State-space stock assessment models for data-moderate fisheries

by

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Abstract

Fish populations are subject to natural growth, environmental pressures, and natural mortality. In addition, they may experience pressure from anthropic fishing mortality. Management of fish stocks requires the collection of suitable data from which population models can be built. Statespace models (SSMs) are one modelling approach, and this project investigates their application to data-moderate stocks. We define data-moderate stocks as those for which there are no survey data, no information on age composition, and fisheries-dependent data are the only available source of information. We find that many existing state-space models are either too simple (e.g., state-space surplus production models) or too complex (e.g., state-space age-structured models) for these stocks, although many fisheries around the world face data-moderate situations.

A state-space model is becoming a favoured choice in modelling fish population dynamics, as it allows one to incorporate both measurement and process errors. However, several studies have found that separation of the two sources of variability can result in estimability problems even in simple state-space models. Using a state-space surplus production model as an example, we found that such estimability problems can occur even in a simple stock assessment model, especially when measurement error is large relative to process error. This problem even exists when constraints are imposed on most of the model parameters. Such findings suggest the limitations of SSMs and the importance of model diagnostics.

Using data collected from South Korean fish stocks as application examples, we developed two stock assessment models in state-space form. The first model is a state-space two-life stage-structured production model which can be applied to stocks where juvenile and adult fish have been separately exploited by different fisheries. The key feature of the model is that in the absence of any composition data (e.g., age and size), demographic relationships between juvenile and adult populations are incorporated using abundance indices collected from different fisheries, each of which selectively targets the two different life stages of fish.

The second model is a state-space length-based age-structured model. This integrated model is developed to utilise length composition data to inform the age structure of a population. Such data are often available in many data-moderate stocks, instead of a direct measure of age composition, such as catch-at-age data. Separating age groups based on length compositions is not a new concept, but most existing models do not allow process error. Thus, the development of such a model in state-space form could provide a more reliable assessment tool for many data-moderate stocks.

This thesis research contributes to the better understanding of potential estimability issues in SSMs for fish stock assessments, as well as development of the two new state-space models for data-moderate fisheries. We also identified several issues associated with our findings which could be useful for future research.

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Chapter 1

Introduction

Fish stock assessment is the process of analysing data collected from either scientific surveys or commercial fisheries or both, to estimate changes in fish stock abundance in response to harvesting (i.e., fish catch), based on a population dynamics approach (Hilborn and Walters, 1992). Harvesting triggers many changes in natural fish populations, which include growth, maturity, population size, age composition, and productivity. Fish population dynamics describes those changes based on basic demographic components: birth and death (in some cases, migration is also considered), using statistical and mathematical models which are generally called stock assessment models in fisheries science (Hilborn and Walters, 1992; Haddon, 2010). The data used for such assessments are typically a relative abundance index (e.g., catch-per-unit-effort: CPUE or fishery-independent survey), yield (e.g., annual catch in biomass), age composition (e.g., catch-at-age), sexual maturity (e.g., maturity-at-age or -length), gear selectivity, and somatic growth (e.g., length-at-age).

Fisheries scientists apply stock assessment models to provide fisheries managers with scientific information that can be used to manage fishing activities. Thus, developing a model that closely approximates the observable behaviour of a fish stock is a key part of a stock assessment process. Such model development is an interdisciplinary task which involves understanding the ecological and biological behaviour of marine species as well as advanced statistical and mathematical techniques.

Numerous stock assessment models have been developed since Fedor Baranov laid a cornerstone of quantitative fisheries science in early 1900s (Baranov and Ricker, 1945; Aeberhard et al., 2018). Those models continue to evolve as more information about fish stocks and implementation of advanced statistical techniques that can integrate various sources of information become available. It is not surprising that as model complexity grows, the model becomes a more realistic representation of a fish stock, thereby providing better quality of assessment results; thus, many previous studies have attempted to develop new models that incorporate more detailed behaviour of a fish stock. In recent decades, a state-space modelling framework has received much attention in fisheries science (Millar and Meyer, 2000; Nielsen and Berg, 2014; Cadigan, 2016; Miller et al., 2016; Miller and Hyun, 2017), especially after the development of new model estimation software, such as ADMB and TMB (Fournier et al., 2012; Kristensen et al., 2016), which largely facilitated computationally efficient implementation and estimation of such complex models by using the Laplace approximation.

State-space modelling is extremely useful for stock assessments as the framework allows us to accommodate both process and observation errors by separately modelling two different time series that appear in most fish population dynamics models (Aeberhard et al., 2018; Auger-Méthé et al., 2021). To be specific, process error refers to stochastic processes affecting the size of a fish population over time (e.g., environmental changes), whereas observation error describes differences between the latent state (e.g., population size) and observed data (e.g., CPUE), caused by uncertainty in sampling (Auger-Méthé et al., 2021). Thus, the first time series is often termed as a state time series which is modelled to reflect a hidden unobserved state of nature, such as actual fish stock size over time.

Most conventional stock assessment models treat those state transitions as a deterministic process, but in state-space models (SSMs), such transitions are modelled as a stochastic process to accomodate the impact of random variation on population abundance, such as environmental changes. The second time series is an observation time series which is modelled to filter out random measurement errors that reflect differences between the unobserved states and the observations. In SSMs, these two stochastic components are hierarchically structured, which allows them to be separately modelled. By fitting a SSM to observed time series data, one can simultaneously estimate both unobserved states and model parameters which include process and observation error variances.

As explained above, because of additional stochasticity incorporated in unobserved states, SSMs are desirable as they better represent actual dynamics of fish stocks compared to conventional models that assume deterministic state transitions. Because of this advantageous property, SSMs have been actively used to assess and manage fish stocks around the world (Aeberhard et al., 2018), but we find the following two major problems that hinder a wider application of these powerful tools in practice:

(i) First, many existing SSMs are age-structured and designed for particular data-rich stocks (Nielsen and Berg, 2014; Cadigan, 2016; Miller et al., 2016; Miller and Hyun, 2017). Thus, they are not applicable for many data-limited or -moderate fish stocks world wide. For example, almost all fish stocks in South Korea are managed under datalimited or -moderate situations where age composition data are either completely lacking or intermittently available. Because of such deficiencies in age composition data, a majority of published studies which used SSMs for assessing Korean fish stocks applied ageaggregated models, such as state-space surplus production models (Choi and Kim, 2019; Choi et al., 2020; An et al., 2021). Although these studies have their own values and made contributions to fisheries management in South Korea, we find that some of those applications have underutilised other existing data, such as length composition and life stage-specific information (e.g., juvenile and adult catch) that can be used to inform more detailed demographic structures of fish stocks.

(ii) Second, SSMs are associated with estimability issues in certain conditions under which some model parameters as well as unobserved states are not estimated well. Such estimation problems seem to arise when SSMs fail to separate out the two different types of errors (i.e., observation and process errors) from each other. Previous studies discovered that those estimation issues tend to occur when observation error is larger than process error (Dennis et al., 2006; Auger-Méthé et al., 2016; Hyun and Kim, 2022), but our preliminary study indicated that the existence of trends in time series data can also affect the estimability of model parameters in SSMs.

The two problems listed above motivated us to investigate the following research questions in this thesis:

- (i) Is one of the simplest SSMs in stock assessments, the state-space surplus production model which has been widely and continuously applied to many data-deficient fisheries world wide, associated with estimability issues? If so, under what conditions do such estimation problems occur?
- (ii) What model validation procedures are required for identifying potential estimation problems in SSMs? What precautions are necessary when deriving conclusions from SSMs?
- (iii) Can we develop new SSMs that can be applied to data-moderate stocks for which popular exisiting SSMs, such as state-space surplus production and age-structured models, are not applicable?

We address these research questions in this thesis in the main three chapters (i.e., Chapters 3 to 5) which investigate different SSMs, using actual fisheries data. Apart from this introductory chapter, the remaining two chapters (i.e., Chapters 2 and 6) respectively discuss the methodology for estimating SSMs and contain the conclusions of this thesis.

To be specific, in Chapter 2, we introduce a maximum marginal likelihood method and the Laplace approximation, which we extensively use throughout the rest of the thesis for inference of SSMs. In Chapter 3, we demonstrate that even a simple SSM in stock assessments has estimability issues, using a state-space surplus production model. We show that such estimation problems can occur in many practical situations, using extensive simulation studies designed based on actual fisheries data. In Chapter 4, we develop a new SSM that is specifically designed for the Korea pollock stock where fisheries information on juvenile and adult stocks is separately available. We evaluate the performance of the new model by comparing it with an existing SSM (i.e., a state-space general surplus production model), based on simulated data which closely mimic the Korea pollock stock. After the performance test, we apply the model to actual pollock data to conduct a stock assessment. We then perform validation tests which identify potential estimability problems associated with this new stock assessment model. In Chapter 5, we develop another new SSM that can be applied to many data-moderate stocks where length composition data are available instead of age composition data. We apply this new length-based state-space model to actual fisheries data collected from the Korea mackerel stock as a case study. After the application, we conduct several model validation tests to evaluate estimability and robustness of the model. Finally, in Chapter 6, we discuss the main conclusions of the thesis, where we suggest several precautions that are associated with the development and application of SSMs in stock assessments. In summary, the original contributions to quantitative fisheries science from this thesis research are as follows:

(i) Identification of estimability issues in a state-space surplus production model that has been extensively applied to many datalimited stocks around the world (Chapter 3).

- (ii) Development of two novel SSMs for data-moderate fish stocks (Chapters 4 and 5)
- (iii) Demonstration of model validation tests in SSMs, which can identify potential estimability problems (Chapters 3, 4, and 5).

We finish this introductory chapter by briefly describing the two most popular existing SSMs (i.e., a state-space surplus production model and a state-space age-structured model) in stock assessments to aid the reader in understanding the concept of stock assessment models and state-space modelling framework.

1.1 Stock assessment models

A range of fish population data are required for reliable stock assessments. These typically include information on length-at-age, length-at-weight, male to female ratio, fecundity, relative abundance (e.g., catch-per-uniteffort), total catch, fishing gears (e.g., gear-selectivity), and spatio-temporal distributions of collected data. Although utilising all of the above information is necessary to accurately assess fish stocks, only a few of them are often available in practice. Under these circumstances, fisheries scientists need to choose the model best suited for the available data, and such a choice is usually made depending on the availability of composition data. In the absence of composition data that can inform the demographic structure of fish stocks, surplus production models (Hilborn and Walters, 1992; Schaefer, 1954; Quinn and Deriso, 1999; Haddon, 2010), which lump the overall effects of biological processes in a single production function, may be a reasonable choice. However, if age composition data are available, age-structured models are used for more detailed assessments (Hilborn and Walters, 1992; Quinn and Deriso, 1999; Haddon, 2010).

1.1. STOCK ASSESSMENT MODELS

In this section, we describe the two most popular stock assessment models, a surplus production model and an age-structured model, as representative examples. To provide the reader with an overview of a general state-space modelling framework in fisheries science, we show how the state-space modelling framework has been applied to these two models. A method for the inference of model parameters and state variables in SSMs is discussed in the next chapter (i.e., Chapter 2), so here we only discuss their fundamental structures.

1.1.1 Surplus production model

The surplus production model (SPM) is one of the simplest stock assessment models. It represents stock dynamics in terms of changing levels of biomass (Quinn and Deriso, 1999; Haddon, 2010). The SPM calculates a new biomass by summing current biomass with surplus production, which is calculated by subtracting the yield (i.e., catch in weight) from the net production:

Next biomass = Current biomass +
$$\underbrace{Production - Yield}_{Surplus production}$$

The main advantage of a SPM is its ease of application because of relatively simple data requirements. However, its simple structure ignores some key biological processes of fish populations that can significantly affect stock productivity (e.g., recruitment, fish growth, etc.). The basis of a SPM is the stock productivity function $g(\cdot)$. Although there are many other versions of formulas available for $g(\cdot)$, the most conventional choice is the logistic growth extended to include yield Y_t (Hilborn and Walters, 1992). Note that we use the term "yield" for fishing catch in biomass units throughout this thesis to differentiate it from that in numbers.

With the productivity function $g(\cdot)$ and the yield term Y_t , the change in

population biomass over time *t* can be expressed as

$$\frac{B_{t+\Delta t} - B_t}{\Delta t} = g(B_t) - Y_t$$
$$= r \cdot B_t \cdot \left(1 - \frac{B_t}{K}\right) - Y_t,$$

where B_t is the biomass at time t, Δt is the duration of a time interval, r is the intrinsic growth rate, and K is the carrying capacity for the population of interest. Then, rearranging the above equation with respect to $B_{t+\Delta t}$ gives

$$\underbrace{B_{t+\Delta t}}_{\text{Next biomass}} = \underbrace{B_t}_{\text{Current biomass}} + \underbrace{\Delta t \cdot \left[r \cdot B_t \cdot \left(1 - \frac{B_t}{K} \right) - Y_t \right]}_{\text{Surplus production}}$$

Since fisheries data are often collected at discrete times (such as daily, monthly, yearly, etc.), we set $\Delta t = 1$, which gives us the following standard form of the surplus production model (also known as the Schaefer production model) (Schaefer, 1954):

$$\underbrace{B_{t+1}}_{\text{Next biomass}} = \underbrace{B_t}_{\text{Current biomass}} + r \cdot B_t \cdot \left(1 - \frac{B_t}{K}\right) - \underbrace{Y_t}_{\text{Yield}}.$$
 (1.1)

1.1.2 State-space surplus production model

In this section, we show how a state-space modelling framework can be applied to the deterministic model in Equation (1.1) (see Figure 1.1 for its overall structure). The data for a SSM mainly consists of the two different time series, a process time series and an observation time series. We explain each component of a state-space surplus production model in the following two subsections.

1.1. STOCK ASSESSMENT MODELS

Process model

It is generally assumed that the natural logarithm of the biomass B_{t+1} in year t + 1 (i.e., $\log(B_{t+1})$) is normally distributed conditional on the previous biomass B_t , and the model parameters (i.e., the intrinsic growth rate r, the carrying capacity K, and the process variance parameter, σ_{η}^2), and the observed yield Y_t (Millar and Meyer, 2000; Punt, 2003):

$$\log(B_{t+1}) = \log\left[B_t + r \cdot B_t \cdot \left(1 - \frac{B_t}{K}\right) - Y_t\right] + \eta_{t+1},$$

where $\eta_t \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{\eta}^2\right)$ is a stochastic process error representing the effect of environmental randomness on population growth and measurement error in observed yield.

Observation model

To estimate the latent states B_t , we need to include an observation model that links those latent states (i.e., B_t) with observed time series data. A common assumption is that the relative abundance index of each time t(i.e., I_t) is related to the latent biomass B_t through a stochastic observation model, where $\log(I_t)$ is normally distributed conditional on the biomass B_t , the catchability parameter q, and the observation variance σ_{ε}^2 :

$$\log(I_t) = \log(q \cdot B_t) + \varepsilon_t,$$

where $\varepsilon_t \stackrel{\text{iid}}{\sim} N(0, \sigma_{\varepsilon}^2)$ is a stochastic observation error representing the difference between the log of the observation (i.e., $\log(I_t)$) and its expected value (i.e., $E[\log(I_t)]$).



Figure 1.1: Directed acyclic graph (DAG) representation of the state-space surplus production model. White circles are non-observed probabilistic nodes (i.e., B_t), and those in gray are observed probabilistic nodes (i.e., I_t). Squares in gray are observed deterministic nodes (i.e., Y_t). Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes

1.1.3 Age-structured model

An age-structured model attempts to describe the composite behavior of cohorts within a population, which involves tracking the development and changes within each cohort separately. Obviously, this is an improvement over an age-aggregated model, such as the surplus production model described above, as different ages of animals tend to grow at varying rates and have varying weights. Depending on the level of information available, an age-structured model could be a better reflection of natural population processes and the impacts of harvesting than simple models.

In theory, after a cohort has recruited, its numbers can only decline (assuming no immigration and emigration). The design of the model depends upon how this decline is modeled. Using an exponential decay model, the changing numbers within a cohort can be expressed as follows:

 $\underbrace{N_{a+1}}_{\text{Numbers at age } a + 1} = \underbrace{N_a}_{\text{Numbers at age } a} \times \underbrace{\exp[-(F_a + M_a)]}_{\text{Survivor rate for fish of age } a} \quad \text{for } 1 < a < A,$

1.1. STOCK ASSESSMENT MODELS

where N_a is the number of fish of age a, M_a and F_a are the instantaneous rates of natural and fishing mortality for fish of age a, and A is the terminal age group.

Modelling an age-structured population through time is a standard problem in fisheries stock assessment. In modern fisheries stock assessments, age-structured models, such as the virtual population analysis (VPA) and the statistical catch-at-age model (SCAA) (Fournier and Archibald, 1982; Quinn and Deriso, 1999; Haddon, 2010), are widely used and considered the most reliable assessment methods as they follow identifiable cohorts. Although estimation procedures are different, the base structure of those methods can be expressed as follows

$$N_{a,t} = \begin{cases} N_{1,t}, \\ N_{a-1,t-1} \cdot \exp[-(M_{a-1,t-1} + F_{a-1,t-1})], & \text{for } 1 < a < A \\ N_{A-1,t-1} \cdot \exp[-(M_{A-1,t-1} + F_{A-1,t-1})] \\ + N_{A,t-1} \cdot \exp[-(M_{A,t-1} + F_{A,t-1})] \end{cases}$$
(1.2)

where $N_{a,t}$ is the number of fish of age *a* for time *t*, $M_{a,t}$ is the instantaneous natural mortality rate (time⁻¹) for fish of age *a* at time *t*, and $F_{a,t}$ is the instantaneous fishing mortality rate for fish of age *a* at time *t* (time⁻¹).

1.1.4 State-space age-structured model

In this section, we show how the age-structured model in Equation (1.2) is commonly modelled in state-space form (see Figure 1.2 for its overall structure). Note that age-structured models generally include numerous sub-models, which parameterise biological traits of a species of interest and selectivity associated with fishing gears and fleets. Details about those sub-structures are discussed in Chapters 4 and 5.

Process model

In state-space age-structured models, it is generally assumed that the natural logarithm of abundance for ages and times are normally distributed (Nielsen and Berg, 2014; Cadigan, 2016; Miller et al., 2016; Miller and Hyun, 2017):

$$\log(N_{a,t}) = \begin{cases} \log(N_{1,t}) + \eta_{1,t} \\ \log(N_{a-1,t-1} \cdot \exp[-(M_{a-1,t-1} + F_{a-1,t-1})]) + \eta_{a,t}, & \text{for } 1 < a < A \\ \log(N_{A-1,y-1} \cdot \exp[-(M_{A-1,t-1} + F_{A-1,t-1})] \\ + N_{A,y-1} \cdot \exp[-(M_{A,t-1} + F_{A,t-1})]) + \eta_{A,t} \end{cases},$$

where $\eta_{a,t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{a,\eta}^2\right)$. To reduce the number of variance parameters $\sigma_{a,\eta}^2$, the process variance for older ages (e.g., a > 1) is assumed to be the same (i.e., $\sigma_{a,\eta}^2 = \sigma_{2,\eta}^2$, for a > 1).

Observation model

To link the unobserved states $N_{a,t}$ with sets of time series observations, the following two observation models can be used. Note that depending on types of data at hand, other alternative observation models can be applied instead of the models given below, which we discuss in Chapter 5. The first observation model assumes that the relative abundance index for each age *a* and time *t* (i.e., $I_{a,t}$) is related to the unobserved abundance $N_{a,t}$ through a stochastic observation model, where $\log(I_{a,t})$ is normally distributed conditional on the abundance $N_{a,t}$, the age-specific catchability parameter q_a , and the observation variance $\sigma_{a,\epsilon}^2$ for the abundance index data (Nielsen and Berg, 2014; Auger-Méthé et al., 2021):

$$\log(I_{a,t}) = \log(q_a \cdot N_{a,t}) + \varepsilon_{a,t}, \quad \text{where } \varepsilon_{a,t} \stackrel{\text{ind}}{\sim} N\left(0, \sigma_{a,\varepsilon}^2\right)$$

....



Figure 1.2: Directed acyclic graph (DAG) representations of the state-space age-structured model: the process model (a) and the observation model (b). White circles are non-observed probabilistic nodes (i.e., $N_{a,t}$), and those in gray are observed probabilistic nodes (i.e., $I_{a,t}$ and $C_{a,t}$). Arrows with solid lines represent conditional probabilistic dependencies between nodes. Dotted rectangular frames with rounded corners indicate repetition of structure over units.

The second observation model links the catch-at-ages for time t (i.e., $C_{a,t}$) with the two types of mortality parameters and the abundance, using the baranov catch equation (Baranov and Ricker, 1945). Again, it is often assumed that the natural logarithm of $C_{a,t}$ (i.e., $\log(C_{a,t})$) is normally distributed (Nielsen and Berg, 2014; Miller and Hyun, 2017; Auger-Méthé et al., 2021):

$$\log(C_{a,t}) = \log\left[\frac{F_{a,t}}{M_{a,t} + F_{a,t}} \cdot \{1 - \exp(-M_{a,t} - F_{a,t})\} \cdot N_{a,t}\right] + \nu_{a,t},$$

where $\nu_{a,t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{a,\nu}^2\right)$.

In the next chapter, we discuss a maximum marginal likelihood method and the Laplace approximation, which are widely used to infer these SSMs in fisheries science.

Chapter 2

Inference in state-space models

In this chapter, we discuss a maximum marginal likelihood estimation approach that is widely used in quantitative fisheries science. In this approach, the approximation of the integral over random effects (e.g., state variables in state-space models) is performed using the Laplace approximation (Skaug and Fournier, 2006; Fournier et al., 2012; Kristensen et al., 2016).

There are two main ways of fitting state-space models (SSMs) to observed data, namely the frequentist and Bayesian approaches. Frequentists infer parameters by maximising the likelihood function, and Bayesians derive a posterior density of the respective unknown quantity by sampling (if the posterior distribution is not analytically tractable). It is important to note that there is a significant difference in how the two statistical frameworks deal with parameters and states. In the frequentist approach, each parameter is considered as an unknown fixed constant, while the hidden states are treated as random variables. In the Bayesian approach, both parameters and states are treated as random variables (Auger-Méthé et al., 2021). Despite these differences between the two approaches, both approaches require dealing with a high-dimensional integration, which is at the core of the problems associated with fitting SSMs to data (Aeberhard et al., 2018; Auger-Méthé et al., 2021).

In this thesis, we use the frequentist approach as our main estimation method because of its superior efficiency in terms of computational speed over Bayesian sampling approaches (Auger-Méthé et al., 2021). In particular, in Chapters 3, 4, and 5, these significant computational advantages allowed us to test the performance of different SSMs using parametric bootstrap, where we run a few hundreds or thousands of bootstrap replicates to obtain robust results.

Therefore, the rest of this chapter is largely devoted to discussing the frequentist approach, where we review the classical and extended likelihoods as well as the Laplace approximation. After the description of the likelihood-based method, we briefly discuss its counterpart, the Bayesian approach, for comparison between the two approaches.

2.1 Frequentist approach

Fitting a state-space model (SSM) to data involves estimating the parameters θ and the latent states v. Since the states are random variables, v has a probability distribution. Thus, it is common to refer to state variables as random effects or latent variables (Auger-Méthé et al., 2021).

The premise of maximum likelihood estimation is to find values of parameters θ and the states v that maximise their joint likelihood. However, direct maximisation of the joint likelihood with respect to both types of unknown quantities is challenging (Aeberhard et al., 2018; Auger-Méthé et al., 2021). Thus, the parameters are commonly estimated by maximising a marginal likelihood instead, which is obtained by integrating out the state variables from the joint likelihood (Aeberhard et al., 2018; Auger-Méthé et al., 2021). This estimation process is the same as the classical maximum likelihood method for a model that has no random effects. However, the difference from the classical method is that there is one more maximisation step for the estimation of state variables.

2.1. FREQUENTIST APPROACH

As explained, the maximum likelihood approach for models with random effects, such as SSMs, can be considered an extension of the classical likelihood method. Thus, in the following sub-sections, we show how the classical likelihood can be extended to incorporate random effects. Note that for clarification, here we use the term "classical likelihood" for a model with no random effects and "extended likelihood" for a model with random effects. We adopt the terminology, extended likelihood, from Pawitan (2001), which has also been referred to as h-likelihood in a mixed effect framework (Lee et al., 2018).

2.1.1 The classical likelihood

Let y and θ be vectors of observations and model parameters, respectively. Then, the probability distribution for the data y conditional on the parameters θ can be denoted as

$$f(\boldsymbol{y}|\boldsymbol{\theta})$$

Support of the data for different values of θ can be expressed using the likelihood function of θ conditional on y, which is equal to $f(y|\theta)$ but written with the argument, revised to emphasise the fact that θ is unknown and the data y are regarded as fixed (Pawitan, 2001):

$$\mathcal{L}(\boldsymbol{\theta}|\boldsymbol{y}) = f(\boldsymbol{y}|\boldsymbol{\theta}).$$

Estimates of θ (i.e., $\hat{\theta}$) can be found by maximising $\mathcal{L}(\theta|y)$ with respect to θ given the data y. In practice, it is computationally more stable to maximise the log-likelihood $\ell(\theta)$ instead of $\mathcal{L}(\theta|y)$:

$$\ell(\boldsymbol{\theta}|\boldsymbol{y}) = \log[\mathcal{L}(\boldsymbol{\theta}|\boldsymbol{y})]$$

since the log-likelihood is less prone to overflow or underflow when evaluated. Moreover, the log-likelihood is often analytically simpler to handle. Thus, maximising the log-likelihood with respect to the parameters θ gives us the maximum likelihood estimator of the parameters θ (Pawitan, 2001):

$$\hat{\boldsymbol{\theta}} = \arg \max_{\boldsymbol{\theta}} \ell(\boldsymbol{\theta}|\boldsymbol{y}).$$

For the maximisation, we use the first derivatives of the log-likelihood $\ell(\boldsymbol{\theta}|\boldsymbol{y})$ with respect to the parameters $\boldsymbol{\theta}$ if the log-likelihood function is reasonably quadratic. This first derivative is commonly referred to as the score function $S(\boldsymbol{\theta})$ (Pawitan, 2001):

$$S(\boldsymbol{\theta}) \equiv \frac{\partial \ell(\boldsymbol{\theta}|\boldsymbol{y})}{\partial \boldsymbol{\theta}}.$$

The maximum likelihood estimates (MLEs) of θ is then the solution of the following vector equation

$$S(\boldsymbol{\theta}) = 0.$$

The Fisher information $I(\theta)$ is defined as the negative of the Hessian matrix and is given by

$$I(\boldsymbol{\theta}) \equiv -\frac{\partial^2 \ell(\boldsymbol{\theta}|\boldsymbol{y})}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}^T}.$$

The inverse of the observed Fisher information $I(\hat{\theta})$, which is obtained by evaluating the Fisher information at $\theta = \hat{\theta}$, gives us the variancecovariance matrix of the estimates $\hat{\theta}$ (Pawitan, 2001):

$$\hat{\operatorname{cov}}(\hat{\boldsymbol{\theta}}) = I(\hat{\boldsymbol{\theta}})^{-1}.$$

2.1.2 The extended likelihood

If we include an additional layer for the unobservable random quantities v in the model with the parameters θ (i.e., $f(y|\theta)$), whose probability distribution function is denoted as $f(v|\theta)$, the joint density $f(y, v|\theta)$ can

be expressed as

$$f(\boldsymbol{y}, \boldsymbol{v}|\boldsymbol{\theta}) = f(\boldsymbol{v}|\boldsymbol{\theta}) \cdot f(\boldsymbol{y}|\boldsymbol{v}, \boldsymbol{\theta})$$
(2.1)

so that

$$f(\boldsymbol{y}|\boldsymbol{\theta}) = \int f(\boldsymbol{v}|\boldsymbol{\theta}) \cdot f(\boldsymbol{y}|\boldsymbol{v},\boldsymbol{\theta}) d\boldsymbol{v}.$$

In terms of the data generation process, the stochastic model in Equation (2.1) can be interpreted as follows (Lee et al., 2018):

- (i) From a probability distribution function $f(v|\theta)$ with known input values for the parameters θ , generate realisations of the random quantities v (e.g., stock abundance in fisheries models, such as B_t , and $N_{a,t}$).
- (ii) Then, from a probability distribution function $f(y|v, \theta)$ where both θ and v are fixed at the values obtained from the process above, generate the observations y.

For inference, similar to the classical likelihood, a joint likelihood for both the parameters θ and the random effects v (i.e., extended likelihood in our terminology) can be expressed as

$$\mathcal{L}(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \equiv f(\boldsymbol{y}, \boldsymbol{v} | \boldsymbol{\theta}).$$

Unlike for the classical likelihood, maximising the extended likelihood with respect to both the parameters θ and the random effects v is challenging. Thus, for inference, the following approach is used instead:

(i) From the extended likelihood $\mathcal{L}(\theta, v|y)$, obtain the marginal log-likelihood $\ell(\theta|y)$ by integrating out the random effects v and take the natural logarithm (Lee et al., 2018):

$$\ell(oldsymbol{ heta}|oldsymbol{y}) = \log\left(\int \mathcal{L}(oldsymbol{ heta},oldsymbol{v}|oldsymbol{y})doldsymbol{v}
ight)$$

(ii) Make inference by maximising the marginal log-likelihood $\ell(\theta|y)$ with respect to the parameters θ :

$$\hat{\boldsymbol{ heta}} = rg\max_{\boldsymbol{ heta}} \ell(\boldsymbol{ heta}|\boldsymbol{y})$$

and

$$\operatorname{cov}(\hat{\boldsymbol{\theta}}) = -\left[\frac{\partial^2 \ell(\boldsymbol{\theta}|\boldsymbol{y})}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}^T}\Big|_{\boldsymbol{\theta} = \hat{\boldsymbol{\theta}}}\right]^{-1}$$

(iii) After $\hat{\theta}$ is found, one can sequentially infer v by maximising the extended log-likelihood $\ell(\hat{\theta}, v | y)$ with respect to v, where θ is fixed at $\hat{\theta}$ (Lee et al., 2018):

$$\hat{\boldsymbol{v}} = \arg \max_{\boldsymbol{v}} \ell(\hat{\boldsymbol{\theta}}, \boldsymbol{v} | \boldsymbol{y}), \quad \text{where } \ell(\hat{\boldsymbol{\theta}}, \boldsymbol{v} | \boldsymbol{y}) = \log[\mathcal{L}(\hat{\boldsymbol{\theta}}, \boldsymbol{v} | \boldsymbol{y})]$$
 (2.2)

and

$$\operatorname{cov}(\hat{\boldsymbol{v}}) = -\left[\frac{\partial^2 \ell(\hat{\boldsymbol{\theta}}, \boldsymbol{v} | \boldsymbol{y})}{\partial \boldsymbol{v} \partial \boldsymbol{v}^T}\Big|_{\boldsymbol{v} = \hat{\boldsymbol{v}}}\right]^{-1}.$$
(2.3)

A major disadvantage of the plug-in method in Equations (2.2) and (2.3) is that it underestimates $cov(\hat{v})$ by ignoring the additional uncertainty that originates from the fact that $\hat{\theta}$ is itself only an estimate. Taking this into account, we use the following formula which is already implemented in statistical software such as ADMB and TMB (Skaug and Fournier, 2006; Fournier et al., 2012; Kristensen et al., 2016):

$$ext{cov}(\hat{m{v}}) = -\left[rac{\partial^2 \ell(\hat{m{ heta}},m{v}|m{y})}{\partialm{v}\partialm{v}^T}\Big|_{m{v}=\hat{m{v}}}
ight]^{-1} + rac{\partial\hat{m{v}}}{\partialm{ heta}}\Big|_{m{ heta}=\hat{m{ heta}}}\cdot ext{cov}(\hat{m{ heta}})\cdot\left(rac{\partial\hat{m{v}}}{\partialm{ heta}}\Big|_{m{ heta}=\hat{m{ heta}}}
ight)^T,$$

where $\partial \hat{v} / \partial \theta$ is the expression for the Jacobian matrix that takes into account the dependence of the likelihood estimator on the parameters θ (Skaug and Fournier, 2006).

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2.1. FREQUENTIST APPROACH

2.1.3 Laplace approximation

To approximate the marginal likelihood of θ (i.e., $\mathcal{L}(\theta|\mathbf{y})$) from the extended likelihood (i.e., $\mathcal{L}(\theta, \mathbf{v}|\mathbf{y})$), we use the Laplace approximation method (Skaug and Fournier, 2006; Fournier et al., 2012; Kristensen et al., 2016). Previously, we showed that

$$\mathcal{L}(\boldsymbol{ heta}|oldsymbol{y}) = \int \mathcal{L}(oldsymbol{ heta},oldsymbol{v}|oldsymbol{y}) doldsymbol{v}$$

which can be written as

$$\mathcal{L}(\boldsymbol{\theta}|\boldsymbol{y}) = \int \exp(\ell(\boldsymbol{\theta}, \boldsymbol{v}|\boldsymbol{y})) d\boldsymbol{v}.$$

Then, the Laplace approximation of the marginal likelihood is obtained by approximating $\ell(\theta, v | y)$, using a second order Taylor polynomial in the random effects v. Thus, by taking a Taylor series approximation of $\ell(\theta, v | y)$ around \hat{v} which maximises the extended log-likelihood $\ell(\theta, v | y)$ with respect to v:

$$egin{split} \mathcal{L}(oldsymbol{ heta}|oldsymbol{y}) &= \int \exp(\ell(oldsymbol{ heta},oldsymbol{v}|oldsymbol{y}))doldsymbol{v} \ &pprox \int \exp\left[\ell(oldsymbol{ heta},oldsymbol{\hat{v}}|oldsymbol{y}) + \ell'(oldsymbol{ heta},oldsymbol{\hat{v}}|oldsymbol{y}) \cdot (oldsymbol{v}-oldsymbol{\hat{v}}) \ &+ rac{1}{2}(oldsymbol{v}-oldsymbol{\hat{v}})^T \cdot \ell''(oldsymbol{ heta},oldsymbol{\hat{v}}|oldsymbol{y}) \cdot (oldsymbol{v}-oldsymbol{\hat{v}})^2
ight] doldsymbol{v}, \end{split}$$

where the vector $\ell'(\theta, \hat{v}|y)$ and matrix $\ell''(\theta, \hat{v}|y)$ are the first and second derivatives with respect to v of the extended log-likelihood, evaluated at the point \hat{v} .

Since by definition $\ell'(\boldsymbol{\theta}, \hat{\boldsymbol{v}} | \boldsymbol{y}) = 0$, we can simplify the above expression

to be

$$egin{split} \mathcal{L}(oldsymbol{ heta}|oldsymbol{y}) &pprox \mathcal{L}(oldsymbol{ heta}, \hat{oldsymbol{v}}|oldsymbol{y}) \cdot \int \exp\left(rac{1}{2}(oldsymbol{v}-\hat{oldsymbol{v}})^T \cdot \ell''(oldsymbol{ heta}, \hat{oldsymbol{v}}|oldsymbol{y}) \cdot (oldsymbol{v}-\hat{oldsymbol{v}})^2
ight) doldsymbol{v} \ &= \mathcal{L}(oldsymbol{ heta}, \hat{oldsymbol{v}}|oldsymbol{y}) \cdot \sqrt{rac{(2\cdot\pi)^n}{\det(-\ell''(oldsymbol{ heta}, \hat{oldsymbol{v}}|oldsymbol{y}))}}, \end{split}$$

where n is the dimension of the vector of random effects v.

2.2 Bayesian approach

In this section, we briefly describe how the Bayesian approach is used to fit SSMs. In the Bayesian approach, the posterior distribution for the hidden states v and parameters θ given the data y and the prior distribution for the parameters θ (i.e., $\pi(\theta)$) is defined by applying Bayes' theorem:

$$f(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) = \frac{\mathcal{L}(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \cdot \pi(\boldsymbol{\theta})}{\iint \mathcal{L}(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \cdot \pi(\boldsymbol{\theta}) d\boldsymbol{v} d\boldsymbol{\theta}},$$
(2.4)

where

$$\begin{split} f(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) &\propto f(\boldsymbol{y} | \boldsymbol{\theta}, \boldsymbol{v}) \cdot f(\boldsymbol{\theta}, \boldsymbol{v}) \\ &= f(\boldsymbol{y} | \boldsymbol{\theta}, \boldsymbol{v}) \cdot f(\boldsymbol{v} | \boldsymbol{\theta}) \cdot \pi(\boldsymbol{\theta}) \\ &= f(\boldsymbol{y}, \boldsymbol{v} | \boldsymbol{\theta}) \cdot \pi(\boldsymbol{\theta}) \\ &= \mathcal{L}(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \cdot \pi(\boldsymbol{\theta}). \end{split}$$

The denominator in Equation (2.4) represents the marginal probability of the data \boldsymbol{y} . The posterior distribution $f(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y})$ provides the basis for the inferences of the random variables $\boldsymbol{\theta}$ and \boldsymbol{v} ; thus, a main objective of a Bayesian analysis is to determine the posterior distribution.

Equation (2.4) contains a denominator that involves high-dimensional integrals that cannot often be expressed analytically and therefore must be approximated. Thus, most of Bayesian inference is concerned with the

computable parts of the posterior:

$$f(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \propto \mathcal{L}(\boldsymbol{\theta}, \boldsymbol{v} | \boldsymbol{y}) \cdot \pi(\boldsymbol{\theta}).$$

Such computational difficulty in Bayesian inference suggests that both frequentist and Bayesian approaches to SSMs have the same challenge in computing integrals of large dimensions. In the frequentist approach, we use Laplace's method to approximate such high-dimensional integration. In the Bayesian approach, simulation-based techniques that approximate the posterior distribution are used instead. The posterior distribution can be approximated with a large sample of dependent draws using various algorithms, such as Markov chain Monte Carlo (MCMC) methods.

MCMC methods are a general category of algorithms that are based upon sampling from a Markov chain rather than sampling directly from the posterior distribution $f(\theta, v|y)$. Different MCMC approaches have been developed, and Hamiltonian dynamics techniques, which are available in MCMC software such as Stan (Stan Development Team, 2016), have been found to be the most efficient for SSMs (Aeberhard et al., 2018). 24 CHAPTER 2. INFERENCE IN STATE-SPACE MODELS

Chapter 3

Estimability of a state-space surplus production model

3.1 Introduction

The surplus production model (SPM) has long been used in fisheries stock assessment, and its utility has been demonstrated by many previous studies (Hilborn and Walters, 1992; Polacheck et al., 1993; Quinn and Deriso, 1999; Mueter and Megrey, 2006; Haddon, 2010). Its simple structure renders it less data-demanding compared to other contemporary stock assessment models, thus it has been applied to many data-moderate fisheries to estimate fish stock status. Despite some structural limitations (Maunder, 2003; Wang et al., 2014), the SPM still remains a popular choice for fisheries modellers possibly due to considerable progress in the improvement of its framework by adapting a state-space approach. Numerous studies have demonstrated the implementation of the state-space framework for a SPM and developed effective software tools for stock assessment scientists (Millar and Meyer, 2000; McAllister, 2014; Winker et al., 2018, 2020).

The state-space surplus production model (SSPM) is a hierarchical model,

which is structured to incorporate both observation and process errors simultaneously, where the time-series of biomass (i.e., B_t , where B is the biomass and t is the time) is treated as a sequence of unobserved states (also known as latent variables), and those unobserved states B_t are linked to observed variables, such as the time series of relative abundance index (often denoted as I_t) collected from either scientific surveys or commercial fisheries (e.g., catch-per-unit-effort: CPUE) (Millar and Meyer, 2000). Unlike a conventional SPM, where the transition of the biomass B_t is deterministic (i.e., no process errors), a SSPM allows a stochastic transition of B_t to capture the effect of environmental randomness on the population changes.

Although a SSPM has a relatively simple structure compared to other contemporary stock assessment models, the likelihood surface may be almost flat or have long level ridges (Hyun and Kim, 2022), so that estimability of its model parameters is often questionable, thus requiring some external aids (e.g., constraints on parameters) for the successful convergence of a model (Millar and Meyer, 2000; McAllister et al., 2001; Punt, 2003; Ono et al., 2012; Parent and Rivot, 2012; Winker et al., 2018, 2020). We consider parameters to be estimable if a unique set of estimates that optimise the likelihood function exists (Auger-Méthé et al., 2016; Auger-Méthé et al., 2021). This condition is almost never satisfied in a SSPM, unless one incorporates extra constraints on the model parameters (Hyun and Kim, 2022). Those constraints are applied through a set of assumptions, or by incorporating strong prior information on model parameters. The assumptions commonly used in the published literature are that (i) the initial biomass is equal to the maximum capacity of the population size ($B_1 = K$, where K is the carrying capacity) (Millar and Meyer, 2000; Punt, 2003; Rankin and Lemos, 2015), and (ii) the observation and process error variances are equal to each other ($\sigma_{\varepsilon}^2 = \sigma_n^2$, where σ_{ε}^2 and σ_n^2 are the observation error and process error variances, respectively) (Ono et al., 2012; Parent and Rivot, 2012; Thorson and Minto, 2015). Alternatively, es-
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pecially in a Bayesian setting, the incorporation of prior knowledge has been used to aid the convergence of a model instead of applying those common assumptions (Millar and Meyer, 2000; McAllister, 2014; Winker et al., 2020). To do so, information available from the published literature on stock levels has been utilised, based on which a probability density function for each of the model parameter is included in a model.

