

SUBMITTED MANUSCRIPT (UNDER REVIEW):

Robust estimation of fish life history parameters from unfished populations

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Abstract

Asymptotic length (L_{∞}) and the ratio of natural mortality to the von Bertalanffy growth coefficient (M/K) underpin fish population dynamics and are central in data-poor stock assessments. These parameters are traditionally generated from length–age keys, mark–recapture studies, or inferred from other life-history traits, yet remain unknown for about 80% of fished species. Because M/K and L_{∞} shape the length distribution of unexploited populations, they should be estimable directly from unfished length distribution. Until recently this was impractical, as most length data came from exploited stocks; however, the rapid growth of diver and camera-based visual surveys now provides thousands of length observations from largely unfished populations. Using simulations, we identified conditions under which direct estimation of M/K and L_{∞} , together with two observational selectivity parameters, is feasible for such fish observation datasets. Parameter estimation was done using a modified widely used length-based assessment model LB-SPR. Our simulation scenarios spanned diverse life-history parameters and realistic sampling regimes with varying selectivity, length binning, and sample sizes. We showed that the model produced unbiased M/K and L_{∞} estimates (<15% and <10% biases respectively) for populations with both continuous and pulsed recruitment, provided the coefficient of variation in length-at-age was specified accurately, length distribution spanned >10 length bins and samples included >500 individuals. The parameter estimation approach presented here enabled reliable estimation of life-history parameters for hundreds of diverse fish species and populations distributed across environmental gradients.

Keywords: data-poor, LB-SPR, life history, population dynamics, stock assessment, underwater survey

Highlights

- Growth and mortality parameters are essential but unknown for most species
- A new method is presented to estimate these parameters from length observations
- Life-history parameters can now be estimated for hundreds of fish populations
- The new method can be used with AI-assisted and citizen science data collections

1. Introduction

Population dynamics of fish are governed by three main processes: growth, mortality, and recruitment (Quinn II and Deriso 1999, Andersen 2020a). Understanding these processes and estimating their associated parameters is an essential component of fisheries research and stock assessment (Allen and Hightower 2010, Sparre and Venema 1998). In the absence of strong environmental variation, the abundance of an unexploited fish population is expected to stabilize at its ecological carrying capacity with recruitment staying relatively constant (Andersen 2020a). Consequently, it is often assumed that for stable populations length structure is predominantly determined and shaped by growth and natural mortality parameters (Hordyk et al. 2015a).

In fisheries models, individual growth is typically modelled using the von Bertalanffy growth function (VBGF) characterized by three parameters - asymptotic length (L_{∞}), the growth coefficient (K), and theoretical age at zero length (a_0). These VBGF parameters have been traditionally estimated from aging studies using otoliths, vertebrae, or spines, but such studies cover only a fraction of fish species, are expensive, and sometimes produce biased estimates due to limited sampling of fish across all age groups (Green et al. 2009, Goldman 2005, Prince, Wilcox and Hall 2023). Likewise, natural mortality, represented by its instantaneous rate per year (M), can be estimated from mark-recapture studies or catch at age data (Maunder et al. 2023, Thorson et al. 2017, Bowlby et al. 2021), however, these methods are also costly and can be imprecise. Consequently, M is often inferred through correlations with other life history (LH) parameters (e.g., maximum age, asymptotic length, and growth coefficient), or environmental conditions (Pauly 1980, Hoenig 1983, Then et al. 2014, Hamel 2014, Dureuil et al. 2021) and is usually modelled as a constant, independent of fish age, length, and time (Maunder et al. 2023, Kai, Yokoi and Fujinami 2023). Despite its critical role in population assessments, M remains one of the most uncertain parameters within fisheries models (Maunder et al. 2023, Miethe, Reece and Dobby 2019, Thorson et al. 2017, Kai et al. 2023).

It has been shown that population length distributions under equilibrium conditions are determined not by the individual parameters M and K , but by their ratio M/K , with L_{∞} serving as a scaling factor (Prince et al. 2014, Hordyk et al. 2015b, Hordyk et al. 2016). Conveniently, M/K ratio varies less among species than the individual M and K values (Prince et al. 2014, Hordyk et al. 2015b, Froese et al. 2018). Recent efforts to estimate M/K values for various fish species include correlative analysis while accounting for evolutionary relatedness (Thorson et al. 2017), as well as compilations of empirically estimated growth rates and maximum age-based natural mortality inferences (Prince et al. 2023). Yet, despite extensive work, validated estimates are available only for a few hundred fish species. Moreover, given that LH parameters are likely to be affected by temperature and other environmental conditions, it is likely that M/K and L_{∞} should be estimated at a local population level (Prince et al. 2023, Audzijonyte et al. 2020). This presents an even bigger challenge to obtain accurate

estimates using traditional approaches. Alternative methods are needed to improve the availability of LH parameters across diverse fish species. One such method could be statistical parameter estimation from unfished population length frequencies.

