Aqua notes 2025:4

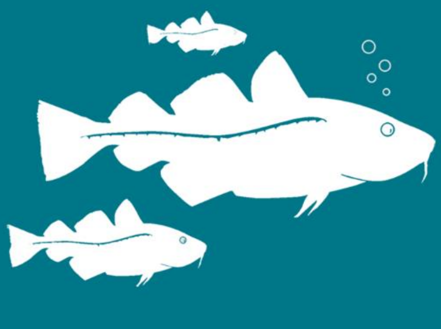
Benchmark of European Lobster (*Homarus gammarus*) in Swedish areas of Skagerrak, Kattegat and Öresund

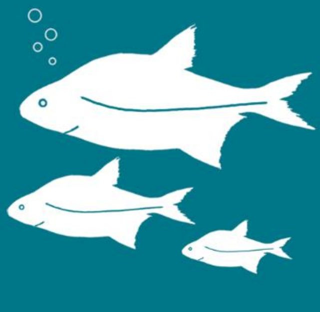
– Stock Annex

Andreas Sundelöf, Massimiliano Cardinale, Hege Sande, Emmelie

Hammenstig-Åström, Henrik Pärn

Sveriges lantbruksuniversitet, SLU
Institutionen för akvatiska resurser





Benchmark of European Lobster (*Homarus gammarus*) in Swedish areas of Skagerrak, Kattegat and Öresund – Stock Annex

*Benchmark of European Lobster (*Homarus gammarus*) in Swedish areas of Skagerrak, Kattegat and Öresund – Stock Annex*

Andreas Sundelöf, https://orcid.org/0000-0001-8577-4379, Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser,

Massimilliano Cardinale, https://orcid.org/0000-0003-1870-38, Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser,

Hege Sande, https://orcid.org/0000-0002-4568-6558, Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser,

Emmelie Hammenstig-Åström, https://orcid.org/0000-0003-2416-7879, Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser,

Henrik Pärn, https://orcid.org/0000-0001-7745-9950, Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser,

Rapportens innehåll har granskats av:

Christopher Griffiths, Sveriges lantbruksuniversitet (SLU), Institutionen för akvatiska resurser
David Gilljam, Sveriges lantbruksuniversitet (SLU), Institutionen för akvatiska resurser
Tonje Knutsen Sørdalen, Universitetet i Agder, Havforskningsinstituttet Flödevigen, Norge

Finansiär: Havs- och vattenmyndigheten, Kunskapsuppbyggnad Fritidsfiske (Dnr 2024-001355, SLU-ID: SLU.aqua.2024.4.2-90), Förvaltningsmål nationellt förvaltade arter (Dnr 2020-23, SLU-ID: SLU.aqua.2023.4.1-197), Bestånds- och ekosystemanalys nationellt reglerade arter (Dnr 2024-002187, SLU-ID: SLU.aqua.2024.4.2-312)

Rekommenderad citering:	Sundelöf, A., Cardinale, M., Sande, H., Hammenstig-Åström, E., Pärn, H. (2025). Benchmark of European Lobster (Homarus gammarus) in Swedish areas of Skagerrak, Kattegat and Öresund – Stock Annex. Aqua notes 2025:4. Lysekil: Institutionen för akvatiska resurser. https://doi.org/10.54612/a.4l1lrggjfs
Publikationsansvarig:	Sara Bergek, Sveriges lantbruksuniversitet (SLU), Institutionen för akvatiska resurser
Redaktör:	Stefan Larsson, Sveriges lantbruksuniversitet (SLU), Institutionen för akvatiska resurser
Utgivare:	Sveriges lantbruksuniversitet, Institutionen för akvatiska resurser
Utgivningsår:	2025
Utgivningsort:	Uppsala
Illustration framsida:	torsk (t.v.): Fredrik Saarkoppel; braxen (t.h.): SLU
Upphovsrätt:	Alla bilder används med upphovspersonens tillstånd.
Serietitel:	Aqua notes
Delnummer i serien:	2025:4
ISBN (elektronisk version):	978-91-8046-591-5
DOI:	https://doi.org/10.54612/a.4l1lrggjfs

Nyckelord: Lobster, Homarus gammarus, assessment, benchmark, stock annex, Stock Synthesis, ensemble, stock status

Sammanfattning

Den här rapporten sammanfattar processen av genomförandet av en riktmärkning för bedömning av europeisk hummer i Svenska Skagerrak, Kattegatt och Öresund. De olika ingående delarna, fångstdata, index och livshistoriedata, som statusbedömningen är avhängig beskrivs sammanfattande i rapporten och i detaljerad form i bifogade appendix. Vidare sammanfattar rapporten modellstrukturen och de känslighetsanalyser som gjorts för att tillslut generera en ensemblemodell för statusbedömningen av hummerbeståndet. Jämfört med tidigare modellverktyg är den nuvarande bedömningen mer optimistisk. Den beståndsanalysmodell som presenteras här bedöms vara en förbättring jämfört med tidigare modeller. Det är på grund av utvecklingen av själva modellverktyget, förbättrat dataunderlag och kunskap om rumslig utbredning och storleksstruktur i beståndet. Beståndet av hummer på svenska västkusten bedöms just nu som på hållbara biologiska nivåer. Efter en period av för stort fiske och liten biomassa har sentida förvaltningsåtgärder sannolikt lyckats begränsa fisket och få beståndets status att förbättras. Under rådande fisketryck kan beståndet utvecklas positivt, men hur framtida fisketryck kan se ut är under rådande förvaltning, utan en begränsning i totalfångst, omöjligt att veta.

Summary

This report summarizes the process of conducting a benchmark for the assessment of European lobster in the Swedish coastal areas of the Skagerrak, Kattegat and Öresund. Catch data, survey indices, commercial catch per unit of effort and life history data, on which the assessment is based on, are described in summary in the report and in detailed form in the attached appendices. Furthermore, the report summarizes the model structure and the sensitivity analyses done to generate an ensemble model that can be used to estimate the stock status of the lobster stock and provide advice. The current assessment is considered an improvement compared to previous modelling. This is due to advances in the modelling tools used, as well as improved data and knowledge on spatial distribution and size composition. The lobster stock on the Swedish west coast is currently assessed as being around sustainable biological levels. After a period of excessive fishing and low biomass, recent management measures have likely succeeded in limiting fishing and improving the status of the stock. Under the current fishing pressure, the stock may develop positively, but what future fishing pressure may look like under current management, without a limitation in total catch, is not possible to predict.

Contents

1. Benchmark process, overview

This Stock annex is the result of the benchmark process for the European lobster (*Homarus gammarus*) stock in the Swedish coastal areas of the Kattegat, Skagerrak and the Sound (ICES subdivisions 20-21 and 23) conducted during 2024. The aim of a benchmark is to agree on a way to perform stock assessment by scrutinizing data and modelling tools. This is usually performed by presenting and comparing data, models and/or management targets. As expert in data collection and stock assessment, the Swedish University of Agricultural Sciences, department of Aquatic resources (SLU Aqua) led this process.

A benchmark framework was formulated to provide information on the development of data collection, data management, assessment model formulation and assessment model evaluation and to decide on a way forward for assessing the stock status. To include a wider perspective on stock biology and utilization of many different data sources, a broad participation of stakeholders is preferred in a benchmark process. Thus, representatives from management bodies, commercial fishing fleets, industry and NGOs (e.g., representing recreational fishing) were invited to actively participate in the meetings. Also, an international reviewer was invited to assist in discussions on biology, assumptions and decisions on how to treat included data and model settings.

Prioritized issues for the assessment were identified during 2022-2023, including e.g. data needs, parameters and model settings, all of which needed to be scrutinized. During 2023, a benchmark process was supported by the Swedish Agency of Marine and Water Management (SWaM), and a meeting was scheduled for the first half of 2024. The original plan was to have one meeting in June 2024 to address all the above aspects and to agree on a model for stock status. However, additional time was needed to standardize indices, and the meeting was adjourned and resumed in October 2024 to finalize the model selection and basis for stock status updates and to provide advice.

Data analyses were performed during spring 2024. An invitation to the international reviewer was sent and accepted during April 2024. Invitations to stakeholders were also sent on 22nd May, 4 weeks prior to the planned meeting. The initial meeting was started on the 17th of June. During the meeting, all data were reviewed, but further data preparations were deemed necessary, and the meeting was adjourned for 18th of June. The meeting was reconvened for model review on the 4th of October. More than 15 people from SLU Aqua, SWaM, the County administrations of Västra Götaland and Halland (Lst VG and Lst Halland) and the Swedish Fishermen Producer Organization (SFPO) attended the benchmark process supported also by the scientific reviewer from University of Agder and Institute of Marine Research in Norway (UiA/HI).

The October meeting was provided with a reference model (a starting point for model assessment and evaluation) and a set of alternative models, each with a different scenario, which were later combined into an ensemble framework for assessment purposes. This model framework was adopted and will serve as the basis for stock status updates from 2025 and onwards. The full details of the assessment and work done to support it are listed in this report. There is also an issue list which details any inconsistencies and needs for further work and will be managed by SLU Aqua until a next benchmark.

2. Background

2.1 Stock definition

The European lobster (*Homarus gammarus*) stock in the Swedish territory of ICES subdivisions 20-21 and 23 is defined as the lobster population along the Swedish west coast. There is no significant genetic differentiation within the Skagerrak, and only weak differentiation within the North Sea (Ellis et al., 2017; Jenkins et al., 2019). Weak genetic differentiation is assumed also for the Swedish Kattegat and the Sound. European lobster is treated as a national stock with Swedish jurisdiction over the Swedish territorial waters inside the trawl border. Overall, the assessed stock includes the Swedish areas of the Sound, Kattegat and Skagerrak. The Danish and Norwegian areas are not considered.

2.2 Spawning and distribution

Although European lobster has a large distribution range (Mediterranean to Northern Norway), spawning and larval distribution occurs on a rather limited scale (Oresland & Ulmestrand, 2013). The pelagic larval stage is limited to only a few weeks of drifting and genetic differentiation is weak in the North Sea area (Ellis et al., 2017; Jenkins et al., 2019). Dispersal by post larval migration is thought to be very limited, and adult lobsters are relatively stationary and occupy small home ranges (Moland et al., 2011).

European lobster has internal fertilization and a brooding time of 9-10 months, when females, after excretion, carry the fertilized eggs under the abdomen. Eggs hatch into a pelagic larval stage with 4 molts before they settle into a bottom dwelling life. Average size at sexual maturity is 78 mm carapace length (L_{50} of females) when the female is around 5-6 years old (Sundelof et al., 2015; Ulmestrand, 2003).

2.3 Factors influencing lobster population development

European lobster is a long-lived species, and although there is currently no precise method of aging lobsters, a max age of 25+ years is suggested based on tagging experiments and anecdotal information suggests that large individuals might be older than that (Fairfield et al., 2021). It grows incrementally by molting its exoskeleton, a process during which they are very vulnerable to predation. Small juvenile lobsters are also likely to be very sensitive to predation by large demersal fish species and other crustaceans. Despite this, the European lobster is thought to have very few natural enemies once it grows to sexual maturity or larger.

Natural mortality decreases dramatically with size and is for larger sizes of lobsters counteracted by being targeted by the fishery that selects individuals larger than the minimum size of landing (MLS). Fishing mortality may be large and is influenced by the number of pots in the fishery, size regulations in the fishery, and the length of the fishing season.

2.3.1 Commercial and recreational fisheries

Lobster fishing has a long history in Sweden (Hasslöf, 1949), with the fishery dating back to at least the 17th century when the Dutch developed a fishery with rudimentary pots for the export market. Around 1730 the earliest demands on regulations were voiced for a summer closure, and in the 1780's minimum landing sizes were suggested. These regulations were not implemented until 1830 and 1879, respectively. Since then, several changes to the regulations such as season closures and a MLS were made.

Until 1994 the fishery was mainly a sustenance fishery with unregulated sales. Fishers were allowed 40 pots each and another 35 pots for every additional person in the boat. In 1994, the lobster fishery was formally separated into a licensed commercial fleet, permitted to fish with 50 pots, and a recreational fleet allowed 14 pots per person. In 2017, the regulation was reformed, and the number of pots were limited to 40 for commercial actors and 6 for recreational fishing.

In 1985, a moratorium on berried females was launched, enforcing the immediate return of any sized female with external eggs to the sea. In addition, the MLS was changed from total length (TL) to carapace length (CL) (22 cm TL corresponding to 80 mm CL). In 1996, escape gaps for the filtering of undersized individuals were introduced to each chamber of pots (least diameter 54 mm). Since 2003, pots have been the only permitted gears for fishing of lobster and each chamber of the pot is regulated since 2018 to have two openings of a minimum diameter of 60 mm.

As there is no mandatory catch reporting for the recreational fleet, the total catch has never been reliably censused. However, in 2007 and 2019, gear counts and interviews on catch rate were performed. The recreational catches were estimated to be 75% and 50% of the total catch in 2007 and 2019, respectively. The importance of recreational fishery to the harvest of lobsters and the worry of reduced stock status warranted a change in regulations between recreational and commercial fishers in 2017.

The revision of the regulation in 2017 confirmed the previous opening date for the fishing season to the first Monday after 20th September (Monday of week 39) but set the closing date on the 1st December for the recreational fishers and 1st January for commercial fishers. In addition to season length and the restrictions in number of pots per fisher, the MLS was increased to 90 mm CL. In a follow up addition in 2022, the date of last live keeping (in holding creels or tanks for storing live lobsters) was changed, and the use of an anti-ghost-fishing device (rotting thread) was regulated. All current regulations are found in (FIFS, 2004)

2.4 Ecosystem aspects

2.4.1 Effects of temperature on biological parameters

Crustacean biology is strongly temperature dependent. European lobsters are no exception, and shifts in temperature are thought to affect several aspects of their biology (Coleman et al., 2021; Goode et al., 2019; Mazur et al., 2022). Although climate related changes in pH and salinity, and the availability of oxygen, may have further implications for lobster larvae and adults, recent studies have focused on temperature.

Strong positive effects of temperature on adult growth rates have been documented for European lobster (Coleman et al., 2021). Furthermore, time to hatching and larval development times were shortened by increased experimental temperatures at least up to 22 °C (Schmalenbach & Franke, 2010), in turn leading to an increased survival through the larval phase by more rapidly growing through the most sensitive stages. What effects such decreased mortality and increased growth rates will have on a harvested stock is not yet predicted.

Although shellfish diseases are not highly prevalent in lobster populations and temperature effects are uncertain (Rowley et al., 2014), diseases have been hypothesized to increase in NTZ although to what extent has not been quantified (Davies et al., 2015). Lack of quantified increases in incidence of shellfish diseases in NTZ is perhaps due to the higher available genetic variability (Le Bris et al., 2018) that can be expected in the more abundant populations in NTZ. Effects of climate on the biology of European lobster was reviewed by (Sundelöf, 2023), and is provided in Appendix I.

2.4.2 Effects of lobster on the ecosystem

Competition between brown crab and lobster is, although only recently documented (Perry et al., 2025), often assumed. Recruitment and survival of juvenile lobster may well be heavily affected by the density of brown crab and other crustacean species. If left unfished however, as they are in NTZs, the density of brown crab is found to be markedly lower than in conventionally fished areas (Oresland et al., 2020). The main reason is assumed to be direct competition (fighting) or competition for food with lobster.

In a large effort to assign the effects of fishing to changes in fish assemblages, scientific fishing inside and outside a Marine Protected Area (MPA) was performed (Perry et al., 2025). Changes in fish assemblages on small spatial scales were not found, however, changes in the abundance of brown crab and lobster were apparent between fished and unfished areas.

In some fisheries with pots, seals are attracted to the smell of bait and if entrances are sufficiently big, small individuals may be captured and drowned. Generally, the pot fishery is very specific to crustaceans with very small bycatches of fish.

2.4.3 Predation from birds and mammals

Studies in NTZs along the Swedish West coast suggest that predation by seals and cormorants on lobsters are negligible. This is because despite large populations of seals and cormorants, the lobster population in the NTZ have increased in recent years (Bergström et al., 2022; Perry et al., 2025).

3. Data

The assessment model for the European lobster stock includes catch data, several indices of abundance, length compositions, and life history parameters (e.g. growth and mortality). The temporal range of the data included in the assessment model is illustrated in Figure 1.

The data sources for abundance indices were either fisheries dependent (data from conventional fishing which depend on variation in fishing pressure due to e.g. new regulations) or fishery independent (not affected by other fishing operations or by changes in management regulations). Six CPUE (Catch Per Unit of Effort) indices exist for five fisheries dependent fleets and one fishery independent fleet (the survey Lobserve).

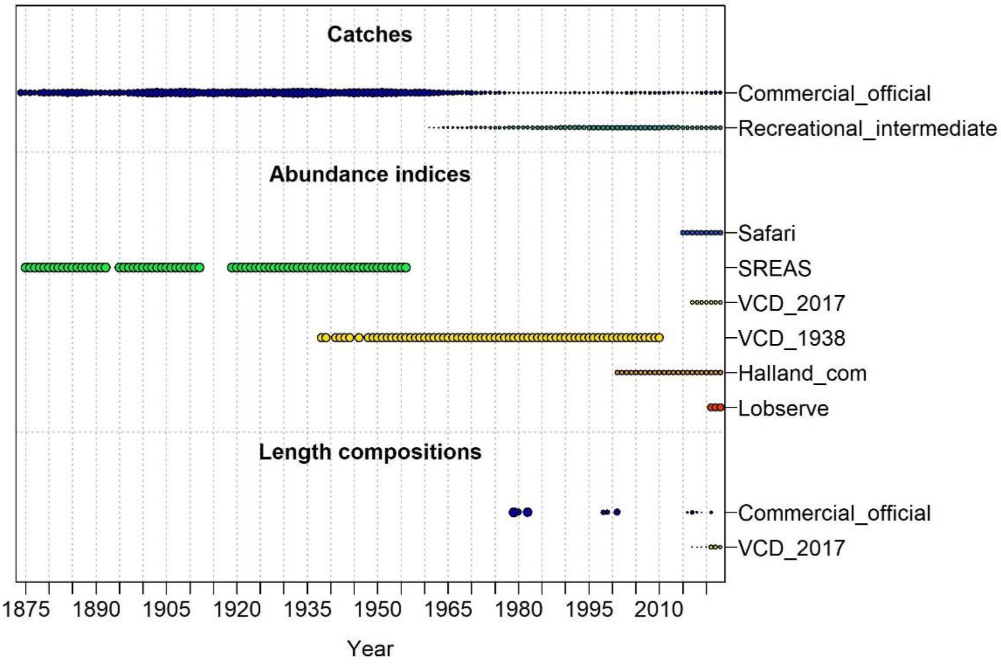


Figure 1. Overview of data on European Lobster stock in ICES subdivisions 20-21 and 23 included in the assessment models. Point size scales with the amount of data that is available.

3.1 Catch

3.1.1 Commercial

Between 1875 and 1956, the Swedish Rural Economic Agricultural Society (SREAS) collected data on the number of fishers, number of pots and number and weight of lobster catch for each year (also used as official statistics on catch by Statistics Sweden).

Since 1978, catch data has been obtained from the sales slips (wholesale receipt) and corrected for by sales on the docks (i.e., "kompletteringstillägg" of landings not sold to wholesale customers). The annual registered landings are published in early June the following year. This is one of the longest known catch series of any marine stock in Europe (Figure 2).

3.1.2 Recreational

In Sweden, recreational catch is not formally registered. Despite attempts to estimate recreational landings from gear counts and interviews, there is no proper census of recreational landings. Instead, catches from the recreational fleet are estimated and the change over time is based on expert judgement and previous studies that have not covered the entire stock area (Ulmestrand & Loo, 2009). Before 1955, all catches from the recreational fishery are assumed to be recorded in the data collected by SREAS. During 1960, the non-recording of some catches is assumed to have started, relating to catches from non-commercial sources (i.e., fish caught for sustenance or recreation). The development of a recreational fleet became important at the same time that the recreational/unregistered part of the landings dominated the total landings (Ulmestrand & Loo, 2009).

Since recreational catches are unreported, the input data has been experimentally tested with different levels of recreational catch - low, intermediate and high (detailed description below). It is formulated to represent recreational catches, but the model handles it as a composite of otherwise unregistered catches. Figure 2 shows registered catches and the assumed additional unregistered catches (defined as Recreational_intermediate in the Reference_run).

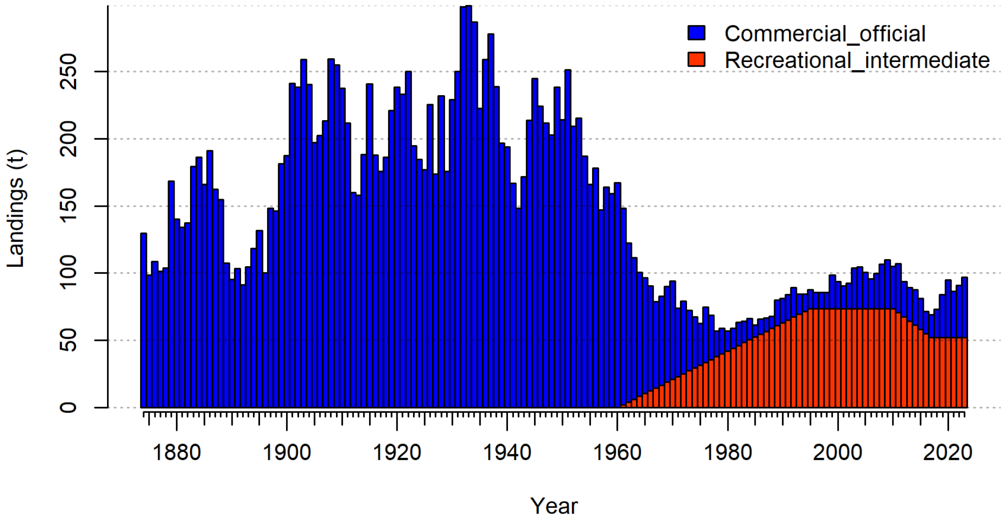


Figure 2. Catch (tonnes) of European lobster stock in ICES subdivisions 20-21 and 23, 1875-2023, in commercial and unreported but estimated recreational (intermediate level) fleets. Data used in the Ry.

3.2 Temporal data selection

Fishing practices tend to change throughout the season. Pots are pulled less frequently later in the season, and catches shift in spatial distribution as recreational fishers have a shorter season, leaving the entire coastal region for commercial fishers from 1st of December.

Information on soak time is very difficult to extract from the journals. However, early in the season pots are pulled a lot more frequently and soak time is assumed to have a lesser effect on catch. Catch rates are also assumed to be impacted by the capture of harvestable individuals which reduces the number of lobsters that are available to the fishery as the season progresses. Catches later in the season may also be over-represented by undersized individuals and berried females that are repeatedly returned to the sea. In combination, these factors led us to assume that for the fisheries dependent indices the first two weeks of the fishery provided the most robust estimate of stock size, and as a result, only the first two weeks of the respective fishery were used in the model. Hence week 39-40 was used for the generic case (used in the SS3 models) and for exploratory purposes weeks 39-41 and 39-44 used for perspective (e.g., Appendix V).

3.3 CPUE

As recreational catches are not formally registered, efforts have been made to study parts of the recreational fleet by voluntary diaries providing CPUE-indices (SREAS, VCD_1938, VCD_2017, Lobserve). Catch journals by sectors of commercial and other licensed fisheries also provide CPUE indices (Tourist, Halland_com). The standardized indices relative to each other are presented in Figure 3.

During the scrutinizing of the data sources and the CPUE-indices, the need for further standardization was recognized during the benchmark. Three indices (Tourist (Safari), VCD_2017 and Halland_com) with supporting fishing operations data (fisher ID, soak information etc.) were updated and differences between nominal CPUE and standardized CPUE are shown in Figure 4. Details on standardizing are given in the respective Appendices (III, IV, V).

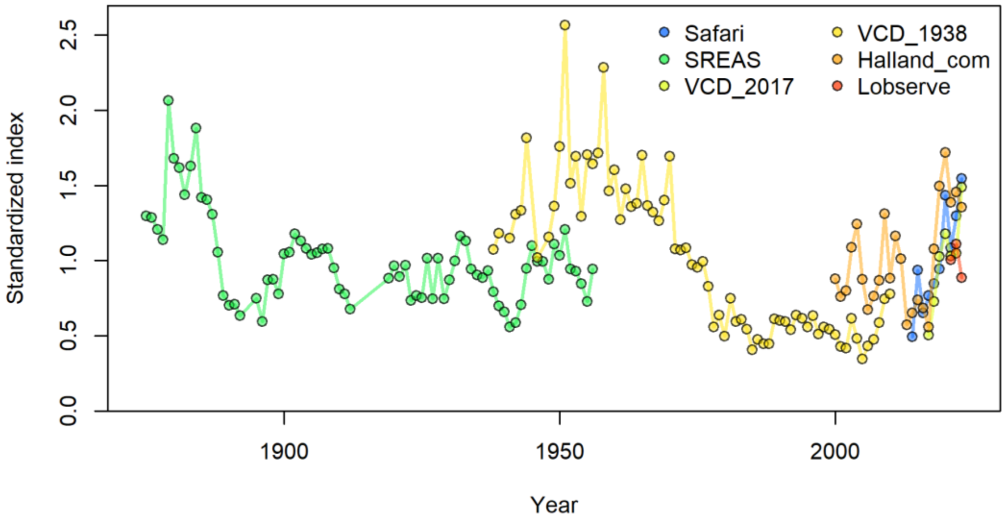


Figure 3. European lobster stock in ICES subdivisions 20-21 and 23. Standardized indices of six different fleets that were used in the assessment models.

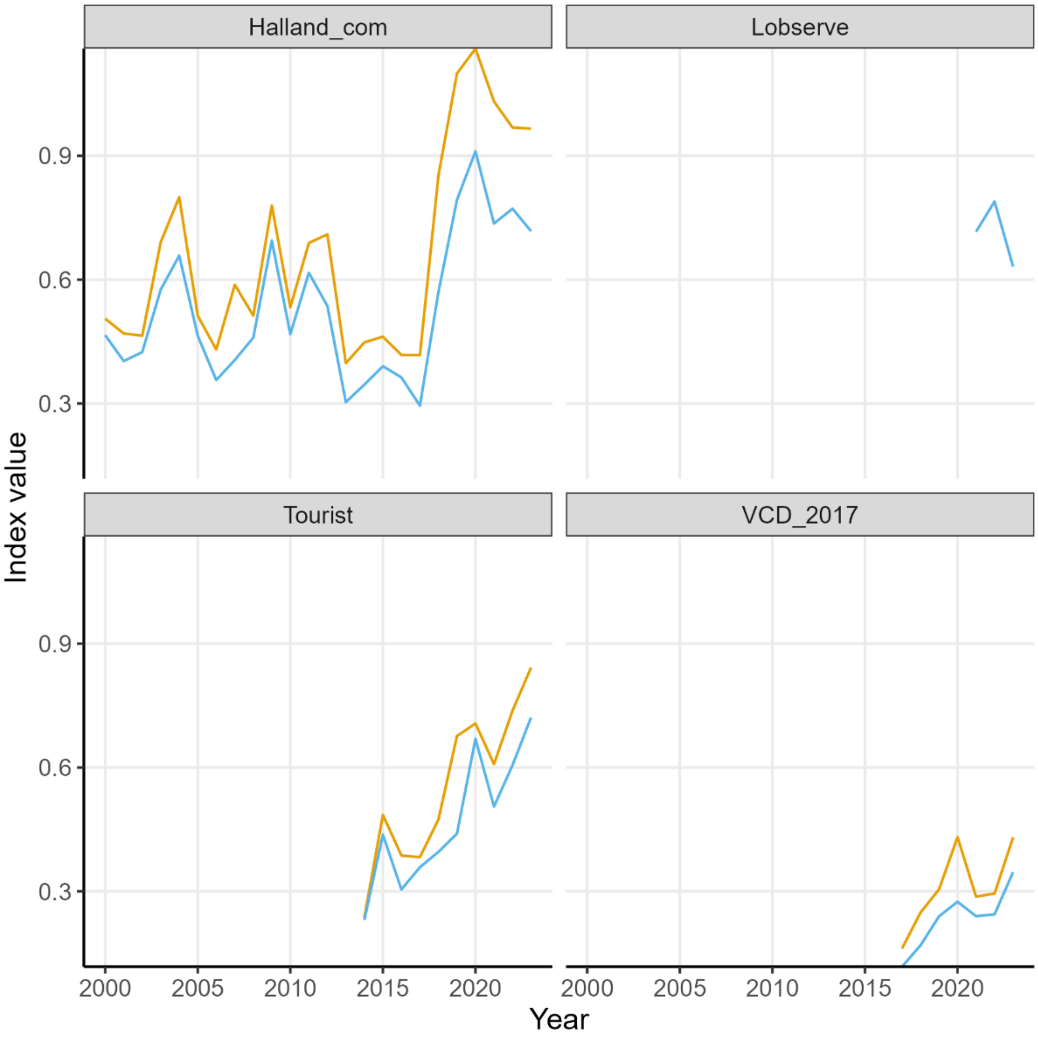


Figure 4. European lobster stock in ICES subdivisions 20-21 and 23. Mean index values, nominal (orange) and standardized (blue) for Halland commercial journals, Tourist fishers and VCD_2017. Lobserve index is only presented with standardized value.

3.3.1 Swedish Rural Economic Agricultural Society (SREAS)

Between 1875 and 1955, the SREAS covered the lobster fishery by census. The number of gears and their catch was recorded per village along the Bohuslän coast. The data were never recorded by actual number of fishing days, but for each season a total number of caught lobsters by the total number of used pots was provided by villagers to the controlling agents. Consequently, a catch per unit effort index can be calculated as the number of landed lobsters divided by the number of used pots. The CPUE was also calculated for each fishing district. Details of standardization are described in Sundelöf et al. (2013) and provided in Appendix II.

3.3.2 Voluntary catch diaries 1938-2010 (VCD_1938)

SLU Aqua-staff had access to data from historical diaries from a number of active lobster fishers along the Bohuslän coast. Fishermen provided catch and effort data from their private fishing operations. Catch per unit effort for each fishing day was calculated and provided a standardized index of abundance for 1938-2010. The participants were assumed to fish predominantly in one area, their "home waters", with a consistent effort and fishing pattern (e.g. type of pots, number of pulls, etc), but with some development of increased efficiency in their catches, a so-called "technical creep". This was included as a linear increase in efficiency of catches during 1970-1980 following a study comparing CPUE in old-style and modern pots (Sundelof et al., 2013). After the change in gear and license regulations in 1994, these fishers were permitted to keep fishing under exemption from the license regulations. These data have been analyzed by fishing district and were published previously (Sundelof et al., 2013) and are provided in Appendix II.

3.3.3 Voluntary catch diaries 2017-2023 (VCD_2017)

VCD_2017 was designed to provide a catch per unit effort index, similar to VCD_1938, but randomized for the entire lobster fishing community. To implement this in the field during lobster fishing season, randomized surveys of lobster pot transects were performed by SLU Aqua. Buoys were counted, and fisher contact information was collected at approximately 5% of the buoys (visit to every 20th buoy). From the collected fisher contact information, 100 were selected to cover the entire area of the coast surveyed. The selected fishers were later interviewed by phone to obtain information on e.g. fishing experience and fishing pattern (number of pots, number of pulls, bait, boat type, etc). The fishers were also asked to participate in data collection on their daily lobster catches by filling in a catch diary. However, more experienced and avid fishers are more likely to participate in the study and submit such catch reports (Thomson, 1991), and they are also less likely to drop out from the study. Together, this creates a bias in the reported catches. This data is therefore not treated as a random subset of the entire fishing community corresponding to an average lobster fisher. Instead, these diaries are assumed to provide a catch index not influenced by changes in effort or participation rates but dominated by experienced fishers with constant fishing habits and therefore comparable effort over time. This produces an index estimate relative to the availability of lobsters to the fishery. Data for VCD_2017 covers 2017-2023 in the benchmark work. Details for VCD_2017 are found in Appendix III.

3.3.4 Tourist charter operators (Safari in SS3 and Tourist elsewhere)

The Swedish Agency for Water and Marine Management (SWaM) issues special permits (and exemptions from the number of gears) for several recreational actors that organize lobster fishing-trips along the Swedish west coast, so-called Tourist fishing. Those fishermen are liable to record their effort and catch in more detail than otherwise necessary. SLU Aqua gets access to data from SWaM, and from this daily effort and catch, a mean catch rate of the first two weeks of the fisheries was calculated giving a catch per unit effort index. This index includes data from 2014-2023 and is called ‘Safari’ in all models runs. Further details are provided in Appendix IV.

3.3.5 Journals for Commercial fishers in Halland (Halland_com)

In the County of Halland, the county board issues special permits (and exemptions from the number of gears) for several commercial actors. Those fishermen are liable to record their effort and catch by fishing day, which is not otherwise necessary by this segment of the commercial fleet. Data on landings and returned berried females is provided. For some years, a few fishermen have also had exemptions for smaller than regulated escape gaps. This made the data more complicated to use. Although an attempt was made to provide catch and landing data irrespective of management rules, this was not successful. Instead, an index of the number of landed lobsters was calculated. This was then combined with data on daily effort to calculate a mean landing rate for the first 2 weeks of the fishery (i.e. an index of landing per unit effort). Data from 2000 to 2023 were available. Further details are provided in Appendix V.

3.3.6 Lobster survey index (Lobserve)

The Lobserve index is based on a research survey performed annually in August before the ordinary lobster fishing season starts. A set of experienced lobster fishers perform a depth stratified catch-measure-release fishery in their specific fishing area. Each fisherman deploys six pots and is liable to pull them at 24-hour intervals at least four times. The pots are set at three different depth strata (6-10 m, 10-20m and >20m), two at each depth. After each pull, the pots are moved to a new set position to minimize the probability of recapturing the same lobsters. The index provides survey quality data on catch rates and size composition. Details are provided in Appendix VI.

3.3.7 Missing data

During the First World War (WWI), the SREAS index has missing values. However, the assessment model can handle data blanks/gaps and make use of whatever data exists in the time series.

3.4 Sizes

Substantial effort has been made to get some representative size samples from both recreational and commercial fisheries. Some incidental size data exist for very early fisheries (1901-1903). However, the documentation of gear selectivity is weak, and data thus deemed unreliable. Sampling of sizes from commercial agents has been made sporadically, and original data sheets have been digitalized in recent years to provide size data for the periods 1979-1982 and 1998-2001. From survey fishing, size composition is available for 2017-2023, with a substantial increase in the number of samples in 2021 with the use of Lobserve data. Some size composition data exist for the Tourist-index for 2016-2021.

Ideally, more size composition data would help inform the assessment model on fishing mortality, age-composition in the stock and recruitment dynamics. Discrepancies in size composition between fishery dependent and fishery independent data sources are notable. Males are on average larger than females in survey data from August but not in size data from fisheries dependent sources later in the year. Large males are effectively filtered from the population during the fishing season.

Size composition data from Lobserve is shown in Figure 5 and from all data sources in Figure 6. Size composition is collated for each data source. “MPA” size composition is from an area protected from fishing and is not included to correspond to a conventional fishery but as a basis for length to weight relationships and von Bertalanffy growth parameters. All available size data are presented in Appendix VII.

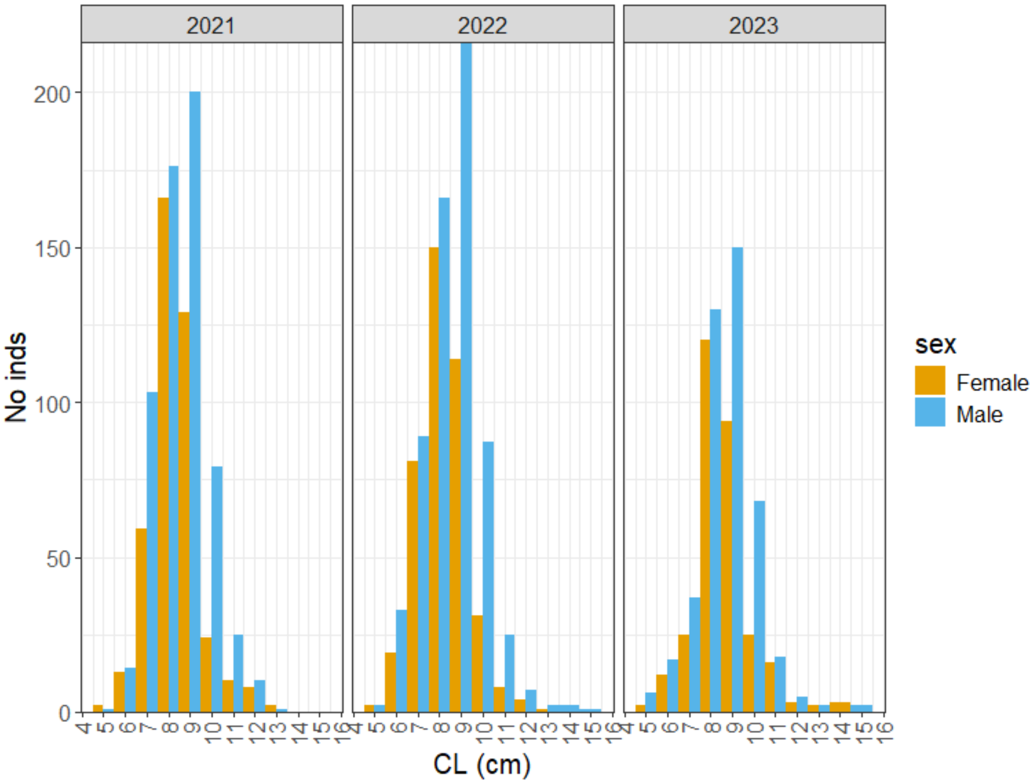


Figure 5. Size composition of European Lobster stock in ICES subdivisions 20-21 and 23. Data from Lobserve projects sampled in August.

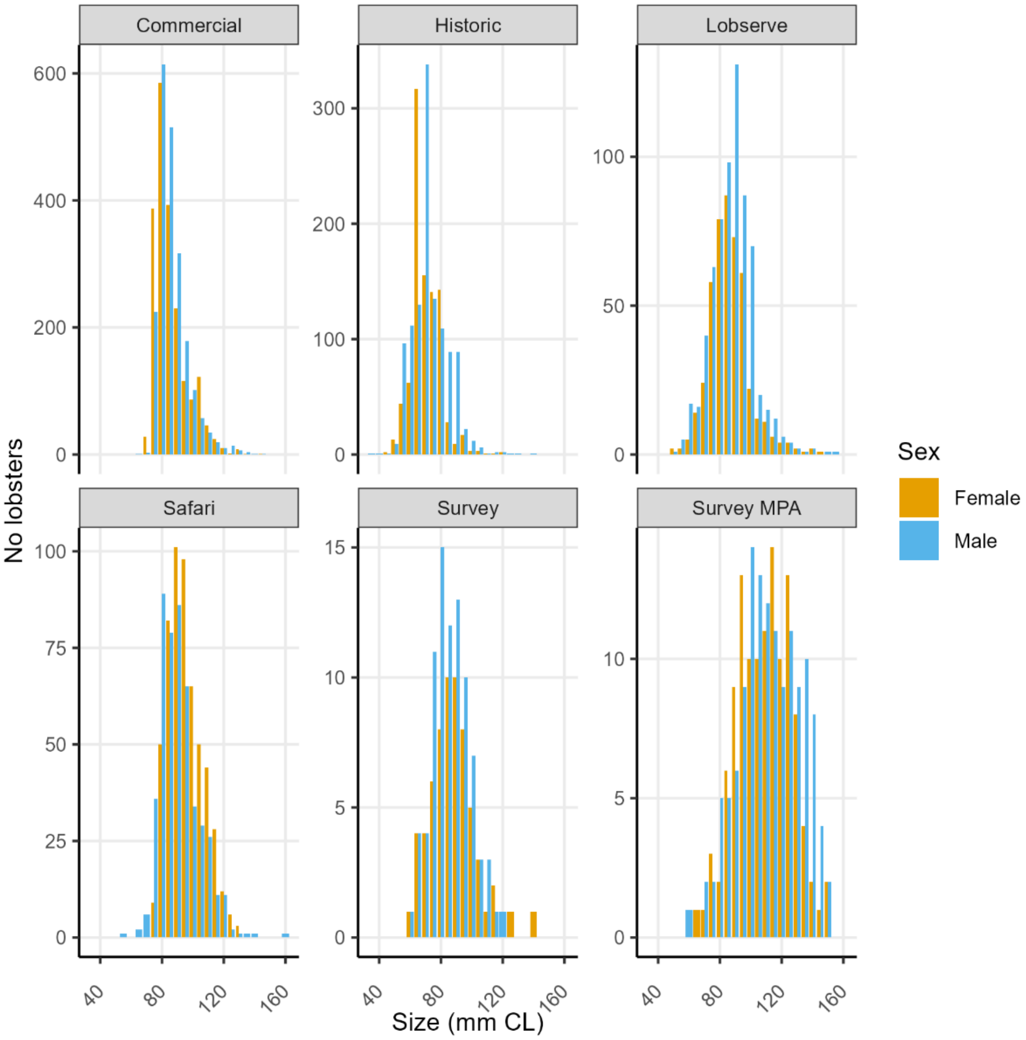


Figure 6. . Size composition of European lobster stock in ICES subdivisions 20-21 and 23, by data source. Historic refers to the period 1901-1903, data not used in the model due to poor documentation.

3.5 Length to Weight conversion

The length to weight relationship was previously calculated using carapace lengths between 50 and 128 mm. This size range was used partly due to the selectivity of the gears and the limited period of sampling. In 2021 and 2022, both standard pots and fish pots were used to sample, measure and weigh individuals in the size range 70-172 mm CL. Total weight depends on sex and whether the individual is missing one or both claws. Standard length to weight relationships by sex use measured individuals with both claws intact.

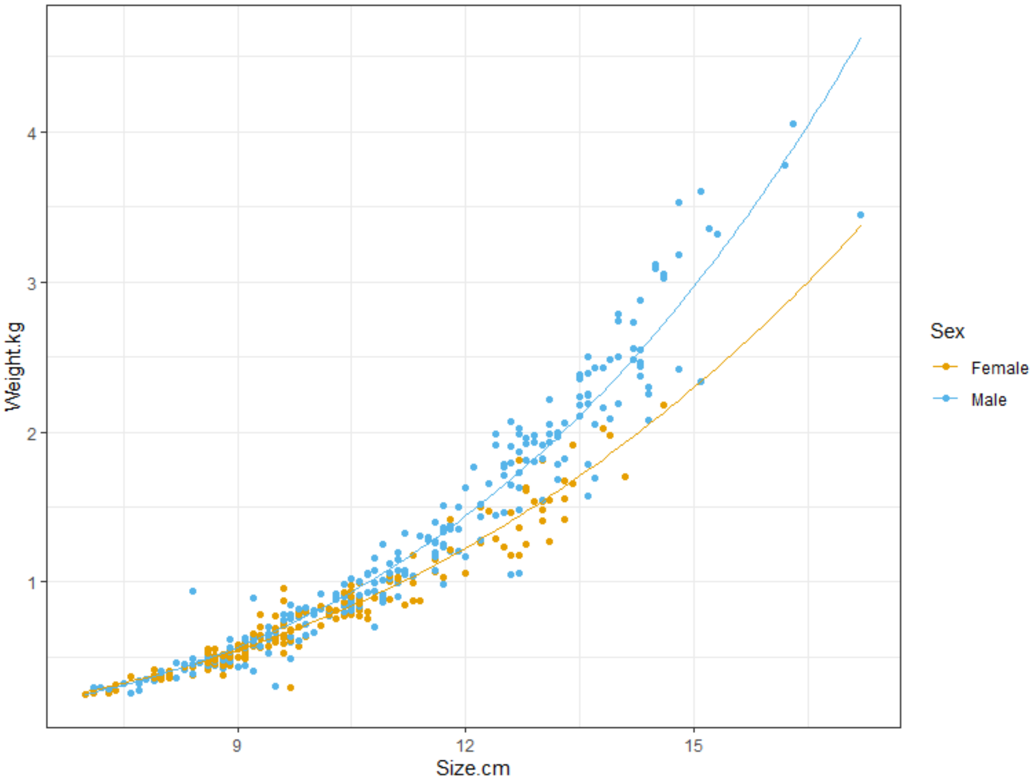


Figure 7. European lobster stock in ICES subdivisions 20-21 and 23. Length (carapace in cm) to weight (in kg) relationship for male and female.

The assessment model was provided with a length to weight relationship expressed in cm CL and kilograms with the following formula

Formula: Weight ~ a * Size^b

and with the following parameters (also shown in Figure 7) by each sex:

	Female	Male
a	0.001165	0.000473
b	2.799602	3.227385

3.6 Discard

Lobster fishing has typically been performed (and since 2003 exclusively) with pots. Inspection of all catch is done during harvesting. For most indices and size compositions, data correspond to catch per unit effort (CPUE) and not Landing per unit effort (LPUE). As all catch has been inspected and is included for the major data components, no separate sampling of discard is warranted. Furthermore, size specific selectivity is used in the model to only harvest individuals above MLS.

3.7 Biological data

3.7.1 Fisheries independent surveying

Mark-recapture-based studies have been performed in the MPA Kåvra since 1989. After a recess in 2010, a survey restarted again in 2017. Survival, fecundity, growth parameters and length to weight relationships were parameterized for modelling purposes as in (Moland et al., 2013; Sundelof et al., 2015). A length-based maturity ogive was fitted using a logistic function (redrawn in (Sundelof et al., 2015)). Survival has been evaluated extensively in (Moland et al., 2013) with mark recapture data from 1994-2007. It has recently been revisited with data from 2017-2023 to verify survival rates, scrutinize the survival of males and females in conventionally fished areas, and to evaluate the effects of a moratorium on the capture of berried females (see Appendix VIII). A von Bertalanffy growth rate (vB) was estimated for each sex (Sundelof et al., 2015), showing typical differences in male and female growth rates (Table 3). Females grow slower than males, particularly after reaching sexual maturity as they start investing in reproduction (L_{50} female; 78 mm CL in size).

3.7.2 Mortality

Sex- and size-dependent mortality rates were estimated from an extensive mark-recapture data set (Moland et al., 2013; Sundelof et al., 2015). Using additional data between 2017 and 2023 did not result in a significantly different sex dependent mortality rate (Appendix VIII). Thus, mortality values from (Moland et al., 2013) were used for the assessment model. See Appendix VIII.

3.7.3 Spawning stock biomass

No independent data available.

3.7.4 Recruitment

No independent data available.

4. Assessment model

The assessment of European Lobster stock in ICES subdivisions 20-21 and 23 was conducted using the Stock Synthesis (SS) model (Methot & Wetzel, 2013; Methot et al., 2024). Stock Synthesis is programmed in the ADMB C++ software and searches for the set of parameter values that maximizes the goodness-of-fit, then calculates the variance of these parameters using inverse Hessian and MCMC methods. The assessment was conducted using the 3.30.22 version of the Stock Synthesis software under the Windows platform. For lobster in 3a, the most feasible structure was a two-sex, length-based model with a time step of one year. A range of plausible scenarios (unreported landings, steepness in stock-recruitment relationships and time varying selectivity, Table 1) were explored using an ensemble modelling approach, which better encapsulates the variability and uncertainty exploring contrasting but plausible ranges of parameter values over choosing a single set of fixed values (Dietterich, 2000; Knutti et al., 2010).

The fitting of the model was satisfactory, with the aggregated length compositions well reconstructed. The model generally showed decent retrospective patterns, weaker predictive skill, but with diagnostic results within the accepted limits used by the ICES framework for international stock assessment models. For an overview of model diagnostics results, see section ‘Model diagnostics’ below. For full details of the evaluation, generality and robustness of the assessment model and the ensemble approach, see the appendices:

Appendix X - Reference model - justifying the set up and structuring of the lobster model in the framework Stock Synthesis.

Appendix XI – Diagnostics - comparing output and diagnostics of several alternative models illustrating the dimensions of uncertainty.

4.1 General model description

A Reference model was formulated based on the best available knowledge of the lobster fishery and its biology. It is described in detail in Appendix X. Such a reference model should be considered the model of choice until another model outcompetes it based on model performance diagnostics. It also provides a metric stick against which other model formulations can be compared to.

Several models were formulated to better represent our uncertainty in parameter estimates or unavailable data. This is referred to as considering multiple dimensions of uncertainty. In this case, we were interested in investigating the effect of unreported catch and the steepness of the stock-recruitment relationship on the fitting and performance of the model.

In particular, we expected the model to react to changes in unreported catch levels and the steepness of the stock recruitment relationship. The model was provided with a long timeseries of catch data within which the most recent part of the time series is underreported largely due to recreational fisheries that are not reported. The potential effect of these underreported catches needed to be tested to understand the models behavior and how they impact estimates of stock status. Steepness, the sensitivity of a stock recruitment function to reductions in biomass, is known to be a parameter that is difficult to parameterize and can have large effects on model output. Thus, steepness was also included in the dimensions of uncertainty.

We did not explore the full grid of uncertainty combinations as some combinations of parameter values might not make ecological sense. Instead, from the reference run we either modified the catch (low -25%, or high + 25%) or the steepness (0.65, 0.90) to investigate directional changes of behavior in model output (run 1-4) and to illustrate variability caused by the uncertainty. As supporting tests, we also tested for time varying selectivity (from 2018) following changes in regulations in 2017 (run 5). Unreported catches are believed to be underestimated, thus most likely being larger than those provided in the reference run. The benchmark group therefore agreed to test the combined effect of higher catches, and low steepness (run 6).

An extra set of models were also tested within SS3 (Table 2) as an add-on to the dimensions of uncertainty. This set of models did not add quantitatively different trends and were not used in the uncertainty grid of the ensemble model but is reported in the Diagnostics section.

Table 1. Dimensions of uncertainty. Model configurations to explore effects of parameter settings.

