Survey-LAndings Model (SLAM): a new length- based Bayesian method for stock-assessment

Silvia Malagoli

First supervisor: Dr Douglas Speirs
Second supervisor: Prof Michael Heath

University of Strathclyde

A thesis submitted for the degree of

Doctor of Philosophy

2023

This thesis is the result of the author's original research. It has been composed by the author and has not been previously submitted for examination, which has led to the award of a degree. The copyright of this thesis belongs to the author under the terms of the United Kingdom copyright Acts as qualified by University of Strathclyde regulations 3.50. Due acknowledgement must always be made of the use of any material contained in, or derived from, this thesis.

Date

Signed

Acknowledgements

This thesis could not be written without the solid, knowledgeable and reassuring guide of my two supervisors, Dr Douglas Speirs and Prof. Michael Heath, more commonly known as Dougie and Mike. A major contribution was given also by Dr. Robin Cook, who in a later stage became my unofficial supervisor. I cannot thank these three people enough - really!!! - for the unlimited patience and the great example of professionalism. I acknowledge also the work of two former colleagues, Dr. Andishesh Bakhsi and Dr. Aidan Hunter, whose work has been setting the base for this thesis. Finally, I acknowledge the Marine Alliance for Science and Technology for Scotland (MASTS) and the University of Strathclyde for funding this project.

Abstract

Full analytical stock-assessment normally relies on age data, but that is not available for most species. Length data are cheaper to collect and is available for all species, and many modern models are being based on that. Length data can be gathered from different sources, for instance, the length distribution of the catches. An alternative source of time series data of length distribution is scientific surveys. Another source of information for species that are not aged is time series of biomass, for both catches and survey, as such can provide a valuable indication of total abundance.

We developed a new length-based model that is able to incorporate data from different sources, survey, landings and discard, and data of two different types, length frequencies and time series of biomass. We called it the Survey-LAndings Model (SLAM), it is based on a growth projection matrix and we fitted it using the Bayesian package Rstan. The model is designed to be flexible and can respond to situations with different data availability. In this thesis it was tested in two versions, a "full model", that fits survey length frequency and abundance, landings length frequency and abundance and discard abundance. The second version includes data from only survey length frequency and abundance. The two different versions are meant to reflect a situation with good data availability, where there is information about the catches and especially there is compositional information from the landings, and a highly data-limited situation, where the assessment can only rely on survey information. In the first research chapter (chapter III) we tested both versions on pseudo data, performed some sensitivity analysis and checked for bias. In the second research chapter (chapter IV) we applied the "full version" of SLAM to a data rich species: Whiting stock from division 6a. We evaluated its performance comparing it to an existent assessment and we assessed its sensitivity to specific assumptions. In the third research chapter (chapter V) we tested the "survey only" version, again we picked Whiting stock from division 6a as a data rich species, as well as Haddock from division 6a, and we compared the results with an existing assessment. In this chapter we applied SLAM to two data limited species from division 6a, which are Grey Gurnards and Lemon Sole.

We conclude that SLAM can be a valid tool for stock assessment because it was able to produce assessments comparable to the ones produced by a well-established

age-based stock assessment model, even by just using length information. Stocks like lemon sole and grey gurnard are currently un-assessed and there could be a benefit for fisheries management of West of Scotland by the adoption of SLAM as a stock assessment tool.

Contents

Appendices

List of Figures

List of Tables

1

Chapter I: introduction to the topic

This chapter will provide the context necessary to understand the thesis. It reviews literature in regards to the science of stock assessment, and it will focus especially on some of the challenges it faces, like dealing with data-limited situations, and it will also provide insights on the advantages of length-based assessment and Bayesian methods. This chapter will also explain how this body of work contributes to the progress in the field.

1.1 What is stock-assessment and what it does

Fisheries play a crucial role in providing food, employment, and economic benefits. They are vital for the livelihoods of many people and, in some cases, even for the survival of entire nations. In the first half of the 20th century, it was widely believed that the fish in the sea were an infinite resource, and fisheries were thought to operate like any other sector of the economy, where increased input of investment would lead to increased output of profit. However, this notion was proven false when industrial fisheries developed unprecedented technological advancements and catches started to decline worldwide. This prompted fisheries agencies to start monitoring changes in the abundance of various fish stocks using different methods, leading to the establishment of the science of stock assessment.

Stock assessment comprises any scientific study to determine the productivity of a fishery resource, the effect of fishing on that resource, and the impact (on the resource and the fishery) of changing the patterns of fishing, e.i., from the implementation of management actions or development of policies. It aims to reconstruct the past abundance of stocks, or understand their current state, or make predictions about the future and construct scenarios (Gulland (1983)). The basic principles of assessing fish stocks are the same general principles of population dynamics. Most stock assessment produce reference points, like for instance the Maximum Sustainable Yield (MSY), that can be used by policy makers to implement, for instance, Total Allowable Catch (TAC). The types of data normally used in stock assessment are the age, size, abundance and effort (used then to calculate Catch Per Unit Effort (CPUE)). The methods of data collection of stock assessment include scientific surveys and tagging programs, which collect fisheries independent data, then there are fisheries dependent data which are collected for instance from market samples, fisheries observers and cameras on board of fishing vessels.

Official statistics on global fisheries, specifically official fisheries catch data, have been compiled since the 1930s. The League of Nations initially attempted to report on the world's economy, and this effort was continued by the United Nations, which was founded in 1945. In the 1950s, the Food and Agriculture Organization of the United Nations began publishing its annual yearbook of fisheries statistics. These yearbooks, with annually updated data, are widely utilized to monitor the development of fisheries at the national, regional, and global levels and to make projections about their future prospects. Additionally, they help identify stocks that have significantly declined in abundance and require conservation measures, such as inclusion in international endangered species listings like CITES or the IUCN Red List. Fisheries management agencies have been tracking changes in the abundance of many stocks using various methods, including scientific surveys, tagging programs, and commercial trends in CPUE. These abundance trend data are now available for over 1,300 fish stocks constituting roughly 50% of global marine fish landings in the RAM Legacy Stock Assessment Database (Hilborn et al. (2020); Ricard et al. (2012)). This effort to keep track of stock biomass does not go only to ensure food security of a growing human population, but also to protect worldwide biodiversity and prevent fisheries to cause the disruption of marine and freshwater ecosystems. Unfortunately, we do not have abundance trend data for thousands of fish stocks, mainly because they have minor economic importance or because they come from developing areas of the world (Kindsvater et al. (2018)). The increasing demand for fish abundance assessment is generating a requirement for better data and for new models that can be used in situations where data are deficient (Hoggarth (2006)).

1.2 Data-limited stocks

We define as data-limited a stock for which there are knowledge gaps such as it is impossible to conduct a comprehensive quantitative, model-based stock assessment to estimate time-series of biomass and fishing mortality relative to their reference points, and to estimate productivity and reconstruct historical abundance trends (N. Dowling et al. (2015b); N. Dowling et al. (2015a); N. A. Dowling et al. (2019)). This is true for the majority of the fish and invertebrate stocks, which have scarce, fragmented, or unreliable information. Data-limited fish stocks pose complex challenges and there is high scientific effort into developing models to asses data-limited stock status, in order to find simple, generic, low-cost solutions for fisheries management (Chrysafi & Kuparinen (2016)).

Normally, a data limited stock does not have information on age, and this is because the practice of aging a fish is expensive, therefore, in general, it is regularly conducted only on stocks of medium-high commercial interest by high-income countries. Moreover, many species are hard or even impossible to age, like for many crustaceans and mollusks species (Punt et al. (2013)). Age is at the base of traditional stock assessment because it provides a precise measure of the fish's life stage and development, and it allows accurate estimates of mortality and recruitment rates (Ricker (1975)).

A solution that does not rely on age data are surplus production models. In this type of models, the dynamic of stock biomass over time is modeled through the surplus production, which is net production of biomass over a given period, which is the difference between the biomass added to the population through growth and reproduction and the biomass removed through natural mortality and fishing. However, these models do not account for internal structuring of the population by age or size, and consider individuals within the stock as homogeneous (Haddon (2011)). Modelling the life-stage of individuals within a stock provides greater realism and more information than simply considering the total abundance and overall mortality rate. It is therefore desirable to model population abundance in a structured form when assessing fish stocks (Kuparinen et al. (2012)).

Length-based models have a high potential for data-limited species, as size is cheap to collect and available for all species. Length based models use abundance-at-length as the state variable, and are a valid alternative to age-based models in terms of biological resolution. Compared to surplus production models, they can provide more detailed information on how fishing affects stocks. Next section will be dedicated to length based models.

1.3 Length-Based Assessments

Full analytical stock assessment is normally based on age rather than length data because age data are more powerful. If the growth rates are not consistent across the population, and this is almost always the case, length alone can be misleading (Ricker (1975)). Growth is subject to seasonality, due to differences in food availability and temperature, it slows down with age, and it is different among individuals of the same species. Age based models are in general more computationally convenient than length based models, because the model is fitted to length classes that normally more numerous than age classes. Also, length classes get promoted not just to one, but several other classes with time.

However, along with many advantages, age data have the considerable disadvantage of being unavailable for many species, including many mollusks, crustacean and elasmobranch species, and this results in a large uncertainty regarding the status of a huge range of the world's fish stocks. On the other hand, length information is accessible for every species. Some biological and fisheries related processes are thought to be better described by length then by age. Kvamme & Bogstad (2007) investigated the benefits of including length data in an assessment, suggesting that the mortality caused by fisheries is size-related rather than age-related.

For the reasons cited above, length-only assessments are growing in popularity (Pauly et al. (1987), Hilborn (2003)). Some of the most prominent methods include Length-Based SPawning Ratio (LBSPR; Hordyk et al. (2015)), Length-Based Integrated Mixed Effects (LIME; Rudd & Thorson (2018)) and Length-Based Bayesian (LBB; Kindong et al. (2020) Froese et al. (2018)). LBSPR is a well-known length-based model that assesses stock status by making use of a quantity called spawning potential. Spawning potential in fisheries stock assessment refers to the estimated reproductive capacity of a fish population at a given time. It's a measure of the potential contribution of adult fish to the next generation through the production of offspring. This model compares the spawning potential as measured through the length composition data to that expected in an unfished stock. LIME can be fit to at least one year of length distribution of the catches, catch records and abundance index (fished biomass for instance). It accommodates fluctuating recruitment and fishing mortality (while assuming constant selectivity) and derives population parameters based on an age-structured model and length compositions. LBB is a Bayesian model that fits only info from the catch and considers differences between gears selectivity. It simplifies data requirements by solely relying on this specific data representing the population structure, with the flexibility for users to refine results by inputting additional parameters like maximum length, initial catch length, and natural mortality rates if available from the literature. These models have been developed especially for data limited situations and they are being largely applied.

None of these models have integrated fisheries independent information like survey. Indeed, fisheries-dependent data such as landings and discard abundance and size composition are essential to estimate the removal from the stock on an absolute scale (Cook (2004)). However, these data are more prone to error or bias originating from various aspects related to misreporting of fisheries catch or changes in fishing technology (Pennino et al. (2016)). Unreported catch and discards create a discrepancy between fish landings used in an assessment model and the actual at-sea fish removals, thereby biasing stock size estimates (Beare et al. (2005)). When fisheries catch rates are used to inform stock trends, many factors that cause changes in fisheries catchability can distort or misrepresent the real trends (Harley et al. (2001); Maunder et al. (2006)). For a state-of-the-art stock assessment model it is fundamental to rely on both these sources of information, the dependent and independent of the fisheries, to describe the stock population dynamics and provide management advice.

1.4 Bayesian approach in stock-assessment

Bayesian inference is an alternative framework to the maximum likelihood (frequentist) approach for conducting statistical inference, although they both share the same likelihood function. The maximum likelihood approach seeks a single point estimate that maximizes the likelihood function. It's a deterministic process aimed at finding the most likely parameter values according to the data. Bayesian inference strictly relies on the Markov Chain Monte Carlo (MCMC), an algorithm that generates samples from a probability distribution when direct sampling is difficult. It's a stochastic process that provides a full probabilistic understanding of the parameter estimates, capturing uncertainties and dependencies (Casella & Berger (2002), Gilks et al. (1996)).

The interpretation of probability of the two methods is fundamentally different: a frequentist probability is the proportion of times an event occurs in an infinite sequence of repeated trials; a Bayesian probability is interpreted as a reasonable expectation of a degree of belief (De Finetti (1989)). In Bayesian statistics there is the possibility to include some prior knowledge about the distribution of a parameter. The prior probability represents our initial belief or knowledge about the likelihood of different values for a parameter before observing any data. It's like having a starting point or an assumption about the parameter's distribution based on existing information, expert opinions, or previous studies. When new data becomes available, Bayes' theorem allows us to update our prior beliefs to obtain the posterior probability. The posterior probability incorporates both the prior knowledge and the new evidence, yielding an updated and refined understanding of the parameter's likelihood. It represents our revised belief about the parameter after considering the observed data.

Bayesian methods are very computationally costly, therefore they have never found a wide application until the early 90's. Along with the progress in computational power, Bayesian method have been steadily growing in popularity, in stock assessment as in many other fields (Hilborn (2003), Punt & Hilborn (1997), McAllister et al. (1994)). The primary rationale behind employing a Bayesian approach in stock assessment lies in its ability to encompass and consider the complete spectrum of uncertainties linked to models and parameter values. In contrast, many decision analyses relying on conditional maximum likelihood or least squares estimation tend to fix or condition on specific parameter values. In Bayesian statistics, instead of fixing a parameter at a specific value, it can be assigned it a prior distribution that reflects the belief or knowledge about that parameter before observing the data. Some of these values might play a crucial role in the final outcome of the assessment, yet they often carry substantial uncertainty, which the Bayesian approach effectively addresses and accommodates.

The use of Bayesian parameter estimation in stock assessment models presents significant unresolved challenges, for instance the choice of which prior to use. In general, the Bayesian approach offers a way of incorporating prior information from previous studies or expert opinion, and is a natural framework for estimating probabilities of hypotheses and performing decision analyses. Nevertheless, as highlighted by Punt & Hilborn (1997), defining prior distributions for model parameters was a struggle since the beginning. They demonstrate that even when employing a seemingly neutral prior on population scale (like a uniform prior on unfished biomass), the resulting prior on the final biomass ratio becomes notably informative. Thorson & Cope (2017) also showed that the arbitrary upper bound on a uniform prior on log-maximum recruitment determines results in 3 of 4 case studies considered. Punt & Butterworth (2000) also warns about specifying priors so that they are not contradictory, which is a problem that has occurred for the bowhead whale assessment. A prior is in conflict with another (or with the likelihood) when the areas where these function have high densities are significantly different (Gagnon (2023)). The other main downside of Bayesian statistics is the long run time. It is extremely intensive computationally to apply Bayes Theorem to complex models, and despite the recent advance in technology and computational power it can take several hours to run.

The alternative to Bayesian statistics in stock assessment is the estimation of Maximum Likelihood (ML). Bayesian and maximum likelihood estimates of stock assessment parameters are both guaranteed to converge on their optimal values as the amount of data increases to infinity (Gelman (2006)), but the main difference between the two methods is how they deal with uncertain or not-so-accurate data. Bayesian estimation involves using a method called “integrating the posterior distribution”, which involves complex computation processes. On the other hand, maximizing the likelihood is also complex, even though not as computationally expensive. However, to conduct defensible decision analyses for assessments based on maximum likelihood estimation, it is usually necessary to conduct a bootstrap analysis (Restrepo et al. (1992)).

Bayesian analyses can be slow for many reasons, especially because the model needs to be iterated a large number of times to converge and produce sufficiently precise shapes of the posterior distributions. This inefficiency comes from different factors. Firstly, the model’s speed, depends on the computer’s power, the programming language used, and how well the code is written. Usually, this isn’t the main reason why the whole process takes a long time. The second factor is the geometric shape of the posterior, which increases run time when the model has many parameters and the posterior has a more complex geometric shape. For instance, efficiency degrades when posterior mass is close to parameter boundaries, or the posterior has fat tails, or there are correlations between parameters that vary over the posterior. Every parameter adds a dimension to the likelihood, making it hard for the model to find the lowest point.

Despite the many difficulties that arise from the use of Bayesian techniques, they still have a vast an constantly increasing application in stock assessment and decision analysis (Hilborn (2003)).

1.5 This thesis

This chapter introduced the science of stock assessment, along with its fundamental concepts, its key challenges, its latest trends, like implementation of Bayesian stock assessment models. The protagonist of this thesis is a length-based Bayesian stock assessment model, thought for, but not limited to, assessing data-limited species. The model is forward running, deterministic, matrix based and length based population model called Survey-LAndings Model (SLAM), and it integrates both fisheries dependent and independent information. It can adapt to different data availability and it incorporates the latest trend in the field to face modern challenges while remaining simple and user friendly. This thesis will show the process of developing of a new stock assessment tool and demonstrate how it is possible to obtain results that are comparable with age-based models by just using length information, even in highly data limited situations where only fisheries independent information is available.

The content of next chapters will be:

- Chapter II gives a detailed overview of all the data sources used during this work and especially focuses on the bias of the data.
- Chapter III introduces SLAM: it describes the structure of the model, the different data sources that it can possibly fit and it reports the results of different tests. In fact, in this chapter the model is tested on pseudo data on the two different configuration that were chosen for this study. The first one is the model “full version” and the second is “survey only”.
- Chapter IV tests SLAM “full version” on whiting data and compares the results

with another stock assessment model.

- Chapter V tests SLAM "survey only" on different stocks: whiting (*Merlangus merlangius*), haddock (*Merlanus aeglefinus*), grey gurnard (*Eutriglia gurnardus*) and lemon sole (*Microstomus kitt*)
- Chapter VI presents and overall discussion and conclusion.

2

Chapter II: the data

In this thesis we will develop and apply a new stock assessment method called Survey-LAndings Model (SLAM). SLAM is a length-based Bayesuan model that can rely on both fisheries dependent (landings and discard) and independent information (scientific surveys). The model, described in details in chapter III, can fit 6 different types of data, survey biomass, landings biomass and discard biomass, and proportions-at-length from survey, landings and discard. SLAM can be configured in different ways in order to face situations with different data availability, in fact SLAM can be fit to all the data simultaneously or just partially. The least requirement to run an assessment with SLAM are survey biomass and survey length distribution, which is what we could consider a data limited situation.

In the present chapter are described in detail the data sources used in this thesis, the species we chose, the area they come from, the advantages and limitations of each data set. Being aware of the biases contained in the fisheries and survey data is fundamental to understand the motivation behind some of the choices that were made, and the content of this chapter will be referred multiple times in the rest of the thesis.

2.1 The stocks

In this thesis are used 4 different stocks, all from West of Scotland (also referred to ICES subarea VIa). The study was limited to this area because it is the only area for which I had access to landings proportions-at-length data for some species. Moreover, differently from the North Sea, there are well assessed stocks along with several unassessed stocks. For this study it was important to pick a couple of assessed stocks to have a reference for the model output, but it was also of interest to assess new stock, which is the ultimate reason why this model was developed.

The first species chose is whiting (*Merlangus merlangius*) from West of Scotland, which is a well assessed stock. Whiting is a commercial species present in the North Atlantic, North Sea and Mediterranean Sea. It is caught in mixed trawl fisheries and in Nephrops fisheries. The maximum size they can reach is 70 cm and there is a great size variability within individual of the same age. A fish of 30 cm can be even 6 years old (Hislop et al. (1991)). Being short is computationally advantageous, because it means a modest number of length classes to fit for the model. This made whiting preferable over cod (*Gadus morhua*). For whiting from subarea VIa there is no evidence of migration to other areas and the international Council for the Exploration of the Sea considers it a closed stock, therefore it is compatible with SLAM's assumption of a closed population. In Scottish waters, Hunter et al. (2016) found that there were significant decreasing trends in asymptotic size, maturity at length and abundance over the last three decades. The main cause driving this trend is the systematic removal of the faster growing individual by the fisheries. This is a well known detrimental effect of fisheries, that goes by the name of the Rosa Lee phenomenon (Lee (1912)). R. M. Cook (2019) also found a decreasing trend over the values of discard at lengths, highlighting as the fisheries is retaining specimens that are smaller and smaller. It is important to be aware of these trends when conducting a stock assessment study. Kraak et al. (2019) investigated the consequences of overlooking the Rosa Lee phenomenon working on simulated data.

As a second well assessed stock we chose haddock (*Merlanus aeglefinus*). It is a commercial species in the North Atlantic and North Sea and it is commonly caught in mixed trawl fisheries alongside cod and whiting. They can grow up to a maximum size of 100 cm, and there is considerable variation in size among individuals. For instance, a haddock measuring 40 cm in length can be around 5 years old (Scott (1988)). They prefer the coarser seabed sediments around the periphery of the muddy *Nephrops* grounds, the adults are found more commonly from 80 to 200 m (Cohen et al. (1990)). Haddock is known for having a considerable variability in recruitment from year to year, therefore we chose it for a comparison with whiting which has a lower variability, to test how the model was dealing with that. Nevertheless, haddock from West of Scotland and haddock from the North Sea were proved to be a single stock, meaning that haddock from area VIa is not a closed population.

We then chose two unassessed and data-limited species: grey gurnard (*Eutriglia gurnardus*) and lemon sole (*Microstomus kitt*). Grey gurnard is the most common gurnard in the North Sea. It is caught as a by-catch in demersal fisheries, and is of limited commercial importance. Juveniles feed on a variety of small crustaceans,the diet of older specimens mainly consists of larger crustaceans and small fish. Spawning takes place in spring and summer. The average length of 8-year-old fish has been estimated at 35cm Damm (1987) and 32cm Pope et al. (2000). Females grow faster and live longer than males Damm (1987). Lemon Sole is a commercial species present in the North Atlantic and North Sea. It is frequently caught in demersal trawl fisheries, where it is encountered alongside other flatfish species. Lemon Sole can grow up to a maximum size of 30 cm, and like the other species mentioned, there can be considerable variability within individuals of the same size. In Scottish waters, lemon sole start to spawn in the northwest of the North Sea in April and spawning spreads south and east as the season progresses. Most spawning occurs between the first and the second quarter of the year (Age et al. (2010)). We chose these two species not only because they are not currently assessed but also because they have quite different morphology and swimming habits, also compared to whiting and haddock. Therefore it was interesting to check if SLAM was able to produce a reliable assessment independently from these characteristics of the stocks.

2.2 The types of data

2.2.1 Pseudo data

The data were generated using SLAM as an operating model. All the parameters were assumed to be known and the model was used to calculate the quantities that we then used to generate the data: total biomass and length distributions. We generated data for survey, discard and landings biomass, landings and survey length frequency. The biomass data were generated by perturbing the model output. Each value was multiplied by a sample withdrawn from a lognormal distribution centered on 0 with standard deviation of 0.3. The length frequency data were generated by withdrawing 50 samples with a multinomial distribution from the model output.

The values of fishing mortality (Ft) used as know values to generate the pseudo data were calculated with a random walk:

$$Ft_{t+1} = Ft_t + \epsilon_t; \quad \epsilon_t \sim N(0, 0.1) \tag{2.1}$$

this is because in SLAM fishing mortality is assumed to follow a random walk, with correlation from one year to the other.

In table 3.1 we report all the parameters and the true values used for the simulations in this chapter, and the type of prior used.

2.2.2 Survey

Scientific surveys are a fundamental source of information for fisheries science. They are designed to catch a representative sample of the real age and length distribution in the sea. In fact, the mesh size of survey net is smaller in comparison to the one of the one of the average demersal trawler, so that the survey is be able to catch small fish. Surveys take samples that are evenly distributed in space, differently

from fishing vessels that go only to places where fish of commercial size are known to gather. On board of scientific surveys all fish are identified and measured, then, according to the survey protocol, a sub-sample of fish is also aged, sexed, and the maturation stage of the gonads is evaluated. Observation error can hide at different stages of the sampling process, as discussed in Gerritsen & McGrath (2006).
The survey data used in this study were downloaded from the DATRAS repository on the ICES website. The data were normalised to fish caught per Km^2, dividing the number of fish caught per haul by the Km towed multiplied by the wingspread. For each of the four species a data set was obtained with the numbers of fish caught for each centimeter of length (per year, from 1989 to 2020). To obtain the proportions at length, the total numbers-at-length was divided by the sum of fish caught by the survey on that year. To obtain the survey biomass, it was necessary to calculate the weight of each fish based on length l. This is done by applying the weight-length relationship:

$$W = \alpha_W \cdot l^{\beta_W} \tag{2.2}$$

Where W is a column vector with size equal to the length classes in the survey data and l is another column vector of the same size. The parameters α_w and β_w are specie-specific and are available in the literature. To calculate the total biomass surveyed each year we multiplied the weight-at-length W by numbers at length Sur and then summed across length classes:

$$W_t = \sum_{l=1} Sur_t \cdot W \tag{2.3}$$

Figure 2.1 shows the proportions-at-length of whiting broke down by quarter in an example year, 1998. We observe how the shape of the distribution changes during the year, this is due to fish somatic growth. Spawning happens in quarter III and fish starts to appear in the catch in the first peak of quarter IV, at about 15 cm long. This recruitment peak is smaller than the second one because the survey does not select well fish that are smaller than this size. The second peak

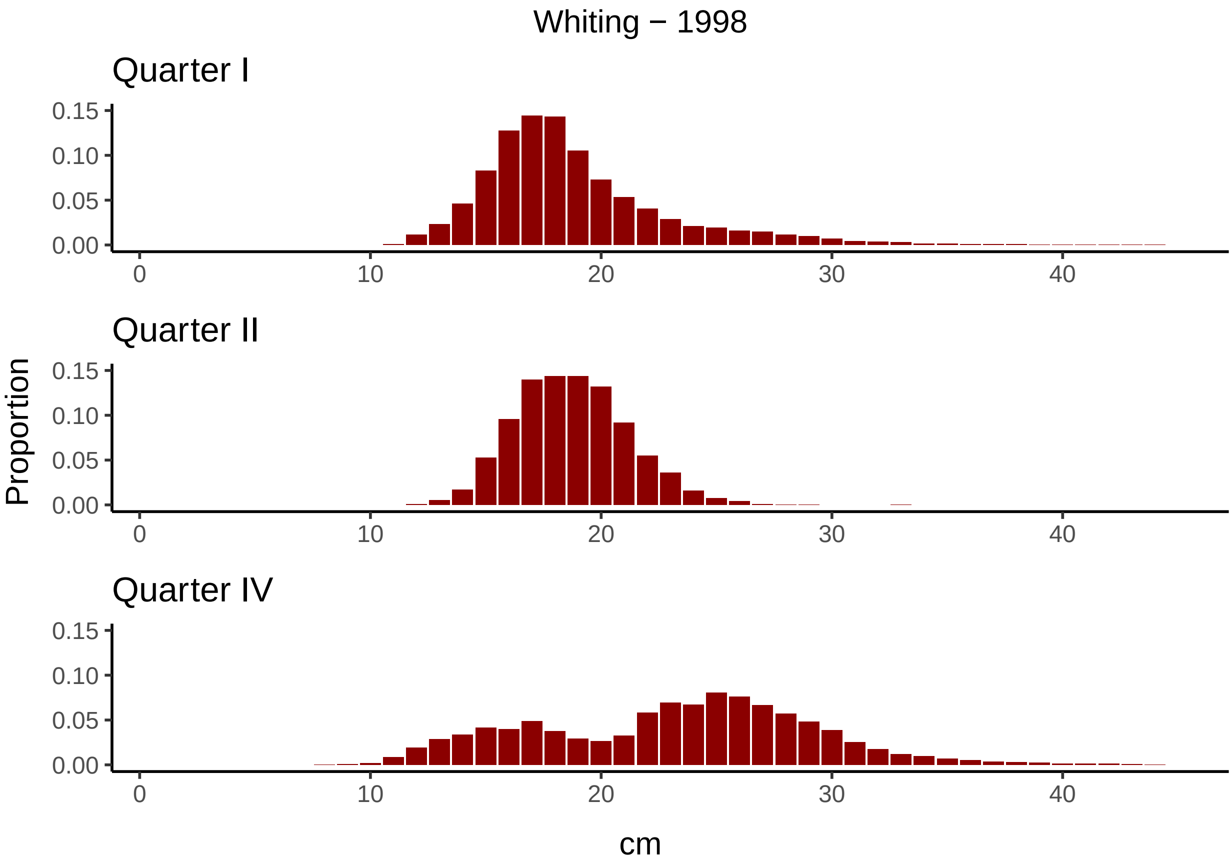


Figure 2.1: The following histograms shows the proportions-at-length of whiting in 1998 broke down by quarter of the year. Quarter 3 was not conducted in 1998. We observe how the shapes of the distribution vary consistently during the year due to the growth of fish.

of quarter IV, with mean at about 25 cm, appeared as the first peak in quarter I with a mean of about 17 cm. We can follow the growth of this cohort in quarter II, where the mean increased of a couple of centimeters. It is of fundamental importance to select fish from only one quarter, otherwise the model will not be able to track the fish cohorts and estimate important quantities, like growth and recruitment. For this study we chose quarter I because it is the only one that was consistent for every year in subarea VIa.

2.2.3 Landings and discard

In this study we focus only on demersal fisheries, where the most of the catch comes from demersal trawlers. Fisheries catches are source of different types of data that can be collected at different stages of the process. Catches can be separated into two components: landings, the part of the catch of commercial value that is took to the port to be sold, and discard, the part of the catch that is thrown back at sea, because because of being too small or too damaged or having no commercial value (bycatch). Fisheries aims at targeting only fish at a commercial size, therefore the mesh sizes of the net is large enough to let the small fish of the target species escape. Moreover, fisheries effort is not evenly distributed in space, but rather focused on specific areas where the target species is known to gather. Moreover, trawlers can fish for many hours and they can easily tire out old and experienced fish, which can swim faster in front of the gear but are not able to escape from the side because of the cloud of sediment that is rising from the trawl wings.

In this study, fisheries dependent data were used only for whiting. Time series of landings biomass and discard biomass are published by the International Council for the Exploration of the sea (ICES) on an annual report (ICES (2022)). This report also breaks down the landed weight by country, and it appears how the majority of the whiting in the area is caught by Scotland. Those values indicate the total weight of fish that were landed or discarded on that particular year.

The landings length frequency data were made available by prof. Heath. The landings length frequency data were collected from year 1989 to 2008 in markets over the coast of West of Scotland. The sample has then been raised to the total landed weight registered for that year. The data set is split between landings coming from Pair Trawls, Nephrops trawl and other gears. This data set is for Scottish gears only, and is missing the landings length frequency from non-Scottish gears. Nevertheless, we saw in the ICES report how non-Scottish landings makes up only a small fraction of the total, therefore this is not a major limitation. We overcame this problem by considering that non-Scottish trawlers fishing in subarea VIa are mainly big trawlers, categorized in the Landings Length Frequency data as "Other Gears". Therefore we could assume that the landings catch at length from non-Scottish fleet has approximately the same shape of Scottish "Other Gears". In the ICES report we found both the total landed biomass and the total Scottish landed biomass, it was possible to calculate the total Non-Scottish Total Landed

Biomass, and then raise the “Other Gears” Scottish Length Frequency according to the ratio between Non-Scottish total landed biomass and total Scottish landed biomass. This step can be more easily read in the formula:

$$non\ ScottishLF_{l,y} = Scottish\ other\ gearsLF_{l,y} * \frac{non\ ScottishW}{ScottishW} \tag{2.4}$$

Where non-Scottish and Scottish LF are a matrix of dimensions $rows = numberoflengths$ and $columns = number\ of\ years$. We then summed non-Scottish and Scottish LF to obtain the landings length frequency.

For the landings and discard we are using annual values and we do not break down by quarter, because the biomass data do not have that resolution. In figure 2.2 we try to break down proportions-at-length landings data by quarter to see if the peaks are very different from one another and if summing them together might mask relevant signal for the model. Each plot in the grid represents a different year, and the four different lines are the different quarters. We observe how for some years the profiles were very similar, like in 1991, while for others there was quite a lot of variability, like 1999. Using annual values is still the better option, since we do not have landings and discard biomass quarterly values, but this is a limitation of the data and we must be aware of that.

Let’s now compare the annual landings proportions-at-length with the survey proportions-at-length from quarter I. Figure 2.3 shows each year of proportions-at-length as a different line. We observe how there are no small fish in the landings, because they are discarded. Also, the peak in the landings comes around 35 cm length, when there are very little fish caught in the survey. This is because the survey trawls only for half an hour (an hour before the change in protocol year 2011) and the bigger fish manage to escape. This is an important source of bias that will need to be considered in chapter IV and V.

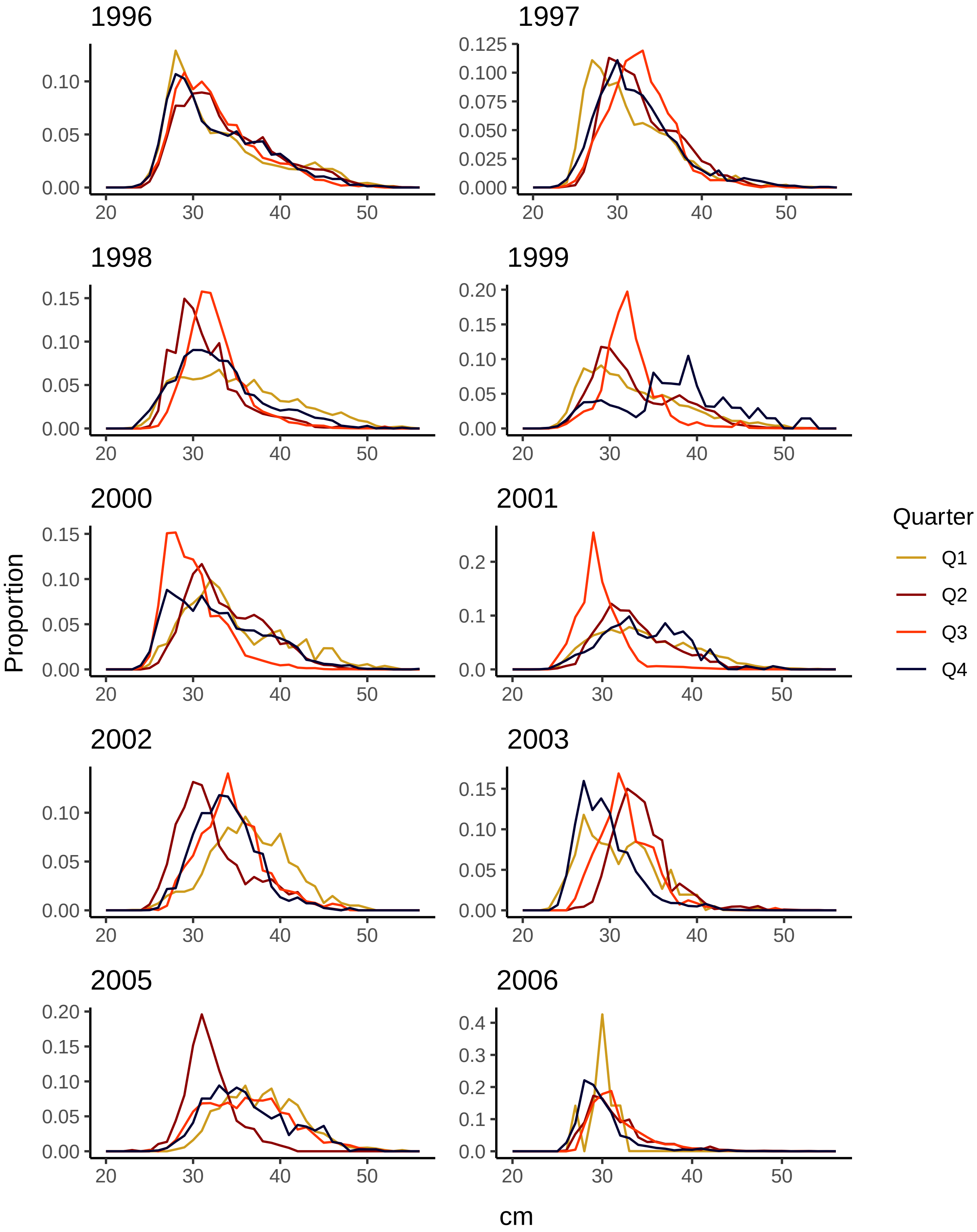


Figure 2.2: The figure shows the breakdown of landings proportions-at-length by quarter, for a part of the years we had available: 1996-2006. We can observe in some years the different quarter had a very similar shape, like year 1996, while for others the shape was quite different, like 1999 or 2003. In the present study we sum over these quartely values to take the yearly values, therefore this might mask some information regarding growth, and create a conflict with the survey proportions-at-length, which comes from quarter 1 only.

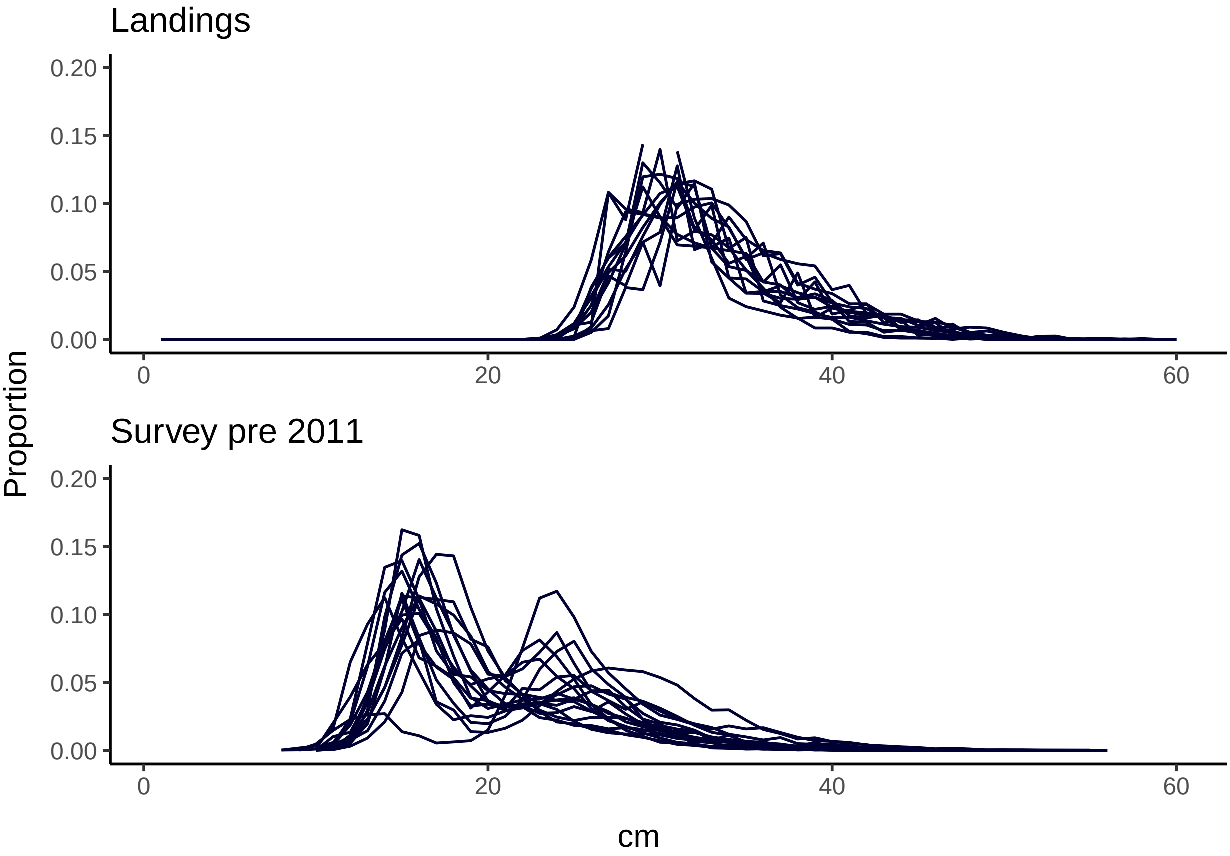


Figure 2.3: Line plot show the whiting proportions-at-length of annual landings and QI survey. We observe how there are no small fish in the landings, because they are discarded, and there are no big fish in the survey, probably because the survey does not sample well big fish.

2.3 West of Scotland fishing area

The West of Scotland fishing area (sometime referred to as subarea VIa), stretches from the West Coast of Scotland over the Outer Hebrides to approximately 5 degrees longitude west of the edge of the continental shelf. The area is exploited for both demersal and pelagic fisheries. It was chose for this study because it was the only one for which I had access to landings compositional data. Moreover, the area has a long and rich survey history. Nevertheless, the geography and the weather conditions of area 6a makes it quite hard to sample uniformly. Furthermore, the survey protocol underwent relevant changes after 2011. A major one was that the haul duration was reduced from 1 hour to 30 minutes, having a significant impact on the survey catchability. Catchability is a concept in fishery biology which reflects the efficiency of a particular fishery (Tanaka (1997)). Moreover, the gear was changed and they changed the design from fixed station to a random stratified design. Table 1.2 is presenting the number of hauls conducted every year during quarter one. We can see how before 2011 the in number of hauls tended to be higher. The mean haul number was roughly 80, with a standard deviation 21.6. This indicate quite high variability, we see for instance year 1999 has two times the number of hauls than year 1995. This could have been for a variety of reasons, even weather conditions. After year 2011 there was an effort to have more consistent with haul numbers, the mean is roughly 61 hauls with a much smaller standard deviation of 2.5. These hauls also had half the duration of hauls before 2011.

Subarea VIa is also known to be difficult to sample, for both the morphology of the seafloor and the harsh weather conditions. We can see in figure 2.4 three maps presenting the spatial distribution of hauls in quarter one. The big map shows all hauls from year 1989 to 2020, and we can observe how there was not one single haul in the area just west of the Outer Hebrides. This is due to the characteristics of the bottom, that is rocky and full of sharp and tall pinnacles, that makes it impossible to practice any kind of demersal fisheries. Furthermore, almost one third of the whole area 6a is occupied by the deep waters outiside the continental shelf, which by protocol are not sampled by demersal survey. The smaller maps compare the distribution of Q1 hauls in 1991, before the protocol was changed, and in 2019. In the first map indeed the hauls are not very uniform in space, with a very clear aggregation of hauls between the Outer Hebrides and the coast. This could be due to an especially bad year in terms of weather, that made it difficult to sample west of the Outer Hebrides for many days. The survey design was based on fixed stations: the operators were given a list of station that they could sample and they could choose from that. If the weather was bad they could just have gone for those hauls that were easy to sample, instead of heading offshore. After the design was changed to random stratified in 2011, we can see that the hauls seems more uniformly spread. The reader is invited to take a look at more maps shown in Appendix II.

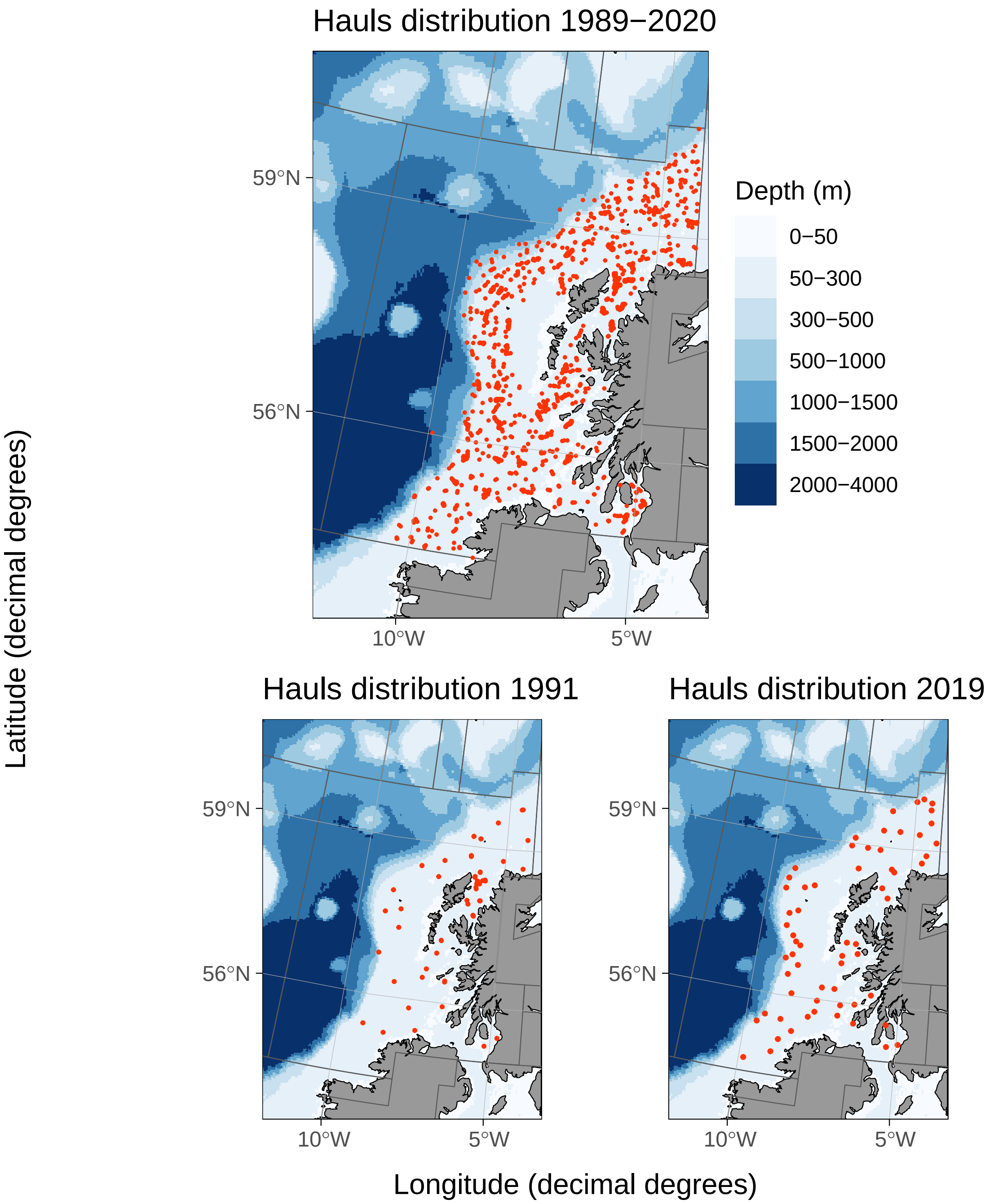


Figure 2.4: The maps above show West of Scotland and the limits of subarea VIa. The larger map represents the distribution of the total hauls that were ever made in quarter 1. We observe how the hauls are not been taken uniformly over the whole area, in fact they are limited to the continental shelf and the area just South West of the Outer Hebrides has never been sampled. The smaller maps display the quarter 1 hauls taken in individual years, 1991 on the left and 2019 on the right. Due to the change in the sampling protocol in 2011, the hauls taken before this year appear to be less spread out, while the ones taken after look more randomised.

Table 2.1: Year and Haul numbers for quarter 1

Year	Haul numbers
1989	82
1990	78
1991	96
1992	76
1993	78
1994	82
1995	54
1996	80
1997	77
1998	72
1999	110
2000	105
2001	76
2002	84
2003	106
2004	92
2005	94
2006	106
2007	130
2008	54
2009	53
2010	57
2011	57
2012	64
2013	64
2014	61
2015	62
2016	63
2017	62
2018	60
2019	62
2020	57

2.4 Summary

In the present thesis we will present a new length-based assessment, the Survey-LAndings Model, and we will test it on different data combinations. Table 1.3 presents the types of data used in each chapter.

Table 2.2: The table summarises the stocks and the types of data used for each chapter.

Chapter	Stock	Source	Type
II	pseudo data	survey	biomass
			length frequency
		landings	biomass
			length frequency
		discard	biomass
III	whiting VIa	survey	biomass
			length frequency
		landings	biomass
			length frequency
		discard	biomass
IV	whiting VIa	survey	biomass
			length frequency
	haddock VIa	survey	biomass
			length frequency
	grey gurnard VIa	survey	biomass
			length frequency
	lemon sole VIa	survey	biomass
			length frequency

3

Chapter III: Description of the Survey-LAndings Model (SLAM) and test on pseudo-data

3.1 Introduction

Most of marine animal species are hard or impossible to age. Length is a measurement that is available for every species and many modern models are being based on that. Length-based population models typically find use when there's a lack of direct aging information but some data on growth is available (Chen et al. (2003), Sullivan et al. (1990), Punt et al. (1997), Hillary (2011)). The three most common types of data used in stock assessment models are catch, abundance indices, and age/length composition, although many integrated models do not simultaneously include all three of these (like Sullivan et al. (1990); Rudd & Thorson (2018); Rudd et al. (2021)). Length data can be gathered from the composition of the catches or of scientific surveys. Catch and abundance indeces are also information that are not dependent on the ageing process, because they are usually a time series of biomass, and can provide a valuable indication of total abundance.

In this chapter we present a forward running, deterministic, matrix based and length based population model called the Survey-LAndings Model (SLAM), which is inspired to Sullivan et al. (1990). Sullivan's model is also a length based model that uses a generalisation of the of the Leslie matrix that uses size classes instead of age (Sullivan et al. (1990), Sainsbury (1982)). In length-based methods, differently from age based methods, the concept of aging revolves around moving through various lengths over time, but in a single time step, an organism can skip multiple length classes or even stay in the same length class. Therefore it is necessary to create a matrix of probabilities of transitions between length classes (Morales-Bojorquez & Nevarez-Martinez (2010), Nevarez-Martinez et al. (2010), Hillary (2011)). In a stock assessment model, the mean growth increment is modeled with the von Bertalanffy curve. Sullivan's model is based on catch-at-length, meaning it relies on information coming from the fisheries and is able to estimate quantities relevant to stock assessment, namely relative abundance, fishing mortality, selectivity, and the von Bertalanffy growth parameters L_∞ and k by using nonlinear least squares approach. The length distribution of the catches is almost never available and this makes Sullivan's model quite limited in its applicability.

Differently from Sullivan's model, SLAM is able to fit both fisheries dependent data (landings and discard) and fisheries independent data (scientific surveys). The types of information required are an index of abundance (total biomass) and compositional information (length frequencies). The minimum requirement to run an assessment with SLAM are survey biomass and length frequencies, which represent a data limited situation. All the other types of data can be added if available. This makes SLAM a flexible tool that can adapt to situations with different data availability. As a further implementation from the Sullivan model, we implemented SLAM in a Bayesian framework, using the software Stan.

This chapter will describe the model in details and will present two different version of the model. The first versions represent a data-rich situations were the model is fitted to survey biomass and length frequency, landings biomass and length frequency and discard biomass. The second version represent a data-limited situation where the model is fitted only to survey biomass and length frequency. The objective of this chapter is to demonstrate that SLAM is unbiased and has low sensitivity to key input values, therefore its output can be fully trusted when applied to a real stock. In order to prove this, both versions of the model will undergo some sensitivity analysis and some tests to show that it is able to retrieve input parameters from sets of pseudo data.

3.1.1 The Survey-LAndings Model (SLAM)

The Survey-LAndings Model (SLAM) is a forward running, deterministic, matrix-based and length-based population model, where the abundances at two different time steps t are related and the length classes are discrete. The time resolution of SLAM is years and the length resolution is centimeters. Equation 1 shows the population dynamic equation underlying of SLAM:

$$N_{t+1} = \mathbf{G} \cdot \mathbf{S}_t \cdot N_t + R_{t+1} \tag{3.1}$$

N is the column vector of length equal to the maximum size modeled (l), the numbers of which indicate the numbers of individuals at each size. **G** (growth) and **S** (survival) are square matrices of dimensions l and R is another column vector of length l that adds recruitment every year.

Stock Growth

The element **G** is the growth projection matrix, which is a generalisation of the Leslie matrix and it is commonly used in many population dynamics models [**?**, **?**, **?**, **?**]. **G** grows each individual for their source length classes and distributes them a set of destination length classes. The mean growth increment $\mu_{\Delta l}$ of fish of length L_i is assumed to follow the Bertalanffy growth curve. Here the subscript i indicates the single length class.

$$\mu_{\Delta l} = (L_\infty - L_i)(1 - e^{-K\Delta t}) \tag{3.2}$$

K is the growth rate coefficient and it is species-specific and influenced by environmental and genetic factors. The spread around the mean length $\sigma_{\Delta l}$ is modeled by a coefficient variation ω that we assume to be constant, therefore:

$$\sigma_{\Delta l} = \omega \mu_{\Delta l} \quad . \tag{3.3}$$

Stock survival

The survival matrix **S** changes in time and is defined by:

$$\mathbf{S}_t = \mathrm{diag}(e^{-\mathbf{Z}_t}) \tag{3.4}$$

Where Z_t is the vector by length l of the total mortality rate. Total mortality is given by the sum of natural mortality (M) and fishing mortality (F_t):

$$Z_t = M + F_t \tag{3.5}$$

where M and F_t are two column vector of dimension l. We assume natural mortality M depends only on the size of the fish and it can be calculated by Lorenzen equation [**?**] expressed in terms of length:

$$M = \alpha_M \cdot l^{\beta_M} \tag{3.6}$$

The assumption of Lorenzen natural mortality is widely used in stock assessment and the parameters α_M and β_M are normally fixed. This is not because these parameters are known, but rather the opposite. Estimating both natural mortality and fishing mortality at the same time without information is impossible without information on both. Since the trend of natural mortality is widely agreed to follow a Lorenzen curve, the parameters are fixed so the model is able to estimate fishing mortality. Fishing mortality F_t represents the mortality of the stock caused by fisheries and will be unpacked in **??**

Stock Reproduction

Recruitment R is a column vector of length l that contains the total number of recruits by length. The shape of the length distribution is controlled by a mean μ_R and a standard deviation σ_R. The total number of recruits is estimated every year, but in case the model is being used to generate data, R_t needs to be calculated. This is done by using Beverton-Holt model:

$$r = \frac{\alpha \cdot SSB}{1 + \beta \cdot SSB} \tag{3.7}$$

Where *SSB* the spawning stock biomass. SSB is calculated by multiplying the weights-at-length by a the maturity ogive and then summing over length:

$$SSB = \sum_{i=1}^{l} N_t W \cdot \frac{1}{1 + \exp(-\beta_{\text{mat}}(L - L_{50\text{mat}}))} \tag{3.8}$$

Where the vector W is a weight-length converter calculated with the following relationship:

$$W = \alpha_W \cdot l^{\beta_W} \cdot w \tag{3.9}$$

α_W and β_W are values are commonly available in the literature, w is parameter used in case the weight needs to be converted from gutted to non-gutted.

The initial Population

The initial population in SLAM is calculated by adding the number-at-length of survival fish from the year before, and the first year of recruitment-at-length. Each component is multiplied by its respective length distribution:

$$N_1 = NS1 \cdot LF1 + R_1 \cdot R_{\text{distr}} \tag{3.10}$$

3.1.2 Modelling the abundance relationship with Landings and Survey

Landings

So far we described the biological process model. Nevertheless, in order to understand the impact that the fisheries has on the population, we need to make some further assumptions on how the data we observe relates to the abundance. We start considering the Baranov equation, commonly referred to as Baranov catch equation, which describes the number of fish caught C_t in relation to fishing mortality F and total mortality Z, already described in the section above:

$$C_t = \frac{F_t}{Z_t} \cdot (1 - e^{-Z_t}) \cdot N_t \tag{3.11}$$

Fishing mortality can be split as a size component, the selectivity s, and a time component F_t:

$$F_t = F_t \cdot s \tag{3.12}$$

F_t is the fishing pressure applied to the population every year. It is assumed to have correlation between one year to the other. The term s is a vector of length l and represents the the fisheries selectivity. The following equation models the fishing selectivity as a logistic:

$$fsel_l = \frac{1}{1 + L50_{f\mathrm{sel}} \cdot \exp\left(-\beta_{f\mathrm{sel}} L\right)} \tag{3.13}$$

This equation is considered to represent a typical selectivity of a standard commercial vessel with a trawl gear. Modelling the selectivity as a logistic depending on length it means assuming that a fish of length 0 cm has 0 probability of being caught, and the probability increases with the size of the fish. The explanation for this is that fishermen prefer to use a mesh size large enough to catch only marketable fish and let the small ones escape through the mesh. The assumption here is that large fish are not able to escape the gear because the vessel will keep trawling for several hours, and in the end, exhausted, will end up in the net. Escaping to the side is unlikely, because the high amount of sediment that gets suspended by the mouth of the net are scary for the fish, which will keep swimming in front of the opening. This is probably the case for some fish species, but not for all of them. We decided to consider a second assumption for the fisheries selectivity that could be included in the model, that fishing selectivity looks as a gamma curve instead of a logistic. This curve also starts at 0 and increase up to a certain size of the fish, but then it decreases when the fish gets bigger. ICES assessment also chose this second version. The practical explanation of this second assumption is that a bigger fish is faster and more experienced, therefore more likely to escape the nets. The shape of the gamma is regulated by two parameters, the mode of the curve ($mode_f$) and the spread (α_f).

$$fsel_l = \frac{L}{\alpha_{fsel} - 1} \cdot \beta_{fsel}^{\alpha_{fsel}-1} \cdot exp\frac{\alpha_{fsel} - 1 - L}{\beta_{fsel}} \tag{3.14}$$

Where:

$$\beta_{fsel} = \frac{mode_{fsel}}{\alpha_{fsel} - 1} \tag{3.15}$$

Sampson & Scott (2012) has explored the shapes and stability of population-selection curves, reporting the dome shape curve as more frequent than other shapes. Now that we know all the components to calculate the catches C_t, we can define another important quantity, the discard D_t. The discard is that proportion of the catch that is being thrown back at sea, because of being too small or too damaged. D_t is a column vector of length l, with a logistic curve defined in terms of two parameters L_{50} and L_{25}:

$$dsel = \frac{1}{1 + L50_{dsel} \cdot \exp\left(-\beta_{dsel} L\right)} \tag{3.16}$$

The discard is shaped like a logistic because small fish have probability equal to 1 of being discarded (or 0 probability of being landed) and this probability gradually increases with size. This selectivity is parametrised in terms of L_{50} and L_{25} because it is more intuitive to assign two lengths as parameters (instead of a length and a steepness). As L_{50} it makes sense to pick the minimum landing size from the fisheries regulation, and as L_{25} maybe 10 or 15 cm less than that. Once the selectivity is defined, the discard numbers-at-length are equal to:

$$D_t = dsel \cdot C_t \tag{3.17}$$

Once we have defined what is thrown back at sea, we can define what is landed ($L_{l,t}$):

$$L_t = C_t - D_t \tag{3.18}$$

This quantity is the length frequency composition of the Landings, so in case data from fish market samples are available, this is a quantity that will be fitted. The vectors L_t and D_t, represent how many fish have been landed or discarded at that specific length on that specific time step. In order to obtain a value of total biomass for each time step, they need to be multiplied by the weight-length relationship W presented in equation 2.2 and summed over length classes:

$$LB_t = \sum_{i=1}^{l} L_t \cdot W; \qquad DB_t = \sum_{i=1}^{l} D_t \cdot W. \tag{3.19}$$

Survey

The fundamental source of information for SLAM are the compositional and abundance data from fisheries independent information, the scientific surveys. The survey is designed to take samples that resemble the real length distribution of fish in the sea as much as possible. The mesh size is smaller than the one used by commercial fisheries, in order to take a representative sample of the population length frequency. We assume that the logistic curve follows a logistic selectivity, starting at 0 for small fish and increasing progressively in size.

$$NSurv_t = N_t \cdot ssel \cdot q \tag{3.20}$$

$$ssel = \frac{1}{1 + \alpha_{ssel} \exp(-\beta_{ssel} L)} \tag{3.21}$$

$$SB_t = \sum_{y=1}^{y_{max}} NSurv_t \cdot W \tag{3.22}$$

Nevertheless, the survey trawling time is quite short, hauls of the ICES NS-IBTS only last half an hour, while a commercial trawler can trawl for hours. This might allow big and fast swimming fish to escape the survey more easily than a commercial fishing vessel. We then leave open the option to describe the survey selectivity as a gamma curve. The shape of the gamma is regulated by two parameters, the mode of the curve ($mode_{surv}$) and the spread (α_{surv}).

$$ssel = \frac{L}{\alpha_{ssel} - 1} \cdot \beta_{ssel}^{\alpha_{ssel}-1} \cdot exp\frac{\alpha_{ssel} - 1 - L}{\beta_{ssel}} \tag{3.23}$$

Where:

$$\beta_f = \frac{mode_f}{\alpha_f - 1} \tag{3.24}$$

Likelihood types

The type of likelihood depends on the type of data and how we assume those data are distributed. In SLAM we use two different types of data, total biomass of landings, survey and discard and length composition from the same sources (even though discard composition will not be used in this thesis, but they can be included by the user).

It is appropriate to assume that the total landed or surveyed biomass follows a log-normal distribution, therefore we chose to apply a lognormal likelihood. It has been applied in similar cases in the literature, even though instead of biomass they had been using CPUE (Maunder (2001); Cook et al. (2021)).

The log-normal distribution is not appropriate for compositional data. Even by assuming that the distribution around that certain length class of that certain year is log-normal, the model would not be able to cope with the many zeros that are commonly present in compositional data. Also, the model would need to calculate the likelihood for every length class of every year, making it too computationally expensive and inefficient. A better choice is the multinomial likelihood, which is the most widely used type of likelihood for length and age data. Nevertheless, multinomial distribution is not the most appropriate (Francis (2014); Thorson et al. (2017)). A strong limitation is that the multinomial assumes that the true proportion at length (or at age) is constant for all samples. This is not the case, because fish are not uniformly distributed in the sea because of schooling and size

segregation. Fish, like humans, tend to create groups where the size or age is uniform. This means that one single sample (a catch from a fishing vessel or a scientific survey) almost certainly will not be representative of the real population, at the exact same way if we want to sample a human population by going to a night club or a retirement home. In fact, set of length distribution does not look smooth, even if it comes from a large number of hauls. The choice of the sample size is very important and cannot be easily guessed. A low sample size will imply a low weight put on the length frequency data, while a high number will put a lot of weight. In the specific case of SLAM, a high sample size will favor the fit to the length frequencies and penalize the fit to the biomass, and the other way around.
Although choosing somewhat arbitrary effective samples sizes is not uncommon Hulson (2012), arbitrariness should be avoided whenever possible, and the literature offers different approaches (Francis (2011), Hulson (2012)). Hulson (2012) suggests a way to overcome the problem by iterating the model many times in order to find the value/s of the sample/s size that lead to the best fit. This approach, however, it is too computationally expensive for a rather complicated model like SLAM.
A possible solution to the problem is offered by Thorson et al. (2017), who introduces the Dirichlet-multinomial likelihood. By combining a Dirichlet with multinomial distribution, he overcomes the problem of the choice of the sample size by the introduction of a new parameter, $D\beta$, which indicate the dispersion of the sample. When the input sample size is increased, $D\beta$ compensates the excess by being reduced, and vice versa. I results, the model becomes less senstitive to the choice of the input sample size.
In this chapter we will apply to compositional data both multinomial and Dirichlet-multinomial likelihood, in order to evaluate which one works best.

Table 3.1: Table summarising all the parameters that can be used for SLAM. The first column stands for the type of parameter, if it is related to time, growth, survival, recruitment or if it is an error term. The second column specifies the abbreviation we attributed to the parameter. The third column provides a brief description of the parameter.

Table 3.1 – continued from previous page

Category	Abbreviation	Description
Time	y_{min}	minimum year present in the dataset
	y_{max}	maximum year present in the dataset
	n_{years}	number of years, used as a dimension for matrices
	Dt	timestep, in the current SLAM version is one year time step
Initial conditions	$NS1$	a single number indicating the size of the initial population
	$LF1_{\text{distr}}$	vector of probabilities indicating the shape of the length frequency of the initial population
Growth	l_{min}	minimum length class
	l_{max}	maximum length class
	n_{len}	number of length classes, length dimension in vector and matrices of the model
	DL	width of length classes
	L_{inf}	infinite length of the Von Bertalanffy growth curve
	K	steepness of the Von Bertalanffy growth curve
	cv	coefficient variation of the growth
	α_{wgt}	alpha of the weight length conversion
	β_{wgt}	beta of the weight length conversion
	w	conversion factor from gutted to ungutted weight
Survival	Ft	vector of length n_{years} with time series of fishing mortality values
	$L50_{\text{fsel}}$	L_{50} of the logistic curve of fishing selectivity
	β_{fsel}	β of the logistic curve of fishing selectivity

Continued on next page

Table 3.1: Table summarising all the parameters that can be used for SLAM. The first column stands for the type of parameter, if it is related to time, growth, survival, recruitment or if it is an error term. The second column specifies the abbreviation we attributed to the parameter. The third column provides a brief description of the parameter.

Table 3.1 – continued from previous page

Category	Abbreviation	Description
	α_{ssel}	spread of the gamma fisheries selectivity
	$mode_{\text{ssel}}$	mode of the gamma fisheries selectivity
	pD	proportion discarded every year, on a logit scale
	$L50_{\text{ssel}}$	L_{50} of the logistic survey selectivity
	β_{ssel}	β of the logistic survey selectivity
	q	survey catchability
	α_{ssel}	spread of the gamma survey selectivity
	$mode_{\text{ssel}}$	mode of the gamma survey selectivity
	α_M	α of Lorenzen natural mortality curve
	β_M	β of Lorenzen natural mortality curve
Recruitment	Rt	a vector of length n_{years} that indicates total recruitment
	μ_{Rt}	Mean length of the recruitment (1 year old fish)
	σ_{Rt}	Standard deviation of the recruitment length
Error terms	σ_{Ft}	log-normal standard error of Ft
	σ_{pD}	log-normal standard error of pD
	σ_{sbiom}	log-normal error term of survey biomass
	σ_{lbiom}	log-normal error term of landings biomass
	σ_{dbiom}	log-normal error term of discard biomass
	$D\beta_{\text{surv}}$	dispersion term of the Dirichelet-Multinomial for the landings
	$D\beta_{\text{land}}$	dispersion term of the Dirichelet-Multinomial for the survey
	σ_{Ft}	log-normal standard error of Ft
	σ_{pD}	log-normal standard error of pD
	σ_{sbiom}	log-normal error term of survey biomass

3.1.3 Stan and the NO-U-Turn Sampler (NUTS) algorithm

SLAM is fitted using Bayesian statistics. The algorithms used in Bayesian statistics tend to be very complicated and slow. To speed up the process, we fitted the model using the software Stan, that is available with an R interface in the package rstan Carpenter (2015). Stan is written is C++ and is a state-of-the-art platform for statistical modeling and thousands of users utilize it for statistical modeling, data analysis, and prediction in many different fields. Stan's high-performance statistical computation makes it rather commonly used in stock assessment, as well as many other ecological fields. Other Bayesian software like BUGS (Spiegelhalter et al. (1996)) and JAGS (`http://mcmc-jags.sourceforge.net`) rely on the classic Markov chain Monte Carlo (MCMC) as a sampling algorithm, but it is very computationally expensive and the time runs for complicated models are prohibitive. Stan uses Hamiltonian Monte Carlo (Neal (2011)), a new family of MCMC algorithm that promises improved efficiency (Brooks et al. (2011)). Neal (2011) provides a good introduction to Hamiltonian Dynamics. HMC has the advantage of efficiently exploring high-dimensional parameter spaces, as it employs gradient information to make intelligent proposals. However, HMC can encounter issues like slow exploration and wasted computation due to rejections. Tuning an HMC sampler in a way that can prevent this to happen require expert hands-on tuning and a priori knowledge (Neal (2011)). Fortunately, Stan does not have this problem because it adopted the NO-U-Turn Sampler (NUTS) algorithm developed by Hoffman et al. (2015). The No U-Turn Sampler (NUTS) addresses these problems by automatically determining the appropriate number of Hamiltonian dynamics steps to take, resulting in a more efficient exploration of the parameter space. NUTS automates this process and provides efficient sampling with minimal or no manual tuning, improving the HMC performance and providing faster convergence (Monnahan et al. (2017)).

3.2 Material and Methods

To check if the Survey-LAnding Model (SLAM) was working as expected, we used it as an operating model to generate data and fit the model to them. The biomass data were perturbed with an error term, one per each: σ_{sbiom}, σ_{lbiom} and σ_{dbiom}. The error is described mathematically in chapter II in equation 2.1. The parameters used to generate the data for each of the two SLAM version are reported in the tables 3.2 and 3.3 as well as the priors and the initial values used. The majority of the priors used were uninformative and centered on the real value with relaxed boundaries. The prior of Ft_1 was set to uniform and the priors of the following years have a lognormal prior centered on the estimate of Ft of the year before. This is because it is assumed that fishing pressure is correlated from one year to the other. The model was fit by running 30,000 iterations with a thinning rate of 300.

Testing the model on only one set of data it is not enough to undestand if the model is subject to systematic bias. Therefore, both for “full model” both for “survey only” we iterated the model 25 times on different sets of pseudo data generated by the same parameters. The model was run every time with the same set of priors, initial values, number of iterations and thinning rate.

3.2.1 Full model

We decided to test SLAM in a data rich situation, with survey biomass and proportions-at-length, landings biomass and proportions-at-length and discard biomass. It is actually not entirely the “full” model, since we did not include the discard proportions-at-length. We did not have any we did not have any data availability from this source. Therefore, within this manuscript it is justifiable to address this version as the full model. The model assumes both the fisheries, the survey and the discard have a logistic selectivity, and fits the proportions at length with a multinomial likelihood. In the results we will show how the use of a Dirichlet-multinomial likelihood can improve the fit when the correct sample size is not known. In the following table we report the true parameters and the type of prior used.

Table 3.2: Table summarising the fixed and fitted parameters used on the full version of SLAM tested on pseudo data. The first column indicates the category, the second the starting value (in the case the parameter was fitted) or the actual fixed value (if the parameter was fixed). The third column specifies if the parameter was fitted and if so what type of prior and what kind of bounds have been set.

Table 3.2 – continued from previous page

Abbreviation	Value	Description
y_{min}	1	fixed
y_{max}	24	fixed
n_{years}	24	fixed
Dt	1	fixed
$NS1$	2670	derived from q, $L50_{ssel}$ and β_{ssel}
$LF1_{\text{distr}}$	fig. 3.2	$Dirichlet \sim (1)$
l_{min}	1	fixed
l_{max}	53	fixed
n_{len}	53	fixed
DL	1	fixed
L_{inf}	53	$lognormal \sim (50; 15)$
K	0.2	$uniform \sim (0.01; 0.9)$
cv	0.1	$uniform \sim (0.01; 0.9)$
α_{wgt}	0.008	fixed
β_{wgt}	250	fixed
w	1	fixed
Ft	fig. 3.1	first year has a uniform prior, later years have a log-normal prior with $\mu = Ft_{t-1}$
$L50_{\text{fsel}}$	18	$uniform \sim (10; 30)$
β_{fsel}	0.25	$uniform(0; 1)$
$L50_{\text{ssel}}$	12	$uniform \sim (5; 20)$
β_{ssel}	0.4	$uniform(0; 1)$
$L50_{\text{dsel}}$	30	fixed
β_{dsel}	0.3	fixed
q	0.9	$uniform \sim (0; 2)$
α_M	0.1	fixed
β_M	-0.3	fixed
Rt	fig 3.1	$uniform \sim (2; 2000)$
μ_{Rt}	10.5	$uniform \sim (5; 20)$
σ_{Rt}	1	$uniform \sim (0.1; 20)$
σ_{Rt}	-	$uniform \sim (0; 2)$
σ_{sbiom}	0.3	$uniform \sim (0; 1)$
σ_{lbiom}	0.3	$uniform \sim (0; 1)$

Continued on next page

Table 3.2: Table summarising the fixed and fitted parameters used on the full version of SLAM tested on pseudo data. The first column indicates the category, the second the starting value (in the case the parameter was fitted) or the actual fixed value (if the parameter was fixed). The third column specifies if the parameter was fitted and if so what type of prior and what kind of bounds have been set.

Table 3.2 – continued from previous page

Abbreviation	Value	Description
σ_{dbiom}	0.3	$uniform \sim (0;1)$
$D\beta_{\text{surv}}$	-	$uniform \sim (0;1000)$
$D\beta_{\text{land}}$	-	$uniform(0;1000)$
n_{land}	100	fixed
n_{surv}	100	fixed

3.2.2 Survey only

The following table summarises all the parameters used in the survey only version, their true value and whether they were kept fixed or they were estimated, and if they were estimated what kind of prior was used. In the survey only version the model has only the survey data which are on a much smaller scale than the fisheries. Therefore, the model will not be able to estimate the real size of the population. Moreover, the model will not be able to estimate the catchability of the survey q, which reflects the efficiency of the survey in sampling the population. The model must then be fitted by fixing q to 1. The same can be said for the survey and fisheries selectivity. The model cannot estimate both selectivity at the same time, therefore we must keep fixed one of the two. By keeping the fisheries selectivity fixed the model would probably be able to estimate well both parameters of the selectivity, let this selectivity have a gamma or a logistic shape. Nevertheless, estimating the survey selectivity parameters is not as meaningful as estimating the fisheries selectivity parameters. Not having any information at all regarding any proportions-at-length coming from the fisheries though, it is unlikely that the model will be able to estimate both parameters, therefore we decided to keep one of the two fixed. In this survey only version we decided to try a gamma curve for fisheries selectivity, indicated by the parameters α_{fsel}, the spread, and $mode_{fsel}$, the peak of the dome. Therefore the mode and the spread estimated. The parameter

α_{fsel} required the use of an informative prior.

This version is less powerful in estimating parameters, because there is no information from the fisheries. Nevertheless, the model will still be able to provide a decent estimate of the trends of meaningful quantities, which might not be precise, but is as far as we can get with the information available.

Table 3.3: Table summarising the fixed and fitted parameters used on the survey only version of SLAM tested on pseudo data. The first column indicates the category, the second the starting value (in the case the parameter was fitted) or the actual fixed value (if the parameter was fixed). The third column specifies if the parameter was fitted and if so what type of prior and what kind of bounds have been set.

Table 3.3 – continued from previous page

Abbreviation	True value/s	Prior
y_{min}	1	fixed
y_{max}	24	fixed
n_{years}	24	fixed
Dt	1	fixed
$NS1$	2670	$lognormal \sim (5.37; 0.9)$
$LF1_{\text{distr}}$	fig. 3.2	$Dirichlet \sim (1)$
l_{min}	1	fixed
l_{max}	53	fixed
n_{len}	53	fixed
DL	1	fixed
L_{inf}	53	$lognormal \sim (50; 15)$
K	0.2	$uniform \sim (0.01; 0.9)$
cv	0.1	$uniform \sim (0; 1)$
α_{wgt}	0.008	fixed
β_{wgt}	250	fixed
Ft	fig 3.1	first year has a uniform prior, later years have a log-normal prior with $\mu = Ft_{t-1}$
α_{fsel}	3	$lognormal \sim (\log(2.4); 0.2)$
$mode_{\text{fsel}}$	25	fixed
α_{ssel}	3	fixed
$mode_{\text{ssel}}$	27	fixed
$L50_{\text{dsel}}$	30	fixed
β_{dsel}	0.3	fixed
q	1	fixed
α_M	0.1	fixed
β_M	-0.3	fixed
Rt	fig 3.1	$loguniform \sim (\log(2); \log(2000))$
μ_{Rt}	10.5	$uniform \sim (5; 20)$

Continued on next page

Table 3.3: Table summarising the fixed and fitted parameters used on the survey only version of SLAM tested on pseudo data. The first column indicates the category, the second the starting value (in the case the parameter was fitted) or the actual fixed value (if the parameter was fixed). The third column specifies if the parameter was fitted and if so what type of prior and what kind of bounds have been set.

Table 3.3 – continued from previous page

Abbreviation	True value/s	Prior
σ_{Rt}	1	$uniform \sim (0.1; 20)$
σ_{Rt}	estimated	$uniform \sim (0.1; 2)$
σ_{Rt}	0.3	$uniform \sim (0; 1)$
$D\beta_{\mathrm{surv}}$	estimated	$uniform \sim (0; 1000)$

3.3 Results

These first results show how the model fitted in the “full-version” was able to retrieve the psedo-data generated running SLAM as an operating model. In this run we are fitting the length frequency data with a multinomial likelihood and the value of the sample size is the same used for generating the data.

The first set of graphs presented in 3.1, shows how the model fits survey, landings and discard biomass, the data are disposed as black dots. The rest of the plots represent the real values of fishing mortality, recruitment and Spawning Stock Biomass (SSB). The real values are presented as ×. The dark line is the model output median and the polygon around it is the 95 credible intervals. We observe as the model fits the data well and can also provide good estimates of Spawning Stock Biomass (SSB), fishing mortality and recruitment, as almost all the points lies between the intervals. The trace plots and histograms of the posteriors for the parameters q, $L50_{ssel}$, β_{ssel}, $L50_{fsel}$, β_{fsel}, μ_R, σ_R, K and L_∞ do not show any particular problem, and can be seen in appendix Chapter III.

The next two plots in 3.2 show the model estimates of the proportions-at-length of the initial population $LF1$ and the recruitment. The symbols × represent the real values, the thick central line is the model median and the shaded area are the credible intervals. The model was able to estimate the values well, and in the case of recruitment proportions-at-length with very low uncertainty.

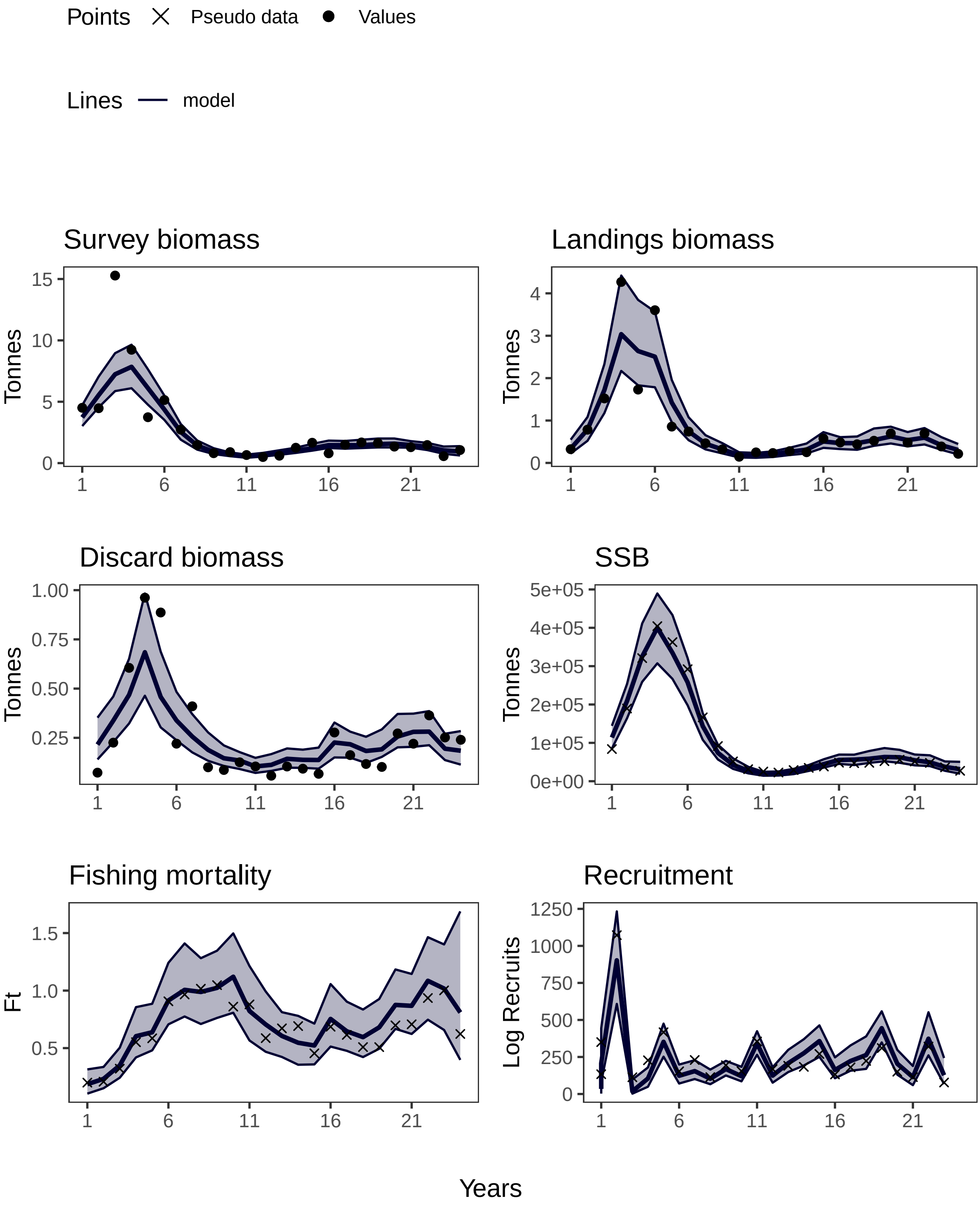


Figure 3.1: The following figures display the model estimates of survey biomass, landings biomass, discard biomass, spawning stock biomass, fisheries mortality and recruitment. The black dots represent the pseudo data that the model is fitting, while the × are the estimated quantities. The central line is the median of the model of the estimates and the shaded area around are the 95% credible intervals.