Our preliminary simulation studies on the estimation performance of a SSPM indicated that the potential estimation problems associated with a SSPM can be two fold. First, a trend in time-series data should show enough contrast to inform model parameters to be estimable (Hilborn and Walters, 1992). Without such contrast in the data, a model would fail to uniquely describe how a stock responds to exploitation, which implies that there could be many other possible explanations for such a monotonic trend. This uninformative data trend is often termed as "one-way-trip" in fisheries science (Hilborn and Walters, 1992; McAllister et al., 2001), and its impact on the estimation of the parameters in a conventional SPM is well-described in Hilborn and Walters (1992), where a relationship between fishing effort, population abundance, and a population growth rate is explained in terms of the amount of contrast in time-series data. In Bayesian analysis of a SSPM, many attempts have already been made to overcome such an estimation problem associated with uninformative data in a SSPM by introducing prior knowledge in the form of a prior probability distribution to the model (Millar and Meyer, 2000; Parent and Rivot, 2012; Rankin and Lemos, 2015; Winker et al., 2018, 2020). However, to our knowledge, its consequences have not yet been thoroughly tested. For example, many studies that applied SSPMs did not test the estimability of model parameters, rather they focused on convergence of the models and validation tests (Millar and Meyer, 2000; Punt, 2003; Parent and Rivot, 2012; Winker et al., 2018, 2020). Although Ono et al. (2012) conducted a model performance test of a Bayesian SSPM, using various metrics, their performance test mainly focused on the comparison of models with different error types.

Second, the ratio between observation and process errors is an important factor for estimability of their variance parameters. Such an estimation problem in state-space models has already been discussed in previous studies (Dennis et al., 2006; Knape, 2008; Auger-Méthé et al., 2016), but they did not investigate the models where parameters are strongly informed by the incorporation of prior knowledge, which are the most common cases in Bayesian SSPMs in real applications (Sant'Ana et al., 2017; Winker et al., 2018; Sant'Ana et al., 2020; Winker et al., 2019, 2020). An estimation problem even in a simple linear state-space model, using a random walk process, has been demonstrated by Auger-Méthé et al. (2016). In their study, it is illustrated that if observation error is larger than process error, even a simple linear state-space model often fails to differentiate those two types of errors as the two variance parameters for the errors become inestimable. Our preliminary studies indicated that such an estimation problem associated with the error ratio can exist even in a Bayesian SSPM where parameters are strongly informed by their priors.

As we discussed in Chapter 2, A SSPM can be fitted using both frequentist and Bayesian approaches. The former can be conducted by a maximum marginal likelihood method, where unobserved states are integrated out through a Laplace approximation technique, and the resultant marginal likelihood is maximised to obtain the maximum likelihood estimates (MLEs) of the parameters (Skaug and Fournier, 2006; Kristensen et al., 2016). In this frequentist approach, constraints on model parameters can be incorporated as penalties on a likelihood function, prior distributions in a Bayesian setting. The latter is analysed by a Markov Chain Monte Carlo (MCMC) sampling method, where random samples from the posterior distribution of the parameters are drawn for inference (Gelman et al., 2013; Monnahan and Kristensen, 2018). For our simulation studies, we mainly use the frequentist approach because of its substantial computational efficiency compared to the Bayesian sampling method, and this

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has allowed us to explore a large number of simulation-estimation runs in a relatively short amount of time. To reassure ourselves that the choice of the estimation method does not affect the results of our simulation studies, we use both frequentist and Bayesian approaches for selected scenarios and compare those results. Since we apply both frequentist and Bayesian paradigms, we use the term "constraints" to refer to both penalties in a frequentist method and priors in a Bayesian method.

The main purpose of this study is to systematically identify the source of the estimation problems in a SSPM, which were detected in our preliminary studies. We conduct comprehensive simulation studies which cover many different possible scenarios in practice. Incorporating constraints into a SSPM becomes a standard technique because of the well-known difficulty in estimating all model parameters and state variables without any external aid; thus, we aim to test model estimation performance under the condition that each model parameter is strongly and correctly informed by its constraint. With such a strong constraint, one may easily expect a successful convergence of a model as well as its good performance (e.g., parameter estimates with low bias and high precision), but our preliminary studies informed us that even the correct application of parameter constraints (e.g., a true value for each parameter is given the most weight) can result in biased estimates of the parameters, which simultaneously affects the prediction of the state variables (i.e., B_t). To construct realistic and convincing scenarios, we obtain input values, which are used to simulate data, from a coventional SPM fitted to the Namibian hake and Atlantic albacore data sets. Such data sets are well studied and widely applied to both SPMs and SSPMs for demonstration purposes in quantitative fisheries science (Hilborn and Walters, 1992; Polacheck et al., 1993; Millar and Meyer, 2000; Punt, 2003; Parent and Rivot, 2012; Rankin and Lemos, 2015).

The rest of this chapter is structured as follows. First, we describe a SSPM and constraints imposed on the parameters of a SSPM. Second, after a mathematical description of the model, the two different estimation

methods are discussed. Third, details of the simulation scenarios and evaluation metrics are described. We also explain a sensitivity analysis used to examine the effect of incorporation of parameter constraints on model performance. Lastly, simulation results are illustrated and discussed.

Notation	Description
t	index for time
T	total number of time steps t
s	index for each simulation scenario
i	index for each simulation run
I_t	abundance index at time t (e.g., catch-per-unit-effort: CPUE)
Y_t	fishery yield at time t (i.e., total catch)
B_t	biomass at time t
H_t	harvest rate at time t (i.e., $H_t = Y_t/B_t$)
P_t	Scaled biomass (or stock status; $P_t = B_t/K$) at time t
ε_t	observation error at time t
η_t	process error at time t
$\sigma_{arepsilon}^2$	variance of the observation error
σ_η^2	variance of the process error
b	proportion of B_1 relative to K
q	catchabiliy coefficient
r	intrinsic growth rate
K	carrying capacity
MSY	maximum sustainable yield (i.e., MSY = $\frac{r \cdot K}{4}$)
heta	vector of the six model parameters (i.e., $\boldsymbol{\theta} = (\sigma_{\eta}, \sigma_{\varepsilon}, b, K, r, q)$)

Table 3.1: Notation summary

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3.2 Methods

In this section, we describe a logistic production model in a state-space framework, which is used throughout this study. This logistic form is the simplest type of a production function considered in a SPM and has been well studied (Hilborn and Walters, 1992; Polacheck et al., 1993; Quinn and Deriso, 1999; Haddon, 2010). Using this form of a SSPM, we explore the estimability of the model parameters under different scenarios which are designed to address various questions that concern the application of a SSPM. In all scenarios, we impose probability density functions on all of the model parameters are used as the modes of those constraints, and their dispersions are set to be 30% of the coefficient of variation (CV). The implementation of those constraints can be considered extreme because in a real world application, such precise information is not known, which would make results of our simulation studies rather conservative.

The data simulation process, a metric used for evaluation of the model performance, and sensitivity analysis are also described. A summary of the notation used in this study can be found in Table 3.1.

3.2.1 State-space surplus production model (SSPM)

Referring to previous studies (Millar and Meyer, 2000; Winker et al., 2018, 2020), we use a logistic production model in the following state-space form, where two sources of variability, observation error ε_t and process error η_t , are separately incorporated:

$$\begin{cases} B_{1} = b \cdot K \cdot \exp(\eta_{1}) \\ B_{t+1} = \left[B_{t} + r \cdot B_{t} \cdot \left(1 - \frac{B_{t}}{K} \right) - Y_{t} \right] \cdot \exp(\eta_{t+1}), & \text{for } 1 \leq t < T \\ I_{t} = q \cdot B_{t} \cdot \exp(\varepsilon_{t}), & \text{for } 1 \leq t \leq T \\ & \text{where } \varepsilon_{t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{\varepsilon}^{2}\right) \text{ and } \eta_{t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{\eta}^{2}\right) \end{cases}$$
(3.1)

where B_t is the biomass at time t, b is the proportion of B_1 relative to the carrying capacity K, η_t is the process error, which is normally distributed with mean 0 and variance σ_{η}^2 , r is the intrinsic growth rate, Y_t is the fishery yield at time t, I_t is the abundance index (e.g., CPUE) at time t, q is the catchability coefficient, and ε_t is the observation error, which is also normally distributed with mean 0 and variance σ_{ε}^2 .

To improve the efficiency of the numerical estimation, we scale down B_t by dividing it by K (i.e., $P_t = B_t/K$) (Millar and Meyer, 2000), and linearise Equation (3.1) by taking the natural logarithm:

$$\begin{cases} \log P_1 = \log b + \eta_1 \\ \log P_{t+1} = \log \left[P_t + r \cdot P_t \cdot (1 - P_t) - \frac{Y_t}{K} \right] + \eta_{t+1}, & \text{for } 1 \le t < T \\ \log I_t = \log q + \log P_t + \log K + \varepsilon_t, & \text{for } 1 \le t \le T \end{cases}$$
(3.2)

In this reparameterised form, P_t is treated as the state variable instead of B_t .

Constraints

We impose constraints on all of the six parameters (i.e., $\theta = (b, K, q, r, \sigma_{\eta}, \sigma_{\varepsilon})$) to aid the convergence of the SSPM. Based on the independence assumption between the parameters θ (Millar and Meyer, 2000; Ono et al., 2012),

the constraints are expressed as a product density of all model parameters:

$$\pi(\boldsymbol{\theta}) = \pi(\sigma_{\varepsilon}^2, \sigma_{\eta}^2, b, K, q, r)$$

= $\pi(\sigma_{\varepsilon}^2) \cdot \pi(\sigma_{\eta}^2) \cdot \pi(b) \cdot \pi(K) \cdot \pi(q) \cdot \pi(r),$

where

$$\begin{cases} \sigma_{\varepsilon}^{2} \sim \text{inverse-gamma}(\alpha_{\varepsilon}, \beta_{\varepsilon}) \\ \sigma_{\eta}^{2} \sim \text{inverse-gamma}(\alpha_{\eta}, \beta_{\eta}) \\ b \sim \text{lognormal}(\mu_{b}, \sigma_{b}^{2}) \\ K \sim \text{lognormal}(\mu_{K}, \sigma_{K}^{2}) \\ q \sim \text{lognormal}(\mu_{q}, \sigma_{q}^{2}) \\ r \sim \text{lognormal}(\mu_{r}, \sigma_{r}^{2}) \end{cases}$$

The choice of the probability distribution for each parameter is based on previous studies (Millar and Meyer, 2000; Ono et al., 2012; Rankin and Lemos, 2015). The domain of all six parameters is the positive real line. Note that imposing a uniform distribution for the natural logarithm of the catchability coefficient q (i.e., log(q)) is a more popular choice than using a lognormal distribution for q in some literature due to a lack of sufficient information to construct a stronger constraint for q (Millar and Meyer, 2000; Ono et al., 2012; Rankin and Lemos, 2015). The values for parameters of the constraints are determined using the mode and coefficient of variation (CV) (see Table 3.2).

3.2.2 Estimation

The penalised likelihood of the parameters (i.e., $\boldsymbol{\theta} = (\sigma_{\varepsilon}, \sigma_{\eta}, b, r, k, q)$) and the state variables (i.e., $\boldsymbol{P} = (P_1, P_2, P_3, ..., P_T)$) is the joint density of those unknowns, constraints (i.e., penalties), and the data $\boldsymbol{I} = (I_1, I_2, I_3, ..., I_T)$,

Table 3.2: Probability densities and their parameters, which are used as the constraints for the six model parameters in the state-space surplus production model (SSPM). The parameters for the distributions are determined, using the true input values of the model parameters, shown in Table 3.3, as the modes of their corresponding probability distributions (denoted by the subscription *o*) and the coefficient of variation (CV).

Distribution	Parameters				
$\sigma_{\varepsilon}^2 \sim \operatorname{inverse-gamma}(\alpha_{\varepsilon}, \beta_{\varepsilon})$	$\alpha_{\varepsilon} = 1/\mathbf{C}\mathbf{V}^2 + 2, \beta_{\varepsilon} = \sigma_{\varepsilon,o}^2 \cdot (\alpha_{\varepsilon} + 1)$				
$\sigma_{\eta}^2 \sim \text{inverse-gamma}(\alpha_{\eta}, \beta_{\eta})$	$\alpha_{\eta} = 1/\mathbf{C}\mathbf{V}^2 + 2, \beta_{\eta} = \sigma_{\eta,o}^2 \cdot (\alpha_{\eta} + 1)$				
$b \sim \text{lognormal}(\mu_b, \sigma_b^2)$	$\mu_b = \log(b_o) + \sigma_b^2, \sigma_b^2 = \log\left(\mathbf{C}\mathbf{V}^2 + 1\right)$				
$K \sim \text{lognormal}(\mu_K, \sigma_K^2)$	$\mu_K = \log(K_o) + \sigma_K^2, \sigma_K^2 = \log\left(\mathbf{C}\mathbf{V}^2 + 1\right)$				
$q \sim \text{lognormal}(\mu_q, \sigma_q^2)$	$\mu_q = \log(q_o) + \sigma_q^2, \sigma_q^2 = \log\left(\mathrm{CV}^2 + 1\right)$				
$r \sim \text{lognormal}(\mu_r, \sigma_r^2)$	$\mu_r = \log(r_o) + \sigma_r^2, \sigma_r^2 = \log\left(\mathrm{CV}^2 + 1\right)$				

which can be written as

$$\mathcal{L}(\boldsymbol{\theta}, \boldsymbol{P} | \boldsymbol{I}) = \pi \left(\sigma_{\varepsilon}^{2}, \sigma_{\eta}^{2}, b, K, q, r \right) \cdot f \left(P_{1} \mid \sigma_{\eta}^{2}, b \right) \cdot \prod_{t=2}^{T} f(P_{t} \mid P_{t-1}, \sigma_{\eta}^{2}, K, r; Y_{t-1}) \\ \times \prod_{t=1}^{T} f(I_{t} \mid P_{t}, \sigma_{\varepsilon}^{2}, q).$$

$$(3.3)$$

To estimate those unknowns (i.e., θ and P), we use both frequentist and Bayesian methods although, as noted in Chapter 2, the former is our primary method due to its considerable computational efficiency.

In a frequentist setting, a marginal maximum likelihood method, where the joint density $\pi(\theta)$ serves as a penalty on the likelihood function, is conducted, using the R package TMB (R Core Team, 2014; Kristensen et al., 2016). The marginal likelihood $\mathcal{L}(\theta \mid I)$ is obtained by integrating out the state variables P:

$$\mathcal{L}(\boldsymbol{\theta} \mid \boldsymbol{I}) = \int \mathcal{L}(\boldsymbol{\theta}, \boldsymbol{P} \mid \boldsymbol{I}) d\boldsymbol{P}.$$

In TMB, this integration is approximated by the Laplace approximation technique (Skaug and Fournier, 2006; Kristensen et al., 2016).

By maximizing the marginal likelihood with respect to θ , using numerical optimisation techniques in R such as a function minimiser like nlminb(), the estimate of θ (i.e., $\hat{\theta}$) can be obtained:

$$\hat{\boldsymbol{ heta}} = rg\max_{\boldsymbol{ heta}} \log[\mathcal{L}(\boldsymbol{ heta} \mid \boldsymbol{I})]$$

Once $\hat{\theta}$ is found, TMB sequentially estimates the state variables P by maximizing the estimated conditional likelihood with respect to P, where θ is fixed at $\hat{\theta}$:

$$\hat{\boldsymbol{P}} = \arg \max_{\boldsymbol{P}} \log[\mathcal{L}(\hat{\boldsymbol{\theta}}, \boldsymbol{P} | \boldsymbol{I})].$$

Furthermore, the uncertainty of parameter estimates is evaluated via the delta method, where the determinant of a Hessian matrix of the marginal likelihood is found via a numerical Cholesky decomposition (Skaug and Fournier, 2006; Kristensen et al., 2016). If the absolute value of the maximum gradient component of the parameters is less than 0.01, and the Hessian matrix is positive definite, we deem that the frequentist model has successfully converged (Kristensen et al., 2016).

In the Bayesian setting, we use a MCMC method to draw random samples from a posterior distribution of the parameters for inference. We use the R package tmbstan to perform the Bayesian inference (Monnahan and Kristensen, 2018), which allows users to implement the MCMC sampling from a TMB object, using the R package rstan (R Core Team, 2014; Stan Development Team, 2016). We conduct MCMC runs of 20,000 iterations and discard the first 5,000 samples as the burn-in period for each chain. For convergence criteria, we check the number of divergent transitions and the potential-scale-reduction statistic \hat{R} (Gelman et al., 2013). We deem that the Bayesian model has successfully converged if there is no divergent transition, and \hat{R} is smaller than 1.01 (Stan Development Team, 2016).

3.2.3 Simulation studies

Harvest rates used for data simulation

For our simulation studies, besides the input values of the six model parameters, we use the time-series of the fishing harvest rate H_t to simulate data on both the relative abundance index I_t and the yield Y_t . The harvest rate H_t is defined as the proportion of the total yield Y_t relative to the total biomass B_t :

$$H_t = \frac{Y_t}{B_t}.$$

To obtain realistic input values for H_t instead of using arbitrarily generated values, we utilise the model estimated H_t (i.e., \hat{H}_t) obtained from a conventional SPM (i.e., $\sigma_{\eta}^2 = 0$) fitted to actual data sets on I_t and Y_t , which are collected from the Namibian hake and Atlantic albacore stocks (see Figure 3.1 (a), (b), (d) and (e)). In this study, we do not aim to assess those two popular stocks, so we do not provide detailed information about them as this information is already available in other publications (Hilborn and Walters, 1992; Polacheck et al., 1993; Millar and Meyer, 2000).

The reason why we use a SPM instead of a SSPM to obtain \hat{H}_t from the actual data sets is because (i) the former can be successfully fitted to the data sets without the aid of the strong constraints which largely affect the estimates of the parameters in the SSPM, and (ii) a previous study by Polacheck et al. (1993) demonstrated the fitting procedure of the SPM, using the same data sets.

To estimate the parameters of the SPM (i.e., $\theta^{\text{SPM}} = (r, K, \sigma_{\varepsilon}, q)$), which are used to derive the estimates of H_t , we use the maximum likelihood estimation (MLE) method:

$$\hat{\boldsymbol{ heta}}^{ ext{SPM}} = rg\max_{\boldsymbol{ heta}^{ ext{SPM}}} \log[\mathcal{L}(\boldsymbol{ heta}^{ ext{SPM}} \mid \boldsymbol{I})],$$

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where

$$\mathcal{L}(\boldsymbol{\theta}^{\text{SPM}}|\boldsymbol{I}) = \prod_{t=1}^{T} f(I_t|r, K, \sigma_{\varepsilon}, q; Y_t).$$

Following Polacheck et al. (1993), we assume that the initial biomass B_1 is equal to the carrying capacity K (i.e., $B_1 = K$), so the parameter b is not estimated, but given as an input (i.e., b = 1).

Using those actual data sets, we obtain the two sets of the model estimated harvest rates \hat{H}_t , which show the two distinct time-series trends, increase-decrease and increase. To consider more trends in H_t for simulation studies, we simply invert those two sets of \hat{H}_t (i.e., $H_t^{\text{inverted}} = -\hat{H}_t + \min(\hat{H}_t) + \max(\hat{H}_t)$), whereby the two additional time-series trends, decrease-increase and decrease, are obtained. We denote the four trends of H_t as HR1, HR2, HR3, and HR4, respectively (see Figure 3.1 (c) and (f)).

Scenario settings

To explore various scenarios systematically, we formulate scenarios, based on two different types of sub-scenario. The first type of sub-scenario concerns the sensitivity to input parameter values. In this sub-scenario, we vary the input values for σ_{η} , σ_{ε} , and r to investigate the impact of those parameter values in the estimation process. The candidate values for σ_{η} and σ_{ε} are selected by referring to previous studies (i.e., σ_{η} , $\sigma_{\varepsilon} \in \{0.05, 0.1, 0.15\}$, and $\sigma_{\eta} + \sigma_{\varepsilon} = 0.2$) (Millar and Meyer, 2000; Parent and Rivot, 2012; Rankin and Lemos, 2015), and those for r are chosen based on biological realism (i.e., $r \in \{0.2, 0.4, 0.6\}$). The values for q and K are arbitrarily chosen as q = 0.01 and K = 100 and kept constant in all simulation scenarios, including a few additional scenarios described in the next section. One should note that q and K only affect the overall scaling of I_t and Y_t ; thus, we do not consider varying these parameter values in our simulation scenarios. The value for b is chosen as b = 1 and kept constant in all 36 scenarios described in this section, but we also test the sensitivity of b by changing



Figure 3.1: Time-series of catch-per-unit-effort (CPUE; panels (a) and (d)), fishery yield (panels (b) and (e)), and estimated harvest rates (panels (c) and (f)) on Namibian hake and Atlantic albacore stocks. Each column of the panels shows those of each data set. The points in panels (a) and (b) are observed CPUEs, and the red lines in the same panels are the model estimated values obtained from a conventional surplus production model (i.e., $\sigma_{\eta} = 0$) fitted to those CPUEs. The solid lines in panels (c) and (f) are the estimated harvest rates, and the broken lines in the same panels are the inverted values of those estimated harvest rates, which are denoted as HR1, HR2, HR3, and HR4, respectively.

it to 0.7 in additional scenarios described in the next section.

Using those candidate values for σ_{η} , σ_{ε} , and r, we design nine different

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cases, which are denoted as S1-S9, respectively (see Table 3.3).

Table 3.3: Nine cases in terms of the input parameter values, which are designed to test the impact of observation and process error variances and the intrinsic growth rate on the model performance. The values for b, q, and K are kept constant in all nine cases.

	Parameter						
Scenario	$\sigma_{arepsilon}$	b	σ_η	K	q	r	
S1	0.05	1.00	0.15	100.00	0.01	0.20	
S2	0.10	1.00	0.10	100.00	0.01	0.20	
S 3	0.15	1.00	0.05	100.00	0.01	0.20	
S4	0.05	1.00	0.15	100.00	0.01	0.40	
S5	0.10	1.00	0.10	100.00	0.01	0.40	
S6	0.15	1.00	0.05	100.00	0.01	0.40	
S7	0.05	1.00	0.15	100.00	0.01	0.60	
S 8	0.10	1.00	0.10	100.00	0.01	0.60	
S9	0.15	1.00	0.05	100.00	0.01	0.60	

The second type of sub-scenario concerns the impact of the trends of the abundance index I_t and the fishery yield Y_t on the model performance. In this sub-scenario, we use the four different sets of time-series of harvest rates H_t , which were described in the earlier section (Figure 3.1). The time-series length of each data set differs by two (i.e., 25 for the hake data and 23 for albacore data), so we discard the last two points of the HR1 and HR2 trends, giving us the same time-series length of 23 for all four harvest rate trends. Those four sets of H_t are then used to simulate both I_t and Y_t in all simulation scenarios considered in this study.

All possible combinations of those two types of sub-scenario are considered, and are denoted jointly as $s \in \{$ HR1.S1, HR1.S2,...,HR1.S9,...,HR4.S1, HR4.S2,...,HR4.S9 $\}$. Thus, a total of 36 scenarios (i.e., $9 \times 4 = 36$) are designed to address the following questions:

(i) Which source of variability between the observation and process errors affects the model estimation more? To test this, we set the ratio of the observation and process error standard deviations differently. Three different ratios are considered for this experiment: $\sigma_{\varepsilon}/\sigma_{\eta} = 1/3$, $\sigma_{\varepsilon}/\sigma_{\eta} = 1$, and $\sigma_{\varepsilon}/\sigma_{\eta} = 3$, where $\sigma_{\varepsilon}, \sigma_{\eta} \in \{0.05, 0.1, 0.15\}$ and $\sigma_{\eta} + \sigma_{\varepsilon} = 0.2$.

- (ii) Do the trends in the time-series of abundance index (i.e., *I_t*) and fishery yield (i.e., *Y_t*) data affect the estimation? For this question, we use the four different trends of the time-series of harvest rates (i.e., HR1-4) and the three different values for the intrinsic growth rate *r* (i.e., *r* ∈ {0.2, 0.4, 0.6}) to simulate the data on *I_t* and *Y_t*.
- (iii) Is the simultaneous estimation of both parameters and state variables a cause of parameter estimation problems in the SSPM? To examine this question, we compare the estimates obtained from the model where both unknowns are simultaneously estimated with those from the models where either the parameters or the state variables are fixed at their true values, and only the remaining unknowns are estimated.

Additional scenarios

Besides these 36 scenarios, we investigate a few more additional scenarios to examine (i) the sensitivity of parameter b, (ii) the impact of the dispersion of the constraints, and (iii) the impact of the incorporation of two more replicated sets of the data on the model performance. For the sensitivity test of the parameter b, we set b = 0.7 instead of b = 1 which is kept constant for all 36 scenarios. For the sensitivity to the dispersion of the constraints, we use either CV = 0.1 or CV = 0.5 instead of CV = 0.3. The incorporation of more data sets is simply conducted by including two more replicated sets of I_t , which are simulated with different seed values, for each simulation-estimation run. All these alternative settings are investigated under the six selected scenarios which are HR4.S1, HR4.S3, HR4.S4, HR4.S6, HR4.S7, and HR4.S9. These six scenarios are chosen be-

cause they seem to well represent the overall results of the 36 simulation scenarios.

Simulation-estimation procedure

For each scenario *s*, we simulate 500 sets of the abundance index and fishery yield data (i.e., $I_{t,i}^s$ and $Y_{t,i}^s$), given the input values described in Table 3.3 and Figure 3.1, where *i* denotes each simulation run (i.e., $i \in \{1, 2, 3, ..., 500\}$):

$$\begin{cases} B_{1,i}^{s} = b^{s} \cdot K^{s} \cdot \exp(\eta_{1,i}^{s}) \\ B_{t+1,i}^{s} = \left[B_{t,i}^{s} + r^{s} \cdot B_{t,i}^{s} \cdot \left(1 - \frac{B_{t,i}^{s}}{K^{s}}\right) - H_{t}^{s} \cdot B_{t,i}^{s} \right] \cdot \exp\left(\eta_{t+1,i}^{s}\right), & \text{for } 1 \leq t < T \\ I_{t,i}^{s} = q^{s} \cdot B_{t,i}^{s} \cdot \exp(\varepsilon_{t,i}^{s}), & \text{for } 1 \leq t \leq T \\ Y_{t,i}^{s} = H_{t}^{s} \cdot B_{t,i}^{s}, & \text{for } 1 \leq t \leq T \\ where \eta_{t,i}^{s} \stackrel{\text{iid}}{\sim} N(0, (\sigma_{\eta}^{s})^{2}) \text{ and } \varepsilon_{t,i}^{s} \stackrel{\text{iid}}{\sim} N(0, (\sigma_{\varepsilon}^{s})^{2}), \\ (3.4) \end{cases}$$

Then, each set of those simulated data is applied to Equation (3.2) to obtain the estimates of the six parameters and the biomass (i.e., $\hat{\theta}^s$ and $\hat{B}_{t,i}^s$). The median trend of those simulated data is shown in Figure 3.2. By comparing those estimates with their true values, we are able to test the model performance for each scenario *s*. A metric used for the performance test is described in the following section.





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Evaluation of model performance

We use the median of relative difference (RD) to investigate if there is any systematic bias in the point estimates of the parameters and the stock status (i.e., B_t/K) for each scenario $s \in \{\text{HR1.S1-9}, \text{HR2.S1-9}, \text{HR3.S1-9}, \text{HR4.S1-9}\}$:

$$\mathrm{RD}_i(\Theta^s) = \frac{\Theta_i^s}{\Theta_i^s} - 1, \qquad (3.5)$$

where $i \in \{1, 2, 3, ..., 500\}$, $\Theta^s \in \{\sigma_{\varepsilon}^s, \sigma_{\eta}^s, b^s, q^s, K^s, r^s, B_1^s/K^s, B_2^s/K^s, ..., B_{23}^s/K^s\}$, Θ_i^s is the true value for the quantity of interest for the *i*th simulated data set under the scenario *s*, and $\hat{\Theta}_i^s$ is the estimate of the quantity.

Since RD can be unstable if the denominator is close to zero, we also evaluate relative difference between the median (RDM) of the estimates of the last biomass B_{23}^s and stock status B_{23}^s/K^s and that of their true values:

$$\text{RDM}(\Psi^s) = \frac{\text{median}(\{\hat{\Psi}_i^s\}_{i=1}^{i=500})}{\text{median}(\{\Psi_i^s\}_{i=1}^{i=500})} - 1,$$

where $\Psi^{s} \in \{B_{23}^{s}, B_{23}^{s}/K^{s}\}.$

To examine if the potential cause of the estimation problem is involved with the simultaneous estimation of the state variables and the parameters, we fit the same model to simulated data sets, where we fix either parameters or state variables at their true values, depending on the purpose of the investigation. For example, to examine the problem in parameter estimation, we fix the state variables (log P_t) at their true values (i.e., values obtained from Equation (3.4)) and only estimate the model parameters. The estimates are then compared with those from the model which simultaneously estimates the state variables and the parameters. Similarly, to examine the problem in state variable estimation, we fix the parameters at their true values (i.e., input parameter values given in Table 3.3) and estimate the state variables, which are compared with those from the model for the simultaneous estimation.

Sensitivity of the parameter estimates to the constraint

To examine the sensitivity of estimates of the model parameters to the constraint $\pi(\theta)$, we reevaluate performance of the SSPM based on the RD of the parameter estimates, where we exclude each of the independent probability densities one by one from the joint penalised likelihood $\mathcal{L}(\theta, P|I)$ in Equation (3.3) and refit the resultant model. The exclusion of each penalty in a frequentist setting is equivalent to imposing a uniform prior on each parameter in a Bayesian setting. This sensitivity analysis is conducted under scenarios HR4.S4 and HR4.S6. We chose these two scenarios because the SSPM showed the poorest performance under scenario HR4.S6 among the 36 scenarios, and scenario HR4.S4 is the counterpart of scenario HR4.S6 in terms of the input values of the two variance parameters (i.e., $\sigma_{\varepsilon}^2 > \sigma_{\eta}^2$ in scenario HR4.S6, and $\sigma_{\varepsilon}^2 < \sigma_{\eta}^2$ in scenario HR4.S4).

We also check the loglikelihood profile of the natural logarithm of each parameter when its corresponding probability distribution is excluded from the model while the other five parameters are still strongly informed by their constraints. This examination allows us to investigate estimability and sensitivity of each parameter. The loglikelihood profiles of the parameters differ in each simulation-estimation run. Thus, in each of the two selected scenarios (i.e., HR4.S4 and HR4.S6), we randomly selected 100 sets of simulation-estimation runs to derive 100 different loglikelihood profiles for each parameter. For visual inspection, the loglikelihood values of the profiles are standardised to lie between 0 and 1.

3.3 Results

3.3.1 Simulation evaluation

All 500 simulation-estimation runs for each scenario *s* have successfully converged with the frequentist approach. The median RD for the six model

parameters and the biomass and the stock status at the last time step (i.e., B_{23} and B_{23}/K) in all 36 scenarios are tabulated in Tables 3.4 and 3.5. In Table 3.4, the estimates are obtained from the models where both the parameters and the state variables are allowed to be estimated, whereas those in Table 3.5 are obtained from the models where either parameters or state variables are fixed at their true values. Overall, the biases in RDM are slightly greater than those in the median RD, but both metrics indicate that the model performs poorly under the HR2 and HR4 scenarios (Table 3.6).

The model generally shows poor performances in terms of the median RD under the scenarios where the observation error variance is equal or greater than the process error variance (S2, S3, S5, S6, S8 and S9; Table 3.4). The worst performance seems to occur when (i) the HR4 trend is involved, and (ii) the observation error variance is greater than the process error variance (i.e., HR4.S3, HR4.S6, and HR4.S9; see Table 3.4 and Figure 3.3). The biases are prominent especially in the parameters *b* and *q*, which showed biases of 12% and -9%, respectively under scenario HR4.S6. However, when the process error variance is larger than the observation error (i.e., Scenario HR4.S4), such biases are reduced to 5% and -3%, which is over twice the performance improvement on average (Table 3.4). The relatively large biases in the estimates of the parameters *b* and *q* induce the positive bias of the stock status B_t/K , which are observed by comparing Figures 3.3 and 3.4 with Figures 3.5 and 3.6.

When either the parameters or the state variables are estimated alone, the biases in the estimates of both parameters and state variables are almost negligible under all 36 scenarios (all absolute biases are less than 5%; see Table 3.5), which suggests that the poor model performance in certain scenarios, such as scenario HR4.S6, is also partially involved with the simultaneous estimation of the parameters and the state variables in the SSPM.

Differences in input values for parameter r are not clearly associated

with the bias of parameter estimates. For example, under the scenarios associated with the HR2 trend (i.e., HR2.S1-S9), when r = 0.2 (i.e., HR2.S1-S3), the model generally shows poor performance, but under the scenarios associated with the HR4 trend (i.e., HR4.S1-S9), the worst performance occurs when r = 0.4 (i.e., HR4.S4-S6). This suggests that the model performance in terms of a trend of time-series data is involved jointly with both H_t and r as those quantities together determine the trend of time-series data.

Table 3.4: Median of relative difference (%) (i.e., a median value of $\text{RD}_i(\cdot)$ of Equation (3.5) in percent) of the estimates of the six model parameters, the biomass at the last time step t = 23 (i.e., \hat{B}_{23}), and the stock status at the last time step t = 23 (\hat{B}_{23}/\hat{K}) under the 36 scenarios. The estimates are obtained from the model for the simultaneous estimation of both the parameters and the s tate variables. Absolute biases greater than 5% are shaded in gray.

			Median Relative difference (%)						
Scenario	$\hat{\sigma}_{arepsilon}$	\hat{b}	$\hat{\sigma}_{\eta}$	\hat{K}	\hat{q}	\hat{r}	MŜY	\hat{B}_{23}	\hat{B}_{23}/\hat{K}
HR1.S1	-0.4	3.4	-3.6	-2.6	-1.1	4.1	1.6	0.2	2.8
HR1.S2	-0.8	3.7	-4.4	-1.1	-2.7	2.0	0.8	2.5	3.7
HR1.S3	-2.1	4.4	-3.3	-0.3	-3.0	-0.5	-0.8	2.7	3.7
HR1.S4	-0.4	4.3	-4.2	-3.4	-0.9	6.8	3.8	1.2	2.9
HR1.S5	-1.0	3.6	-4.3	-1.1	-2.1	4.8	3.3	1.7	2.2
HR1.S6	-2.2	2.6	-3.2	-0.2	-1.2	2.0	1.7	2.1	1.2
HR1.S7	-0.5	2.7	-4.0	-2.3	-0.0	6.0	5.2	0.3	1.2
HR1.S8	-1.4	2.4	-3.8	-1.3	-1.3	5.6	4.0	0.7	1.4
HR1.S9	-2.5	1.5	-2.4	-1.0	0.3	3.7	2.3	-0.7	0.6
HR2.S1	-0.4	3.2	-3.3	-1.7	-1.6	3.5	0.0	1.1	3.6
HR2.S2	-0.8	6.0	-4.1	-1.7	-4.4	1.2	-2.5	3.9	6.5
HR2.S3	-1.5	8.6	-3.3	-2.4	-5.2	-0.5	-4.3	6.7	10.0
HR2.S4	-0.5	3.7	-3.7	-1.7	-2.8	5.7	3.5	2.0	3.8
HR2.S5	-1.0	5.6	-4.0	-0.5	-5.4	5.6	4.2	5.5	5.8
HR2.S6	-2.2	6.2	-3.2	-0.2	-4.4	4.4	4.0	5.7	6.5
HR2.S7	-0.5	1.8	-4.0	-0.1	-1.5	4.6	4.1	1.5	1.6
HR2.S8	-1.5	3.2	-3.8	1.0	-3.0	5.2	5.3	3.3	2.1
HR2.S9	-2.8	1.7	-2.3	1.0	-1.9	3.8	3.3	2.6	1.8
HR3.S1	-0.4	3.7	-3.5	-1.9	-2.2	5.2	2.3	1.4	2.9
HR3.S2	-0.9	5.4	-3.9	-0.7	-3.7	3.1	0.9	4.5	4.1
HR3.S3	-1.6	5.0	-3.2	-0.1	-4.1	0.0	-0.5	5.6	5.7
HR3.S4	-0.5	3.8	-3.8	-1.6	-2.1	6.5	5.8	2.2	3.0
HR3.S5	-1.3	5.1	-3.6	-0.4	-3.6	6.1	5.6	4.1	3.4
HR3.S6	-2.0	3.8	-2.8	-0.1	-2.6	4.2	2.7	3.8	4.2
HR3.S7	-0.5	2.3	-3.6	-0.7	-1.1	6.1	5.4	1.2	1.5
HR3.S8	-1.6	3.3	-3.2	-0.1	-2.3	6.6	6.3	2.5	1.9
HR3.S9	-2.6	1.0	-1.8	-0.4	-1.4	4.5	3.2	2.1	2.3
HR4.S1	-0.5	2.6	-3.5	-1.2	-1.4	1.3	-0.6	1.7	2.9
HR4.S2	-0.8	5.1	-4.1	-0.9	-3.8	-2.2	-4.2	4.0	6.0
HR4.S3	-1.7	7.3	-2.9	-2.0	-5.9	-6.7	-8.7	5.5	8.1
HR4.S4	-0.5	5.3	-3.7	-2.3	-3.1	3.4	0.7	2.8	4.8
HR4.S5	-1.0	9.2	-4.2	-1.1	-6.9	1.0	-0.5	6.0	7.4
HR4.S6	-1.8	12.2	-3.1	-0.9	-9.4	-1.7	-2.7	8.8	9.1
HR4.S7	-0.5	3.3	-3.6	-0.5	-2.9	3.9	3.3	1.9	2.3
HR4.S8	-1.2	6.5	-3.6	1.3	-6.3	3.8	4.1	5.2	3.8
HR4.S9	-2.2	6.6	-2.5	1.4	-6.2	3.3	3.4	4.5	3.9

Table 3.5: Median of relative difference (%) (i.e., a median value of $\text{RD}_i(\cdot)$ of Equation (3.5) in percent) of the estimates of the six model parameters, the biomass at the last time step t = 23 (i.e., \hat{B}_{23}), and the stock status at the last time step t = 23 (\hat{B}_{23}/\hat{K}) under the 36 scenarios. The estimates are obtained from the models where either the parameters or the state variables are fixed at their true values and only the remaining unknowns are allowed to be estimated.

			Median Relative difference (%)						
Scenario	$\hat{\sigma}_{arepsilon}$	\hat{b}	$\hat{\sigma}_{\eta}$	\hat{K}	\hat{q}	\hat{r}	MŜY	\hat{B}_{23}	\hat{B}_{23}/K
HR1.S1	-1.6	0.9	-3.5	-1.4	1.2	2.3	1.6	-0.2	-0.2
HR1.S2	-1.6	0.7	-3.8	-1.2	1.4	2.5	1.6	-0.5	-0.5
HR1.S3	-1.6	0.4	-4.1	-0.8	0.7	1.6	0.8	-0.7	-0.7
HR1.S4	-1.6	0.9	-3.5	-1.8	2.0	3.5	1.5	-0.1	-0.1
HR1.S5	-1.6	0.7	-3.7	-2.1	1.9	3.5	1.0	-0.6	-0.6
HR1.S6	-1.6	0.4	-4.0	-1.6	1.0	1.9	0.8	-0.5	-0.5
HR1.S7	-1.6	0.9	-3.5	-2.2	2.2	3.3	1.3	-0.2	-0.2
HR1.S8	-1.6	0.7	-3.8	-2.3	2.2	3.4	0.9	-0.4	-0.4
HR1.S9	-1.6	0.4	-4.0	-1.8	2.0	2.6	0.5	-0.4	-0.4
HR2.S1	-1.6	0.9	-3.5	-0.9	0.9	3.4	2.0	-0.1	-0.1
HR2.S2	-1.6	0.7	-3.8	-0.6	0.7	2.7	1.6	-0.6	-0.6
HR2.S3	-1.6	0.4	-4.1	-0.2	0.2	1.2	0.9	-0.8	-0.8
HR2.S4	-1.6	0.9	-3.5	-1.2	1.2	2.9	1.1	-0.2	-0.2
HR2.S5	-1.6	0.7	-3.8	-0.9	0.5	1.8	0.6	-0.7	-0.7
HR2.S6	-1.6	0.4	-4.0	-0.2	-0.1	0.8	0.4	-0.8	-0.8
HR2.S7	-1.6	0.9	-3.5	-1.2	0.9	2.2	0.8	-0.2	-0.2
HR2.S8	-1.6	0.7	-3.7	-0.5	0.1	1.6	0.6	-0.5	-0.5
HR2.S9	-1.6	0.4	-3.9	0.1	-0.1	0.8	0.2	-0.5	-0.5
HR3.S1	-1.6	0.9	-3.3	-0.3	0.3	3.5	2.5	-0.1	-0.1
HR3.S2	-1.6	0.7	-3.5	-0.6	0.8	3.4	2.0	-0.5	-0.5
HR3.S3	-1.6	0.4	-4.0	-0.8	0.5	2.1	1.3	-0.5	-0.5
HR3.S4	-1.6	0.9	-3.3	-1.2	1.1	3.2	2.1	-0.2	-0.2
HR3.S5	-1.6	0.7	-3.5	-1.3	1.3	3.2	1.6	-0.6	-0.6
HR3.S6	-1.6	0.4	-3.9	-1.0	1.0	1.5	0.9	-0.9	-0.9
HR3.S7	-1.6	0.9	-3.5	-1.3	1.3	2.7	1.5	-0.1	-0.1
HR3.S8	-1.6	0.7	-3.5	-1.4	1.2	2.1	1.2	-0.7	-0.7
HR3.S9	-1.6	0.4	-3.7	-0.8	0.9	0.9	0.7	-0.7	-0.7
HR4.S1	-1.6	0.9	-3.5	-0.8	1.1	2.9	1.6	-0.2	-0.2
HR4.S2	-1.6	0.7	-3.8	-0.6	0.8	2.1	1.4	-0.6	-0.6
HR4.S3	-1.6	0.4	-3.9	-0.2	0.5	1.0	0.8	-0.5	-0.5
HR4.S4	-1.6	0.9	-3.7	-1.1	1.4	3.6	0.8	-0.1	-0.1
HR4.S5	-1.6	0.7	-3.8	-0.9	1.3	2.4	0.7	-0.6	-0.6
HR4.S6	-1.6	0.4	-3.9	-0.5	0.5	0.9	0.4	-0.4	-0.4
HR4.S7	-1.6	0.9	-3.7	-1.1	1.1	3.1	0.3	-0.2	-0.2
HR4.S8	-1.6	0.7	-3.8	-1.2	1.0	2.2	0.4	-0.4	-0.4
HR4.S9	-1.6	0.4	-3.9	-0.7	0.2	1.0	0.2	-0.4	-0.4

3.3. RESULTS

Table 3.6: Relative difference between the median (RDM) of the estimates of the last biomass B_{23}^s and stock status B_{23}^s/K^s and that of their true values in percent under the 36 scenarios. Those in the first two columns (denoted as "Estimated") are the RDM of the estimates obtained from the model for the simultaneous estimation of both the parameters and the state variables, and those in the last two columns (denoted as "Fixed") are the RDM of the estimates obtained as "Estimates obtained from the model as "Estimates obtained from the last two columns (denoted as "Fixed") are the RDM of the estimates obtained from the model where the parameters are fixed at their true values and only the biomass is allowed to be predicted. Absolute biases greater than 5% are shaded in gray.