The use of length data to infer LH (e.g., growth) and fisheries (e.g., fishing mortality rate) parameters is a well-established practice in fisheries science (Gulland and Rosenberg 1992, Andersen 2020b). However, the existing approaches either rely on length compositions derived from catch or focus on evaluating the impacts of fishing to populations (Hordyk et al. 2015a, Froese et al. 2018, Beverton and Holt 1956, Pauly 1983, Pauly and David 1980, Taylor and Mildenerberger 2017). Among these approaches, length-based, data-poor stock assessment methods typically estimate fisheries-related parameters, using the length composition from catches, and *a priori* estimates of LH parameters (e.g., M/K and L_{∞}). Yet, by removing the fishing component, these methods could, in theory, be adapted to estimate LH parameters from length composition data of unfished populations. Such length composition data is now available through rapid accumulation of diver and camera operated visual surveys (e.g., Edgar and Stuart-Smith 2014). These datasets include hundreds of fish species with diverse LH and represent thousands of populations from around the globe. Importantly, many of the surveyed fish species are not subject to fishing pressure, providing an opportunity to apply length-based methods to estimate LH parameters. Ultimately, having better estimates of LH parameters will help subsequent assessments of fished populations.

In this study, we introduce a modified version of the length-based spawning potential ratio method (LB-SPR, Hordyk et al. 2015a, Hordyk et al. 2015b), with the focus on LH parameter estimation in unfished populations. Fitting is performed using Bayesian methods and the performance is tested using simulated datasets with realistic sampling regimes. Our analysis focuses on identifying conditions that will affect the estimation accuracy and precision of the method, and we offer recommendations for applying this approach to real-world datasets.

2. Materials and methods

To develop the method to estimate LH parameters, we modified the LB-SPR method introduced by Hordyk et al. (2015a) and tested the performance of the newly developed method using a range of simulated datasets, across various LH and sampling conditions. LB-SPR applies user-provided LH (M/K and L_{∞}) parameters to estimate fishing mortality, fisheries selectivity, and spawner potential ratio using length composition data from catch. In contrast, our LH estimation method removes the fishing component of the model and estimates M/K and L_{∞} and two observation selectivity parameters (length at 50% and 95% observed in logistic function) using length composition samples from unfished populations.

2.1. Model structure of our LH estimation method

Our LH estimation method assumes an unfished population with a stationary age distribution, which in turn yields a stationary length distribution. Stationarity arises from the model assumption of constant and continuous recruitment, age-invariant natural mortality, and time-invariant growth parameters. Growth is described by the VBGF model.

A constant natural mortality implies an exponentially declining abundance with age. Just like in LB-SPR, our model tracks individuals to a maximum age (a_{\max}), by discretising lifespan into X equally spaced age classes of arbitrary time length, $x = 0, 1, \dots, X - 1$. The annual natural mortality rate (M) is replaced by a generic natural mortality rate (\dot{M}) expressed in the same time unit as x . We obtain \dot{M} from the assumed number of cohorts X and the cohort survivorship at a_{\max} , denoted ε , which allows age and length distribution to be modelled without specifying the true M and a_{\max} .

The relative abundance at age x satisfies the following equation:

$$\dot{N}_x = e^{-\dot{M}x} \quad (1)$$

Note that the recruitment rate is arbitrarily set to 1, because the model uses relative abundances.

Age distribution is then converted to length distribution facilitated by VBGF model. In this VBGF model, we set the theoretical age at zero length (a_0) to 0 (Table 1; see also Hordyk et al. 2015a to see why this assumption is necessary) and treat L_∞ as the population mean asymptotic length. Asymptotic length for individual fish is normally distributed around L_∞ with coefficient of variation CV . These lead to a growth equation parameterized by L_∞ and M/K :

$$L_x = L_\infty \left(1 - \varepsilon^{\frac{x}{M/K(X-1)}} \right) \quad (2)$$

with L_x the population mean length at age x and that individual length at age (l_x) is also normally distributed about the mean L_x and coefficient of variation CV :

$$l_x \sim \text{Normal}(L_x, (CV L_x)^2). \quad (3)$$

In practice, lengths are usually allocated to length bins which partition the length range of individuals and have either equal or varying bin widths. Combining (1) to (3), the relative abundances in ages can be transformed to relative abundances in length bins. Specifically, suppose there are J length bins, where the j^{th} bin is bounded by lengths l_{j-1} and l_j . The relative abundance of fish expected to be associated with j^{th} length bin (\dot{N}_j) is given by:

$$\dot{N}_j = \begin{cases} \sum_{x=0}^{X-1} \dot{N}_x \Phi\left(\frac{l_j - L_x}{CV L_x}\right), & \text{if } j = 1; \\ \sum_{x=0}^{X-1} \dot{N}_x \left(\Phi\left(\frac{l_j - L_x}{CV L_x}\right) - \Phi\left(\frac{l_{j-1} - L_x}{CV L_x}\right) \right), & \text{if } 1 < j < J; \\ \sum_{x=0}^{X-1} \dot{N}_x \left(1 - \Phi\left(\frac{l_j - L_x}{CV L_x}\right) \right), & \text{if } j = J \end{cases} \quad (4)$$

where Φ is the cumulative probability density function of the standard normal distribution.