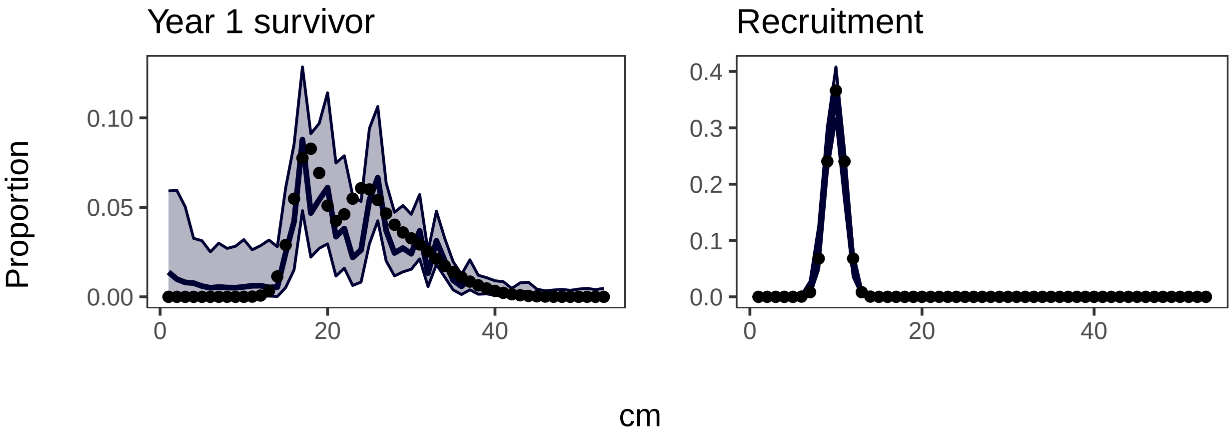


Figure 3.2: The figure shows the model estimates of the proportions-at-length for the initial population ($LF1$) and the proportions at length of the recruitment. The black dots represent data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The model was able to estimate the all the values correctly.

Figure 3.3 and 3.4 show how the model fits the proportions-at-length of survey and landings respectively. The graphs are disposed in a grid where each single plot represents one year. The black dots represent the data, the thick central line is the model median and the credible intervals around it are really thin, meaning the model fits the data with low uncertainty.

3.3.1 Sensitivity to the Effective Sample Size

The choice of the sample size is know to be critical in stock assessment model when using a multinomial likelihood. Therefore, we decided to test the sensitivity of the model to this value. In figure 3.5 we compare the previous model run, where the two input sample sizes were equal to 100 (the same value used to generate the data), with a new run where the two effective sample sizes were raised to to 1000. The output of the run with the correct value is presented with the dark line, while the other in red. The estimates of fishing mortality appear to be quite different, even though the trends are still picked up and the difference is not drastic. The fit to survey and landings biomass does not seem to be particularly affected, differently from the discard biomass. The estimates of recruitment and spawning stock biomass are not particularly affected.

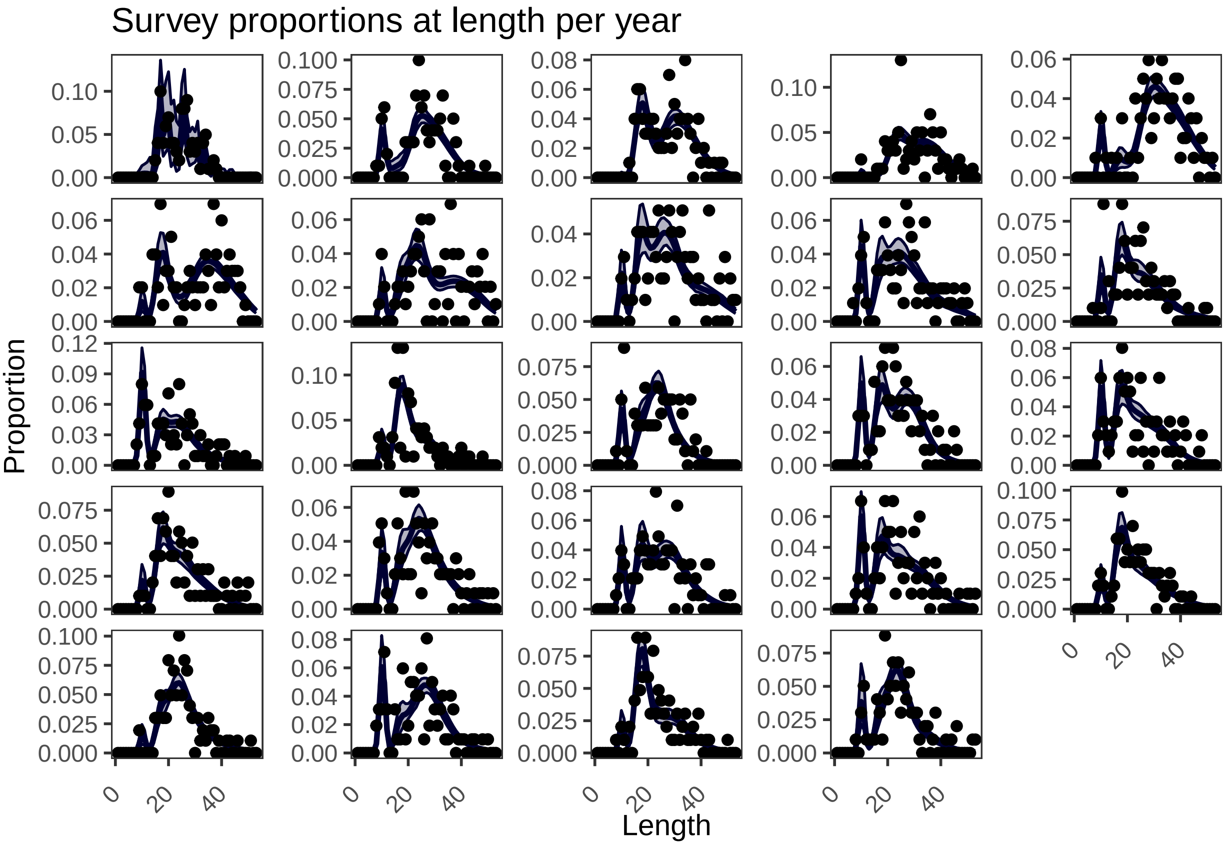


Figure 3.3: The figure shows a series of yearly plot of survey proportions at length. The black dots represent data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The model fits well the data.

In the next two sets of plots, 3.6) and 3.7), we observe the fit of the two models to landings and survey proportions-at-length. The model does not look particularly sensitive to the sample size in this case, and the red and the black line are overlapping almost at every point.

Despite these tests on pseudo data did not reveal a high sensitivity to the choice of the sample size, we still decided to implement the Dirichlet-multinomial likelihood, because when dealing with real data the situation gets more complicated and the model could become more sensitive.

3.3.2 Implementation of the Dirichlet-multinomial likelihood

In order to remove the sensitivity to the effective sample size, we replaced the multinomial likelihood with a Dirichlet-multinomial likelihood as described by

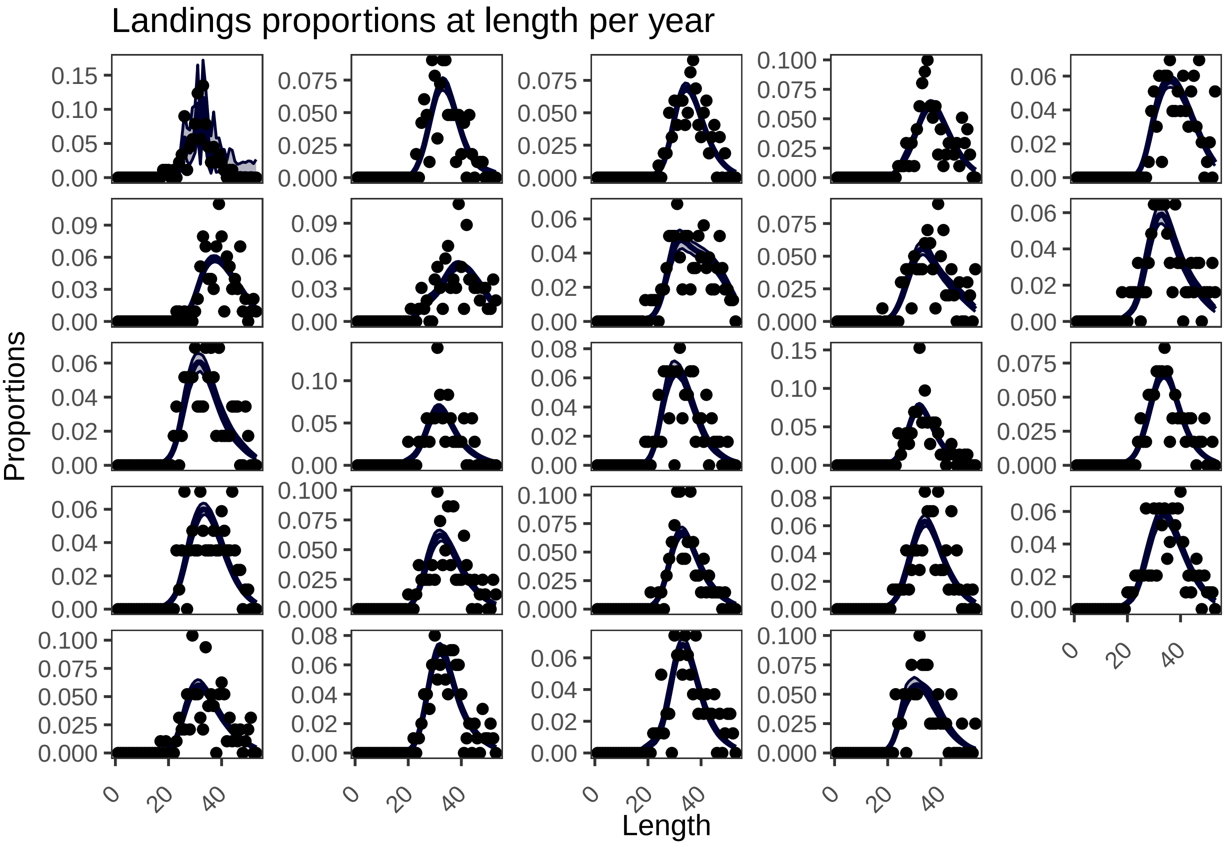


Figure 3.4: The figure shows a series of yearly plot of landings proportions at length. The black dots represent data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The model fits well the data.

Thorson et al. (2017). In 3.8 we see the fit to survey, landings and discard biomass, and the estimates of fishing mortality, recruitment and Spawning Stock Biomass. The black line is the model run with $n_{eff} = 100$ while the red line $n_{eff} = 1000$, for both survey and landings. The data are presented as black dots and the real values of Ft, Rt and SSB with the symbols ×. The dark and the red line are almost completely overlapping so it looks as if the Dirichlet-multinomial likelihood managed to reduce the model's sensitivity to the sample size.

Similarly, in the next two sets of plots 3.9 and 3.10 presenting landings and survey proportions-at-length, the red and the black line are almost completely overlapping, meaning the model is not sensitive to the sample size.

The histograms in figure 3.11 represent the posterior distributions of the Dirichlet β parameters, $D\beta$. The top ones were run with effective sample size equal to

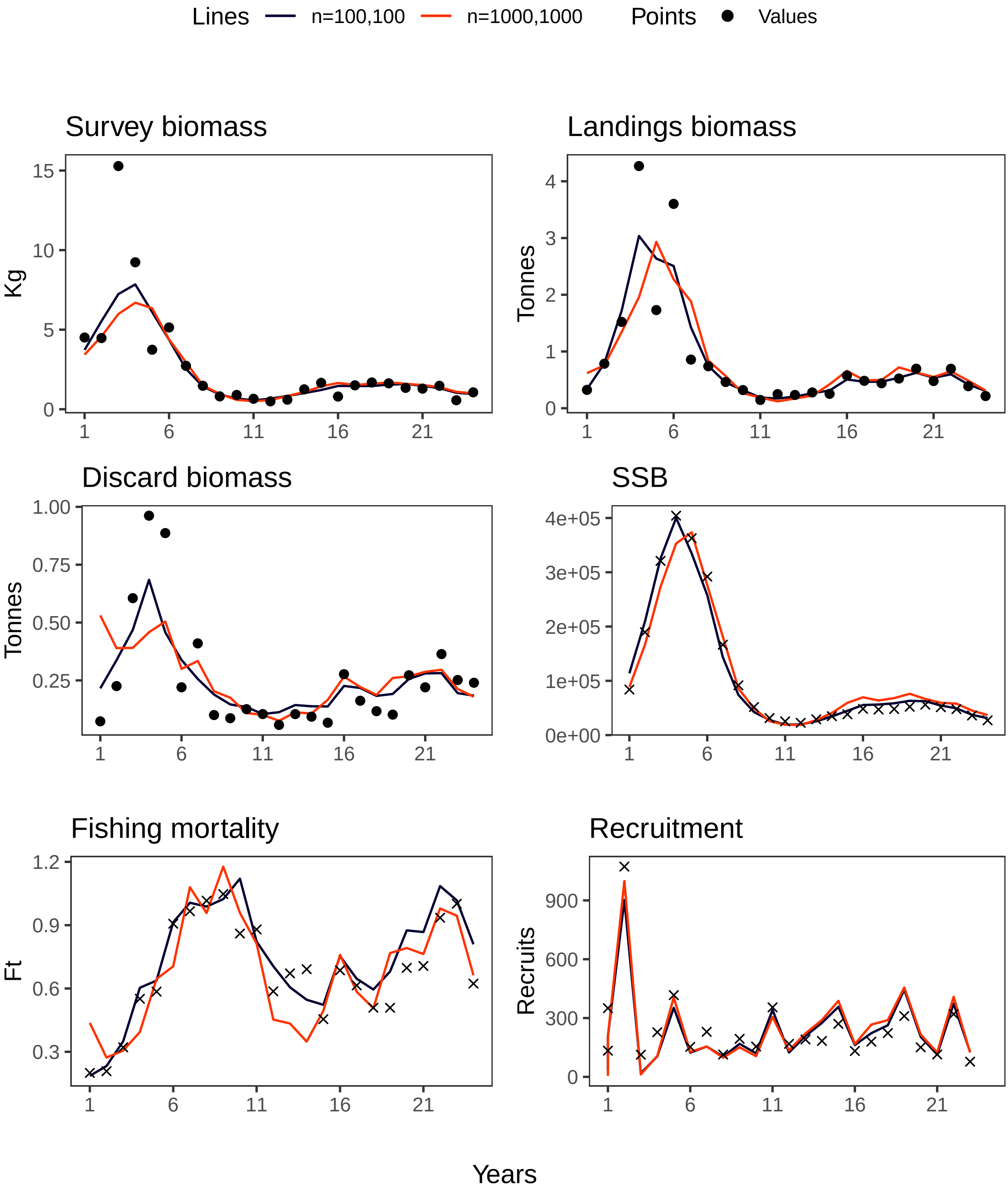


Figure 3.5: The following figures display the median of the model estimates when the sample size for the survey and the landings is set to the true value in dark blue (n_{land} and $n_{surv} = 100$) and when it is set to a much higher value in red (n_{land} and $n_{surv} = 1000$). The plot displays the estimates for survey biomass, landings biomass, discard biomass, spawning stock biomass, fisheries mortality and recruitment. The symbols × represent the actual data the model is being fitted to, while the black dots are estimates calculated by the space assessment model. The difference between the two models is not dramatic, even though there is some difference in the estimates of some values, especially fisheries mortality.

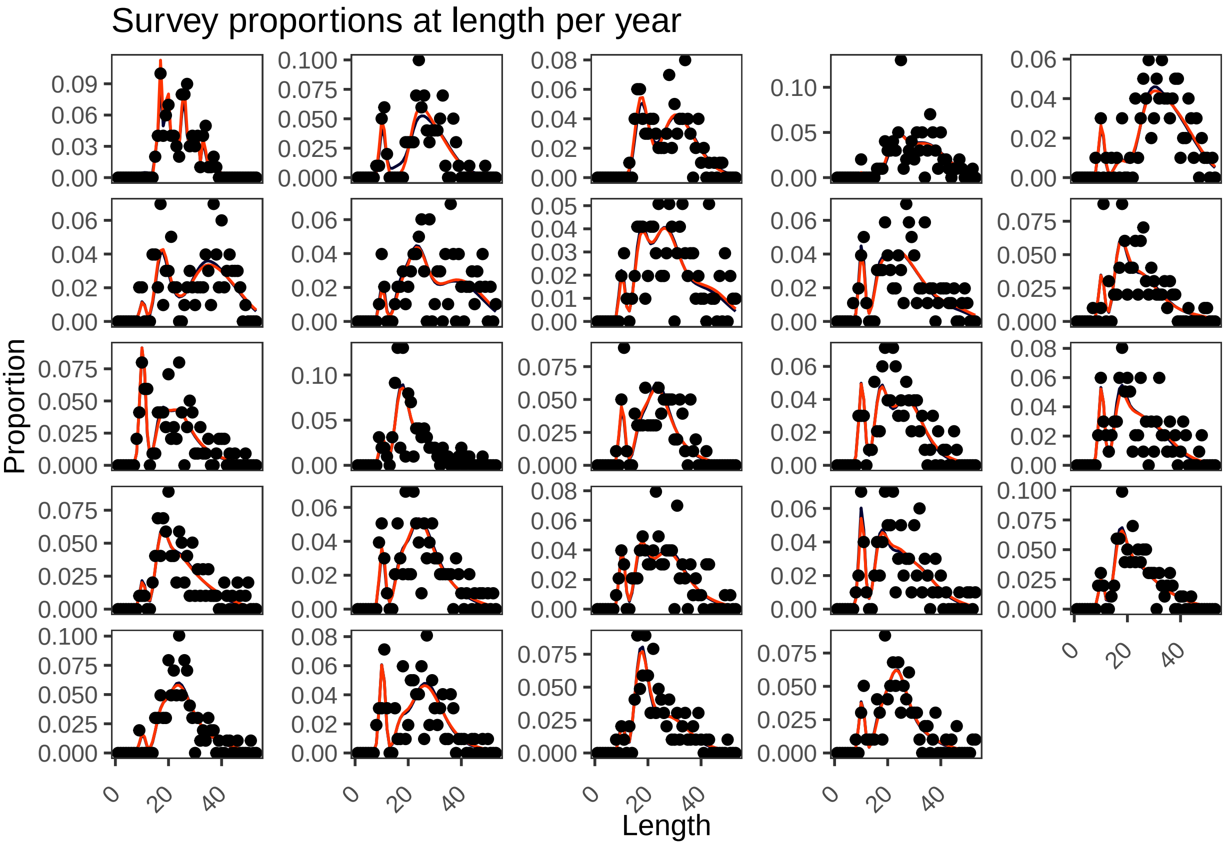


Figure 3.6: The figure shows a series of yearly plot of landings proportions at length. The dark line represents the median of the estimates for the proportions-at-length when the sample size corresponds to the true value (n_{land} and n_{surv} = 100) and when the sample size is set to a much higher value in red (n_{land} and n_{surv} = 1000).The black dots are pseudo data. We observe that the lines are close and the model does not seem to be sensible to this assumption when estimating the proportions-at-length.

100, while the bottom ones with sample size equal to 1000. The left histograms represent the posterior for the survey β and the right ones for the fisheries β. We observe how when the sample size is increased respect to the right value, the parameter β compensates the excess by being reduced.

Since this modification was proved to be effective, we decided to adopt the Dirichlet-multinomial for SLAM. The rest of the run from here on wards have this implementation.

3.3.3 Check for bias in "full model"

In this and the next section we present the results of the test we made to see if the full model was biased. The first box plots we present (3.12), represent the

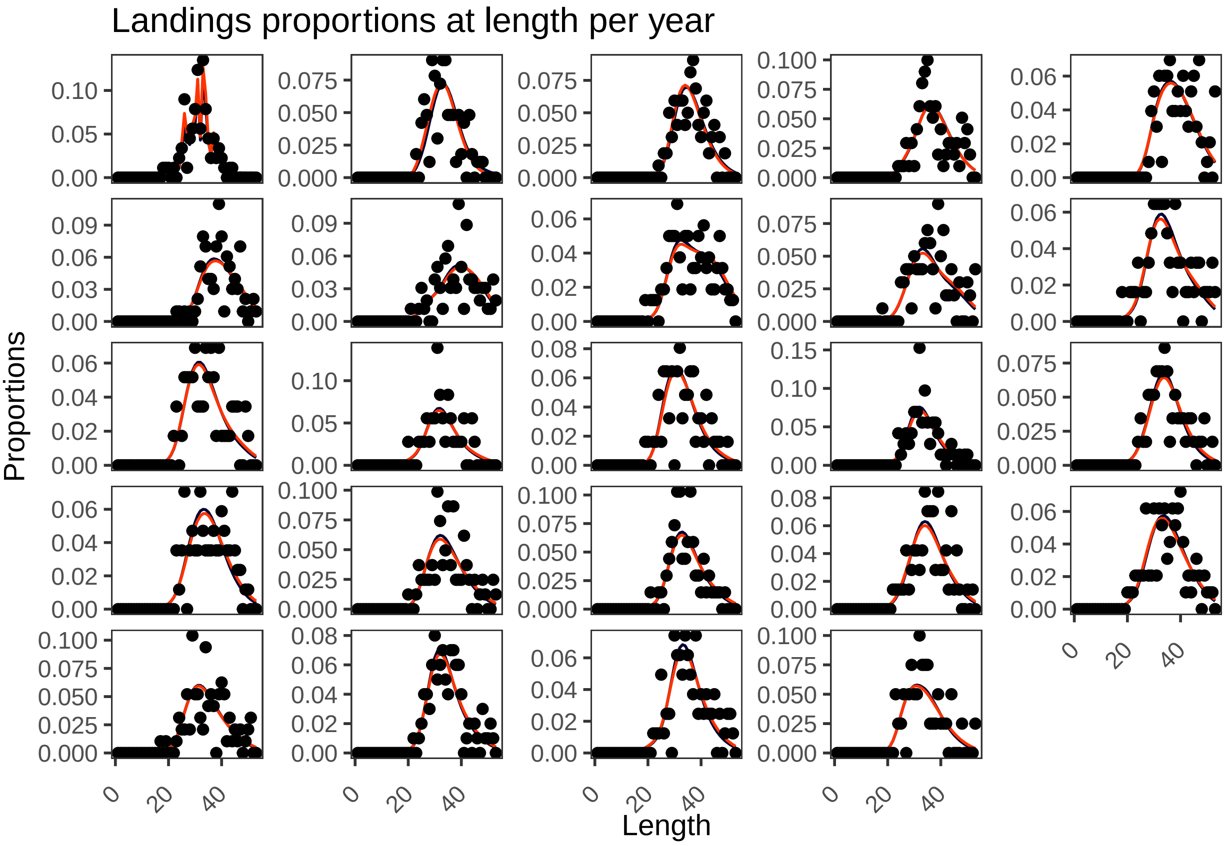


Figure 3.7: The figure shows a series of yearly plot of landings proportions at length. The dark line represents the median of the estimates for the proportions-at-length when the sample size corresponds to the true value (n_{land} and n_{surv} = 100) and when the sample size is set to a much higher value in red (n_{land} and n_{surv} = 1000).The black dots are pseudo data. We observe that the lines are close and the model does not seem to be sensible to this assumption when estimating the proportions-at-length.

median values of the 25 different runs on 25 different survey, landings and discard biomass pseudo data. The real values (black dots), were perturbed every time with 3 constant error terms, a different one for each set of data (σ_{sbiom}, σ_{dbiom}, σ_{lbiom}). The central values of the box is the median of the medians and the upper and lower bounds are the highest and the lowest medians generated by the model. We can observe how all the parameters lie in the grey area, meaning that the model fits all the data without bias.

We will now see if SLAM is able to retrieve the parameters used to generate the pseudo data. The first box plot in figure (3.13) shows the median, the maximum and the minimum values calculated by SLAM for the parameters: q, β_{ssel}, β_{fsel}, σ_R, K, cv, σ_{sbiom} and σ_{dbiom}. The parameters

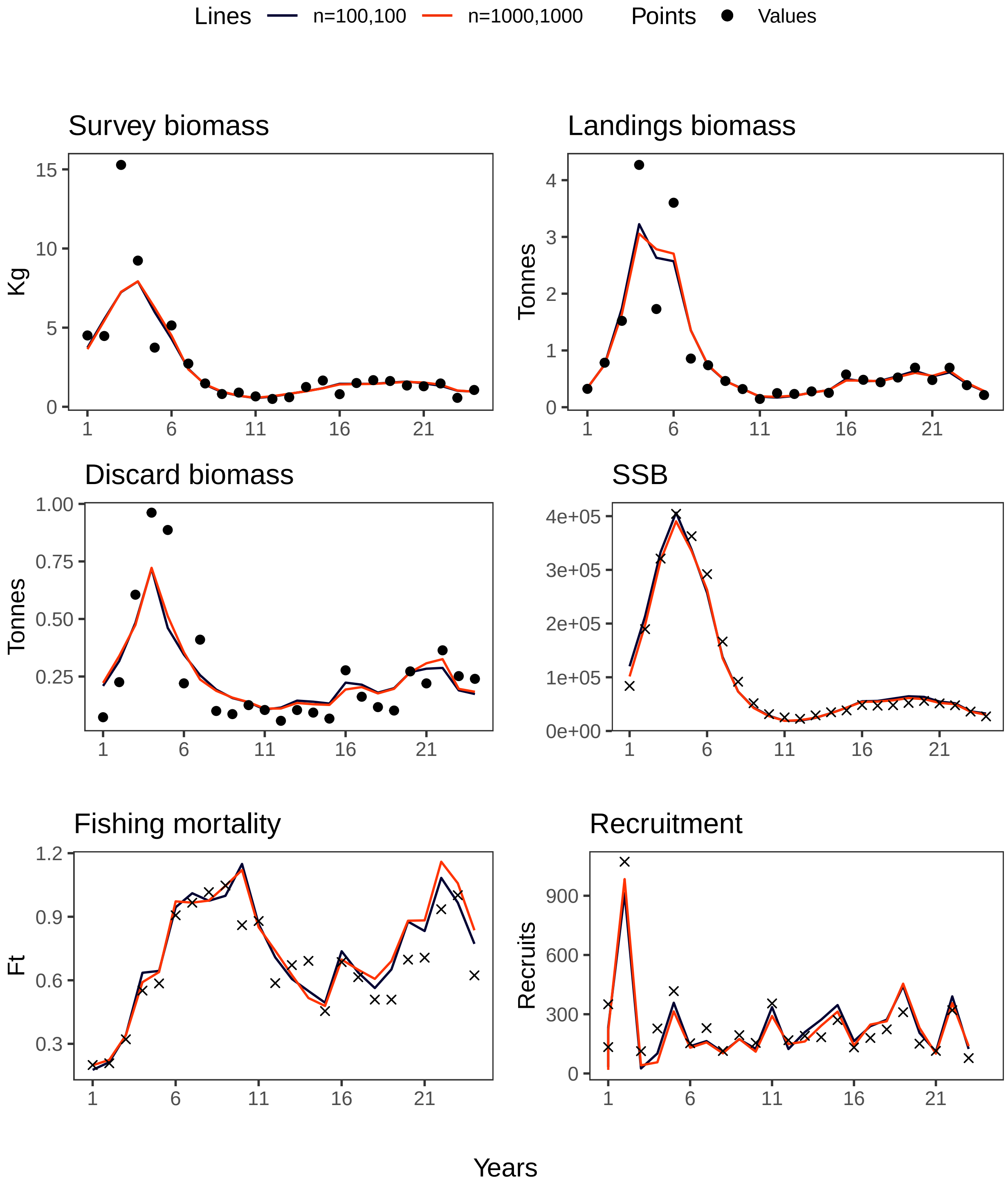


Figure 3.8: The following figures display the median of the model estimates when the sample size for the survey and the landings is set to the true value in dark blue (n_{land} and $n_{surv} = 100$) and when it is set to a much higher value in red (n_{land} and $n_{surv} = 1000$). The plot displays the estimates for survey biomass, landings biomass, discard biomass, spawning stock biomass, fisheries mortality and recruitment. The x represent the actual data the model is being fitted to, while the black dots are estimates calculated by the space assessment model. We observe that the lines are close and the model does not seem to be sensible to this assumption.

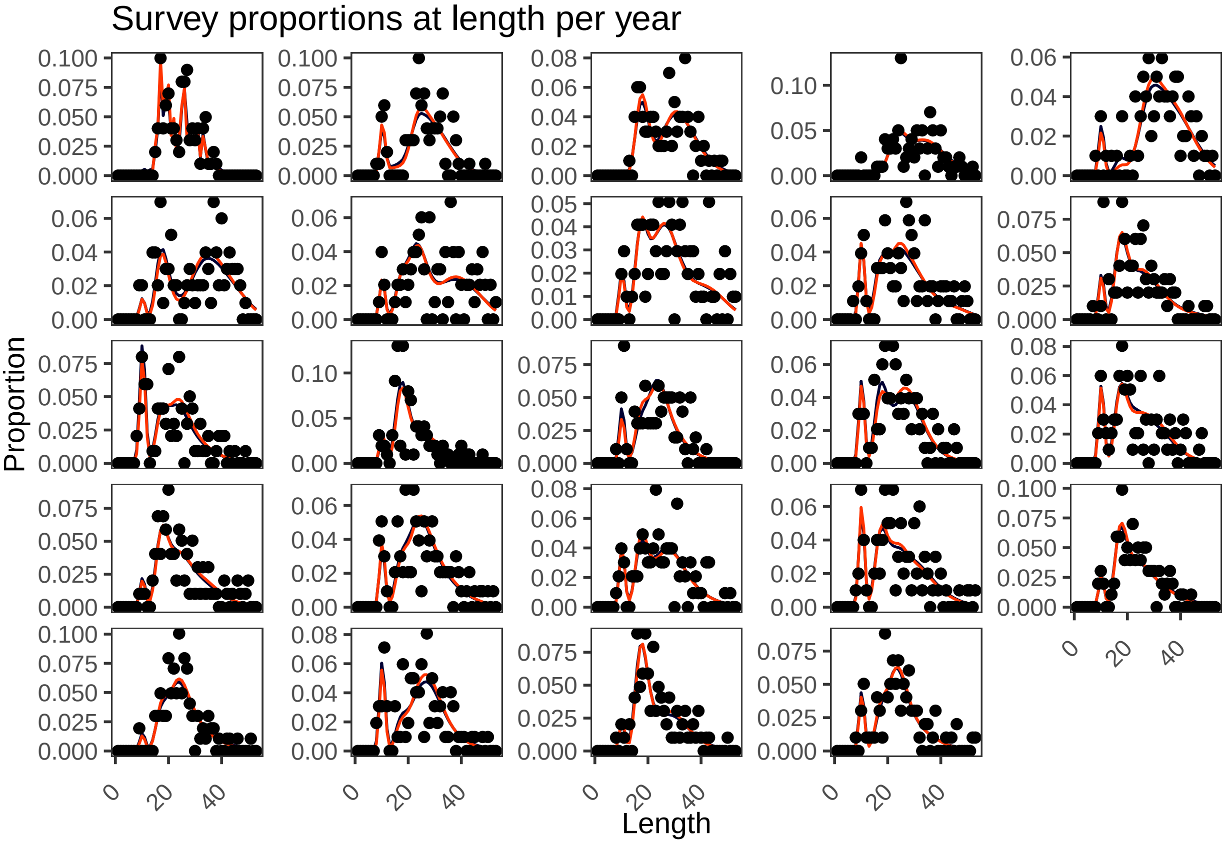


Figure 3.9: The figure shows a series of yearly plot of landings proportions at length. The dark blue line represents the median of the estimates for the proportions-at-length when the sample size corresponds to the true value (n_{land} and $n_{surv} = 100$) and when the sample size is set to a much higher value in red (n_{land} and $n_{surv} = 1000$).The black dots are estimates calculated by the space assessment model. We observe that the line are close and the model does not seem to be sensible.

mu_R, $L50_{fsel}$, $L50_{ssel}$ and L_∞ have been grouped in the second box plot (3.14) for scaling reasons. In both graphs, the symbols × indicate the real value for each parameter. We observe how the model manages to retrieve well all the parameters, except for a slight overestimation of the slope of the logistic curve of the survey selectivity.

The last figure of this paragraph (3.15) shows three similar box plots with fisheries mortality, recruitment and SSB. SLAM managed to retrieve correctly all the parameters of recruitment and fishing mortality and the generated quantity SSB. For all points the symbol × lies ot just outside of it. The only really biased value seems to be the first year of recruitment, which is underestimated.

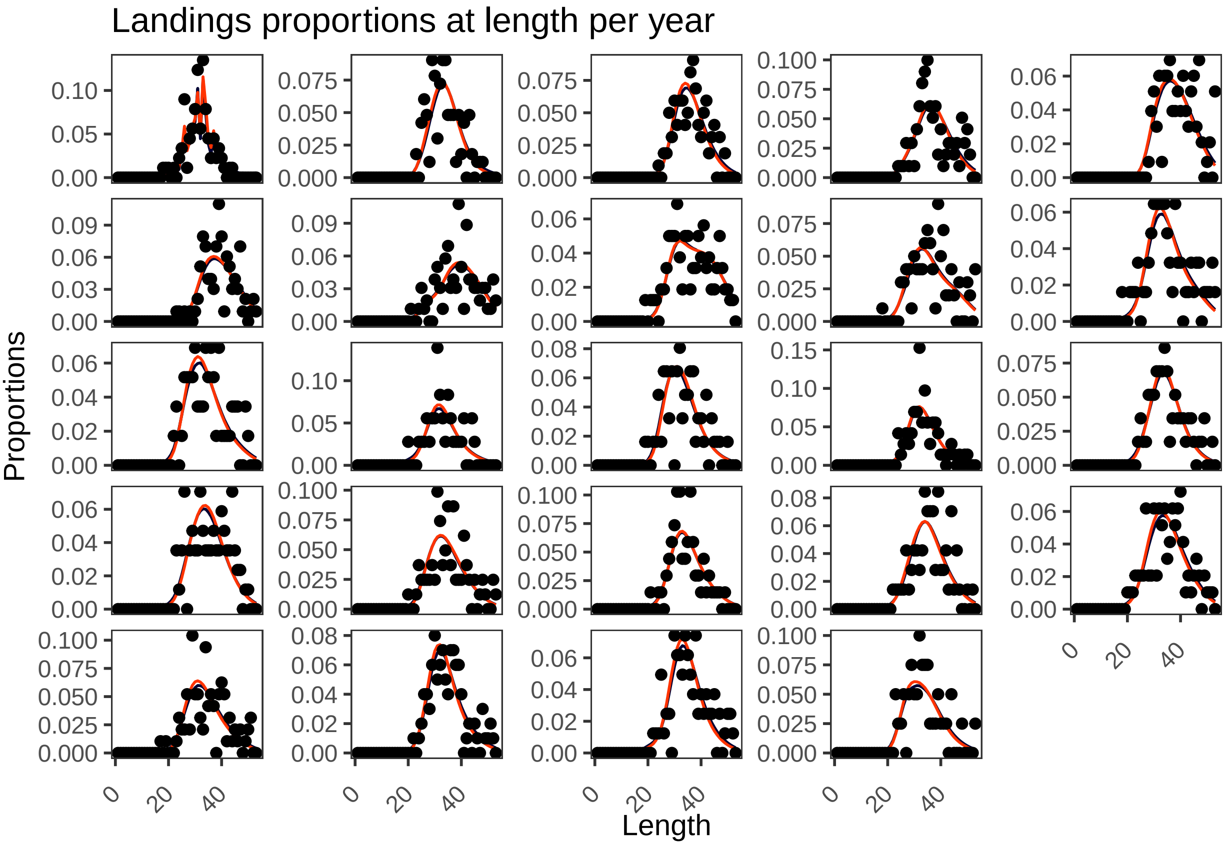


Figure 3.10: The figure shows a series of yearly plot of landings proportions at length. The dark blue line represents the median of the estimates for the proportions-at-length when the sample size corresponds to the true value (n_{land} and $n_{surv} = 100$) and when the sample size is set to a much higher value in red (n_{land} and $n_{surv} = 1000$).The black dots are estimates calculated by the space assessment model. We observe that the line are close and the model does not seem to be sensible.

3.4 Survey only model

This session will present the Survey-LAndings Model (SLAM) fitted in its survey only version to pseudo data of survey biomass and proportions-at-length. The trace plots and histograms of the posteriors for the parameters μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, σ_{Ft} and NS_1 do not show any particular problem, and can be found in appendix Chapter III. 3.16 shows the fit to survey biomass and the estimates of spawning stock biomass, fisheries mortality and recruitment. Data are represented as black dots, while real values used for comparison are indicated with the symbol ×. The dark line is the model output median and the polygon around it is the 95 credible intervals. We observe as the result is quite satisfactory as almost all the

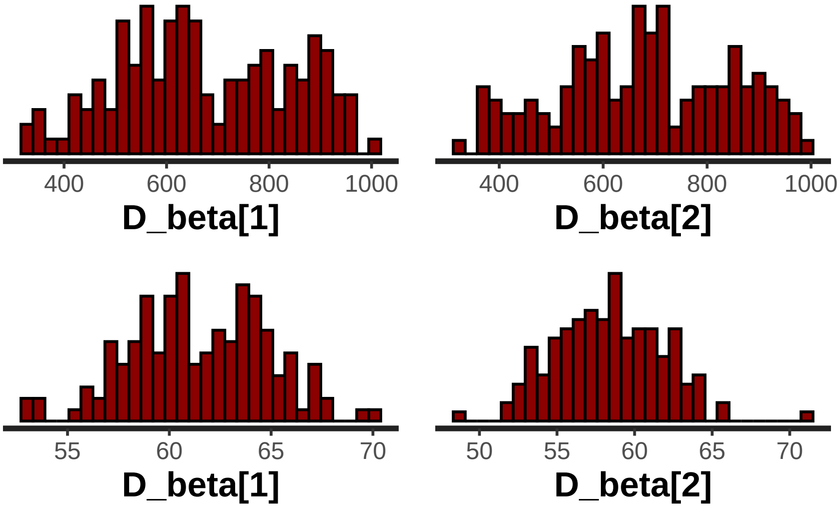


Figure 3.11: The four histograms shows the posterior distribution of the posterior parameters $D\beta_s$, on the left, and $D\beta_l$ on the right. The top histograms were run with the two values of sample size set to 100 (the true value), while the bottom ones were run with effective sample size set to 1000. We observe how the parameter $D\beta$ compensate the excess in sample size by being reduced.

points lies between the intervals. The only parameters that might be biased are the first year recruitment and the first two years of spawning stock biomass.

The two plots in 3.17 show the model estimates of the proportions-at-length of the initial population $LF1$ and the recruitment. The symbols × represent the real values, the thick central line is the model median and the shaded area are the credible intervals. The model was able to estimate the values well, and in the case of recruitment proportions-at-length with very low uncertainty.

3.18 shows how the model fits the proportions-at-length of surveys. The graphs are disposed in a grid where each single plot represents one year. The black dots represent the data, the thick central line is the model median and the credible intervals around it are very thin, meaning the model fits the data with really low uncertainty.

3.4.1 Check for bias in "survey only"

We are now going to check if the survey only model is biased. In 3.19 is shown a box plot of the median values of the 25 different runs on 25 different survey biomass pseudo data. The real values (black dots), were perturbed every time

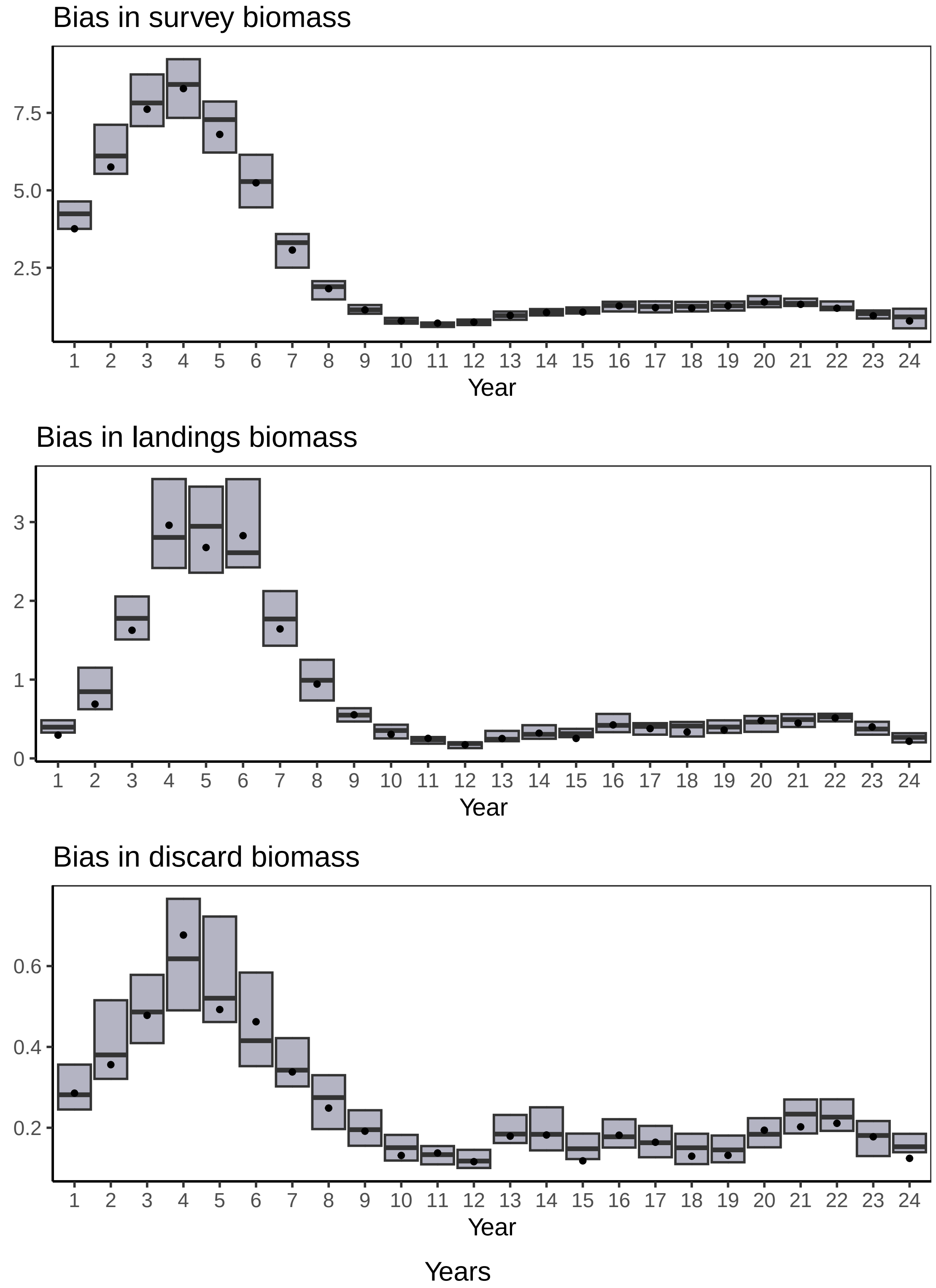


Figure 3.12: The boxplot at the top shows the bias in the yearly values of survey biomass, the one at the centre shows the bias in the yearly values of landings biomass and the one at the bottom shows the bias in the yearly values of landings biomass. In every boxplot, the central value of each box shows the median values, the upper is the maximum value estimated by the model and the lower is the minimum. The dots represent the true values. The model fits the pseudo data ok. We run it for 25 times and fitted every time to a different set of data perturbed with a random error.

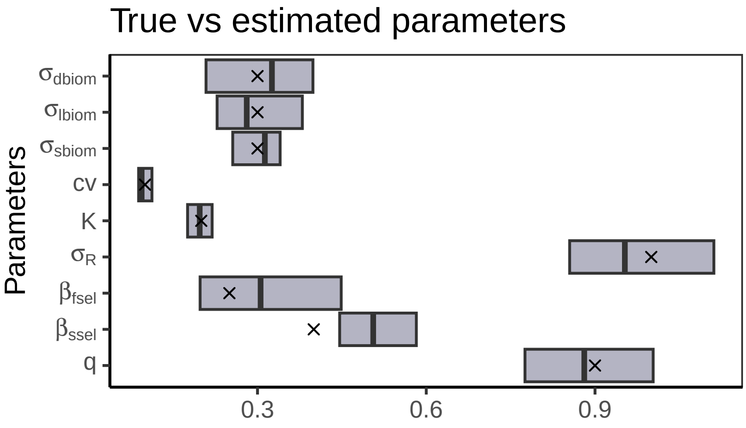


Figure 3.13: Box plot showing the median, the maximum and the minimum values calculated by SLAM for the parameters: q, β_{ssel}, β_{fsel}, σ_R, K, cv, σ_{sbiom} and σ_{dbiom}. The symbol × stands for the values of the parameter that was used to generate the pseudo data. The model was run for 25 times and fitted every time to a different set of data perturbed with a random error.

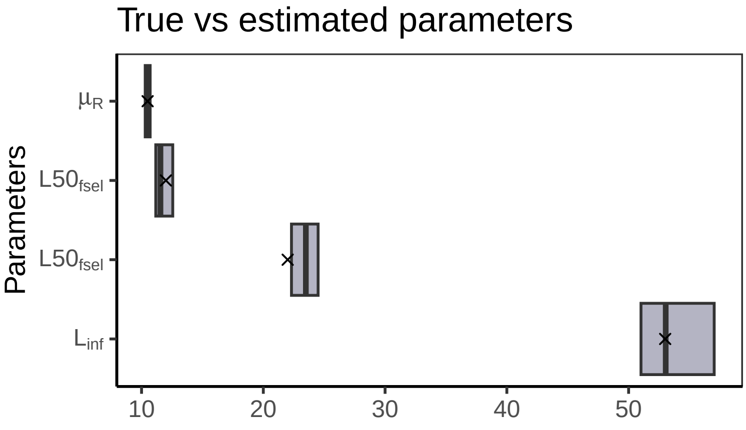


Figure 3.14: Box plot showing the median, the maximum and the minimum values calculated by SLAM for the parameters: μ_R, $L50_{fsel}$, $L50_{ssel}$, L_∞. The symbols × represent the values of the parameter that was used to generate the pseudo data. The model was run for 25 times and fitted every time to a different set of data perturbed with a random error.

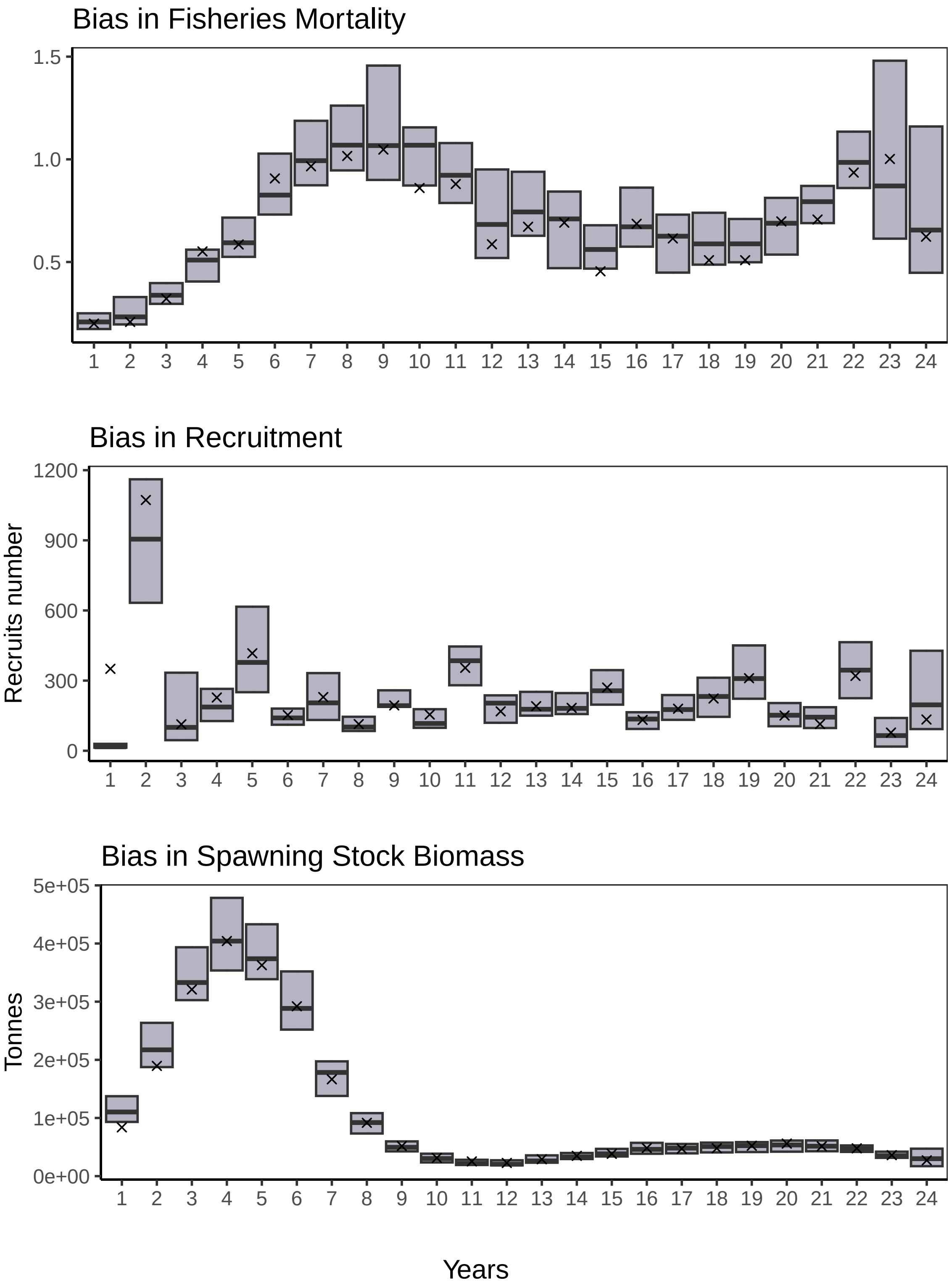


Figure 3.15: The boxplot at the top shows the bias in the yearly values of fishing mortality, the one at the centre shows the bias in the yearly values of recruitment and the one at the bottom shows the bias in the yearly values of spawning stock biomass. In every boxplot, the central value of each box shows the median values, the upper is the maximum value estimated by the model and the lower is the minimum. The symbols × represent the true values. The model retrieves the generated quantities generated with the pseudo data ok. The model was run for 25 times and fitted every time to a different set of data perturbed with a random error.

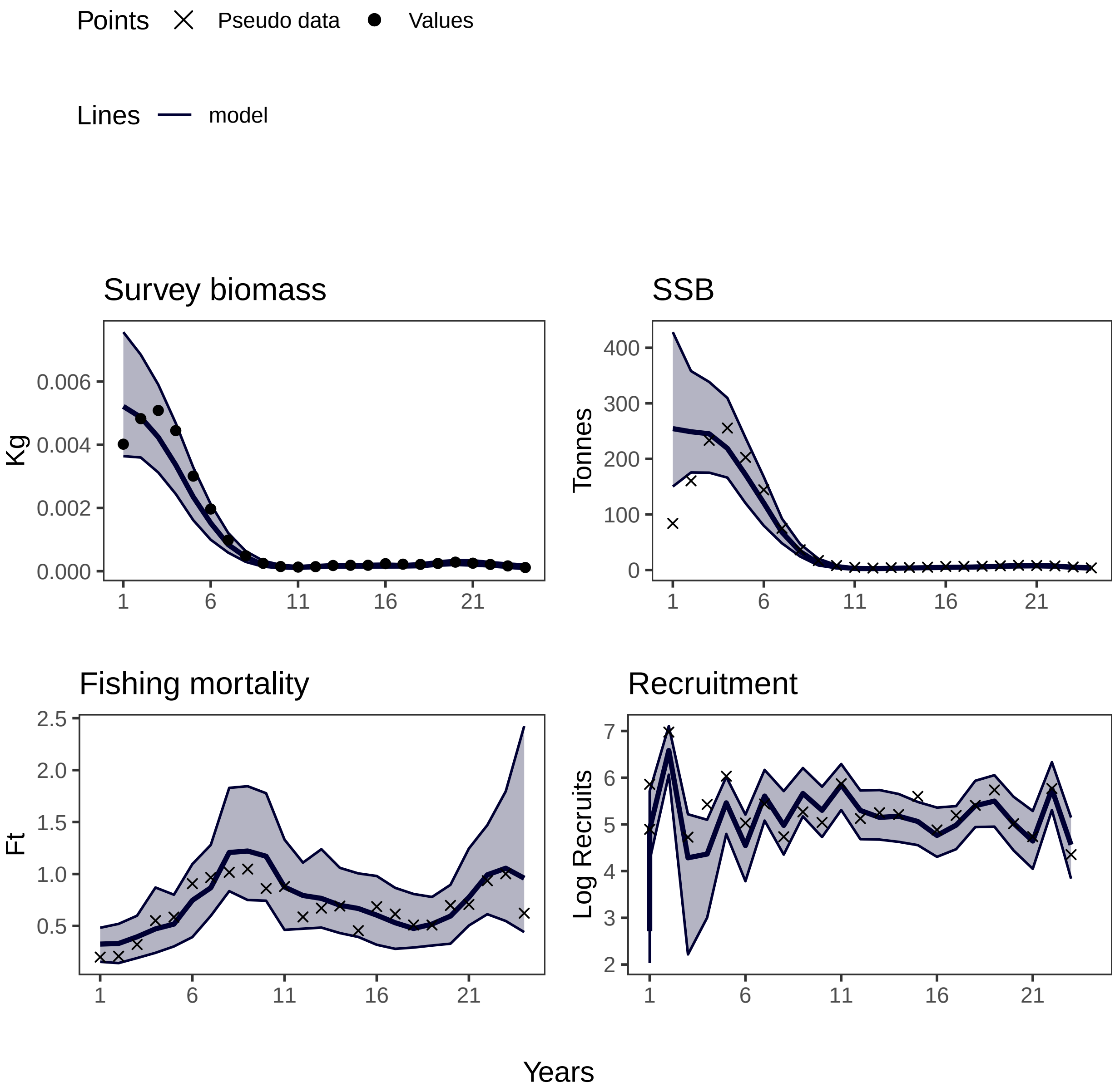


Figure 3.16: The following figures display the model estimates of survey biomass, spawning stock biomass, fisheries mortality and recruitment. The symbols x represent the actual data the model is being fitted to, while the black dots are estimates calculated by the space assessment model. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

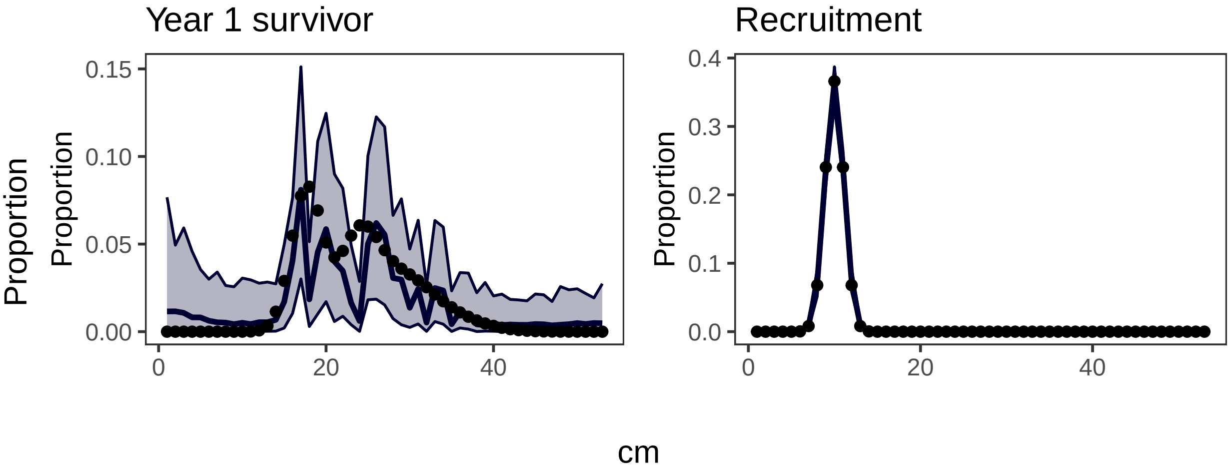


Figure 3.17: The following figures display the model estimates of the proportions-at-length of the initial population and the proportions-at-length of the recruitment. The symbols x represent the actual data the model is being fitted to, while the black dots are estimates calculated by the space assessment model. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

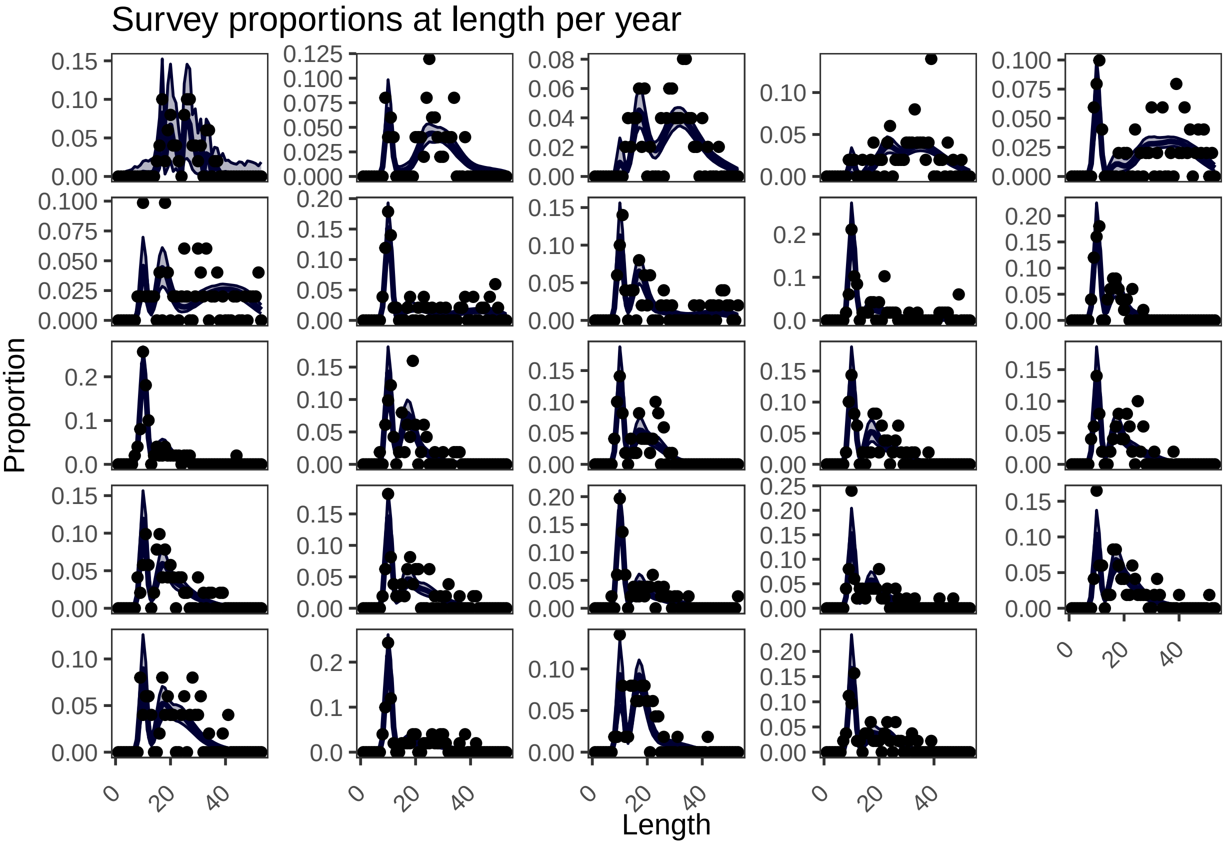


Figure 3.18: The figure shows a series of yearly plot of survey proportions at length. The black dots represent data points, the thick line is the median of the model output and the shaded area represent the 95% credible intervals. The model fits well the data.

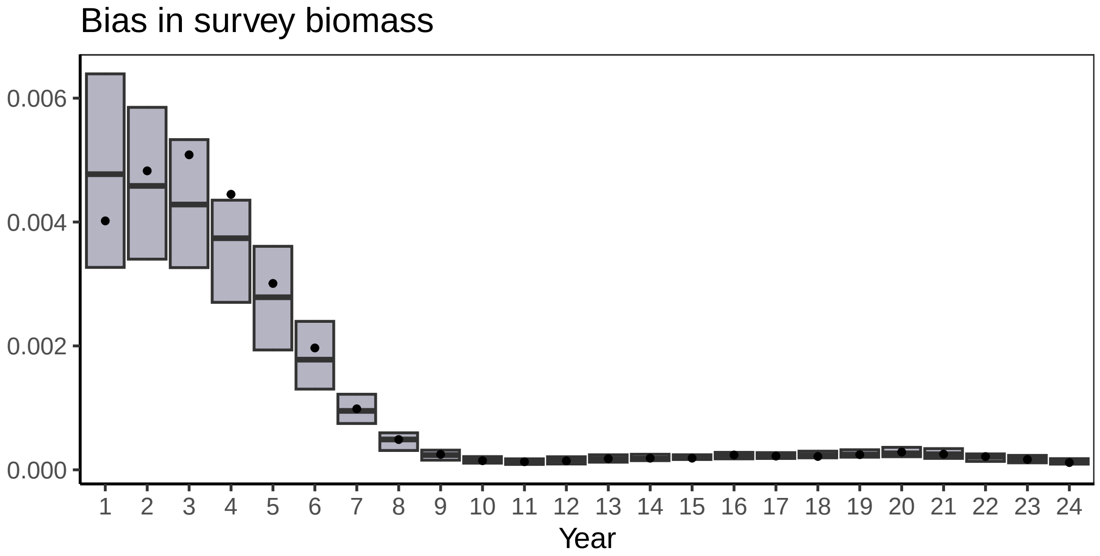


Figure 3.19: Box plot showing the median, the maximum and the minimum values calculated by SLAM for the survey biomass. The model has been run for 25 times.

with a constant error term (σ_{sbiom}). The central value of the box is the median of the medians and the upper and lower bounds are the highest and the lowest medians generated by the model. We can observe how all but one data points lie in the grey area, meaning that the model fits survey well and with little to no bias. Nevertheless, the model seems to smooth out the trend of the data in the early years.

We will now see if SLAM is able to retrieve the parameters used to generate the pseudo data. The first box plot (3.20) shows the median, the maximum and the minimum values calculated by SLAM for the parameters: α_{fsel}, σ_R, K, cv and σ_{sbiom}. The parameters μ_R and L_∞ have been grouped in the second box plot (3.21) for scaling reasons. In both graphs, the symbols × indicate the real value for each parameter. We observe how the model manages to retrieve well all the parameters, except for α_{fsel}, which seems slightly underestimated. This is likely due to the fact that we set 2.7 was the value chosen for the mean of the lognormal prior, as reported on table 3.3. It looks as if the estimate of the posterior is prior driven.

Three similar box plot show the bias in estimation of fisheries mortality, recruitment and SSB (3.22). SLAM managed to retrieve correctly all the values for fishing mortality as for both estimates all × lie in the grey area except for one, which is

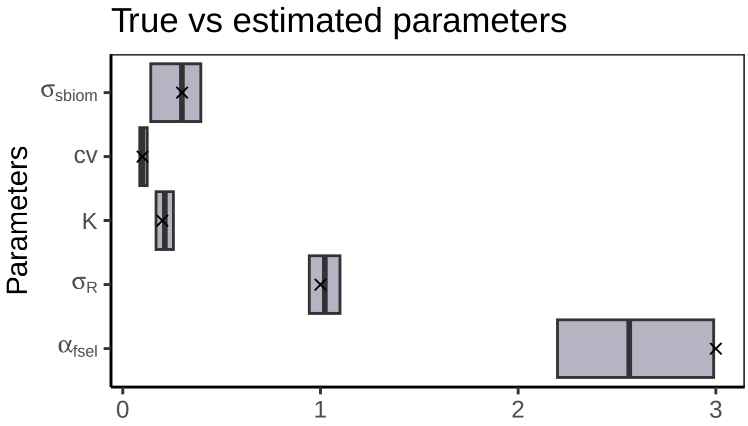


Figure 3.20: Box plot showing the median, the maximum and the minimum values calculated by SLAM for the parameters: α_{Ft}, σ_R, K, cv and σ_{sbiom}. The model has been run for 25 times.

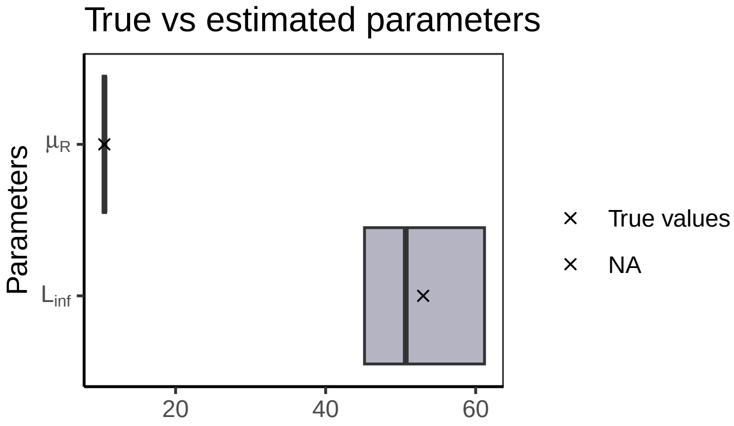


Figure 3.21: Box plot showing the median, the maximum and the minimum values calculated by SLAM for the parameters: μ_R, L_∞. The model has been run for 25 times.

nevertheless lying just outside of it. SLAM performed well even on recruitment, but as observed in the full model, there seem to be an underestimation of the first year recruitment. Regarding SSB, SLAM seems biased in the first two years of estimates. This is likely because it is basing the estimates of SSB on the fit to survey abundance, which we have already noticed to be slightly smoothed in the first years.

3.5 Discussion

This chapter described the theory behind Survey-LAndings Model (SLAM) and presented two possible configurations, one called full model and the other survey

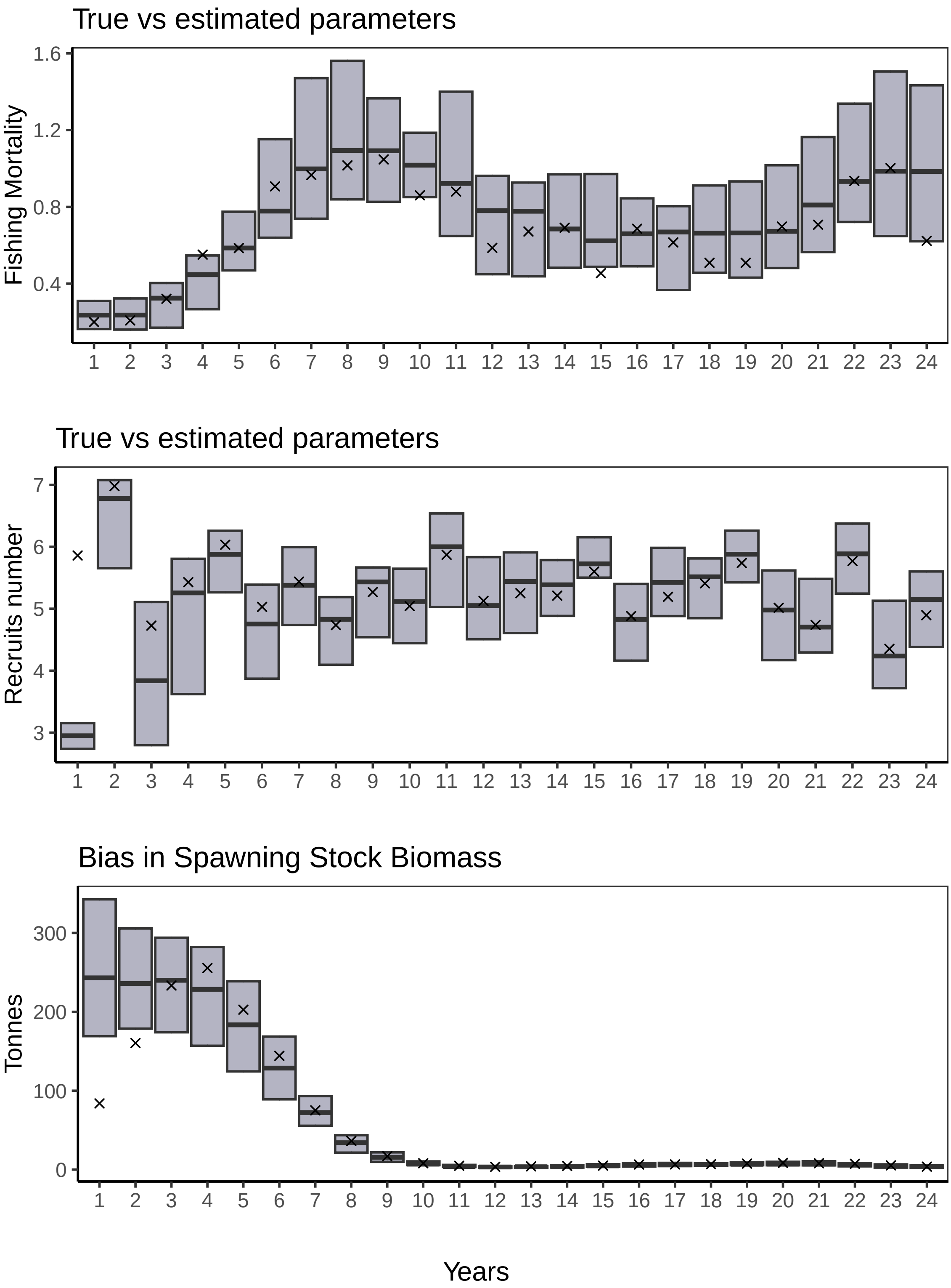


Figure 3.22: The boxplot at the top shows the bias in the yearly values of fishing mortality, the one at the centre shows the bias in the yearly values of recruitment and the one at the bottom shows the bias in the yearly values of spawning stock biomass. In every boxplot, the central value of each box shows the median values, the upper is the maximum value estimated by the model and the lower is the minimum. The symbols × represent the true values. The model retrieves the generated quantities generated with the pseudo data, except for a slight bias in the early years of SSB. The model has been run for 25 times and fitted every time to a different set of data perturbed with a random error.

only. Then, by fitting the model to pseudo data, it was tested if both versions were able to retrieve parameter values. Overall, the results can be considered satisfactory, because SLAM was able to retrieve almost all the parameters with little bias and a very little use of informative priors, and it can be considered valid and reliable.

Nevertheless, the aim of this chapter was also to flag the model's weaknesses. For some of those it was possible to implement a correction, as we did after testing the model's sensitivity to the effective sample size when the proportions-at-length were fitted with a multinomial likelihood. The model showed a moderate sensitivity to the choice of sample size: it was still able to fit the survey and landings biomass and estimate accurately recruitment and spawning stock biomass. The fisheries mortality estimates appeared to be more sensitive. The model also fit worse the discard biomass. This can be explained by the fact the whenever we increase the sample size, we also increase the "weight" we attribute to the proportions-at-length. Since the full-model version was not fitted to any discard proportions-at-length, the model fits better the landings and survey biomass compared to discard biomass, because more weight went to landings and survey proportions-at-length. Age- and length-composition data are often fitted using a multinomial distribution and then reweighted iteratively. However, this method is not advisable with SLAM that is a computationally costly model. Therefore, even though the sensitivity was not high, we decided to act precautionary by replacing the multinomial likelihood with a Dirichlet-multinomial likelihood, as suggested by Thorson et al. (2017). In fact, the sensitivity could increase when switching from pseudo data to real data and cause problems. The Dirichlet-multinomial likelihood visibly reduced the sensitivity to the sample size. The Dirichlet-multinomial likelihood provides a model-based alternative that estimates an additional parameter and thereby "self-weights" data.

The survey only version of the model also managed to fit well the data and retrieve most of the parameters without bias. The survey only version of the model tended to smooth out through the survey biomass data. Understanding the exact causes of this would require more investigation, which we decided not to undertake because it was not something major. Nevertheless, we noticed how the Spawning Stock Biomass tended to follow the exact same pattern of the survey biomass. This is because the model has only this information available to estimate the abundance of the stock. The model had produced biased estimates for SSB only for the first two years, nevertheless, we expect this to be a limitation that is important to consider when apply the model to real data, because if the survey data are unreliable so will be the estimates of the model.

It is important to remark how the fewer information available, the stronger the model assumptions have to be. This chapter demonstrated how removing stock information from the model (by going from the full-version to the survey only), means to fix more information, use more informative priors and make stronger assumptions. For instance we had to fix the survey selectivity, fix the mode of the fishing selectivity and assume that $q = 1$. It was necessary to fix entirely one of the two selectivity because the model did not have enough information to estimate both selectivity curves at the same time, since it only had information from one type of data. It was also necessary to fix one of the two parameters of the fishing selectivity because estimating fisheries parameters from survey only data it was too hard for the model. Even when fixing all this information, the spread of the fishing selectivity resulted to be prior driven, which means the model does not have enough information in the survey length composition data to estimate this parameter correctly and relies on the prior information that were provided. The situation was solved by using an informative (lognormal) prior, because when a uniform was used, the model could not converge on a value for the parameter. This should be accounted for when applying the model to real data, because if the data are not very informative, the result will be conditioned by the input value chosen by the user. This problem could be addressed by trying different priors parameters and input values for the selectivity and conduct some sensitivity analysis. The assumption that $q = 1$ is also quite limiting in a real stock situation, because it means that values of recruitment and SSB will be returned in the survey scale. This means it will be possible to trust the trends, but not the numbers. Anyway, it is still important to remember that stock assessment needs to have simplifying assumptions, especially in situations whew, like in this case, there are strong constraints on data availability (A. Cotter et al. (2004)).

Even though the survey only version resulted to be less powerful compared to the full model version, it is important to keep in mind that length composition of the catches are almost never available, therefore the full version is likely to find much less applicability than the survey only. As the introduction stressed, the majority of the world's stock are unassessed because of the lack of data availability and developing model like this survey only version is of vital importance. It is impossible to reach the same level of assessment quality of a data-rich, age-based assessment with a model like the survey only version of SLAM, but an assessment with limitation is always better than no assessment at all.

4

Chapter IV: Full-model version applied to Whiting VIa

4.1 Introduction

In stock assessment, using fisheries-dependent data such as landings and discard abundance and size composition can provide detailed information on removals from the stock, thereby allowing the provision of catch advice on an absolute scale (Cook (2004)). However, these data are more prone to error or bias originating from various aspects related to misreporting of fisheries catch or changes in fishing technology (Pennino et al. (2016)). Unreported catch and discards create a discrepancy between fish landings used in an assessment model and the actual at-sea fish removals, thereby biasing stock size estimates (Beare et al. (2005)). When fisheries catch rates are used to inform stock trends, many factors that cause changes in fisheries catchability can distort or misrepresent the real trends (Harley et al. (2001); Maunder et al. (2006)).

A state-of-the-art stock assessment model relies on both these sources of information, the dependent and independent of the fisheries, to describe the stock population dynamics and provide management advice.

In this chapter we are testing on a real stock the “full-version” of the Survey-

Landings Stock Assessment Model (SLAM), which is a version that incorporates both fisheries dependent and fisheries independent information. It is fitted to a 5 sets of data: survey biomass and length frequency, landings biomass and length frequency and discard biomass. In this chapter are performed also sensitivity analysis to different assumptions. As a species for this study we picked whiting (*Merlangus merlangius*) from West of Scotland, that identifies as ICES area VIa.

4.2 Materials and Methods

The description of stock, the area, the data collection process and the potential bias in the data can be found in chapter II.

The bias in the data lead some structural changes to the version we tested on pseudo data. We needed to consider the surveys before and after 2011 as two different surveys, because of the change in protocol described in 2.4. This means the parameters must be estimated separately, meaning that we needed two different selectivity, catchability, error terms, as well as two separate likelihood functions. The change in the survey protocol and especially the reduction of the haul duration had undoubtedly impacted the survey catchability and the selectivity. After few trials, we concluded that the model's best fit was given by adopting a logistic curve for the fishery selectivity, a logistic for the survey pre 2011 and a gamma for the selectivity post 2011. In this chapter, the survey parameters labeled with the number 1 refers to the survey pre 2011 and the ones labeled with the number 2 to the survey post 2011.

All the model output presented here were run for 100,000 iterations, 3 chains and thinning of 1,000, on data from 1996 to 2020. The shape of the priors, the initial values and the parameter bound used in this version of the model can be found in table 4.1. To have an idea if the results were on a reasonable scale we compared them with the results with an existing assessment for Whiting from subarea VIa. This assessment is conducted by using the State Space Stock Assessment Model (SAM), the results are presented in ICES (2022). The two models are based on different assumptions and fit to different data sources, so this is not a comparison where we expect to see the two outputs to overlap completely, but rather to see if SLAM is able to pick up the relevant trends highlighted by SAM (i.e major decreases or increases in fishing mortality or spawning stock biomass).

Table 4.1: Table summarises the fixed and fitted parameters used on the full model test on real whiting data. The first column indicates the parameter abbreviation pr symbol, the second the starting value (in the case the parameter was fitted) or the actual fixed value (if the parameter was fixed). The third column specifies if the parameter was fitted and if so what type of prior and what kind of bounds have been set.

Abbreviation	Initial value/s	Prior
y_{min}	1990	fixed
y_{max}	2020	fixed
n_{years}	30	fixed
Dt	1	fixed
$LF1_{\text{distr}}$	$\frac{\text{data\_surv\_distr}_{l,1}}{\sum_{l=1}\text{data\_surv\_distr}_{l,1}}$	$Dirichlet \sim (1)$
$NS1$	$100,000$	$Uniform \sim (90,000; 500,000)$
l_{min}	10	fixed
l_{max}	55	fixed
n_{len}	46	fixed
DL	1	fixed
L_{inf}	58	$lognormal \sim (58; 10)$
K	.34	$Uniform \sim (.34; .2)$
cv	.1	$Uniform \sim (0; 1)$
α_{wgt}	.0093	fixed
β_{wgt}	2.9456	fixed
w	1.13	fixed
$Ft_{l,1}$	.2	$Uniform \sim (0, 1)$
$Ft_{l,y+1}$	.2	$lognormal \sim (Ft_{l,y}, \sigma_{Ft})$
$L50_{\text{fsel}}$	30	$lognormal \sim (30; 3.5)$
β_{fsel}	.35	$lognormal \sim (.35; .2)$
$L50_{\text{dsel}}$	values reported by [?]	fixed
β_{dsel}	.3	0.3
$L50_{\text{ssel1}}$	20	$Uniform \sim (10; 50)$
β_{ssel1}	.3	$Uniform \sim (0; 1)$
$mode_{\text{ssel2}}$	35	$Uniform \sim (10; 100)$
α_{ssel2}	2	$Uniform \sim (1; 80)$
q^1	.01	$Uniform \sim (0.001; 1)$
q^2	.01	$Uniform \sim (0.001; 1)$
α_M	.1	fixed
β_M	$-.3$	fixed

Continued on next page

Table 4.1 – continued from previous page

Abbreviation	Initial value/s	Fixed or fitting
Rt	recruitment values reported in [?]	$Uniform \sim (\log(50,000); \log(2,000,000))$
Rt_{μ}	15	$Uniform \sim (5; 30)$
Rt_{σ}	1	$Uniform \sim (.1; 3)$
σ_{Ft}	.1	$Uniform \sim (0; 1)$
σ_{lbiom}	.2	$Uniform \sim (0; 1)$
σ_{dbiom}	.2	$Uniform \sim (0; 1)$
σ_{sbiom}	.2	$Uniform \sim (0; 1)$
$D\beta_{\text{surv1}}$	50	$Uniform \sim (0; 1000)$
$D\beta_{\text{surv2}}$	50	$Uniform \sim (0; 1000)$
$D\beta_{\text{land}}$	50	$Uniform \sim (0; 1000)$
n_{surv1}	70	fixed
n_{surv2}	70	fixed
n_{land}	70	fixed

We performed different types of sensitivity analysis to check how the model reacted to some key specific assumptions. We tried to change the assumptions on fixed parameters, the input sample size (n_{surv1}, n_{surv2}, n_{land}) and the $L50$ of the discard selectivity ($L50_{dsel}$). The input sample sizes were decreased from 70 to 30. $L50_{dsel}$ was changed from the increasing trend reported by R. M. Cook (2019) to a fixed number: the highest at the end of the time series (38) and the lowescorresponding to the beginning of the time series 26. As an analysis of the sensitivity to the model structure we changed the shape of the fisheries and survey selectivity. For testing the model sensitivity to the shape of the fishing selectivity we replaced the logistic selectivity with a gamma selectivity, for which we estimated both the mode and the spread. For the sensitivity to the survey selectivity shape we tried two different combinations: both surveys (pre and post 2011) are assumed to have a logistic selectivity and both the surveys are assumed to have a dome-shaped selectivity. The last type of sensitivity we tried is the sensitivity to parameter bounds. In particular we decreased the lower bound of the parameter from log(7500) to log(200).