Model name	**Description**	**Ecological/biological relevance**
Reference_run	Average catches, steepness 0.80	Assumed reference run formulated from previous experience
Run1	Reference run, low catches - 25%	Assumed reduced level of unreported catches, reduced productivity
Run2	Reference run, high catches + 25%	Assumed elevated level of unreported catches, increased productivity
Run3	Reference run, low steepness 0.65	Recruitment sensitive to overfishing
Run4	Reference run, high steepness 0.90	Recruitment insensitive to overfishing
Run5	Reference run, time varying selectivity	Selectivity of the commercial fleet since 2018, using time-blocks to separate selectivity patterns
Run6	Run 2 but with low steepness	Run to inform on a model that would be sensitive to overfishing and experience elevated harvest

Table 2. Set of additional standard model configurations suggested by SS3 to be run for diagnostic purposes. Reference_run model set up was used for modifications

Model name	**Description**	**Ecological/biological relevance**
sigmaR06	Variability around stock recruitment relationship set to 0.6. Instead of 0.5	Model more flexible to deviations from average recruitment
High catches	Assumed elevated level of unreported catches	Increased catch must be matched by increased recruitment or growth and survival to mitigate an increase in productivity of the stock
Recdev2	The deviations do not have an explicit constraint to sum to zero, although they still should end up having close to a zero-sum. Option (2) instead of option (1).	Recruitment deviations allow for larger fluctuations and may result in a more positive intrinsic growth rate

TVsel	Time-varying selectivity of the commercial and recreational fleets, estimated within the model for each year	Selectivity fitted by year. Making the model more influenced by size composition.
M-estimated	Natural mortality estimated within the model	Tagging work not included as an independent estimation of mortality. Test of how the tagging data performed for estimating M
ExtraSd_estimated	Additional standard error is estimated within the model for survey indices	Model more influenced by other factors than indices (catch and life-history parameters)

4.2 Model settings

Full model formulation is provided in Appendix X. Here follows a summary.

The benchmark model is a one-area yearly model where the population is comprised of 25+ age-classes with two sexes (males and females are considered as separated). The model is a length-based model where the numbers at length in the fisheries and survey data are converted into ages using the von Bertalanffy growth function. The population was modelled as sex-structured with sex-specific parameterization for somatic growth and M-at-age. Stock fecundity was assumed to be proportional to female spawning stock biomass. The model starts in 1875 and includes 8 fleets: 1 commercial fisheries, 1 recreational fishery and 6 surveys. LFDs are available for 2 of the fleets.

4.2.1 Key settings

- Maximum age in the population set to 25 years (population plus group)
- Growth parameters separated for females and males using the von Bertalanffy function
- Fixed CV young and old individuals at 0.15 and 0.10 respectively
- Fixed age varying, time unvarying M for females and males separately
- Estimated selectivity for the commercial fleet and VCD_2017 survey
- Early recruitment era starts in 1875
- Extra standard deviation was assumed for several surveys

4.2.2 Model specifications

- For the reference model, the sex specific growth is fixed for both sexes using Von Bertalanffy model. L_{atAmin} and L_{atAmax} were specified as 0.5 and 25 years, respectively. The CVs for L_{atAmin} were set to 0.15 and for L_{atAmax} to 0.1.
- Female maturity was assumed to have the form of a logistic ogive with a length at 50% maturity (L_{m50}) being attained 7.8 cm and a slope of -0.971 cm (Figure 7). L_{m50} corresponds approximately to a female of age-5.
- Sex-specific natural mortality at age (M_a) was set for age 0, 1, 4, 5, 10 and 20 and were based on tagging carried out in the Kåvra marine reserve
- Nominal spawning and settling time were set to 1st January. The expected mean recruitment was assumed to follow a Ricker stock recruitment relationship. For the base-case a steepness of $h = 0.8$ was assumed.
- Recruitment deviations were estimated for 2010-2017 as main recruitment deviations and for the preceding years 1875-2009 as early recruitment deviations. Recruitment deviations were assumed to have a penalty of 0.5 on the standard deviation (sigmaR).
- All fleets were assumed to have a double-normal (dome-shaped) selectivity (option 24).
- A time-varying selectivity was enabled for the commercial fleet (Figure 9).
- Fishing mortality was modeled using a fleet-specific hybrid F method (Option 4), which is consistent with best practice. Option five was selected for the fishing mortality (F) report basis; this option corresponds to the simple unweighted average of the F of the age classes chosen to represent the F_{bar} (ages 8–13).

Table 3 lists all inserted parameters.

Table 3. Life-history parameters as input into SS3. Negative phase indicates that these parameters are fixed and thus not estimated within the model. Min, Max and Bounds is SS3-language used in the estimation process when active.

Label	Value	Phase	Min	Max	Bounds
NatM_break_1_Fem_GP_1	1.11	-3	0.15	3	(0.15, 3)
NatM_break_2_Fem_GP_1	0.747	-3	0.15	1.4	(0.15, 1.4)
NatM_break_3_Fem_GP_1	0.356	-3	0.15	0.4	(0.15, 0.4)
NatM_break_4_Fem_GP_1	0.343	-3	0.15	0.4	(0.15, 0.4)
NatM_break_5_Fem_GP_1	0.305	-3	0.15	0.4	(0.15, 0.4)
NatM_break_6_Fem_GP_1	0.247	-3	0.15	0.4	(0.15, 0.4)
L_at_Amin_Fem_GP_1	1.7	-3	1	15	(1, 15)
L_at_Amax_Fem_GP_1	15.2	-3	10	20	(10, 20)
VonBert_K_Fem_GP_1	0.089	-3	0.05	0.22	(0.05, 0.22)
CV_young_Fem_GP_1	0.15	-3	0.05	0.45	(0.05, 0.45)
CV_old_Fem_GP_1	0.1	-3	0.03	0.45	(0.03, 0.45)
Wtlen_1_Fem_GP_1	0.00116	-99	-3	3	(-3, 3)
Wtlen_2_Fem_GP_1	2.8	-99	-3	4	(-3, 4)
Mat50%_Fem_GP_1	7.8	-3	5	20	(5, 20)
Mat_slope_Fem_GP_1	-0.97	-99	-1	3	(-1, 3)
Eggs/kg_inter_Fem_GP_1	1	-99	-3	3	(-3, 3)
Eggs/kg_slope_wt_Fem_GP_1	0	-99	-3	3	(-3, 3)
NatM_break_1_Mal_GP_1	1.11	-3	0	3	(0, 3)
NatM_break_2_Mal_GP_1	0.747	-3	0	1.5	(0, 1.5)
NatM_break_3_Mal_GP_1	0.39	-3	0	0.5	(0, 0.5)
NatM_break_4_Mal_GP_1	0.363	-3	0	0.5	(0, 0.5)
NatM_break_5_Mal_GP_1	0.286	-3	0	0.5	(0, 0.5)
NatM_break_6_Mal_GP_1	0.239	-3	0	0.5	(0, 0.5)
L_at_Amin_Mal_GP_1	1.7	-3	1	15	(1, 15)
L_at_Amax_Mal_GP_1	17.3	-3	10	20	(10, 20)
VonBert_K_Mal_GP_1	0.139	-3	0.08	0.25	(0.08, 0.25)
CV_young_Mal_GP_1	0.15	-3	0.05	0.5	(0.05, 0.5)
CV_old_Mal_GP_1	0.1	-3	0.03	0.5	(0.03, 0.5)
Wtlen_1_Mal_GP_1	5.00E-04	-99	3.00E-04	0.02	(3e-04, 0.02)
Wtlen_2_Mal_GP_1	3.15	-99	2	4	(2, 4)
CohortGrowDev	1	-1	0.1	10	(0.1, 10)
FracFemale_GP_1	0.5	-99	1.00E-05	0.99999	(1e-05, 1)
SR_Ricker_beta	0.8	-2	0.2	1	(0.2, 1)
SR_sigmaR	0.5	-2	0	5	(0, 5)
SR_regime	0	-2	-5	5	(-5, 5)
SR_autocorr	0	-99	0	0	(0, 0)

The formulated model has 18 parameters to be estimated. Table 4 shows initial values, sequence of estimation, range of values and estimates for those 18 parameters as they were estimated in Run2. Run2 will be presented below as an example for model fitting.

Table 4. European Lobster stock in ICES subdivisions 20-21 and 23. Parameters fitted by the model with values for Run2 as example. Fitted value, in which phase of the model parameter estimation is done, range of value of estimates, parameter initial value and status of estimation process et cetera. 18 parameters were estimated, all models converged, and gradients were acceptable.

Parameter	Value	Phase	Min	Max	Init	Status	Parm_StDev	Gradient	Pr_type	Prior	Pr_SD	Pr_Like	Afterbound
SR_LN(R0)	11.11	1	8	15	12.03	OK	0.10	-1.78E-05	No_prior	NA	NA	NA	OK
Q_extraSD_VCD_1938(6)	0.05	4	0	1	0.07	OK	0.02	1.90E-05	No_prior	NA	NA	NA	OK
Size_DblN_peak_Commercial_official(1)	8.65	5	7.4	15	8.65	OK	0.03	-2.72E-08	No_prior	NA	NA	NA	OK
Size_DblN_top_logit_Commercial_official(1)	-4.37	6	-5	3	-4.41	OK	1.24	5.88E-07	No_prior	NA	NA	NA	OK
Size_DblN_ascend_se_Commercial_official(1)	-4.50	6	-12	3	-4.50	OK	0.26	-7.20E-06	No_prior	NA	NA	NA	OK
Size_DblN_descend_se_Commercial_official(1)	2.05	6	-5	12	2.05	OK	0.11	1.20E-05	No_prior	NA	NA	NA	OK
SzSel_MaleatDogleg_Commercial_official(1)	-0.23	6	-10	3	-0.27	OK	0.09	-2.74E-06	No_prior	NA	NA	NA	OK
SzSel_MaleatMaxage_Commercial_official(1)	-2.53	6	-15	10	-2.45	OK	0.60	-2.53E-05	No_prior	NA	NA	NA	OK
Size_DblN_peak_VCD_2017(5)	8.29	5	7.4	15	8.31	OK	0.05	7.69E-06	No_prior	NA	NA	NA	OK
Size_DblN_ascend_se_VCD_2017(5)	-2.00	6	-5	12	-1.96	OK	0.14	-4.62E-06	No_prior	NA	NA	NA	OK
Size_DblN_descend_se_VCD_2017(5)	1.90	6	-13	16	1.97	OK	0.15	2.44E-06	No_prior	NA	NA	NA	OK
SzSel_MaleatDogleg_VCD_2017(5)	-0.44	6	-10	3	-0.49	OK	0.15	2.03E-06	No_prior	NA	NA	NA	OK
SzSel_MaleatMaxage_VCD_2017(5)	-0.87	6	-15	10	-1.25	OK	0.92	-3.36E-06	No_prior	NA	NA	NA	OK
ln(DM_theta)_Len_P1	-1.52	7	-5	5	-1.54	OK	0.09	-5.48E-07	Normal	0	2	0	OK
ln(DM_theta)_Len_P2	-0.58	7	-5	5	-0.59	OK	0.14	5.33E-08	Normal	0	2	0	OK
Size_DblN_peak_Commercial_official(1)_BLK1repl_1875	7.96	5	6	15	7.96	OK	0.01	1.49E-05	No_prior	NA	NA	NA	OK
Size_DblN_peak_Commercial_official(1)_BLK1repl_1985	8.21	5	6	15	8.21	OK	0.01	4.97E-06	No_prior	NA	NA	NA	OK
Size_DblN_peak_Commercial_official(1)_BLK1repl_2017	8.23	5	6	15	8.23	OK	0.02	-4.33E-07	No_prior	NA	NA	NA	OK

4.3 Model diagnostics

Full diagnostics are provided in Appendix XI.

4.3.1 Model fit

Selectivity and catchability are both estimated in the model (Table 3) and the model fits to size compositions are crucial to understand the quality of the model fit. Sizes compositions fit well, and the Pearson residuals by sex do not show any apparent trend (Figure 8).

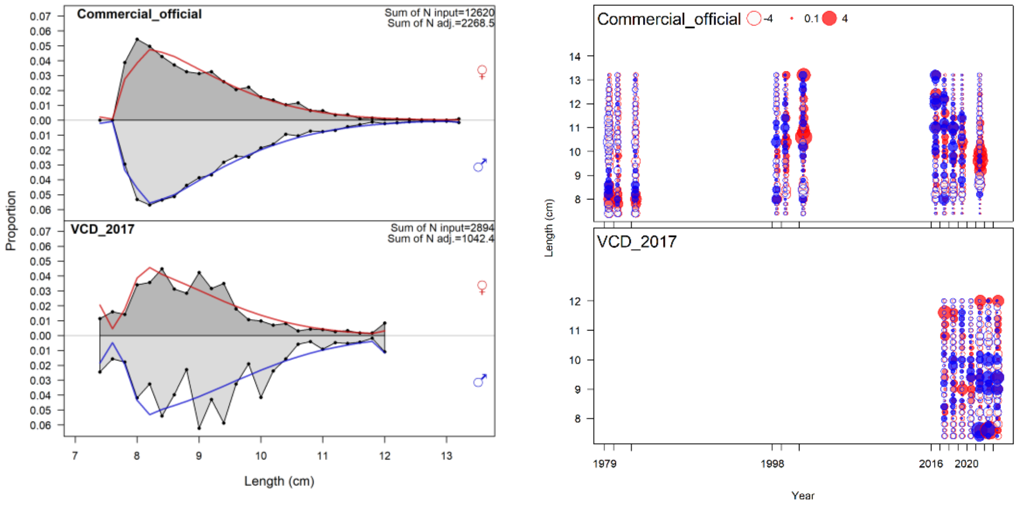


Figure 8. European Lobster stock in ICES subdivisions 20-21 and 23. Residuals of the size compositions by sex in Run2, which is used here for illustration.

The trajectories estimated by all models showed similar trends with some quantitative differences (Figure 9). The largest differences were displayed in recent years in terms of F, which is driven by assumptions on the levels of unreported catch. Inflated catches inform the model of an assumed larger productivity, and the model responds with increased recruitment deviations, decreased SSB and increased F in the later years to compensate.

Inflated catches in the later years are seen by the model as a productivity change historically, through a complex integration between relative SSB and relative F. The model does not have a lot of information on historical productivity and has to compensate for by increasing relative SSB and with a decreased relative F.

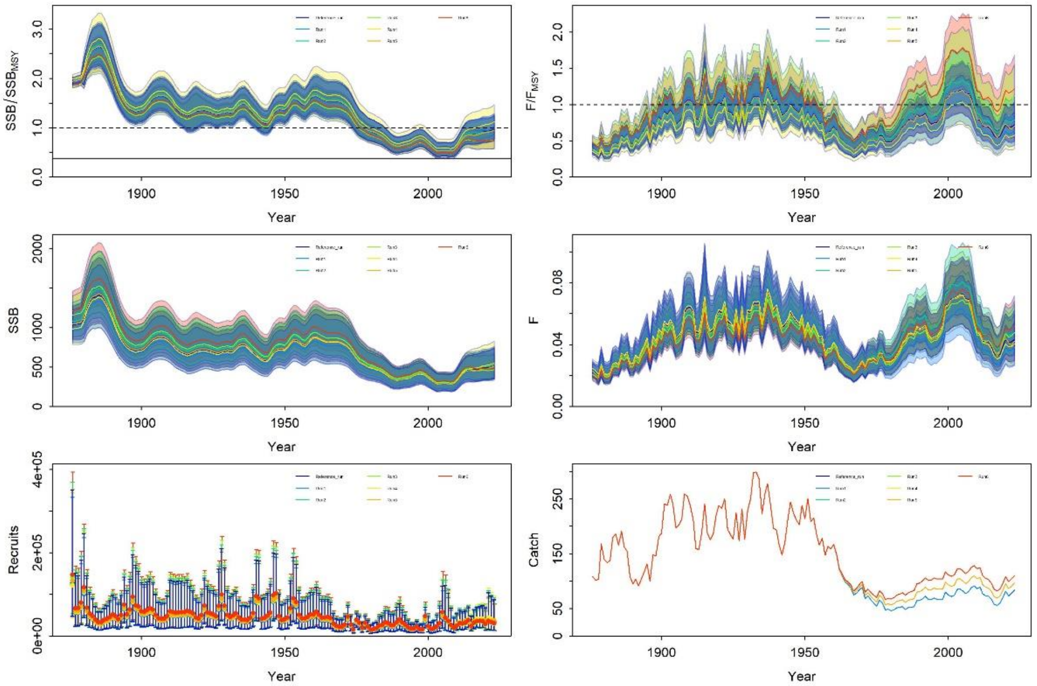


Figure 9. European Lobster stock in ICES subdivisions 20-21 and 23. Trajectories of all models as dimensions of uncertainty.

4.3.2 Retrospective analysis

Retrospective analyses were performed showing acceptable results (Figure 10). This is based on ICES standards for which values of Mohn's rho higher than 0.20 or lower than -0.15 for longer-lived species (upper and lower bounds of the 90% simulation intervals for the flatfish base case) indicate a cause for concern and the presence of a retrospective pattern. However, Mohn's rho values within the proposed range should not be taken as confirmation that a given assessment does not present a retrospective pattern, and the choice of a 90% interval means that a "false positive" will occur 10% of the time. In both cases, model misspecification would be correctly detected more than half the time. SSB appears to have been consistently underestimated. A substantial part of the lobster fishery catches is not documented (reported) hence an improved documentation of unreported fishing may provide a better basis for the model to analyze biomass trends.

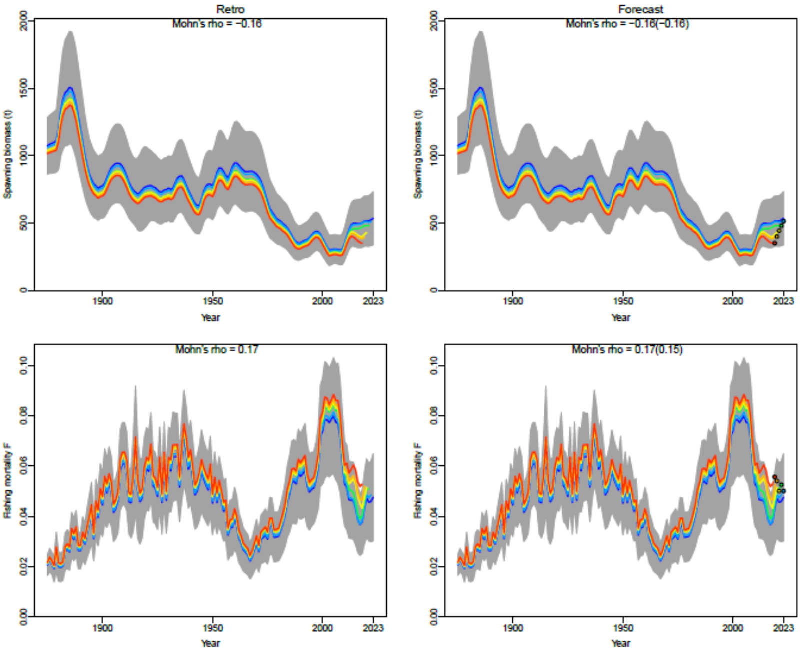


Figure 14: Retrospective analysis and retrospective forecasts for the Run2

Figure 10. European Lobster stock in ICES subdivisions 20-21 and 23. Retrospective analysis of Run 2.

4.3.3 Predictive analysis

Mean Absolute Scaled Error (MASE-) indices showed that the model is not able to accurately predict the indices (MASE > 1, Figure 11). This is most likely due to a conflict in indices and catch trends between North and Southern areas of the stock distribution, which is known for European Lobster stock in ICES subdivisions 20-21 and 23 and because some of the time series are short. Such conflicts are not rare in stock assessment work but may be difficult to resolve. A more reliable sampling of landings as well as the introduction of an area specific model could potentially disentangle this conflict and perhaps achieve a better predictive power for the model. However, we would need to distinguish the landings data on an appropriate spatial level.

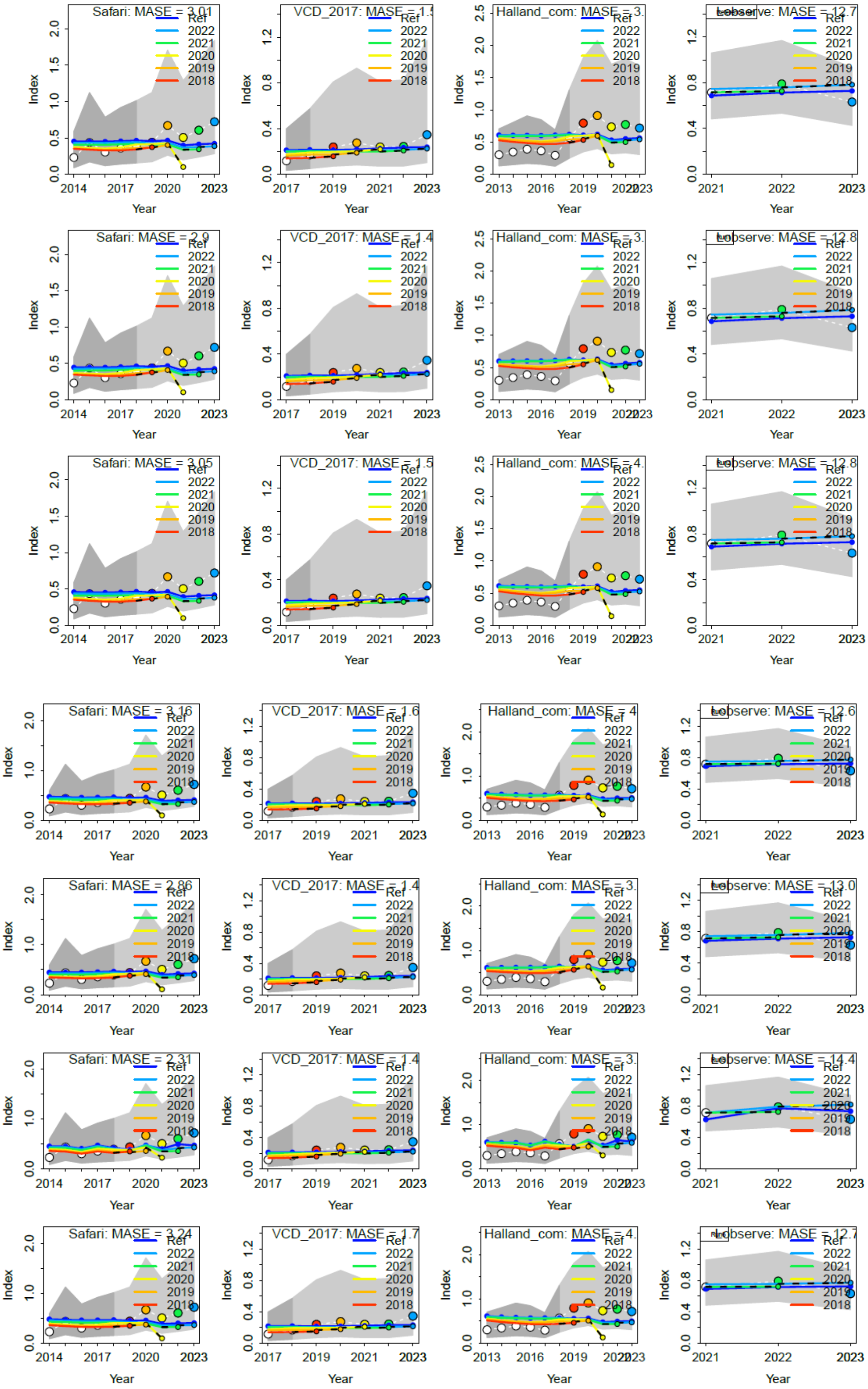


Figure 11. European Lobster stock in ICES subdivisions 20-21 and 23. Hindcast cross-validations for the survey indices of the Reference_run (top) and Run1 to Run6 (bottom).

4.4 Alternative models tested

The set of additional models (see Table 2 for details) that were tested as supporting sensitivity runs did not add any qualitative trends that differed from what was already captured by the set of dimensions of uncertainty (Figure 12). Some aspects were not dealt with in the dimensions of uncertainty (e.g., fitting of natural mortality, M). However, this did not introduce additional trends in the trajectories, and no further models were suggested by the benchmark meeting.

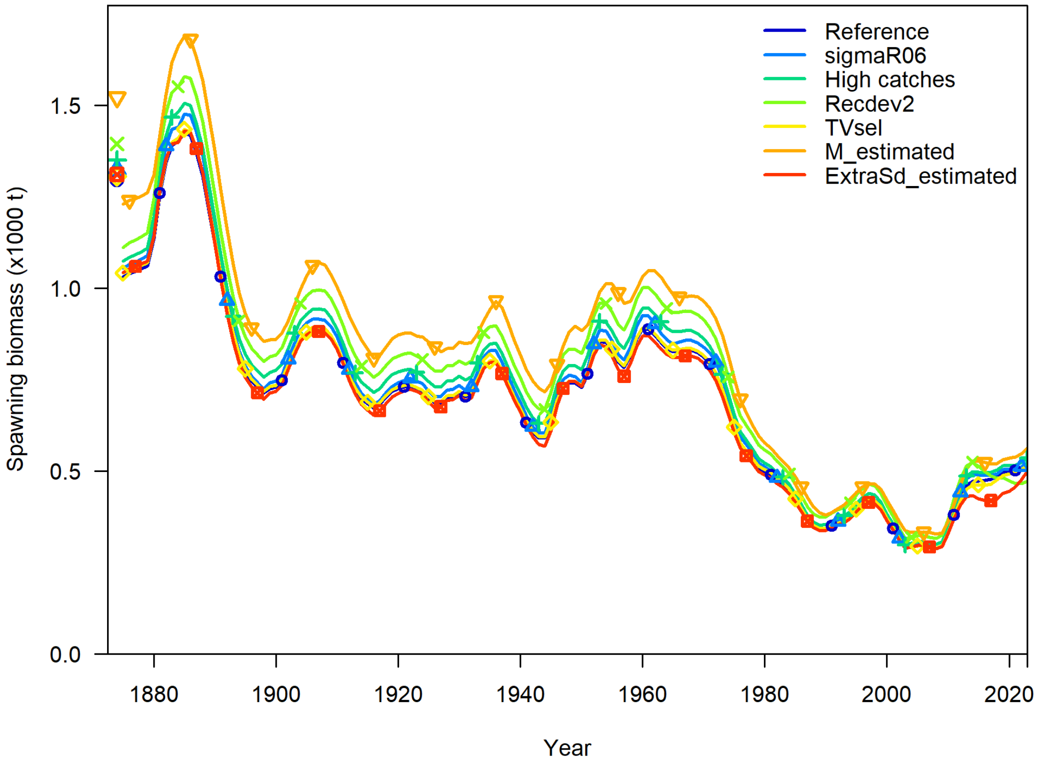


Figure 12. European Lobster stock in ICES subdivisions 20-21 and 23. Trajectory of alternative models fitted as supporting sensitivity analysis.

Diagnostics could not identify one best model, the differences in diagnostics between models are very small. Each model may capture the relevant behavior of the data and help inform us on the development of the stock. Limiting the modelling work to selecting only one model may lead to an underestimation of the total variability in data and model fits. Instead, by using an ensemble model framework it is possible to incorporate all model output weighted by the diagnostic output (Table 5).

4.4.1 Model selection

It is good practice that an objective methodology for selecting, pruning and weighting hypotheses is pre-agreed, to overcome artifacts and biases introduced by a ”cherry-picking” approach (Pechlivanidis et al., 2018). This is particularly important since divergent views and opinions mean that uncertainties can be used to support stakeholder positions and to strengthen or weaken management measures (Fromentin et al., 2014).

Stock assessment models are deeply scrutinized for model misspecification during their development within benchmark workshops. Traditionally in ICES, diagnostics have been based on retrospective and visual analysis of the residuals. However, recent papers by (Carvalho et al., 2021) showed that when several diagnostic tests are considered together, the power to detect model misspecification improves without a substantial increase in the probability of incorrectly rejecting a correctly specified model (Carvalho et al., 2017; Carvalho et al., 2021). Consequently, several available diagnostics should be applied routinely during benchmarks. For example, residual analyses were easily the best detector of misspecification in the observation model, while the retrospective analysis had low rates of detection of misspecified models (Carvalho et al., 2017; Carvalho et al., 2021), although retrospective analysis is effective in detecting un-modelled temporal variation (Hurtado-Ferro et al., 2015).

4.4.2 Model diagnostics

The different plausible model configurations to be used in the ensemble were compared using model diagnostics (Carvalho et al., 2017; Carvalho et al., 2021; Kell et al., 2021; Merino et al., 2022). The key model diagnostics used were convergency (which includes checking of parameters at the bounds, final gradient and inversion of the Hessian matrix for uncertainty estimation), runs test and RMSE, retrospective analysis, and hindcasting cross-validation (Table 3). Estimates and trends in SSB, F, and R were used at the last step and only as a plausibility check.

Convergence

The first step for checking model convergence is to verify if parameters are estimated at a bound, which can suggest problems with data or the assumed model structure. The second is checking that the final gradient of the model is relatively small (e.g., ≤ 1.00E-04 or smaller). The third is to determine whether the Hessian (i.e., the matrix of second derivatives of the log-likelihood concerning the parameters, from which the asymptotic standard error of the parameter estimates is derived) is positive definite (Carvalho et al., 2021). Other convergence diagnostics include (i) examining the correlation matrix for highly correlated (e.g., > 0.95) parameter pairs; and (ii) examining parameters for excessively high variance as an indication that they do not influence the fit to the data (Carvalho et al., 2021).

Residuals test

A non-random pattern of residuals may indicate that some heteroscedasticity is present, or there is some leftover serial correlation (serial correlation in sampling/observation error or model misspecification). Several well-known nonparametric tests for randomness in a time-series include: the runs test, the sign test, the runs up and down test, the Mann-Kendall test, and Bartel's rank test (Gibbons & Chakraborti, 1992). Standardized residuals are commonly used, although recent analysis showed that one-step-ahead (OSA) should be used instead in stock assessment model diagnostics (Trijoulet et al., 2023). Here we used the runs test to evaluate whether residuals of the surveys, and the length frequency distributions, were normally distributed and/or displayed any temporal trends. The runs test was chosen as this test has recently been used to diagnose fits to indices and other data components in other assessment models (e.g., (Carvalho et al., 2021; FAO-GFCM, 2021; Winker et al., 2018).

The RMSE runs test (see (Carvalho et al., 2021) for details) could indicate the presence of a random pattern in the length frequency distributions and in the survey indices. The RMSE plot is frequently used as a tool for identifying trends in residuals, and if the standard deviation is small on a given year this means the fleets included in the model agree, even if not fitting well, which is a useful diagnostic. Its purpose is to visualize multiple residuals at once, pick up on periods of substantial data conflicts and systematic departures in median residuals (loess smoothers). The fit is considered satisfactory if no residuals are larger than 1 and the RMSE is below 30%.

Retrospective analyses

Retrospective analysis is a diagnostic approach to evaluate the reliability of parameter and reference point estimates and to reveal systematic bias in the model estimation. It involves fitting a stock assessment model to the full dataset. The same model is then fitted to truncated datasets where the data for the most recent years are sequentially removed. The retrospective analysis was conducted for the last 5 years of the assessment time horizon to evaluate whether there were any strong changes in model results. Given that the variability of Mohn's rho index depends on life history, and that the statistic appears insensitive to F, (Hurtado-Ferro et al., 2015) proposed the following rule of thumb when determining whether a retrospective pattern should be addressed explicitly. Values of Mohn's rho index higher than 0.20 or lower than -0.15 for long-lived species (upper and lower bounds of the 90% simulation intervals for the flatfish base case), or higher than 0.30 or lower than -0.22 for short-lived species (upper and lower bounds of the 90%

simulation intervals for the sardine base case) should be cause for concern and taken as indicators of retrospective patterns.

Hindcasting

The provision of fisheries management advice requires the assessment of stock status relative to reference points, the prediction of the response of stock to management, and checking that predictions are consistent with reality. A major uncertainty in stock assessment models is the difference between model estimates and reality. To evaluate this uncertainty, it is common for several scenarios to be considered, whereby scenarios correspond to alternative model structures and/or dataset choices (Hilborn, 2016). It is difficult, however, to empirically validate model predictions, as fish stocks can rarely be observed and counted. Various criteria are available for estimating prediction skill (see (Hyndman & Koehler, 2006). One commonly used measure is a root-mean-square error (RMSE). RMSE, however, is an inappropriate and misinterpreted measure of average error (Willmott and Matsuura, 2005). On the other hand, mean absolute error (MAE) is a more natural measure of average error, and unlike RMSE is unambiguous. Scaling the average errors using the Mean Absolute Scaled Error (MASE) allows forecast accuracy to be compared across a series at different scales. MASE values greater than one indicates that in-sample one-step forecasts from the naïve method perform better than the forecast values under consideration. MASE also penalizes positive and negative errors and errors in large forecasts and small forecasts equally.

(Carvalho et al., 2021; Kell et al., 2016; Kell et al., 2021) showed that hindcasting can be used to evaluate the model prediction skill of the CPUE time series. When conducting hindcasting, a model is fitted to the first part of a time series and then projected over the period omitted in the original fit. Prediction skill can then be evaluated by comparing the predictions from the projection with the observations using, for example, the MASE indicator (Hyndman & Athanasopoulos, 2013). If a model is used for prediction, the specific tool used for model selection is less important than the approach used to validate predictions. Quantifying predictive skills using independent data in ecology is therefore essential (Tredennick et al., 2021).

4.4.3 Model weights

Table 5 summarizes the model diagnostics that were used to evaluate the reference and candidates' alternative model configurations that were used in the ensemble. The table is an attempt to sum up a multidimensional space and thus it needs to be seen as a guidance more than as a definitive result. All models invert the hessian matrix and have a good to moderate convergence. Most of the models did not pass the runs test (Table 5). The RMSE is below 30% for all models. However, most of the MASE-tests fail.

The estimated Hurtado-Ferro et al. (2015) variant of the Mohn´s rho (of SSB) indices were inside the bounds of recommended values for long-lived species for model Reference_run and for Run1 (however not for the forecast), Run3 and Run5. For F Mohn´s rho was acceptable for all models.

Table 5. European Lobster stock in ICES subdivisions 20-21 and 23. Table of model diagnostics and weights

Run	**Reference_run**	**Run1**	**Run2**	**Run3**	**Run4**	**Run5**	**Run6**
Convergence	9.57E-05	5.51E+00	9.25E-05	8.28E+00	6.21E-05	1.46E+01	1.08E+01
Total_LL	2142.56	2142.58	2143.11	2136.98	2146.47	2116.82	2138.53
N_Params	170	170	170	170	170	178	170
Runs_test_cpue1	Failed	Failed	Failed	Failed	Failed	Failed	Failed
Runs_test_cpue2	Passed	Passed	Passed	Passed	Passed	Passed	Passed
Runs_test_cpue3	Failed	Failed	Failed	Failed	Failed	Failed	Failed
Runs_test_cpue4	Failed	Failed	Failed	Passed	Failed	Failed	Passed
Runs_test_cpue5	Failed	Failed	Failed	Failed	Failed	Failed	Failed
Runs_test_len1	Failed	Failed	Failed	Failed	Failed	Failed	Failed
Runs_test_len2	Passed	Passed	Passed	Passed	Passed	Passed	Passed
RMSE_Perc	19.7	19.6	19.9	19.9	19.8	19.1	20.1
RMSE_Perc_1	3.1	3.1	3.1	3	3.1	2.3	3
Retro_Rho_SSB	-0.15	-0.14	-0.16	-0.15	-0.16	-0.14	-0.16
Forecast_Rho_SSB	-0.16	-0.14	-0.16	-0.15	-0.16	-0.14	-0.16
Retro_Rho_F	0.17	0.15	0.17	0.16	0.17	0.16	0.17
Forecast_Rho_F	0.14	0.12	0.15	0.14	0.14	0.16	0.15
MASE_cpue1	3.01	2.90	3.05	3.16	2.86	2.31	3.24
MASE_cpue2	1.50	1.45	1.55	1.67	1.43	1.47	1.72
MASE_cpue3	3.95	3.71	4.09	4.60	3.54	3.21	4.79
MASE_cpue4	18.49	18.57	18.66	18.38	18.94	20.84	18.43
MASE_cpue5	4.30	4.19	4.38	4.55	4.17	4.09	4.64
MASE_len1	1.39	1.39	1.37	1.38	1.34	0.69	1.38
MASE_len2	0.16	0.16	0.16	0.16	0.16	0.16	0.16
MASE_len3	0.51	0.51	0.50	0.51	0.50	0.31	0.51
Summary Weight	0.48	0.48	0.48	0.52	0.48	0.52	0.52

The summary weight is calculated as the number of passed tests divided by the total, resulting in a proportion.

4.5 Ensemble model

The models in the set of dimensions of uncertainty provide alternative sources of uncertainty and variability in model fitting. Including them all in the ensemble and allowing them to influence the model outputs saves us from limiting ourselves to only one model representation. The trajectories in Figure 13 include trends and variability from all model representations. The fluctuations coincides well with previous descriptions of developments of effort, catch and CPUE (Sundelof et al., 2013). The large decline beginning in the 1960’s is well described since before, but not entirely understood. However, it is followed by a continued decline as fishing mortality increased during the 1980’s to 2000’s. The many regulations on lobster fishing since 1971 onwards, eventually reduced fishing mortality and a rebuilding of biomass followed. Details on ensemble are provided in Appendix XI.

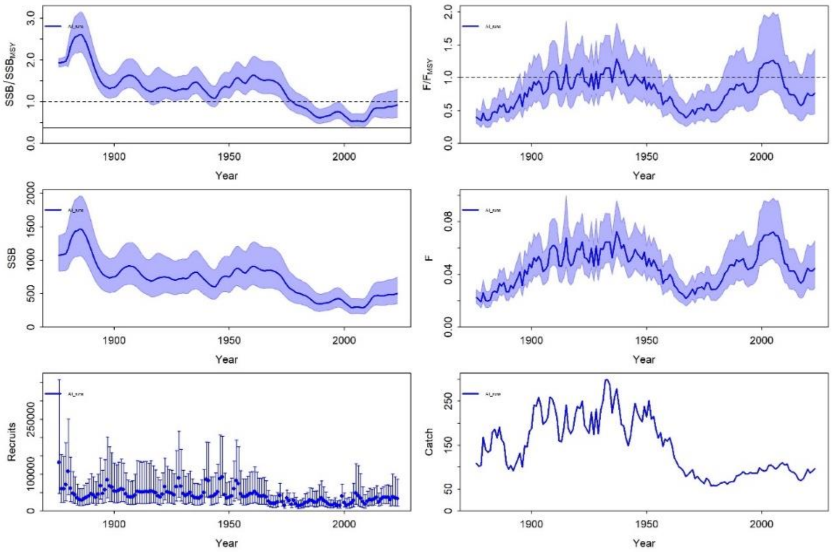


Figure 13. European Lobster stock in ICES subdivisions 20-21 and 23. Trajectories of ensemble model. Catches are expressed as median of the 3 scenarios tested.

4.6 Stock status

The final ensemble model is a development and scrutinization of a model first developed with data up to 2022. The ensemble model is more optimistic than the model of 2023 (Figure 14). This may have several causes, and no single reason can be pointed out as the integrated model balances changes in data and parameters. The current model has better fit to inflated levels of unreported catches. Also, a couple of the index series have positive trends and some changes towards larger size compositions cause the model to reduce F and increase SSB relatively.

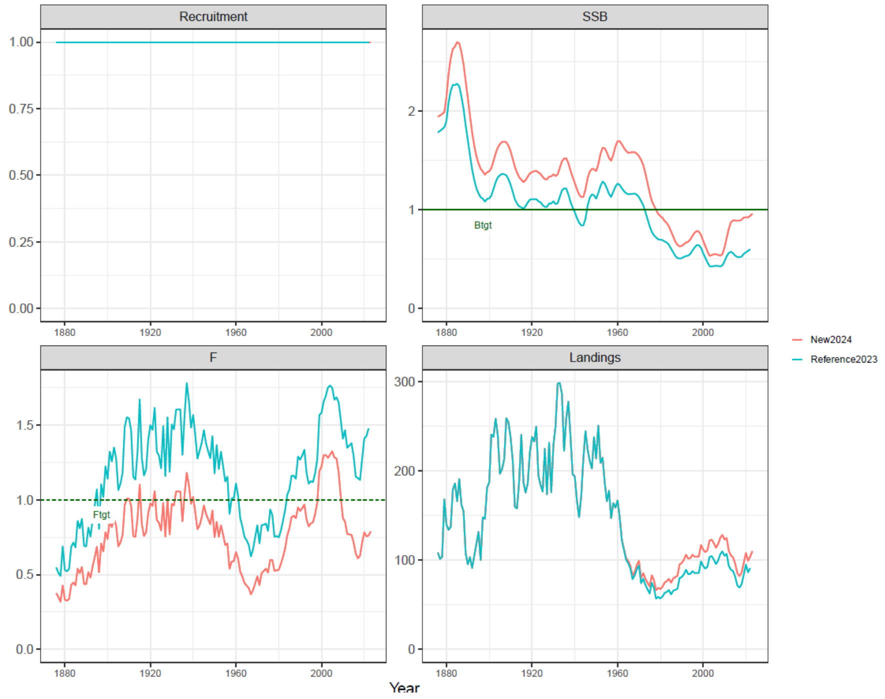


Figure 14. European Lobster stock in ICES subdivisions 20-21 and 23. Comparison between the relative stock status estimates from the new reference run and the last previous advice model update from 2023. Landings are an input of the models. There is no reference point for recruitment and the comparison is therefore flat.

The Kobe plot of the ensemble model shows the density of outcomes from the bootstrapped Hessian variance-covariance matrix (Figure 15 for each model, Figure 16 for the ensemble). For each model every parameter has a variance-covariance estimate to the other parameters in the specific model. The bootstrapping methodology uses the entire parameter space (one value chosen at random from each of the parameter variability) to illustrate the statistical possibilities of the variability in all parameters These realizations are depicted as coloured dots in the kobe plot (Figure 15). Some model configurations provide more optimistic status than other (see Figure 9). Generally, assumed larger unreported catches provide more optimistic output, and higher steepness showing more pessimistic output (legend for model colours).

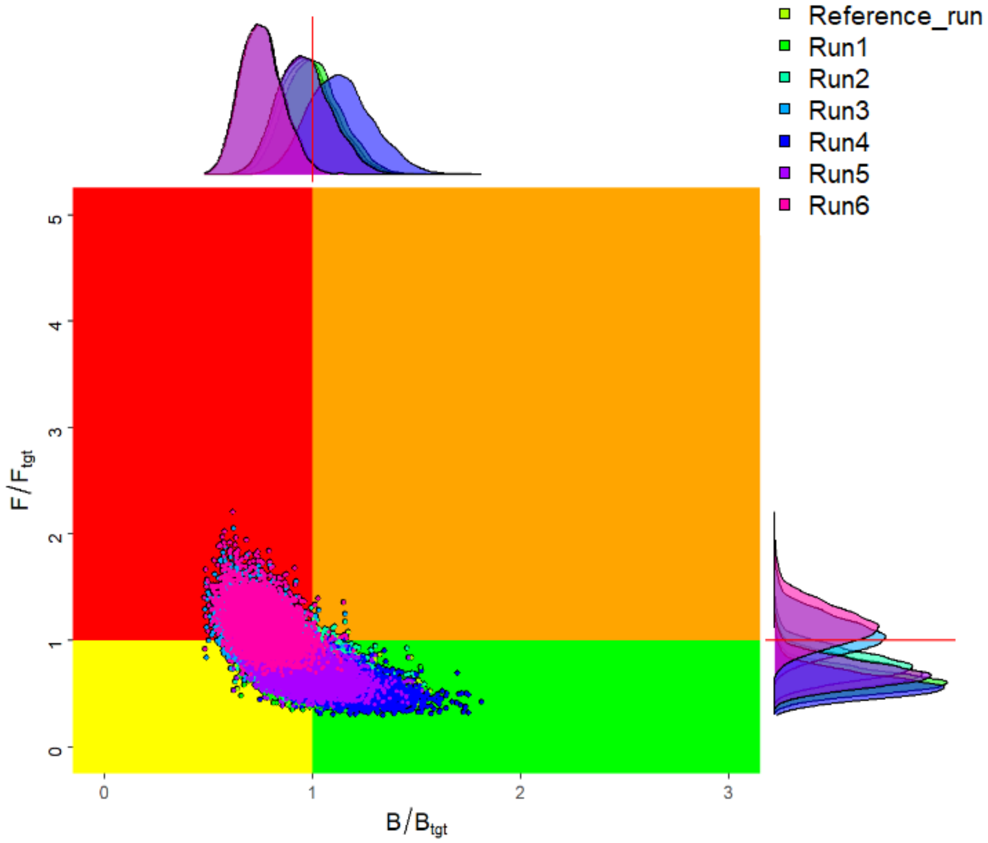


Figure 15. European Lobster stock in ICES subdivisions 20-21 and 23. Kobe plot of terminal year estimate from all bootstrapped alternative models.

Plotting relative F against relative SSB also provides the trajectory of the stock over time (Figure 16), which is defined as the Kobe plot (Kell et al., 2016; also called the phase plot). It provides an intuitive way of visualising stock status in the context of biomass and fishing mortality. It is based on the concept that if fishing mortality (F) is above F_{MSY}, overfishing is judged to be occurring, whereas if the biomass (B; or some measure of spawning output) is below B_{MSY}, the stock is judged to be overfished. The Kobe plot shows B/B_{MSY} on the x-axis and F/F_{MSY} on the y-axis such that vertical and horizontal lines at 1.0 split the plot into four sections. The upper left represents a phase which is not desirable: overfishing occurring and an overfished stock; and the lower right represents a healthy stock: overfishing not occurring and an underfished stock. The trajectory of the stock over time is plotted such that the historical status of the stock can be followed. Typically, a stock starts in the lower right as the fishery develops, then moves into the upper left as the population becomes overexploited, and finally, as appropriate management is applied, it cycles around the centre of the plot.

The current (2023) status of the lobster stock following the ensemble approach is described by probabilities relating to different phases, where the probability of being in the red (overfishing and overfished), orange (overfishing), yellow (overfished) and green zone (no overfishing, not overfished) is 25, 2, 40 and 33 percent, respectively. The mean point estimate in 2023 shows that F is below FMSY, and spawning stock biomass is just below BMSY. However, for 25% of the bootstrapped model outputs the lobster stock is in the red phase, which indicates the probability of overfishing occurring and the stock being overfished. The status of the stock has changed substantially over 145 years, from a high abundance and low fishing regime to a high fishing and low abundance regime which matches published historical sources of lobster fishing (e.g., (Sundelof et al., 2013)).

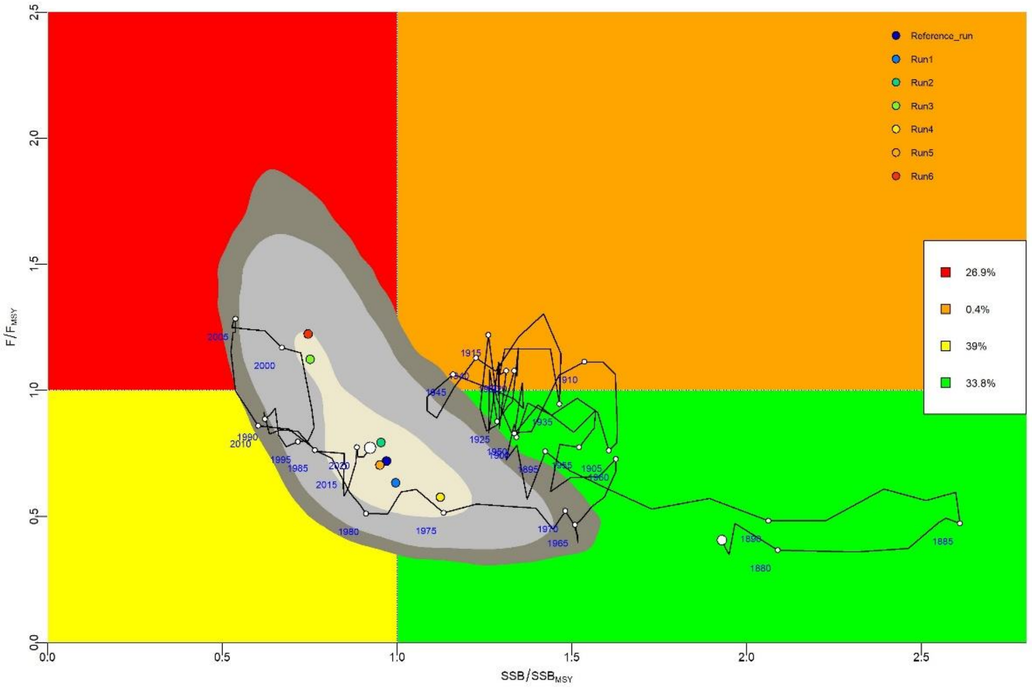


Figure 16. European Lobster stock in ICES subdivisions 20-21 and 23. Kobe plot of ensemble trajectory of the stock from 1875-2023. 2023 is denoted by a large white open circle in the yellow quadrant.

4.7 Conclusions and recommendations

The benchmark was attended by research scientists, managers and commercial fishermen. Data was provided from several segments of the fishery where each concerned segment can interact in the provisioning of data. The benchmark workshop put light on discrepancies between these different segments of fishers and the formal requisition of catch data from national authorities. The models provide a robust assessment of the European Lobster stock in ICES subdivisions 20-21 and 23.

Further developments in quality of catch data, standardizing of indices and development of spatial aspects of the model may improve the model performance and better inform on differences between areas. These are not new challenges but have been manifested by the benchmark. Securing the data provisioning from the different catch indices is a prerequisite for future updates of this ensemble model framework.

4.8 Forecast not performed

Without specific management goals or a deductible quota, there is no reference point for this model against which a forecast can be made. However, the current model is evaluated against the MSY concept. It is implemented in the modelling framework and provides a useful basis for sustainability.

4.9 Reference points

No reference points were suggested before the benchmark. The previous use of B_{target} of 40% of B_0 was extended to use the MSY approach estimated within SS3. B_{MSY} and B_{target} were very similar and no further discussion on the use of reference points were made.

The current management of lobster is not concerned with a catch limit and the capping of catches is not a viable option. Instead, regulations are placed on individual fishers and are very indirect in the purpose of limiting catch to a relative level over time. Sustainability is therefore analysed in hindsight relating to some reference level. It may be possible to evaluate the effects of increased regulations on number of pots (per person), season length or minimum landing size. This will affect F but may also affect fishing habits and practices with implications for the final F acting on the stock. Minimum landing size and a moratorium on berried females are the most likely used management practices to protect the lobster population. How these options affect the size composition and productivity of the stock, and how their implementation may be traced in the assessment model, have not been developed.

