.ccsbt.org/ja/system/files/resource/ja/ 4d93fe45b53f2/18.pdf

Bravington, M.V., Skaug, H.J. and Anderson, E.C., 2016. Close-kin mark-recapture. Stat. Sci. 31, 259–274. doi: 10.1214/16-STS552

Bruce, B., Bradford, R., Bravington, M., Feutry, P., Grewe, P., Gunasekera, R., et al. 2018. “A national assessment of the status of white sharks,” in National environmental science programme (Marine Biodiversity Hub, CSIRO, Australia), 64pp. Available at: https://www.nespmarine.edu.au/system/files/NESP-A3-A\_ national\_assessment\_of\_the\_status\_of\_white\_sharks\_Feb\_2018.pdf

Casas, L. and Saborido-Rey, F., 2023. A review of an emerging tool to estimate population parameters: the close-kin mark-recapture method. Front. Mar. Sci. 10:1087027. doi: 10.3389/fmars.2023.1087027

Conn, P.B., Bravington, M.V., Baylis, S. and Ver Hoef, J.M., 2020. Robustness of close‐kin mark–recapture estimators to dispersal limitation and spatially varying sampling probabilities. *Ecology and Evolution*, *10*(12), pp.5558-5569.

Davies, C., Bravington, M., & Thomson, R. 2017. Advice on close-kin mark-recapture for estimating abundance of eastern Atlantic blue-fin tuna: a scoping study. Atlantic-Wide Research Programme on Bluefin Tuna (ICCAT GBYP-PHASE 5) GBYP 07c/2015. International Commission for the Conservation of Atlantic Tuna.

Dichmont, C.M., Deng, R.A., Punt, A.E., Brodziak, J., Chang, Y.-J., Cope, J.M., Ianelli, J. N., Legault, C.M., Methot, R.D., Porch, C.E., Prager, M.H., Shertzer, K.W., 2016. A review of stock assessment packages in the United States. Fish. Res. 183, 447–460. https://doi.org/10.1016/j.fishres.2016.07.001.

Francis, R.I.C.C., 2014. Replacing the multinomial in stock assessment models: a first step. Fish. Res. 151, 70–84. https://doi.org/10.1016/j.fishres.2013.12.015.

Hillary, R.M., Bravington, M.V., Patterson, T.A., Grewe, P., Bradford, R., Feutry, P., Gunasekera, R., Peddemors, V., Werry, J., Francis, M.P. and Duffy, C.A.J., 2018. Genetic relatedness reveals total population size of white sharks in eastern Australia and New Zealand. *Scientific reports*, *8*(1), p.2661.

Hordyk, A.R., Huynh, Q.C. and Carruthers, T.R., 2019. Misspecification in stock assessments: common uncertainties and asymmetric risks. *Fish and Fisheries*, *20*(5), pp.888-902.

Hurtado-Ferro, F., Szuwalski, C.S., Valero, J.L., Anderson, S.C., Cunningham, C.J., Johnson, K.F., Licandeo, R., McGilliard, C.R., Monnahan, C.C., Muradian, M.L. and Ono, K., 2015. Looking in the rear-view mirror: bias and retrospective patterns in integrated, age-structured stock assessment models. *ICES Journal of Marine Science*, *72*(1), pp.99-110.

Kristensen K., Nielsen A., Berg C. W., Skaug H., Bell B. M. 2016. TMB: automatic differentiation and laplace approximation. Journal of Statistical Software, 70: 1–21.

Mace, P.M., Bartoo, N.W., Hollowed, A.B., Kleiber, P., Methot, R.D., Murawski, S.A., Powers, J.E., Scott, G.P., 2001. National Marine Fisheries Service Stock Assessment Improvement Plan. Report of the NMFS National Task Force for Improving Fish Stock Assessments. NOAA Technical Memorandum NMFS-F SPO-56. 76pp

Maunder, M. N., Lennert-Cody, C. E., Aires-da-Silva, A. M., and Xu, H. (2021) Considerations for conducting close kin mark recapture of stocks managed by the IATCC. Available at: https://www.iattc.org/GetAttachment/ddc8410e-4de7-401c-87a9-73fb33090f23/ SAC-12-14\_Considerations-for-conducting-Close-Kin-Mark-Recapture-of-stocksmanaged-by-IATTC.pdf

Maunder, M.N., Punt, A.E., 2013. A review of integrated analysis in fisheries stock assessment. Fish. Res. 142, 61–74.

McAllister, M.K., Ianelli, J.N., 1997. Bayesian stock assessment using catch-age data and the sampling - importance resampling algorithm. Can. J. Fish. Aquat. Sci. 54, 284–300. https://doi.org/10.1139/f96-285.

Nielsen, R., Mattila, D. K., Clapham, P. J., and Palsbøll, P. J. 2001. Statistical approaches to paternity analysis in natural populations and applications to the north Atlantic humpback whale. Genetics. 157, 1673–1682. doi: 10.1093/genetics/157.4.1673

Nielsen, A., & Berg, C. W. (2014). Estimation of time-varying selectivity in stock assessments using state-space models. *Fisheries Research, 158*, 96-101.

Ono, K., Licandeo, R., Muradian, M.L., Cunningham, C.J., Anderson, S.C., Hurtado-Ferro, F., Johnson, K.F., McGilliard, C.R., Monnahan, C.C., Szuwalski, C.S. and Valero, J.L., 2015. The importance of length and age composition data in statistical age-structured models for marine species. *ICES Journal of Marine Science*, *72*(1), pp.31-43.

Pennington, M., Volstad, J.H., 1994. Assessing the effect of intra-haul correlation and variable density on estimates of population characteristics from marine surveys. Biometrics 50, 725. <https://doi.org/10.2307/2532786>

Rodriguez-Ezpeleta, N., Patterson, T. A., Pereda, I., Grande, M., Davies, C. R., Lezama-Ochoa, N., et al. (2020). Feasibility study on applying close-kin mark recapture abundance estimates to Indian ocean tuna commission shark species. Final Report to IOTC. San Sebastian, Spain: AZTI; 2020. csiro:EP2022-2718.

Skaug, H. J. 2001. Allele-sharing methods for estimation of population size. Biometrics 57, 750–756. doi: 10.1111/j.0006-341X.2001.00750.x

Stock, B. C., & Miller, T. J. (2021). The Woods Hole Assessment Model (WHAM): a general state-space assessment framework that incorporates time-and age-varying processes via random effects and links to environmental covariates. *Fisheries Research, 240*, 105967.

Swenson, J.D., Brooks, E.N., Kacev, D., Boyd, C., Kinney, M., Marcy-Quay, B., Sévêque, A., Feldheim, K. and Komoroske, L.M., *in-review*. Accounting for unobserved population dynamics and aging error in close-kin mark-recapture assessments. *Ecology and Evolution*.

Trenkel, V. M., Charrier, G., Lorance, P., and Bravington, M. V. (2022). Close-kin mark–recapture abundance estimation: practical insights and lessons learned. ICES J. Mar. Sci. 79, 413–422. doi: 10.1093/icesjms/fsac002

Xu, H., Thorson, J. T., Methot, R. D., & Taylor, I. G. (2019). A new semi-parametric method for autocorrelated age-and time-varying selectivity in age-structured assessment models. *Canadian* *Journal of Fisheries and Aquatic Sciences*, 76, 268-285.