4.3 Results

4.3.1 SLAM full version

In this section we show the results of the model fitted to Whiting IVa data. The trace plots and histograms of the posterior distributions for the most important parameters are reported in the Appendix IV. In 4.1 we can observe the model fit to survey, landings and discard biomass, the estimates for Spawning Stock Biomass, fisheries mortality and recruitment. The black dots are the data the model is being fitted to, while the × are the estimates calculated by SAM. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the data, it produces estimates of fishing mortality very close to the ones produced by SAM, it picks up well the trends in SSB and the ones in recruitment, despite this last one seems to be underestimated.

Figure 4.2 shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

In the next two plot grids 4.3 and 4.4 we observe how the model fits the proportions-at-length of survey and landings of whiting from subarea VIa. Each single plot in the grid represents one year, from 1996 to 2020. The dark line is the model output median and the polygon around it is the 95 credible intervals. The black dots represents the data. The landings data are missing from 2009 onwards. The model was fitted only to the available data and with the parameters estimated from those it calculated the expected landings for the following years. Except for few exceptional years in the survey, both the model fits the data quite well.

We now have a look at the estimates of the fisheries and survey selectivity in 4.5. The three plots show the logistic selectivity of the fisheries on the right, the model estimated $L50_{fsel} = 28.7$ and $\beta_{fsel} = 0.6$. At the centre there is the survey pre

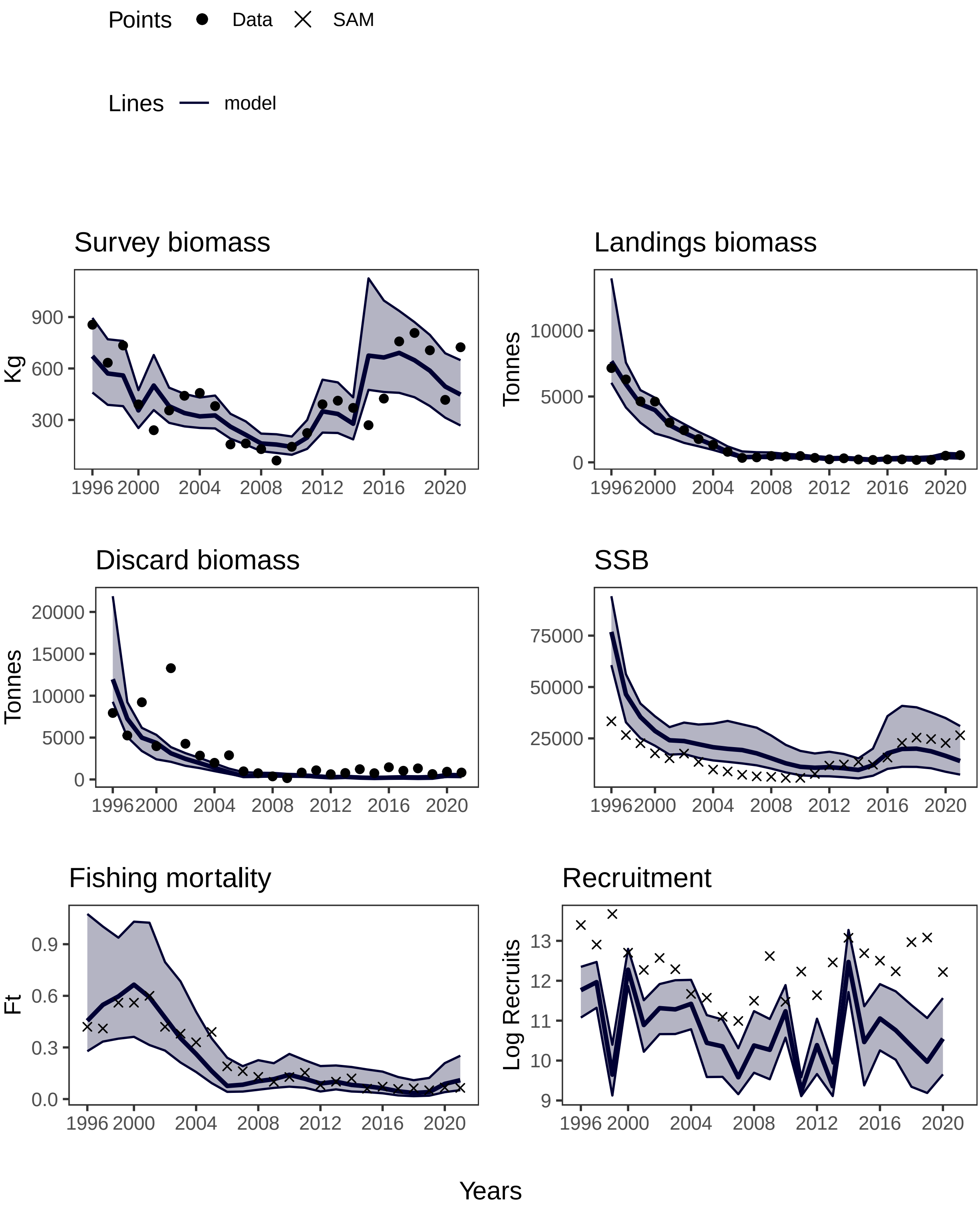


Figure 4.1: In this set of graphs we can observe the model fit to survey, landings and discard biomass, the estimates for Spawning Stock Biomass, fisheries mortality and recruitment. The black dots are the data the model is being fitted to, while the × are the estimates calculated by SAM. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the data, it produces estimates of fishing mortality very close to the ones produced by SAM, it picks up well the trends in SSB and the ones in recruitment, despite this last one seems to be underestimated.

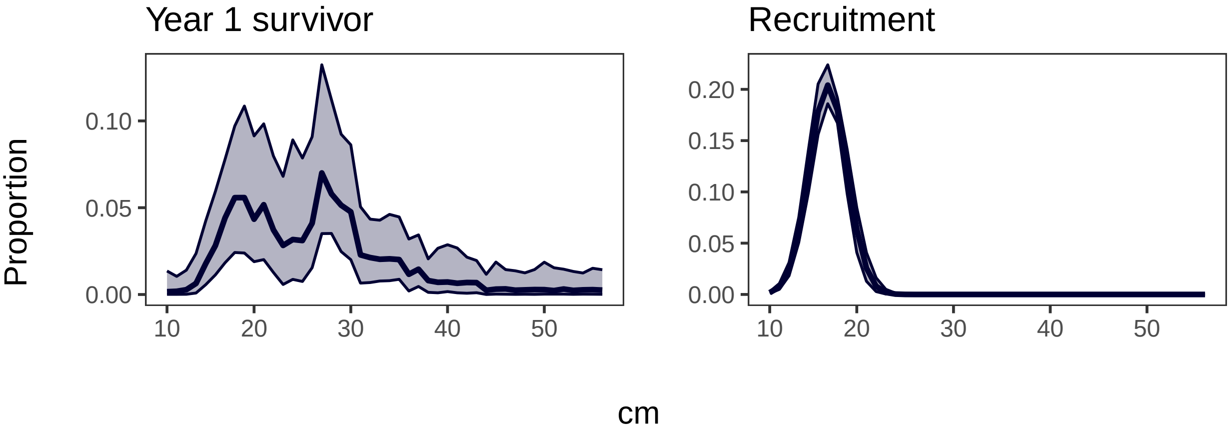


Figure 4.2: The two graphs shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

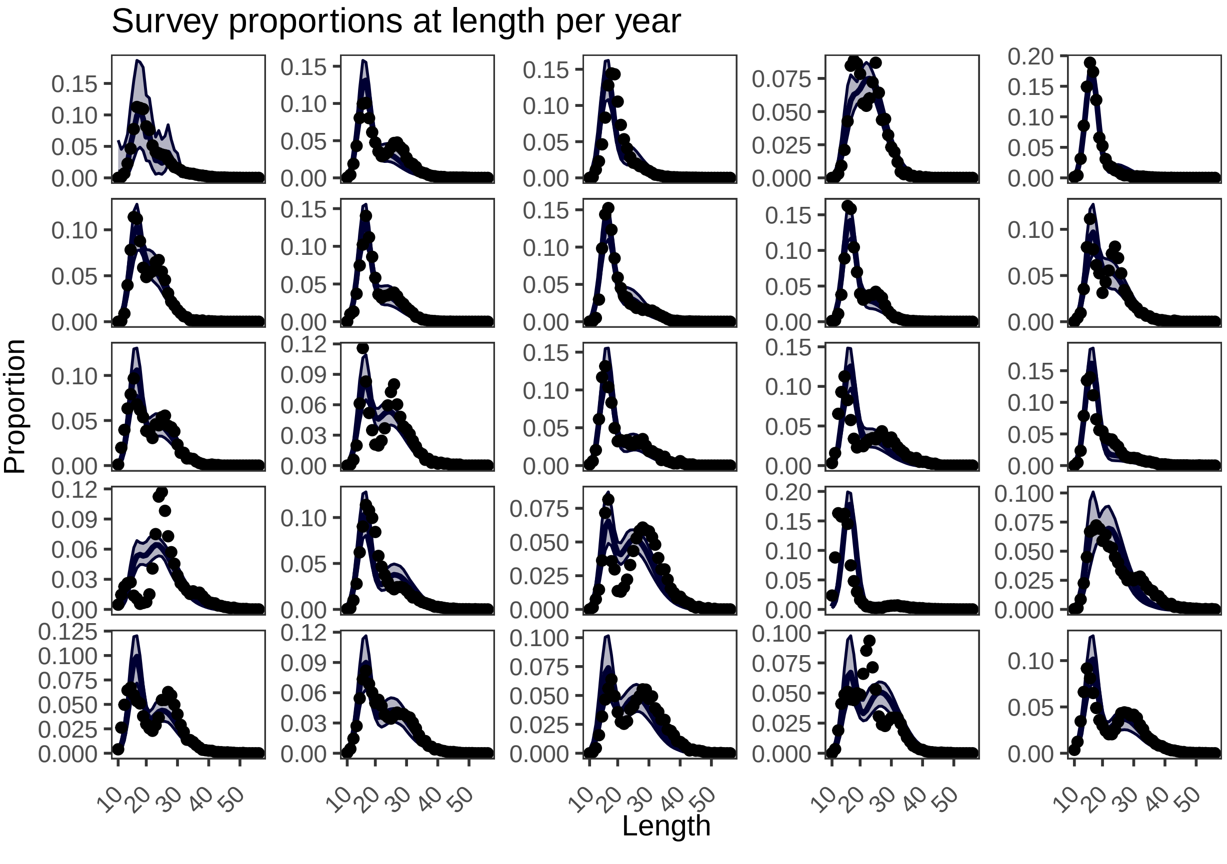


Figure 4.3: The figure shows a series of yearly plot of survey proportions at length. The black dots represents data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The data has been fitted by using two separate surveys, with different parameters and likelihood. The first survey runs until 2010, while the second from 2011 onwards. The model fits well the data.

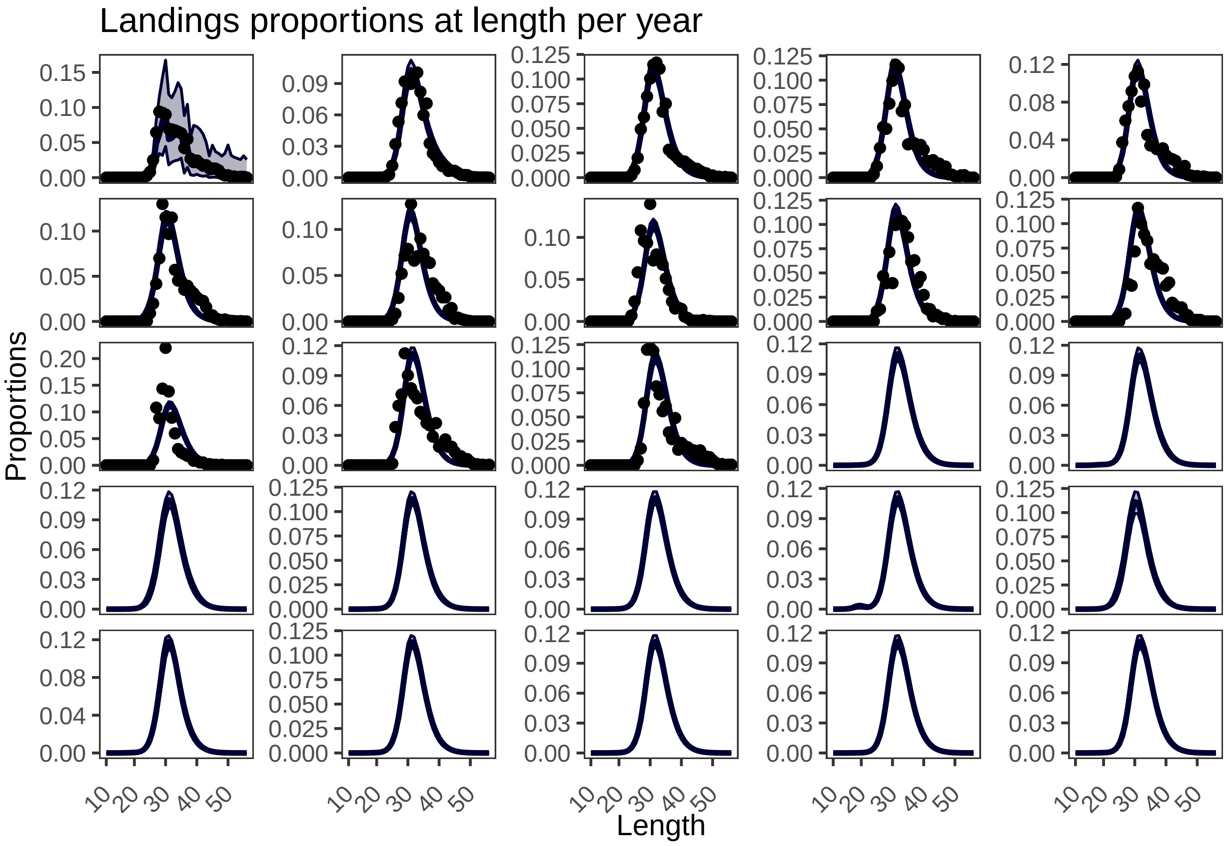


Figure 4.4: The figure shows a series of yearly plot of landings proportions at length. The thick line is the median of the model output and the shaded area represents the 95% credible intervals. The black dots represents data, which are available only untile 2009. The model fits well the data.

2011, the model estimated the parameters to be $L50_{ssel1} = 40$ and $\beta_{fsel} = 0.17$. The gamma selectivity of the survey post 2011 is shown on the right, the parameters are $mode_{ssel2} = 39$ and $\alpha_{ssel2} = 5.5$ The estimates are sensible, except that in general we would expect the $L50$ of the fisheries to be higher that the one of the survey.

4.3.2 Sensitivity Analysis

In the following paragraphs we will present the sensitivity analysis performed on the model. First we present the sensitivity to parameter values, then the sensitivity to model structure and lastly to parameter bounds. In every plot, the output presented in the previous paragraph, that we con sider the best fit, is compared to the output with modified features.

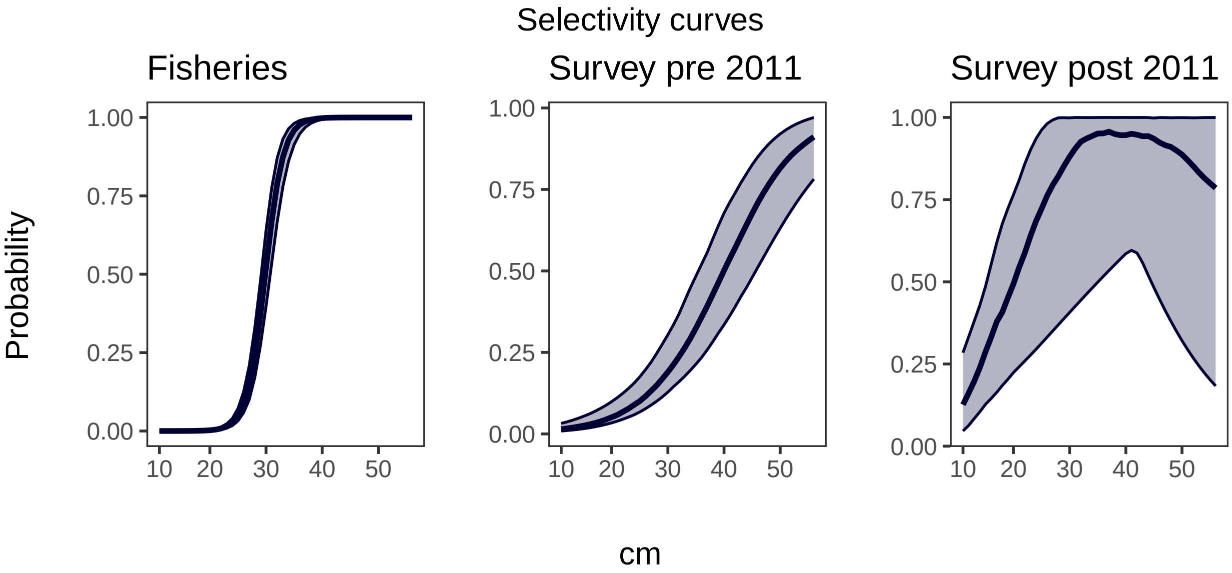


Figure 4.5: The first figure on the left shows the logistic fisheries selectivity, the one in the centre the logistic survey selectivity pre 2011 and the last plot shows the gamma survey selectivity post 2011. The three curves seem sensible.

Sensitivity to parameter values I: sample size

In this paragraph we present the results of the sensitivity analysis we performed on SLAM by trying to decrease the three input sample sizes (n_{surv1}, n_{surv2} and n_{land}) from 70 to 30. The results for the estimated (4.6) quantities like recruitment, SSB and fishing mortality are shown in the next plot, as well as the fit to biomass data. The median of the model output of the "original" model is represented as a black line, while the red line is the run with the decreased sample size. The difference between the two lines is not dramatic overall, but it is notable, especially in the estimates of fishing mortality and SSB. We can say that the model with $n = 70$ fits the data better and produces estimates closer to SAM. We would not expect to observe sensitivity to the sample size after replacing the multinomial likelihood with the Dirichlet-multinomial likelihood. When we decrease the sample size we are putting less weight on the compositional data therefore the model will fit better the abundance data. This is not really visible, it actually seems that the model fits better discard biomass when the sample size is higher.

The fit to proportions-at-length of landings and survey is shown in figure 4.7 and 4.8 respectively. Again the black line is the median of the model where the

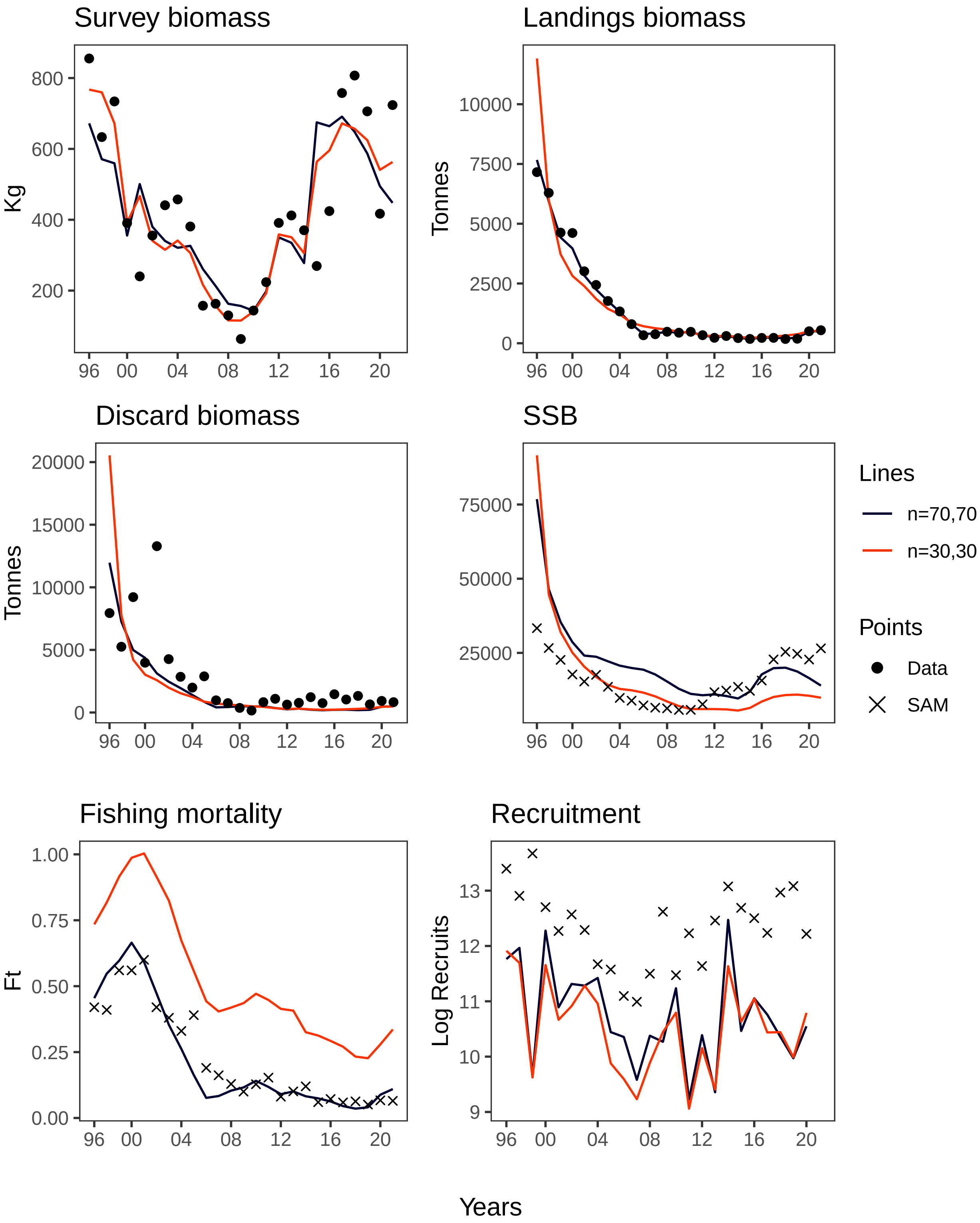


Figure 4.6: This set of plots shows as a dark line the sample size that was used in the previous model run, while in red a lower sample size. The black dots represents data points and the symbols × represents the SAM estimates. The difference between the two lines is not dramatic overall, but it is notable, especially in the estimates of fishing mortality and SSB.

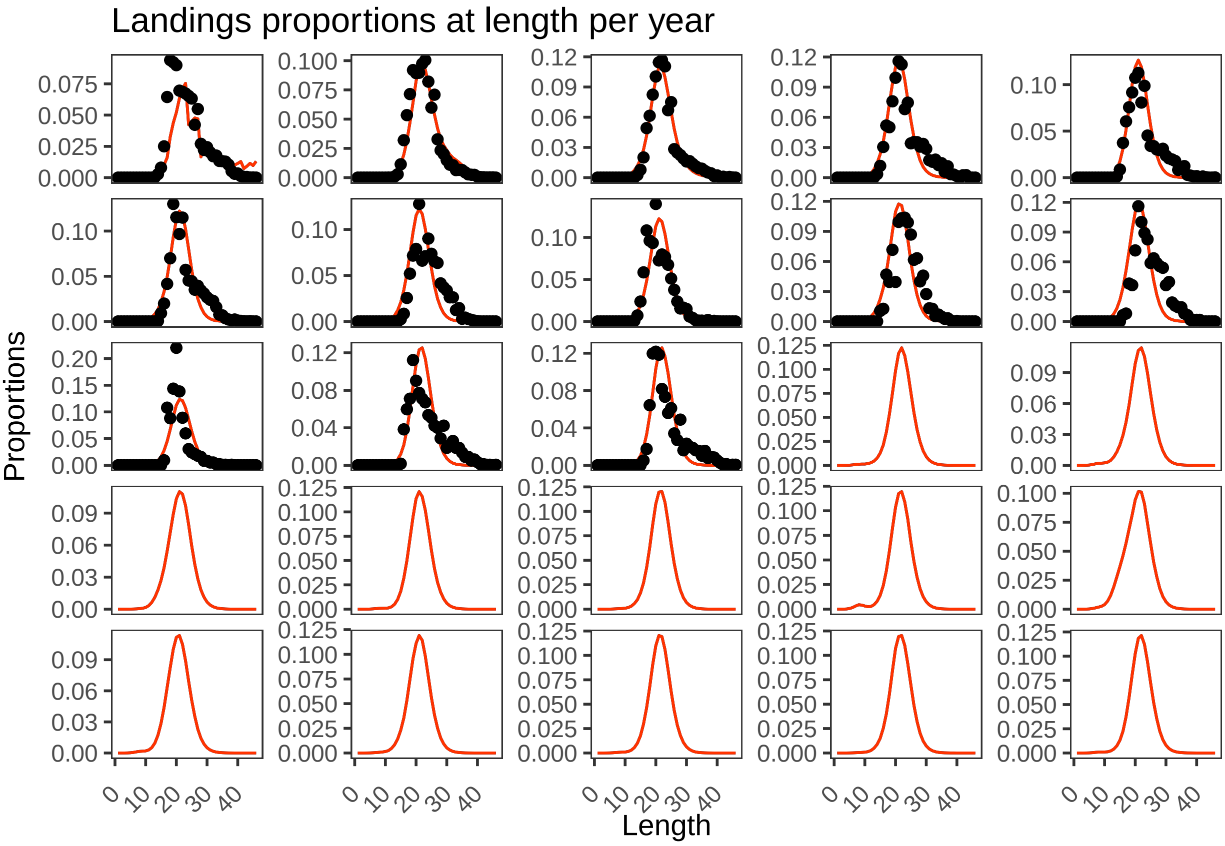


Figure 4.7: The figure shows a series of yearly plot of landings proportions at length. The black line is the median of the model where the input sample sizes were equal to 70 and the red line is the median of the model with sample sizes equal to 30. The black dots represents data, which are available only untile 2009. Both model fits well the data and only the red line on top is visible because the two estimates are completely overlapping.

input sample sizes were equal to 70 and the red line is the median of the model with sample sizes equal to 30. The black dots are data points, which for landings are available only until 2009. In this case the two models are completely overlapping.

From the fishing mortality plot shown in 4.6 we would expect an effect on the fishing selectivity. In 4.9 we compare the fishing selectivity curves of the two models. The two curves are basically the same, even though the fishing selectivity with lower input sample size has higher uncertainty and higher $L50_{fsel}$ (31>28.7).

Sensitivity to parameter values II: discard $L50_{dsel}$

In this section we present the results of the analysis we performed to investigate the sensitivity of the model to the values picked as the L_{50} of the discard selectivity.

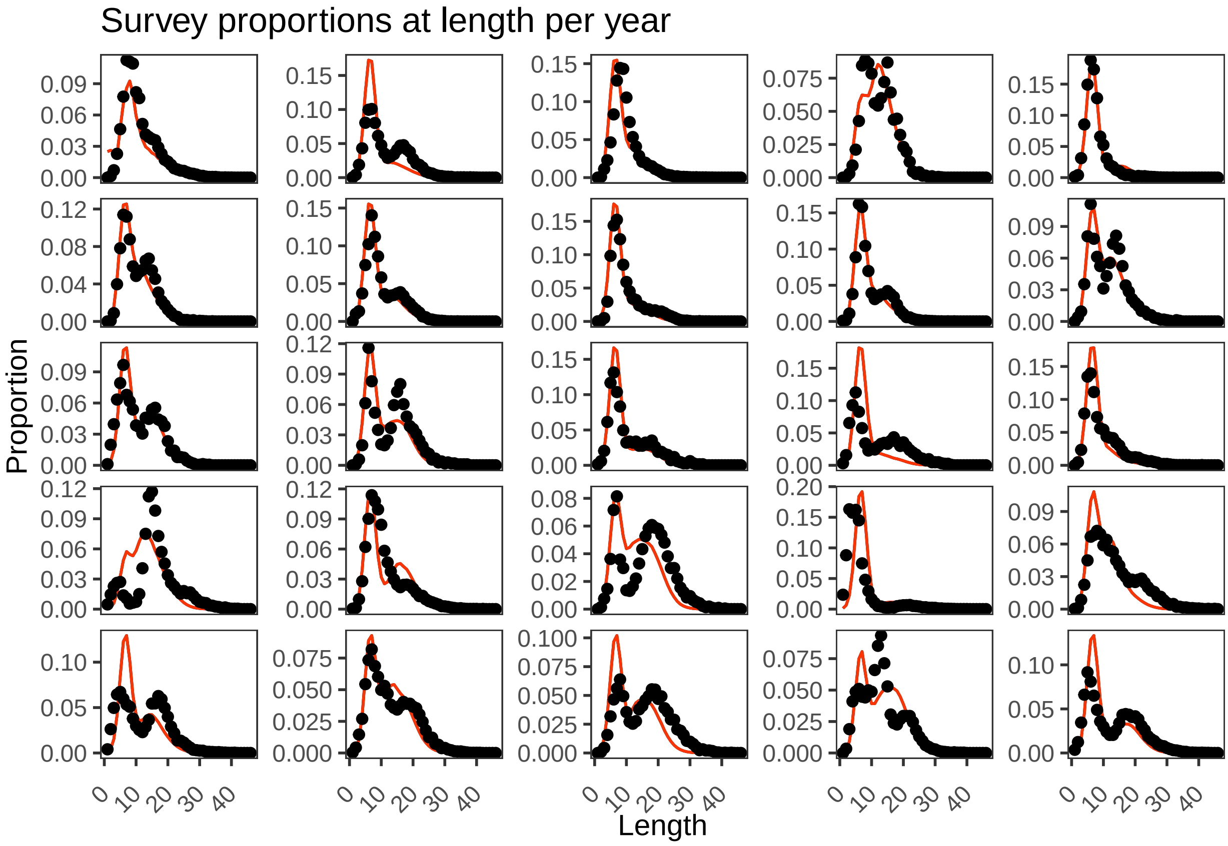


Figure 4.8: The figure show a series of yearly plot of landings proportions at length. The black line is the median of the model where the input sample sizes were equal to 70 and the red line is the median of the model with sample sizes equal to 30. The data has been fitted by using two separate surveys, with different parameters and likelihood. The first survey runs until 2010, while the second from 2011 onwards. Both model fits well the data and only the red line on top is visible because the two estimates are completely overlapping.

We compared the version described in paragraph 4.3.1 with other two versions where we replaced the series of increasing values of $L50_{dsel}$ calculated in R. M. Cook (2019) with a single value: a supposedly low $L50$, $L50_{dsel} = 26$, and what we hypothesise could be a high $L50$, $L50_{dsel} = 36$. These two values are the highest (most recent) and the lowest (older) calculated in R. M. Cook (2019). Figure 4.10 shows the median values of the three different models as a line. The model that has the increasing trends of $L50_{dsel}$ is represented in dark blue, $L50_{dsel} = 26$ in red, $L50_{dsel} = 38$ in dark red. The black dots represents data points and the symbols × represents the SAM estimates. The lines are all very close between each other, highlighting that the model does not have high sensitivity to the choice if the

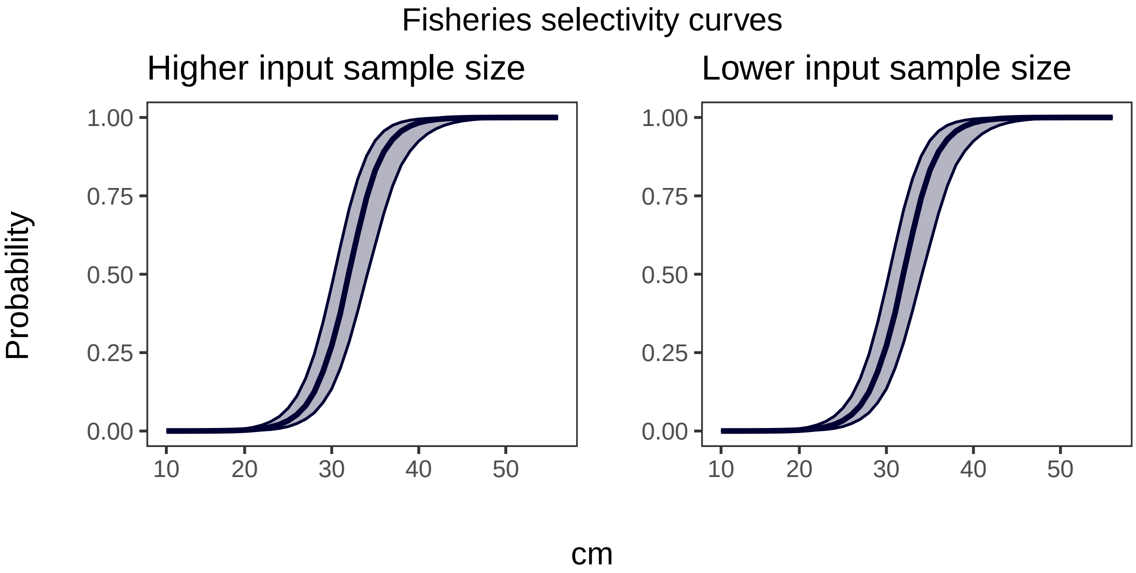


Figure 4.9: This figure compares the fishing selectivity curves of the two models. The two curves are basically the same, even though the fishing selectivity with lower input sample size has higher uncertainty and higher $L50_{fsel}$

parameter $L50_{dsel}$. The greatest difference between the models can be observed in fishing mortality, but it is still not very relevant.

Figure 4.11 shows SLAM sensitivity in the fit to landings proportions-at-length. The model that has the increasing trends of $L50_{dsel}$ is represented in dark blue, $L50_{dsel} = 26$ in red and $L50_{dsel} = 38$ in dark red. The black dots represents data points. The lines are overlapping, confirming that the model does not have high sensitivity to the choice if the parameter $L50_{dsel}$, as we have already observed in the previous figure. Figure 4.12 shows a similar situation for the survey proportions-at-length. The lines are overlapping here too.

Sensitivity to model structure: the shape of the survey selectivity

This section shows the results of the sensitivity analysis on the shape of the survey selectivity. We compared the model presented in 4.3.1, that assumes that the survey pre 2011 has a logistic selectivity while the survey post 2011 has a dome-shaped selectivity with other two versions, one both surveys (pre and post 2011) are assumed to have a logistic selectivity and one where both the surveys are assumed to have a dome-shaped selectivity. In 4.13 we compare the three versions performance

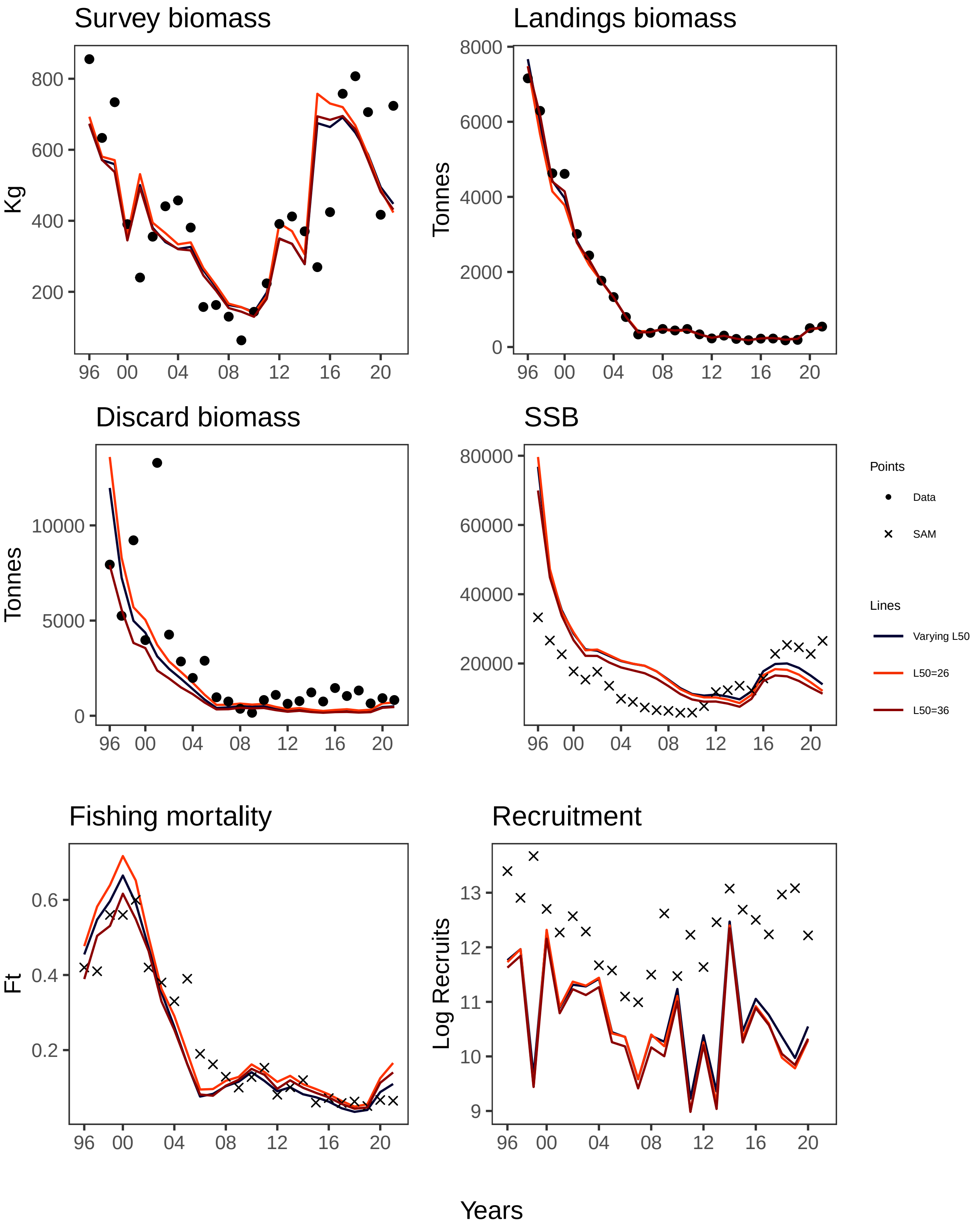


Figure 4.10: The figure shows different values of the parameter $L50_{dsel}$ have influenced the fit to abundance indexes and the estimates of SSB, fishing mortality and recruitment. The model that has the increasing trends of $L50_{dsel}$ is represented in dark blue, $L50_{dsel} = 26$ in red and $L50_{dsel} = 38$ in dark red. The black dots represents data points and the symbols × represents the SAM estimates. The lines are all very close between each other, highlighting that the model does not have high sensitivity to the choice if the parameter $L50_{dsel}$.

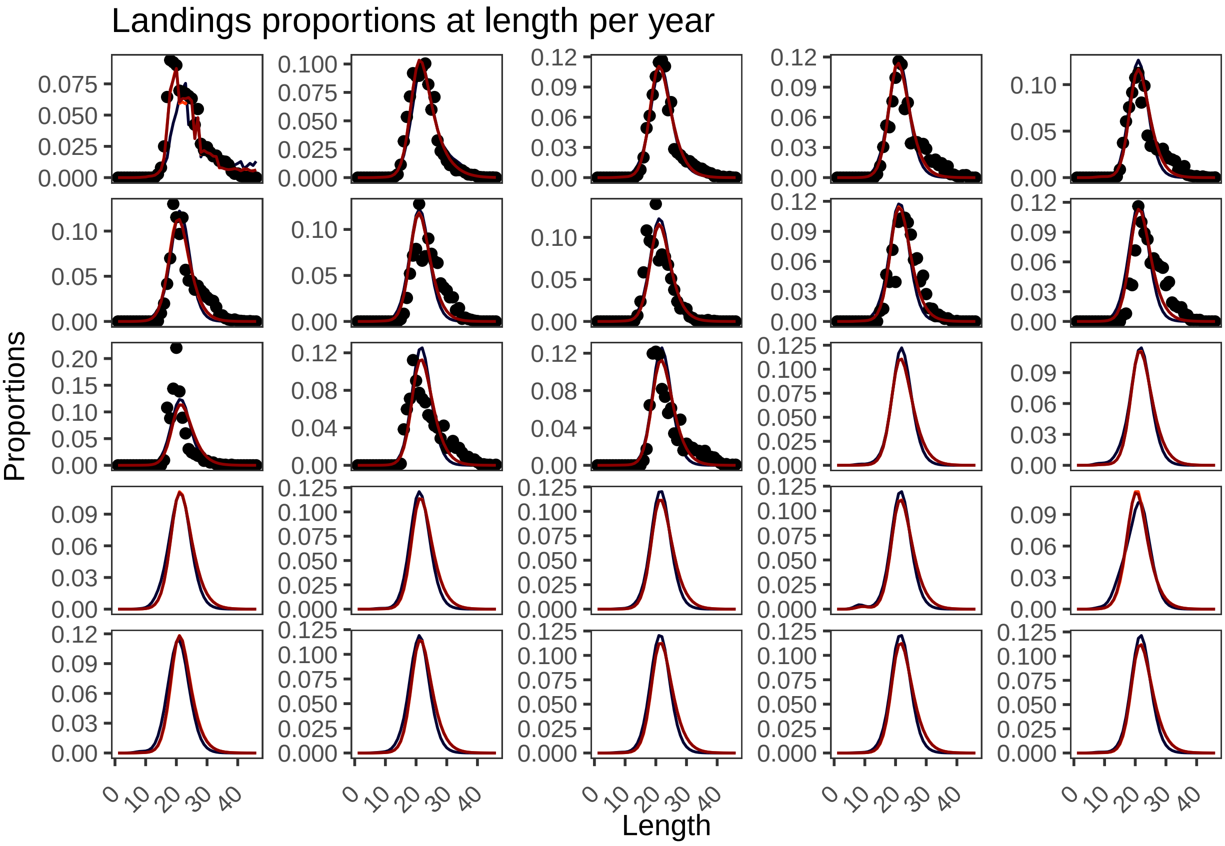


Figure 4.11: The figure shows SLAM sensitivity to the parameter $L50_{dsel}$ in the fit to landings proportions-at-length. The model that has the increasing trends of $L50_{dsel}$ is represented in dark blue, $L50_{dsel} = 26$ in red and $L50_{dsel} = 38$ in dark red. The black dots represents data points, which are available only until 2009. The lines are overlapping, suggesting that the model does not have high sensitivity to the choice if the parameter $L50_{dsel}$.

on fitting the survey, landings and discard biomass and estimating fishing mortality, recruitment and SSB. The black dots represents data points and the symbols × represents the SAM estimates. The combination logistic+gamma, the one we use as a reference, is colored in dark blue, the combination gamma+gamma is presented in red and the combination logistic+logistic in dark red. The combination gamma+gamma has a very similar performance to the reference model, while the combination logistic+logistic goes quite off track on the early years of estimate of discard and landings biomass. The estimates of recruitment and SSB are acceptable, but the model overestimates the values of fishing mortality and fails to capture the initial peak and overestimating the values in the recent years.

Figure 4.14 shows SLAM sensitivity in the fit to landings proportions-at-length.

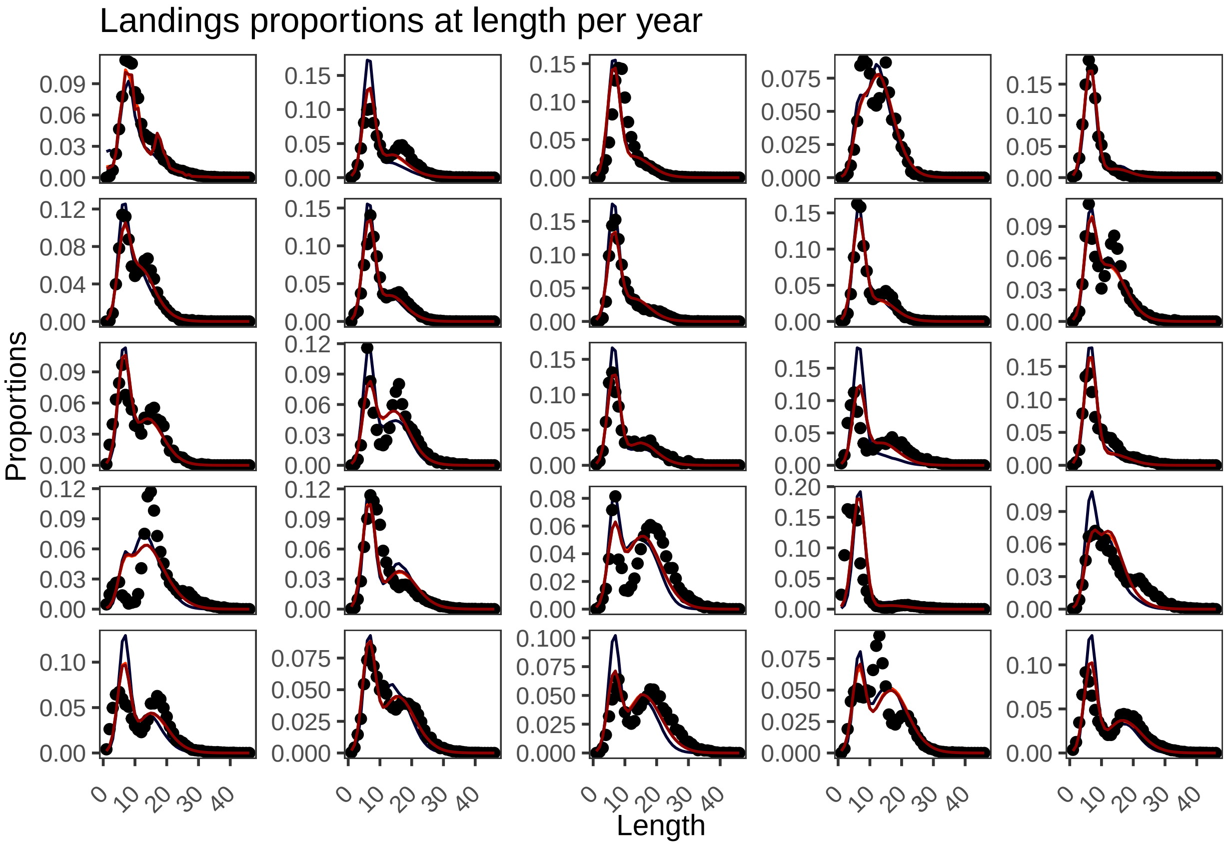


Figure 4.12: The figure shows SLAM sensitivity to the parameter $L50_{dsel}$ in the fit to survey proportions-at-length. The model that has the increasing trends of $L50_{dsel}$ is represented in dark blue, $L50_{dsel} = 26$ in red and $L50_{dsel} = 38$ in dark red. The black dots represents data points. The lines are overlapping, suggesting that the model does not have high sensitivity to the choice if the parameter $L50_{dsel}$. The data has been fitted by using two separate surveys, with different parameters and likelihood. The first survey runs until 2010, while the second from 2011 onwards.

The dark blue line is the model with the logistic+gamma combination, the red line is the gamma+gamma and the dark red line is the logistic+logistic. The black dots represents data points, which are available until 2009. The model is not sensitive to the shape of the survey selectivity in the fit to landings proportions-at-length. Figure 4.15 shows the same situation for the survey proportions-at-length.

From what we observed in the fishing mortality estimate in figure 4.13 we would expect the fisheries selectivity of the model with two logistics to look different compared to the other two. In 4.16 we show the logistic selectivity of the fisheries for the three combinations of survey selectivity, from the left is shown the fisheries selectivity when the survey selectivity is assumed to be logistic before year 2011

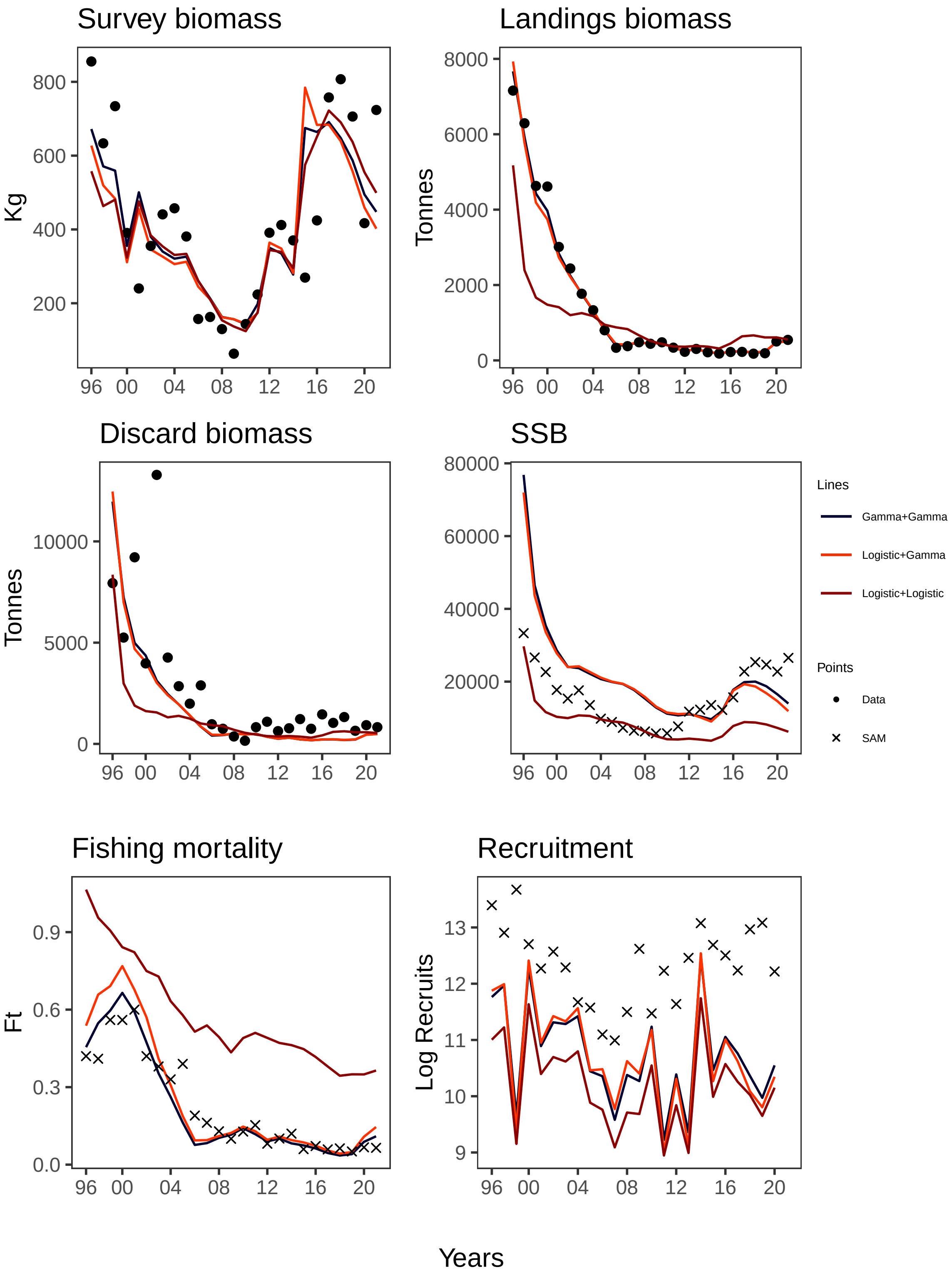


Figure 4.13: The black dots represents data points and the symbols × represents the SAM estimates. The dark line represents the median of the model output with the logistic selectivity and the red line is the median of model with the gamma selectivity. The gamma model fits well discard and landings biomass, and the estimates of SBB and recruitment are not too far from the logistic model, but the estimates of fishing mortality are too high and not credible, and the early years of the survey biomass are clearly overestimated.

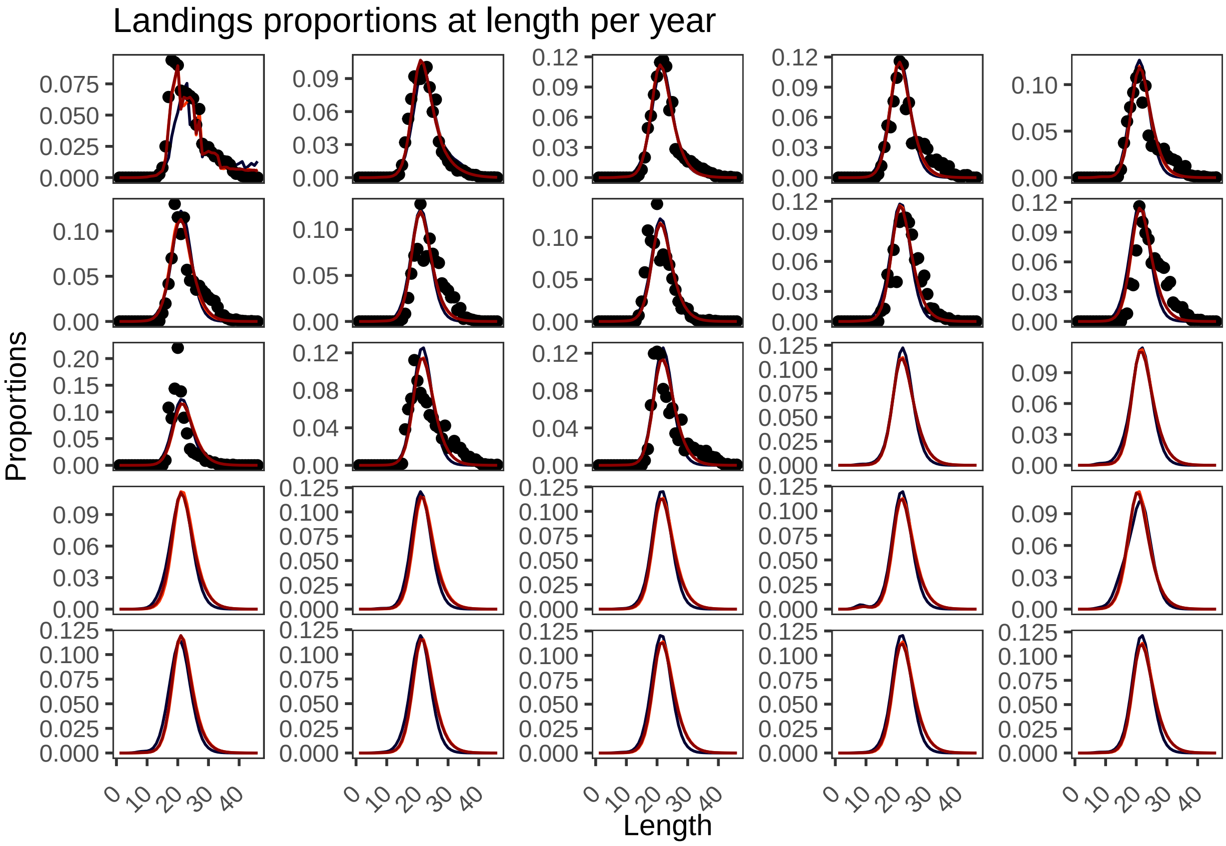


Figure 4.14: The figure shows a series of yearly plot of survey proportions at length. The dark blue line is the median of the model with the the logistic+gamma combination, the red line is the gamma+gamma and the dark red line is the logistic+logistic. The black dots represents data points, which are available until 2009. The three models fit well the data and there is no relevant difference between the three.

and gamma after 2011, at the centre when it is assumed to be gamma for both surveys, and lastly when it is assumed to be logistic. The three curves look identical, therefore we assume that the difference in the estimates of fishing mortality must be due to some other processes.

Sensitivity to model structure: the shape of the fishing selectivity

This paragraph shows the results of the sensitivity analysis performed on SLAM by replacing the logistic selectivity of the fisheries with a gamma curve. Figure 4.17 shows the fit to the abundance indexes and the estimates of SSB, fishing mortality and recruitment. The black dots represents data points and the symbols × represents the SAM estimates. The dark line represents the median of the model

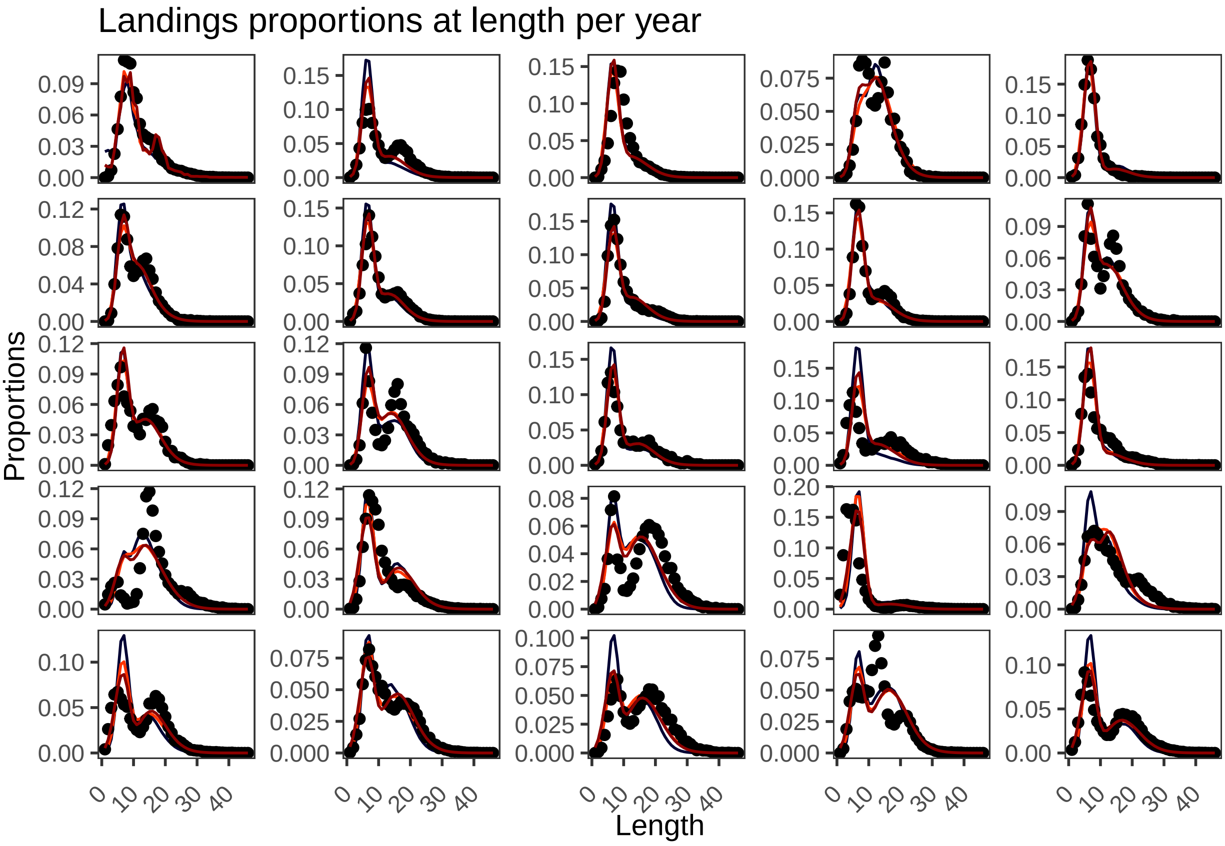


Figure 4.15: The figure shows a series of yearly plot of survey proportions at length. The dark blue line is the median of the model with the the logistic+gamma combination, the red line is the gamma+gamma and the dark red line is the logistic+logistic. The black dots represents data points. The first survey runs until 2010, while the second from 2011 onwards. The three models fit well the data and there is no relevant difference between the three.

output with the logistic selectivity and the red line is the median of model with the gamma selectivity. Despite the fact that the gamma model fits well the biomass data, and the estimates of SBB and recruitment are not too far from the logistic model, the estimates of fishing mortality are clearly too high. We keep in mind that SAM is a soft reference, but fishing mortality of whiting in West of Scotland is surely not above 1. Therefore fishing mortality is overestimated. Nevertheless the estimates did not change in trend, but they changed in scale.

Figure 4.18 shows SLAM sensitivity in the fit to landings proportions-at-length. The logistic model is represented in black while the gamma model is represented in red. The black dots represents data points. The lines are almost overlapping, suggesting that the structural change does not particularly affect the model fit to

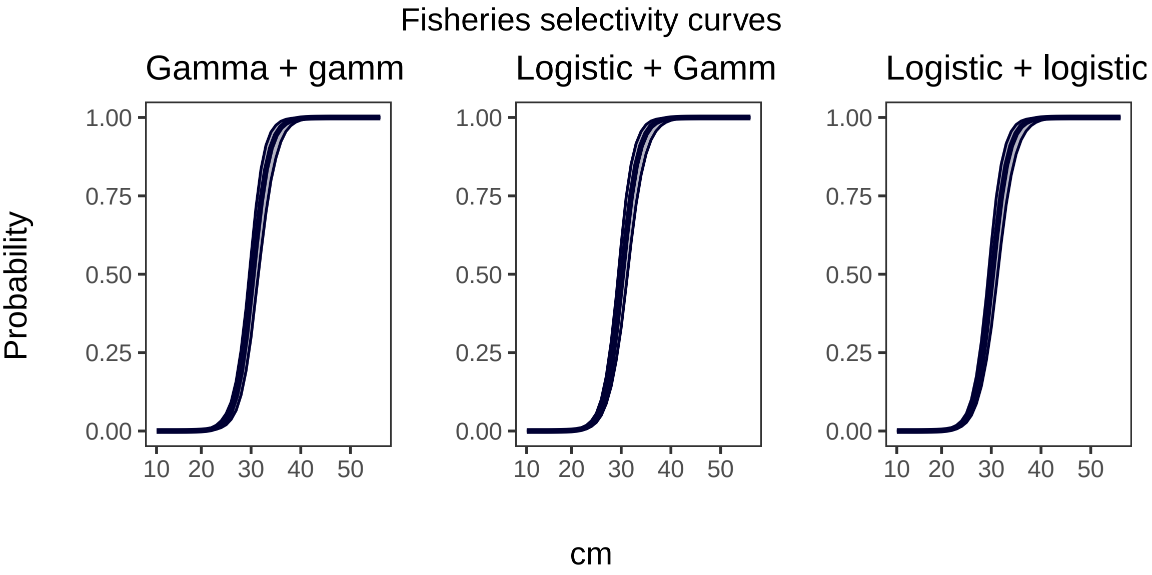


Figure 4.16: The three plots show the logistic selectivity of the fisheries for the three combinations of survey selectivity, from the left is shown the fisheries selectivity when the survey selectivity is assumed to be logistic before year 2011 and gamma after 2011, at the centre when it is assumed to be gamma for both surveys, and lastly when it is assumed to be logistic. The three curves look identical, even though we would expect to see the last one on the right to be different to the other two.

proportions-at-length. A similar situation is shown in 4.19, which shows the fit to survey proportions-at-length.

In order to understand further the reason of the overestimation of the fishing mortality, we have a look at the posterior of the two parameters of the fishing selectivity, $mode_{fsel}$ and α_{fsel}, reported in the upper half of figure 4.20. While $mode_{fsel}$ seems reasonable, α_{fsel} is far too high. The graph at the bottom left corner shows the estimated shape of the selectivity curve with its credible intervals. From the graph emerges that the high value of α_{fsel} makes the spread of the gamma curve really narrow. The plot at the bottom right of the figure reports the median of the fishing selectivity in comparison to one year of landings proportions-at-length. It seems that the gamma curve is trying to over-fit the landings distribution.

Sensitivity to parameter bounds: Recruitment

The last sensitivity analysis we conducted was on recruitment parameter bounds. In this test we compared the reference model with one where the lower bound of the

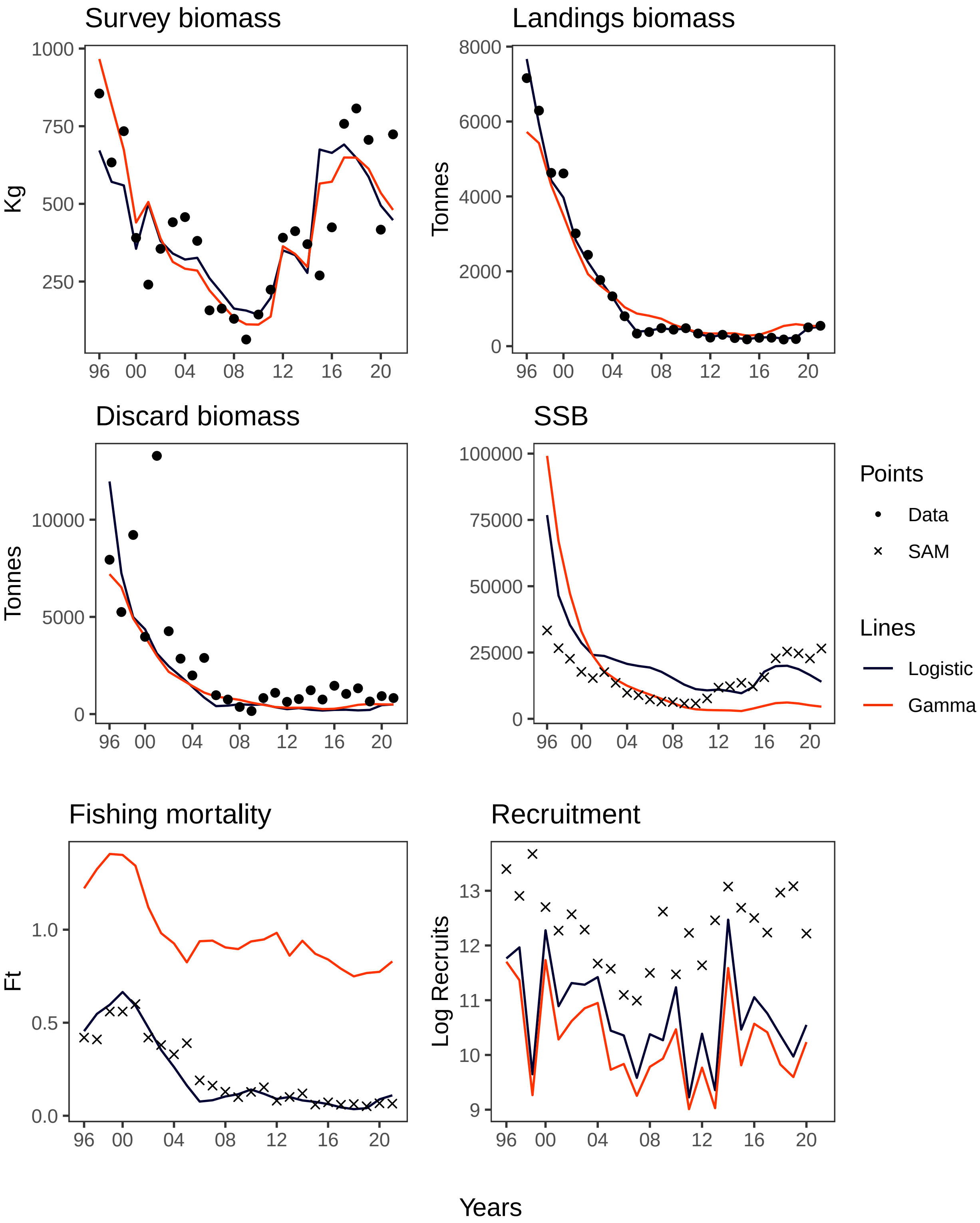


Figure 4.17: The black dots represents data points and the symbols × represents the SAM estimates. The dark line represents the median of the model output with the logistic selectivity and the red line is the median of model with the gamma selectivity. The gamma model fits well discard and landings biomass, and the estimates of SBB and recruitment are not too far from the logistic model, but the estimates of fishing mortality are too high and not credible, and the early years of the survey biomass are clearly overestimated.

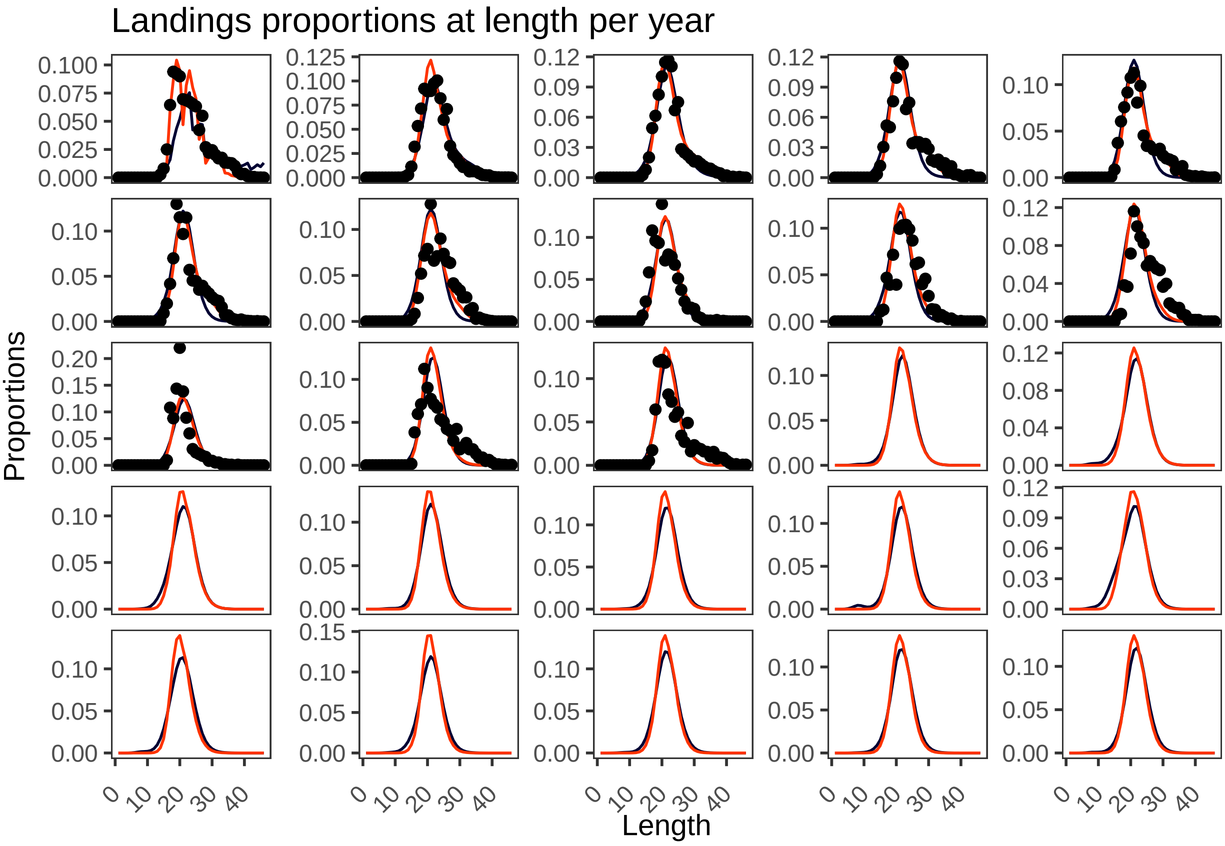


Figure 4.18: The figure shows a series of yearly plot of landings proportions at length. The black line is the median of the model with the fisheries logistic selectivity, while the red line is the median of the model with the gamma. The black dots represents data, which are available only untile 2009. Both model fits well the data and there is no relevant difference between the two.

log-uniform prior of the recruitment was lowered. Figure 4.21 shows the fit to the abundance indexes and the estimates of SSB, fishing mortality and recruitment. The black dots represents data points and the symbols × represents the SAM estimates. The dark line represents the median of the model output with the higher lower bound ($\log 7500$) and the red line is the median of model with the lower lower bound ($\log 200$). The fit to abundance index is consistent, but the recruitment and SSB a bit underestimated and fishing mortality has some bizarre peaks in the recent years. Sensitivity to recruitment bounds could mean that the model does not find a lot information in the data to estimate recruitment, especially in the last years.

The fit to proportions-at-length of landings and survey is shown in figure 4.22 and 4.23 respectively. Again the black line is the median of the model with the

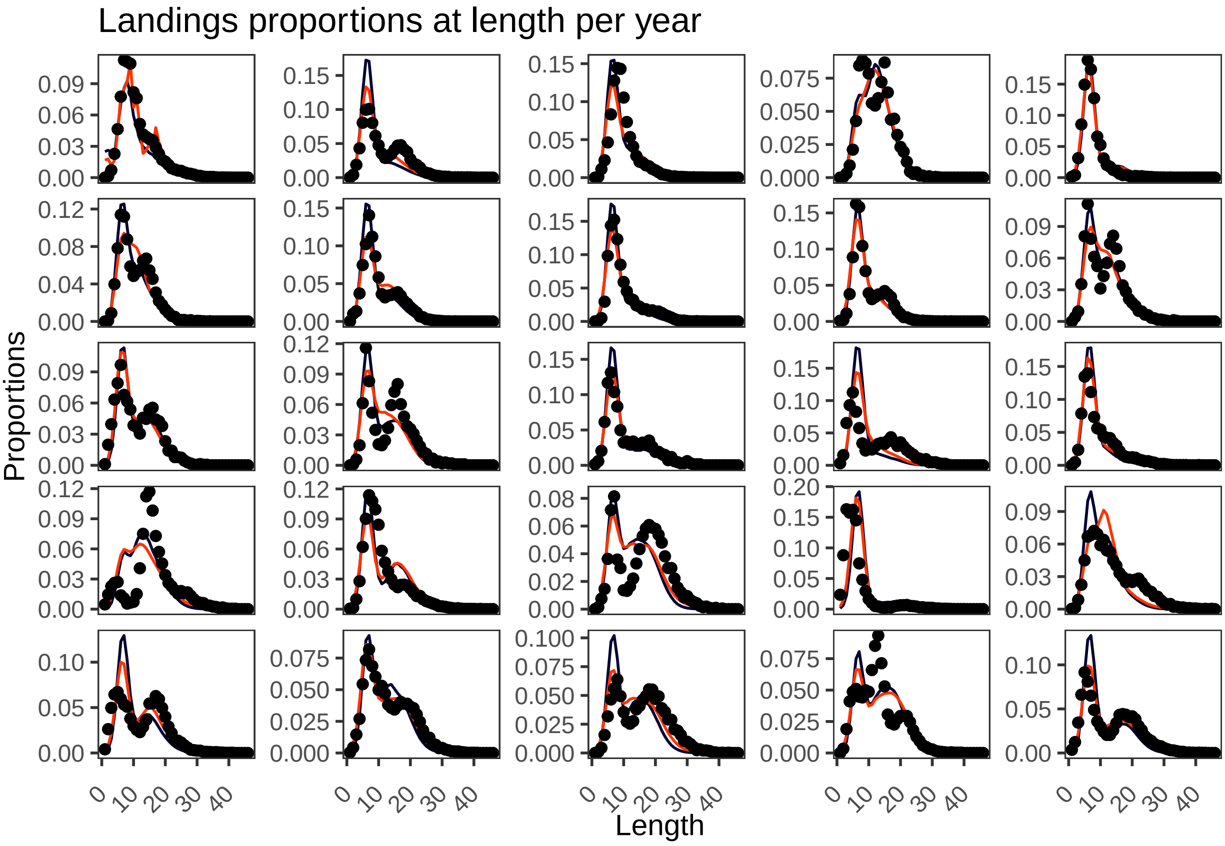


Figure 4.19: The figure shows a series of yearly plot of survey proportions at length. The black line is the median of the model with the fisheries logistic selectivity, while the red line is the median of the model with the gamma. The data has been fitted by using two separate surveys, with different parameters and likelihood. The first survey runs until 2010, while the second from 2011 onwards. Both model fits well the data and there is no relevant difference between the two.

higher lower bound and the red line is the median of the model with the lower lower bound. The black dots are data points, which for landings are available only until 2009. In this case the two models are completely overlapping and only the red line is visible.

4.4 Discussion

In this chapter we applied the “full version” of the Survey-LAndings Model (SLAM) to the whiting stock of subarea VIa. SLAM’s output was compared to the State Space Assessment Model (SAM), the stock currently used to assess whiting in this area (ICES (2022)). It is important to remark that the aim of the comparison with

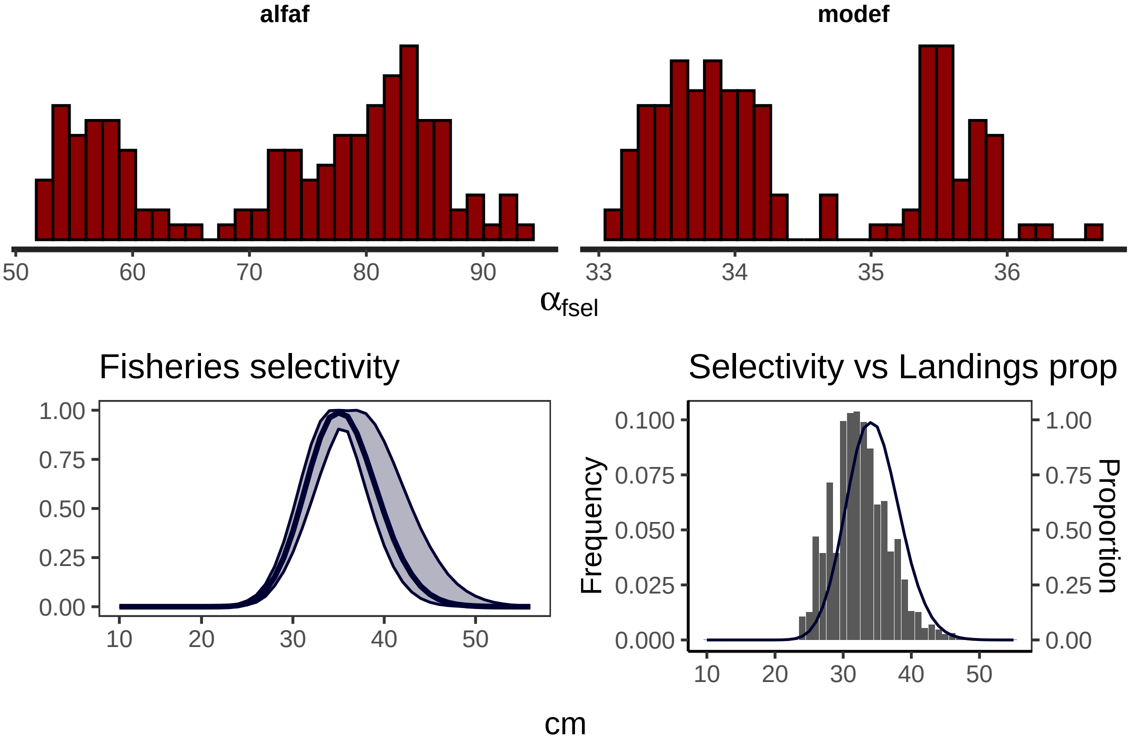


Figure 4.20: The upper half of the figure shows the posterior distribution of the parameters $mode_{fsel}$ and α_{fsel}. The distributions looks as if the model converged on two different values, the upper bound of α_{fsel} should have probably have set to 70 in order to avoid a bivariate distribution. The plots at the bottom left shows the shape of the selectivity, the line at the centre being the median and the shaded area around being the 95% credible interval. The high value(s) of α_{fsel} causes the angle of the curve to be very narrow. The plot at the bottom right compares on year of landings proportions-at-length with the median of the curve. It seems that the curve is almost trying to overfit the distribution of lengths.