	Esti	imated	Fixed		
Scenario	\hat{B}_{23}	\hat{B}_{23}/\hat{K}	\hat{B}_{23}	\hat{B}_{23}/K	
HR1.S1	3.9	7.1	1.3	1.3	
HR1.S2	2.9	5.2	1.6	1.6	
HR1.S3	2.4	4.3	-0.5	-0.5	
HR1.S4	2.4	5.9	0.4	0.4	
HR1.S5	2.5	4.5	0.2	0.2	
HR1.S6	1.4	2.3	0.1	0.1	
HR1.S7	-1.5	2.0	-0.5	-0.5	
HR1.S8	0.6	1.7	-0.1	-0.1	
HR1.S9	-0.6	0.5	-0.3	-0.3	
HR2.S1	1.6	3.3	0.8	0.8	
HR2.S2	4.6	8.2	0.5	0.5	
HR2.S3	6.7	11.3	-0.1	-0.1	
HR2.S4	3.7	6.6	-0.6	-0.6	
HR2.S5	7.4	7.2	0.4	0.4	
HR2.S6	7.1	8.5	0.3	0.3	
HR2.S7	1.7	3.0	-0.6	-0.6	
HR2.S8	4.0	3.5	0.2	0.2	
HR2.S9	3.1	3.3	0.1	0.1	
HR3.S1	1.2	3.0	-0.7	-0.7	
HR3.S2	4.7	7.1	-0.0	-0.0	
HR3.S3	4.7	6.5	-0.4	-0.4	
HR3.S4	1.4	5.0	-0.6	-0.6	
HR3.S5	5.0	5.9	0.3	0.3	
HR3.S6	5.0	5.4	0.3	0.3	
HR3.S7	1.5	3.1	-0.3	-0.3	
HR3.S8	2.9	3.9	-0.2	-0.2	
HR3.S9	2.9	2.8	-0.0	-0.0	
HR4.S1	2.0	4.5	-0.6	-0.6	
HR4.S2	4.3	7.7	-0.4	-0.4	
HR4.S3	5.0	7.4	-0.7	-0.7	
HR4.S4	5.2	9.3	1.1	1.1	
HR4.S5	8.7	10.2	1.0	1.0	
HR4.S6	8.5	10.3	0.3	0.3	
HR4.S7	3.3	4.8	-0.3	-0.3	
HR4.S8	5.9	5.7	0.5	0.5	
HR4.S9	47	4.5	01	0.1	



Figure 3.3: Relative difference (RD) of the estimates of each parameter under the scenarios where the process error variance is smaller than the observation error variance (i.e., $\sigma_{\eta} = 0.05$ and $\sigma_{\varepsilon} = 0.15$). The red boxplots denote the RD of the parameter estimates obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the parameter estimates obtained from the model where the state variables are fixed at their true values, and only the parameters are estimated. Each column of panels shares the simulation condition associated with the trend of harvest rates, which is denoted at the top of each column (i.e., HR1, HR2, HR3, and HR4). Each row of panels shares the simulation condition associated with input values of the six parameters, which is denoted at the right side of each row (i.e., S3, S6, and S9)



Figure 3.4: Relative difference (RD) of the estimates of the stock status at time t (\hat{B}_t/\hat{K}) under the scenarios where the process error variance is smaller than the observation error variance (i.e., $\sigma_{\eta} = 0.05$ and $\sigma_{\varepsilon} = 0.15$). The red boxplots denote the RD of the stock status at time t obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the estimates of the stock status at time t obtained from the model where the parameters are fixed at their true values and only the state variables are estimated. Each column of panels shares the simulation condition associated with the trend of harvest rates, which is denoted at the top of each column (i.e., HR1, HR2, HR3, and HR4). Each row of panels shares the simulation condition associated with input values of the six parameters, which is denoted at the right side of each row (i.e., S3, S6, and S9)



Figure 3.5: Relative difference (RD) of the estimates of each parameter under the scenarios where the observation error variance is smaller than the process error variance (i.e., $\sigma_{\eta} = 0.15$ and $\sigma_{\varepsilon} = 0.05$). The red boxplots denote the RD of the parameter estimates obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the parameter estimates obtained from the model where the state variables are fixed at their true values and only the parameters are estimated. Each column of panels shares the simulation condition associated with the trend of harvest rates, which is denoted at the top of each column (i.e., HR1, HR2, HR3, and HR4). Each row of panels shares the simulation condition associated with input values of the six parameters, which is denoted at the right side of each row (i.e., S1, S4, and S7)



Figure 3.6: Relative difference (RD) of the estimates of the stock status at time t (\hat{B}_t/\hat{K}) under the scenarios where the observation error variance is smaller than the process error variance (i.e., $\sigma_\eta = 0.15$ and $\sigma_{\varepsilon} = 0.05$). The red boxplots denote the RD of the stock status at time t obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the estimates of the stock status at time t obtained from the model where the parameters are fixed at their true values and only the state variables are estimated. Each column of panels shares the simulation condition associated with the trend of harvest rates, which is denoted at the top of each column (i.e., HR1, HR2, HR3, and HR4). Each row of panels shares the simulation condition associated with input values of the six parameters, which is denoted at the right side of each row (i.e., S1, S4, and S7)

3.3.2 Additional scenarios

The sensitivity to the constraints with the different dispersion levels is illustrated in Figures 3.7 - 3.10. In the case of the strong constraints (CV =0.1), the bias of the estimates of the parameter and the stock status is almost non-existent, regardless of the scenarios considered (the first column of Figures 3.7 - 3.10), which implicitly verifies the correct implementation of our simulation studies. However, in the case of the weaker constraints (CV = 0.5), the bias patterns observed in Figure 3.3 (j)-(l) are even more prominently shown when the observation error variance is larger than the process error variance (Figure 3.7 (d)-(f)), which also induces the large positive bias of the estimates of the stock status (i.e., B_t/K) (Figure 3.8 (d)-(f)). This large bias is substantially reduced when the process error variance is larger than the observation error variance (Figure 3.9 (d)-(f) and Figure 3.10 (d)-(f)). The same bias patterns as those in Figure 3.3 (j)-(l) are produced even though the different value for b is used (b = 0.7) (Figure 3.7 (g)-(i)). The incorporation of two more replicated data sets on I_t does not significantly improve the model performance compared to the case where a single set of I_t is applied, which can be observed by comparing the last column of Figures 3.7 and 3.8 with that of Figures 3.3 and Figures 3.4.



Figure 3.7: Relative difference (RD) of the estimates of the parameters under additional scenarios coupled with sub-scenario S3, S6, and S9 (i.e., $\sigma_{\eta} = 0.05$ and $\sigma_{\varepsilon} = 0.15$), where the CV of the penalties is set to be either 0.1 (the first column: panels (a)-(c)) or 0.5 (the second column: panels (d)-(f)), the value of the parameter *b* is set to be 0.7 (the third column: panels (g)-(i)), and the two additional sets of I_t are incorporated into the model (the fourth column: panels (j)-(l)). The red boxplots denote the RD of the parameter sand state variables. The blue boxplots denote the RD of the parameter estimates obtained from the model from the model where the state variables are fixed at their true values and only the parameters are estimated.



Figure 3.8: Relative difference (RD) of the estimates of the stock status at time t (\hat{B}_t/\hat{K}) under additional scenarios coupled with sub-scenario S3, S6, and S9 (i.e., $\sigma_{\eta} = 0.05$ and $\sigma_{\varepsilon} = 0.15$), where the CV of the penalties is set to be either 0.1 (the first column: panels (a)-(c)) or 0.5 (the second column: panels (d)-(f)), the value of the parameter b is set to be 0.7 (the third column: panels (g)-(i)), and the two additional sets of I_t are incorporated into the model (the fourth column: panels (j)-(l)). The red boxplots denote the RD of the stock status at time t obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the estimates of the stock status at time t obtained from the model form the parameters are fixed at their true values and only the state variables are estimated.



Figure 3.9: Relative difference (RD) of the estimates of the parameters under additional scenarios coupled with sub-scenario S1, S4, and S7 (i.e., $\sigma_{\eta} = 0.15$ and $\sigma_{\varepsilon} = 0.05$), where the CV of the penalties is set to be either 0.1 (the first column: panels (a)-(c)) or 0.5 (the second column: panels (d)-(f)), the value of the parameter *b* is set to be 0.7 (the third column: panels (g)-(i)), and the two additional sets of I_t are incorporated into the model (the fourth column: panels (j)-(l)). The red boxplots denote the RD of the parameter sand state variables. The blue boxplots denote the RD of the parameter estimates obtained from the model from the model where the state variables are fixed at their true values and only the parameters are estimated.



Figure 3.10: Relative difference (RD) of the estimates of the stock status at time t (\hat{B}_t/\hat{K}) under additional scenarios coupled with sub-scenario S1, S4, and S7 (i.e., $\sigma_\eta = 0.15$ and $\sigma_{\varepsilon} = 0.05$), where the CV of penalties is set to be either 0.1 (the first column: panels (a)-(c)) or 0.5 (the second column: panels (d)-(f)), the value of the parameter *b* is set to be 0.7 (the third column: panels (g)-(i)), and the two additional sets of I_t are incorporated into the model (the fourth column: panels (j)-(l)). The red boxplots denote the RD of the stock status at time *t* obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the estimates of the stock status at time *t* obtained from the model form the model form the model where the parameters are fixed at their true values and only the state variables are estimated.

3.3.3 Frequentist vs. Bayesian

With both frequentist and Bayesian approaches, all 500 simulation-estimation runs under the selected scenarios (i.e., HR4.S1-S9 and the additional scenarios associated with the different CVs for the constraints) have successfully converged. There are slight differences between the frequentist and Bayesian estimates of the parameters in terms of the relative differences, but both types of estimates show similar bias patterns (Figures 3.11 and 3.12), which reassure us that the choice of estimation method does not affect the overall results of our simulation studies. Such differences in estimates are expected, considering use of the Laplace approximation method and the inherent bias of the variance of the maximum likelihood estimate in the frequentist approach.



HR4

Figure 3.11: Relative difference (RD) of the estimates of each parameter under the scenarios associated with the HR4 trend. The red boxplots denote the RD of the parameter estimates obtained from the model for the simultaneous estimation of the parameters and state variables, using the frequentist approach. The light blue boxplots denote the RD of the parameter estimates obtained from the same model, using the Bayesian approach.



Figure 3.12: Relative difference (RD) of the estimates of each parameter under the additional scenarios associated with the different dispersion levels (i.e., the first two columns of panels: CV=0.1; the last two columns of panels: CV=0.5), which are coupled with sub-scenario S1, S3, S4, S6, S7, and S9. The red boxplots denote the RD of the parameter estimates obtained from the model for the simultaneous estimation of the parameters and the state variables, using the frequentist approach. The light blue boxplots denote the RD of the parameter estimates obtained from the Bayesian approach.

3.3.4 Sensitivity analysis

The two variance parameters (i.e., σ_{ε}^2 and σ_{η}^2) are highly sensitive to inclusion of the constraints in the model. The other four parameters are less sensitive to the constraints and often estimable without the constraints. However, the estimates tend to be more biased when they are obtained without such constraints. The sensitivity and estimability of the two variance parameters depend on the ratio of those two parameter values. When either of them is larger than the other, the one with a larger value is inestimable without the aid of its own penalty.

To be specific, when the penalty for the process error variance (i.e., $\pi(\sigma_{\eta}^2)$) is excluded under scenario HR4.S6 ($\sigma_{\varepsilon}^2 > \sigma_{\eta}^2$), which is the same as imposing a uniform prior on σ_{η}^2 in a Bayesian setting, the median RD of the estimates of all other parameters become close to 0, whereas the median RD of σ_{η} becomes largely biased (Figure 3.13 (g)-(l)). This large bias indicates that the parameter σ_{η} is not identifiable without a strong constraint, which is supported by its corresponding loglikelihood profile depicted in Figure 3.14 (g).

Similarly, when the penalty for the observation error variance (i.e., $\pi(\sigma_{\eta}^2)$) is excluded under scenario HR4.S4 ($\sigma_{\varepsilon}^2 < \sigma_{\eta}^2$), the median RD of the estimates of all other parameters become less biased, but the median RD of σ_{ε} becomes more biased (Figure 3.13 (a)-(f)). However, in contrast to σ_{ε}^2 in scenario HR4.S6, depending on simulated data, the observation error variance σ_{ε}^2 in scenario HR4.S4 is partially estimable even without its penalty (Figure 3.14 (b)).

As visually illustrated in Figure 3.13, estimability of the variance parameters is more problematic when the observation error variance is greater than the process error variance. This problem is also investigated by the loglikelihood profile of each parameter, shown in Figure 3.14.


Figure 3.13: Relative difference (RD) of the estimates of the parameters obtained from the models fitted to the data simulated under scenarios HR4.S4 (panels (a)-(f)) and HR4.S6 (panels (g)-(l)), where the penalties for the parameters are excluded one by one (denoted by the legend "Without $\pi(\cdot)$ " at the top right corner of each panel). The red boxplots denote the RD of the parameter estimates obtained from the model for the simultaneous estimation of the parameters and state variables. The blue boxplots denote the RD of the parameter estimates obtained from the model where the state variables are fixed at their true values and only the parameters are estimated. The legend "Without $\pi(\cdot)$ " can be interpreted as imposing a uniform prior on the parameter in the Bayesian approach.



Figure 3.14: Loglikelihood profiles of the natural logarithm of the six parameters (gray curves) evaluated after their corresponding penalties are excluded one by one (denoted by the legend "Without $\pi(\cdot)$ " at the top right corner of each panel), while other five parameters are constrained by their strong penalties. Those in the first two columns are evaluated with the data sets simulated under scenario HR4.S4, and those in the last two columns are evaluated with the data sets simulated with the data sets simulated under scenario HR4.S6. The vertical solid black line of each panel is the true input value of the parameter. The legend "Without $\pi(\cdot)$ " can be interpreted as imposing a uniform prior on the parameter in the Bayesian approach.

3.4 Discussion

In this study, we show the estimation problem of the SSPM even under the setting that all model parameters are strongly informed by their constraints. We demonstrated that successful convergence of the model aided by such strong constraints does not guarantee good performance in terms of relative difference, and some significant biases in parameter estimates can occur, depending on the values of the two variance parameters σ_{η}^2 and σ_{ε}^2 as well as the trend of the time-series data applied to the model.

The SSPM used in this study is considered one of the simplest forms in stock assessment models. We show that even this simple model can have the parameter estimation problem, which consequently induces bias of the estimates of both parameters and state variables. An estimation problem is relatively well studied for a conventional SPM, which is known to occur when time series data show a lack of contrast (Hilborn and Walters, 1992; McAllister et al., 2001), but the problem associated with its statespace form seems to be not well understood. This could be because in many previous studies, one of the conditions for the occurrence of the estimation problem (i.e., $\sigma_{\varepsilon}^2 > \sigma_{\eta}^2$) is prevented by an assumption that constrains the values of the two variance parameters (Punt, 2003; Ono et al., 2012; Rankin and Lemos, 2015; Thorson et al., 2015). For example, published studies, which applied the Namibian hake data to the SSPM for demonstration purposes, assumed that the process error variance is either smaller than or equal to the observation error variance (Punt, 2003; Parent and Rivot, 2012; Rankin and Lemos, 2015). These settings are similar to some of our scenarios, such as scenarios HR1.S4, HR1.S5, HR3.S4, and HR4.S5, under which the estimation problem is hardly detectable or almost non-existent.

From our stimulation studies, we also illustrate that the trend of I_t and Y_t is an important factor, which seems to largely determine the estimability of the variance parameters. For instance, the scenarios associated with the HR4 trend show the most biased results, where both I_t and Y_t show almost a monotonic decrease with little contrast (see Figure 3.2). However, one should note that the data trend alone cannot explain the bias of the estimates because such bias is substantially reduced when the observation error is smaller than the process error while the overall data trend remains the same. Moreover, when the state variables are fixed at their true values, and only the parameters are estimated, the bias of the parameter estimates almost disappears in all 36 scenarios (see Table 3.5). These experiments indicate that the estimation problem of the SSPM could originates from the state-space framework of the model and the general difficulty in differentiating between observation and process errors in state-space models. This finding is consistent with Auger-Méthé et al. (2016), but our study further demonstrates that such an estimation problem can arise even in models with strong parameter constraints.

Although our simulation studies are extensively designed, more focused simulation scenarios for testing the impact of the two variance parameters on parameter estimability could be considered for future research to better identify which variance parameter is the cause of the bias. For example, one can consider fixing either the process or observation error variances at their true values and estimate other remaining parameters.

The practical usefulness of the SSPM is well supported in the fisheries science community as it has been applied often by Regional Fishery Management Organizations (RFMOs) (Winker et al., 2019; Sant'Ana et al., 2020). However, our study raises a question about reliability of the model in terms of the performance. Although the SSPM still remains a useful tool for data-moderate fish stocks, our study demonstrates that the model could provide biased results under certain conditions (i.e., $\sigma_{\varepsilon}^2 > \sigma_{\eta}^2$ and the one-way trip trend of the time-series data), which seems to be not well understood. Our finding emphasises the importance of a model performance check in the SSPM and the general difficulty of the model estimation in state-space models.

Chapter 4

A two-life stage-structured production model

4.1 Introduction

Age-structured models (ASMs) are the preferred choice of most fisheries modellers as those models explicitly incorporate the composite behaviour of different cohorts of fish (Hilborn and Walters, 1992; Haddon, 2010). However, in many data-moderate situations where compositional data are lacking, simpler models, such as surplus production models (SPMs) have been used as alternative methods (Polacheck et al., 1993; Winker et al., 2020).

SPMs are considered the most simple and least data-demanding stock assessment models in fisheries, where the dynamic process of population growth in biomass is simply expressed as a function of age-aggregated biomass. These production models require two types of information, a time-series of relative abundance index (e.g., catch-per-unit-effort: CPUE) and total yield (e.g., annual catch in weight). Although such fisheries data are often available and relatively easy to collect, one should be aware that

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acquiring such information does not always ensure applicability of these simple models. This is because there are some practical situations where these models are not appropriate, mainly because of their simplistic structure that ignores demographic impact on population productivity.

Changes in the demographic structure of a population subsequently affect the productivity of a population. Such an effect is easily reflected in age-structured dynamics where age-specific contributions to reproduction and density dependence in recruitment are explicitly modelled. In SPMs, however, this demographic phenomenon is neglected because population productivity is simply expressed as a function of age-aggregated biomass, using a single production function (Wang et al., 2014; Winker et al., 2020). Despite this critical drawback, fisheries scientists still apply SPMs to many fish stocks due to a lack of sufficient composition data that allow them to apply more complex and detailed representation of the dynamics models, such as ASMs.

The choice of using a SPM over other more reliable options tends to be made when only a time-series of relative abundance index and yield are available in the absence of any auxiliary information on population structure. Although such a compromise is necessary for most data-limited cases, we observed an exceptional case from the Korean walleye pollock (*Gadus Chalcogrammus*) fisheries, in which a demographic effect on population growth could be modelled, based only on information on fisheries yields and relative abundance indices, collected from multiple fisheries. Those pollock fisheries in South Korea have targeted adults and juveniles separately in different fishing locations; thus, such fishery-dependent data provide information on fish at each life stage.

Since CPUE data, collected from commercial fisheries, are often available in many data-limited or -moderate stocks, many researchers have applied SPMs where they assumed that multiple sets of CPUE data collected from different fisheries are independent to each other (Hyun, 2018; An et al., 2021). However, in the case of the pollock fisheries, we find that such an application violates the underlying assumption about the proportionality between the total (or exploitable) biomass and CPUE (e.g., CPUE = catchability × Biomass), often used in SPMs, since each set of CPUE data is for either juvenile or adult stocks alone (e.g., adult CPUE = adult catchability×adult Biomass; juvenile CPUE = juvenile catchability× juvenile Biomass;).

Spatial separations of juvenile and adult populations are well-known ecological behaviours of many marine fish species, including walleye pollock, since they show ontogenetic migration patterns and seasonal differences in habitat use (Honda et al., 2004; Smart et al., 2013; Barbeaux and Hollowed, 2018) (e.g., juveniles tend to inhabit in nearshore areas and migrate toward offshore areas as they grow). Thus, depending on fishing location, each fishery may show a distinct pattern of life stage-specific selectivity, from which information on separate yields and CPUEs from fish in different life stages can be obtained. The Harden-Jones' migration triangle of marine fishes, which is illustrated in Figure 4.1, effectively describes how such life stage-specific migratory patterns (Harden Jones, 1968) are associated with selectivity in the Korea pollock fisheries (Kim and Hyun, 2018).

The main purpose of this research is to develop a two-life stage-structured production model (TSPM) that is applicable to the Korea pollock fisheries, which does not require composition data, but allows us to separately match those multiple sets of abundance indices with their corresponding sub-groups (i.e., juvenile and adult) of a population. We develop this new model by bifurcating a general surplus production model (GSPM), based on a life stage-structured matrix model, known as a Lefkovich matrix model in demographic analysis (Caswell, 2000). We also incorporate a density-dependent term following the method by Jensen (1995) and make necessary modifications. This new model is specifically designed for stocks where both juveniles and adults are targeted by multiple fisheries; thus, information on separate yields from the two life stages are required.



Figure 4.1: Diagram depicting the Harden-Jones migration triangle with hypothetical life stage-selective catches.

Such a specific design may limit its usability, but capturing both juvenile and adult fish is not uncommon in some open-access fisheries (Jung et al., 2008; Najmudeen and Sathiadhas, 2008; Kim and Hyun, 2018).

To accommodate environmental noise and uncertainty in harvest rate as process error, we formulate a TSPM in a state-space framework. Furthermore, to check strength of a TSPM over a GSPM, we conduct a simulation test where we use an ASM as an operating model to generate pollocklike age-structured data which are fitted to both a GSPM and a TSPM for performance comparison. For clarity of presentation and ease of reading, mathematical details of the model development process are given in the Appendix. Thus, the rest of this chapter is organised as follows: First, background information on the Korea pollock fisheries is discussed, which provides readers with a better understanding of the necessity of our new model and the motivation for the model development. Second, we conduct a simulation test to investigate how a TSPM performs compared to a GSPM by fitting both models to data generated from an ASM. We introduce both a GSPM and a TSPM in state-space forms as estimation models. Lastly, we fit a TSPM to the actual pollock data and perform model validation, based on which we discuss the status of the pollock fisheries and some possible issues associated with parameter estimability of the model.

4.2 Korean pollock fisheries

In this section, we describe some background information on the Korean pollock fisheries. This information provides readers with a fundamental research question that we attempt to solve by developing a new model which is applicable to situations similar to the Korea pollock stock.

The Korea pollock stock has collapsed since the late 1990s. Korean fisheries scientists conjecture that such a collapse would have occurred due to some environmental changes in Korean waters and overexploitation of both juvenile and adult populations, but no reliable scientific analysis is available due to limited data available and a lack of stock assessment (Kim and Hyun, 2018).

Interestingly, juvenile and adult pollock were considered different species until the early 1970s, and both of them were caught until the late 1990s. This misconception launched two separate data collection schemes on the species, where individuals smaller than 27 cm were categorised as juveniles, and those equal or larger than 27 cm were considered adults (Kim and Hyun, 2018). Although annual time series data for adult and juvenile stocks were separately collected from commercial fisheries (details are given in the following section), having only this information without annual composition data still seems to limit analysis to use of a simple stock assessment model, such as a GSPM.

Despite being an applicable option because of the limited data, it should be noted that a GSPM may not be the correct model for separate CPUEs on juvenile and adult stocks, as each set of those CPUEs does not represent a trend of the total exploitable biomass well. Moreover, a GSPM cannot reflect a demographic response to such selective fishing mortality as there is no demographic structure in the model. Instead, age-aggregated total yield is simply subtracted from the total exploitable biomass to incorporate the impact of fishing mortality on population growth.

Such modelling issues for the pollock stock motivated us to develop a TSPM where separate information on juvenile and adult stocks is correctly and fully utilised. In the next section, we describe more details about the data collected from the Korea pollock fisheries.

4.2.1 Data

Spatial separation of juvenile and adult stocks is indicated by the different fishing location of each fishery (Figure 4.2). Such ontogenetic spatial separation of walleye pollock is also reported by Honda et al. (2004). Longline and gillnet fisheries have exclusively captured adults, whereas Danish seine fishery has primarily caught juveniles (Kim and Hyun, 2018). Thus, we refer to CPUEs collected from longline and gillnet fisheries as adult CPUEs and that from Danish seine fishery as juvenile CPUE.

A single set of juvenile CPUE collected from Danish seine fishery and two sets of adult CPUEs collected from gillnet and longline fisheries are available along with separate yields from juvenile and adult stocks (see Figure 4.3) (Kim and Hyun, 2018). We refer to these CPUE and yield series using I_t^j , $I_{1,t}^a$, $I_{2,t}^a$, Y_t^j , and Y_t^a , respectively, where *I* denotes the relative abundance index (i.e., CPUE), subscript *t* denotes the time (in year), *Y* denotes the yield (in biomass), and superscripts *j* and *a* denote juvenile and adult stocks, respectively. The subscript values 1 and 2 on $I_{1,t}^a$ and $I_{2,t}^a$ refer to gillnet and longline fisheries, respectively.



Figure 4.2: Spatial locations where three major pollock fisheries operated. The red shaded area indicates where longline and gillnet fisheries operated, exclusively targeting adult fish (i.e., fish equal or larger than 27 cm in length). The blue shaded area indicates where Danish seine fishery operated, mostly capturing juvenile fish (i.e., fish smaller than 27 cm in length).



Figure 4.3: Data on catch per unit effort (CPUE) collected from gillnet, longline, and Danish seine fisheries (from top to bottom) and yield from juvenile and adult stocks (the bottom panel). A sheet is a unit area of the gillnet whose width ranges from 45 m to 72 m and whose height ranges from 4 m to 4.125 m. One basket in the longline contains approximately 300 hooks.

4.3 State-space production models

Throughout this section, we describe both a GSPM and a TSPM in statespace form, which we also reparameterise in terms of derived quantities that can be matched with those from ASMs for construction of parameter constraints. Functional relationships between the two production models and ASMs can be derived by matching optimum equilibrium characteristics of those models, such as biological reference points (BRPs). BRPs reflect a combination of demographic components (e.g., recruitment, mortality, growth, etc.) of fish stock dynamics in single indices, such as maximum sustainable yield (MSY), the biomass at which MSY is obtained (B_{MSY}), and the harvest fraction required to achieve the MSY (H_{MSY} ; note that these BRPs are theoretical concepts; thus not necessarily equivalent to management objectives). Hence, mathematically, these reference points can be viewed as derived quantities, which can potentially provide functional links between different types of stock assessment models.

Our preliminary study as well as the simulation studies in Chapter 3 indicated that those state-space production models require constraints on parameters to be estimated. Thus, we construct parameter constraints for those two state-space models, using ASMs with Monte-Carlo simulations, where input values for parameters of ASMs are obtained from previous studies. Distributional assumptions on natural mortality and productivity parameters of ASMs are made to reflect uncertainties in model inputs when performing Monte-Carlo simulations with ASMs. This method for construction of parameter constraints for a GSPM has already been used by Winker et al. (2020), but that for a TSPM is newly developed in this study. We discuss these methods in the next section for more details (i.e., Section 4.4), but readers should bear in mind that the purpose of reparameterisations in the two production models is to incorporate parameter constraints that are derived from ASMs.

We use a GSPM to demonstrate why a GSPM is not an appropriate

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model for the pollock stock and to show how a TSPM is different from a GSPM. Moreover, in Section 4.6, we evaluate performance of a TSPM by comparing it with that of a GSPM, using two different types of simulated data for each model. Thus, we present a total of four models in this section, which we refer to as GSPM1, GSPM2, TSPM1, and TSPM2, respectively. The numbers, 1 and 2, after the name of each model indicate what type of data are applied to those models. For example, in GSPM1 and TSPM1, life stage-specific data, such as separate CPUEs collected from juvenile and adult fisheries, are used, whereas in GSPM2 and TSPM2, CPUEs collected from fisheries targeting a combined stock (i.e., juvenile stock + adult stock) are used. Through the comparison of GSPM2 and TSPM2, we aim to investigate whether or not accounting for different fishing pressures on juvenile and adult stocks improves model performance in terms of accuracy of estimates. To compare the performance of the two production models, we use data simulated from an ASM which has a more realistic and complex structure than those of the two production models. We obtain input values for ASMs from previous studies, which is discussed in detail in Section 4.6.1. After the simulation test, we fit a TSPM1 to the actual pollock data as a case study in Section 4.7.

To reproduce the condition of the Korean pollock stock in terms of data availability, we assume three different sets of CPUE data for each of the four models are available. For example, for GSPM1 and TSPM1, we use a single set of juvenile CPUE and two sets of adult CPUE (i.e., I_t^j , $I_{1,t}^a$, and $I_{2,t}^a$), which is the case for the pollock stock, but for GSPM2 and TSPM2, we use three sets of CPUE for a combined stock (i.e., $I_{1,t}$, $I_{2,t}$, and $I_{3,t}$). The differences between four models are illustrated in Figures 4.4 and 4.5.



Figure 4.4: DAG representations of GSPM1 (a) and TSPM1 (b). White circles are non-observed probabilistic nodes (i.e., B_t^j , B_t^a , and B_t), and those in colour are observed probabilistic nodes (i.e., $I_{d^j,t}^j$, $I_{d^a,t}^a$, and $I_{d,t}$). Squares in colour are observed deterministic nodes (i.e., Y_t^j , Y_t^a , and Y_t). Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes. Dotted rectangular frames with rounded corners indicate repetition of structure over units. Colouring the nodes blue, red, and blue-red gradient compositionally represents juvenile, adult, and both juvenile and adult biomasses, respectively.



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Figure 4.5: DAG representations of GSPM2 (a) and TSPM2 (b). White circles are non-observed probabilistic nodes (i.e., B_t^j , B_t^a , and B_t), and those in colour are observed probabilistic nodes (i.e., $I_{d,t}$). Squares in colour are observed deterministic nodes (i.e., Y_t^j , Y_t^a , and Y_t). Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes. Dotted rectangular frames with rounded corners indicate repetition of structure over units. Colouring the nodes blue, red, and blue-red gradient compositionally represents juvenile, adult, and both juvenile and adult biomasses, respectively.

 $I_{d,i}$

 $d \in \{1, 2, 3\}$

4.3.1 General surplus production model (GSPM)

Base structure

The logistic production model, which we used in Chapter 3, has been criticised because the maximum growth rate always occurs when the population is at half of the carrying capacity K, which is not the case for most fish species (Hilborn and Walters, 1992; Maunder, 2003; Haddon, 2010). Thus, a few studies generalised the production function $g(B_t)$ by including one more parameter which gives flexibility in the shape of $g(B_t)$ (Pella and Tomlinson, 1969; Fletcher, 1978; Polacheck et al., 1993). Among those, we use the form reparametrised by Polacheck et al. (1993):

$$B_{t+1} = B_t + g(B_t) - Y_t; \qquad g(B_t) = \frac{r}{n-1} \cdot B_t \cdot \left[1 - \left(\frac{B_t}{K}\right)^{n-1}\right], \quad (4.1)$$

where B_t is the biomass at time t, r is the intrinsic growth rate, and n is the inflection point of the production function $g(B_t)$ relative to the carrying capacity K. Using n, one can express any particular form of a production model. For example, with n = 2, Equation (4.1) becomes identical to the logistic production model (Schaefer, 1954), and with $n \rightarrow 1$, it becomes the Fox model (Fox Jr, 1970; Polacheck et al., 1993).

Since the harvest rate for the maximum sustainable yield (i.e., H_{MSY}) of the GSPM is calculated by $H_{MSY} = r/n$, the above equation can be reparameterised as a function of H_{MSY} (Winker et al., 2020):

$$B_{t+1} = B_t + \frac{H_{\text{MSY}} \cdot n}{n-1} \cdot B_t \cdot \left[1 - \left(\frac{B_t}{K}\right)^{n-1}\right].$$
(4.2)

We use the above reparameterised form to utilise functional links between the GSPM and an ASM, where H_{MSY} is approximated by that derived from an ASM.

Process equations

By incorporating a multiplicative error term $\exp(\varepsilon_{p,t})$, where the subscript p indicates that it is a process error term, in Equation (4.2), the process equations of the GSPM can now be expressed in the following state-space form, where the initial biomass B_1 is scaled by introducing the scaling coefficient b to estimate the ratio of the initial biomass to the carrying capacity K:

$$B_{t} = \begin{cases} b \cdot K \cdot \exp(\varepsilon_{p,t}), & \text{for } t = 1\\ \\ \left[B_{t-1} + \frac{H_{\text{MSY}} \cdot n}{n-1} \cdot B_{t-1} \cdot \left[1 - \left(\frac{B_{t-1}}{K}\right)^{n-1} \right] - Y_{t-1} \right] \cdot \exp(\varepsilon_{p,t}), & \text{for } t > 1 \end{cases}$$

where $Y_t = Y_t^j + Y_t^a$, and $\varepsilon_{p,t} \stackrel{\text{iid}}{\sim} N(0, \sigma_p^2)$. We define the scale free relative biomass $P_t = B_t/K$ for numerical efficiency when estimating the parameters (Millar and Meyer, 2000; Hyun, 2018):

$$P_t = \begin{cases} b \cdot \exp(\varepsilon_{p,t}), & \text{for } t = 1\\ \\ \left[P_{t-1} + \frac{H_{\text{MSY}} \cdot n}{n-1} \cdot P_{t-1} \cdot \left[1 - (P_{t-1})^{n-1}\right] - \frac{Y_{t-1}}{K} \right] \cdot \exp(\varepsilon_{p,t}), & \text{for } t > 1 \end{cases}$$

Observation equations

In the majority of previous studies that used a GSPM, a relative abundance index I_t was assumed to be proportional to the total exploitable biomass B_t with multiplicative observation error (i.e., $I_t \propto B_t \cdot \exp(\varepsilon_{o,t})$, where the subscript o indicates that it is an observation error term) (Polacheck et al., 1993; Millar and Meyer, 2000; Thorson and Minto, 2015). If multiple CPUE indices are available, they are assumed to be conditionally independent on B_t . Thus, for the case of the Korean pollock stock, we have the following observation equations:

$$\begin{cases} I_t^j &= q^j \cdot P_t \cdot K \cdot \exp(\varepsilon_{o,t}^j) \\ I_{d^a,t}^a &= q_{d^a}^a \cdot P_t \cdot K \cdot \exp(\varepsilon_{o,d^a,t}^a) \end{cases},$$
(4.3)

where $d^a \in \{1,2\}$, $\varepsilon_{o,t}^j \stackrel{\text{iid}}{\sim} N(0, (\sigma_o^j)^2)$, $\varepsilon_{o,d^a,t}^a \stackrel{\text{iid}}{\sim} N(0, (\sigma_{o,d^a}^a)^2)$, $(\sigma_o^j)^2$ is the observation error variance for the juvenile CPUE, and $(\sigma_{o,d^a}^a)^2$ is the observation error variance for the d^a th adult CPUE. We label the GSPM, where the observations are modelled by Equation (4.3), as GSPM1 (see Figure 4.4a).

Additionally, for the purpose of testing the sole impact of not accounting for the life stage-specific fishing pressures in the GSPM compared to a TSPM, we assume another possible case that CPUEs collected from the total exploitable stock are available instead of those from separate substocks. In this alternative case, the observation equations are given by

$$I_{d,t} = q_d \cdot P_t \cdot K \cdot \exp(\varepsilon_{o,d,t}); \quad \varepsilon_{o,d,t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{o,d}^2\right), \tag{4.4}$$

where $d \in \{1, 2, 3\}$, and $\sigma_{o,d}^2$ is the observation error variance for the *d*th index data. We label the GSPM, where the observations are modelled by Equation (4.4), as GSPM2 (see Figure 4.5a).

4.3.2 Two-life stage-structured production model (TSPM)

Base structure

In the absence of density-dependent effect and fishing mortality, relationships between the two sub-stocks in biomass can be modelled using the following simple matrix equation:

$$\underbrace{\begin{bmatrix} B_{t+1}^{j} \\ B_{t+1}^{a} \end{bmatrix}}_{B_{t+1}} = \underbrace{\begin{bmatrix} g^{j} & R^{j} \\ R^{a} & g^{a} \end{bmatrix}}_{D} \underbrace{\begin{bmatrix} B_{t}^{j} \\ B_{t}^{a} \end{bmatrix}}_{B_{t}}, \qquad (4.5)$$

where g^j is the net growth rate for B_{t+1}^j (e.g., somatic growth, emigration after sexual maturation, and natural mortality), R^j is the recruitment rate for B_{t+1}^j (e.g., spawning), R^a is the recruitment rate for B_{t+1}^a (e.g., immigration from the juvenile stock after sexual maturation), and g^a is the net growth rate for B_{t+1}^a (e.g., somatic growth and natural mortality).

Similar to the derivation of the GSPM from an exponential growth model (i.e., $B_{t+1} = B_t + r \cdot B_t$), we may extend Equation (4.5) by incorporating a density dependent effect (i.e., K_t in the equation below) and life stage-specific fishing mortality (i.e., Y_t in the equation below) after rewriting the matrix model in a discrete time form:

$$\underbrace{\begin{bmatrix} B_{t+1}^{j} \\ B_{t+1}^{a} \end{bmatrix}}_{B_{t+1}} = \underbrace{\begin{bmatrix} B_{t}^{j} \\ B_{t}^{a} \end{bmatrix}}_{B_{t}} + \underbrace{\begin{bmatrix} \left[1 - \left(\frac{B_{t}^{j}}{K^{j}} \right)^{n^{j}-1} \right] / (n^{j}-1) & 0 \\ 0 & 1 \end{bmatrix}}_{K_{t}} \underbrace{\begin{bmatrix} g^{j}-1 & R^{j} \\ R^{a} & g^{a}-1 \end{bmatrix}}_{G=D-I} \underbrace{\begin{bmatrix} B_{t}^{j} \\ B_{t}^{a} \end{bmatrix}}_{B_{t}} - \underbrace{\begin{bmatrix} Y_{t}^{j} \\ Y_{t}^{a} \end{bmatrix}}_{Y_{t}},$$

$$(4.6)$$

where K^j is the carrying capacity for the juvenile biomass, n^j is the shape parameter for a productivity curve of the juvenile biomass, and Y_t^j and Y_t^a are the yields from the juvenile and adult stocks, respectively (i.e., $Y_t^j = H_t^j \cdot B_t^j$, and $Y_t^a = H_t^a \cdot B_t^a$). Note that in a majority of ASMs, density dependence is introduced via a stock recruitment relationship (e.g., Beverton-Holt, Ricker, etc.) where the maximum number of recruits is limited, not the spawning stock size. Thus, we include the density dependent term only in the juvenile biomass.

We further reparameterise Equation (4.6), based on the dominant eigenvalue and eigenvector of the matrix G (i.e., r_m and ψ in the equation below;

see Appendix A.3 for the derivation), which provides us with the form that can be functionally linked to the dominant eigenvalue and eigenvector of an age-structured density-independent matrix model (e.g., Leslie Matrix Model: LMM):

$$\begin{cases} B_{t+1}^{j} = B_{t}^{j} + \frac{r_{m}}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}} \right)^{n^{j} - 1} \right] \\ + \frac{R^{j}}{n^{j} - 1} \cdot \left(B_{t}^{a} - \frac{1}{\psi} \cdot B_{t}^{j} \right) \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}} \right)^{n^{j} - 1} \right] - Y_{t}^{j}, \quad (4.7)$$
$$B_{t+1}^{a} = B_{t}^{a} + r_{m} \cdot B_{t}^{a} + R^{a} \cdot \left(B_{t}^{j} - \psi \cdot B_{t}^{a} \right) - Y_{t}^{a}$$

where r_m is the dominant eigenvalue of the matrix G, which is calculated as $r_m = g^j - 1 + R^j/\psi = g^a - 1 + \psi \cdot R^a$ (see Appendix A.3.3 for the proof), and ψ is the ratio of the two elements in the dominant eigenvector of the matrix G.