5. Report from the reviewer

5.1 Overview

The benchmark assessment of the European lobster (*Homarus gammarus*) in ICES Division 3a was conducted in a series of meetings in 2024. The objective was to improve data integration, develop a stock assessment model, and provide a foundation for future management advice. The work considers data from scientific surveys, landing statistics and fishery-dependent survey data, from both commercial and recreational fishers. The assessment was presented and discussed over two workshops (17-18th of June and 3rd of October), with the primary goals of addressing the quality of input data (indices and biological data) and key uncertainties related to stock productivity, recruitment, and fishing mortality and reviewing the base case model. I have reviewed the benchmark based on participation in meetings and the received documentation, and I find that the assessment work is solid and grounded in the best available data.

5.2 Data sources and standardization

The lobster stock model utilizes a comprehensive selection of data sources and incorporates available life history parameters. The assessment uses landings data from both commercial and recreational fisheries (2), and surveys (6), enabling a robust assessment of stock status. One of the main strengths of this assessment is the use of historical data in conjunction with more recent fishery-independent surveys to inform the model. A long-standing historical time series from Hushållningssällskapet (SREAS1), dating back to 1875 provides catch data from the commercial fishery, including seasonal total catch and catch per unit effort (CPUE) indices, standardized to account for effort creep. More recent data are available from the Lobserve survey, a three-year scientific initiative where recruited fishermen conduct depth-stratified catch-and-release surveys before the start of the official fishing season.

Integrating shorter surveys with other indices presents challenges due to differences in data standardization, variations in recorded data types (e.g., full catch vs. landed catch only), and changes in fishing pressure and selectivity curves influenced by shifts in regulations over time. Some limitations in data availability were noted, especially for recreational catches. However, the working group revised input data and standardized CPUE across indices to enhance comparability where possible. For instance, for *Lobserve*, a survey with high-resolution data, a generalized linear mixed model (GLMM) was fitted with a Poisson distribution of errors (to handle the skewed zero-catch data) while adjusting for fishing effort by an offset term and fisher-specific differences. Data sources with higher variability receive lower weight within the model to reduce their influence.

The data used in the assessment are:

- Landings data: The assessment uses landings data from both commercial and recreational fisheries. This includes commercial data from *vcd_2017*, along with landings from *Halland* introduced in later stages of the assessment process. The data had undergone a rigorous review for accuracy and consistency.
- Survey indices: The model includes fishery-independent survey indices, which were standardized to account for variables such as depth, soak time, and fisher ID to improve consistency, where available.
- Size composition data: Data on size structure derived from commercial logbooks, *vcd_2017* and some from *Lobserve* surveys. Discrepancies in size compositions between commercial catches and survey data introduce some uncertainty in the model.

5.3 Assessment Model

The Stock Synthesis 3 (SS3) model was chosen as the base for the assessment, incorporating sex-specific population dynamics and length-based models to track the stock over 25+ age classes. One of the strengths of SS is that it allows for mixing a range of different data sources, which this benchmark has. It should provide a robust and flexible environment for modelling population dynamics which should suit the European lobster. Although this framework is outside of my area of expertise, assessment team members have previous experience with handling SS from stock assessments and I entrust their expertise and knowledge to the best use.

The model integrates much biological detail, accounting for lobsters' biennial egg-laying and differences in fecundity with size (egg mass estimates not included). By setting the max age at 25+ years, the model treats all lobsters older than this age as a plus group, accounting for the longevity of this species while managing data limitations on older individuals. Some of the key settings for the reference model were:

Growth: Sex-specific growth was estimated by von Bertalanffy's growth function based on mark-recapture data. By controlling the level of uncertainty associated with growth at various ages, the coefficient of variation (CV) was set slightly differently for younger (0.15) and older (0.10) lobsters (higher variability in young individuals is expected, while older individuals have more consistent growth patterns).

Mortality: Age-specific mortality estimates for males and females were obtained from mark-recapture data from Kåvra lobster reserve. This is assumed to reflect the natural mortality (N) of an unfished population not confounded by fishery-related causes. Further, N was set to be constant over time, but differentiates between six age classes (0, 1, 2, 4, 5, 10, 20) and sexes, which is a sound assumption for lobsters.

Maturity: Female maturity was modelled with logistic regression, with the length at 50% maturity (Lm50) set at 7.8 cm, (appr. age 5). The maturity curve estimates the reproductive contributions of female lobsters based on size and age.

Recruitment resilience: The model infers recruitment trends from size structure data since information on recruitment remains sparse for lobsters. The assessment used a Ricker stock-recruitment relationship which regards recruitment as a function of spawning stock biomass (SSB) that eventually levels off due to density-dependence. Steepness of h = 0.8 was assumed as a baseline, implying the assumption of moderate resilience to lower stock levels. Considering lobsters have complex mating behaviour, low stock densities may proportionally reduce recruitment levels if lobsters have difficulties finding mates (depensation). It was therefore a wise choice of the team to explore the sensitivity to lowering the steepness (h= 0.45 − 0.95).

Selectivity: The model assumed time-varying selectivity for the commercial fleet based on known changes in fishing effort and behaviour. A double-normal (dome-shaped) selectivity was assumed and means the catchability of lobsters increases to a peak size, then declines for larger lobsters. It is reasonable in this case because scientific mark-recapture surveys often show higher catch rates for medium-sized lobsters and lower rates for small and larger individuals. Compulsory escape openings for juveniles, and because larger lobsters may be deterred from entering the trap opening (or easier escape), likely contribute to this pattern.

5.4 Diagnostics, ensemble approach and stock status

Multiple model configurations (seven in total, including the base model) were tested in the assessment, with “run2” identified as the most robust. This run demonstrated strong convergence and gave a balanced view of the uncertainties within the stock's dynamics (recruitment, fishing mortality). However, the decision was made to pursue an ensemble model, as it provides a more balanced view of uncertainty than a single model run. Weighted averages of models should offer a more realistic representation of the stock's status, thus improving risk assessment.

The model uses various diagnostic tools (e.g., residual tests, RMSE evaluations and retrospective analysis) to evaluate model stability and conflicts in surveys. Size structure data from the vcd_2017 survey and commercial catches displayed reasonable fits, while residual patterns in some surveys like *Safari* and *Halland* highlighted potential spatial inconsistencies, which could be explained by differences in trends between northernmost and southernmost areas (latitudinal gradients). Retrospective analyses showed stable performance, with Mohn's Rho below the threshold of 0.2. The hindcast cross-validation showed that the model has limited predictive abilities for CPUE indices, suggesting issues with the model's ability to capture trends in stock CPUE accurately. However, the predictive performance of mean lengths was better so the size structure data might be more reliably modelled than CPUE trends (although low accuracy for *Lobserve* and *Halland*).

The steepness is an important parameter for inferring recruitment trends and can have a large effect on the model results. The testing of different levels showed that the model better supports slightly lower steepness values (h= 0.45 − 0.65) based on log-likelihood, but that this parameter had minimal impact on the stock status estimates. The ensemble approach adds confidence by capturing uncertainties across the tested range, but it is somewhat unclear how the steepness values have been weighted. If the ensemble primarily reflects the reference run (h= 0.8), this value appears to be a reasonable middle ground given the lack of data. That said, it would be interesting to explore alternative stock-recruitment functions, especially ones that account for depensation at low stock densities.

The biomass reference points were defined based on the female spawning stock biomass (SSB) set to SSB_{40} (40% of unfished biomass, SSB_0) and F_{40} (fishing mortality at SSB_{40}) to limit the risk of overfishing. Model estimates of reference points indicate that the lobster stock has shown signs of recovery, with SSB trending upward over the last ten years after having declined since the 60s. Yet, the SSB remains below the maximum sustainable yield (BMSY), suggesting the stock has yet to reach optimal levels. Fishing mortality was found to be above sustainable thresholds so current fishing pressure continues to exert considerable pressure on the stock. This is further reflected in the kobe plots, which mostly place the stock in yellow zone (40-45% of unfished biomass), indicating a moderate risk of overfishing of what is interpreted as currently stable biomass. This highlights the need for a cautious approach, especially given the uncertainties surrounding recruitment and the impact of the recreational fishery. Better reporting from the recreational fishery would likely benefit future assessments by addressing all sources of fishing mortality.

5.5 Conclusions and future recommendations

The purpose of this benchmark assessment was to determine if a model could present a realistic and reasonable representation of the Swedish lobster population, aiming to reflect dynamics and trends over time. I commend the working group for a thorough job in assembling and weighing the various data sources, paying attention to the limitations and potential biases of each source of data, the sampling design, and standardization decisions. Attention is also paid to the importance of life history traits and the values chosen are based on the best available knowledge, and the ensemble modelling approach and thorough diagnostic testing give confidence in the results while acknowledging areas of uncertainty.

5.5.1 Recommendations for future assessments:

- A potential limitation identified in the current data usage is the absence of corrections for technological improvements (technological creep) in fishing efficiency, such as the transition to two-chambered traps, which could inflate historical catch rates. It would be beneficial to include such corrections in future assessments to help avoid potential overestimations of stock abundance, as similar findings have been highlighted in studies like Kleiven *et al.* (2022).
- There is still room for continued refinement of data sources, particularly regarding recreational catches and the inclusion of more size data. Improving recreational fishery data collection through expanded *Lobserve* participation and user-friendly electronic logbook systems could help validate catch-based indices and improve model parameterization.
- Consider including video surveys as additional data sources as they give valuable fishery-independent data on density/relative abundance and size distributions (with potentially being less size selective than traps).
- The changing climate already increases the water temperature which can affect feeding behaviour and spatial distribution of lobster, which in turn can affect catchability in the fishery and scientific surveys. Temperature monitoring through trap-mounted loggers is recommended to develop temperature-dependent catchability models. The current assumption of constant catchability likely misses out on an important relationship between environmental conditions (temperature, salinity) and catch rates. Combining temperature data with existing depth-stratified sampling could improve CPUE standardization.
- Exploring alternative stock-recruitment relationships that account for depensation effects at low stock densities.

Tonje Knutsen Sørdalen (*PhD*)

6. Model code

The running of the models is outlined in Appendices IX and X. Model settings and input as well as output can be shared on request. However, the code is not implemented in GitHub or other repositories for executing code. At the publication of this reports it was not yet decided how this would be pursued.

References

Bergström, U., Berkström, C., Sköld, M., & Börjesson, P., Eggertsen, M., Fetterplace., L.,Florin, A.B., Fredriksson, R., Fredriksson, S., Kraufvelin, P., Lundström, K., Nilsson, J., Ovegård, M., Perry, D., Sacre, E., Sundelöf, A., Wikström, A., Wennhage, H.,. (2022). *Long-term effects of no-take zones in Swedish waters* (2022:20). S. U. o. A. S. Department of Aquatic Resources.

Carvalho, F., Punt, A. E., Chang, Y. J., Maunder, M. N., & Piner, K. R. (2017). Can diagnostic tests help identify model misspecification in integrated stock assessments? *Fisheries Research*, *192*, 28-40. https://doi.org/10.1016/j.fishres.2016.09.018

Carvalho, F., Winker, H., Courtney, D., Kapur, M., Kell, L., Cardinale, M., Schirripa, M., Kitakado, T., Yemane, D., Piner, K. R., Maunder, M. N., Taylor, I., Wetzel, C. R., Doering, K., Johnson, K. F., & Methot, R. D. (2021). A cookbook for using model diagnostics in integrated stock assessments. *Fisheries Research*, *240*. https://doi.org/ARTN 105959
10.1016/j.fishres.2021.105959

Coleman, M. T., Agnalt, A. L., Emmerson, J., Laurens, M., Porter, J. S., & Bell, M. C. (2021). From the Adriatic to Northern Norway-geographic differences in moult increment and moult probability of the European lobster (Homarus gammarus), across the natural range. *Ices Journal of Marine Science*, *78*(2), 611-620. https://doi.org/10.1093/icesjms/fsaa172

Davies, C. E., Johnson, A., Wootton, E. C., Greenwood, S. J., Clark, K. F., Vogan, C. L., & Rowley, A. F. (2015). Effects of population density and body size on disease ecology of the European lobster in a temperate marine conservation zone. *Ices Journal of Marine Science*, *72*, 128-138. https://doi.org/10.1093/icesjms/fsu237

Dietterich, T. G. (2000). Ensemble methods in machine learning. *Multiple Classifier Systems*, *1857*, 1-15. https://doi.org/Doi 10.1007/3-540-45014-9_1

Ellis, C. D., Hodgson, D. J., Daniels, C. L., Collins, M., & Griffiths, A. G. F. (2017). Population genetic structure in European lobsters: implications for connectivity, diversity and hatchery stocking. *Marine Ecology Progress Series*, *563*, 123-137. https://doi.org/10.3354/meps11957

Fairfield, E. A., Richardson, D. S., Daniels, C. L., Butler, C. L., Bell, E., & Taylor, M. (2021). Ageing European lobsters (Homarus gammarus) using DNA methylation of evolutionarily conserved ribosomal DNA. *Evolutionary Applications*, *14*(9), 2305-2318. https://doi.org/10.1111/eva.13296

FAO-GFCM. (2021). *Report of the Working Group on Stock Assessment of Demersal Species (WGSAD) – Benchmark session for the assessment of common sole in GSA 17, Scientific Advisory Committee on Fisheries (SAC)*.

FIFS. (2004). *Fiskeriverkets föreskrifter (FIFS 2004:36) om fiske i*

Skagerrak, Kattegatt och Östersjön. Havs- och Vattenmyndigheten Retrieved from https://www.havochvatten.se/download/18.387f3a3018e62ceb8856fa1c/1711635579945/HVMFS-FIFS%202004-36%20keu%20240401.pdf

Fromentin, J. M., Bonhommeau, S., Arrizabalaga, H., & Kell, L. T. (2014). The spectre of uncertainty in management of exploited fish stocks: The illustrative case of Atlantic bluefin tuna. *Marine Policy*, *47*, 8-14. https://doi.org/10.1016/j.marpol.2014.01.018

Gibbons, J., & Chakraborti, S. (1992). *Nonparametric Statistical Inference*. Marcel Dekker.

Goode, A. G., Brady, D. C., Steneck, R. S., & Wahle, R. A. (2019). The brighter side of climate change: How local oceanography amplified a lobster boom in the Gulf of Maine. *Global Change Biology*, *25*(11), 3906-3917. https://doi.org/10.1111/gcb.14778

Hasslöf, O. (1949). *Svenska Västkustfiskarna: Studier i en Yrkesgrupps Näringsliv och Sociala Kultur.* . Svenska Västkustfiskarnas Centralförbund.

Hilborn, R. (2016). Correlation and Causation in Fisheries and Watershed Management. *Fisheries*, *41*(1), 18-25. https://doi.org/10.1080/03632415.2016.1119600

Hurtado-Ferro, F., Szuwalski, C. S., Valero, J. L., Anderson, S. C., Cunningham, C. J., Johnson, K. F., Licandeo, R., McGilliard, C. R., Monnahan, C. C., Muradian, M. L., Ono, K., Vert-Pre, K. A., Whitten, A. R., & Punt, A. E. (2015). Looking in the rear-view mirror: bias and retrospective patterns in integrated, age-structured stock assessment models. *Ices Journal of Marine Science*, *72*(1), 99-110. https://doi.org/10.1093/icesjms/fsu198

Hyndman, R., & Athanasopoulos, G. (2013). *Forecasting: principles and practice* http://otexts.com/fpp/

Hyndman, R. J., & Koehler, A. B. (2006). Another look at measures of forecast accuracy. *International Journal of Forecasting*, *22*(4), 679-688. https://doi.org/10.1016/j.ijforecast.2006.03.001

Jenkins, T. L., Ellis, C. D., Triantafyllidis, A., & Stevens, J. R. (2019). Single nucleotide polymorphisms reveal a genetic cline across the north-east Atlantic and enable powerful population assignment in the European lobster. *Evolutionary Applications*, *12*(10), 1881-1899. https://doi.org/10.1111/eva.12849

Kell, L. T., Kirnoto, A., & Kitakado, T. (2016). Evaluation of the prediction skill of stock assessment using hindcasting. *Fisheries Research*, *183*, 119-127. https://doi.org/10.1016/j.fishres.2016.05.017

Kell, L. T., Sharma, R., Kitakado, T., Winker, H., Mosqueira, I., Cardinale, M., & Fu, D. (2021). Validation of stock assessment methods: is it me or my model talking? *Ices Journal of Marine Science*, *78*(6), 2244-2255. https://doi.org/10.1093/icesjms/fsab104

Knutti, R., Furrer, R., Tebaldi, C., Cermak, J., & Meehl, G. A. (2010). Challenges in Combining Projections from Multiple Climate Models. *Journal of Climate*, *23*(10), 2739-2758. https://doi.org/10.1175/2009jcli3361.1

Le Bris, A., Mills, K. E., Wahle, R. A., Chen, Y., Alexander, M. A., Allyn, A. J., Schuetz, J. G., Scott, J. D., & Pershing, A. J. (2018). Climate vulnerability and resilience in the most valuable North American fishery. *Proceedings of the National Academy of Sciences of the United States of America*, *115*(8), 1831-1836. https://doi.org/10.1073/pnas.1711122115

Mazur, M. D., Tanaka, K. R., Shank, B., Chang, J. H., Hodgdon, C. T., Reardon, K. M., Friedland, K. D., & Chen, Y. (2022). Incorporating spatial heterogeneity and environmental impacts into stock-recruitment relationships for Gulf of Maine lobster. *Ices Journal of Marine Science*, *79*(2), 362-372. https://doi.org/10.1093/icesjms/fsab266

Merino, G., Urtizberea, A., Fu, D., Winker, H., Cardinale, M., Lauretta, M. V., Murua, H., Kitakado, T., Arrizabalaga, H., Scott, R., Pilling, G., Minte-Vera, C., Xu, H. K., Laborda, A., Erauskin-Extramiana, M., & Santiago, J. (2022). Investigating trends in process error as a diagnostic for integrated fisheries stock assessments. *Fisheries Research*, *256*. https://doi.org/ARTN10647810.1016/j.fishres.2022.106478

Methot, R. D., & Wetzel, C. R. (2013). Stock synthesis: A biological and statistical framework for fish stock assessment and fishery management. *Fisheries Research*, *142*, 86-99. https://doi.org/10.1016/j.fishres.2012.10.012

Methot, R. D., Wetzel, C. R., Taylor, I. G., Perl, E. F., Doering, K. L., & Johnson, K. F. (2024). Stock Synthesis User Manual Version 3.30.23. In: NOAA Fisheries.

Moland, E., Olsen, E. M., Knutsen, H., Knutsen, J. A., Enersen, S. E., André, C., & Stenseth, N. C. (2011). Activity patterns of wild European lobster in coastal marine reserves: implications for future reserve design. *Marine Ecology Progress Series*, *429*, 197-207. https://doi.org/10.3354/meps09102

Moland, E., Ulmestrand, M., Olsen, E. M., & Stenseth, N. C. (2013). Long-term decrease in sex-specific natural mortality of European lobster within a marine protected area. *Marine Ecology Progress Series*, *491*, 153-+. https://doi.org/10.3354/meps10459

Oresland, V., Oxby, G., & Oxby, F. (2020). Abundance and Size of European Lobsters (*Homarus gammarus*) and Brown Crabs (*Cancer pagurus*) inside and Outside the Kavra Lobster Reserve (West Coast of Sweden). *Crustaceana*, *93*(2), 157-169. https://doi.org/10.1163/15685403-bja10001

Oresland, V., & Ulmestrand, M. (2013). European lobster subpopulations from limited adult movements and larval retention. *Ices Journal of Marine Science*, *70*(3), 532-539. https://doi.org/10.1093/icesjms/fst019

Pechlivanidis, I. G., Gupta, H., & Bosshard, T. (2018). An Information Theory Approach to Identifying a Representative Subset of Hydro-Climatic Simulations for Impact Modeling Studies. *Water Resources Research*, *54*(8), 5422-5435. https://doi.org/10.1029/2017wr022035

Perry, D., Wikström, A., Sköld, M., Wennhage, H., & Sundelöf, A. (2025). Lobster-specific MPA offers little refuge for fish: Long-term closure does not compensate for insufficient size. *Ocean and Coastal Management*, *261*. https://doi.org/https://doi.org/10.1016/j.ocecoaman.2024.107535

Rowley, A. F., Cross, M. E., Culloty, S. C., Lynch, S. A., Mackenzie, C. L., Morgan, E., O'Riordan, R. M., Robins, P. E., Smith, A. L., Thrupp, T. J., Vogan, C. L., Wootton, E. C., & Malham, S. K. (2014). The potential impact of climate change on the infectious diseases of commercially important shellfish populations in the Irish Sea-a review. *Ices Journal of Marine Science*, *71*(4), 741-759. https://doi.org/10.1093/icesjms/fst234

Schmalenbach, I., & Franke, H. D. (2010). Potential impact of climate warming on the recruitment of an economically and ecologically important species, the European lobster (Homarus gammarus) at Helgoland, North Sea. *Marine Biology*, *157*(5), 1127-1135. https://doi.org/10.1007/s00227-010-1394-8

Sundelöf, A. (2023). European lobster. In V. Bartolino, B. Koehler, & L. Bergström (Eds.), *Climate effects on fish in Sweden – Species-Climate Information Sheets for 32 taxa in marine and coastal waters* (Vol. 17). Department of Aquatic Resources. . https://doi.org/https://doi.org/10.54612/a.4lmlt1tq5j

Sundelof, A., Bartolino, V., Ulmestrand, M., & Cardinale, M. (2013). Multi-Annual Fluctuations in Reconstructed Historical Time-Series of a European Lobster (Homarus gammarus) Population Disappear at Increased Exploitation Levels. *Plos One*, *8*(4). https://doi.org/ARTN e5816010.1371/journal.pone.0058160

Sundelof, A., Grimm, V., Ulmestrand, M., & Fiksen, O. (2015). Modelling harvesting strategies for the lobster fishery in northern Europe: the importance of protecting egg-bearing females. *Population Ecology*, *57*(1), 237-251. https://doi.org/10.1007/s10144-014-0460-3

Thomson, C. J. (1991). Effects of the Avidity Bias on Survey Estimates of Fishing Effort and Economic Value. *Creel and Angler Surveys in Fisheries Management*, *12*, 356-366. <Go to ISI>://WOS:A1991BX31V00043

Tredennick, A. T., Hooker, G., Ellner, S. P., & Adler, P. B. (2021). A practical guide to selecting models for exploration, inference, and prediction in ecology. *Ecology*, *102*(6). https://doi.org/ARTN e03336
10.1002/ecy.3336

Trijoulet, V., Albertsen, C. M., Kristensen, K., Legault, C. M., Miller, T. J., & Nielsen, A. (2023). Model validation for compositional data in stock assessment models: Calculating residuals with correct properties. *Fisheries Research*, *257*. https://doi.org/ARTN 10648710.1016/j.fishres.2022.106487

Ulmestrand, M. (2003). Reproduction of female lobsters (Homarus gammarus) on the Swedish west coast.*Can Tech Rep Fish Aquat Sci* Workshop on lobster (Homarus americanus and H. gammarus) reference points for fishery management held in Tracadie-Sheila New Brunswick,

Ulmestrand, M., & Loo, L.-O. (2009). *Fritidsfisket efter hummer hösten 2007* (I Fem studier av fritidsfiske 2002-2007., Issue. Fiskeriverket.

Winker, H., Carvalho, F., & Kapur, M. (2018). JABBA: Just Another Bayesian Biomass Assessment. *Fisheries Research*, *204*, 275-288. https://doi.org/10.1016/j.fishres.2018.03.010

Acknowledgement

The authors are grateful for the participation and contribution to the meetings from management bodies and industry representatives as well as from colleagues at SLU Aqua. The meetings were productive and all participants provided support to advance the assessment tools for lobster in Skagerrak, Kattegat and the Sound. A special thank you to Tonje Knutsen Sørdalen for sharing her immense knowledge on lobster ecology and management aspects from across Skagerrak as a scientific reviewer during this work. Thank you also to Johan Lövgren, SLU Aqua, for chairing the first of the two benchmark meetings, letting the authors concentrate on the details. Also a big thank you to Chris Griffiths and David Gilljam, SLU Aqua, for their insightful revision and development of a previous versions of this report.

Over the years many colleagues at Havsfiskelaboratoriet have provided knowledge, support, sweat and tears for the data collection on lobster, lobster catches or lobster fisheries. This work is built on your shoulders! Thank you!

7. Appendices

7.1 Appendix I - Climate effects on Lobster in Sweden

European lobster, *Homarus gammarus*, is a long-lived decapod crustacean living in rocky subtidal environments in the Mediterranean and Eastern Atlantic primarily down to 40 meters depth. It is a marine species distributed from the Mediterranean to the Northern Norwegian Sea. Adults are sensitive to elevated temperatures (above 22ºC) for physiological excretion of ammonium and larvae are sensitive to low salinity. These limitations result in the curbed distribution of European lobster in Swedish waters to Skagerrak, Kattegat and parts of Öresund and primarily distributed around or below the summer halocline.

European lobster has internal fertilization and a brooding time of 9-10 months, when females after excretion carry the fertilized eggs under the abdomen. Eggs hatch into a pelagic larval stage with 4 moults before it settles to a bottom dwelling life. Average size at sexual maturity is 78 mm carapax length (L50 of females) when the female is around 5-6 years old (Sundelof et al., 2015).

Crustacean biology is strongly temperature dependent. European and American lobsters (*Homarus gammarus*, *H. americanus*) are no exceptions and shifts in temperature may potentially affect several aspects of their biology (Coleman et al., 2021; Goode et al., 2019; Mazur et al., 2022). Although climate related changes in pH and salinity and availability of oxygen may have implications for lobster larvae and adults recent studies have focused on temperature.

Many studies during the past 10-15 years have been performed on American lobster, while fewer have covered the European lobster. Their life histories are very similar and inference on European lobster is assumed relevant from studies also on American lobster.

Increased temperature stress lobster larvae and narrows the settling habitat available at 12-16 degrees Celsius (Steneck & Wahle, 2013). This effect has been more pronounced in the southern distribution range for *H. americanus*, and less so in the more northern, due to colder ocean currents but also depending on the mixing due to large tidal amplitudes in the Gulf of Maine (Goode et al., 2019). Incorporating environmental variability and projections of future change has predicted decadal declines even in the northern range (Oppenheim et al., 2019). This seems to be, at least partly, driven by temperature effects on food items of the larvae (Calanus, (Greenan et al., 2019)).

Strong positive effects of temperature on adult growth rates have been documented on *H. gammarus* (Coleman et al., 2021). Furthermore time to hatching and larval development times were shortened by increased experimental temperatures at least up to 22 degrees Celsius (Schmalenbach & Franke, 2010), in turn leading to an increased survival through the larval phase. What effects such decreased mortality and increased growth rates will have on a harvested stock is not yet predicted. Warmer temperatures enhance growth rates at the expense of physiological stress that may cause loss of genetic variability and adaptability of *H. americanus* through temperature induced genetic erosion (Harrington et al., 2019). It has been suggested that maximum size limits for landing mitigates loss of adaptability through preservation of genetic variability on larger individuals and secured reproduction and recruitment (Le Bris et al., 2018).

More individuals with less genetic variability are thus assumed to reach post larval phase and affect recruitment positively. However, many individuals will by a faster individual growth rate more quickly recruit into the fishery. This may in turn lead to a fishery on fewer year classes and the average age of a reproducing individual to be younger.

Restrictive harvesting regulations may mitigate the effects of climate change. No-take-zones (NTZ) have strong local effects on population abundance (Knutsen et al., 2022) and will help preserve adaptability. Although shellfish diseases are not highly prevalent in lobster populations and temperature effects are uncertain (Rowley et al., 2014) diseases have been hypothesized to increase in NTZ although it has not been quantified (Davies et al., 2015). Lack of quantified increases in incidence of shellfish diseases in NTZ is perhaps due to the higher available genetic variability (Le Bris et al., 2018) that can be expected in the more abundant populations in NTZ.

Increased freshwater runoff may have detrimental effects on suitable settling grounds as the larval development is sensitive to a salinity below 17 ppt (Charmantier et al., 2001) affecting potential settling through a gradient of salinities. Settling at salinities below 17 ppt will be nonexistent and the geographical limit for 17 ppt may shift in the future due to increased runoff.

Table 6.10. Climate change processes and responses, key conclusions

European lobster

Process	Response to climate change	Reference
Mortality	Temperature provokes early hatching Faster larval growth decreases early life stage mortality	Schmalenbach & Franke (2010)
Maturation	Warming increases growth rate and implicitly early maturation	Coleman et al (2021)
Growth	Faster larval growth and genetic erosion Faster adult growth rates, anticipates recruitment to fishery	Schmalenbach & Franke (2010), Harrington et al. (2019) Coleman et al (2021)
Settling	Warmer water compresses available habitat for settling Reduced salinity below 17 ppt inhibits settling	Steneck & Wahle (2013) Charmantier et al. (2001)

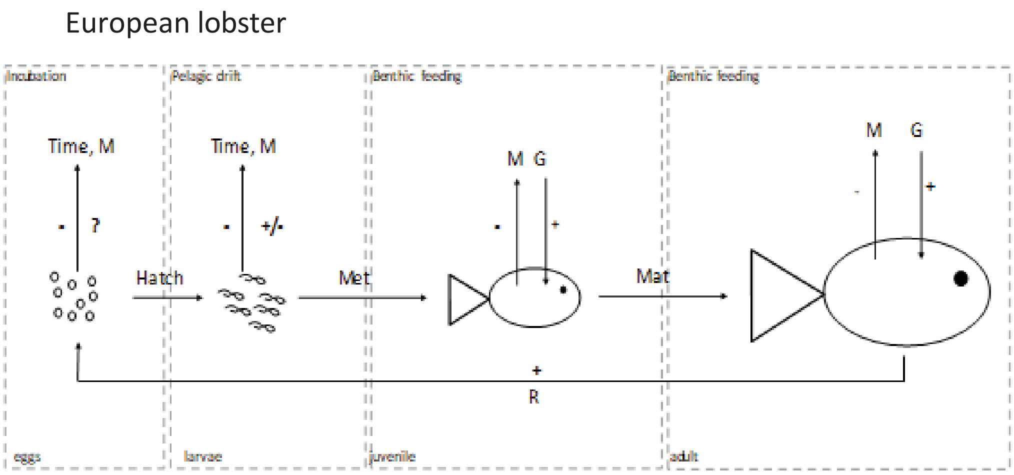


Figure 6.10. Schematic of expected impact of warming on main life stages and processes. The elements included are hatching (Hatch), metamorphosis (Met), maturity (Mat), natural mortality (M), growth (G) and recruitment (R). A plus sign (+) refers to an expected increase in the rate of the process as a consequence of climate change, a minus sign (-) to an expected decrease, (~) to no expected change, (±) to contrasting effects with uncertain net effect, and (?) to an unknown effect.

Key references

Charmantier, G., Haond, C., Lignot, J. H., & Charmantier-Daures, M. (2001). Ecophysiological adaptation to salinity throughout a life cycle: A review in homarid lobsters. Journal of Experimental Biology, 204(5), 967-977. <Go to ISI>://WOS:000167568800016

Coleman, M. T., Agnalt, A. L., Emmerson, J., Laurens, M., Porter, J. S., & Bell, M. C. (2021). From the Adriatic to Northern Norway-geographic differences in moult increment and moult probability of the European lobster (Homarus gammarus), across the natural range. Ices Journal of Marine Science, 78(2), 611-620. https://doi.org/10.1093/icesjms/fsaa172

Davies, C. E., Johnson, A., Wootton, E. C., Greenwood, S. J., Clark, K. F., Vogan, C. L., & Rowley, A. F. (2015). Effects of population density and body size on disease ecology of the European lobster in a temperate marine conservation zone. Ices Journal of Marine Science, 72, 128-138. https://doi.org/10.1093/icesjms/fsu237

Goode, A. G., Brady, D. C., Steneck, R. S., & Wahle, R. A. (2019). The brighter side of climate change: How local oceanography amplified a lobster boom in the Gulf of Maine. Global Change Biology, 25(11), 3906-3917. https://doi.org/10.1111/gcb.14778

Greenan, B. J. W., Shackell, N. L., Ferguson, K., Greyson, P., Cogswell, A., Brickman, D., Wang, Z. L., Cook, A., Brennan, C. E., & Saba, V. S. (2019). Climate Change Vulnerability of American Lobster Fishing Communities in Atlantic Canada. Frontiers in Marine Science, 6. https://doi.org/ARTN 57910.3389/fmars.2019.00579

Harrington, A. M., Tudor, M. S., Reese, H. R., Bouchard, D. A., & Hamlin, H. J. (2019). Effects of temperature on larval American lobster (Homarus americanus): Is there a trade-off between growth rate and developmental stability? Ecological Indicators, 96, 404-411. https://doi.org/10.1016/j.ecolind.2018.09.022

Knutsen, J. A., Kleiven, A. R., Olsen, E. M., Knutsen, H., Espeland, S. H., Sordalen, T. K., Thorbjornsen, S. H., Hutchings, J. A., Fernandez-Chacon, A., Huserbraten, M., Villegas-Rios, D., Halvorsen, K. T., Kleiven, P. J. N., Langeland, T. K., & Moland, E. (2022). Lobster reserves as a management tool in coastal waters: Two decades of experience in Norway. Marine Policy, 136. https://doi.org/ARTN 10490810.1016/j.marpol.2021.104908

Le Bris, A., Mills, K. E., Wahle, R. A., Chen, Y., Alexander, M. A., Allyn, A. J., Schuetz, J. G., Scott, J. D., & Pershing, A. J. (2018). Climate vulnerability and resilience in the most valuable North American fishery. Proceedings of the National Academy of Sciences of the United States of America, 115(8), 1831-1836. https://doi.org/10.1073/pnas.1711122115

Mazur, M. D., Tanaka, K. R., Shank, B., Chang, J. H., Hodgdon, C. T., Reardon, K. M., Friedland, K. D., & Chen, Y. (2022). Incorporating spatial heterogeneity and environmental impacts into stock-recruitment relationships for Gulf of Maine lobster. Ices Journal of Marine Science, 79(2), 362-372. https://doi.org/10.1093/icesjms/fsab266

Oppenheim, N. G., Wahle, R. A., Brady, D., Goode, A. G., & Pershing, A. J. (2019). The cresting wave: larval settlement and ocean temperatures predict change in the American lobster harvest. Ecological Applications, 29(8). https://doi.org/10.1002/eap.2006

Rowley, A. F., Cross, M. E., Culloty, S. C., Lynch, S. A., Mackenzie, C. L., Morgan, E., O'Riordan, R. M., Robins, P. E., Smith, A. L., Thrupp, T. J., Vogan, C. L., Wootton, E. C., & Malham, S. K. (2014). The potential impact of climate change on the infectious diseases of commercially important shellfish populations in the Irish Sea-a review. Ices Journal of Marine Science, 71(4), 741-759. https://doi.org/10.1093/icesjms/fst234

Schmalenbach, I., & Franke, H. D. (2010). Potential impact of climate warming on the recruitment of an economically and ecologically important species, the European lobster (Homarus gammarus) at Helgoland, North Sea. Marine Biology, 157(5), 1127-1135. https://doi.org/10.1007/s00227-010- 1394-8

Steneck, R. S., & Wahle, R. A. (2013). American lobster dynamics in a brave new ocean. Canadian Journal of Fisheries and Aquatic Sciences, 70(11), 1612-1624. https://doi.org/10.1139/cjfas-2013-0094

Sundelof, A., Grimm, V., Ulmestrand, M., & Fiksen, O. (2015). Modelling harvesting strategies for the lobster fishery in northern Europe: the importance of protecting egg-bearing females. Population Ecology, 57(1), 237-251. https://doi.org/10.1007/s10144-014-0460-3

Authored by Andreas Sundelöf

Original reference is:

Sundelöf, A. (2023) European lobster. In Bartolino, V., Koehler, B., Bergström, L. (2023). Climate effects on fish in Sweden – Species-Climate Information Sheets for 32 taxa in marine and coastal waters. Aqua notes 2023:17. Uppsala: Department of Aquatic Resources. https://doi.org/10.54612/a.4lmlt1tq5j

From the proceedings:

Bartolino, V., Koehler, B., Bergström, L. (2023). Climate effects on fish in Sweden – Species Climate Information Sheets for 32 taxa in marine and coastal waters. Aqua notes 2023:17. Uppsala: Department of Aquatic Resources. https://doi.org/10.54612/a.4lmlt1tq5j

7.2 Appendix II – Sundelöf et al. PLOS 2013

Original reference is:

Sundelöf A, Bartolino V, Ulmestrand M, Cardinale M (2013) Multi-Annual Fluctuations in Reconstructed Historical Time-Series of a European Lobster (Homarus gammarus) Population Disappear at Increased Exploitation Levels. PLoS ONE 8(4): e58160. doi:10.1371/journal.pone.0058160

Can be freely downloaded from:

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0058160

7.3 Appendix III – VCD2017 - recent recreational diaries

Emmelie Hammenstig-Åström

In Sweden, fishery-dependent lobster fishing data and catch records are collected from several sources. One of these sources was initiated by SLU-Aqua which includes voluntary journals, e.g. diary records, written by professional fishermen, or recreational fishermen. These journals, i.e. catch logs, have been compiled and used to provide support for additional parameters (see this report) which are then included in the stock analysis that forms the basis for the status assessment in the presentation of "Fiskbarometern" (Larsson et al. 2024).

Since 2017, SLU assembles voluntary catch journals e.g. diaries, where contact information to recreational fishermen and a few professional lobster fisheries are collected using the information on the floating buoys of the fishing gear. This is followed by an interview where individuals are invited to participate in track record of providing journals of their lobster fishing and catches. This is entirely based on voluntary participation and the goal is to complement the weaker data records from the commercial logbook. During 2022, the collection of information from recreational fishers slightly changed based on the results from a few assumptions that were made (see specifics below). We will go through these assumptions and explain their influence on the provided data that can be used in the stock analysis model (Stock Synthesis 3, SS3).

Thanks to this type of fishery-dependent data, trends and fishing patterns provide increased information first and foremost about the recreational lobster fisheries in Sweden, as well as index calculations that later can be used in the SS3 model.

The journals that SLU obtain from the voluntary catch records are relatively few in the light of how many recreational lobster fishermen that every season join the fishery. As there is no register before or after fishing starts, estimates are based on the number of floatation buoys. Since the new VCD2017 started, there has been approximately 24-40 participants annually that contribute to the records. The VCD2017-logs may also include more than one person per submitted journal, i.e. two people fish with 12 pots, and family and relatives can report as one group, household etc. The main regulation of six pots per fishing person is used to back-calculate the effort.

In the VCD2017, fishermen report their catches (figure 1) as above minimum size length (MSL), below MSL (these have to be released immediately) and berried females (female carrying eggs underneath the tail, these have to be released immediately as well). The provided information has a high accuracy in terms of how often fishermen pull their pots during a season, catch distribution, rates between the size classes and berried females and for how long fisheries continues in the autumn. This information can be used to get average of fishery patterns, and this information forms the basis for calculations of fishing effort and catch per draw as well as the fishery indices such as catch and landings per unit effort (CPUE and LPUE).

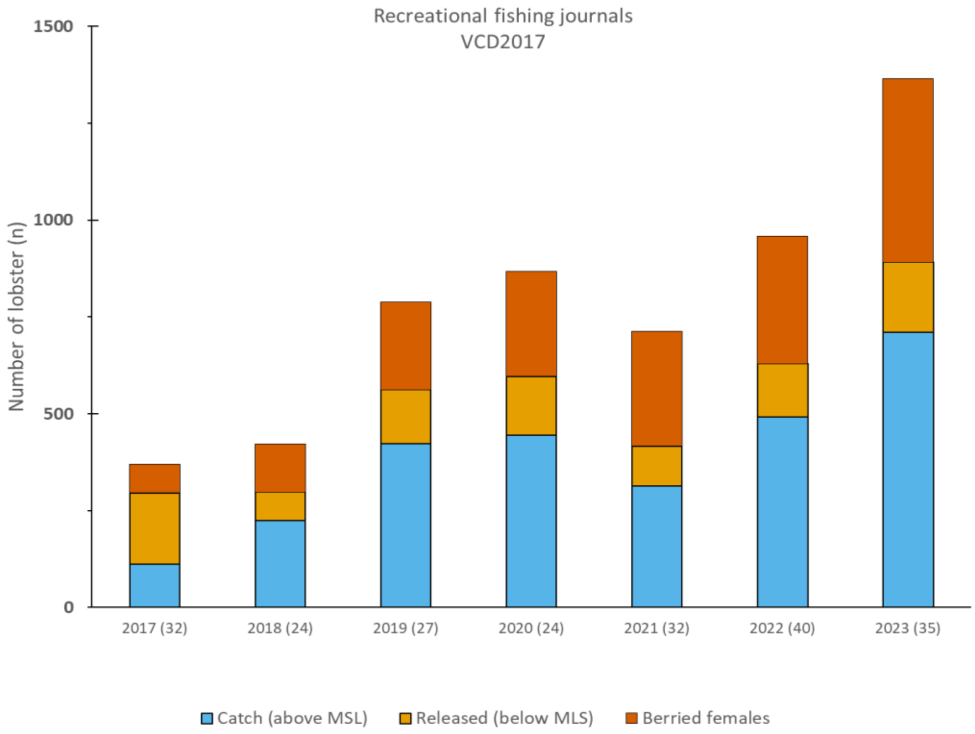


Figure 1. Number of lobsters reported in VCD2017 fishing, separated into the three different categories, above minimum size length (MSL), below MSL, and berried females. The number in parenthesis behind the years at the x-axis indicate the number of journals returned to SLU, at the Institute of marine research in Lysekil.

The length of the lobster fishing season varies annually and can differ up to a week because of the variable start date (first Monday 7 o’clock, after September 20th). As an example, the premiere 2020 took place Sep. 21st whereas the year after, 2022, the premiere was Sep 27th instead. The end of the season is November 30th for recreational fishers, and December 31st for professional, licenced lobster fishermen, regardless of the starting date. The weeks 39 to 40 captures the same period annually.

Assumptions to the modelled work

Fishing practices changes through the season, the pots being pulled less frequently later in the season and shifts in spatial distribution as recreational fishers have a shorter season opening up the entire coastal region for commercial fishers from 1st December (figure 2). Also catch rates are assumed to be affected by the extraction of harvest, leaving fewer lobsters available to the fishery. Soak time is very difficult to extract from the journals. However, early in the season pots are pulled a lot more frequently and soak time is assumed to have a lesser effect on catch. It is a rapid decrease in fishing intensity (number of pulled pots), after the first weeks and many fishermen end their fishing season early. The combination of these factors leads to a general conclusion to focus on a subset of the information in the journals, using only the first two weeks of the fishery after season opening.

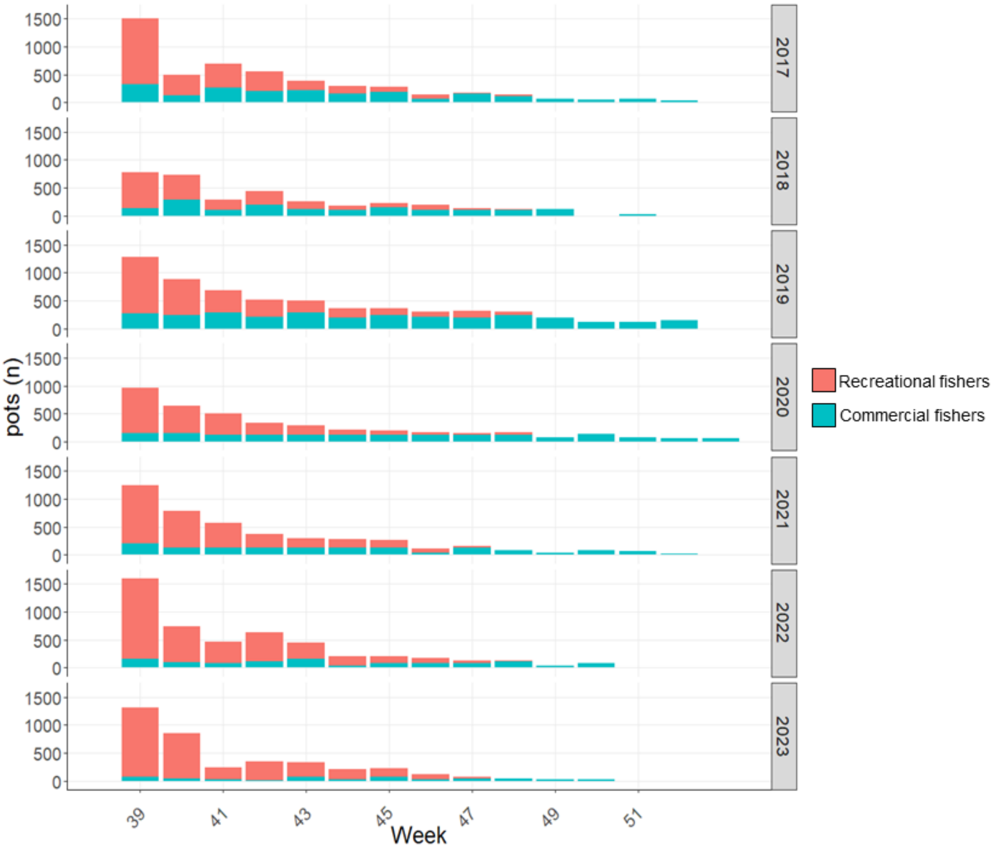


Figure 2. Number of pulled pots per week. The first week of the fishing season tend to have the greatest number of pulled pots and then the intensity in the fisheries decreases.

As the length of the season to the index was set to two weeks, we further tested potential variability in experience, geographical knowledge and fishery-patterns, and if this would influence the index used for the SS3 model. Á priori set ups of data were analyzed to determine the potential difference among the level of experience of fishermen that report their catches to SLU (Table 1). Level of experience was documented from previous interviews with reporting fishermen. The following groups were compared: 1] randomly selected lobster fishers, recruited from previously counted buoys and the information from these. 2] all lobster fishers (regardless of year and how much experience they previously had, before the recruitment), 3] less experienced lobster fishermen, (fishermen with less experience in terms of both lobster fisheries <5 years and little geographical knowledge of the area). Table 1 shows the small difference (2nd decimal) in nominal CPUE of both total catch and landed catch between the different sub groups of fishers.

Table 1. The outcome in the a priori tests represents no major difference in catch per unit effort (CPUE), based on the two first weeks of the Swedish recreational lobster fisheries).

	1] Randomly selected		**2] All lobster fishers**		**3] Less experience**	
	CPUE (above MSL)	*CPUE (all catches)*	*CPUE mål (above MSL)*	*CPUE (all catches)*	*CPUE mål (above MSL)*	*CPUE (all catches)*
2017	0.06	0.16	0.06	0.16	0.06	0.15
2018	0.15	0.26	0.14	0.25	0.16	0.25
2019	0.16	0.31	0.16	0.30	0.15	0.28
2020	0.22	0.44	0.22	0.43	0.23	0.44
2021	0.12	0.26	0.12	0.28	0.11	0.24
2022	0.15	0.30	0.15	0.30	0.15	0.28

Hence, table 1 indicates that the previous recruitment of VCD’s through the buoy-counting and randomly collected information of fishermen as well as experienced lobster fishers does not have a strong impact on the index of catch per unit effort. This is most likely an effect of fisher avidity, and the more active and engaged fishers, that generally have more experience, are the ones that voluntarily report catch diaries to SLU. The less avid fishers often drop out before they even start reporting. It implies that the recruitment of fishermen and their journals could be performed by more efficient methods. Also, despite a large effort to randomize information from fishermen and their lobster catches, we see that the recruits from the voluntary catch diaries are experienced lobster fishers and most likely engaged in the fisheries and monitoring of the species as they chose to participate in the survey and also return their diaries to SLU in Lysekil.

The number of pots pulled per week decreases sharply as the season progresses (figure 2). There is also a risk that CPUE per week decreases, fluctuates and become influenced by the few numbers of fishermen that continue through-out the late season.

From the potential scenarios of selecting data depending on

- Length of the season (i.e. full season, or a limited number of weeks).
- Skills and experience among recreational lobster fishers that participate in the VCD- work (presented in table 1).

It was decided, based on the analyses and arguments above, to limit the data for standardization of CPUE to weeks 39 and 40, including soak nights for that period (the first two weeks of the season) and include all of the reporting fishermen.

Model formulation

As the lobster catch data are counts of lobsters, with many zeros and typically poisson distributed variance the standardization was done with a generalized linear model with a Poisson model as variance estimator using Year as a fixed factor, fisher_id as a random variable and offsetting number of pots and soak nights. The final model formulation was:

```
   lob_num ~ factor(Year) + (1 | fisher_id) + offset(log(pots)) +
offset(log(soak_nights))
```

Coding and analysing was done in R using R-Studio. The output estimate was on log scale and transformed back to normal scale (Table 2).

Table 2: Output of the glm-model on lobster counts in pots. Estimate and Standard Error (SE) of the fixed factor Year is on log scale. SE on log scale is used in SS3 but estimates are back transformed to normal scale for use in SS3.