SAM was not to check if SLAM could reproduce the results of ICES assessment exactly, but rather if SLAM's output was on a reasonable scale and could pick up SAM's relevant trends (i.e decrease/increase…). The two models are fitted to different data and are based on different assumptions. Overall it can be concluded that SLAM performed well against SAM.

SLAM fitted well both the compositional and the abundance data, and provided estimates of fishing mortality that were really close to SAM's. Fishing mortality for the two models express slightly different quantities: for SLAM fishing mortality is a fishing pressure which is constant for fish of every size. The fishing mortality reported by ICES (2022) is the one experienced by fish of age 1 to 3. The estimates of Spawning Stock Biomass (SSB) were also satisfactory. The model managed to

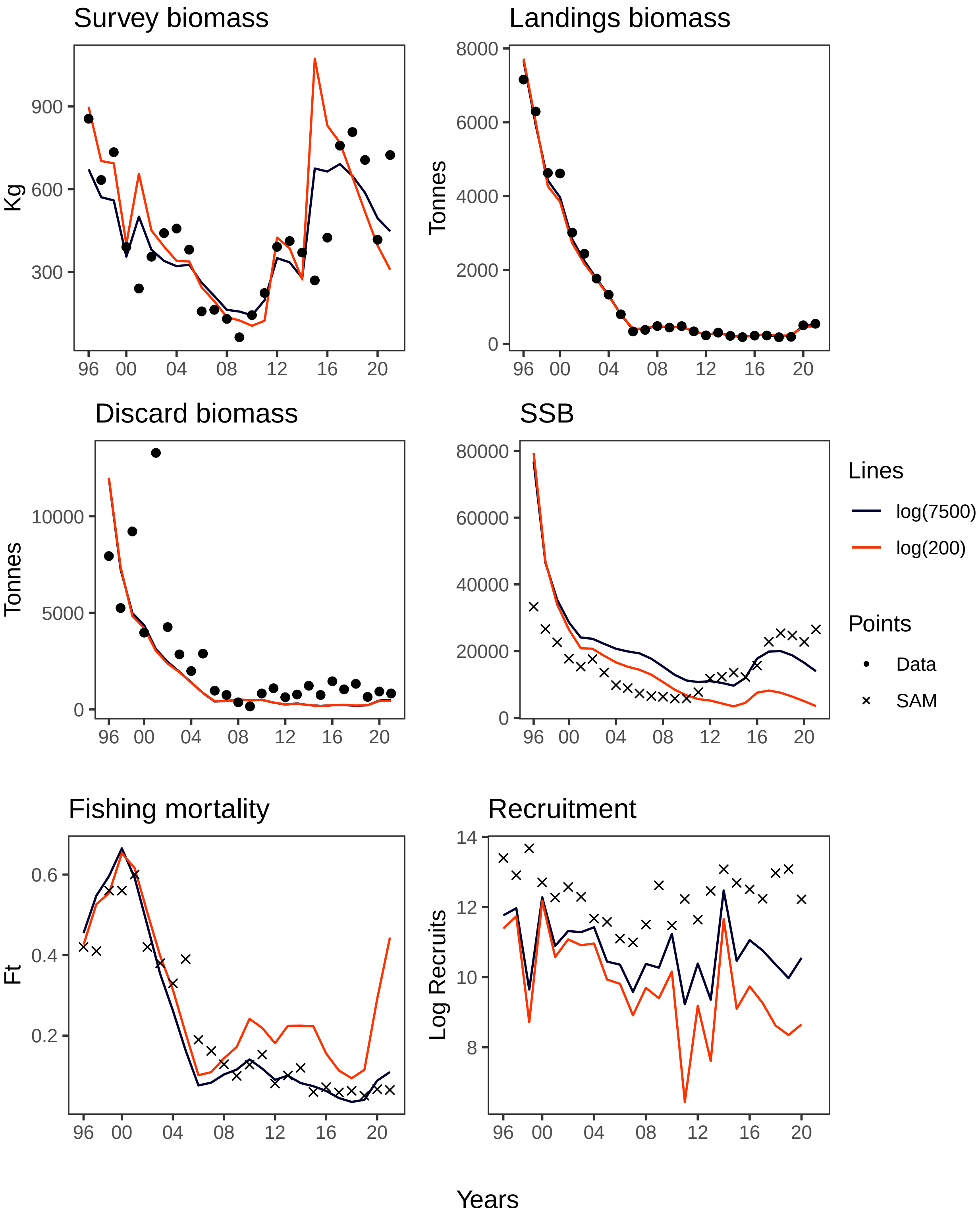


Figure 4.21: The figure shows the fit to the abundance indexes and the estimates of SSB, fishing mortality and recruitment. The black dots represents data points and the symbols × represents the SAM estimates. The dark line represents the median of the model output with the higher lower bound ($\log 7500$) and the red line is the median of model with the lower lower bound ($\log 200$). The fit to abundance index is consistent, but the recruitment and SSB a bit underestimated and fishing mortality has some bizarre peaks in the recent years. Sensitivity to recruitment bounds could mean that the model does not find a lot information in the data to estimate recruitment.

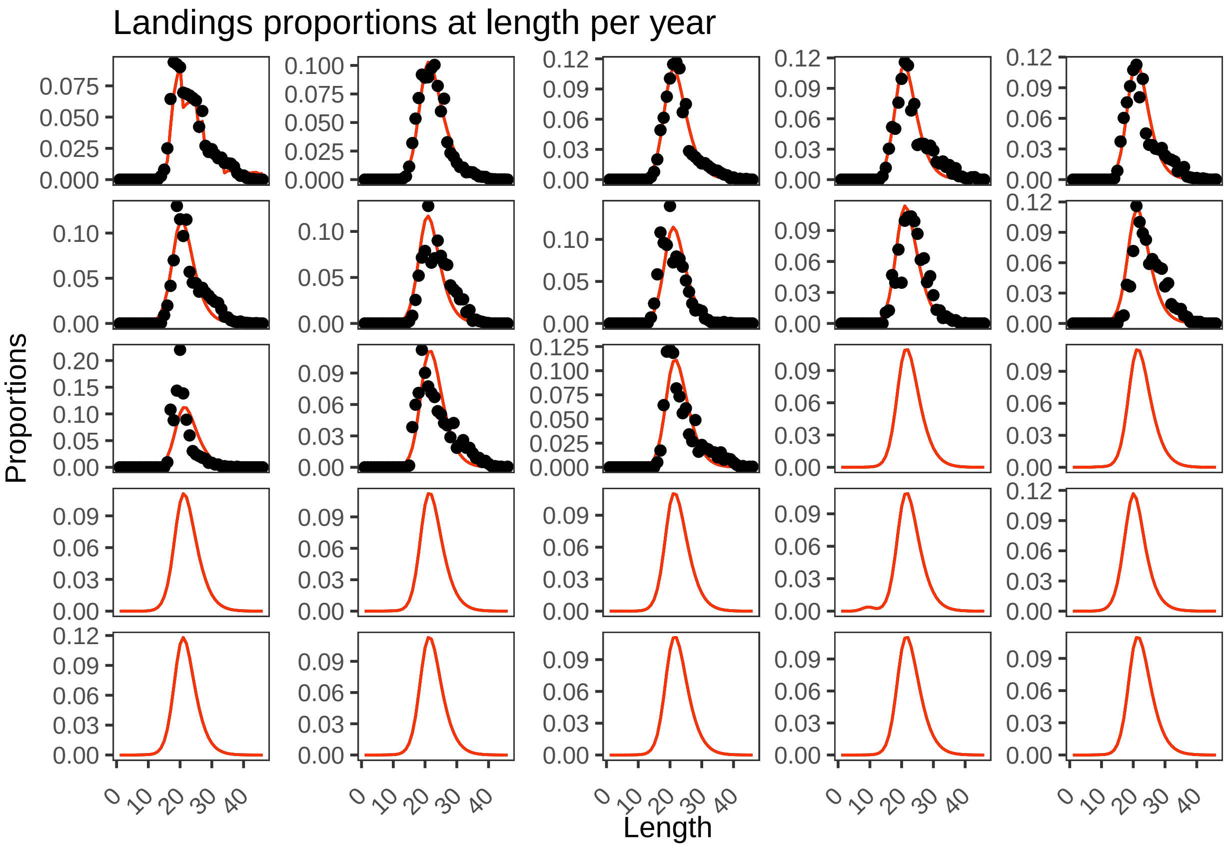


Figure 4.22: The figure shows a series of yearly plot of landings proportions at length. The black line is the median of the model with the higher lower bounds and the red line is the median of the model with the lower lower bound. The black dots represents data, which are available only untile 2009. Both model fits well the data and only the red line on top is visible because the two estimates are completely overlapping.

estimate well all parameters' posteriors even by using almost exclusively uninformative priors, meaning that the data were sufficiently informative. The estimates of recruitment were slightly lower compared to SAM's, but this is not a major concern. The reasons for this discrepancy could be several: first of all, SAM is an age based model that assumes recruitment as year fish of one year old. SLAM is a length-based model and as such it interprets recruitment as the first consistent length peak appearing in survey data. This is a major difference in the two model's assumption, that might lead to difference in the estimates. Moreover, length data are renowned to provide weak information about recruitment and this could result into being a problem for producing a reliable estimate. A possible way to improve the estimates of recruitment could be assume they follow a time series. This is

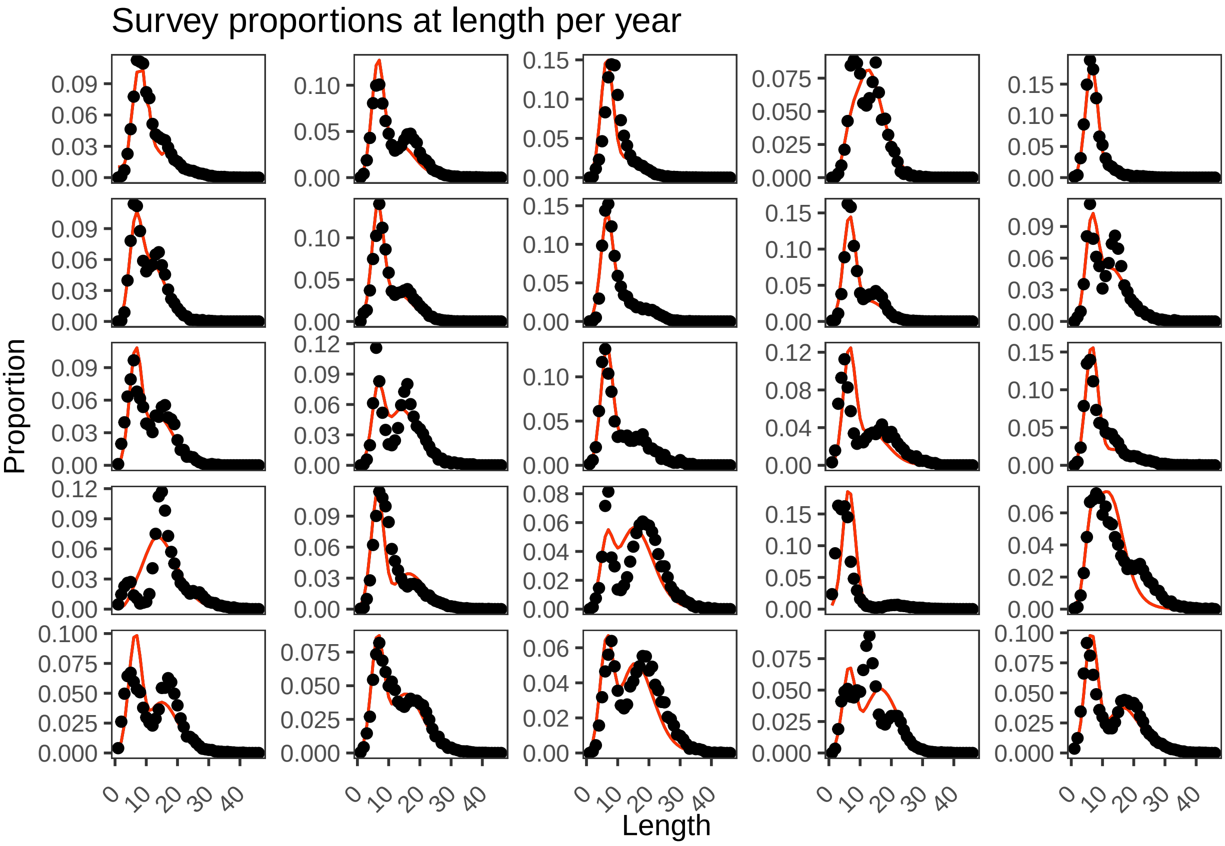


Figure 4.23: The figure shows a series of yearly plot of landings proportions at length. The black line is the median of the model with the higher lower bound and the red line is the median of the model with the lower lower bound. The data has been fitted by using two separate surveys, with different parameters and likelihood. The first survey runs until 2010, while the second from 2011 onwards. Both model fits well the data and only the red line on top is visible because the two estimates are completely overlapping.

the assumption in SAM, and it is fair to assume correlation between years for species with low recruitment variability like whiting (Nielsen & Berg (2014)). This would probably not help to improve the scale, but would still help the model in the estimate.

In order to fit the model, the survey was split into two, pre and post 2011. We needed to specify different parameters, different likelihood functions and even two different selectivity shapes. The fact that the model estimated different parameters for the two survey and even two different selectivity shapes confirms that the change in the survey protocol had a significant impact on the sampling. Before fitting the model, we were not intended to use a dome-shaped selectivity for the survey. Often, in stock assessment the selectivity of the survey is assumed to be logistic and the selectivity of the fisheries is assumed to be dome shaped. Nevertheless, after the data visualization process made in chapter II (2.3), it was evident that the survey was not efficient in catching big fish, because the large length classes found in the landings composition were absent in the survey. Finding SLAM's best fit was not an easy process, it required a lot of trial and error to find the best configuration, even though we already have experience with fitting it to pseudo data. This reminds how real data can be extremely complex and conducting a stock assessment should always be preceded by a detailed investigation on the stock characteristics.

The priors used were largely uniform, with the only exception of fishing mortality. Here the mean of the log-normal of each prior is set to the mean of the posterior of the year before. This is because fishing mortality is expected to be correlated from one year to the other. It was also necessary to put recruitment on a log scale and then apply a log-uniform prior. Many Bayesian stock assessments specify a uniform prior on the logarithm of the parameter governing carrying capacity in the log-unfished recruits, but Thorson & Cope (2017) demonstrated as this is not always advisable, especially in data limited situations. In 3 of 4 case studies considered, the arbitrary upper bound on a uniform prior on log-maximum recruitment determined the results of the assessment. We tried to estimate the real value of recruitment using a uniform prior, but the result was not satisfactory. Further investigation is required to better understand the influence of the shape of the priors and the initial values chose for SLAM.

This chapter also explored SLAM's sensitivity to some key assumptions. We analysed the sensitivity to two fixed parameter values, the first of which was the sensitivity to input sample size. The model showed low-to-moderate sensitivity to the input sample size when we decreased the values from 70 to 30 ($n_{\text{surv1}} = n_{\text{surv2}} = neff_{\text{land}} = 70$ to $neff_{\text{surv1}} = neff_{\text{surv2}} = n_{\text{land}} = 30$). We were not expecting to observe sensitivity to the choice of sample size after implementing the Dirichlet-multinomial likelihood. The sensitivity to sample size showed by the model was definitely higher than the sensitivity in found on pseudo chapter III (see 3.8). Moreover, in the previous chapter the input sample size was set 10 times higher than the real value, while here the input sample size was only halved. The reason is not obvious, we might speculate that it is related to the fact that the Dirichlet-multinomial likelihood assumes no correlation between the length classes within one year. This was true for the pseudo data, that were generated by sampling the population by a multiomial random sample, but it is not true for the data. Length observation in the data are correlated because fish tends to distribute in space and aggregate in schools by size. This violates the Dirichlet-multinomial assumption of independent observation and might be the cause of the sensitivity we observed. Jim Thorson, the same author who implemented the Dirichlet-multinomial likelihood for stock assessment (Thorson et al. (2017)), recently came up with a multivariate-Tweedie likelihood (Thorson et al. (n.d.)). The multivariate Tweedie has three main advantages. The first one is that it can identify both overdispersion (downweighting) or underdispersion (upweighting) relative to the input sample size. Second, proportional changes in the input sample size are exactly offset by parameters. The last one is that it arises naturally when expanding data arising from a hierarchical sampling design. A future implementation for SLAM could be replacing the Dirichlet-multinomial likelihood with a Tweedie-multinomial. The second sensitivity analysis on fixed parameter assumption we performed was the one to the $L50$ of the discard selectivity ogive. In the reference model we used values calculated by R. M. Cook (2019), who found a decreasing trend in this value for whiting in West of Scotland. When we tried to assumed fixed values, either high or low, the model showed basically no sensitivity. This is excellent, because it means that for a case in which we do not have information about the value of this parameter, we do not have to worry about finding a precise value.

The other class of sensitivity analysis regarded structural assumptions. Firstly the sensitivity of the model to the shape of the survey selectivity was investigated. The reference model used a logistic and a gamma, so the test assumed both selectivities to be logistic in one case and both selectivities to be gamma in the other. The model was proved to perform equally well when the two selectivities were assumed to be gamma, but its performance was much worse when both selectivities were assumed to be logistic. Especially, it mis-fitted the early years of landings and discard biomass, underestimating them, and it provided different estimates of fishing mortality and SSB compared to the reference model. While estimates of SSB are lower but still acceptable, fishing mortality is poorly estimated, not just in scale but also in shape. Nevertheless, this sensitivity is caused by the characteristics of the data rather than the model's ability of estimating the curves. As seen in 2.3, there are contrasting information between the maximum size in the length composition of the landings and the one of the survey. The logistic selectivity is much less flexible than a gamma and assumes the highest probability is always at the highest lengths. Having a logistic selectivity in both of the surveys means that the survey has the highest probability of catching big fish, if it cannot find them it is because they are being wiped out by the fisheries. This explains the higher values of fishing mortality. However, it does not provide an obvious explanation to the underestimation to the early years of discard and landings biomass data. This might require further investigation. The sensitivity of the model to the shape of the fisheries selectivity was also tested by replacing the logistic selectivity of the reference model with a gamma selectivity. The model resulted to be insensitive in the fit to the data and the estimates of recruitment and SSB, but it was quite sensitive in the estimates of fishing mortality, which resulted to be quite overestimated, even though the shape was right. It is known that the fishing selectivity likely has a dome-shaped curve in reality, which is the shape assumed by SAM. Nevertheless, the model already applies a gamma curve to the survey post 2011, and the model struggles to estimate two gammas at the same time, due to their high flexibility. As shown in figure 4.20, the spread of the gamma selectivity tends to grow larger, seeming to try to over-fit the landings length frequency. Having a logistic model works better because the logistic manages to "pin down" the gamma. We must also keep in mind that selectivity shape have been demonstrated to be inconstant over time, and sometimes are even subject to drastic changes (Sampson & Scott (2012)). This is another potential limitation for the model and might be object to further investigation in the future.

The last sensitivity analysis regard the lower parameter bound of the log-uniform prior of the recruitment. The model showed notable sensitivity in the estimates of fishing mortality and recruitment of the later years when the lower bound las decreased from log(7500) to log(200). Estimating recruitment in length based models is a problem, as length data do not include information as powerful as age data. If the model does not have clear information regarding recruitment, it might be that playing around with parameter bounds pulls the mean of the posterior from one side to the other. This might be what is happening in the later years of recruitment, which appear to be underestimated in later years when the lower bound of the prior is set to a lower value. This problem then propagates to the estimates of fishing mortality, which in the later years are slightly overestimated and show some peaks that are unlikely true.

The sensitivity analysis of this chapter helped to determine the robustness of a SLAM's qualitative conclusions. In this thesis we evaluated the model performance was evaluated only by visually inspecting the different lines of the model outputs against the data or SAM's estimate. Considering the relevance of these tests, a more accurate evaluation could be considered for publishing the study. A possible solution could be offered by Morris method, also called the elementary effects method, which is based on the ratio of the change in an output variable to the change in an input parameter. The Morris method is easy to understand, does not depend on assumptions about the model and is computationally inexpensive, however, it cannot quantify the contribution of a parameter to the variability of the output (Wu et al. (2013), Morris et al. (2014)).

5

Chapter V: survey-only version applied to four VIa stocks

Traditional methods of evaluating fish stocks heavily rely on commercial catch information. However, there's a growing need for alternative assessment approaches in various scenarios, for instance or bycatch or collapsed stocks. In the first case the species might have low to no commercial values, and a large part might be discarded. If discard information are inaccessible, the information goes lost. Misreporting and unrecorded discards are an issue, as they make it hard to accurately convert landings into actual sea catches. In collapsed stocks the catch data can be unreliable or unavailable because the fishery might shut down. Moreover, there's an increasing demand for advice on numerous data limited stocks.

In this context, research-based surveys conducted at sea using standardized methods and controlled conditions offer invaluable fishery-independent data crucial for conducting assessments. In the latest years, several assessments have been conducted using only information coming from research vessels (Cook (2004), Cook (1997), Cook (2013)). The most renowned survey only method is the SURvey-BAsed stock assessment model (SURBA), which has quite a long history and was first used to analyze the major fish stocks of the North Sea (Cook (1997)). Since then, it has been extensively used in assessments conducted by the International

Council for the Exploration of the Sea (ICES) for various bottom-dwelling fish stocks (Beare et al. (2005); Needle (2002)). It's been applied to evaluate cod stocks in Northwest Atlantic Fisheries Organization (NAFO) regions like Divisions 2J3KL (DFO, 2013) and Subdivision 3Ps (Cadigan (2010)). Additionally, even a state-space variation called the SSURBA model (Space SURvey-BAsed) has been implemented and applied to the Grand Banks stock of American plaice (*Hippoglossoides platessoides*) (Kumar et al. (2020)). SURBA and other survey only models have been proved to be able to capture effectively fluctuations in survey biomass, nevertheless these models normally cannot offer precise estimates of absolute abundance, but they rather offer relative values on a scale without a fixed reference point. In general, survey-based methods might offer quicker updates on the stock's condition compared to methods relying on catch data (Mesnil et al. (2009), J. Cotter et al. (2009)).

In this chapter we test the Survey-LAndings-Model (SLAM) in its “survey only version” for data-limited species. For this purpose we chose two well assessed species from subarea VIa, one of which is again whiting (*Merlangus merlangius*), and the other one is haddock (*Merlanus aeglefinus*). These two species have a similar body type but haddock has much bigger variability in recruitment. We also chose two un-assessed species from the same area, grey gurnard (*Eutriglia gurnardus*) and lemon sole (*Microstomus kitt*). These two species do not have a stock assessment available, and they have completely different body types and swimming habits. Stocks with different characteristics will be targeted differently by the survey and the fisheries, and this might imply different gear selectivity that may affect as well the model's assumptions. Therefore, it is important to test SLAM's behavior on different species.

5.1 Materials and Methods

In this chapter we used survey data from subarea VIa for four species: whiting (*Merlangus merlangius*), haddock (*Merlanus aeglefinus*), grey gurnard (*Eutriglia gurnardus*) and lemon sole (*Microstomus kitt*). Information about the species biology and how the data were prepared can be found in Chapter II.

Whiting and haddock from subarea VIa are already assessed by the International Council for the Exporation of the Sea (ICES). The results are published online on reports that are regularly updated (ICES (2022), ICES (2023)). Haddock assessment is available only until 2013, because after that year ICES decided to incorporate the assessment of subarea VIa with the rest of the North Sea. This is because scientific investigations proved that what was considered to be two separate stock is actually a single stock. The assessments are conducted with the State-space stock-Assessment Model (SAM). SAM has different assumptions and relies on full catch and age data, therefore we do not expect the models to overlap, but we are interested to see if SLAM can pick up the relevant trends.

Since SLAM is fitted to survey data only, and the survey samples a very small proportion of the population, the survey catchability parameter q cannot be estimated because the model has no information from the fisheries to reconstruct the real size of the population. The parameter q was fixed to 1, meaning that we're assuming that the survey samples the population with the maximum possible efficiency. The estimates of Spawning Stock Biomass (SSB) and recruitment will then be returned in the same order of magnitude of the survey biomass, and in order to make them comparable with SAM results we divided each time series by its mean. This means that it will be only possible to compare the trends of the output and not the absolute scale. This approach is the same used in Cook (2013).

The absence of information from the fisheries impacts also the model's ability to estimate the selectivities, in particular it is impossible for the model to estimate both survey and fisheries selectivity simultaneously. Therefore one must be treated as known, and since fisheries selectivity is more interesting from the stock assessment's point of view, the two survey selectivity (pre and post 2011) were assumed to be known. One of the two parameters controlling the shape of the fishing selectivity, which depending on the stock could be logistic or dome-shaped, was also fixed. For whiting, for instance, it was applied a logistic function where the inclination β_{fsel} is assumed to be known and $L50_{fsel}$ is estimated. The information regarding the input values were taken from the results presented in chapter IV For the other stocks there was no prior knowledge about what the fishing selectivity nor the survey selectivity. The the survey selectivities were assumed to be known and dome shaped, and the fisheries selectivity a dome-shaped curve with a known $mode_{fsel}$ and an estimated α_{fsel}. It was possible to use three gamma curves because two of them are fixed, therefore the model has no problem of convergence relative to the excessive flexibility of the gamma curve, as observed in the previous chapter (4.17 and 4.20). The reason behind preferring a dome-shaped curve is that this is likely the true shape of the fisheries selectivity. This is because the bigger fish the more likely they are to escape the trawlers, since they are faster and more experienced, and the probability of catching them decreases after a certain size. SAM too assumes the fisheries selectivity to be dome-shaped.

The simulations in this chapter were made by running SLAM in the survey-only version for all the four species, using 3 chains, 50,000 iterations and a thinning of 500.

The fixed values used for every stock are reported in table 1.1, while the priors and initial values used for the fitting parameters are reported in table 1.2.

Table 5.1: The table summarises the values we used for the fixed parameters in the survey-only test on whiting, haddock, lemon sole and grey gurnard.

Parameter	**Whiting**	**Haddock**	**Grey Gurnard**	**Lemon sole**
y_{min}	1989	1989	1989	1989
y_{max}	2020	2020	2020	2020
$nyears$	31	31	31	31
Dt	1	1	1	1
l_{min}	8	8	8	8
l_{max}	52	52	42	42
$nlen$	45	45	35	35
DL	1	1	1	1
$L0$	1	1	1	1
α_{wgt}	.0093	.0157	.007	.0238
β_{wgt}	2.9456	2.8268	3.05	2.7643
c_{wgt}	1.13	1.16	1	1.04
α_M	.2	.2	.2	.2
β_M	$-.3$	$-.3$	$-.3$	$-.3$

Continued on next page

Table 5.1 – continued from previous page

Abbreviation	Initial value/s	Fixed or fitting		
$L50_{mat}$	20.5	20	25.25	18.5
β_{mat}	.3	.6	.3	.3
$mode_{ssel}1$	26	25	30	35
$\alpha_{ssel}1$	3.6	3.5	3.5	8.5
$mode_{ssel}2$	29	27	27	32
$\alpha_{ssel}2$	3	2.5	3	8
$mode_{fsel}$	–	25	30	25
β_{fsel}	.6	–	–	–
q	1	1	1	1

5.2 Results

5.2.1 Whiting (*Merlangus merlangius*)

The trace plots and the histograms for some of the most important parameters can be found in the appendix of chapter V under the paragraph whiting. The chains have mixed well and do not highlight any serious issue. There are no obvious signs of autocorrelation, even if some parameters are likely auto-correlated, like L_∞ and K. Figure 5.1 shows SLAM in its survey only version fitted to whiting data from subarea VIa (West of Scotland). The dark line is the model output median and the shaded area around it is the 95% credible intervals. We observe that the model fits the survey biomass data, displayed as black dots, quite well. Almost all the points lie between the intervals. The symbols × in the graphs of Spawning Stock Biomass (SSB), fishing mortality and recruitment, represent the quantities estimated by the State-Space Stock Assessment Model (SAM). Values of recruitment and SSB have been scaled to be comparable with the survey scale. We notice how the estimated quantities of SSB resembles the pattern of the survey biomass. This is expected, because the model does not have any other information out of survey abundance to estimate SSB. The values of fishing mortality are much higher than SAM's, and even though the trend is picked up correctly, values of 1.2 for whiting VIa are too high. Recruitment trends are also approximately right, even though there is high uncertainty.

Table 5.2: Table showing the prior and initial values chose for the fitting parameters of whiting, haddock, grey gurnard and lemon sole.

Parameter	**Whiting**	**Haddock**	**Grey Gurnard**	**Lemon sole**
$Ft_{l,1}$	prior: $U \sim (0,1)$ inits: .2	prior: $U \sim (0,1)$ inits: .2	prior: $U \sim (0,1)$ inits: .2	prior: $U \sim (0,1)$ inits: .2
$Ft_{l,y+1}$	prior: $log(N) \sim (Ft_{l,y}, \sigma_{Ft})$ inits: .2	prior: $log(N) \sim (Ft_{l,y}, \sigma_{Ft})$ inits: .2	prior: $log(N) \sim (Ft_{l,y}, \sigma_{Ft})$ inits: .2	prior: $log(N) \sim (Ft_{l,y}, \sigma_{Ft})$ inits: .2
σ_{Ft}	prior: $U \sim (.01,1)$ inits: .2	prior: $U \sim (.01,1)$ inits: .2	prior: $U \sim (.01,1)$ inits: .2	prior: $U \sim (.01,1)$ inits: .2
α_{fsel}	– –	prior: $log(N) \sim (1.3,.2)$ inits: 1	prior: $N \sim (2.8,.2)$ inits: 2.8	prior: $N \sim (2.3,.2)$ inits: 2
$L50_{fsel}$	prior: $log(N) \sim (29,3)$ inits: 1.5	– –	– –	– –
Rt	prior: $log(U) \sim (5,17)$ inits: values in ICES, 2022	prior: $log(U) \sim (5,17)$ inits: values in ICES, 2023	prior: $log(U) \sim (5,17)$ inits: $log(\sum \text{dat\_lf}_{1:15,y+1})$	prior: $log(U) \sim (5,17)$ inits: $log(\sum \text{dat\_lf}_{1:15,y+1})$
μ_R	prior: $U \sim (5,20)$ inits: 15	prior: $U \sim (5,20)$ inits: 7.5	prior: $N \sim (4,13)$ inits: 15	prior: $N \sim (11,.3)$ inits: 11
σ_R	prior: $U \sim (.1,1.5)$ inits: 1	prior: $U \sim (.1,1.5)$ inits: 1	prior: $U \sim (.1,1.5)$ inits: 1	prior: $U \sim (.1,1.5)$ inits: 1
L_∞	prior: $N \sim (35,3)$ inits: 30	prior: $N \sim (35,.1)$ inits: 35	prior: $N \sim (30,3)$ inits: 30	prior: $N \sim (27,2)$ inits: 30
K	prior: $N \sim (.25,.1)$ inits: 0.34	prior: $N \sim (.35,.01)$ inits: 0.4	prior: $N \sim (.45,.1)$ inits: 0.41	prior: $N \sim (.5,.09)$ inits: 0.48
cv	prior: $U \sim (.01,.9)$ inits: 0.1	prior: $U \sim (.01,.9)$ inits: 0.1	prior: $U \sim (.01,.9)$ inits: 0.1	prior: $U \sim (.01,.9)$ inits: 0.1
$LF1$	prior: $Dir \sim (1)$ inits:	prior: $Dir \sim (1)$ inits:	prior: $Dir \sim (1)$ inits:	prior: $Dir \sim (1)$ inits:
$NS1$	prior: $log(N) \sim \sum(\text{dat\_lf}_{1,y}), 20)$ inits: $\sum(\text{dat\_lf}_{1,y})$	prior: $log(N) \sim \sum(\text{dat\_lf}_{1,y}), 20)$ inits: $\sum(\text{dat\_lf}_{1,y})$	prior: $log(N) \sim \sum(\text{dat\_lf}_{1,y}), 20)$ inits:$\sum(\text{dat\_lf}_{1,y})$	prior: $log(N) \sim \sum(\text{dat\_lf}_{1,y}), 20)$ inits:$\sum(\text{dat\_lf}_{1,y})$
σ_{sbiom}	prior: $U \sim (0,1)$ inits: 0.2	prior: $U \sim (0,1)$ inits: 0.2	prior: $U \sim (0,1)$ inits: 0.2	prior: $U \sim (0,1)$ inits: 0.2
$D\beta_{surv}$	prior: $U \sim (0,1000)$ inits: 250	prior: $U \sim (0,1000)$ inits: 250	prior: $U \sim (0,1000)$ inits: 250	prior: $U \sim (0,1000)$ inits: 250

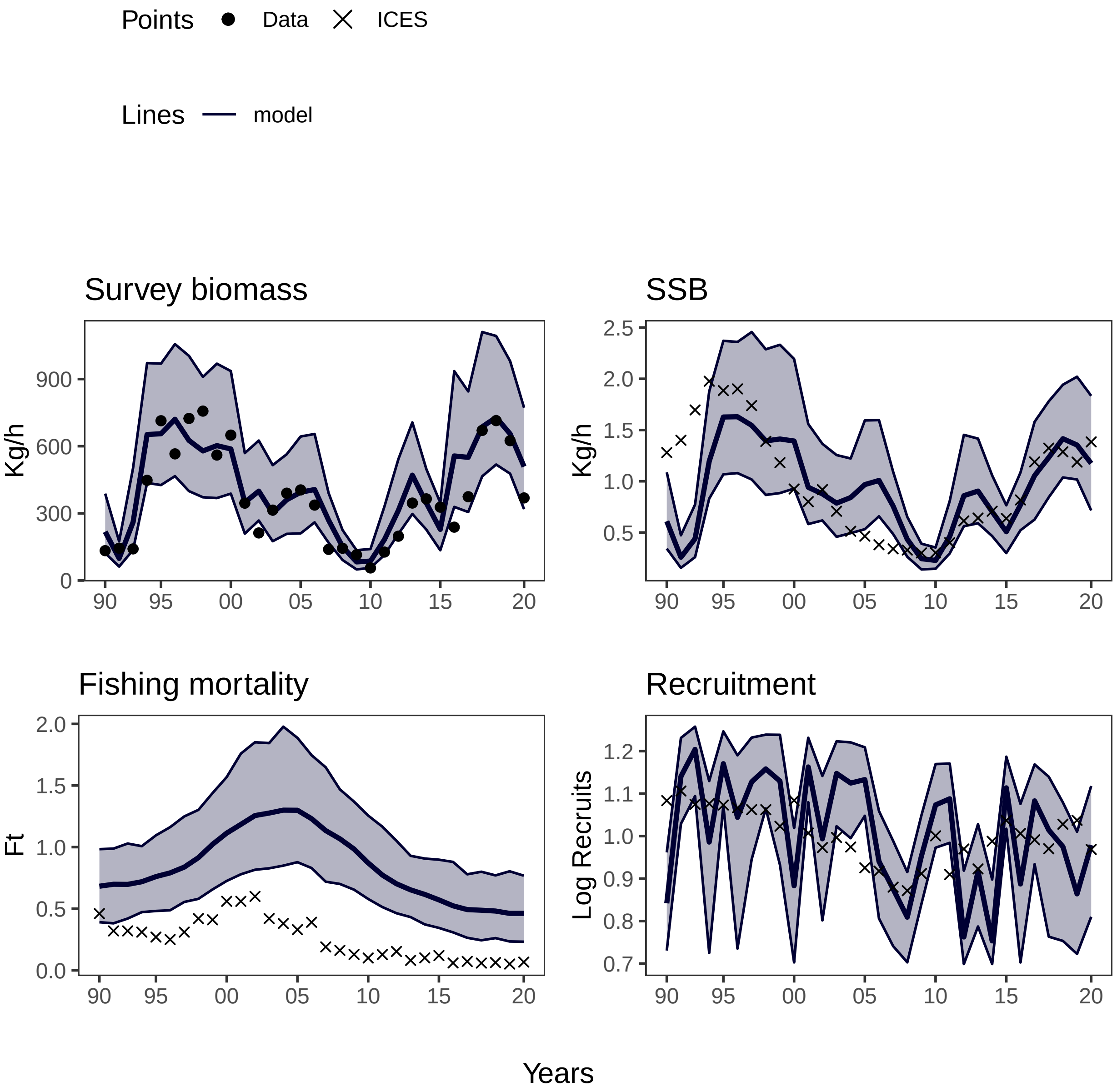


Figure 5.1: Whiting - The following figures display the model estimates of survey biomass, SSB, fisheries mortality and recruitment. The black dots are the data the model is being fitted to, while the × are estimates calculated by SAM (the values of recruitments and SSB are scaled to be comparable to SLAM). The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the data in the case of survey biomass and SLAM can pick up the trends of the estimates of SSB, fisheries mortality and recruitment calculated by SAM. Nevertheless, recruitment appears to be very variable and fishing mortality is too high.

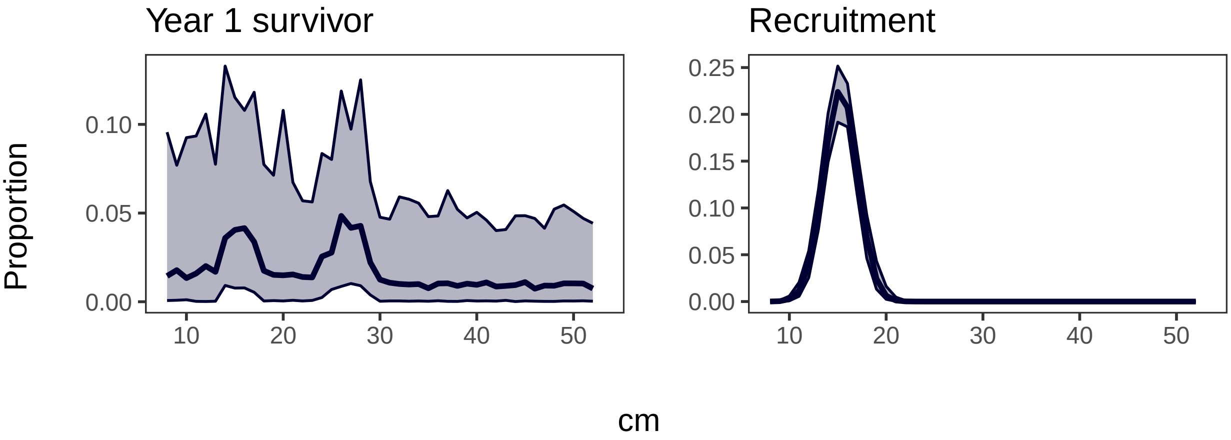


Figure 5.2: Whiting - The two graphs shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The model has high uncertainty and the proportions at length are not well estimated. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals, in this case they are very thin, meaning very low uncertainty.

Figure 5.2 shows two graphs with proportions-at-length. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. Still, the central line is the median of the estimates and the shaded area around are the 95% credible intervals. The first thing to notice is the high uncertainty of the estimates. It is clear that the model does not have much information about the state of the initial population. We notice how the first peak of the survivors of the initial population coincides perfectly with the peak in recruitment at 20. The initial population has also a very clear second peak at around 30 cm, which represents the second cohort, and then declines. In the recruitment proportions-at-length we observe how the credible intervals are very thin, this means the model has very little uncertainty on these values.

In the next plot, 5.3 grid we observe the model fit to proportions-at-length of survey for whiting from subarea VIa. Each graph represents the length distribution of a single year, form 1990 to 2000. The dark line is the model output median and

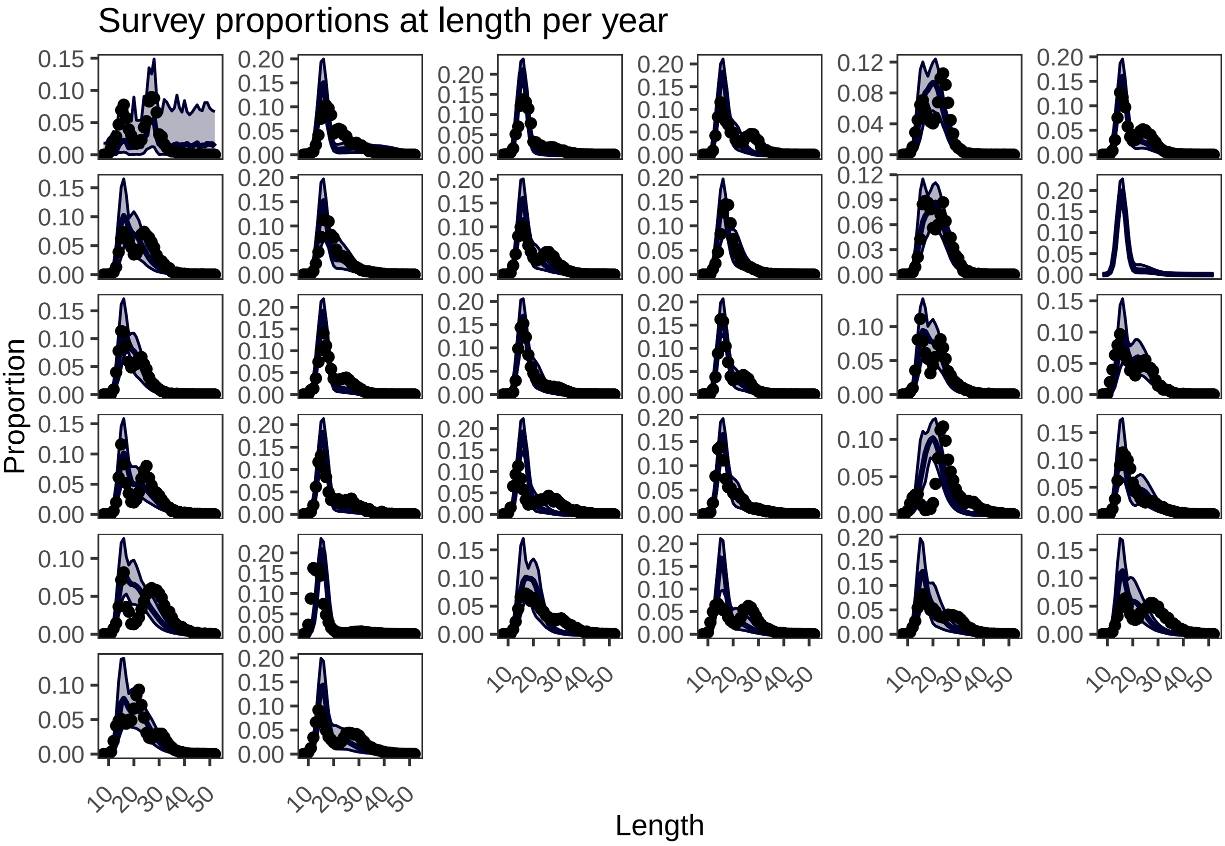


Figure 5.3: Whiting - The figure shows a series of yearly plot of survey proportions at length. The black dots represents data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. There is bigger uncertainty around the estimate of the first year. The model fits well the data.

the polygon around it is the 95% credible intervals. We notice how the credible intervals around the first years estimate are larger than for the other years, but the model fits the rest of the data well and with very little uncertainty.

Figure 5.4 shows the estimated logistic fishing selectivity curve. The inclination was kept fixed ($\beta_{fsel} = 0.6$) and $L50_{fsel}$ was estimated. The value of β_{fsel} and the mean of the log-normal prior of $L50_{fsel}$ was taken from the estimates provided by the full model version applied to whiting in chapter IV. Despite setting up a strong prior, the median of the parameter $L50_{fsel}$ sets at around 10, a very low value.

5.2.2 Haddock (*Melanogrammus aeglefinus*)

The trace plots and the histograms can be found in the Appendix V under the paragraph haddock. The chains have mixed well and does not highlight any serious

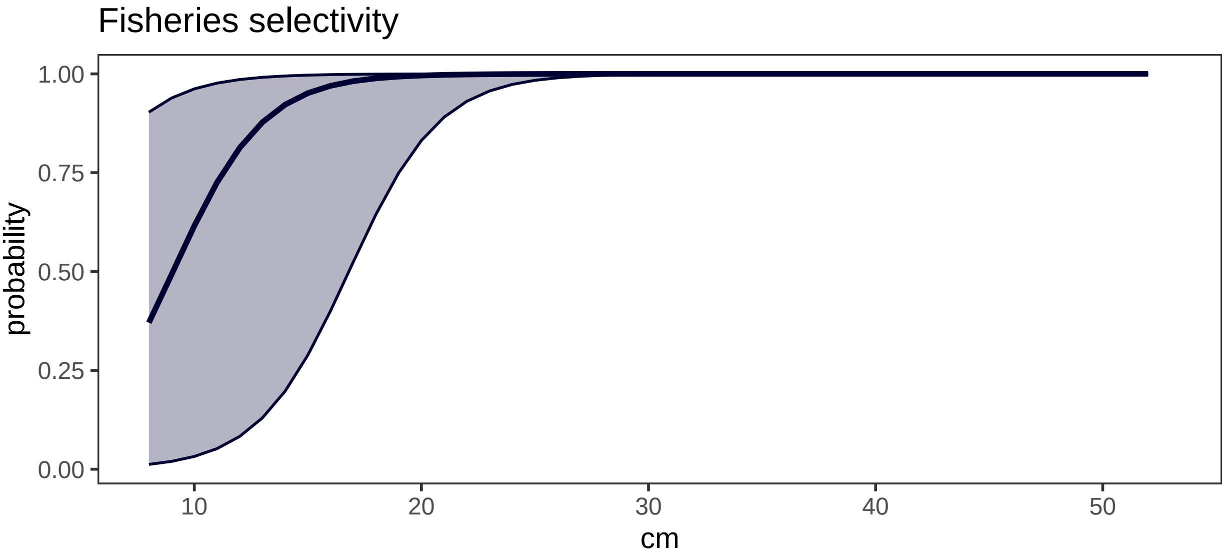


Figure 5.4: Whiting - The graph shows the gamma-shaped fisheries selectivity estimated by the model from 10 to 50 cm. The thick line is the median of the model output and the shaded area represents the 95% credible intervals. In this run, the mode of the gamma ($mode_{fsel}$) was kept fixed and only the width α_{fsel} was estimated. The estimate looks quite reasonable, with a minimum probability of being caught at 10 cm, then increasing to peak at around 29 to 31 cm, and then decreasing again.

issue. L_∞ and μ_R show some signs of autocorrelation and σ_R is clearly hitting a bound. other than that there are no signs of major issues and the model seem to have converged on these parameters. The second figure shows the histograms of the porteriors for the same parameters cited above. For haddock, K does not show any sign of auto-correlation with other parameters. Figure 5.5 shows SLAM in its survey only version fitted to haddock data from subarea VIa. The dark line is the model output median and the shaded area around it is the 95% credible intervals. We observe that the model fits quite well the survey biomass data, displayed as black dots. Almost all the points lies between the intervals. The symbols × in the graphs of SSB, fishing mortality and recruitment, represent the quantities estimated by SAM. Values of recruitment and SSB have been scaled to 1 be comparable, since the two models work on different scales. As for the run on whiting, we do not expect the two assessments to overlap, since the models have different assumptions and rely on different data sources. We notice how the estimated quantities of SSB resembles the pattern of the survey biomass, but even so the trends of SLAM's estimate are comparable with SAM's. SLAM and SAM's estimate of recruitment overlap. SLAM's estimate of fisheries mortality in the early years are probably a bit too low, but from 2000 onward SLAM manages to produce a fairly good estimate, comparable with ICES's assessment.

Figure 5.6 shows two graphs with proportions-at-length. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions-at-length for the recruitment across all years. Still, the central line is the median of the estimates and the shaded area around are the 95% credible intervals. We notice how the first peak of the survivors of the initial population coincides perfectly with the peak in recruitment at 20 cm. The initial population has also a very clear second peak at around 28 cm, which represents the second cohort, and then gradually declines. The model has high uncertainty regarding the initial population and it is not very estimated. In the recruitment proportions-at-length we observe how the credible intervals are very thin, this means the model has very little uncertainty regarding the value of this quantity.

The grid plot in figure 5.7 shows the model fit to proportions-at-length of survey for haddock. Each graph represents the length distribution of a single year, form 1990 to 2000. The dark line is the model output median and the polygon around it is the 95% credible intervals. Differently than whiting, the credible intervals around the first years estimate are not larger than for the other years, meaning that the model have little uncertainty regarding the distribution of the first year of survey length frequency and the length frequency of the initial population.

Figure 5.8 shows the estimated fishing selectivity curve. In this run, the mode of the gamma was kept fixed ($mode_{fsel} = 25$) and only the width α_{fsel} was estimated. The curve has a minimum for fish of 10 cm, it has a long peak at 1 from approximately 28 cm to 40 cm and then decrease slighly. overall it looks quite flat. The upper credible interval on the left part of the graph is not likely, since it estimates values for the selectivity (a probability) that are bigger than one.

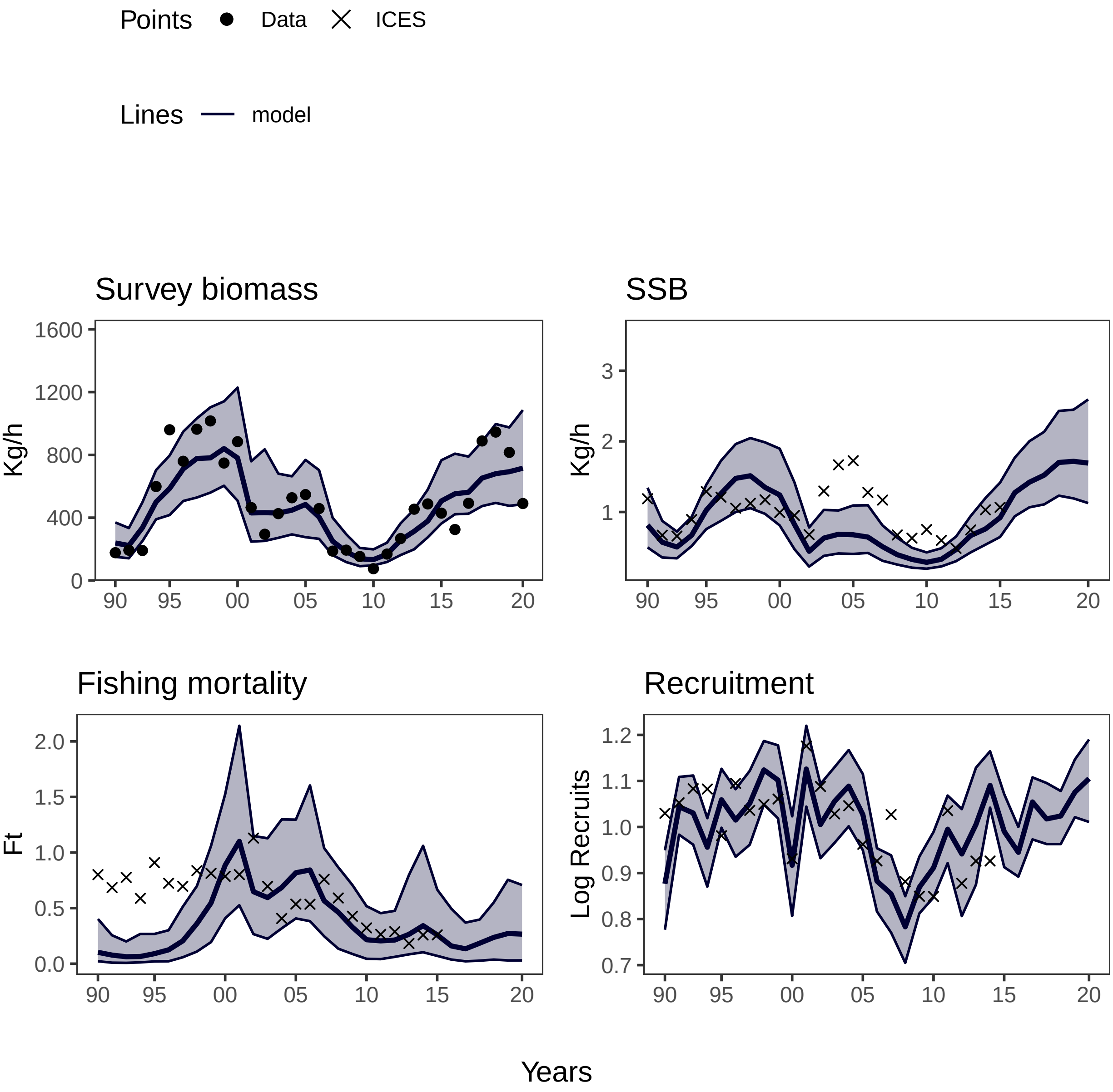


Figure 5.5: Haddock - The following figures display the model estimates of survey biomass, Spawning Stock Biomass, fisheries mortality and recruitment. The black dots are the data the model is being fitted to, while the symbols × are estimates calculated by SAM (the values of recruitments and SSB are scaled to be comparable to SLAM). The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the data and the estimates of SSB, recruitment and fishing mortality are comparable with the ICES's assessment, even though fishing mortality in the early years are probably a bit too low.

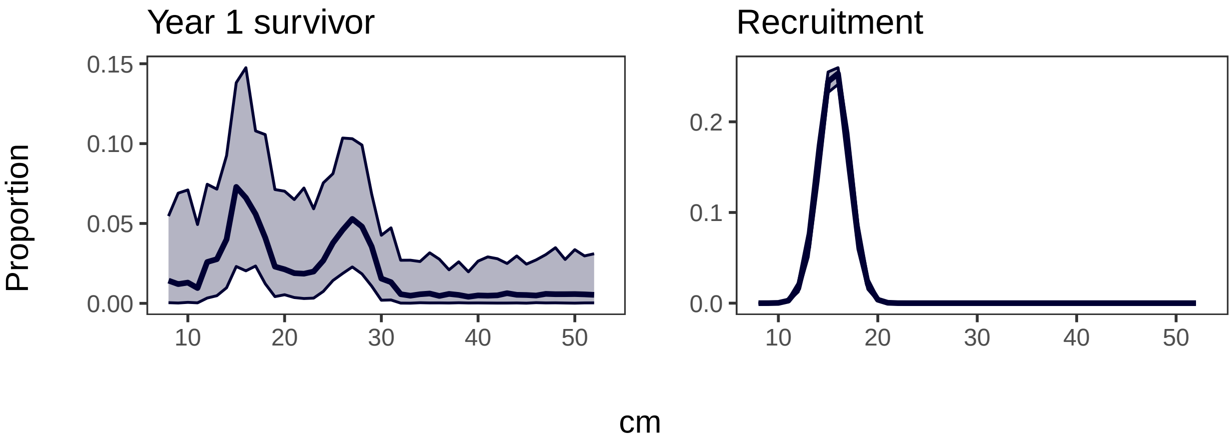


Figure 5.6: Haddock - The two graphs shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

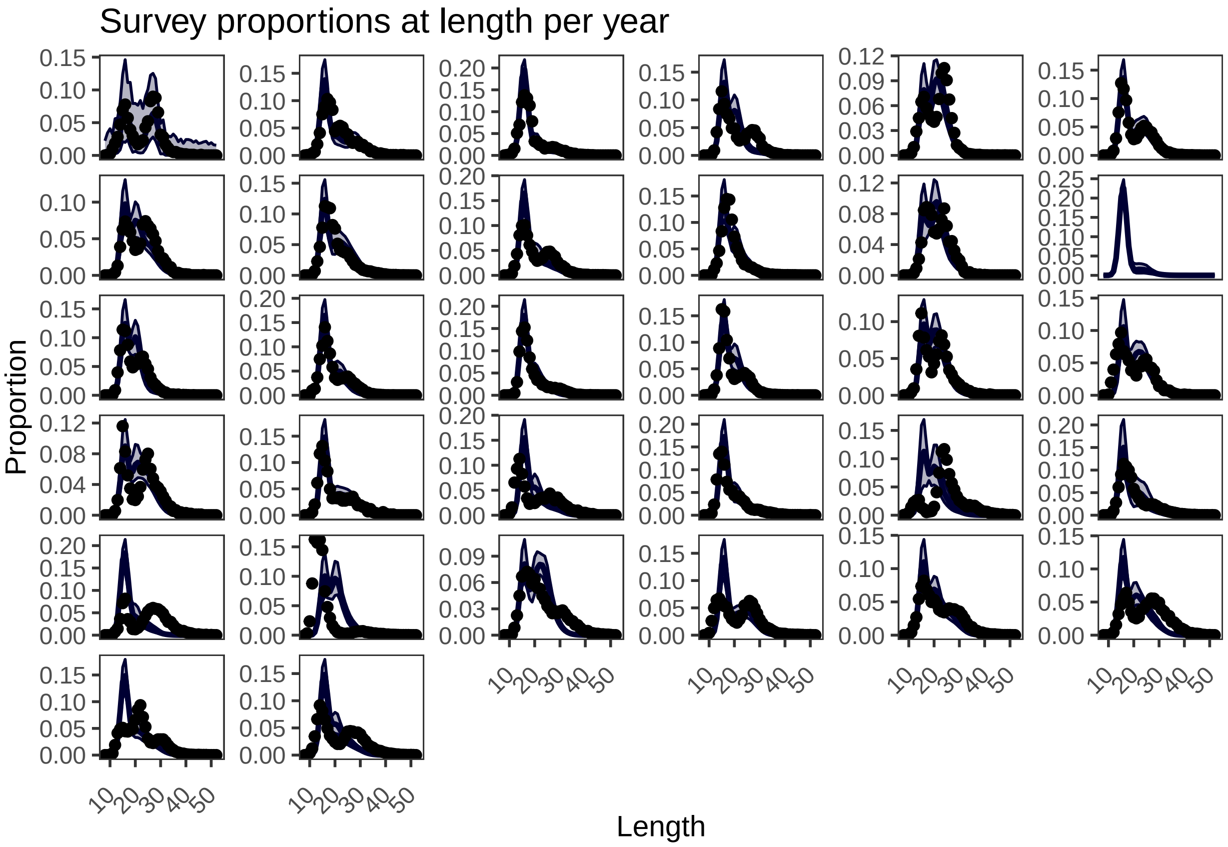


Figure 5.7: Haddock - The figure shows a series of yearly plot of survey proportions at length. The black dots represents data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The credible intervals around the first years estimate are not larger than the intervals around the other years. In general, the model fits well the data.

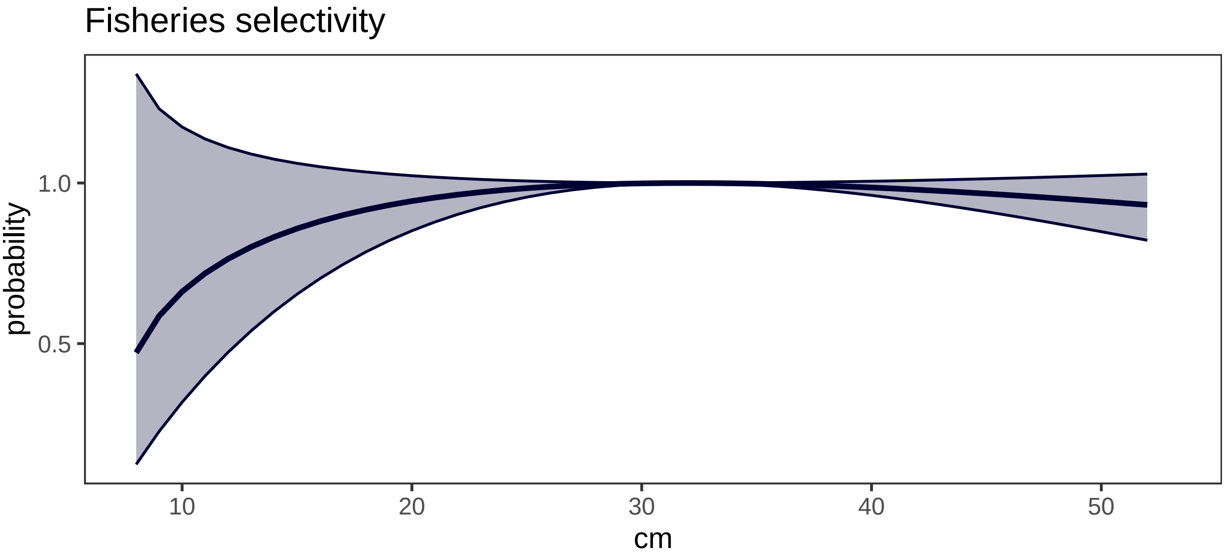


Figure 5.8: Haddock - The graph shows the gamma-shaped fisheries selectivity estimated by the model for haddock from 10 to 50 cm. The thick line is the median of the model output and the shaded area represents the 95% credible intervals. In this run, the mode of the gamma ($mode_{fsel}$) was kept fixed and only the width α_{fsel} was estimated. The curve looks quite flat, having a long peak at 1 from approximately 28 cm to 40 cm. The upper credible interval on the left part of the graph does not seem very likely, in fact it estimates values for the selectivity bigger than one. The median and the lower credible interval though, are plausible.

5.2.3 Lemon Sole (*Microstomus kitt*)

The trace plots and the histograms can be found in the Appendix V under the paragraph lemon sole. The chains have mixed well and does not highlight any serious issue. There are no obvious signs of autocorrelation. The next set of plots 5.9 shows some of the model estimates for SLAM applied to lemon sole. The dark line is the model output median and the shaded area around it is the 95% credible intervals. We observe that the model fits well the survey biomass data, disposed as black dots. All the points lies between the intervals. For this species there is no SAM assessment available for comparison of Ft, recruitment and SSB. As for the other species, we see how the estimated quantities of recruitment and especially SSB resembles the pattern of the survey biomass. Values of Ft seem reasonable and resemble the patterns of whiting and haddock fisheries mortality.

Figure 5.15 shows two graphs with proportions-at-length. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was

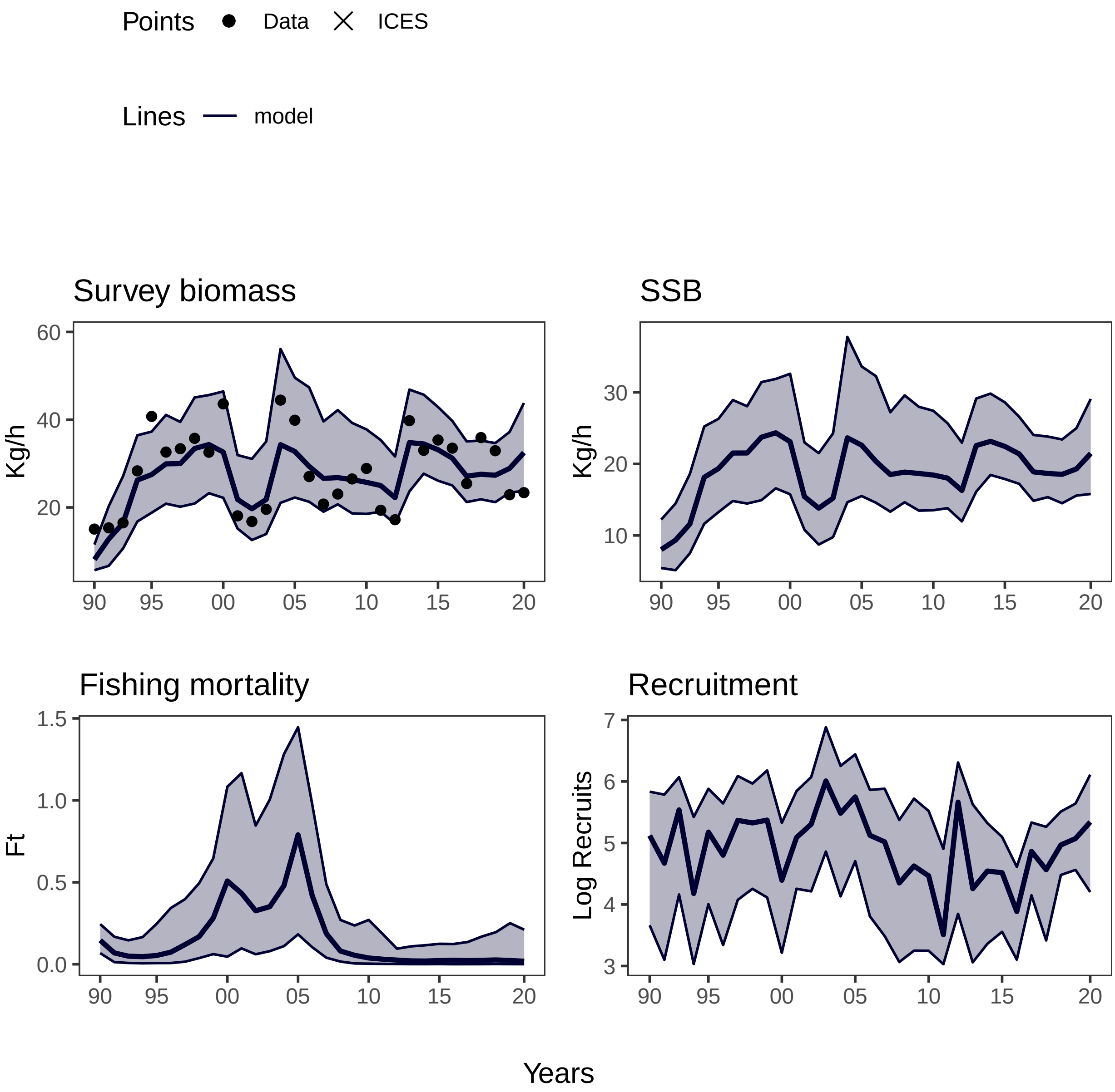


Figure 5.9: Lemon sole - The following figures display the model estimates of survey biomass, Spawning Stock Biomass, fisheries mortality and recruitment. The black dots are the data the model is being fitted to. For this model there is no SAM assessment available for comparison. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the survey biomass data. SSB resembles almost perfectly the trends in survey biomass. The medians of fishing mortality and recruitment seems plausible, fishing mortality tends to be higher in central years like the other two species and recruitment follows more or less the trend of survey biomass.

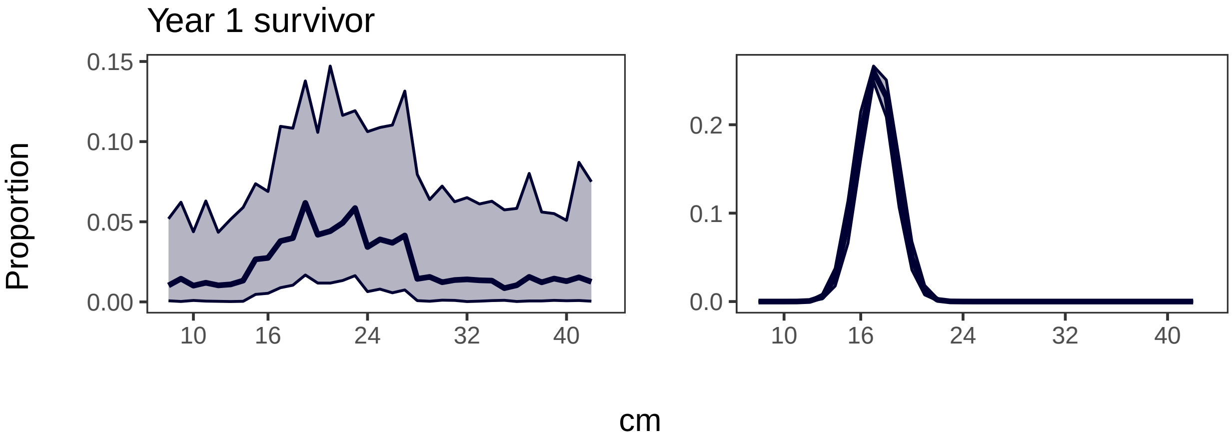


Figure 5.10: Lemon sole - The two graphs shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

applied and before recruitment was added, representing the survivors from the year before. The graph on the right shows the proportions-at-length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The initial population does not very clear peaks, and this reflects the situation in the survey proportions-at-length. In fact, fish appear quite late in the survey, probably when they are already two years old, that is why μ_R is quite high. Because of how the species grows, the length classes in the later years merge and it is no longer possible to distinguish cohorts.

Figure 5.11 shows the model fit to survey proportions-at-length. Each graph represents the length distribution of a single year, form 1990 to 2000. The dark line is the model output median and the polygon around it is the 95% credible intervals. The credible intervals have approximately all the same width around every year. Overall, the fit is good and the uncertainty is quite low. We observe how lemon sole does not have clearly distinct cohorts, but rather a single peak.

Figure 5.12 shows the estimated fishing selectivity curve. In this run, the mode of the gamma was kept fixed ($mode_{fsel} = 35$) and only the width α_{fsel} was estimated. The curve has a minimum for fish of 10 cm, it peaks at the maximum probability of 1 from approximately 24 cm to 36 cm and then decrease again.

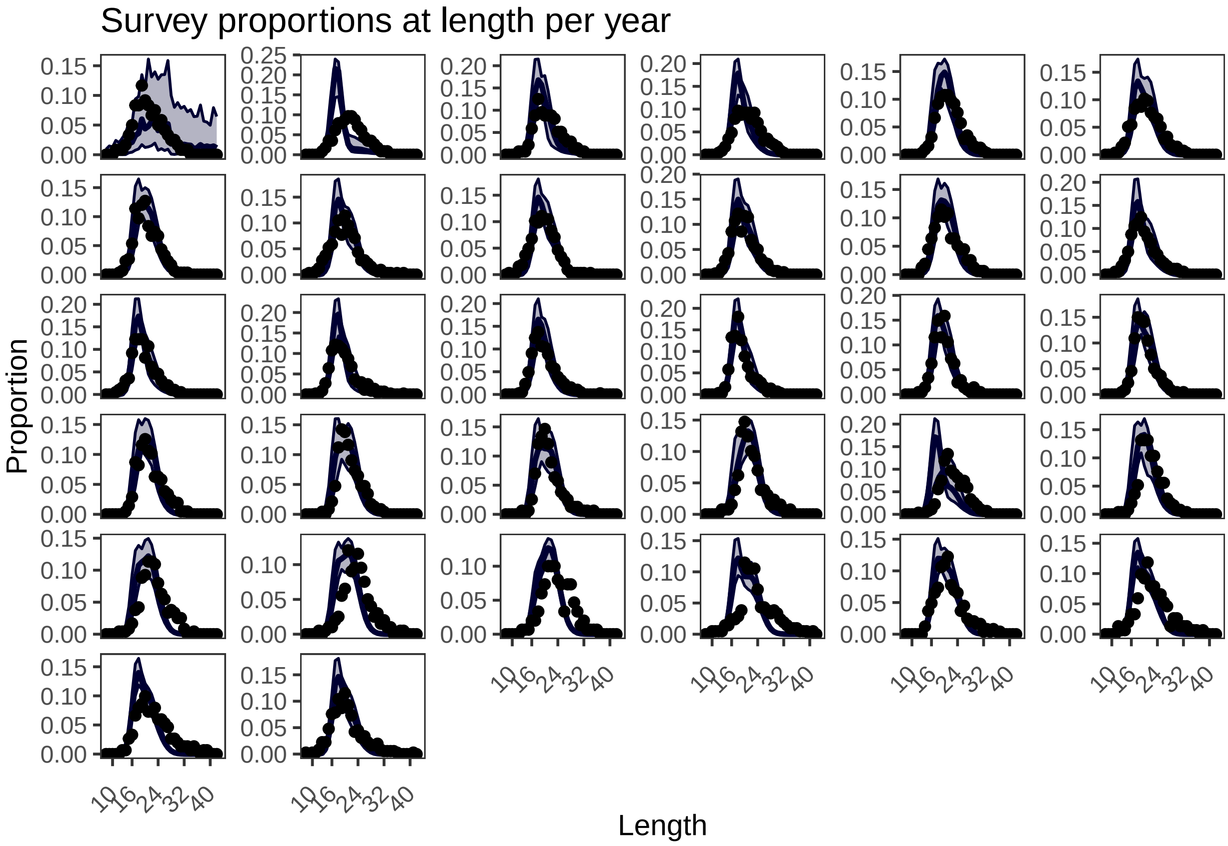


Figure 5.11: Lemon sole - The figure shows a series of yearly plot of survey proportions at length. The black dots represents data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The credible intervals around the first years estimate are not larger than the intervals around the other years. In general, the model fits well the data.

5.2.4 Grey Gurnard (*Eutriglia gurnardus*)

The model could fit gurnard's biomass and proportions-at-length quite well, but it could not provide a very reasonable estimation of fishing mortality. The right graph in figure 5.13 shows how the median is very low and almost flat, while the upper credible interval is sky rocketing at the center. This is because the model has no clue about what could be the value of σ_{Ft}, as shown by the trace plot on the right. The model was given a uniform prior for σ_{Ft}, $U \sim (0, 1)$. The left graph shows that the model is returning a uniform posterior that resembles the prior, meaning that the model has no clue of the value of σ_{Ft}. This lead us to to make a new trial keeping this parameter fixed to 0.2.

The trace plots and the histograms of the run with $\sigma_{Ft} = 0.2$ can be found in the

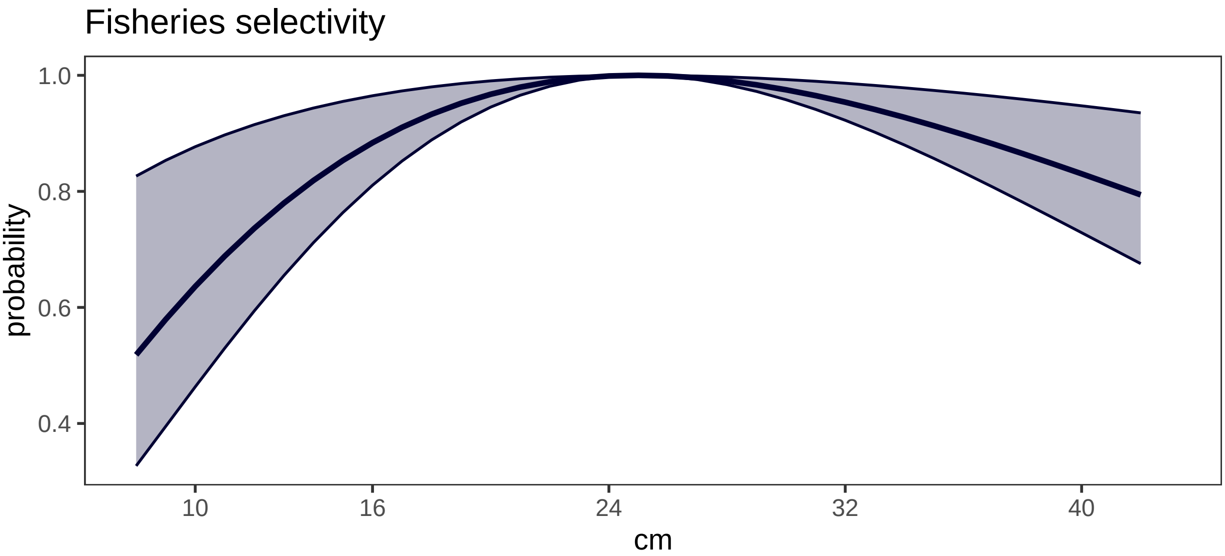


Figure 5.12: Lemon sole - The graph shows the gamma-shaped fisheries selectivity estimated by the model for lemon sole from 10 to 42 cm. The thick line is the median of the model output and the shaded area represents the 95% credible intervals. In this run, the mode of the gamma ($mode_{fsel}$) was kept fixed and only the width α_{fsel} was estimated. The estimate looks quite reasonable, with a minimum probability of being caught at 10 cm, then increasing to peak at around 24 to 26 cm, and then decreasing again.

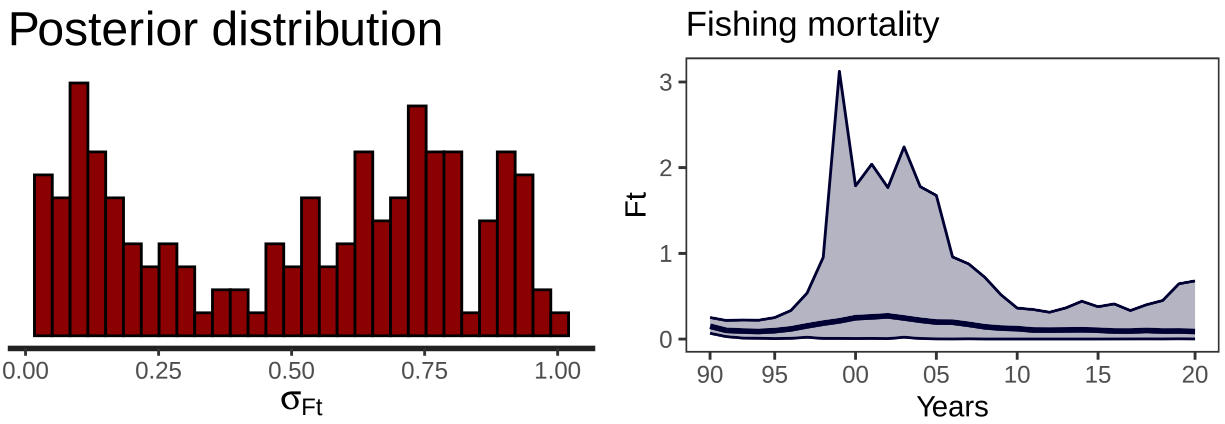


Figure 5.13: Grey gurnard - Posterior of σ_{Ft} and estimates of Ft. The posterior resembles the prior and the model does not find a solution for this parameter. This means that the model cannot find out the value of σ_{Ft}, and the reason is the data do not contain enough information.

Appendix V under the paragraph grey gurnard. The chains have mixed well but almost every parameters show signs of autocorrelation, like μ_R and L_∞, or inverse autocorrelation, like L_∞ and K. Figure 5.14 shows some of the model estimates for SLAM applied to grey gurnard. The dark line is the model output median and the shaded area around it is the 95% credible intervals. We observe that the model fits well the survey biomass data, disposed as black dots, all data the points lie between the intervals. For this species there is no SAM assessment available for comparison of Ft, recruitment and SSB. We observe how SSB trends resembles the trends of the survey biomass. Recruitment have quite a lot of variability from one year to the other, and interestingly, the model have high uncertainty regarding recruitment values from 2009 onward. Comparing the estimates of fishing mortality with the right graph of figure 5.13, we can see how fixing σ_{Ft} helped the model to produce a more reasonable estimate of Ft. Nevertheless, the values are quite low and the curve almost flat, leading us to think that the survey data do not contain much information about Ft.

Figure 5.15 shows two graphs with proportions-at-length. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied and before recruitment was added, representing the survivors from the year before. The graph on the right shows the proportions-at-length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The initial population does not very clear peaks, and this reflects the situation in the survey proportions-at-length. In fact, fish appear quite late in the survey, probably when they are already two years old, that is why μ_R is quite high. Because of how the species grows, the length classes in the later years merge and it is no longer possible to distinguish cohorts.

Figure 5.16 shows the model fit to survey proportions-at-length. Each graph represents the length distribution of a single year, form 1990 to 2000. The dark line is the model output median and the polygon around it is the 95% credible intervals. The credible intervals have approximately all the same width around every year. Overall, the fit is good and the uncertainty is quite low.