Process equations

Similar to the GSPM, we incorporate multiplicative error terms (i.e., $\exp(\varepsilon_{p,t}^{j})$ and $\exp(\varepsilon_{p,t}^{a})$) in Equation (4.7) and assume that the total exploitable biomass for the initial time step (i.e., B_1) is a fraction of the carrying capacity K, which is further divided into the two sub-groups (i.e., B_1^{j} and B_1^{a}) by the initial juvenile proportion c. That is, for the juvenile stock, the process

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equations of the state-space TSPM are given as

$$B_{t}^{j} = \begin{cases} b \cdot c \cdot K \cdot \exp(\varepsilon_{p,t}^{j}), & \text{for } t = 1 \\ \left[B_{t-1}^{j} + \frac{r_{m}}{n^{j} - 1} \cdot B_{t-1}^{j} \cdot \left[1 - \left(\frac{B_{t-1}^{j}}{K^{j}} \right)^{n^{j} - 1} \right] \\ + \frac{R^{j}}{n^{j} - 1} \cdot \left(B_{t-1}^{a} - \frac{1}{\psi} \cdot B_{t-1}^{j} \right) \cdot \left[1 - \left(\frac{B_{t-1}^{j}}{K^{j}} \right)^{n^{j} - 1} \right] \\ - Y_{t-1}^{j} \right] \cdot \exp(\varepsilon_{p,t}^{j}), & \text{for } t > 1 \end{cases}$$

(4.8)

,

where $\varepsilon_{p,t}^{j} \stackrel{\text{iid}}{\sim} N(0, \sigma_{p}^{2})$, and σ_{p}^{2} is the process error variance. The total carrying capacity K can be expressed as the sum of the two seperate stage-specific carrying capacities, K^{j} and K^{a} (i.e., $K = K^{a} + K^{j}$, where $K^{a} = K^{j}/(\psi - r_{m}/R^{a})$), Then, for the adult stock, we have the following process equations

$$B_{t}^{a} = \begin{cases} b \cdot (1-c) \cdot K \cdot \exp(\varepsilon_{p,t}^{a}), & \text{for } t = 1 \\ \\ \begin{bmatrix} B_{t-1}^{a} + r_{m} \cdot B_{t-1}^{a} + R^{a} \cdot \left(B_{t-1}^{j} - \psi \cdot B_{t-1}^{a}\right) - Y_{t-1}^{a} \end{bmatrix} \cdot \exp(\varepsilon_{p,t}^{a}), & \text{for } t > 1 \\ \\ \end{cases}$$
(4.9)

where $\varepsilon_{p,t}^a \stackrel{\text{iid}}{\sim} N\left(0, \sigma_p^2\right)$.

For numerical efficiency in model estimation, we form the relative biomass by dividing B_t^j and B_t^a by K^j and K^a , respectively, denoted by P_t^j and P_t^a (i.e., $P_t^j = B_t^j/K^j$ and $P_t^a = B_t^a/K^a$). Thus, we can reexpress Equations (4.8) and (4.9) in terms of P_t^j and P_t^a as follows

$$P_t^j = \begin{cases} b \cdot c \cdot \left(\frac{K^a}{K^j} + 1\right) \cdot \exp(\varepsilon_{p,t}^j), & \text{for } t = 1\\ \left[P_t^j + \frac{r_m}{n^j - 1} \cdot P_t^j \cdot \left[1 - \left(P_t^j\right)^{n^j - 1}\right] \\ + \frac{R^j}{n^j - 1} \cdot \left(P_t^a \cdot \frac{K^a}{K^j} - \frac{1}{\psi} \cdot P_t^j\right) \cdot \left[1 - \left(P_t^j\right)^{n^j - 1}\right] \\ - \frac{Y_{t-1}^j}{K^j} \right] \cdot \exp(\varepsilon_{p,t}^j), & \text{for } t \ge 1 \end{cases}$$

$$P_t^a = \begin{cases} b \cdot (1-c) \cdot \left(1 + \frac{K^j}{K^a}\right) \cdot \exp(\varepsilon_{p,t}^a), & \text{for } t = 1\\ \\ \left[P_{t-1}^a + r_m \cdot P_{t-1}^a + R^a \cdot \left(P_{t-1}^j \cdot \frac{K^j}{K^a} - \psi \cdot P_{t-1}^a\right) - \frac{Y_{t-1}^a}{K^a}\right] \cdot \exp(\varepsilon_{p,t}^a), & \text{for } t > 1 \end{cases}$$

Observation equations

For observation equations of the TSPM, we also consider the two situations, depending on availability of the relative abundance data. If we have the data separately collected from the juvenile and adult stocks (i.e., I_t^j and $I_{d^a,t}^a$), which are used in GSPM1, we formulate the following observation equations:

$$\begin{cases} I_t^j &= q^j \cdot P_t^j \cdot K^j \cdot \exp(\varepsilon_{o,t}^j) \\ I_{d^a,t}^a &= q_{d^a}^a \cdot P_t^a \cdot K^a \cdot \exp(\varepsilon_{o,d^a,t}^a) \end{cases},$$
(4.10)

where $d^a \in \{1,2\}$, $\varepsilon_{o,t}^j \stackrel{\text{iid}}{\sim} N(0, (\sigma_o^j)^2)$, and $\varepsilon_{o,d^a,t}^a \stackrel{\text{iid}}{\sim} N(0, (\sigma_{o,d^a}^a)^2)$. We label the TSPM, where the observations are modelled by Equation (4.10), as TSPM1 (see Figure 4.4b).

If we have the data collected from the total exploitable biomass B_t (i.e., $I_{d,t}$), we use the same observation equations as those of GSPM2:

$$I_{d,t} = q_d \cdot P_t \cdot K \cdot \exp(\varepsilon_{o,d,t}); \quad \varepsilon_{o,d,t} \stackrel{\text{iid}}{\sim} N\left(0, \sigma_{o,d}^2\right), \tag{4.11}$$

where $P_t = (B_t^j + B_t^a)/(K^j + K^a)$. We label the TSPM, where the observations are modelled by Equation (4.11), as TSPM2 (see Figure 4.5b)

4.4 Parameter constraints

Estimating all the model parameters of a GSPM without any constraints (e.g., priors in a Bayesian approach or penalties in a frequentist approach) is notoriously difficult (Maunder, 2003), which is a problem also found in a TSPM. Thus, we impose multivariate constraints on parameters of each state-space production model, which are derived based on relationships between the two production models and ASMs.

Following a prior construction method suggested by Winker et al. (2020), we construct a bivariate constraint for H_{MSY} and n of the GSPM, using Monte-Carlo simulations with a conventional density-dependent equilibrium age-structured model, which we simply refer to as an equilibrium ASM. However, for the TSPM, we develop a novel method to construct a multivariate constraint for r_m , n^j , ψ , R^j , and R^a , using Monte-Carlo simulations with two different types of ASMs (i.e., an equilibrium ASM and a Leslie matrix model (LMM)). Input values for life-history and fisheries parameters associated with ASMs are obtained from previous studies (see Tables 4.1 and 4.2 for a summary of key notation and input values used in ASMs). In Figure 4.6, we plot the curves for quantities calculated from sub-models nested in ASMs, given the input values listed in Table 4.2. Details about those sub-models are discussed in the following subsection.

Some of those input values in Table 4.2 are roughly chosen, based on information provided in Kim and Hyun (2018) as exact values for those

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parameters are unable to be obtained from other published studies. For example, the input values for the parameters for the age at 50% selectivity for juvenile and adult fish (i.e., $i_{sel50}^j = 1.5$ and $i_{sel50}^a = 2.7$) are determined, based on the length frequency samples shown in Kim and Hyun (2018).

We could not find any input values for the slope parameters of the two selectivity curves (i.e., ν_{sel}^{j} and ν_{sel}^{a}) and the maturity curve (i.e., ν_{mat}) from previous studies; thus, we simply assume the value of 2 for those parameters. Other input values, such as the female proportion (i.e., ϕ) and the unfished age-1 recruitment at equilibrium (i.e., $R_*(0)$), are arbitrarily chosen because values of those parameters do not change distributions of parameter constraints.

The rest of this section is organised as follows: First, we discuss an equilibrium ASM and derive BRPs of the model, from which we find functional links between the two production models and an ASM. Second, we describe a LMM (i.e., a density-independent age-structured matrix model), a dominant eigenvalue and eigenvector of which are functionally linked to r_m and ψ of the TSPM. Lastly, using functional links derived from the two ASMs, we describe how multivariate constraints for the two production models can be derived.

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Notation	Description	Dimension
a, j	superscripts indexing adult (a) and juvenile (j)	
c	superscript denoting a stable distribution	
i	subscript indexing age	time
A	maximum age	time
t	discrete time	time
T	final time step	time
*	subscript denoting an equilibrium state	
$N_{i,t}$	numbers-at-age at time t	count
Y_t	yield at time t	mass
H_t	harvest fraction at time t	dimensionless
B_t	exploitable biomass at time t	mass
K	exploitable unfished biomass	mass
R_t	recruitment at time t	count
Egg_t	total egg production at time t	count
α	Beverton-Holt SR parameter	dimensionless
β	Beverton-Holt SR parameter	$count^{-1}$
h	steepness parameter	dimensionless
M	instantaneous rate of natural mortality	$time^{-1}$
ϕ	female proportion	dimensionless
Fec_i	fecundity-at-age	count
η_1	length-fecundity relationship parameter	count/length
η_2	length-fecundity relationship parameter	dimensionless
MSY	maximum sustainable yield	mass
B_{MSY}	biomass that provides MSY	mass
H_{MSY}	long-term constant harvest fraction for MSY	dimensionless
Mat_i	maturity-at-age	dimensionless
$\nu_{\rm mat}$	slope steepness parameter of a maturity curve	$time^{-1}$
i _{mat50}	age at 50% maturity	time
v_i	selectivity-at-age	dimensionless
$\nu_{\rm sel}$	slope steepness parameter of a gear selectivity curve	$time^{-1}$
i_{sel50}	age at 50% selectivity	time
L_a	length-at-age	length
k	growth parameter in the von Bertalanffy growth function (VBGF)	$time^{-1}$
i_0	theoretical age at length 0 in the VBGF	time
L_{∞}	asymptotic length in the VBGF	length
w_i	weight-at-age	mass
ω_1	length-weight relationship parameter	mass/length
ω_2	length-weight relationship parameter	dimensionless
b	scaling coefficient for the initial exploitable biomass B_1 (i.e., $b = B_1/K$)	dimensionless
I_t	relative abundance index at time t	mass/effort

Table 4.1: A summary of the key notation used in the ASMs

parameter	value	unit	range	reference
L_{∞}	46	cm	$(0,\infty)$	Kooka (2012)
k	0.31	year ⁻¹	$(0,\infty)$	Kooka (2012)
i_0	-0.17	year	$(-\infty,\infty)$	Kooka (2012)
A	18	year	$(0,\infty)$	Kooka (2012)
i_{mat50}	4.6	year	$(0,\infty)$	Kooka (2012)
$ u_{\mathrm{mat}}$	2	year ⁻¹	$(0,\infty)$	
ω_1	$0.134\cdot10^{-3}$	gram/cm	$(0,\infty)$	Kooka (2012)
ω_2	2.47		$(0,\infty)$	Kooka (2012)
η_1	0.16	egg/cm	$(0,\infty)$	Kooka (2012)
η_2	3.72		$(0,\infty)$	Kooka (2012)
M , M_0	0.22	year ⁻¹	$(0,\infty)$	Kooka (2012)
$i_{ m sel50}^{j}$	1.5	year	$[0,\infty)$	Kim and Hyun (2018)
$ u_{ m sel}^j$	2	year ⁻¹	$[0,\infty)$	
$i^a_{ m sel50}$	2.7	year	$[0,\infty)$	Kim and Hyun (2018)
$ u^a_{ m sel}$	2	year ⁻¹	$[0,\infty)$	
ϕ	0.5		(0,1)	
$R_*(0)$	1000	recruit	$(0,\infty)$	
h , h_0	0.647		(0.2, 1]	A'mar et al. (2008)
q_1, q_2, q_3	10^{-5}	$effort^{-1}$	$(1/\infty, 1]$	
q^j	10^{-5}	$effort^{-1}$	$(1/\infty, 1]$	
q_1^a , q_2^a	10^{-5}	$effort^{-1}$	$(1/\infty, 1]$	
$\sigma_{p,1}$	0.4		$[0,\infty)$	
$\sigma_{p,2}$	0.2		$[0,\infty)$	
$\sigma_{o,1}$, $\sigma_{o,2}$, $\sigma_{o,3}$	0.1		$[0,\infty)$	
σ_o^j	0.1		$[0,\infty)$	
$\sigma^a_{o,1}$, $\sigma^a_{o,2}$	0.1		$[0,\infty)$	

 Table 4.2: Input parameter values used for the age-structured models (ASMs)



Figure 4.6: Plotted curves for quantities calculated from the sub-models nested in the ASMs, given the input values listed in Table 4.2. The dashed lines in panels (a) and (b) (i.e., v_i^j and v_i^a) are gear selectivities assumed for each juvenile and adult fisheries. Details about the structure of those sub-models are provided in Section 4.4.1

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4.4.1 Equilibrium age-structured model

The equilibrium population abundance for age *i* under a given constant harvest fraction *H* (i.e., $N_{i,*}(H)$, where the subscript * denotes the population is at equilibrium) is equal to the equilibrium survivor rate per recruit at *H* (i.e., $\tilde{N}_{i,*}(H)$) multiplied by the equilibrium recruitment at *H* (i.e., $R_*(H)$):

$$N_{i,*}(H) = \widetilde{N}_{i,*}(H) \cdot R_*(H).$$

The equilibrium survivor rate per recruit at *H* (i.e., $\widetilde{N}_{i,*}(H)$) is given by

$$\widetilde{N}_{i,*}(H) = \begin{cases} 1 & \text{for } i = 1 \\ \widetilde{N}_{i-1,*}(H) \cdot \exp(-M) \cdot (1 - H_{i-1}), & \text{for } 1 < i < A \\ \frac{\exp(-M) \cdot (1 - H_{A-1})}{1 - \exp(-M) \cdot (1 - H_A)} \cdot \widetilde{N}_{A-1,*}(H), & \text{for } i = A \end{cases}$$
(4.12)

where A is the maximum age group (the "plus group"; see Appendix A.2 for the derivation of the starting condition), M is the instantaneous rate of natural mortality, and H_i is the harvest fraction for fish of age i.

Using the separability assumption (Doubleday, 1976), the harvest fraction for fish of age *i* (i.e., H_i) is expressed as the products of the constant harvest fraction *H* and the age-dependent vulnerability V_i (note that *H* defines the fully selected harvest fraction; thus, $H \neq \sum_{i=1}^{A} H_i$):

$$H_i = V_i \cdot H, \tag{4.13}$$

The age-dependent vulnerability V_i is then calculated, based on the stock-specific age-gear selectivities, v_i^j and v_i^a , and the maturity-at-age, Mat_a:

$$V_i = v_i^j \cdot (1 - \operatorname{Mat}_i) + v_i^a \cdot \operatorname{Mat}_i.$$

The two stock-specific age-dependent gear selectivities (i.e., v_i^j and v_i^a) are computed from the following logistic curve:

$$v_i^{\text{st}} = \frac{1}{1 + \exp\left[-\nu_{\text{sel}}^{\text{st}} \cdot \left(i - i_{\text{sel}50}^{\text{st}}\right)\right]},\tag{4.14}$$

where the superscript st identifies which sub-stock (i.e., st $\in \{j, a\}$) is associated with the gear selectivity curve, i_{sel50}^{st} is the age at 50% selectivity, and ν_{sel}^{st} is the slope steepness of the selectivity curve. Similarly, for the maturity-at-age (i.e., Mat_i), the following logistic curve is used:

$$\mathsf{Mat}_{i} = \frac{1}{1 + \exp\left[-\nu_{\mathsf{mat}} \cdot (i - i_{\mathsf{mat50}})\right]},$$

where i_{mat50} is the age at 50% maturity, and ν_{mat} is the slope steepness of the maturity curve.

The equilibrium recruitment at H (i.e., $R_*(H)$) is expressed in terms of eggs, using the following Beverton-Holt stock-recruitment (BHSR) relationship (Beverton and Holt, 1993):

$$R_*(H) = \frac{\alpha \cdot \operatorname{Egg}_*(H)}{1 + \beta \cdot \operatorname{Egg}_*(H)},$$

where α/β defines the maximum recruitment level, $1/\beta$ defines the number of eggs which will result in 50% of the maximum recruitment, and $\text{Egg}_*(H)$ is the equilibrium total annual egg production (in numbers) at H, which can be further expressed as

$$\operatorname{Egg}_{*}(H) = R_{*}(H) \cdot \operatorname{Egg}_{*}(H),$$

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where $\operatorname{Egg}_{*}(H)$ is the number of eggs produced per recruit at equilibrium:

$$\widetilde{\mathrm{Egg}}_{*}(H) = \sum_{i}^{A} \mathrm{Fec}_{i} \cdot \mathrm{Mat}_{i} \cdot \phi \cdot \widetilde{N}_{i,*}(H).$$

The female fraction ϕ of the population is assumed to be constant over age groups. Fec_i is the fecundity-at-age, which is defined as the number of eggs that are likely to be laid by a fish during the spawning season. Fec_i is assumed to be related to the mean length-at-age (i.e., L_i):

$$\operatorname{Fec}_i = \eta_1 \cdot L_i^{\eta_2},$$

where η_1 and η_2 are the length-fecundity relationship parameters. Then, the mean length at age *i* (i.e., L_i) can be modelled by using the von Berta-lanffy growth function (von Bertalanffy, 1938):

$$L_i = L_{\infty} \cdot [1 - \exp(-k \cdot (i - i_0))],$$

where L_{∞} is the asymptotic length, k is the growth coefficient which describes how quickly L_{∞} is achieved, and i_0 is the theoretical age at length-0.

Note that the two BHSR parameters are often expressed in terms of the steepness parameter *h*, which is defined as the fraction of recruitment from an unfished population when the total egg production is 20% of its unfished level (Mace and Doonan, 1988) (see Appendix A.1 for the derivation):

$$\alpha = \frac{4 \cdot h \cdot R_*(0)}{(1-h) \cdot \text{Egg}_*(0)}; \quad \beta = \frac{5 \cdot h - 1}{(1-h) \cdot \text{Egg}_*(0)},$$
(4.15)

where $R_*(0)$ is the equilibrium unfished recruitment, and $\text{Egg}_*(0)$ is the equilibrium unfished eggs (in numbers).

Since the production models are expressed in terms of biomass, we

need to derive the following quantities from the equilibrium ASM:

$$\begin{cases} B_{*}(H) = R_{*}(H) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(H) \cdot w_{i} \cdot V_{i} \\ B_{*}^{j}(H) = R_{*}(H) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(H) \cdot w_{i} \cdot v_{i}^{j} \cdot (1 - \operatorname{Mat}_{i}) \\ B_{*}^{a}(H) = R_{*}(H) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(H) \cdot w_{i} \cdot v_{i}^{a} \cdot \operatorname{Mat}_{i} \\ K = R_{*}(0) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(0) \cdot w_{i} \cdot V_{i} \\ K^{j} = R_{*}(0) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(0) \cdot w_{i} \cdot v_{i}^{j} \cdot (1 - \operatorname{Mat}_{i}) \\ K^{a} = R_{*}(0) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(0) \cdot w_{i} \cdot v_{i}^{a} \cdot \operatorname{Mat}_{i} \\ Y_{*}(H) = B_{*}(H) \cdot H \\ Y_{*}^{j}(H) = B_{*}^{j}(H) \cdot H \\ Y_{*}^{a}(H) = B_{*}^{a}(H) \cdot H \end{cases}$$

$$(4.16)$$

The mean weight-at-age (i.e., w_i) is modelled by a length-weight relationship function:

$$w_i = \omega_1 \cdot L_i^{\omega_2},$$

where ω_1 and ω_2 are the two parameters which govern the above allometric curve.

We evaluate those derived quantities in Equation (4.16) at the optimum harvest rates to obtain BRPs. Then, those BRPs from the ASM are matched with corresponding ones from the two production models to derive functional links between the three different models. The BRPs from the ASM are defined as

$$\begin{cases} MSY &= Y_{*}(H_{MSY}) \\ Y_{MSY}^{j} &= Y_{*}^{j}(H_{MSY}) \\ Y_{MSY}^{a} &= Y_{*}^{a}(H_{MSY}) \\ MSY^{j} &= Y_{*}^{j}(H_{MSY}) \\ B_{MSY} &= MSY/H_{MSY} \\ B_{MSY}^{j} &= Y_{MSY}^{j}/H_{MSY} \\ B_{MSY}^{a} &= Y_{MSY}^{a}/H_{MSY} \\ B_{MSY}^{j} &= MSY^{j}/H_{MSY} \\ B_{MSY^{j}}^{j} &= MSY^{j}/H_{MSY^{j}} \\ B_{MSY^{j}}^{a} &= R_{*}(H_{MSY^{j}}) \cdot \sum_{i=1}^{A} \widetilde{N}_{i,*}(H_{MSY^{j}}) \cdot w_{i} \cdot v_{i} \cdot Mat_{i} \end{cases}$$

where H_{MSY} and H_{MSY^j} can be obtained by solving

$$\left. \frac{dY_*(H)}{dH} \right|_{H_{\rm MSY}} = 0; \qquad \left. \frac{dY_*^j(H)}{dH} \right|_{H_{\rm MSY}^j} = 0.$$

We numerically obtain the solutions for the above equations, but those can also be analytically solved (Forrest et al., 2008).

By substituting MSY, B_{MSY} , and K of the GSPM with those derived from the equilibrium ASM, the two parameters (i.e., H_{MSY} and n) in the GSPM can be approximated as follows

$$\begin{cases} H_{\rm MSY} = \frac{\rm MSY}{B_{\rm MSY}} \\ n = \left(\frac{B_{\rm MSY}}{K}\right)^{1-n} \end{cases}, \qquad (4.18)$$

where the quantities on the left-hand side (i.e., H_{MSY} and n) are the parameters of the GSPM, while MSY, B_{MSY} , and K on the right-hand side

are of the equilibrium ASM. Similarly, for the TSPM, the three parameters (i.e., n^j , R^a , and R^j) are approximated as follows (see Appendix A.4 for the derivation)

$$\begin{cases} n^{j} = \left(\frac{B_{\text{MSY}^{j}}^{j}}{K^{j}}\right)^{1-n^{j}} \\ R^{a} = \frac{r_{m}}{\psi - \frac{K^{j}}{K^{a}}} , \qquad (4.19) \\ R^{j} = \frac{n^{j} \cdot H_{\text{MSY}^{j}} - r_{m}}{\frac{B_{\text{MSY}^{j}}^{a}}{B_{\text{MSY}^{j}}^{j}} - \frac{1}{\psi}} \end{cases}$$

where $B_{MSY^j}^j$, H_{MSY^j} , $B_{MSY^j}^a$, K^a , and K^j are those obtained from the equilibrium ASM, not from the TSPM.

4.4.2 Leslie matrix model (LMM)

In this section, we show how the two parameters r_m and ψ in the TSPM can be approximated by corresponding values derived from a density-independent age-structured matrix model, also known as a Leslie matrix model (LMM) in demographic analysis.

Using the same life history parameters of the ASM, a LMM can be expressed as follows (Mangel et al., 2010)

$$\begin{bmatrix}
N_{1,t+1} \\
N_{2,t+1} \\
\vdots \\
N_{A-1,t+1} \\
N_{A,t+1}
\end{bmatrix} = \begin{bmatrix}
f_1 & f_2 & \cdots & f_{A-1} & f_A \\
S_1 & 0 & \cdots & 0 & 0 \\
0 & S_2 & \cdots & 0 & 0 \\
\vdots & \vdots & \ddots & \vdots & \vdots \\
0 & 0 & \cdots & S_{A-1} & S_A
\end{bmatrix} \begin{bmatrix}
N_{1,t} \\
N_{2,t} \\
\vdots \\
N_{A-1,t} \\
N_{A,t}
\end{bmatrix},$$
(4.20)

where f_i is the per capita average number of offspring from individuals of age *i*, which is given by

$$f_i = \alpha \cdot \operatorname{Fec}_i \cdot \operatorname{Mat}_i \cdot \phi$$

Note that the BHSR parameter α can be derived from the steepness parameter *h*, using Equation (4.15).

In the matrix model above, because the transition matrix L has constant elements, the population N_t tends to reach a stable age structure over time, from which age proportions of N_t remains in equilibrium. Once the population reaches its stable age structure, the age-aggregated abundance N (i.e., $N = \sum_{i=1}^{A} N_i$) grows according to the following differential equation (McAllister et al., 2001):

$$\frac{\mathrm{d}N}{\mathrm{d}t} = \log(\Lambda_1) \cdot N,$$

where Λ_1 is the dominant eigenvalue of *L*.

In the absence of the density-dependent effect and fishing mortality, the matrix model shown in Equation (4.6) also tends to reach a stable lifestage structure, from which the ratio of juvenile and adult biomasses remains in equilibrium. Then, after reaching a stable structure, the biomass B grows at the rate of r_m (recall that r_m is the dominant eigenvalue of the matrix G in Equation (4.6)):

$$\frac{B_{t+\Delta t} - B_t}{\Delta t} = r_m \cdot B_t$$

Although the LMM describes population abundance in numbers, the dominant eigenvalue Λ_1 remains the same in biomass (see Appendix A.3.4 for the proof). Thus, the following approximate relationship can be satisfied:

$$r_m \approx \log(\Lambda_1).$$
 (4.21)

Then, the dominant eigenvector of the matrix L can be used to approximate ψ of the TSPM as follows

$$\psi = \frac{\sum_{i}^{A} C_{i} \cdot w_{i} \cdot (1 - \operatorname{Mat}_{i}) \cdot v_{i}^{j}}{\sum_{i}^{A} C_{i} \cdot w_{i} \cdot \operatorname{Mat}_{i} \cdot v_{i}^{a}},$$
(4.22)

where C_i is the proportion of age-*i* fish (in numbers) at the stable age structure, which is obtained by normalising elements in the dominant eigenvector of the matrix L.

4.4.3 Multivariate normal constraints

Using Equations (4.18), (4.19), (4.21), and (4.22) derived from equilibrium ASM and the LMM described in the previous sections, multivariate constraints for the parameters of the GSPM and the TSPM can be constructed. We use Monte-Carlo simulations to reflect uncertainties in inputs of the natural mortality parameter M and the steepness parameter h. To do that, we randomly draw 5000 input values for M and h from gamma and beta distributions, respectively (Michielsens and McAllister, 2011; Winker et al., 2020), where modes of the distributions, denoted by M_0 and h_0 (i.e., $M_0 = 0.22$ and $h_0 = 0.647$), are the point estimates obtained from previous studies, which are given in Table 4.2 (A'mar et al., 2008; Kooka, 2012), while variances of those distributions are determined by the coefficient of variation (CV). We use 25% and 15% of CV for the gamma and beta distributions, respectively; thus, the resulting distributions correspond to 2.5th and 97.5th percentiles for M of 0.13 and 0.36 and those for h of 0.51 and 0.77.

To be more specific, we illustrate several steps involved with the construction of multivariate parameter constraints for the GSPM and the TSPM as follows, which is also depicted in Figure 4.7:


Figure 4.7: Diagram depicting the process of constructing multivariate constraints for the GSPM and TSPM, using the two ASMs (i.e., the equilibrium ASM and the LMM) with input values for the parameters of the ASMs. The boldface symbols and grey ellipses indicate sets of 5000 quantities for each parameter. Those in the grey rectangles have a single input value.

(i) We assume the natural mortality M follows a gamma distribution with shape parameter κ and the scale parameter τ , from which we randomly draw 5000 samples of M (i.e., M_{ℓ} , where $\ell \in \{1, 2, 3, ..., 5000\}$):

$$M_{\ell} \stackrel{\text{iid}}{\sim} \text{Gamma}(\kappa, \tau), \quad \text{where } \ell \in \{1, 2, 3, ..., 5000\},$$

where we derive κ and τ , based on the mode of M (i.e., M_0) and its coefficient of variation (CV_M), which are given as 0.22 and 0.25, respectively:

$$\kappa = \frac{M_0}{\tau} + 1 \quad \text{and} \quad \tau = \frac{M_0}{\text{CV}_M^{-2} - 1}.$$

(ii) For the steepness parameter h, we draw 5000 random samples of h (i.e., h_{ℓ} , where $\ell \in \{1, 2, 3, ..., 5000\}$) from a beta distribution, where we rescale the distribution to constrain h_{ℓ} to lie within the defined range of h (i.e., $0.2 \le h_{\ell} \le 1$) (Michielsens and McAllister, 2011):

$$h_{\ell} = V_{\ell} \cdot 0.8 + 0.2,$$

where

$$V_{\ell} \stackrel{\text{iid}}{\sim} \text{Beta}(\xi, \zeta).$$

The two shape parameters, ξ and ζ , are derived given the mode and coefficient of variation (i.e., $h_0 = 0.647$ and $CV_V = 0.15$):

$$\zeta = rac{(2 \cdot V_0 + (1 - V_0) \cdot \xi - 1)}{V_0}, \quad ext{where} \quad V_0 = rac{h_0 - 0.2}{0.8},$$

and

$$\xi = \sqrt{\frac{V_0^2 \cdot \xi \cdot (2 \cdot V_0 + \xi - 1 - V_0 \cdot \xi)}{(2 \cdot V_0 + \xi - 1)^2 \cdot (3 \cdot V_0 + \xi - 1)}} \cdot \frac{\xi + \zeta}{CV_V}.$$

The above implicit equation for ξ is derived from the following rela-

tionship:

$$\begin{aligned} \text{Var}[V] = (\text{CV}_V \cdot E[V])^2, \\ \text{where} \quad \text{Var}[V] = \frac{V_0^2 \cdot \xi \cdot (2 \cdot V_0 + \xi - 1 - V_0 \cdot \xi)}{(2 \cdot V_0 + \xi - 1)^2 \cdot (3 \cdot V_0 + \xi - 1)} \\ \text{and} \quad E[V] = \frac{\xi}{\xi + \zeta}. \end{aligned}$$

(iii) Using M_{ℓ} , h_{ℓ} and the input values for the other parameters of the equilibrium ASM, provided in Table 4.2, we calculate MSY_{ℓ} , $B_{MSY,\ell}$, and K_{ℓ} from the equilibrium ASM. Then, using the following equations, we obtain $H_{MSY,\ell}$ and n_{ℓ} :

$$\begin{cases} H_{\text{MSY},\ell} = \frac{\text{MSY}_{\ell}}{B_{\text{MSY},\ell}} \\ \\ n_{\ell} = \left(\frac{B_{\text{MSY},\ell}}{K_{\ell}}\right)^{1-n_{\ell}} \end{cases}$$

,

where $\ell \in \{1, 2, 3, ..., 5000\}$

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Similarly, for the TSPM, we obtain $r_{m,\ell}$, ψ_{ℓ} , n_{ℓ}^{j} , R_{ℓ}^{a} , and R_{ℓ}^{j} as follows:

$$\begin{cases} r_{m,\ell} = \log(\Lambda_{1,\ell}) \\ \psi_{\ell} = \frac{\sum_{i}^{A} C_{i,\ell} \cdot w_{i} \cdot (1 - \operatorname{Mat}_{i}) \cdot v_{i}^{j}}{\sum_{i}^{A} C_{i,\ell} \cdot w_{i} \cdot \operatorname{Mat}_{i} \cdot v_{i}^{a}} \\ n_{\ell}^{j} = \left(\frac{B_{\mathrm{MSY}^{j},\ell}^{j}}{K_{\ell}^{j}}\right)^{1 - n_{\ell}^{j}} , \qquad (4.23) \\ R_{\ell}^{a} = \frac{r_{m,\ell}}{\psi_{\ell} - \frac{K_{\ell}^{j}}{K_{\ell}^{a}}} \\ R_{\ell}^{j} = \frac{n_{\ell}^{j} \cdot H_{\mathrm{MSY}^{j},\ell} - r_{m,\ell}}{\frac{B_{\mathrm{MSY}^{j},\ell}^{a}}{B_{\mathrm{MSY}^{j},\ell}^{j}} - \frac{1}{\psi_{\ell}}} \end{cases}$$

where $\Lambda_{1,\ell}$ and $C_{i,\ell}$ are derived from the LMM, and $B^j_{MSY^j,\ell'}$, $B^a_{MSY^j,\ell'}$, $H_{MSY^j,\ell'}$, K^a_ℓ , and K^j_ℓ are derived from the equilibrium ASM.

(iv) Then, we parameterise the joint distribution of $\log(H_{\text{MSY},\ell})$ and $\log(n_{\ell})$, where $\ell \in \{1, 2, 3, ..., 5000\}$, using a multivariate normal (MVN) distribution with mean vector $\boldsymbol{\theta}_{\text{GS},0}$ and covariance matrix $\boldsymbol{\Sigma}_{\text{GS}}$:

$$\boldsymbol{\theta}_{\mathrm{GS}} \sim \mathrm{MVN}(\boldsymbol{\theta}_{\mathrm{GS},0}, \boldsymbol{\Sigma}_{\mathrm{GS}}),$$

where

$$\boldsymbol{\theta}_{\mathrm{GS},0} = \left[\overline{\log(H_{\mathrm{MSY}})}, \overline{\log(n)}\right]^{\mathrm{T}}$$
(4.24)

and

$$\Sigma_{\rm GS} = \begin{bmatrix} {\rm Var}[\log(H_{\rm MSY})] & {\rm Cov}[\log(H_{\rm MSY}), \log(n)] \\ {\rm Cov}[\log(H_{\rm MSY}), \log(n)] & {\rm Var}[\log(n)] \end{bmatrix}.$$
(4.25)

The bar symbol means the average of the 5000 samples for each parameter, and Var and Cov are the variance and covariance of the 5000 samples of stated parameters. The operator T is the transpose operator.

For the TSPM, we parameterise the joint distribution of $\log(r_{m,\ell})$, $\log(n_{\ell}^{j})$, $\log(R_{\ell}^{j})$, $\log(R_{\ell}^{a})$, and $\log(\psi_{\ell})$, where $\ell \in \{1, 2, 3, ..., 5000\}$, using a multivariate normal (MVN) distribution with mean vector $\boldsymbol{\theta}_{\text{TS},0}$ and covariance matrix $\boldsymbol{\Sigma}_{\text{TS}}$:

$$\boldsymbol{\theta}_{\mathrm{TS}} \sim \mathrm{MVN}(\boldsymbol{\theta}_{\mathrm{TS},0}, \boldsymbol{\Sigma}_{\mathrm{TS}}),$$

where

$$\boldsymbol{\theta}_{\mathrm{TS},0} = [\overline{\log(r_m)}, \overline{\log(n^j)}, \overline{\log(R^j)}, \overline{\log(R^a)}, \overline{\log(\psi)}]^{\mathrm{T}}, \qquad (4.26)$$

and

$$\Sigma_{\mathrm{TS}} = \begin{bmatrix} \mathrm{Var}[\log(r_m)] & \mathrm{Cov}[\log(r_m), \log(n^j)] & \cdots & \mathrm{Cov}[\log(r_m), \log(\psi)] \\ \mathrm{Cov}[\log(r_m), \log(n^j)] & \mathrm{Var}[\log(n^j)] & \cdots & \mathrm{Cov}[\log(n^j), \log(\psi)] \\ \vdots & \vdots & \ddots & \vdots \\ \mathrm{Cov}[\log(r_m), \log(\psi)] & \mathrm{Cov}[\log(n^j), \log(\psi)] & \cdots & \mathrm{Var}[\log(\psi)] \\ & (4.27) \end{bmatrix}$$

(v) We also impose a normal distribution on the parameter $\log(b)$ with

mean μ_b and variance σ_b^2 :

$$\log(b) \sim N(\mu_b, \sigma_b^2),$$

where $\mu_b = \log(b_0) + \sigma_b^2$, $\sigma_b^2 = \log(\text{CV}_b^2 + 1)$, and CV_b is the coefficient of variation for $\log(b)$. We use $\text{CV}_b = 0.3$ for both simulation and application studies, but the value of b_0 varies depending on the study settings. For a simulation study, discussed in Section 4.6, we use the true value for *b* as b_0 for each scenario. For a case study, discussed in Section 4.7, we use $b_0 \in \{0.3, 0.5, 0.7\}$ for three alternative models.

4.5 Estimation methods

To estimate the parameters of the four models, a marginal maximum likelihood method is used, using the TMB package (Kristensen et al., 2016). In TMB, one needs to specify a joint likelihood function for the model parameters (see the following subsections). TMB takes care of approximating the marginal likelihood (i.e., $\mathcal{L}_{Model}(\Psi_{Model}|Data)$, where Model \in {GSPM1, GSPM2, TSPM1, TSPM2}, and Ψ_{Model} denotes a vector of the model parameters), by integrating out the state variables (i.e., P for the GSPM and P^{j} , P^{a} for the TSPM), using a Laplace appoximation technique (Skaug and Fournier, 2006; Kristensen et al., 2016). That is, the marginal likelihoods for the four estimation models can be expressed as follows

$$\begin{split} \mathcal{L}_{\text{GSPM1}}(\boldsymbol{\Psi}_{\text{GSPM1}} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ &= \int \mathcal{L}_{\text{GSPM1}}(\boldsymbol{\Psi}_{\text{GSPM1}}, \boldsymbol{P} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}, \\ \mathcal{L}_{\text{GSPM2}}(\boldsymbol{\Psi}_{\text{GSPM2}} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ &= \int \mathcal{L}_{\text{GSPM2}}(\boldsymbol{\Psi}_{\text{GSPM2}}, \boldsymbol{P} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}, \\ \mathcal{L}_{\text{TSPM1}}(\boldsymbol{\Psi}_{\text{TSPM1}} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ &= \iint \mathcal{L}_{\text{TSPM1}}(\boldsymbol{\Psi}_{\text{TSPM1}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{j} d\boldsymbol{P}^{a}, \\ \mathcal{L}_{\text{TSPM2}}(\boldsymbol{\Psi}_{\text{TSPM2}} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ &= \iint \mathcal{L}_{\text{TSPM2}}(\boldsymbol{\Psi}_{\text{TSPM2}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{j} d\boldsymbol{P}^{a}, \end{split}$$

where the parameters of the each estimation model are given by

$$\begin{split} \Psi_{\text{GSPM1}} &= (b, r, n, K, \sigma_p, \sigma_o^j, \sigma_{o,1}^a, \sigma_{o,2}^a, q^j, q_1^a, q_2^a), \\ \Psi_{\text{GSPM2}} &= (b, r, n, K, \sigma_p, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, q_1, q_2, q_3), \\ \Psi_{\text{TSPM1}} &= (b, c, r_m, n^j, K, \psi, R^j, R^a, \sigma_p, \sigma_o^j, \sigma_{o,1}^a, \sigma_{o,2}^a, q^j, q_1^a, q_2^a), \\ \Psi_{\text{TSPM2}} &= (b, c, r_m, n^j, K, \psi, R^j, R^a, \sigma_p, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, q_1, q_2, q_3). \end{split}$$

Then, by maximizing the marginal likelihoods with respect to Ψ_{Model} , using numerical optimisation techniques in R (R Core Team, 2014), the estimates of Ψ_{Model} (i.e., $\hat{\Psi}_{\text{Model}}$) can be obtained:

$$\begin{split} \hat{\boldsymbol{\Psi}}_{\text{GSPM1}} &= \arg \max_{\boldsymbol{\Psi}_{\text{GSPM1}}} \log[\mathcal{L}_{\text{GSPM1}}(\boldsymbol{\Psi}_{\text{GSPM1}} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \\ \hat{\boldsymbol{\Psi}}_{\text{GSPM2}} &= \arg \max_{\boldsymbol{\Psi}_{\text{GSPM2}}} \log[\mathcal{L}_{\text{GSPM2}}(\boldsymbol{\Psi}_{\text{GSPM2}} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \\ \hat{\boldsymbol{\Psi}}_{\text{TSPM1}} &= \arg \max_{\boldsymbol{\Psi}_{\text{TSPM1}}} \log[\mathcal{L}_{\text{TSPM1}}(\boldsymbol{\Psi}_{\text{TSPM1}} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \\ \hat{\boldsymbol{\Psi}}_{\text{TSPM2}} &= \arg \max_{\boldsymbol{\Psi}_{\text{TSPM2}}} \log[\mathcal{L}_{\text{TSPM2}}(\boldsymbol{\Psi}_{\text{TSPM2}} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \end{split}$$

Once $\hat{\Psi}_{Model}$ is found, TMB sequentially infers the state variables by maximizing the estimated conditional likelihoods, where Ψ_{Model} is fixed at $\hat{\Psi}_{Model}$:

$$\begin{split} \hat{\boldsymbol{P}}_{\text{GSPM1}} &= \arg\max_{\boldsymbol{P}} \log[\mathcal{L}_{\text{GSPM1}}(\hat{\boldsymbol{\Psi}}_{\text{GSPM1}}, \boldsymbol{P} | \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \\ \hat{\boldsymbol{P}}_{\text{GSPM2}} &= \arg\max_{\boldsymbol{P}} \log[\mathcal{L}_{\text{GSPM2}}(\hat{\boldsymbol{\Psi}}_{\text{GSPM2}}, \boldsymbol{P} | \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a})] \\ \hat{\boldsymbol{P}}_{\text{TSPM1}}^{j} &= \arg\max_{\boldsymbol{P}^{j}} \log\left[\int \mathcal{L}_{\text{TSPM1}}(\hat{\boldsymbol{\Psi}}_{\text{TSPM1}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} | \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{a}\right] \\ \hat{\boldsymbol{P}}_{\text{TSPM1}}^{a} &= \arg\max_{\boldsymbol{P}^{a}} \log\left[\int \mathcal{L}_{\text{TSPM1}}(\hat{\boldsymbol{\Psi}}_{\text{TSPM1}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} | \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{j}\right] \\ \hat{\boldsymbol{P}}_{\text{TSPM2}}^{j} &= \arg\max_{\boldsymbol{P}^{a}} \log\left[\int \mathcal{L}_{\text{TSPM2}}(\hat{\boldsymbol{\Psi}}_{\text{TSPM2}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} | \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{a}\right] \\ \hat{\boldsymbol{P}}_{\text{TSPM2}}^{a} &= \arg\max_{\boldsymbol{P}^{a}} \log\left[\int \mathcal{L}_{\text{TSPM2}}(\hat{\boldsymbol{\Psi}}_{\text{TSPM2}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} | \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) d\boldsymbol{P}^{a}\right] \end{aligned}$$

Furthermore, the uncertainty of parameter estimates is evaluated via the delta method, where the determinant of a Hessian matrix of the marginal likelihood is found via a numerical Cholesky decomposition (Skaug and Fournier, 2006; Kristensen et al., 2016).