Year	Estimate on log scale	Back transformed to real scale	Estimated SE on log scale	z value	Pr(>|z|)	
2017	-2.1418	0.11744	0.398	4.133	3.58E-05	***
2018	-1.7775	0.16906	0.3968	5.064	4.12E-07	***
2019	-1.4295	0.23943	0.3956	5.959	2.54E-09	***
2020	-1.2917	0.27480	0.3958	6.304	2.89E-10	***
2021	-1.4283	0.23972	0.396	5.956	2.59E-09	***
2022	-1.4097	0.24422	0.3962	6	1.98E-09	***
2023	-1.0597	0.34656	0.3956	6.893	5.45E-12	***

Diagnostics

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) ['glmerMod']
```

```
   Family: poisson  ( log )
   Formula: lob_num ~ factor(Year) + (1 | fisher_id) + offset(log(pots))
+                                            offset(log(soak_nights))
Data:                                                                tmp
     AIC                  BIC          logLik    deviance    df.resid
  7972.6        8092.8      -3963.3        7926.6                1352

Scaled                                                     residuals:
    Min                1Q      Median              3Q              Max
-5.0677     -0.9480           0.0506          1.0322           9.2906

Random                                                       effects:
 Groups Name                      Variance    Std.Dev.
 fisher_id (Intercept)            0.2544      0.5044

Number     of     obs:     1375,     groups:         fisher_id,     98
```

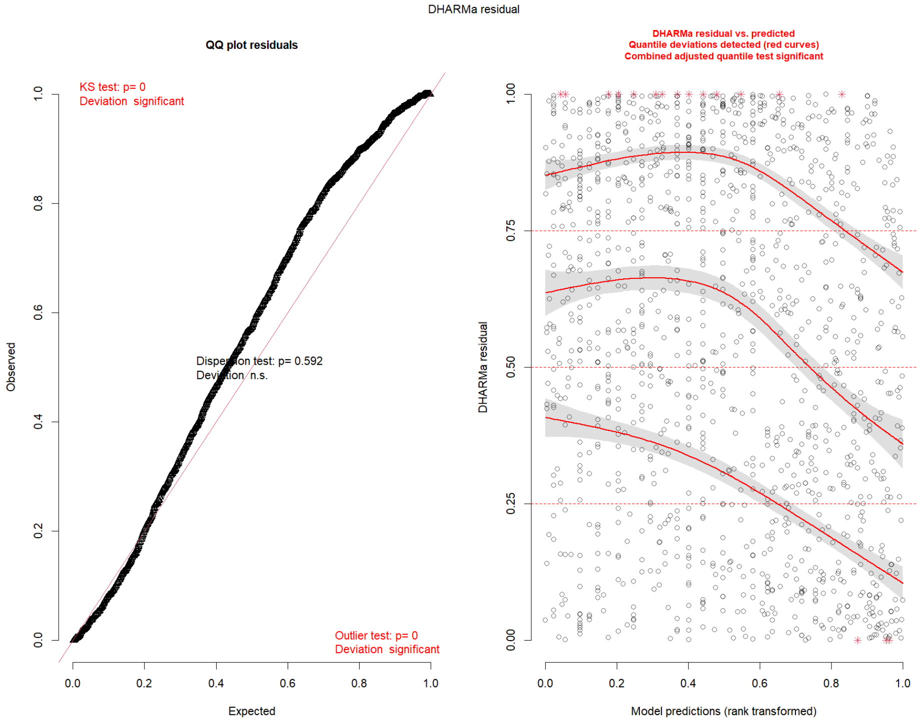


Figure 3. Residual analyses. Dispersion test insignificant but KS- and outlier test significant.

We ran a DAHRMa-residual (Hartig, 2024) to check the diagnostics to the Poisson model (Figure 3) and the non-significant result (p = 0.592) from the dispersion test indicates that there is no strong evidence for over-dispersion of our VCD data. Hence, it also supports that the Poisson model is appropriate in terms of variance structure. Regarding the significant deviation of the KS-test, this could indicate that the residuals are not matching perfectly a Poisson distribution. Further, outliers are expected in our data set and the Poisson model can be relatively robust to outliers, in particular if these have a minor influence on parameter estimates. The Poisson model was chosen based on the abovementioned conclusions to include both variables; soak time and pots in the analysis.

References

Hartig, F. 2024. DHARMa: Residual Diagnostics for Hierarchial (Multi-Level / Mixed) Regression Models. R package version 0.4.7, http://florianhartig.github.io.DHARMa/

Larsson, S., Svensson F., Wennhage, H., Olsson, J. (2024). Indikatorrapportering för “Hållbart nyttjande av fisk- och skaldjursbestånd i kust och hav”: bedömningsåret 2023. Aqua notes 2024:6. Uppsala: Sveriges lantbruksuniversitet. https://doi.org/10.54612/a.1p05qqkdqa

Posit team (2024). RStudio: Integrated Development Environment for R. Posit Software, PBC, Boston, MA. URL http://www.posit.co/.

7.4 Appendix IV - Tourist journals

Emmelie Hammenstig Åström

The Swedish Agency for Water and marine Management (SwAM) may issue special permits for fishing, and exemptions from regulations. Tourist fishing operators, fishing as recreational fishers but with customers on-board, may apply for such exemptions, in order to use more than six pots in their fishing operations. Conditions for these exemptions from the regulations include keeping a detailed journal of catch and effort. Instead of six pots per fisher used in the recreational lobster fishery, these Tourist fishers can use as many as 50 pots per registered person or operator. Apart from the number of gears, these operators follow the regulations of recreational fishers concerning season length and the non-sale of landing with an addition of a baglimit of landing a maximum of 2 lobsters per guest. This segment of the lobster fishing fleets is called Tourist fishers, and in the SS3 model it is called Safari.

At SLU-Aqua, there is information of lobster catches from commercial tourist permits since 2014. Monthly, operators need to report information about their trips and number of guests as well as the number of pulled pots and lobster catches (above MSL, released and berried females) to SwAM.

The detailed catch log for tourist permits, is used to calculate a catch per unit effort index, and as all operators need to report their trips, the basis provides a total number of all catch, and we get an absolute number for the amount of lobster caught in the Tourist fisheries annually. Annual lobster catches from all categories are presented below (figure 1).

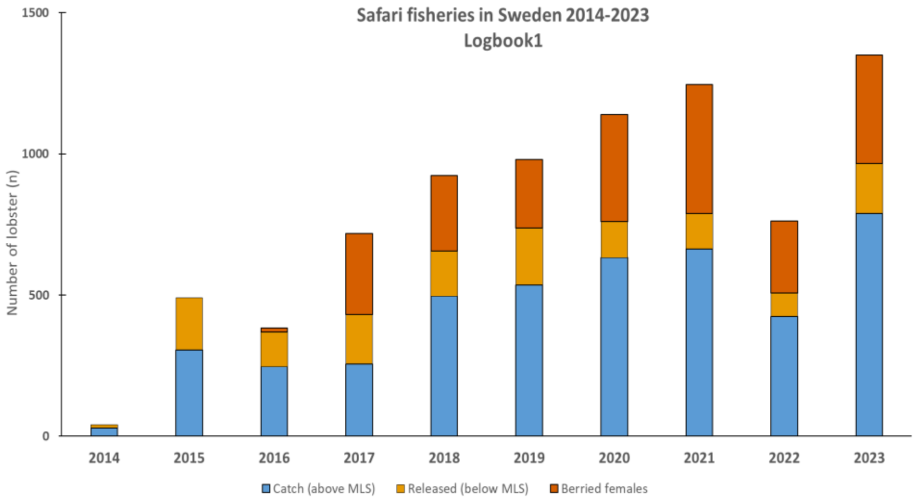


Figure 1. Total number of lobsters caught in the Swedish Tourist fishery annually.

In 2023, there were 55 permits from SwAM to Tourist operators along the Swedish west-coast. Similarly, as for the VCD_2017 journals, there is an intense start at the week of the lobster premiere, and then a decrease in number of pulled pots per week (figure 2). For some years, there is a steep decline in the fisheries and further, notable is also week 44 which pop up for a few years as this week is known to be the autumn holiday for elementary schools in Sweden.

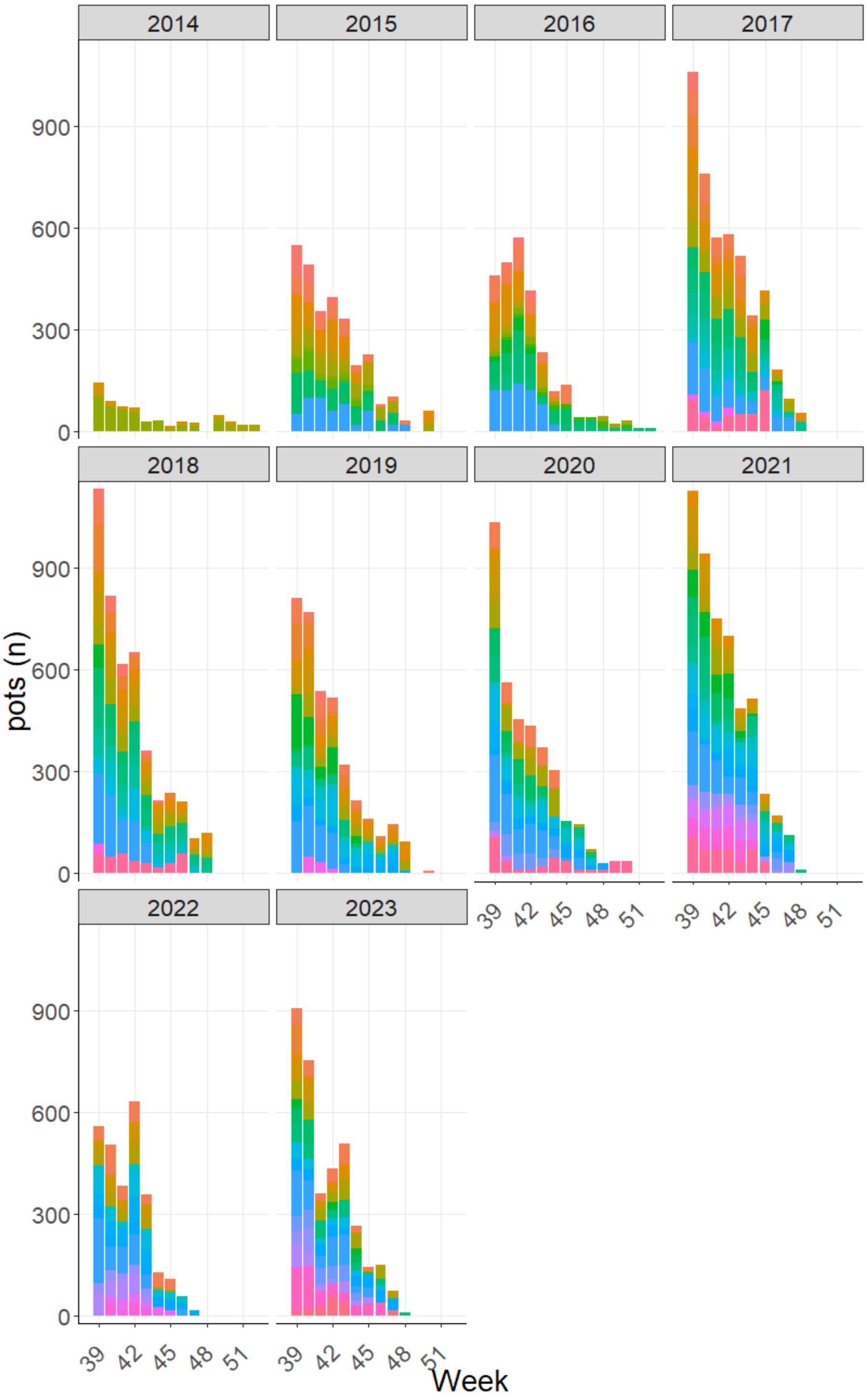


Figure 2. Number of pulled pots per week in the stipulated commercial Tourist fishery. The different colours correspond to operator permits (in total 55 permits for 2023).

Assumptions

Fishing practices changes through the season, the pots being pulled less frequently later in the season and shifts in spatial distribution as recreational fishers have a shorter season opening up the entire coastal region for commercial fishers from 1st December. Also catch rates are assumed to be affected by the extraction of harvest, leaving fewer lobsters available to the fishery. Soak time was not possible to extract from the Tourist journals. Depending on the demand on the operators, they may pull variable number of pots per fishing day. This quickly leads to a loss of precise soak time information in the journals. However, early in the season pots are pulled a lot more frequently and soak time is assumed to be more uniform, also for the Tourist fleet, and have a lesser effect on catch.

Following the same reasoning of how the lobster fishery progresses over the season (above and in Appendix III and V) the catch data was not used in its entirety. It was decided, based on the analyses and arguments above (and in Appendix III and V), to limit the data for standardization of CPUE to weeks 39 and 40, and not include soak nights for that period (the first two weeks of the season).

Model formulation

As the lobster catch data are counts of lobsters, with many zeros and typically Poisson distributed variance the standardization was done with a generalized linear model with a Poisson model as variance estimator using Year as a fixed factor, fisher_id as a random variable and offsetting number of pots. The final model formulation was:

```
lob_num ~ factor(Year) + (1 | fisher_id) + offset(log(pots))
```

Coding and analysing was done in R using R-Studio. The output estimate was on log scale and transformed back to normal scale (Table 1).

Table 1. Output of the glm-model on lobster counts in pots. Estimate and Standard Error (SE) of the fixed factor Year is on log scale. SE on log scale is used in SS3 but estimates are back transformed to normal scale for use in SS3.

Year	Estimate on log scale	Backtransform to real scale	Estimated SE	z value	Pr(>|z|)	
2014	-1.4674	0.2305	0.2271	-6,462	1.03E-10	***
2015	-0.8271	0.4373	0.229	2,791	0.005253	**
2016	-1.1893	0.3044	0.23	1,209	0.226754	
2017	-1.0259	0.3585	0.2273	1,943	0.05205	
2018	-0.9273	0.3956	0.2268	2,381	0.017244	*
2019	-0.8216	0.4397	0.2266	2.85	0.004372	**
2020	-0.4013	0.6694	0.2257	4,724	2.32E-06	***
2021	-0.6824	0.5054	0.2254	3,483	0.000496	***
2022	-0.5019	0.6054	0.2268	4,257	2.07E-05	***
2023	-0.3269	0.7212	0.2254	5,059	4.21E-07	***

Diagnostics

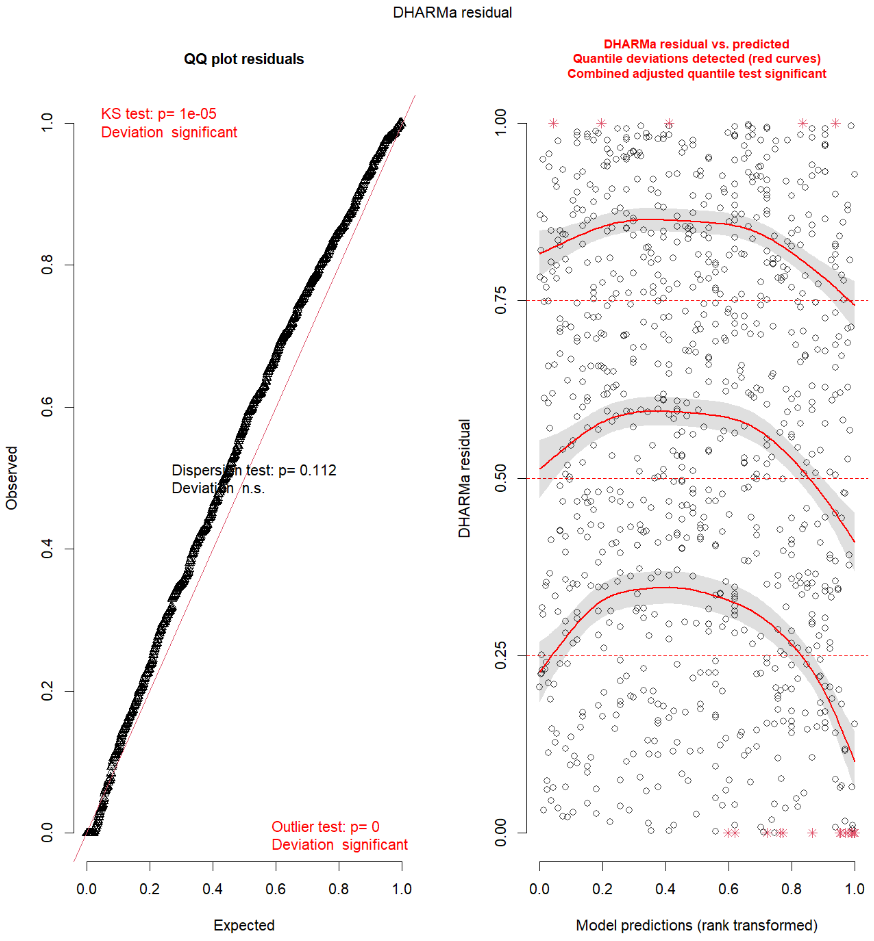


Figure 3. Residual analyses. Dispersion test insignificant but KS- and outlier test significant.

We standardized the data for the Tourist-fisheries and used a Poisson-model where the dispersion test (DHARMa package R, Hartig, 2024) indicates no significant overdispersion (p = 0.112) and where the variance structure support that we can proceed using a Poisson model.

The deviations in the KS test and outlier test indicate minor imperfections in the residuals, however, does not necessarily nor substantially affect the model's overall validity.

Our model provides reliable inferences about the relationships between the predictors and our outcome, even if the residuals does not align perfectly with a Poisson distribution. Additionally, the model's performance in terms of prediction and inference remains strong, and thus, support the idea that our choice to use the Poisson model is reasonable despite the minor residual deviations.

References

Hartig, F. 2024. DHARMa: Residual Diagnostics for Hierarchial (Multi-Level / Mixed) Regression Models. R package version 0.4.7, http://florianhartig.github.io.DHARMa/

Posit team (2024). RStudio: Integrated Development Environment for R. Posit Software, PBC, Boston, MA. URL http://www.posit.co/

7.5 Appendix V - Commercial lobster fishermen in Halland with stipulated journals

Andreas Sundelöf

Since 2000 a number of commercial fishermen have filled a compulsory journal as a terms for the exemption of rules for number of allowed gears. Originally the journal reported on legal individuals and berried individuals. In 2017 the regulation on minimum landing size changed (80 mm to 90 mm) but not size of escape gaps (maximum diameter 54 mm), resulting in a larger part of the catch to be released. The regulation of escape gaps was later changed to a larger diameter (60 mm) and some exemptions included the small escape gaps providing an opportunity to inspect and record size categories of lobsters such that the original categories of MLS = 80mm could be recalculated also for the years after 2017. Although the journal is ambitious the reporting has not been error free, and the true size categories prove difficult to recalculate. For example the data 2000 to 2016 does not report undersized returns. And from 2017 and afterwards the size categories risk to be difficult to interpret.

From the 2017 journal the following column names and meanings exist

Number	Column name	renaming	issue
1	Antalet lovliga humrar	above_MLS	some years only LPUE exist!!
2	Återutsatt (CL 80-900mm)	returned_8090	
3	Åter 80-90 Hona	returned_8090_female	could be double counted females
4	Åter 80-90mm Hanne	returned_8090_male	
5	åter 80-90 varav romhona	returned_8090_berried	
6	Antalet återutsatta romhumrar (över 90mm 2017-18)	management rule, returned_berried	after 2017 some should be reported in 5
7	Totalt återsatta humrar inkl romhona(2017-18)	returned_1718	not exist before 2017
8	total fångst inkl romhonnor	Total catch	Not total catch until 2017

As the reporting was not provided for all returned individuals this document outlines the calculation of an index following the same assumptions on the data, but a change in the size composition due to regulation change in 2017.

Management dependent index CPUE: above_MLS+returned_17_18/pots

Management dependent index LPUE: above_MLS/pots

The catch per unit effort (CPUE) is not a true catch as it lacks number of undersized individuals. The landing per unit effort (LPUE) however, is a true LPUE following the minimum landing size (MLS) change in 2017

Data

Landings (and partly catch) data by fishing day is provided by the county administration of Halland.

A lot of effort was put into trying to salvage the size category data but in the end time constraints forced the dismissal of the more detailed data. Going through the data line by line may result in something more useful from 2017 onwards. To not risk calculating an index with double counted individuals, inflating the possible biomass, a management dependent index was calculated. An LPUE can be readily used, and the CPUE is calculated by combining legal and returned berried females.

Management index LPUE was calculated as: aboveMLS/pots

Management index CPUE was calculated as: aboveMLS+returned1718/pots

Data was inspected for consistency and then proceeded with conversions of data for later modelling purposes.

Date conversions

Adding days and weeks for filtering of catch data. Harvest of lobsters during seasonal fishery removes individuals above a certain size and without external eggs. As fishing intensity has been high for a long time, an assumption is that the proportion returned individuals will increase during the season. To get comparable indices between years only the first weeks of the fishery are used for index calculations. The season always open on a Monday, thus number of weeks is a neat variable to used for index calculation. Periods of different lengths and their effect on the index are evaluated.

Summary statistics

Catch and effort

Weekly data show the change in fishery over time. Soak time was cleaned from NAs and Catch and effort by week shows fishing patterns through the year and was recorded only since 2017 (Figure 1).

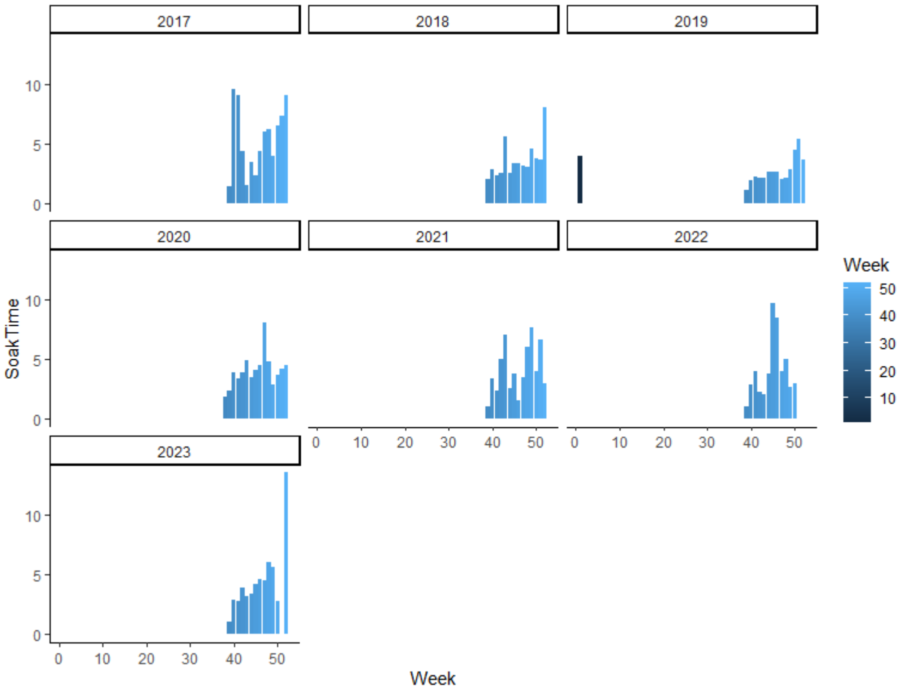


Figure 1. Available data on soak time.

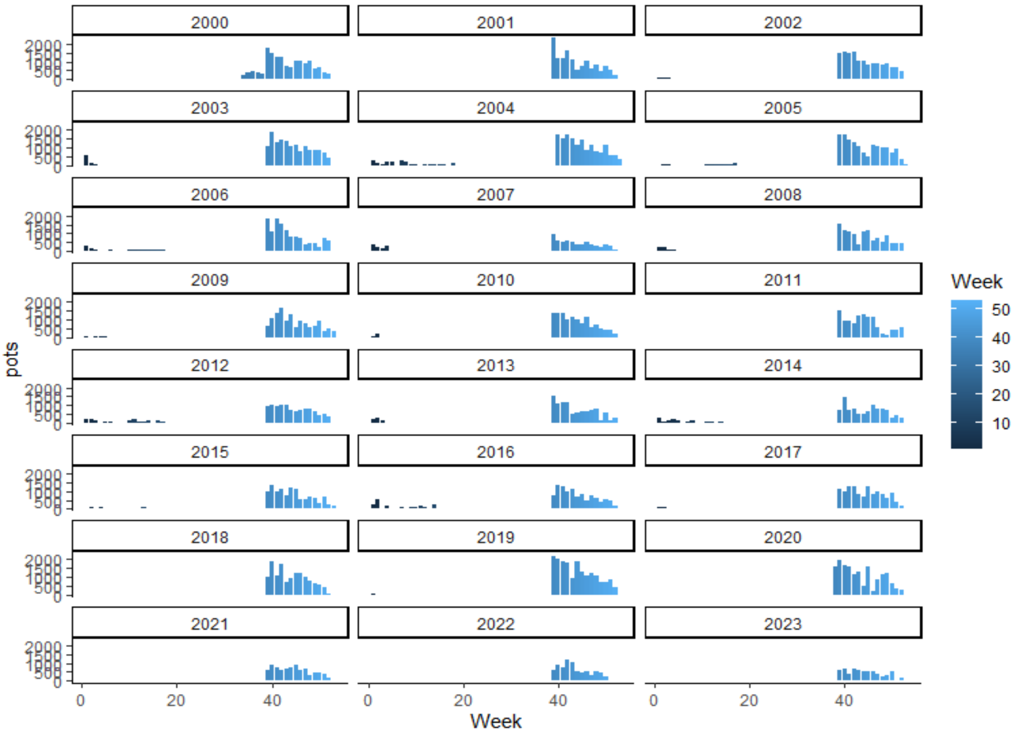


Figure 2. Number of pots pulled per week.

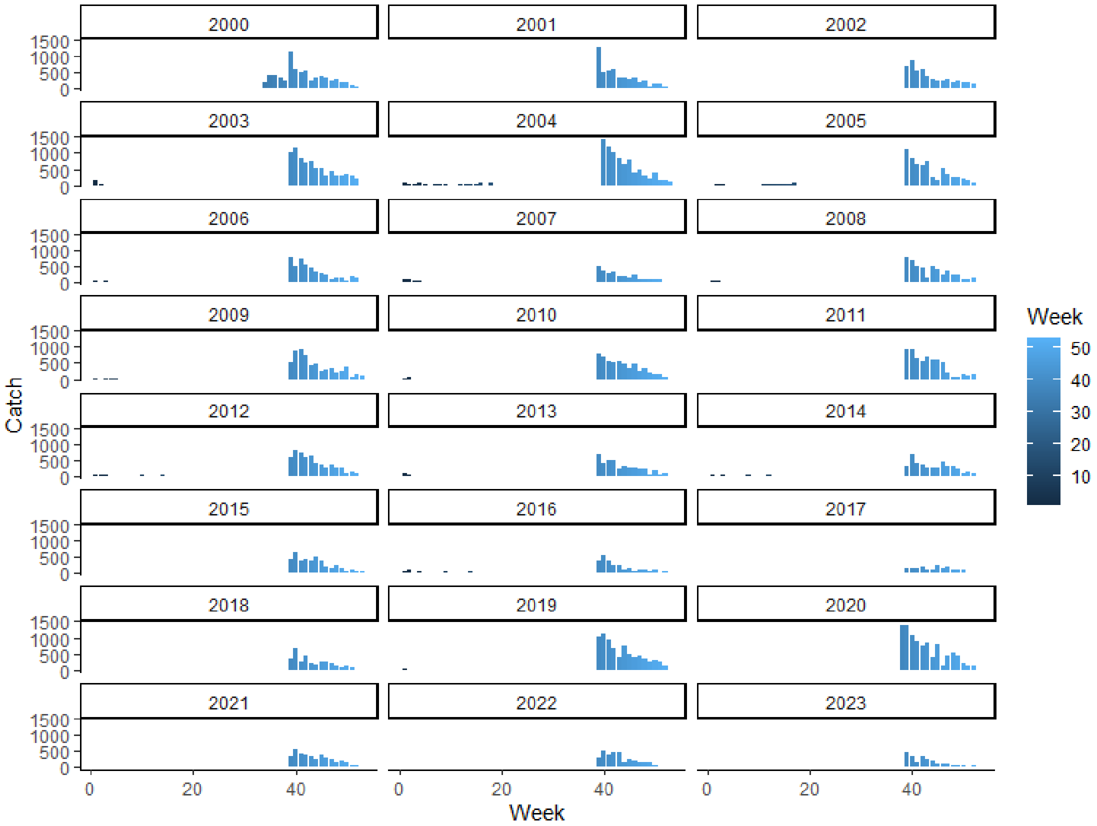


Figure 3. Number of lobsters caught by week.

Proportion berried can be looked at by week to asses seasonal change and by year for temporal trends. Trends in effort is shown by aggregation of weekly number of pots, but shows only the commercial trends, and may be strongly influenced by weather/weekday etc

An overview of amount of records in the data. Count of pots and lobsters (landed) per week per year (Figure 2 and 3). Same data tabulated below by fishers, pots, caught (landed + berried females) and landed.

Table 2. Number of Fishers, Pots, LST Total (landed + berried females), total reg (test on all types of registered lobsters), Landed (used for index)

Year	Fishers	Pots	LST Total	total reg	Landed
2000	7	14894	9031	6798	6798
2001	7	13226	6543	5016	5016
2002	7	14564	6501	5148	5148
2003	7	15536	10064	7898	7898
2004	7	16958	10925	8825	8825
2005	7	15327	8414	6554	6554
2006	7	13888	6339	4776	4776
2007	4	7052	4104	3030	3030
2008	7	12166	6263	5035	5035
2009	7	12657	7859	6178	6178
2010	7	12032	7273	5662	5662
2011	5	11081	7645	6247	6247
2012	4	12377	7603	5865	5865
2013	4	10818	5434	4096	4096
2014	4	11122	5935	4400	4400
2015	6	11971	6330	4403	4403
2016	6	12219	4089	3079	3079
2017	10	12427	5632	5462	1949
2018	9	13220	8679	8661	3386
2019	9	18179	16795	16795	7524
2020	10	16211	18184	18184	9538
2021	7	8213	7358	7358	3733
2022	5	7624	5667	5667	3204
2023	4	6280	4197	4197	2318

Proportion berried

The sex biased fishery removes more males than females from the population. It thus may have detrimental effects on the proportion of berried females and potential reproduction. Proportion females may increase over the season as they are returned, and may be increasingly recaptured. Below the proportion berried in all of the journal records (entire season) is described (with small differences per year), and also per week to illustrate the within season temporal trends.

Table 2. Halland commercial journals. Proportion berried by season.

Year	prop_berried
2000	0.24725944
2001	0.23337918
2002	0.20812183
2003	0.21522258
2004	0.19221968
2005	0.22106014
2006	0.24656886
2007	0.26169591
2008	0.19750918
2009	0.21389490
2010	0.22150419
2011	0.18286462
2012	0.22859398
2013	0.24622746
2014	0.25863521
2015	0.30442338
2016	0.24700416
2017	0.19957386
2018	0.11268579
2019	0.07079488
2020	0.08952926
2021	0.10641479
2022	0.12511029
2023	0.07815106

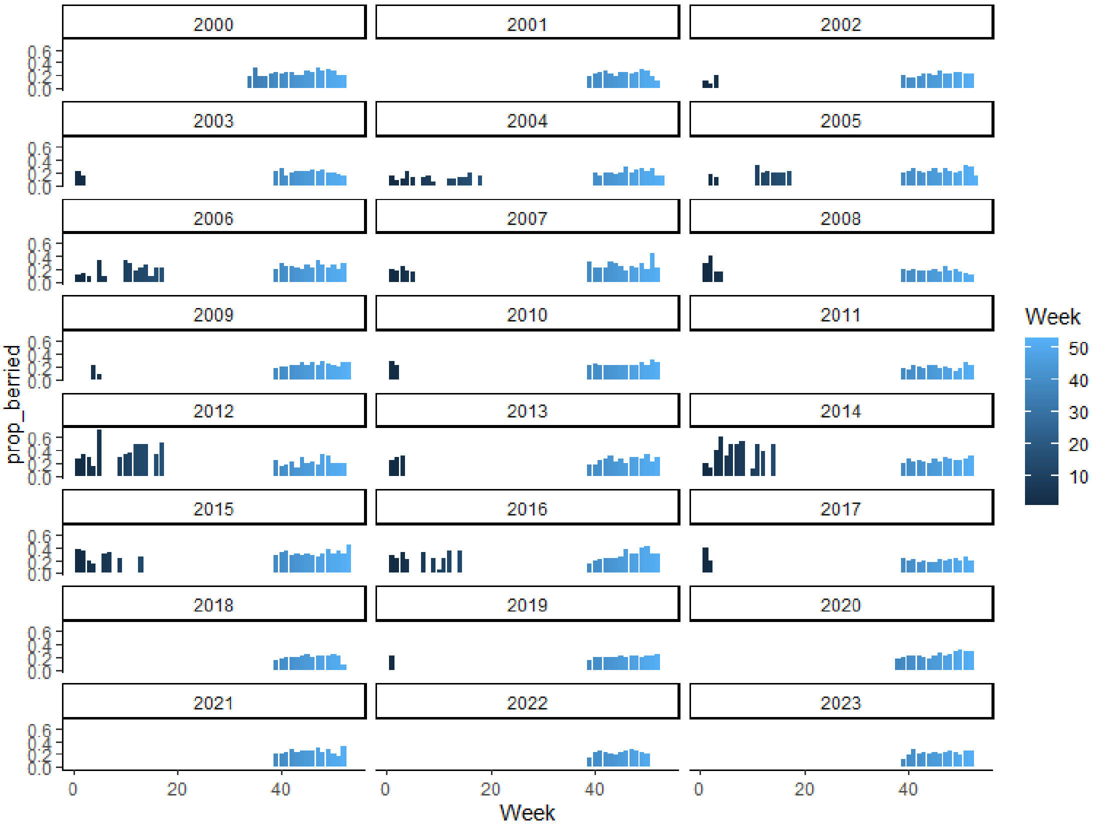


Figure 4. Proportion berried rarely below 0.2 before 2017. After 2017, berried females have been reported in a different way, only legal size being noted.

Nominal CPUE/LPUE

LPUE was thus calculated as the AboveMLS divided by number of pulled pots per day per fisher. CPUE accordingly was calculated as aboveMLS plus returned berried females per pulled pot per day per fisher. Fishing practices changes through the season, the pots being pulled less frequently later in the season and shifts in spatial distribution as recreational fishers have a shorter season opening up the entire coastal region for commercial fishers from 1st December. Also catch rates are assumed to be affected by the extraction of harvest, leaving fewer lobsters available to the fishery. Soak time is very difficult to extract from the journals. However, early in the season pots are pulled a lot more frequently and soak time is assumed to have a lesser effect on catch. Also, lobster activity is temperature dependent leading to less activity as the sea temperature drops, introducing yet another factor potentially influencing catch rate of lobsters. The combination of these factors leads to a general conclusion to use only a subset of the journals, focusing on the first two weeks of the fishery. Hence week 39-40 was used for generic case and for exploratory purposes weeks 39-41 and weeks 39-44 used for perspective.

Table 3. Nominal CPUE by year, accompanied by standard deviation, Standard Error, CV and Standard Error on log scale.

Year	management_CPUE	man_CPUE_sd	man_CPUE_se	man_CPUE_CV	man_CPUE_se_log
2000/2001	0.5055484	0.3172618	0.0448676	0.0887503	0.0885763
2001/2002	0.4696520	0.2661550	0.0372692	0.0793548	0.0792303
2002/2003	0.4641013	0.2985220	0.0445010	0.0958865	0.0956671
2003/2004	0.6910234	0.3320721	0.0512398	0.0741507	0.0740490
2004/2005	0.7999153	0.3658679	0.0746825	0.0933630	0.0931605
2005/2006	0.5125971	0.2451644	0.0346715	0.0676389	0.0675617
2006/2007	0.4306506	0.2064240	0.0304356	0.0706734	0.0705854
2007/2008	0.5875226	0.3672229	0.0842467	0.1433931	0.1426641
2008/2009	0.5127910	0.2424176	0.0374058	0.0729456	0.0728488
2009/2010	0.7795913	0.4213453	0.0769268	0.0986758	0.0984368
2010/2011	0.5333660	0.2425360	0.0353775	0.0663288	0.0662560
2011/2012	0.6887542	0.3707372	0.0601415	0.0873193	0.0871535
2012/2013	0.7097228	0.2501515	0.0490588	0.0691238	0.0690415
2013/2014	0.3977388	0.1788398	0.0298066	0.0749402	0.0748353
2014/2015	0.4480278	0.2071859	0.0350208	0.0781666	0.0780476
2015/2016	0.4618228	0.1947820	0.0315978	0.0684198	0.0683399
2016/2017	0.4175467	0.2738578	0.0484117	0.1159432	0.1155563
2017	0.4171800	0.3390759	0.0565126	0.1354635	0.1348481
2018	0.8526491	0.3815483	0.0575206	0.0674610	0.0673844
2019	1.0993977	0.4720732	0.0604428	0.0549781	0.0549366
2020	1.1598563	0.4940889	0.0622493	0.0536699	0.0536313
2021	1.0315852	0.7034959	0.1263516	0.1224829	0.1220273
2022	0.9686637	0.5450339	0.1112546	0.1148537	0.1144776
2023	0.9658897	0.5050064	0.1076677	0.1114700	0.1111260

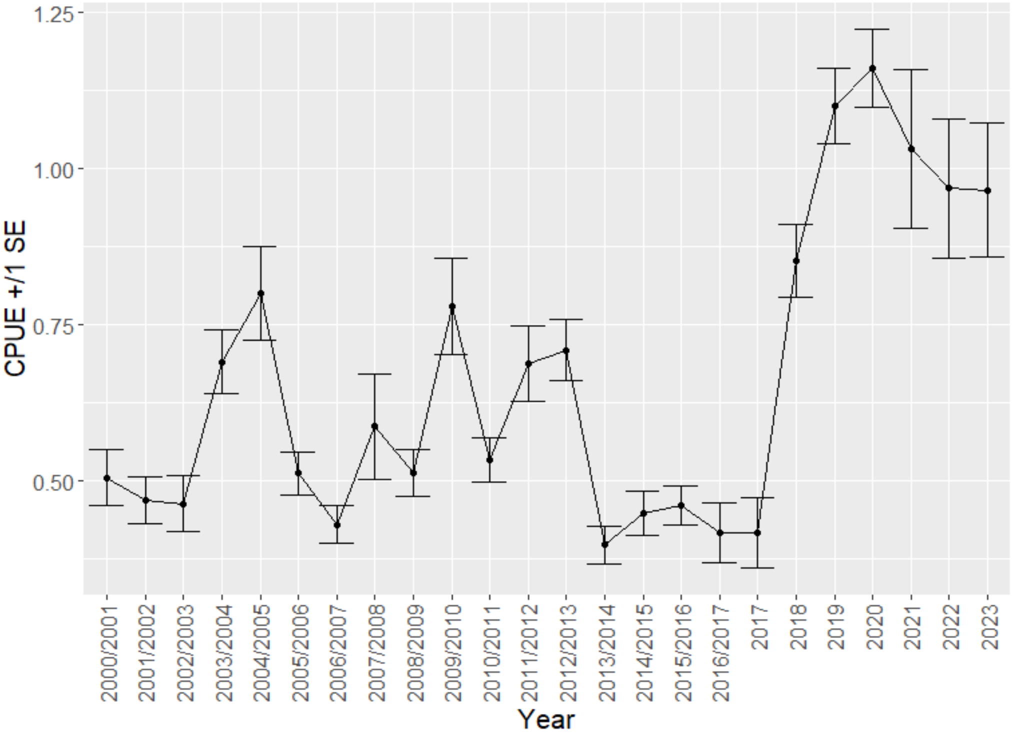


Figure 5. Nominal CPUE for week 39-40.

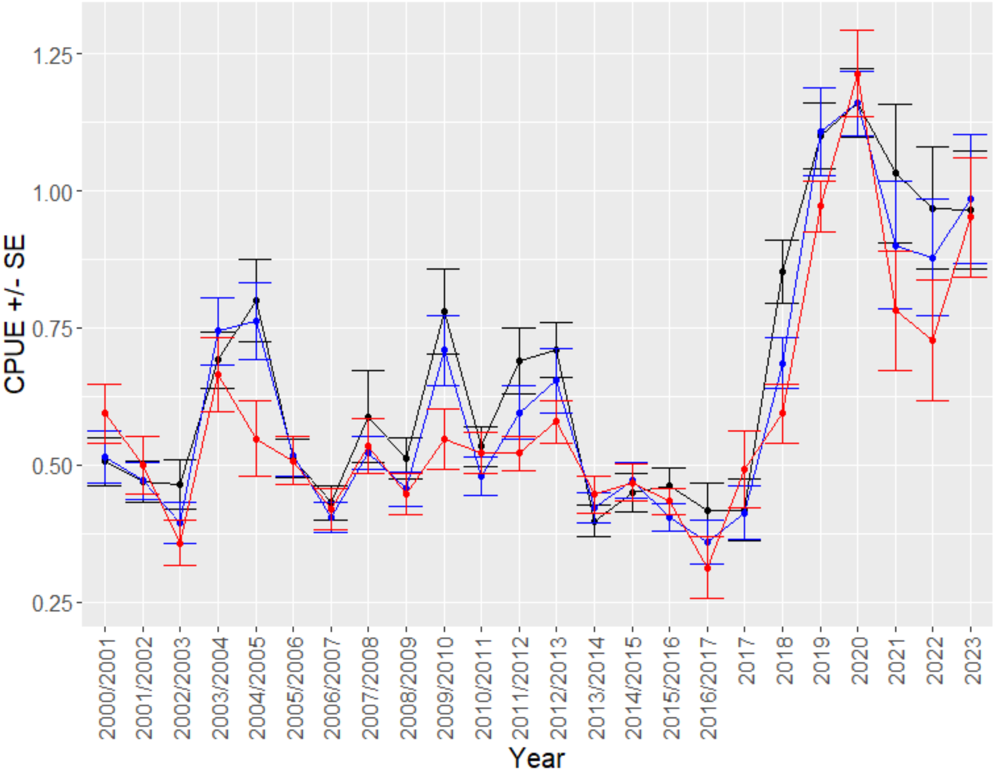


Figure 6. Nominal CPUE for different periods of the season. Week 39-40 (black), 39-41 (blue) and weeks 39-44 (red). Index drops slightly as the season goes on.

Standardization

Nominal cpue was insufficient for the stock assessment model. Available parameters for standardization was fisher_id, pull time. Further work may provide positioning of fishing practice but it was not available at the time of data processing.

Standardizing for a captain effect is common practice in fisheries cpue standardization. This was introduced in a glmm as a random effect to compensate for the bias in fisher activity over time.

Fishers differ in activity patterns, geographic location, intensity in fishing etc. standardizing the counts of catches to the fisher identity and estimating a mean catch is useful for assessment purposes. In count models it is possible to offset the intensity in the fishery (corresponds to effort in number of pots used for each fishing event) thus converting the estimate to a rate, namely a catch per unit effort (cpue) commonly used as index of abundance. This is accommodated using mixed models with both fixed and random effects by predictor variables to the response variable.

Competeing models

Models were set up to standardize for several parameters and compare results and diagnostics. Year was a factor and fisher_id as a random variable. Number of pots and soak time were modelled as offsets to compensate the model fit for variability in those parameters. Soak time is preferrably included as it has strong effects on catch. However, in many fishing practices concerning pots it may be poorly documented and thus very difficult to extract from journals. Two models were formulated to illustrate the inclusion of soak time for this particular fishery.

model.cpue.poisson <- glmer(lobCount ~ factor(Year) + (1|fisher_id) + offset(log(pots)), data, family=poisson

model.cpue.poisson.soak <- glmer(lobCount ~ factor(Year) + (1|fisher_id) + offset(log(pots) + offset(log(SoakTime))), data, family=poisson)

GLM using soak time (data only available 2018-2023). Both models converged and provided model summaries:

model.cpue.poisson

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: poisson  ( log )
Formula: lobCount ~ factor(Year) + (1 | fisher_id) + offset(log(p
ots))
   Data: dat[!(is.na(pots) | pots == 0) & Week %in% c(39, 40)]

     AIC      BIC   logLik deviance df.resid
 11339.3  11460.2  -5644.6  11289.3      907
```

```
Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-7.5617 -1.7842 -0.2548  1.4263 14.8986 

Random effects:
 Groups    Name        Variance Std.Dev.
 fisher_id (Intercept) 0.2922   0.5406  
Number of obs: 932, groups:  fisher_id, 15

Fixed effects:
                  Estimate Std. Error z value Pr(>|z|)    
(Intercept)      -0.764422   0.142275  -5.373 7.75e-08 ***
factor(Year)2001 -0.144917   0.033940  -4.270 1.96e-05 ***
factor(Year)2002 -0.092771   0.035126  -2.641  0.00826 ** 
factor(Year)2003  0.212807   0.032487   6.550 5.74e-11 ***
factor(Year)2004  0.346287   0.035819   9.668  < 2e-16 ***
factor(Year)2005 -0.003465   0.033277  -0.104  0.91706    
factor(Year)2006 -0.266261   0.037059  -7.185 6.73e-13 ***
factor(Year)2007 -0.138826   0.042343  -3.279  0.00104 ** 
factor(Year)2008 -0.012941   0.035814  -0.361  0.71784    
factor(Year)2009  0.399832   0.036030  11.097  < 2e-16 ***
factor(Year)2010  0.004801   0.035619   0.135  0.89278    
factor(Year)2011  0.280917   0.033935   8.278  < 2e-16 ***
factor(Year)2012  0.141422   0.036339   3.892 9.95e-05 ***
factor(Year)2013 -0.428380   0.039132 -10.947  < 2e-16 ***
factor(Year)2014 -0.297513   0.040119  -7.416 1.21e-13 ***
factor(Year)2015 -0.176389   0.039247  -4.494 6.98e-06 ***
factor(Year)2016 -0.248688   0.041461  -5.998 2.00e-09 ***
factor(Year)2017 -0.457602   0.042859 -10.677  < 2e-16 ***
factor(Year)2018  0.202255   0.032830   6.161 7.25e-10 ***
factor(Year)2019  0.532669   0.030163  17.660  < 2e-16 ***
factor(Year)2020  0.670993   0.029834  22.491  < 2e-16 ***
factor(Year)2021  0.457772   0.039305  11.647  < 2e-16 ***
factor(Year)2022  0.505585   0.039766  12.714  < 2e-16 ***
factor(Year)2023  0.432486   0.045277   9.552  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

model.cpue.poisson.soak

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: poisson  ( log )
Formula: lobCount ~ factor(Year) + (1 | fisher_id) + offset(log(p
ots) +  
    offset(log(SoakTime)))
   Data: 
dat[!(is.na(pots) | pots == 0) & Week %in% c(39, 40) & !is.na(Soa
kTime)]

     AIC      BIC   logLik deviance df.resid 
```

```
  3722.7   3748.2  -1853.4   3706.7      171 

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-8.1412 -2.0505  0.3347  3.5561 13.0939 

Random effects:
 Groups    Name        Variance Std.Dev.
 fisher_id (Intercept) 0.5615   0.7493  
Number of obs: 179, groups:  fisher_id, 13

Fixed effects:
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      -2.13731    0.21784  -9.811   <2e-16 ***
factor(Year)2018  0.66044    0.06676   9.892   <2e-16 ***
factor(Year)2019  1.47013    0.06305  23.318   <2e-16 ***
factor(Year)2020  1.27305    0.07474  17.033   <2e-16 ***
factor(Year)2021  0.13353    0.12942   1.032    0.302    
factor(Year)2022  1.13557    0.07500  15.141   <2e-16 ***
factor(Year)2023  0.99663    0.08293  12.017   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) f(Y)2018 f(Y)2019 f(Y)2020 f(Y)2021 f(Y)2022
fctr(Y)2018 -0.251                                             
fctr(Y)2019 -0.258  0.907                                      
fctr(Y)2020 -0.240  0.808    0.830                             
fctr(Y)2021 -0.143  0.460    0.480    0.482                    
fctr(Y)2022 -0.234  0.789    0.833    0.747    0.462           
fctr(Y)2023 -0.221  0.708    0.754    0.688    0.434    0.728  
```

Conclusion

Estimates are provided for both models. However, information on soak time was only available for a small part of the time series. Also, differences in estimates are substantial, both in absolute numbers and in trend. The main explanation is that number of soak nights is a very complex variable and not easily used to standardize cath. Fishermen are often not pulling all of their pots at the same time, leaving some due to weather, distance, prices etc. This renders a mismatch between catch related to number of pots and soak nights and a glm-model has not sufficient information to be fitted properly. Soak time may vary a lot during season but most fishermen are eager to pull their pots often in the beginning of the season. With the lack of detailed effort information on soak time, positioning of gears etc we make the assumption that soak time is most similar between pots, areas and fishermen during the first two weeks of the season when availability and market prices of lobster are highest. Modelling catch data per pull, given fisher_ID as a random factor and number of pots as an offset only using landings from week 39 and 40 minimizes the potential bias coming from soak time. Here we accept the original model without the offset SoakTime parameter which is provided to the assessment model.

Transformed index values

Transformation back to normal scale was done for the estimates, however SE was inputted in SS3 as SE on log scale.

Year	Index	LPUE	SE on logscale
2000	Halland_journals	0.465602972	0.142275
2001	Halland_journals	0.402791186	0.03394
2002	Halland_journals	0.424352416	0.035126
2003	Halland_journals	0.57601994	0.032487
2004	Halland_journals	0.658274672	0.035819
2005	Halland_journals	0.463993377	0.033277
2006	Halland_journals	0.356763922	0.037059
2007	Halland_journals	0.405252074	0.042343
2008	Halland_journals	0.459617342	0.035814
2009	Halland_journals	0.694482719	0.03603
2010	Halland_journals	0.467844642	0.035619
2011	Halland_journals	0.616619586	0.033935
2012	Halland_journals	0.536334095	0.036339
2013	Halland_journals	0.303370636	0.039132
2014	Halland_journals	0.345786758	0.040119
2015	Halland_journals	0.390311945	0.039247
2016	Halland_journals	0.363088744	0.041461
2017	Halland_journals	0.294633815	0.042859
2018	Halland_journals	0.569973734	0.03283
2019	Halland_journals	0.793143591	0.030163
2020	Halland_journals	0.910804504	0.029834
2021	Halland_journals	0.735909595	0.039305
2022	Halland_journals	0.771950384	0.039766
2023	Halland_journals	0.717534679	0.045277

Residuals, dispersion and zero inflation of poisson model

Diagnostics of the model not containing soak time.

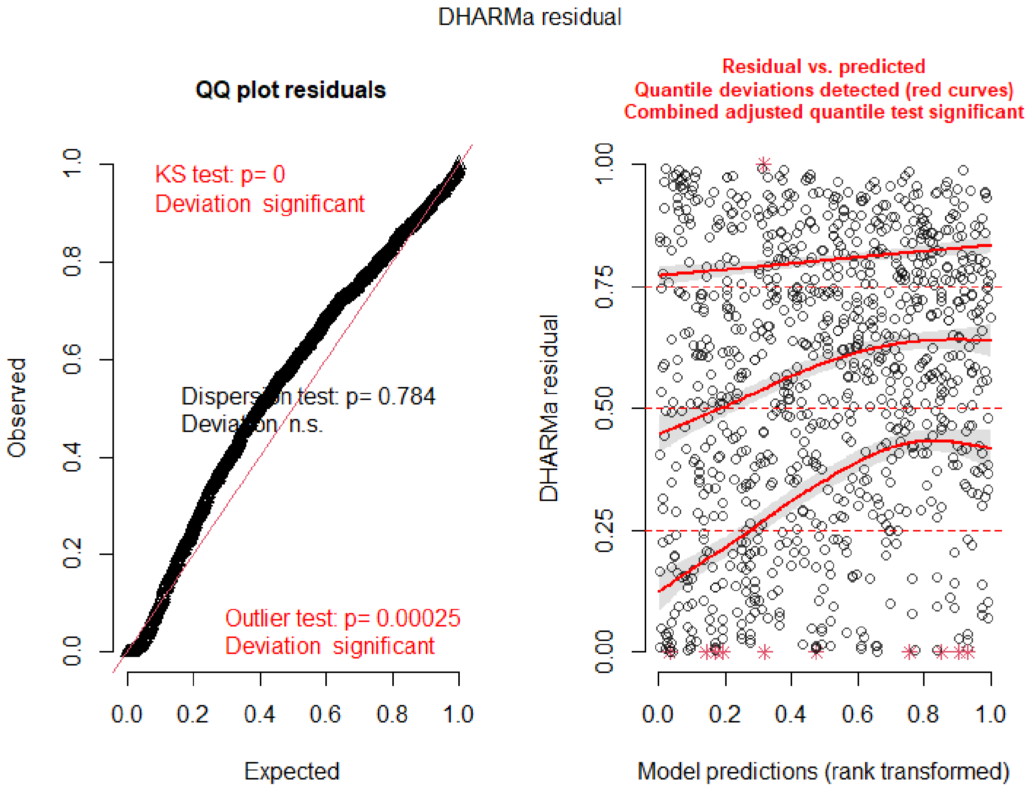


Figure. Residual tests of model not including soak time. Outliers significant but not adjusted as they are thought to be true observations.