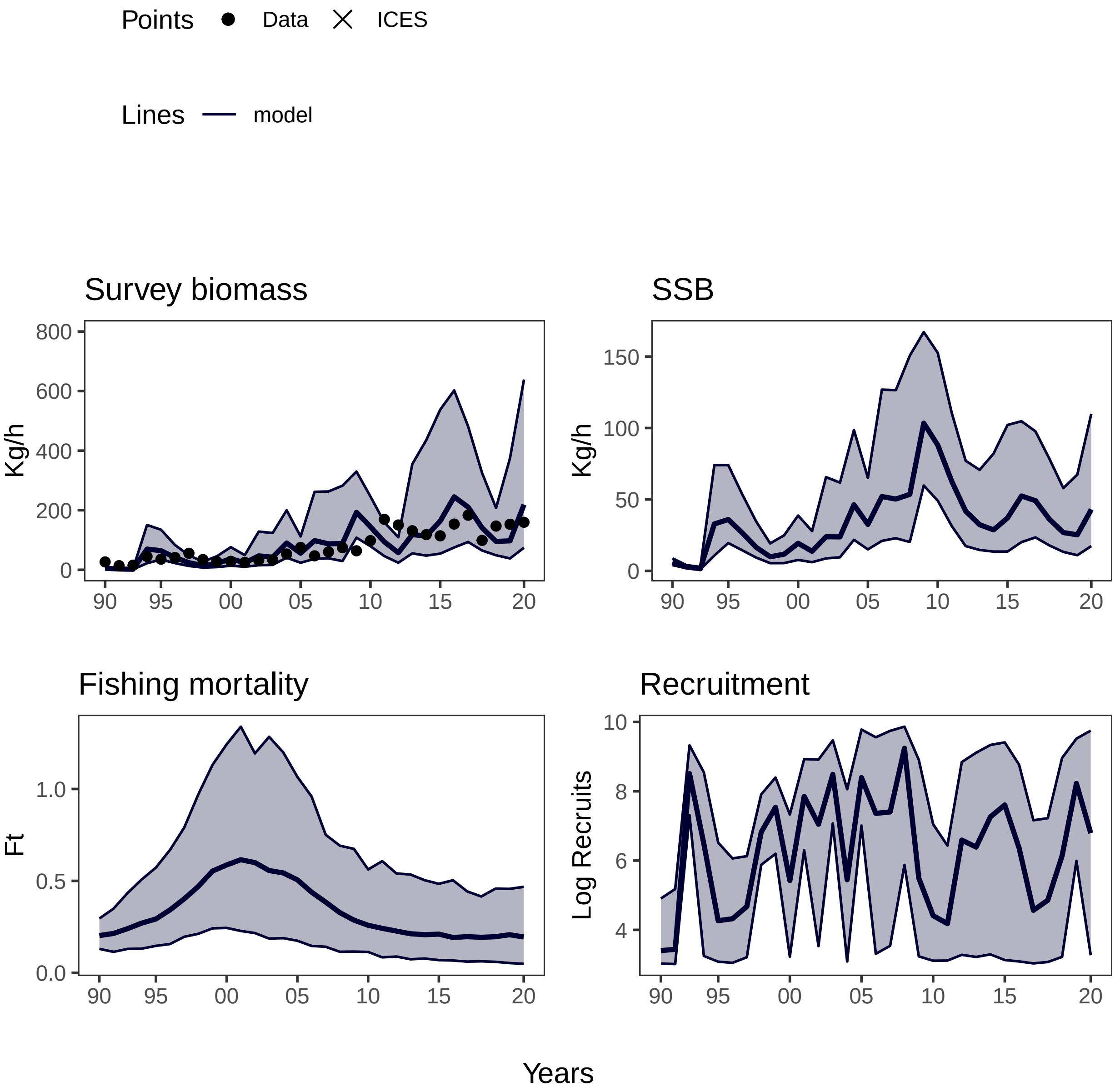


Figure 5.14: Grey gurnard - The following figures display the model estimates of survey biomass, Spawning Stock Biomass, fisheries mortality and recruitment. The black dots are the data the model is being fitted to. For this model there is no SAM assessment available for comparison. The central line is the median of the estimates and the shaded area around are the 95% credible intervals. The model fits well the survey biomass data. SSB resembles almost perfectly the trends in survey biomass. The mean for fishing mortality and recruitment seems plausible, but the upper credible interval for fishing mortality is very high in the central years.

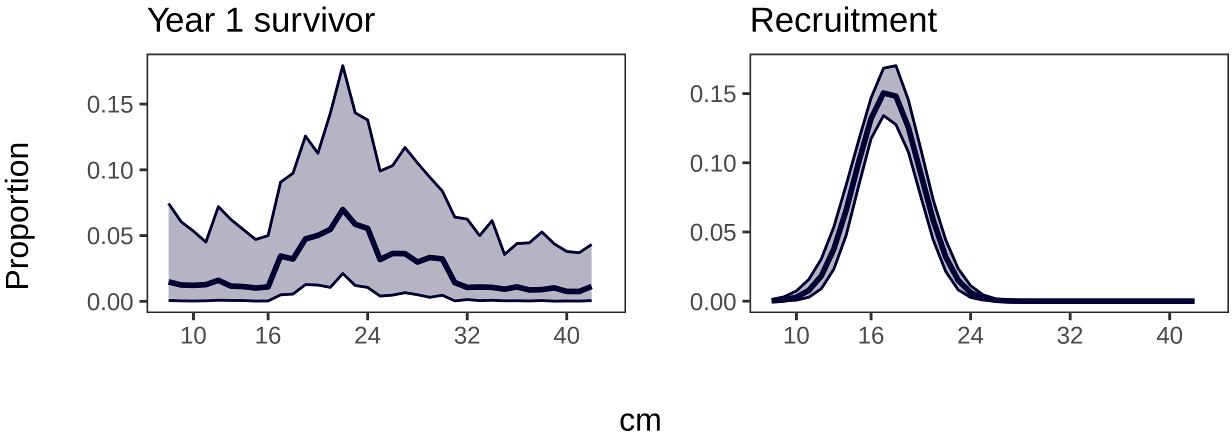


Figure 5.15: Grey gurnard - The two graphs shows two different proportions-at-length estimated by the model. The graph on the left shows the proportions-at-length of the initial population NS_1 after mortality was applied, this means it is representative of the survivors from the year before. The graph on the right shows the proportions at length for the recruitment across all years. The central line is the median of the estimates and the shaded area around are the 95% credible intervals.

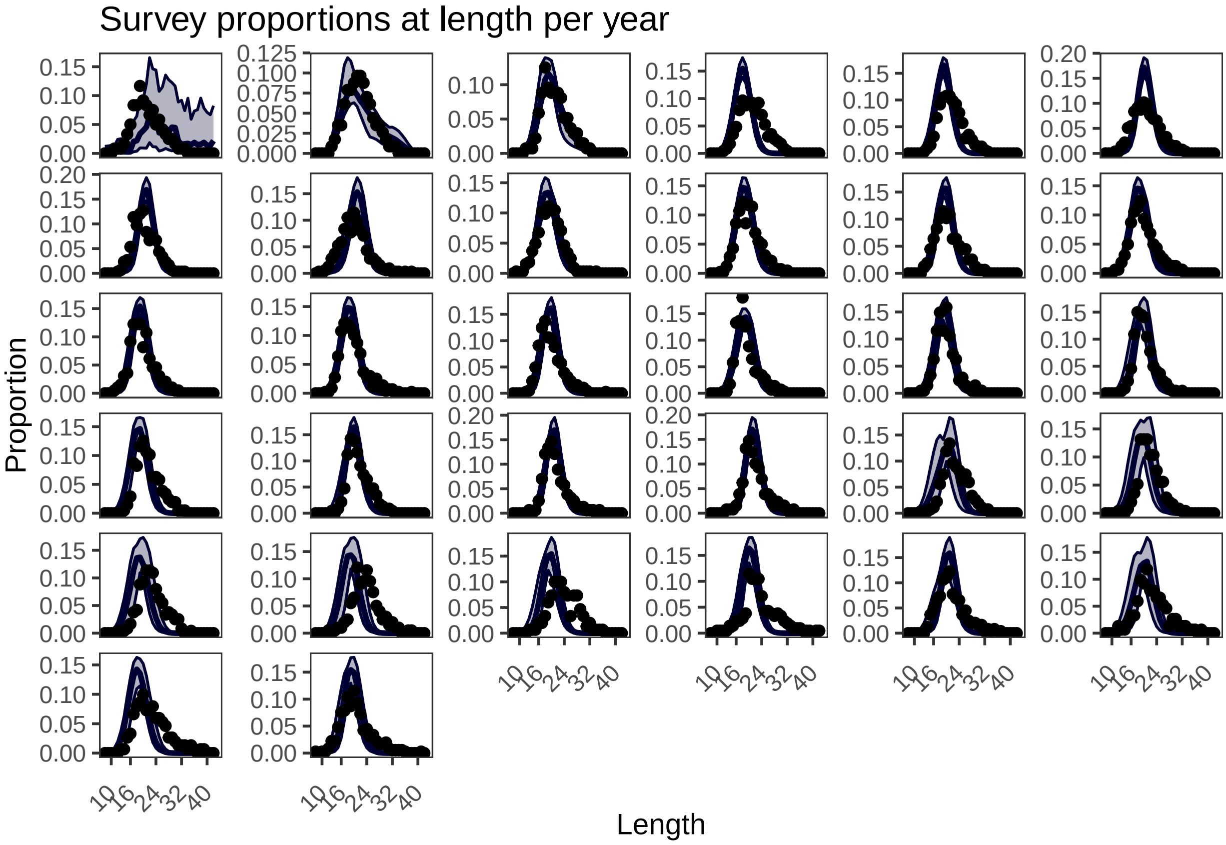


Figure 5.16: Grey gurnard - The figure shows a series of yearly plot of survey proportions at length. The black dots represents data points, the thick line is the median of the model output and the shaded area represents the 95% credible intervals. The credible intervals around the first years estimate are not larger than the intervals around the other years. In general, the model fits well the data.

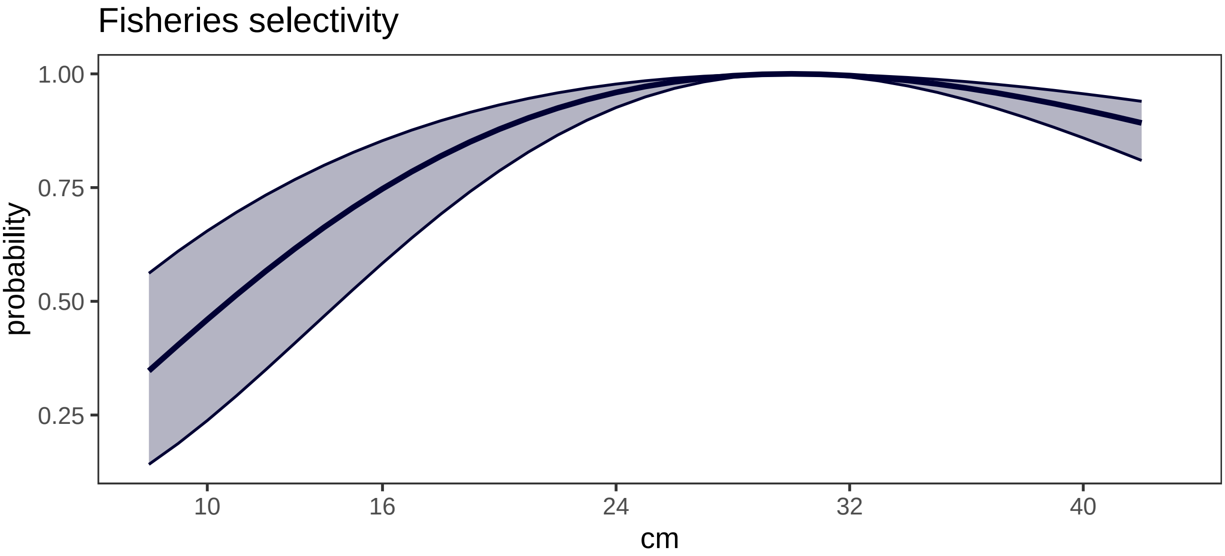


Figure 5.17: Grey gurnard - The graph shows the gamma-shaped fisheries selectivity estimated by the model for grey gurnard from 10 to 42 cm. The thick line is the median of the model output and the shaded area represents the 95% credible intervals. In this run, the mode of the gamma ($mode_{fsel}$) was kept fixed and only the width α_{fsel} was estimated. The estimate looks quite reasonable, with a minimum probability of being caught at 10 cm, then increasing to peak at around 28 to 32 cm, and then decreasing again.

Figure 5.17 shows the estimated fishing selectivity curve. In this run, the mode of the gamma was kept fixed ($mode_{fsel} = 35$) and only the width α_{fsel} was estimated. The curve has a minimum for fish of 10 cm, it peaks at the maximum probability of 1 from approximately 28 cm to 32 cm and then decrease again.

5.3 Discussion

Overall, the analysis of this chapter can be considered satisfactory. Nevertheless, as survey only method, this version of the model has some consistent limitations. The model has no information on abundance coming from the catches, and this data is fundamental for the model to know the real scale of the population and consequentially to estimate the survey catchability q. In this study q was fixed to 1, which means assuming that the survey samples uniformly and completely the population. The estimates of the model output will then be returned in the survey scale, which is much lower than the real population size. Nevertheless the trends are still valid and they still provide important information on the stock.

Another limitation of the survey only version of SLAM is that with no other information from abundance, quantities like SSB completely resemble the shape of the survey biomass. This was observed in every species tested: The estimates of SSB can be completely overlapped to the estimates of survey biomass. In case the survey is reliable this would not be a major issue, but in the case of West of Scotland, where the survey quality is limited (as explained in chapter II), the assessment becomes less reliable. The model also seemed to struggle to estimate initial population for every species. This should not be ignored, but estimating the initial population is a general problem of many stock assessment models, because normally the data are not very informative regarding this quantity.

When fitted to whiting, the model managed to pick up the relevant trends of recruitment, SSB and fishing mortality. The values estimated for fishing mortality were overestimated compared to SAM's, and even if we do not expect the two model to produce the same results, the highest value of fishing mortality estimated by SLAM, roughly 1.2, is too high for whiting VIa. Having applied the model to the same stock with catch data, we were able to feed the model the estimates of selectivity parameters. The inclination α_{fsel} was kept fixed and the $L50_{fsel}$ was estimated with an informative prior with the mean coming from the full model version in chapter IV. Nevertheless, the $L50_{fsel}$ was considerably underestimated. The reason for this likely hides in the fact that the full model version was fitted to landings composition that had bigger fish in them compared to the survey (this was described in chapter II, 2.3) Since in the survey only version is using only length information from the survey, the model thinks that the highest length in the population are the only one present in the survey. This hypothesis is supported also by the estimates of L_{inf}. The value estimated in the full model (**??**) is higher than the one estimated by the survey only version (**??**). Since with a low $L50_{fsel}$ the fishing mortality happens at a smaller size, the overall fishing mortality results to be higher and this could also explain why the estimate resulted to be higher than SAM's. For other species we did not have the landings distribution to compare, but likely the survey has the same problem in sampling the biggest length classes.

The trial on haddock was also satisfactory. The model fitted the data well and managed to estimate trends of recruitment, SSB and fishing mortality that were in line with the ones provided by SAM. The model just missed the second peak in SSB because it was not well captured by the survey. The early estimates of fishing mortality are underestimated. The reason for this are not as immediately obvious, but it is still probably due to some inconsistency in the early years of the survey. Also we must keep in mind that haddock VIa was demonstrated to be connected with North Sea stock and this violates SLAM's assumption of close population. Anyway, this can compromise the quality of the assessment overall, but not the comparison with SAM, as it makes the same assumptions. This two models can buffer the immigration and emigration of the population through recruitment and natural mortality respectively, but it is fundamental to be aware of this limitation because it influence the quality of the assessment.

The quality of results of lemon sole and grey gurnard is a bit harder to evaluate since we do not have an assessment of reference. Anyway, the model fitted the data of both species well, provided estimates of SSB that are similar to the the fit to survey biomass and the estimates of fishing mortality are consistent with the ones of whiting and haddock. The fishing mortality of all species were increasing, reaching one (or two peaks), and then decreasing to a lower value than the start. These are all demersal stocks caught by the same gears, therefore observing similar patterns of fishing mortality is encouraging. For grey gurnard it was necessary to fix the standard error of fishing mortality σFt, because the model was returning a bivariate posterior. This suggests that the model does not have much information about fishing mortality from the data, but still the fishing mortality is low, as we would expect for a species of no commercial interest like grey gurnard, which is not actively targeted and caught only as bycatch.

The reason why the model worked better for some species than others is that the survey does not sample all the species at the same way. In fact, the quality of the survey data is influenced by things like the species abundance, behavior and body type. The numbers-at-length we had for haddock were around 10 times the numbers-at-length we had for gurnard and lemon sole, meaning the model has more observations and can produce estimates that are more robust. Also, haddock, as well as whiting, had distinct peaks in the length distribution, that makes it possible to track down the cohorts. Gurnard and lemon sole on the other hand, had one single peak in the survey length frequency, probably of 2 years old fish. The absence of the peak of 1 year old fish means that the model interprets 2 years old as recruitment. Furthermore, for a length based model it is important to recognise at least two peaks in the length distribution in order to read the signals for growth and survival. Although both lemon sole and gurnard suffered of this limitation, SLAM produced performed fairly well, especially for lemon sole. Grey gurnard had a slightly worse performance, this could be again related to the data collection process. It is possible that grey gurnard has quite a strong size segregation, meaning that the survey is never able to sample more than one size in one haul, and this would make the sample not very informative. Also, grey gurnard might be confunded with other two species of gurnard, the red gurnard (*Aspitrigla cuculus*) and tub gurnard (*Chelidonichthys lucerna*).

Another limitation for this study is that SLAM assumes that somatic growth is constant, but in Chapter II we have seen there are strong evidence for long term decreasing term in L_∞ in whiting and haddock from subarea VIa (Hunter et al. (2016)). Another study conducted on plaice (Ciotti et al. (n.d.)) found the same evidence, and it could be possible that something similar is happening to lemon sole and grey gurnard. The long term trends are caused by external stressors like climate change (Lindmark et al. (2022)) or the Rosa Lee phenomenon, by which fishing pressure removes individuals that grow bigger and mature slower (Lee (1912); Enberg et al. (2012)). Growth is also variable during the year, due to the water temperature that affects the fish metabolism. It could be possible to implement a SLAM version that fits data from the four quarter, nevertheless it is very rare to have survey data available for every quarter. West of Scotland, for instance, does not have this data availability. Accounting for interannual variation instead opens up to the necessity of estimating one growth parameter or more for every year of model run, and this adds a considerable level of complexity. The existence of trends in growth, either seasonal or long-term, is a violation of SLAM's assumptions, but accounting for it might be impossible to do, or too complex to be worth it, leading to overparametrisation of the model. Also, we recall that in the bias test conducted in chapter III, the survey only model was proved to be underestimating α_{fsel} (3.20). If this bias in the parameter might be affecting the fishing mortality estimates requires further investigation.

SLAM has indeed several limitations, but it must also be considered that it is a method developed for data limited species. These species are often of minor commercial interest and are not a direct target of the fisheries. A precise and accurate stock assessment is then less necessary than for commercially important stocks, which experience a high fishing pressure. This study showed that in a data limited situation with survey only it is possible to capture the trends in abundance and fishing mortality, and even though they are not reliable in an absolute scale, they are still able to inform the assessor regarding the state of the stock. This monitoring could highlight, for example, a decrease in abundance to dangerously low levels, and it could lead up to the implementation of policies for the protection of the species.

6

Final discussion and conclusion

This thesis focused on the development of the The Survey-LAndings Stock Assessment Model, a new length based forward running, deterministic, matrix based and length based population model, thought for data limited species, but not limited to that. Chapter III, the first of the research chapters, was dedicated to the implementation of two different versions of the model. SLAM is designed to be a flexible tool, able to fit different data sources at the same time. The first version, called "full-model", is thought for data rich stocks, and the other version, called "survey only", was thought for data limited stocks with good survey information. The full-model version fits 5 sets of data, survey, landings and discard abundance and survey and landings proportions-at-length. The survey only fits only survey biomass and survey length frequency. The two versions were then tested on pseudo data, with sensitivity analysis and check for bias. The testing phase was fundamental to highlight some of the model's fault and identify the first of the adaptations necessary when stepping from theory to practice. Stepping from equations to data is a key step during model development, because some issues cannot be evident until the model is put into practice. For instance, after the analysis on sensitivity to sample size, it emerged that it would have been better to replace the multinomial likelihood with a Dirichlet-multinomial. The full-model correctly retrieve all the fitting parameters, even when using a majority of uninformative priors. The bias test proved this version of the model to be unbiased. The “survey only” version also performed well, retrieving all parameters with no bias, except for the early years of Spawning Stock Biomass (SSB). The cause of this bias hides in the fact that the only source of information on stock abundance is survey biomass, therefore the trends of SSB will follow the trends of survey biomass. The model also revealed bias in estimating α_{fsel}, the spread of the gamma fishing selectivity curve, despite making use of an informative prior. An important take home message of this chapter is that when data are removed, the model needs to be aided by making use of more informative priors and by fixing more information. In fact, if this version $mode_{fsel}$ resulted to be prior driven, and instead of a uniform prior it was necessary to adopt a log-normal.

Chapter IV tested the full-version of SLAM with a real stock, for this purpose it was chosen whiting from ICES subarea VIa. Stepping from pseudo data to real data is another key step in model development, because real data are much more complex. It was necessary to distinguish two different surveys, before and after 2011. As explained in the data chapter (chapter II), the survey protocol for West of Scotland was subject to major changes in 2011 that had a serious impact on the characteristics of the data. Different shapes of selectivity were investigated and in the end were selected a logistic for the fisheries, another logistic for the survey pre 2011 and a gamma for the survey post 2011. Survey selectivity is normally assumed to be logistic but during the data visualization process emerged that the survey fails to sample large length classes, which appear in the landings instead (2.3). After these implementations, the model fitted well the data, produced good estimates of fishing mortality and SSB and reasonable estimates of recruitment, as well as of all other parameters. The chapter proceeded with sensitivity analysis on fixed parameter values, structural assumptions and parameter bounds. The sensitivity to the input sample size (n_{surv1}, n_{surv2}, n_{land}) was also checked, as well as the sensitivity to $L50$ of the discard selectivity ($L50_{dsel}$). It was analysed the sensitivity to the shape of the fisheries and survey selectivity and finally the sensitivity to recruitment parameter bounds. The only assumption that the model is clearly insensitive to is the value of $L50_{dsel}$. To all other assumption the model resulted to be moderately sensitive, and the only estimate that was always affected was fishing mortality. In some cases the sensitivity is not caused by some underlying processes of the model itself, but rather from the properties of the data, like in the case of the assumptions on the survey selectivity shapes. In some other cases, the sensitivity analysis highlighted a model's fault, like the sensitivity to the input sample size. Another important result from these analysis is the sensitivity to recruitment prior bounds. The fact that the model is sensitive to the width of the log-uniform prior suggests that in the data there is not much information to estimate this quantity, and the model relies also on the information that we input. Therefore, extra care needs to be applied when we apply the model to new unassessed species for which the scale of the recruitment is not known. These are only few of the many possible sensitivity test. In the future, the analysis could be extended to the choice of priors and on the initial values.

The last of the research chapters, chapter V, was dedicated to fitting the survey only version of SLAM on four groundfish stocks from subarea VIa. The stocks picked for this chapter have different characteristics. Whiting and haddock have similar body types and swimming habits, but they have a very different recruitment signal. Grey gurnard and lemon sole were selected because they have completely different body types and swimming habits, therefore we assume the survey to sample all these species in a different way. The first two stocks are assessed by ICES and the results were compared with the pre-existing stock assessment. The other two stocks are unassessed and SLAM provided the first stock assessment that was ever conducted for these two species in area 6a. We are partially satisfied by the results of this chapter: in whiting and haddock the model managed to pick up the trends of SAM, but in whiting the fishing mortality was considerably overestimated and in haddock was underestimated for the first two years. The other two assessments are harder to evaluate, because there is no available assessment for a comparison. This version of SLAM requires more investigation before being published, but indeed it has the potential to become the model used to assess these two species and other currently unassessed flatfish stocks in West of Scotland.

There are still few improvements that could be developed before SLAM gets adopted as a stock assessment tool. During stock assessment meetings models need to be re-fitted many times in just a couple of days, and in general assessors prefer models that take under half an hour to run. This is why Bayesian models are not commonly used for official assessments. SLAM full version takes slightly more than 1 hour to run and it could be rejected because considered too slow. A possibility could be implementing a non-Bayesian version with RTMB. Another possible way to improve SLAM could be account for misreported landings. SLAM makes no attempt to account for potential misreported landings and this may be considered in future formulations of the model as landings of West of Scotland for cod and whiting are suspected to be subject to significant misreporting Patterson (1998). Finally, in order to make SLAM more user friendly, it would be ideal to develop a well documented R package.

As a length based model, SLAM has several limitations, but there could be different approaches to mitigate them. Length-based models are very complicated, they need many assumptions, including the one that growth is constant over time. This might be the case for few stocks, but not for the majority. It is important to account for potential changes in growth rate within stock assessment models because trends in growth can influence estimates of stock biomass (Lorenzen (2016)). In fish, growth is influenced by the external condition, and we can consider this as an year effect depending on things like temperature, food availability), but it is also pretty much defined at the birth of the fish, so there is also a cohort effect. For correctly modelling growth, it is necessary to take into account a cohort and a year effect. At the moment, the only way to account for growth variability in SLAM is through the parameter cv, and it can buffer only for the difference in growth during the year. The year effect at the moment is not accounted for, but it should, as we saw that whiting and haddock from subarea VIa are subject to the Rosa Lee phenomenon (Hunter et al. (2016)), by which fishing pressure removes individuals that grow bigger and mature slower (Lee (1912); Enberg et al. (2012)).

A possible other use of SLAM that goes beyond stock assessment could be the incorporation of its outputs into to analyse the predator-prey interactions in a multi-species context. There are several food chain, ecological or end-to-end models that requires input about fish stocks. SLAM could be used in one of its possible configurations, depending on data availability, as source for fishing mortality, biomass trends, recruitment, SSB, or more. SLAM is able to capture trends in the state of the stocks, and serve as a source of information on network changes and stressors that have a potential importance for ecosystem based management.

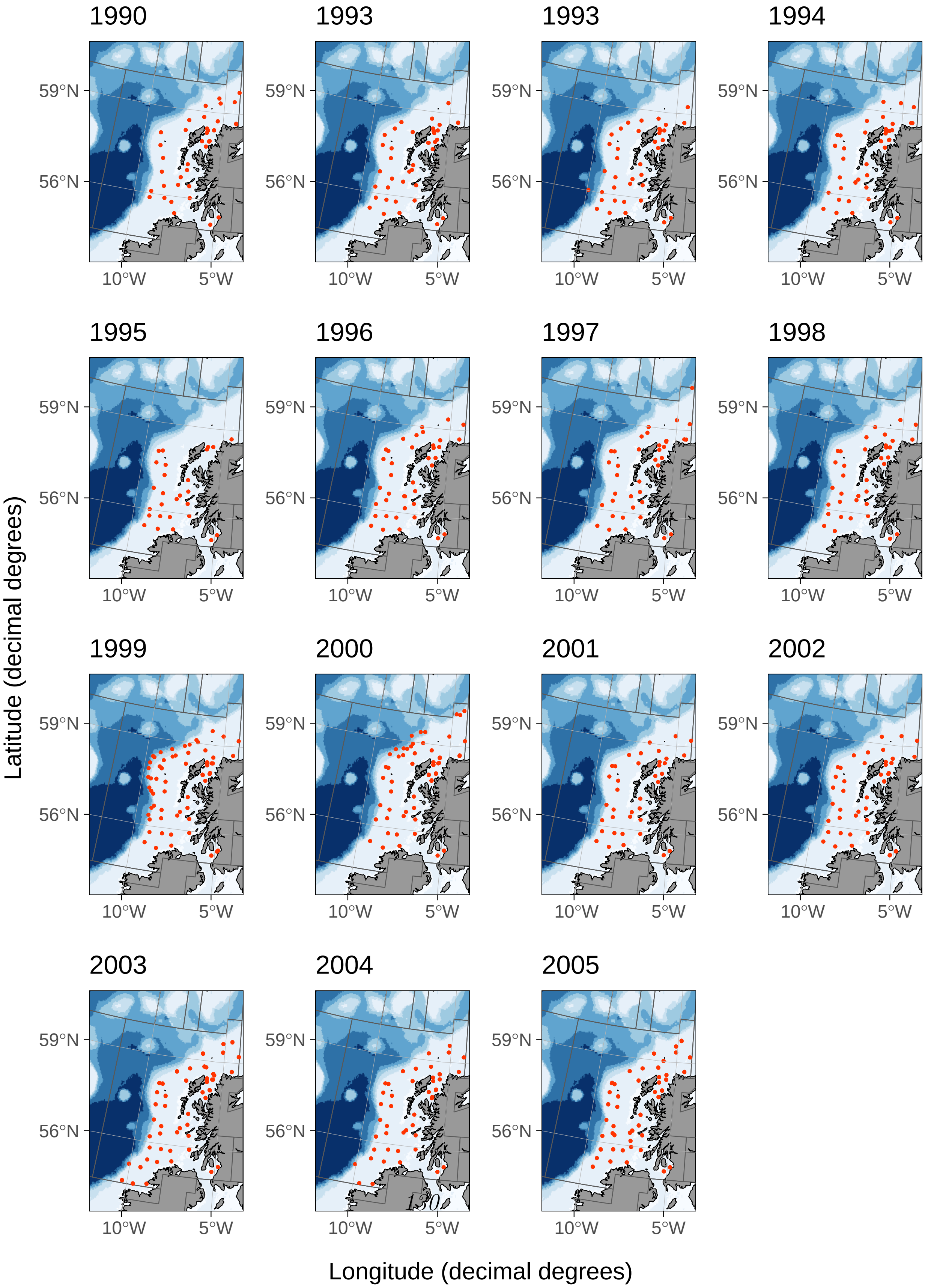
In this thesis emerged another fundamental concept, which is the importance of data availability and quality for correctly managing fisheries. Chapter IV, for instance, showed how the shape of the survey selectivity could be heavily impacted by the change in protocol, and especially by halving the trawling time. This study highlighted that going back to 1 hour trawling time could be advisable. Chapter III, IV and V showed how removing data sources from a model, going from a data rich to a data limited situation, impact the amount of information that is possible to get out of an assessment. When the model has only information coming from scientific survey, it becomes impossible to provide values on an absolute scale, and to make estimates without assuming as known several parameters. For management purposes, it would be ideal to include always both fisheries dependent and independent information, and use survey only assessments only when it is really impossible to have access to one or the other. In the next future it is likely that catch-at-length information will become easier to collect. New tools like image recognition with AI on board of vessels, but also in the net itself, can provide an enormous amount of information on the size composition of catch. With this technology it will also be possible to monitor what is landed and what discarded, and even collect data on bycatch. These kinds of fisheries compositional information are almost impossible to find online so far. An important step towards accessibility and transparency would also be to provide open access to these data around the world, as it is already for some scientific surveys. Stock assessment nowadays seems to be much more oriented towards the developing and improving models, which are becoming more and more complex, rather than what is truly important: the collection of data and the understanding of biological processes Rose (1997). Few scientists are working on biology and new data; and few scientists are in touch with the fishery and what is actually happening on the water Hilborn (2003). For the future of stock assessment and for the correct management of the sea, it is desirable that data stay at the centre of management procedures.

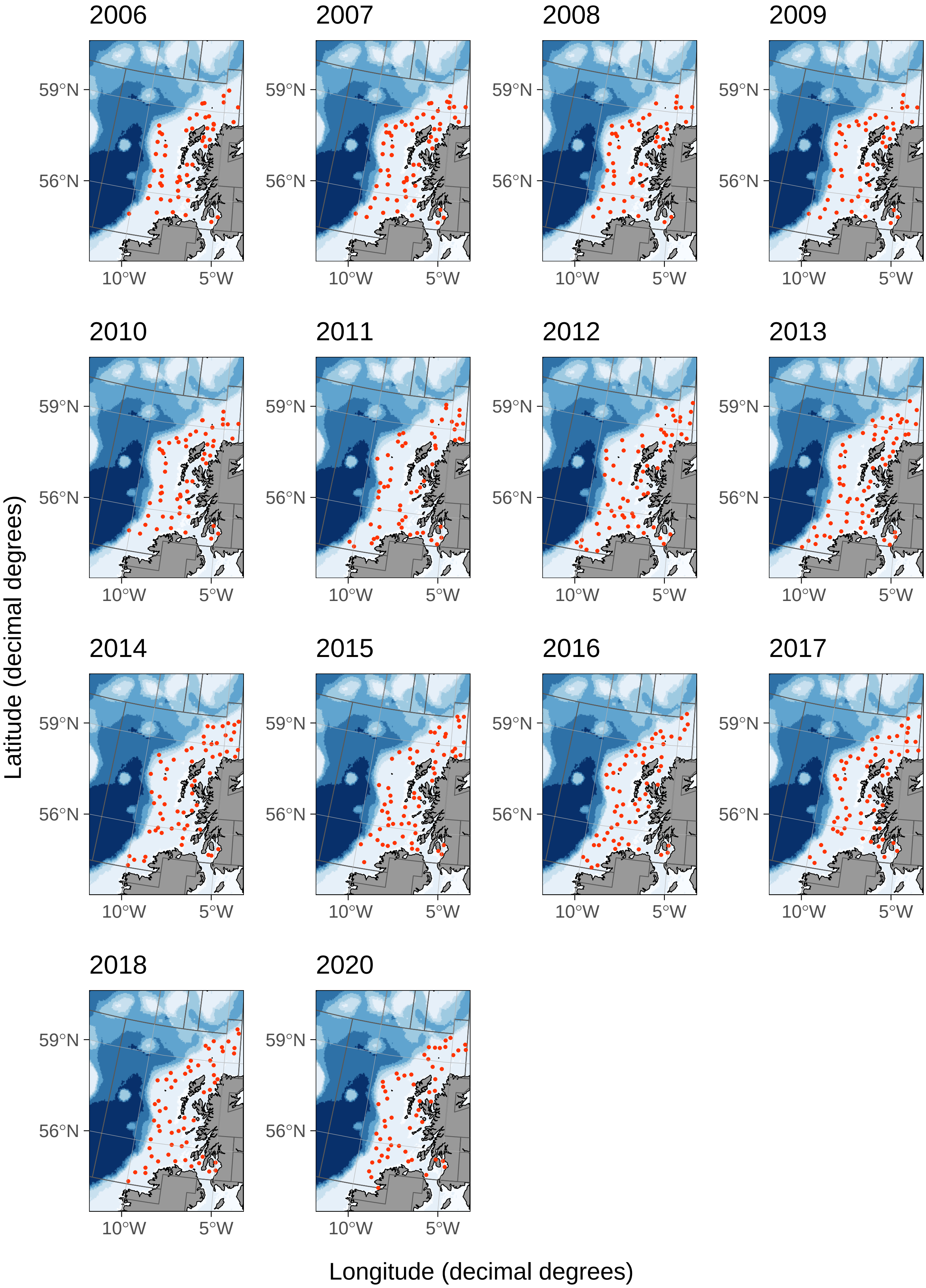
Appendices

A

Appendix

A.1 Chapter II




2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2020
59°N
56°N
10°W
5°W
Latitude (decimal degrees)
Longitude (decimal degrees)

A.2 Chapter III

A.2.1 Fully annotated code of supplementary functions called in the mode: file INTERNAL.R

```
library(latticeExtra)


# function to create a generic logistic function
logistic <- function(x,x0,k) {
return(1/(1+exp(-k(x-x0))))
}


# function to create a logistic that varies in time
time_varying_logistic <- function(x,x0,k) {
M <- matrix(NA, nrow=length(x), ncol=length(x0))
for (i in 1:length(x0)){
M[,i] <- 1/(1+exp(-k(x-x0[i])))
}
return(M)
}


# gamma function
gamsel <- function(alpha,beta,len){
return((len/((alpha-1)* beta))^(alpha-1)exp(alpha-1-len/beta));
}


# Von Bertalanffy growth function


Von_B <- function (L0,Linf,K,Dt){
# function returning the new length of fish of length L after timestep Dt (von Bertalanffy growth)
```

```
return(Linf - (Linf-L0) exp(-KDt))
}

# Length-weight conversion. Transforms a vector of lengths in a vector of weights.

# divide by 1e6 converts grams into tons
wgt_at_len <- function (L,alpha,beta,gut_wgt_conv) {
return((alpha  L^beta)* gut_wgt_conv1e-3)
}

# Natural mortality function transforms a vector of weigth in mortality at length.
# (Lorenzen 1996, Journal of Fish Biology 49, 627-647).
Lorenzen <- function(W, M_u, d) {
return(M_u  W^d)
}

# I create a function for calculating the differences between pnorms, which is
# necessary in order to create some normal distribution around a length class.
# the mean of these pnorms on each column is defined by VB growth function. The mean
# is a function and also sd is a function (Coefficient Variation 10% of the new
# destination length), as in the original model Sullivan et al.
Get_G <- function(nlen, L, Linf, K, Dt, lmax, DL, cv) {
newL <- Von_B(L0=L,Linf=Linf,K=K,Dt=Dt) # the mean of pnorm (mu)
sd <- cvnewL
G <- matrix(0,nrow=nlen,ncol=nlen)
for (j in 1:nlen) { # loop through the columns (i.e. length classes)...
newL <- Von_B(L[j],Linf=Linf,K=K,Dt=Dt) # new mean length after timestep Dt
G[,j] <- pnorm(L + DL, mean = newL, sd = sd) - pnorm(L, mean = newL, sd =
```

```
sd)
}
G <- sweep(G,2,colSums(G),'/') # normalise column sum to 1. in order not to
loose individuals
return(G)
}

# these are the function to get recruitment. I have three different ones: one to get
the
# spawning stock biomass, one for generating the normal distribution around the
mean length
# and one for the Beverton_Holt. They are expliceted below in the right order of
application

Get_SSB_new <- function(N, Mat, W) {
SSB <- sum((Mat  N) * W)
return(SSB)
}

Beverton_Holt <- function(SSB, alpha_recr, beta_recr) {
return((alpha_recr*SSB)/(beta_recr + SSB))
}

### Fully annotated code of supplementary functions called in the mode: file
FUNCTIONS.R
    source("INTERNAL.R")

# in this document are presented the functions to get the matrices and the
# main function of the survey-landings model. The general functions, like
# the Beverton-Holt and the Von Bertalanffy etc, are soucerd through
```

```
# INTERNAL.R.

# create the initial population, the population that exists before the model starts.
get_pop_start <-function(no_at_age,cv,nlen,DL,L0,Linf,K){
# population total of input data
tot <- sum(no_at_age)
# proportion of population at each age
pr_at_age <- no_at_age/tot
# N.B. assumes input adist starts at age 1
MaxAge <- length(no_at_age)
mean_len_at_age <- Von_B(L0,Linf,K,1:MaxAge)

# get sd of length at age assuming a constant coefficient of variation
sd_len_at_age <- cvmean_len_at_age
# vector of lengths for output
L <- seq(1,nlen,DL)
# initialise the population length distribution
ldist <- rep(0,length(L))
for (a in 1:length(no_at_age)){
# get length distribution of the cohort of age a...
ldist_at_age <-pnorm(L+DL,mean_len_at_age[a],sd_len_at_age[a])
-pnorm(L,mean_len_at_age[a],sd_len_at_age[a])
# add that to the population length distribution after weighting by the proportion
at the current age..
ldist <- ldist + pr_at_age[a]ldist_at_age

}
# normalise (not strictly necessary) and scale up to total population
ldist<-ldist/sum(ldist)tot
return(ldist)
```

```
}

# function that gets the recruitment matrix
Get_R <- function(totR, muR, cv, nlen, L, DL) {
sd <- cvmuR
Rdistr <- pnorm(L + DL, mean = muR, sd = sd) - pnorm(L, mean = muR, sd = sd)
Rdistr <- Rdistr/sum(Rdistr)
Rdistr <- RdistrtotR
return(Rdistr)
}

Get_R_stan <- function(muR, cv, nlen, L, DL) {
sd <- cvmuR
Rdistr <- pnorm(L + DL, mean = muR, sd = sd) - pnorm(L, mean = muR, sd = sd)
Rdistr <- Rdistr/sum(Rdistr)
return(Rdistr)
}

# MODEL FUNCTION
Survey_Landings_run <- function(parms_fixed, parms_fitting) {
with(c(parms_fixed, parms_fitting), {

# create the initial population
pop_start <-get_pop_start(no_at_age, cv, nlen, DL, L0, Linf, K)
# (the sum of popstart must be equal to the sum of no_at_age)

# Growth
G <- Get_G(nlen, L, Linf, K, Dt, lmax, DL, cv)
```

```
# Recruitment
Mat <- logistic(L,L50R,k)

# Survivorship
s <- logistic(L,L50_fish_sel,beta_fish_sel) # fishing selectivity
# outer product performs all the possible multiplication in a matrix
F <- s%o%Ft # fishing mortality at length and year
Z <- F + M # total mortality
S <- exp(-Z) # survivorship dt

# empty population matrix
N <- matrix(0,nlen,nyears)
R <- matrix(0,nlen,nyears)
SSB <- rep(0, nyears)
Survey <- matrix(0,nlen,nyears)
R[,1] <- Get_R(Rt[1], muR, cv, nlen, L, DL)
N[,1] <- R[,1] + pop_start
Survey[,1] = theta logistic(L, L50_surv_sel, beta_surv_sel)N[,1]

# model function
# Population
for(i in 1:(nyears-1)){

# recruitment
SSB[i] <- Get_SSB_new(N[,i], Mat, W)
totR <- Beverton_Holt(SSB[i], alpha_recr, beta_recr)
# model is use with Rt[i] as a first index for this function when recr is fitted
# and with totR when recr is used to generate data.
R[,i+1] <- Get_R(Rt[i+1], muR, cv, nlen, L, DL) #totR
```

```
N[,i+1] <- G % % (N[,i] * S[,i])
Survey[,i+1] = theta* logistic(L, L50_surv_sel, beta_surv_sel)N[,i+1]
N[,i+1] <- N[,i+1] + R[,i+1]
}
# next step switch off recr and check growth. 17 cm first peak

# Generate catch data
# catch numbers at length and year
C = F/Z {1-S}N
# catch retention fraction
sD = logistic(L,L50_discard_sel,log(9)/beta_discard_sel)
# landed numbers at length and year
Landed_N = sD  C
# discarded numbers
Discard_N = C-Landed_N
# total landed biomass (model expectation)
Landed_B = colSums(W * Landed_N)
# total discarded biomass (model expectation)
Discard_B = colSums(W * Discard_N)
# caught biomass
Caught_B = colSums(W * C)
# distribution of landings over lengths each year
Landed_Distr = sweep(Landed_N,2,colSums(Landed_N),‘/’)
# distribution of discards over lengths each year
Discard_Distr = sweep(Discard_N,2,colSums(Discard_N),‘/’)
Catch_Distr = sweep(C,2,colSums(C),‘/’)
Survey_Distr = sweep(Survey,2,colSums(Survey),‘/’)

return(list(N=N, C=C, sD=sD, Landed_N=Landed_N, Discard_N=Discard_N,
```

```
Landed_B=Landed_B, Discard_B=Discard_B, Landed_Distr=Landed_Distr, Discard_Distr=Discard_Distr, parms_fixed=parms_fixed, parms_fitting=parms_fitting, Caught_B=Caught_B, Survey_Distr=Survey_Distr, sD=sD, Catch_Distr=Catch_Distr, Survey=Survey, G=G, S=S, R=R, F=F, Z=Z, M=M, Rt=Rt, pop_start=pop_start, SSB=SSB))
})
}
```

A.2.2 Fully annotated code used to generate the pseudo data

```
# in this file I am plotting a time series for showing biomass and numbers of discard and landings over years and compare with SAM output.
source(“FUNCTIONS.R”)
set.seed(38)

##### other values coming from ICES model (from 1963 till 2019) #####
# recruitment
r <- matrix(c(397633000, 650569000, 871808000, 1059734000, 891641000, 448119000, 391338000, 1319269000, 1740206000, 43186000, 635677000, 632510000, 1092931000, 75228000, 1842843000, 1122754000, 1399884000, 2254006000, 877285000, 1414554000, 784294000, 1436937000, 350975000, 1597931000, 609972000, 421805000, 733346000, 294268000, 341888000, 780266000, 395474000, 951238000, 544657000, 350372000, 1072352000,112966000, 227641000, 416935000, 152852000, 229713000, 113961000, 193972000, 154826000, 354524000, 168447000, 190527000, 183333000, 270365000, 131827000, 179746000, 223389000, 310228000, 150660000, 114185000, 320063000, 77677000, 133583000), byrow = TRUE, ncol = 1)

#### MODEL PARAMETRS ####
ymin = 1995
```

```
ymax = 2018
# Number of years with both catch and survey data
nyears = ymax-ymin+1
# fixed parameters
parms_fixed = list(

##### GROWTH RELATED #####
DL = 1,
# maximum length represented in matrix model (cm)
lmax = 53,
# minimum length modeled
L0 = 1,

# minimum that appears in model
lmin = 8,
# Year index
years = 1:nyears,
# timestep (years)
Dt = 1,
# L_infinity
Linf = 53,
# growth rate (1/year)
K = 0.2,
# coefficient variation. estimated to be 0.1 for many biological processes
cv = 0.1,

##### RECRUITMENT RELATED #####
# L50 of the maturity ogive
L50R = 40,
# Inclination of the maturity ogive
```

```
k = 0.14,
# mean length of recr
muR = 10.5,
# coefficient variation. estimated to be 0.1 for many biological processes
cv = 0.1,
# parameter of the Beverton-Holt
alpha_recr = 175000,
# parameter of the Beverton-Holt
beta_recr = 250,

##### SURVIVORSHIP RELATED #####
# parameter of Lorenzen
d = -0.3, # parameter of Lorenzen
M_u = 0.1,
# parameter for the weight-length conversion
alpha_wgt_len = 0.008,
# parameter for the weight-length conversion
beta_wgt_len = 3.0669,

   ##### GENERATE THE CATCHES AND SURVEY LENGTH-DISTR #####

# Length at which 50% of the fishery catch is retained as landings, and the other
50% is discarded
L50_discard_sel = 30,
# As above, controls the steepness of the retention fraction curve
beta_discard_sel = 7,

# sample size to scale
neff_surv = 50,
# sample size for landings
```

```
neff_land = 50


)


# I add the derived parameters to the list
parms_fixed$ymin <- ymin
parms_fixed$ymax <- ymax
parms_fixed$nyears <- nyears
parms_fixed$L <- seq(parms_fixed$L0, parms_fixed$lmax, parms_fixed$DL)
parms_fixed$nlen <- length(parms_fixed$L)
parms_fixed$W <- wgt_at_len(parms_fixed$L, parms_fixed$alpha_wgt_len, parms_fixed$beta_
gut_wgt_conv = 1)
parms_fixed$M <- Lorenzen(parms_fixed$W, parms_fixed$M_u, parms_fixed$d)
# fitting parameters
parms_fitting = list(

no_at_age = c(0,1e+3,9e+02,500,200,70),

# Length at 50% fishery selectivity
L50_fish_sel = 22,
# Difference in length between fish that are 75% and 25% selected by the fishery,
betaF=L75F-L25F.
# Controls the steepness of selectivity curve.
beta_fish_sel = 0.25,
alfa_f = 2,
mode_f = 25,
# Length at 50% survey selectivity
L50_surv_sel = 12,
# As above, controls the steepness of the survey selectivity curve.
beta_surv_sel = 0.4,
```

```
alfa_s = 3,
mode_s = 27,
# Survey catchability
q = 1,

# Vector parameters
Ft = c(0.2000000, 0.2081258, 0.3212827, 0.5513396, 0.5851095, 0.9068046, 0.9661099,
1.0161163, 1.0474364, 0.8603230, 0.8797522, 0.5865069, 0.6715918, 0.6915008, 0.4545992,
0.6859463, 0.6146628, 0.5088190, 0.5086527, 0.6975478, 0.7068113, 0.9353432, 1.0017207,
0.6231272),
Rt = r[34:57]/1e6

)

##################### MODEL ########################


# FUNCTION
Survey_Landings_trial <- function(parms_fixed, parms_fitting) {
with(c(parms_fixed, parms_fitting), {

# Growth
G <- Get_G(nlen, L, Linf, K, Dt, lmax, DL, cv)

# initial population
pop_init <-get_pop_start(no_at_age, cv, nlen, DL, L0, Linf, K)

# Survivorship
#s <- logistic(L,L50_fish_sel,beta_fish_sel) # fishing selectivity
beta_s=mode_s/(alfa_s-1)
```

```
beta_f=mode_f/(alfa_f-1)
s <- gamsel(alfa_f,beta_f,L)
# outer product performs all the possible multiplication in a matrix
F <- s%o%Ft
Z <- F + M # total mortality
S <- exp(-Z) # survivorship dt

# Recruitment
Mat <- logistic(L,L50R,k)

# empty population matrix
N <- matrix(0,nlen,nyears)
R <- matrix(0,nlen,nyears)
Survey <- matrix(0,nlen,nyears)
R[,1] <- Get_R(Rt[1], muR, cv, nlen, L, DL)
N[,1] <- pop_init
Survey[,1] = q gamsel(alfa_s,beta_s,L)N[,1]

# Population
for(i in 1:(nyears-1)){
# recruitment
R[,i+1] <- Get_R(Rt[i+1], muR, cv, nlen, L, DL)
N[,i+1] <- G %  % (N[,i] * S[,i]) + R[,i+1]
Survey[,i+1] = q* gamsel(alfa_s,beta_s,L)N[,i+1]
}

# Generate catch data
# catch numbers at length and year
C = F/Z  {1-S} * N
# catch retention fraction
```

```
sD = logistic(L,L50_discard_sel,log(9)/beta_discard_sel)
SSB=colSums(Mat * N * W)
# landed numbers at length and year
Landed_N = (sD * C)
# discarded numbers
Discard_N = C-Landed_N
# total landed biomass (model expectation)
Landed_B = colSums(W * Landed_N)/10e4
# total discarded biomass (model expectation)
Discard_B = colSums(W * Discard_N)
# caught biomass
Caught_B = colSums(W * C)
Survey_B = colSums(W * Survey)/10e4
# normalise the surveys
Survey_Distr = sweep(Survey,2,colSums(Survey),‘/’)
# distribution of landings over lengths each year
Landed_Distr = sweep(Landed_N,2,colSums(Landed_N),‘/’)
# distribution of discards over lengths each year
Discard_Distr = sweep(Discard_N,2,colSums(Discard_N),‘/’)

data_surv_distr <- matrix(0,nlen,nyears)
for (i in 1:nyears) {
# divide by three hundred and multiply
data_surv_distr[,i] <- rmultinom(1, neff_surv, Survey[,i])
data_surv_distr[,i] <- (data_surv_distr[,i]/neff_surv) * sum(Survey[,i])
}

# generate data with lognormal distribution
data_surv_biom <- matrix(0,1,nyears)
for (i in 1:nyears) {
```

```
data_surv_biom[i] <- Survey_B[i] * rlnorm(1, 0, 0.3)
}

# output the initial population to use as initial condition in the model
pop_start <- rep(0, nlen)
pop_start <- N[,1]

return(list(N=N, C=C, G=G, sD=sD, Landed_N=Landed_N, Discard_N=Discard_N,
Landed_B=Landed_B, Discard_B=Discard_B, Landed_Distr=Landed_Distr, Discard_Distr=Discard_Distr,
parms_fixed=parms_fixed, parms_fitting=parms_fitting,
Caught_B=Caught_B, SSB=SSB, Survey_Distr=Survey_Distr, Survey=Survey,
data_surv_distr=data_surv_distr, Survey_B=Survey_B, data_surv_biom=data_surv_biom,
R=R, pop_start=pop_start, pop_init=pop_init))
})
}

generate_data <- Survey_Landings_trial(parms_fixed, parms_fitting)
data_surv_distr <- round(generate_data$data_surv_distr)
data_surv_biom <- as.vector(generate_data$data_surv_biom)
pop_start <- as.vector(generate_data$pop_start)
SSB <- as.vector(generate_data$SSB)
surv_biom_true <- as.vector(generate_data$Survey_B)
surv_distr_true <- as.vector(generate_data$Survey_Distr)
write.table(data_surv_distr, ‘surv_only_data_surv_distr.txt’)
write.table(data_surv_biom, ‘surv_only_data_surv_biom.txt’)
write.table(pop_start, ‘surv_only_pop_start.txt’)
write.table(surv_biom_true, ‘surv_only_surv_biom_true.txt’)
write.table(surv_distr_true, ‘surv_only_surv_distr_true.txt’)
write.table(SSB, ‘surv_only_SSB.txt’)
```

```
### Fully annotated R code of the full model tested on pseudo data
#source(“GENERATE DATA.R”)
source(“FUNCTIONS.R”)
library(rstan)
#### FIXED PARAMETERS AND DATA ####
#### RECR VALUES ####
r <- matrix(c(397633000, 650569000, 871808000, 1059734000, 891641000, 448119000,
391338000, 1319269000, 1740206000, 43186000, 635677000, 632510000, 1092931000,
75228000, 1842843000, 1122754000, 1399884000, 2254006000, 877285000, 1414554000,
784294000, 1436937000, 350975000, 1597931000, 609972000, 421805000, 733346000,
294268000, 341888000, 780266000, 395474000, 951238000, 544657000, 350372000,
1072352000, 112966000, 227641000, 416935000, 152852000, 229713000, 113961000,
193972000, 154826000, 354524000, 168447000, 190527000, 183333000, 270365000,
131827000, 179746000, 223389000, 310228000, 150660000, 114185000, 320063000,
77677000, 133583000), byrow = TRUE, ncol = 1)

#### PARAMETERS ####
# many parameters of this block are not used directly in the model in stan, but
rather used in
# functions to calculate values that will enter the stan model as parameters.
ymin = 1989 # first year of data
ymax = 2008 # last year of data
y_land = 2008
y_D_beta = 2011
nyears = ymax-ymin+1 # number of years
nyears_land = ymax-y_land+1
nyears_D_beta_pre2011 = ymax-y_D_beta+1
Dt = 1 # timestep
```

```
L0 = 1 # minimum length modeled
lmax = 66 # maximum length modeled
DL = 1 # length class width
L = L0:lmax
# coefficient variation (used to calculate the sd around length class)
cv = 0.1

nlen = length(L) # number of length classes
alpha_wgt_len = 0.0093 # alpha in length-weight conversion
beta_wgt_len = 2.9456 # beta in length-weight conversion
M_u = 0.1 # parameter in natural mortality
d = -0.3 # parameter in natural mortality
L50_Mat = 40 # L50 of the maturity logistic
L25_Mat = 0.14 # steepness of the maturity logistic
muR = 12.7 # mean length of the recruitment

# call to functions to calculate derived fixed parameters
W = wgt_at_len(L, alpha_wgt_len, beta_wgt_len) # vector of weight at length

M = Lorenzen(W, M_u, d) # natural mortality at length
Mat = logistic(L,L50_Mat,L25_Mat) # maturity at length
R_distr = Get_R_stan(muR, cv, nlen, L, DL) # probability of recruitment length


#### DATA ####
data_disc_biom <- read.table(‘data_disc_biom_whiting.txt’)
data_land_biom <- read.table(‘data_land_biom_whiting.txt’)
data_surv_biom <- read.table(‘data_surv_biom_whiting.txt’)
data_surv_distr <- read.table(‘data_surv_distr_whiting.txt’)
data_surv_distr[is.na(data_surv_distr)] <- 0
```

```
data_land_distr <- round(read.table(‘data_land_distr_whiting.txt’))

#### LIST THAT IMPUTS THE DATA ####
input.data = list(
# see above for definitions
#~~~~~ PARAMETERS ~~~~~
# TIME
nyears = nyears,
# GROWTH
nlen = nlen,
L = L,
W = W,
Dt = 1, # timestep
L0 = 1, # minimum length modeled
lmax = 66, # maximum length modeled
DL = 1, # length class width
Linf = 38, # maximum length for the Von Bertalanffy
# RECRUITMENT
# R_distr = R_distr,
# used only in generated quantities (a posteriori calculations)
Mat = Mat,

# SURVIVORSHIP
M = M,
q = 0.9,
# EFFECTIVE SAMPLE SIZE
neff_surv = 1000, # effective sample size of the survey
neff_land = 1000,

# discard selectivity
```

```
L25_disc_sel = 22, # L25 of the discard selectivity
L50_disc_sel = 27, # L50 of the discard selectivity

#~~~~ DATA ~~~~
data_land_distr = as.matrix(data_land_distr),
data_surv_distr = as.matrix(data_surv_distr),
data_surv_biom = data_surv_biom[,1],
data_land_biom = data_land_biom[,1],
data_disc_biom = data_disc_biom[,1],

    #~~~~ FITTING PARAMETERS BOUNDS ~~~~~
Rt_mean = log(200),# lower bound for Rt
Rt_sd = log(200000), # Upper bound for Rt
q_mean = 0,
q_sd = 2,
L50_fish_sel_mean = 5,
L50_fish_sel_sd = 35,
beta_fish_sel_mean = 0,
beta_fish_sel_sd = 3,
L50_surv_sel_mean = 5,
L50_surv_sel_sd = 20,
beta_surv_sel_mean = 0,
beta_surv_sel_sd = 3,
L50_surv_sel_bounds = c(2,40),
beta_surv_sel_bounds = c(0.1,3),
Ft_bounds = c(0.01,3),
sd_Ft_bounds = c(0.01,2),
sd_surv_biom_bounds = c(0,50),
sd_disc_biom_bounds = c(0,50),
sd_land_biom_bounds = c(0,50),
```

```
NS1_mean=mean(log(2colSums(as.matrix(data_land_distr)))),
NS1_sd=0.9,
alpha=rep(1,nlen),
rd_lim=c(5,20),
rd_sd_lim=c(.1,20),
lf=c(1:nlen),
cv_bounds = c(0.01,0.9),
K_bounds = c(0.01,0.9),
L_bound=c(38,.338),
D_beta_bounds = c(0,900)
# steepness of the discard selectivity
#L25_disc_sel_bounds = c(5,40),
# L50 of the discard selectivity
#L50_disc_sel_bounds = c(5,50)
)

#### FITTING PARAMETERS ####
# initial values
inits1 <- list(

#Rt = rep((250),(nyears)), # recruitment per year
Rt=log(colSums(data_surv_distr[1:15,]*3)),
Ft = c(0.1,rep(0.5,(nyears-1))), # fishing effort per year
beta_surv_sel = 0.2, # steepness of the survey selectivity
L50_surv_sel = 10, # L50 of the survey selectivity
L50_fish_sel = 23, # L50 of fishing selectivity curve
beta_fish_sel = 0.19, # steepness of fishing selectivity curve
q =(0.1), # survey catchability
sd_surv_biom=0.6, # error around the survey biomass
sd_land_biom=0.2, #error around the landings biomass
```

```
sd_disc_biom=0.6,
sd_Ft=0.2,
NS1=exp(input.data$NS1_mean),
LF1_distr=(data_land_distr[,1]+1)/sum(data_land_distr[,1]+1),
R_distr_mean=12,
R_distr_sd=1.2,
cv = 0.1,
K = 0.1,
Linf=38,
D_beta_pre2011=c(50,50),
D_beta_post2011=c(50,50)
)

inits2<-inits3<-inits1

iter<-30000
chains<-3
thin<-300
model<-“whiting_slam_v4.02_DM.stan”
init<-list(inits1,inits2,inits3)#

t1<-Sys.time()
fitted <- stan(file = model, data = input.data, thin=thin, diagnostic_file = “parameter values”,
init=init, cores=4, seed = “38”, #algorithm = “Fixed_param”,
iter =iter, chains = chains, verbose=FALSE, init_r=.5)
t2<-Sys.time()
t2-t1
```

A.2.3 Fully annotated Stan code of the full model tested on pseudo data

```
functions {
// function to calculate log probability for a Dirichlet-multinomial distribution
real DM_lpmf(int [] n, vector alpha) {
int N = sum(n);
real A = sum(alpha);
return lgamma(A) - lgamma(N + A)
+ sum(lgamma(to_vector(n) + alpha))
- sum(lgamma(alpha));
}
}

// data and fixed parameters
data {
int nyears; // number of years
real Dt; // time step
real L_bound[2]; // bounds on Linf
real DL; // length bin size
int nlen; // number of length bins
vector[nlen] W; // weight at length vector
vector[nlen] L; // length classes
vector[nlen] alpha; // Dirichlet parameter vector
vector[nlen] M; // natural mortality
vector[nlen] sD; // discard selection at length
vector[nlen] Mat; // maturity
// bounds for survey q
real q_mean;
real q_sd;
// values for fishery selection parameter priors,
```

```
real L50_fish_sel_mean;
real L50_fish_sel_sd;
real beta_fish_sel_mean;
real beta_fish_sel_sd;
// values for survey selection parameter priors
real L50_surv_sel_mean;
real L50_surv_sel_sd;// = 0.3,
real beta_surv_sel_mean;// = 0.25,
real beta_surv_sel_sd;// = 0.1,
// values for prior on initial population survivors
real NS1_mean;
real NS1_sd;
// observations
int data_land_distr[nlen,nyears]; // landings number at length
int data_surv_distr[nlen,nyears]; // survey number at length
real data_surv_biom[nyears]; // survey biomass
real data_land_biom[nyears]; // landings biomass
// effective sample sizes for survey and landings distributions
int neff_surv;
int neff_land;
// Bounds for prior on growth parameters
real K_bounds[2];
real cv_bounds[2];
// Bounds for prior on recruitment
real Rt_mean;
real Rt_sd;
// bounds or prior on Ft
real Ft_bounds[2];
// bounds for prior on suvey biomass
real sd_surv_biom_bounds[2];
```

```
// bounds for std dev prior on landings observations
real sd_land_biom_bounds[2];
// bounds for std dev process error on Ft
real sd_Ft_bounds[2];
// bounds of priors on recruitment distribution parameters
real rd_lim[2]; // bounds for mean of distribution
real rd_sd_lim[2]; // bounds for sd of distribution
}
// end block

transformed data {
int data_land_scaled[nlen,nyears];
int data_surv_scaled[nlen,nyears];
// re-scale survey distribution to effectove sample size
for (l in 1:nlen){
for (y in 1:nyears){
data_surv_scaled[l,y] = data_surv_distr[l,y]*
neff_surv/sum(data_surv_distr[,y]);
}
}
// re-scale landings distribution to effective sample size
for (l in 1:nlen){
for (y in 1:nyears){
data_land_scaled[l,y] = data_land_distr[l,y]*
neff_land/sum(data_land_distr[,y]);
}
}
}
// end block
```

```
// fitting parameters
// see R document for definitions
parameters {
vector[nyears] Rt; // Annual recruitment
vector[nyears] Ft; // Annual fishing mortality year effect
simplex[nlen] LF1_distr; // proportion at length surviving in first year
real NS1; // total number of survivirs in first year
real sd_surv_biom; //observation error on survey biomass
real sd_land_biom; // observation error on landings biomass
real sd_Ft; // process error on fishing morality year effect
// growth parameters
real cv;
real K;
real Linf;
// survey slectivity parameters
real L50_surv_sel;
real beta_surv_sel;
// fishery selectivity parameters
real L50_fish_sel;
real beta_fish_sel;
// survey catchability
real q;
// recruitment length frequency parameters
real R_distr_mean;
real R_distr_sd;
// Dirichlet scalar
real D_beta[2];
}
// end block
```

```
transformed parameters {
matrix[nlen, nlen] G; // growth projection matrix
vector[nlen] newL;
vector[nlen] sd_growth;
vector[nlen] s; // fishing selectivity curve
matrix[nlen, nyears] F; // fishing mortality matrix
matrix[nlen, nyears] Z; // total mortality matrix
matrix[nlen, nyears] S; // survival matrix
matrix[nlen, nyears] N; // population matrix
vector[nlen] NS; // population matrix * survival matrix
// survey proportion at length x years
matrix[nlen, nyears] Survey_Distr;
// survey numbers at length x years
matrix[nlen, nyears] Survey;
// landings proportion at length x years
matrix[nlen, nyears] Land_Distr;
// caught numbers at length x years
matrix[nlen, nyears] Catches;
// discarded numbers at length x years
matrix[nlen, nyears] Discard;
// landed numbers at length x years
matrix[nlen, nyears] Landings;
// biomass landed per length per year
matrix[nlen, nyears] Landings_biom_xlen;
// total biomass landed per year
vector[nyears] Land_Biomass;
// biomass surveyed per length per year
matrix[nlen, nyears] Survey_biom_xlen;
```

```
// total biomass surveyed per year
vector[nyears] Surv_Biomass;
// recruitmet length frequency distribution
vector[nlen] R_distr;

// calculate recruitment length distribution from a normal distribution
for(i in 1:nlen){
R_distr[i] = normal_cdf(L[i]+DL,R_distr_mean,R_distr_sd)-
normal_cdf(L[i],R_distr_mean,R_distr_sd);
}

// construct initial population from survivors in initial year and recruitment
for(l in 1:nlen){
N[l,1]=NS1* LF1_distr[l]+ (Rt[1])R_distr[l];
}
newL = Linf - (Linf-L) exp(-KDt);
for (l in 1:nlen) {
sd_growth[l] = cv  newL[l];
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = normal_cdf(L[l]+DL,newL[y],sd_growth[l])-
normal_cdf(L[l],newL[y],sd_growth[l]);
}
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = G[l,y] / sum(G[,y]);
}
}
```

```
// define S: survival at length
s = 1 ./ (1+exp(-beta_fish_sel(L-L50_fish_sel)));
for (l in 1:nlen) {
for (y in 1:nyears) {
F[l,y] = s[l]  Ft[y];
Z[l,y] = F[l,y] + M[l];
}
}
S = exp(-(Z));
// Calculate survivors into the next year
for (y in 1:(nyears-1)) {
for (l in 1:nlen) {
NS[l] = N[l,y] * S[l,y];
}
// Project the population at length one year ahead from suvivors and growth matrix
N[,y+1] = G * NS; // double check with length distribution plot
for (l in 1:nlen) {
N[l,y+1] = N[l,y+1] + (Rt[y+1])
R_distr[l]; // note Rt is on a log scale
}
}
// Calculate fitted survey numbers at length from catchability q and survey size
selection
for (y in 1:nyears){
for (l in 1:nlen){
Survey[l,y] = q N[l,y]/ (1+exp(-beta_surv_sel(L[l]-L50_surv_sel))); }
}
// calculate discard, catches and landings
// catch numbers at length and year
Catches = F ./ Z . (1-S) .* N;
```

```
for (l in 1:nlen) {
for (y in 1:nyears) {

// landings dervided from a retention ogive sD
Landings[l,y] = sD[l] * Catches[l,y];
}
}
Discard = Catches - Landings; // discarded numbers
for (y in 1:nyears) {
for (l in 1:nlen) {
// landed weight at length and year
Landings_biom_xlen[l,y] = W[l] * Landings[l,y];
}

Land_Biomass[y] = sum(Landings_biom_xlen[,y])/10e4;
}
for (y in 1:nyears) {
for (l in 1:nlen) {
// survey weight at length and year
Survey_biom_xlen[l,y] = W[l] * Survey[l,y];

}
// fitted survey biomass
Surv_Biomass[y] = sum(Survey_biom_xlen[,y])/10e4;
}
// calculate fitted landing and survey length frequency
for (y in 1:nyears) {
for (l in 1:nlen) {
Land_Distr[l,y] = Landings[l,y] / sum(Landings[,y]);
Survey_Distr[l,y] = Survey[l,y] / sum(Survey[,y]);
```

```
}
}
}
// end block

model {
// Priors
// Fishing mortality year effect in first year
Ft[1]~uniform(Ft_bounds[1],Ft_bounds[2]);
// Annual recruitment
for (y in 1:(nyears)) {
Rt[y]~uniform(Rt_mean,Rt_sd);
}
// total survivors in first year
NS1~lognormal(NS1_mean,NS1_sd);
//survivors proportion at length
LF1_distr~dirichlet(alpha);
// survey catcability
q~uniform(q_mean,q_sd);
// fishery and survey selection parameters
beta_surv_sel~uniform(beta_surv_sel_mean, beta_surv_sel_sd);
L50_surv_sel~uniform(L50_surv_sel_mean, L50_surv_sel_sd);
L50_fish_sel~uniform(L50_fish_sel_mean, L50_fish_sel_sd);
beta_fish_sel~uniform(beta_fish_sel_mean, beta_fish_sel_sd);
// growth parameters
cv~uniform(cv_bounds[1],cv_bounds[2]);
K~uniform(K_bounds[1],K_bounds[2]);
Linf~normal(L_bound[1],L_bound[2]);
// Dirichlet scalar
D_beta~uniform(0,1000);
```

```
// observation errors
sd_land_biom~uniform(sd_land_biom_bounds[1],sd_land_biom_bounds[2]);
sd_surv_biom~uniform(sd_surv_biom_bounds[1],sd_surv_biom_bounds[2]);
// process error on fishing mortality
sd_Ft~uniform(sd_Ft_bounds[1],sd_Ft_bounds[2]);
// recruitmnet proiportins at length
R_distr_mean~uniform(rd_lim[1],rd_lim[2]);
R_distr_sd~uniform(rd_sd_lim[1],rd_sd_lim[2]);
// construct a randon walk for fishing mortality
for (y in 1:(nyears-1)) {
Ft[y+1]~lognormal(log(Ft[y]),sd_Ft);
}
// Likelihoods
for(y in 1:(nyears)){
// biomass observations
data_surv_biom[y]~lognormal(log(Surv_Biomass[y]),sd_surv_biom);
data_land_biom[y]~lognormal(log(Land_Biomass[y]),sd_land_biom);
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y]|Survey_Distr[,y]D_beta[1]);
target+=DM_lpmf(data_land_scaled[,y]|Land_Distr[,y]D_beta[2]);
}
}
// end block

generated quantities {
matrix[nlen,nyears] SSB_Mat;
vector[nyears] SSB;
vector[nyears] Discard_Biomass;
vector[nyears] Caught_Biomass;
matrix[nlen, nyears] Catches_biom_xlen;
```

```
matrix[nlen, nyears] Discard_biom_xlen;
matrix[nlen, nyears] Catch_Distr;
matrix[nlen, nyears] Discard_Distr;
real eff_smpl_size[2]; // effective sample size
// Distribution of the catches and of the discard
for (y in 1:nyears) {
for (l in 1:nlen) {
Discard_Distr[l,y] = Discard[l,y] / sum(Discard[,y]);
Catch_Distr[l,y] = Catches[l,y] / sum(Catches[,y]);
}
}
// Discard and Catches weight
for (y in 1:nyears) {
for (l in 1:nlen) {
// landed numbers at length and year
Catches_biom_xlen[l,y] = W[l] * Catches[l,y];
}
Caught_Biomass[y] = sum(Catches_biom_xlen[,y]);
}
for (y in 1:nyears) {
for (l in 1:nlen) {
// landed numbers at length and year
Discard_biom_xlen[l,y] = W[l] * Discard[l,y];

}
Discard_Biomass[y] = sum(Discard_biom_xlen[,y]);
}
// Spawning Stock Biomass (SSB)
for (y in 1:nyears) {
for (l in 1:nlen) {
```

```
SSB_Mat[l,y] = Mat[l] * N[l,y]; // caught biomass


}
}
for (y in 1:nyears) {
for (l in 1:nlen) {
SSB_Mat[l,y] = SSB_Mat[l,y] * W[l]; // caught biomass
}
}
for (y in 1:nyears) {
SSB[y] = sum(SSB_Mat[,y]);


}
// calculate effective sample size
eff_smpl_size[1]=neff_surv* (1+D_beta[1])/(neff_surv+D_beta[1]);
eff_smpl_size[2]=neff_land* (1+D_beta[2])/(neff_land+D_beta[2]);
}
// end block
```

A.2.4 Supplementary plots: Full model

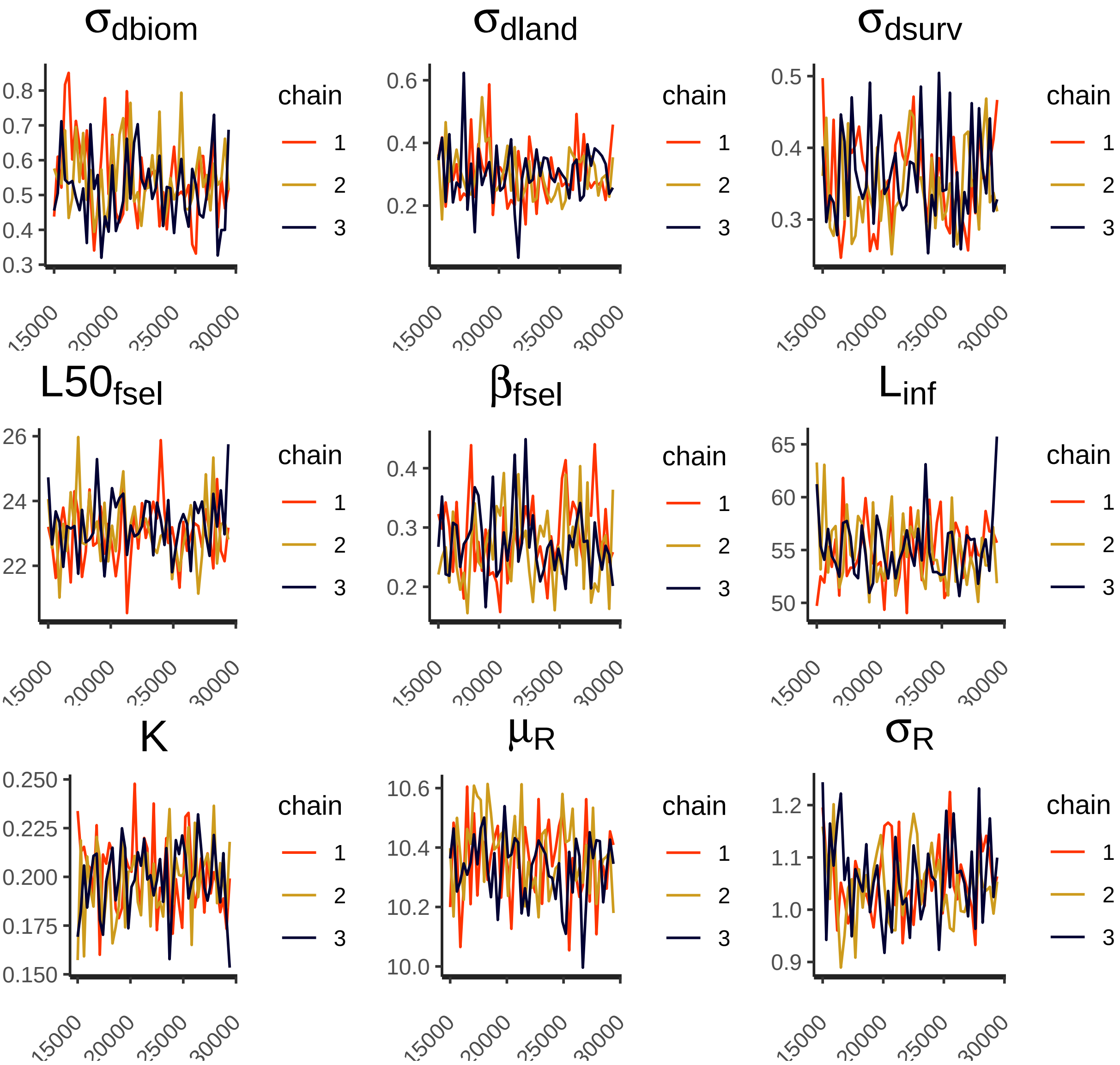


Figure A.1: Chapter III full model - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

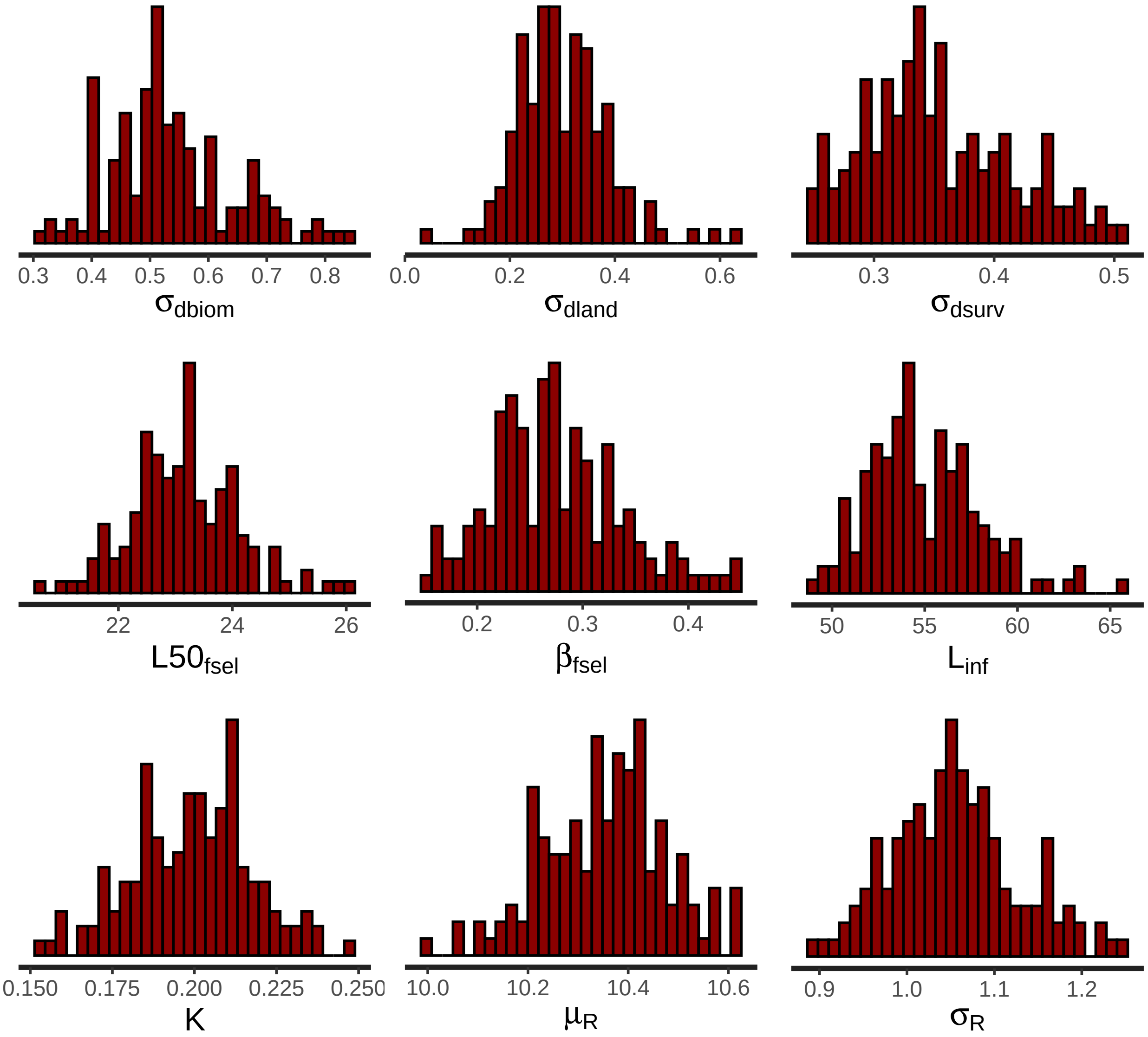


Figure A.2: Chapter III full model - Posterior distribution of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

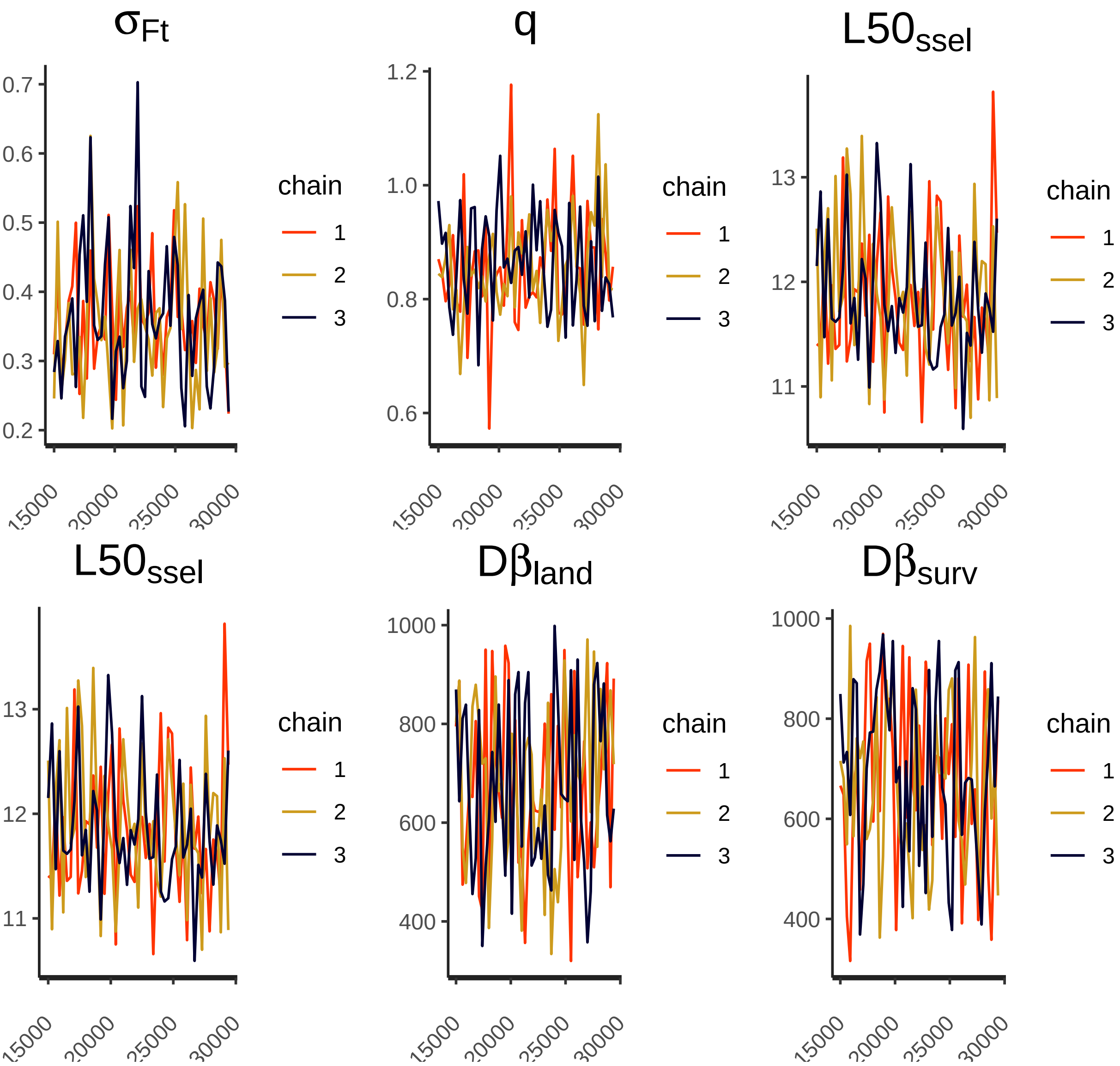


Figure A.3: Chapter III full model - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