The proportion of fish observed in j^{th} length bin (\tilde{N}_j^o) will differ from the expected proportion ($\tilde{N}_j / \sum_{j=1}^J \tilde{N}_j$) if the probability of observing fish (observation selectivity) is affected by their length. Usually, smaller fish are more difficult to observe than larger fish. Therefore, similar as with fishing selectivity in LB-SPR, we model observation selectivity with a logistic function defined by parameters L_{50} and L_{95} , representing the lengths at which fish have 50% and 95% chances of being observed. For the j^{th} length bin with midpoint $\frac{l_{j-1}+l_j}{2}$, selectivity (s_j) is given by:

$$s_j = \left(1 + \exp \left(-\frac{\ln 19}{L_{95}-L_{50}} \left(\frac{l_{j-1}+l_j}{2} - L_{50} \right) \right) \right)^{-1}. \quad (5)$$

Given this length-dependent selectivity, the expected proportion of fish observed in the j^{th} length bin is given by:

$$\tilde{N}_j = \frac{s_j \tilde{N}_j}{\sum_{j=1}^J s_j \tilde{N}_j} \quad (6)$$

We used $X = 200$ age classes to balance a good approximation to continuous recruitment with computational efficiency. Consistent with LB-SPR, our LH estimation method assumes that 1% of fish survive to the maximum age ($\varepsilon = 0.01$) and that coefficient of variation of l_x is 10% ($CV = 0.1$) (Table 1). We examined sensitivity to ε and CV as well as to a_0 in the simulations. More complete description of the model structure of our LH estimation method is provided in Supplementary Materials.

2.2. Parameter estimation

Our LH estimation method uses length composition sample provided by the user and assumptions described above, to estimate four parameters. The model requires a dataset where the lengths of N fish are assigned to J length bins and N_j^o is the number of fish observed in each of the j^{th} length bin ($N = \sum_{j=1}^J N_j^o$). We expect proportion \tilde{N}_j to be associated with j^{th} length bin. Given counts across multiple length bins, our LH estimation method will estimate four parameters: $\theta = \{M/K, L_{\infty}, L_{50}, L_{95}\}$ using Bayesian method that fits the expected and observed proportions of fish in each length bin. Observed fish counts are assumed to follow a Dirichlet-multinomial distribution. This distribution allows for overdispersion of observational data compared to a Multinomial distribution, that would normally be used to model observed fish proportions across length bins. The overdispersion arises because in practice fish are sampled non-independently, leading to greater variation in the observed proportions \tilde{N}_j^o compared to the expected proportions \tilde{N}_j . Non-independence may arise from samples being collected at multiple times or across multiple locations. Additional variation may also arise because the model does not fully describe the processes that generate the length frequency data in natural populations.

The Dirichlet-multinomial distribution requires the estimation of an additional positive parameter, θ_0 , that quantifies the level of overdispersion. Therefore, the likelihood function of the model parameters given the data can be written as:

$$L(\theta, \theta_0 | N_1^o \dots N_J^o) = \frac{\Gamma(\theta_0)\Gamma(N+1)}{\Gamma(\theta_0+N)} \times \prod_{j=1}^J \frac{\Gamma(\theta_0 \tilde{N}_j + N_j^o)}{\Gamma(\theta_0 \tilde{N}_j) \Gamma(N_j^o + 1)}. \quad (7)$$

Bayesian analysis was implemented using the *rstan* package (Stan Development Team 2024), which applies Hamiltonian Monte-Carlo (HMC) algorithms. Estimations were conducted using one chain with 3,000 posterior samples and 500 burn-in samples to be discarded from the final posterior estimates. Full details of parameter estimation procedure are provided in Supplementary Materials.

2.3. Data-generating model

To evaluate the performance of our LH estimation method and its sensitivity to violations of underlying assumptions, we used a simulation-estimation procedure. Data-generating models (DGMs) were developed to simulate length composition samples from unfished populations across a range of LH and sampling parameters (Fig. 1, Table 2). The simulated data were then fed to the estimation model (EM; i.e., our LH estimation method) that returns the estimates of two LH (M/K and L_∞) and two observation selectivity (L_{50} and L_{95}) parameters. To assess the sensitivity of parameter estimates to the violation of the assumed continuous recruitment, DGMs incorporated both continuous and pulsed (annual) recruitment. A summary of these DGMs is provided below, with methodological details available in Supplementary Materials.

Briefly, the continuous-recruitment DGM shared the same assumptions as the EM, except that a_0 of the VBGF was not always fixed at zero. As in the EM, the DGM generated length composition sample from age structure defined in X equally spaced classes where we set $X = 1,000$ to obtain smooth length distributions. In the DGM, age (a) was defined in years, instead of arbitrary unit as in the EM. The relative numbers of fish at each age were computed assuming a particular value of annual instantaneous mortality rate M . The M was set to an arbitrary value of 0.3 year^{-1} , but this value does not affect results since length distributions are largely determined by M/K , rather than on M and K individually. The exception occurs when a_0 is not 0 (see Hordyk et al. 2015b), which we examined in sensitivity analyses. From this, length at age was computed using the original VBGF equation parameterized by K , L_∞ and a_0 , with K obtained from the target M/K and $M = 0.3$.

Both EM and DGMs produce length compositions, but the length binning differs. The EM binned lengths directly into observational length bins, either equal or variable in width (see below). In contrast, DGMs first binned the simulated data into 0.5 cm equal-width bins, to represent “true population length structure”. This length structure was then randomly sampled using the specified sampling parameters (Table 2), and then re-binned into the observational length bins.

The pulsed-recruitment DGM assumed recruitment occurred only for three months each year (February-April), altering age structure relative to continuous recruitment. In this pulsed-recruitment DGM, we used the same $X \approx 1,000$ time steps, but the effective number of populated age groups was considerably smaller because most time steps lacked recruits. Once the age structure was established, length composition was generated in the same manner as with continuous-recruitment DGM.