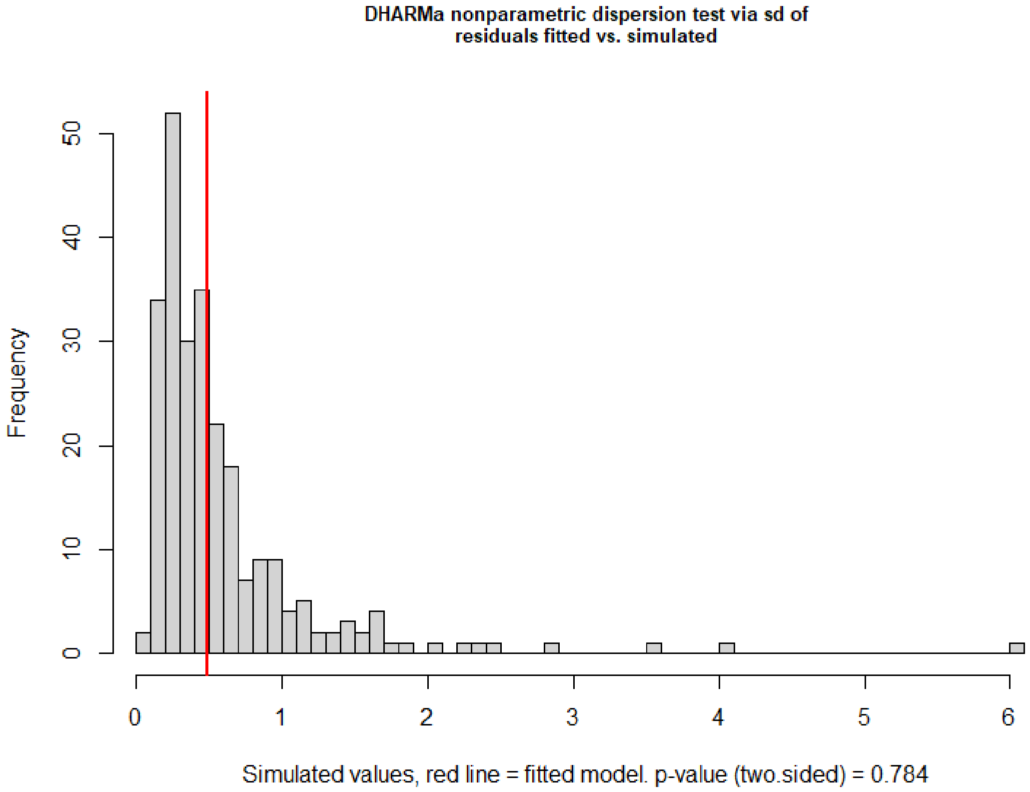


Figure. Dispersion test of glm not including soak time.

```
	DHARMa nonparametric dispersion test via sd of residuals fitt
ed vs.
	simulated

data:  simulationOutput
dispersion = 0.82644, p-value = 0.784
alternative hypothesis: two.sided
```

Test of dispersion was insignificant and overdispersion thus not an issue.

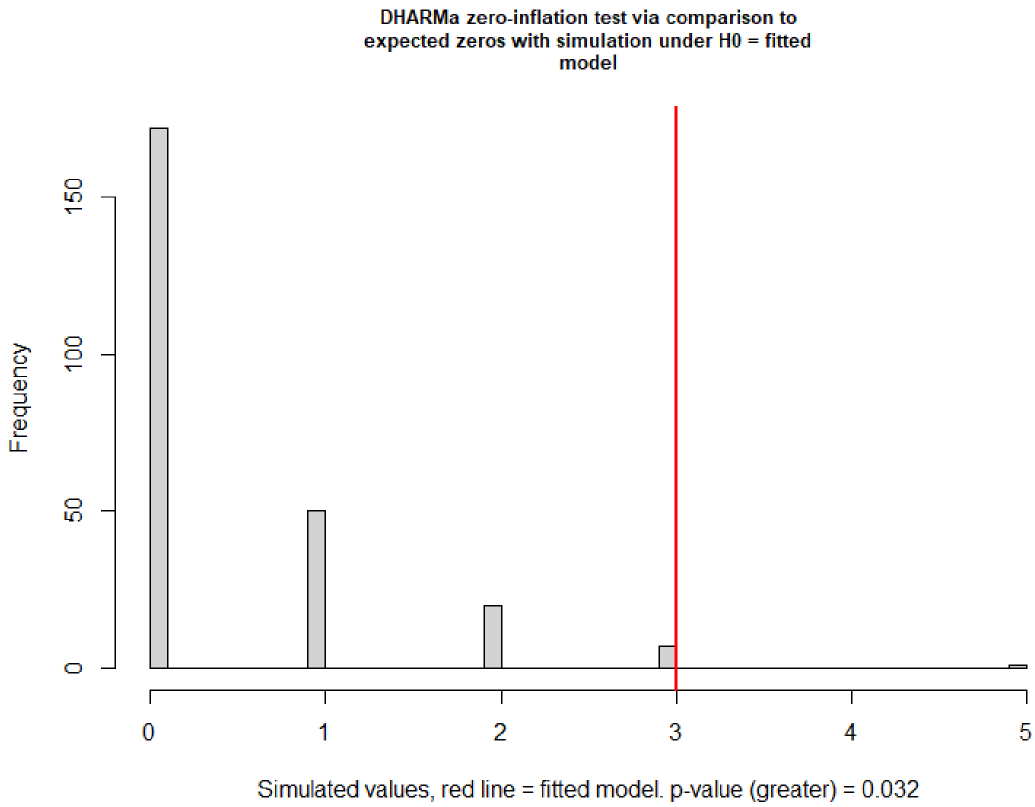


Figure. Zero-inflation test of model including soak time.

```
    DHARMa zero-inflation test via comparison to expected zeros w
ith
    simulation under H0 = fitted model

data:  simulationOutput
ratioObsSim = 6.4655, p-value = 0.032
alternative hypothesis: greater
```

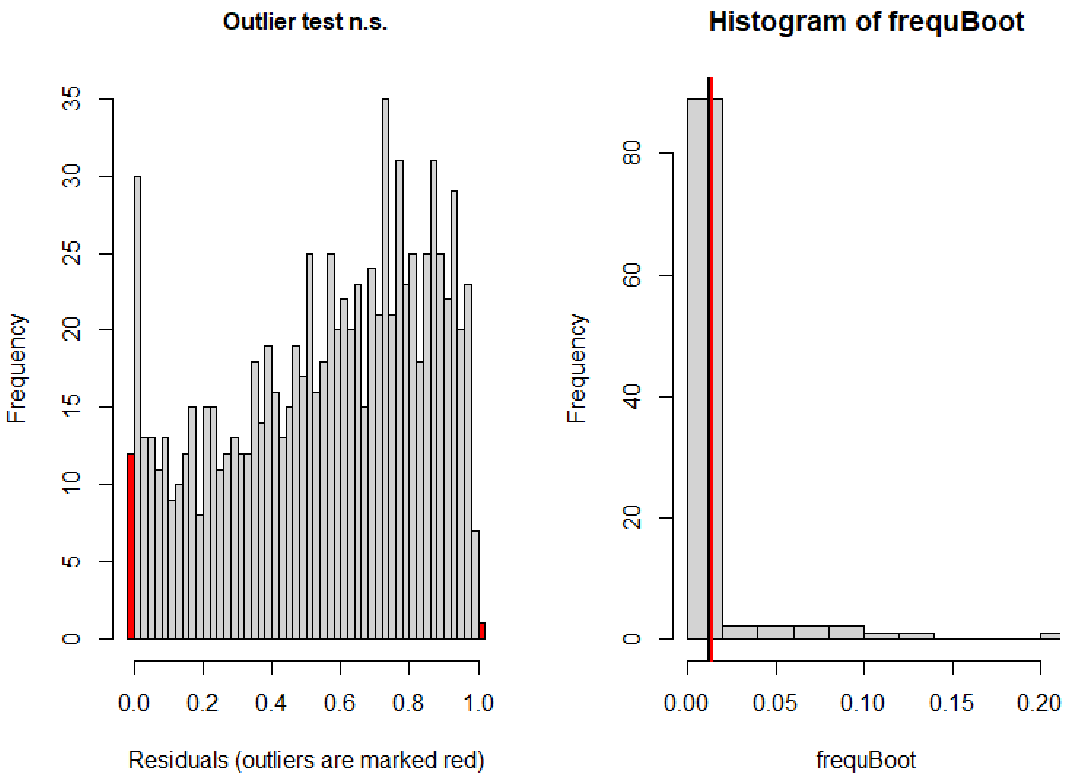


Figure. Outlier test of model not including soak time.

```
    DHARMa bootstrapped outlier test

data:  model.cpue.poisson
outliers at both margin(s) = 13, observations = 932, p-value = 0.
18
alternative hypothesis: greater
 percent confidence interval:
 0.00000000 0.09648605
sample estimates:
outlier frequency (expected: 0.0122854077253219 )
                                       0.0139485
```

Outlier test is insignificant when bootstrapped, but there seem to be some trend in the residuals. Whether this is due to a shift in the fishery, abundance or management is untested at the moment.

7.6 Appendix VI - Lobserve

Hege Sande

Lobserve, a citizen science project where volunteers perform a survey fishery similar to SLU Aquas own survey, occurs annually during 3-4 weeks in August since 2021.

The fishing is stratified on 3 depth-intervals to ensure coverage between 6m and 20+m, with 2 pots deployed at each depth every fishing event (6-10m, 10-20m, 20+m). Each participant (=fisher) deploy 6 pots at least 4 times, within a determined area (where they normally fish during lobster season and hence know the area). Pots are placed on bottoms suitable for lobster fishery, as well as they can, using sonar, and GPS to record position.

Catch is reported per pot, lobsters are measured (carapax length), sex is determined, presence of external eggs noted, and all catch is released after measurements. The pots are moved to a new location to avoid recapturing the same lobsters. Position and depth of the pot are noted using GPS and echo-sounder, as are date and time of setting and pulling of the pots.

Weather data are obtained from SMHI open data accessed 2024-04-05, matched with catches based on distance to 7 available weather station.

Setting up environment and loading data

Standardizing depth (mean centered and standardized)

The variable Depth (the depth at which the pot was deployed) is included in the models. Using unstandardized depth leads to issues when interpreting the data, as the intercept represent the average catch when depth equals zero. This is not a meaningful reference point (there is no meaningful catch at depth = zero), hence depth is centered around the mean so that the intercept instead represents catch at the mean depth (Goldstein 2015). Additionally, depth is standardized by dividing by the standard deviation, so that depth has a mean of 0 and a standard deviation of 1. The beta-coefficient shows the effect on catch of an increase in depth of 1 sd.

Variables included

The response variable is lobCount - the number of lobsters per pot (or in case of aggregating on biomass, “kg”). Variables are labelled in Swedish in the dataset, and are explained and translated below;

- “År” - Year (always included in model regardless of significance)

- “Datum” - date of catch (i.e. pull pot) (fishing occurs during 3 weeks in August - no seasonal effect is to be expected, there are too few participants to expect high fishing pressure, and catch is released so no risk of “fishing out”, i.e. reduced catch with time)

- “Fiskare” - The fishers name. Must be combined with other variable (such as area) as names might occur several times for different people. Random effect.

- “Lat”, “Lon”, “Område” - Positional data: Område = 5 km wide transects or circular areas (3 km radius). Lat and Lon are gps coordinates = wgs84/sweref99 (spatial component of spatial glms)

- “Djup_std” - depth standardized (mean 0 sd 1)

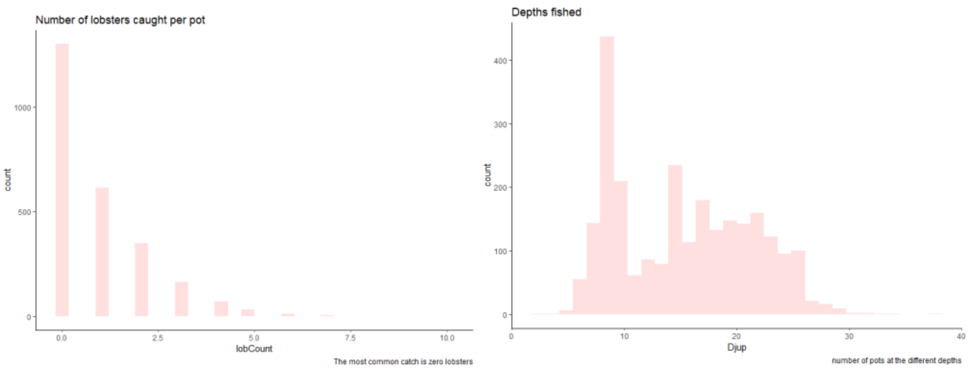
- “FiskadTid” - soak time - number of days pots are left in the water.

- “WS_0”, “WS_1”, “WS_2” wind in m/s, “_0” = at day of catch, “_1” = one day before catch, “_2” = two days before catch

- “WD_0”, “WD_1”, “WD_2” - wind direction (circular, i.e. degrees), “wd_0”, “wd_1”, “wd_2” = wind direction categorical (specified as the wind rose quadrant of the wind direction; NE, ES, SW, WN) with number indicating days before catch (“_0” = at day of catch, “_1” = one day before catch, “_2” = two days before catch).

Summary statistics

- Number of lobsters caught per pot = the most frequent catch n., Depth fished, Wind direction, Wind speed, Soak time


Number of lobsters caught per pot

The most common catch is zero lobsters

Depths fished

number of pots at the different depths

Figure. Number of caught lobsters per pot indicating zero as the most common catch (left) and number of pots per depth (right)

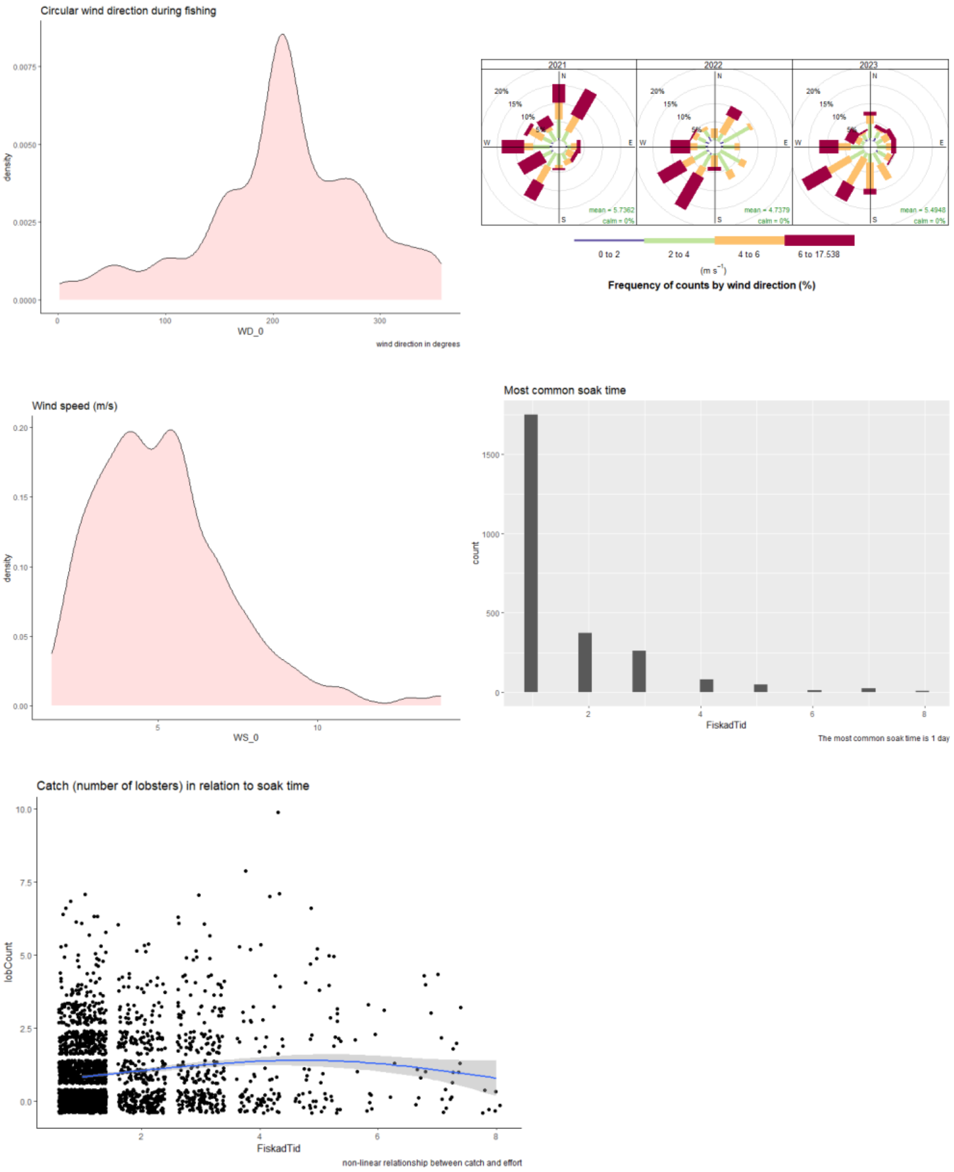


Figure. Overview of meteorological data (wind direction - top left, wind speed - mid left, combined as wind rose - top right), counts of soak time (mid right), counts of catch of lobster against soak time with model results (bottom right).

- Factors; Area, anonymized Fisher, Wind direction (day of, 1 and 2 days prior to pulling pot)

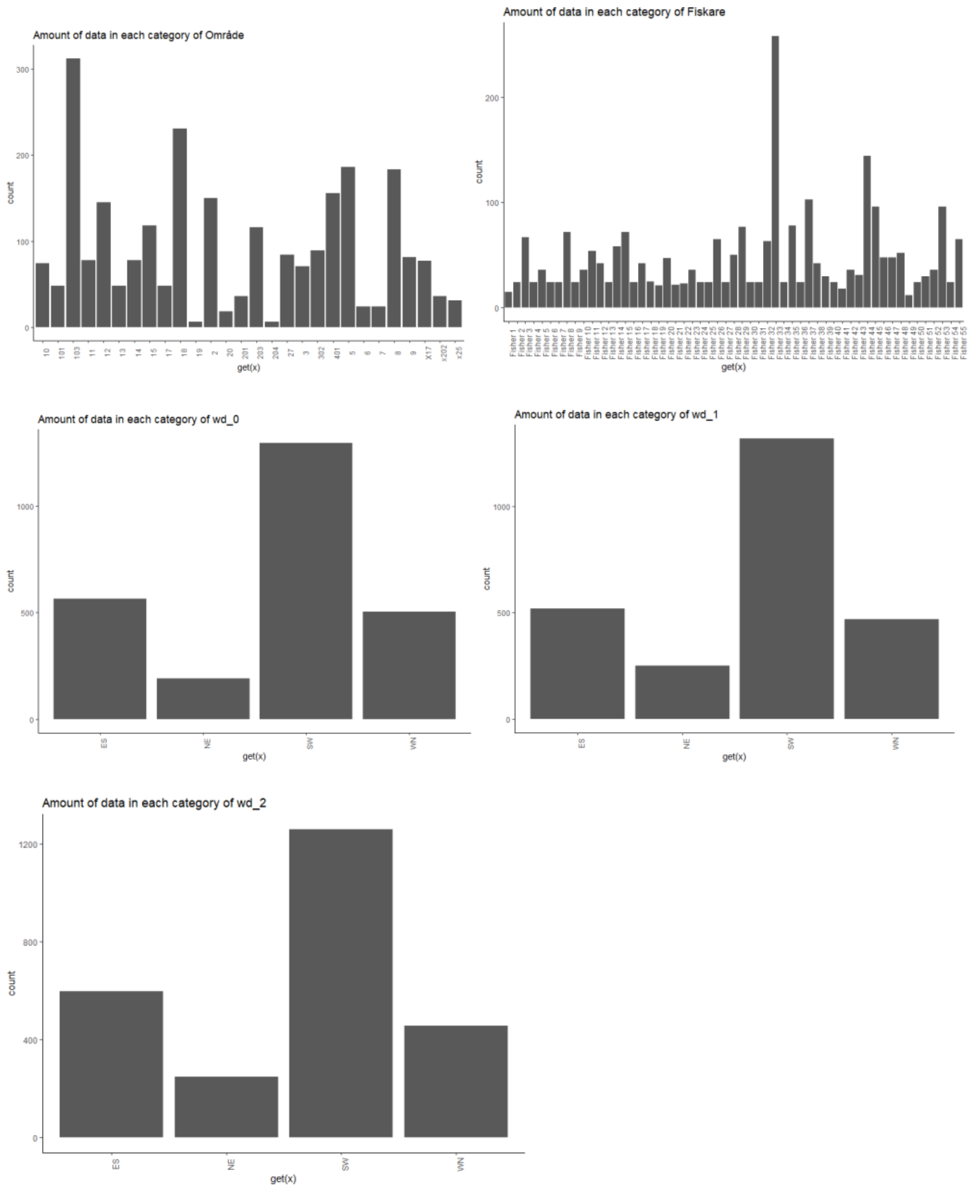


Figure. Counts of data related to some variables. Område (Area, top left), fiskare (Fisher_ID, top right), wind without lag (mid left), wind with lag 1 (mid right), wind with lag 2 (bottom left)

Models

All modelling is carried out in R version 4.3.0.

Model diagnostics are performed with the R package {DHARMa} where possible (Hartig 2024), and selection among the models is by BIC (Bayesian Information Criterion) and AIC (Akaikes Information Criterion).

GLM

Initial {DHARMa} diagnostics show issues with overdispersion (for poisson distribution the mean and variance are assumed to be equal). A negative binomial model is therefore fitted, as this allows for overdispersion.

glm.nb (Negative binomial)

Two negative binomial models are fitted, one with Area and one with GPS position (Lat*Lon) specifying the geographical component. While modelling catches by area enables us to compare specific regions (the fished lobserve areas), finer spatial variation is lost and generalizability might be reduced. We therefore model catches with latitude and longitude as well, potentially catching trends within or across areas.

- glm_nb_w <- glm.nb(lobCount ~ År + Område + Djup_std + FiskadTid + wd_0 + wd_1 + wd_2 + WS_0 + WS_1 + Fiskare, data=tmp1)

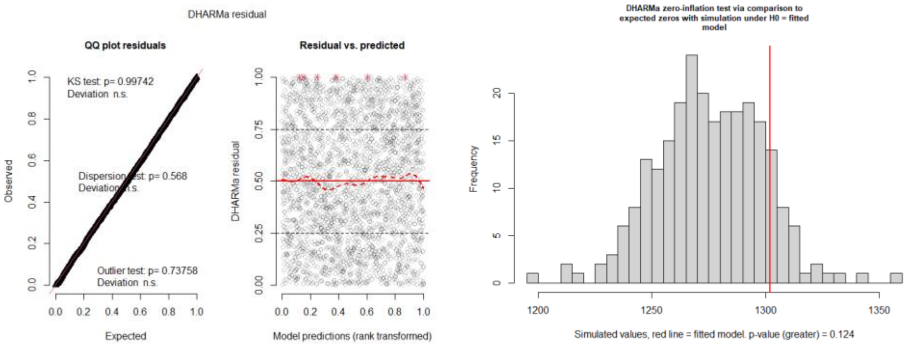


Figure. Dispersion test (left) and zero-inflation test (right) of the negative binomial area model

```
    DHARMa zero-inflation test via comparison to expected zeros w
ith
    simulation under H0 = fitted model

data:  simulationOutput
ratioObsSim = 1.0206, p-value = 0.124
alternative hypothesis: greater
```

- with GPS position (Lat * Lon) instead of area

  glm_nb_w2 <- glm.nb(lobCount ~ År + Djup_std + Lat*Lon + FiskadTid+ wd_0 + wd_1 + wd_2 + WS_0 + WS_1 + WS_2 + Fiskare, data=tmp1)

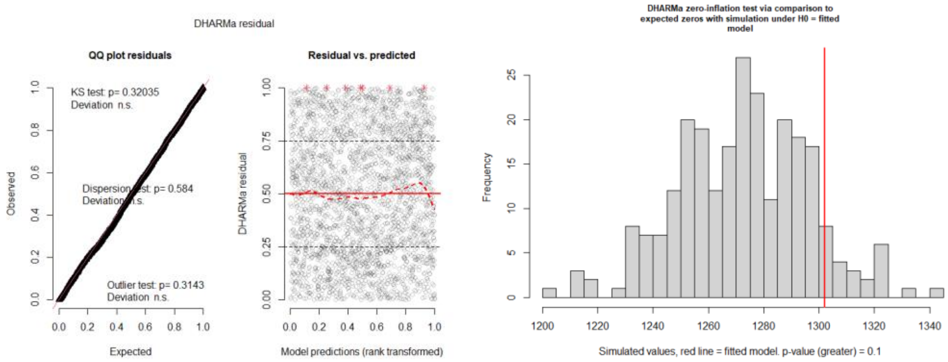


Figure. Dispersion test (left) and zero-inflation test (right) of the negative binomial model with position as Lat*Lon

```
    DHARMa zero-inflation test via comparison to expected zer
os with
    simulation under H0 = fitted model

data:  simulationOutput
ratioObsSim = 1.0229, p-value = 0.1
alternative hypothesis: greater
```

Diagnostics with {DHARMa} show both models to perform well with regards to deviation, dispersion or outliers.

Although the negative binomial models allow for overdispersion, there is a slight concern about the possibility of zero inflation.

sdmTMB

While a negative binomial model can account for overdispersion (i.e. large variability), it assumes that observations are independent of each other. That is usually not the case, as neighboring areas can be spatially correlated (similar to each other) (Anderson et al. 2024). The same is true for the temporal aspect, the current status can depend on the past status.

{sdmTMB} models these spatial and temporal dependencies by adding random fields to the model, and provides a function for index standardization once a model has been fitted and predictions made.

The R package {sdmTMB} fits spatial and spatiotemporal Generalized Linear Mixed Effects Models (GLMMs) using R packages TMB for model fitting (Template Model Builder TMB), R-INLA (Integrated nested Laplace approximation, a method for Bayesian inference) to set up stochastic partial differential equation (SPDE) matrices, and Gaussian Markov random fields. The package is particularly well suited for species distribution models (SDMs) (Anderson et al. 2024).

The sdmTMB model requires spatial coordinates, and to make sure the distance remains constant throughout the study region, the spatial coordinates are converted to an equidistant projection (UTM).

Index standardization is developed for biomass/area, as calculated from catch biomass, net characteristics, and time on bottom. However, lobster fishing is performed with pots and catch is counted as number per pot in 1 day fishing, so for the purpose of lobster Index we use the response variable lobCount = lobster per pot, and include the variable soak time (number of days the pot is left fishing) in the model.

Make mesh

To approximate the spatial variability in observations, sdmTMB uses a triangualted mesh with “knots” (vertices) including the spatial components as random fields. A continuous spatial field is approximated by bilinear interpolation (Rue et al., 2009; Lindgren et al., 2011) from estimated value at knots to other locations, with spatial random effects assumed to be drawn from Gaussian Markov random fields (Lindgren et al., 2011).

The minimum distance between knots before a new mesh vertex is added, called the “cutoff”, can be chosen depending on the speed or accuracy needed.

Cutoff is in the units of X and Y (UTM in this case), and here set at 0.5 km.

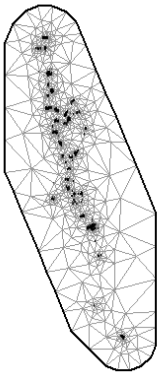


Figure. Prediction mesh

sdmTMB models

All models are constructed in the same way but with different family (family = poisson(), nbinom1(link = "log"), delta_gamma(), delta_gamma(type = "poisson-link")).

```
mod_sdm <- sdmTMB(lobCount ~  0 + as.factor(År) + s(Djup_std) + s(FiskadTid,
k=3) +  wd_0 + wd_1 + wd_2 + WS_0 + WS_1 + (1|Fiskare), time =
"År",data=tmp1, mesh=mesh, family= poisson(),spatial="on",anisotropy = T)
```

1. Poisson

   This model pass sanity checks, diagnostics are ok with residuals distribution and Q-Q plot (quantiles of residuals against quantiles of predicted values).

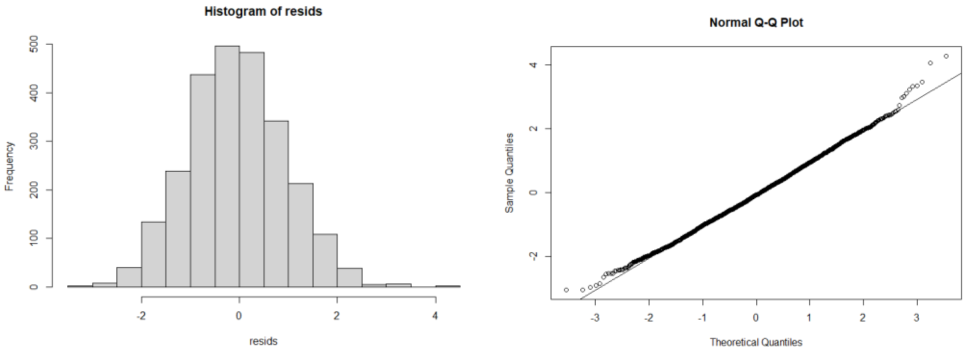


   Figure. Residuals of poisson model.

2. Negative binomial

   The model pass sanity checks, diagnostics are ok.

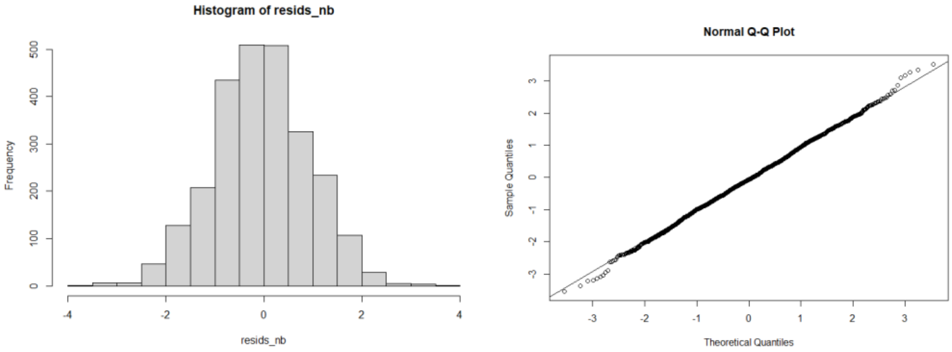


   Figure. Residuals of negative binomial model.

3. Delta Gamma

With family = delta_gamma(), the presence absence model is binomial (link = “logit”), and the positive catch model is Gamma (link = “log”)

The model pass sanity checks, diagnostics ok

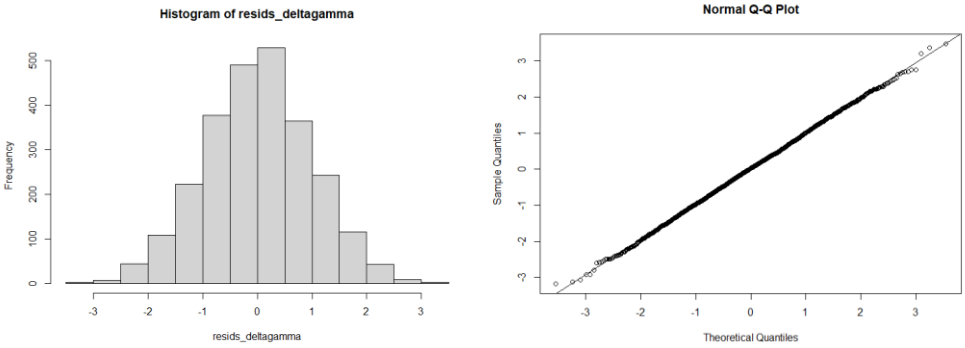


Figure. Residuals of Delta Gamma model.

- with poisson link

The default type = “standard” (specifying the Delta/hurdle family type) is changed to “poisson-link”, which can be used in the same instances you would a Tweedie, when you have positive continuous data with zeroes (Thorson 2018).

The model does not pass all sanity checks (large standard error), qq plot ok

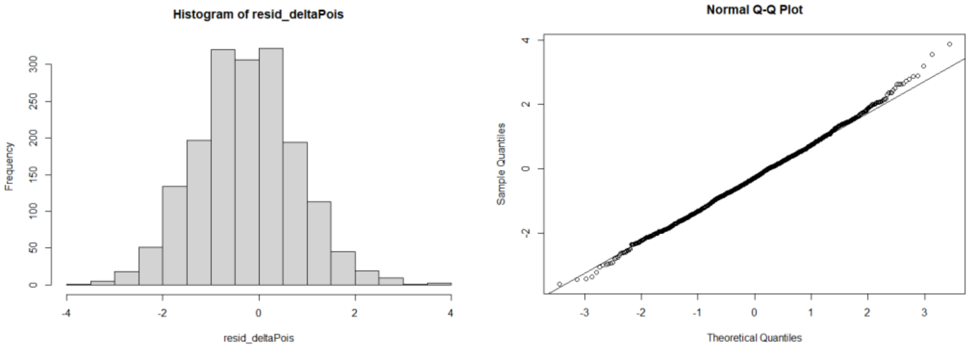


Figure. Residuals of model with poisson link.

All sdmTMB models pass the sanity checks except the deltaGamma with Poisson link (“mod_deltaPois”), which is excluded from further consideration.

Simulations from fitted model with simulation-based randomized quantile residuals

Simulating data based on the different models should produce a number of zero catches as close to the observed data as possible.

The observed proportion of zeros (no catch):

```
[1] 0.5097886
```

Zero frequency was calculated for simulated data from each of the models, and compared in table 1.

The difference in observed and modeled zeros for the 3 remaining sdmTMB models, as well as the 2 glm models:

Model performance and selection

The model performing best with regards to diagnostics, AIC, BIC and ability to predict proportion of zeroes closest to what is observed, is the spatiotemporal model with negative binomial distribution (mod_sdm_nb).

Table 1 The models listed all passed the diagnostic tests. The model performing best with regards to diagnostics, AIC, BIC and ability to predict proportion of zeroes closest to what is observed, is the spatiotemporal model with negative binomial distribution (mod_sdm_nb, in bold)

Model	Family	AIC	BIC	Loglikelihood	Diff prop 0
mod_sdm_nb	Nbinom1	6150.771	6296.906	-3050.385	0.0048
mod_sdm	Poisson	6167.681	6307.971	-3059.840	0.0324
mod_deltaGamma	binomial	6187.200	6445.998	-3038.632	-0.0062
glm_nb_w	Neg binom	6187.200	6637.298	-3016.600	0.0095
glm_nb_w2	Neg binom	6200.467	6633.028	-3026.234	0.0108

Prediction

Prepare prediction grid

To predict with the fitted sdmTMB model, a data frame to predict on needs to be created. This dataframe (prediction grid) contains the same covariates (i.e. predictor columns) as the fitted data (and for spatiotemporal models, a column for time), and provides a fine scale grid on which to predict (Anderson et al. 2024).

Here we create a prediction grid using the UTM coordinates in the fitted data, a base world map (R packages {rnaturalearth}, {rnaturalearthdata}), and a depth raster (avoids predicting on any part of the grid covering land) downloaded from

EMODnet (https://emodnet.ec.europa.eu/en). The R package {terra} was used to rasterize and extract depth data.

Add variables

For the prediction grid, variables are set as follows;

- fiskadTid = 1 (fishing time 1 day)
- wd_0, wd_1 and wd_2 = “SW” (the most common wind direction our volunteers went fishing in)
- WS_0 and WS_1 = 5 (wind speed 5 m/s)

Prediction on grid

The model to be used for prediction is selected in section “Model performance and selection”.

The model used for predictions:

```
[1] "mod_sdm_nb"
```

Prediction is performed using the function predict(). We predict on the prediction grid, and set re_form_iid to NA to predict on a population level.

The Index

The function get_index() {sdmTMB} is used to extract the calculation of biomass or numbers as well as the standard errors. Since some of the grid cells we created are on land, we will set the area argument to a vector of areas instead of a fixed area (the length of which matches the length of the predictions).

```
    År       est         lwr      upr    log_est       se
1 2021 0.7625669 0.007745858 75.07345 -0.2710650 2.341641
2 2022 0.8455727 0.008454685 84.56769 -0.1677412 2.349683
3 2023 0.6948273 0.007084808 68.14370 -0.3640919 2.339691
```

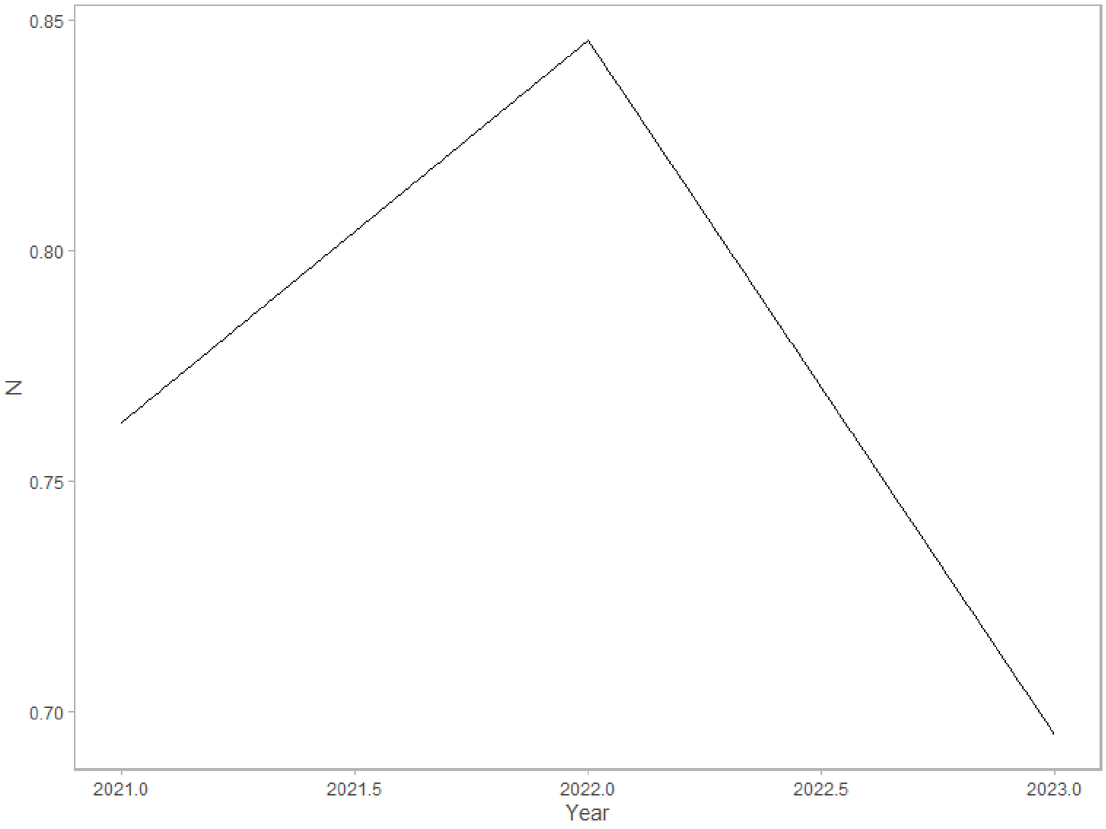


Figure. Modelled average cpue 2021-2023.

Conclusion

The index provided is calculated as number of lobsters per pot in one day fishing and is the result of a multimodel approach where the best performing model is selected according to determined criteria. The model is Incorporating variables assumed to have an effect on the CPUE such as weather and depth, as well as taking into account the possibility of spatiotemporal differences. It is expected that the associated standard error, and hence upper and lower limits of the confidence interval, can be significantly reduced if more relevant variables can be included in the data collection and analysis. Work towards achieving this is ongoing.

References

Anderson, S.C., E.J. Ward, P.A. English, L.A.K. Barnett, J.T. Thorson. 2024. sdmTMB: an R package for fast, flexible, and user-friendly generalized linear mixed effects models with spatial and spatiotemporal random fields. bioRxiv 2022.03.24.485545; doi: https://doi.org/10.1101/2022.03.24.485545

Goldstein ND. The why and when of centering continuous predictors in regression modeling. Nov 19, 2015. DOI: 10.17918/goldsteinepi

Hartig, F. 2024. DHARMa: Residual Diagnostics for Hierarchial (Multi-Level / Mixed) Regression Models. R package version 0.4.7, http://florianhartig.github.io.DHARMa/

Rue, H., Martino, S., Chopin, N., 2009. Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. Journal of the Royal Statistical Society: Series B (Statistical Methodology) 71, 319–392. https://doi.org/10.1111/j.1467-9868.2008.00700.x

Thorson, J.T., 2018. Three problems with the conventional delta-model for biomass sampling data, and a computationally efficient alternative. Can. J. Fish. Aquat. Sci. 75, 1369–1382. https://doi.org/10.1139/cjfas-2017-0266

Supplement

The following plots show the four different predictions the model has produced (All fixed and random effects, fixed effects, spatial random effects, and spatiotemporal random effects).

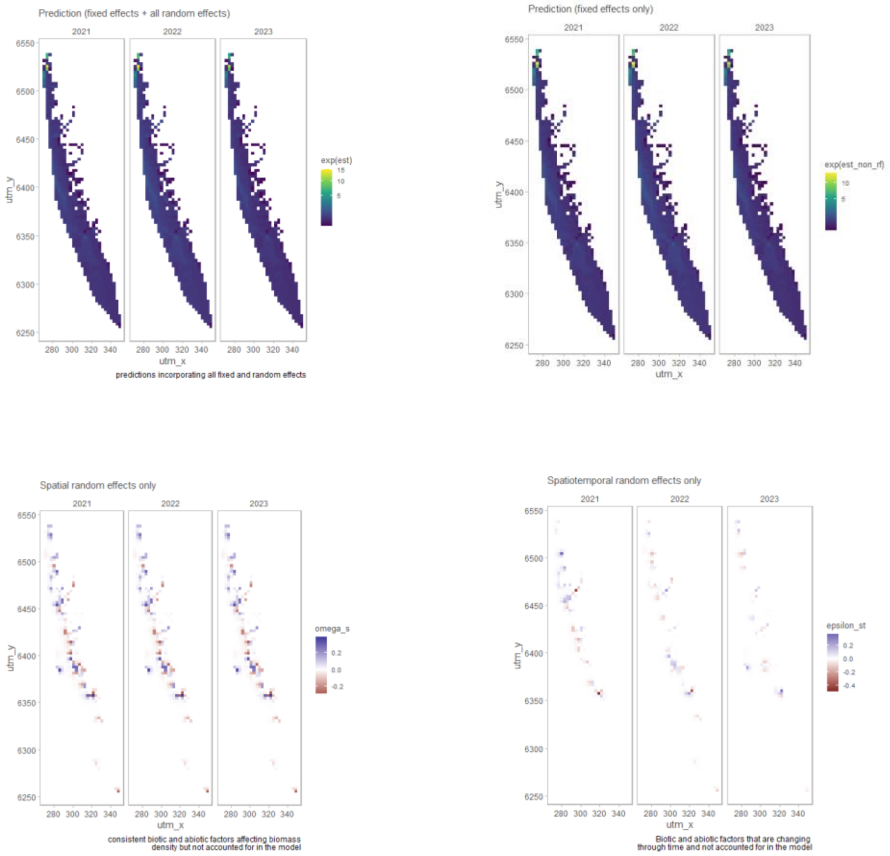


Figure. Predictions of the model `mod_sdm_nb` . Fixed and random effects (top left), fixed effects (top right), spatial random effects (bottom left), and spatiotemporal random effects (bottom right)

7.7 Appendix VII - Size compositions in lobster data sources

Andreas Sundelöf

Size composition and their sources

Sizes of lobster catches are hard to come by. Commercial sources do not exist, and voluntary or stipulated journals usually provide only size categories, not measurements of individual sizes. Some voluntary rapporteurs have been recruited for some data sources, and some targetted studies have been performed to, for some years, get size information from large scale lobster dealers providing size data on the catch.

In the designated survey fishery LOBSERVE all lobster catches are individually measured, securing size data in a fisheries independent study. This document presents size composition data available to the SS3 model up to 2023.

Commercial dealers data

Some commercial dealers have been sampled on site

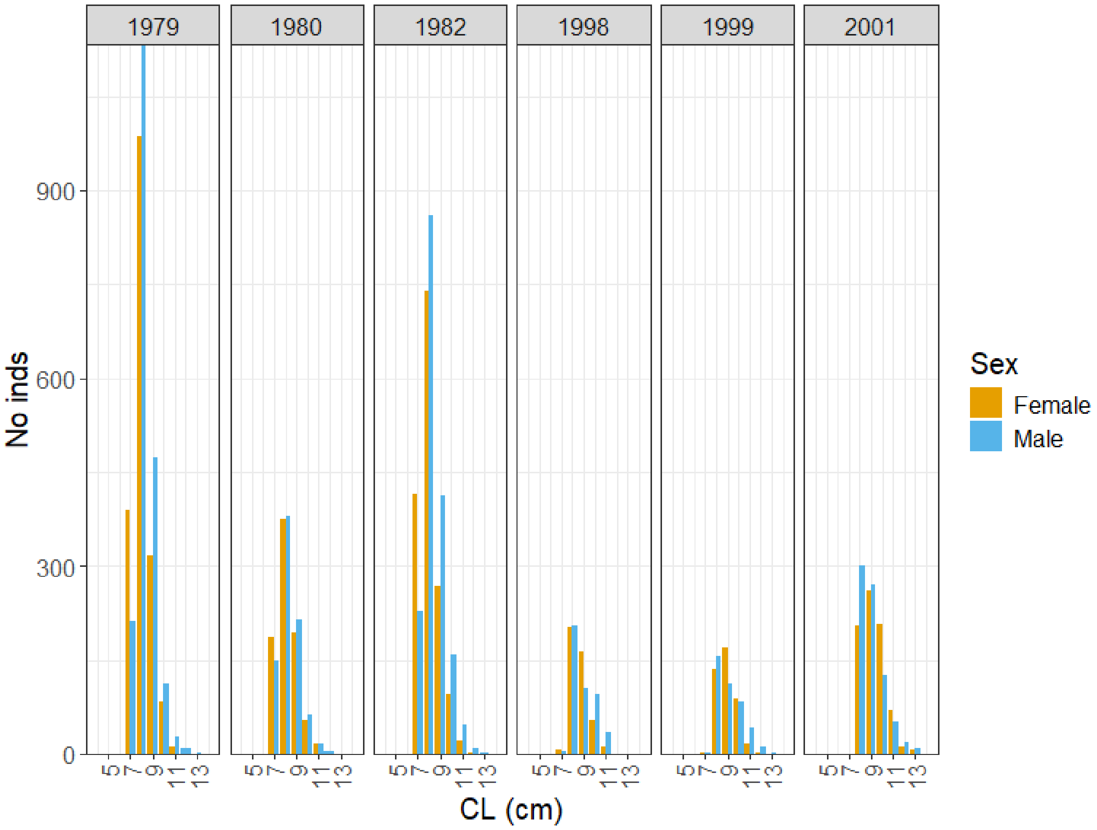


Figure. Size composition from commercial dealers.

Tourism fishing sizes

To the for hire business Swedish Agency for Marine and Water Management imay ssue exemtions from the rules of number of fishing gears to be used by recreational fishers. Thus operators running fishing trips for lobster fishing may do so with more than 6 pots (up to 40) without a commercial license (Tourism or Safari fishing). One term is to fill a stipulated journal of the catches. Some operators have been approached by SLU to voluntarily also record sizes of catch, data that is usually difficult to get by. Although number of reporting operators and total effort (number of pulled pots) vary over time these observations of sizes in one sector of the fishery is available and useful to inform the model of availability/selectivity/catchability.

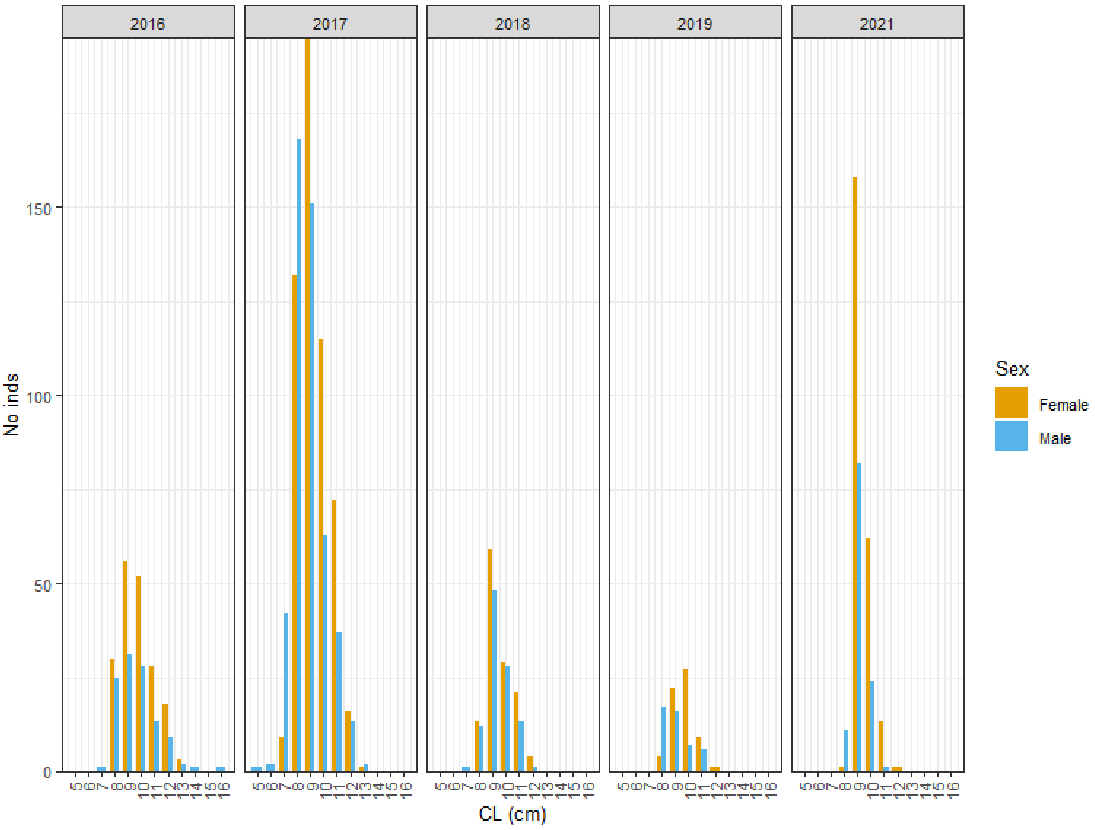


Figure. Size composition from Tourism fishing operators.