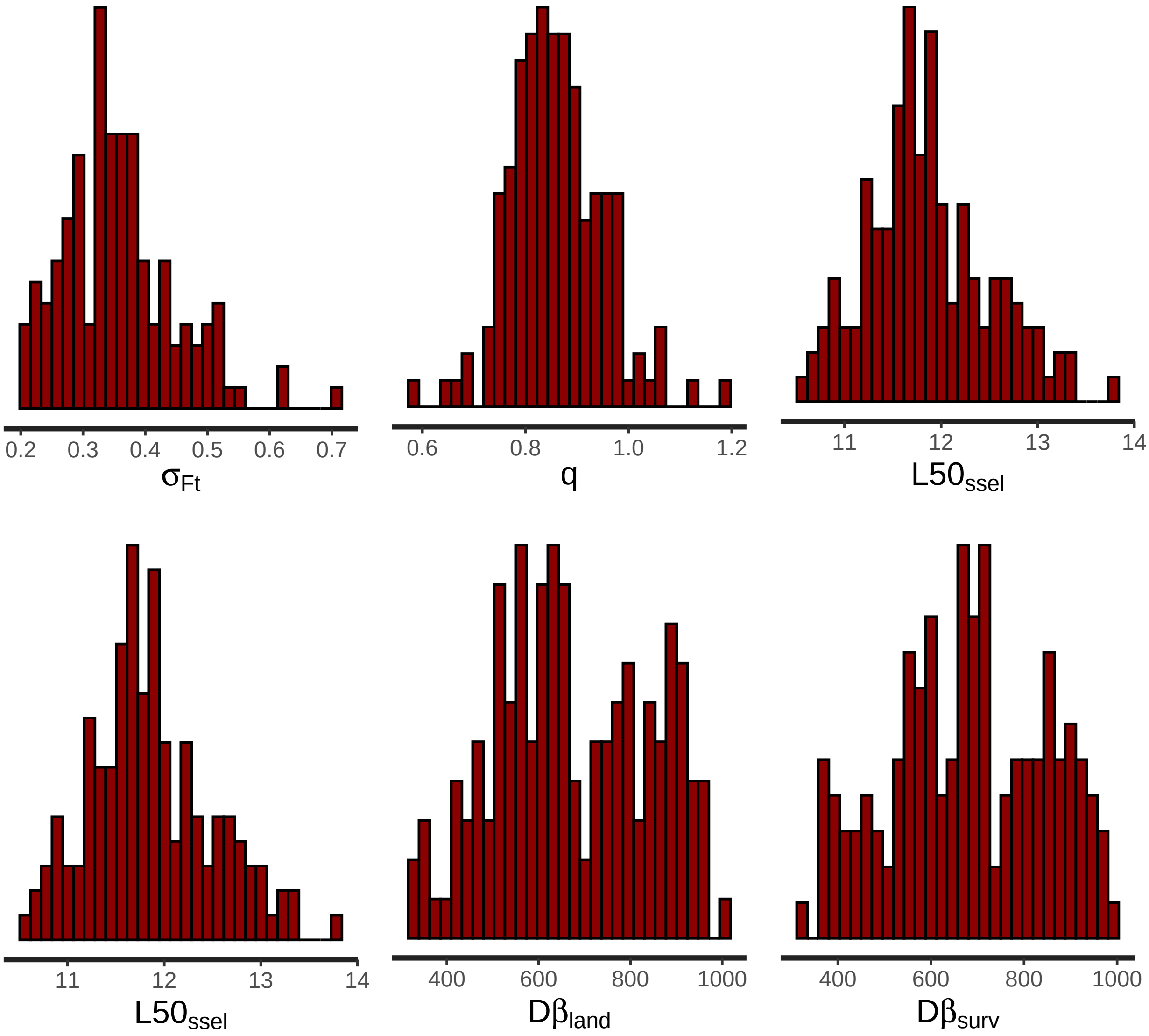


Figure A.4: Chapter III full model - Posterior distribution of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

```
### Survey only
### Fully annotated R code of the survey only model tested on pseudo data
source(“FUNCTIONS.R”)
library(rstan)
#### FIXED PARAMETERS AND DATA ####
#### RECR VALUES ####
r <- matrix(c(397633000, 650569000, 871808000, 1059734000, 891641000, 448119000,
391338000, 1319269000, 1740206000, 43186000, 635677000, 632510000, 1092931000,
75228000, 1842843000, 1122754000, 1399884000, 2254006000, 877285000, 1414554000,
784294000, 1436937000, 350975000, 1597931000, 609972000, 421805000, 733346000,
294268000, 341888000, 780266000, 395474000, 951238000, 544657000, 350372000,
1072352000, 112966000, 227641000, 416935000, 152852000,229713000, 113961000,
193972000, 154826000, 354524000, 168447000, 190527000, 183333000, 270365000,
131827000, 179746000, 223389000, 310228000, 150660000, 114185000, 320063000,
77677000, 133583000), byrow = TRUE, ncol = 1)
r = r[34:57]/1e6
#### PARAMETERS ####
# many parameters of this block are not used directly in the model in stan, but
rather used in
# functions to calculate values that will enter the stan model as parameters.
ymin = 1995 # first year of data
ymax = 2018 # last year of data
nyears = ymax-ymin+1 # number of years
Dt = 1 # timestep
L0 = 1 # minimum length modeled
lmax = 53 # maximum length modeled
DL = 1 # length class width
Linf = 53 # maximum length for the Von Bertalanffy
L = L0:lmax
Linf = 53 # maximum length for the Von Bertalanffy
```

```
L = L0:lmax
K = 0.2 # K for the Von Bertalanffy
# coefficient variation (used to calculate the sd around length class)
cv = 0.1
nlen = length(L) # number of length classes
alpha_wgt_len = 0.008 # alpha in length-weight conversion
beta_wgt_len = 3.0669 # beta in length-weight conversion
M_u = 0.1 # parameter in natural mortality
d = -0.3 # parameter in natural mortality
L50Mat = 40 # L50 of the maturity logistic
kMat = 0.14 # steepness of the maturity logistic
beta_discard_sel = 7 # steepness of the discard selectivity
L50_discard_sel = 30 # L50 of the discard selectivity
muR = 10.5 # mean length of the recruitment

    # call to functions to calculate derived fixed parameters
# vector of weight at length
W = wgt_at_len(L, alpha_wgt_len, beta_wgt_len, gut_wgt_conv = 1)
M = Lorenzen(W, M_u, d) # natural mortality at length
Mat = logistic(L,L50Mat,kMat) # maturity at length
# probability of discard at length
sD = 1 / (1+exp(-log(9)/beta_discard_sel(L-L50_discard_sel)))
alfa_s = 3
mode_s = 27
beta_s=mode_s/(alfa_s-1)
sS = gamsel(alfa_s,beta_s,L)
# probability of recruitment length
R_distr = Get_R_stan(muR, cv, nlen, L, DL)
#### DATA ####
# survey length distribution, total number at length
```

```
data_surv_distr <- (read.table(‘surv_only_data_surv_distr.txt’))
data_surv_biom <- read.table(‘surv_only_data_surv_biom.txt’)
#### LIST THAT IMPUTS THE DATA ####
input.data = list(
# see above for definitions
#~~~~~ PARAMETERS ~~st
# TIME
nyears = nyears,
# GROWTH
nlen = nlen,
L = L,
W = W,
Dt = 1, # timestep
L0 = 1, # minimum length modeled
lmax = 53, # maximum length modeled
DL = 1, # length class width
Linf = 53, # maximum length for the Von Bertalanffy
# RECRUITMENT
Mat = Mat, # used only in generated quantities (a posteriori calculations)
# SURVIVORSHIP
M = M,
sD = sD,
sS = sS,
q = 1,
# EFFECTIVE SAMPLE SIZE
neff_surv = 100, # effective sample size of the survey
neff_land = 100,
#~~ DATA ~st
data_surv_distr = as.matrix(data_surv_distr),
data_surv_biom = data_surv_biom[,1],
```

```
#~~ FITTING PARAMETERS BOUNDS ~~~
Rt_mean = (70),# lower bound for Rt
Rt_sd = (1500), # Upper bound for Rt
#L50_fish_sel_mean = 5,
#L50_fish_sel_sd = 50,
mode = 27,
Ft_bounds = c(0.01,.5),
sd_Ft_bounds = c(0.01,2),
sd_surv_biom_bounds = c(0,1),
sd_land_biom_bounds = c(0,1),
NS1_mean=mean(log(2colSums(as.matrix(data_surv_distr)))),
NS1_sd=0.9,
alpha=rep(1,nlen),
rd_lim=c(5,20),
rd_sd_lim=c(.1,20),
lf=c(1:nlen),
cv_bounds = c(0.01,0.9),
K_bounds = c(0.01,0.9),
L_bound=c(50,0.3*50),
alfa_bounds=c(2.4,0.2)
#beta_fish_sel_mean = 0.1,
#beta_fish_sel_sd = 0.9 # steepness of fishing selectivity curve
)

#### FITTING PARAMETERS ####
# initial values
inits1 <- list(
#Rt = rep((250),(nyears)),
Rt=(r),
Ft = c(0.1,rep(0.5,(nyears-1))), # fishing effort per year
```

```
#L50_fish_sel= 20, # L50 of fishing selectivity curve
sd_surv_biom=0.6, # error around the survey biomass
sd_Ft=0.2,
#beta_fish_sel=0.3,
alfa = 2.5,
NS1=exp(input.data$NS1_mean),
LF1_distr=(data_surv_distr[,1]+1)/sum(data_surv_distr[,1]+1),
R_distr_mean=12,
R_distr_sd=1.2,
cv = 0.1,
K = 0.1,
Linf=55,
D_beta=500
)

inits2<-inits3<-inits1
iter<-30000
chains<-3
thin<-300
model<-“slam_v5.stan”
init<-list(inits1,inits2,inits3)
t1<-Sys.time()
fitted0 <- stan(file = model, data = input.data, thin=thin, diagnostic_file =
“parameter values”, init=init, cores=4, seed = “38”, iter =iter, chains = chains,
verbose=FALSE, init_r=.5)
t2<-Sys.time()
```

A.2.5 Fully annotated Stan code of the survey only model tested on pseudo data

```
functions {
// function to calculate log probability for a Dirichlet-multinomial distribution
real DM_lpmf(int [] n, vector alpha) {
int N = sum(n);
real A = sum(alpha);
return lgamma(A) - lgamma(N + A)
+ sum(lgamma(to_vector(n) + alpha))
- sum(lgamma(alpha));
}
real gamsel(real alpha,real beta,real len){
return((len/((alpha-1)* beta))^(alpha-1)* exp(alpha-1-len/beta));
}
}

// data and fixed parameters
data {
int nyears; // number of years
real Dt; // time step
real L_bound[2]; // bounds on Linf
real DL; // length bin size
int nlen; // number of length bins
vector[nlen] W; // weight at length vector
vector[nlen] L; // length classes
vector[nlen] alpha; // Dirichlet parameter vector
vector[nlen] M; // natural mortality
vector[nlen] sD; // discard selection at length
real sS[nlen];
vector[nlen] Mat; // maturity
```

```
// values for fishery selection parameter priors,
//real beta_fish_sel_mean;
//real beta_fish_sel_sd;
//real L50_fish_sel_mean;
//real L50_fish_sel_sd;
real mode;
real alfa_bounds[2];

// values for prior on initial population survivors
real NS1_mean;
real NS1_sd;

// observations
int data_surv_distr[nlen,nyears]; // survey number at length
real data_surv_biom[nyears]; // survey biomass

// effective sample sizes for survey and landings distributions
int neff_surv;

// Bounds for prior on growth parameters
real K_bounds[2];
real cv_bounds[2];

// Bounds for prior on recruitment
real Rt_mean;
real Rt_sd;

// bounds or prior on Ft
real Ft_bounds[2];
```

```
// bounds for prior on suvey biomass
real sd_surv_biom_bounds[2];

// bounds for std dev process error on Ft
real sd_Ft_bounds[2];

// bounds of priors on recruitment distribution parameters
real rd_lim[2]; // bounds for mean of distribution
real rd_sd_lim[2]; // bounds for sd of distribution
}
// end block

transformed data {
int data_surv_scaled[nlen,nyears];
// re-scale survey distribution to effectove sample size
for (l in 1:nlen){
for (y in 1:nyears){
data_surv_scaled[l,y] = data_surv_distr[l,y]* neff_surv/sum(data_surv_distr[,y]);
}
}
}
// end block

// fitting parameters
// see R document for definitions
parameters {
vector[nyears] Rt; // Annual recruitment
vector[nyears] Ft; // Annual fishing mortality year effect
simplex[nlen] LF1_distr; // proportion at length surviving in first year
```

```
real NS1; // total number of survivirs in first year
real sd_surv_biom; //observation error on survey biomass
real sd_land_biom; // observation error on landings biomass
real sd_Ft; // process error on fishing morality year effect
real alfa;

// growth parameters
real cv;
real K;
real Linf;

// fishery selectivity parameters
real L50_fish_sel;
real beta_fish_sel;

// recruitment length frequency parameters
real R_distr_mean;
real R_distr_sd;

// Dirichlet scalar
real D_beta;
}
// end block

// place here anything for which you want to plot a posterior distribution.
// The actual ecologycal model must go here.
transformed parameters {
matrix[nlen, nlen] G; // growth projection matrix
vector[nlen] newL;
vector[nlen] sd_growth;
```

```
vector[nlen] s; // fishing selectivity curve
matrix[nlen, nyears] F; // fishing mortality matrix
matrix[nlen, nyears] Z; // total mortality matrix
matrix[nlen, nyears] S; // survival matrix
matrix[nlen, nyears] N; // population matrix
vector[nlen] NS; // population matrix * survival matrix
// survey proportion at length x years
matrix[nlen, nyears] Survey_Distr;
// survey numbers at length x years
matrix[nlen, nyears] Survey;
// landings proportion at length x years
matrix[nlen, nyears] Land_Distr;
// caught numbers at length x years
matrix[nlen, nyears] Catches;
// discarded numbers at length x years
matrix[nlen, nyears] Discard;
// landed numbers at length x years
matrix[nlen, nyears] Landings;
// biomass landed per length per year
matrix[nlen, nyears] Landings_biom_xlen;
// total biomass landed per year
vector[nyears] Land_Biomass;
// biomass surveyed per length per year
matrix[nlen, nyears] Survey_biom_xlen;
// total biomass surveyed per year
vector[nyears] Surv_Biomass;
// recruitmet length frequency distribution
vector[nlen] R_distr;
real beta;
```

```
// calculate recruitment length distribution from a normal distribution
for(i in 1:nlen){
R_distr[i] = normal_cdf(L[i]+DL,R_distr_mean,R_distr_sd)-
normal_cdf(L[i],R_distr_mean,R_distr_sd);
}
// construct initial population from survivors in initial year and recruitment
for(l in 1:nlen){
N[l,1]=NS1* LF1_distr[l]+exp(Rt[1])R_distr[l];
}
newL = Linf - (Linf-L) exp(-KDt);
for (l in 1:nlen) {
sd_growth[l] = cv  newL[l];
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = normal_cdf(L[l]+DL,newL[y],sd_growth[l])-
normal_cdf(L[l],newL[y],sd_growth[l]);
}
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = G[l,y] / sum(G[,y]);
}
}
// define S: survival at length
//s = 1 ./ (1+exp(-beta_fish_sel(L-(L50_fish_sel))));
beta=mode/(alfa-1);
for (l in 1:nlen) {
for (y in 1:nyears) {
s[l] = gamsel(alfa,beta,L[l]);
```

```
F[l,y] = s[l]  Ft[y];
Z[l,y] = F[l,y] + M[l];
}
}
S = exp(-(Z));
// Calculate survivors into the next year
for (y in 1:(nyears-1)) {
for (l in 1:nlen) {
NS[l] = N[l,y] * S[l,y];
}
// Project the population at length one year ahead from suvivors and growth matrix
N[,y+1] = G * NS; // double check with length distribution plot
for (l in 1:nlen) {
// note Rt is on a log scale
N[l,y+1] = N[l,y+1] + exp(Rt[y+1])R_distr[l];
}
}
// Calculate fitted survey numbers at length from catchability q and survey size
selection
for (y in 1:nyears){
for (l in 1:nlen){
Survey[l,y] = N[l,y]sS[l];
}
}
// calculate discard, catches and landings
// catch numbers at length and year
Catches = F ./ Z .* (1-S) .* N;

for (y in 1:nyears) {
for (l in 1:nlen) {
```

```
// survey weight at length and year
Survey_biom_xlen[l,y] = W[l] * Survey[l,y];

}
// fitted survey biomass
Surv_Biomass[y] = sum(Survey_biom_xlen[,y])/10e4;

}
// calculate fitted landing and survey length frequency
for (y in 1:nyears) {
for (l in 1:nlen) {
Survey_Distr[l,y] = Survey[l,y] / sum(Survey[,y]);
}
}
}
// end block

model {
// Priors
// Fishing mortality year effect in first year
Ft[1]~uniform(Ft_bounds[1],Ft_bounds[2]);
// Annual recruitment
for (y in 1:(nyears)) {
Rt[y]~uniform(Rt_mean,Rt_sd);
}
// total survivors in first year
NS1~lognormal(NS1_mean,NS1_sd);
//survivors proportion at length
LF1_distr~dirichlet(alpha);
// fishery and survey selection parameters
```

```
//L50_fish_sel~uniform(L50_fish_sel_mean,L50_fish_sel_sd);
//beta_fish_sel~uniform(beta_fish_sel_mean,beta_fish_sel_sd);
alfa~lognormal(log(alfa_bounds[1]),alfa_bounds[2]);
// growth parameters
cv~uniform(cv_bounds[1],cv_bounds[2]);
K~uniform(K_bounds[1],K_bounds[2]);
Linf~normal(L_bound[1],L_bound[2]);
// Dirichlet scalar
D_beta~uniform(0,1000);
// observation errors
sd_surv_biom~uniform(sd_surv_biom_bounds[1],sd_surv_biom_bounds[2]);
// process error on fishing mortality
sd_Ft~uniform(sd_Ft_bounds[1],sd_Ft_bounds[2]);
// recruitmnet proiportins at length
R_distr_mean~uniform(rd_lim[1],rd_lim[2]);
R_distr_sd~uniform(rd_sd_lim[1],rd_sd_lim[2]);
// construct a randon walk for fishing mortality
for (y in 1:(nyears-1)) {
Ft[y+1]~lognormal(log(Ft[y]),sd_Ft);
}

// Likelihoods
for(y in 1:(nyears)){
// biomass observations
data_surv_biom[y]~lognormal(log(Surv_Biomass[y]),sd_surv_biom);
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y]|Survey_Distr[,y]*D_beta);
}
}
```

```
// end block

    generated quantities {
matrix[nlen,nyears] SSB_Mat;
vector[nyears] SSB;
vector[nyears] Discard_Biomass;
vector[nyears] Caught_Biomass;
matrix[nlen, nyears] Catches_biom_xlen;
matrix[nlen, nyears] Discard_biom_xlen;
matrix[nlen, nyears] Catch_Distr;
matrix[nlen, nyears] Discard_Distr;
real eff_smpl_size; // effective sample size
// Distribution of the catches and of the discard
for (y in 1:nyears) {
for (l in 1:nlen) {
Discard_Distr[l,y] = Discard[l,y] / sum(Discard[,y]);
Catch_Distr[l,y] = Catches[l,y] / sum(Catches[,y]);
}
}
// Discard and Catches weight
for (y in 1:nyears) {
for (l in 1:nlen) {
// landed numbers at length and year
Catches_biom_xlen[l,y] = W[l] * Catches[l,y];

}
Caught_Biomass[y] = sum(Catches_biom_xlen[,y]);
}
for (y in 1:nyears) {
for (l in 1:nlen) {
```

```
// landed numbers at length and year
Discard_biom_xlen[l,y] = W[l] * Discard[l,y];

}
Discard_Biomass[y] = sum(Discard_biom_xlen[,y]);
}
// Spawning Stock Biomass (SSB)
for (y in 1:nyears) {
for (l in 1:nlen) {
// caught biomass
SSB_Mat[l,y] = Mat[l] * N[l,y];
}
}
for (y in 1:nyears) {
for (l in 1:nlen) {
// caught biomass
SSB_Mat[l,y] = SSB_Mat[l,y] * W[l];
}
}
for (y in 1:nyears) {
SSB[y] = sum(SSB_Mat[,y]);
}
// calculate effective sample size
eff_smpl_size=neff_surv*(1+D_beta)/(neff_surv+D_beta);
}
// end block
```

A.2.6 Supplementary plots: survey only model

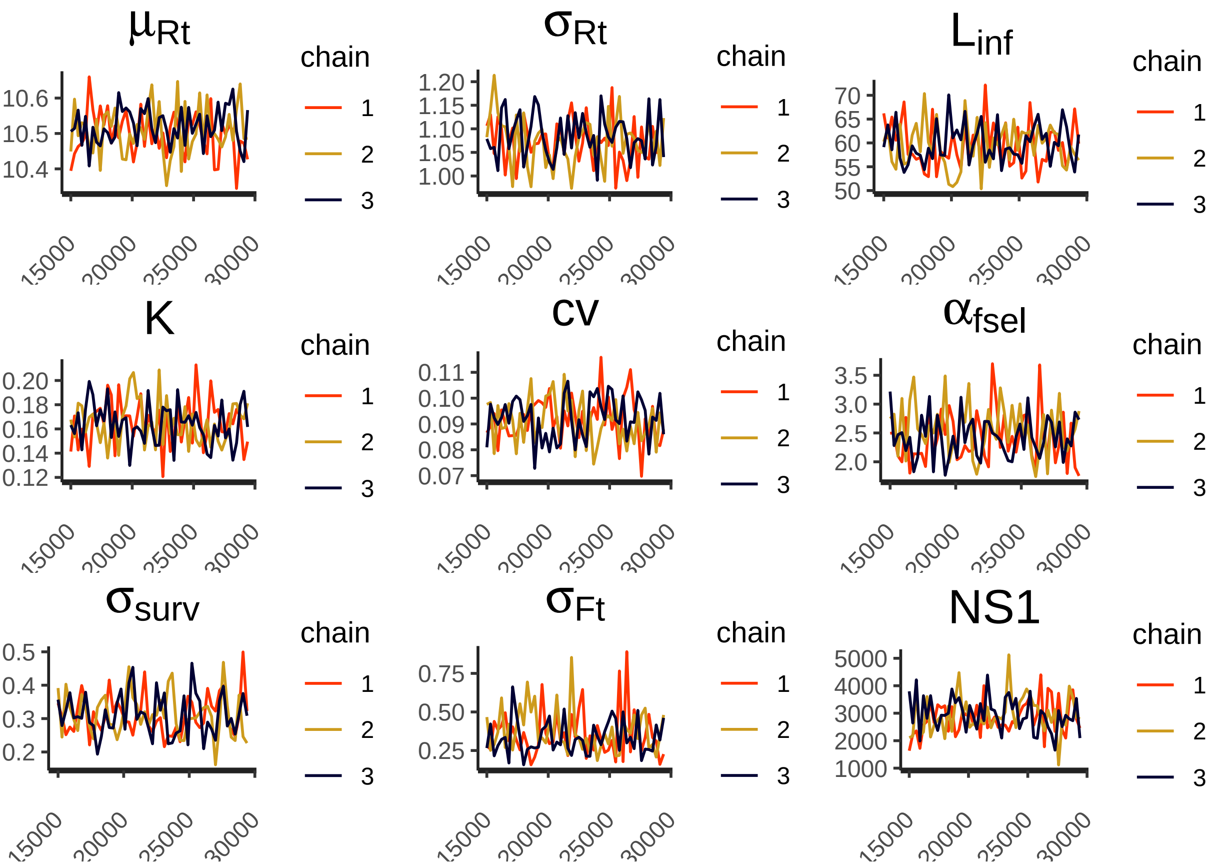


Figure A.5: Chapter III survey only model - Trace plots for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, σ_{Ft}, NS_1

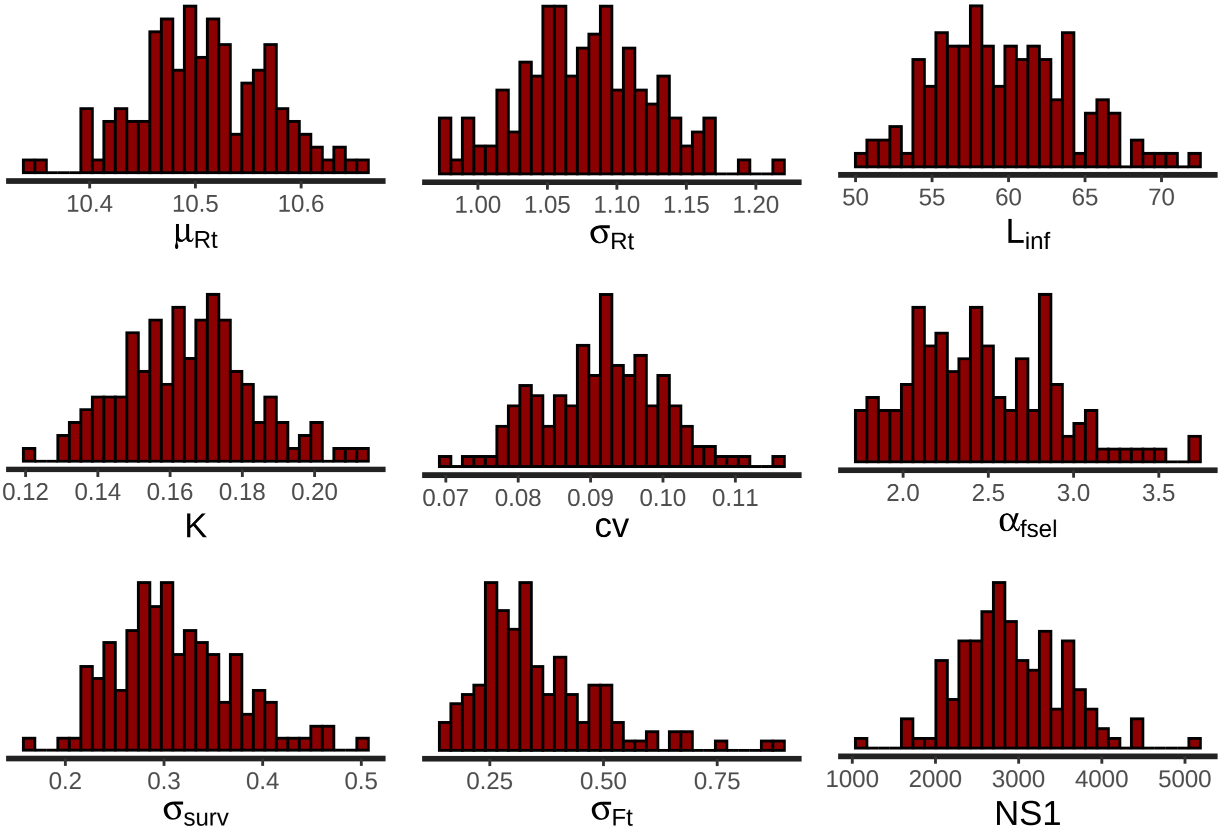


Figure A.6: Chapter III survey only model - Plot showing the posterior for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, σ_{Ft}, NS_1

A.3 Chapter IV

A.3.1 Fully annotated R code of the reference model tested on whiting data

```
library(rstan)
#### FIXED PARAMETERS AND DATA ####
#### RECR VALUES ####
r <- c(657216, 860236, 1145112, 771780, 785939, 755366, 696054, 657609, 657222,
402613, 866442, 328494, 213390, 287758, 217260, 117059, 106349, 65960, 59396,
98577, 302352, 96013, 204747, 113307, 257644, 477394, 324234, 268962, 206089,
427777, 480698, 202293)
r <- r[9:32]

#### PARAMETERS ####
ymin1 = 1996 # first year of data
ymax1 = 2010 # last year of the first survey
ymin2 = 2011 # first year of the new survey
ymax2 = 2020 # last year of data
nyears1 = ymax1-ymin1+1
nyears2 = ymax2-ymin2+1 # number of years
nyears_tot = ymax2-ymin1+1
Dt = 1 # timestep
L0 = 1
lmin = 10 # minimum length modeled
lmax = 55 # maximum length modeled
DL = 1 # length class width
L = lmin:lmax
# coefficient variation (used to calculate the sd around length class)
cv = 0.1
```

```
nlen = length(L) # number of length classes
alpha_wgt_len = 0.0093 # alpha in length-weight conversion
beta_wgt_len = 2.9456 # beta in length-weight conversion
M_u = 0.2 # parameter in natural mortality
d = -0.31 # parameter in natural mortality
L50_Mat = 20 # L50 of the maturity logistic
L25_Mat = 0.14 # steepness of the maturity logistic
muR = 15.4 # mean length of the recruitment

# internal functions to get weight-at-length, natural mortality, maturity ogive.
# This quantities are calculated with quantities assumed to be known,
# therefore they are calculated externally from the Stan model

# Length-weight conversion. Transforms a vector of lengths in a vector of weights.
# divide by 1e6 converts grams into tons
wgt_at_len <- function (L, alpha, beta) {
return((alpha * L^beta)* 1.131e-3)
}
M = Lorenzen(W, M_u, d) # natural mortality at length

# Natural mortality function transforms a vector of weigth in mortality at length.
# (Lorenzen 1996, Journal of Fish Biology 49, 627-647).
Lorenzen <- function(W, M_u, d) {
return(M_u  W^d)
}

# multipurpose logistic function that can be used to calculate the maturity ogive
logistic <- function(x,x0,k) {
return(1/(1+exp(-k(x-x0))))
}
```

```
Mat = logistic(L,L50_Mat,L25_Mat) # maturity at length

#### DATA ####
data_disc_biom <- read.table('data_disc_biom_whiting.txt')
data_land_biom <- read.table('data_land_biom_whiting.txt')
data_surv_biom <- read.table('data_surv_biom_whiting.txt')
data_surv_distr <- round(read.table('data_surv_distr_whiting.txt'))
data_surv_distr[is.na(data_surv_distr)] <- 0
data_surv_distr <- data_surv_distr[10:55,]
data_land_distr <- round(read.table('data_land_distr_whiting.txt'))
data_land_distr <- (data_land_distr[11:56,])
data_land_distrX26 < −rep(0, 46)data_land_distrX27 <- rep(0,46)
#### LIST THAT IMPUTS THE DATA ####
input.data = list(
# see above for definitions
#~~~~~ PARAMETERS ~~~~
# TIME
nyears1 = nyears1,
nyears2 = nyears2,
nyears_tot = nyears_tot,
# GROWTH
nlen = nlen,
L = L,
W = W,
Dt = Dt, # timestep
L0 = L0, # minimum length modeled
lmax = lmax, # maximum length modeled
DL = DL, # length class width
# RECRUITMENT
# used only in generated quantities (a posteriori calculations)
```

```
Mat = Mat,
# SURVIVORSHIP
M = M,
# EFFECTIVE SAMPLE SIZE
neff_surv = 30,
neff_land = 40,

# discard selectivity
L25_disc_sel = 0.3, # L25 of the discard selectivity
L50_disc_sel = c(28.55163, 29.29826, 29.89666, 30.20272, 30.01695, 29.92714,
29.84362, 31.08411, 31.22390, 31.46994, 31.80673, 31.93525, 31.82081, 31.93169,
32.08761, 32.73832, 32.63299, 33.54136, 34.31517, 34.67922, 34.76380, 35.20056,
35.27752, 35.2, 35.2),

#~~~~ DATA ~~~~
data_land_distr = as.matrix(data_land_distr),
data_surv_distr = as.matrix(data_surv_distr),
data_surv_biom = data_surv_biom[,1],
data_land_biom = data_land_biom[,1],
data_disc_biom = data_disc_biom[,1],

#~~~~ FITTING PARAMETERS BOUNDS ~~~
Rt_mean = log(200),# lower bound for Rt
Rt_sd = log(20000000), # Upper bound for Rt
q_mean = 0,
q_sd = 2,
L50_fish_sel_mean=30,
L50_fish_sel_sd=3.5,
beta_fish_sel_mean=0.35,
beta_fish_sel_sd=0.1,
```

```
Ft_bounds = c(0.01,2),
sd_Ft_bounds = c(0.01,1),
sd_surv_biom_bounds = c(0,1),
sd_disc_biom_bounds = c(0,1),
sd_land_biom_bounds = c(0,1),
alpha=rep(1,nlen),
rd_lim=c(5,20),
rd_sd_lim=c(.1,1.5),
lf=c(1:nlen),
cv_bounds = c(0.01,0.9),
K_bounds = c(0.34,0.2),
L_bound=c(58,.330),
D_beta_bounds = c(0,900),
md2 = c(1.5,50),
al2 = c(1.5,10),
md1 = c(1.5,50),
al1 = c(1.5,10)
)

#### FITTING PARAMETERS ####
# initial values
inits1 <- list(

Rt=log(r),
Ft = c(rep(0.2,(nyears_tot))), # fishing effort per year
q1=0.01, # survey catchability before 2011
q2=0.01, # survey catchability after 2011
L50_fish_sel = 30,
beta_fish_sel = 0.35,
sd_surv_biom=0.2, # error around the survey biomass
```

```
sd_land_biom=0.2, # error around the landings biomass
sd_disc_biom=0.2,
sd_Ft=0.1,
LF1_distr=(data_surv_distr[,1]+1) / sum(data_surv_distr[,1]+1),
R_distr_mean=15,
R_distr_sd=1,
cv=0.1,
K=0.34,
Linf=58,
D_beta=c(50,50,50),
mode1=30,
alfa1=3,
mode2=35,
alfa2=2

)

inits2<-inits3<-inits1

iter<-100000
chains<-3
thin<-1000
model<-“whiting_slam_v5.03.stan”
init<-list(inits1,inits2,inits3)

t1<-Sys.time()
fitted <- stan(file = model, data = input.data, thin=thin, diagnostic_file = “parameter values”, init=init, cores=4, seed = “38”, #algorithm = “Fixed_param”,
iter =iter, chains = chains, verbose=FALSE, init_r=.5)
t2<-Sys.time()
```

```
t2-t1
```

A.3.2 Fully annotated Stan code of the reference model tested on whiting data

```
// slam full model version: reference model
// initial N is estimated the sum of Rt[1] and NS1,
// the survivors from year 0 (first data year -1)
// recruitment length distribution is estimated
// recruitment drawn from uniform distribution - not log uniform
// Ft follows a random walk
// estimates growth parameters
// removed initial zeroing of G matrix calculation
// uses Dirichlet-multinomial with Beta dispersion parameter D_beta
// two surveys: pre and post 2011
// fisheries logistic selectivity and survey gamma selectivity

functions {
// function to calculate log probability for a Dirichlet-multinomial distribution
real DM_lpmf(int [] n, vector alpha) {
int N = sum(n);
real A = sum(alpha);
return lgamma(A) - lgamma(N + A)
+ sum(lgamma(to_vector(n) + alpha))
- sum(lgamma(alpha));
}
// gamma selectivity function
real gamsel(real alpha,real beta,real len){
return((len/((alpha-1) * beta))^(alpha-1))exp(alpha-1-len/beta);
}
```

```
}

// data and fixed parameters

data {

int nyears1; // number of years
int nyears2; // number of years
int nyears_tot; // number of years

real Dt; // time step
real L_bound[2]; // bounds on Linf
real DL; // length bin size
int nlen; // number of length bins
vector[nlen] W; // weight at length vector
vector[nlen] L; // length classes
vector[nlen] alpha; // Dirichlet parameter vector
vector[nlen] M; // natural mortality
vector[nlen] Mat; // maturity

// bounds for survey q
real q_mean;
real q_sd;

// values for fishery selection parameter priors,
real L50_fish_sel_mean;
real L50_fish_sel_sd;
real beta_fish_sel_mean;
real beta_fish_sel_sd;
```

```
// discard selectivity parameters
real L25_disc_sel;
real L50_disc_sel[nyears_tot];

// values for survey selection parameter priors
real md2[2];
real al2[2];
real md1[2];
real al1[2];

// observations
int data_land_distr[nlen,nyears1]; // landings number at length
int data_surv_distr[nlen,nyears_tot]; // survey number at length
real data_surv_biom[nyears_tot]; // survey biomass
real data_land_biom[nyears_tot]; // landings biomass
real data_disc_biom[nyears_tot]; // discard biomass

// effective sample sizes for survey and landings distributions
int neff_surv;
int neff_land;

// Bounds for prior on growth parameters
real K_bounds[2];
real cv_bounds[2];

// Bounds for prior on recruitment
real Rt_mean;
real Rt_sd;

// bounds or prior on Ft
```

```
real Ft_bounds[2];

// bounds for prior on suvey biomass
real sd_surv_biom_bounds[2];

// bounds for std dev prior on landings observations
real sd_land_biom_bounds[2];

// bounds for std dev process error on Ft
real sd_Ft_bounds[2];

// bounds for std dev discard biomass
real sd_disc_biom_bounds[2];

// bounds for dispersion parameter Dirichlet
real D_beta_bounds[2];

// bounds of priors on recruitment distribution parameters
real rd_lim[2]; // bounds for mean of distribution
real rd_sd_lim[2]; // bounds for sd of distribution

}
// end block

transformed data {

int data_land_scaled[nlen,nyears1];
int data_surv_scaled[nlen,nyears_tot];

// re-scale survey distribution to effectove sample size
```

```
for (l in 1:nlen){
for (y in 1:nyears_tot){
data_surv_scaled[l,y] = data_surv_distr[l,y] neff_surv/sum(data_surv_distr[,y]);
}
}

// re-scale landings distribution to effective sample size
for (l in 1:nlen){
for (y in 1:(nyears1-2)){
data_land_scaled[l,y] = data_land_distr[l,y] * neff_land/sum(data_land_distr[,y]);
}
}

}
// end block

// fitting parameters
// see R document for definitions
parameters {
vector[nyears_tot-1] Rt; // Annual recruitment
vector[nyears_tot] Ft; // Annual fishing mortality year effect
simplex[nlen] LF1_distr; // proportion at length surviving in first year
real sd_surv_biom; //observation error on survey biomass
real sd_land_biom; // observation error on landings biomass
real sd_disc_biom; // observation error on discard biomass
real sd_Ft; // process error on fishing morality year effect

// growth parameters
real cv;
real K;
```

```
real Linf;

// fishery selectivity parameters
real L50_fish_sel;
real beta_fish_sel;

// survey catchability
real q1;
real q2;

// recruitment length frequency parameters
real R_distr_mean;
real R_distr_sd;



// Dirichlet scalar
real D_beta[3];

// survey selectivity parameter
real mode1;
real alfa1;
real mode2;
real alfa2;

}
// end block

transformed parameters {

matrix[nlen, nlen] G; // growth projection matrix
```

```
vector[nlen] newL;
vector[nlen] sd_growth;
matrix[nlen, nyears_tot] F; // fishing mortality matrix
matrix[nlen, nyears_tot] Z; // total mortality matrix
matrix[nlen, nyears_tot] S; // survival matrix
matrix[nlen, nyears_tot] N; // population matrix
vector[nlen] NS; // population matrix * survival matrix
// survey proportion at length x years
matrix[nlen, nyears_tot] Survey_Distr;
// survey numbers at length x years
matrix[nlen, nyears_tot] Survey;
// survey numbers at length x years
matrix[nlen, nyears1] Survey1;
// survey numbers at length x years
matrix[nlen, nyears2] Survey2;
// landings proportion at length x years
matrix[nlen, nyears_tot] Land_Distr;
// caught numbers at length x years
matrix[nlen, nyears_tot] Catches;
// discarded numbers at length x years
matrix[nlen, nyears_tot] Discard;
// landed numbers at length x years
matrix[nlen, nyears_tot] Landings;

// biomass landed per length per year
matrix[nlen, nyears_tot] Landings_biom_xlen;
// total biomass landed per year
vector[nyears_tot] Land_Biomass;
vector[nyears_tot] Disc_Biomass;
vector[nyears_tot] Caught_Biomass;
```

```
matrix[nlen, nyears_tot] Catches_biom_xlen;
matrix[nlen, nyears_tot] Discard_biom_xlen;
// biomass surveyed per length per year
matrix[nlen, nyears_tot] Survey_biom_xlen;
// total biomass surveyed per year
vector[nyears_tot] Surv_Biomass;
// recruitmet length frequency distribution
vector[nlen] R_distr;
real NS1; // total number of survivirs in first year
vector[nlen] sF; // fishing selectivity curve
vector[nlen] sS1;
vector[nlen] sS2;
real beta1;
real beta2;

// calculate recruitment length distribution from a normal distribution
for(i in 1:nlen){
R_distr[i] = normal_cdf(L[i]+DL,R_distr_mean,R_distr_sd)-
normal_cdf(L[i],R_distr_mean,R_distr_sd);
}

// survey gamma selectivity
beta1=mode1/(alfa1-1);
beta2=mode2/(alfa2-1);
for (l in 1:nlen) {
sS1[l]=gamsel(alfa1,beta1,L[l]);
sS2[l]=gamsel(alfa2,beta2,L[l]);
}

// construct initial population from survivors in initial year and recruitment
```

```
NS1=0;
for(l in 1:nlen){
NS1=NS1+data_surv_distr[l,1]/(q1sS1[l]);
}
for(l in 1:nlen){
N[l,1]=NS1LF1_distr[l];
}
// total biomass
newL = Linf - (Linf-L)* exp(-KDt);

for (l in 1:nlen) {
sd_growth[l] = cv  newL[l];
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = normal_cdf(L[l]+DL,newL[y],sd_growth[l])-
normal_cdf(L[l],newL[y],sd_growth[l]);
}
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = G[l,y] / sum(G[,y]);
}
}

// fishing logistic selectivity
sF = 1 ./ (1+exp(-beta_fish_sel* (L-L50_fish_sel)));
// define S: survival at length
for (l in 1:nlen) {
for (y in 1:nyears_tot) {
```

```
F[l,y] = sF[l] * Ft[y];
Z[l,y] = F[l,y] + M[l];
}
}
S = exp(-(Z));

// Calculate survivors into the next year
for (y in 1:(nyears_tot-1)) {
for (l in 1:nlen) {
NS[l] = N[l,y] * S[l,y];
}

// Project the population at length one year ahead from suvivors and growth matrix
N[,y+1] = G * NS; // double check with length distribution plot
for (l in 1:nlen) {
// note Rt is on a log scale
N[l,y+1] = N[l,y+1] + exp(Rt[y])R_distr[l];
}
}

// Calculate fitted survey numbers at length from catchability q and survey size
selection
for (y in 1:nyears1){
for (l in 1:nlen){
Survey1[l,y] = q1N[l,y]/sS1[l];
}
}
for (y in 1:nyears2){
for (l in 1:nlen){
Survey2[l,y] = q2N[l,y+nyears1]/sS2[l];
```

```
}
}
Survey = append_col(Survey1,Survey2);

// calculate discard, catches and landings
// catch numbers at length and year
Catches = F ./ Z . (1-S) .* N;

for (y in 1:nyears_tot) {
for (l in 1:nlen) {
// landed weight at length and year
Discard[l,y] = (1 / (1+exp((log(3)/ (L25_disc_sel-L50_disc_sel[y]))*
(L[l]-L50_disc_sel[y])))) * Catches[l,y];
}
}

Landings = Catches - Discard;

for (y in 1:nyears_tot) {
for (l in 1:nlen) {
Landings_biom_xlen[l,y] = W[l] * Landings[l,y];
Catches_biom_xlen[l,y] = W[l] * Catches[l,y];
Discard_biom_xlen[l,y] = W[l] * Discard[l,y];
Survey_biom_xlen[l,y] = W[l] * Survey[l,y];
}
Caught_Biomass[y] = sum(Catches_biom_xlen[,y]);
Land_Biomass[y] = sum(Landings_biom_xlen[,y]);
Disc_Biomass[y] = sum(Discard_biom_xlen[,y]);
Surv_Biomass[y] = sum(Survey_biom_xlen[,y]);
}
```

```
// calculate fitted landing and survey length frequency
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
Land_Distr[l,y] = Landings[l,y] / sum(Landings[,y]);
Survey_Distr[l,y] = Survey[l,y] / sum(Survey[,y]);
}
}
//print("N =",N);
//print("LB =",Land_Biomass);
//print("SB =",Surv_Biomass);
}
// end block

model {
// Priors
// Fishing mortality year effect in first year
Ft[1]~uniform(Ft_bounds[1],Ft_bounds[2]);

// Annual recruitment
for (y in 1:(nyears_tot-1)) {
Rt[y]~uniform(Rt_mean,Rt_sd);
}

//survivors proportion at length
LF1_distr~dirichlet(alpha);

// survey catcability
q1~uniform(q_mean,q_sd);
q2~uniform(q_mean,q_sd);
```

```
// fishery, discard and survey selection parameters
L50_fish_sel~lognormal(log(L50_fish_sel_mean),L50_fish_sel_sd);
beta_fish_sel~lognormal(log(beta_fish_sel_mean),beta_fish_sel_sd);

// survey selection parameters
mode1~uniform((md1[1]),md1[2]);
alfa1~uniform((al1[1]),al1[2]);
mode2~uniform(md2[1],md2[2]);
alfa2~uniform((al2[1]),al2[2]);

// growth parameters
cv~uniform(cv_bounds[1],cv_bounds[2]);
K~lognormal(log(K_bounds[1]),K_bounds[2]);
Linf~lognormal(log(L_bound[1]),L_bound[2]);

// Dirichlet scalar
D_beta[1]~uniform(D_beta_bounds[1],D_beta_bounds[2]);
D_beta[2]~uniform(D_beta_bounds[1],D_beta_bounds[2]);

    // observation errors
sd_land_biom~uniform(sd_land_biom_bounds[1],
sd_land_biom_bounds[2]);
sd_surv_biom~uniform(sd_surv_biom_bounds[1],
sd_surv_biom_bounds[2]);
sd_disc_biom~uniform(sd_disc_biom_bounds[1],
sd_disc_biom_bounds[2]);

// process error on fishing mortality
sd_Ft~uniform(sd_Ft_bounds[1],sd_Ft_bounds[2]);
```

```
// recruitmnet proiportins at length
R_distr_mean~uniform(rd_lim[1],rd_lim[2]);
R_distr_sd~uniform(rd_sd_lim[1],rd_sd_lim[2]);

// construct a randon walk for fishing mortality
for (y in 1:(nyears_tot-1)) {
Ft[y+1]~lognormal(log(Ft[y]),sd_Ft);
}

// Likelihoods functions
for(y in 1:(nyears_tot)){
// biomass observations
data_surv_biom[y]~lognormal(log(Surv_Biomass[y]), sd_surv_biom);
data_land_biom[y]~lognormal(log(Land_Biomass[y]), sd_land_biom);
data_disc_biom[y]~lognormal(log(Disc_Biomass[y]), sd_disc_biom);
}

for(y in 1:(nyears1)){
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y]|Survey_Distr[,y]* D_beta[1]);
}

for(y in 1:(nyears2)){
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y+nyears1]|
Survey_Distr[,y+nyears1] D_beta[2]);
}
```

```
for(y in 1:(nyears1-2)){
// length frequency observations
target+=DM_lpmf(data_land_scaled[,y]|
Land_Distr[,y]D_beta[3]);
}
}
// end block

generated quantities {


matrix[nlen,nyears_tot] SSB_Mat;
vector[nyears_tot] SSB;
matrix[nlen, nyears_tot] Catch_Distr;
matrix[nlen, nyears_tot] Discard_Distr;
//real eff_smpl_size_post2011[2]; // effective sample size
//real eff_smpl_size_pre2011[2];

// Distribution of the catches and of the discard
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
Discard_Distr[l,y] = Discard[l,y] / sum(Discard[,y]);
Catch_Distr[l,y] = Catches[l,y] / sum(Catches[,y]);
}
}

// Spawning Stock Biomass (SSB)
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
SSB_Mat[l,y] = Mat[l] * N[l,y]; // caught biomass
```

```
}
}
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
SSB_Mat[l,y] = SSB_Mat[l,y] * W[l]; // caught biomass

}
}
for (y in 1:nyears_tot) {
SSB[y] = sum(SSB_Mat[,y]);

}
// calculate effective sample size before 2011
eff_smpl_size_pre2011[1]=neff_surv(1+D_beta_pre2011[1])/
(neff_surv+D_beta_pre2011[1]);
eff_smpl_size_pre2011[2]=neff_land(1+D_beta_pre2011[2])/
(neff_land+D_beta_pre2011[2]);
// calculate effective sample size after 2011
eff_smpl_size_post2011[1]=neff_surv(1+D_beta_post2011[1])/
(neff_surv+D_beta_post2011[1]);
eff_smpl_size_post2011[2]=neff_land(1+D_beta_post2011[2])/
(neff_land+D_beta_post2011[2]);
}
// end block
```

A.3.3 Supplementary plots

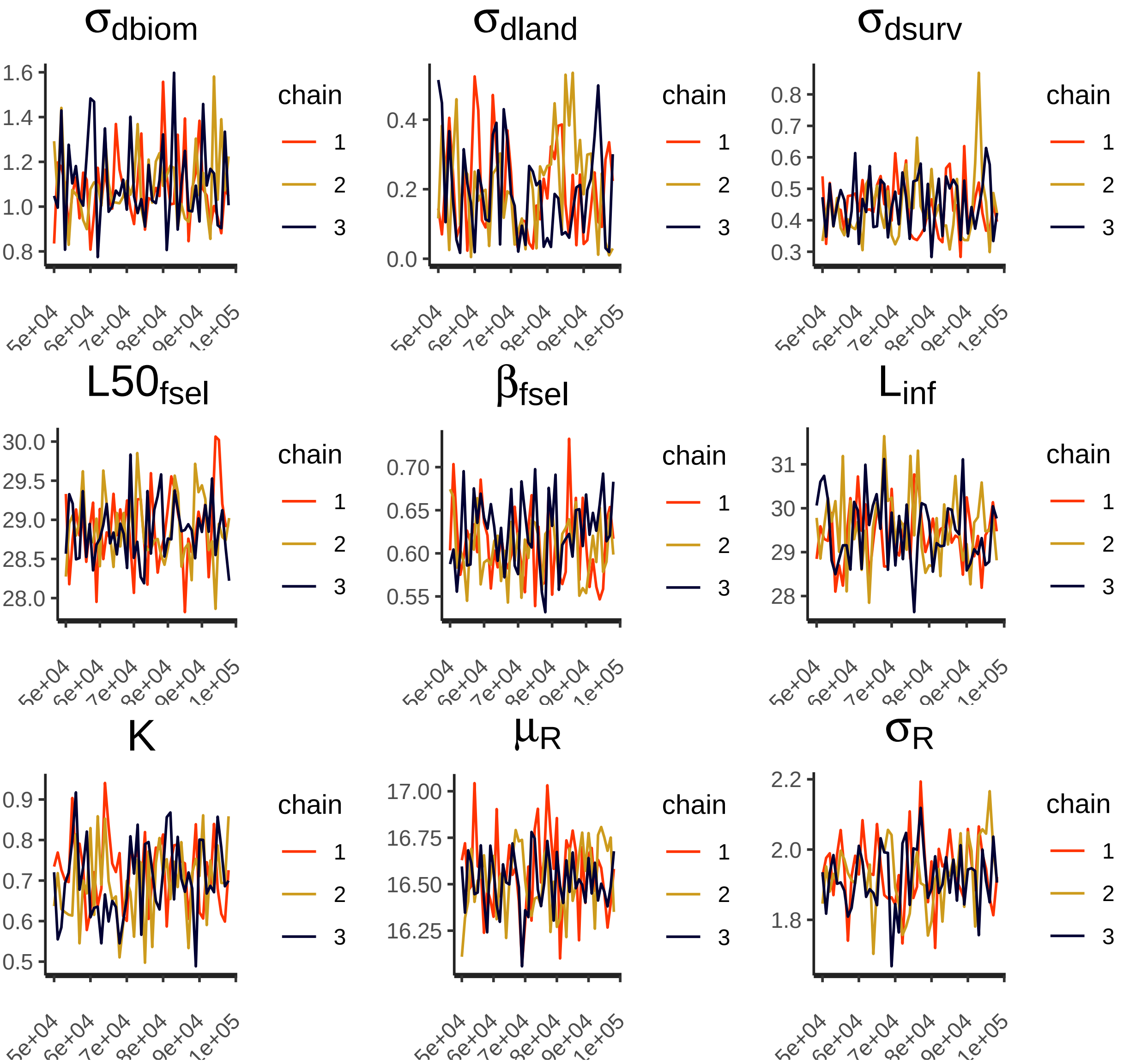


Figure A.7: Chapter IV reference model - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

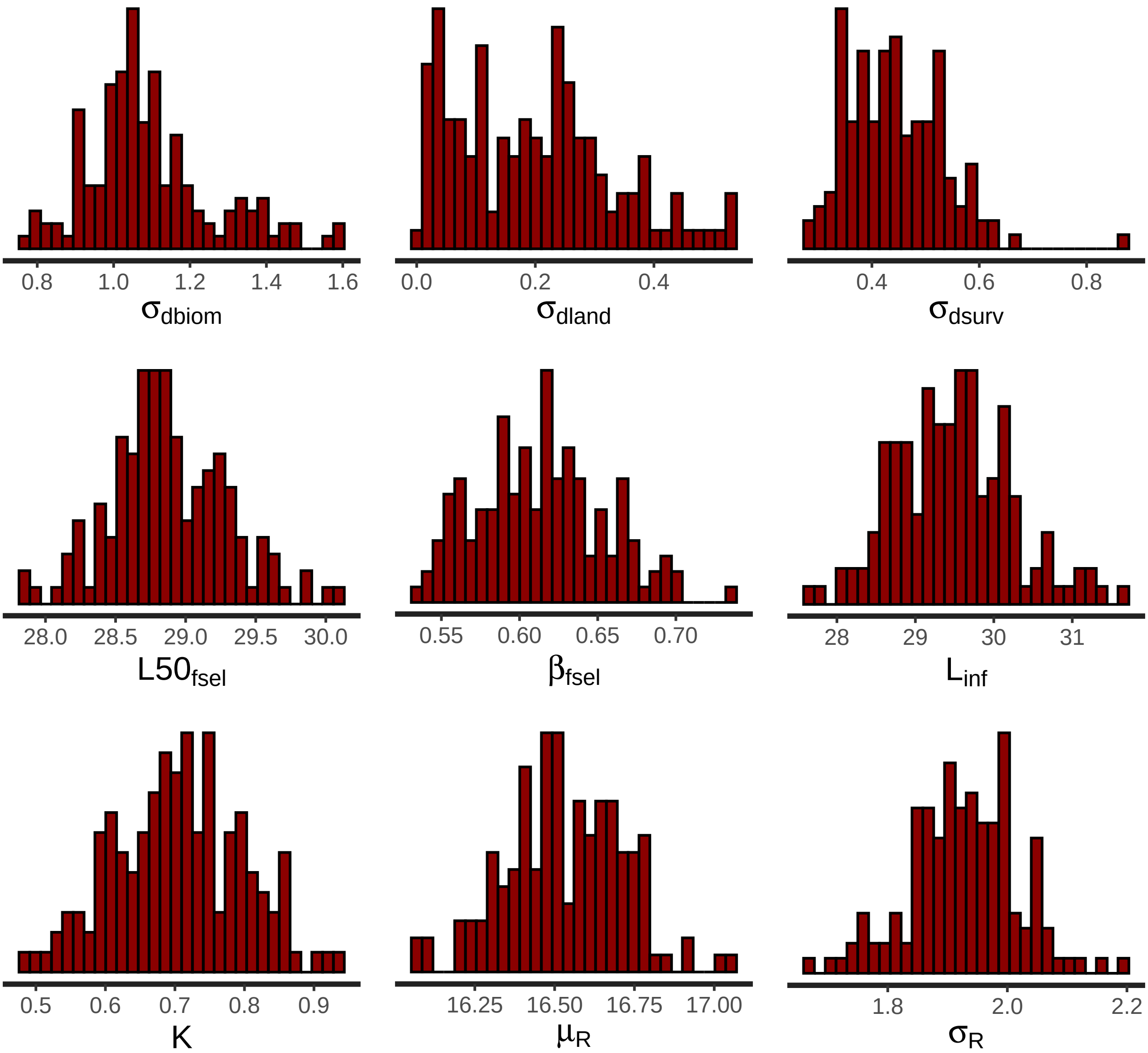


Figure A.8: Chapter IV reference model - Posteriors for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

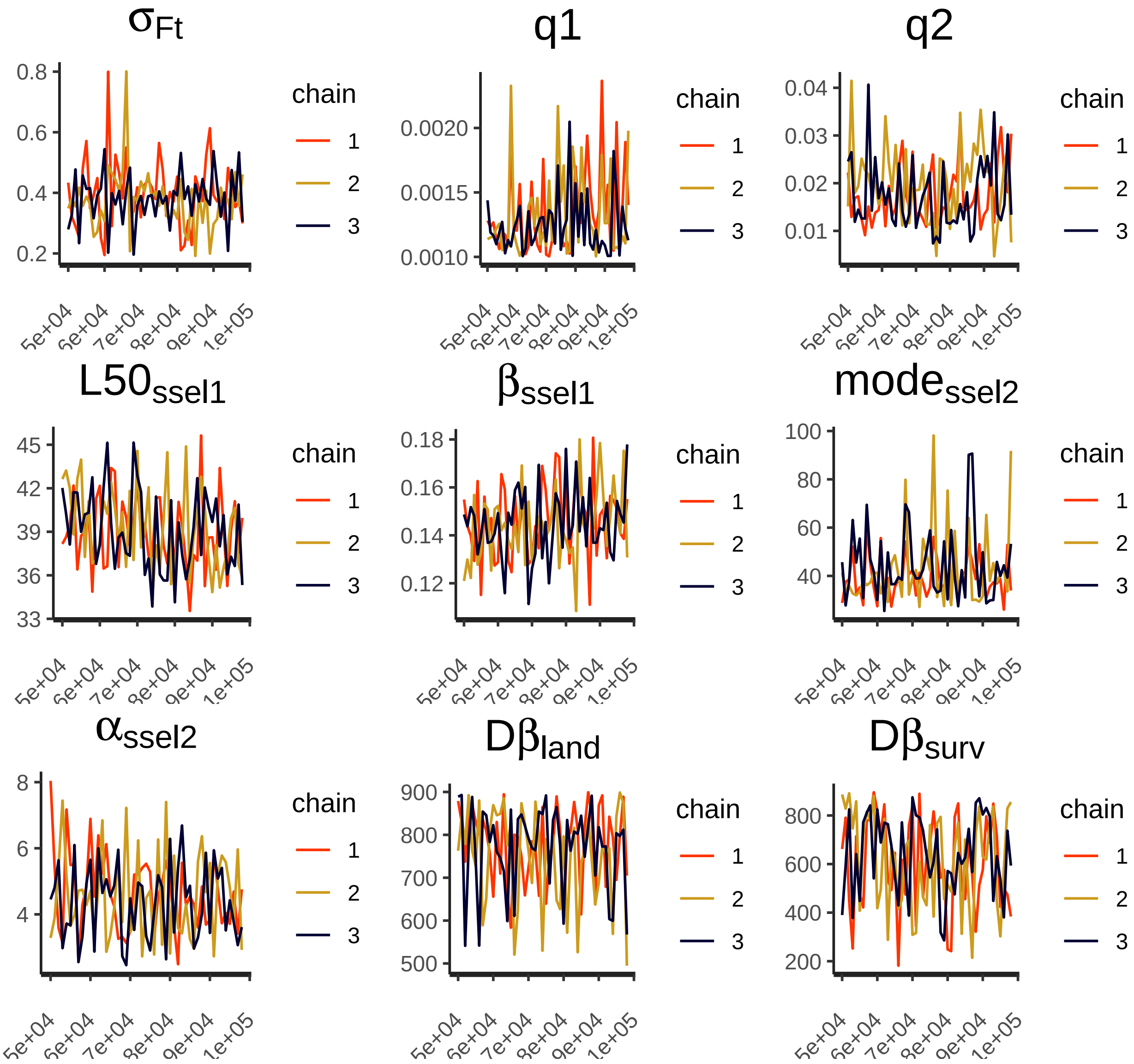


Figure A.9: Chapter IV reference model - Trace plots for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $L50_{ssel1}$, β_{ssel1}, α_{ssel2}, $mode_{ssel2}$, $D\beta1$, $D\beta$

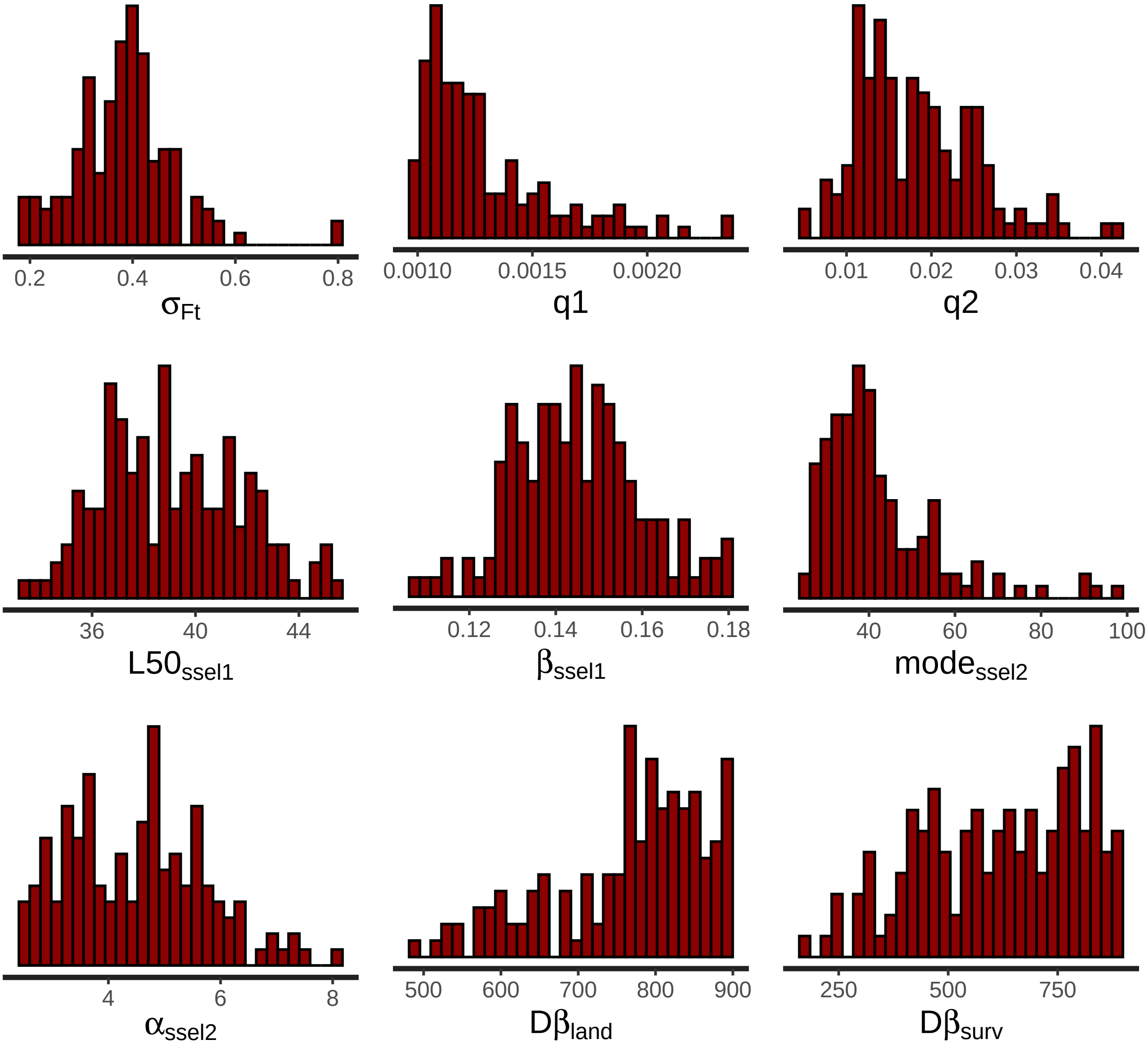


Figure A.10: Chapter IV reference model - Posteriors for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $L50_{ssel1}$, β_{ssel1}, α_{ssel2}, $mode_{ssel2}$, $D\beta1$, $D\beta2$

A.3.4 Sensitivity to parameter values I: sample size

Input sample size = 30,30

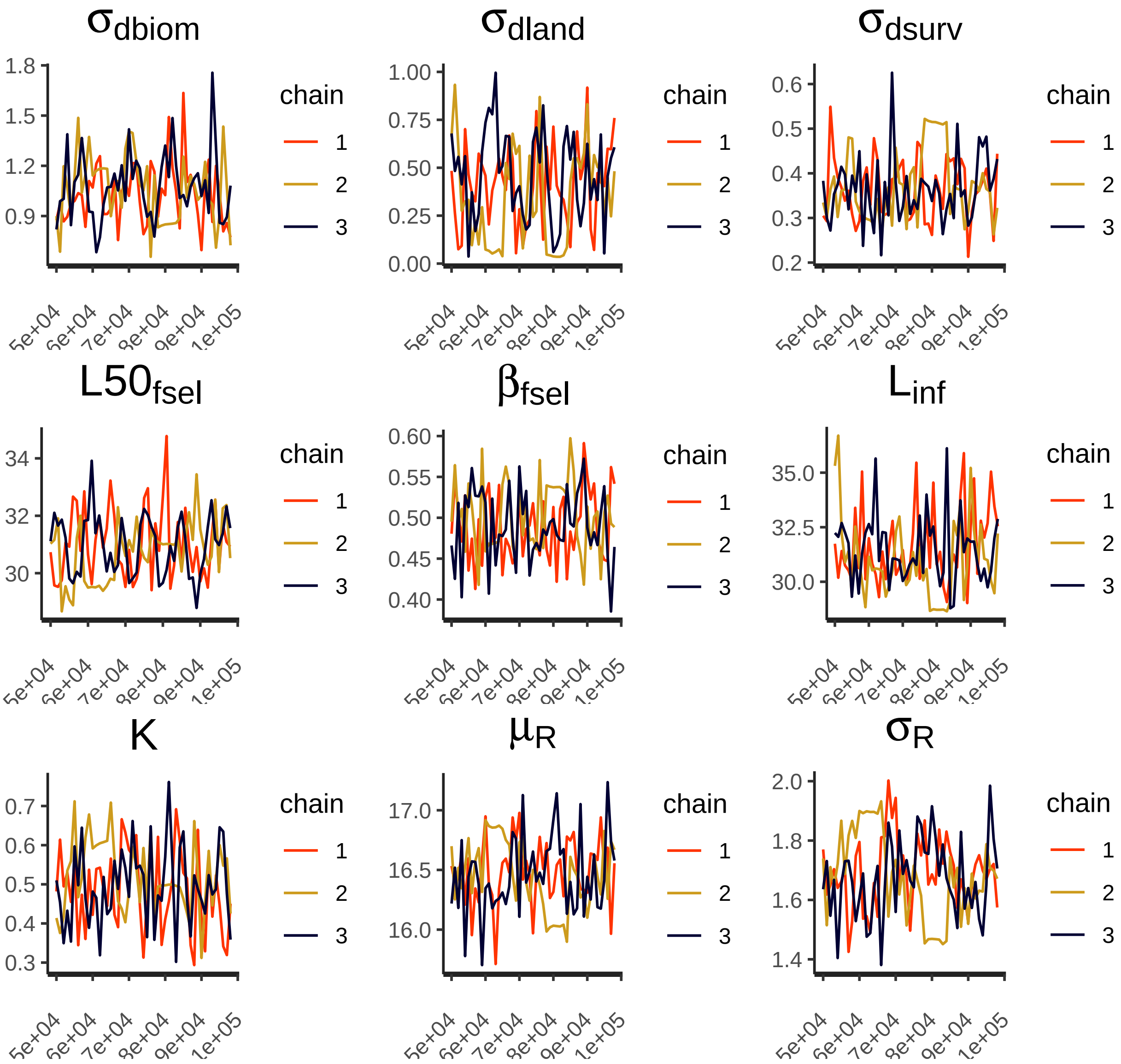


Figure A.11: Chapter IV sensitivity to sample size - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

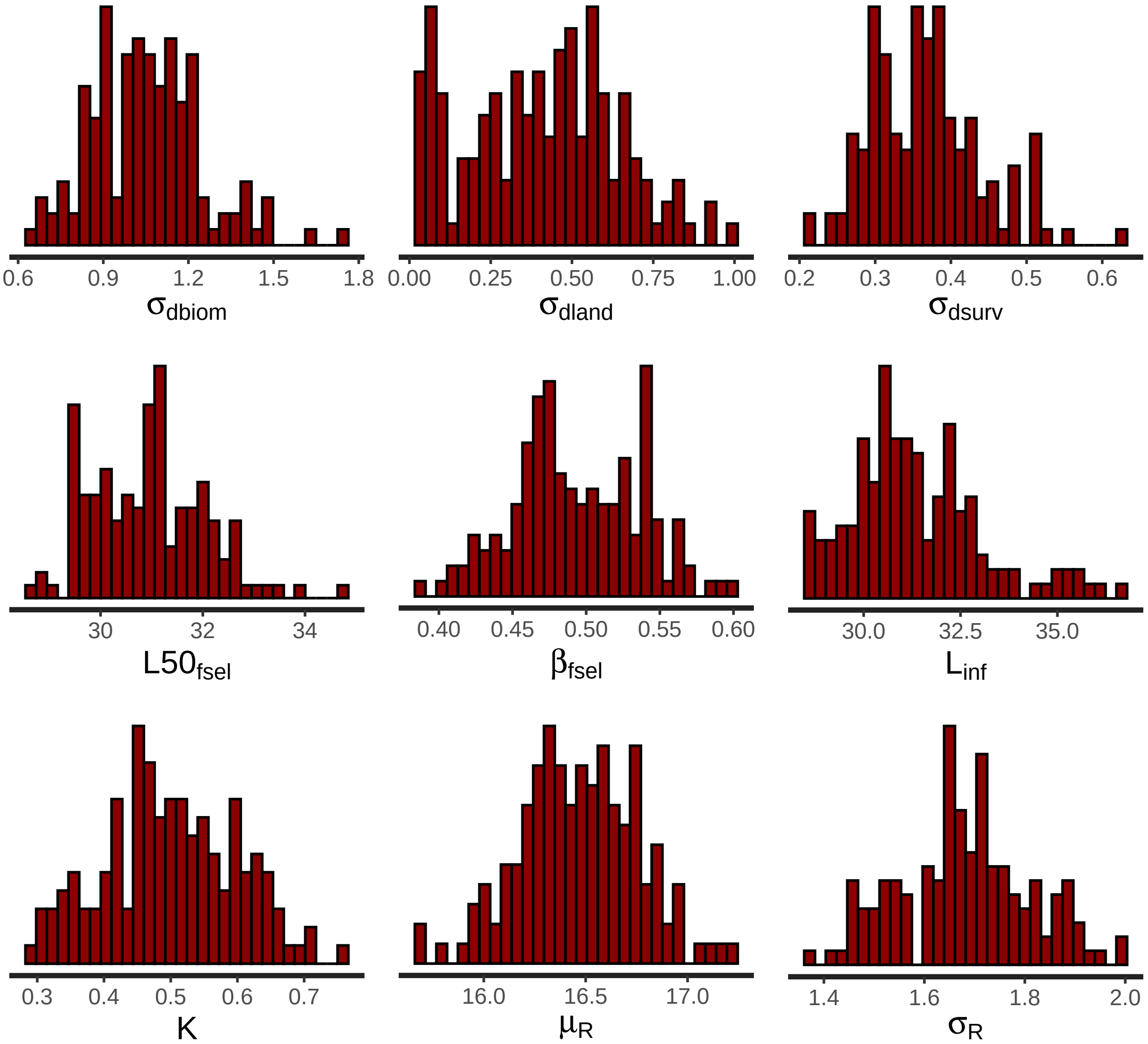


Figure A.12: Chapter IV sensitivity to sample size - Posterior distribution of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

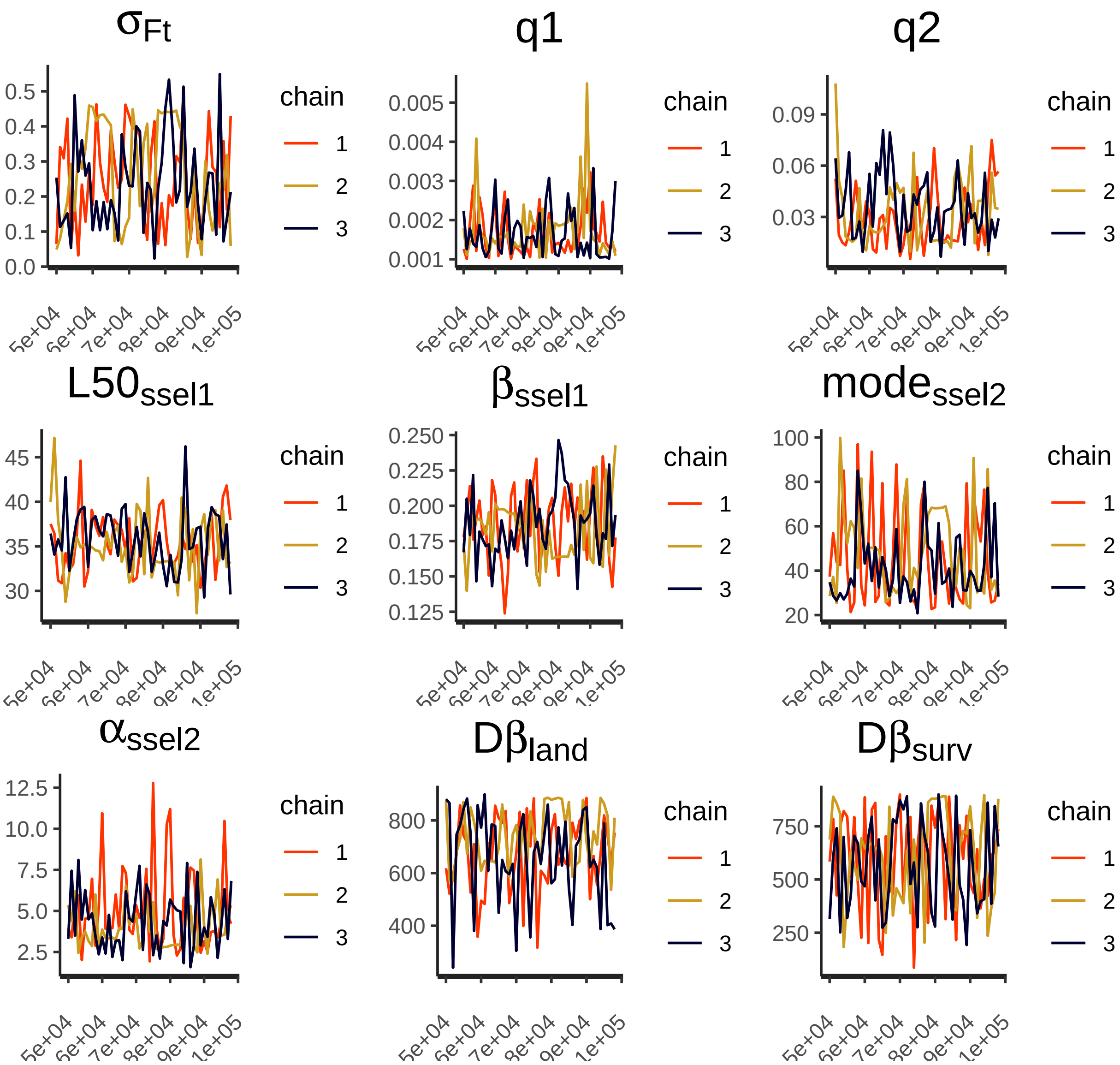


Figure A.13: Chapter IV sensitivity to sample size - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

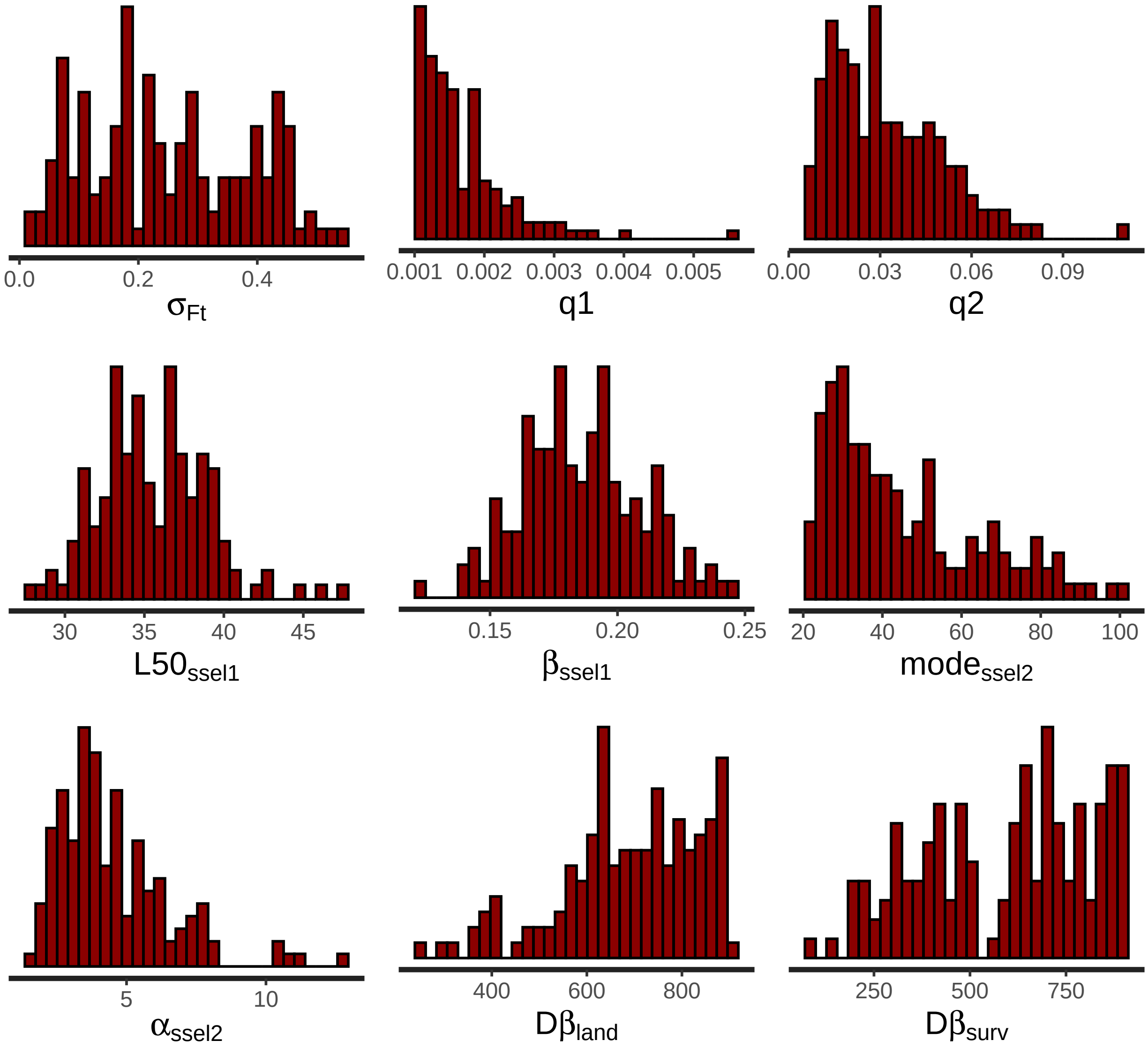


Figure A.14: Chapter IV sensitivity to sample size - Posterior distribution of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