2.4. Simulations and evaluations

Fig. 1 outlines the general structure of simulations, with parameters listed in Table 2. In the base simulations, we explored the ability of the EM to estimate LH and selectivity parameters from populations characterized by M/K values of 0.5, 1.0, 1.5, 2.3, and 3.5. These values span most empirical estimates of M/K ratios (Prince et al. 2023) and were also used in previous studies (Prince et al. 2014, Hordyk et al. 2015a, Prince et al. 2023). In the base simulations, we assumed continuous recruitment, $a_0 = 0$, $\varepsilon = 0.01$, $CV = 0.1$, i.e. the same as in the EM. We also assumed L_∞ of 40 cm, a common maximum length of fish observed in coastal rocky and coral reefs (Audzijonyte et al. 2020). For each of the five M/K scenarios, the true population length distribution in I bins $\{N_1^o, \dots, N_I^o\}$ was sampled 10 times with a sample size (N) of 5,000 length observations per sample, using observation selectivity parameters of $L_{50} = 5$ cm and $L_{95} = 7.5$ cm (representative of underwater visual surveys, Ackerman and Bellwood 2000). Sampled fish lengths were then re-binned into J length bins (in base scenario resulting in 2 cm equally spaced bins), representing the observed length distribution.

First, we tested the sensitivity of the EM to violations of assumptions about LH parameters a_0 , ε , and CV . The a_0 , specifying fish length at zero age (L_0) and assumed to be 0 in the EM, was varied from 0 to 20% of L_∞ ($L_0 = 0$ to 8 cm as $L_\infty = 40$ cm) in the DGMs. For ε , which was set to 1% in the EM, we explored values ranging from 0.1% to 2%. Finally, we simulated data using CV values ranging from 0.05 to 0.2 (0.1 in the EM). Since we found that violation of CV assumption strongly affected parameter estimates, we also explored whether estimates can be improved when EM assumed different CV values (0.05 to 0.2).

Second, we explored how observation selectivity might affect accuracy and precision of LH parameter estimation. For each of the five M/K scenarios described above (other parameters following baseline values), we sampled fish with L_{50} values ranging from 2 to 20 cm (5% to 50% of L_∞) and L_{95} ranging from 1.2 to 2 times L_{50} . We also explored the effects of bin width by sampling into equal and unequal binning schemes. For equal bin widths, we tested bin sizes ranging from 1 to 8 cm. For unequal bin widths, we used increasing bin sizes, as is commonly used in underwater visual surveys. Specifically, we used the Reef Life Survey (RLS) binning, where bin width starts from 2 cm in the smallest fish, increasing to 3.75, 5, etc (see Table 2). For the base scenario of $L_\infty = 40$ cm, the RLS binning resulted in 10-12 length bins, depending on M/K ratio. Sensitivity of parameter

estimation to sample sizes was evaluated by varying sample size from 200 to 20,000 length observations, reflecting the variability observed for common fish species in the RLS data.

In theory, length structure is only sensitive to the M/K ratio and not its L_∞ value (Prince et al. 2014, Hordyk et al. 2016). However, because observational data is usually collected in a fixed length binning (e.g., RLS binning), resolution of observational data will be different depending on the L_∞ of the species, and this will affect model's ability to estimate LH parameters. Therefore, for each of the five M/K scenarios in base simulations, we also tested the accuracy of parameter estimation for L_∞ values ranging from 10 to 90 cm. To examine potential effects from where the maximum observed length falls within a bin, we perturbed L_∞ by $\pm 10\%$, yielding five evenly spaced L_∞ values within each of 10 to 90 cm above.

Finally, we explored the performance of the EM to the violation of the continuous recruitment assumption. For this we used the length frequency data simulated using five M/K values and baseline values of other parameters, but using recruitment only for three months (February-April). The simulated populations were then sampled with the frequency of 1, 2, 6, or 12 times. In cases where sampling occurred only once, we compared sampling during the recruitment event (March) versus six months later (September). When sampling occurred 2, 6 and 12 times, we spaced sampling events evenly across months with the initial sampling occurring in March. The timing of sampling matters because pulsed recruitment leads to non-stationary length structures through the year.

The sensitivity analysis described above results in 380 tested parameter combinations, each replicated 10 times, giving 3,800 simulated length distributions provided to the EM for parameter estimation. From this we generated posterior distributions for each of the four estimated parameters $\theta = \{M/K, L_\infty, L_{50}, L_{95}\}$ and quantified the relative error (RE) following equation

$$RE = \frac{\hat{\theta} - \theta}{\theta} \quad (8)$$

where $\hat{\theta}$ is the median of the posterior estimate and θ is the true value used in the simulation (Hordyk et al. 2015b, Rudd and Thorson 2018). All analyses were conducted in R (R Core Team 2024). Data and code are available on GitHub at <https://github.com/wanw001> and will be archived on Zenodo upon the acceptance of this publication.

3. Results

3.1. M/K and L_∞ could be estimated accurately when observations include small fish

The shape of the observed length distribution in unfished population strongly depended on the M/K ratio and observation selectivity parameters (Fig. 2). The length distribution transitioned from left-skewed to right-skewed as M/K ratio goes from <1 to >1 (see also Miethe et al. 2019). Above M/K

of 2, the general shape of the distribution was highly right-skewed and less sensitive to M/K values, but very high M/K ratios (3.5) resulted in lower maximum length, relative to L_{∞} .

