

Accounting for Age Measurement Errors in Fish Growth Model Estimation Using Length-Stratified Age Sampling Data

by

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Abstract

Fish growth models are crucial for fisheries stock assessments and are commonly estimated using fish length-at-age data. This data is widely collected using length-stratified age sampling (LSAS), a cost-effective two-phase response-selective method. The data may contain age measurement errors. We propose a methodology that remarkably reduces the bias in the estimation of fish growth for LSAS data with age measurement errors. The proposed methods use empirical proportion likelihood methodology for LSAS and the structural errors in variables methodology for age measurement errors. We provide a measure of uncertainty for parameter estimates and standardized residuals for model validation.

To model the age distribution, we employ a continuation ratio-logit model consistent with the random nature of the true age distribution. We also apply a discretization approach for age and length distributions, which significantly improves computational efficiency and is consistent with the discrete age and length data typically encountered in practice. The simulation study shows that neglecting age measurement errors can lead to significant bias in growth estimation, even with small but nonnegligible age measurement errors. However, our new approach performs well regardless of the magnitude of age measurement errors and accurately estimates standard errors of parameter estimates. Real data analysis demonstrates the effectiveness of the proposed model validation device. Computer codes to implement the methodology are provided.

KEYWORDS: Covariate measurement error; Fish growth model; Length-stratified age sampling; Pseudoconditional likelihood; Response-selective sampling; Structural errors in variables.

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Chapter 1

Introduction

Fish growth modelling is a scientific approach that involves developing mathematical or statistical models to understand and predict fish length at different ages. Predicting the length of fish at different ages is necessary for converting fish age to length and vice versa in fisheries stock assessment [e.g. 43]. This process considers various factors that influence fish growth, including species-specific characteristics, populations of a species (i.e. stocks), and year classes within a population (i.e. cohorts) [e.g. 21].

Researchers use fish growth models to gain insights into the health of fish stocks and fisheries. These models can help assess the impact of environmental changes, manage fisheries, and make informed decisions for sustainable fishing practices. In order to make informed decisions about sustainable harvest rates and predict the effects of future fishing quotas on stock mortality, it is essential to have reliable information on body growth rates [e.g. 73]. Therefore, growth model estimation is pivotal in assessing and managing fisheries stocks.

The statistical inference about fish growth is based on the paired length-at-age data

[e.g. 39, 47], which we also refer to it as growth data in this thesis. Such growth data are widely available through large-spatial-scale multiyear surveys conducted by various countries, which provide valuable insights into fish growth and ocean ecosystems. For example, Fisheries and Oceans Canada (DFO) has been conducting seasonal multispecies surveys for over four decades, accumulating vast growth data for various fish species in the north-west Atlantic Ocean. As explained subsequently, fish growth data are often collected using response-selective sampling [see, e.g. 45] with substantial errors in age determination. The objective of this research is to develop an effective methodology to accurately estimate fish growth that takes into account both the sampling scheme and age measurement errors. Additionally, this methodology includes a measure of uncertainty for parameter estimates and provides a validation device for model fitting. To our knowledge, such a methodology has not been proposed before.

Fish age measurement involves examining the structures in a fish's body that accumulate growth increments over time. The most common method for determining the age of a fish is by analyzing otoliths found in the fish's inner ear. The analysis involves extracting the otoliths and examining the growth rings under a microscope. In some cases, it is necessary to slice the otolith across the core to see all the annuli. Other structures, such as scales, vertebrae, and fin rays, may also be used depending on the species and the researcher's preference. All these processes make age determination far more time-consuming and expensive than length measurement. Therefore, fisheries surveys commonly use a two-phase length-stratified age sampling (LSAS) method to obtain fish length and age data. In the first phase, a large number of fish are randomly caught. The captured fish are then measured for their length and divided into length strata, such as 2 centimeters (cm). For example, all fish within the range of 10-12 cm would fall into one length stratum, and those in the range of

12-14 cm would be in another stratum, and so on. In the second phase, a fixed number of fish from each length stratum are randomly selected for age measurement. In this way, with only a small number of age measurements, the selected fish are evenly distributed across different length bins, which aligns with the actual growth curve of the fish population. The actual growth curve refers to the real pattern of fish growth that fish exhibit over time. The two-phase Length-Stratified Age Sampling (LSAS, acronyms for key methods and terms are outlined in Table 1.1) method in fisheries surveys offers additional advantages, such as greatly reducing age sampling costs, improving population representativeness, and enhancing measurement manageability. However, LSAS can significantly bias growth model estimation if not properly considered [e.g. 31, 53, 79]. [49] offers an extensive review of fish growth models, which typically treat age as the covariate and length as the response variable. Treating age as the response and length as the covariate can be mathematically inconvenient because fish length is confined below a certain asymptotic length. LSAS is thus a kind of basic stratified sampling (BSS) in response-selective sampling (RSS) as defined in [45]. To introduce the methodology for addressing LSAS, I will begin by providing a review of the statistical inference of RSS.

1.1 Inference for response-selective sampling (RSS)

Consider a random sample from a target population of N observational units, where each unit has a response y_i and a vector of covariates \mathbf{x}_i , $i = 1, \dots, N$. These responses and covariates are generated from the joint distribution $f(y, \mathbf{x}|\theta)$, which based on chain rule probability theorem can be broken down into a conditional distribution of y given \mathbf{x} , de-

noted by $f(y|\mathbf{x}; \theta)$, and a distribution of \mathbf{x} , denoted as $g(\mathbf{x})$,

$$f(y, \mathbf{x}|\theta) = f(y|\mathbf{x}; \theta)g(\mathbf{x}). \quad (1.1)$$

The parameters θ include all the parameters describing the conditional distribution of y given \mathbf{x} .

Response-selective sampling (RSS) is widely used in various fields such as epidemiology, finance, and social studies. In RSS, the partitioning of the range of (y, \mathbf{x}) into K strata labelled as S_1, S_2, \dots, S_k , the process is influenced partially by the values of the response variable y . In one of the simplest examples, this approach deals with a binary response y that can be 1 or 0. We take separate samples from the population of units with $y = 1$ and another one from the population with $y = 0$, then measure \mathbf{x} for all sampled units. In contrast to prospective sampling, which involves selecting samples during the study, RSS chooses samples based on outcomes established at the study's beginning. This makes it particularly advantageous in clinical studies due to its effectiveness in saving time and costs.

Now, I review the semi-parametric maximum likelihood and pseudo-likelihood estimations of θ for RSS in the literature. Let $G(\cdot)$ denote the corresponding distribution function of $g(\cdot)$, and define the following inclusion probabilities,

$$\begin{aligned} Q_j(\theta, G) &= pr \{(Y, \mathbf{X}) \in S_j\} \\ Q_j^*(\mathbf{x}; \theta) &= pr \{(Y, \mathbf{x}) \in S_j|\mathbf{x}\} \end{aligned} \quad (1.2)$$

In the context of RSS, the response and covariate vector (y, \mathbf{x}) are only available for a subset of size n out of the total N units, referred to as complete data. In contrast, for the remaining $N - n$ units, only a partial subset of (y, \mathbf{x}) is observed, making them incomplete data. Let N_j and n_j represent the number of observational units and complete data in the j th stratum, so it is obvious that $\sum_{j=1}^K N_j = N$ and $\sum_{j=1}^K n_j = n$. The set of fully observed

units in the j th stratum is referred to as D_j . The full likelihood for RSS samples is provided by [45] as follows,

$$L_F(\theta, G) = \prod_{j=1}^K \left\{ \prod_{i \in D_j} f(y_i | \mathbf{x}_i; \theta) g(\mathbf{x}_i) \right\} Q_j(\theta, G)^{N_j - n_j}. \quad (1.3)$$

To make an inference about θ using the full likelihood (1.3), I briefly describe a semi-parametric maximum likelihood approach as outlined in [45]. The full likelihood function $L_F(\theta, G)$ depends on the parameter θ and the distribution of function G , both of which need to be estimated. By holding θ fixed, we can maximize L_F over all discrete distributions in the data and obtain the profile likelihood for θ . When θ is fixed, we can ignore the constant $\ln f(y_i | \mathbf{x}_i; \theta)$. The resulting profile log-likelihood function is [see, e.g. 66]

$$l_{\text{FP}}(\theta) = h\{\theta, Q(\theta)\}, \quad (1.4)$$

where $h(\theta, Q)$ is defined by

$$h(\theta, Q) = \sum_{i: R_i=1} [\ln f(y_i | \mathbf{x}_i; \theta) - \ln \sum_{l=1}^K \tilde{p}_l Q_l^*(\mathbf{x}_i; \theta)] + \sum_{j=1}^K (N_j - n_j) \ln(Q_j) \quad (1.5)$$

with

$$\tilde{p}_j = 1 - (N_j - n_j) / N Q_j \quad (1.6)$$

Then, $\partial h / \partial Q = 0$ can be solved for an estimation of Q 's. The resulting score function from profile likelihood is

$$S_{\text{FP}}(\theta) = \frac{\partial l_{\text{FP}}}{\partial \theta}. \quad (1.7)$$

The semi-parametric maximum likelihood estimates of θ are obtained by solving the score equation $S_{\text{FP}}(\theta) = 0$ using the Newton-Raphson algorithm. The observed Hessian matrix of l_{FP} is detailed in [45].

For problems that involve response-selective data, besides the likelihood approach, there are several estimating function methods based on pseudo-likelihoods in the literature. One of these pseudo-likelihoods is the “estimated pseudo-likelihood” [see, e.g. 36] which is based on an empirical estimator $\tilde{G}(\cdot)$ of the covariate distribution $G(\cdot)$,

$$\tilde{G}(\mathbf{x}) = \sum_{j=1}^K \tilde{G}_j(\mathbf{x}) \frac{N_j}{N}, \quad (1.8)$$

where $\tilde{G}_j(\mathbf{x})$ represents the empirical cumulative distribution function derived from the observed covariate values \mathbf{x}_i of the complete observations in the j th stratum. Substituting Eq. (1.8) into the logarithm of Eq. (1.3), and obtain the logarithm of the pseudo-likelihood,

$$l_p(\theta) = \sum_{i:R_i=1} \log \{f(y_i|\mathbf{x}_i; \theta)\} + \sum_{j=1}^K (N_j - n_j) \log \left\{ \sum_{l=1}^K \tilde{p}_l^{-1} \sum_{i \in D_l} Q_j^*(\mathbf{x}_i; \theta) \right\} \quad (1.9)$$

where $\tilde{p}_j = n_j/N_j$, and $R_i = 1$ if the unit i is completely observed, and 0 otherwise.

When all of the N units had been observed completely, the log-likelihood function would be

$$\sum \ln f(y_i|\mathbf{x}_i; \theta) \quad (1.10)$$

An estimation of this value can be calculated by considering only the fully observed units and adjusting their impacts using weights according to the selection probabilities [see, e.g. 76]. In the pseudo-likelihood function, when each element of the dataset is assigned a specific weight, it refers to “weighted pseudo-likelihood” and is given by

$$l_w(\theta) = \sum_{j=1}^K \tilde{p}_j^{-1} \sum_{i \in D_j} \ln \{f(y_i|\mathbf{x}_i; \theta)\}, \quad (1.11)$$

which has been studied since the 1980’s for response-selective sampling. This method utilizes the Horvitz-Thompson technique to address issues related to differential sampling rates [see, e.g. 6].

Another method is the pseudoconditional likelihood [9, 76], for which the log pseudo-likelihood function is

$$l_C(\theta) = \sum_{i:R_i=1} \left[\ln \{f(y_i|\mathbf{x}_i; \theta)\} - \ln \left\{ \sum_{l=1}^K \tilde{p}_l Q_l^*(\mathbf{x}_i; \theta) \right\} \right]. \quad (1.12)$$

Alternatively, the mean score pseudo-likelihood method can be obtained by applying the EM algorithm to maximize the full likelihood $L_F(\theta, G)$ [see, e.g. 25, 62]. Here the complete-data likelihood $l_{\text{com}}(\theta, G)$ is defined as the log-likelihood based on complete observation of all \mathbf{x}_i , $i = 1, 2, \dots, N$ (conditional observation of y_i only when $R_i = 1$),

$$l_{\text{com}}(\theta, G) = \sum_{i=1}^N (R_i [\ln \{f(y_i|\mathbf{x}_i; \theta)\} + \ln \{dG(\mathbf{x}_i)\}] + (1 - R_i) [\ln \{Q_{j_i}^*(\mathbf{x}_i; \theta)\} + \ln \{dG(\mathbf{x}_i)\}]). \quad (1.13)$$

where j_i denotes the stratum that unit i has taken. The EM algorithm iterates between an E-step and an M-step. In E-step, it calculates the expected value of $l_{\text{com}}(\theta, G)$ based on the current estimates θ and G , given the observed data. The expectation of l_{com} is

$$\sum_{i=1}^N (R_i [\ln f(y_i|\mathbf{x}_i; \theta) + \sum_{j=1}^K \sum_{i \in (S_j - D_j)} \mathbb{E}[\ln Q_j^*(\mathbf{X}_i; \theta) | (Y_i, \mathbf{X}_i) \in S_j]). \quad (1.14)$$

Then the M-step adjusts the values of θ and G to maximize this function resulting from the E-step and gives [for details, see, e.g. 44, 45]

$$l_M(\theta) = \sum_{j=1}^K \sum_{i \in D_j} (\ln f(y_i|x_i; \theta) + \sum_{j=1}^K (N_j - n_j)/n_j \sum_{i \in D_j} \ln Q_j^*(x_i; \theta)) \quad (1.15)$$

Subsequently, the estimating equation is obtained from Eq. (1.15).