Lobserve

A fisheries independent citizen science survey data source using pots without escape gaps. All catch from all pulled pots were measured and sexed. Available size information provides availability estimates for the survey fishery August. Catch below

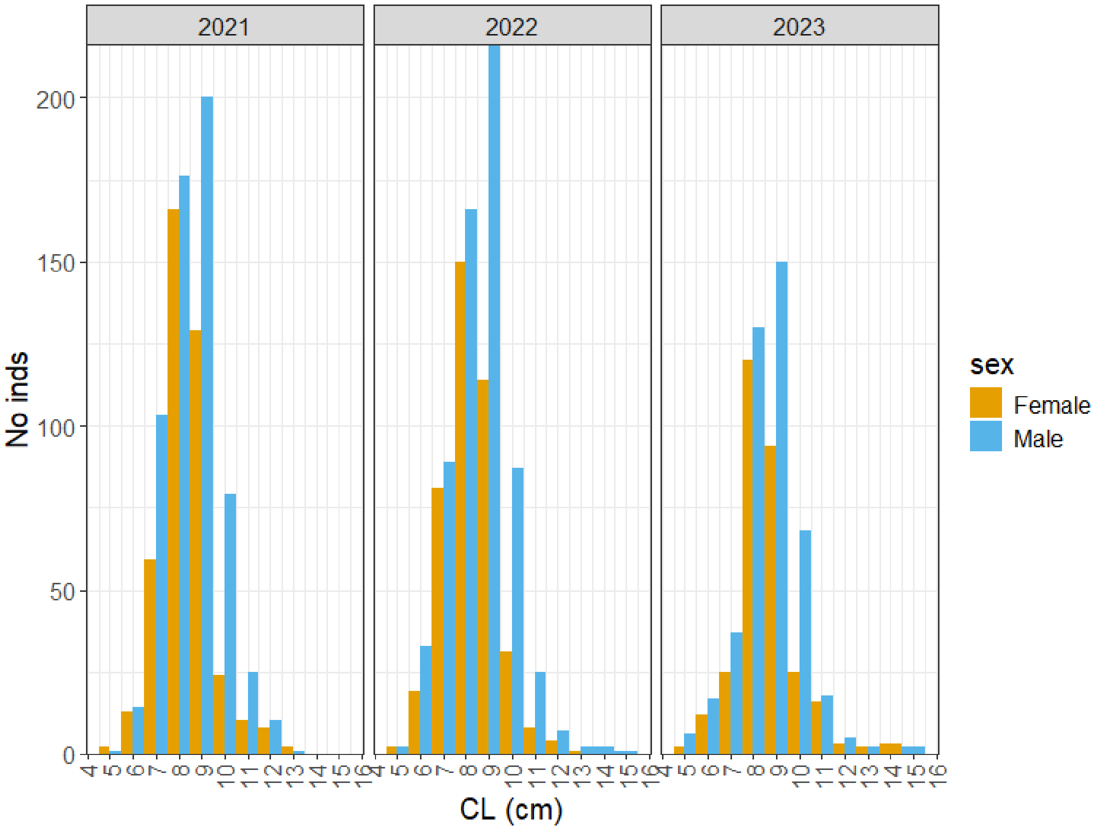


Figure. Size composition from the Lobserve survey.

Survey fishery

From Kåvra and adjacent fished reference areas there are several years of accumulated size data. It may be used as comparison between fished and unfished size composition and also add to size composition in conventionally fished areas.

Counts of sizes and sex by area from catches in lobster pots reveal large differences in size and abundance. It is suggested by these data that males are more common as catch in the larger sizes. This is seen in Kåvra (MPA) as large sizes are more common. Males grow faster and larger, and if left unharvested the sex ratio for lobsters larger than 14 cm CL is highly skewed to males.

Sizes data plotted by area for several different gears reveal the remarkable difference size composition between fished and unfished areas.

This is further substantiated by CPUE of kilogram lobster for lobster pots and fish pots.

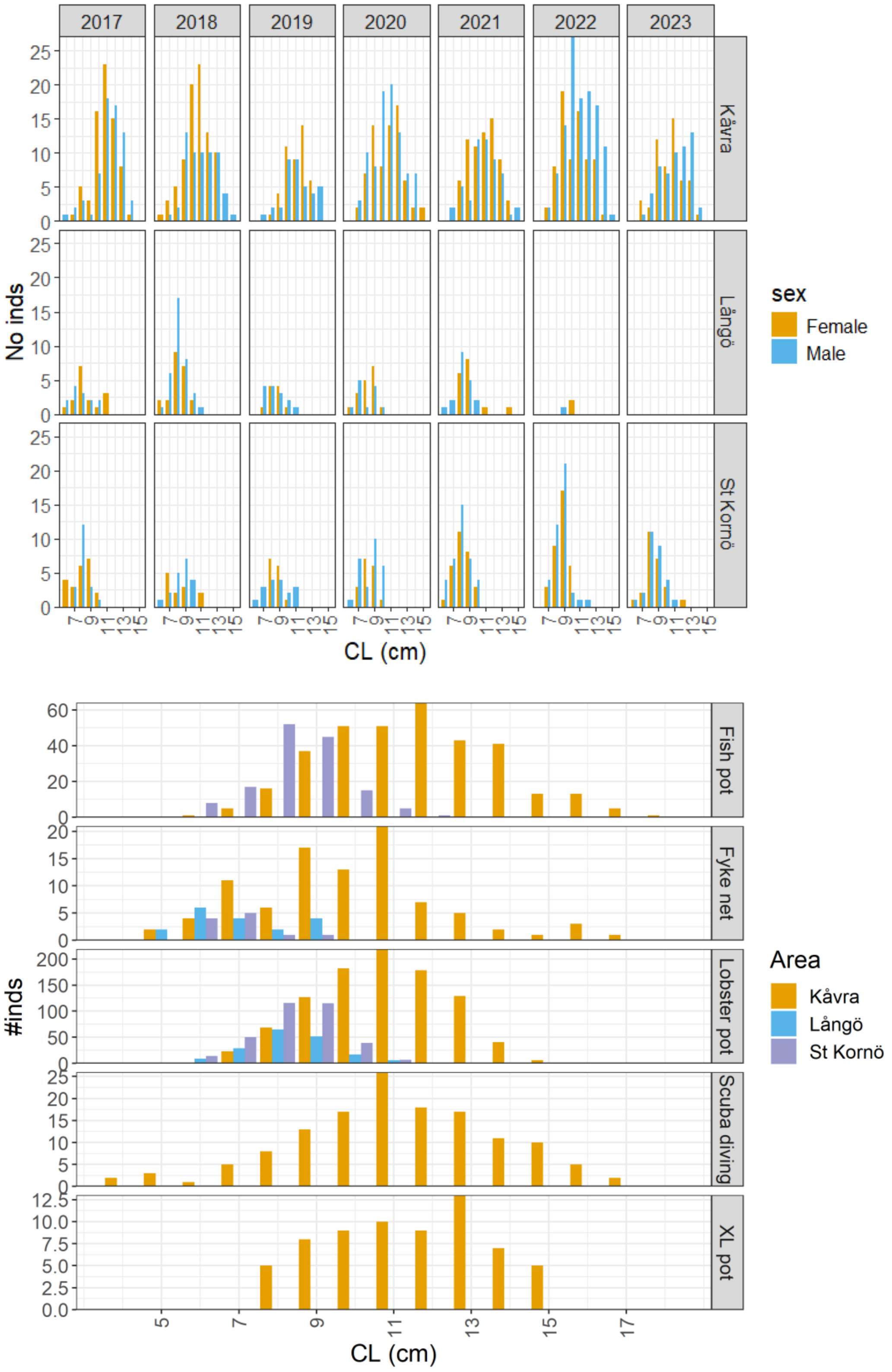


Figure. Size composition of lobster in SLU survey, by years and areas for lobster pots(top) and areas and gear (bottom).

Length to weight

Lobsters have been captured, measured, weighed, tagged and released. A generic length to weight relationship was based on individuals with both clawes intact. However, both females with or without external eggs were used. For use in SS3 the fitted model needs to be of the form _Weight (kg) = a*Size(cm CL)^b_ model outputs for males and females respectively.

```
    Size    Sex    Tag Streemer Weight LeftClaw RightClaw Berried
Size.cm
   <int> <char> <char>   <char>  <int>    <int>     <int>  <char>
<num>
1:    70 Female                    250       25        30
7.0
2:    73 Female             479    260       27        34
7.3
3:    71 Female             558    260       34        22
7.1
4:    76   Male             642    265       29        36
7.6
5:    74 Female             549    276       27        35
7.4
6:    71 Female             744    279       26        33
7.1
   Weight.kg
       <num>
1:     0.250
2:     0.260
3:     0.260
4:     0.265
5:     0.276
6:     0.279
```

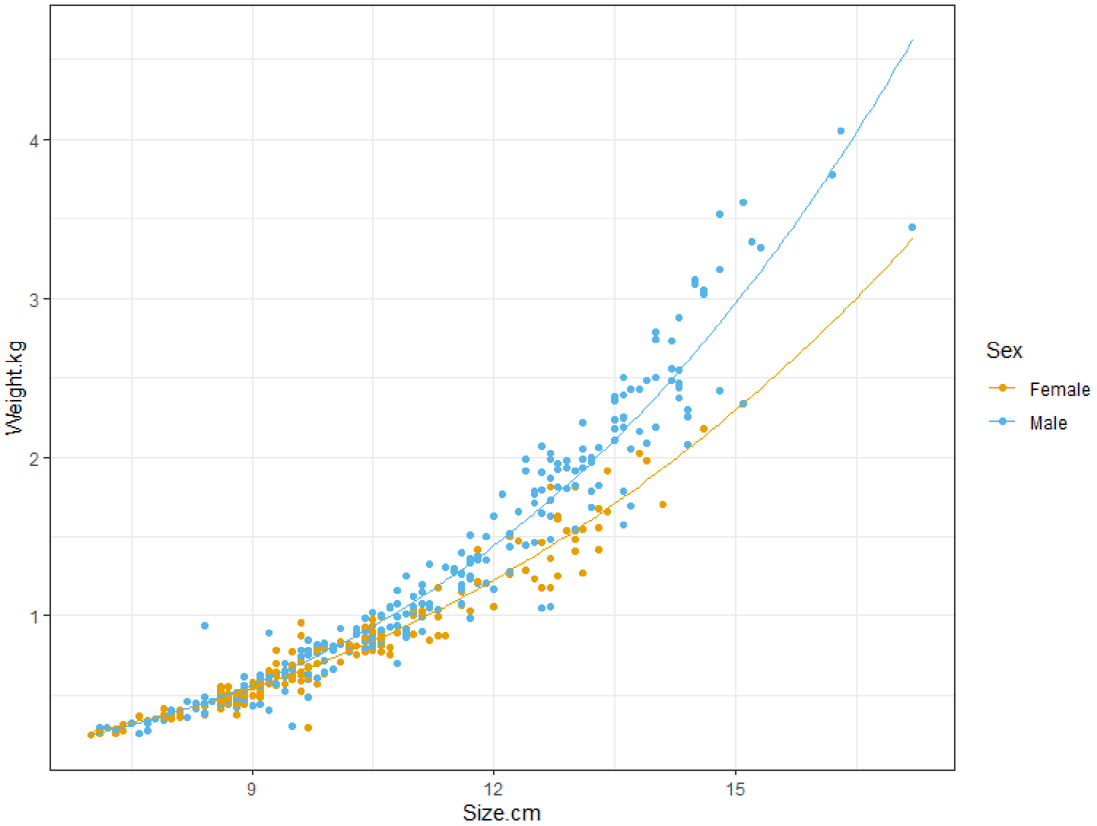


Figure. Length to weight relationship of male and female lobsters.

Model outputs (summary(fm0)) for table mm to gramms

Has been updated with data not available to the SS3 model, with minor changes to the parameters. The model formulation in R was: (Weight.kg) ~ a * (Size.cm)^b

Model fits were:

	Female	Male
a	0.00114	0.000459
b	2.80935	3.240244

Conversion for mm to grams affected the parameter of both Males and females. This length to weight conversion is not used for modelling, but useful for calculating weights in data sets were size in mm is handled.

Male Parameters

	Estimate	Std. Error	t value	Pr(>
a	2.639e-04	7.344e-05	3.594	0.000388 ***
b	3.240e+00	5.690e-02	56.945	< 2e-16 ***

Residual standard error: 199.2 on 263 degrees of freedom Number of iterations to convergence: 41 Achieved convergence tolerance: 2.451e-06

Female parameters

	Estimate	Std. Error	t value	Pr(>
a	0.0017686	0.0004929	3.588	0.00044 ***
b	2.8093464	0.0585916	47.948	< 2e-16 ***

Residual standard error: 104.3 on 163 degrees of freedom Number of iterations to convergence: 29 Achieved convergence tolerance: 2.26e-08

7.8 Appendix VIII - Survival of European lobster *Homarus gammarus* in protected and non-protected areas

Henrik Pärn & Andreas Sundelöf

Background

During 1989-2007 European lobsters *Hommarus gammarus* were individually marked and recaptured annually in a Marine Protection Area (MPA; Kåvra) off the coast of Lysekil, by the Swedish Agricultural University SLU, to estimate survival (Moland et al. 2013). In 2017, the study was resumed, and capture sessions have been performed annually in the MPA during 1-2 weeks in August. Two non-MPAs have also been included in the study (Stora Kornö, 2017-ongoing; Långö, 2017-2022). In addition, recaptures have been reporterted from a citizen science projects (“Lobserve”, an annual survey fishery by volunteers), or by other private fishers.

In the SLU projects, lobsters are caught, individually marked with a tag, and released alive. For a more detailed description of field procedures (see Moland et al. 2013). Given that a marked lobster is recaptured in the MPA, it can be in the following states: (1) encountered alive and released alive; or (2) recovered dead in pot. In addition, if a lobster is captured by private fishers outside the MPA, it may be reported as (3) encountered alive and then harvested (by non-Lobserve private fishers). The outcome for 2 and 3 is the same: dead (“loss on capture”). In this report, both causes of death are treated in the same way, i.e. as “loss on capture”, and cause-specific mortality is not estimated.

The two main objectives of this report are to estimate: (1) sex-specific survival for the MPA during 2017-2023; (2) sex-specific differences in survival between the MPA (Kåvra) and the two non-MPAs (Stora Kornö and Långö) during 2017-2023.

Methods

Mark recapture analyses

In the analyses, the R package `RMark` (Laake 2013) was used. Individual encounter histories for 2017-2023 were created, i.e. a sequence of `1` and `0`, where each number represent the individual state in each annual capture session; `1` indicates that an individual was recaptured, and `0` indicates the individual was not recaptured (or otherwise seen). In addition, a `"."` in the capture history was used for missing occasions, i.e. at Långö 2023. To account for “loss on capture” (see above), the `freq` field in the capture history was set to -1, to indicate that the individual was removed after the last occasion.

Covariates

In a previous study in the same study area (Moland et al. 2013), models included sex-specific survival (φ). The reason for this were that (1) management rules are sex-specific (ban on capture of egg-bearing females), and (2) available information on longevity suggests that females might have higher survival probabilities in the wild. Thus, sex is included as a predictor variable in the models.

Surival in a Marine Protection Area (Kåvra) and two non-MPA (Stora Kornö & Långö) were compared. Some individuals have been recorded at several sites. However, in the analyses, site is treated as a "fixed" covariate and site at first capture was used. In addition, several recapture occasions are captures by private fishers who have not registered a 'site', but only coordinates. Thus, for each individual, the site of first capture is assigned to all rows.

Results

Sex-specific survival in the MPA (Kåvra), 2017-2023

Parameter estimates, β

parameter	estimate	se	lcl	ucl
Phi:(Intercept)	0.405	0.152	0.107	0.702
Phi:sex_m	0.141	0.169	-0.191	0.473
p:(Intercept)	-1.505	0.132	-1.764	-1.246

Real parameters

Contrary to the expectations, survival rate of females seems slightly lower than for males. However, it should be noted that the 95% confidence intervals of the estimates are mostly overlap. The estimates are similar to those reported by Moland et al. (2013).

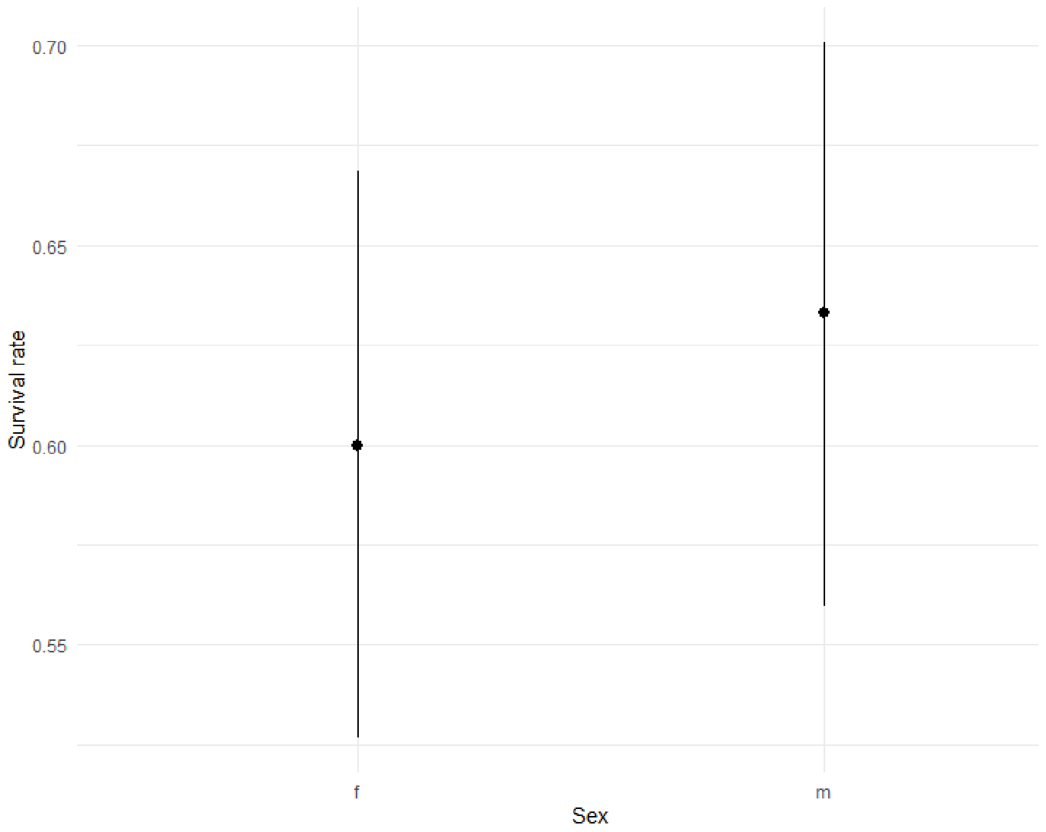


Figure 1: Survival rate of male and female European lobster a marine protected area (Kåvra).

*Sex-specific influence of MPA vs non-MPA on survival (**φ**: sex * MPA + time; **ρ**: MPA)*

Survival in a Marine Protection Area (Kåvra) is compared with two non-MPAs pooled (Långö and Stora Kornö). The influence of MPA is allowed to vary between males and females by including the interaction `sex * MPA` in the model.

Parameter estimates, β

parameter	estimate	se	lcl	ucl
Phi:(Intercept)	0.492	0.409	-0.309	1.293
Phi:sex_m	-1.494	0.374	-2.226	-0.761
Phi:mpaTRUE	-0.888	0.397	-1.667	-0.109
Phi:time2018	0.018	0.406	-0.778	0.814
Phi:time2019	1.186	0.485	0.235	2.137
Phi:time2020	1.613	0.552	0.530	2.696
Phi:time2021	1.033	0.457	0.137	1.930
Phi:time2022	1.442	0.609	0.249	2.635
Phi:sex_m:mpaTRUE	1.540	0.415	0.727	2.353
p:(Intercept)	-1.530	0.231	-1.982	-1.078
p:mpaTRUE	0.082	0.262	-0.431	0.596

In females, the estimate of φ for the non-MPA, Långö and Stora Kornö, are both positive. That is, φ is higher for the non-MPA than for the MPA, Kåvra. However, the CI of the estimate for Långö includes zero. Thus, the difference between non-MPA and MPA is not obvious for females. The `sex * mpa` interaction is positive. Thus, in males, the survival in the MPA seems to be higher. One possible explanation for the sex-specific effect of MPA, may be that egg-bearing females are protected also in the non-MPA anyway. In addition, higher densities of lobster in the MPA together with density-dependent dispersal may reduce the apparent survival (joint effect of true survival and fidelity to the study area) estimated within the MPA. Again, note that harvesting in non-MPA are not distinguised from ‘loss on capture’ in MPA.

Real parameters

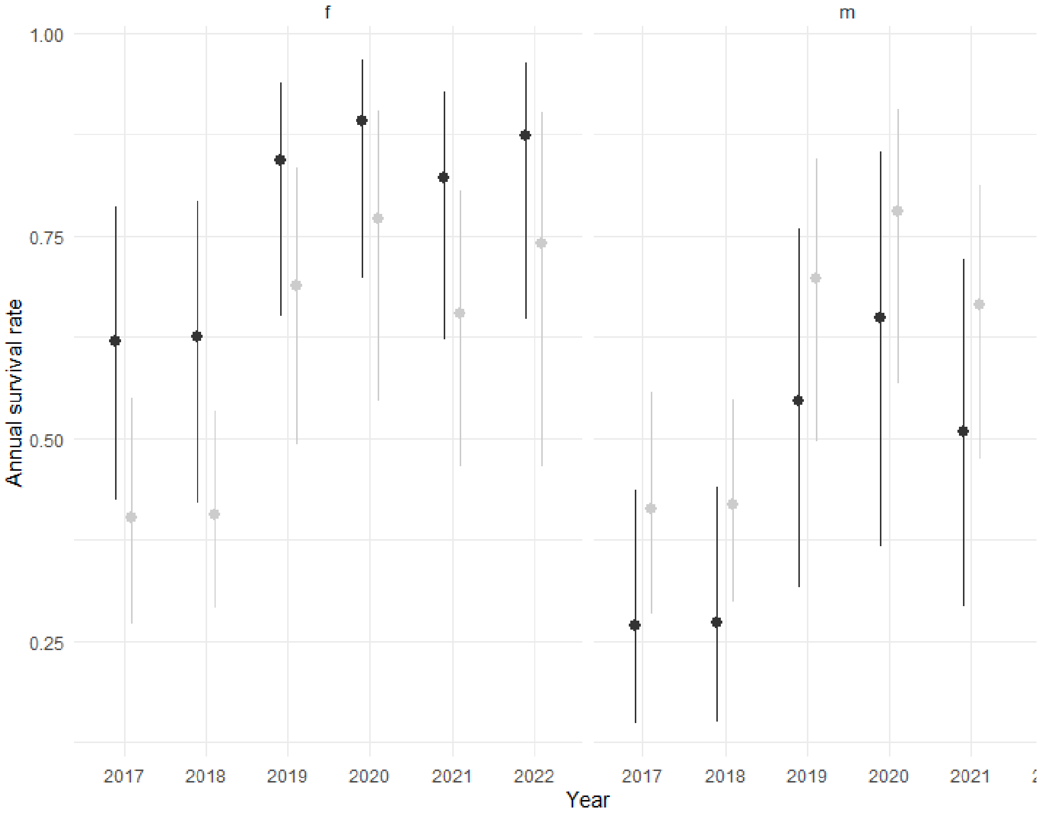


Figure 2: Annual survival rate of male and female European lobster in a marine protected area (grey points and error bars), and outside the MPA (black points and error bars).

References

Laake, J. L. 2013. "RMark: An R Interface for Analysis of Capture-Recapture Data with MARK." {AFSC} {Processed} {Rep}. 2013-01. Seattle, WA: Alaska Fish. Sci. Cent., NOAA, Natl. Mar. Fish. Serv. https://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2013-01.pdf.

Moland, Even, Mats Ulmestrand, Esben Moland Olsen, and Nils Chr Stenseth. 2013. "Long-Term Decrease in Sex-Specific Natural Mortality of European Lobster Within a Marine Protected Area." *Marine Ecology Progress Series* 491 (October): 153–64. https://doi.org/10.3354/meps10459.

7.9 Appendix XI – List of Participants Benchmark lobster 2024

Data meeting, Havs- och Vattenmyndigheten, Göteborg, 2024-06-05

Andreas Sundelöf, SLU Aqua
Max Cardinale (digital), SLU Aqua
Johan Lövgren, SLU Aqua
Henrik Pärn, SLU Aqua
Hege Sande, SLU Aqua
Richard Yngwe (digital), SLU Aqua
Emmelie Hammenstig-Åström, SLU Aqua
Tonje Knutsen Sørdalen, Havforskningsinstitutet och Universitetet i Agder, Norge
Kristian Nilsson, SFPO
Martin Zackrisson, SFPO
Martin Karlsson, HaV
Martin Rydgren, HaV
Erika Axelsson (digital), Länsstyrelsen Halland
Therese Jansson (digital), Länsstyrelsen Västra Götaland
Lars Molander (digital), Länsstyrelsen Västra Götaland
Björn Fagerholm (digital), Länsstyrelsen Västra Götaland

Model diagnostics, SLU Aqua Havsfiskelaboratoriet, Lysekil, 2024-10-03

Andreas Sundelöf, SLU Aqua
Max Cardinale, SLU Aqua
Henrik Pärn, SLU Aqua
Hege Sande, SLU Aqua
Emmelie Hammenstig-Åström, SLU Aqua
Valerio Bartolino (digital), SLU Aqua
Daniel Valentinsson (digital), SLU Aqua
Tonje Knutsen Sørdalen, Havforskningsinstitutet och Universitetet i Agder, Norge
Martin Zackrisson, SFPO
Martin Karlsson (digital), HaV
Martin Rydgren (digital), HaV
Erika Axelsson (digital), Länsstyrelsen Halland

7.10 Appendix X - Candidate benchmark model for European lobster in 3a

Separate page numbering: 1 – 50

Candidate benchmark model for European lobster in 3a

Max Cardinale (SLU)

06 September, 2024

Contents

1 Draft conclusions and recommendations

- The benchmark assessment of European lobster in ICES division 3a was conducted in June-October 2024 using the Stock Synthesis (SS) model (Methot & Wetzel 2013)
- Benchmark was conducted comparing 7 different model configurations, which were evaluated through diagnostic
- The Working Group on Stock Assessment of Lobster in 3a proposed Run2 as the final model configuration to be used for stock assessment and management. Run2 has the same diagnostic score than Run3 and Run6 but a better convergence and therefore was chosen as the final run
- Forecast settings: R from the Beverton & Holt stock-recruitment curve, biology and selectivity as the average of the last 5 years, Ftarget is FMSY. BMSY is about 41% of unfished SSB

2 Base Case Model Development

The previous advice concluded that the stock was in overfishing and overfished; however SSB shows a positive trend in the last five years but below the target reference point ($BMSY$). Fishing pressure was estimated to be above F/F_{MSY}.

- The benchmark model is a one-area yearly model where the population is comprised of 25+ age-classes with two sexes (males and females are considered as separated). The model is a length-based model where the numbers at length in the fisheries and survey data are converted into ages using the von Bertalanffy growth function. The model started in 1875 and it includes 8 fleets: 1 commercial fisheries, 1 recreational fisheries and 6 surveys. LFDs are available for 2 of the fleets.
- This document presents the candidate benchmark model run. This model was initially set up based on the discussions held during the data preparation meeting, which was held in June 2024. This new set of models includes revised survey indices after standardisation.

2.1 Data revisions

- All modern surveys were standardised
- Revision of lenght composition data

2.2 Model setting

- Maximum age in the population set to 25 years (population plus group)
- Growth parameters separated for females and males using the von Bertallanfy function
- Fixing of CV young and old individuals at 0.15 and 0.10 respectively
- Fixing age varying, time unvarying M for females and males separately
- Estimating selectivity for the commercial fleet and VC_2017 survey
- Early recruitment era start in 1875
- Extra standard deviation was assumed for several surveys

2.3 Benchmark trial runs

Model Directory

- Reference run
- Run1 : As Reference run but assuming low catches
- Run2 : As Reference run but assuming high catches
- Run3 : As Reference run, low steepness
- Run4 : As Reference run, high steepness
- Run5 : As Reference run, time varying selectivity of the commercial fleet since 2018
- Run6 : As Reference run, high catches, low steepness

2.4 Work flow

- Run first the file Ensemble_grid_Lobster3a.R, which creates input files for the files (Lobster3a_basecase model.Rmd) and the Diags_Compare_refruns_lobster3a.Rmd. The latter visualize the comparison between the different model alternatives, the first instead focus on the basecase model as selected by diagnostic (Run2 in this case).

Load R packages

```
library(r4ss)
library(ss3diags)
library(ggplot2)
library(ggpubr)
library(FLCore)
library(ggplotFL)
library(FLSRTMB)
library(FLRef)
library(ss3om)
library(png)
library(parallel)
library(doParallel)
cl <- makeCluster(10, type = "PSOCK")
registerDoParallel(cl)
```

Some system specific setups (Linux vs Windows)

```
if (Sys.info()["sysname"] == "Windows") {

    ss.exe <- "~/Max/Stock_synthesis/ss3_3.22.1/ss3.exe"
    main.dir <- "~/Max/Commitees/National stocks/Lobster 3a"
    MC.CORES <- 3
    print("mc.cores set to 1, NO PARALLELISATION on Windows :( ")

} else {

    SS_EXE <- "~/Max/Executives_SS/ss_linux"
    main.dir <- "~/Max/WKBENCH 2023/Central Baltic herring/Ensemble"
}
   [1] "mc.cores set to 1, NO PARALLELISATION on Windows :( "
```

Load reference run

```
# 2024 reference case
load("rdata_runs/Lobster3a_Run2.rdata", verbose = F)
ref = ss3rep

# load retrospective runs
load("rdata_retros/RetroModels_Run2.rdata", verbose = F)

# load steepness profile
load("Reference_run/profile/profile_h.ref.rdata", verbose = F)
```

2.5 Fishery Data

- Catch data were available for commercial and recreational fleets.
- Alternative time series of recreational catches were tested

```
mod = ref
df.catch = mod$catch
df.catch$Season = factor(df.catch$Seas)

pc1 = ggplot(df.catch, aes(Yr, Obs, fill = Fleet_Name)) + theme_bw() +
```

```
    geom_bar(position = "stack", stat = "identity") + ylab("Catch") +
    xlab("Year") + scale_x_continuous(expand = c(0.01, 0)) +
    scale_y_continuous(expand = c(0.01, 0)) + scale_fill_manual(values = sscol(length(unique(df.catch$F

pc1
```

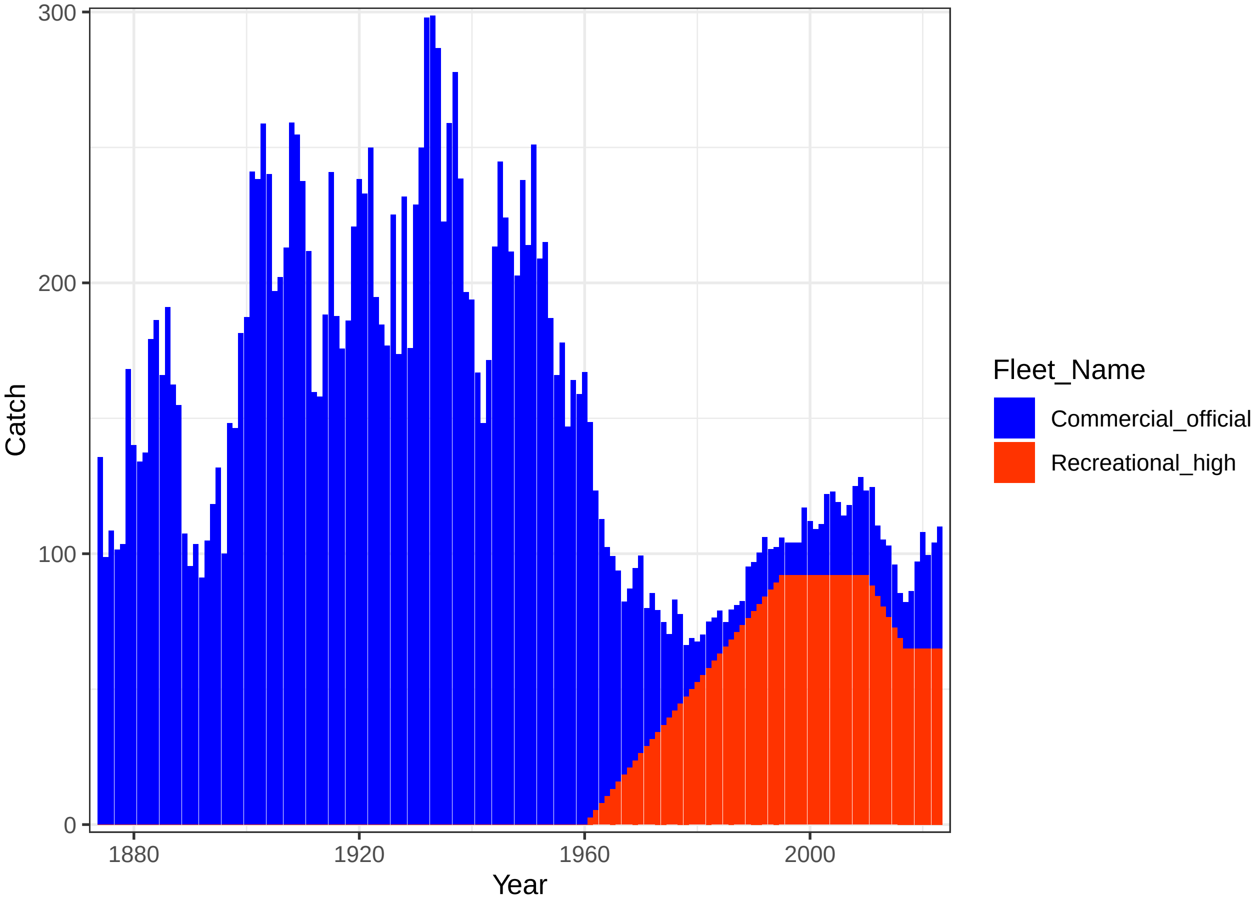


Figure 1: Time series of annual total catches for European lobster in 3a, illustrated as disaggregated by Season (top) and Fleets (bottom) through 2023

- Sex-structured length data (LFDs) were available for commercial catches and VCD_2017. The final cleaned and revised available input data time series are shown in Figure 2.
-

```
SSplotData(ref, subplots = 2)
```

2.6 Survey

- Six survey indices were include in the model. All modern surveys were standardised.
- The survey LFD data were available only for VCD_2017 survey.

```
knitr::include_graphics("index9_standcpueall.png")
```

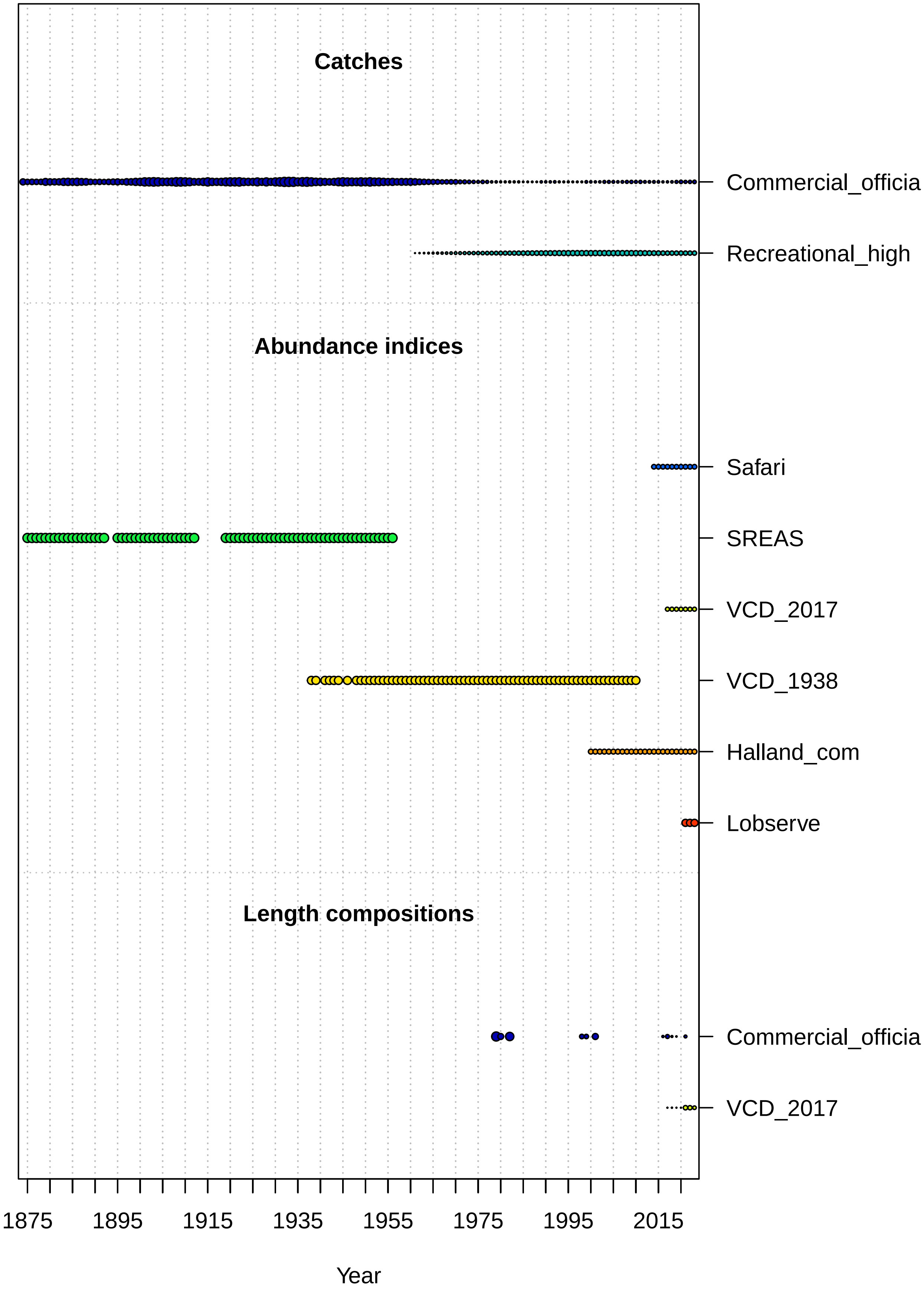


Figure 2: Illustration of time series data for catches, LFDs and the survey indeces that were adopted as input for the Stock Synthesis model during the benchmark session for the 2024 reference model.

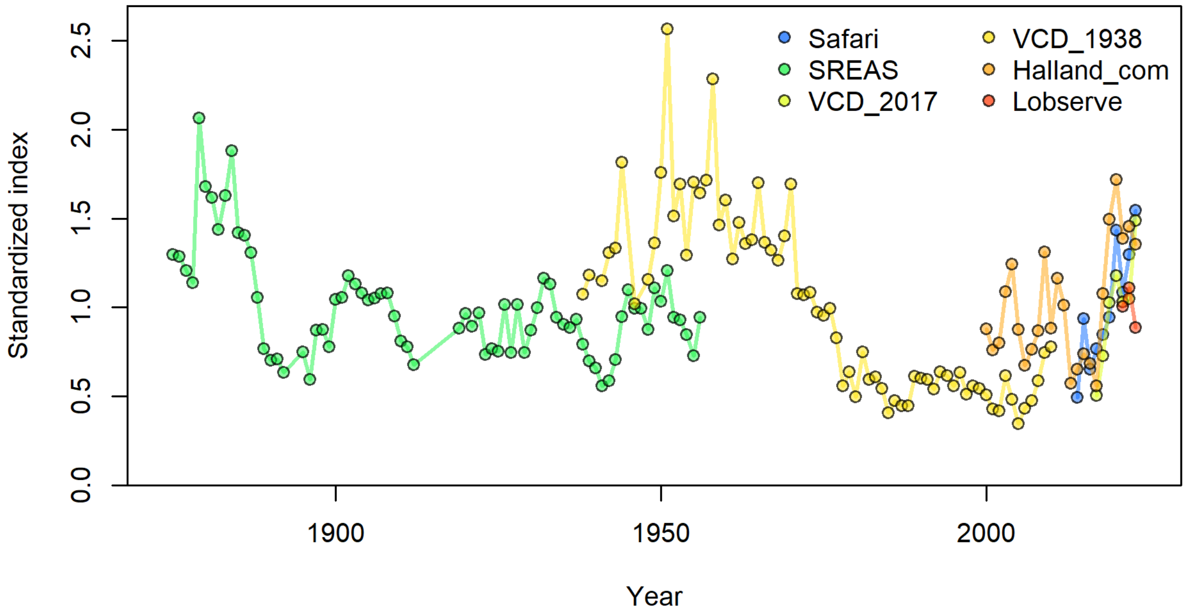


Figure 3: Survey indices

2.7 Model specifications

- The reference model for European lobster in 3a is an annual, sex-structured length-based Stock Synthesis model. The underlying age-structured dynamics is set up to comprise ages 0-25, where age 25 was treated as a plus group. The population was modeled as sex-structured with sex-specific parameterisations for somatic growth and $M - at - age$. Stock fecundity was assumed to be proportional to female spawning stock biomass.
- For the reference model, the sex specific growth is fixed for both sexes using Von Bertalanffy model (Figure 6). $L_a t_A min$ and $L_a t_A max$ were specified as 0.5 and 25 years, respectively. The CVs for $L_a t_A min$ were set to 0.15 and for $L_a t_A max$ to 0.1.

```
sspar(mfrow = c(1, 1), plot.cex = 0.7)
SSplotBiology(mod, subplots = 1, main = F)
```

- Female maturity was assumed to have the form of a logistic ogive with a length at 50% maturity ($L_{m_{50}}$) being attained 7.8 cm and a slope of -0.97 1/cm (Figure 7). $L_{m_{50}}$ corresponds approximately to a female of age-5.

```
sspar(mfrow = c(1, 1), plot.cex = 0.7)
SSplotBiology(mod, subplots = 6, main = F)
```

- Sex-specific natural mortality at age (M_a) were inputed for age 0, 1, 4, 5, 10 and 20 and were based on tagging carried out in the Kåvra marine reserve

```
sspar(mfrow = c(1, 1), plot.cex = 0.7)
SSplotBiology(ref, subplots = 21, main = F)
```

- Nominal spawning and settling time were set to January. The expected mean recruitment was assumed

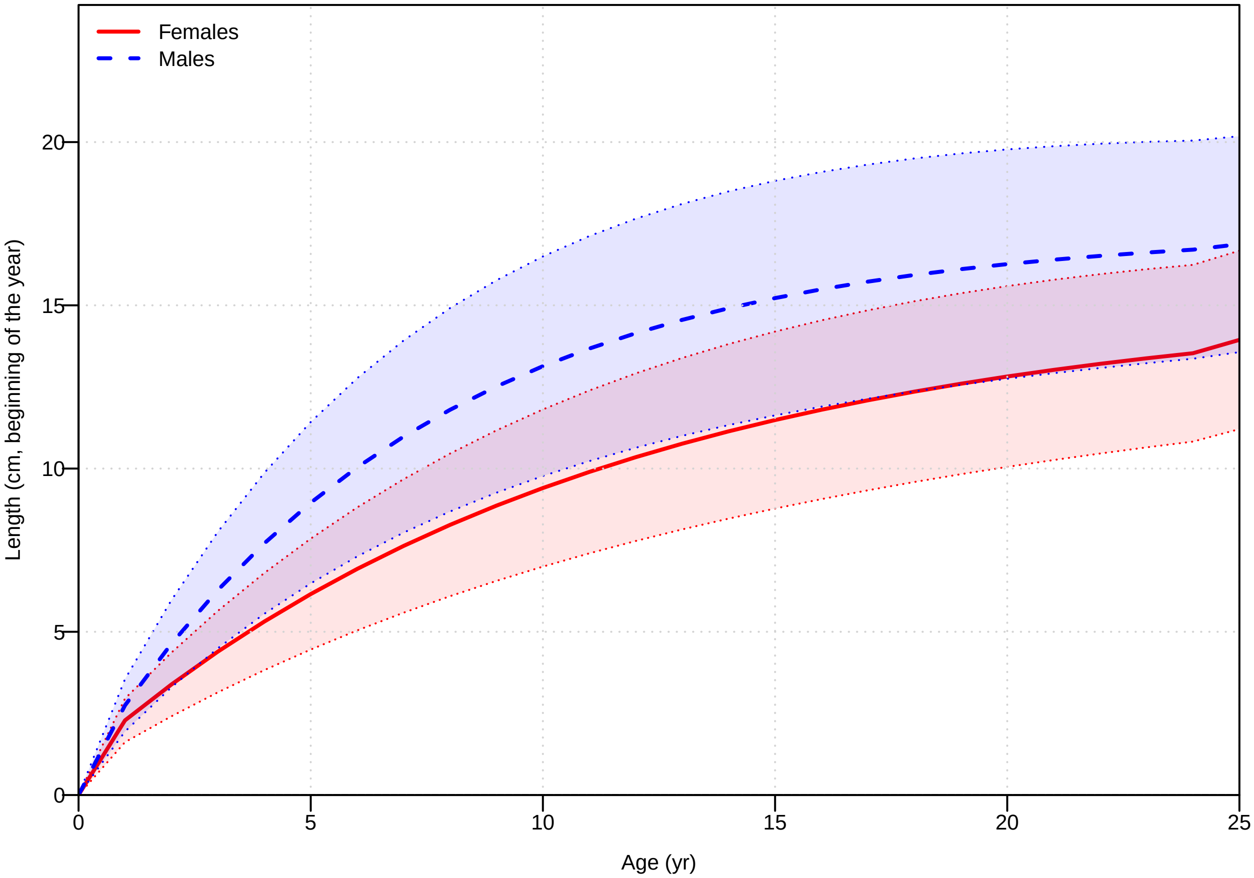


Figure 4: Growth functions for Female and Males.

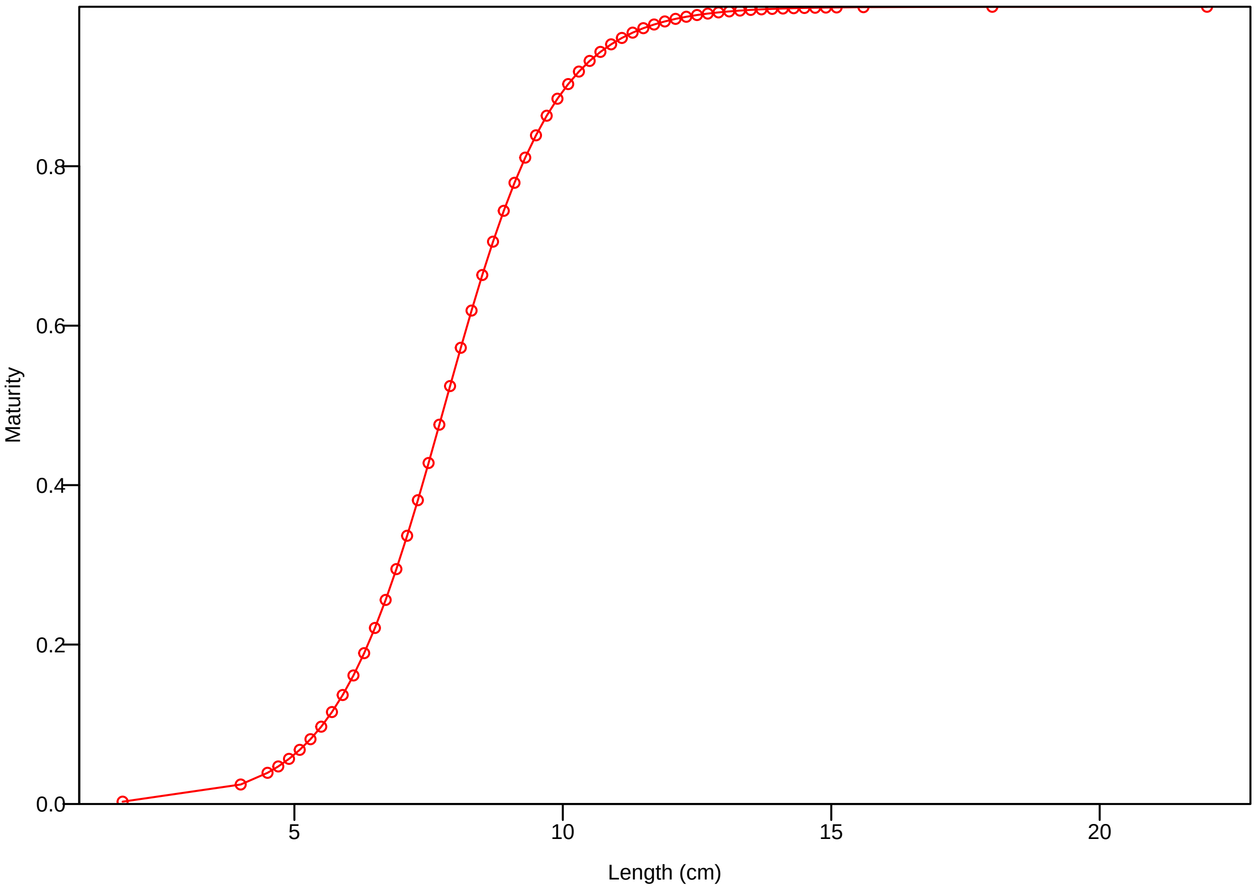


Figure 5: Assumed Maturity ogive for females.