The EM gave accurate and precise estimates of both M/K and L_{∞} parameters when selectivity parameters were sufficiently low (Fig. 3). Specifically, when L_{50} was no more than 25% of L_{∞} , the estimates of M/K and L_{∞} were within 25% and 10% of their true values for all M/K ratios, respectively. However, when L_{50} was set at half of L_{∞} , estimates were within the same error ranges only in cases when the logistic selectivity curve was very steep (i.e., L_{95} was 120% of L_{50}). For all selectivity parameters, the bias in both M/K and L_{∞} estimates generally increased with increasing M/K . This bias was mostly positive but became negative for M/K of 3.5 at high selectivity parameters. The negative bias at M/K of 3.5 occurs because the overall shape of the length distribution was similar to that of M/K of 2.3, but maximum observed lengths were small relative to their L_{∞} values (Fig. 2), hence our method estimated smaller M/K and L_{∞} values relative to the true values.

Accuracy of L_{50} and L_{95} estimates showed a slightly different pattern from that of M/K and L_{∞} . The estimates of L_{50} were slightly negatively biased for low true L_{50} and positively biased for high L_{50} , especially for low M/K values. Meanwhile, the biases of L_{95} estimates tended to be higher for low L_{50} , especially for low M/K values (Fig. 3).

3.2. M/K and L_{∞} estimates were accurate for >10 length bins, sample sizes > 500 and $L_{\infty} \geq 30$ cm

Accurate and precise estimates of M/K and L_{∞} were obtained when observations were done in equal length bin widths of 4 cm or smaller, as well as for progressively increasing bin widths as adopted in RLS surveys (Fig. 4, left column). The relative errors of M/K and L_{∞} were within 12% and 7% of their true values respectively. For the baseline case of L_{∞} 40 cm, the 4 cm equal bin, and the RLS bins resulted in 10 to 13 actual observed length bins, depending on the M/K ratio. Using 8 cm equal length bins led to a large decline in the accuracy and precision of parameter estimates, with large positive errors in estimated values (Fig. 4, left column).

As expected, increasing sample size decreased bias and increased precision for all four estimated parameters (Fig. 4, middle column; see also Fig. S1 for non-truncated plot). Sample sizes of 5,000 resulted in very accurate and precise M/K and L_{∞} estimates, i.e. the estimates were within 9% and 6% of their true values. However, even a sample size of 500 provided reasonable accuracy, with nearly all estimates within 30% of their true values. For a sample size of 200, parameter estimates were generally inaccurate. Generally, for simulations exploring length bin and sample sizes, higher M/K values resulted in higher positive errors in M/K and L_{∞} estimates, except for M/K of 3.5, where the bias was reduced and errors became negative. Estimates of selectivity parameters behaved

similarly to M/K and L_∞ estimates in that parameter values were estimated accurately for all except 8 cm length bins and smallest sample sizes of 200.

Finally, given that the use of finite and especially progressively larger length bins is likely to affect parameter estimation accuracy depending on the absolute length of the fish, we assessed the accuracy of parameter estimates for L_∞ ranging from 10 to 90 cm (Fig. 5 & S2). Results showed that when increasing bin widths are used to record observations, estimates of M/K and L_∞ were strongly biased for L_∞ of 10 cm. However, when true L_∞ was at 20 cm and especially 30 cm or larger, all parameter estimates improved rapidly. Accuracy improvements were also observed in the estimates of L_{50} and L_{95} as the true L_∞ increased. The only exception was the case of L_∞ at 90 cm, where biases of L_{50} and L_{95} increased for the low M/K of 0.5. In some cases we observed abrupt changes in the accuracy of M/K and L_∞ estimates with small changes in L_∞ , for example when L_∞ was increased from 19 to 20 cm for M/K of 3.5.

3.3. M/K and L_∞ could be estimated accurately for fish with pulsed recruitment when sampling was conducted over multiple months

Pulsed recruitment diminished the accuracy of M/K and L_∞ when estimates were made from just a single sample (Fig. 4, right column), although sampling in the middle of recruitment time (March), yielded slightly better results than estimates from a single sampling event in September. Even two sampling events separated by 6 months produced considerably better estimates of M/K and L_∞ , except for the smallest M/K values of 0.5. When sampling frequency was higher, parameter estimates were generally reliable and similar to those of continuous recruitment.

3.4. M/K and L_∞ estimates were sensitive to the misspecification of CV

Overall, the estimates of M/K and L_∞ were robust to violation of the assumption that age at zero length was 0 ($a_0 = 0$) (Fig. 6, left column). Even when a_0 corresponded to a high L_0 , i.e. 20% of L_∞ , the two parameters were estimated within 20% accuracy, with highest positive bias at high M/K values. In contrast, estimates of the two selectivity parameters were more sensitive to the violation of $a_0 = 0$, and were highly biased when a_0 corresponded to an L_0 higher than 10% of L_∞ . Misspecification to cohort survivorship at maximum age ε (proxy for a_{\max}) had the opposite effect of parameter estimates in that it mostly affected M/K and L_∞ estimates, leading to positive bias for values lower than the default, i.e., $\varepsilon = 1\%$, and low M/K ratios, but having negligible impact on selectivity parameter estimates. Finally, M/K and L_∞ estimates were highly sensitive to the misspecification of CV (Fig. 6, right column; see also Fig. S3 for non-truncated plot). Deviations from the default assumption of 0.1 strongly biased M/K and L_∞ estimates, in either negative or positive

direction, depending on the values of true CV . Estimates of selectivity parameters were less affected, except for cases with the lowest M/K values.