To estimate θ based on these pseudo-likelihood methods, we need to solve $S(\theta) = 0$, where $S(\theta) = \partial l / \partial \theta$ represents the score function associated with a log-pseudolikelihood $l(\theta)$. In all cases considered here, the Newton-Raphson algorithm can be employed to solve the estimating equations [for details, see, e.g., 45].

1.2 Inference for length-stratified age sampling (LSAS)

LSAS typically involves a large amount of first-phase length data and a relatively small number of second-phase length-at-age data. To utilize the full likelihood given by Eq. (1.3), it is necessary to accurately model the covariate (i.e., age) distribution to obtain the distribution of first-phase length data by integrating age from the joint distribution of length and age. However, due to the highly variable nature of fish recruitment, the age distribution of a fish stock is often complex, with multiple modes and substantial skewness and can change significantly over time.

As a result, no valid parametric or non-parametric model has been identified, so that involving the distribution of first-phase length data in the likelihood can improve the inference of growth model parameters [53]; that is, the full likelihood is not suitable for growth model estimation with LSAS data. In the remaining part of this thesis, we will consider only the distribution of the second-phase length-at-age data. Inference for RSS data in other fields, such as health and medicine, also involves only the distribution of the second-phase response-at-covariate data [e.g. 67, 19]. Nevertheless, without the first-phase data, the RSS cannot be addressed. The first-phase data is incorporated into the likelihood via weights or inclusion proportions [45, 53].

Conditional likelihood [see, e.g., Eq. 1 in 67], given that the individuals are selected for covariate measurement when their true covariate values are known, has been implemented for RSS data in various fields, such as econometrics [35], biostatistics [9], case-control study [76], and survey sampling [54]. In these implementations, the conditional probability of an individual present in the second phase sample, given its true covariate value, is approximated using the observed sampling proportions of all response strata (see, Eq. 2.8).

The resulting approximation to the conditional likelihood is referred to as the pseudoconditional likelihood (Eq. 1.12). [14] applied the pseudoconditional likelihood approach to estimate growth models in fisheries. Their method for addressing trawl fishing selectivity differs somewhat from the pseudoconditional likelihood approach defined by Eq. (16) of [45]. To address LSAS data [53] conducted simulation studies to compare nine approaches found in statistical and fisheries science literature. The results showed that the pseudoconditional likelihood approach had substantially better performance than the other methods. In fisheries' LSAS data, some length strata include small and long lengths, but these strata often do not contain any observations. To address this issue, [81] extended the pseudoconditional likelihood method. Their approach was also more consistent with Eq. (16) of [45] in terms of incorporating research gear selectivity, as compared to the method used in [14].

1.3 Age measurement errors

The conditional and pseudoconditional likelihood methods do not consider any errors that may occur during covariate measurement. Unfortunately, such errors are quite common in fisheries age determination, due to process and subjective factors [27, 12]. For instance, one year's growth may not always correspond to a single distinguishable ring on an otolith [3]. Additionally, age readers and laboratories may show significant variation in the preparation and interpretation of periodic features in otoliths [7, 13]. In both cases, it led to subjective errors. Here, both types of errors in age determination are referred to as age measurement errors. For nonlinear models, covariate measurement errors have been shown to cause biased and inconsistent parameter estimates, leading to inaccurate conclusions in subsequent analyses to varying degrees [17, 29]. In addition, it is widely acknowledged

that age and length measurement errors can substantially impact the accuracy of estimates for fish growth, mortality, and recruitment patterns [e.g. 8, 60].

There are two primary methods used to address age measurement errors: functional errors-in-variables (FEV) and structural errors-in-variables (SEV) [e.g. 69]. In FEV models, the actual unobservable covariates of the fish are treated as fixed unknown constants (i.e., parameters), while SEV models consider them as random variables, which vary in repeated sampling. The SEV approach is highly efficient and suitable for likelihood-based inferences, while likelihood-based inference can be more challenging with FEV models due to the numerous parameters involved [e.g. 17]. Even though the SEV approach requires the specification and estimation of the distribution of unobserved covariates, SEV models are widely used in comparison to FEV models because of their versatility, straightforward computational process, and potential for improved efficiency. To further strengthen the robustness of SEV models, two strategies have been proposed: semiparametric models [e.g. 71] and flexible parametric models [e.g. 16]. It is worthwhile to mention that accurately estimating the variances of age and length measurement errors can be difficult without additional information regarding the precision of at least one of them. [65] utilized a hierarchical Bayesian growth model to integrate age measurement error as a random effect. The variance of age measurement error was considered known in this model. Later, [34] extended this approach by introducing a true age prior distribution to the hierarchical Bayesian model, and claimed that this approach allows for the estimation of age measurement error variance using data with only one age read per individual. However, the effectiveness of this method was not evaluated through a simulation study.

[24] addressed a situation in which a smaller sample of fish with multiple age measurements exists to estimate aging error variance. They proposed a SEV model with a gamma

distribution for the unobserved true ages. The results of their simulation study showed that this method provided more accurate estimations of von Bertalanffy (vonB) model parameters than the conventional ‘errors-in-length’ non-linear least squares method. However, validation or repeated age measurement data is generally not readily available.

The model proposed by [50] builds upon the work of [24] by incorporating a gamma distribution for unobserved ages, accounting for length measurement error variance as a known parameter, and introducing between-individual variation in the growth model. [50] also estimated the aging error variance. Results from the simulation study of [50] revealed that the misspecification of the distribution of unobserved ages did not introduce bias in the estimation of parameters for the vonB growth model. However, the estimated aging error variance in [50] was very small. The von Bertalanffy growth model is a mathematical formula used to describe the growth of living organisms over time. The model has been widely used in fisheries science to estimate growth parameters and understand the growth patterns of various species.

[11] employed a hierarchical model of growth that utilized a gamma distribution for the age distribution. The model accounted for between-individual variability and measurement errors in age and length, with known variances obtained from external sources. The study found that a more flexible parametric age distribution did not significantly affect the vonB parameter estimation. [37] revealed that the asymptotic bias of parameter estimators in SEV models is close to zero when the covariate measurement error is low. However, model misspecification and the magnitude of covariate measurement errors can introduce bias, which was not considered in previous studies such as [24], [50], and [11]. [37] introduced a method to evaluate bias arising from the misspecification of random-effects distribution in SEV models.

1.4 Previous studies on LSAS and age measurement errors

[26] recommends the use of the SEV approach, which is also called structural modelling strategy [e.g. 78], due to its high efficiency and the ability to perform likelihood-based inference. SEV considers both the observed and true covariates as random variables that vary in repeated sampling, as described by [17]. Therefore, for the SEV approach, it is necessary to have an effective model of the covariate distribution. However, the irregularities often found in fisheries age distribution, such as multi-modality and skewness, can make this challenging. To address this issue, [26] proposed a parametric normal mixture distribution for the true age and demonstrated through simulation studies that this model can improve growth model estimation even with the misspecification of the true age distribution. However, [26] considered a random sample. Preliminary simulation tests conducted by [53] showed that the normal mixture model does not perform well when applied to LSAS data, even in the absence of age measurement errors. [53] introduced an empirical proportion (EP) likelihood method for LSAS data (see, Eq. 2.6). This method is similar to the pseudoconditional likelihood, but instead involves the joint distribution of length and age, and hence requires an age distribution model. For variable probability sampling (VPS), the EP likelihood is also similar to the complete-data likelihood [Eq. 11 in 45] by replacing the specified selection probability for full observation with the observed sample proportion. Ages are typically represented as integers rather than continuous numbers, making the age distribution a type of distribution for compositional data. The simulation studies in [53] found that the EP likelihood method performed better than alternative approaches when applying the continuation ratio-logit (CRL) model to analyze the age distribution in LSAS

data. Compositional data cannot be independent due to the fixed total. Neutrality, as introduced by [23], is the concept of independence for compositional data; complete neutrality represents the highest level of independence.

In CRL, parameters are independent if the compositional data is completely neutral. Given the high variability in yearly recruitments of a fish population, it is reasonable for the sizes of cohorts (or age groups) to possess some degree of independence, resulting in neutrality in age composition. This may be the reason for the popularity of the CRL transformation in modelling age distribution in fisheries literature [e.g. 5, 10]. [53] did not account for age measurement errors. We will evaluate the performance of the EP likelihood method in the presence of age measurement errors. Additionally, we will introduce a combined approach that utilizes both EP likelihood and SEV methods to address age measurement errors in LSAS data.

When modelling age measurement errors, the variance of age measurement error is difficult to determine. It is frequently assumed known [e.g. 65, 11] or proportional to that of length measurement error [e.g. 40], which is an inconvenient limitation. For growth model estimation, the variance of age measurement error is a nuisance parameter. My study also aims to investigate the precision of estimating this parameter and its impact on the inference of growth model parameters.

1.5 Model validation

To ensure the accuracy of the statistical models, it is crucial to validate their fitting to the data. Measures such as Akaike Information Criterion [AIC, e.g. 70], Bayesian Information Criterion [BIC, e.g. 77], and likelihood-ratio test [e.g. 46] can provide insight into the

relative quality of models for a given dataset. It is necessary to have a means of assessing the absolute quality of the model fitting. One commonly used method is to examine the residuals, which can indicate how well the model fits the data. [81] discussed that the conventional random-sample-based residual is unsuitable for LSAS data, and proposed a residual evaluation method for LSAS data in cases where age measurement error is negligible. The residual formula in [81] requires knowledge of the true age values, as it involves the conditional expectation of response given the true age. In cases with age measurement errors, the true ages are unknown; hence, the residuals in [81] cannot be applied. In Sec. 2.4, we will introduce a new set of standardized residuals that can be used for LSAS data with nonnegligible age measurement errors.

As part of my MSc training, I gained expertise in utilizing TMB [Template Model Builder; e.g. 41], a powerful modelling package. In this thesis, I successfully implemented various methods using TMB, and I would like to provide a concise introduction to TMB in the upcoming section.

1.6 Template Model Builder (TMB)

The calculation of derivatives plays a vital role in computational statistics. Automatic differentiation [AD; e.g. 32] is a technique to compute derivatives of a function when giving the computer algorithm to evaluate the function. This method is being integrated into statistical software, e.g., C++ packages ADMB [e.g. 28], Stan [e.g. 72] and Ceres Solver [e.g. 1]. In particular, the R [58] package TMB [Template Model Builder; e.g. 41] uses the state-of-the-art AD package CppAD [e.g. 4] to calculate first, second, and third-order derivatives of a user-defined function written in C++. The package facilitates the solving of complex

nonlinear mixed-effects models. It calculates the marginal likelihood through the integration of random effects automatically using the Laplace approximation. This approximation and its derivatives are achieved by using automatic differentiation of the joint likelihood function. These computations are optimized for speed, especially for dealing with problems containing a substantial number of random effects ($\approx 10^6$) and parameters ($\approx 10^3$). The structure of TMB is shown in Fig. 1.1.

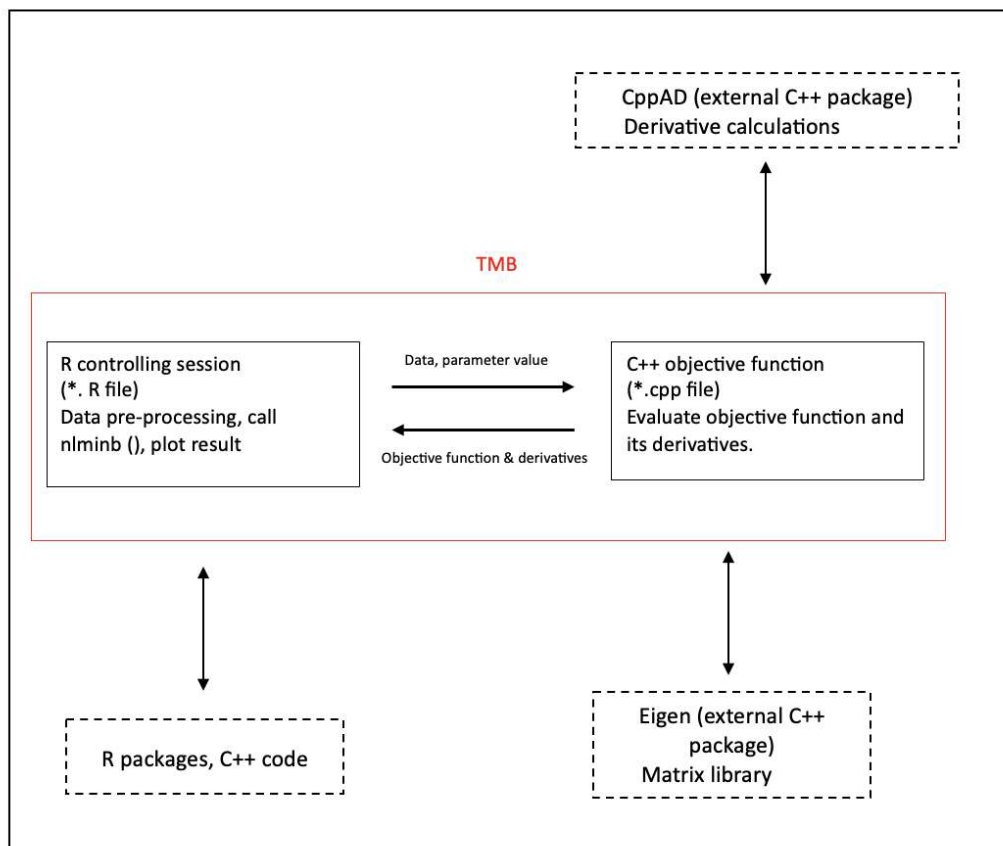


Figure 1.1: The structure of Template Model Builder (TMB).

