Inclusion of ageing error and growth variability in the estimation of age composition input sample size

Pete Hulson1,\*, and Benjamin Williams1

1 Auke Bay Laboratories, Alaska Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 17109 Point Lena Loop Rd., Juneau, AK 99801

\* Correspondence: [Pete Hulson <[pete.hulson@noaa.gov](mailto:pete.hulson@noaa.gov)>](mailto:pete.hulson@noaa.gov)

# Abstract

*Why are you doing this? [context and aim]*

*What did you do?* [*methods*](#methods)

*What did you find? [core results – say something useful – no motherhood statements or deference to the main text!]*

*What does this mean? [interpretation in context]*

*What is it good for? [application]*

# Introduction

Compositional information on age and length comprise critical data products used in statistical catch-at-age assessment models, as they facilitate the tracking of year classes and size-structure over time and improve our understanding of the population dynamics (Quinn and Deriso 1999). There are two primary sources for age and length composition data used in statistical catch-at-age models: fishery-independent sources, which include some level of randomized and standardized collection of samples in a non-targeted framework, and fishery-dependent sources, in which collection of age and length samples are also randomized at some level but are obtained from hauls that are not random but rather targeted within a specific fishery. Regardless of the source of age and length composition data, it is commonly accepted that overdispersion of collections are inherent to the data due to intra-haul correlation (e.g., Pennington et al. 2000). The concept of ‘effective sample size’ has since been developed, that is smaller than the sample size collected, to reflect the increased uncertainty due to this overdispersion (e.g., McAllister and Ianelli 1997). Since modern statistical catch-at-age stock assessment models integrate multiple sources of data related to catch (e.g., fisheries catch-per-unit-effort, survey indices of abundance), life history (e.g., size-at-age, maturity-at-age, selectivity-at-age), and composition (e.g., length and age), it is imperative to consider the relative information content these data products provide to the model employed.

Because fisheries often depend on the periodic production of strong year-classes and subsequent recruitment into fishery catch, sampling efforts for age and length data, scaling of these data to the population level (‘compositional expansion’), and the weight assigned to these data products in assessment models are highly important in order to provide accurate advice for management. This is often handled through the use of data-weighting methods, checking the fit of compositional data in the model, and ensuring a good match between the variance of the data and the variance implied by the model (Francis 2017). The weight assigned to annual compositions (the ‘input sample size’) can follow a myriad of methods (e.g., fixed values as in Monnahan et al. (2021), number of samples or tows sampled upon as in Hulson et al. (2021) or Spencer and Ianelli (2022), bootstrapping compositions as in Stewart and Hamel (2014)). The primary consideration when assigning a weight to age or length composition data is to account for the potential variability and correlation in the sampling process. The method developed by Stewart and Hamel (2014) allows for resampling techniques to be employed at each level of the sampling design, and provides an objective avenue to determine input sample size that is smaller than the actual sample size based on the observation variability contained within the sampling process.

In addition to intra-haul correlation, for every fish species sampled for which age is capable of being determined from otoliths there is resulting variability in the ageing of the otolith, often called ‘ageing error’ (e.g., Punt et al. 2008). There are a number of factors that can influence the magnitude of ageing error (Nesslage et al. 2022), but inherent to obtaining ages from otoliths is variability in the age readings. To account for this source of variability, ageing laboratories regularly evaluate precision through obtaining multiple readings of the same otolith across different age readers (Morison et al. 2005). Several methods have been developed to account for ageing error in statistical catch-at-age models when fitting age composition through the use of an ageing error matrix (Punt et al. 2008, Candy et al. 2012). The essence of this approach is that the numbers-at-age estimated by the assessment model are ‘corrected’ through multiplication with an ageing error matrix, which assigns estimated numbers-at-age to adjacent age-classes depending on the magnitude of the ageing error within the specific age-class. Since the development and implementation of ageing error matrices a number of studies have been devoted to quantifying the effects of ageing error on assessment model estimates Liao et al. (2013). Within each of these studies, and in each application of an ageing error matrix within a stock assessment model, the age composition data fit will be weighted by an input sample size. As described previously, the input sample size selected would reflect the variability in the sampling process, which would also include the variability in the age readings themselves.