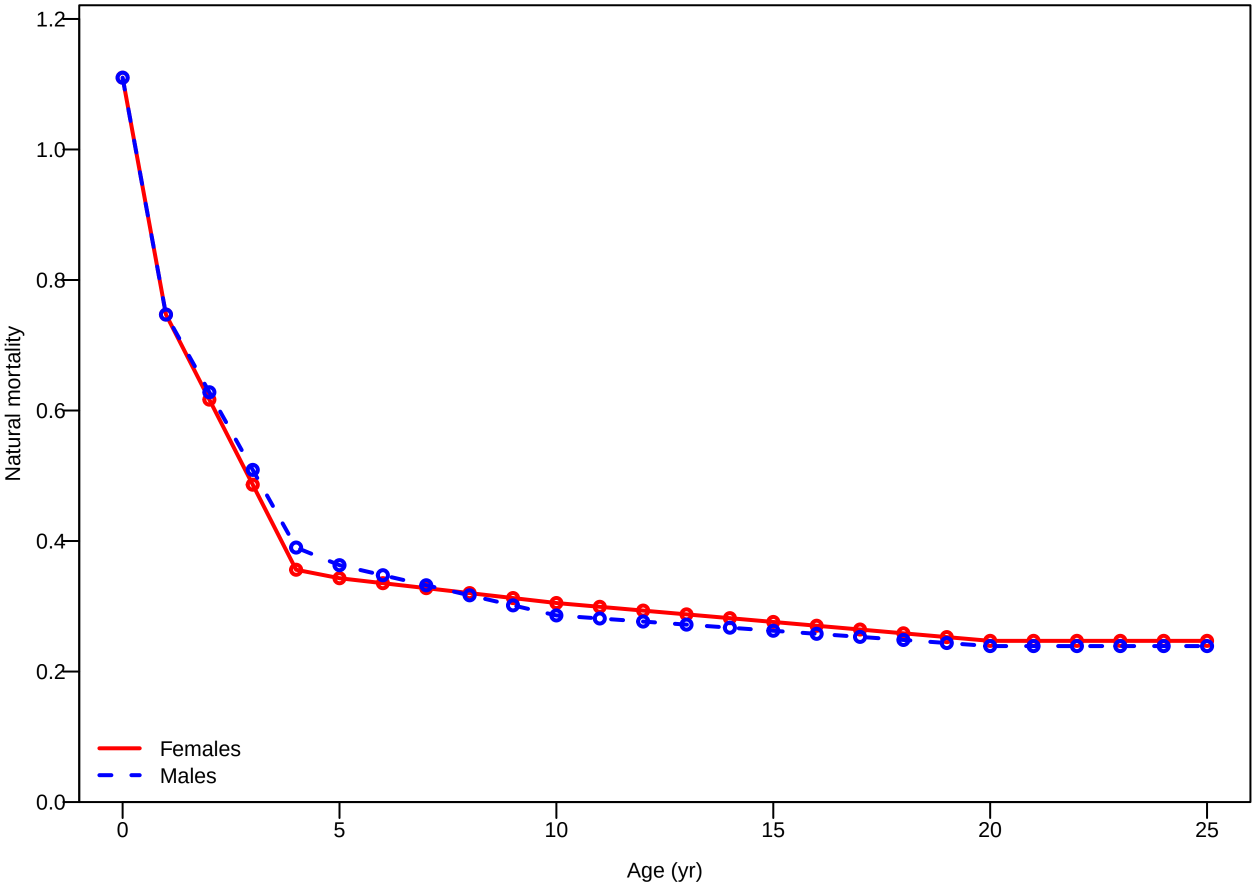


Figure 6: Assumed age-specific natural mortality vectors for females and males.

to follows a Beverton and Holt stock recruitment relationship. For the base-case a steepness of $h = 0.8$ was assumed. Recruitment deviations were estimated for 2010-2017 as main recruitment deviations and for the preceding years 1875-2009 as early recruitment deviations. Recruitment deviations were assumed to have a penalty of 0.5 on the standard deviation (sigmaR).

- All fleets assumed a double-normal (dome-shaped) selectivity (option 24).
- A time-varying selectivity was enabled for the commercial fleet (Figure 9).
- Fishing mortality was modeled using a fleet-specific hybrid F method (Option 4), which is consistent with best practice. Option five was selected for the fishing mortality (F) report basis; this option corresponded to the simple unweighted average of the F of the age classes chosen to represent the Fbar (age 8–13).

2.8 Model Diagnostics

Prepare outputs of retrospective runs (see Supplement)

```
retro.idx = r4ss::SSsummarize(retroModels, verbose = F)
retro.len = ss3diags::SSretroComps(retroModels)
```

2.8.1 Survey indeces

The reference-case model fitted all indices moderately well, with runs tests indicating mixed evidence for a systematic residual pattern (Figure 10).

```
sspar(mfrow = c(3, 2), plot.cex = 0.7)
for (i in 1:5) {
    SSplotIndices(ref, subplots = 2, fleets = i + 8)
    r = SSplotRunstest(ref, add = T, verbose = F, indexselect = i)
}
```

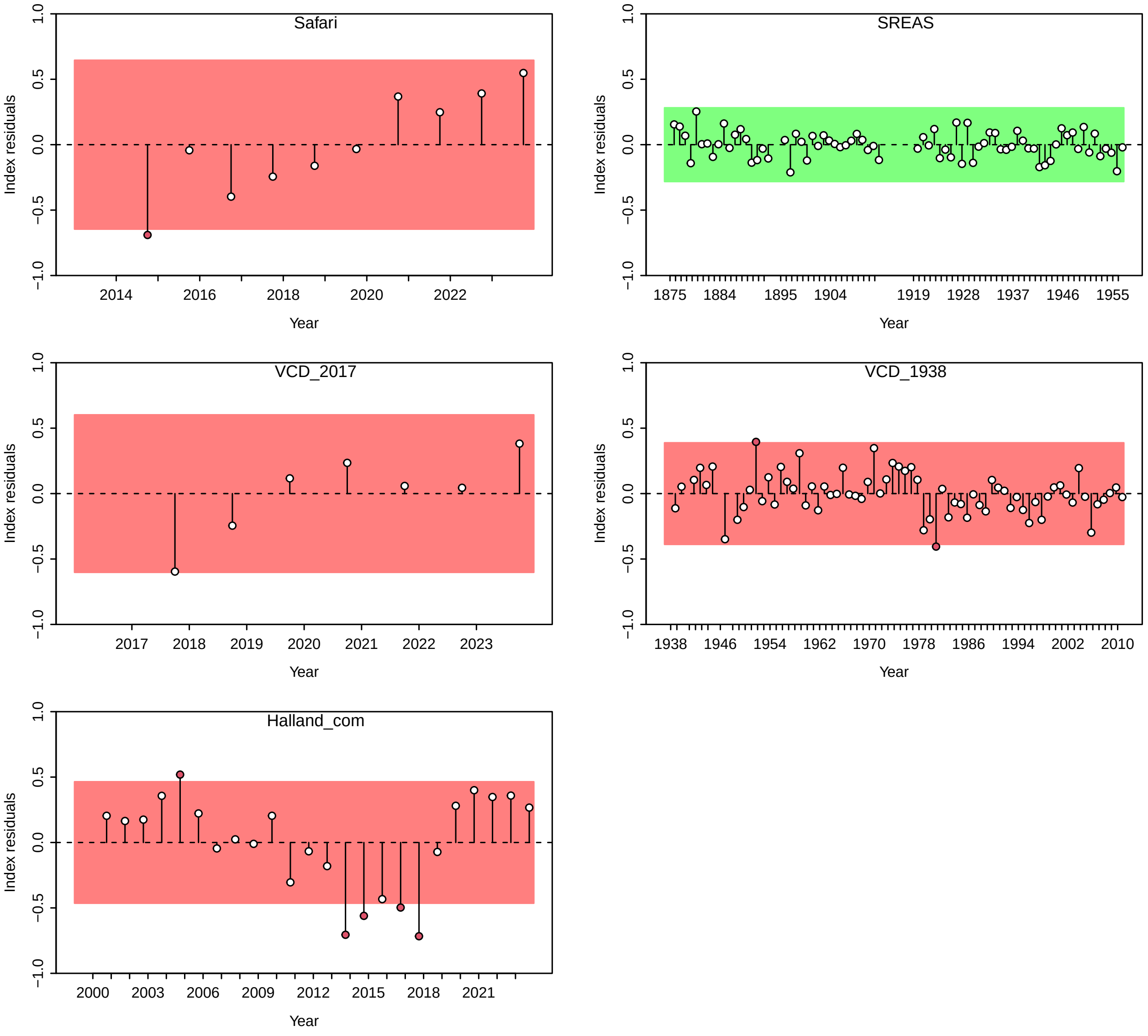


Figure 7: Fit, residual diagnostics and hindcast cross-validations for Survey Index

- Figure 7 check conflict between indices and mean length. As the value are under 30%, no major conflicts were found

```
sspar(mfrow = c(1, 2), plot.cex = 0.8)
SSplotJABBAres(ss3rep, subplots = "cpue", add = T, col = sscol(3)[c(1,
    3, 2)])
   Plotting JABBA residual plot

   RMSE stats by Index:
         indices RMSE.perc nobs
   1      Safari      37.0   10
   2       SREAS       9.7   74
   3    VCD_2017      30.1    7
   4    VCD_1938      15.5   70
   5 Halland_com      35.6   24
   6    Lobserve      10.3    3
   7    Combined      19.9  188
SSplotJABBAres(ss3rep, subplots = "len", add = T, col = sscol(3)[c(1,
    3, 2)])
   Plotting JABBA residual plot
```

```
   RMSE stats by Index:
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.3    7
   3            Combined       3.1   18
```

2.8.2 Size composition

- The estimated selectivity curves are shown in Figure 11, with time-varying selectivity patterns for illustrated in Figure 12.
- The fits to the size composition data and conditional age-length-key appeared overall adequate and only showed evidence for non-random residual patterns in few instances. Sex ratio at length by the current reference case is also satysfying.

```
sspar(mfrow = c(1, 1), plot.cex = 0.8)
SSplotSelex(ref, subplots = 1)
```

```
SSplotComps(ref, subplots = 21)
```

```
SSplotComps(ss3rep, subplots = 24)
```

```
sspar(mfrow = c(3, 3), plot.cex = 0.5)
for (i in 1:2) {
    r = SSplotRunstest(ref, subplots = "len", add = T, indexselect = i,
        verbose = F)
}
```

```
SSplotSexRatio(ss3rep, kind = "LEN")
```

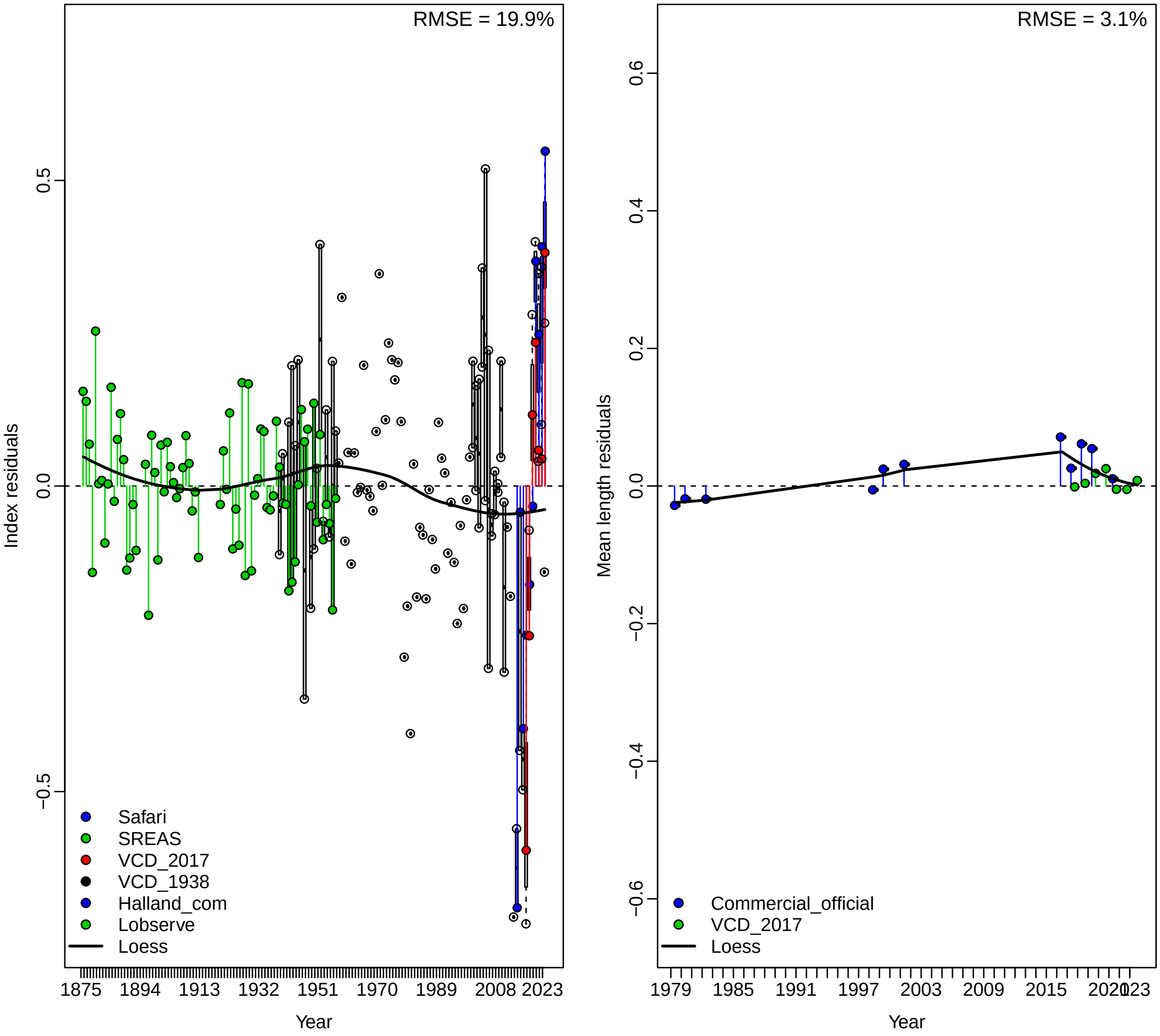


Figure 8: Joint residuals

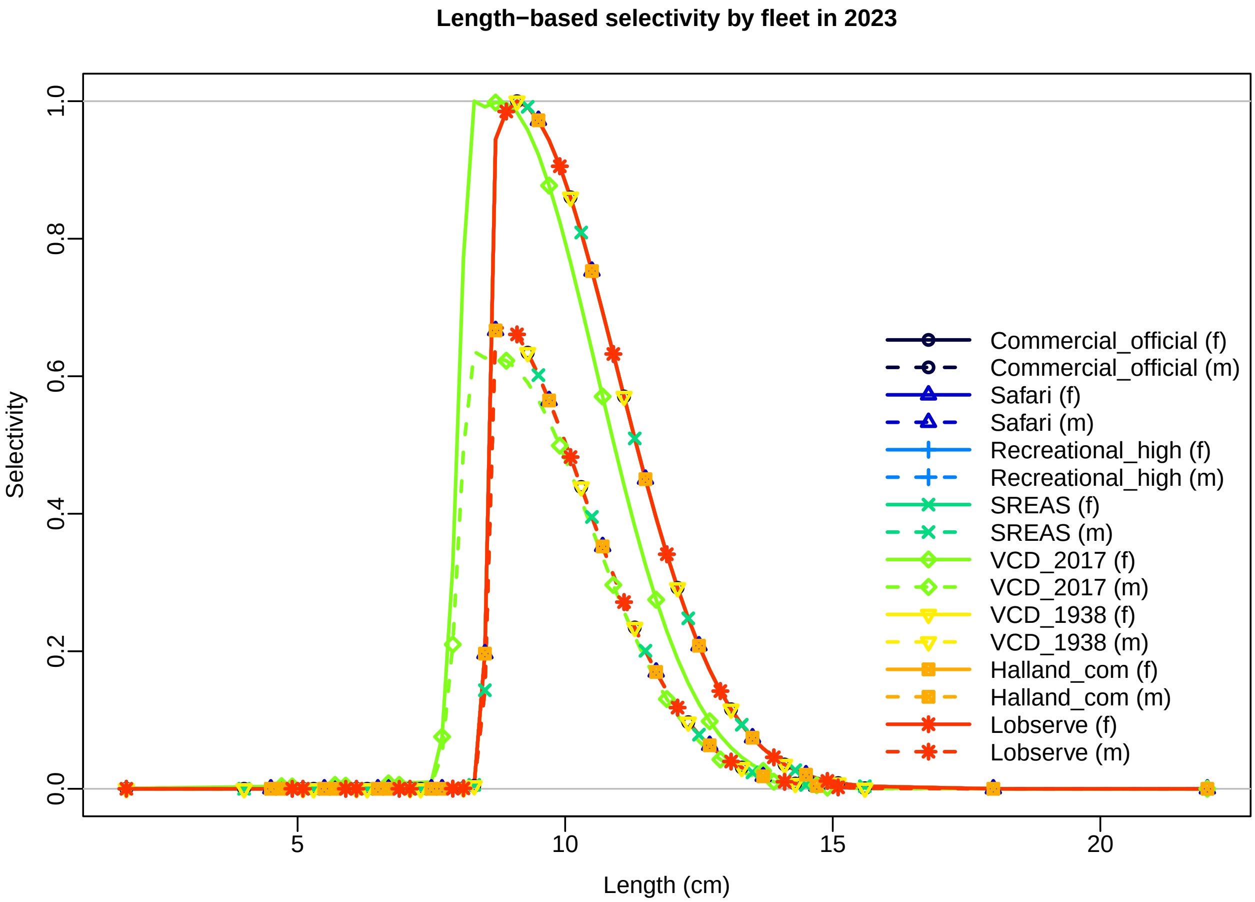


Figure 9: Estimated logistic selectivity curves by fleet

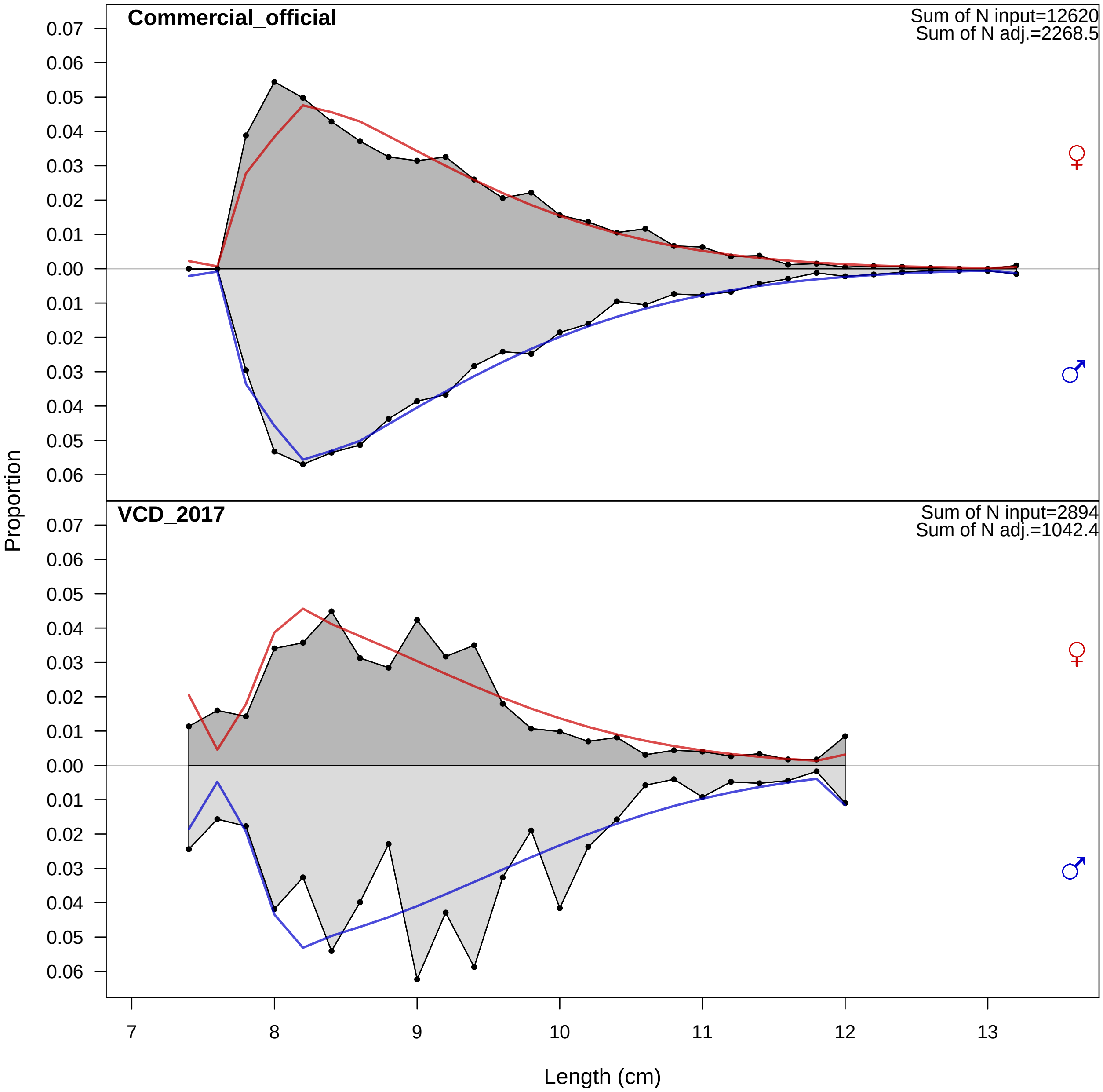


Figure 10: Summary of observed and expected composition data aggregated across years

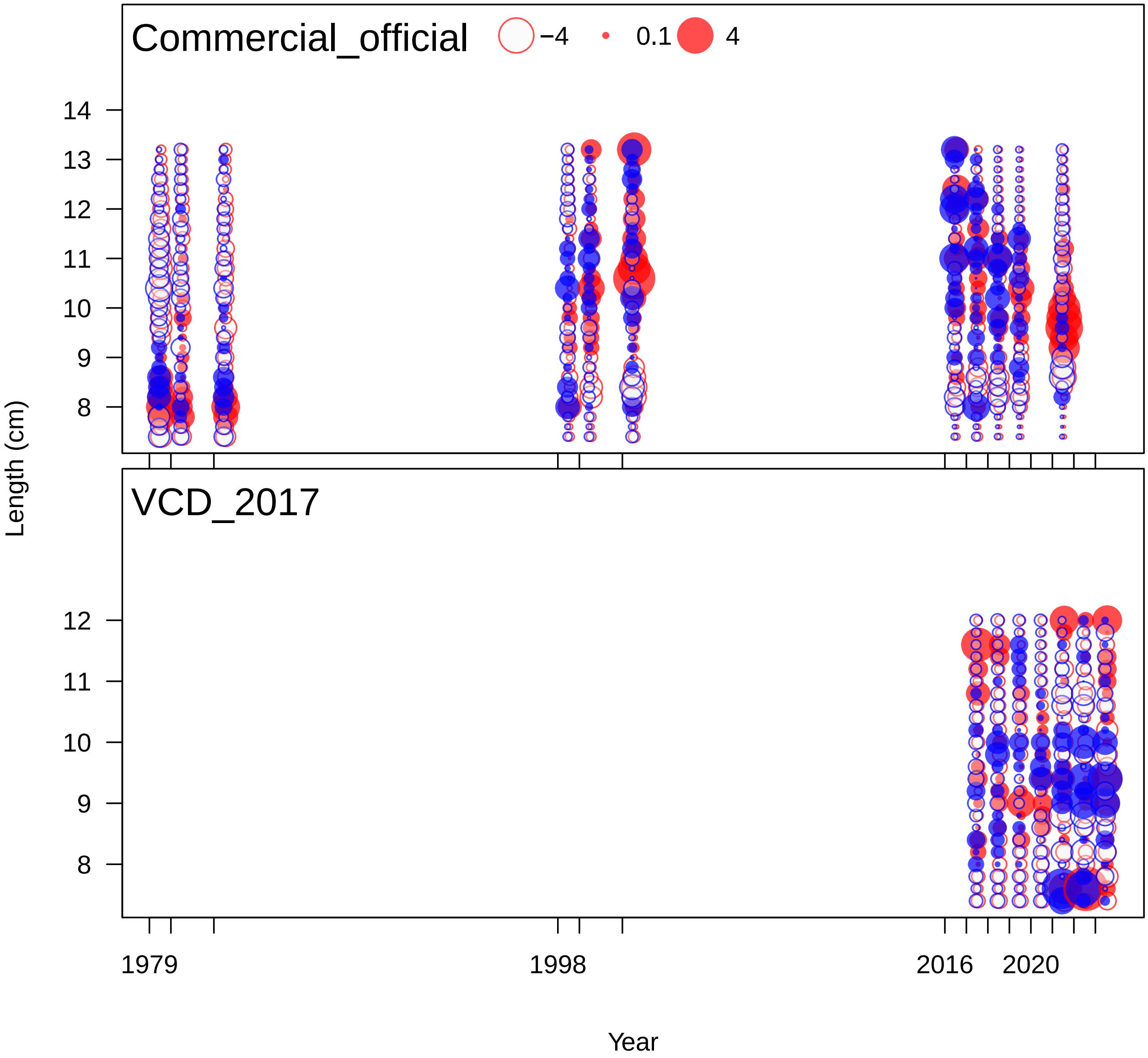


Figure 11: Residuals for mean lengths of size composition data from fishing fleets and surveys

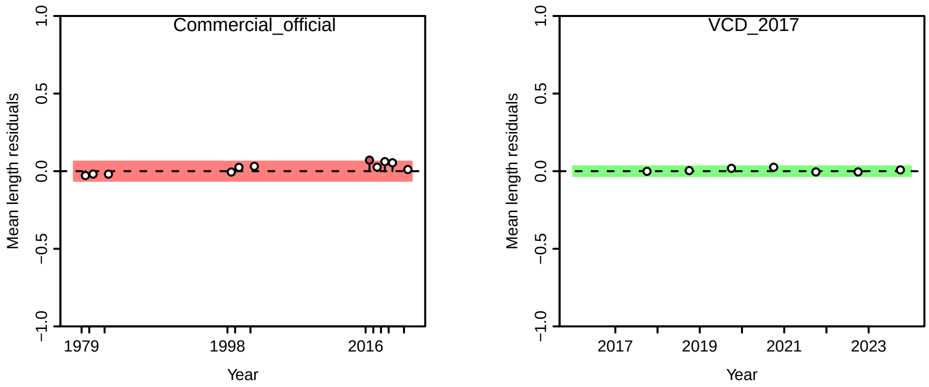


Figure 12: Run test for mean lengths of size composition data from fishing fleets and surveys

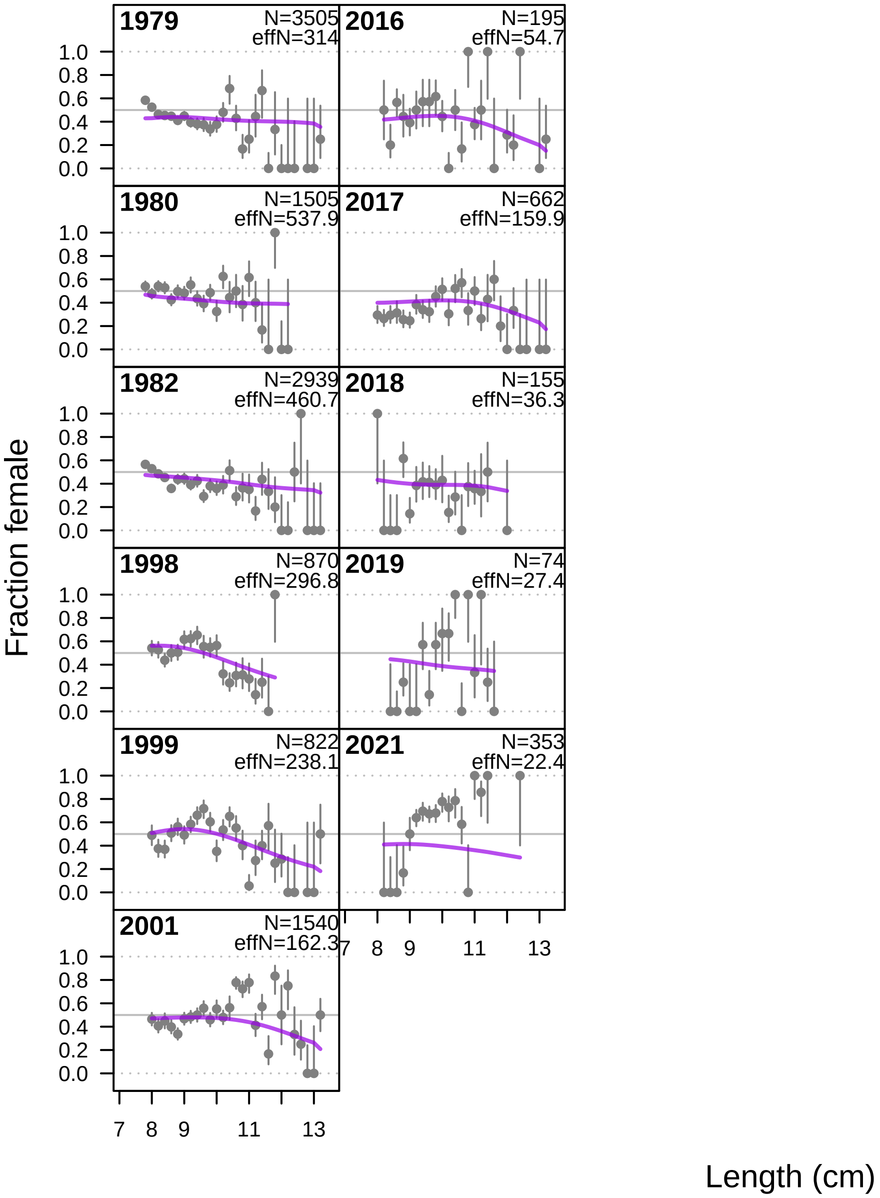


Figure 13: Observed and predicted sex ratio by length

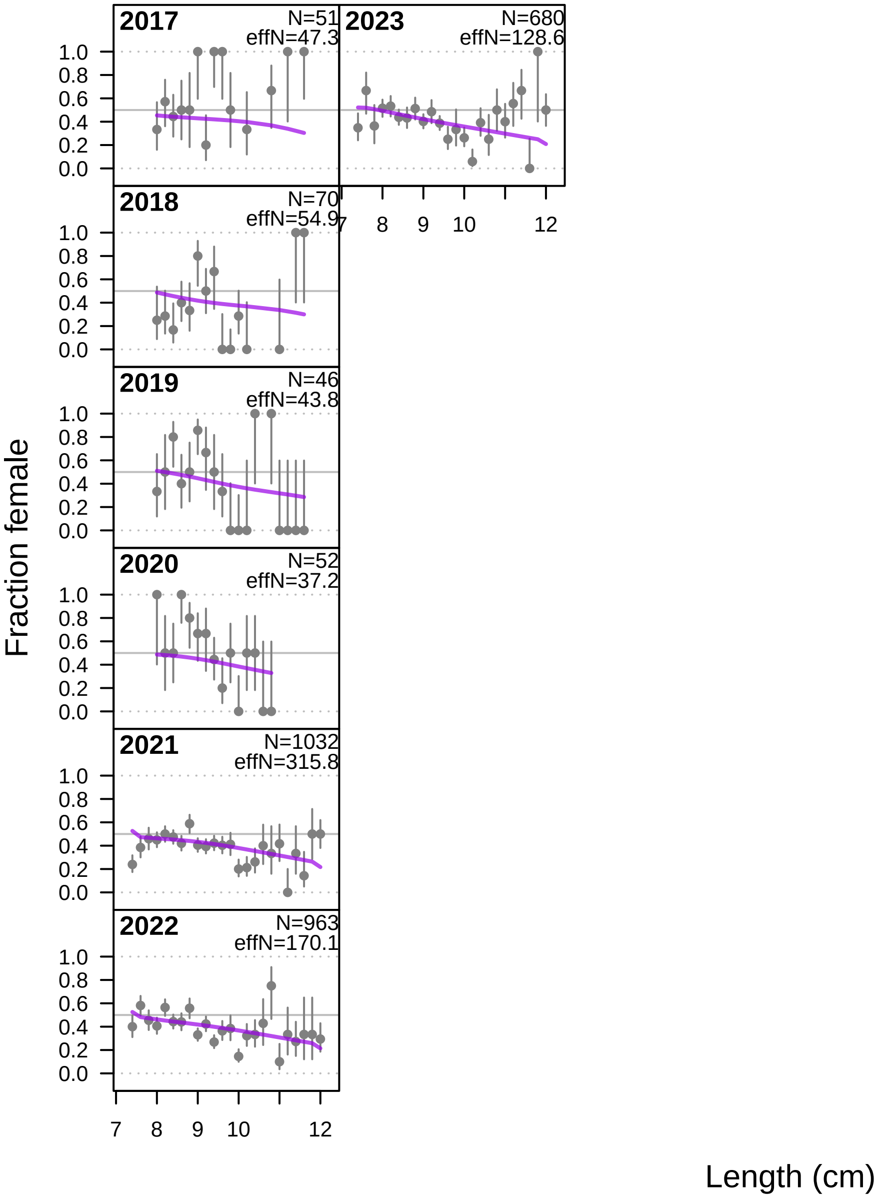


Figure 14: Observed and predicted sex ratio by length

2.8.3 Restropective Analysis with Forecasting

- The retrospective analysis showed a slightly retrospective pattern on *SSB* from Mohn's Rho of -0.17, while the *F* bias was -0.16. Forecast bias were the same as retrosective bias. All retrospective peels fell within the 95% confidence intervals of the full model

```
sspar(mfrow = c(2, 2), plot.cex = 0.65)
r = SSplotRetro(retro.idx, add = T, legend = F, forecast = F,
    verbose = F)
r = SSplotRetro(retro.idx, add = T, forecastrho = T, legend = F,
    verbose = F, xlim = c(2005, 2023))
r = SSplotRetro(retro.idx, subplots = "F", add = T, legend = F,
    forecast = F, verbose = F)
r = SSplotRetro(retro.idx, subplots = "F", add = T, forecastrho = T,
    legend = F, verbose = F, xlim = c(2005, 2023))
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3,
    0.8), cex = 0.8)
```

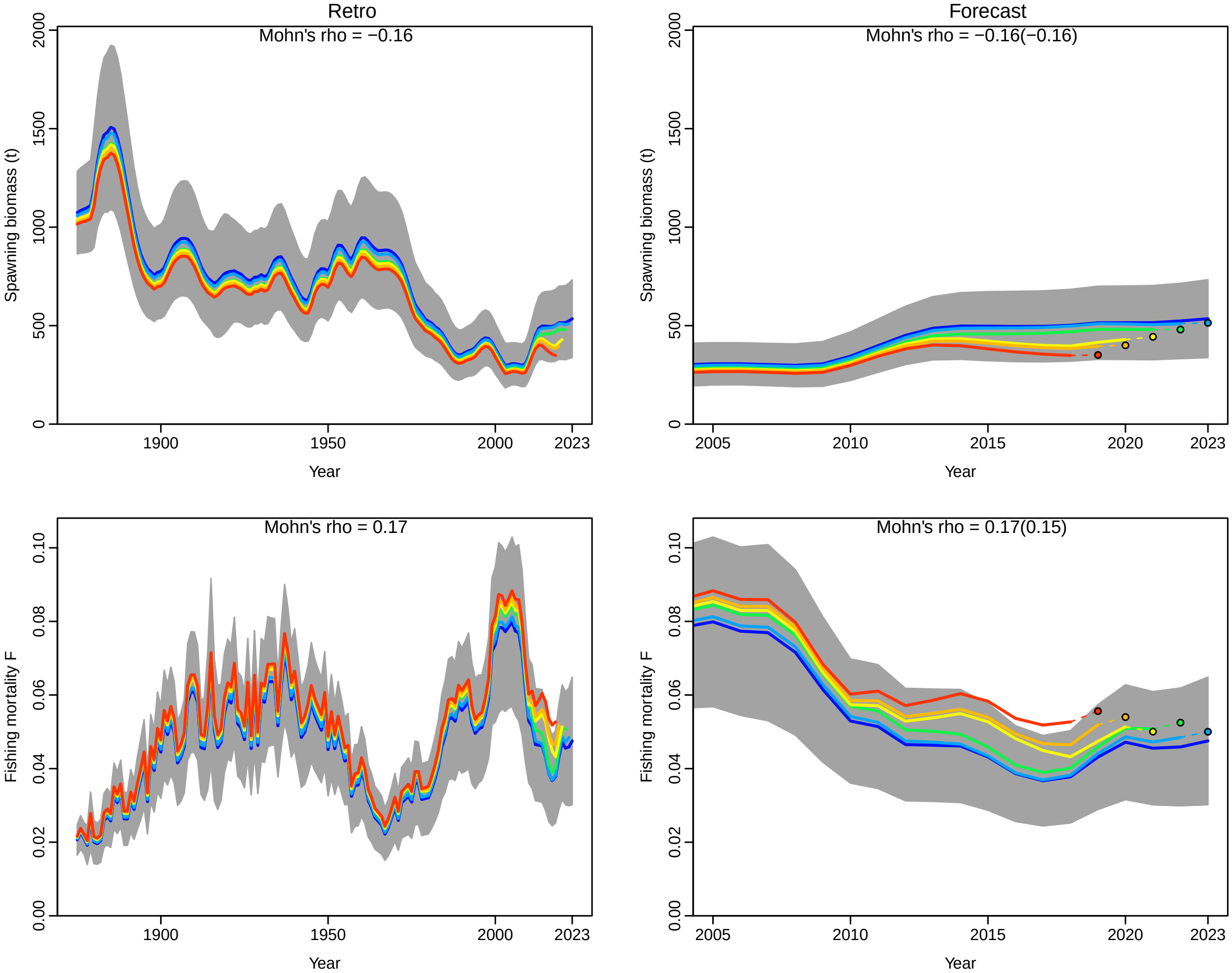


Figure 15: Retrospective analysis and retrospective forecasts for the 2024 base-case model

2.8.4 Hindcast Cross-Validations

Hindcast cross-validations indicated that the model has limited prediction skill for all indices. By contrast, both the indeces indicated prediction skill for mean lengths (Figure 19).

```
sspar(mfrow = c(1, 2), plot.cex = 0.5)
SSplotHCxval(retro.len, subplots = "len", add = T, verbose = FALSE)
```

```
                  Index Season      MASE     MAE.PR    MAE.base  MASE.adj n.eval
   1 Commercial_official      1 26.215262 0.13653419 0.005208195 1.3653419      2
   2            VCD_2017      1  1.220097 0.01580474 0.012953671 0.1580474      5
```

Hindcast with Cross-Validation of CPUE observations

```
sspar(mfrow = c(2, 2), plot.cex = 0.9)
SSplotHCxval(retroSummary, xmin = 2006, add = T, legendcex = 0.6,
    Season = 1)
   Plotting Hindcast Cross-Validation (one-step-ahead)

    Computing MASE with all 5 of 5  prediction residuals for Index Safari
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf

   No observations in evaluation years to compute prediction residuals for Index SREAS

    Computing MASE with all 5 of 5  prediction residuals for Index VCD_2017

   No observations in evaluation years to compute prediction residuals for Index VCD_1938

    Computing MASE with all 5 of 5  prediction residuals for Index Halland_com

    Computing MASE with only 2 of 5  prediction residuals for Index Lobserve

    Warning:  Unequal spacing of naive predictions residuals may influence the interpretation of MASE
```

```
   MASE stats by Index:
           Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
   1      Safari      1  3.053345 0.7099632 0.2325198  3.053345      5
   2       SREAS      1        NA        NA        NA        NA      0
   3    VCD_2017      1  1.548711 0.3069549 0.1982003  1.548711      5
   4    VCD_1938      1        NA        NA        NA        NA      0
   5 Halland_com      1  4.094495 0.6574687 0.1605738  4.094495      5
   6    Lobserve      1 12.876485 2.0627023 0.1601914 12.876485      2
```

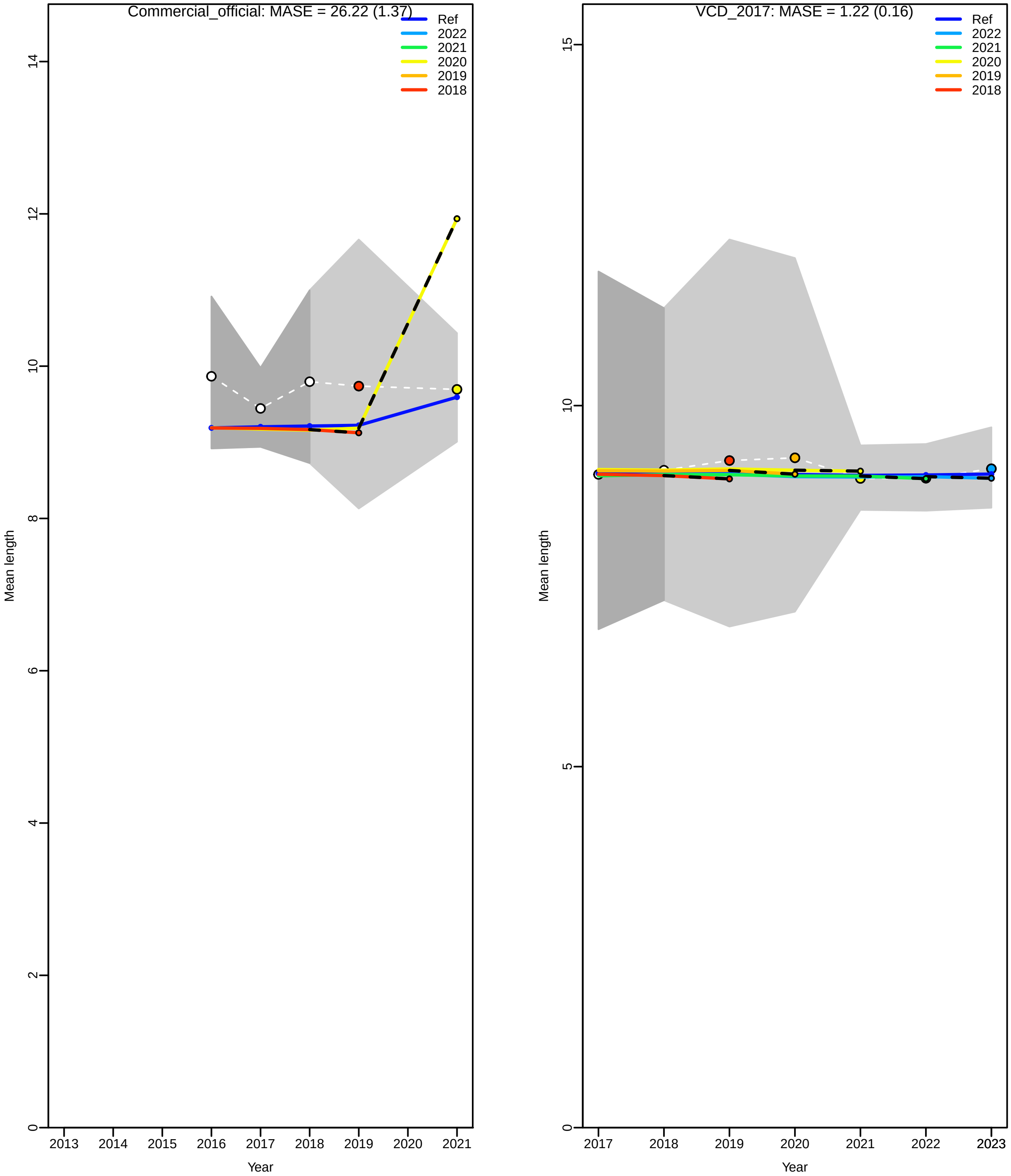


Figure 16: Fit and hindcast cross-validations for Survey size compositions of the base-case model

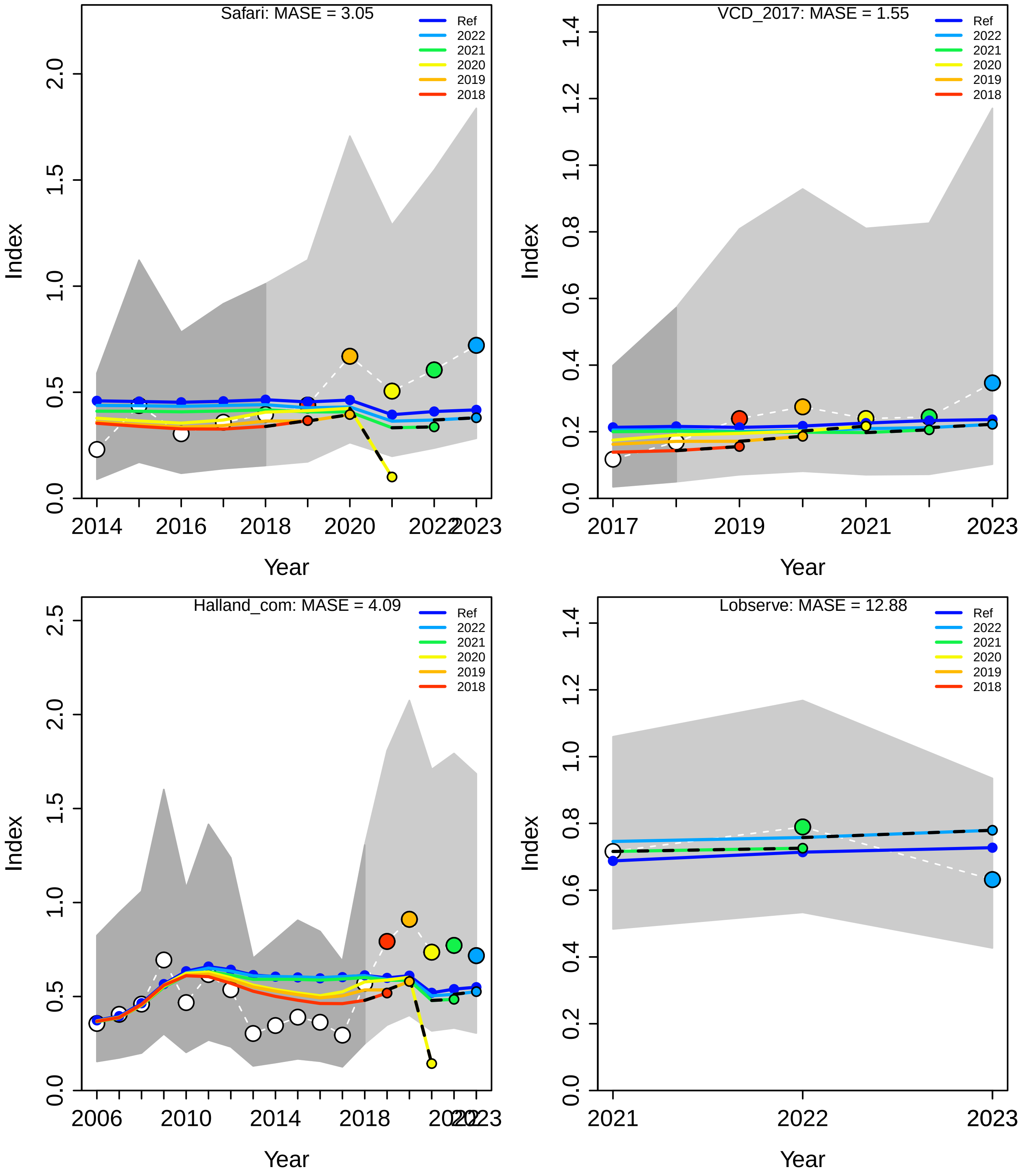


Figure 17: Hindcast with Cross-Validation of CPUE observations

2.8.5 Profiling of steepness

The reference case was further evaluated through profiling it over a range of steepness values $h = 0.45 - 0.95$.

Figure 22 shows that a lower range of $h = 0.45 - 0.65$ is supported by the total negative log-likelihood.