Table 1.1: Definition of the acronyms. In the definition of RSS, the terminology two-phase stratified sampling is used. In a two-phase stratified sampling, the sampling units are partially observed and classified based on their response and/or covariate in the first phase. The classes formed are used as strata in the second phase, where the sampling units are selected for full observation.

Acronym	Full name	Brief definition
BSS	Basic stratified sampling	A RSS where in the second phase, a prespecified number or proportion of units in each first phase stratum are randomly selected and observed fully.
CEP	Conditional empirical proportion	Defined by Eq. (2.7).
CRL	Continuation ratio-logit	Defined by Eq. (2.13).
EP	Empirical proportion	Defined by Eq. (2.6).
LSAS	Length-stratified age sampling	A BSS where the response length is observed for all the sampling units in the first phase, but the covariate age is observed only for the selected second phase subsamples.
RSS	Response selective sampling	A two-phase stratified sampling where the probability that a unit is fully observed depends on the response.
SEV	Structural errors in variables	A method to address measurement errors in covariates by modelling the true covariates as random effects.
VPS	Variable probability sampling	A RSS where the units are observed sequentially and independently, and their strata are identified. In the second phase, a unit in a stratum is selected for full observation with the specified stratum probability.

In order to perform maximum likelihood estimation and hybrid MCMC (Markov Chain Monte Carlo) sampling, first-order derivatives are often sufficient. For example, the Stan package utilizes first-order derivatives [e.g. 72]. However, in complex models with random effects, computing higher-order derivatives using automatic differentiation can greatly simplify the optimization process of the Laplace approximation for the marginal likelihood [e.g. 68]. This method has been implemented in the TMB package and is particularly useful for random effects models and Gaussian Markov Random Fields (GMRF). The TMB package combines several high-performance libraries, including CppAD for automatic differentiation in C++, Matrix [e.g. 2] for sparse and dense matrix calculations in R, Eigen for sparse and dense matrix calculations in C++, and OpenMP for parallelization in C++ and Fortran. Utilizing these packages results in better performance and simpler code.

Due to the good performance of TMB, the theory and methodologies in my thesis are all implemented with TMB.

My thesis is structured as follows. In Chapter 2, I extend the SEV and EP likelihood methods for two-phase LSAS data with age measurement errors. I also provide standard errors for the parameter estimators and introduce standardized residuals for model validation. In Chapter 3, I evaluate the performance of the proposed methods through extensive simulation studies. In Chapter 4, I apply the proposed methods to a set of growth data for American plaice. Finally, I provide my conclusions and further discussions in Chapter 5.

Chapter 2

Methods

2.1 Notations and background

Suppose there is a sample of N fish with individual length l and age a_t , generated independently from the joint distribution

$$f(l, a_t | \boldsymbol{\theta}) = f(l | a_t; \boldsymbol{\theta}_g) p(a_t | \boldsymbol{\theta}_t), \quad (2.1)$$

where $\boldsymbol{\theta}$ is a vector of unknown parameters, subscripts indicating distinct subsets within $\boldsymbol{\theta}$. Here, a_t indicates the true age of a fish, which is equivalent to the measured age in the absence of age measurement error. This joint distribution may represent the population distribution filtered by trawl fishing selectivity. The conditional density, denoted as $f(l, a_t | \boldsymbol{\theta}_g)$, models the length distribution of caught fish given their true age. This includes various growth models, trawl selectivities, and accounting errors for both process and measurement of the length data. During the first phase of the two-phase LSAS, length measurements are obtained for all N fish. Based on their lengths, the first phase sample is then classified into J exclusive length strata, S_1, S_2, \dots, S_J . The probability of a fish with

length (l) falling into the j th stratum (i.e., $l \in S_j$, where $j = 1, 2, \dots, J$) is determined by the inclusion probability $Q_j(\boldsymbol{\theta})$. This probability can be calculated by integrating over length and summing over discrete age as follows:

$$Q_j(\boldsymbol{\theta}) = \Pr[(l, a_t) \in S_j | \boldsymbol{\theta}] = \int_{l \in S_j} \left[\sum_{a_t} f(l, a_t | \boldsymbol{\theta}) \right] dl. \quad (2.2)$$

A conditional version of the inclusion probability given the true age a_t is defined as

$$Q_j^*(a_t; \boldsymbol{\theta}_g) = \Pr(l \in S_j | a_t; \boldsymbol{\theta}_g) = \int_{l \in S_j} f(l | a_t; \boldsymbol{\theta}_g) dl. \quad (2.3)$$

The number of fish in a stratum is denoted by N_j , where $N = \sum_{j=1}^J N_j$.

Only a subsample of size n from the N fish is measured for age in the second phase of LSAS. Thus, only a subset of size n out of the N fish have their full length and age information (l_i, a_i) , where subscript i indexes individual fish. In each stratum j , the maximum number of fish to be sampled for age is denoted by m_j . The true sample size n_j for this stratum is determined by the following equation:

$$n_j = \begin{cases} N_j, & \text{if } N_j < m_j, \\ m_j, & \text{if } N_j \geq m_j, \end{cases} \quad (2.4)$$

which is a random variable. We define the indicator variable R_i for all individuals $i = 1, \dots, N$ in the first-phase sample as

$$R_i = \begin{cases} 1, & \text{if } (l_i, a_i) \text{ is fully observed,} \\ 0, & \text{if some information on } (l_i, a_i) \text{ is missing.} \end{cases} \quad (2.5)$$

Here age is missing at random in the terminology of [64] since $\Pr(R_i = 1 | l_i, a_i) =$

$\Pr(R_i = 1|l_i)$. Further, define the stratum indicator

$$\delta_{ij} = \begin{cases} 1, & \text{if } l_i \in S_j, \\ 0, & \text{otherwise,} \end{cases} \quad i = 1, 2, \dots, N, \quad j = 1, 2, \dots, J,$$

and denote the set of indices of all fully observed units in stratum S_j by

$$D_j = \{i : \delta_{ij} = 1, R_i = 1\}.$$

[53] introduced the following EP joint density of length and age for LSAS data,

$$f_{\text{EP}}(l, a_t | R = 1; \boldsymbol{\theta}) = \frac{(n_j/N_j) f(l, a_t | \boldsymbol{\theta})}{\sum_{k=1}^{J_{\text{obs}}} (n_k/N_k) Q_k(\boldsymbol{\theta}) + \sum_{k=J_{\text{obs}}+1}^{J_{\text{total}}} Q_k(\boldsymbol{\theta})}, \quad (2.6)$$

where $l \in S_j$, $k = 1, 2, \dots, J_{\text{obs}}$ enumerates the length strata with observed data, and $J_{\text{obs}} + 1, \dots, J_{\text{total}}$ count the strata without data. [81] utilized the following conditional EP density of length $l \in S_j$ given true age a_t for LSAS data under the assumption that age measurement error is negligible,

$$f_{\text{CEP}}(l | a_t, R = 1; \boldsymbol{\theta}) = \frac{(n_j/N_j) f(l | a_t; \boldsymbol{\theta}_g)}{\sum_{k=1}^{J_{\text{obs}}} (n_k/N_k) Q_k^*(a_t; \boldsymbol{\theta}_g) + \sum_{k=J_{\text{obs}}+1}^{J_{\text{total}}} Q_k^*(a_t; \boldsymbol{\theta}_g)}. \quad (2.7)$$

The conditional and unconditional EP likelihoods are obtained by multiplying the corresponding conditional and unconditional EP densities over the n second phase length-at-age data. [53] also implemented the pseudoconditional likelihood method with individual density given by

$$f_{\text{pseudo}}(l | a_t, R = 1; \boldsymbol{\theta}) = \frac{(n_j/N_j) f(l | a_t; \boldsymbol{\theta}_g)}{\sum_{k=1}^{J_{\text{obs}}} (n_k/N_k) Q_k^*(a_t; \boldsymbol{\theta}_g)} \quad \text{for } l \in S_j. \quad (2.8)$$

In their simulation studies, [53] demonstrated that based on densities (2.6) and (2.8), the EP likelihood and pseudoconditional likelihood approaches outperformed other methods

for LSAS data, when age measurement errors are negligible. The conditional EP likelihood is expected to be an improvement over the pseudoconditional likelihood because the conditional EP likelihood accounts for empty length strata in the denominator, while the pseudoconditional likelihood omits them. In this study, we extend the conditional and unconditional EP likelihood methods to address age measurement errors using SEV.

2.2 SEV methods for LSAS data

Let $p(a|a_t; \boldsymbol{\theta}_e)$ be the probability mass function (pmf) of the measured age a given the true age a_t . In SEV, the unobserved true ages are treated as random effects (REs) that must be summed out to obtain the marginal distribution for observed length-at-age data. The SEV densities based on the EP and conditional EP densities are, respectively,

$$f_{\text{SEV EP}}(l, a | R = 1; \boldsymbol{\psi}) = \frac{(n_j/N_j) \sum_{a_t} f(l|a_t; \boldsymbol{\theta}_g) p(a_t | \boldsymbol{\theta}_t) p(a|a_t; \boldsymbol{\theta}_e)}{\sum_{k=1}^{J_{\text{obs}}} (n_k/N_k) Q_k(\boldsymbol{\theta}) + \sum_{k=J_{\text{obs}}+1}^{J_{\text{total}}} Q_k(\boldsymbol{\theta})}, \quad (2.9)$$

$$f_{\text{SEV CEP}}(l, a | R = 1; \boldsymbol{\psi}) = \sum_{a_t} \frac{(n_j/N_j) f(l|a_t; \boldsymbol{\theta}_g) p(a_t | \boldsymbol{\theta}_t) p(a|a_t; \boldsymbol{\theta}_e)}{\sum_{k=1}^{J_{\text{obs}}} (n_k/N_k) Q_k^*(a_t; \boldsymbol{\theta}_g) + \sum_{k=J_{\text{obs}}+1}^{J_{\text{total}}} Q_k^*(a_t; \boldsymbol{\theta}_g)}, \quad (2.10)$$

where $l \in S_j$, and $\boldsymbol{\psi}^\top = (\boldsymbol{\theta}^\top, \boldsymbol{\theta}_e^\top)^\top$. The vector $\boldsymbol{\psi}$ include the entire set of parameters for estimation, comprising $\boldsymbol{\theta}_g$ (growth and gear selectivity parameters), $\boldsymbol{\theta}_t$ (parameters for the true age distribution), and $\boldsymbol{\theta}_e$ (age measurement error parameter).

In the rest of this thesis, we will use the terms ‘‘SEV EP’’ and ‘‘SEV CEP’’ to denote the SEV methods that utilize the EP and conditional EP densities, respectively. To obtain the log-pseudoconditional likelihoods, the corresponding individual log-densities are summed over the n second phase length-at-age data,

$$l_{\text{SEV EP}}(\boldsymbol{\psi}) = \sum_{i=1}^N R_i \log f_{\text{SEV EP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi}), \quad (2.11)$$

$$l_{\text{SEV CEP}}(\boldsymbol{\psi}) = \sum_{i=1}^N R_i \log f_{\text{SEV CEP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi}). \quad (2.12)$$

Note that the SEV based on density (2.9) may be more efficient to implement, as the denominator is evaluated once for all a_t .

Following [53], we apply the CRL transformation to model the pmf of true ages,

$$p(a_t | \boldsymbol{\theta}_t) = \begin{cases} \frac{e^{\lambda_{a_t}}}{\prod_{i=1}^{a_t} \{1 + e^{\lambda_i}\}} & \text{if } a_t = 1, 2, \dots, A_{\max} - 1, \\ \frac{1}{\prod_{i=1}^{A_{\max}-1} \{1 + e^{\lambda_i}\}} & \text{if } a_t = A_{\max}, \end{cases} \quad (2.13)$$

where A_{\max} is the maximum age in the data. It is easy to verify that the CRL model satisfies the two probability rules: $p(a_t | \boldsymbol{\theta}_t) \geq 0$ and $\sum_{a_t=1}^{A_{\max}} p(a_t | \boldsymbol{\theta}_t) = 1$. The parameters λ_i , where $i = 1, 2, \dots, A_{\max} - 1$, can take any value between $-\infty$ to ∞ , making them suitable for estimation through optimization techniques. The inverse transformation of Eq. (2.13) is

$$\lambda_{a_t} = \log \left[\frac{p(a_t | \boldsymbol{\theta}_t)}{p(a_t + 1 | \boldsymbol{\theta}_t) + \dots + p(A_{\max} | \boldsymbol{\theta}_t)} \right], \quad a_t = 1, 2, \dots, A_{\max} - 1. \quad (2.14)$$

When implementing the various methods discussed in this section, the function of λ_{a_t} values in Eq. (2.13) should be used in place of $p(a_t | \boldsymbol{\theta}_t)$, and the λ_{a_t} values are estimated along with the other model parameters.