In the process of compositional expansion, it is often the case that an age-length key (ALK) is employed to expand population numbers-at-length to population numbers-at-age (Ailloud and Hoenig 2019). It is through the age-length key, and the subsequent age expansion, that observations of age composition are derived from fishery-independent and fishery-dependent sources. Conditional age-at-length (CAAL), in which paired age-length data are used as in indication of the age distribution for a specific length, is used to inform length-at-age and it’s related uncertainty (Taylor and Methot 2013). CAAL data can be used directly within statistical catch-at-age models to inform estimates of growth as well as composition data (Lee et al. 2019) and has been implemented in a number of operational stock assessments (e.g., McGilliard et al. 2019, Hulson et al. 2022). An intrinsic component to both the ALK and CAAL is the variability in length for a given age. Further, when using CAAL data as an additional likelihood component to a statistical catch-at-age model one must determine the input sample size to be used to weight this information.

Despite the acceptance of requiring an input sample size to weight age composition data in statistical catch-at-age models that reflects the added uncertainty caused by overdispersion common to age sampling, and the recognition of the inherent variability in the ageing process when reading otoliths and in the growth process upon which age-length keys are based, these sources of uncertainty have not been previously integrated in an objective estimation method for input sample size. In this study, we use the methods of Stewart and Hamel (2014) to estimate age composition input sample size that includes both ageing error and growth variability in the estimation process. We show, in a step-wise process, the added variability in age composition sample size from including ageing error and growth variability across a number of species that reflect differing life histories and levels of ageing difficulty. Using a current statistical catch-at-age models that are used for assessment and management as case studies we then show the effects of this added uncertainty on assessment model results.

# Methods

## Data: age collections and reader-tester agreement

In this study we used historical data collected from bottom trawl surveys conducted by the Alaska Fisheries Science Center (AFSC) in the Eastern Bering Sea (EBS: Lauth et al. 2019), Aleutian Islands (AI: von Szalay et al. 2017), and Gulf of Alaska (GOA: von Szalay and Raring 2018). Within the AFSC bottom trawl surveys both length frequency data and age specimen data are collected (in addition to other data sources including catch, effort, location, etc.). To facilitate age estimation, individual fish are processed at sea to record sex, length and weight and to remove sagittal otoliths that are sent to the AFSC Age and Growth laboratory for age determination. Periodically, a subset of these otoliths are selected for reader-tester agreement tests, which evaluates the reproducability of an age reading when two different age readers age the same fish, without knowledge of the other reader’s age (Kimura and Lyons 1991). The average annual bottom trawl survey age sample sizes for the species selected for this analysis by region, along with the total number of otoliths that have been selected for reader-tester agreement tests across these regions is shown in Table @ref(tab:species\_samples)). Besides that they are the most frequently sampled species for age, these species were selected because they are all assessed with statistical catch-at-age models that require input sample sizes to ‘weight’ the age composition data fit in the stock assessment models. Details of how the length frequency and age collections are expanded to population abundance-at-length and age at AFSC to then subsequently used as compositional data in stock assessment models are provided in Hulson et al. (in review).

## Simulation-Bootstrap framework

To evaluate the inclusion of ageing error and growth variability on uncertainty in age compostion datasets we developed a bootstrap-simulation framework that allowed for the addition of these sources of error. In simple terms, the simulation framework that we developed resamples the hauls, then lengths and ages collected within the resampled hauls following from the method introduced by Stewart and Hamel (2014). To implement ageing error, the ages that were resampled are then resampled again based on the reader-tester dataset, that is, for a specific resampled age, the set of tester ages for that reader age were pooled and a new age was resampled from that set. To implement growth variability, for a given resampled age the lengths observed for that age were pooled, and then a new length was resampled from that set of lengths. The bootstrap-simulation framework is composed of a suite of nested resampling protocols. Functions to run the sampling protocols were developed in a compartmentalized manner to provide for substantial flexibility in exploring desired resampling protocols. The order of operations (Figure @ref(fig:bs\_flows) *ben - we need to add where we’re doing tha geing error and growth resampling to this figure*) has the following schedule, with steps 1-2 and 4-6 being optional switches:

1. Resample hauls from the set of hauls with associated catch per unit effort (in numbers)
2. Within the resampled hauls from step 1, resample the observed lengths
3. With the resampled length frequency data from step 2, calculate population abundance-at-length
4. Within the resampled hauls from step 1, resample the observed ages from the specimen data
5. For the resampled ages in step 4, resample a length from the set of lengths observed for the given age
6. For the resampled ages in step 4, resample an age from the set of tester ages for the given age
7. With the resampled age data in steps 4-6 and the population abundance-at-length in step 3, calculate the population abundance-at-age

The core of the bootstrap-simulation function (steps 5 and 6 above) were designed to explore inclusion of ageing error and growth variability. The bootstrap-simulation then repeated steps 1-7 iteratively providing iterated population abundance-at-age that was then compared to the historical (the full sample without any resampling of data) population abundance-at-age determined by the bottom trawl surveys.