Given that misspecification in CV had a large impact on parameter estimates, we further tested whether assuming a different CV value in the EM (currently set at 0.1) could give better estimates of the four parameters. As expected, parameter estimates were most accurate when the CV assumed in the EM was the same as the value used to simulate the data (Fig. 7; see also Fig. S4 for non-truncated plot). Yet, when the CV value was mis-specified, using a CV of 0.15 in the EM resulted in the least biased parameter estimates. Notably, for low M/K values, estimates of L_{50} and L_{95} were often highly biased.

4. Discussion

4.1. Overall performance of our method

Building on a widely popular LB-SPR method described by Hordyk et al. (2015a), we developed a method to estimate two LH (M/K and L_{∞}) and two observational selectivity (L_{50} and L_{95}) parameters, using length data from unfished populations. Overall, we found that the new method performs reasonably well, typically estimating parameters with less than 15% and 10% bias for M/K and L_{∞} respectively (30% and 20% bias in extreme data cases), assuming that the observation data was generated by processes that do not strongly violate the model assumptions. Good performance of the method required moderate observation selectivity (L_{50} and $L_{95} < 0.5L_{\infty}$), sufficient number of length bins (≥ 10) and reasonable sample sizes (≥ 500). These conditions are necessary for the data to accurately reflect the shape of the underlying length distribution. We found that our method was sensitive to the misspecification of the variation of length at age, CV (assumed to be 0.1 in the method, but other values can also be used), but violations to the assumed theoretical age at length zero (a_0) or fish survivorship at the maximum modelled age (ϵ) had smaller effects. Performance was best for fish species that exhibit continuous recruitment, although continuous recruitment throughout the year rarely occurs in nature. However, even under pulsed recruitment, pooling samples from different seasons smoothed the composite length distribution and improved the accuracy and precision of parameter estimates.

The M/K and L_{∞} parameters are central to describing the expected unfished length structure needed for population assessments. Two most widely used length-based methods – LB-SPR (Hordyk et al. 2015a) and LBB (Froese et al. 2018) – require M/K and L_{∞} to generate expected unfished length distributions and estimate reference points for evaluating population status. However, estimating reliable values for M , K , and L_{∞} through traditional approaches such as aging or tagging studies remains challenging and costly. With the rapid growth in underwater monitoring, either

through underwater surveys, deployments of underwater cameras, or AI-assisted data extraction, fish length observations from both fished and unfished populations are becoming increasingly available. Our method is designed to utilize these data to estimate M/K and L_∞ across a broad range of species and populations.

4.2. Comparison with other LH estimation methods and with original LB-SPR

The estimation of LH parameters using length-frequency data has a long history in fisheries science, with examples including electronic length frequency analysis (ELEFAN, Pauly and David 1981) and Bayesian growth model (BGM, Zhou et al. 2022). Both ELEFAN and BGM infer VBGF parameters (L_∞ and K) from length data by analysing modal or mean-length shifts across cohorts, either from a single snapshot or a time-series sample. Alternative methods (Ebert 1973, Sparre 1987) estimate growth and total mortality (Z) parameters, with Z derived from the right-hand limb of the length distribution. Broader adoption of these methods is sometimes hindered by the lack of clear separable cohorts due to low sampling resolution or extended recruitment times. In fact, a large scale study spanning 800 species and nearly 3,000 populations from mostly unfished populations, showed that, when pooled over temporal scales, most length compositions are largely unimodal (Heather et al. 2025). Another limitation of previous LH estimation methods is that they typically estimate growth and mortality separately, using different parts of length distribution - growth from cohort spacing and mortality from the slope of the right-hand limb. Estimating growth and mortality parameters individually is more prone to bias, as they tend to exhibit higher variability than their ratio (Prince et al. 2014, Prince et al. 2023).

Until recently, LH parameter estimation, including using methods above, typically use length data from fished population or catch, which is already affected by length-selective fishing (Hordyk et al. 2016). When used in estimation, the “distorted” length distribution can bias the parameter estimates. The LH estimation method presented here avoids reliance on length progression or the slope of the right-hand limb of length distribution. Instead, it uses the overall shape of length distribution from unfished population, building on the modelling foundation established by Hordyk et al. (2015a) in the development of the LB-SPR method.

Developed from LB-SPR framework, our method retains the same underlying model structure and assumptions. Both approaches use the shapes of the length distribution to infer growth to mortality ratio and selectivity. In our method it is the relative natural mortality rate and observation selectivity, whereas in LB-SPR it is the relative total mortality rate, which translates to relative fishing mortality rate (F/M), and fishing selectivity. Importantly, our method also estimates L_∞ , a parameter that determines the absolute scale of the length distribution. In contrast to fishing selectivity in LB-SPR, observation selectivity in our method does not impact population length structure. Methodologically, our method employs Bayesian inference (as in LBB; Froese et al. 2018), allowing

the incorporation of prior knowledge and direct quantification of uncertainty (Hoff 2009), while LB-SPR employs maximum likelihood. It should also be noted that we followed the original version of LB-SPR introduced by Hordyk et al. (2015a), rather than the Growth-Type-Group (GTG LB-SPR) extension (Hordyk et al. 2016), which addresses the Rosa Lee's phenomenon, where length-at-age distribution in older age groups become increasingly skewed due to selective removal of fastest growing fish. The GTG modification, while important for fished populations, is unnecessary here because we focus on unfished populations with length-independent natural mortality.