2.3 Asymptotics

We estimate the entire set of parameters, represented by $\boldsymbol{\psi}$, by solving the score equation,

$$S_c(\boldsymbol{\psi}) = \sum_{i=1}^N R_i \frac{\partial l_{ci}(\boldsymbol{\psi})}{\partial \boldsymbol{\psi}} = 0, \quad (2.15)$$

where $l_{ci}(\boldsymbol{\psi})$ can be $\log f_{\text{SEV EP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi})$ or $\log f_{\text{SEV CEP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi})$, depending on which log-pseudoconditional likelihood is being optimized, SEV EP or SEV CEP.

According to [45], under mild regularity conditions on the model, the estimator $\hat{\boldsymbol{\psi}}$ obtained from solving Eq. (2.15) for BSS is consistent, and $\sqrt{N}(\hat{\boldsymbol{\psi}} - \boldsymbol{\psi})$ is asymptotically normal with covariance matrix estimated with

$$\widetilde{\text{ACOV}}_{\text{BSS}} = A(\hat{\boldsymbol{\psi}})^{-1} \hat{B}_{\text{BSS}} A(\hat{\boldsymbol{\psi}})^{-T}, \quad (2.16)$$

where

$$A(\hat{\boldsymbol{\psi}}) = -\frac{1}{N} \frac{\partial S_c(\boldsymbol{\psi})}{\partial \boldsymbol{\psi}^\top} \Big|_{\boldsymbol{\psi}=\hat{\boldsymbol{\psi}}}.$$

To replicate the formula for \hat{B}_{BSS} derived in [45], we first define $\hat{U}_i = \partial l_{ci}(\hat{\boldsymbol{\psi}}) / \partial \hat{\boldsymbol{\psi}}$ and

$$\tilde{U}^{(j)} = \sum_{i \in D_j} \hat{U}_i / n_j \quad \text{for } j = 1, \dots, J.$$

Using these values, we can compute

$$\hat{B}_{\text{BSS}} = \frac{1}{N} \sum_{j=1}^J \tilde{p}_j \sum_{i \in D_j} \hat{U}_i \hat{U}_i^\top + \frac{1}{N} \sum_{j=1}^J n_j (1 - \tilde{p}_j) \hat{V}_j(\mathbf{U}), \quad (2.17)$$

where $\tilde{p}_j = n_j / N_j$, and

$$\hat{V}_j(\mathbf{U}) = \frac{1}{n_j - 1} \sum_{i \in D_j} (\hat{U}_i - \tilde{U}^{(j)}) (\hat{U}_i - \tilde{U}^{(j)})^\top.$$

Standard error (SE) estimates of parameter estimators based on Fisher information are usually provided by popular modelling packages such as TMB [Template Model Builder, 42] package in R [59]. Therefore, we also consider the asymptotic covariance estimator of $\sqrt{N}(\hat{\boldsymbol{\psi}} - \boldsymbol{\psi})$ given by

$$\widetilde{\text{ACOV}}_{\text{FI}} = A(\hat{\boldsymbol{\psi}})^{-1}, \quad (2.18)$$

where the subscript FI denotes the ‘‘Fisher information’’.

2.4 Residuals

As previously mentioned in the Introduction, the residual formula presented in [81] requires knowledge of the true age values. However, when age measurement errors are not negligible, the true ages are unknown, and using their residual formula requires estimating the true ages. In SEV, the true ages are regarded as REs, and are frequently estimated using the posterior modes with model parameters at the maximum likelihood estimates (MLEs) [e.g. 38]. Nevertheless, the true ages are fixed values treated as REs because they are unobserved. Posterior mode RE estimators are biased and variable in this situation [80]. Therefore, we define LSAS residual error based on the conditional distribution of length given the observed age as

$$\begin{aligned} e_i &= l_i - \chi_i, \\ \chi_i &= E(l_i | a_i, R_i = 1; \boldsymbol{\psi}), \end{aligned} \tag{2.19}$$

where χ_i is evaluated with the conditional distributions of l_i given a_i ,

$$\frac{f_{\text{SEV EP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi})}{\int f_{\text{SEV EP}}(l, a_i | R_i = 1; \boldsymbol{\psi}) dl} \quad \text{and} \quad \frac{f_{\text{SEV CEP}}(l_i, a_i | R_i = 1; \boldsymbol{\psi})}{\int f_{\text{SEV CEP}}(l, a_i | R_i = 1; \boldsymbol{\psi}) dl},$$

for SEV EP and SEV CEP, respectively. Here, the denominators are integrated over the support of length l . Note that the marginal distribution of observed age is not $\sum_{a_t} p(a_i | a_t; \boldsymbol{\theta}_e) p(a_t | \boldsymbol{\theta}_t)$ under LSAS.

The residuals, or estimated errors, can be calculated using Equation

$$\begin{aligned} r_i &= l_i - \hat{\chi}_i, \\ \hat{\chi}_i &= \frac{\int l f_{\text{SEV EP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl}{\int f_{\text{SEV EP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl} \quad \text{or} \\ \hat{\chi}_i &= \frac{\int l f_{\text{SEV CEP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl}{\int f_{\text{SEV CEP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl}, \end{aligned} \tag{2.20}$$

where the symbol $\hat{\cdot}$ indicates that the estimated parameters are used, and $\hat{\chi}_i$ is estimated using the SEV density based on either the EP or conditional EP method. The standard errors (SEs) of the residuals can be calculated with

$$\begin{aligned} \text{SE}(r_i) &= \sqrt{\frac{\int l^2 f_{\text{SEV EP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl}{\int f_{\text{SEV EP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl} - \hat{\chi}_i^2} \quad \text{or} \\ \text{SE}(r_i) &= \sqrt{\frac{\int l^2 f_{\text{SEV CEP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl}{\int f_{\text{SEV CEP}}(l, a_i | R_i = 1; \hat{\boldsymbol{\psi}}) dl} - \hat{\chi}_i^2}. \end{aligned} \quad (2.21)$$

The standardized residual for the i th observation can then be evaluated as $r_i/\text{SE}(r_i)$.

Chapter 3

Simulation studies

The simulation study uses a revised version of the widely recognized von Bertalanffy growth function [vonB; 74], which effectively approximates growth for many fish species [20, 57] by assuming a linear decrease in growth rate as the fish size increases. The model based on the vonB growth function for the observed length $l(a_t)$, given the true age a_t , is expressed as

$$\begin{aligned}l(a_t) &= \mu_a + \epsilon, \\ \mu_a &= L_\infty \left[1 - \left(1 - \frac{l_0}{L_\infty} \right) e^{-k a_t} \right], \\ \epsilon &\sim N(0, \sigma_a^2), \\ \sigma_a &= \mu_a \text{ CV},\end{aligned}\tag{3.1}$$

where L_∞ is the theoretical length at which the growth rate stops, k is the growth coefficient, l_0 is the length at age 0, CV is the coefficient of variation, $N(\mu, \sigma^2)$ denotes normal distribution with mean μ and variance σ^2 . The Gaussian error term ϵ represents the combined effect of between-individual variation (or process error) resulting from individual growth parameter variability and the length measurement error, as described in [55]. The

commonly used parameter of age at length 0 is usually negative and is an extrapolation that should be avoided, as fish length cannot be zero. Therefore, this parameter is replaced with l_0 , which can usually be determined from existing larval studies in the literature [see 81, for an example].

Model (3.1) states that the conditional distribution of length l given age a_t is $f(l|a_t; \boldsymbol{\theta}_g) \sim N(\mu_a, \sigma_a^2)$. In practice, since the real length data is discrete and represented as integers, the corresponding probability mass function (pmf) can be approximated as [Eq. 5 in 55]

$$p(l|a_t; \boldsymbol{\theta}_g) = \frac{N(l, \mu_a, \sigma_a^2)}{\sum_{l'} N(l', \mu_a, \sigma_a^2)}. \quad (3.2)$$

Here the pmf $p(l|a_t; \boldsymbol{\theta}_g)$ is obtained by normalizing the probability density function (pdf) of $N(l, \mu_a, \sigma_a^2)$ over all possible values of l , with $N(l, \mu, \sigma^2)$ denoting a normal pdf with mean μ and variance σ^2 evaluated at l .

The integrals in Eqs. (2.2) and (2.3) should be replaced with summations over all the length values falling in the length stratum S_j , and the integrals in Eqs. (2.19)-(2.21) should be replaced with summations over all possible values of length.

In order to ensure comparability with the results presented in [53], we replicated their methodology of simulating population dynamics to obtain population distributions for length and age and collect LSAS data from the simulated fish population. The population simulation utilizes the structure of the stock assessment model, Stock Synthesis [48]. The simulation procedure is illustrated in Fig 3.1.

Figure 1: Diagram of steps used in population simulations; LSAS is length-stratified age sampling

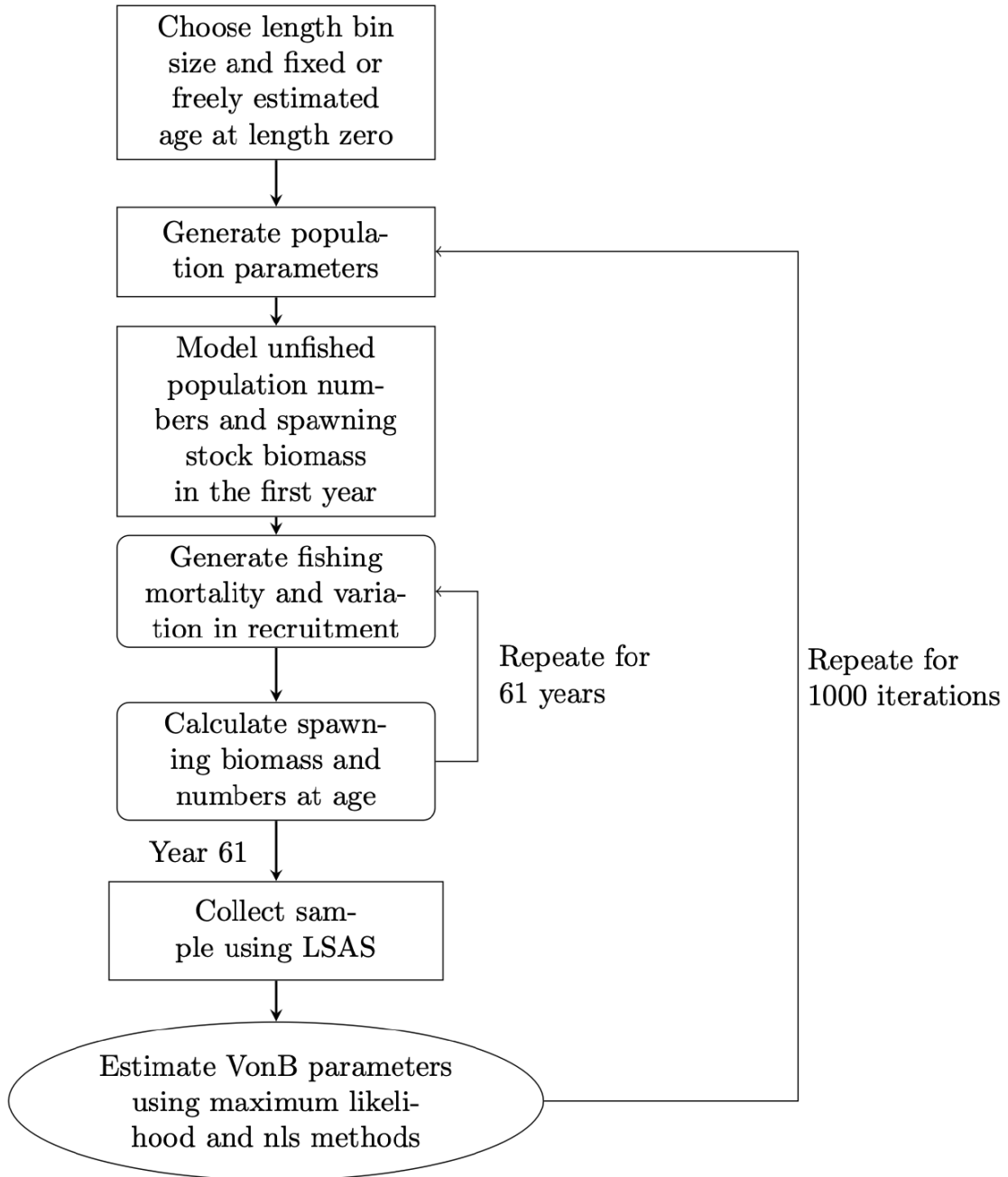


Figure 3.1: Illustration of the simulation steps used in population dynamics and LSAS data collection.