We applied the bootstrap-simulation in a step-wise manner to evaluate the consequences of adding each source of additional error to the age composition estimates.  
First, we ran the bootstrap-simulation with the historical data without adding any extra error, thus, omitting steps 5 and 6 above. Next, we added ageing error and growth variability separately, thus, omitting either step 5 or 6 depending on the source of uncertainty that we wanted to include. Finally, we added both ageing error and growth variability to the bootstrap-simulation framework. To allow for the largest number of samples from which the consequences of these sources of uncertainty could be evaluated we included reader-tester data that was pooled across these three regions. To evaluate the inclusion of growth variability we pooled the age-length pairs across all the years of the survey in order to provide the maximum influence of growth variability on the replicated age composition estimates. We ran the bootstrap-simulation for 500 iterations, which was a level for which the variability in population abundance-at-age results had stabilizeds. The bootstrap-simulation was developed in R (R Core Team 2022) and is available via GitHub as an R package (<https://github.com/BenWilliams-NOAA/swo> *will need to change this to the surveyISS package*).

## Computing effective and input sample size

A useful statistic that can quantify the variability in age composition is effective sample size, introduced by McAllister and Ianelli (1997). This statistic evaluates the amount of uncertainty in an estimated composition compared to an observed composition and is given by:

where is the estimated proportion for category-*c* (which can be age or any other arbitrary category across which proportions are computed) and is the observed proportion.

Here, the underlying age composition derived from the historical bottom trawl surveys with the full and unsampled data was treated as the observed proportions in equation (1). For each iteration of the bootstrap-simulation we computed an estimated proportion () that was then compared to the underlying historical age composition () to determine the effective sample size of the resampled age composition. Thus, across each iteration of the bootstrap-simulation we computed an effective sample size that indicated the amount of uncertainty in the resampled age composition. To summarize effective sample size across iterations we used the harmonic mean, which has been shown to reduce bias in recovering the true sample size in simulations for a multinomial distribution. Due to this reduction in bias the harmonic mean has also been recommended to determine the ‘input sample size’ that is used in stock assessment models to fit compositional data (Stewart and Hamel 2014). Herein, when we use the term ‘effective sample size’ we are referring to the effective sample sizes that were computed for each iteration of the bootstrap-simulation, when we use the term ‘input sample size’ we are referring to the harmonic mean of the iterated effective sample sizes.

## Evaluating life-history relationships to consequences of subsampling

[add text here describing what was done to compare reductions to life history]

# Results

[length results for selected species, including samples saved, ess and iss reductions - Pete and Ben/Meaghan]

[age results, including ess and iss reductions - Pete and Ben/Meaghan]

# Discussion

[Summary para of main results]

[Cost-benefit of precision compared to survey injuries]

[Still thinking on other paras]

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# Tables

(#tab:species\_sample)Average age samples from the AFSC bottom trawl surveys by region, and total reader-tester age pairs for the species evaluated in the bootstrap-simulation.

| Stock | Scientific name | AI | EBS | GOA | R-T |
| --- | --- | --- | --- | --- | --- |
| Alaska plaice | Pleuronectes quadrituberculatus | – | 407 | – | 2,781 |
| arrowtooth flounder | Atheresthes stomias | 451 | 476 | 849 | 6,073 |
| Atka mackerel | Pleurogrammus monopterygius | 601 | – | – | 12,864 |
| Dover sole | Microstomus pacificus | – | – | 392 | 2,384 |
| flathead sole | Hippoglossoides elassodon | – | 558 | 515 | 9,409 |
| Greenland turbot | Reinhardtius hippoglossoides | – | 283 | – | 3,227 |
| Kamchatka flounder | Atheresthes evermanni | – | 471 | – | 1,447 |
| northern rock sole | Lepidopsetta polyxystra | – | 456 | 449 | 8,883 |
| northern rockfish | Sebastes polyspinis | 532 | – | 452 | 6,366 |
| Pacific cod | Gadus macrocephalus | 804 | 1071 | 648 | 21,152 |
| Pacific ocean perch | Sebastes alutus | 942 | – | 1032 | 13,525 |
| rex sole | Glyptocephalus | – | – | 473 | 2,571 |
| southern rock sole | Lepidopsetta billineta | – | – | 514 | 1,745 |
| walleye pollock | Gadus chalcogrammus | 793 | 1534 | 1291 | 84,361 |
| yellowfin sole | Limanda aspera | – | 747 | – | 10,279 |

# Figures



(#fig:bs\_flows)Bootstrap-simulation flow chart, the steps refer to the order of operations as described in the *Bootstrap-simulation framework* section.