In the next following subsections, we provide details about the joint likelihood for each estimation model.

4.5.1 Joint likelihoods for GSPM1 and GSPM2

The joint likelihoods for GSPM1 and GSPM2 are

$$\mathcal{L}_{\text{GSPM1}}(\boldsymbol{\Psi}_{\text{GSPM1}}, \boldsymbol{P} \mid \boldsymbol{I}^{j}, \boldsymbol{I}^{a}_{1}, \boldsymbol{I}^{a}_{2}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) = f_{\boldsymbol{I},\text{GSPM1}}(\boldsymbol{I}^{j}, \boldsymbol{I}^{a}_{1}, \boldsymbol{I}^{a}_{2} \mid \boldsymbol{P}, q^{a}_{1}, q^{a}_{2}, q^{j}, \sigma^{j}_{o}, \sigma^{a}_{o,1}, \sigma^{a}_{o,2}, K) \\ \times f_{\boldsymbol{P}}(\boldsymbol{P} \mid r, K, b, n, \sigma_{p}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ \times f_{\boldsymbol{\theta}_{\text{GS}}}(\boldsymbol{\theta}_{\text{GS}}) \cdot f_{b}(b),$$

 $\begin{aligned} \mathcal{L}_{\text{GSPM2}}(\boldsymbol{\Psi}_{\text{GSPM2}}, \boldsymbol{P} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) = & f_{\boldsymbol{I},\text{GSPM2}}(\boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3} \mid \boldsymbol{P}, q_{1}, q_{2}, q_{3}, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, K) \\ & \times f_{\boldsymbol{P}}(\boldsymbol{P} \mid r, K, b, n, \sigma_{p}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ & \times f_{\boldsymbol{\theta}_{\text{GS}}}(\boldsymbol{\theta}_{\text{GS}}) \cdot f_{b}(b), \end{aligned}$

where

$$\begin{split} f_{P}(\boldsymbol{P}|r, K, b, n, \sigma_{p}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) \\ &= \prod_{t=1}^{T-1} \left[\frac{1}{\sigma_{p} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{[\log(P_{t+1}) - \log(E(P_{t+1}|P_{t}, r, K, b, n, \sigma_{p}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}))]^{2}}{2 \cdot \sigma_{p}^{2}} \right\} \right] \\ &\times \frac{1}{\sigma_{p} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{[\log(P_{1}) - \log(b)]^{2}}{2 \cdot \sigma_{p}^{2}} \right\}, \\ f_{I,\text{GSPM1}}(\boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}|\boldsymbol{P}, q_{1}^{a}, q_{2}^{a}, q^{j}, \sigma_{o}^{j}, \sigma_{o,1}^{a}, \sigma_{o,2}^{a}, K) \\ &= \prod_{d^{a}=1}^{2} \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o,d^{a}}^{a} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{d^{a},t}^{a}) - \log(q_{d^{a}}^{a} \cdot P_{t} \cdot K))^{2}}{2 \cdot (\sigma_{o,d^{a}}^{a})^{2}} \right\} \right] \\ &\times \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o}^{j} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{t}^{j}) - \log(q^{j} \cdot P_{t} \cdot K))^{2}}{2 \cdot (\sigma_{o}^{j})^{2}} \right\} \right], \\ f_{I,\text{GSPM2}}(\boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}|\boldsymbol{P}, q_{1}, q_{2}, q_{3}, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, K) \\ &= \prod_{d=1}^{3} \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o,d} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{d,t}) - \log(q_{d} \cdot P_{t} \cdot K))^{2}}{2 \cdot (\sigma_{o,d}^{j})^{2}} \right\} \right], \\ f_{\boldsymbol{\theta}_{\text{GS}}}(\boldsymbol{\theta}_{\text{GS}}) = \frac{1}{\sqrt{(2 \cdot \pi)^{2} \cdot |\boldsymbol{\Sigma}_{\text{GS}}|}} \exp\left\{ -\frac{1}{2} \cdot (\boldsymbol{\theta}_{\text{GS}} - \boldsymbol{\theta}_{\text{GS},0})' \cdot \boldsymbol{\Sigma}_{\text{GS}}^{-1} \cdot (\boldsymbol{\theta}_{\text{GS}} - \boldsymbol{\theta}_{\text{GS},0}) \right\}, \end{split}$$

and

$$f_b(b) = \frac{1}{\sigma_b \cdot \sqrt{2\pi}} \cdot \exp\left\{-\frac{(\log(b) - \mu_b)^2}{2 \cdot \sigma_b^2}\right\}.$$

4.5.2 Joint likelihoods for TSPM1 and TSPM2

The joint likelihoods for TSPM1 and TSPM2 are

$$\begin{split} \mathcal{L}_{\text{TSPM1}}(\Psi_{\text{TSPM1}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} \mid \boldsymbol{I}^{j}, \boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) = & f_{\boldsymbol{I}^{j}}(\boldsymbol{I}^{j} | q^{j}, \boldsymbol{P}^{j}, \sigma_{o}^{j}, K^{j}) \\ & \times f_{\boldsymbol{I}^{a}}(\boldsymbol{I}_{1}^{a}, \boldsymbol{I}_{2}^{a} | q_{1}^{a}, q_{2}^{a}, \boldsymbol{P}^{a}, \sigma_{o,1}^{a}, \sigma_{o,2}^{a}, K^{a}) \\ & \times f_{\boldsymbol{P}^{j}}(\boldsymbol{P}^{j} | \boldsymbol{P}^{a}, r_{m}, b, c, n^{j}, R^{j}, K^{j}, \psi, \sigma_{p}; \boldsymbol{Y}^{j}) \\ & \times f_{\boldsymbol{P}^{a}}(\boldsymbol{P}^{a} | \boldsymbol{P}^{j}, r_{m}, R^{a}, \psi, b, c, \sigma_{p}, K^{j}; \boldsymbol{Y}^{a}) \\ & \times f_{\boldsymbol{\theta}_{\text{TS}}}(\boldsymbol{\theta}_{\text{TS}}) \cdot f_{b}(b), \end{split}$$

$$\begin{aligned} \mathcal{L}_{\text{TSPM2}}(\Psi_{\text{TSPM2}}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a} \mid \boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3}; \boldsymbol{Y}^{j}, \boldsymbol{Y}^{a}) = & f_{\boldsymbol{I}}(\boldsymbol{I}_{1}, \boldsymbol{I}_{2}, \boldsymbol{I}_{3} | q_{1}, q_{2}, q_{3}, \boldsymbol{P}^{j}, \boldsymbol{P}^{a}, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, K) \\ & \times f_{\boldsymbol{P}^{j}}(\boldsymbol{P}^{j} | \boldsymbol{P}^{a}, r_{m}, b, c, n^{j}, R^{j}, K^{j}, \psi, \sigma_{p}; \boldsymbol{Y}^{j}) \\ & \times f_{\boldsymbol{P}^{a}}(\boldsymbol{P}^{a} | \boldsymbol{P}^{j}, r_{m}, R^{a}, \psi, b, c, \sigma_{p}, K^{j}; \boldsymbol{Y}^{a}) \\ & \times f_{\boldsymbol{\theta}_{\text{TS}}}(\boldsymbol{\theta}_{\text{TS}}) \cdot f_{b}(b), \end{aligned}$$

where

$$\begin{split} f_{\boldsymbol{P}^{j}}(\boldsymbol{P}^{j}|\boldsymbol{P}^{a},r_{m},b,c,n^{j},R^{j},K^{j},\psi,\sigma_{p};\boldsymbol{Y}^{j}) \\ &= \prod_{t=1}^{T-1} \left[\frac{1}{\sigma_{p}\cdot\sqrt{2\cdot\pi}} \cdot \exp\left\{ -\frac{[\log(P_{t+1}^{j}) - \log(E(P_{t+1}^{j}|P_{t}^{j},P_{t}^{a},K^{j},n^{j},r_{m},R^{j};Y_{t}^{j}))]^{2}}{2\cdot\sigma_{p}^{2}} \right\} \right] \\ &\times \frac{1}{\sigma_{p}\cdot\sqrt{2\cdot\pi}} \cdot \exp\left\{ -\frac{[\log(P_{1}^{j}) - \log(b\cdot c\cdot(K^{a}/K^{j}+1)]^{2}}{2\cdot\sigma_{p}^{2}} \right\}, \\ f_{\boldsymbol{P}^{a}}(\boldsymbol{P}^{a}|\boldsymbol{P}^{j},r_{m},R^{a},\psi,b,c,\sigma_{p},K^{j};\boldsymbol{Y}^{a}) \\ &= \prod_{t=1}^{T-1} \left[\frac{1}{\sigma_{p}\cdot\sqrt{2\cdot\pi}} \cdot \exp\left\{ -\frac{[\log(P_{t+1}^{a}) - \log(E(P_{t+1}^{a}|P_{t}^{a},P_{t}^{j},r_{m},R^{a},\psi,K^{j};Y_{t}^{a}))]^{2}}{2\cdot\sigma_{p}^{2}} \right\} \right] \\ &\times \frac{1}{\sigma_{p}\cdot\sqrt{2\cdot\pi}} \cdot \exp\left\{ -\frac{[\log(P_{1}^{a}) - \log(b\cdot(1-c)\cdot(K^{j}/K^{a}+1))]^{2}}{2\cdot\sigma_{p}^{2}} \right\}, \end{split}$$

$$f_{\mathbf{I}^{j}}(\mathbf{I}^{j}|q^{j}, \mathbf{P}^{j}, \sigma_{o}^{j}, K^{j}) = \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o}^{j} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{t}^{j}) - \log(q^{j} \cdot P_{t}^{j} \cdot K^{j}))^{2}}{2 \cdot (\sigma_{o}^{j})^{2}} \right\} \right],$$

$$\begin{split} f_{I^{a}}(I_{1}^{a}, I_{2}^{a} | q_{1}^{a}, q_{2}^{a}, P^{a}, \sigma_{o,1}^{a}, \sigma_{o,2}^{a}, K^{a}) \\ &= \prod_{d^{a}=1}^{2} \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o,d^{a}}^{a} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{d^{a},t}^{a}) - \log(q_{d^{a}}^{a} \cdot P_{t}^{a} \cdot K^{a}))^{2}}{2 \cdot (\sigma_{o,d^{a}}^{a})^{2}} \right\} \right], \\ f_{I}(I_{1}, I_{2}, I_{3} | q_{1}, q_{2}, q_{3}, P^{j}, P^{a}, \sigma_{o,1}, \sigma_{o,2}, \sigma_{o,3}, K) \\ &= \prod_{d=1}^{3} \prod_{t=1}^{T} \left[\frac{1}{\sigma_{o,d} \cdot \sqrt{2 \cdot \pi}} \cdot \exp\left\{ -\frac{(\log(I_{d,t}) - \log(q_{d} \cdot P_{t} \cdot K))^{2}}{2 \cdot (\sigma_{o,d})^{2}} \right\} \right], \\ f_{\theta_{\mathsf{TS}}}(\theta_{\mathsf{TS}}) = \frac{1}{\sqrt{(2 \cdot \pi)^{5} \cdot |\boldsymbol{\Sigma}_{\mathsf{TS}}|}} \cdot \exp\left\{ -\frac{1}{2} \cdot (\theta_{\mathsf{TS}} - \theta_{\mathsf{TS},0})' \cdot \boldsymbol{\Sigma}_{\mathsf{TS}}^{-1} \cdot (\theta_{\mathsf{TS}} - \theta_{\mathsf{TS},0}) \right\}, \end{split}$$

and

$$f_b(b) = \frac{1}{\sigma_b \cdot \sqrt{2\pi}} \cdot \exp\left\{-\frac{(\log(b) - \mu_b)^2}{2 \cdot \sigma_b^2}\right\}$$

The next two sections (i.e., Sections 4.6 and 4.7) describe procedures for simulation study and application to pollock data, respectively. Results and discussions of those simulation and application studies follow in Section 4.8.

4.6 Simulation study

In this section, we investigate the performance of the TSPM compared to the GSPM, using simulated data imitating those collected from the Korean pollock fisheries. We use a dynamic ASM, which has the same structure as that of the equilibrium ASM, but the harvest fractions are age-specific and time-varying, as an operating model to simulate an age-structured pollock-like population, from which data on relative abundance indices (i.e., I_t^j , $I_{d^a,t'}^a$ and $I_{d,t}$) and yields (i.e., Y_t^j and Y_t^a) are generated. We con-

sider eight different scenarios to investigate the effects of trends in population size and harvest regimes on model performances, which is discussed in more detail in the following sections.

Although we attempt to mimic the situation in the Korean pollock fisheries for the simulation (discussed in Sections 4.6.1 and 4.6.2 for more details), where both juveniles and adults have been caught by multiple fisheries, and only a 20-year-long time series of CPUEs and yields on both sub-stocks are available, in this simulation study, we assume the length of the time series is 40 instead of 20 to improve reliability and robustness of simulation results. One should note that the main purpose of this simulation study is to investigate how the TSPM and GSPM perform when the same set of data is given to each model; thus, the simulation settings are not necessarily required to be the exact imitation of the pollock fisheries.

This section is organised as follows: First, we describe an operating model (i.e., a dynamic ASM), designed to generate relative abundance indices and yields for juvenile and adult stocks. Second, we describe the scenarios and performance metrics, used for this simulation study.

4.6.1 **Operating Model**

Based on the equilibrium ASM with the input values given in Table 4.2, we simulate pollock-like age-structured data. We make the equilibrium ASM dynamic by simulating changes in numbers-at-ages at time t (i.e., $N_{i,t}$) with the age-specific time-varying harvest rates, $H_{i,t}$, where we consider normal process errors for transitions in log-abundance for times and ages (i.e., $\varepsilon_{p,1,t} \stackrel{\text{iid}}{\sim} N(0, \sigma_{p,1}^2)$ and $\varepsilon_{p,i,t} \stackrel{\text{iid}}{\sim} N(0, \sigma_{p,2}^2)$, for i > 1). Furthermore, to initialise a population, we assume that only the initial population (i.e., $N_{i,1}$) is at equilibrium, which is calculated by $N_{i,1}(H_{\text{init}}) = R_*(H_{\text{init}}) \cdot \tilde{N}_{i,*}(H_{\text{init}})$, where H_{init} is the constant harvest rate at times t < 1. The dynamic ASM

is then given by

$$N_{i,t} = \begin{cases} R_*(H_{\text{init}}) \cdot \tilde{N}_{i,*}(H_{\text{init}}), & \text{for } 1 < i \le A, \text{ and } t = 1 \\ \\ \frac{4 \cdot h \cdot R_*(0) \cdot \text{Egg}_{t-1}}{\text{Egg}_*(0) \cdot (1 - h) + (5 \cdot h - 1) \cdot \text{Egg}_{t-1}} \\ \times \exp(\varepsilon_{p,1,t-1}), & \text{for } i = 1, \text{ and } t > 1 \end{cases}$$

$$N_{i,t} = \begin{cases} N_{i-1,t-1} \cdot \exp(-M_{i-1}) \cdot (1 - H_{i-1,t-1}) \\ \times \exp(\varepsilon_{p,i,t-1}), & \text{for } 1 < i < A, \text{ and } t > 1 \end{cases}$$

$$[N_{A-1,t-1} \cdot \exp(-M_{A-1}) \cdot (1 - H_{A-1,t-1}) \\ + N_{A,t-1} \cdot \exp(-M_A) \cdot (1 - H_{A,t-1})] \\ \times \exp(\varepsilon_{p,A,t-1}), & \text{for } i = A, \text{ and } t > 1 \end{cases}$$

To mimic the harvest regimes on the Korean pollock fisheries where both juvenile and adult fish were targeted under different fishing pressures over time with the stock-specific selectivity-at-ages (i.e., v_i^j and v_i^a), we derive the time-varying age-specific harvest fraction $H_{i,t}$ by substituting the fully selected harvest fraction H in Equation (4.13) with the life stage-specific harvest fractions H_t^j and H_t^a accordingly:

$$H_{i,t} = v_i^j \cdot (1 - \operatorname{Mat}_i) \cdot H_t^j + v_i^a \cdot \operatorname{Mat}_i \cdot H_t^a,$$

where both v_i^j and v_i^a are calculated using the logistic curve in Equation (4.14) with corresponding parameters (i.e., ν_{sel}^j and i_{sel50}^j for v_i^j , and ν_{sel}^a and i_{sel50}^a for v_i^a) whose input values are given in Table 4.2.

The exploitable biomass of juvenile, adult, and total stocks at time t

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(i.e., B_t^j , B_t^a , and B_t , respectively) can be computed by

$$\begin{cases} B_t^j = \sum_i^A v_i^j \cdot (1 - \operatorname{Mat}_i) \cdot N_{i,t} \cdot w_i \\ B_t^a = \sum_i^A v_i^a \cdot \operatorname{Mat}_i \cdot N_{i,t} \cdot w_i \\ B_t = B_t^j + B_t^a \end{cases}$$

,

from which the relative abundance and yield data can be obtained as follows

$$\begin{cases}
I_t^j = q^j \cdot B_t^j \cdot \exp(\varepsilon_{o,t}^j) \\
I_{d^a,t}^a = q_{d^a}^a \cdot B_t^a \cdot \exp(\varepsilon_{o,d^a,t}^a) \\
I_{d,t} = q_d \cdot B_t \cdot \exp(\varepsilon_{o,d,t}) \\
Y_t^j = H_t^j \cdot B_t^j \\
Y_t^a = H_t^a \cdot B_t^a
\end{cases}$$

We repeat this data simulation process for each simulation-estimation run in each scenario.

4.6.2 Simulation scenarios and performance metrics

To compare the model performance between the four estimation models, we vary the harvest rates for both H_t^j and H_t^a , based on the H_{MSY} of the simulation model, which allows us to systematically investigate different trajectories of relative abundance data (e.g., $I_{d,t}$, I_t^j , and $I_{d^a,t}^a$), according to different harvest regimes (Table 4.3). For example, to simulate a population, where a juvenile population is heavily caught, we set $H_t^j > H_{MSY}$ and $H_t^a < H_{MSY}$. In addition, we also vary H_{init} , depending on the scenarios, along with H_t^j and H_t^a , as it largely affects an overall trend of a population trajectory. We set eight different simulation scenarios for these various conditions.

Under each scenario, we generate six sets of relative abundance data for each simulation run: $I_{d,t}^{j}$, $I_{d^{a},t}^{a}$, and $I_{d,t}$, where $d^{a} \in \{1,2\}$, and $d \in$ {1,2,3}) and separate yields on juvenile and adult stocks: Y_t^j and Y_t^a . In each simulation-estimation run, those simulated data are fitted to the four estimation models, depending on the model assumption and configuration (see Figures 4.4, 4.5, and 4.8). We repeat this simulation-estimation procedure thousands of times for each scenario until 500 converged runs for all four estimation models are obtained. In each simulation-estimation run, we deem the model has successfully converged if the maximum gradient component (mgc) of the parameters is close to 0 (i.e., less than 0.01), and the Hessian matrix is positive definite. If at least one of the four models fails to fulfil that criteria, we discard entire results of that particular simulation-estimation run.

To quantify the model performance, we use two performance metrics: the median relative difference (MRD) to measure bias of the estimates, and median absolute relative difference (MARD) to evaluate accuracy of the estimates (Ono et al., 2012; Winker et al., 2020). To obtain the values of those metics, in each converged simulation run, we record the relative difference (RD) of the quantity of interest Θ :

$$\mathrm{RD}_{\ell}(\Theta) = \frac{\hat{\Theta}_{\ell}}{\Theta} - 1,$$

where $\hat{\Theta}_{\ell}$ is the estimated quantity in the ℓ th converged run (i.e., $\ell \in \{1, 2, ..., 500\}$), and Θ is the corresponding true value (i.e., B_{MSY} , H_{MSY} , MSY, B_t , B_t/K , H_t , and H_t/H_{MSY} ; note that no analytical solutions for BRPs of the TSPM are available, thus we numerically calculate those quantities.). Additionally, we record the RD for B^j , B^a , B^j_t/K^j , B^a_t/K^a , H^j_t , and, H^a_t when TSPM1 and TSPM2 are evaluated. Once $RD_{\ell}(\Theta)$ is obtained, the MRD of $\hat{\Theta}$ is calculated as

$$MRD(\Theta) = Median(RD_{\ell}(\Theta)).$$

Similarly, the MARD is obtained by

$$MARD(\Theta) = Median(|RD_{\ell}(\Theta)|).$$

Table 4.3: Input harvest values used for eight different simulation scenarios which are denoted as S1-S8. Note that harvest values are expressed as fractions of H_{MSY} ($H_{\text{MSY}} = 0.126$).

	Scenarios							
parameters	S1	S2	S3	S4	S5	S6	S7	S8
H_t^j for $1 \le t \le 20$	1	$\frac{3}{2}$	$\frac{1}{2}$	$\frac{3}{2}$	1	$\frac{3}{2}$	$\frac{1}{2}$	$\frac{3}{2}$
H_t^j for $20 < t \le 40$	1	$\frac{1}{2}$	$\frac{3}{2}$	$\frac{3}{2}$	1	$\frac{1}{2}$	$\frac{3}{2}$	$\frac{3}{2}$
$H_t^a \text{for } 1 \le t \le 20$	1	$\frac{1}{2}$	$\frac{3}{2}$	$\frac{3}{2}$	1	$\frac{1}{2}$	$\frac{3}{2}$	$\frac{3}{2}$
H_t^a for $20 < t \le 40$	1	$\frac{3}{2}$	$\frac{1}{2}$	$\frac{3}{2}$	1	$\frac{3}{2}$	$\frac{1}{2}$	$\frac{3}{2}$
H_{init}	0	0	0	0	1	1	1	1



Figure 4.8: Schematic overview of the simulation study. The data simulation is represented by a directed acyclic graph (DAG). White circles are non-observed probabilistic nodes (e.g., state variables in the estimatation models), simulated from the ASM, and those in colour are observed probabilistic nodes (i.e., relative abundance indices: $I_{d,t}$, I_t^j , and, $I_{d^a,t}^a$; yields: Y_t^j and Y_t^a), fitted to the estimation models. Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes. Dotted rectangular frames with rounded corners indicate repetition of structure over units. Colouring the nodes blue, red, and blue-red gradient compositionally represents juvenile, adult, and both juvenile and adult biomasses, respectively. Note that the size of each node indicates the relative magnitude of values.

4.7 Application to the Korea pollock stock

In this section, we apply the state-space TSPM (i.e., TSPM1) to the actual data collected from the Korean pollock fisheries to investigate the applicability of the model and the stock status. For this case study, we fit the TSPM with three different assumptions on the constraints of the parameter *b*, which is discussed in the next section.

After fitting the three models to the actual data, we perform three model validation tests, jitter analysis (i.e., sensitivity of model fit to initial parameter values), residual analysis, and parametric bootstrap.

4.7.1 Estimation

For estimation, the joint likelihood given in Equation (4.28) is used (i.e., TSPM1), as we have information on yields and abundance indices collected from both juvenile and adult stocks. For parameter constraints, the same multivariate constraint as used in the simulation study is applied, but for the constraint on the scaling coefficient *b*, we try three candidate values as the modes of *b* (i.e., $b_0 \in \{0.3, 0.5, 0.7\}$) since information on the initial population size (i.e., $B_{t=1975}$) is not obtainable from other studies. We label the models with three different constraints for *b* as M1 ($b_0 = 0.3$), M2 ($b_0 = 0.5$), and M3 ($b_0 = 0.7$), respectively.

4.7.2 Model validation

Jitter analysis

To evaluate the stability of the model, we perform a "jitter" analysis (i.e., sensitivity to initial parameter values) (Cass-Calay et al., 2014), using all three models (i.e., M1-M3) considered in our study, for which we generate different initial random values for the model parameters and use them for parameter estimation with the pollock data. We repeat this procedure until

200 sets of converged results are obtained. We generate such random values using uniform distributions, where a reasonably wide range of lower and upper limits for each parameter is chosen. We visually inspect if all 200 converged results show a unique set of parameter estimates. A wellbehaved model should converge to a global solution regardless of initial values (Cass-Calay et al., 2014).

Residual analysis

To assess the validity of the model assumptions associated with the state equations, we use a single sample approach suggested by Thygesen et al. (2017). We randomly draw samples of a time series of P_t^j and P_t^a from their posterior distributions and calculate the standardized process errors (details about the calculation are given in Equation 4.7.2 below). In our frequentist approach, the posterior modes of those state variables in log-scale (i.e., $\log(P_t^j)$ and $\log(P_t^a)$) are found by maximising the joint likelihood discussed in Section 4.5, and the Hessian of the model is obtained by using the automatic differentiation technique with TMB (Kristensen et al., 2016; Thygesen et al., 2017), from which the precision matrix for the state variables can be identified. Then, with the modes and precision matrix, we approximate the posteriors of $\log(P_t^j)$ and $\log(P_t^a)$ using a MVN distribution, which allows us to draw random samples for P_t^j and P_t^a .

For a correct model, we expect that those standardised process residuals are normally distributed with mean 0 and variance 1 (Thygesen et al., 2017). Thygesen et al. (2017) used a Kolmogorov Smirnov (K-S) test to check the normality assumption of those process residuals, but such a test is known to be conservative if one or more parameters of a distribution is estimated (Lilliefors, 1967). Thus, in our study, instead of using a K-S test, we visually check the normality assumption of those residuals, using a normal quantile-quantile plot. Our preliminary study showed that using a single set of the residuals for checking the normality can be misleading as the distribution of those residuals also depends on the random variability in sample drawing. Therefore, we use 200 sets of standardised process residuals to find any systematic patterns, which are obtained by using the following equations, where $e_{t,s}^j$ and $e_{t,s}^a$ denote the standardised process residuals associated with juvenile and adult stocks, respectively, and the subscript *s* denotes the sample index of the process residuals (i.e., $s \in \{1, 2, 3, ..., 200\}$):

$$e_{t,s}^{j} = \begin{cases} \frac{\log P_{1,s}^{j} - \log\left[\hat{b} \cdot \hat{c} \cdot \left(\frac{\hat{K}^{a}}{\hat{K}^{j}} + 1\right)\right]}{\hat{\sigma}_{p}}, & \text{for } t = 1\\ \\ \log P_{t+1,s}^{j} - \log\left[P_{t,s}^{j} + \frac{\hat{r}_{m}}{\hat{n}^{j} - 1} \cdot P_{t,s}^{j} \cdot \left[1 - (P_{t,s}^{j})^{\hat{n}^{j} - 1}\right]\right] \\ + \frac{\hat{R}^{j}}{\hat{n}^{j} - 1} \cdot \left(P_{t,s}^{a} \cdot \frac{\hat{K}^{a}}{\hat{K}^{j}} - \frac{1}{\hat{\psi}} \cdot P_{t,s}^{j}\right) \cdot \left[1 - (P_{t,s}^{j})^{\hat{n}^{j} - 1}\right] - \frac{Y_{t}^{j}}{\hat{K}^{j}} \\ \frac{\hat{\sigma}_{p}}{\hat{\sigma}_{p}}, & \text{for } t \ge 1 \end{cases}$$

and

$$e^a_{t,s} = \begin{cases} \frac{\log P^a_{1,s} - \log\left[\hat{b} \cdot (1-\hat{c}) \cdot \left(1 + \frac{\hat{K}^j}{\hat{K}^a}\right)\right]}{\hat{\sigma}_p}, & \text{for } t = 1 \\ & , \end{cases}$$

$$\left(\frac{\log P_{t+1,s}^a - \log \left[P_t^a + \hat{r}_m \cdot P_t^a + \hat{R}^a \cdot \left(P_t^j \cdot \frac{\hat{K}^j}{\hat{K}^a} - \hat{\psi} \cdot P_t^a\right) - \frac{Y_t^a}{\hat{K}^a}\right]}{\hat{\sigma}_p}, \quad \text{for } t \ge 1$$

Parametric bootstrap

We employ a parametric bootstrap approach to test the estimability of the model parameters. State-space models can be associated with estimability problems if a model is overparameterized or both observation and process variances are attempted to be estimated (Dennis et al., 2006; Auger-Méthé et al., 2016; Auger-Méthé et al., 2021). Non-estimable parameters are often biased with large variances (Auger-Méthé et al., 2021).

To simulate data on the annual relative abundance and yield, we use the estimates obtained from fitting the models (i.e., M1-M3) to the actual pollock data as true input values. We fit the same model to these generated data and repeat this procedure 2000 times.

In each simulation and estimation run, we check the convergence by examining the maximum gradient component (mgc) and the Hessian matrix (i.e., mgc < 0.01, and the Hessian matrix is positive definite). In each converged run, we calculate the median relative difference (RD) for the model parameters (i.e., Ψ_{TSPM1}), BRPs (i.e., BRPs $\in \{B_{\text{MSY}}, B_{\text{MSY}}^{j}, B_{\text{MSY}}^{a}, M_{\text{SY}}, Y_{\text{MSY}}^{j}, Y_{\text{MSY}}^{a}, 1\}$), and biomasses (i.e., B_{t}^{j}, B_{t}^{a} , and B_{t}):

$$\mathrm{RD}_s(\mathbf{\Phi}) = \frac{\hat{\mathbf{\Phi}}_s}{\mathbf{\Phi}_s} - 1,$$

where $\hat{\Phi}$ is the estimated set of quantities of interest (i.e., $\Phi \in \{\Psi_{\text{TSPM1}}, B_t^j, B_t^a, B_t, BRPs\}$), Φ is the set of true values for those quantities of interest, and *s* denotes the simulation run (i.e., $s \in \{1, 2, 3, ..., 2000\}$).

The difficulty of estimating variance parameters in state-space models has already been discussed by previous studies (Dennis et al., 2006; Auger-Méthé et al., 2016). In Chapter 3 of this thesis, we demonstrated that such estimation problems occur when observation error is larger than process error. Thus, we have done additional experiments to detect if setting the values of the observation error variances to be smaller than the process error variance improves model performance. We also investigate the impact of simultaneous estimation of both process and observation error variances. To do that, we additionally consider three alternative parametric bootstrap tests for each estimation model (i.e., M1-M3), which are denoted by the suffixes 'V1', 'V2', and 'V3', respectively (e.g., M1.V1, M1.V2, M1.V3, ..., M3.V3). These additional tests are designed as follows:

- (i) 'V1' is designed to investigate the effect of the simultaneous estimation of both observation and process error variances. Thus, we fit the model to the data generated with the estimates obtained from fitting the models to the actual pollock data as input values, where we treat all observation error variances as known.
- (ii) 'V2' is designed to investigate the effect of the large observation error variances in parameter estimation. Thus, we fit the model to data generated with low observation error standard deviations (i.e., σ_{o}^{j} , $\sigma_{o,1}^{a}$, and $\sigma_{o,2}^{a}$), where we set all of those standard deviations as 0.1, which is less than half of the process error standard deviation estimated in each model. We estimate both observation and process error variances.
- (iii) 'V3' is designed to investigate performance of the models when both 'V1' and 'V2' conditions are met (this is known to be an ideal condition, where state-space models show the best performance). We fit the models to the same data used in V2 test, but treat those observation error standard deviations as known.

4.8 **Results and discussion**

4.8.1 Parameter constraints

Overall, multivariate constraints on the parameters of the GSPM and the TSPM in the log-scale are well approximated by multivariate normal distributions, which are visually demonstrated in Figures 4.9, 4.10, and 4.11. The Monte-Carlo samples for the parameters n and H_{MSY} of the GSPM are derived from Equation (iii), and those for the parameters n^j , R^a , R^j , ψ , and r_m of the TSPM are calculated from Equation 4.23. Those approximated distributions for the constraints of the parameters in the original scale are given in Figure 4.12.

4.8. RESULTS AND DISCUSSION

We visually evaluate the performance of the functional links between the two production models and the equilibrium ASM by comparing the yield curve of each model at different depletion levels, which is depicted in Figure 4.13. For the yield curve of the equilibrium ASM, we use the input values given in Table 4.2, but for the yield curves of the GSPM and TSPM, we use the input values given in Table 4.4, which are obtained from Equations (4.18), (4.19), (4.21), and (4.22). In terms of approximating the total yield of the ASM, the GSPM slightly outperforms the TSPM. However, it should be noted that the TSPM is able to account for the yields of two separate sub-stocks of the ASM, which is not possible with the GSPM. The closeness between the three different types of curves in Figure 4.13 confirms the derivations of Equations (4.18), (4.21), and (4.22).

Table 4.4: Input values for the parameters of the GSPM and the TSPM, which are derived from Equations (4.18), (4.19), (4.21), and (4.22) with the equilibrium ASM where the input values for the parameters are given in Table 4.2.

n	H_{MSY}	r_m	n^j	ψ	R^{j}	R^a
1.165	0.126	0.238	2.313	1.088	0.452	0.322



Figure 4.9: Distributions of 5000 samples for the natural mortality M and the steepness h (i.e., M_{ℓ} and h_{ℓ} , where $\ell \in \{1, 2, 3, ..., 5000\}$, which are drawn from gamma and beta distributions, respectively; see Section 4.4.3 for more details) and those for the parameters of the GSPM (i.e., $\log(H_{MSY,\ell})$ and $\log(n_{\ell})$) and the TSPM (i.e., $\log(r_{m,\ell})$, $\log(\psi_{\ell})$, $\log(n_{\ell}^{j})$, $\log(R_{\ell}^{a})$, and $\log(R_{\ell}^{j})$) in log-scale. The purple curves show the sample distributions, and the black curves represent corresponding MVN approximations.



Figure 4.10: Scatter plot (bottom left) between the samples of $\log(H_{\text{MSY}})$ and $\log(n)$ (i.e., $\log(H_{\text{MSY},\ell})$ and $\log(n_{\ell})$, where $\ell \in \{1, 2, 3, ..., 5000\}$; purple points). The black points underlaid in the scatter plot are 5000 samples drawn from a multivariate normal distribution with mean vector $\theta_{\text{GS},0}$ and covariance matrix Σ_{GS} , obtained from Equations (4.24) and (4.25). The top right panel shows the correlation coefficient between the two parameters.



Figure 4.11: Pair-wise scatter plots (panels in the lower triangle) of the samples for the five parameters of the TSPM (i.e., $\log(r_{m,\ell})$, $\log(\psi_{\ell})$, $\log(n_{\ell}^{j})$, $\log(R_{\ell}^{a})$, and $\log(R_{\ell}^{j})$, where $\ell \in \{1, 2, 3, ..., 5000\}$; purple points). The black points underlaid in the scatter plot are 5000 samples drawn from a multivariate normal distribution with mean vector $\theta_{\text{TS},0}$ and covariance matrix Σ_{TS} , obtained from Equations (4.26) and (4.27). The panels in the upper triangle show the pair-wise correlation coefficients between the parameters.



Figure 4.12: Constraints imposed on the parameters of the GSPM (a, b, and h) and the TSPM (c, d, e, f, g, and h). Those in panels a-g are used for both the simulation and application studies. Constraints on the parameter b (panel h) are varying by scenario in the simulation study (the red line for S1-S4, and the blue line for S5-S8) or by model (i.e., the purple broken line for M1, the brown broken line for M2, and the orange broken line for M3) in the application study.



Figure 4.13: Yield curves derived from the equilibrium ASM (solid curves), GSPM (dotted curve), and TSPM (broken curves). The red and blue colours represent juvenile and adult yields, respectively, and the black colour represents a total combined yield (i.e., juvenile yield + adult yield).

4.8.2 Simulation study

Overall, TSPM1 performs the best among the four models in our simulation settings although under S2 and S4, the estimates of B_{MSY} are more biased than those of other models. Especially, under S1-S4 (Figures 4.14-4.17), where the initial biomass is at the carrying capacity K (i.e., $H_{\text{init}} = 0$), it is shown that TSPM1 presents the least biased results (i.e., close to 0) in most of the derived quantities, except for those of H_{MSY} . However, under S6-S8 (Figures 4.19-4.21), where the initial biomass is at B_{MSY} (i.e., $H_{\text{init}} = H_{\text{MSY}}$), TSPM2 shows less biased results than those of TSPM1 although most of the differences are quite marginal. In other words, TSPM shows better performance than GSPM in all eight scenarios tested, which demonstrates that the incorporation of demographic relationships between the two life stages, using the life stage-specific yield information, can result in more accurate and less biased estimation.

The convergence rate varies among the four estimation models (Table 4.5). GSPM2 converged most frequently followed by TSPM1, GSPM1, and TSPM2, but the differences between those four models are not significant as all four models show the good convergence rates (the lowest convergence rate is 74%) although TSPM2 has the lowest convergence rates in all eight scenarios (recall that in this simulation study, the operating model has more complex structure than those of the estimation models; so, we deem that the over 70% of convergence rates are satisfactory results). Such low convergence rates of TSPM2 compared to those of TSPM1 indicate that the incorporation of separate CPUEs increases the robustness of the TSPM.

Under S5-S8 (Figures 4.18-4.21), because of a relatively low initial biomass (i.e., $B_1 = 0.39 \cdot K$) compared to that of S1-S4 (i.e., $B_1 = K$), the overall trend of population biomass is less affected by the harvest fractions (i.e., H_t^j and H_t^a), whereby less distinct performance differences among the four models are observed.

One of the interesting results is that even under S1, S4, S5, and S8 (Fig-

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ures 4.14, 4.17, 4.18, and 4.21), where H_t^j and H_t^a share the same harvest fractions to imitate situations where a stock has been exploited by a single fishery which simultaneously targets both juveniles and adults, both TSPM1 and TSPM2 generally outperform GSPM1 and GSPM2. Such results indicate that even without the fishery-induced demographic changes (i.e., different life stage-specific fishing pressures), the single production function of the GSPM cannot fully capture the effect of demographic changes on population growth.

GSPM1 shows the worst performance in all eight scenarios, showing the largest biases in MRD and MARD of almost all quantities investigated. Such results are expected as the structure of the model does not correctly account for the separate relative abundance indices for each sub-stock. Especially, the estimates of the initial biomass show large biases in all eight scenarios, which affects those in subsequent time points.

In the estimates of the BRPs, those of B_{MSY} show the most biased and inaccurate results in all four models. Such biases and inaccuracies tend to be larger when the values of H_t^j and H_t^a differ. However, the estimates of H_{MSY} show the least biased and most accurate results, which is consistent in all scenarios regardless of the values of H_t^j and H_t^a assigned.

verged results for all four models under each scenario.							
Scenario (total)	GSPM1	GSPM2	TSPM1	TSPM2			
S1 (606)	99	100	96	87			
S2 (710)	98	100	93	77			
S3 (677)	98	100	95	79			
S4 (683)	84	94	92	74			
S5 (584)	98	100	94	92			
S6 (654)	98	100	94	84			
S7 (666)	98	99	94	81			
S8 (932)	76	94	92	76			

Table 4.5: Convergence rate in percent for each of the four estimation models under all eight scenarios (i.e., S1-S8). The numbers in the parentheses are the total number of simulation-estimation runs required for 500 mutual converged results for all four models under each scenario.



Figure 4.14: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 1, where exploitation rates for both juveniles and adults are set to be equal at H_{MSY} (i.e., $H_t^j = H_{MSY}$ and $H_t^a = H_{MSY}$, $\forall t$), and the initial biomass is at the maximum capacity K (i.e., b = 1). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Scenario2 (S2)

Figure 4.15: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 2, where exploitation rates for both juveniles and adults are set to differ (i.e., $H_t^j =$ $1.5 \cdot H_{MSY}$ and $H_t^a = 0.5 \cdot H_{MSY}$ for $1 \le t \le 20$, and $H_t^j = 0.5 \cdot H_{MSY}$ and $H_t^a = 1.5 \cdot H_{MSY}$ for $20 < t \le 40$), and the initial biomass is at the maximum capacity K (i.e., b = 1). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Figure 4.16: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 3, where exploitation rates for both juveniles and adults are set to differ (i.e., $H_t^j = 0.5 \cdot H_{MSY}$ and $H_t^a = 1.5 \cdot H_{MSY}$ for $1 \le t \le 20$, and $H_t^j = 1.5 \cdot H_{MSY}$ and $H_t^a = 0.5 \cdot H_{MSY}$ for $20 < t \le 40$), and the initial biomass is at the maximum capacity K (i.e., b = 1). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Scenario4 (S4)

Figure 4.17: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 4, where exploitation rates for both juveniles and adults are set to be equal at $1.5 \cdot H_{MSY}$ (i.e., $H_t^j = 1.5 \cdot H_{MSY}$ and $H_t^a = 1.5 \cdot H_{MSY}$, $\forall t$), and the initial biomass is at the maximum capacity K (i.e., b = 1). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Figure 4.18: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 5, where exploitation rates for both juveniles and adults are set to be equal at H_{MSY} (i.e., $H_t^j = H_{MSY}$ and $H_t^a = H_{MSY}$, $\forall t$), and the initial biomass is at B_{MSY} (i.e., b = 0.39). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Scenario6 (S6)

Figure 4.19: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 6, where exploitation rates for both juveniles and adults are set to differ (i.e., $H_t^j =$ $1.5 \cdot H_{MSY}$ and $H_t^a = 0.5 \cdot H_{MSY}$ for $1 \le t \le 20$, and $H_t^j = 0.5 \cdot H_{MSY}$ and $H_t^a = 1.5 \cdot H_{MSY}$ for $20 < t \le 40$), and the initial biomass is at B_{MSY} (i.e., b = 0.39). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).