4.3. Conditions for high performance of our LH estimation method

Overall, we found that, despite the challenge of estimating four parameters from relatively low-resolution length data (e.g., unequal bin widths from 2 to 10 cm), our LH estimation method performed surprisingly well. As expected, parameter inference generally improved with increasing sample size. When total sample size fell below 500 length observations, the length distribution often failed to adequately represent the underlying population length-structure, resulting in reduced method performance (see Fig. S7). Although 500 lengths may seem large, the assumption of equilibrium in the population allows data pooling across temporal and spatial scales. This makes sample sizes of 500 to 1,000 lengths achievable for many commonly observed species in underwater surveys.

The binning resolution is another key factor influencing the accuracy of parameter estimation, as it determines how well the underlying shape of the length distribution is captured by the data (see Figs. S6 & S10). We found that binning with 10 length bins, whether of equal 2 cm width or increasing width (as in RLS surveys), provided good accuracy and precision, with minimal improvement beyond 13 bins. This minimum bin count also sets the lowest L_{∞} for which the method remains effective. When we considered RLS binning we found that our method performed well for species where L_{∞} is at least 30 cm, as it resulted in 9 to 11 length bins containing counts. Smaller L_{∞} (e.g., ~10–20 cm) produced only 5–9 bins that leads to lower accuracy. The abrupt changes of bias shown in Fig. 5 arise when small shifts in L_{∞} move the maximum observed length (L_{\max}) across bins, changing the number of informative bins (e.g., shift of L_{∞} from 19 to 20 cm at M/K of 3.5 increases the number of bins from 6 to 7). When the bin count remains unchanged, accuracy is largely unaffected even if L_{\max} shifts from lower to higher end of the bin.

For similar reasons, our method may produce highly biased parameter estimates when observational selectivity excludes fish of sizes up to half of L_{∞} . Such extreme selectivity - either due to inability of the observer to see small fish present within the study site or because young fish occur in different habitats - obscures the left side of the length distribution (Fig. 2; see also Fig S5). As a result, the model is unable to distinguish whether the absence of small fish is caused by selectivity or a low M/K ratio. Consequently, our method is not suitable for estimating LH parameters for species

that undergo pronounced ontogenetic habitat shifts, unless standardised length frequency data can be collected across all relevant habitats.

Finally, our simulation also showed that for species with high M/K ratios, where length distributions are strongly right-skewed, the model tended to produce more biased estimates of M/K and L_∞ . This bias is again linked to the number of informative length bins. Higher M/K ratios result in fewer larger fish, reducing L_{\max} and the number of informative bins. However, it is unclear why the bias tends to be increasingly positive. This is possibly due to differences in how observation selectivity and age resolution are implemented in the DGM and the EM. For example, the DGM uses $X \sim 1,000$, while EM uses $X = 200$. Interestingly, when the true M/K reaches 3.5, the bias suddenly drops or becomes negative. Two mechanisms likely explain this pattern: (i) length distributions become increasingly similar for $M/K > 2$ (Fig. 2), so the method may ascribe the distribution to a lower M/K and L_∞ combination; and (ii) with finite samples, observations in the upper right-tail become increasingly rare, reducing the observed L_{\max} . When sample sizes are very large (e.g., 20,000; Fig. 4 right column), more observations capture the upper right-tail, reinforcing the trend of increasing positive bias. Therefore, counterintuitively, smaller sample sizes can sometimes reduce bias at high M/K values by limiting the influence of rare large individuals.

4.4. Violations of model assumptions and impacts on LH parameter estimates

Like all models, the LH estimation method presented here relies on a set of assumptions about the processes that generated the observed length data, and violations of these assumptions can affect the accuracy of the model results. A common assumption in data-poor approaches is constant and continuous recruitment. While we did not explore the impact of varying recruitment intensity, we found that pulsed recruitment can impair parameter estimation accuracy when observations are drawn from a single time period. This is because the shape of the length distribution varies depending on the timing of sampling relative to the recruitment event (see Fig. S8). However, our sensitivity analyses showed that pooling even two samples collected by six months apart is sufficient to smooth the length distribution toward that expected under continuous recruitment, thereby improving our method's performance (Figs. 4, S8, & S9).

Three additional assumptions in our method are related to a_0 , ϵ , and CV . Both LB-SPR and our method require that $a_0 = 0$, even though it is well known that good fits of VBGF are obtained mostly when a_0 is negative, corresponding to positive length at zero age ($L_0 > 0$) (e.g., Shih, Hsu and Chen 2014, Wilson and Nieland 2001, Pardee, Wiley and Springer 2021). Fortunately, our simulations show the violation to $a_0 = 0$ assumption has minimal impact, consistent with findings from LB-SPR (Hordyk et al. 2015b). Varying ϵ between 0.1% to 2% also had limited effect on parameter estimates (Fig. 6), indicating robustness to model misspecification. While species-specific values of ϵ have been

suggested (e.g., 1-2% in some Teleost and Elasmobranch, Dureuil and Froese 2021, Nadon and Ault 2016), our method adopted $\varepsilon = 1\%$ following the original LB-SPR formulation. Although Dureuil and Froese (2021) estimated an average ε of 1.5% across species, our simulations show that using $\varepsilon = 1\%$ has a negligible influence on M/K and L_∞ estimates.