For the first year, an unfished stationary population is created based on a recruitment value of R_0 ; that is, the number of fish at a given age a is calculated as $R_0 e^{-Ma}$ for $a = 1, 2, \dots, A = 60$. The natural mortality rate M is randomly generated from a uniform distribution with a mean of 0.3 and a standard deviation (SD) of 0.11. The natural mortality refers to the loss of fish within the population resulting from factors unrelated to fishing activities. For the growth parameters, we fix $l_0 = 3$, but for each simulation run, the asymptotic length L_∞ is randomly generated from a normal distribution with mean 50 and SD 8, and the growth rate k is determined by the life-history-invariant $k = M/1.65 + \varepsilon_k$ [18], where ε_k is randomly generated from a normal distribution with mean 0 and SD $0.10 \times M/1.65$. The number of mature fish in the population is evaluated using a logit maturity model

$$m(a) = \frac{1}{1 + e^{\frac{-\log(19)(a-A_{50})}{A_{95}-A_{50}}}}, \quad (3.3)$$

where the age at 50% maturity $A_{50} = \log(3)/k$, and the age at 95% maturity $A_{95} = A_{50} + 4$. The weight (w) of age a fish is calculated based on the mean length μ_a in (3.1) using a cubic relationship, expressed as $w(\mu_a) = 0.20 \times \mu_a^3$. Then the Spawning stock biomass (SSB) is evaluated by $SSB(y) = \sum_{a=1}^A w(\mu_a) \times m(a) \times N(y = 1, a)$, where $N(y, a)$ is the number of age a fish in year y . The recruitment R , namely the number of fish at age 0 for the upcoming year, is determined by SSB using the Beverton and Holt spawner-recruit relationship

$$R(y) = \frac{SSB(y-1) e^{-M} e^{\varepsilon_R}}{1 - \left(\frac{5h-1}{4h}\right) \left[1 - \frac{SSB(y-1)}{SSB_{eq}}\right]}, \quad (3.4)$$

where $SSB_{eq} = ((5h-1)/(4h)) \times R_0$, the steepness h is randomly generated from a normal distribution with a mean of 0.75 and a SD of 0.07, and the random deviation ε_R is

generated from a normal distribution with a mean of 0 and a standard deviation of σ_{Rec} , which is also randomly generated from a truncated normal distribution with a mean of 0.6 and a standard deviation of 0.15. To evaluate the number of fish at ages 1 to A for the second year, we utilize the population dynamics model given by:

$$N(y, a) = N(y - 1, a - 1)e^{-[M+F(y)]}, \quad (3.5)$$

where F represents fishing mortality or the death of fish due to fishing activities. F is generated from a normal distribution with a mean of 0.2 and a standard deviation of 0.08, truncated at 0 to ensure that it remains positive. Using $N(y = 2, a)$, we evaluate the recruitment for the third year and continue this process iteratively. This simulation of population dynamics is repeated for 61 years so that the joint distribution of length and age in the 61st year closely approximates the natural distribution. Table 3.1 lists the distributions and models used. Each year, new fishing mortality (F) and variation in recruitment (ε_R) are drawn from their corresponding distributions; all other population values are generated once per simulation run.

Table 3.1: Population dynamics models and parameter distributions used to generate population simulation. Fishing mortality (F) and log recruitment deviation (σ_{Rec}) are generated randomly on a yearly basis, while other parameters are generated randomly for each simulation iteration.

<i>Parameter</i>	<i>Distribution</i>	<i>Mean</i>	<i>SD</i>
Natural mortality (M)	Uniform	0.3	0.11
Fishing mortality (F)	TruncNorm	0.20	0.08
Steepness (h)	Normal	0.75	0.07
Log recruitment deviation (σ_{Rec})	TruncNorm	0.60	0.15
Asymptotic length (L_∞)	Normal	50	8
Growth coefficient error (ϵ)	Normal	0	0.10(1.65/M)
CV length-at-age	TruncNorm	0.10	0.04
Log unfished recruitment [$\log(R_0)$]	Fixed	9.0	—
Length at age 0 (L_0)	Fixed	3	—
Age at length 0 (a_0)	Fixed	-0.07	—

Parameter	Model
Recruitment	$R(y) = \frac{SSB(y-1)}{1 - (\frac{5h-1}{4h})[1 - \frac{SSB(y-1)}{SSB_{eq}]}$
Weight	$w(\mu_a) = 0.20 \times \mu_a^3$
Maturity	$m(a) = \{1 + e^{\frac{[-\log(19)(a-A_{50})]}{A_{95}-A_{50}}}\}^{-1}$
Numbers at age	$N(y, a) = N(y-1, a-1)e^{-[M+F(y)]}$
Numbers in first year	$N(1, a) = R_0(e^{-a \cdot M})$
Spawning stock biomass	$SSB(y) = \sum_{a=1}^A w[l(a)] \cdot m(a) \cdot N(y, a)$

Note: Minimum = 0.10 and maximum = 0.50 for the uniform distribution; TruncNorm is the truncated normal distribution with minimum = 0 , maximum = ∞ to prevent generating negative values.

We use the simulated population in the 61st year as the first-phase sample. Its age composition is the true age distribution $p(a_t)$, which is modelled with CRL in Eqs. (2.9) and (2.10). Subsequently, we draw the second-phase LSAS sample from this first-phase sample. The LSAS aims to regulate the number of age measurements and acquire evenly distributed length-at-age data across the growth curve. Following [53], we assume that the target stratum sample size m_j is proportional to the length bin size, such that $m_j = 10 \times \text{bin size}$, where the bin size is chosen from a set of commonly used values in practice, namely 1, 2, 3, and 5 cm [e.g. 51]. This target stratum sample size choice is consistent with the sampling strategies used in DFO surveys for American plaice, where $m_j = 20$ for each length bin of size 2 cm.

In data generation and model fitting, we assume that the measured age a equals the true age a_t plus a Gaussian random error with mean 0 and SD σ_u , rounded to the nearest positive integer. This approach is a discrete analog to the Gaussian age measurement error model used by [63] and [56]. The conditional pmf $p(a|a_t)$ in Eqs. (2.9) and (2.10) are evaluated accordingly. To specify σ_u , we consider three different levels: small (0.1), medium (0.5, 1), and large (2).

Table 3.2: Sample size summary statistics for the 1000 simulated first-phase and second-phase LSAS samples in the simulation studies. Length bin size is 2 cm.

	Min.	1st Quartile	Median	Mean	3rd Quartile	Max.
First phase	5452	12950	18041	20364	25277	100441
Second phase	193	392.0	446.0	446.7	500.0	714

For each simulation classified by σ_u and bin size, we repeated the data generation and parameter estimation process 1000 times. To ensure that the resulting sample sizes for the first and second phases of LSAS are comparable to the actual data, we have implemented an initial recruitment of $R_0 = e^9$. The sample size of the 1000 simulated first-phase and second-phase LSAS samples, using a length bin size of 2cm, are presented in Table 3.2. The assessment of various approaches involves comparing the calculated values of L_∞ , K and CV from each method to the true values in the simulation model. We evaluate the estimation performance using two metrics: relative root mean squared error (RRMSE)

$$\text{RRMSE} = \frac{\text{RMSE}}{|\text{true}^*|} \times 100, \quad \text{where RMSE} = \sqrt{\frac{\sum_{i=1}^{1000} (\text{est}_i - \text{true}_i)^2}{1000}},$$

and relative bias (RelBias)

$$\text{RelBias} = \frac{\text{Bias}}{|\text{true}^*|} \times 100, \quad \text{where Bias} = \frac{\sum_{i=1}^{1000} (\text{est}_i - \text{true}_i)}{1000}.$$

Here, we use true_i to denote the parameter value in the i th simulation, and true^* to denote the mean value of the parameter distribution. As mentioned earlier, the parameters for L_∞ , CV, and k were drawn randomly from their respective distributions, resulting in variations across iterations.

To evaluate the log-pseudoconditional likelihood functions and their gradients, we utilized the TMB package in R. We performed the likelihood maximization using the R function `nlminb()`.

The simulation results are presented in Tables 3.3 – 3.4 and Fig. 6.1. “EP” refers to the EP likelihood methods based on density (2.6), where the age measurement errors are ignored. SEV EP and SEV CEP exhibit nearly identical RRMSEs and RelBias for estimating all the model parameters in all simulation scenarios. When the age measurement

errors are small ($\sigma_u = 0.1$), all three methods perform similarly well in estimating L_∞ , k and CV, as measured by their RRMSEs and RelBias. However, when the age measurement errors are not negligible ($\sigma_u = 0.5, 1, 2$), the EP likelihood method shows poor performance with large RRMSEs and RelBias, while the RRMSEs and RelBias remain small for the SEV EP and SEV CEP approaches. Overall, the RRMSEs of the SEV EP and SEV CEP methods for estimating L_∞ , k and CV tend to increase with age measurement error (σ_u) and bin width. However, their RelBias show less variation and trend. When the age measurement error is small to moderate ($\sigma_u = 0.1, 0.5, 1$), it is difficult to estimate σ_u accurately, as indicated by large RRMSEs and RelBias. However, as the age measurement error increases, the RRMSE and RelBias tend to decrease. Despite poor estimation of σ_u at small and moderate age measurement errors, the SEV EP and SEV CEP methods still perform well in estimating the growth model parameters L_∞ , k and CV. Simulation studies for log-normal length-at-age and age measurement error models, detailed in Tables 6.1 – 6.4, reveal consistent findings.

Fig. 3.2 displays the LSAS data, the fitted growth curves, and the true growth curve to illustrate the performance of various methods in estimating growth curves. The LSAS data were generated randomly with a bin size of 2 cm, a commonly used bin size, and a moderate age measurement error of $\sigma_u = 1$. The growth curves estimated using SEV EP (dashed black curve) and SEV CEP (dashed green curve) approaches are nearly identical and almost overlap with the true growth curve (the red curve). This demonstrates that both approaches perform well in estimating the growth curve. However, the EP likelihood method (dashed orange curve) exhibits a notable bias in its estimates when age measurement errors are present, which starkly contrasts the results presented in Fig. 4 of [53]. In that study, the estimated growth curve using the EP likelihood method closely aligned with the true growth

curve in the absence of age measurement errors.

Table 3.3: Relative root mean squared errors (RRMSEs) for vonB parameter estimates from 1000 simulations with length at age 0 fixed at 3 cm, for various length bin sizes and measurement error SDs (σ_u).

σ_u Method	0.1			0.5			1			2		
	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP
RRMSE												
1 cm												
L_∞	1.7	1.7	1.7	1.9	2.1	14.2	2.1	2.1	27.3	2.3	2.3	39.0
k	2.5	2.5	2.5	2.7	2.8	33.4	2.9	2.9	97.4	3.1	3.1	>100
CV	3.7	3.7	3.8	3.9	4.4	47.4	4.3	4.3	94.8	4.7	4.7	>100
σ_u	64.6	64.7	—	25.6	27.2	—	12.4	12.6	—	7.3	7.7	—
2 cm												
L_∞	1.7	1.7	1.7	1.9	2.1	14.6	2.1	2.1	27.5	2.4	2.4	39.1
k	2.5	2.5	2.5	2.9	2.9	34.1	3.2	3.2	99.5	3.4	3.4	>100
CV	3.5	3.6	3.6	3.6	4.3	48.9	4.2	4.2	96.2	4.8	4.8	>100
σ_u	62.7	62.9	—	26.1	27.5	—	12.7	12.7	—	7.3	7.3	—
3 cm												
L_∞	1.8	1.8	1.8	2.0	2.1	14.7	2.2	2.2	27.3	2.5	2.5	38.6
k	2.6	2.6	2.6	3.0	3.0	35.7	3.3	3.3	100.4	3.8	3.8	>100
CV	3.7	3.7	3.7	4.0	4.4	51.4	4.4	4.4	98.2	5.2	6.1	>100
σ_u	66.2	63.6	—	26.7	27.6	—	12.9	12.9	—	7.2	7.5	—
5 cm												
L_∞	1.7	1.7	1.7	2.0	2.3	15.4	2.3	2.3	27.8	2.7	2.8	39.5
k	2.7	2.7	2.6	3.4	3.5	38.5	3.9	3.9	101.2	4.6	4.6	>100
CV	3.6	3.6	3.6	4.3	5.2	55.7	4.7	4.7	100.8	5.7	6.0	>100
σ_u	69.0	67.5	—	27.9	28.8	—	13.5	13.5	—	7.7	7.8	—

Note: >100 are results that are greater than 100% .

Table 3.4: Relative bias (RelBias) for vonB parameter estimates from 1000 simulations with length at age 0 fixed at 3 cm, for various length bin sizes and measurement error SDs (σ_u).