A.3.5 Sensitivity to parameter values II: discard $L50_{dsel}$

Discard $L50_{dsel}$ $=$ **26**

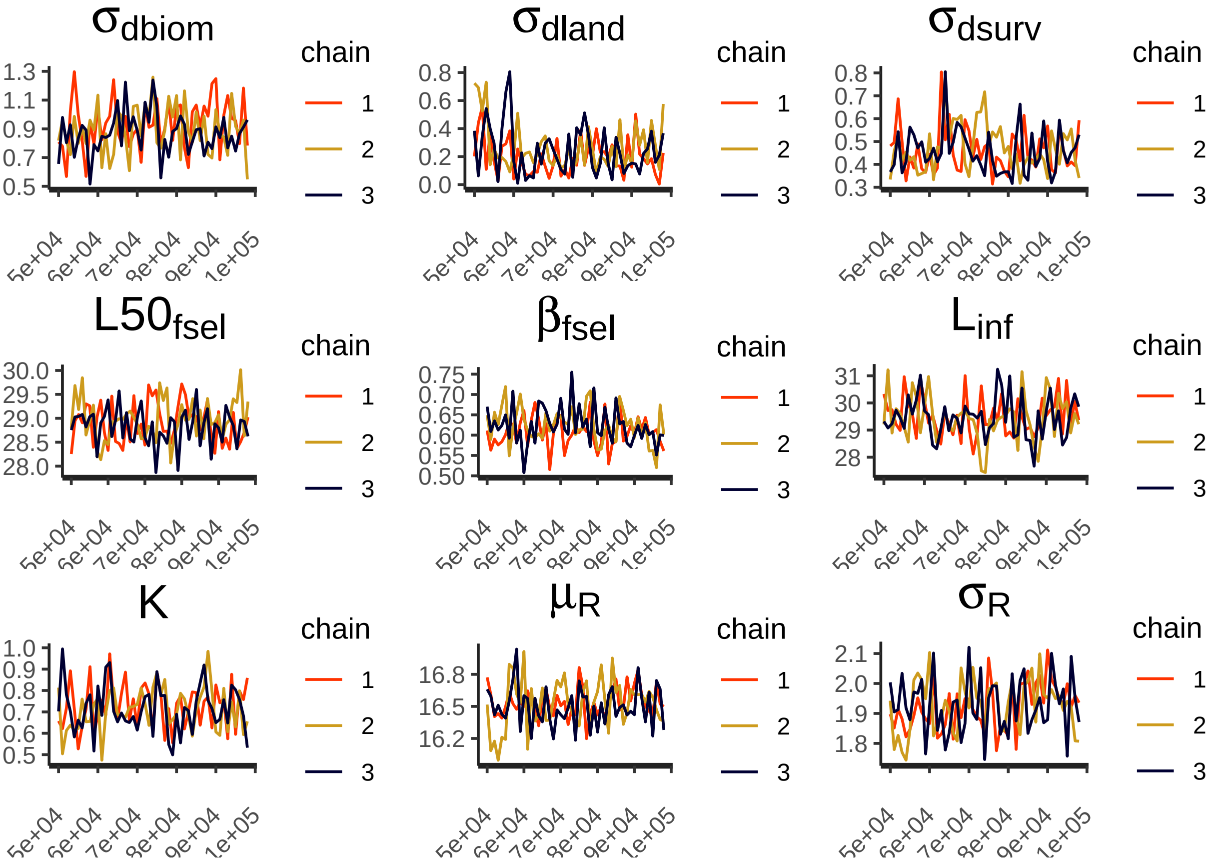


Figure A.15: Chapter IV sensitivity to L50 of discard selectivity (26) - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

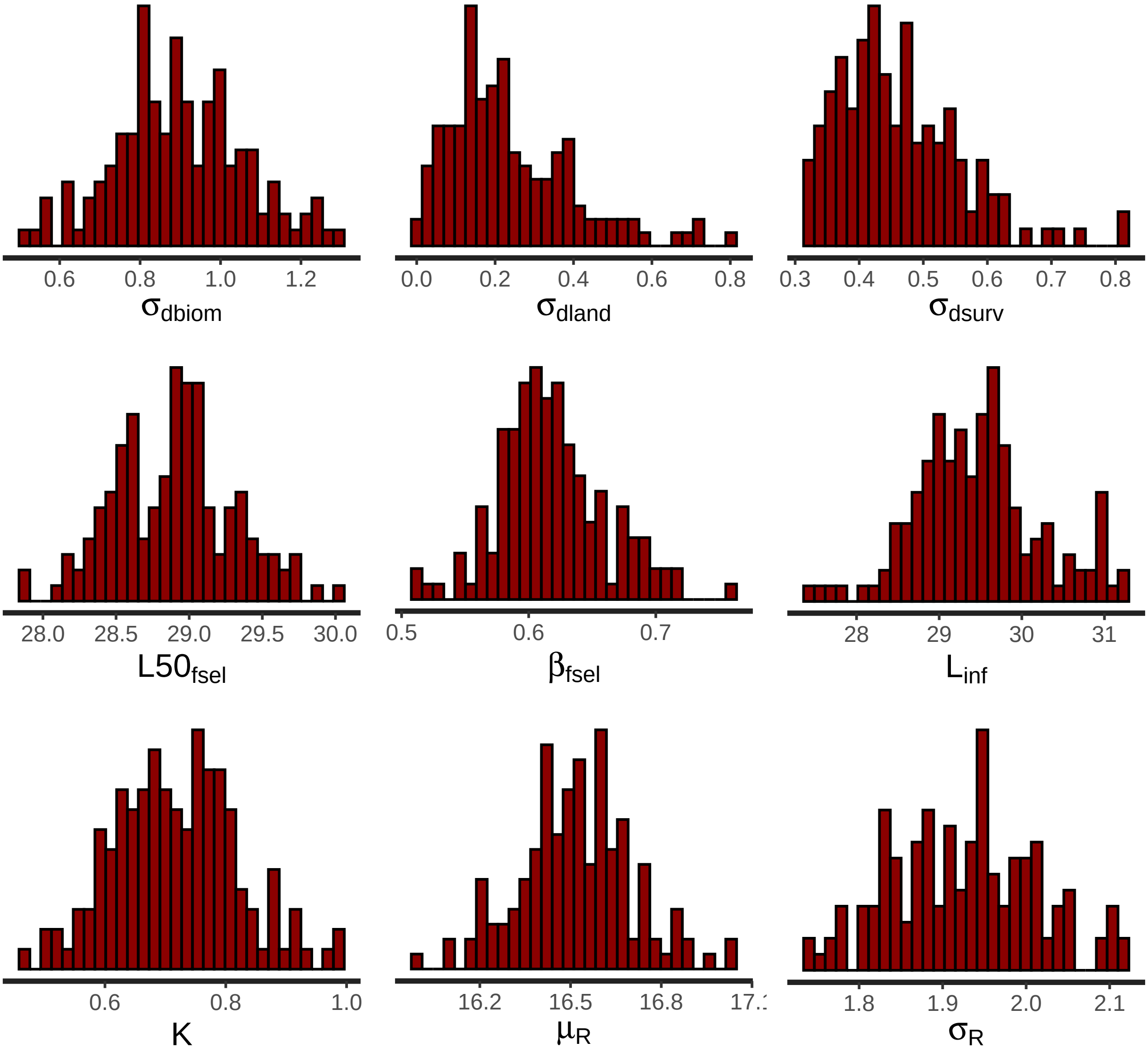


Figure A.16: Chapter IV sensitivity to L50 of discard selectivity (26) - Posterior distribution of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

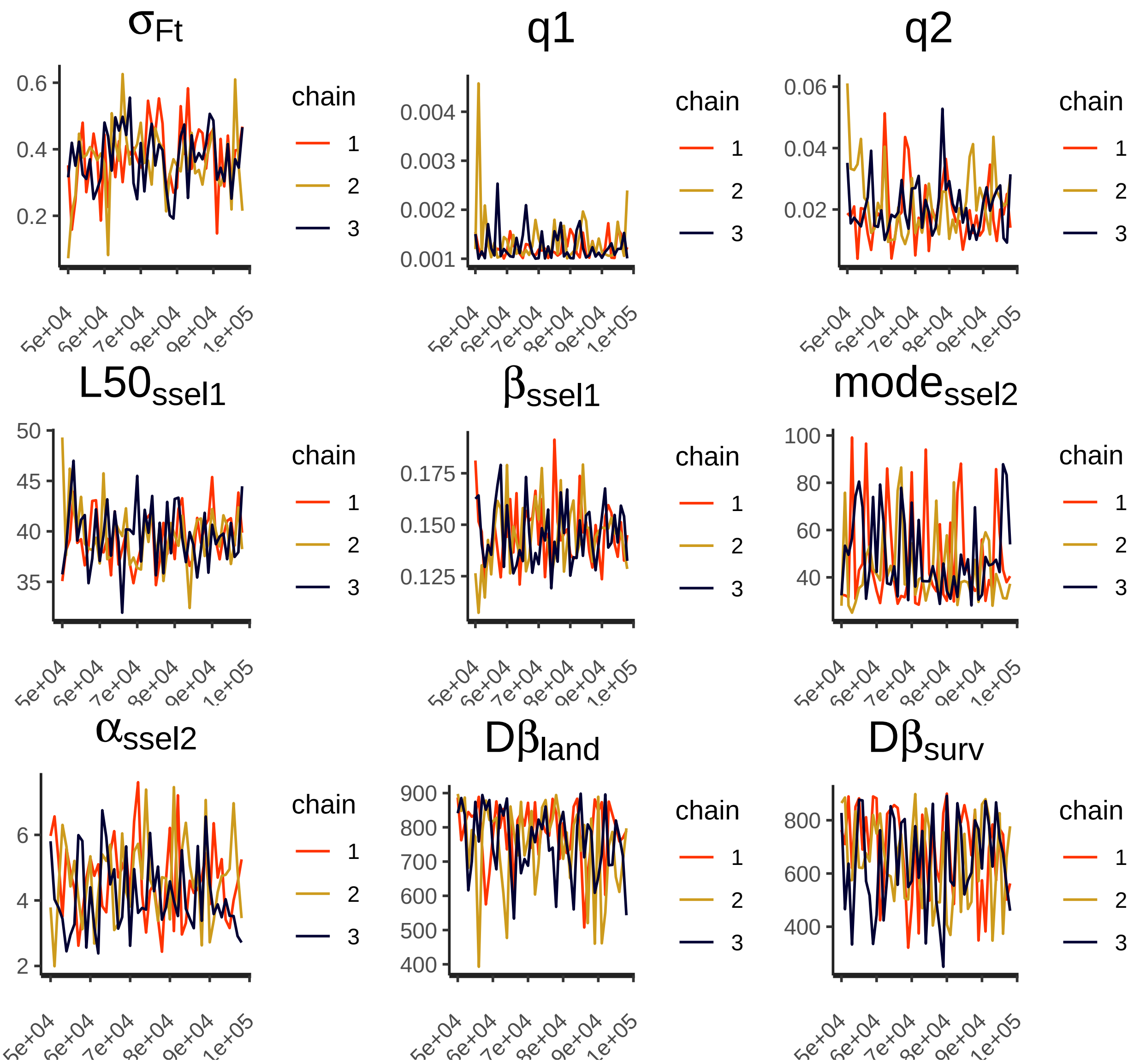


Figure A.17: Chapter IV sensitivity to L50 of discard selectivity (26) - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

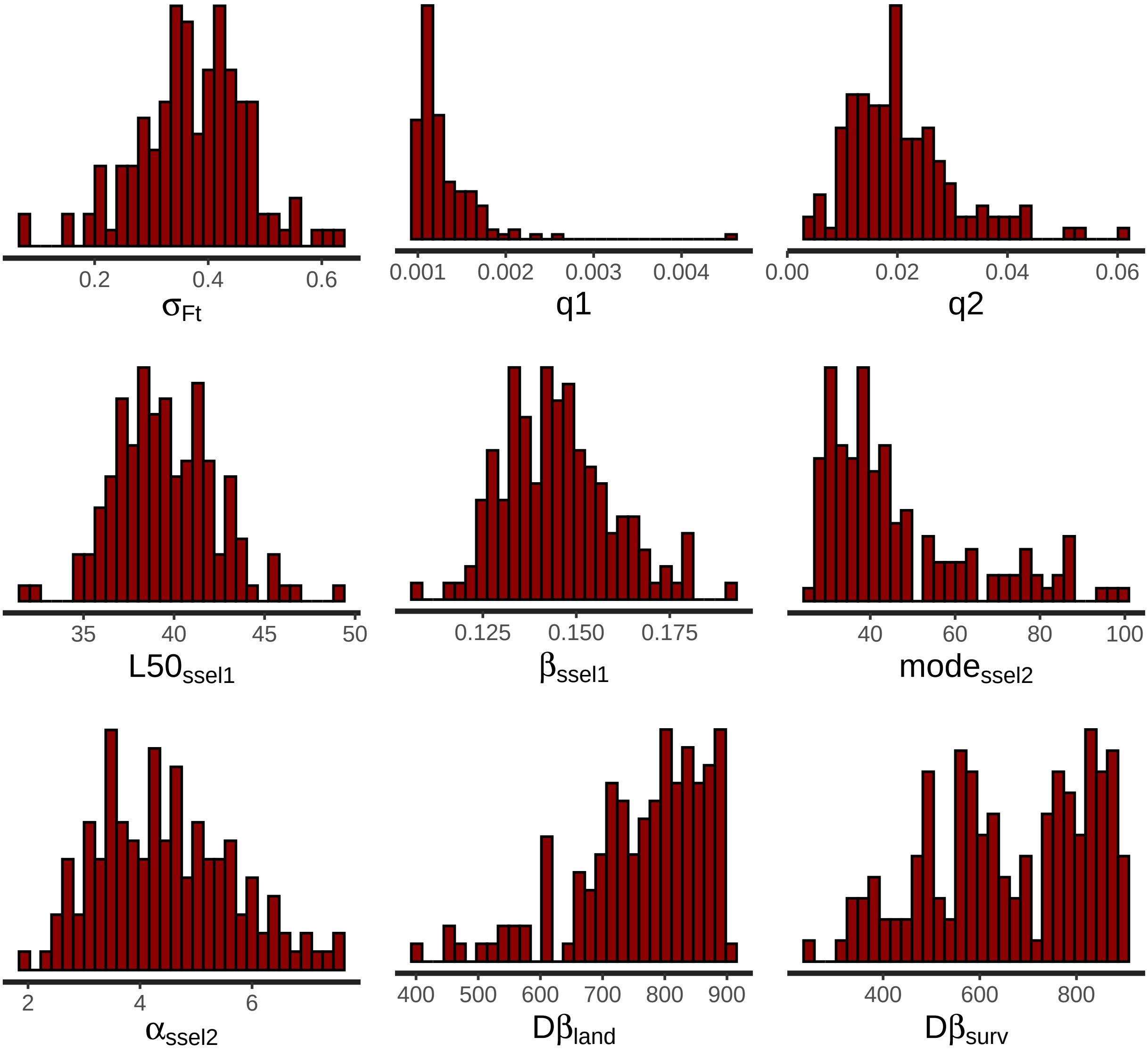


Figure A.18: Chapter IV sensitivity to L50 of discard selectivity (26) - Posterior distribution of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

Discard $L50_{dsel}$ **= 38**

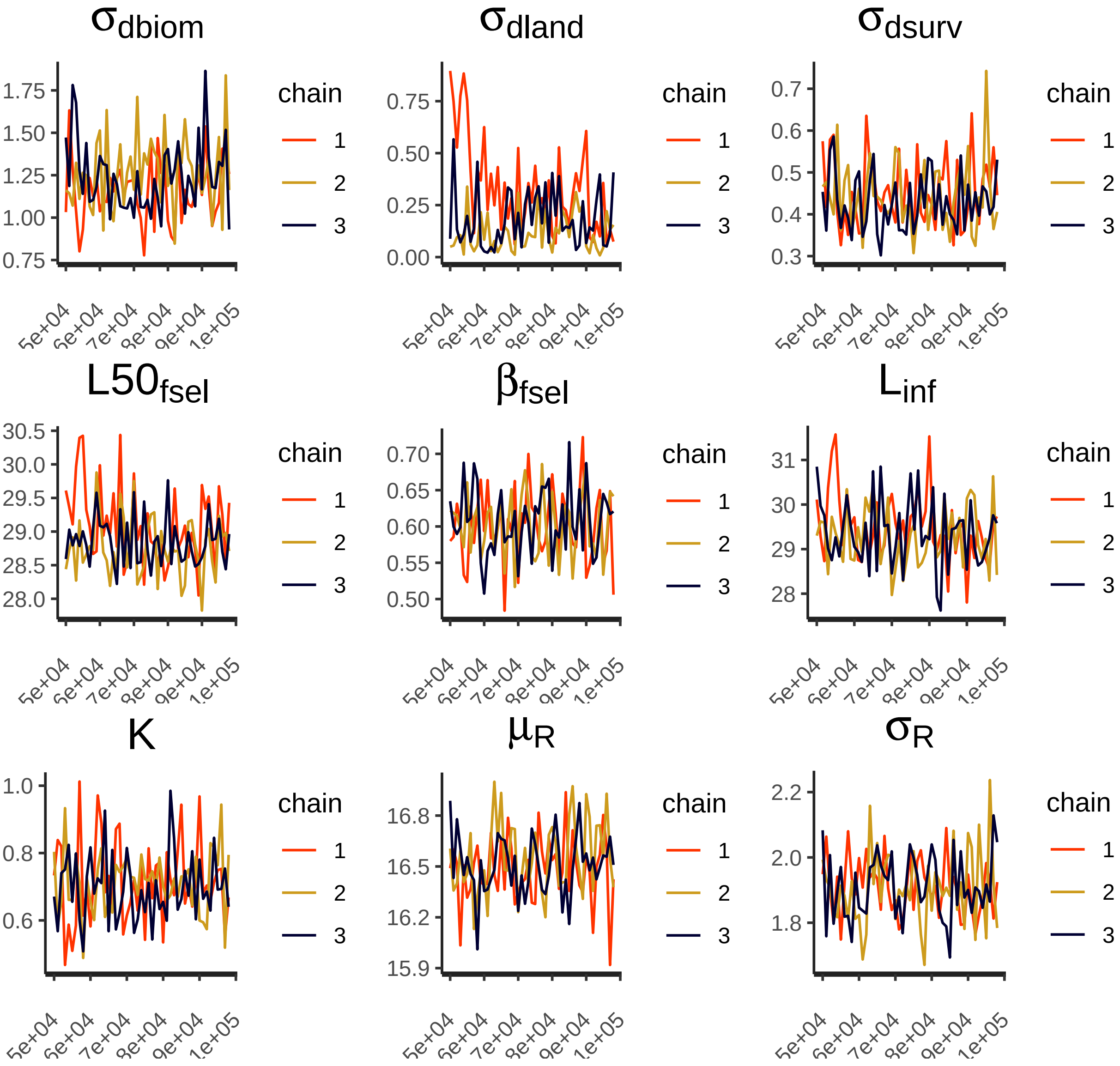


Figure A.19: Chapter IV sensitivity to L50 of discard selectivity (38) - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

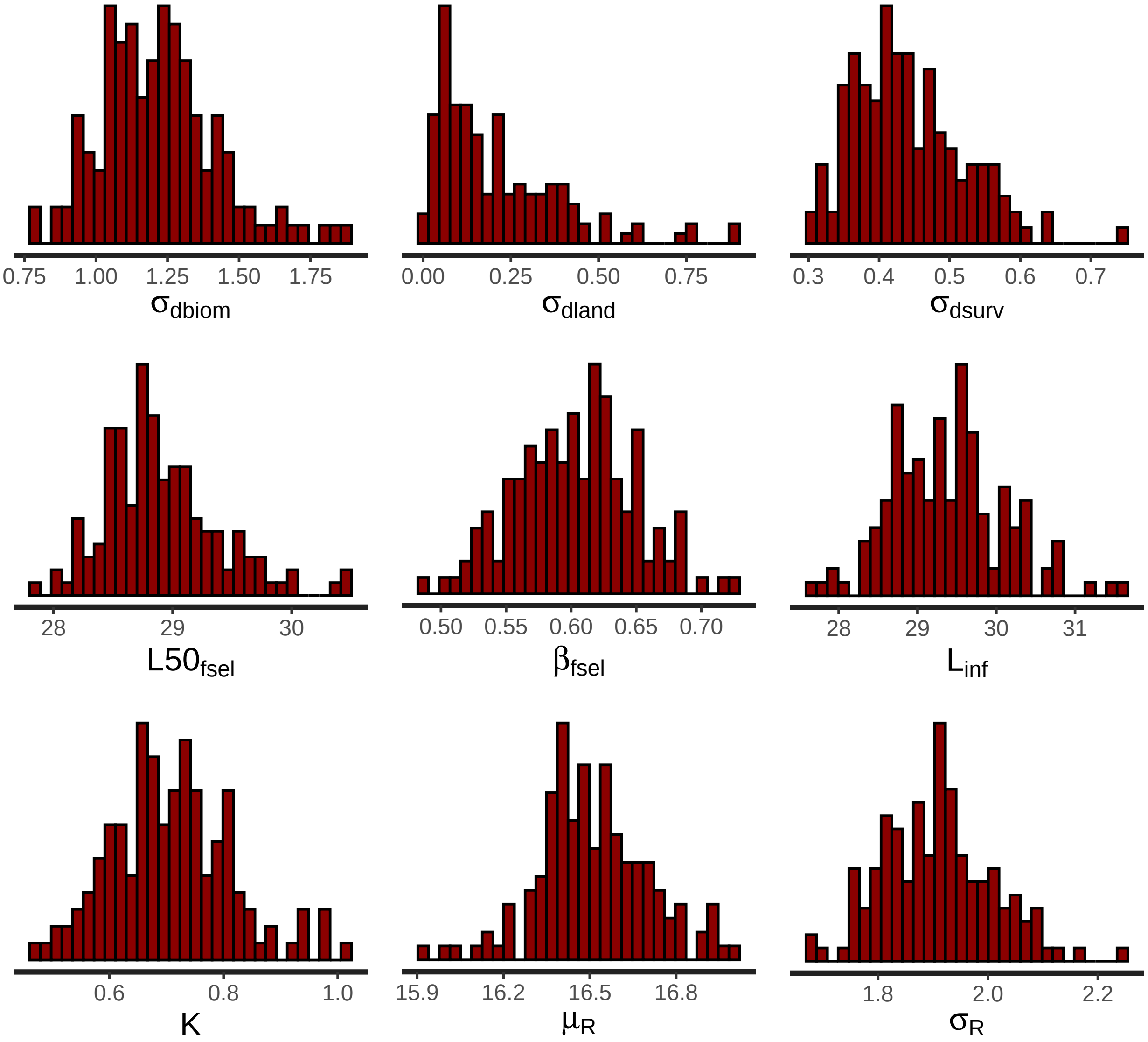


Figure A.20: Chapter IV sensitivity to L50 of discard selectivity (38) - Posterior distribution of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

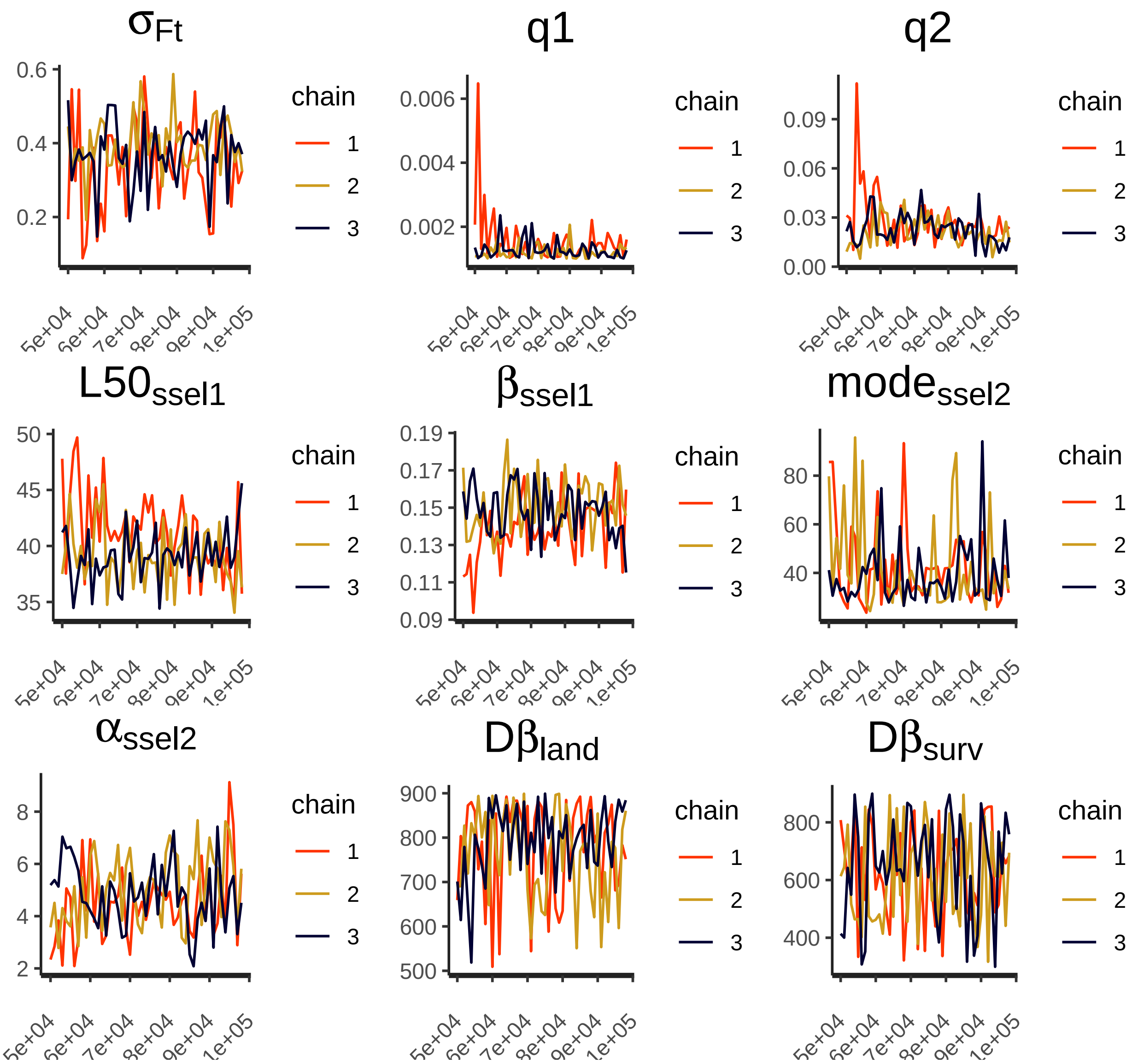


Figure A.21: Chapter IV sensitivity to L50 of discard selectivity (38) - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

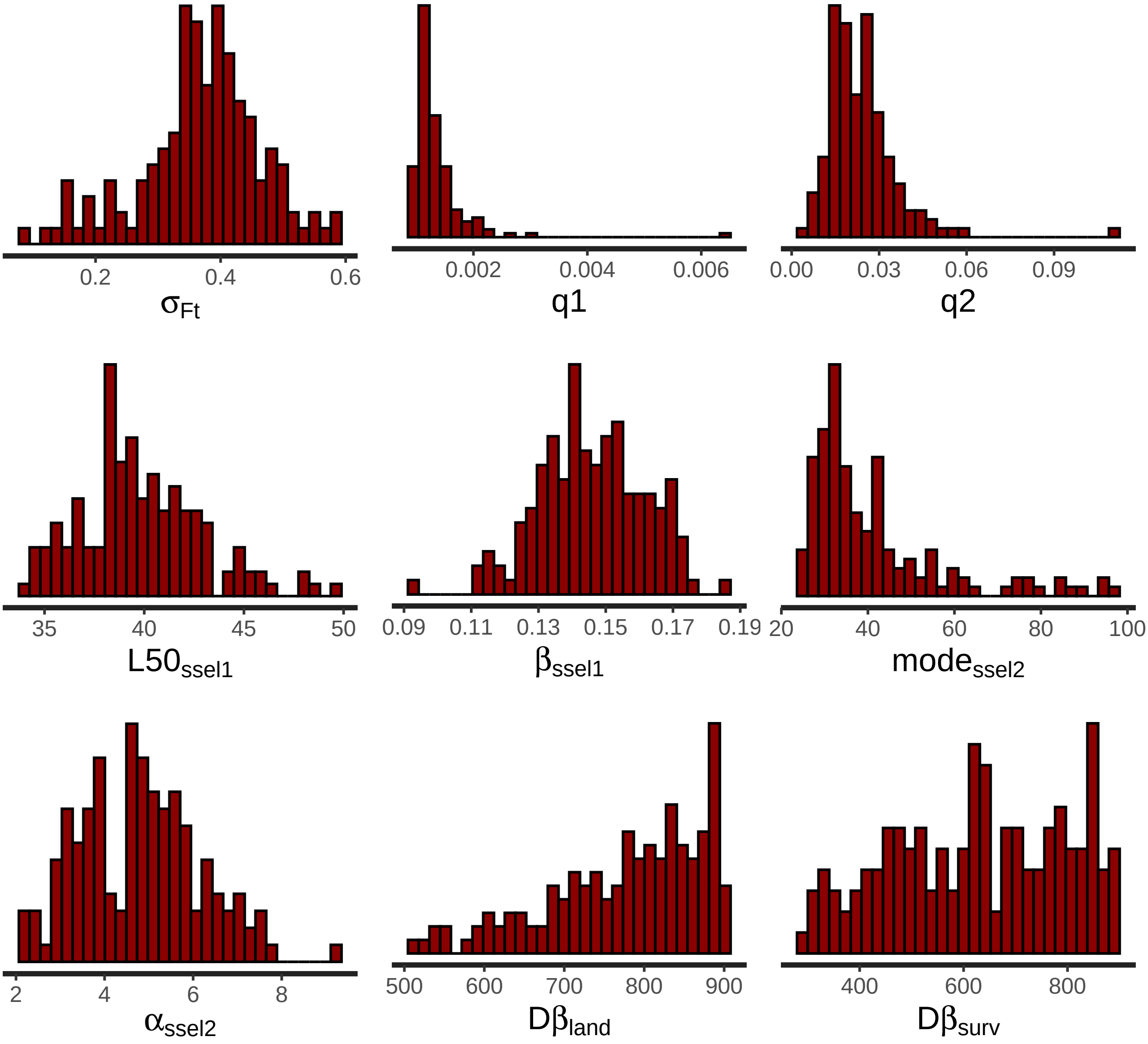


Figure A.22: Chapter IV sensitivity to L50 of discard selectivity (38) - Posterior distribution of some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

A.3.6 Sensitivity to model structure: the shape of the survey selectivity

Logistic + logistic

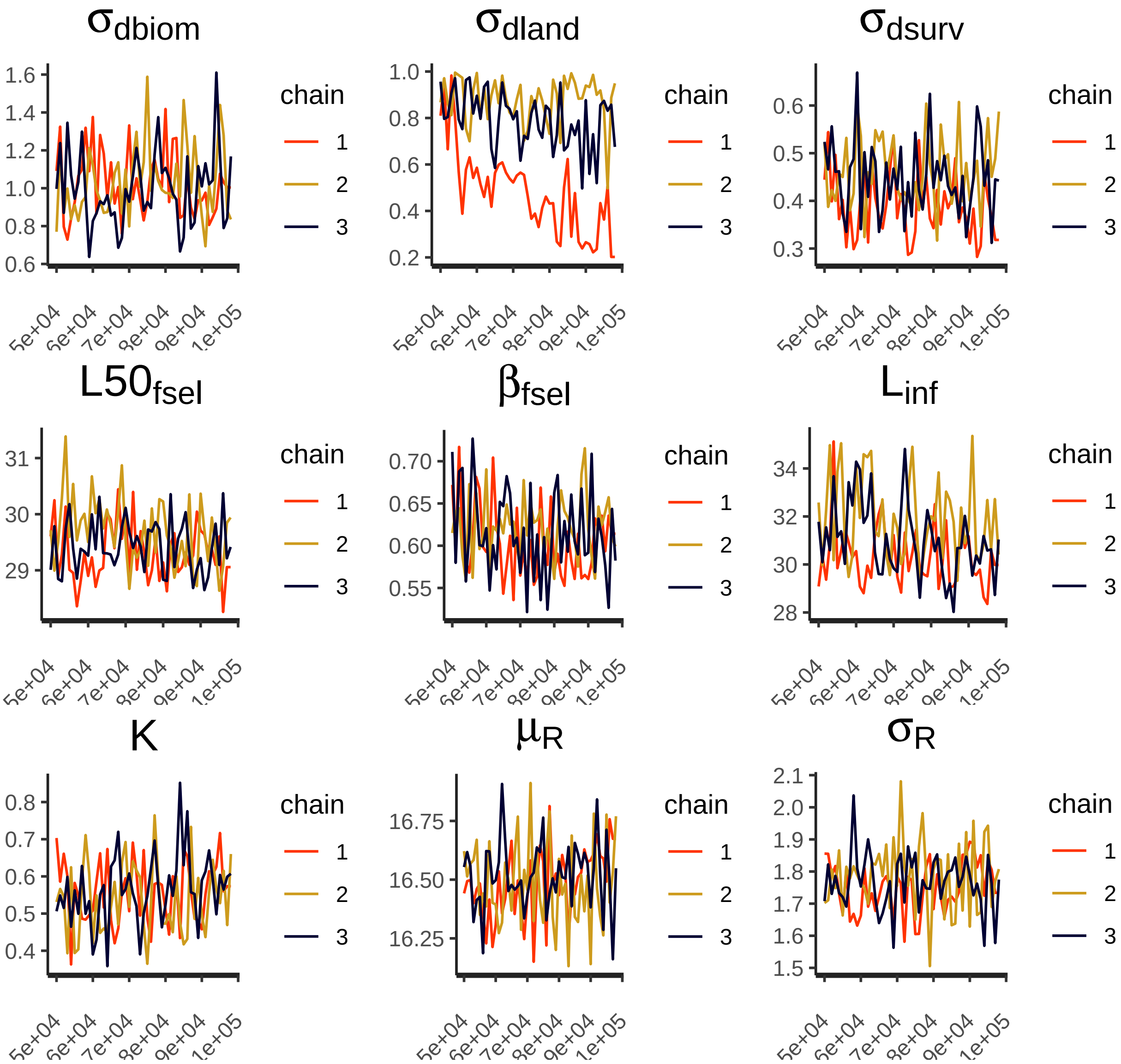


Figure A.23: Chapter IV sensitivity to survey selectivity logistic and logistic - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

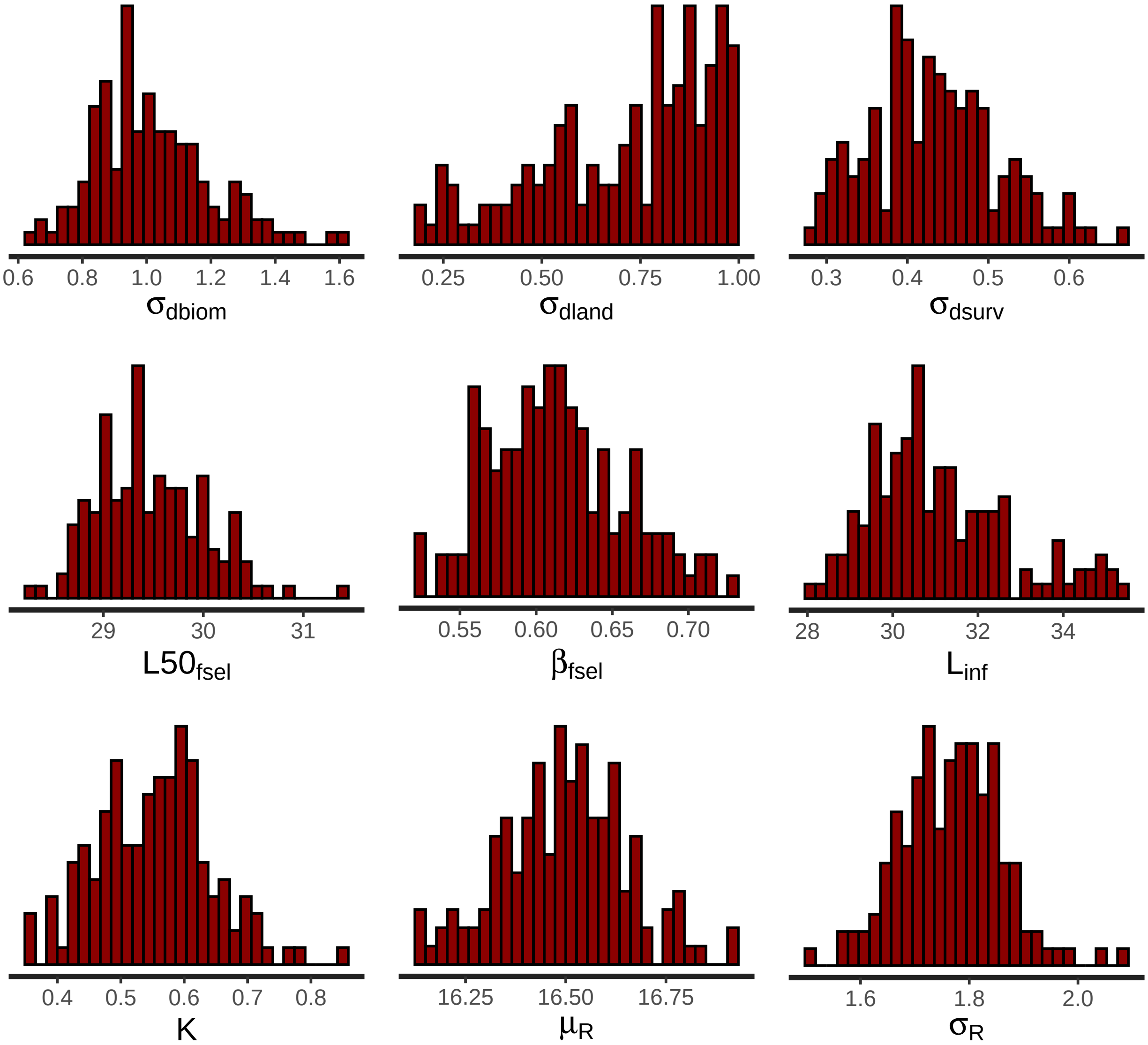


Figure A.24: Chapter IV sensitivity to survey selectivity logistic and logistic - Posterior distribution of some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

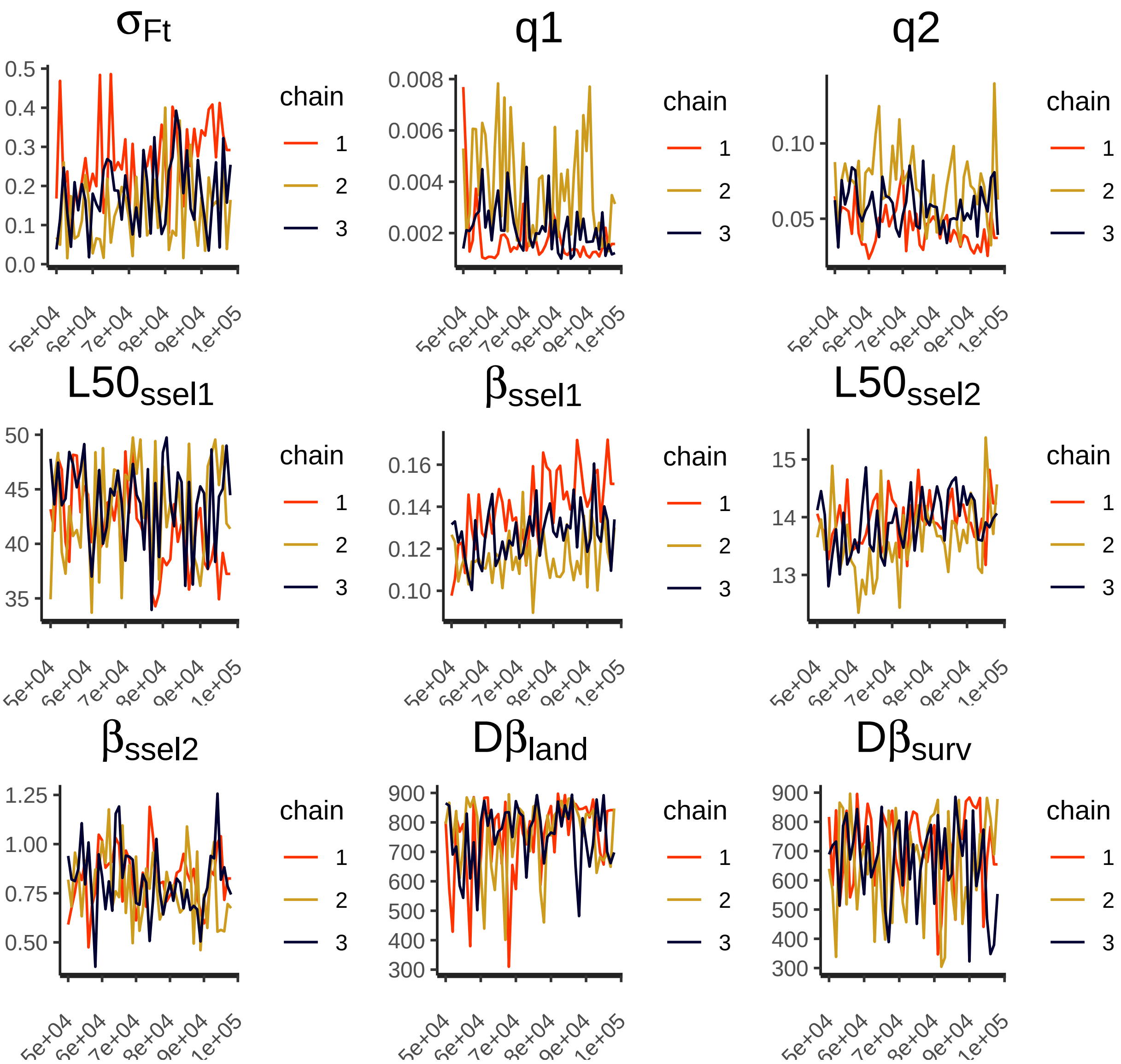


Figure A.25: Chapter IV sensitivity to survey selectivity logistic and logistic - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $L50_{ssel1}$, β_{ssel1}, $L50_{ssel2}$, β_{ssel2}, $D\beta1$, $D\beta$

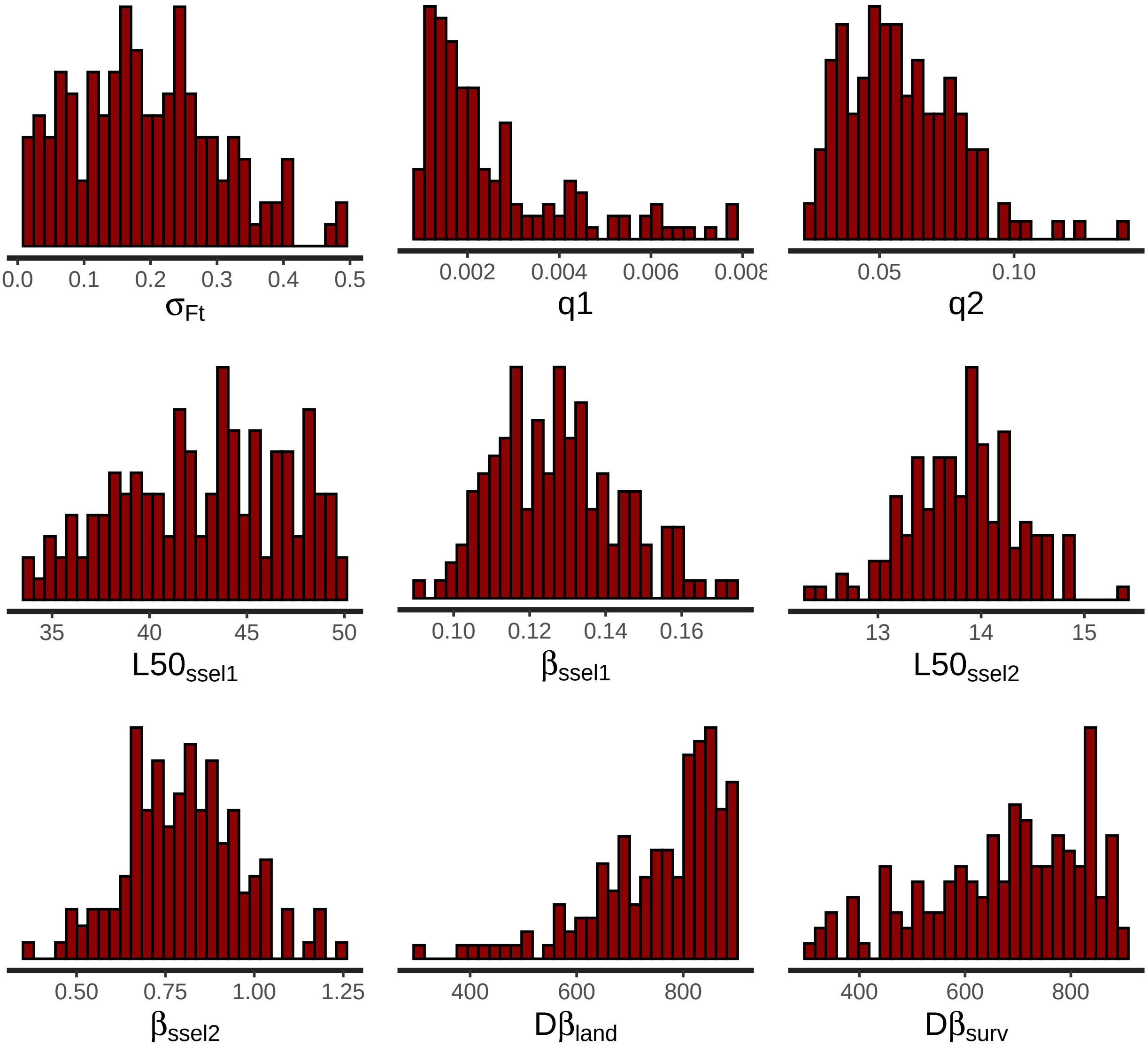


Figure A.26: Chapter IV sensitivity to survey selectivity logistic and logistic - Posterior distributions for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $L50_{ssel1}$, β_{ssel1}, $L50_{ssel2}$, β_{ssel2}, $D\beta 1$, $D\beta$

Gamma + gamma

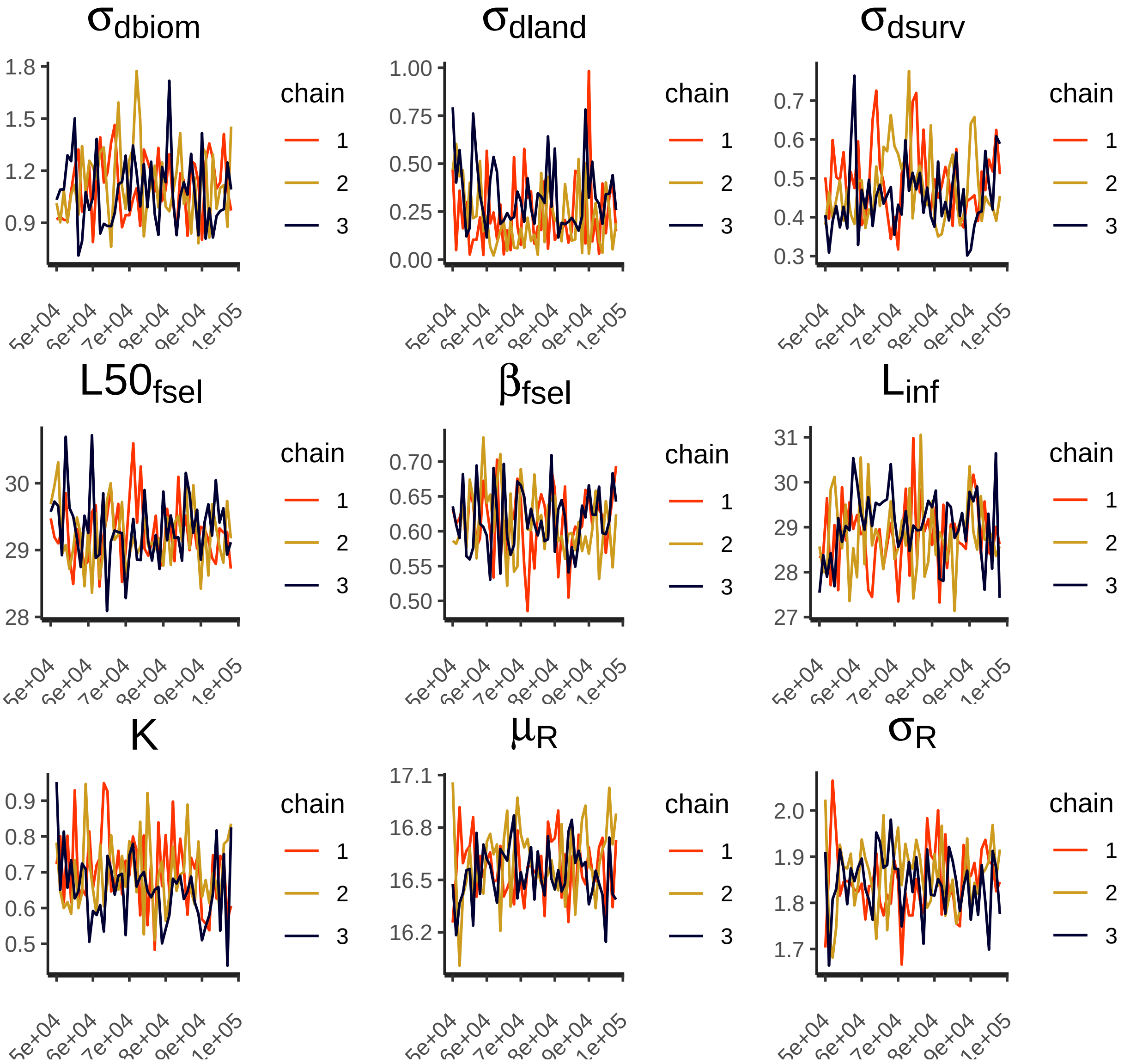


Figure A.27: Chapter IV sensitivity to survey selectivity gamma and gamma - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

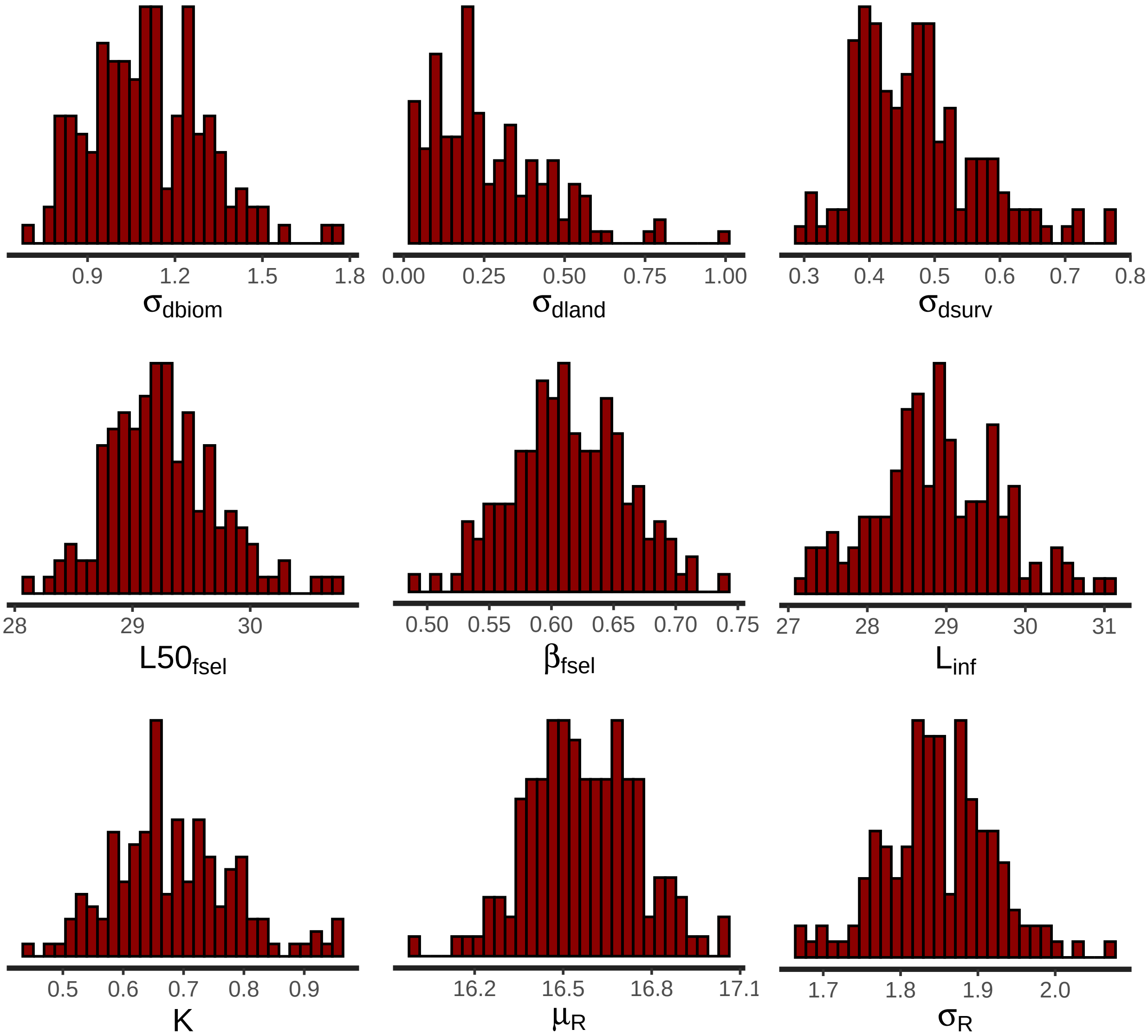


Figure A.28: Chapter IV sensitivity to survey selectivity gamma and gamma - Posterior distributions for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

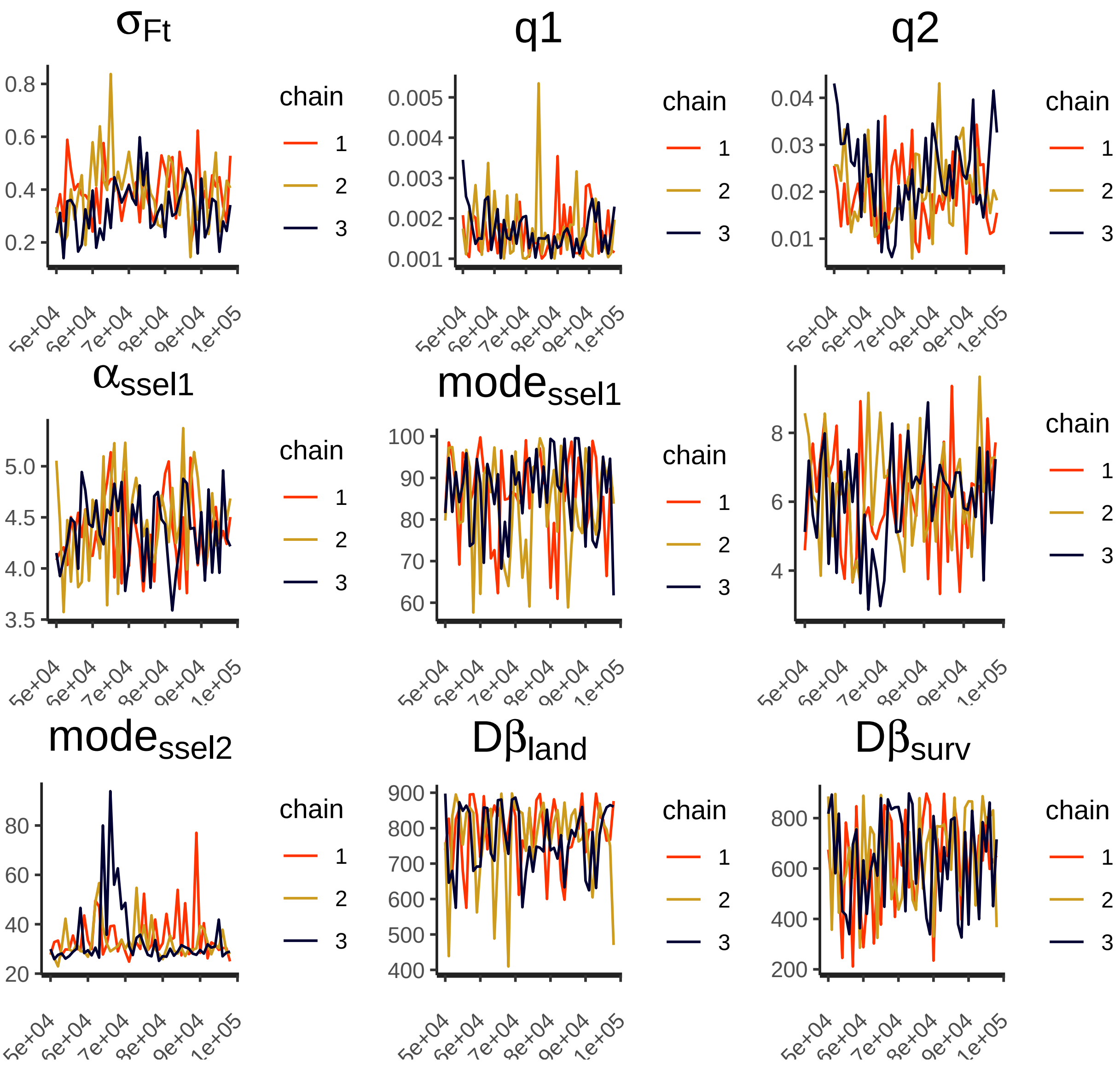


Figure A.29: Chapter IV sensitivity to survey selectivity gamma and gamma - Trace plots of some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

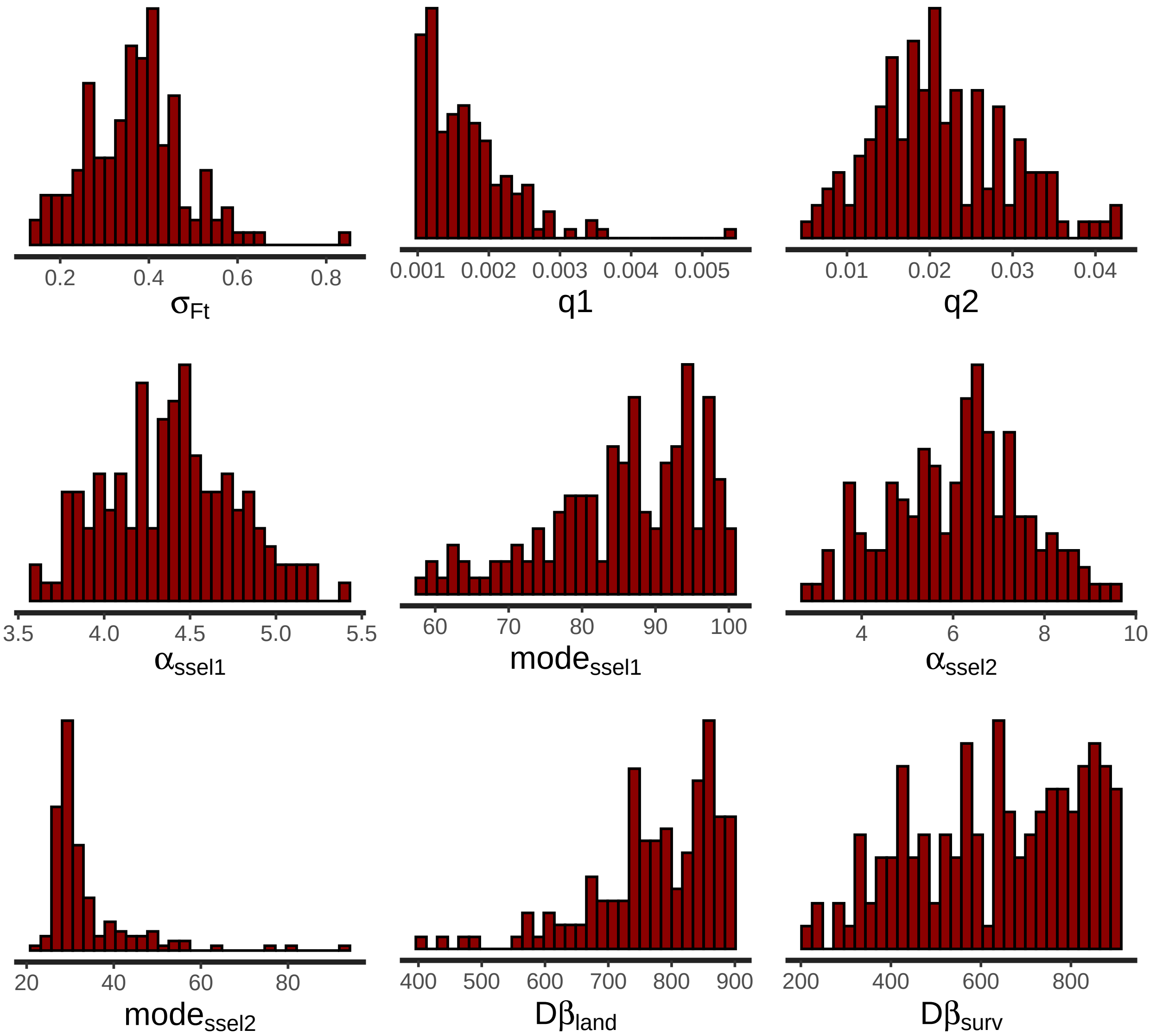


Figure A.30: Chapter IV sensitivity to survey selectivity gamma and gamma - Posterior distributions for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

A.3.7 Sensitivity to model structure: the shape of the fishing selectivity

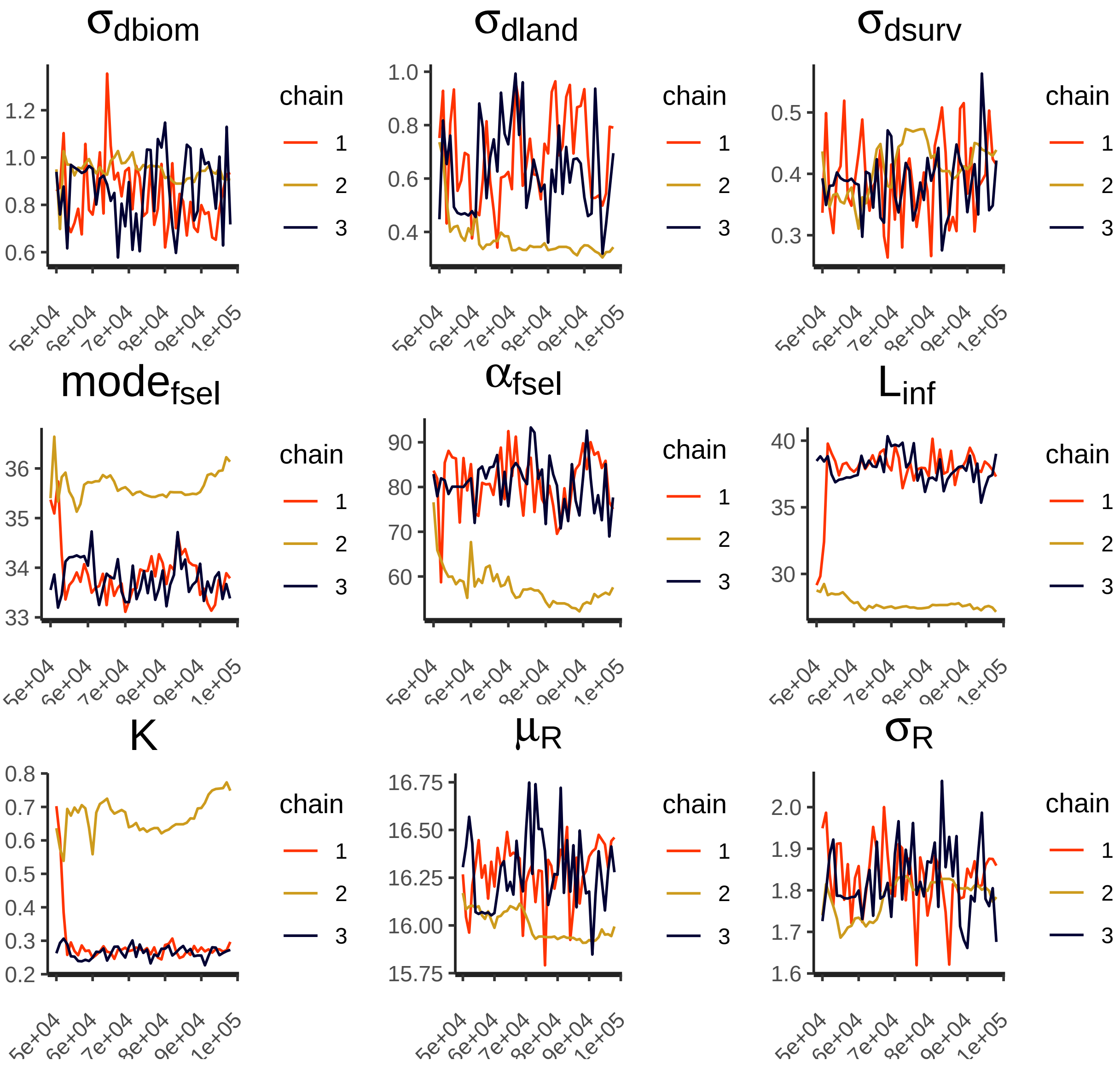


Figure A.31: Chapter IV sensitivity to fishing selectivity - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

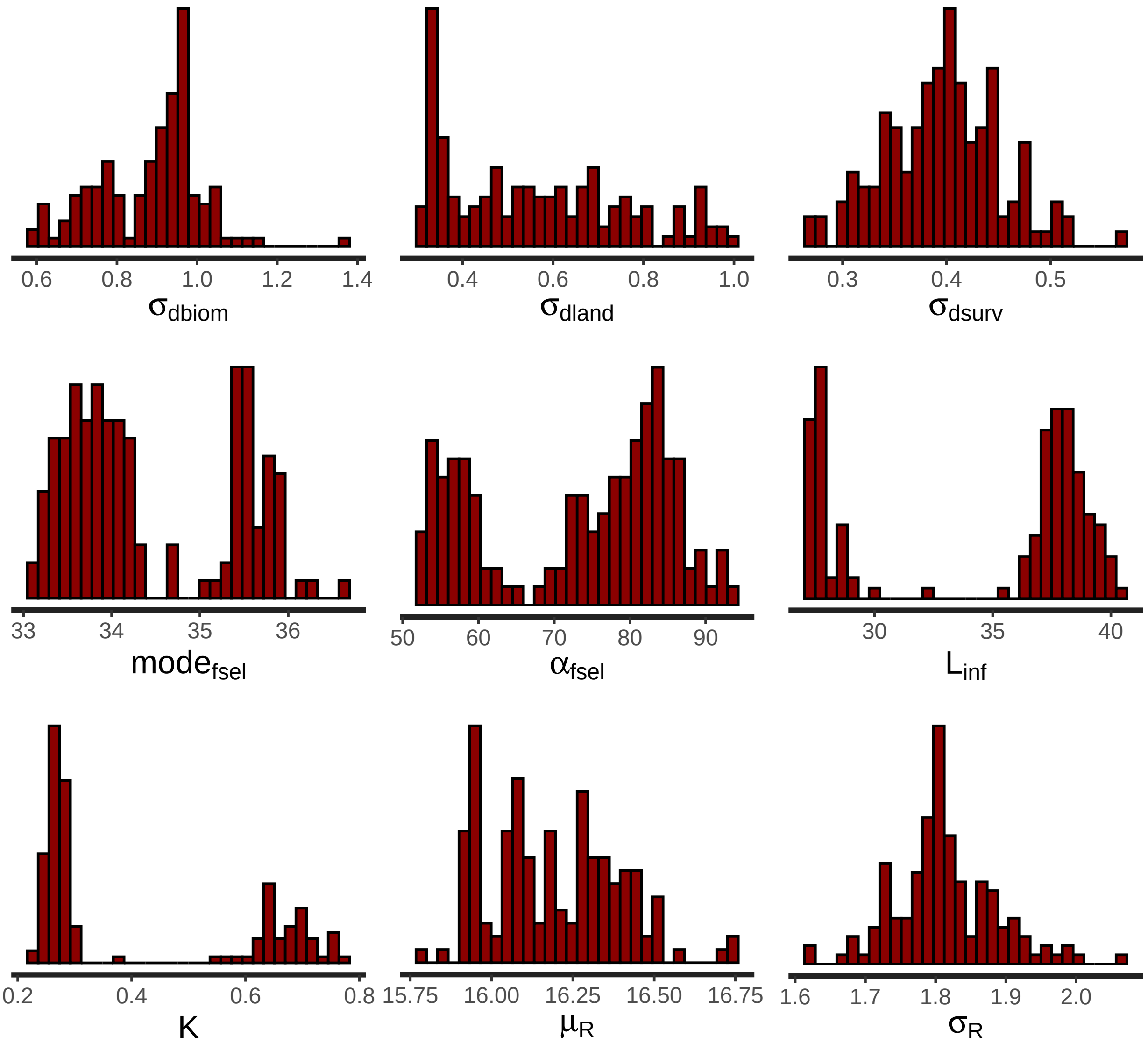


Figure A.32: Chapter IV sensitivity to fishing selectivity - Posterir distributions of some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_∞, K, μ_R, σ_R

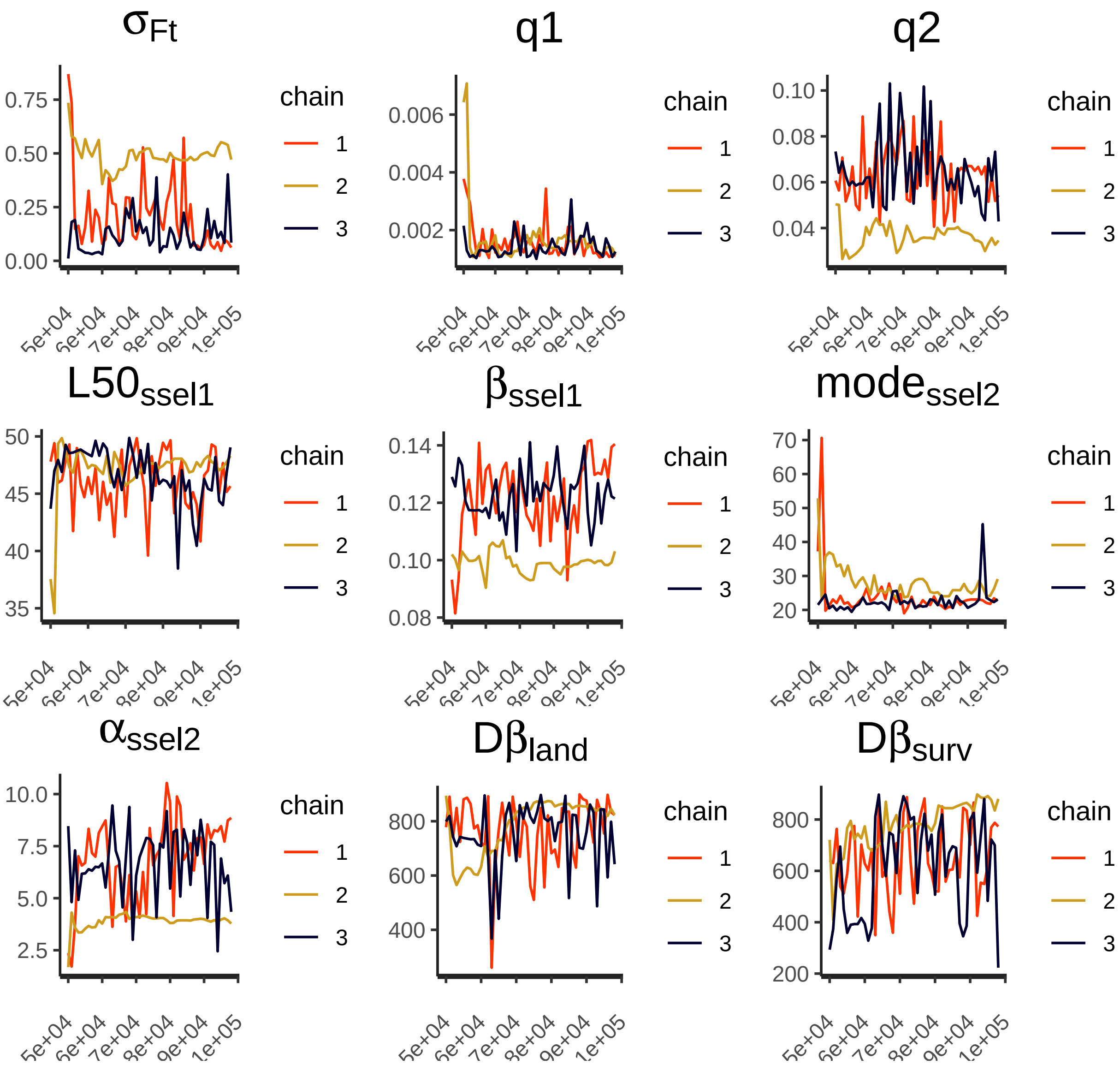


Figure A.33: Chapter IV sensitivity to fishing selectivity - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

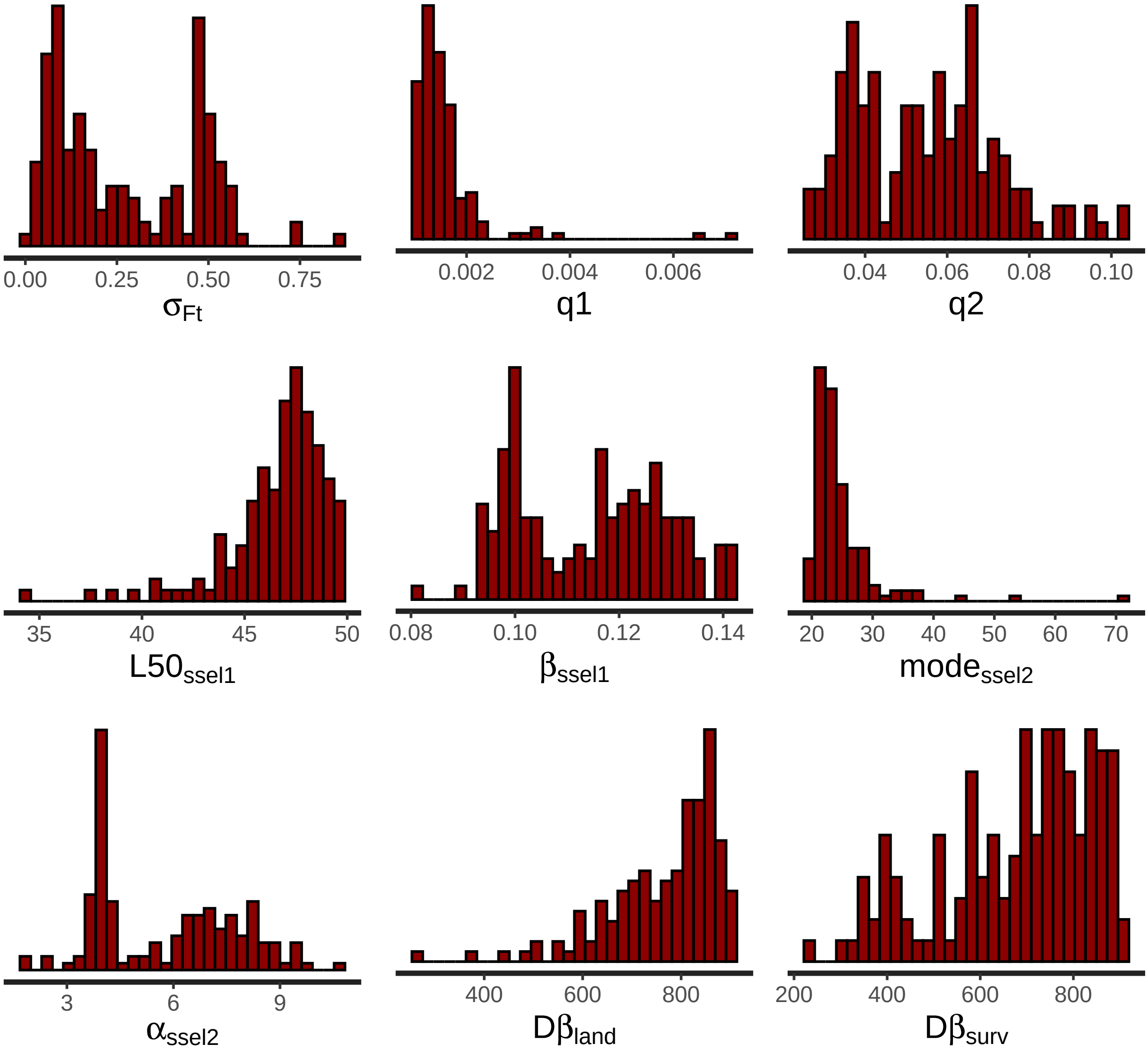


Figure A.34: Chapter IV sensitivity to fishing selectivity - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta 1$, $D\beta$

A.3.8 Sensitivity to parameter bounds: Recruitment

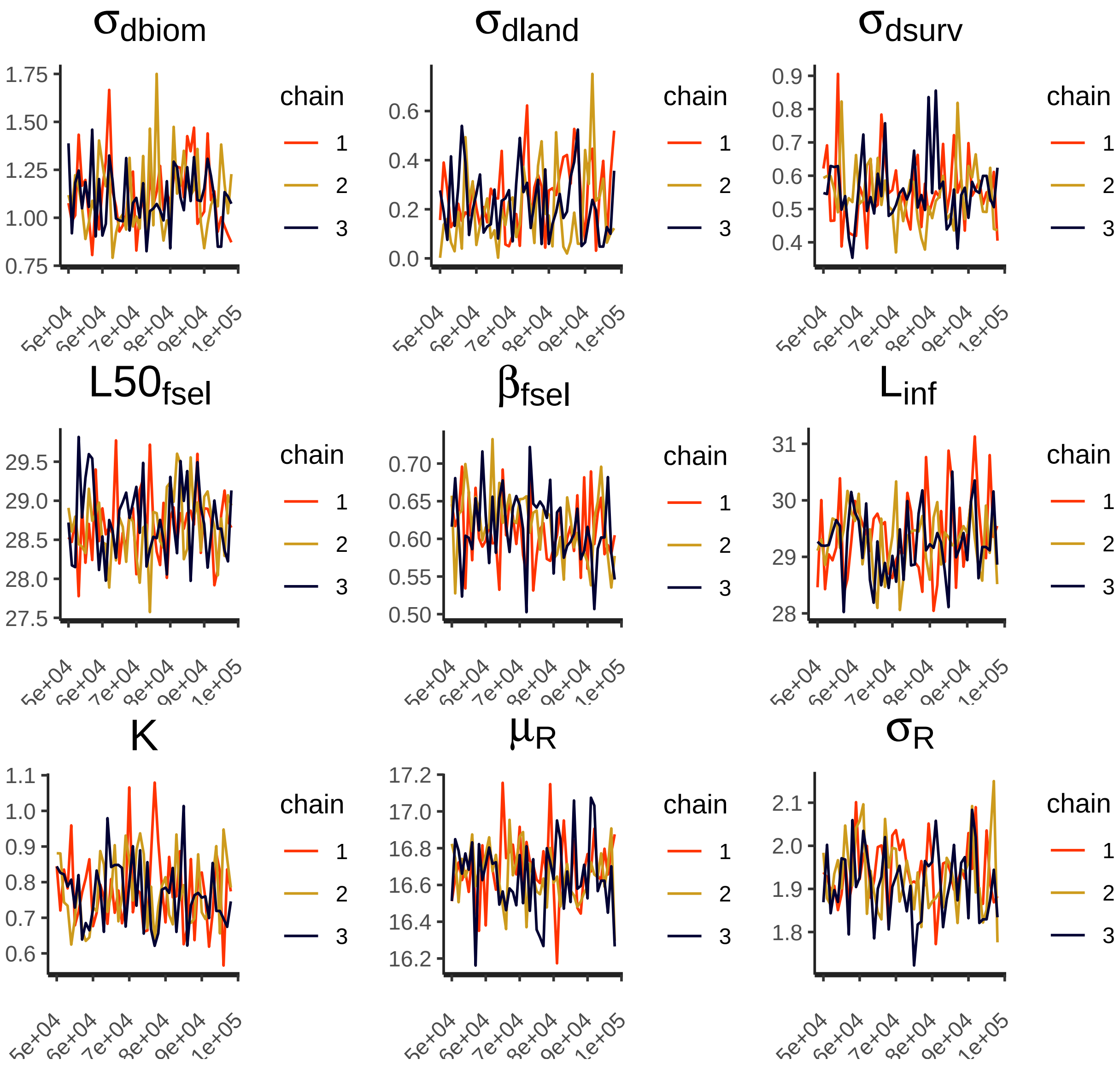


Figure A.35: Chapter IV sensitivity to recruitment lower parameter bound - Trace plot for some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