In contrast to the relatively minor effects of misspecifying a_0 and ε , we found that inaccurate assumption about CV can lead to substantial bias in LH parameter estimates. Our method, following LB-SPR, assumed a baseline CV of 10%. However, if the true value was 20%, estimates were positively biased by 35-100% for M/K and 18-40% for L_∞ . In comparison, LB-SPR is reported to be insensitive to CV (Hordyk et al. (2015b), though this conclusion was made based on a narrower range of CV (0.075-0.125), compared to our study (0.05-0.20). Interestingly, when comparing our results with Fig. 2 in Hordyk et al. (2015b) for the same CV value, the relative errors in our LH parameter estimates were generally smaller. It remains to be determined which baseline CV value performs best with our method, or whether the CV parameter should also be estimated together with main LH parameters.

Notably, errors in M/K and L_∞ estimates are positively correlated - overestimation in one parameter often accompanies overestimation in the other and *vice versa*. However, observation selectivity (L_{50} and L_{95}) trades off negatively with M/K and L_∞ , such that improving the accuracy of one pair can lead to reduced accuracy in the other. When applied to assess the status of fished population, LB-SPR is sensitive to M/K and L_∞ (Hordyk et al. 2015b). Overestimating M/K tends to result in an underestimation of F/M and inflation of the SPR, whereas overestimating L_∞ has the opposite effect. This interaction can be beneficial when M/K and L_∞ estimates from our method are used for LB-SPR to assess the population status of the same species. If M/K and L_∞ are both overestimated, their opposing effects in LB-SPR could partly offset each other, leading to more accurate estimates of F/M and SPR. Naturally, the overall reliability of LB-SPR-based assessments depends on the magnitude of bias in LH parameters and potential misspecifications of other model parameters.

4.5. Limitations and future work

Estimating LH parameters from length frequency data alone is challenging, and any method applied to address it must rely on a set of assumptions and simplifications. A key assumption of our method, as in other length-based methods, is that the M/K ratio is defined under the conditions that fish growth follows VBGF and natural mortality is independent of both length and age. These conditions are often violated (Lorenzen, Camp and Garlock 2022, Fahmi et al. 2021). While the VBGF provides a reasonable approximation for many species, it can misrepresent juvenile growth (Quinn II and Deriso 1999, Lester, Shuter and Abrams 2004), and mortality is unlikely to be length-independent. When

body growth follows a different model, or mortality changes across length, M/K may lose interpretability. We did not test sensitivity of L_{∞} estimate to departures from VBGF or length-independent M , but such violations will likely bias L_{∞} .

In our DGM, we used a steady-state, one-snapshot population with constant recruitment, rather than dynamic populations through time (cf. Hordyk et al. 2015b, Rudd and Thorson 2018, Huynh et al. 2018). This choice is reasonable, as we did not explore variable recruitment effect on parameter estimation. Like LB-SPR, our model treats recruitment as constant, although it is well known that in natural populations recruitment can fluctuate dramatically around its average level (Hordyk et al. 2015b, Rudd and Thorson 2018). Our random sampling design might not have sufficiently represented this fluctuation, potentially leading to weaker performance of our LH estimation method in real-world applications.

Finally, just like fishing selectivity in LB-SPR, our method assumes logistic observation selectivity. Yet, some species or observation methods may have dome-shaped selectivity, where largest fish are harder to observe. In such cases, our method will likely underestimate L_{∞} and bias M/K . Unfortunately, accounting for dome-shaped selectivity in LH parameter estimation is challenging (Hordyk et al. 2015a). If large individuals are absent, it is difficult to identify whether this is caused by the LH parameters, or selectivity. Hence, the model should not be applied in cases where observational selectivity is likely to be strongly dome-shaped.

Despite these limitations, the LH parameter estimation method presented here offers valuable potential for estimating M/K and L_{∞} across a wide range of fish and invertebrate species, where growth can be reasonably described by the VBGF and other model assumptions are approximately met. With the increasing availability of length data from citizen science, automatic monitoring and other emerging sources, the method could help illuminate variable LH traits across hundreds of species and support data-poor stock assessments. Importantly, the method presented here requires data from a largely unfished population, which may be obtained from well-managed marine reserves, remote ecosystems, or historical surveys conducted prior to the onset of fishery.

Future studies could extend the current LH estimation method to incorporate environmental gradients using hierarchical models that allow population-specific estimates of M/K and L_{∞} . Another extension could be reformulating our method with dome-shaped observation selectivity particularly for species with clear ontogenetic shift in habitat for oldest individuals.

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6. Author contributions: CRediT

WK: Conceptualization, Methodology, Formal analysis, Writing-original draft. **SAR:** Conceptualization, Methodology, Writing – review and editing. **PB-B:** Methodology, Writing – review and editing. **AA:** Conceptualization, Methodology, Writing – review and editing, Funding acquisition.

7. Declaration of generative AI and AI-assisted technologies in the manuscript preparation process

During the preparation of this work the authors used ChatGPT in order to improve the wording and overall clarity of the text. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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