σ_u	0.1			0.5			1			2		
	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP
RelBias												
1 cm												
L_∞	-0.2	-0.2	-0.3	-0.1	-0.2	-13.5	-0.1	-0.1	-26.6	-0.2	-0.2	-38.2
k	0.2	0.2	0.2	0.2	0.2	28.1	0.1	0.1	83.8	0.2	0.1	>100
CV	2.4	2.4	2.5	1.9	2.0	44.7	2.44	2.44	91.8	3.1	3.1	>100
σ_u	-27.0	-27.4	—	21.7	21.1	—	9.3	9.4	—	4.4	4.5	—
2 cm												
L_∞	-0.2	-0.2	-0.3	-0.1	-0.1	-13.9	-0.5	-0.5	-26.7	-0.2	-0.2	-38.3
k	0.2	0.2	0.2	0.2	0.2	29.1	0.0	0.0	85.3	0.1	0.1	>100
CV	2.1	2.1	2.2	1.4	1.6	46.3	2.0	2.0	93.0	2.7	2.7	>100
σ_u	-25.0	-26.8	—	22.7	21.8	—	9.8	9.8	—	4.4	4.4	—
3 cm												
L_∞	-0.1	-0.1	-0.2	0.0	0.0	-14.0	0.0	0.0	-26.5	0.0	0.0	-37.7
k	0.1	0.1	0.2	0.0	0.0	30.4	0.0	0.0	86.5	0.0	0.0	>100
CV	1.8	1.9	2.1	1.0	1.1	48.7	1.5	1.5	95.3	2.3	2.4	>100
σ_u	-18.9	-24.4	—	23.6	23.0	—	10.3	10.3	—	4.6	4.6	—
5 cm												
L_∞	0.0	-0.1	-0.1	0.1	0.1	-14.8	0.1	0.1	-27.1	0.0	0.1	-38.8
k	0.0	0.0	0.1	-0.2	-0.2	32.3	-0.2	-0.2	86.8	0.0	0.0	>100
CV	1.6	1.6	1.9	0.5	0.7	52.6	1.0	1.0	97.6	1.9	1.9	>100
σ_u	-16.3	-18.2	—	24.4	23.7	—	11.2	11.2	—	5.4	5.4	—

Note: >100 are results that are greater than 100% .

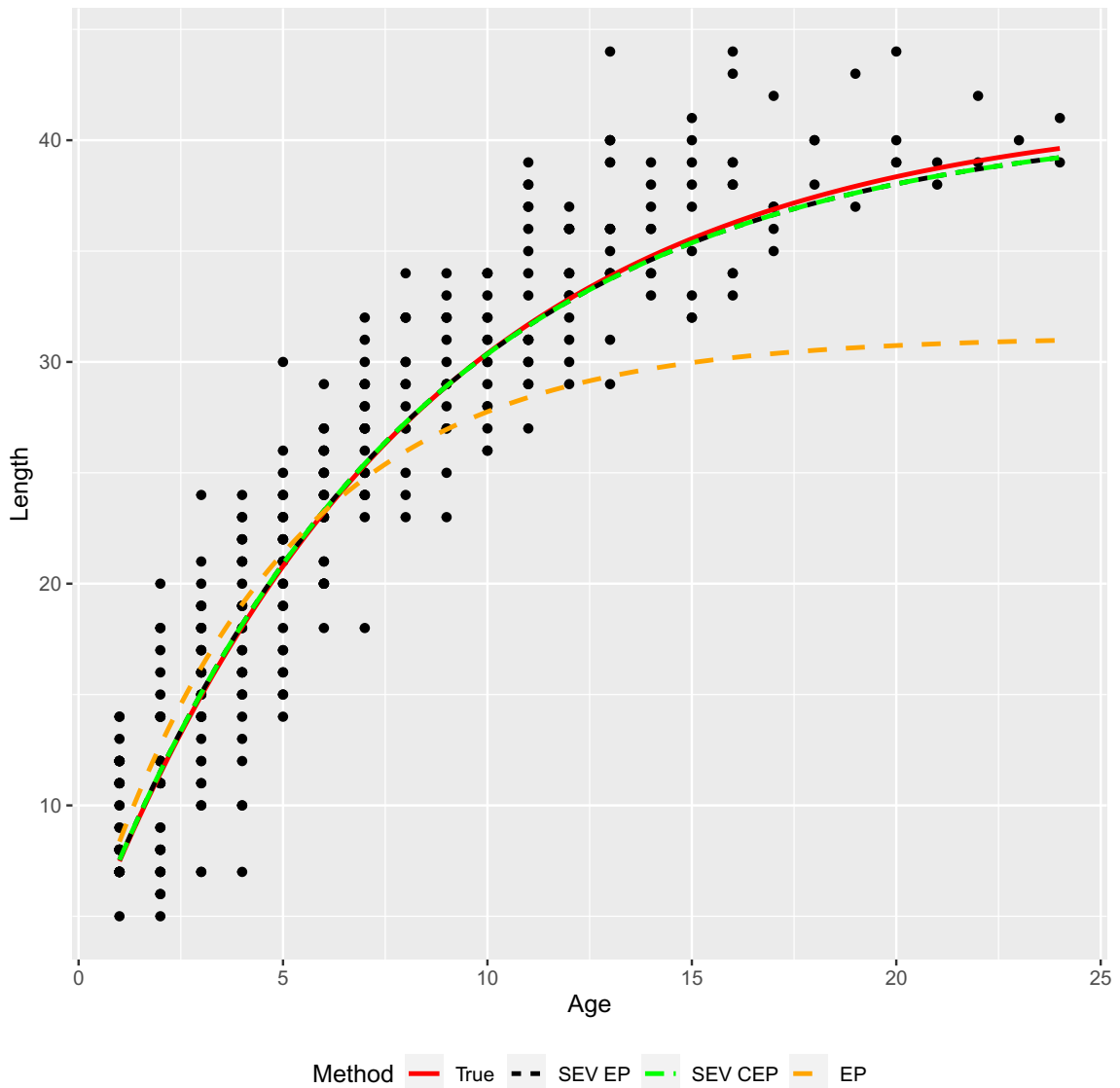


Figure 3.2: Plot of a simulated length-stratified age sampling (LSAS) sample with estimated von Bertalanffy growth models from the sample. The length-at-age data are simulated with length bin size equal to 2 cm and age measurement error standard deviation $\sigma_u = 1$. Points are subtly perturbed in random directions to mitigate overlapping observations. In the legend, “True” indicates the true growth model, “SEV EP” and “SEV CEP” indicate the estimated growth models by maximizing the likelihoods (2.11) and (2.12), respectively, and “EP” indicates the estimated growth model by maximizing the likelihood constructed from density (2.6).

In order to evaluate the performance of the two standard error (SE) estimators described in Sec. 2.3 for the SEV EP and SEV CEP parameter estimators, we conduct simulation studies. To do this, we first set the growth model parameters to $L_\infty = 50, k = 0.30/1.65$ and $CV = 0.1$. Then, we generate an age distribution using the population dynamics simulation, which is also used to examine parameter estimators. With the growth model parameters and age distribution fixed, we randomly generated 500 LSAS data sets for analysis, then applied SEV EP and SEV CEP approaches to each data set and evaluated the resulting two SE estimators separately. As some age categories have little data, the estimates of the corresponding age distribution parameter λ_a in Eq. (2.14) approach the lower bound of $-\infty$, which can result in a singular $A(\hat{\psi})$ in the covariance estimators. To address this issue, we employ Moore-Penrose inverse [52] for $A(\hat{\psi})$. Table 3.5 displays the means of the 500 SE estimates. The BSS and FI SE estimators are based on Eqs. (2.16) and (2.18), respectively. The “True” value represents the SD of the 500 parameter estimates. We conducted this simulation procedure five times. In each simulation, we fixed growth model parameters but randomly generated and then fixed age distribution during the 500 iterations. As a result, Table 3.5 contains five groups of results, separated by horizontal lines. To illustrate the variability among the 500 SE estimates for each parameter and approach, we present their boxplots for a single set of 500 simulation iterations in Fig. 3.3. $\hat{\sigma}_{L_\infty}, \hat{\sigma}_k$ and $\hat{\sigma}_{CV}$ denote the SE estimators for L_∞, k and CV respectively. These results suggest that the BSS SE estimator is fairly accurate, while FI estimator is not as reliable.

Table 3.5: Comparison of standard error (SE) estimators for parameter estimators with true SE values. BSS and FI SE estimators are based on Eqs. (2.16) and (2.18), respectively. Each group of results, separated by horizontal lines, represents a simulation of 500 iterations with $L_\infty = 50, k = 0.30/1.65, CV = 0.1$, and a randomly generated and then fixed age distribution. The “True” SE values refer to the standard deviations of parameter estimates obtained from each set of 500 iterations.

	SEV EP			SEV CEP		
	FI	BSS	True	FI	BSS	True
L_∞	0.87	0.73	0.70	0.87	0.73	0.70
k	0.0054	0.0040	0.0039	0.0054	0.0040	0.0039
CV	0.0031	0.0028	0.0027	0.0031	0.0028	0.0027
L_∞	1.15	1.01	1.01	1.15	1.01	1.01
k	0.0064	0.0052	0.0053	0.0064	0.0052	0.0053
CV	0.0032	0.0028	0.0029	0.0032	0.0028	0.0029
L_∞	1.24	1.08	1.02	1.24	1.08	1.02
k	0.0069	0.0055	0.0053	0.0069	0.0055	0.0053
CV	0.0036	0.0032	0.0032	0.0036	0.0032	0.0032
L_∞	1.11	0.93	0.90	1.11	0.93	0.90
k	0.0065	0.0048	0.0047	0.0065	0.0048	0.0047
CV	0.0041	0.0036	0.0034	0.0041	0.0036	0.0034
L_∞	0.83	0.70	0.68	0.83	0.70	0.68
k	0.0053	0.0041	0.0039	0.0053	0.0041	0.0039
CV	0.0027	0.0023	0.0021	0.0027	0.0023	0.0021

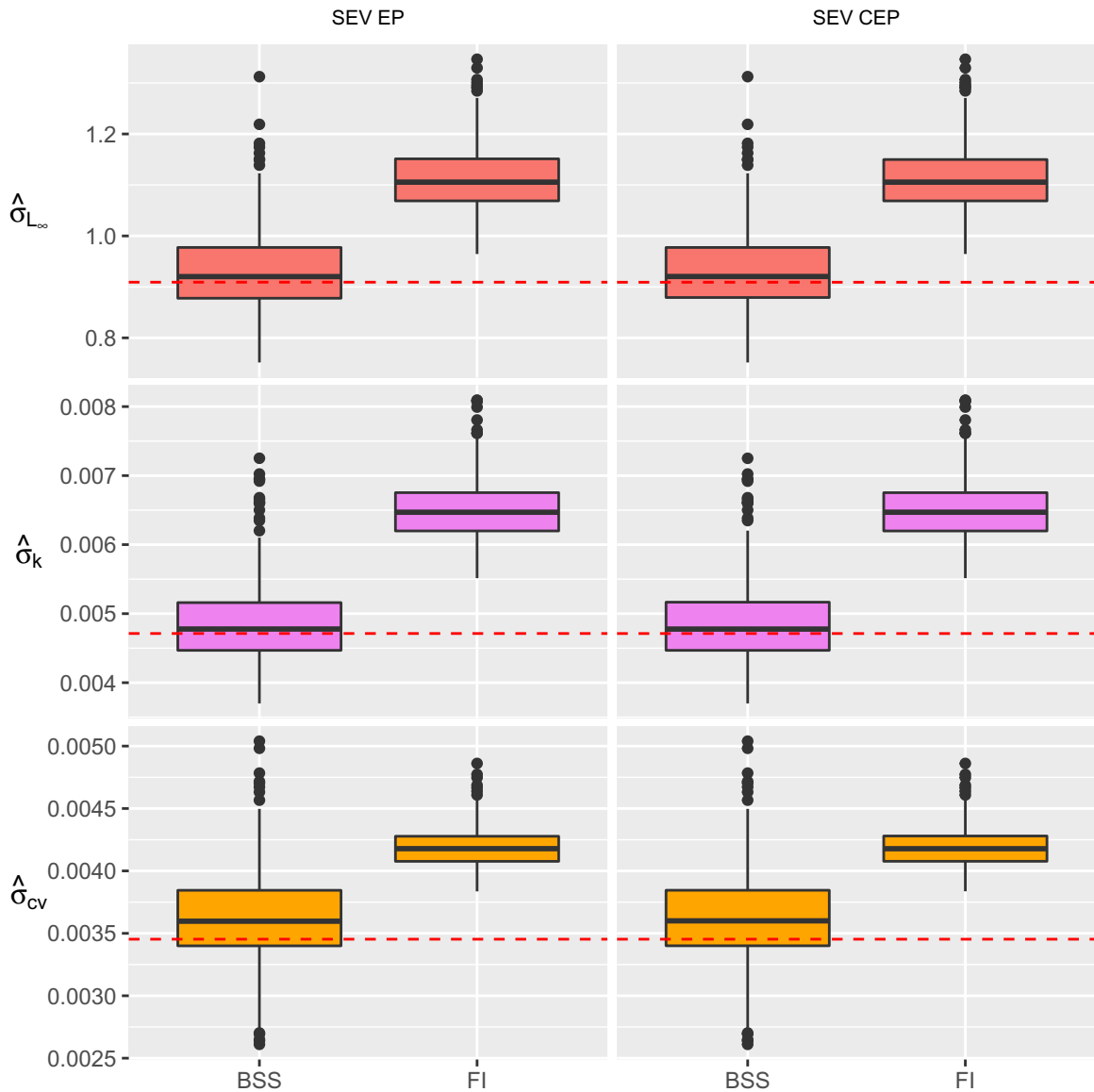


Figure 3.3: Boxplots of the standard error (SE) estimates of parameter estimators for 500 simulated length-at-age data sets generated with $L_\infty = 50$, $k = 0.30/1.65$, $CV = 0.1$, and the age distribution was randomly generated once and then fixed for the 500 simulation iterations. BSS and FI SE estimators are based on Eqs. (2.16) and (2.18), respectively. “SEV EP” and “SEV CEP” refer to the estimators obtained by maximizing the likelihoods (2.11) and (2.12), respectively.