Figure 4.20: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 7, where exploitation rates for both juveniles and adults are set to differ (i.e., $H_t^j = 0.5 \cdot H_{\text{MSY}}$ and $H_t^a = 1.5 \cdot H_{\text{MSY}}$ for $1 \leq t \leq 20$, and $H_t^j = 1.5 \cdot H_{\text{MSY}}$ and $H_t^a = 0.5 \cdot H_{\text{MSY}}$ for $20 < t \leq 40$), and the initial biomass is at B_{MSY} (i.e., b = 0.39). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).



Scenario8 (S8)

Figure 4.21: Median relative difference (MRD) and median absolute relative difference (MARD) of 500 sets of estimates under Scenario 8, where exploitation rates for both juveniles and adults are set to be equal at $1.5 \cdot H_{MSY}$ (i.e., $H_t^j = 1.5 \cdot H_{MSY}$ and $H_t^a = 1.5 \cdot H_{MSY}$, $\forall t$), and the initial biomass is at B_{MSY} (i.e., b = 0.39). TS and GS represent the type of model used (i.e., abbreviation of TSPM and GSPM), respectively, and the numbers "1" and "2" represent the type of abundance indices used for estimation (i.e., "1" indicates those collected separately from juvenile and adult stocks, and "2" indicates those collected from a combined stock).

4.8.3 Application to the Korea pollock stock

Estimation

All three models (i.e., M1-M3) successfully converged. The parameter estimates and their associated uncertainties in each model are given in Table 4.6. Given the parameter estimates in Table 4.6, we numerically calculate the BRPs from each model (Table 4.7). Based on those estimated BRPs, we evaluate the status of the Korea pollock stock.

The biomasses (i.e., juvenile, adult, and the total biomasses) estimated under all three models, illustrated in Figures 4.22-4.24, show that the Korea pollock stock continuously decreased since the early 1980s. The fitted results of the three models in Figures 4.22-4.24 also show that large observation errors are involved with I_t^j and $I_{1,t}^a$, which are collected from Danish seine and gillnet fisheries, respectively. The configurations of the three models only differ in the assumption on the constraint for the scaling coefficient *b* (i.e., $b_0 = 0.3$ for M1, $b_0 = 0.5$ for M2, and $b_0 = 0.7$ for M3; see Figure 4.12h); thus, the estimated biomass trends in all three models are almost identical, but such differences affect the estimates for the initial biomasses, which determine the overall scale of the other biomass estimates in each model.

According to all three models, both juvenile and adult stocks were either overfished or were in the overfishing phase, or both. Especially since the early 1980s, the stock had been severely overfished and remained in the overfished status (Figure 4.25).

Parameters	M1	M2	M3
\hat{b}	0.332 (0.098)	0.553 (0.159)	0.756 (0.212)
\hat{c}	0.624 (0.176)	0.623 (0.162)	0.641 (0.152)
\hat{r}_m	0.206 (0.044)	0.213 (0.047)	0.216 (0.046)
$\hat{\psi}$	0.946 (0.335)	1.004 (0.365)	1.040 (0.368)
\hat{R}^{a}	0.338 (0.065)	0.328 (0.064)	0.321 (0.061)
\hat{R}^{j}	0.362 (0.202)	0.397 (0.227)	0.421 (0.234)
\hat{n}^{j}	2.307 (0.024)	2.304 (0.025)	2.303 (0.024)
\hat{K}^{j} (×10 ⁵)	5.366 (2.126)	3.995 (1.242)	3.841 (1.580)
\hat{q}^{j} (×10 ⁻³)	1.448 (0.716)	1.218 (0.714)	0.994 (0.760)
$\hat{q}_{1}^{a}~(imes 10^{-3})$	0.085 (0.041)	0.071 (0.040)	0.059 (0.043)
\hat{q}_{2}^{a} (×10 ⁻³)	0.041 (0.019)	0.035 (0.019)	0.029 (0.020)
$\hat{\sigma}_p$	0.278 (0.162)	0.277 (0.163)	0.299 (0.182)
$\hat{\sigma}_{o}^{j}$	1.403 (0.278)	1.447 (0.270)	1.460 (0.267)
$\hat{\sigma}^a_{o,1}$	0.678 (0.117)	0.680 (0.117)	0.680 (0.115)
$\hat{\sigma}^a_{o,2}$	0.160 (0.181)	0.159 (0.182)	0.131 (0.244)

Table 4.6: Estimates of the parameters of the three models (i.e., M1-M3). Numbers in the parenthesis indicate standard error.

Table 4.7: Biological reference points (BRPs) estimated from the three models fitted to the Korea pollock data (i.e., M1-M3)

BRPs	M1	M2	M3	
\hat{H}_{MSY}	0.104	0.108	0.110	
\hat{B}_{MSY}	981724	703778	661235	
МŜҮ	102099	76008	72736	
\hat{B}^{j}_{MSY}	384650	285827	274498	
\hat{Y}^j_{MSY}	40004	30869	30195	
\hat{B}^a_{MSY}	597074	417951	386737	
\hat{Y}^a_{MSY}	62095	45139	42541	



Figure 4.22: Assessment results of the Korea pollock stock under M1. The red lines represent the point estimates, and the red shaded areas represent (95%) uncertainties of the estimates. The horizontal dotted lines are the corresponding BRPs.



Figure 4.23: Assessment results of the Korea pollock stock under M2. The red lines represent the point estimates, and the red shaded areas represent (95%) uncertainties of the estimates. The horizontal dotted lines are the corresponding BRPs.



Figure 4.24: Assessment results of the Korea pollock stock under M3. The red lines represent the point estimates, and the red shaded areas represent (95%) uncertainties of the estimates. The horizontal dotted lines are the corresponding BRPs.



Figure 4.25: Kobe-plots for the Korea pollock stock. Stock trajectories shown in each column of the panels are estimated from the model, denoted at the top of each column (i.e., M1-M3). The panels in each row show the trajectories of the juvenile (B_t^j ; first row), adult (B_t^a ; second row), and total (B_t ; third row) exploitable biomasses, respectively. Each panel is divided into four coloured zones. The red zone indicates that a stock is overfished and in the overfishing phase, where biomass is lower than its optimum level, but fishing mortality is greater than 1. The green zone indicates that a stock is in a safe status where fishing mortality is below 1 and the biomass is above B_{MSY} . The two yellow zones characterise intermediate situations (either overfishing or overfished). The open circles represent the annual trajectory of the Korea pollock stock.

4.8. RESULTS AND DISCUSSION

Model validation

Our jitter analysis results demonstrate that all three models have converged to a unique set of parameter estimates, regardless of the initial guess values used for the model estimation (see Figures 4.26). The distributions of standardised process residuals in Figure 4.27 show that there is insufficient evidence for a significant violation of the normality assumption for the process error in all three models.

In the parametric bootstrap test, because of the short time series of data and the large observation errors involved with I_t^j and $I_{1,t}^a$, all three models show low convergence rates (i.e., 348/2000 (17.4%) with M1, 365/2000 (18.3%) with M2, and 411/2000 (20.6%) with M3). Although we imposed some strong constraints on the five model parameters, the median relative difference of some parameters show biased results, especially standard deviation parameters (σ_{o}^j , $\sigma_{o,1}^a$, $\sigma_{o,2}^a$, and σ_p), R^j , and ψ (see Figures 4.28, 4.30, and 4.32), which indicates that estimability issues exist in those parameters. However, it should be noted that since the bias of those paramters is not significantly large (mostly less than 20%), the biomass predicted and some of the estimated BRPs still show somewhat reliable estimation performance (i.e., the biases of those derived quantities are mostly less than 20%; see Figures 4.28-4.33), which supports the use of those estimated quantities to analyse the status of the Korea pollock stock.

From the additional bootstrap tests (those denoted by the suffixes 'V1', 'V2', and 'V3'), we confirm that such biases in relative difference of some model parameters are associated with the large observation error variances as well as the simultaneous estimation of both observation and process error variances. For example, under V1 (i.e., M1.V1, M2.V1, and M3.V1, where large observation error variances are treated as known), performance improvement in terms of relative difference is negligible, but when the observation error standard deviations are set to be smaller under 'V2' and 'V3', significant performance improvement is observed although the relative difference of the observation and process error standard devi-

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ations gets worse under 'V2' (see Figures 4.28-4.33).



Figure 4.26: Box plots for 200 estimates of parameters from the three alternative models (first row; the name of the model is denoted at the top of each column) and the corresponding 200 sets of initial guess values used for the parameter estimation of each of the three models (second row).

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Figure 4.27: Normal quantile plots for 200 sets of process residuals, obtained from the three models (red points; the name of the model is denoted at the top of each panel). The blue points, which are given as a comparative reference, in the last panel are generated from the standard normal distribution.



Figure 4.28: Relative difference (RD) of the parameters (i.e., Ψ_{TSPM1}) and the BRPs under M1 (first column), M1.V1 (second column), M1.V2 (third column), and M1.V3 (fourth column).



Figure 4.29: Relative difference (RD) of the juvenile (i.e., B_t^j), adult (i.e., B_t^a), and total (i.e., B_t) exploitable biomasses under M1 (first column), M1.V1 (second column), M1.V2 (third column), and M1.V3 (fourth column).



Figure 4.30: Relative difference (RD) of the parameters (i.e., Ψ_{TSPM1}) and the BRPs under M2 (first column), M2.V1 (second column), M2.V2 (third column), and M2.V3 (fourth column).



Figure 4.31: Relative difference (RD) of the juvenile (i.e., B_t^j), adult (i.e., B_t^a), and total (i.e., B_t) exploitable biomasses under M2 (first column), M2.V1 (second column), M2.V2 (third column), and M2.V3 (fourth column).



Figure 4.32: Relative difference (RD) of the parameters (i.e., Ψ_{TSPM1}) and the BRPs under M3 (first column), M3.V1 (second column), M3.V2 (third column), and M3.V3 (fourth column).



Figure 4.33: Relative difference (RD) of the juvenile (i.e., B_t^j), adult (i.e., B_t^a), and total (i.e., B_t) exploitable biomasses under M3 (first column), M3.V1 (second column), M3.V2 (third column), and M3.V3 (fourth column).

4.9 Conclusion

Through the simulation study, we demonstrated problems with the GSPM when the age-aggregated model is naively applied to data collected from separate sub-groups (e.g., juveniles and adults) of a population. Those problems that we found are consistent with previous studies (Maunder, 2003; Wang et al., 2014):

- (i) Taking catch from the wrong component of the population (i.e. small fish grow faster than large fish so their removal has a different effect).
- (ii) Associating indices of abundance with the wrong component of the population (e.g., link the juvenile index I_t^j to the total exploitable biomass B_t).
- (iii) Assuming the production function stays the same over time when multiple fisheries operate and the effort allocation among them changes.
- (iv) Can not explicitly model time varying recruitment, particularly when there is information (e.g. a juvenile index).

Conversely, the key advantages of using the TSPM are as follows: first, the model is capable of accounting for the impacts of demographic changes on population growth; second, catch (i.e., fishing mortality) is taken from the appropriate component of the population; third, recruitment variation is informed by the juvenile index; fourth, more detailed assessment results are provided compared to the GSPM (e.g., estimated biomasses for juvenile and adult stocks); and lastly, since the model is formulated in a state-space form, it is able to capture both observation and process errors, which is a desirable property in modern stock assessment.

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Chapter 5

A state-space length-based age-structured model

5.1 Introduction

In modern fisheries stock assessment, age-structured models such as statistical catch-at-age models (SCAAMs) are widely used and considered the most reliable assessment methods. These models have continuously evolved, and in a recent decade, state-space age-structured models (SSAMs) have received much attention in the fisheries science community. A SSAM is becoming a more favoured choice for fisheries scientists because its state-space framework allows the model to differentiate between process and observation errors, providing a more realistic representation of a fish population dynamics than that of a SCAAM. The development of new software such as TMB (Kristensen et al., 2016) facilitates the efficient implementation and estimation of such large-scale parametric models in statespace form, where log-abundance for ages and years are treated as state variables with normal process errors to account for demographic stochasticity (Cadigan, 2016; Miller et al., 2016; Miller and Hyun, 2017; Aeberhard et al., 2018). Thus, many data-rich stocks around the world are actively managed using SSAMs (Aeberhard et al., 2018). However, these methods have a high data demand, which cannot be fulfilled in many fisheries where information on age composition is not available.

Age-structured models typically require catch-at-age data (Fournier and Archibald, 1982; Methot and Wetzel, 2013), obtained from age determination methods such as the analysis of annuli on the scales, otoliths, and vertebrae. Despite the importance of fish age information, the costly examination on such ageing parts and lack of technical expertise often restrict its availability. Under these circumstances, fish length data are often the only composition information available to researchers. Thus, as alternatives to age-structured models, numerous length-based models have been developed and widely used for many fisheries stock assessments (Fournier et al., 1998; Quinn et al., 1998; Punt et al., 2016).

Measuring fish length is an easy way to collect biological information on fish populations, and its cost and labour-effectiveness have probably made length data one of the most abundantly used fisheries information globally. These advantageous properties of fish length data led to the gradual development of length-based age-structured models (LBASMs), where length frequency samples are utilised to infer the age composition of a population as an alternative to direct observations such as catch-atage data (Fournier et al., 1998; Quinn et al., 1998). Except for the length frequency analysis component, the overall structure of LBASMs is almost identical to conventional SCAAMs as both types of models are designed to account for age-structured dynamics of a fish population (Fournier and Archibald, 1982; Deriso and Parma, 1988; Parma and Deriso, 1990; Fournier et al., 1991, 1998; Quinn et al., 1998). Such structural similarity between those models suggests a possible extension of LBASMs to state-space forms as demonstrated in previous studies which developed SSAMs from conventional SCAAMs (Cadigan, 2016; Miller et al., 2016; Miller and Hyun, 2017; Aeberhard et al., 2018).

5.2. DEVELOPMENT OF THE STATE-SPACE LBASM

Therefore, the main purpose of this research lies in the development of a LBASM in a state-space form. We evaluate goodness-of-fit and estimability of parameters to test the impact of the additional complexity on model performance. For a state-space framework of LBASM, we adopt an exisiting LBASM which has been gradually developed by Deriso and Parma (1988); Parma and Deriso (1990); Quinn et al. (1998) and extend the model into a state-space form, where process errors between transitions in abundance for ages and years are newly incorporated. Furthermore, we include the Dirichlet-multinomial distribution to account for overdispersion in length composition data (Thorson et al., 2017), which allows us to avoid a subjective choice of data weighting. As an example application, we fit our model to observations on the Korea chub mackerel stock, testing different assumptions on natural mortality and the number of age groups of the stock. Lastly, to evaluate model performance, goodness-of-fit, and estimability of parameters, we conduct simulation studies.

5.2 Development of the state-space LBASM

To effectively describe the development process of a LBASM in state-space form, we first introduce the basic structure of a LBASM for a single year class, which has no state-space framework (Quinn et al., 1998). After introducing the structure and concept of the model, we expand it into a statespace form, which is applicable to multiple year classes. All notation we use throughout this study is defined in Table 5.1.

5.2.1 LBASM for a single year-class

In this section, we describe Quinn et al. (1998)'s LBASM (hereafter referred to as Quinn's LBASM) which we use as the underlying structure of our state-space LBASM. Here, we consider only a single year class to effectively describe the concept and the basic structure of the model.

Parameter	Description
i, j	index for length class bins
w	length bin width
Ι	number of length class bins
a	index for ages
A	last age group
r	recruitment age
y	index for years
T	number of years
d	index for replicated data sets (i.e., those in simulation study)
\overline{L}_i	mid-point of length class <i>i</i>
$Effort_y$	fishing effort in year y
q	catchability coefficient
F_y	fully-selected fishing mortality in year y (i.e., $F_y = q \cdot \text{Effort}_y$)
Mat_i	sexual maturity for fish of length $ar{L}_i$
v_i	selectivity for fish of length \bar{L}_i
$F_{i,y}$	fishing mortality rate for fish of length \overline{L}_i in year y (i.e., $F_{i,y} = v_i \cdot F_y$)
au	scale factor to account for the plus group accumulation for the last age group of the initial year class, which is given as 0
M_i	natural mortality rate for fish of length $ar{L}_i$
$Z_{i,y}$	total mortality rate for fish of length \bar{L}_i in year y (i.e., $Z_{i,y} = M_i + F_{i,y}$)
μ_r	expected length for recruits
$\mu_{i,a+1}$	expected length at age $a + 1$ for fish of length \bar{L}_i at age a
σ_{a+1}	standard deviation for a length distribution of fish at age $a + 1$
k , L_{∞}	parameters associated with $\mu_{i,a+1}$ (i.e., $\mu_{i,a+1} = L_{\infty} \cdot (1-\rho) + \rho \cdot \overline{L}_i$, where $\rho = \exp(-k)$ and L_{∞} is given as 40.6)
\bar{R}	average number of recruitment
W_i	weight of fish of length $ar{L}_i$
b_0, b_1	parameters of the Lorenzen equation (i.e., $M_i = b_0 \cdot W_i^{-b_1}$, where b_1 is given as 0.305)
ω_0,ω_1	parameters of the length-weight relationship equation (i.e., $W_i = \omega_0 \cdot \bar{L}_i^{\omega_1}$), which are given as 0.003 and 3.425, respectively
$\sigma_{N,1}$	standard deviation of annual log-recruitment deviations from $ar{R}$
$\sigma_{N,2}$	standard deviation in stochastic annual transition of abundance at age $2/(a+1-a)$
σ_r, σ_L	parameters associated with σ_{a+1}^2 (i.e., $\sigma_{a+1}^2 = \sigma_L^2 \cdot \frac{1 - \rho^{2 \cdot (a+1-r)}}{1 - \sigma_r^2} + \rho^{2 \cdot (a+1-r)} \cdot \sigma_r^2$)
σ_Y	inter annual deviation in yield
$\gamma_{\rm Mat}, l_{50,\rm Mat}$	parameters associated with Mat _i (i.e., Mat _i = $\frac{1}{1 + \exp[-\gamma_{Mat} \cdot (\bar{L}_i - l_{50,Mat})]}$), which are given as 0.70 and 20.11, respectively
γ , l_{50}	parameters associated with v_i (i.e., $v_i = \frac{1}{1 + \exp[-\gamma \cdot (\bar{L}_i - l_{50})]}$)
E_y	sample size for length frequency samples in year y
E_y^{eff}	effective sample size for length frequency samples in year y
θ	parameter that governs the linear relationship between E_y^{eff} and E_y (i.e., $E_y^{\text{eff}} = \frac{1}{1+\theta} + E_y \cdot \frac{\theta}{1+\theta}$)
$n_{i,y}$	observed length frequency for length bin i in year y
$oldsymbol{n}_y$	vector of observed length frequencies in year y (i.e., $n_y = (n_{1,y}, n_{2,y}, n_{3,y},, n_{I,y})$)
$N_{a,y}$	number of fish at age a in year y
B_y	biomass in year y
SSB_y	spawning stock biomass in year y
ϕ	fraction of the year elapsed when spawning occurs, which is given as 0.33.
φ	average female proportion, which is given as 0.6.

Table 5.1: Notation summary

 $\hat{C}_{i,y}$ model predicted catch-at-length i in year y

 Y_y observed total yield in year \boldsymbol{y}

 \hat{Y}_y model predicted total yield in year \boldsymbol{y}

 $\hat{oldsymbol{P}}_y$ vector of model predicted length composition proportions in year \boldsymbol{y}

vector of concentration parameters in year y for a Dirichlet-multinomial distribution (i.e., $\alpha_y = (\alpha_{1,y}, \alpha_{2,y}, \alpha_{3,y}, ..., \alpha_{I,y})$) \pmb{lpha}_y

5.2. DEVELOPMENT OF THE STATE-SPACE LBASM

In Quinn's LBASM, survivorship of individual fish is length-dependent; thus, modelling individual growth in length is one of the key components in the model. To do so, Quinn et al. (1998) adopted Cohen and Fishman (1980)'s stochastic growth model which was derived from the von Bertalanffy growth model by simple reparameterisation. Using Cohen and Fishman (1980)'s model allows the modelling of transition probabilities of individual growth in length to be both age- and length-specific. We discuss this brief description of the model in the following subsections.

Length growth model

The von Bertalanffy growth equation is frequently used when modelling growth of a fish in length (von Bertalanffy, 1938):

$$L_a = L_{\infty} \cdot [1 - \exp\{-k \cdot (a - a_0)\}], \tag{5.1}$$

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where L_a is the length of a fish at age a, L_{∞} is the asymptotic length, k is the growth parameter, and a_0 is the theoretical age at length 0. This deterministic form has been applied in several length-based methods when modelling the mean length of fish in each age group (Fournier et al., 1990, 1998; Taylor et al., 2005). However, in those models, size (e.g., length or weight) transitions between age groups were not explicitly modelled, thus failing to incorporate cumulative impact of length-dependent mortality (e.g., bigger individuals are more susceptible to being caught, therefore the mean length of fish in a population becomes smaller over time) on the length distribution of a population.

Following Quinn et al. (1998), we use an alternative form of Equation (5.1), which was reparameterised by Cohen and Fishman (1980) (see Appendix B.1 for derivation), to account for stochastic growth transitions of individuals in length between age groups:

$$L_{a+1} = L_{\infty} \cdot (1-\rho) + \rho \cdot L_a + \varepsilon_a, \quad \text{for} \quad r \le a < A, \tag{5.2}$$

where *r* is the age at recruitment, *A* is the maximum age, ρ is the Brody coefficient (i.e., $\rho = \exp(-k)$), and ε_a denotes a normally distributed error term with mean 0 and variance σ_L^2 .

For the initial condition of the equation above (i.e., a = r), we assume that the length of a fish recruited to a population at age a = r is normally distributed with mean μ_r and variance σ_r^2 :

$$L_r \sim N(\mu_r, \sigma_r^2). \tag{5.3}$$

Then, the expected length and variance at age a + 1 for an individual of length x at age a in Equation (5.2) can be expressed as (see Appendix B.1 for derivation)

$$E[L_{a+1}|x] = \mu_{a+1}(x) = L_{\infty} \cdot (1-\rho) + \rho \cdot x, \quad \text{for } r \le a < A_{2}$$

and

$$\operatorname{Var}[L_{a+1}] = \sigma_{a+1}^2 = \sigma_L^2 \cdot \frac{1 - \rho^{2 \cdot (a+1-r)}}{1 - \rho^2} + \rho^{2 \cdot (a+1-r)} \cdot \sigma_r^2, \quad \text{for } r \le a < A.$$
(5.4)

Another possible assumption on the standard deviation (SD) of the error term ε_a in Equation (5.2) is that the SD for each age *a* (i.e., $\sigma_{a,L}$) is proportional to the expected length increment ΔL_a (Haddon et al., 2008):

$$\sigma_{a,L} = \zeta \cdot \Delta L_a,\tag{5.5}$$

where

 $\Delta L_a = L_{a+1} - L_a, \quad \text{ for } r \le a < A,$

and ζ is the proportionality coefficient ($\zeta > 0$).

Then, the variance of L_{a+1} under this proportionality assumption be-

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comes (see Appendix B.1 for derivation)

$$\operatorname{Var}[L_{a+1}] = \sigma_{a+1}^2 = \zeta^2 \cdot \sum_{i=0}^{a-r} \rho^{2 \cdot i} \cdot \Delta L_{a-i}^2 + \rho^{2 \cdot (a+1-r)} \cdot \sigma_r^2, \quad \text{for } r \le a < A.$$
(5.6)

Despite its biologically more reasonable assumption on fish growth in length, the alternative form in Equation (5.6) for the variance σ_{a+1}^2 is not considered in this study because of its restricted form compared to that in Equation (5.4). The variance curve in Equation (5.6) only takes a form of a decreasing curve in older age groups, whereas that in Equation (5.4) can model both decreasing and increasing trends in those age groups (see Figure B.1 in Appendix B.1). We attempted to fit the model, using the variance curve from Equation (5.6), but observed failure in estimation with the mackerel data. Note that a gradual increase in length variance over age is a common assumption in previous studies on length-based stock assessment models (Fournier et al., 1990, 1998; Quinn et al., 1998).

In theory, stochastic growth trajectories of all individual fish can be recursively obtained by Equation (5.2) with the initial condition given in Expression (5.3). However, one should note that this calculation entails two major problems:

- (i) Incorporating individual-specific growth curves into a model requires excessive computational power, which is further inflated when calculating length-dependent mortality, based on those individual length growth models.
- (ii) The error term in Equation (5.2) allows for negative growth, which is not possible for most fish species.

To account for the modelling issues listed above, we use a discretised approximation method, where we discretise the continuous variable for an individual length (i.e., x) into a number of bins with a width of Δw . Then, we keep track of length growth trajectories of individuals by age on a bin-

by-bin basis. For example, individuals of the same age, whose lengths belong to the same bin, are assumed to follow the same stochastic growth trajectory for their next length increments, where any negative growth is restricted by assigning a zero probability to bins for lengths smaller than their current size.

We use the subscripts *i* and *j*, both of which denote the same prespecified length bins (i.e., $i, j \in \{1, 2, 3, ..., I\}$, where *I* denotes a total number of bins), to express growth transition probabilities between length bins. To be specific, since we assume that the midpoint of each length bin, denoted as either \overline{L}_i or \overline{L}_j , represents the length of all individuals that fall in the same length bin, the probability that an individual of age *a* in length bin *i* falls in length bin *j* at age a + 1 is given by

$$\Pr(\bar{L}_j|\mu_{a+1,i},\sigma_{a+1}) = \int_{\bar{L}_j - w/2}^{\bar{L}_j + w/2} h(L|\mu_{a+1,i},\sigma_{a+1}) dL, \quad \text{for } 1 \le i, j \le I \text{ and } j \ge i,$$
(5.7)

where $h(\cdot)$ is a normal probability density function, w is the length bin width, and

$$\mu_{a+1,i} = L_{\infty} \cdot (1-\rho) + \rho \cdot \bar{L}_i.$$

Growth transition probabilities

As explained in the earlier section, for computational efficiency, we discretise a normal length distribution of recruits, given in Expression (5.3), into a number of bins. Thus, the probability that those of age a = r fall in the length bin *i* (i.e., $\pi_{i|r}$) can now be approximated by

$$\pi_{i|r} = \frac{\exp\left[-\frac{(\bar{L}_i - \mu_r)^2}{2 \cdot \sigma_r^2}\right]}{\sum_{i'=1}^{I} \exp\left[-\frac{(\bar{L}_{i'} - \mu_r)^2}{2 \cdot \sigma_r^2}\right]}$$

Similarly, the growth transition probabilities between the length bins (i.e., $\pi_{j|i,a}^{G}$) can be expressed through discrete approximation of Expression (5.7) as follows

$$\pi_{j|i,a}^{G} = \frac{\exp\left[-\frac{(\bar{L}_{j} - \mu_{i,a+1})^{2}}{2 \cdot \sigma_{a+1}^{2}}\right] \cdot \mathbf{1}_{\{j \ge i\}}}{\sum_{j'=i}^{I} \exp\left[-\frac{(\bar{L}_{j'} - \mu_{i,a+1})^{2}}{2 \cdot \sigma_{a+1}^{2}}\right]}, \quad \text{for } r \le a < A,$$

where we incorporate the indicator function $\mathbf{1}_{\{j \ge i\}}$ to omit the possibility of the negative growth of individual fish.

In the absence of mortality, the length distribution of fish at subsequent ages is recursively updated by

$$\pi_{j|a+1} = \sum_{i=1}^{I} \pi_{i|a} \cdot \pi_{j|i,a}^{G}, \quad \text{for } r \le a < A,$$
(5.8)

However, in the presence of mortality, where mortality is assumed to be length-dependent, the length distribution must vary, depending on the survivorship of individuals, and such changes accumulate through the recursive property in Equation (5.8). Thus, by assuming that individuals only survived from length-dependent mortality processes have a chance to grow in length for their subsequent ages, we can rewrite Equation (5.8) as follows

$$\pi_{j|a+1} = \frac{\sum_{i} \pi_{i|a} \cdot \exp(-Z_{i}) \cdot \pi_{j|i,a}^{G}}{\sum_{j'} \sum_{i'} \pi_{i'|a} \cdot \exp(-Z_{i'}) \cdot \pi_{j'|i',a}^{G}}, \quad \text{for } r \le a < A,$$
(5.9)

where Z_i is the length-dependent total mortality rate for those in length bin *i*, which we discuss in the next section for more details.

Length-dependent mortality

The length-dependent total mortality rate Z_i consists of length-dependent natural and fishing mortality rates, denoted by M_i and F_i , respectively:

$$Z_i = M_i + F_i$$

For the natural mortality M_i , we consider three different assumptions by referring to previous studies. The first assumption is that natural mortality is length-dependent, which is expressed by the allometric relationship of natural mortality to the body mass of fish in each length bin *i* (Lorenzen, 1996):

$$M_i = b_0 \cdot W_i^{-b_1}.$$

Here b_0 is the natural mortality rate at unit weight, b_1 is the allometric scaling factor, and W_i is the weight of fish of length \bar{L}_i . This weight W_i is also assumed to have an allometric relationship:

$$W_i = \omega_0 \cdot \bar{L}_i^{\omega_1},$$

where ω_0 and ω_1 are the two length-weight relationship parameters. The second assumption is that natural mortality is constant across all length groups (i.e., $M_i = M$); thus, the parameter M here is treated as a single free parameter to be estimated (or given if not estimable). The third assumption is that natural mortality is constant at 1.5 times the von Bertalanffy growth parameter k (i.e., $M_i = 1.5 \cdot k$) (Jensen, 2011), where the parameters k and M simultaneously constrain each other when estimated. We test those assumptions when we apply our model to actual data sets collected from the Korea chub mackerel stock.

For the length-dependent fishing mortality F_i , we use the following

separability assumption (Doubleday, 1976):

$$F_i = v_i \cdot F,$$

where v_i is the selectivity for fish of length L_i , and F is the fully selected instantaneous fishing mortality rate.

The fully-selected fishing mortality F is assumed to be proportional to the total effort (i.e., Effort):

$$F = q \cdot \text{Effort},$$

where q is the catchability coefficient.

For the selectivity v_i , we use a two-parameter logistic function

$$v_i = \frac{1}{1 + \exp\left[-\gamma \cdot \left(\bar{L}_i - l_{50}\right)\right]},$$

where γ is the slope parameter, and l_{50} is the length at 50% selectivity.

5.2.2 State-space LBASM for multiple year classes

In this section, we describe the full structure of our state-space LBASM. We divide the model into two parts, namely the population model and data model. In the population model part, we formulate age-structured dynamics of a population, where abundances for ages and years are treated as state variables. In the data model part, we relate those state variables to observations (i.e., the time series of yield and length frequency samples), where we assume a Dirichlet-multinomial distribution for the length frequency samples and a normal distribution for the natural logarithm of yield.

In the following subsections, we describe the two parts of the model.

Population model

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Fisheries data, such as total yield and fishing effort, are often collected annually. Thus, we expand the single year-class model to be applicable for such annual time series data. With year-specific fishing mortality rates (i.e., $F_{i,y} = v_i \cdot q \cdot \text{Effort}_y$), Equation (5.9) can be written as

$$\pi_{j|a+1,y} = \frac{\sum_{i} \pi_{i|a,y} \cdot \exp[-(F_{i,y} + M_{i})] \cdot \pi_{j|i,a}^{G}}{\sum_{j'} \sum_{i'} \pi_{i'|a,y} \cdot \exp[-(F_{i',y} + M_{i'})] \cdot \pi_{j'|i',a}^{G}}, \quad \text{for } r \le a < A.$$

The recursive process for the length composition proportions for ages and years (i.e., $\pi_{i|a,y}$) in Equation 5.2.2 is illustrated in Figure 5.1a. Although mortality is length-dependent, our length-based model is designed to account for the age-structured dynamics of a population (see Equation (5.10) below), where transitions in abundance occur between ages and years. Thus, we derive the annual survival fraction for age *a* in year *y* (i.e., $S_{a,y}$) from the length-dependent mortality rates $Z_{i,y}$ as follows

$$S_{a,y} = \sum_{i=1}^{I} \pi_{i|a,y} \cdot \exp(-Z_{i,y}),$$

To account for the impact of demographic stochasticity and random environmental changes on abundance, we assume that the natural logarithm of abundances for ages and years (i.e., $\log(N_{a,y})$) are normally distributed conditional on those at previous time steps, where the log of abundance for the initial age group in each year class (i.e., recruitment) is also normally distributed around the mean $\log(\overline{R})$ (Miller and Hyun, 2017). Note that for the first A - r years (i.e., $1 \le y < A + 1 - r$), not all age groups exist because their corresponding length composition proportions, where the cumulative effect of fishing mortality cannot be incorporated, are not

modelled (Figure 5.1). Thus, the population model is given by

$$\log(N_{a,y}) = \begin{cases} \log(\bar{R}) + \varepsilon_{a,y}^{p}, & \text{for } (1 \le y \le T) \land (a = r) \\ \log(N_{a-1,y-1} \cdot S_{a-1,y-1}) + \varepsilon_{a,y}^{p}, & \text{for } (1 < y < A + 1 - r) \land (r < a < y + r) \\ \text{or } (A + 1 - r \le y \le T) \land (r < a < A) \end{cases}$$
$$\log[N_{a-1,y-1} \cdot S_{a-1,y-1} \\ \times (1 + \tau)] + \varepsilon_{a,y}^{p}, & \text{for } (y = A + 1 - r) \land (a = A) \\ \log(N_{a-1,y-1} \cdot S_{a-1,y-1} \\ + N_{a,y-1} \cdot S_{a,y-1}) + \varepsilon_{a,y}^{p}, & \text{for } (A + 1 - r < y \le T) \land (a = A) \end{cases}$$
$$(5.10)$$

where τ is the scale factor ($\tau \ge 0$) to account for the plus group accumulation for the maximum age group of the initial year class (see Figure 5.1), and $\varepsilon_{a,y}^p$ are normal process errors with mean 0 and variance $\sigma_{N,a}^2$ (i.e., $\varepsilon_{a,y}^p \stackrel{\text{iid}}{\sim} N(0, \sigma_{N,a}^2)$). We assume two different variance parameters for stochastic changes in abundance at age: one for the recruitment (i.e., $\sigma_{N,a=r}^2 = \sigma_{N,1}^2$) and the other for those older than age r (i.e., $\sigma_{N,a>r}^2 = \sigma_{N,2}^2$). If $\sigma_{N,2}^2 = 0$, the transitions in abundance at age are deterministic, similar to a conventional SCAAM.

Once the state variables N_y are estimated, the derived quantities for management decisions, such as an annual total biomass and spawning stock biomass, can be obtained. For instance, the total biomass in year y is calculated by

$$B_{y} = \sum_{i=1}^{I} \sum_{a=r}^{A} N_{a,y} \cdot \pi_{i|a,y} \cdot W_{i}, \text{ for } A + 1 - r \le y \le T.$$

Then, the spawning stock biomass SSB_y is calculated by

$$SSB_{y} = \varphi \cdot \sum_{i=1}^{I} \sum_{a=r}^{A} N_{a,y} \cdot \pi_{i|a,y} \cdot W_{i} \cdot \operatorname{Mat}_{i} \cdot \exp(-\phi \cdot Z_{i,y}), \quad \text{for } A + 1 - r \le y \le T,$$

where ϕ is the fraction of the year elapsed when spawning occurs, φ is the average female proportion of the population.

For the length-dependent maturity Mat_i , we use the logistic functional form:

$$\operatorname{Mat}_{i} = rac{1}{1 + \exp\left[-\gamma_{\operatorname{Mat}} \cdot \left(ar{L}_{i} - l_{\operatorname{50,Mat}}
ight)
ight]},$$

where γ_{Mat} is the slope parameter, and $l_{50,Mat}$ is the length at 50% maturity.



Figure 5.1: Directed acyclic graph (DAG) representing the length composition proportions for ages (rows) and years (columns) ($\pi_{i|a,y}$; panel a) and the abundances for ages (rows) and years (columns) ($N_{a,y}$; panel b). White circles are non-observed probabilistic nodes. Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes. The dotted rectangular frame with rounded corners indicates repetition of structure over units.

Data model

The data model relates observations to the state variables (i.e., N_y) in Equation (5.10) (see Figure 5.2 for an overview). We assume a Dirichletmultinomial distribution (see Appendix B.2 for derivation) for the vector of observed length frequencies in year y (i.e., $n_y = (n_{1,y}, n_{2,y}, n_{3,y}, ..., n_{I,y})$):

$$\boldsymbol{n}_y \sim \text{Dirichlet-multinomial}(E_y, \boldsymbol{\alpha}_y, \hat{\boldsymbol{P}}_y), \text{ for } A + 1 - r \leq y \leq T,$$

where E_y is the sample size in year y (i.e., $E_y = \sum_{i=1}^{I} n_{i,y}$), α_y is the vector of concentration parameters in year y (i.e., $\alpha_y = (\alpha_{1,y}, \alpha_{2,y}, \alpha_{3,y}, ..., \alpha_{I,y})$, and \hat{P}_y are the vector of model predicted length composition proportions in year y, whose elements are calculated from the model predicted catch in year y (i.e., $\hat{C}_{i,y}$):

$$\hat{P}_{i,y} = \frac{\hat{C}_{i,y}}{\sum_{i'=1}^{I} \hat{C}_{i',y}}, \text{ for } A + 1 - r \le y \le T,$$

where $\hat{C}_{i,y}$ is modelled using the Baranov catch equation:

$$\hat{C}_{i,y} = \sum_{a=r}^{A} N_{a,y} \cdot \pi_{i|a,y} \cdot \frac{F_{i,y}}{M_i + F_{i,y}} \cdot [1 - \exp(-M_i - F_{i,y})], \text{ for } A + 1 - r \le y \le T,$$

where $F_{i,y} = q \cdot v_i \cdot \text{Effort}_y$.

The advantage of using a Dirichlet-multinomial distribution for compositional data over a multinomial distribution (which is often used in an integrated assessment model) is that the former can account for overdispersion of such data within a model by estimating the concentration parameters of a Dirichlet distribution (Thorson et al., 2017). Overdispersion in compositional data, such as length frequency samples, arises because those data mostly have greater variance than those predicted by a multinomial distribution. This larger variance occurs mainly because sampling
processes in fisheries are often involved with fish behaviours (e.g., ontogenetic distribution, schooling, etc.) which violate the statistical independence assumed in the multinomial distribution. For this reason, fisheries scientists usually consider a sample size smaller than an actual input sample size when maximising likelihood for compositional data. The smaller sample size is often termed as the effective sample size.

Following Thorson et al. (2017), we define the effective sample size of a Dirichlet-multinomial distribution (i.e., E_y^{eff}) for the vector of observed length composition proportions (i.e., P_y) as the sample size of a multinomial distribution for P_y . Thus, the variance of the observed length composition proportion for bin *i* in year *y* (i.e., $P_{i,y}$) from a multinomial distribution is defined as

$$\operatorname{Var}(P_{i,y}|E_y^{\operatorname{eff}}, \hat{\boldsymbol{P}}_y) = \frac{\hat{P}_{i,y} \cdot (1 - \hat{P}_{i,y})}{E_y^{\operatorname{eff}}}, \quad \text{for } A + 1 - r \le y \le T.$$

Then, the variance of $P_{i,y}$ from a Dirichlet-multinomial distribution is given by

$$\operatorname{Var}(P_{i,y}|E_y, \boldsymbol{\alpha}_y) = \frac{\alpha_{i,y}}{E_y \cdot \alpha_y^o} \cdot \left(1 - \frac{\alpha_{i,y}}{\alpha_y^o}\right) \cdot \left(\frac{E_y + \alpha_y^o}{1 + \alpha_y^o}\right),$$
(5.11)

where $\alpha_y^o = \sum_{i=1}^I \alpha_{i,y}$.

By assuming that the concentration parameter $\alpha_{i,y}$ is proportional to E_y and $\hat{P}_{i,y}$ (Thorson et al., 2017), $\alpha_{i,y}$ in Equation 5.11 can be further modeled as follows

$$\alpha_{i,y} = \theta \cdot E_y \cdot \hat{P}_{i,y}, \quad \text{for } A + 1 - r \le y \le T,$$

where θ is the scaling parameter for overdispersion caused by the Dirichlet distribution.

We can rewrite Equation (5.11) as follows

$$\operatorname{Var}(P_{i,y}|E_y, \hat{\boldsymbol{P}}_y, \theta) = \frac{\hat{P}_{i,y} \cdot (1 - \hat{P}_{i,y}) \cdot (1 + \theta)}{1 + \theta \cdot E_y}, \quad \text{for } A + 1 - r \le y \le T,$$

which then provides the following relationship between E_y^{eff} , θ , and E_y :

$$E_y^{\rm eff} = \frac{1+\theta\cdot E_y}{1+\theta} = \frac{1}{1+\theta} + E_y\cdot \frac{\theta}{1+\theta}, \quad \text{for } A+1-r \leq y \leq T.$$

The above equation describes that E_y^{eff} is a linear function of the input sample size E_y , where the intercept and the slope are determined by θ , and if $\theta \to \infty$, $E_y^{\text{eff}} = E_y$ (Thorson et al., 2017).

The log of the observed total yield in year y (i.e., $\log(Y_y)$) is assumed to be normally distributed:

 $\log(Y_y) \sim N[\log(\hat{Y}_y), \sigma_Y^2], \quad \text{for } A + 1 - r \le y \le T,$

where

$$\hat{Y}_y = \sum_i \hat{C}_{i,y} \cdot W_i.$$



Figure 5.2: Directed acyclic graph (DAG) illustrating the linkage between the population model and the data model. White circles are non-observed probabilistic nodes, and those in gray are observed probabilistic nodes. Squares in gray are observed deterministic nodes. Arrows with solid lines represent conditional probabilistic dependencies, and those with dotted lines represent deterministic dependencies between nodes.