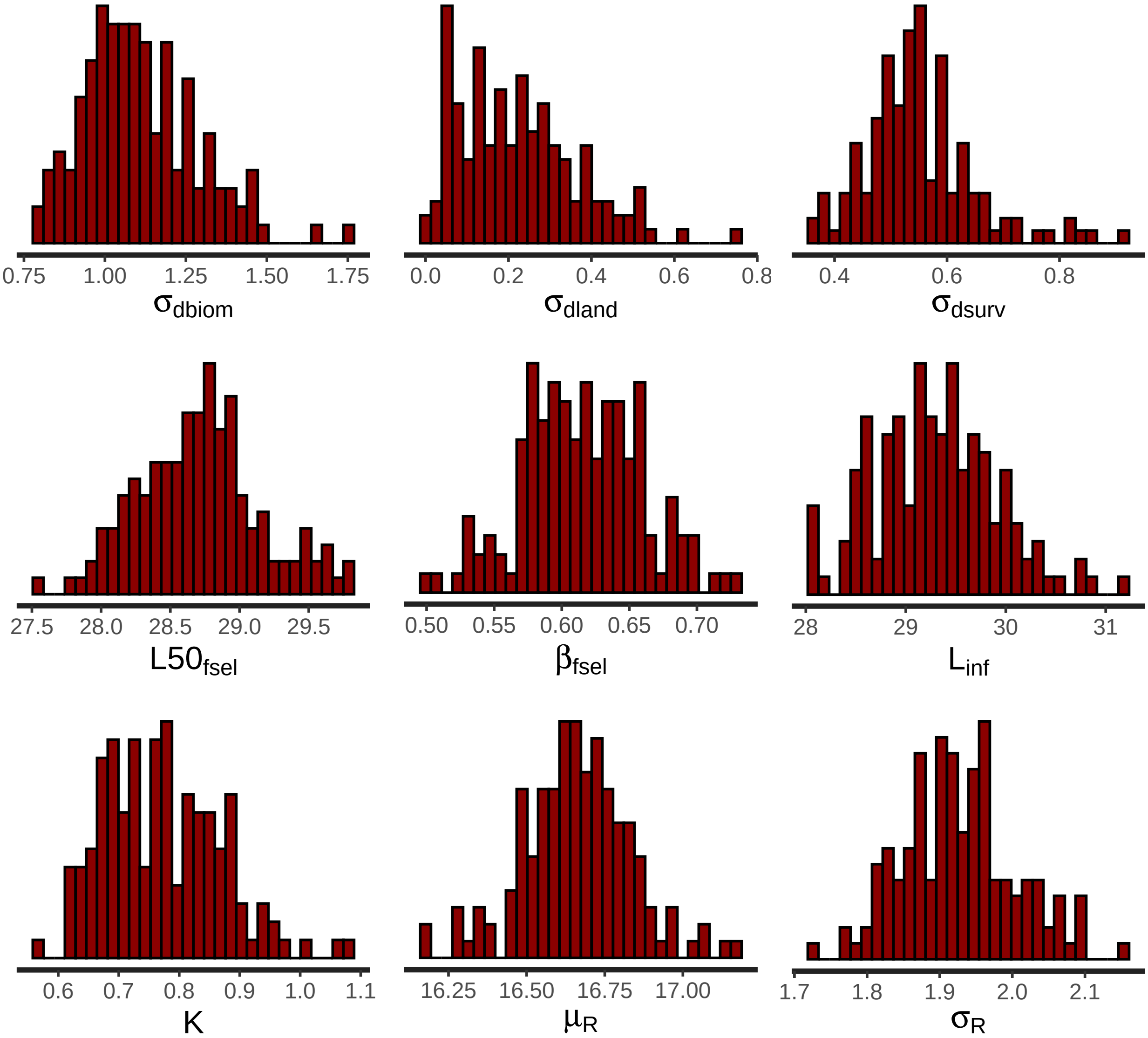


Figure A.36: Chapter IV sensitivity to recruitment lower parameter bound - Posterior distribution of some of the most important parameters: σ_{dbiom}, σ_{lbiom}, σ_{sbiom}, α_{fsel}, $L50_{fsel}$, β_{fsel}, L_{∞}, K, μ_R, σ_R

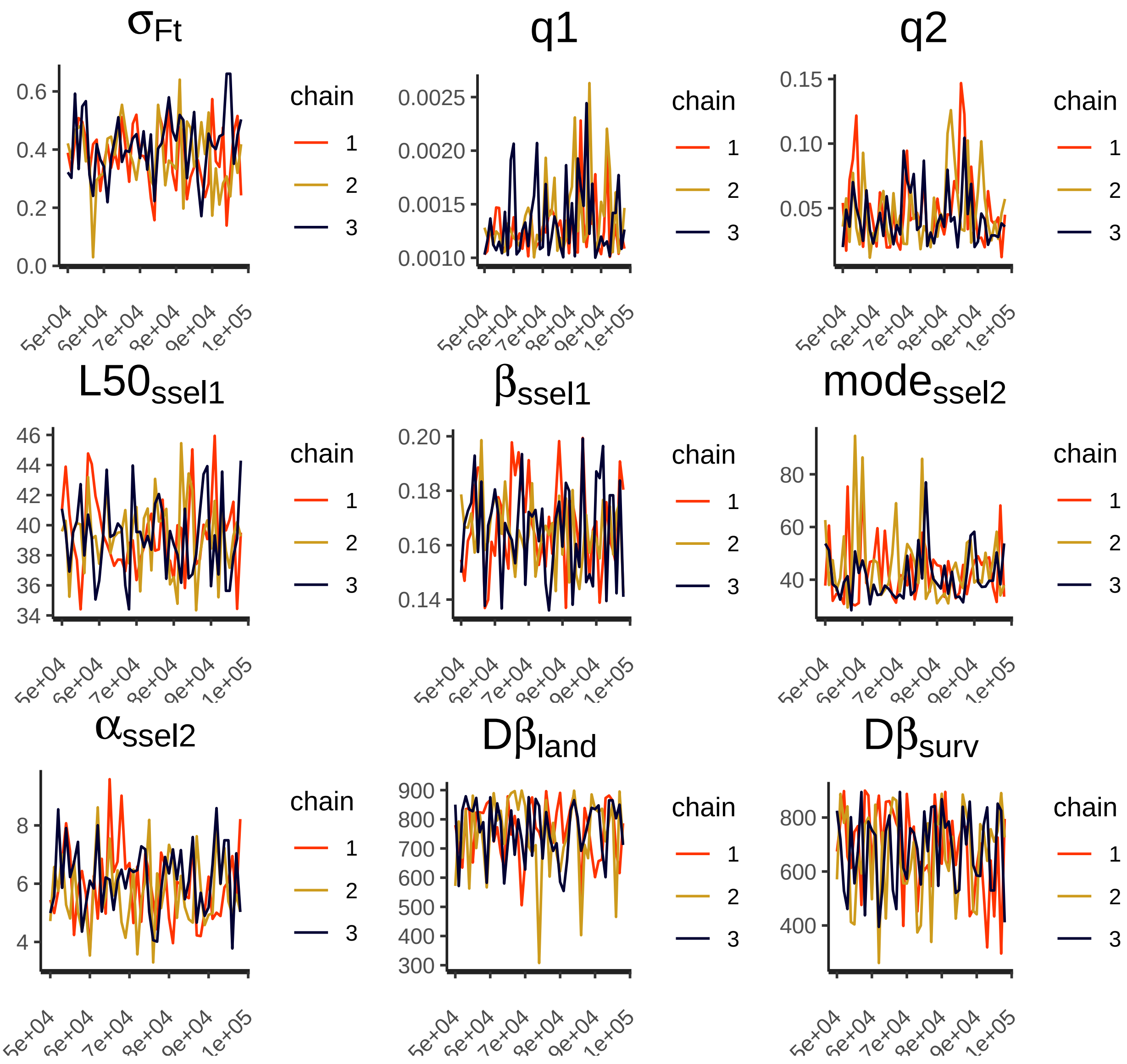


Figure A.37: Chapter IV sensitivity to recruitment lower parameter bound - Trace plot for some of the most important parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

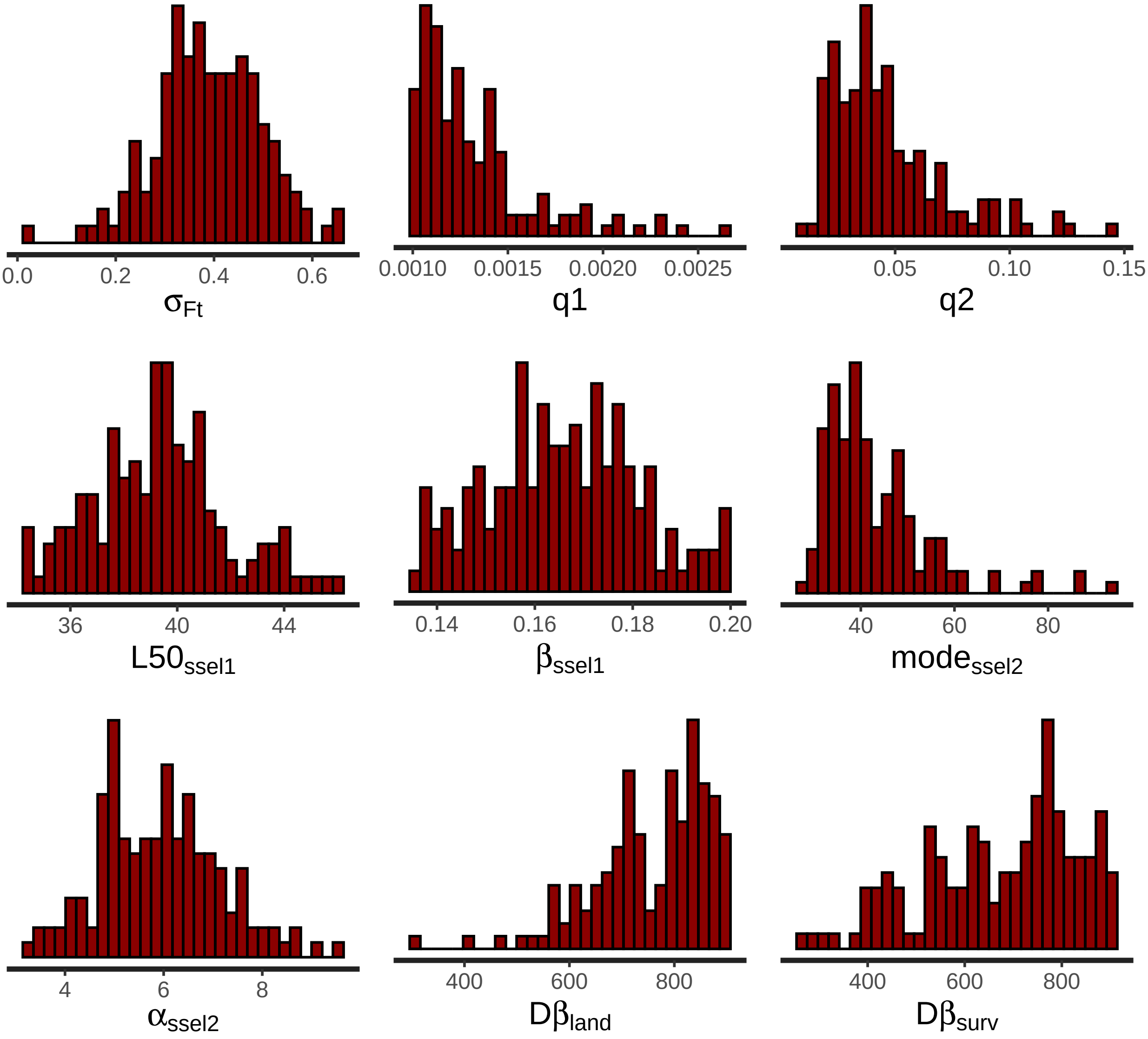


Figure A.38: Chapter IV sensitivity to recruitment lower parameter bound - Posterior distributions of some example parameters: σ_{Ft}, $q1$, $q2$, $mode_{ssel1}$, $mode_{ssel2}$, α_{ssel1}, α_{ssel2}, $D\beta1$, $D\beta$

A.4 Chapter V

```
### Fully annotated R code
source(“FUNCTIONS.R”)
library(rstan)
#### FIXED PARAMETERS AND DATA ####
#### PARAMETERS ####
# many parameters of this block are not used directly in the model in stan, but
rather used in
# functions to calculate values that will enter the stan model as parameters.
ymin1 = 1989 # first year of data
ymax1 = 2010 # last year of data
ymin2 = 2011
ymax2 = 2020
nyears1 = ymax1-ymin1+1
nyears2 = ymax2-ymin2+1 # number of years
nyears_tot = ymax2-ymin1+1
nyears = nyears_tot
Dt = 1 # timestep
L0 = 1
lmin=8
lmax = 52 # maximum length modeled
DL = 1 # length class width
L = lmin:lmax
cv = 0.1 # coefficient variation (used to calculate the sd around length class)
nlen = length(L) # number of length classes
alpha_wgt_len = 0.0093 # alpha in length-weight conversion
beta_wgt_len = 2.9456 # beta in length-weight conversion
M_u = 0.2# parameter in natural mortality
d = -0.31 # parameter in natural mortality
```

```
L50M = c(19.9, 19.8, 19.7, 19.6, 19.5, 19.3, 19.2000, 19.0875, 18.9750, 18.8625,
18.7500, 18.6375, 18.5250, 18.4125, 18.3000, 18.1875, 18.0750, 17.9625, 17.8500,
17.7375, 17.6250, 17.5125, 17.4000, 17.2875, 17.1750, 17.0625, 16.9500, 16.8375,
16.7250, 16.6125, 16.5000, 16.5000) # L50 of the maturity logistic
L50F = c(24, 23.9, 23.8, 23.7, 23.5, 23.4, 23.3000, 23.1625, 23.0250, 22.8875,
22.7500, 22.6125, 22.4750, 22.3375, 22.2000, 22.0625, 21.9250, 21.7875, 21.6500,
21.5125, 21.3750, 21.2375, 21.1000, 20.9625, 20.8250, 20.6875, 20.5500, 20.4125,
20.2750, 20.1375, 20.0000, 20.0000)
beta_Mat = 0.3 # steepness of the maturity logistic
muR = 15 # mean length of the recruitment
# call to functions to calculate derived fixed parameters
# Length-weight conversion. Transforms a vector of lengths in a vector of weights.
# divide by 1e6 converts grams into tons
wgt_at_len <- function (L, alpha, beta) {
return((alpha * L^beta)* 1.131e-3)
}
# Natural mortality function transforms a vector of weigth in mortality at length.
# (Lorenzen 1996, Journal of Fish Biology 49, 627-647).
Lorenzen <- function(W, M_u, d) {
return(M_u  W^d)
}
M = Lorenzen(W, M_u, d) # natural mortality at length
# multipurpose logistic function that can be used to calculate the maturity ogive
logistic <- function(x,x0,k) {
return(1/(1+exp(-k(x-x0))))
}
Mat = logistic(L,L50_Mat,L25_Mat) # maturity at length
# calculation of the survey selectivity
alfa1=.17
mode1=20
```

```
sS1 <- logistic(1:52,mode1,alfa1)
alfa2=6
mode2=20
beta2=mode2/(alfa2-1);
sS2 <- gamsel(alfa2,beta2,1:52)
W = W[-(1:7)];M = M[-(1:7)];sS1 = sS1[-(1:7)];sS2 = sS2[-(1:7)]
# maturity at length for males
MatM = time_varying_logistic(1:52,L50M,beta_Mat)
# maturity at length for females
MatF = time_varying_logistic(1:52,L50F,beta_Mat)
MatM = MatM[-(1:7),];MatF = MatF[-(1:7),]
# function to get the distribution of recruitment
Get_R_stan <- function(muR, cv, nlen, L, DL) {
sd <- cvmuR
Rdistr <- pnorm(L + DL, mean = muR, sd = sd) -
pnorm(L, mean = muR, sd = sd)
Rdistr <- Rdistr/sum(Rdistr)
return(Rdistr)
}
# probability of recruitment length
R_distr = Get_R_stan(muR, cv, nlen, 1:52, DL)
R_distr = R_distr[-(1:7)]

    #### DATA ####
data_surv_biom <- read.table(‘data_surv_biom_whiting.txt’)
data_surv_distr <- round(read.table(‘data_surv_distr_whiting.txt’))
data_surv_distr[is.na(data_surv_distr)] <- 0

    #### LIST THAT IMPUTS THE DATA ####
input.data = list(
```

```
# see above for definitions
#~~~~ PARAMETERS ~~~~
# TIME
nyears1 = nyears1,
nyears2 = nyears2,
nyears_tot = nyears_tot,
# GROWTH
nlen = nlen,
L = L,
W = W,
Dt = Dt, # timestep
L0 = L0, # minimum length modeled
lmax = lmax, # maximum length modeled
DL = DL, # length class width
# note that at least one parameter of the fishing selectivity must be fixed
alfa=0.2,
sd_Ft=0.1, # note that in survey only sd_Ft is fixed
#Linf=40,
# RECRUITMENT
# used only in generated quantities (a posteriori calculations)
MatM = MatM,
MatF = MatF,
# SURVIVORSHIP
M = M,
sS1 = sS1,
sS2 = sS2,
# EFFECTIVE SAMPLE SIZE
neff_init = 15,
#~~~ DATA ~~st
data_surv_distr = as.matrix(data_surv_distr),
```

```
data_surv_biom = data_surv_biom[,1],
#~~ FITTING PARAMETERS BOUNDS ~~~~
Rt_mean = log(400),# lower bound for Rt
Rt_sd = log(500000), # Upper bound for Rt
Ft_bounds = c(0.01,1),
#sd_Ft_bounds = c(0.01,3),
sd_surv_biom_bounds = c(0,1),
alpha=rep(1,nlen),
rd_lim=c(5,20),
rd_sd_lim=c(.1,5),
lf=c(1:nlen),
NS1_bounds = c(600,5000),
cv_bounds = c(0.01,1.2),
K_bounds = c(0.25,0.1),
L_bound=c(35,3),
D_beta_bounds = c(0,10000),
md = c(3,35)
)

#### FITTING PARAMETERS ####
# initial values
inits1 <- list(
Rt=log(colSums(data_surv_distr[1:15,-1])),
Ft = c(rep(0.2,(nyears_tot))), # fishing effort per year
sd_surv_biom=0.2, # error around the survey biomass
LF1_distr=(data_surv_distr[,1]+1)/sum(data_surv_distr[,1]+1),
R_distr_mean=7.5,
R_distr_sd=1,
cv=0.1,
K=0.34,
```

```
Linf=40,
D_beta=c(150,150),
mode=29,
NS1=sum(data_surv_distr[15:45,1])
)

inits2<-inits3<-inits1
iter<-100000
chains<-3
thin<-1000
model<-“whiting_slam_v5.00.stan”
init<-list(inits1,inits2,inits3)
t1<-Sys.time()
surv_only_whiting <- stan(file = model, data = input.data, thin=thin, diagnostic_file = “parameter values”, init=init, cores=4, seed = “38”, #algorithm = “Fixed_param”, iter =iter, chains = chains, verbose=FALSE, init_r=.5)
t2<-Sys.time()
t2-t1
```

A.4.1 Fully annotated Stan code

```
// slam full model version: reference model
// initial N is estimated the sum of Rt[1] and NS1,
// the survivors from year 0 (first data year -1)
// recruitment length distribution is estimated
// recruitment drawn from uniform distribution - not log uniform
// Ft follows a random walk
// estimates growth parameters
// removed initial zeroing of G matrix calculation
// uses Dirichlet-multinomial with Beta dispersion parameter D_beta
```

```
// two surveys: pre and post 2011
// fisheries logistic selectivity and survey gamma selectivity
functions {
// function to calculate log probability for a Dirichlet-multinomial distribution
real DM_lpmf(int [] n, vector alpha) {
int N = sum(n);
real A = sum(alpha);
return lgamma(A) - lgamma(N + A)
+ sum(lgamma(to_vector(n) + alpha))
- sum(lgamma(alpha));
}
// gamma selectivity function
real gamsel(real alpha,real beta,real len){
return((len/((alpha-1) * beta))^(alpha-1)
exp(alpha-1-len/beta));
}
}

// data and fixed parameters
data {
int nyears1; // number of years of first survey
int nyears2; // number of years of second survey
int nyears_tot; // total number of years
real Dt; // time step
real L_bound[2]; // bounds on Linf
real DL; // length bin size
int nlen; // number of length bins
vector[nlen] W; // weight at length vector
vector[nlen] L; // length classes
vector[nlen] alpha; // Dirichlet parameter vector
```

```
vector[nlen] M; // natural mortality
matrix[nlen,nyears_tot] MatM; // maturity for males
matrix[nlen,nyears_tot] MatF; // maturity for females
real NS1_bounds[2];
// values for survey selection parameter priors
real alfa;
real sd_Ft; // process error on fishing morality year effect
real md[2];
// observations

int data_surv_distr[nlen,nyears_tot]; // survey number at length
real data_surv_biom[nyears_tot]; // survey biomass
// effective sample sizes for survey and landings distributions
int neff_init;
// Bounds for prior on growth parameters
real K_bounds[2];
real cv_bounds[2];
// Bounds for prior on recruitment
real Rt_mean;
real Rt_sd;
// bounds or prior on Ft
real Ft_bounds[2];
// bounds for prior on suvey biomass
real sd_surv_biom_bounds[2];
// bounds for std dev process error on Ft
//real sd_Ft_bounds[2];
// bounds for dispersion parameter Dirichlet
real D_beta_bounds[2];
// bounds of priors on recruitment distribution parameters
real rd_lim[2]; // bounds for mean of distribution
```

```
real rd_sd_lim[2]; // bounds for sd of distribution
// survey selectivity
real sS1[nlen];
real sS2[nlen];
}
// end block

transformed data {
int data_surv_scaled[nlen,nyears_tot];
// re-scale survey distribution to effectove sample size
for (l in 1:nlen){
for (y in 1:nyears_tot){
data_surv_scaled[l,y] = data_surv_distr[l,y]
neff_init/sum(data_surv_distr[,y]);
}
}
}
// end block

// fitting parameters
parameters {
vector[nyears_tot-1] Rt; // Annual recruitment
vector[nyears_tot] Ft; // Annual fishing mortality year effect
simplex[nlen] LF1_distr; // proportion at length surviving in first year
real sd_surv_biom; //observation error on survey biomass
real NS1; // total number of survivirs in first year
// growth parameters
real cv;
real K;
real Linf;
```

```
// fishery selectivity parameters
real mode;
// recruitment length frequency parameters
real R_distr_mean;
real R_distr_sd;
// Dirichlet scalar
real D_beta[2];
}
// end block

transformed parameters {
matrix[nlen, nlen] G; // growth projection matrix
vector[nlen] newL;
vector[nlen] sd_growth;
matrix[nlen, nyears_tot] F; // fishing mortality matrix
matrix[nlen, nyears_tot] Z; // total mortality matrix
matrix[nlen, nyears_tot] S; // survival matrix
matrix[nlen, nyears_tot] N; // population matrix
// population matrix * survival matrix
vector[nlen] NS;
// survey proportion at length x years
matrix[nlen, nyears_tot] Survey_Distr;
// survey numbers at length x years
matrix[nlen, nyears_tot] Survey;
// survey numbers at length x years
matrix[nlen, nyears1] Survey1;
// survey numbers at length x years
matrix[nlen, nyears2] Survey2;
// caught numbers at length x years
matrix[nlen, nyears_tot] Catches;
```

```
vector[nyears_tot] Caught_Biomass;
matrix[nlen, nyears_tot] Catches_biom_xlen;
// biomass surveyed per length per year
matrix[nlen, nyears_tot] Survey_biom_xlen;
// total biomass surveyed per year
vector[nyears_tot] Surv_Biomass;
// recruitmet length frequency distribution
vector[nlen] R_distr;
vector[nlen] sF; // fishing selectivity curve
// calculate recruitment length distribution from a normal distribution
for(i in 1:nlen){
R_distr[i] = normal_cdf(L[i]+DL,R_distr_mean,R_distr_sd)-
normal_cdf(L[i],R_distr_mean,R_distr_sd);
}
// construct initial population from survivors in initial year and recruitment
for(l in 1:nlen){
N[l,1]=NS1LF1_distr[l];
}
newL = Linf - (Linf-L)  exp(-KDt);
for (l in 1:nlen) {
sd_growth[l] = cv  newL[l];
}
for (y in 1:nlen){
for (l in 1:nlen) {
G[l,y] = normal_cdf(L[l]+DL,newL[y],sd_growth[l])-
normal_cdf(L[l],newL[y],sd_growth[l]);
}
}
for (y in 1:nlen){
for (l in 1:nlen) {
```

```
G[l,y] = G[l,y] / sum(G[,y]);
}
}
// logistic survey selectivity
sF=1 ./ (1+exp(-alfa(L-mode)));
// define S: survival at length
for (l in 1:nlen) {
for (y in 1:nyears_tot) {
F[l,y] = sF[l]  Ft[y];
Z[l,y] = F[l,y] + M[l];
}
}
S = exp(-(Z));
// Calculate survivors into the next year
for (y in 1:(nyears_tot-1)) {
for (l in 1:nlen) {
NS[l] = N[l,y] * S[l,y];
}
// Project the population at length one year ahead from suvivors and growth matrix
N[,y+1] = G * NS; // double check with length distribution plot
for (l in 1:nlen) {
// note Rt is on a log scale
N[l,y+1] = N[l,y+1] + exp(Rt[y])R_distr[l];
}
}
// Calculate fitted survey numbers at length from catchability q and survey size selection
for (y in 1:nyears1){
for (l in 1:nlen){
Survey1[l,y] = N[l,y]sS1[l];
```

```
}
}
for (y in 1:nyears2){
for (l in 1:nlen){
Survey2[l,y] = N[l,y+nyears1]sS2[l];
}
}
Survey = append_col(Survey1,Survey2);
// calculate discard, catches and landings
Catches = F ./ Z . (1-S) .* N; // catch numbers at length and year
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
Catches_biom_xlen[l,y] = W[l] * Catches[l,y];
Survey_biom_xlen[l,y] = W[l] * Survey[l,y];
}
Caught_Biomass[y] = sum(Catches_biom_xlen[,y]);
Surv_Biomass[y] = sum(Survey_biom_xlen[,y]);
}
// calculate fitted landing and survey length frequency
for (y in 1:nyears_tot) {
for (l in 1:nlen) {
Survey_Distr[l,y] = Survey[l,y] / sum(Survey[,y]);
}
}
//print("N =",N);
//print("LB =",Land_Biomass);
//print("SB =",Surv_Biomass);
}
// end block
```

```
model {
// Priors
// Fishing mortality year effect in first year
Ft[1]~uniform(Ft_bounds[1],Ft_bounds[2]);
// Annual recruitment
for (y in 1:(nyears_tot-1)) {
Rt[y]~uniform(Rt_mean,Rt_sd);
}
//survivors proportion at length
LF1_distr~dirichlet(alpha);
//initial population size
NS1~uniform(NS1_bounds[1],NS1_bounds[2]);
// survey selection parameters
mode~uniform(md[1],md[2]);
//alfa~lognormal(log(al[1]),al[2]);
// growth parameters
cv~uniform(cv_bounds[1],cv_bounds[2]);
K~lognormal(log(K_bounds[1]),K_bounds[2]);
Linf~normal((L_bound[1]),L_bound[2]);
// Dirichlet scalar
D_beta[1]~uniform(D_beta_bounds[1],D_beta_bounds[2]);
D_beta[2]~uniform(D_beta_bounds[1],D_beta_bounds[2]);
// observation errors
sd_surv_biom~uniform(sd_surv_biom_bounds[1], sd_surv_biom_bounds[2]);
// process error on fishing mortality
//sd_Ft~uniform(sd_Ft_bounds[1],sd_Ft_bounds[2]);
// recruitment proiportins at length
R_distr_mean~uniform(rd_lim[1],rd_lim[2]);
R_distr_sd~uniform(rd_sd_lim[1],rd_sd_lim[2]);
// construct a randon walk for fishing mortality
```

```
for (y in 1:(nyears_tot-1)) {
Ft[y+1]~lognormal(log(Ft[y]),sd_Ft);
}
// Likelihoods
for(y in 1:(nyears_tot)){
// biomass observations
//if(data_surv_biom[y]>0)
if(data_surv_biom[y]>0) data_surv_biom[y]~lognormal(log(
Surv_Biomass[y]),sd_surv_biom);
}
for(y in 1:(nyears1)){
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y]|Survey_Distr[,y]* D_beta[1]);
}
for(y in 1:(nyears2)){
// length frequency observations
target+=DM_lpmf(data_surv_scaled[,y+nyears1]|
Survey_Distr[,y+nyears1]D_beta[2]);
}
}

generated quantities {
matrix[nlen,nyears_tot] SSB_MatF;
matrix[nlen,nyears_tot] SSB_MatM;
vector[nyears_tot] SSB;
//matrix[nlen, nyears_tot] Catch_Distr;
//matrix[nlen, nyears_tot] Discard_Distr;
real neff[2]; // effective sample size
// Spawning Stock Biomass (SSB) for males and for females
for (y in 1:nyears_tot) {
```

```
for (l in 1:nlen) {

SSB_MatF[l,y] = ((MatF[l,y]  N[l,y]) * W[l])/2;

SSB_MatM[l,y] = ((MatM[l,y] * N[l,y]) * W[l])/2;

}

SSB[y] = sum(SSB_MatF[,y])+sum(SSB_MatM[,y]);

}

// calculate effective sample size

neff[1]=neff_init(1+D_beta[1])/(neff_init+D_beta[1]);

neff[2]=neff_init(1+D_beta[2])/(neff_init+D_beta[2]);

}

// end block
```

A.4.2 Supplementary plots: whiting

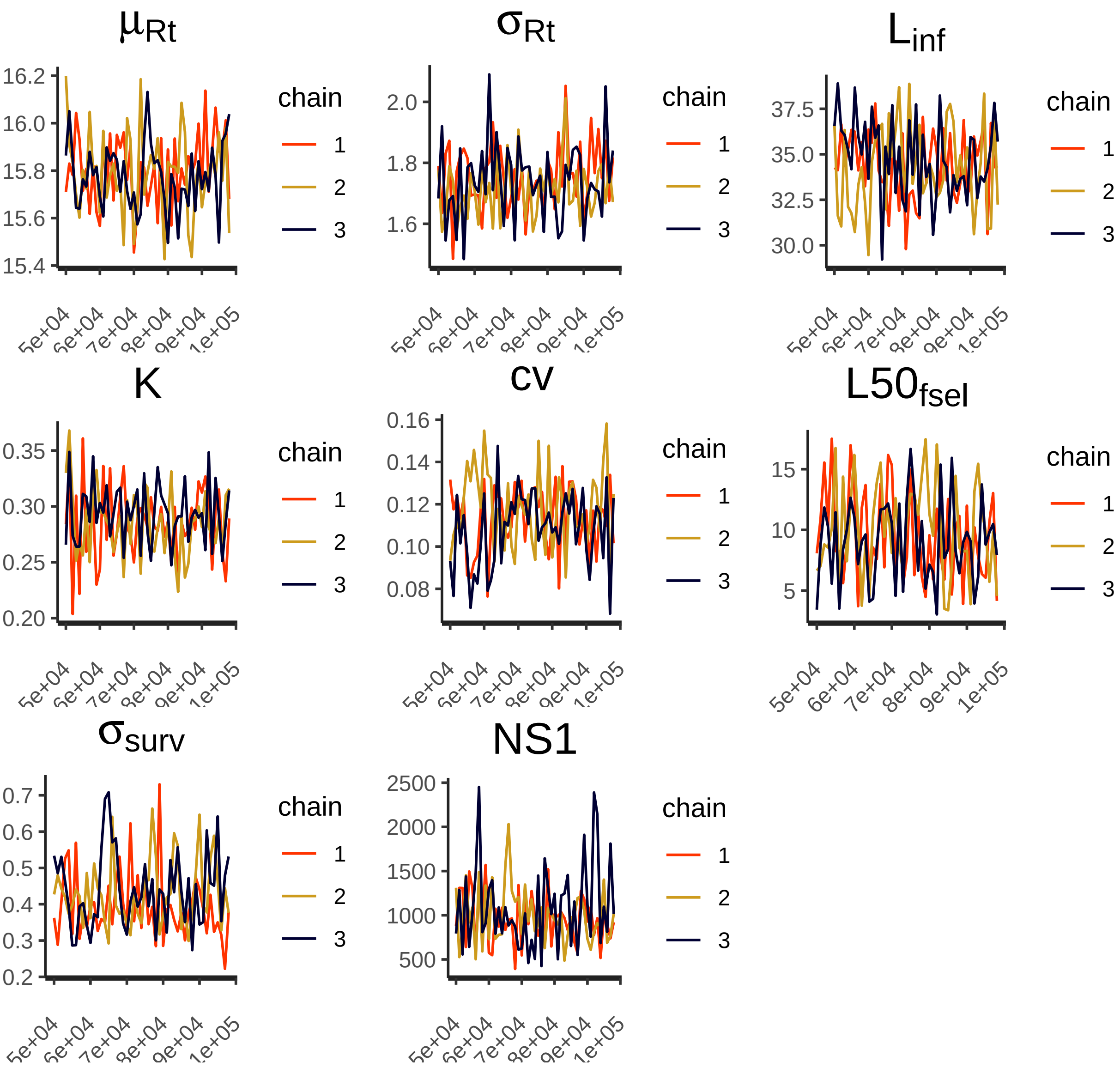


Figure A.39: Chapter V whiting - Trace plots for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

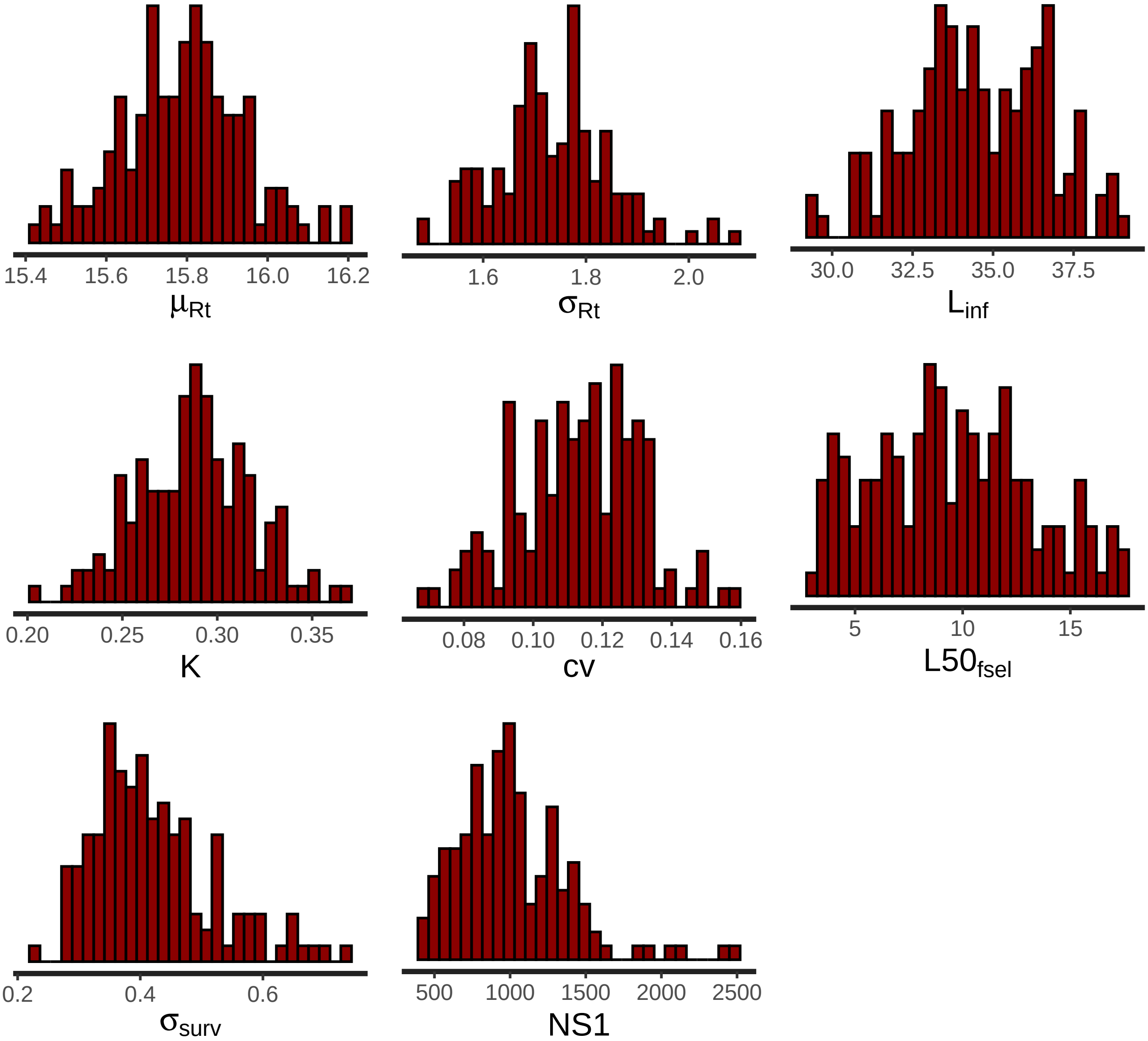


Figure A.40: Chapter V whiting - Posterior distributions of some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

A.4.3 Supplementary plots: haddock

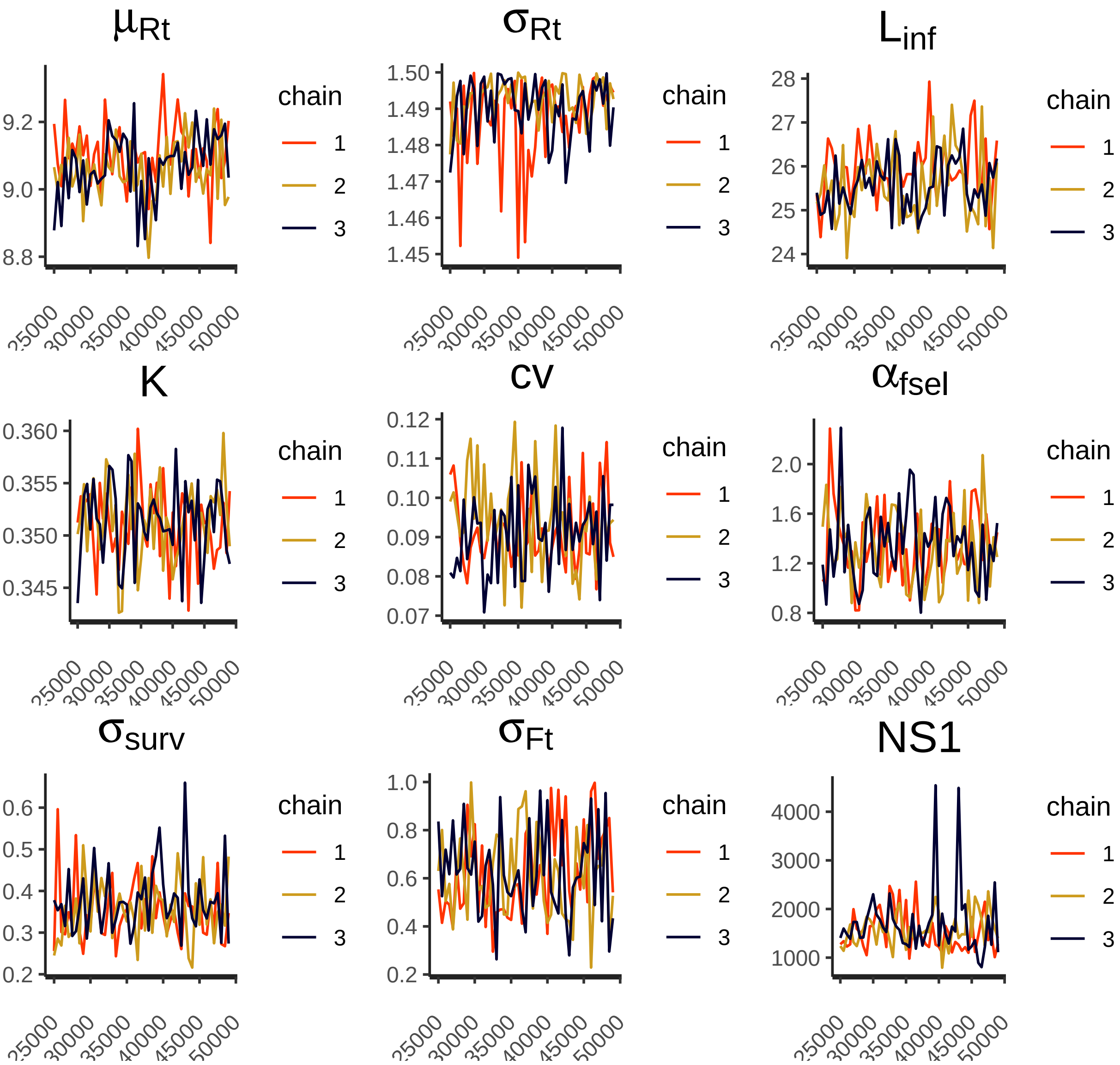


Figure A.41: Chapter V haddock - Trace plots for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

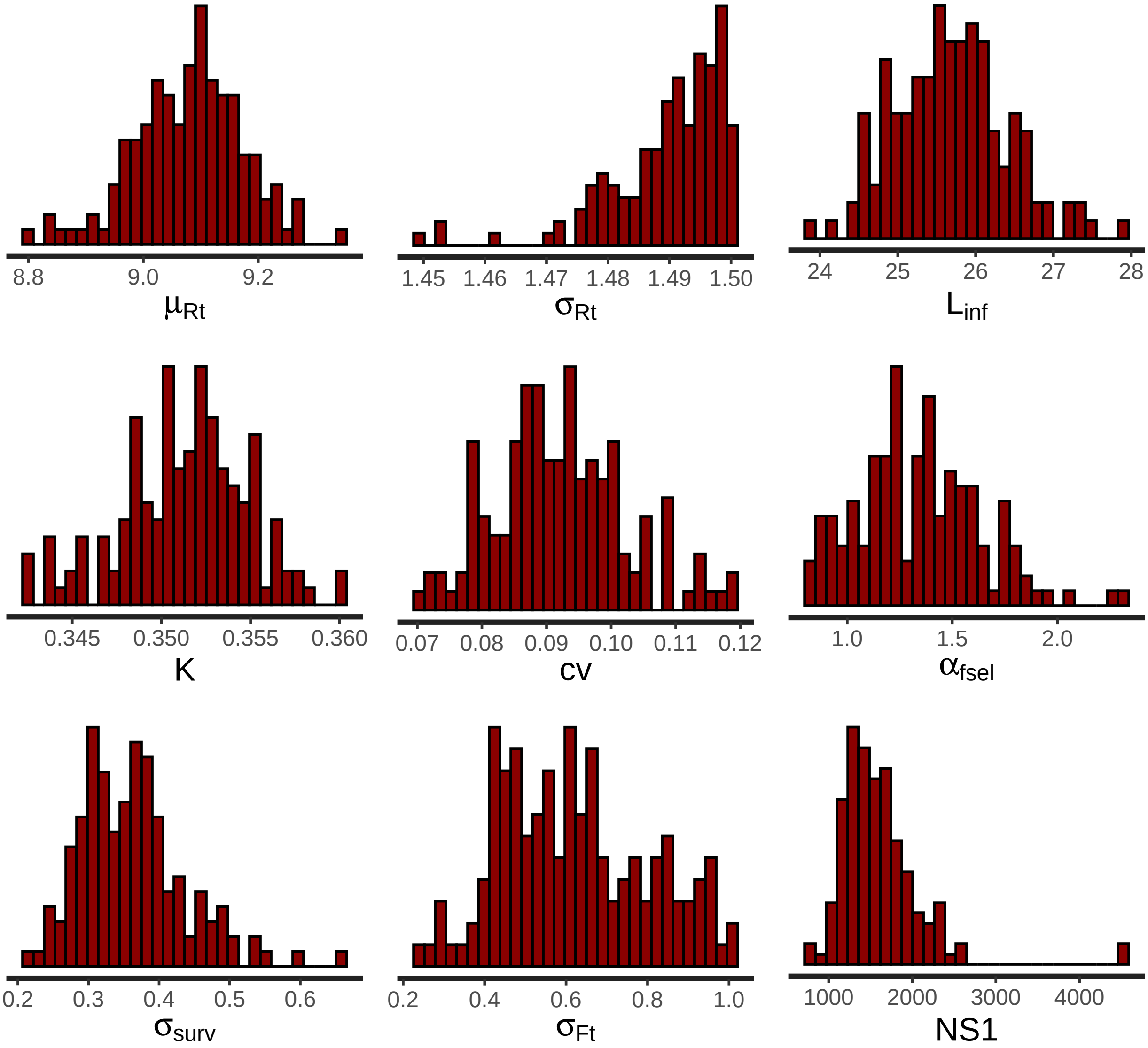


Figure A.42: Chapter V haddock - Plot showing the posterior distributions for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

A.4.4 Supplementary plots: lemon sole

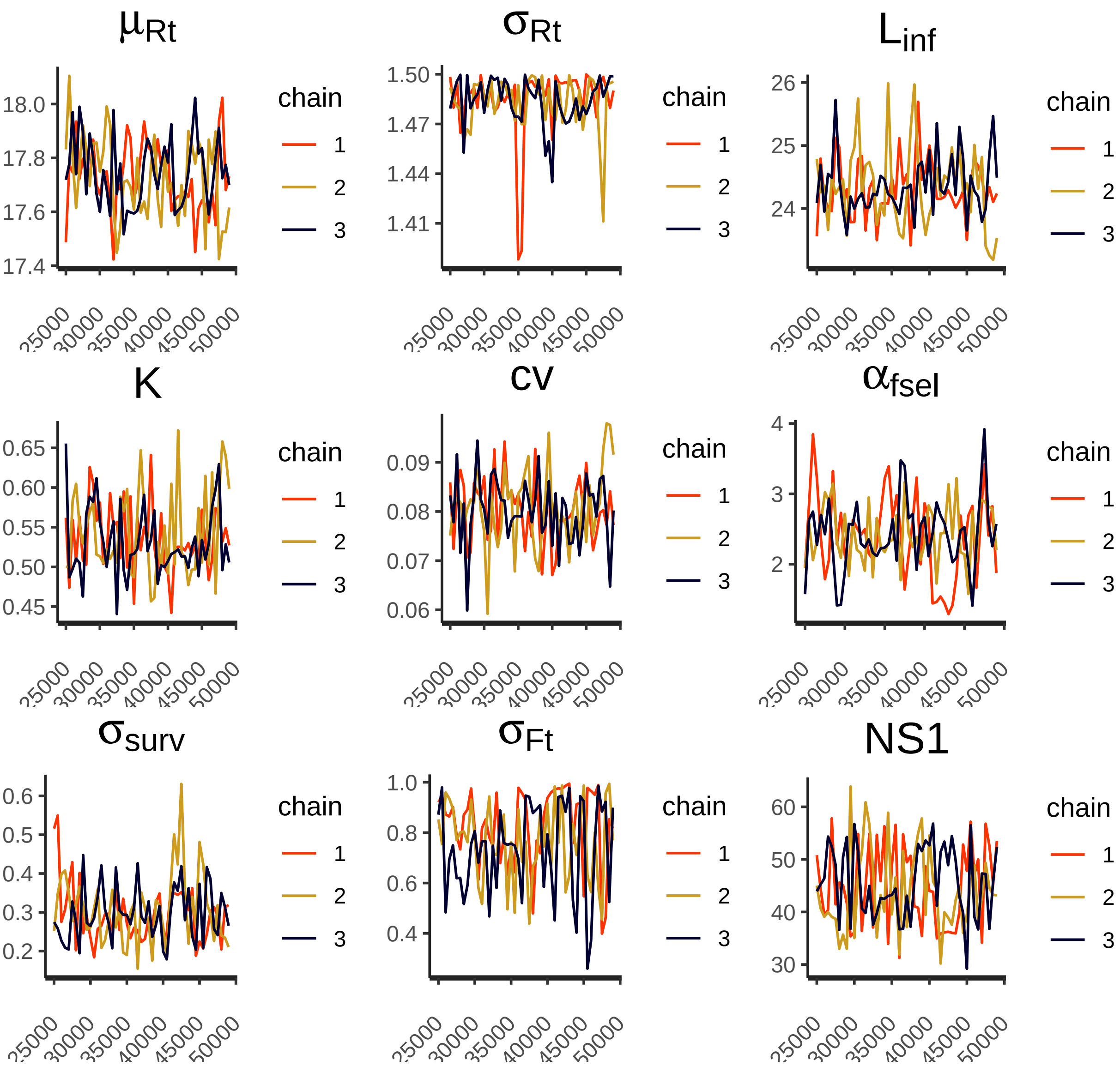


Figure A.43: Chapter V lemon sole - Trace plots for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

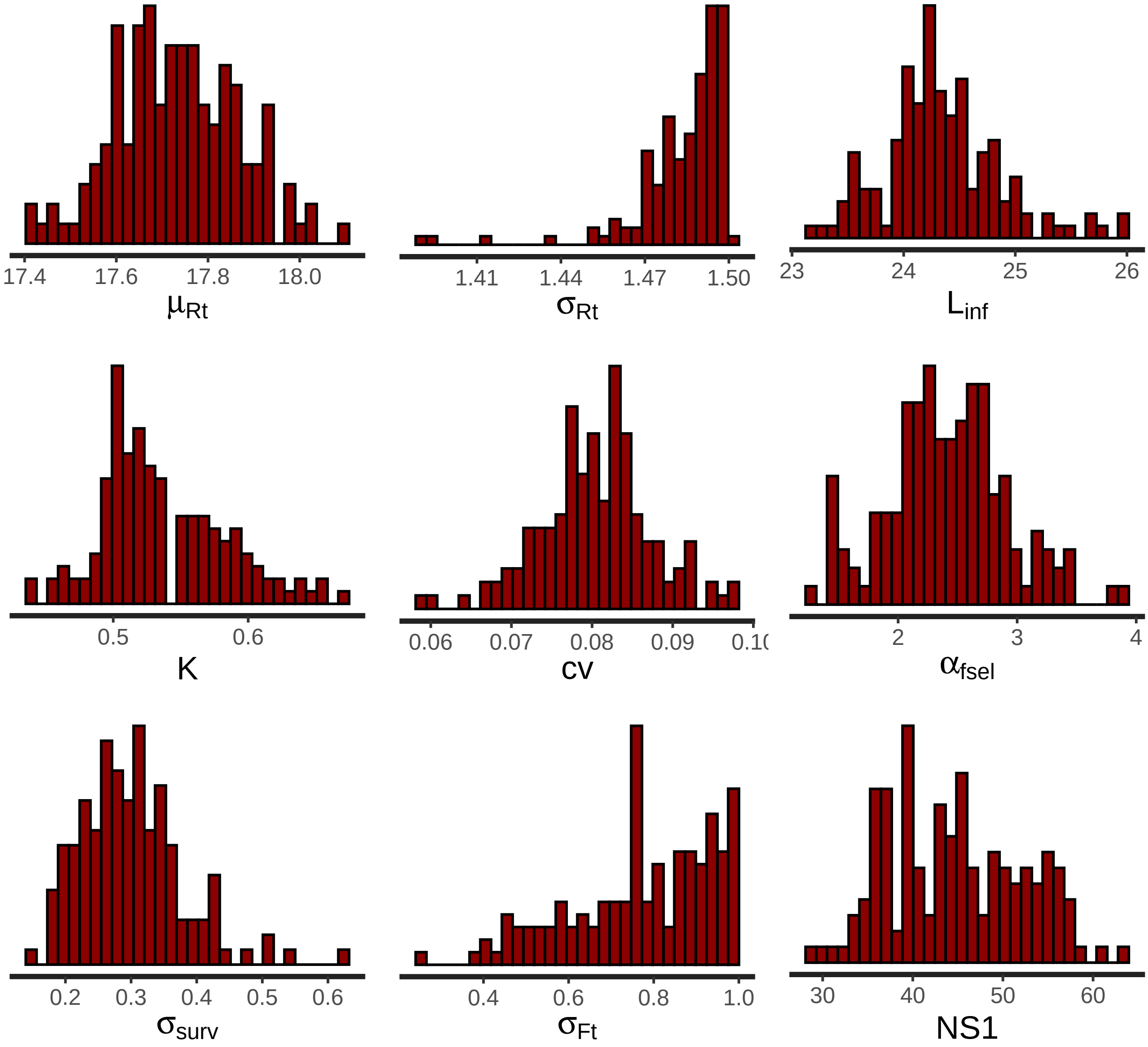


Figure A.44: Chapter V lemon sole - Plot showing the posterior distributions for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

A.4.5 Supplementary plots: grey gurnard

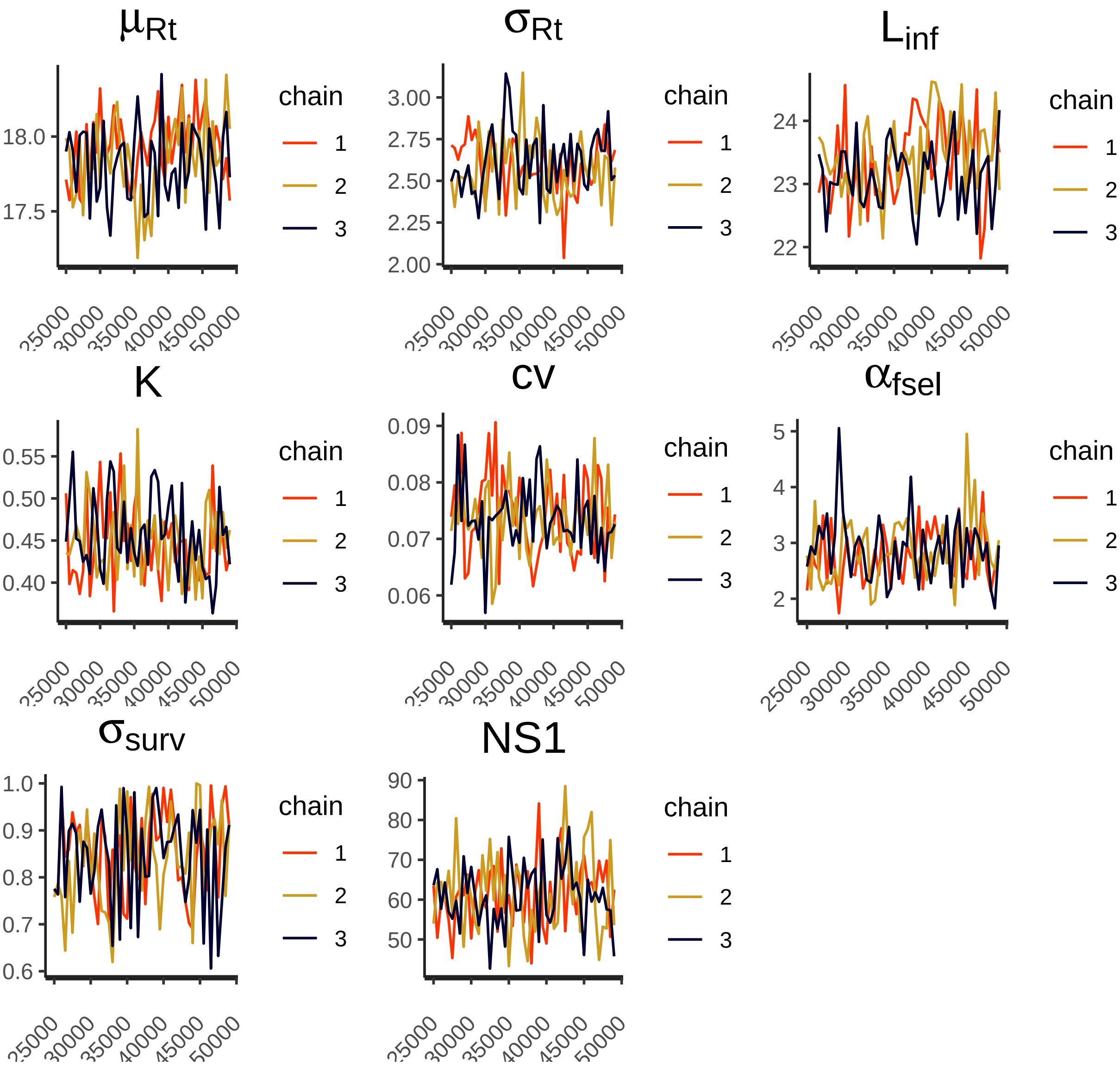


Figure A.45: Chapter V grey gurnard - Trace plots for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

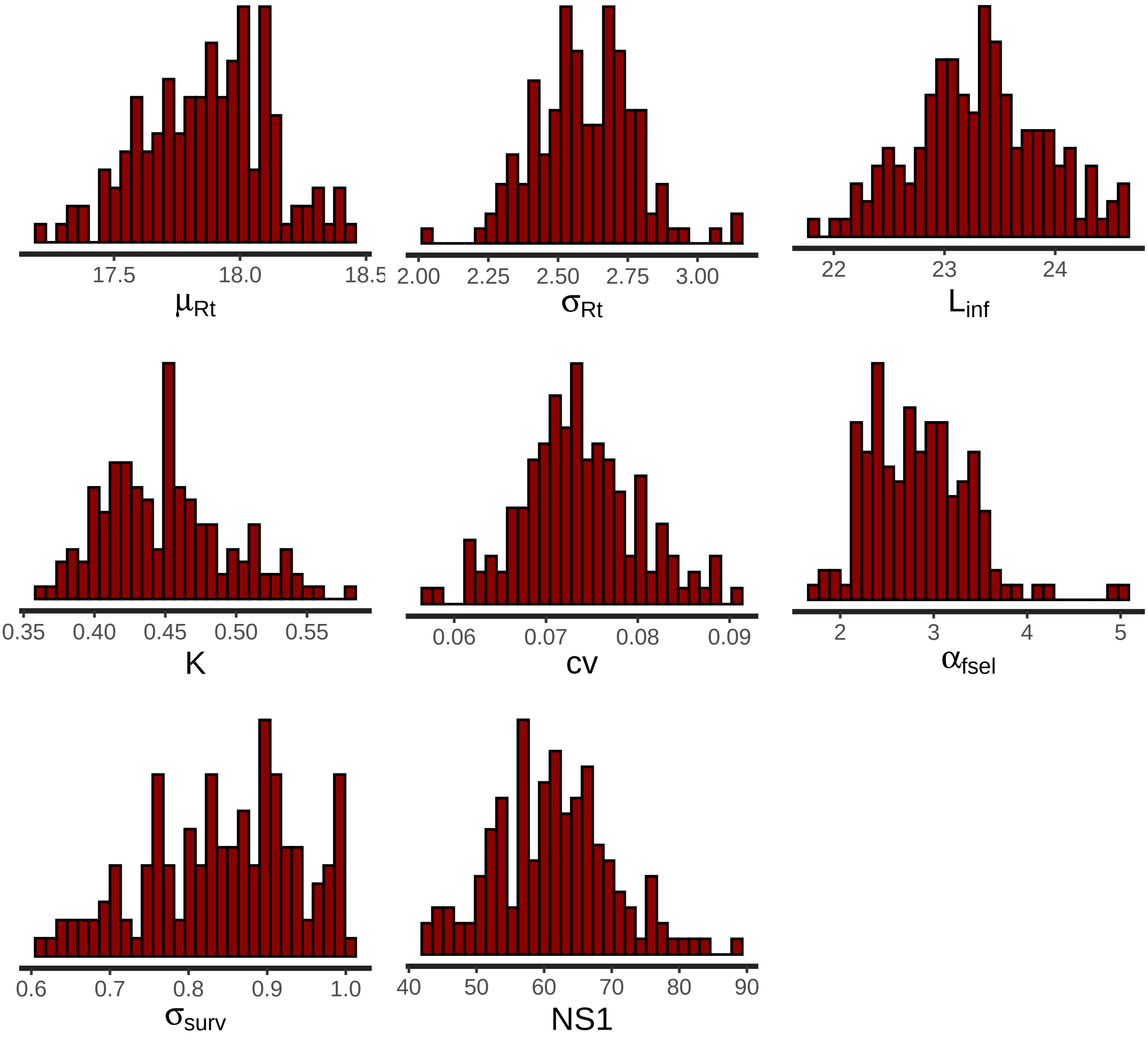


Figure A.46: Chapter V grey gurnard - Plot showing the posterior for some example parameters: μ_R, σ_R, L_∞, K, cv, α_{fsel}, σ_{sbiom}, NS_1

References

Age, Celtic Sea, G. of the lemon sole (Microstomus kitt) in the, & North Sea, the. (2010). Mahe, kelig and elleboode, romain and persohn, cecile and dufour, jean-louis. *Journal of Oceanography, Research and Data*, *3*, 12–18.

Beare, D., Needle, C., Burns, F., & Reid, D. (2005). Using survey data independently from commercial data in stock assessment: An example using haddock in ICES division VIa. *ICES Journal of Marine Science*, *62*(5), 996–1005.

Brooks, S., Gelman, A., Jones, G., & Meng, X.-L. (2011). *Handbook of markov chain monte carlo*. CRC press.

Cadigan, N. G. (2010). *Trends in northwest atlantic fisheries organization (NAFO) subdivision 3Ps cod (gadus morhua) stock size based on a separable total mortality model and the fisheries and oceans canada research vessel survey index*. Fisheries; Oceans Canada, Science.

Carpenter, B. (2015). Stan: A probabilistic programming language. *Journal of Statistical Software*.

Casella, G., & Berger, R. L. (2002). *Statistical inference* (2nd ed.). Duxbury.

Chen, Y., Hunter, M., Vadas, R., & Beal, B. (2003). *Developing a growth-transition matrix for the stock assessment of the green sea urchin (strongylocentrotus droebachiensis) off maine*.

Chrysafi, A., & Kuparinen, A. (2016). Assessing abundance of populations with limited data: Lessons learned from data-poor fisheries stock assessment. *Environmental Reviews*, *24*(1), 25–38.

Ciotti, B. J., Targett, T. E., & Burrows, M. T. (n.d.). Decline in growth rate of juvenile european plaice (pleuronectes platessa) during summer at nursery beaches along the west coast of scotland. *Canadian Journal of Fisheries and Aquatic Sciences*, *70*(5), 720–734.

Cohen, D. M., Inada, T., Iwamoto, T., & Scialabba, N. (1990). Gadiform fishes of the world. *FAO Fisheries Synopsis*, *10*(125), I.

Cook, R. (1997). Stock trends in six north sea stocks as revealed by an analysis of research vessel surveys. *ICES Journal of Marine Science*, *54*(5), 924–933.

Cook, R. (2004). Estimation of the age-specific rate of natural mortality for shetland sandeels. *ICES Journal of Marine Science*, *61*(2), 159–164.

Cook, R. (2013). A fish stock assessment model using survey data when estimates of catch are unreliable. *Fisheries Research*, *143*, 1–11.

Cook, R. M. (2019). Inclusion of discards in stock assessment models. *Fish and Fisheries*, *20*(6), 1232–1245.

Cook, R., Acheampong, E., Aggrey-Fynn, J., & Heath, M. (2021). A fleet based surplus production model that accounts for increases in fishing power with application to two west african pelagic stocks. *Fisheries Research*, *243*, 106048.

Cotter, A., Burt, L., Paxton, C., Fernandez, C., Buckland, S., & Pan, J.-X. (2004). Are stock assessment methods too complicated? *Fish and Fisheries*, *5*(3), 235–254.

Cotter, J., Petitgas, P., Abella, A., Apostolaki, P., Mesnil, B., Politou, C.-Y., Rivoirard, J., Rochet, M.-J., Spedicato, M. T., Trenkel, V. M., et al. (2009). Towards an ecosystem approach to fisheries management (EAFM) when trawl surveys provide the main source of information. *Aquatic Living Resources*, *22*(2), 243–254.

Damm, U. (1987). Growth of the grey gurnard, eutrigla gurnardus l., in the north sea. *ICES Document CM.*

De Finetti, B. (1989). Probabilism: A critical essay on the theory of probability and on the value of science. *Erkenntnis (1975-)*, *31*(2/3), 169–223.

Dowling, N. A., Smith, A. D., Smith, D. C., Parma, A. M., Dichmont, C. M., Sainsbury, K., Wilson, J. R., Dougherty, D. T., & Cope, J. M. (2019). Generic solutions for data-limited fishery assessments are not so simple. *Fish and Fisheries*, *20*(1), 174–188.

Dowling, N., Dichmont, C., Haddon, M., Smith, D., Smith, A., & Sainsbury, K. (2015a). Empirical harvest strategies for data-poor fisheries: A review of the literature. *Fisheries Research*, *171*, 141–153.

Dowling, N., Dichmont, C., Haddon, M., Smith, D., Smith, A., & Sainsbury, K. (2015b). Guidelines for developing formal harvest strategies for data-poor species and fisheries. *Fisheries Research*, *171*, 130–140.

Enberg, K., Jørgensen, C., Dunlop, E. S., Varpe, Ø., Boukal, D. S., Baulier, L., Eliassen, S., & Heino, M. (2012). Fishing-induced evolution of growth: Concepts, mechanisms and the empirical evidence. *Marine Ecology*, *33*(1), 1–25.

Francis, R. C. (2011). Data weighting in statistical fisheries stock assessment models. *Canadian Journal of Fisheries and Aquatic Sciences*, *68*(6), 1124–1138.

Francis, R. C. (2014). Replacing the multinomial in stock assessment models: A first step. *Fisheries Research*, *151*, 70–84.

Froese, R., Winker, H., Coro, G., Demirel, N., Tsikliras, A. C., Dimarchopoulou, D., Scarcella, G., Probst, W. N., Dureuil, M., & Pauly, D. (2018). A new approach for estimating stock status from length frequency data. *ICES Journal of Marine Science*, *75*(6), 2004–2015.

Gagnon, P. (2023). Robustness against conflicting prior information in regression. *Bayesian Analysis*, *18*(3), 841–864.

Gelman, A. (2006). Prior distributions for variance parameters in hierarchical models (comment on article by Browne and Draper). *Bayesian Analysis*, *1*(3), 515–534. `https://doi.org/10.1214/06-BA117A`

Gerritsen, H., & McGrath, D. (2006). *An overview of sources of bias and uncertainty in fisheries surveys.* `https://doi.org/10.17895/ices.pub.25258795.v1`

Gilks, W. R., Richardson, S., & Spiegelhalter, D. J. (Eds.). (1996). *Markov chain monte carlo in practice.* Chapman; Hall/CRC.

Gulland, J. A. (1983). *Stock assessment: why?* Training Department, Southeast Asian Fisheries Development Center.

Haddon, M. (2011). *Modelling and quantitative methods in fisheries.* Chapman; Hall/CRC.

Harley, S. J., Myers, R. A., & Dunn, A. (2001). Is catch-per-unit-effort proportional to abundance? *Canadian Journal of Fisheries and Aquatic Sciences*, *58*(9), 1760–1772.

Hilborn, R. (2003). The state of the art in stock assessment: Where we are and where we are going. *Scientia Marina*, *67*(S1), 15–20.

Hilborn, R., Amoroso, R. O., Anderson, C. M., Baum, J. K., Branch, T. A., Costello, C., Moor, C. L. de, Faraj, A., Hively, D., Jensen, O. P., et al. (2020). Effective fisheries management instrumental in improving fish stock status. *Proceedings of the National Academy of Sciences*, *117*(4), 2218–2224.

Hillary, R. (2011). A new method for estimating growth transition matrices. *Biometrics*, *67*(1), 76–85.

Hislop, J., Robb, A., Bell, M., & Armstrong, D. (1991). The diet and food consumption of whiting (merlangius merlangus) in the north sea. *ICES Journal of Marine Science*, *48*(2), 139–156.

Hoffman, M. D., Gelman, A., et al. (2015). The no-u-turn sampler: Adaptively setting path lengths in hamiltonian monte carlo. *J. Mach. Learn. Res.*, *15*(1), 1593–1623.

Hoggarth, D. D. (2006). *Stock assessment for fishery management: A framework guide to the stock assessment tools of the fisheries management and science programme*. Food & Agriculture Org.

Hordyk, A., Ono, K., Valencia, S., Loneragan, N., & Prince, J. (2015). A novel length-based empirical estimation method of spawning potential ratio (SPR), and tests of its performance, for small-scale, data-poor fisheries. *ICES Journal of Marine Science*, *72*(1), 217–231.

Hulson, P.-J. F. (2012). *Dealing with uncertainties in integrated age-structured assessment models*. University of Alaska Fairbanks.

Hunter, A., Speirs, D. C., & Heath, M. R. (2016). Investigating trends in the growth of five demersal fish species from the firth of clyde and the wider western shelf of scotland. *Fisheries Research*, *177*, 71–81.

ICES. (2022). *Whiting (Merlangius merlangus) in Division 6.a (West of Scotland)*. `https://doi.org/10.17895/ices.advice.19457426.v1`

ICES. (2023). *Haddock (Melanogrammus aeglefinus) in Subarea 4, Division 6.a, and Subdivision 20 (North Sea, West of Scotland, Skagerrak). Replacing advice provided in 2022*. `https://doi.org/10.17895/ices.advice.22269400.v2`

Kindong, R., Gao, C., Pandong, N. A., Ma, Q., Tian, S., Wu, F., & Sarr, O. (2020). Stock status assessments of five small pelagic species in the atlantic and pacific oceans using the length-based bayesian estimation (LBB) method. *Frontiers in Marine Science*, *7*, 592082.

Kindsvater, H. K., Dulvy, N. K., Horswill, C., Juan-Jordá, M.-J., Mangel, M., & Matthiopoulos, J. (2018). Overcoming the data crisis in biodiversity conservation. *Trends in Ecology & Evolution*, *33*(9), 676–688.

Kraak, S. B., Haase, S., Minto, C., & Santos, J. (2019). The rosa lee phenomenon and its consequences for fisheries advice on changes in fishing mortality or gear selectivity. *ICES Journal of Marine Science*, *76*(7), 2179–2192.

Kumar, R., Cadigan, N. G., Zheng, N., Varkey, D. A., & Morgan, M. J. (2020). A state-space spatial survey-based stock assessment (SSURBA) model to inform spatial variation in relative stock trends. *Canadian Journal of Fisheries and Aquatic Sciences*, *77*(10), 1638–1658.

Kuparinen, A., Mäntyniemi, S., Hutchings, J. A., & Kuikka, S. (2012). Increasing biological realism of fisheries stock assessment: Towards hierarchical bayesian methods. *Environmental Reviews*, *20*(2), 135–151.

Kvamme, C., & Bogstad, B. (2007). The effect of including length structure in yield-per-recruit estimates for northeast arctic cod. *ICES Journal of Marine Science*, *64*(2), 357–368.

Lee, R. M. (1912). An investigation into the methods of growth determination in fishes. *Publ. Circonst. Cons. Int. Explor. Mer.*, *63*, 35.

Lindmark, M., Audzijonyte, A., Blanchard, J. L., & Gårdmark, A. (2022). Temperature impacts on fish physiology and resource abundance lead to faster growth but smaller fish sizes and yields under warming. *Global Change Biology*, *28*(21).

Lorenzen, K. (2016). Toward a new paradigm for growth modeling in fisheries stock assessments: Embracing plasticity and its consequences. *Fisheries Research*, *180*, 4–22.

Maunder, M. N. (2001). *A general framework for integrating the standardization of catch per unit of effort into stock assessment models*. *58*(4), 795–803.

Maunder, M. N., Sibert, J. R., Fonteneau, A., Hampton, J., Kleiber, P., & Harley, S. J. (2006). Interpreting catch per unit effort data to assess the status of individual stocks and communities. *Ices Journal of Marine Science*, *63*(8), 1373–1385.

McAllister, M. K., Pikitch, E. K., Punt, A. E., & Hilborn, R. (1994). A bayesian approach to stock assessment and harvest decisions using the sampling/importance resampling algorithm. *Canadian Journal of Fisheries and Aquatic Sciences*, *51*(12), 2673–2687.

Mesnil, B., Cotter, J., Fryer, R. J., Needle, C. L., & Trenkel, V. M. (2009). A review of fishery-independent assessment models, and initial evaluation based on simulated data. *Aquatic Living Resources*, *22*(2), 207–216.

Monnahan, C. C., Thorson, J. T., & Branch, T. A. (2017). Faster estimation of bayesian models in ecology using hamiltonian monte carlo. *Methods in Ecology and Evolution*, *8*(3), 339–348.

Morales-Bojorquez, E., & Nevarez-Martinez, M. O. (2010). Catch-at-size analysis for dosidicus gigas in the central gulf of california, mexico in 1996–2002. *Fisheries Research*, *106*(2), 214–221.

Morris, D. J., Speirs, D. C., Cameron, A. I., & Heath, M. R. (2014). Global sensitivity analysis of an end-to-end marine ecosystem model of the north sea: Factors affecting the biomass of fish and benthos. *Ecological Modelling*, *273*, 251–263.

Neal, R. M. (2011). New monte carlo methods based on hamiltonian dynamics. *MaxEnt Workshop, Number July*.

Needle, C. (2002). Preliminary analyses of survey indices for whiting in IV and VIId. *Working Document WD2 to the ICES Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak, Copenhagen*.

Nevarez-Martinez, M. O., Morales-Bojórquez, E., Cervantes-Valle, C., Santos-Molina, J. P., & López-Martnez, J. (2010). Population dynamics of the jumbo squid (dosidicus gigas) in the 2002–2008 fishing seasons off guaymas, mexico. *Fisheries Research*, *106*(2), 132–140.

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

Patterson, K. (1998). Assessing fish stocks when catches are misreported: Model, simulation tests, and application to cod, haddock, and whiting in the ICES area. *ICES Journal of Marine Science*, *55*(5), 878–891.

Pauly, D., Morgan, G., et al. (1987). *Length-based methods in fisheries research* (Vol. 13). WorldFish.

Pennino, M. G., Conesa, D., López-Qulez, A., Munoz, F., Fernández, A., & Bellido, J. M. (2016). Fishery-dependent and-independent data lead to consistent estimations of essential habitats. *ICES Journal of Marine Science*, *73*(9), 2302–2310.

Pope, J. G., Macdonald, D. S., Daan, N., Reynolds, J. D., & Jennings, S. (2000). Gauging the impact of fishing mortality on non-target species. *ICES Journal of Marine Science*, *57*(3), 689–696.

Punt, A. E., & Butterworth, D. S. (2000). Why do bayesian and maximum likelihood assessments of the bering-chukchi-beaufort seas stock of bowhead whales differ? *Journal of Cetacean Research and Management*, *2*(2), 125–133.

Punt, A. E., & Hilborn, R. (1997). Fisheries stock assessment and decision analysis: The bayesian approach. *Reviews in Fish Biology and Fisheries*, *7*, 35–63.

Punt, A. E., Huang, T., & Maunder, M. N. (2013). Review of integrated size-structured models for stock assessment of hard-to-age crustacean and mollusc species. *ICES Journal of Marine Science*, *70*(1), 16–33.

Punt, A. E., Kennedy, R. B., & Frusher, S. D. (1997). Estimating the size-transition matrix for tasmanian rock lobster, jasus edwardsii. *Marine and Freshwater Research*, *48*(8), 981–992.

Restrepo, V. R., Hoenig, J., Powers, J. E., Baird, J. W., & Turner, S. C. (1992). A simple simulation approach to risk and cost analysis, with applications to swordfish and cod fisheries. *Fishery Bulletin*, *90*(4), 736–748.

Ricard, D., Minto, C., Jensen, O. P., & Baum, J. K. (2012). Examining the knowledge base and status of commercially exploited marine species with the RAM legacy stock assessment database. *Fish and Fisheries*, *13*(4), 380–398.

Ricker, W. E. (1975). *Computation and interpretation of biological statistics of fish populations*. Department of the Environment, Fisheries; Marine Service.

Rose, G. A. (1997). Points of view: The trouble with fisheries science! *Reviews in*

Fish Biology and Fisheries, *7*(3), 365–370. https://doi.org/10.1023/A:1018495929784

Rudd, M. B., Cope, J. M., Wetzel, C. R., & Hastie, J. (2021). Catch and length models in the stock synthesis framework: Expanded application to data-moderate stocks. *Frontiers in Marine Science*, *8*, 663554.

Rudd, M. B., & Thorson, J. T. (2018). Accounting for variable recruitment and fishing mortality in length-based stock assessments for data-limited fisheries. *Canadian Journal of Fisheries and Aquatic Sciences*, *75*(7), 1019–1035.

Sainsbury, K. (1982). Population dynamics and fishery management of the paua, haliotis iris: II. Dynamics and management as examined using a size class population model. *New Zealand Journal of Marine and Freshwater Research*, *16*(2), 163–173.

Sampson, D. B., & Scott, R. D. (2012). An exploration of the shapes and stability of population–selection curves. *Fish and Fisheries*, *13*(1), 89–104.

Scott, W. B. (1988). Atlantic fishes of canada. *Can. Bull. Fish. Aqua. Sci.*, *218*, 1–731.

Spiegelhalter, D., Thomas, A., Best, N., & Gilks, W. (1996). BUGS 0.5: Bayesian inference using gibbs sampling manual (version ii). *MRC Biostatistics Unit, Institute of Public Health, Cambridge, UK*, 1–59.

Sullivan, P. J., Lai, H.-L., & Gallucci, V. F. (1990). A catch-at-length analysis that incorporates a stochastic model of growth. *Canadian Journal of Fisheries and Aquatic Sciences*, *47*(1), 184–198.

Tanaka, E. (1997). A model of catchability of developing fishery. *Fisheries Science*, *63*(4), 496–502.

Thorson, J. T., & Cope, J. M. (2017). Uniform, uninformed or misinformed?: The lingering challenge of minimally informative priors in data-limited bayesian stock assessments. *Fisheries Research*, *194*, 164–172.

Thorson, J. T., Johnson, K. F., Methot, R. D., & Taylor, I. G. (2017). Model-based estimates of effective sample size in stock assessment models using the dirichlet-multinomial distribution. *Fisheries Research*, *193*, 84–93.

Thorson, J. T., Miller, T. J., & Stock, B. C. (n.d.). The multivariate-tweedie: A self-weighting likelihood for age and length composition data arising from hierarchical sampling designs. *ICES Journal of Marine Science*, *2022*, fsac159.

Wu, J., Dhingra, R., Gambhir, M., & Remais, J. V. (2013). Sensitivity analysis of infectious disease models: Methods, advances and their application. *Journal of The Royal Society Interface*, *10*(86), 20121018.