Chapter 4

Real data analysis

To demonstrate the impact of accounting for age measurement errors on growth estimation, we apply the EP and SEV EP methods to estimate vonB growth parameters. We do not include SEV CEP in this real data analysis as it provides almost identical growth model estimation as SEV EP. We use a dataset for female American plaice collected by DFO in Northwest Atlantic Fisheries Organization (NAFO) Divisions 3L, 3N, and 3O for 2012. The data were collected at various sites across each division to ensure spatial representativeness. The sampling goal in each division was to obtain approximately 25 age measurements per 2 cm length stratum by sex if the length was greater than or equal to 10 cm, and about 15 age measurements per stratum without distinguishing sex if the length was less than 10 cm. For simplicity, we assume no spatial variation in fish growth and therefore neglect the spatial structure of the sampling scheme, treating the whole sample in each division as an LSAS sample [see Appendix C of 53]. The total first-phase sample size is 59627, and the second-phase sample size is 942.

To determine the length at age 0, l_0 , we referred to [61] that reported American plaice

larvae to be 0.62–0.75 cm long five days after hatching when yolk absorption is complete. We used the midpoint of this range, which is 0.685 cm, as the value for l_0 .

Since the fall of 1995, the survey gear used by DFO has been the Campelen trawl. We assume a linear logistic model for the trawl selectivity,

$$s(l) = \frac{1}{1 + \exp(-\log(19)[l - l_{50}]/[l_{95} - l_{50}])}, \quad (4.1)$$

where $s(l)$ is the selectivity at length l , and l_{50} and l_{95} are the lengths at which 50% and 95% of fish are retained, respectively. The values of l_{50} and l_{95} were estimated by [81] using 38 years of data and the results of DFO trawl selectivity comparative studies [30, 75]. For this data analysis with only a relatively small sample, we adopt the estimation of [81] that $l_{50} = 11.01$ with SE = 0.049 and $l_{95} = 12.65$ with SE = 0.075.

We continue to use the model (3.1) to determine the population conditional distribution of length given age. However, by incorporating gear selectivity $s(l)$, the sample conditional distribution $f(l|a_t; \boldsymbol{\theta}_g)$ in (2.1) takes on a different form,

$$f(l|a_t; \boldsymbol{\theta}_g) = \frac{s(l)N(l, \mu_a, \sigma_a^2)}{\sum_{l'} s(l')N(l', \mu_a, \sigma_a^2)}, \quad (4.2)$$

which is proven in Appendix B of [81] and utilizes the discretization method outlined in Eq. (3.2).

Table 4.1 displays the estimated growth model parameters and their corresponding SEs obtained through SEV EP and EP methods. The estimated value of $\sigma_u = 0.70$ suggests the presence of age measurement errors. The standardized residuals are assessed using Eqs. (2.20)–(2.21) and visualized in Fig. 4.1. We assume the estimated σ_u of 0.70 as the standard deviation of age measurement errors when evaluating residuals for both methods.

Ideally, the mean of residuals at each age (solid red lines in Fig. 4.1) should be equal to 0, and the standard deviation (SD) of the standardized residuals at each age (dashed red

lines in Fig. 4.1) should be equal to 1 if the model is correct. For SEV EP, the means of the standardized residuals at each age, except ages 2 and 3, follow the zero reference line (green line at 0), and SDs follow the one reference line (green line at 1), indicating a good fit of the model to the data. However, for EP, the residual means deviate from 0 after age 13, suggesting a lack of fit. Both methods show overestimation for ages 2 and 3, which may be attributed to the research gear selectivity and an improper length variability model, as discussed in [81]. Specifically, the misspecification of the length variability model $\sigma_a(\mu_a)$ in (3.1) may result in this pattern in residual plots. To address this issue, [81] proposed a more sophisticated length variability model. However, exploring the length variability model is beyond the scope of this thesis.

Table 4.1: Estimations of growth model (3.1) for female American plaice length-at-age data collected by Fisheries and Oceans Canada (DFO) using length-stratified age sampling in 2012 in NAFO (Northwest Atlantic Fisheries Organization) Divisions 3L, 3N and 3O. The EP likelihood method based on (2.6) and neglecting age measurement errors is denoted by “EP”. “SEV EP” denotes the growth estimation obtained by maximizing likelihood (2.11). The parameter estimates are denoted as “Est.” and their corresponding standard errors are denoted as “SE”. SEs are based on the BSS asymptotic covariance given by Eq. (2.16).

Method	Quantity	L_∞	k	CV	σ_u
SEV EP	Est.	82.30	0.066	0.066	0.70
	SE	1.92	0.0021	0.0030	0.039
EP	Est.	64.62	0.091	0.11	—
	SE	1.17	0.0024	0.0022	—

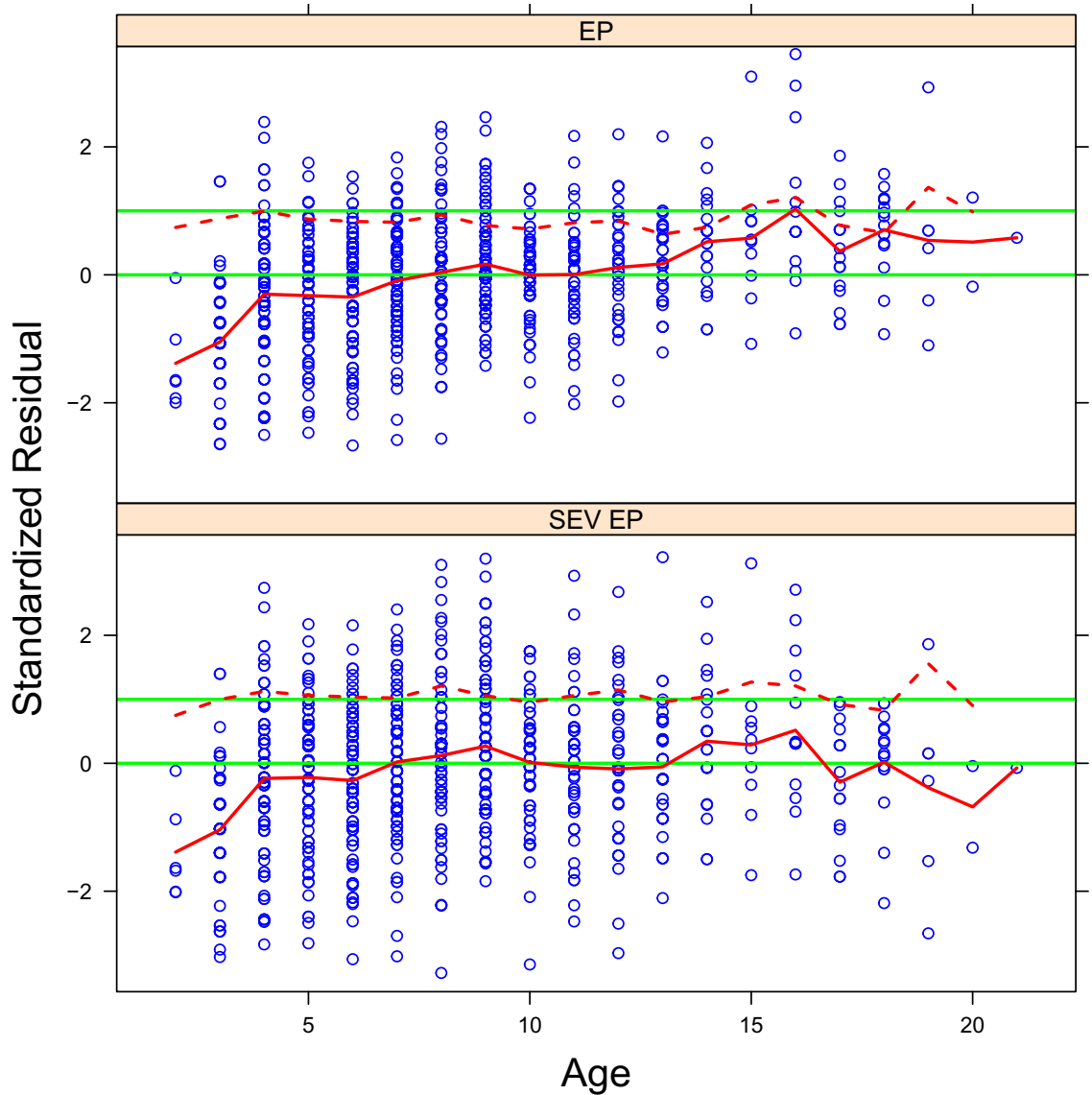


Figure 4.1: Standardized residuals for fitting 3LNO female American plaice growth data using SEV EP (lower panel) and EP (upper panel) methods, as assessed by Eqs. (2.20)–(2.21). Here “EP” refers to the EP likelihood method based on (2.6) and neglecting age measurement errors, while “SEV EP” denotes the growth estimation method achieved by maximizing likelihood (2.11). The points have added transparency to represent the density of the observations better. The solid red lines indicate the residual means at age, while the dashed red lines represent the standard deviations of the residuals at age. The green reference lines are at 0 and 1.

Chapter 5

Discussion

In this work, we developed two methods to estimate growth parameters using fisheries survey data while accounting for length-stratified age sampling (LSAS) design and age measurement errors. These methods are extensions of the empirical proportion (EP) likelihood method [53, 81] for LSAS and the structural errors in variables [SEV; 17] method for covariate measurement errors. The two approaches, which are denoted as “SEV EP” and “SEV CEP”, optimize (2.11) and (2.12), respectively.

Effectively modelling covariate distribution is challenging when dealing with either response-selective sampling design [45] or covariate measurement errors, such as age measurement errors [26]. To address this issue, we treat ages as ordered categorical data (integers) and use the continuation ratio-logit (CRL) model for age distribution. This approach aligns with the limitation that fish ages can only be determined in years and effectively handles the wild variation, multiple modes, and significant skewness present in the true population age distribution. As a random sample can be considered a special case of LSAS when the second phase subsample size within each length stratum is significantly large, the

impressive performance of CRL for LSAS data implies its appropriateness in modelling age distribution while dealing with age measurement errors for a random length-at-age sample, for which we suggest further studies.

To accelerate the evaluation of the inclusion probabilities $Q_j(\boldsymbol{\theta})$ and $Q_j^*(a_t; \boldsymbol{\theta}_g)$ defined in (2.2) and (2.3) respectively, we applied a discretized normal distribution (3.2) for length distribution modeling. This approach converts integration over length into summation and is consistent with the fact that fish lengths are commonly recorded as integers in practice. To optimize the algorithm for implementing the proposed approaches, it is crucial to minimize or avoid duplicated evaluations, particularly those of the inclusion probabilities $Q_j(\boldsymbol{\theta})$ and $Q_j^*(a_t; \boldsymbol{\theta}_g)$. The codes provided along with this thesis can demonstrate my efforts in this regard.

The simulation results indicate that inadequate consideration of age measurement errors can severely bias growth model estimations, even when using inferential methods that have been proven optimal under the assumption of negligible age measurement errors. A notable advantage of the proposed SEV EP and SEV CEP methods is their ability to perform well regardless of the presence or magnitude of age measurement errors. Although the estimation of σ_u , the standard deviation of age measurement errors, may not be precise when σ_u is small, it does not affect the accurate estimation of growth model parameters using the SEV EP and SEV CEP methods. We also believe that the σ_u estimates produced by these methods can still be useful in identifying the presence or magnitude of age measurement errors. This information can be valuable in monitoring and improving age measurements. Further exploration of this topic is left for future research.

This thesis aims to develop a general methodological framework for accounting for age measurement errors in LSAS data. In addition to the discretized normal age mea-

surement error model used in this thesis, my methodology can also incorporate other age measurement error models, such as the symmetrical geometric model of [22], asymmetrical two-sided geometric model of [33], and continuation ratios model of [15]. However, my focus is not on investigating a comprehensive age measurement error model that can accommodate bias, asymmetry, and skewness in age measurement errors or the impact of incorrectly specifying age measurement errors. These topics will be explored in future research.

The simulation and case studies suggest using the BSS asymptotic covariance estimator (2.16) and the standardized residual estimators proposed in Eqs. (2.20)–(2.21) for measuring uncertainty in parameter estimates and validating model fittings, respectively.

Chapter 6

Appendix

6.1 Simulation results for log-normal growth model

The simulations in Tables 6.1 – 6.2 replicated the thesis’s specifications and procedures, deviating solely in the growth model presented in Eq. 3.1. While Eq. 3.1 in the original model adopts a normal distribution for length-at-age with a mean of μ_a and a standard deviation of $\mu_a CV$, the revised version here employs a log-normal model with a median of μ_a and a coefficient of variation set to CV .