5.2.3 Parameter estimation

To estimate the model parameters, a marginal maximum likelihood method is used, using the TMB package (Kristensen et al., 2016). In TMB, one needs to specify a joint likelihood function for both fixed effect parameters and random effects. The joint likelihood $\mathcal{L}(\Theta, N|D)$ is the product of three likelihood functions, where we define Θ as fixed effect parameters to be estimated in the model (i.e., $\Theta = \{\bar{R}, q, \mu_r, k, l_{50}, \gamma, M(\text{or } b_0), \sigma_L, \sigma_r, \sigma_{N,1}, \sigma_{N,2}, \sigma_Y, \theta\}$), N as random effects (i.e., state variables: $N_{a,y}$), and Y, Effort, and n as observed yield, effort, and length composition data, respectively:

$$\begin{aligned} \mathcal{L}(\boldsymbol{\Theta}, \boldsymbol{N} | \boldsymbol{Y}, \boldsymbol{n}; \mathbf{Effort}) = & f_N(\boldsymbol{N} | \bar{R}, q, \mu_r, k, l_{50}, \gamma, M(\text{or } b_0), \sigma_L, \sigma_r, \sigma_{N,1}, \sigma_{N,2}; \mathbf{Effort}) \\ & \times f_Y(\boldsymbol{Y} | \sigma_Y, \hat{\boldsymbol{Y}}) \\ & \times f_{LF}(\boldsymbol{n} | \theta, \hat{\boldsymbol{P}}), \end{aligned}$$

where

$$\begin{split} f_{N}(\boldsymbol{N} | \bar{R}, q, \mu_{r}, k, l_{50}, \gamma, M(\text{or } b_{0}), \sigma_{L}, \sigma_{r}, \sigma_{N,1}, \sigma_{N,2}; \text{Effort}) \\ &= \left[\prod_{y=1}^{T} \frac{1}{\sqrt{2\pi}\sigma_{N,1}} \exp\left[-\frac{(\log(N_{r,y}) - \log(\bar{R}))^{2}}{2\sigma_{N,1}^{2}} \right] \right] \\ &\times \left[\prod_{a=r+1}^{y+r-1} \prod_{y=2}^{A-r} \frac{1}{\sqrt{2\pi}\sigma_{N,2}} \exp\left[-\frac{(\log(N_{a,y}) - \log(N_{a-1,y-1} \cdot S_{a-1,y-1}))^{2}}{2\sigma_{N,2}^{2}} \right] \right] \\ &\times \frac{1}{\sqrt{2\pi}\sigma_{N,2}} \exp\left[-\frac{(\log(N_{A,A+1-r}) - \log(N_{A-1,A-r} \cdot (1+\tau))^{2}}{2\sigma_{N,2}^{2}} \right] \\ &\times \left[\prod_{y=A+1-r}^{T} \prod_{a=r+1}^{A-1} \frac{1}{\sqrt{2\pi}\sigma_{N,2}} \exp\left[-\frac{(\log(N_{a,y}) - \log(N_{a-1,y-1} \cdot S_{a-1,y-1}))^{2}}{2\sigma_{N,2}^{2}} \right] \right] \\ &\times \left[\prod_{y=A+2-r}^{T} \frac{1}{\sqrt{2\pi}\sigma_{N,2}} \exp\left[-\frac{(\log(N_{A,y}) - \log(N_{A-1,y-1} \cdot S_{A-1,y-1} + N_{A,y-1} \cdot S_{A,y-1}))^{2}}{2\sigma_{N,2}^{2}} \right] \right] \end{split}$$

$$f_Y(\boldsymbol{Y}|\sigma_Y, \hat{\boldsymbol{Y}}) = \prod_{y=A+1-r}^T \frac{1}{\sqrt{2\pi}\sigma_Y} \exp\left[-\frac{(\log(Y_y) - \log(\hat{Y}_y)^2}{2\sigma_Y^2}\right],$$

and

$$f_{\rm LF}(\boldsymbol{n}|\boldsymbol{\theta}, \hat{\boldsymbol{P}}) = \prod_{y=A+1-r}^{T} \left[\frac{\Gamma(E_y+1)}{\prod_{i=1}^{I} \Gamma(n_{i,y}+1)} \cdot \frac{\Gamma(\boldsymbol{\theta} \cdot E_y)}{\Gamma(E_y+\boldsymbol{\theta} \cdot E_y)} \cdot \prod_{i=1}^{I} \frac{\Gamma\left(n_{i,y}+\boldsymbol{\theta} \cdot E_y \cdot \hat{P}_{i,y}\right)}{\Gamma\left(\boldsymbol{\theta} \cdot E_y \cdot \hat{P}_{i,y}\right)} \right].$$

Then, TMB takes care of approximating the marginal likelihood $\mathcal{L}(\Theta \mid \boldsymbol{Y}, \boldsymbol{n}; \text{Effort})$ by integrating out the random effects N:

$$\mathcal{L}(\Theta|\boldsymbol{Y}, \boldsymbol{n}; \boldsymbol{ ext{Effort}}) = \int \mathcal{L}(\Theta, \boldsymbol{N}|\boldsymbol{Y}, \boldsymbol{n}; \boldsymbol{ ext{Effort}}) d\boldsymbol{N},$$

using a Laplace appoximation method (Skaug and Fournier, 2006; Kristensen et al., 2016).

By maximizing the marginal likelihood with respect to Θ , using numerical optimisation techniques in R, the estimate of Θ (i.e., $\hat{\Theta}$) can be obtained:

$$\hat{\boldsymbol{\Theta}} = \arg\max_{\boldsymbol{\Theta}} \log[\mathcal{L}(\boldsymbol{\Theta} \mid \boldsymbol{Y}, \boldsymbol{n}; \boldsymbol{\mathsf{Effort}})].$$

Once $\hat{\Theta}$ is found, TMB sequentially infers the random effects N by maximizing the estimated conditional likelihood with respect to N, where Θ is fixed at $\hat{\Theta}$:

$$\hat{N} = \arg \max_{N} \log[\mathcal{L}(\hat{\Theta}, N | Y, n; \text{Effort})].$$

Furthermore, the uncertainty of parameter estimates is evaluated via the delta method, where the determinant of the Hessian matrix of the marginal likelihood is found via a numerical Cholesky decomposition (Skaug and Fournier, 2006; Kristensen et al., 2016).

5.3 Application to the Korea chub mackerel stock

For demonstration purposes, we apply our model to the Korea chub mackerel stock. The two main purposes of this demonstration are (i) to suggest the application of our length-based model for the future stock assessment of the Korea mackerel stock (or similar stocks to which conventional agestructured models are not applicable, which are most stocks in Korean fisheries) and (ii) to show the applicability of our state-space LBASM to data-moderate stocks where information on a time-series of total yield, fishing effort (or CPUE), and length composition is available.

5.3.1 Background information

The chub mackerel stock in Korea is regulated by government issued quotas of total allowable catch (TAC) for large purse seine (LPS) fishery. More than six fisheries (e.g., large purse seine, small purse seine, gillnet, trawl, etc.) target the mackerel stock, but over 90% of the annual total catch of chub mackerel in Korea is from LPS fishery (Jung et al., 2021). The Korean National Institute of Fisheries science (NIFS) has periodically collected fishing effort of LPS fishery (number of hauls) since 1976, and previous studies on a quantitative assessment of this stock used this fisherydependent information. Besides the fishing effort data, the NIFS has also collected samples of fish from landed catches by LPS fishery to sample biological parameters of the species, including length, weight, and sexual maturity. The characteristics of the stock, including major fishing grounds for LPS fishery in Korean waters, spawning grounds, and migratory patterns, are depicted in Figure 5.3.



Figure 5.3: Characteristics of the Korea mackerel stock. The green and red shaded areas indicates the spawning ground and the major fishing grounds for LPS fishery in Korean waters, respectively. The dotted arrows show the migratory patterns of the stock.

Length and weight of the samples have been periodically measured, whereas age determination has been intermittently conducted (Hwang et al., 2008; Kang et al., 2015). Thus, those age-length data were pooled to obtain a single age-length key (ALK) (Kang et al., 2015). Many published studies reported that applying a single ALK to other years of length frequency data results in severe bias as this application fails to account for temporal changes in age composition of a population (Kimura, 1977; Westrheim and Ricker, 1978; Aanes and Vølstad, 2015; Ailloud and Hoenig, 2019) (e.g., an age composition of fish in length bin *i* in year *y* most likely varies in year y + 1 due to recruitment and mortality, meaning that probability of age given length must be year-specific). Despite this problem of using a single ALK, according to published reports on this stock, this application seems to have long been used for mackerel stock assessment in Korea (Kang et al., 2015; Gim et al., 2020).

The fishery data described above are not publicly available, thus we extract the time series of CPUE and length composition from published figures (Kim et al., 2018; Gim and Hyun, 2019; Gim et al., 2020; Jung et al., 2021) using Web Plot Digitizer (Rohatgi, 2020) (Figures 5.4-5.6). Data on annual yields are publicly available from Statistics Korea (Figure 5.4). We make the simplifying assumption that the annual fishing effort of LPS fishery is proportional to the total annual fishing effort of the mackerel stock because (i) both the CPUE and length composition data were collected only from LPS fishery which accounts for over 90% of the total annual yield of chub mackerel in Korea, (ii) other data on this stock are not available, and (iii) the relatively short time series of the data set challenge the use of the CPUE as an abundance index, which typically requires introducing two more variance parameters to be estimated: one for observation errors of the CPUE and the other for transitions in fishing mortality rate.

Based on the assumption about the effort, we back-calculated the annual total effort from the LPS CPUE and total yield (i.e., Effort=Yield/CPUE) from 1995 to 2017 (Figure 5.4). The CPUE data from 1976 to 2017 were able to be extracted from several previous studies (Choi et al., 2004; Gim et al., 2020; Jung et al., 2021), but the length composition data only exist from 2000 to 2017 in the figures of a few recent studies (Kim et al., 2018; Gim and Hyun, 2019). We assume either five or six age groups as the total number of age groups for the mackerel stock by referring to previous studies on the age determination of the species with samples collected from LPS fishery (Hwang et al., 2008; Kang et al., 2015), treating the last age group as the "plus group" in both cases. Note that our model requires a longer time series of effort by A - r than those of length composition and yield; thus, we use the effort data from 1996 to 2017 when five age groups are assumed, but those from 1995 to 2017 are used when six age groups are assumed instead (Figure 5.4).



Figure 5.4: Annual total yields of the chub mackerel stock in South Korea (top panel) and the annual mackerel CPUE (middle panel) and effort (bottom panel) collected from a large purse seine fishery. Coloured dots indicate the data used for the eight models. The red dot in the effort data is only used for Models M5-M8 which require one more additional data point on effort as those models assume six age groups (Models M1-M4 assume five age groups).



Figure 5.5: Length frequency samples collected from large purse seine fishery for chub mackerel during 2000-2008. Yr is the abbreviation of year.



Figure 5.6: Length frequency samples collected from large purse seine fishery for chub mackerel during 2009-2017. Yr is the abbreviation of year.

5.3.2 Estimation

We consider a total of eight alternative models (i.e., two assumptions for the number of age groups \times four assumptions for natural mortality; see Table 5.2) for the mackerel stock. For the first four models (i.e., M1-M4), we assume five age groups, and for the last four model (i.e., M5-M8), we assume six age groups. Differences within the two sets of four models are the assumptions on natural mortality. To be specific, we allow models M1 and M5 to estimate the scale parameter b_0 in the allometry relationship for the length-dependent natural mortality, while we constrain b_1 to 0.305 which was estimated by Lorenzen (1996) for marine species. The other six models (M2-M4 and M6-M8) assume natural mortality to be constant across all length bins. Models M2 and M6 estimate the natural mortality M. The constant natural mortality M in models M3 and M7 are fixed at 0.45, which is the average value of constant natural mortality rates of chub mackerel, obtained from previous studies (Hiyama et al., 2002; Cerna and Plaza, 2014). In models M4 and M8, the natural mortality is assumed to have a relationship with the von Bertalanffy growth parameter k (i.e., M = $1.5 \cdot k$) (Jensen, 2011).

Our preliminary study showed that the scaling parameter τ for the plus group accumulation of the initial year class is inestimable with the mackerel data, indicated by an extremely large value for the standard error and almost flat likelihood profile of the parameter. We assume that this estimation problem occurs because of insufficient information obtained from unimodal-like distributions of the length frequency samples as well as the small sample size of the first year length data (i.e., $E_{y=2000}$) compared to others. Thus, we assume no plus group accumulation for the initial year class (i.e., $\tau = 0$) in all eight models by visually investigating the length frequency samples in year 2000, where we observe that the samples in year 2000 have a significantly narrower range of a fish length distribution than that in other years in the absence of large size individuals.

Besides the scaling parameter τ , some of the life-history parameters as-

sociated with the maturity (i.e., γ_{Mat} and $l_{50,\text{Mat}}$), weight (i.e., ω_0 and ω_1), and length models (i.e., L_{∞}) as well as the average female proportion (i.e., φ) are also assumed to be known, which is a standard treatment for estimation of a large number of parameters in fully-integrated assessment models in fisheries (Nielsen and Berg, 2014; Cadigan, 2016; Miller and Hyun, 2017). We obtain the input values of 0.70 and 20.11 for the two maturity parameters, γ_{Mat} and $l_{50,\text{Mat}}$, from Kim et al. (2020) and those of 0.003 and 3.425 for the two length-weight relationship parameters, ω_0 and ω_1 , from Gim and Hyun (2019). The input value of 40.6 for the asymptotic length, L_{∞} , was obtained from Shiraishi et al. (2008), and that of 0.6 for the average female proportion, φ , was obtained from Gim et al. (2020).

We have no information on the observation error variance as the data we use were collected from a commercial LPS fishery; thus, we estimate all three observation and process error variance parameters (i.e., σ_Y^2 , $\sigma_{N_1}^2$, and $\sigma_{N_2}^2$) within the model. An estimation problem associated with observation and process error variances in state-space models has been investigated by previous studies which suggested that using an input value for a parameter of observation error variance can enhance parameter estimability (Dennis et al., 2006; Auger-Méthé et al., 2016; Auger-Méthé et al., 2021). Some previous studies in fisheries also treated the observation error parameter as known (Miller et al., 2016; Miller and Hyun, 2017), but one should note that this treatment is not applicable to most data-moderate fisheries where survey data to inform such a variance parameter are not available. We investigate a possible estimation problem in our state-space LBASM, using a parametric bootstrap method, which we discuss in more detail in the next section.

We check the convergence of the model by examining the maximum gradient component (mgc) and the Hessian matrix. We deem the model has successfully converged if mgc is less than 0.1 and the Hessian is positive definite (Kristensen et al., 2016).

Table 5.2: Description of the eight models (M1-M8) considered for the Korea chub mackerel stock

Model	Description
M1	Five age groups (0 to 4) assumed with the length-dependent natural mortality
	(i.e., $M_i = b_0 \cdot W_i^{b_1}$, where b_0 is estimated, but b_1 is fixed at 0.305 based on Lorenzen (1996))
M2	Five age groups (0 to 4) assumed with the constant natural mortality M estimated
M3	Five age groups assumed with the constant natural mortality M fixed at 0.45
M4	Five age groups (0 to 4) assumed with the constant natural mortality M ,
	which is derived from the relationship: $M = 1.5 \cdot k$
M5	Six age groups (0 to 5) assumed with the length-dependent natural mortality
	(i.e., $M_i = b_0 \cdot W_i^{b_1}$, where b_0 is estimated, but b_1 is fixed at 0.305 based on Lorenzen (1996))
M6	Six age groups (0 to 5) assumed with the constant natural mortality M estimated
M7	Six age groups (0 to 5) assumed with the constant natural mortality M fixed at 0.45
M8	Six age groups (0 to 5) assumed with the constant natural mortality M ,
	which is derived from the relationship $M = 1.5 \cdot k$

5.4 Simulation studies

We perform simulation studies to validate the statistical behaviour of the eight models (i.e., M1-M8; see Table 5.2). To evaluate stability, goodness-of-fit, distributional assumptions, and estimability of the model, we use four model checking methods, namely (i) jitter analysis, (ii) posterior predictive check, (iii) residual analysis, and (iv) parametric bootstrap. Initially, we also attempted performing a retrospective analysis, but because of the short time-series of the data, estimation results were highly sensitive to removal of even a single observation, and therefore not considered in this study.

5.4.1 Jitter analysis

To evaluate the stability of the model, we perform the "jitter" analysis (Cass-Calay et al., 2014), using all eight models (i.e., M1-M8) considered in our study, for which we randomly generate different initial values for the

model parameters and use them for parameter estimation with the mackerel data. This analysis is to test the sensitivity of initial guess values for parameter estimation. A well-behaved model should converge to a global solution regardless of the initial values (Cass-Calay et al., 2014).

We repeat this procedure until 100 sets of converged results are obtained. We generate such random values using uniform distributions, where a reasonably wide range of lower and upper limits for each parameter is chosen (see Table 5.3). We visually inspect if all 100 converged results show a single unique set of parameter estimates.

Table 5.3: Lower and upper bounds of the model parameters, based on which we draw initial random values for the parameters from uniform distributions (note that these bounds are not parameter constraints).

Parameter	Lower	Upper
l_{50}	20.00	30.00
γ	0.20	2.00
k	0.20	0.60
μ_r	13.00	20.00
σ_r	1.00	3.00
σ_L	1.00	3.00
σ_Y	0.10	1.00
$\sigma_{N,1}$	0.10	1.00
$\sigma_{N,2}$	0.10	1.00
θ (×10 ⁻³)	0.02	0.20
$q (\times 10^{-3})$	0.12	2.47
M	0.20	2.00
b_0	2.00	6.00
$ar{R}$ (×10 ⁶)	100.00	10000.00

5.4.2 **Posterior predictive check**

For the goodness-of-fit measure, we use a frequentist version of the posterior predictive check (PPC) (Thygesen et al., 2017; Auger-Méthé et al., 2021). The principal concept of this method is that if a model fits the observed data well, the data generated from the model should be similar to the observed data (Gelman et al., 2013). Using the parameter estimates obtained from fitting the model to the Korea chub mackerel data as the true input values of the model parameters, we randomly replicate 1000 sets of time series of yield and length frequencies (i.e., $Y_{y,d}^{\text{rep}}$, and $n_{i,y,d}^{\text{rep}}$, where *d* denotes the replicated set: $d = \{1, 2, 3, ..., 1000\}$). Then, we compare the replicated data with the observed data to assess the goodness-of-fit of the models. In fisheries stock assessment, the last few years of prediction are of special interest for managers; thus, we use the last three years of yield and length models, we use the median relative difference (RD) as the performance metric (i.e., $\text{RD}_{y,d} = Y_{y,d}^{\text{rep}}/Y_{y,d}^{\text{obs}} - 1$) for yield, and the root mean squared error (RMSE) for length composition (i.e., $\text{RMSE}_{y,d} = \sqrt{\sum_{i=1}^{I} (n_{i,y,d}^{\text{rep}} - n_{i,y})^2/I}$).

5.4.3 Residual analysis

To assess the validity of the model assumptions associated with the state equations, we use a single sample approach suggested by Thygesen et al. (2017). We randomly draw samples of a time series of $N_{a,y}$ from their posterior distributions and calculate the standardized process errors (details about the calculation are given in Equations 5.4.3 and 5.4.3 below). In our frequentist approach, the posterior modes of those state variables in log-scale (i.e., $\log(N_{a,y})$) are found by maximising the joint likelihood discussed in Section 5.2.3, and the Hessian of the model is obtained by using the automatic differentiation technique with TMB (Kristensen et al., 2016; Thygesen et al., 2017), from which the precision matrix for the state variables can be identified. Then, with the modes and precision matrix, we approximate the posteriors of $\log(N_{a,y})$ using a MVN distribution, which allows us to draw random samples for $N_{a,y}$.

For a correct model, we expect that those standardised process residuals are normally distributed with mean 0 and variance 1 (Thygesen et al., 2017). Thygesen et al. (2017) used a Kolmogorov Smirnov (K-S) test to check the normality assumption of those process residuals, but such a test is known to be conservative if one or more parameters of a distribution is estimated (Lilliefors, 1967). Thus, in our study, instead of using a K-S test, we visually check the normality assumption of those residuals, using a normal quantile-quantile plot. Our preliminary study showed that using a single set of the residuals for checking the normality can be misleading as the distribution of those residuals also depends on the random variability in sample drawing. Therefore, we use 200 sets of standardised process residuals to find any systematic patterns.

Since we assume two different variance parameters for $N_{a,y}$ (i.e., $\sigma_{N,1}^2$ and $\sigma_{N,2}^2$), we separately calculate a time series of standardized process errors for recruitment ($e_{r,y,d}$) and abundances after recruitment ($e_{a,y,d}$, where a > r) for each replicate $d \in \{1, 2, 3, ..., 200\}$ as follows

$$e_{r,y,d} = \frac{\log(N_{r,y,d}) - \log(\bar{R})}{\hat{\sigma}_{N,1}}, \quad \text{for } 1 \le y \le T$$

and

$$e_{a,y,d} = \begin{cases} \frac{\log(N_{a,y,d}) - \log(N_{a-1,y-1,d} \cdot \hat{S}_{a-1,y-1})}{\hat{\sigma}_{N,2}}, & \text{for } (1 < y < A + 1 - r) \land (r < a < y + r) \\ & \text{or } (A + 1 - r \le y \le T) \land (r < a < A) \end{cases}$$
$$\frac{\log(N_{a,y,d}) - \log[N_{a-1,y-1,d}}{\hat{\sigma}_{N,2}}, & \text{for } (y = A + 1 - r) \land (a = A) \\ \frac{\log(N_{a,y,d}) - \log(N_{a-1,y-1,d} \cdot \hat{S}_{a-1,y-1})}{\hat{\sigma}_{N,2}}, & \text{for } (A + 1 - r < y \le T) \land (a = A) \end{cases}$$

where \bar{R} , $\hat{S}_{a,y}$, $\hat{\sigma}_{N,1}$, $\hat{\sigma}_{N,2}$, and $\hat{\tau}$ denote the parameters estimated from the

models fitted to the mackerel data.

5.4.4 Parametric bootstrap

We employ a parametric bootstrap approach to test estimability of the model parameters. State-space models (SSMs) can have estimability problems if a model is overparameterized or both observation and process variances are estimated (Dennis et al., 2006; Auger-Méthé et al., 2016; Auger-Méthé et al., 2021). These problems also lead the models to be non-identifiable, meaning that there would be more than one set of parameter estimates that maximize the likelihood. Parameter estimates from such problematic models are often biased with large variances (Auger-Méthé et al., 2021).

We simulate the abundances for ages and years (i.e., $N_{a,y}$) using the estimates from fitting models to the Korea chub mackerel stock, from which we generate the observation time series of total yield and length compositions. We fit the same model to these generated data and repeat this procedure 1000 times.

In each simulation and estimation run, we check the convergence by examining the maximum gradient component (mgc) and the Hessian matrix. In each converged run, we calculate the median relative difference (RD) for the fixed effect parameters (Θ), biomass (B_y), and spawning stock biomass (SSB_{*u*}) to estimate the bias of those quantities:

$$\mathrm{RD}_d(\Phi) = \frac{\hat{\Phi}_d}{\Phi_d} - 1$$

where $\hat{\Phi}$ is the estimated set of quantities of interest (i.e., $\Phi \in {\{\Theta, B_y, SSB_y\}}$), Φ is the set of true values for those quantities of interest, and d denotes the simulated data set (i.e., $d \in {\{1, 2, 3, ..., 1000\}}$).

5.5 Results

5.5.1 Application to the mackerel stock

All eight models fitted to the mackerel data successfully converged. Estimates and standard errors of the parameters from all eight models are provided in Tables 5.4 and 5.5. Given the estimates in Table 5.4, we calculated key derived quantities associated with the sub-models for each estimation models, which are illustrated in Figures 5.7-5.9.

We present a series of plots, which compare the observed data with the model fitted values, for visual inspection of goodness-of-fit of the models. Those for length frequency samples are shown in Figures 5.10-5.17, and those for yield data are presented in Figures 5.19 and 5.20. Bubble charts for the normalised residuals for the fits to the mackerel length frequency data under each estimation models are illustrated in Figure 5.18, which are used to compare the details of the differences in fit for the different models. The visual inspection show good fits for all observed data under all eight models.

The estimates of annual biomass (\hat{B}_y) , spawning stock biomass (SSB_y), and recruitment (\hat{R}_y) vary by model, but overall trends of those estimates are similar in all eight models (see Figures 5.19 and 5.20). The assumption on the different number of age groups (i.e., five for M1-M4 and six for M5-M8) does not significantly affect the estimates. However, the assumption on natural mortality strongly affects the population estimates. For example, \hat{SB}_y from M2 and M6, where the constant natural mortality M is estimated, are almost twice as larger as those from the other models (see Figures 5.19 and 5.20).

er <u>el data.</u>								
Parameter	M1	M2	M3	M4	M5	M6	M7	M8
\hat{l}_{50}	30.42	30.45	30.14	30.11	30.54	30.59	30.17	30.17
ý	0.59	09.0	0.51	0.51	0.57	0.59	0.47	0.48
\hat{k}	0.28	0.29	0.34	0.34	0.30	0.30	0.36	0.36
$\hat{\mu}_r$	15.16	15.26	15.57	15.54	15.24	15.36	15.67	15.63
$\hat{\sigma}_r$	1.78	1.73	1.79	1.79	1.83	1.79	1.86	1.86
$\hat{\sigma}_L$	2.35	2.40	2.35	2.35	2.18	2.22	2.16	2.17
$\hat{\sigma}_Y$	0.28	0.31	0.32	0.32	0.26	0.27	0.36	0.34
$\hat{\sigma}_{N,1}$	1.59	1.55	1.66	1.64	1.58	1.56	1.57	1.57
$\hat{\sigma}_{N,2}$	1.34	1.25	1.34	1.32	1.34	1.26	1.36	1.35
$\hat{ heta}$ ($ imes 10^{-3}$)	35.19	34.92	36.72	36.70	36.60	36.46	38.05	37.96
$\hat{q}~(imes 10^{-3})$	0.20	0.12	0.23	0.23	0.21	0.13	0.23	0.21
\hat{M}	l	1.50	0.45	0.51	I	1.45	0.45	0.54
\hat{b}_0	5.57				5.55			
$\hat{ar{R}}$ ($ imes 10^6$)	11792.16	22949.09	1175.16	1262.72	9613.25	17500.95	916.90	1100.86

Table 5.4:	Point ∈	estimates	of the f	fixed e	effect]	parameter	s of al	l eight	models	(M1-M8)	fitted to	the Ko
mackerel (data.											

$\begin{array}{cccccccccccccccccccccccccccccccccccc$
$\begin{array}{cccccccccccccccccccccccccccccccccccc$
2.85 2.84 2.82 2.83 0.04 0.04 0.04 0.05 0.03 0.27 1.14
$\begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$
$\begin{array}{rrrrr} & 0.03 & & 0.27 \\ & & 1.14 & \end{array}$
1.14

le 5.5: Estimates of the standard errors (SE) of the fixed effect parameters of to the Korea mackerel data.	ameters of all eight mode	lels (M1-M8)
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Figure 5.7: Mean length (a), mean weight (b), and length variance (c) as a function of age, derived from each model (i.e., M1-M8). The estimates of the associated parameters are listed in Table 5.4.



Figure 5.8: Selectivity (a) and maturity (b) as a function of length, derived from each model (i.e., M1-M8). The estimates of the selectivity parameters (i.e., \hat{l}_{50} and $\hat{\gamma}$) for each model are listed in Table 5.4. The same maturity curve is used for all eight models, where the values of the maturity parameters are given as inputs (i.e., $l_{50,mat} = 20.11$ and $\gamma_{mat} = 0.70$).



Figure 5.9: Fishing mortality (a) and natural mortality (b) rates, derived from each model (i.e., M1-M8). The estimates of the associated parameters for each model are listed in Table 5.4. Note that the estimated fishing mortality rates in panel a are fully selected fishing mortality rates.



Figure 5.10: Model M1 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M1 assumes five age groups (from age-0 to age-4), where the last age group (i.e., age-4) accumulates those older than age-4 (i.e., the "plus group").



Figure 5.11: Model M2 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M2 assumes five age groups (from age-0 to age-4), where the last age group (i.e., age-4) accumulates those older than age-4 (i.e., the "plus group").



Figure 5.12: Model M3 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M3 assumes five age groups (from age-0 to age-4), where the last age group (i.e., age-4) accumulates those older than age-4 (i.e., the "plus group").



Figure 5.13: Model M4 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M4 assumes five age groups (from age-0 to age-4), where the last age group (i.e., age-4) accumulates those older than age-4 (i.e., the "plus group").



Figure 5.14: Model M5 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M5 assumes six age groups (from age-0 to age-5), where the last age group (i.e., age-5) accumulates those older than age-5 (i.e., the "plus group").



Figure 5.15: Model M6 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M6 assumes six age groups (from age-0 to age-5), where the last age group (i.e., age-5) accumulates those older than age-5 (i.e., the "plus group").



Figure 5.16: Model M7 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M7 assumes six age groups (from age-0 to age-5), where the last age group (i.e., age-5) accumulates those older than age-5 (i.e., the "plus group").



Figure 5.17: Model M8 fitted to the observed length frequencies collected during 2000-2017. Yr is the abbreviation of year. Note that M8 assumes six age groups (from age-0 to age-5), where the last age group (i.e., age-5) accumulates those older than age-5 (i.e., the "plus group").



Figure 5.18: Normalised residuals for the fits to the mackerel length frequency data under M1-M8, given in Figures 5.10-5.17.



Figure 5.19: Annual estimates of biomass, spawning stock biomass (SSB), recruitment, and yields for each of the four models, where five age groups are assumed (i.e., models M1 to M4). The red shaded areas indicate 95% confidence intervals. The open circles depicted in the plots of the last column are the observed annual yields.



Figure 5.20: Annual estimates of biomass, spawning stock biomass (SSB), recruitment, and yields for each of the four models, where six age groups are assumed (i.e., models M5 to M8). The red shaded areas indicate 95% confidence intervals. The open circles depicted in the plots of the last column are the observed annual yields.
5.5.2 Simulation studies

Jitter analysis

Our jitter analysis (i.e., sensitivity of model fit to initial parameter values) results demonstrate that there exists more than a single set of estimates when six age groups are assumed (M5-M8) depending on initial guess values used for the parameter estimation, whereas models with five age groups (M1-M4) converge to a unique set of parameter estimates regardless of initial guess values. These results are depicted in Figures 5.21 and 5.22.

In Figure 5.23, we visually demonstrate that assuming six age groups (M5-M8) for the mackerel length frequency samples is redundant. In the figure, we illustrate two different fitted results with M5-M8 for the length frequency data collected in year 2001, where the first three age groups (i.e., from age-0 to age-2) estimated from the models take up a large part of length composition proportion, but those older than age 2 only share a small remaining proportion. It is shown that the two different fitted lines for each age groups largely differ in older age groups (i.e., those older than age-2).



Figure 5.21: Box plots for 100 estimates of each parameters from M1-M4 (first column; the name of the model is denoted on the left side of each row) and the corresponding 100 sets of initial guess values used for the parameter estimation of each of the four models (second column).



Figure 5.22: Box plots for 100 estimates of each parameters from M5-M8 (first column; the name of the model is denoted on the left side of each row) and the corresponding 100 sets of initial guess values used for the parameter estimation of each of the four models (second column).



Figure 5.23: Two different fitted results of models M5 to M8 for the length frequency samples collected in year 2001.

5.5. RESULTS

Posterior predictive check

Model M2 provides the best performance in terms of goodness-of-fit for both the yield (i.e., the relative differences of M2 are closest to 0; see the panels in the first column of Figure 5.24) and length frequency data (i.e., the RMSEs of M2 are the lowest values; see the panels in the second column of Figure 5.24) among the eight alternative models.

The inclusion of one additional age group (M5-M8) results in poorer performance for fitting the length frequency data, which is observed by comparing M1-M4 with M5-M8 in the second column of Figure 5.24. For the yield data, the models with natural mortality fixed or constrained (M3, M4, M7, and M8) show relatively poorer performance than those with natural mortality estimated (M1, M2, M5, and M6) (see the panels in the first column of Figure 5.24).

This goodness-of-fit test demonstrates that (i) the length-dependent natural mortality assumption (M1 and M5) is not supported as the constant natural mortality models (M2 and M5) show better performance for both the yield and length frequency data, and (ii) the models with five age groups (M1-M4) show better performance than those with six age groups (M5-M6) for the length frequency data.



Figure 5.24: Median relative difference and root mean square error (RMSE) for each of the eight models (i.e., models M1 to M8), obtained from a frequentist version of the posterior predictive check. Plots in the first column show the median relative differences between the simulated yields of the last three years (i.e., from 2015 to 2017) and the corresponding observed yields. Those in the second column show the RMSE obtained by comparing the simulated length frequencies of the last three years (i.e., from 2015 to 2017) with the corresponding observed length frequencies.

Residual analysis

The results of the jitter analysis and posterior predictive check show that the models with six age groups (M5-M8) have issues (i.e., multiple sets of parameter estimates and the poorer performance for fitting the length frequency data) and were dropped for further analysis. Thus, residual analysis is only conducted for those with five age groups (M1-M4).

The panels in the first column of Figure 5.25 show that the normality assumption for the recruitment variability in all four models is satisfied. However, those in the second column of Figure 5.25 demonstrate that the normality assumption for the stochastic transitions in abundance for ages and years are only satisfied under M1 and M2. The residuals for the abundances under M3 and M4 (i.e., the panels in the third and fourth rows in the second column) show systematic biases because the residual points in the centre of the panels do not lie in the dashed straight lines.



Figure 5.25: Normal quantile plots for 200 sets of the standardised process residuals of M1-M4 (red points; the name of the model is denoted on the left side of each row). The panels in the last row, which have blue points generated from the standard normal distribution, are given as comparative references (denoted as Ref). The panels in the first column are the residuals for the recruitment process in each model (see Equation 5.4.3), and those in the second column are the residuals for the abundances after the recruitment (see Equation 5.4.3).

Parameter estimability

Median relative difference of the fixed effect parameters and derived quantities of all four models show satisfactory results, most of which are close to 0 (see Figures 5.26-5.29). The model convergence rate for M2 is the highest among the four models, but those convergence rates are similar to each other (Table 5.6).

The slight negative bias in variance parameters (see the top panel in the second column of Figures 5.26-5.29), shown in all four models, is expected as they are obtained from maximum likelihood estimation (MLE of variance is known to be biased) (Cadigan, 2016; Miller and Hyun, 2017). The bimodal distribution of the bootstrap samples of σ_Y in all four models (see the bottom panel in the second column of Figures 5.26-5.29) indicates that the observation variance parameter has an estimability problem (Auger-Méthé et al., 2016; Auger-Méthé et al., 2021), which is also detected from its likelihood profiles shown in Figures 5.30-5.33.

Table 5.6: Convergence rate in percent for each estimation model. A total of 1000 simulation-estimation runs were performed for parametric boot-strapping for each estimation model.

M1	M2	M3	M4
44.2	49.8	45.6	44.3



Figure 5.26: Median relative difference (RD) of the fixed effect parameters (i.e., Φ), biomass (i.e., B_y), spawning stock biomass (i.e., SSB_y), and recruitment (i.e., $N_{r,y}$), which are estimated from fitting model M1 to data sets simulated from the same model M1, using the estimates obtained from fitting M1 to the data on the Korea mackerel stock as input parameter values.



Figure 5.27: Median relative difference (RD) of the fixed effect parameters (i.e., Φ), biomass (i.e., B_y), spawning stock biomass (i.e., SSB_y), and recruitment (i.e., $N_{r,y}$), which are estimated from fitting model M2 to data sets simulated from the same model M2, using the estimates obtained from fitting M2 to the data on the Korea mackerel stock as input parameter values.



Figure 5.28: Median relative difference (RD) of the fixed effect parameters (i.e., Φ), biomass (i.e., B_y), spawning stock biomass (i.e., SSB_y), and recruitment (i.e., $N_{r,y}$), which are estimated from fitting model M3 to data sets simulated from the same model M3, using the estimates obtained from fitting M3 to the data on the Korea mackerel stock as input parameter values.



Figure 5.29: Median relative difference (RD) of the fixed effect parameters (i.e., Φ), biomass (i.e., B_y), spawning stock biomass (i.e., SSB_y), and recruitment (i.e., $N_{r,y}$), which are estimated from fitting model M4 to data sets simulated from the same model M4, using the estimates obtained from fitting M4 to the data on the Korea mackerel stock as input parameter values.



Figure 5.30: Profile log-likelihoods for the fixed effect parameters of model M1 fitted to the data on the Korea mackerel stock. Blue vertical lines represent 95% confidence intervals (CIs) derived from the profile log-likelihoods. Red vertical lines represent 95% Wald CIs derived based on the asymptotic normality theory.



Figure 5.31: Profile log-likelihoods for the fixed effect parameters of model M2 fitted to the data on the Korea mackerel stock. Blue vertical lines represent 95% confidence intervals (CIs) derived from the profile log-likelihoods. Red vertical lines represent 95% Wald CIs derived based on the asymptotic normality theory.



Figure 5.32: Profile log-likelihoods for the fixed effect parameters of model M3 fitted to the data on the Korea mackerel stock. Blue vertical lines represent 95% confidence intervals (CIs) derived from the profile log-likelihoods. Red vertical lines represent 95% Wald CIs derived based on the asymptotic normality theory.



Figure 5.33: Profile log-likelihoods for the fixed effect parameters of model M4 fitted to the data on the Korea mackerel stock. Blue vertical lines represent 95% confidence intervals (CIs) derived from the profile log-likelihoods. Red vertical lines represent 95% Wald CIs derived based on the asymptotic normality theory.

5.6 Discussion

In this research, we show that the state-space LBASM we developed can be applied to data-moderate fisheries, using the data collected from the Korea chub mackerel stock. The model can successfully estimate all model parameters even with a relatively short time series of data, including variance parameters ($\sigma_{N,1}^2$, $\sigma_{N,2}^2$, and σ_Y^2) for process and observation errors and the parameter for overdispersion (θ) in length frequency samples. We also show the successful implementation of a Dirichlet-multinomial distribution for length composition proportions to estimate effective sample size within the state-space model, which allows us to avoid subjective choice of data-weighting between likelihoods (Thorson et al., 2017).

From the parametric bootstrap analysis, we find that the models (i.e., M1 to M4) are not robust since less than half of the bootstrap runs converged (from 44.2% to 49.8%), but such low convergence rates are not surprising as the models attempt to estimate both observation and process error variances, as well as other fixed effect parameters, which are known to be challenging even in simple state-space models (Auger-Méthé et al., 2016; Auger-Méthé et al., 2021). If we fix some of those fixed effect parameters at some assumed values, the model performance would greatly improve. Such treatment is not uncommon in state-space stock assessment models even for data-rich stocks. For example, in previous papers on state-space age-structure models (Miller et al., 2016; Miller and Hyun, 2017), observation error variance was fixed at some assumed value and not estimated.

We believe a place of possible improvement in our current length-based model to be in the deterministic relationship between fishing mortality and effort (i.e., $F_y = q \cdot \text{Effort}_y$). In our current approach, it is assumed that the annual yield data Y_y have observation error; thus, the model is fitted to the yield data while conditioning on the annual fishing effort. To avoid using such a simplelistic deterministic structure in the fishing mortality model, one can consider that observation error in the yield data is small, and model temporal variation in the fishing mortality-effort relationship to incorporate random deviation in effort (Fournier et al., 1998).

Our simulation studies show that the model with constant natural mortality assumption (M2) performs better than that with length-dependent natural mortality assumption (M1) for the mackerel stock, but it should be noted that the mackerel data were collected from a commercial fishery, and the data were not standardised. Moreover, we assume the catchability is constant to avoid overparameterisation, although it is probably more likely to be varying over time. We initially attempted to incorporate a time-varying catchability, using a random walk model, but observed a failure in estimation, which we attribute to the short time series length of the data.

We found that the constant natural mortality estimated from M2 (i.e., M = 1.5) is approximately two or three times the values estimated from other models with different assumptions on the natural mortality and those from previous studies (e.g., M typically ranges from 0.4 to 0.6). This high natural mortality rate in M2 occurs because it freely estimates the natural mortality parameter, whereas other models have some constraints associated with the natural mortality rate. Moreover, it is possible that the higher estimated R compensates for the higher estimated M.

Such a high natural mortality rate estimated from a state-space agestructured model was previously reported by Miller and Hyun (2017), although their model was not length-based and was applied to the Acadian redfish stock in the Gulf of Maine. However, Miller and Hyun (2017) found that a model with a constant natural mortality estimated shows the best performance in their simulation studies, which is consistent with our simulation results.

The other possible explanation for the high estimate for the natural mortality M in our study is the age range considered in the models. We included the age-0 group in our models, which typically undergoes the

highest natural mortality rate. The inclusion of this early life-stage group in the models could increase the overall natural mortality rate.

From a fisheries perspective, such a large value for *M* could originate from various processess such as emigration of the species from the area where the fishery-dependent data were collected and underreported catch. In fact, the mackerel stock has been heavily and jointly harvested by fisheries from three neighbouring countries, South Korea, China, and Japan, while the species highly migrate around the waters of those countries (Hiyama et al., 2002; Hwang et al., 2008). Thus, our study results may not well represent the stock status of the species, until more information from two other countries are incorporated in the model.