Table 6.1: Relative root mean squared error (RRMSE) for von Bertalanffy growth model parameter estimates from 1000 simulation iterations. Log-normal model is used for length-at-age. The length at age 0 was fixed at 3 cm. The simulation study considered different length bin sizes indicated with “cm” in the first column and various age measurement error standard deviations (σ_u) indicated in the first row.

σ_u	0.1			0.5			1			2		
Method	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP
RRMSE												
1 cm												
L_∞	1.8	1.8	1.8	2.0	2.0	13.5	2.3	2.3	28.8	2.6	2.7	45.9
k	2.4	2.4	2.4	2.8	2.8	30.1	3.2	3.2	96.0	3.5	3.6	>100
CV	4.1	4.1	4.1	4.4	4.6	44.7	4.9	5.2	95.4	5.8	6.3	>100
σ_u	58.4	58.2	—	25.1	25.7	—	12.4	12.7	—	7.6	7.7	—
2 cm												
L_∞	1.9	1.9	1.9	2.2	2.3	13.8	2.5	2.5	29.2	3.0	3.0	46.5
k	2.8	2.8	2.9	3.2	3.2	30.6	3.6	3.6	96.3	4.2	4.5	> 100
CV	3.7	3.8	3.8	4.0	4.5	47.3	4.5	4.5	97.8	5.5	5.9	> 100
σ_u	60.1	61.4	—	26.4	27.4	—	12.7	12.7	—	7.5	7.5	—
3 cm												
L_∞	1.9	1.9	1.9	2.2	2.3	14.0	2.7	2.7	29.2	3.1	3.1	46.5
k	2.7	2.7	2.7	3.3	3.3	31.3	3.8	3.8	94.4	4.7	4.4	>100
CV	3.7	3.7	3.8	4.5	4.8	50.1	4.7	4.7	>100	6.2	6.1	>100
σ_u	61.1	60.1	—	26.9	27.8	—	13.1	13.1	—	7.6	7.9	—
5 cm												
L_∞	1.9	1.9	1.9	2.2	2.4	14.6	2.5	2.5	29.5	3.0	3.1	47.5
k	2.9	2.9	2.9	3.3	3.3	31.0	3.8	3.8	90.7	4.5	4.5	>100
CV	4.0	4.0	4.0	4.4	5.5	56.5	5.1	5.1	>100	6.1	6.4	>100
σ_u	62.7	61.2	—	27.1	28.1	—	12.9	12.9	—	7.4	7.5	—

Note: >100 are results that are greater than 100% .

Table 6.2: Relative bias (RelBias) for von Bertalanffy growth model parameter estimates from 1000 simulation iterations. Log-normal model is used for length-at-age. The length at age 0 was fixed at 3 cm. The simulation study considered different length bin sizes indicated with “cm” in the first column and various age measurement error standard deviations (σ_u) indicated in the first row.

σ_u	0.1			0.5			1			2		
Method	SEV	EP	CEP	SEV	EP	CEP	SEV	EP	CEP	SEV	EP	CEP
RelBias												
1 cm												
L_∞	0.0	0.0	0.0	0.0	0.0	-12.7	0.0	0.0	-27.9	-0.1	-0.1	-44.8
k	-0.1	-0.1	-0.1	-0.1	-0.1	24.6	-0.4	-0.4	79.7	-0.2	-0.2	>100
CV	2.7	2.7	2.8	2.5	2.6	42.7	2.9	2.9	92.7	3.8	3.9	>100
σ_u	-31.1	-32.6	—	20.8	20.5	—	9.0	8.9	—	4.2	4.2	—
2 cm												
L_∞	0.0	0.0	0.0	0.1	0.1	-13.0	0.1	0.1	-28.2	0.0	0.0	-45.5
k	-0.2	-0.2	-0.1	-0.3	-0.2	25.1	-0.4	-0.4	80.2	0.0	-0.1	>100
CV	2.2	2.3	2.4	1.7	1.8	45.2	2.1	2.1	95.3	3.0	3.1	>100
σ_u	-27.3	-32.3	—	22.7	22.0	—	9.9	9.9	—	4.5	4.5	—
3 cm												
L_∞	0.0	0.0	0.0	0.3	0.2	-13.2	0.3	0.3	-28.2	0.0	0.1	-45.5
k	-0.1	-0.1	-0.1	-0.4	-0.4	25.4	-0.5	-0.5	78.3	-0.2	-0.3	>100
CV	2.0	2.0	2.1	1.2	1.3	47.8	1.5	1.5	97.8	2.4	2.4	>100
σ_u	-24.6	-28.0	—	23.3	22.6	—	10.5	10.5	—	4.9	5.0	—
5 cm												
L_∞	0.0	0.0	0.0	0.3	0.3	-13.8	0.3	0.3	-28.5	0.1	0.1	-46.6
k	-0.3	-0.3	-0.2	-0.6	-0.6	24.7	-0.6	-0.6	73.7	-0.3	-0.3	>100
CV	1.8	1.8	2.0	0.8	1.0	53.5	1.2	1.3	>100	2.1	2.1	>100
σ_u	-25.6	-27.8	—	24.0	23.3	—	10.4	10.4	—	4.9	4.9	—

Note: >100 are results that are greater than 100% .

6.2 Simulation results for log-normal growth and age measurement error models

The simulation analysis presented in Tables 6.3 – 6.4 maintains the log-normal model for length-at-age as that of Tables 6.1 – 6.2 but incorporates a log-normal model for age measurement errors. Specifically, the relationship between observed age a and true age a_t is defined as $a = a_t e^{\varepsilon_a}$ rounded to the nearest positive integer, where ε_a follows a normal distribution with mean 0 and standard deviation σ_u . σ_u values exceeding 0.5 yield unrealistically large age measurement errors and are therefore excluded from consideration. All other specifications and procedures align with those outlined in the thesis.

Table 6.3: Relative root mean squared error (RRMSE) for von Bertalanffy growth model parameter estimates from 1000 simulation iterations. Log-normal model is used for both length-at-age and age measurement error. The length at age 0 was fixed at 3 cm. The simulation study considered different length bin sizes indicated with “cm” in the first column and various σ_u 's for age measurement error indicated in the first row.

σ_u	0.1			0.3			0.5		
Method	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP
RRMSE									
1 cm									
L_∞	2.6	2.6	4.5	3.6	3.6	25.4	3.9	3.9	37.9
k	3.3	3.2	5.7	5.3	5.3	64.7	6.6	6.6	>100
CV	6.7	6.5	12.5	7.2	7.2	74.6	7.1	7.1	>100
σ_u	35.4	32.4	—	14.9	14.8	—	12.6	12.6	—
2 cm									
L_∞	2.7	2.7	4.5	3.8	3.8	25.4	4.0	4.0	38.6
k	3.8	3.8	6.1	5.8	5.8	64.5	6.9	6.9	>100
CV	6.3	6.5	12.7	7.4	7.4	75.1	6.8	6.8	>100
σ_u	36.6	36.2	—	15.7	15.6	—	12.9	12.9	—
3 cm									
L_∞	2.7	2.6	4.6	3.7	3.7	25.5	4.0	4.0	38.4
k	3.6	3.6	6.4	5.8	6.6	63.8	6.5	6.5	>100
CV	6.2	6.1	13.7	6.9	6.9	76.2	6.6	6.6	>100
σ_u	34.1	32.5	—	15.6	16.9	—	13.1	13.1	—
5 cm									
L_∞	2.7	2.7	4.7	3.7	3.6	25.7	4.1	4.1	38.8
k	3.7	3.7	6.4	5.4	5.4	61.7	7.0	7.0	160.9
CV	6.5	6.3	14.8	7.1	7.1	80.5	6.8	6.8	133.4
σ_u	33.7	31.7	—	15.7	15.7	—	13.6	13.6	—

Note: >100 are results that are greater than 100% .

Table 6.4: Relative bias (RelBias) for von Bertalanffy growth model parameter estimates from 1000 simulation iterations. Log-normal model is used for both length-at-age and age measurement error. The length at age 0 was fixed at 3 cm. The simulation study considered different length bin sizes indicated with “cm” in the first column and various σ_u 's for age measurement error indicated in the first row.

σ_u	0.1			0.3			0.5		
Method	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP	SEV EP	SEV CEP	EP
RelBias									
1 cm									
L_∞	-1.1	-1.1	-3.7	-1.1	-1.1	-24.5	-0.7	-0.7	-36.8
k	1.2	1.1	4.8	1.7	1.7	61.1	1.6	1.6	>100
CV	5.0	4.9	11.0	5.0	5.0	72.2	5.0	5.0	>100
σ_u	-20.1	-18.4	—	11.2	11.1	—	10.7	10.7	—
2 cm									
L_∞	-1.1	-1.1	-3.8	-1.1	-1.1	-24.6	-0.6	-0.6	-37.6
k	1.3	1.3	5.1	1.7	1.7	60.8	1.4	1.4	>100
CV	4.5	4.6	11.1	4.5	4.5	73.0	4.4	4.4	>100
σ_u	-20.5	-20.2	—	12.1	12.1	—	11.2	11.2	—
3 cm									
L_∞	-1.0	-1.0	-4.0	-0.7	-0.7	-24.6	-0.1	-0.1	-37.3
k	1.2	1.2	5.5	1.3	1.2	60.0	0.8	0.8	>100
CV	4.2	4.2	12.0	3.5	3.5	74.2	3.3	3.4	>100
σ_u	-18.4	-17.5	—	12.6	12.8	—	11.5	11.5	—
5 cm									
L_∞	-0.9	-0.9	-4.0	-0.2	-0.2	-24.9	0.1	0.1	-37.9
k	1.0	1.0	5.4	0.4	0.5	57.5	0.3	0.3	>100
CV	4.2	4.1	12.8	2.6	2.6	78.1	2.7	2.7	>100
σ_u	-18.4	-17.3	—	13.0	13.0	—	12.2	12.2	—

Note: >100 are results that are greater than 100% .

6.3 Summary figure for Tables 3.3 – 3.4

In the simulation results detailed in Tables 3.3 – 3.4, diverse methods exhibit consistent trends in the variations of Relative Root Mean Squared Error (RRMSE) and Relative Bias (RelBias) vs the age measurement error standard deviation (σ_u) across different growth model parameters (L_∞, k, CV), and various length bin sizes. This shared trend is illustrated by plotting RRMSE and RelBias against σ_u specifically for L_∞ and the 1cm length bin in Fig. 6.1.

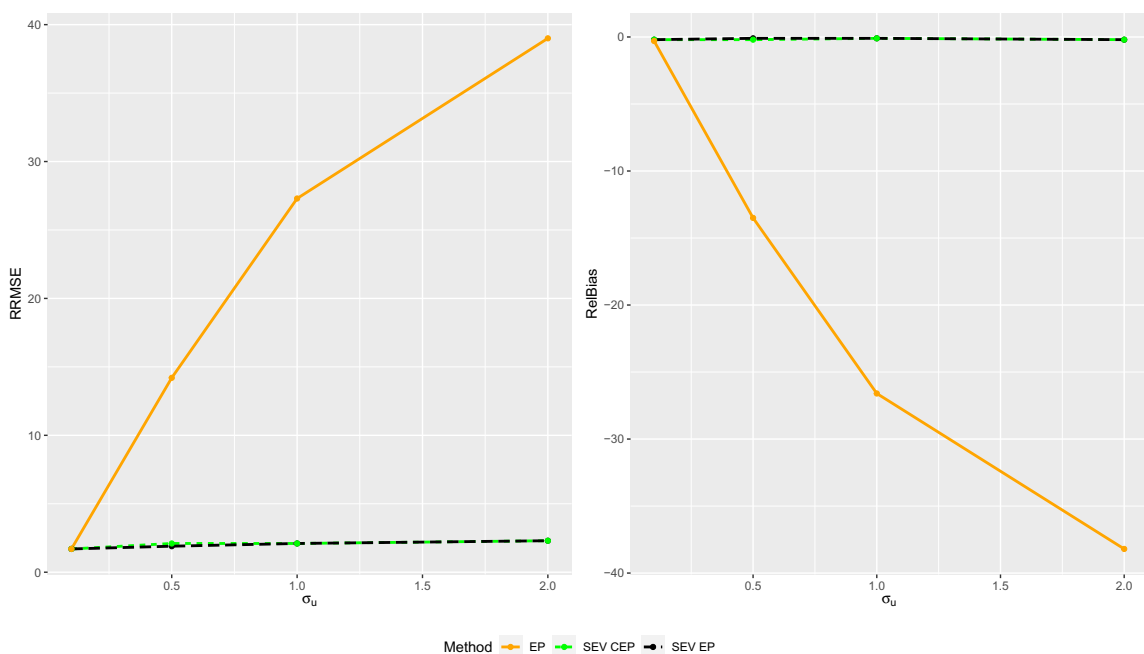


Figure 6.1: Comparisons of relative root mean squared errors (RRMSEs) and relative bias (RelBias) against the age measurement error standard deviation (σ_u) in the simulation results corresponding to L_∞ and the 1cm length bin, as presented in Tables 3.3 – 3.4.

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