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Chapter 6

Conclusion

Management of fish stocks requires the collection of suitable data from which population models can be built. State-space models (SSMs) are one modelling approach, and this thesis investigates their application to datamoderate stocks. We define data-moderate stocks as those for which there are no survey data, no information on age composition, and fisheriesdependent data are the only available source of information. We find that many existing state-space models are either too simple (e.g., statespace surplus production models) or too complex (e.g., state-space agestructured models) for these stocks, although many fisheries around the world face data-moderate situations. Complex models can suffer from significant estimability problems.

In this thesis we have developed two state-space models (SSMs) for fish stock assessment and applied those models to the data-moderate stocks (i.e., the Korea pollock and chub mackerel stocks) where relatively short time-series of data on relative abundance (e.g., catch-per-unit-effort: CPUE), yield (i.e., catch in weight), and some indirect demographic information (e.g., life-stage and length composition data) are available. We have also shown how performance of those SSMs can be investigated using several model checking methods, such as jitter analysis (i.e., test hundreds sets of initial values for parameter estimation and compare their corresponding estimates to determine if those estimates converge to the same set), parametric bootstrapping, and process error residual analysis. From this work, we have three main conclusions:

- (i) Separation of observation and process error can be problematic even in simple SSMs, such as state-space surplus production models. This estimation problem can occur even when correct and narrow constraints (i.e., priors in a Bayesian approach and penalties in a frequentist approach) on most model parameters are imposed.
- (ii) The availability of alternative demographic information (e.g., life stage and length composition data) in data-moderate fisheries enables the development of new stock assessment models in statespace form, which allows one to take full advantage of existing data. We developed two new state-space assessment models which were applied to the two data-moderate stocks (i.e., the pollock and chub mackerel stocks) in South Korean waters.
- (iii) SSMs can be tested using several existing methods, each of which detects different issues, so their combined use is essential.

We discuss each of these findings in more detail below, where we identify what literature gaps are fulfilled by this thesis research.

6.1 Estimability of the variance parameters

In Chapter 3, we showed that even a simple SSM has estimation issues, using the state-space surplus production model. From our simulation studies, we conclude that parameter estimation for a state-space surplus production model (SSPM) is sensitive to the ratio between process and observation error as well as trends in the time series data. Imposing strong constraints on model parameters did not completely address the issues, unless one uses extremely narrow constraints (e.g., CV=0.1) which are almost impossible to obtain in real world situations.

We found that simultaneous estimation of both unobserved state variables and model parameters in the SSPM is the main cause of this estimation problem, which suggests that the flexible structure of the SSPM due to the incorporation of process variability often cannot be informed by observation data even with some strong constraints imposed on the parameters (e.g., strong informative priors in a Bayesian approach). The results of the simulation studies in Chapter 3 demonstrated that the SSPM tends to show good performance (i.e., nearly unbiased estimates of the parameters and state variables in bootstrap runs) when the following two conditions are met:

- (i) The parameter for the standard deviation of observation error is not greater than that of process error (i.e., $\sigma_o \leq \sigma_p$, where the subscripts o and p indicate observation and process errors, respectively).
- (ii) The time series of abundance index and yield data does not follow the "one-way trip" trend (e.g., monotonic increasing or decreasing), but mostly fluctuates over time.

Although many previous studies have used SSPMs, most of them have not examined parameter estimability during their model checking process and tend to focus on model convergence instead (Millar and Meyer, 2000; Parent and Rivot, 2012; Winker et al., 2019, 2020). Our simulation studies in Chapter 3, however, demonstrated using parametric bootstrapping that even converged models produce biased results in parameter estimates. The importance of checking estimability of parameters in SSMs has been discussed in previous ecological studies (Dennis et al., 2006; Auger-Méthé et al., 2016; Auger-Méthé et al., 2021), but those studies assume either uninformative priors (in a Bayesian setting) or no constraints (in a frequentist setting) for parameters. In fisheries stock assessments, some parameters are often treated as known or constrained, based on some previous information. Thus, we initially thought that those treatments could not only help models to converge, but also aid parameter identifiability. Surprisingly, our simulation tests in Chapter 3 showed that even with such external aids, certain parameters (particularly, the two variance parameters) had biased point estimates, which brings us to the question about the robustness of the almost ubiquitous application of SSPMs in fisheries stock assessments.

The findings of our study suggest that future studies on stock assessments using SSMs should verify estimability of the parameters before the results are presented. Particularly for data-limited or data-moderate fisheries, observed data collected from commercial fisheries may contain large errors, making it even more difficult for SSMs to distinguish process error from observation error. In our study, we found that parametric bootstrapping was the simplest method for evaluating parameter estimability.

6.2 The two new stock assessment models

In Chapters 4 and 5, we developed two new SSMs for stock assessment, which are applicable to data-moderate fisheries where age composition data are not available. Instead, these models can be used when alternative demographic information, such as life stage and length composition data, is available. These new models were applied to the Korea walleye pollock and chub mackerel stocks as case studies in order to demonstrate their applicability.

Most of South Korea's managed fisheries, including those for the pollock and mackerel stocks, are data-moderate. In our view, the stock assessment models used for these fisheries in South Korea either underused existing data or modelled the data incorrectly. Thus, Chapters 4 and 5 of this thesis have developed new stock assessment models that are more suitable for these types of data-moderate fisheries. In the following subsections, an overview of these two chapters, conclusions, and recommendations for future research are discussed.

6.2.1 The two-life stage-structured model in Chapter 4

The Korea pollock stock collapsed in the late 1990s and has not recovered. Some Korean fisheries scientists postulate that the collapse was caused by a combination of environmental changes in Korean waters and overexploitation of both juvenile and adult pollock stocks. However, a reliable scientific report supporting this hypothesis could not be produced due to the limited available data and the lack of stock assessments on this stock (Kim and Hyun, 2018).

In fact, even one of the simplest stock assessment models, a surplus production model, was not valid for the pollock stock because data on stock abundance were specific to life stages (i.e., juveniles and adults). As already discussed in Chapter 4, such a model misspecification problem was addressed by developing the state-space two-life stage-structured production model, which offers the following advantages:

- (i) The two-life stage model has a simple structure, but the model incorporates demographic relationships between juveniles and adults, which cannot be achieved with a simple age-aggregated model (e.g., a surplus production model).
- (ii) The model is constructed in state-space form, which allows transitions between the two life stages (i.e., juvenile and adult stages) to be stochastic. This demographic stochasticity in process equations allows the model to incorporate unobserved variability, such as environmental changes.
- (iii) Constraints (e.g., priors in a Bayesian approach and penalties in a frequentist approach) on the model parameters can be derived from an age-structured model where input values for life-history parameters

are obtained from previous studies. Such parameter constraints, derived from finer scale models (e.g., age-structured models), not only aid all the model parameters to be estimable, but also allows those parameters to remain within biologically reasonable boundaries.

While the advantages highlighted above are attractive, we caution that future research should also consider the following limitations:

- (i) The model parameters are reparameterised, based on the dominant eigenvalue and eigenvector of the transition matrix. Thus, compared to an age-structured model, direct biological interpretation of each parameter is unclear. However, it still offers more detailed information than a surplus production model.
- (ii) Due to the state-space structure of the model, an estimability issue may arise. We found that this estimation issue cannot be overcome by parameter constraints, but rather is more related to the two conditions discussed in Section 6.1.

6.2.2 The length-based age-structured model in Chapter 5

According to the Korean Coastal and Offshore Fishery Census reports, the Korea chub mackerel stock has been assessed using virtual population analysis (VPA). Based on published articles on this stock (Hwang et al., 2008; Kang et al., 2015; Gim et al., 2020), we could assume that such an age-structured assessment was conducted by converting length frequency data into age composition proportions. The problem of this conversion process is that only a single age-length key (ALK; probability of age given length) estimated from length-at-age data collected during a certain period of time was applied to all years of length frequency data (Gim et al., 2020).

Several studies have demonstrated that applying a single ALK to length frequency data across all years leads to substantial bias (Kimura, 1977;

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Westrheim and Ricker, 1978; Aanes and Vølstad, 2015; Ailloud and Hoenig, 2019). This naive approach does not take into account changes in age composition of populations over time, and is likely to preserve the proportions described by the single ALK used. Despite those previous studies, this obvious flaw in the naive application of ALK seems not to be well-understood by local fisheries scientists as age composition data on the mackerel stock have only been collected intermittently (Hwang et al., 2008; Kang et al., 2015).

Therefore, we believe that the state-space length-based age-structured model we developed in Chapter 5 can be used as a better alternative to the VPA method used for the mackerel stock assessment because of the following reasons:

- (i) The new length-based model does not require an ALK and instead, infers age compositions directly from length composition data within the model. In addition, the model takes into account temporal changes in age composition and allows for the propagation of errors in estimating age proportions from length frequency data.
- (ii) The state-space modelling considers transitions for ages and years to be stochastic, which is a more realistic representation of fish stocks than those used in VPA (or other contemporary age-structured models), which assume deterministic transitions.
- (iii) The new model is capable of estimating an overdispersion parameter within the model, which allows one to avoid the subjective choice of data-weighting between the likelihood of the observed yield data and that of the observed length frequency samples.

However, we note that in addition to the advantages highlighted above, the following limitations need to be considered in future research:

(i) Due to a lack of information, the CPUE data we applied to the model was not standardised. Therefore, collecting more information for

standardizing the CPUE data would be necessary for a more accurate assessment of the mackerel stock.

(ii) We assumed that the catchability was constant to avoid overparameterisation, although it is probably more likely to be varying over time. We initially attempted to incorporate a time-varying catchability, using a random walk model, but observed a failure in estimation, which we attribute to the short time series length of the data and possible confounding in two variance parameters, each of which is for the random walk and the likelihood for the yield data, respectively.

6.3 Model checking methods

Throughout this thesis, we have demonstrated how SSMs can be validated using various model checking methods, such as parametric bootstrapping, jitter analysis, and process error residual analysis. Our study found that the collective use of these model checking methods is helpful in diagnosing SSMs because each method identifies a different type of problem.

In Chapter 3, we showed that parametric bootstrapping can identify issues with estimability of parameters as inestimable parameters (e.g., variance parameters) were biased in terms of relative difference between their point estimates and true values. We used the parametric bootstrap method to test the two new models in Chapters 4 and 5, and found that even the new models potentially have estimability problems. However, we showed that such an estimation issue associated with model parameters did not always produce unreliable estimates for state variables. Since state variables are often of primary interest (e.g., population abundance), in addition to checking parameters, we recommend examining the bias of estimates for state variables.

We found that jitter analysis is useful for checking stability of SSMs. In Chapter 5, we demonstrated that the excessive flexibility of the model could be detected by jitter analysis. When we tested the length-based model using mackerel data under two assumptions about the number of age groups (five and six), we found that the model became too flexible when six age groups are assumed, resulting in multiple sets of estimates for parameters. It should be noted, however, that jitter analysis cannot detect estimability of parameters, which we found in Chapter 4 when testing the two-stage model using both jitter and bootstrap analyses.

In Chapters 4 and 5, we used process error residuals to check model assumptions following the method from Thygesen et al. (2017). Although the method has proven to be effective in testing model assumptions in SSMs, we found that a single check using a Kolmogorov-Smirnov (K-S) test, which was used in Thygesen et al. (2017), may lead to misleading results because

- (i) The distribution of process residuals can also be affected by sampling variability, so using a single set of residuals for checking normality can be misleading.
- (ii) A K-S test is known to be conservative if one or more parameters of a distribution is estimated (Lilliefors, 1967), but the method by Thygesen et al. (2017) uses estimates of parameters when calculating process residuals.

Thus, we applied the following methods to resolve the issues above and suggest that they be considered for future research:

- (i) Use hundreds of sets of process residuals to generalise overall patterns rather than relying on a single set.
- (ii) Visually check the normality of all those sets of residuals to detect any systematic patterns, using a normal quantile-quantile plot.

In summary, this thesis research contributes to the better understanding of the potential estimability issues in SSMs for fish stock assessments, as well as the development of the two new state-space models for datamoderate fisheries. We also identified several issues associated with our findings which could be useful in future research.

Appendix A

A two-life stage-structured production model (TSPM)

A.1 Beverton-Holt steepness formulation

In this section, we show how the Beverton-Holt stock-recruitment model (BHSR) can be expressed in terms of the steepness parameter h (Mace and Doonan, 1988).

In the absence of fishing mortality and recruitment variability, using the BHSR, the relationship between the equilibrium unfished recruitment, $R_*(0)$, and the equilibrium unexploited egg production, Egg_{*}(0), is expressed as

$$R_*(0) = \frac{\alpha \cdot \operatorname{Egg}_*(0)}{1 + \beta \cdot \operatorname{Egg}_*(0)}.$$
(A.1)

Although α and β have vague biological meanings, this parameterization is not suitable for exploring a relationship between $R_*(0)$ and $\text{Egg}_*(0)$, because changes in α and β result in a change to $R_*(0)$. To circumvent this problem, we use the steepness formulation devised by Mace and Doonan (1988), where the parameters α and β are expressed in terms of $R_*(0)$ and the steepness parameter *h*:

$$\begin{cases} \alpha = \frac{4 \cdot h \cdot R_*(0)}{(1-h) \cdot \text{Egg}_*(0)} \\ \beta = \frac{5 \cdot h - 1}{(1-h) \cdot \text{Egg}_*(0)} \end{cases},$$
(A.2)

where $\operatorname{Egg}_{*}(0) = \widetilde{\operatorname{Egg}}_{*}(0) \cdot R_{*}(0)$, and $\widetilde{\operatorname{Egg}}_{*}(0) = \sum_{i}^{A} \operatorname{Fec}_{i} \cdot \operatorname{Mat}_{i} \cdot \phi_{i,*} \cdot \widetilde{N}_{i,*}(0)$. Since the dynamic version of the BHSR is given by

$$R_{t+1} = \frac{\alpha \cdot \mathrm{Egg}_t}{1 + \beta \cdot \mathrm{Egg}_t},$$

substituting β and α with those expressed in Equations (A.4) and (A.5) yields the following reparameterised form:

$$R_{t+1} = \frac{4 \cdot h \cdot R_*(0) \cdot \operatorname{Egg}_t}{\operatorname{Egg}_*(0) \cdot (1-h) + (5 \cdot h - 1) \cdot \operatorname{Egg}_t}.$$

In the following subsection, we show how Equation (A.2) is derived.

A.1.1 Reparameterisation of α and β in terms of *h*

By definition, the steepness parameter *h* is the fraction of $R_*(0)$ to be expected when $\text{Egg}_*(0)$ is reduced to 20% of its pristine level (i.e., $0.2 \cdot \text{Egg}_*(0)$) (Mace and Doonan, 1988). That is,

$$h \cdot R_*(0) = \frac{\alpha \cdot 0.2 \cdot \operatorname{Egg}_*(0)}{1 + \beta \cdot 0.2 \cdot \operatorname{Egg}_*(0)}.$$
(A.3)

After rearranging Equation (A.1) for α , we have

$$\alpha = \frac{R_*(0) \cdot (1 + \beta \cdot \operatorname{Egg}_*(0))}{\operatorname{Egg}_*(0)},$$

By substituting the above equation into Equation (A.3) and rearranging it for β , we can express β in terms of *h* as follows:

$$\beta = \frac{5 \cdot h - 1}{\operatorname{Egg}_*(0) \cdot (1 - h)}$$
(A.4)

Similarly, to obtain the equation for α , we substitute

$$\beta = \frac{\alpha \cdot \operatorname{Egg}_{*}(0) - R_{*}(0)}{R_{*}(0) \cdot \operatorname{Egg}_{*}(0)}$$

into Equation (A.3). Then, rearranging it for α gives us

$$\alpha = \frac{4 \cdot h \cdot R_*(0)}{\operatorname{Egg}_*(0) \cdot (1-h)}$$
(A.5)

A.2 Plus group starting condition (i.e., t = 1)

In this section, we show how the plus group starting condition in Equation (4.12) is derived. Let $\ell_{a,*} = (1 - v_a \cdot H) \cdot S_a$. Then,

$$\widetilde{N}_{A,*} = \widetilde{N}_{A-1,*} \cdot \ell_{A-1,*} + \widetilde{N}_{A-1,*} \cdot \ell_{A-1,*} \cdot \ell_{A,*} + \widetilde{N}_{A-1,*} \cdot \ell_{A-1,*} \cdot l_{A,*}^2 + \dots$$

$$= \widetilde{N}_{A-1,*} \cdot \ell_{A-1,*} \cdot (1 + \ell_{A,*} + \ell_{A,*}^2 + \dots).$$
(A.6)

Note that the above equation is a geometric series.

If we substitute $U = 1 + \ell_{A,*} + \ell_{A,*}^2 + \dots$, the following relationship can be derived:

$$U = 1 + U \cdot \ell_{A,*} = \frac{1}{1 - \ell_{A,*}},$$

which is then substituted back into Equation (A.6) to yield the form:

$$\widetilde{N}_{A,*} = \frac{\ell_{A-1,*}}{1-\ell_{A,*}} \cdot \widetilde{N}_{A-1,*}$$
$$= \frac{S_{A-1} \cdot (1-v_{A-1} \cdot H)}{1-\cdot S_A \cdot (1-v_A \cdot H)} \cdot \widetilde{N}_{A-1,*}.$$

A.3 Reparameterisation of the TSPM

The four composite parameters in the matrix G of Equation (4.6) (i.e., R^j , R^a , g^j , and g^a) together represent demographic relationships between juvenile and adult populations in biomass. In the absence of density dependence and fishing mortality (i.e., without the carrying capacity K_t and the yield Y_t), the population eventually reaches a stable stage structure, from which the ratio of the juvenile and adult biomasses (i.e., the ratio of the two elements in a dominant eigenvector) remains in equilibrium, which we denote as ψ :

$$\psi = \frac{X_1}{X_2},\tag{A.7}$$

where X_1 and X_2 are the two elements of the dominant eigenvector of the matrix G.

Then, using the equation above, we can express B_t^j and B_t^a in terms of ψ :

$$\begin{cases} B_t^j = \psi \cdot B_t^a + \delta_t^j \\ B_t^a = \frac{1}{\psi} \cdot B_t^j + \delta_t^a \end{cases},$$
(A.8)

where δ_t^j and δ_t^a denote the amount of juvenile and adult biomass at time t, deviated from the stable stage ratio ψ .

In the following sections, based on the relationships given in Equation (A.8), we show how the models in Equation (4.6) can be reparameterized in terms of the dominant eigenvalue and eigenvector. The final reparameterised form is given in Equation (4.7).

A.3.1 Reparameterization process for the juvenile model

For the juvenile biomass, we have the following model, which is obtained from Equation (4.6):

$$B_{t+1}^{j} = B_{t}^{j} + \frac{\left(g^{j} - 1 + R^{j} \cdot \frac{B_{t}^{a}}{B_{t}^{j}}\right)}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j}$$

Substituting B_t^a with $(1/\psi) \cdot B_t^j + \delta_t^a$ of Equation (A.8) and rearranging it gives us

$$\begin{split} B_{t+1}^{j} = & B_{t}^{j} + \frac{\left(g^{j} - 1 + \frac{R^{j}}{\psi} + R^{j} \cdot \frac{\delta_{t}^{a}}{B_{t}^{j}}\right)}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j} \\ = & B_{t}^{j} + \frac{\left(g^{j} - 1 + \frac{R^{j}}{\psi}\right)}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] \\ & + \frac{R^{j}}{n^{j} - 1} \cdot \delta_{t}^{a} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j} \end{split}$$

Since $\delta^a_t = B^a_t - (1/\psi) \cdot B^j_t$ by Equation (A.8), we have

$$B_{t+1}^{j} = B_{t}^{j} + \frac{\left(g^{j} - 1 + \frac{R^{j}}{\psi}\right)}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] + \frac{R^{j}}{n^{j} - 1} \cdot \left(B_{t}^{a} - \frac{1}{\psi} \cdot B_{t}^{j}\right) \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j}.$$
(A.9)

Equation (A.9) shows that when the population reaches the stable stage

structure (i.e., $B_t^j = \psi \cdot B_t^a$), the above equation reduces to

$$B_{t+1}^{j} = B_{t}^{j} + \frac{\left(g^{j} - 1 + \frac{R^{j}}{\psi}\right)}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j},$$

which becomes the exact same form as the GSPM, where the term corresponding to the intrinsic growth rate r in the GSPM (i.e., $g^j - 1 + R^j/\psi$) is the dominant eigenvalue of the matrix G (see the proof given in Appendix A.3.3 below). Then, by substituting $g^j - 1 + R^j/\psi$ with r_m , we finally have the form shown in Equation (4.7):

$$B_{t+1}^{j} = B_{t}^{j} + \frac{r_{m}}{n^{j} - 1} \cdot B_{t}^{j} \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] + \frac{R^{j}}{n^{j} - 1} \cdot \left(B_{t}^{a} - \frac{1}{\psi} \cdot B_{t}^{j}\right) \cdot \left[1 - \left(\frac{B_{t}^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - Y_{t}^{j}.$$

A.3.2 Reparameterization process for the adult model

For the adult biomass, we obtain the following model from Equation (4.6):

$$B_{t+1}^{a} = B_{t}^{a} + \left(g^{a} - 1 + R^{a} \cdot \frac{B_{t}^{j}}{B_{t}^{a}}\right) \cdot B_{t}^{a} - Y_{t}^{a}.$$

Substituting B_t^j with $\psi \cdot B_t^a + \delta_t^j$ and rearranging it gives us

$$B_{t+1}^{a} = B_{t}^{a} + \left(g^{a} - 1 + \psi \cdot R^{a} + R^{a} \cdot \frac{\delta_{t}^{j}}{B_{t}^{a}}\right) \cdot B_{t}^{a} - Y_{t}^{a}$$
$$= B_{t}^{a} + (g^{a} - 1 + \psi \cdot R^{a}) \cdot B_{t}^{a} + R^{a} \cdot \delta_{t}^{j} - Y_{t}^{a}.$$
Since $\delta_t^j = B_t^j - \psi \cdot B_t^a$ by Equation (A.8), we have

$$B_{t+1}^{a} = B_{t}^{a} + (g^{a} - 1 + \psi \cdot R^{a}) \cdot B_{t}^{a} + R^{a} \cdot (B_{t}^{j} - \psi \cdot B_{t}^{a}) - Y_{t}^{a}$$

When the population reaches the stable stage structure (i.e., $B_t^j = \psi \cdot B_t^a$), the above equation reduces to

$$B_{t+1}^{a} = B_{t}^{a} + (g^{a} - 1 + \psi \cdot R^{a}) \cdot B_{t}^{a} - Y_{t}^{a}.$$

where the term in the parentheses (i.e., $g^a - 1 + \psi \cdot R^a$) is also the dominant eigenvalue of the matrix *G* (see the proof below). Hence, the finial structure of the model is given by

$$B_{t+1}^a = B_t^a + r_m \cdot B_t^a + R^a \cdot \left(B_t^j - \psi \cdot B_t^a\right) - Y_t^a,$$

which is the same as that in Equation (4.7)

A.3.3 Proof that $r_m = g^j - 1 + R^j / \psi = g^a - 1 + \psi \cdot R^a$

In this section, we show the proof that $r_m = g^j - 1 + R^j/\psi = g^a - 1 + \psi \cdot R^a$.

In Equation (4.6), the matrix G is given as

$$\boldsymbol{G} = \left[egin{array}{ccc} g^j - 1 & R^j \ R^a & g^a - 1 \end{array}
ight].$$

To find the eigenvalues and eigenvectors of G, we set the following equation:

$$\boldsymbol{G}\cdot\boldsymbol{X}=\lambda\cdot\boldsymbol{X}.$$

Then, solving $det(\boldsymbol{G} - \lambda \cdot \boldsymbol{I}) = 0$ gives

$$0 = \begin{vmatrix} g^j - 1 - \lambda & R^j \\ R^a & g^a - 1 - \lambda \end{vmatrix}$$
$$= \lambda^2 + (2 - g^j - g^a) \cdot \lambda$$
$$- g^j - g^a + g^j \cdot g^a + 1 - R^j \cdot R^a$$

Using the quadratic formula, we find the dominant eigenvalue λ_1 as

$$\lambda_1 = \frac{g^j + g^a - 2 + \sqrt{(g^j - g^a)^2 + 4 \cdot R^j \cdot R^a}}{2}$$

Note that $\sqrt{(g^j - g^a)^2 + 4 \cdot R^j \cdot R^a} > 0$ as $g^j, R^j, R^a, g^a > 0$, so there is no complex eigenvalue in this case.

For a dominant eigenvector, we solve the following matrix equation:

$$\begin{bmatrix} g^j - 1 - \lambda_1 & R^j \\ R^a & g^a - 1 - \lambda_1 \end{bmatrix} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

By expanding,

$$\begin{cases} (g^{j} - 1 - \lambda_{1}) \cdot X_{1} + R^{j} \cdot X_{2} = 0\\ R^{a} \cdot X_{1} + (g^{a} - 1 - \lambda_{1}) \cdot X_{2} = 0 \end{cases}$$

which yields

$$\frac{X_1}{X_2} = -\frac{R^j}{g^j - 1 - \lambda_1} = -\frac{g^a - 1 - \lambda_1}{R^a}$$

Since $X_1/X_2 = \psi$ by Equation (A.7),

$$r_m = g^j - 1 + \frac{R^j}{\psi}$$
$$= g^j - 1 - R^j \cdot \frac{g^j - 1 - \lambda_1}{R^j}$$
$$= \lambda_1$$

and

$$r_m = g^a - 1 + R^a \cdot \psi$$
$$= g^a - 1 - R^a \cdot \frac{g^a - 1 - \lambda_1}{R^a}$$
$$= \lambda_1$$

A.3.4 Population growth in numbers or biomass?

Although the matrix models describe population abundance in numbers, the demographic analysis method is also applicable to population abundance in biomass (McAllister et al., 2001). As shown above, in the absence of fishing mortality, the population would eventually reach a stable (age or stage) structure and exponentially grows at a rate of the dominant eigenvalue Λ_1 . That is,

$$N_{t+1} = \Lambda_1 \cdot N_t$$
, where $N_t = \sum_i^A N_{i,t}$

or

$$\Lambda_1 = \frac{N_{t+1}}{N_t},\tag{A.10}$$

where the corresponding dominant eigen vector x_1 is given by

$$\boldsymbol{x}_1 = \begin{bmatrix} x_1 & x_2 & \cdots & x_A \end{bmatrix}'.$$

If we assume that the same population at the stable structure in biomass also grows exponentially at a rate of Λ_1 , we have

$$\Lambda_1 = \frac{B_{t+1}}{B_t}$$

Since $B_t = \sum_i^A w_i \cdot N_{i,t}$, we can rewrite the above equation as

$$\Lambda_1 = \frac{\sum_i^A w_i \cdot N_{i,t+1}}{\sum_i^A w_i \cdot N_{i,t}}.$$
(A.11)

At the stable age structure, the proportion of each age group (i.e., C_i) in the population is independent of the total population size N_t as it remains the same regardless of the total population size:

$$N_{i,t} = C_i \cdot N_t, \tag{A.12}$$

where

$$C_i = \frac{x_i}{\sum_i^A x_i}.$$

Then, substituting Equation (A.12) into Equation (A.11) yields

$$\Lambda_1 = \frac{N_{t+1} \cdot \sum_i^A w_i \cdot C_i}{N_t \cdot \sum_i^A w_i \cdot C_i}$$
$$= \frac{N_{t+1}}{N_t},$$

which becomes the same as Equation (A.10).

A.4 Functional links between the two ASMs and TSPM

In this section, we show how we derive the functional links between the two age-structured models (i.e., the LMM and the ASM) and TSPM, which are given in Equation (4.23).

First, the parameters r_m and ψ of the TSPM can be approximated by

the LMM using the following equations, which we show in Section 4.4.2:

$$\begin{cases} r_m = \log(\Lambda_1) \\ \psi = \frac{\sum_i^A C_i \cdot w_i \cdot (1 - \operatorname{Mat}_i) \cdot v_i^j}{\sum_i^A C_i \cdot w_i \cdot \operatorname{Mat}_i \cdot v_i^a} \end{cases},$$

where Λ_1 is the dominant eigenvalue of the matrix L in Equation (4.20), and C_i is the proportion of age-*i* fish at a stable age structure, which is obtained by normalising the dominant eigenvector of L (i.e., $\sum_i C_i = 1$).

Second, for the approximation of R^a , we derive the change in adult biomass ΔB^a from Equation (4.7) as follows:

$$\Delta B^a = r_m \cdot B^a + R^a \cdot \left(B^j - \psi \cdot B^a\right) - H \cdot B^a$$

Then, setting $\Delta B^a = 0$ gives

$$0 = r_m \cdot B^a_*(H) + R^a \cdot \left(B^j_*(H) - \psi \cdot B^a_*(H) \right) - H \cdot B^a_*(H).$$

Rearranging the above equation for R^a with H = 0 (i.e., no fishing mortality) gives the equation for R^a , which we show in Equation (4.23):

$$R^a = \frac{r_m}{\psi - \frac{K^j}{K^a}},$$

where K^{j} and K^{a} are obtained from the equilibrium ASM (see Equation (4.16)).

Third, for the approximation of R^{j} , we derive the change in juvenile biomass ΔB^{j} from Equation (4.7) as follows:

$$\Delta B^{j} = \frac{\left(r_{m} + \frac{B^{a}}{B^{j}} \cdot R^{j} - \frac{1}{\psi} \cdot R^{j}\right)}{n^{j} - 1} \cdot B^{j} \cdot \left[1 - \left(\frac{B^{j}}{K^{j}}\right)^{n^{j} - 1}\right] - H \cdot B^{j}.$$

Setting $\Delta B^j = 0$ and rearranging it for the equilibrium yield $Y^j_*(H)$ give

$$Y_*^j(H) = H \cdot B_*^j(H) \\ = \frac{\left(r_m + \frac{B_*^a(H)}{B_*^j(H)} \cdot R^j - \frac{1}{\psi} \cdot R^j\right)}{n^j - 1} \cdot B_*^j(H) \cdot \left[1 - \left(\frac{B_*^j(H)}{K^j}\right)^{n^j - 1}\right]$$

Since the above form is the same as that derived from the GSPM for the equilibrium yield, the analytical solutions for the BRPs of the GSPM (see Equation (4.18)) can be applied for estimating n^j and R^j of the TSPM. Thus, for the shape parameter n^j , we use the following equation:

$$n^j = \left(\frac{B^j_{\mathrm{MSY}^j}}{K^j}\right)^{1-n^j},$$

where K^{j} and $B^{j}_{MSY^{j}}$ are obtained from the equilibrium ASM (i.e., see Equations (4.16) and (4.17)).

Similarly, for R^j , we use the following equation for H_{MSY^j} (recall that $H_{MSY} = r/n$ in the GSPM):

$$H_{\mathrm{MSY}^j} = \frac{\left(r_m + \frac{B^a_*(H_{\mathrm{MSY}^j})}{B^j_*(H_{\mathrm{MSY}^j})} \cdot R^j - \frac{1}{\psi} \cdot R^j\right)}{n^j},$$

where

$$B^j_{\mathrm{MSY}^j} = B^j_*(H_{\mathrm{MSY}^j}), \quad \text{and} \quad B^a_{\mathrm{MSY}^j} = B^a_*(H_{\mathrm{MSY}^j}),$$

which we rearrange for R^j as follows

$$R^{j} = \frac{n^{j} \cdot H_{\mathrm{MSY}^{j}} - r_{m}}{\frac{B_{\mathrm{MSY}^{j}}^{a}}{B_{\mathrm{MSY}^{j}}^{j}} - \frac{1}{\psi}}$$

Appendix **B**

A state-space length-based age-structured model

B.1 Cohen and Fishman (1980)'s growth model

In this section, we show how the Cohen and Fishman (1980)'s growth function (CFGF) is derived from the von Bertalanffy growth function (VBGF). Furthermore, after showing the derivation, we derive equations for the expected value and variance of CFGF.

First of all, the VBGF for the length of a fish at age a (i.e., L_a) is given by

$$L_a = L_{\infty} \cdot [1 - \exp\{-k \cdot (a - a_0)\}],$$
(B.1)

where L_{∞} is the asymptotic length, a_0 is the theoretical age at length 0, and k is the growth parameter. Then, for a fish of age $a + \Delta a$, where Δa denotes the age increment, Equation (B.1) can be written as

$$L_{a+\Delta a} = L_{\infty} \cdot [1 - \exp\{-k \cdot (a + \Delta a - a_0)\}]$$

= $L_{\infty} - L_{\infty} \cdot \exp\{-k \cdot (a - a_0)\} \cdot \exp(-k \cdot \Delta a)$

We define the length increment ΔL_a as the difference between $L_{a+\Delta a}$ and L_a :

$$\Delta L_a = L_{a+\Delta a} - L_a$$

= $L_{\infty} - L_{\infty} \cdot \exp\{-k \cdot (a - a_0)\} \cdot \exp(-k \cdot \Delta a) - L_{\infty} \cdot [1 - \exp\{-k \cdot (a - a_0)\}]$
= $L_{\infty} \cdot \exp\{-k \cdot (a - a_0)\} \cdot \{1 - \exp(-k \cdot \Delta a)\}$
= $[L_{\infty} - L_{\infty} + L_{\infty} \cdot \exp\{-k \cdot (a - a_0)\}] \cdot \{1 - \exp(-k \cdot \Delta a)\}$
= $(L_{\infty} - L_a) \cdot \{1 - \exp(-k \cdot \Delta a)\}$

Then, rearranging the above equation with respect to $L_{a+\Delta a}$ yields

$$L_{a+\Delta a} = L_a + \Delta L_a$$

= $L_a + (L_\infty - L_a) \cdot \{1 - \exp(-k \cdot \Delta a)\}$
= $L_\infty \cdot \{1 - \exp(-k \cdot \Delta a)\} + L_a \cdot \exp(-k \cdot \Delta a).$

Letting $\Delta a = 1$, $\rho = \exp(-k)$, and including the normal error term ε_a finally give us

$$L_{a+1} = L_{\infty} \cdot \{1 - \exp(-k)\} + L_a \cdot \exp(-k) + \varepsilon_a$$

= $L_{\infty} \cdot (1 - \rho) + L_a \cdot \rho + \varepsilon_a$, (B.2)

where $\varepsilon_a \stackrel{iid}{\sim} N(0, \sigma_L^2)$.

B.1.1 Expected value and variance of the Cohen and Fishman's growth model

The expected value of Equation (B.2) can be simply obtained by

$$E[L_{a+1}] = \mu_{a+1} = L_{\infty} \cdot (1-\rho) + L_a \cdot \rho.$$

Note that Equation (B.2) is a geometric series:

$$L_{a+1} = L_{\infty} \cdot \{1 - \exp(-k)\} + L_a \cdot \exp(-k) + \varepsilon_a$$
$$= \alpha + L_a \cdot \rho + \varepsilon_a$$
$$= \alpha \cdot \sum_{i=0}^{a-1} \rho^i + L_1 \cdot \rho^a + \sum_{i=0}^{a-1} \rho^i \cdot \varepsilon_{a-i}$$

Thus, the variance of Equation (B.2) (i.e., $Var(L_{a+1})$) can then be expressed as follows

$$\operatorname{Var}(L_{a+1}) = \operatorname{Var}\left(\alpha \cdot \sum_{i=0}^{a-1} \rho^i + L_1 \cdot \rho^a + \sum_{i=0}^{a-1} \rho^i \cdot \varepsilon_{a-i}\right)$$
$$= \sigma_r^2 \cdot \rho^{2 \cdot a} + \operatorname{Var}\left(\sum_{i=0}^{a-1} \rho^i \cdot \varepsilon_{a-i}\right)$$
$$= \sigma_r^2 \cdot \rho^{2 \cdot a} + \sigma_L^2 \cdot \frac{1 - \rho^{2 \cdot a}}{1 - \rho^2} \quad \because \operatorname{Var}(\varepsilon_a) = \sigma_L^2.$$

With the proportionality assumption in Equation (5.5) (i.e., $Var(\varepsilon_a) = \zeta^2 \cdot \Delta L_a^2$), the variance of Equation (B.2) becomes

$$\operatorname{Var}(L_{a+1}) = \sigma_r^2 \cdot \rho^{2 \cdot a} + \operatorname{Var}\left(\sum_{i=0}^{a-1} \rho^i \cdot \varepsilon_{a-i}\right)$$
$$= \sigma_r^2 \cdot \rho^{2 \cdot a} + \zeta^2 \cdot \sum_{i=0}^{a-1} \rho^{2 \cdot i} \cdot \Delta L_{a-i}^2.$$



Figure B.1: Length variance curves formulated based on the two different assumptions on the standard deviation of the error term ε_a in Equation (5.2). The panels in the first column (denoted as "Original form") are obtained from Equation (5.4) where $\sigma_L \in \{2.5, 1.5, 0.5\}$, and those in the second column (denoted as "Alternative form") are from Equation (5.4) where $\zeta \in \{0.5, 0.3, 0.1\}$. Input values for other associated parameters are obtained from the estimates (or given values) of M2 (i.e., $\sigma_r = 1.73$, $\rho = \exp(-0.29)$, A = 5, $L_{\infty} = 40.6$, and $\mu_r = 15.26$; see Table 5.4).

B.2 Derivation of a Dirichlet-multinomial distribution

A Dirichlet distribution for length composition proportion $P_{i,y}$ is given as

$$f\left(\boldsymbol{P}_{y}|\boldsymbol{\alpha}_{y}\right) = \frac{\Gamma\left(\sum_{i=1}^{I}\alpha_{i,y}\right)}{\prod_{i=1}^{I}\Gamma\left(\alpha_{i,y}\right)} \cdot \prod_{i=1}^{I}P_{i,y}^{\alpha_{i,y}-1}$$

where $\alpha_{i,y}$ is the concentration parameter.

A multinomial distribution for length composition proportion $P_{i,y}$ is given as

$$f(\boldsymbol{n}_{y}|\boldsymbol{P}_{y}) = \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I} \Gamma(n_{i,y}+1)} \cdot \prod_{i=1}^{I} P_{i,y}^{n_{i,y}}$$

where $n_{i,y}$ is the sample size for length bin *i* in year *y*, and E_y is the total sample size of those collected in year *y* (i.e., $E_y = \sum_{i=1}^{I} n_{i,y}$, where *I* is the total number of length bins).

Multiplying the above two distributions and integrating across the length composition proportion P_y yield the following marginal probability den-

sity function $f(\boldsymbol{n}_y|\boldsymbol{\alpha}_y)$ for a Dirichlet-multinomial distribution:

$$\begin{split} f(\boldsymbol{n}_{y}|\boldsymbol{\alpha}_{y}) &= \int f\left(\boldsymbol{n}_{y}|\boldsymbol{P}_{y}\right) \cdot f\left(\boldsymbol{P}_{y}|\boldsymbol{\alpha}_{y}\right) d\boldsymbol{P}_{y} \\ &= \int \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I}\Gamma\left(n_{i,y}+1\right)} \cdot \prod_{i=1}^{I}P_{i,y}^{n_{i,y}} \cdot \frac{\Gamma\left(\sum_{i=1}^{I}\alpha_{i,y}\right)}{\prod_{i=1}^{I}\Gamma\left(\alpha_{i,y}\right)} \cdot \prod_{i=1}^{I}P_{i,y}^{\alpha_{i,y}-1}d\boldsymbol{P}_{y} \\ &= \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I}\Gamma\left(n_{i,y}+1\right)} \cdot \frac{\Gamma\left(\sum_{i=1}^{I}\alpha_{i,y}\right)}{\prod_{i=1}^{I}\Gamma\left(\alpha_{i,y}\right)} \cdot \int \prod_{i=1}^{I}P_{i,y}^{n_{i,y}+\alpha_{i,y}-1}d\boldsymbol{P}_{y} \\ &= \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I}\Gamma\left(n_{i,y}+1\right)} \cdot \frac{\Gamma\left(\sum_{i=1}^{I}\alpha_{i,y}\right)}{\prod_{i=1}^{I}\Gamma\left(\alpha_{i,y}\right)} \cdot \frac{\prod_{i=1}^{I}\Gamma\left(n_{i,y}+\alpha_{i,y}\right)}{\Gamma\left(E_{y}+\sum_{i=1}^{I}\alpha_{i,y}\right)} \\ &= \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I}\Gamma\left(n_{i,y}+1\right)} \cdot \frac{\Gamma\left(\sum_{i=1}^{I}\alpha_{i,y}\right)}{\Gamma\left(E_{y}+\sum_{i=1}^{I}\alpha_{i,y}\right)} \cdot \prod_{i=1}^{I}\frac{\Gamma\left(n_{i,y}+\alpha_{i,y}\right)}{\Gamma\left(\alpha_{i,y}\right)} \end{split}$$

Since we assume that $\alpha_{i,y} = \theta \cdot E_y \cdot \hat{P}_{i,y}$, the above equation can be rewritten as

$$\begin{split} f(\boldsymbol{n}_{y}|\boldsymbol{\theta}, \hat{\boldsymbol{P}}_{y}) = & \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I} \Gamma(n_{i,y}+1)} \cdot \frac{\Gamma\left(\sum_{i=1}^{I} \boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)}{\Gamma\left(E_{y} + \sum_{i=1}^{I} \boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)} \\ & \times \prod_{i=1}^{I} \frac{\Gamma\left(n_{i,y} + \boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)}{\Gamma\left(\boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)} \\ = & \frac{\Gamma(E_{y}+1)}{\prod_{i=1}^{I} \Gamma(n_{i,y}+1)} \cdot \frac{\Gamma\left(\boldsymbol{\theta} \cdot E_{y}\right)}{\Gamma\left(E_{y} + \boldsymbol{\theta} \cdot E_{y}\right)} \\ & \times \prod_{i=1}^{I} \frac{\Gamma\left(n_{i,y} + \boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)}{\Gamma\left(\boldsymbol{\theta} \cdot E_{y} \cdot \hat{P}_{i,y}\right)} \quad \because \sum_{i=1}^{I} \hat{P}_{i,y} = 1, \quad \forall y \end{split}$$

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