The stock status estimates appear insensitive to alternative assumption about the steepness h values under the value assumed for the reference case ($h = 0.80$) (Figure 22)

```r
# summarize output
profilesummary <- SSsummarize(profilemodels, verbose = F)
results <- SSplotProfile(profilesummary, add_cutoff = TRUE, verbose = F,
    profile.string = "Ricker_beta", profile.label = "Stock-recruit steepness (h)")
```

```r
h = c(seq(0.45, 0.6, 0.05), seq(0.7, 0.95, 0.05))

mvns = Map(function(x, y) {
    SSdeltaMVLN(x, add = T, run = paste0("h=", y), Fref = "MSY",
        catch.type = "Exp", years = 1875:2023, verbose = F, plot = F)
}, x = profilemodels, y = h)
   Warning in mapply(FUN = f, ..., SIMPLIFY = FALSE): longer argument not a
   multiple of length of shorter

sspar(mfrow = c(3, 2), plot.cex = 0.7)
SSplotEnsemble(mvns, uncertainty = T, add = T, legendcex = 0.65,
    legendloc = "topright", verbose = F)
```

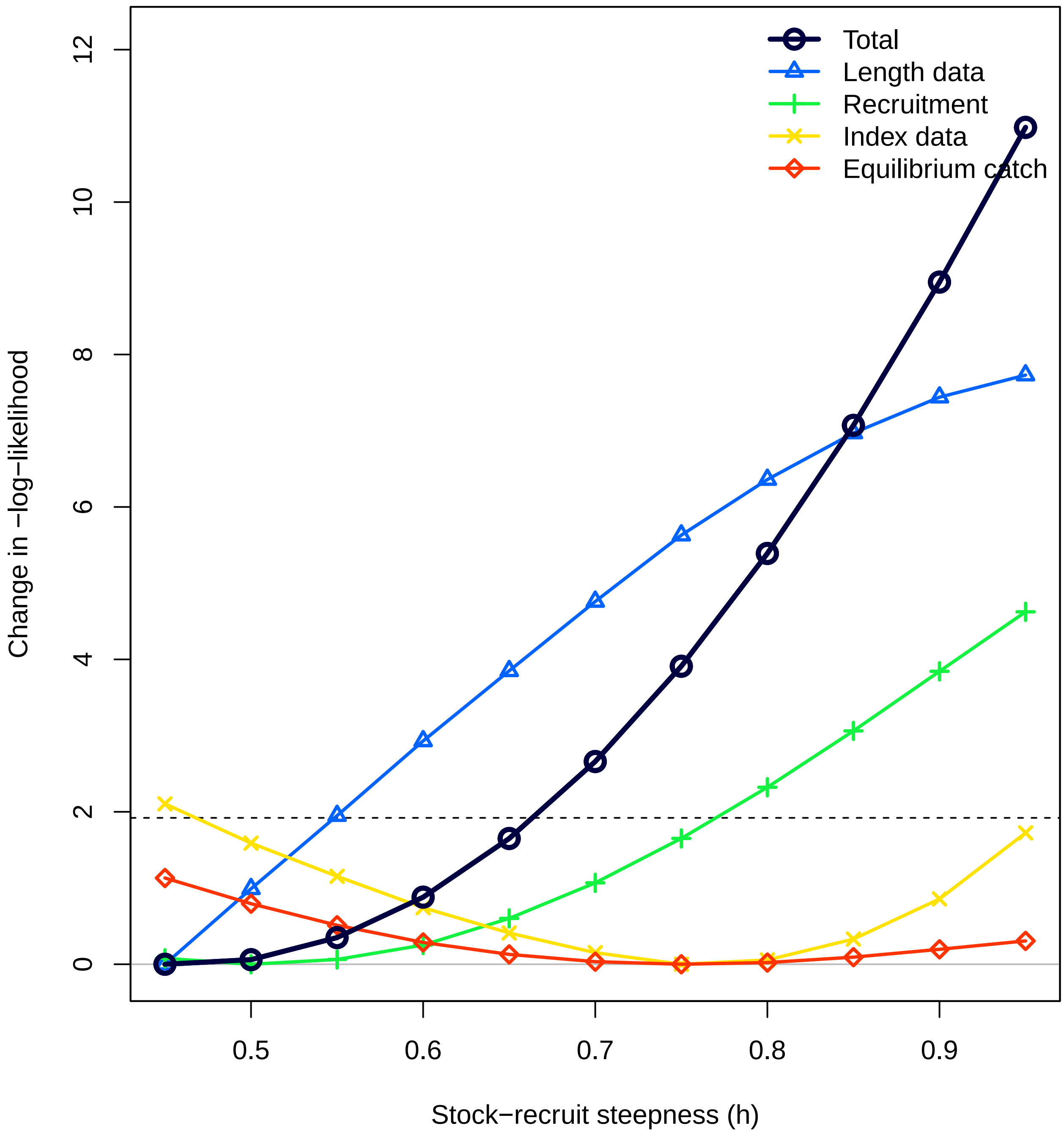


Figure 18: Negative log-likelihood profiles over a range of steepness values (h = 0.45-0.95)

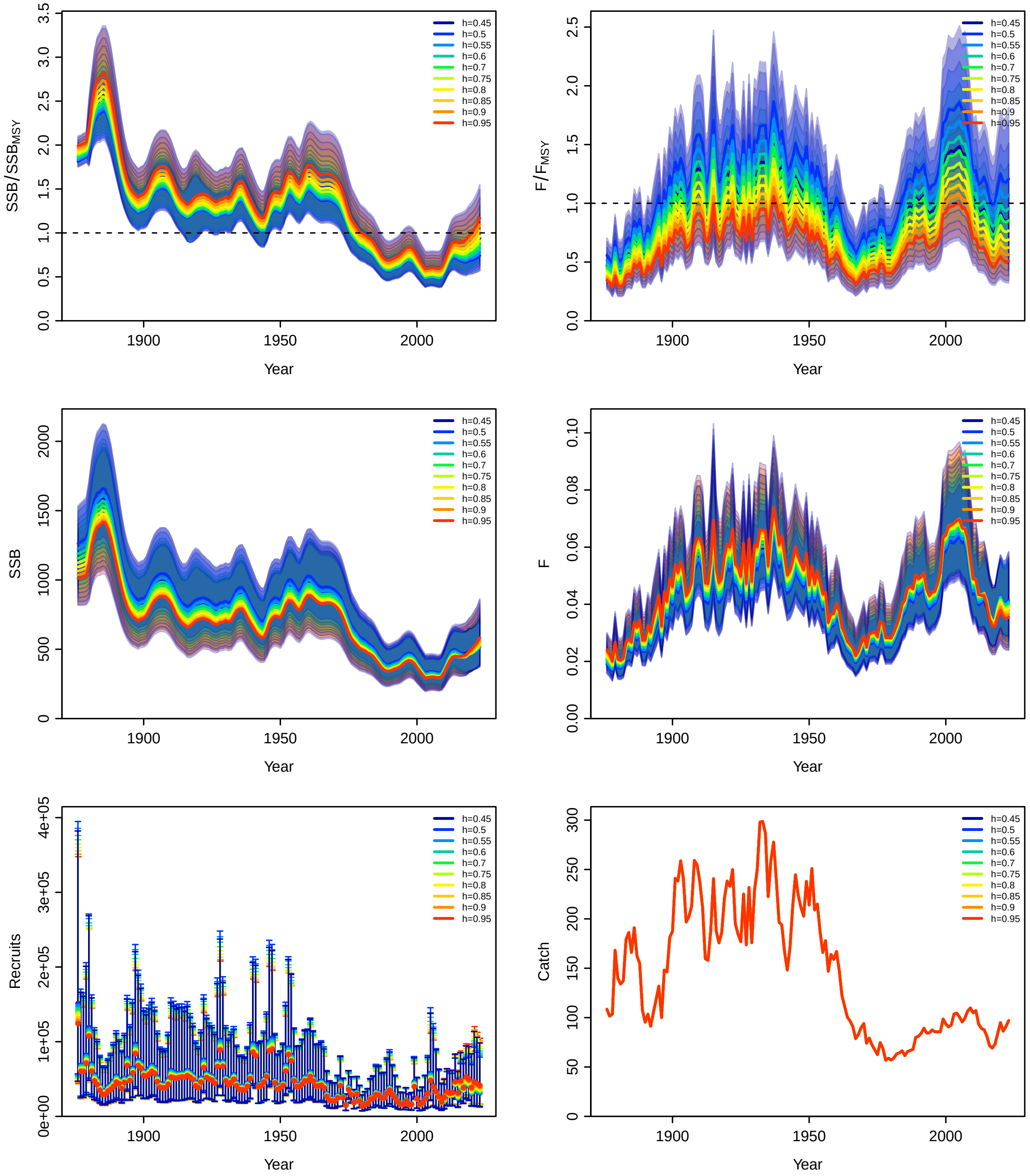


Figure 19: Comparison of stock trajectories with alternative stepness values (h = 0.45-0.95)

3 Assessment outcome

3.1 Reference Points

- Reference points were estimated within the Stock Synthesis model, where the biomass reference points are considered as SSB for females. Following the precautionary approach, target reference points of $B_{tgt} = SSB_{40}$ (biomass equal to 40 percent of unfished biomass SBB_0) and $F_{tgt} = F_{SB40}$ (fishing mortality level at SSB_{40}) were proposed to serve a preliminary as proxies for B_{MSY} and F_{MSY}. In the light of uncertainty about the underlying stock recruitment relationship, this choice of precautionary MSY proxies is likely to reduce the asymmetric risk of overfishing, while still attaining more than 95% of the theoretical MSY at FMSY and ensuring that about more 40% more SBB is left in the water to ensure both future recruitment and catch opportunities. However, as the ratio between SSB_{MSY} and SBB_0 is similar to SSB_{40}, it was decided to use SSB_{MSY} as biomass reference point and F_{MSY} as target fishing mortality F_{tgt}. Moreover, the group proposed trigger ($B_{trigger}$) and limit (B_{lim}) biomass reference points. Accordingly, $B_{trigger}$ was set to SSB_{MSY} and B_{lim} to 50% of SSB_{MSY} ($B_{lim} = 0.50B_{tgt}$).

```r
sspar(mfrow = c(1, 2), plot.cex = 0.7)
SSplot_eqcurves(ref, Fref = "MSY", msyline = 0.95)
```

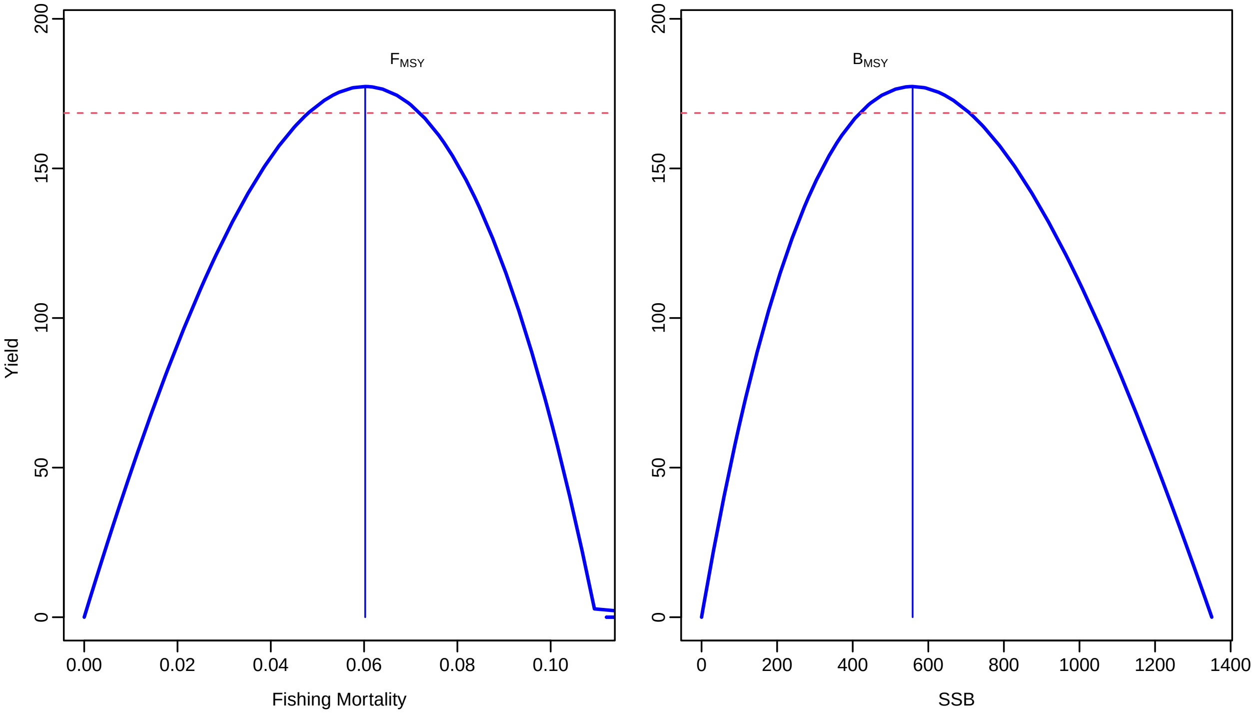


Figure 20: Equilibrium yield curves relative to fishing mortality and spawning stock biomass (SSB). The vertical lines indicate the location of the precautionary target reference points FSB35 and SSB35 relative to the theoretical FMSY and BMSY. The horizontal red dashed line denotes 95% of the theoretical maximum surplus production relative to MSY.

```
       Fmsy     Bmsy      MSY       B0      R0
1 0.0602354 558.536 177.379 1350.06 66587.8
```

3.2 Stock Status

```
mvnbase = FLRef::ssmvln(ref, Fref = "MSY", years = 1875:2023,
    verbose = T)

    starter.sso with Bratio: SSB/SSBMSY and F: _abs_F

stk = ss2FLStockR(mvnbase)
# Add Btrigger + Blim
stk@refpts = rbind(stk@refpts, FLPar(Btrigger = stk@refpts[[2]] *
    1, Blim = stk@refpts[[2]] * 0.5))
# with uncertainty
stki = ss2FLStockR(mvnbase, output = "iters")
stki@refpts = stk@refpts
```

```
plotAdvice(stki)
```

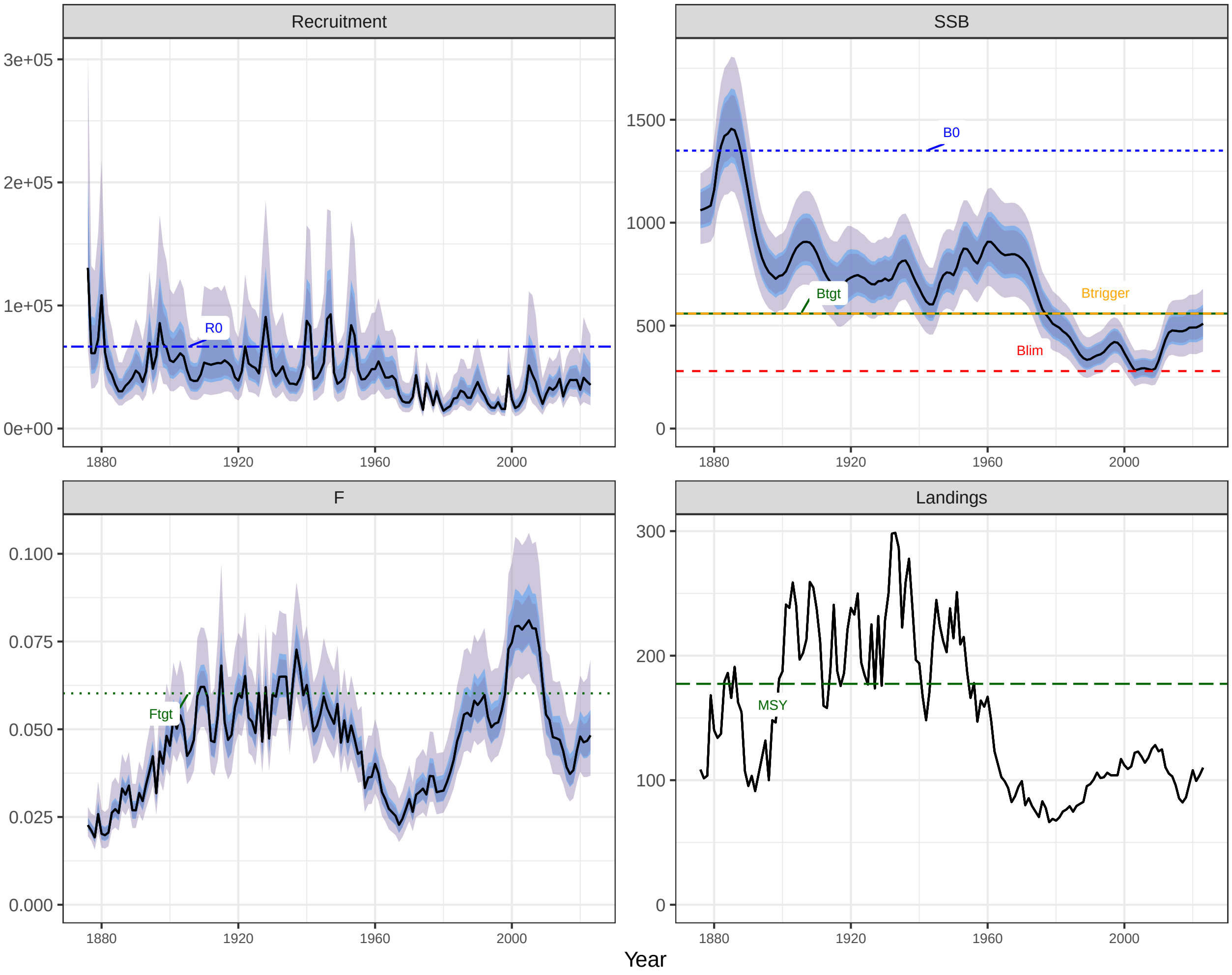


Figure 21: Estimated stock status trajectories with associated reference points for the 2024 base-case scenario of European lobster in 3a

3.3 Comparison with previous model (optional)

```
load("Reference_2023/Lobster_3a_Reference_2023.RData", verbose = T)
   Loading objects:
     ss3rep
bm = FLRef::ssmvln(ss3rep, Fref = "MSY", verbose = F)
stk.bm = ss2FLStockR(bm)

plot(FLStocks(New2024 = stk, Reference2023 = stk.bm)) + facet_wrap(~qname,
    scales = "free_y") + theme_bw()
```

Figure 22: Comparison between the estimated stock status trajectories from the new reference run and the last previous advice model update from 2023

```
stks = FLStocks(New2024 = stock2ratios(stk), Reference2023 = stock2ratios(stk.bm))
stks[[1]]@refpts = stks[[1]]@refpts[1:2]
stks[[2]]@refpts = stks[[2]]@refpts[1:2]
plotAdvice(stks)
```

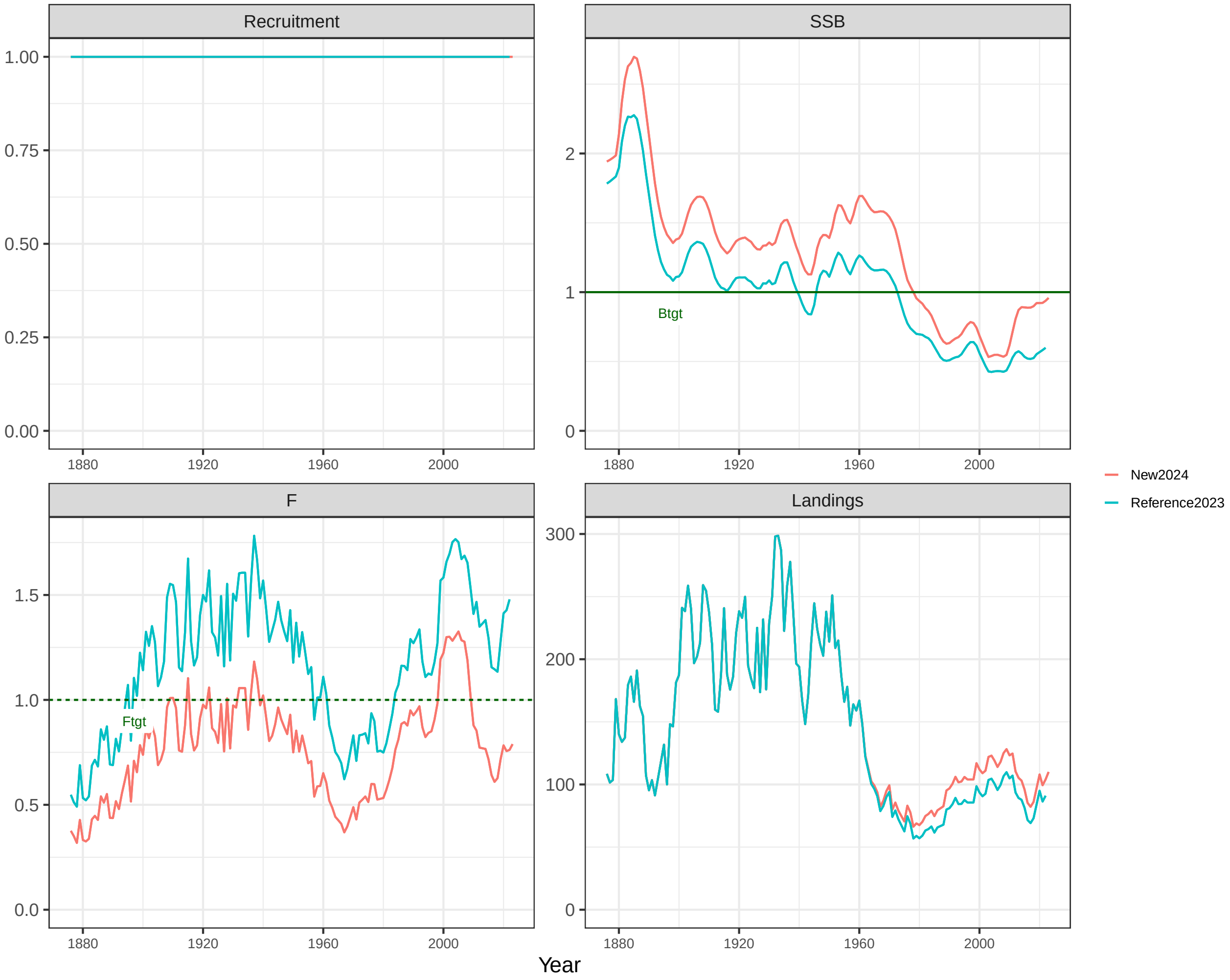


Figure 23: Comparison between the relative stock status estimates from the new reference run and the last previous advice model update from 2023

```
knitr::kable(FLRef::flr2stars(stk)$refpts, "pipe", align = "lc",
    caption = "Summary of estimated reference points
      for 2024 preliminary reference case model of European lobster in 3a")
```

Table 1: Summary of estimated reference points for 2024 preliminary reference case model of European lobster in 3a

RefPoint	Value
Ftgt	0.060
Btgt	558.537
MSY	177.379
B0	1350.060
R0	66587.800
Btrigger	558.537
Blim	279.269
Fcur	0.048
Bcur	535.253
B0.33	630.019
B0.66	833.572

Save

```
out = FLRef::flr2stars(stki)$timeseries
mles = FLRef::flr2stars(stk)

# replace medians with mles (TODO: automise)
out$Rec = mles$timeseries$Rec
out$SSB = mles$timeseries$SSB
out$Bratio = mles$timeseries$Bratio
out$F = mles$timeseries$F
out$Fratio = mles$timeseries$Fratio

write.csv(out, file = "Lobster3a.stars.csv", row.names = F)
write.csv(mles$refpts, file = "Lobster3a.refpts.stars.csv", row.names = F)
```

4 F-based forecasting

F_{apic} is used for good reason in forecasts in order to account for multi- fleet selectivity. Comparing the partial impacts selectivity pattern requires setting the instantaneous rate of fishing mortality F at comparable constant levels. For this purpose, it is important to consider that the definition of selectivity differs across regions (e.g. $Fbar$ or exploitation rate). With regards to temporal compatibility of partial fleet selectivity effects, F_{bar} has the undesirable property that its scale depends on the pre-specified age range across which F_a is averaged. For example, if F_{bar} is set to ages 1-4 to represent the dominant age classes under the current selectivity regime, but the goal is to evaluate the effect of selecting fish only at age-5, a common F_{bar} would result in disproportionately high F_a on ages 5+. This is because F_{bar} is computed for age ranges that are hardly selected for the definition $S_a = F_a/max(F_a)$. For this reason, it is more straight forward to use F_{apical} as the standardized quantity F quantify to account for partial impacts of fleet selectivity.

In the following, step-by-step guidelines are provided to setup an F_{apic}, so that it correctly corresponds to the F_{bar} baseline for F_{tgt} across multiple fleets and seasons.

4.1 Step 1: Basic setup

In this a case, a folder with the reference model run is created and the model outputs are loaded with `r4ss::SS_output`

Define name of reference model folder with the fitted ss3 model. Here you need to choose the model of the grid that is selected as best case

```
model = "Run2"
```

Load reference model

```
ss3rep = SS_output(model)
```

Next a folder `forecast` is created

```
dir.create(paste0("forecast.", model), showWarnings = F)
```

A new helper function `SSnewrun` was added to `ss3diags` to easily create subfolders for the forecast scenarios. First a `Ftgt` reference folder is created for initial cross-checks

Specify subfolder path

```
ftgtdir = file.path(paste0("forecast.", model), "Ftgt")
```

Create new F forecast model folder. Note that the data and control file and ss.exe names need to be specified if these diverge from the defaults `data.ss`, `control.ss` and `ss3.exe`

```
dat = "Lobster_dat.dat"
ctl = "Lobster_ctl.ss"
par = "ss3.par"
ss.exe = "ss3.exe"

SSnewrun(model = model, dat = dat, ctl = ctl, par.file = "ss3.par",
    newdir = ftgtdir, ss.exe = "ss3.exe")
```

Now the forecast file can be read be read with `r4ss`

```
fc <- SS_readforecast(file.path(ftgtdir, "forecast.ss"), verbose = F)
```

4.2 Step 2: Initial F exploitation calculations for Fapic forecast

Extract the `$exploitation` output from the report file

```
Fexp = ss3rep$exploitation
```

Importantly, the `annual_F` are scaled to the F-basis (here F_{bar}), whereas fleet specific F values are always given as F_{apic}

Next compute the combined F_{apic} generically across fleets

```
Fexp$Fapic = apply(as.matrix(ss3rep$exploitation[, -c(1:6)]),
    1, sum, na.rm = T)
```

and aggregate across seasons, by taking the `mean` and not the `sum`.

```
Fapic = aggregate(Fapic ~ Yr, Fexp, mean)
```

Next compute the corresponding annual F_{bar} values from the `annual_F`

```
Fbar = aggregate(annual_F ~ Yr, Fexp, mean)
```

To work out exact ratio between F_{apic} and F_{bar} so that it is consistent with the benchmark calculations with ss3, it is necessary to extract the reference years for selectivity from the `forecast.ss` file.

The information required for the average selectivity conditions can be found in the `forecast.ss` file under `$Bmark_years`. The third and fourth position define the time horizon for the average selectivity across fleet, a value of -999 (here) indicates that the whole time series is use, but more commonly averages are taken, e.g. over the last 3 years, which can be specified as -2 0 or 2019 2021. The following code attempts to compute this generically.

```
endyr = ss3rep$endyr
if (fc$Bmark_years[3] < -90) {
    nfc = length(min(ss3rep$exploitation$Yr + 1):endyr)  # excluded init year
} else {
    # if specified (e.g. -2, 0)
    nfc = fc$Bmark_years[4] - fc$Bmark_years[3] + 1
}

# Benchmark reference years
bmyrs = (endyr - nfc + 1):endyr
```

```
Fratio = mean(Fapic$Fapic[Fapic$Yr %in% max(bmyrs)]/Fbar$annual_F[Fbar$Yr %in%
    max(bmyrs)])
Fratio
   [1] 3.05232
```

`Fratio` defines the ratio of F_{apic} to F_{bar} for the reference period

Get the F_{tgt} reference point, here defined as $F_{B_{40}}$. Therefore, the `annF_Btgt` is extracted.

```
Fref = c("annF_Btgt", "annF_MSY", "annF_SPR")[1]
Ftgt = ss3rep$derived_quants$Value[ss3rep$derived_quants$Label ==
    Fref]
Ftgt.apic = Ftgt * Fratio
Ftgt  # Fbar
   [1] 0.0617631
Ftgt.apic
   [1] 0.1885208
```

4.3 Setting up the manual F forecast input structure

First, do some basic house keeping for the model structure

```
nseas = length(unique(ss3rep$exploitation$Seas))  # number of seasons
fleets = unique(ss3rep$fatage$Fleet)  # fleets
nfleets = length(fleets)  # number of fleet
```

Next, the mean Fapic by fleet and season is calculated

```
# subset to benchmark years for selectivity
fexp = ss3rep$exploitation[ss3rep$exploitation$Yr %in% bmyrs,
    ]
fexp = cbind(fexp[, 1:2], fexp[, -c(1:5)])[, -3]  #><>  single fleet trick

# flip
fexp = reshape2::melt(fexp, id.vars = c("Yr", "Seas"), variable.name = "Fleet",
    value.name = "Fapic")
head(fexp)
       Yr Seas               Fleet     Fapic
   1 1875    1 Commercial_official 0.0641473
   2 1876    1 Commercial_official 0.0700632
   3 1877    1 Commercial_official 0.0651366
   4 1878    1 Commercial_official 0.0589406
   5 1879    1 Commercial_official 0.0792504
   6 1880    1 Commercial_official 0.0616395
```

The forecast file requires Fleet IDs not names. In the next step these are extracted and fleet names are converted in to Fleet IDs

```
fleet = data.frame(Fleet = ss3rep$FleetNames, ID = ss3rep$fleet_ID)
fexp$Fleet = fleet[match(fexp$Fleet, fleet$Fleet), 2]
```

Then, the relative proportions of F_{apic} by fleet and season can be computed

```
Fap = aggregate(Fapic ~ Seas + Fleet, fexp, mean)
Fap$prop = Fap$Fapic/sum(Fap$Fapic) * nseas
Fap
     Seas Fleet      Fapic      prop
   1    1     1 0.10310839 0.7010579
   2    1     3 0.04396704 0.2989421
```

In the next step, status quo F_{sq} for forecasting over the intermediate year(s) is defined. This can be relatively easily changed to intermediate catch years. Here, the F_{sq} of the average of the last 3 years is used as average, and the intermediate years are set to 2, account for 1 data lag year and an additional management lag year.

```
# F status q
nfsq = 3
nint = 2
```

Compute the F_{sq} as F_{apic} vector by season and fleet

```
fsq = ss3rep$exploitation[ss3rep$exploitation$Yr %in% ((endyr -
    nfsq + 1):endyr), ]
fsq = cbind(fsq[, 1:2], fsq[, -c(1:5)])[, -3]  #><>  single fleet trick
fsq = reshape2::melt(fsq, id.vars = c("Yr", "Seas"), variable.name = "Fleet",
    value.name = "Fapic")
Fsq = aggregate(Fapic ~ Seas + Fleet, fsq, mean)
```

Now, the forecast horizon can be defined in the loaded `starter.ss` object `fc`. Note that the forecast years muct match the same as in the forecast file of the reference run

```
fc$Nforecastyrs = 10
nfyrs = fc$Nforecastyrs
fyrs = endyr + c(1:nfyrs)
```

The F-vector that is passed on the forecast file comprises the season/fleet structure replicates for `ninit` for F_{sq} and the forecast years under F_{tgt} that is scaled to F_{apic} by the `Fratio` and partioned by season and fleets.

```
fvec = c(rep(Fsq$Fapic, nint), rep(Ftgt * Fratio * Fap$prop,
    nfyrs - nint))
```

Given the fleet, season, intermediate year and forecast years structures, the forecast table for the `forecast.ss` file can finally be constructed.

```
fc$ForeCatch = data.frame(Year = rep(fyrs, each = nseas * nfleets),
    Seas = 1:nseas, Fleet = rep(fleets, each = nseas), `Catch or F` = fvec,
    Basis = 99)
head(fc$ForeCatch, 9)
     Year Seas Fleet Catch.or.F Basis
   1 2024    1     1 0.05331410    99
   2 2024    1     3 0.08805547    99
   3 2025    1     1 0.05331410    99
   4 2025    1     3 0.08805547    99
   5 2026    1     1 0.13216396    99
   6 2026    1     3 0.05635679    99
   7 2027    1     1 0.13216396    99
   8 2027    1     3 0.05635679    99
   9 2028    1     1 0.13216396    99
```

Note that the `Basis` 99 specifies that Fs are inputted (2 would be Catch). Finally, the forecast options need to be adjusted for manual input

```
fc$eof = TRUE
fc$InputBasis = -1
```

and then the modified `starter.ss` file can be saved

4.4 Running Ftgt forecasts with checks

In principle, the `Ftgt` can serve as a reference and the model does not have to be run if the goal is set up a number forecasts relative to F_{tgt}.

However, for illustration, the `Ftgt` forecast is run to check that the F_{apic} will produce F_{bar} estimates that are consistent with F_{tgt}.

To run

```
# Edit 'starter.ss'
starter.file <- readLines(file.path(ftgtdir, "starter.ss", sep = ""))
linen <- NULL
linen <- grep("# 0=use init values in control file; 1=use ss.par",
    starter.file)
starter.file[linen] <- paste0("0 # 0=use init values in control file; 1=use ss.par")
# tells it to use the estimate parameters
write(starter.file, paste(file.path(ftgtdir, "starter.ss", sep = "")))
r4ss::run(ftgtdir, skipfinished = T, show_in_console = F, exe = "ss3.exe")
```

After the run is finished, the output can be loaded again.

```
ftgtrep = SS_output(ftgtdir)
save(ftgtrep, file = "rdata_forecast/ftgtref_Run2.rdata")
```

```
load("rdata_forecast/ftgtref_Run2.rdata")
```

For testing, `SSdeltaMVLN` is used to computed the trajectories with CIs, but this time the option `addprj=T` needs to be added to also include the forecast years

```
ftgt.test = SSdeltaMVLN(ftgtrep, Fref = "MSY", run = "Ftgt",
    addprj = T, plot = F, verbose = F)
```

```
sspar(mfrow = c(3, 2), plot.cex = 0.8)
SSplotEnsemble(ftgt.test, add = T, verbose = F, legendloc = "topleft")
```

It can be readily seen that the F_{apic} based F_{tgt} forecast corresponds indeed to the F_{tgt} estimate on F_{bar} scale.

```
library(FLRef)
mvn = FLRef::ssmvln(ftgtrep, Fref = "MSY", addprj = T, verbose = F)

stkf = ss2FLStockR(mvn)
rps = stkf@refpts
stkf@refpts = rbind(rps, FLPar(Bpa = rps["Btgt"] * 1, Blim = rps["Btgt"] *
    0.5))
```

```
plotAdvice(stkf) + geom_vline(xintercept = 2022.5, linetype = 2)
```

```
sspar(mfrow = c(1, 1), plot.cex = 0.8)
SSplotEnsemble(ftgt.test, add = T, subplots = "harvest", verbose = F,
    legendloc = "topleft", ylabs = expression(F/F[BMSY]))
```

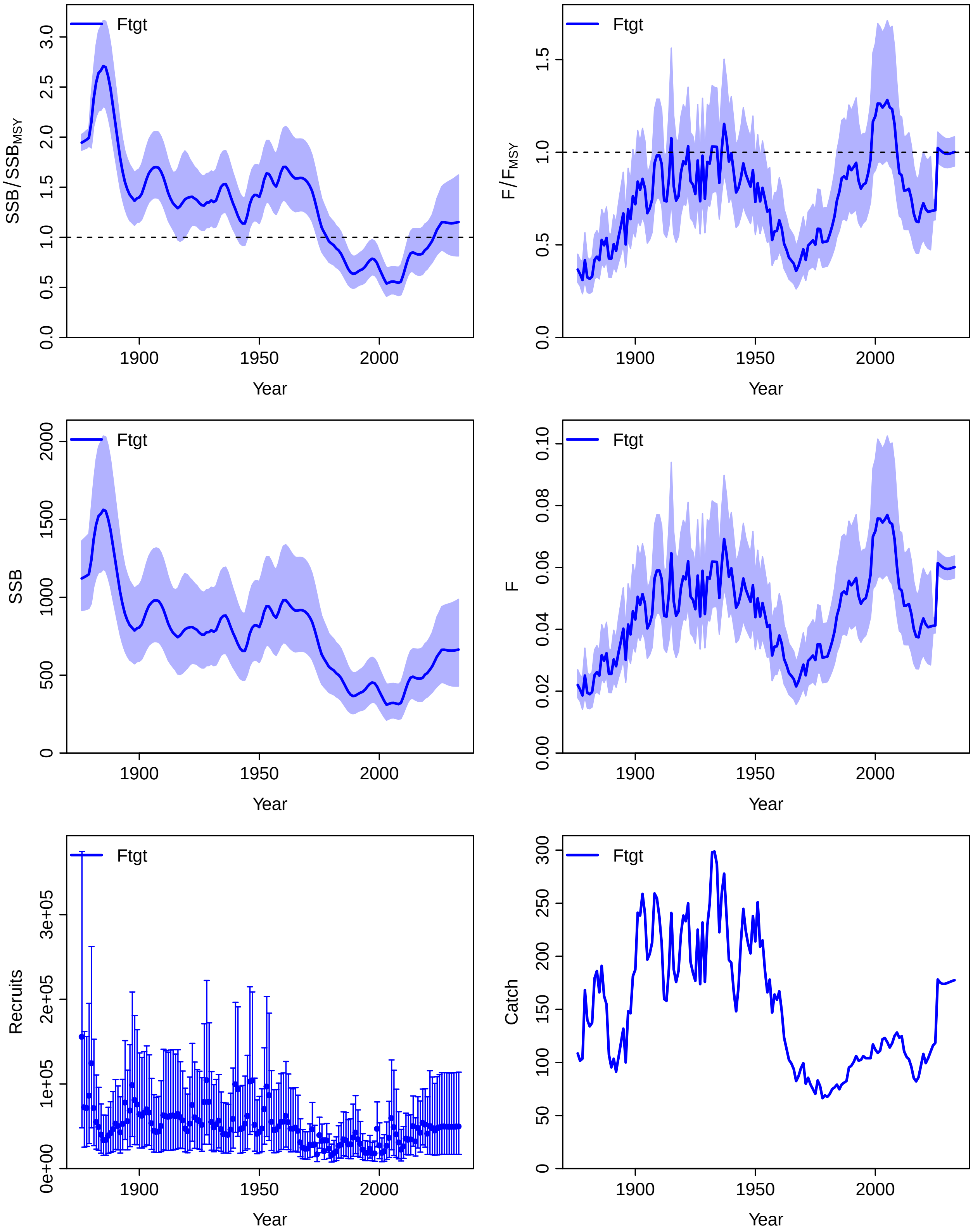


Figure 24: Stock trajectories with 95% CIs for basecase run and a F_{tgt} forecast

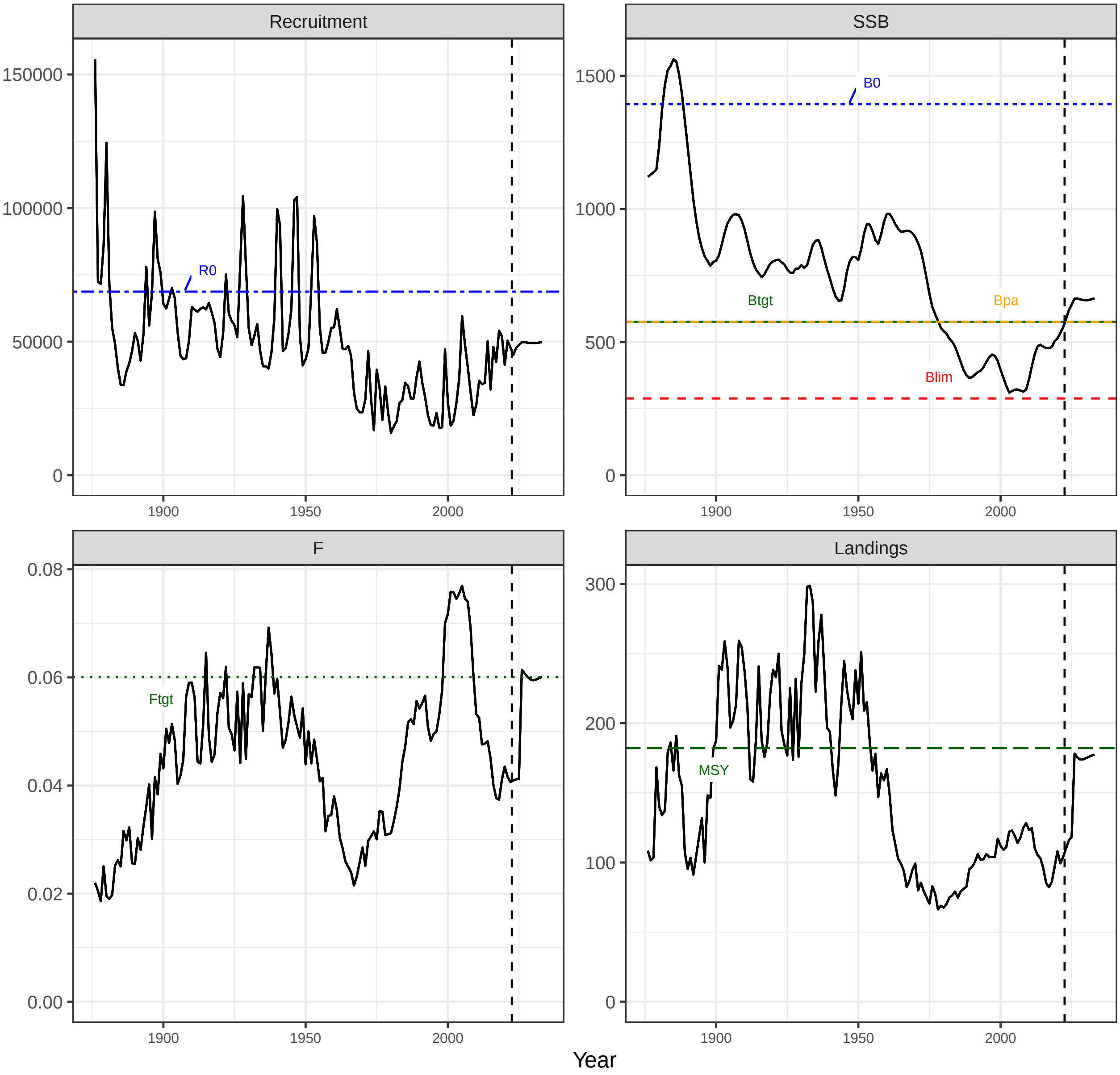


Figure 25: Stock trajectories for basecase run and a F_{tgt} forecast, relative to reference points

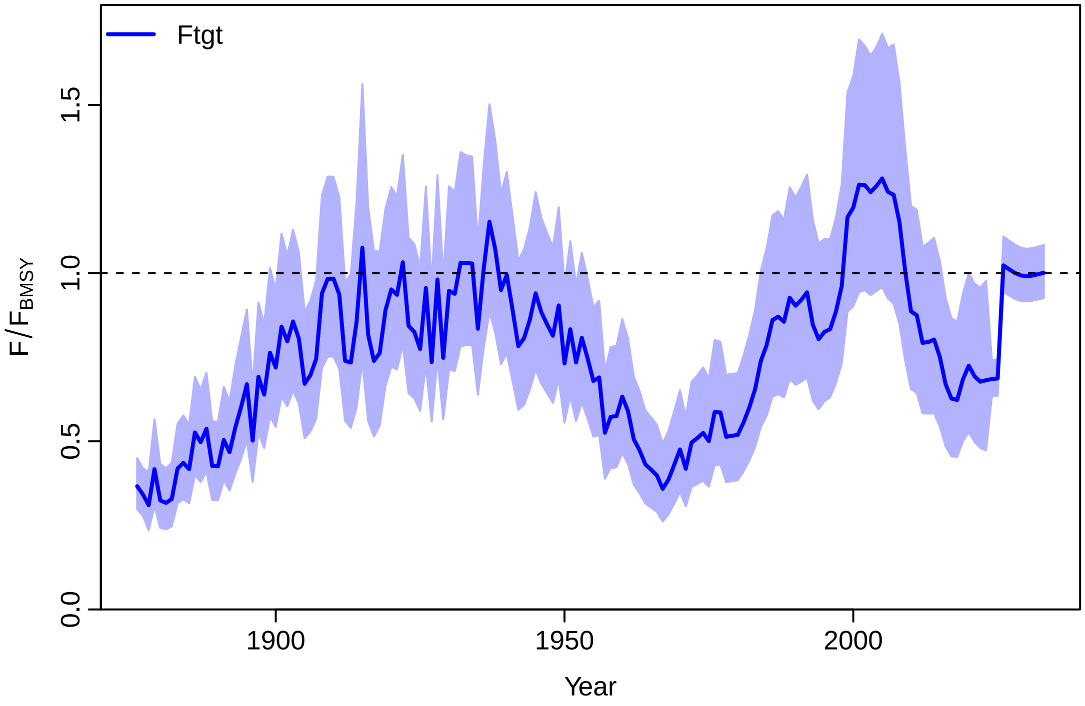


Figure 26: Stock trajectories with 95% CIs for basecase run and a F_{tgt} forecast

4.5 Looping through forecast scenarios

Set up ratios relative to F_{sq} in this case

```
Ffrac = c(0.01, seq(0.6, 1.1, 0.1))
```

Specify forecast folders

```
fcdirs = file.path(paste0("forecast.", model), paste0("Fsq",
    Ffrac))
```

Loop through the process of modifying the `forecast.ss` file iteratively. The `Ffrac` is applied to apportioned F_{tgt} vector.

Create the forecast batch list

```
foreBatch <- list()

for (i in 1:length(Ffrac)) {
    dir.tacN <- paste0(main.dir, "/forecast.Run2/", "Fsq", Ffrac[i],
        "/")

    ## Create the forecast batch list
    foreBatch <- c(foreBatch, as.list(dir.tacN))
}

library(parallel)
library(doParallel)
cl <- makeCluster(20, type = "PSOCK")
registerDoParallel(cl)
```

```
for (i in 1:length(Ffrac)) {
    # create model folder
    SSnewrun(model = ftgtdir, dat = dat, ctl = ctl, par.file = "ss3.par",
        newdir = fcdirs[i], ss.exe = "ss3.exe")
    # Edit 'starter.ss'
    starter.file <- readLines(file.path(fcdirs[i], "starter.ss",
        sep = ""))
    linen <- NULL
    linen <- grep("# 0=use init values in control file; 1=use ss.par",
        starter.file)
    starter.file[linen] <- paste0("1 # 0=use init values in control file; 1=use ss.par")
    # tells it to use the estimate parameters
    write(starter.file, paste(file.path(fcdirs[i], "starter.ss",
        sep = "")))
    # Read Forecast file
    fc <- SS_readforecast(file.path(fcdirs[i], "forecast.ss"))
    # Apply Ffrac Create F forecast vector (generic) Change
    # to Fsq
    fvec = c(rep(Fsq$Fapic, nint), rep(Fsq$Fapic * Ffrac[i],
        nfyrs - nint))
    # Create F forecast table in forecast.ss
    fc$ForeCatch = data.frame(Year = rep(fyrs, each = nseas *
        nfleets), Seas = 1:nseas, Fleet = rep(fleets, each = nseas),
        `Catch or F` = fvec, Basis = 99)
    SS_writeforecast(fc, file = file.path(fcdirs[i], "forecast.ss"),
        overwrite = T)
}
```

```
foreach(i = 1:length(Ffrac), .packages = "r4ss") %dopar% {
    cat("core:", i + 1, "\n")
    r4ss::run(foreBatch[[i]], skipfinished = F, show_in_console = FALSE,
        exe = ss.exe)
    # r4ss::run(fcdirs[i], extras = '-maxfn 0 -phase 50',
    # skipfinished = F, show_in_console = TRUE, exe=ss.exe)

}
```

Load all runs in one go with `SSgetoutput`

```
fcs = SSgetoutput(dirvec = c(fcdirs, ftgtdir))
save(fcs, file = "rdata_forecast/ftgtref_Run2.rdata")
```

Create list with outputs from `SSdeltaMVLN`

```
sspar(mfrow = c(3, 3), plot.cex = 0.8)

fmvns = Map(function(x, y) {
    out = SSdeltaMVLN(x, Fref = "MSY", verbose = F, run = y,
        addprj = T, plot = T)
    mtext(y, outer = F, cex = 0.8)
    return(out)
}, x = fcs, y = as.list(c(paste0("Fsq", Ffrac), "Ftgt")))
```

Plot forecasts with `SSplotEnsemble`

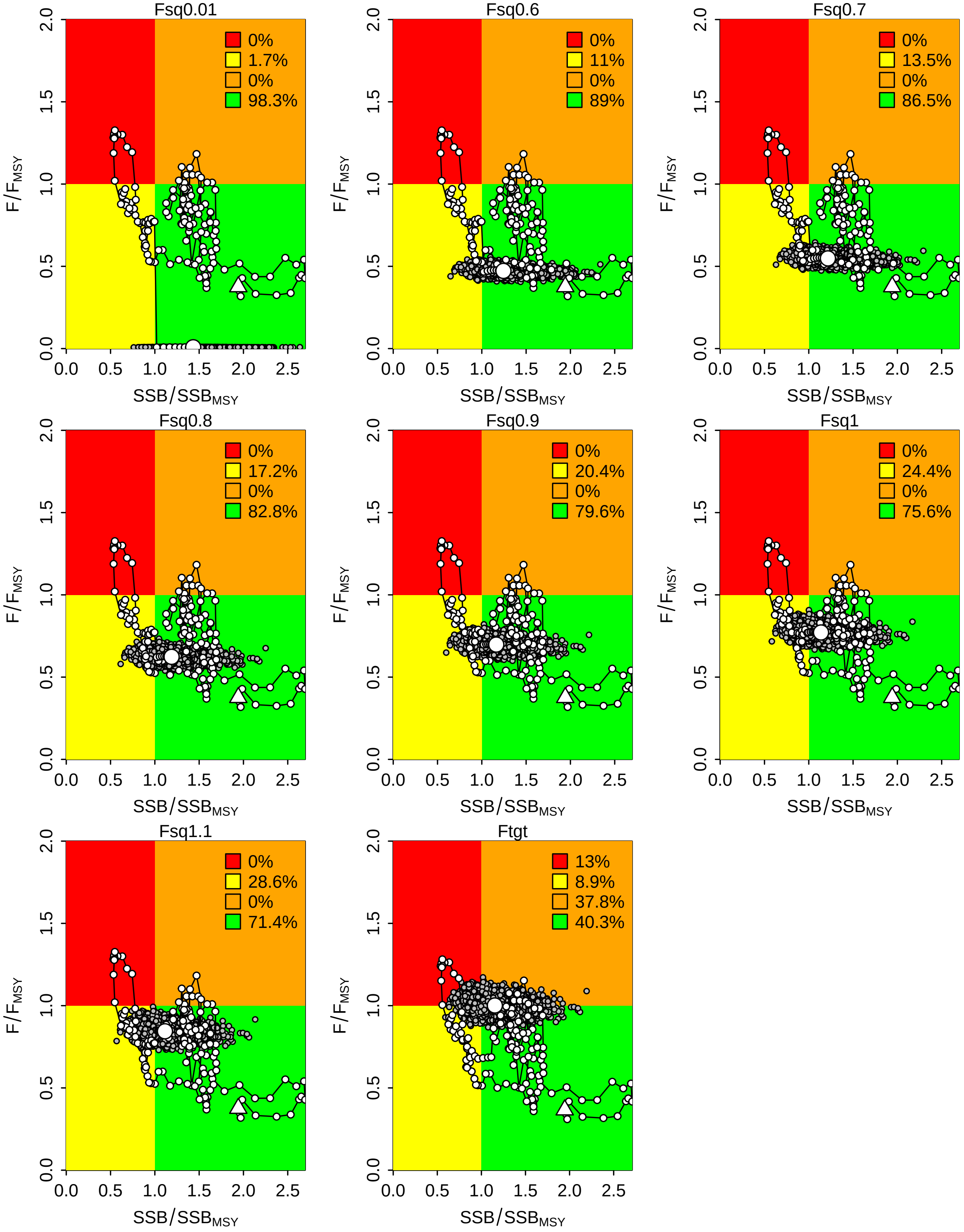


Figure 27: Kobe plot checks for the final forecast year

```r
sspar(mfrow = c(3, 2), plot.cex = 0.8)
SSplotEnsemble(fmvns, add = T, verbose = F, legendloc = "topleft")
```

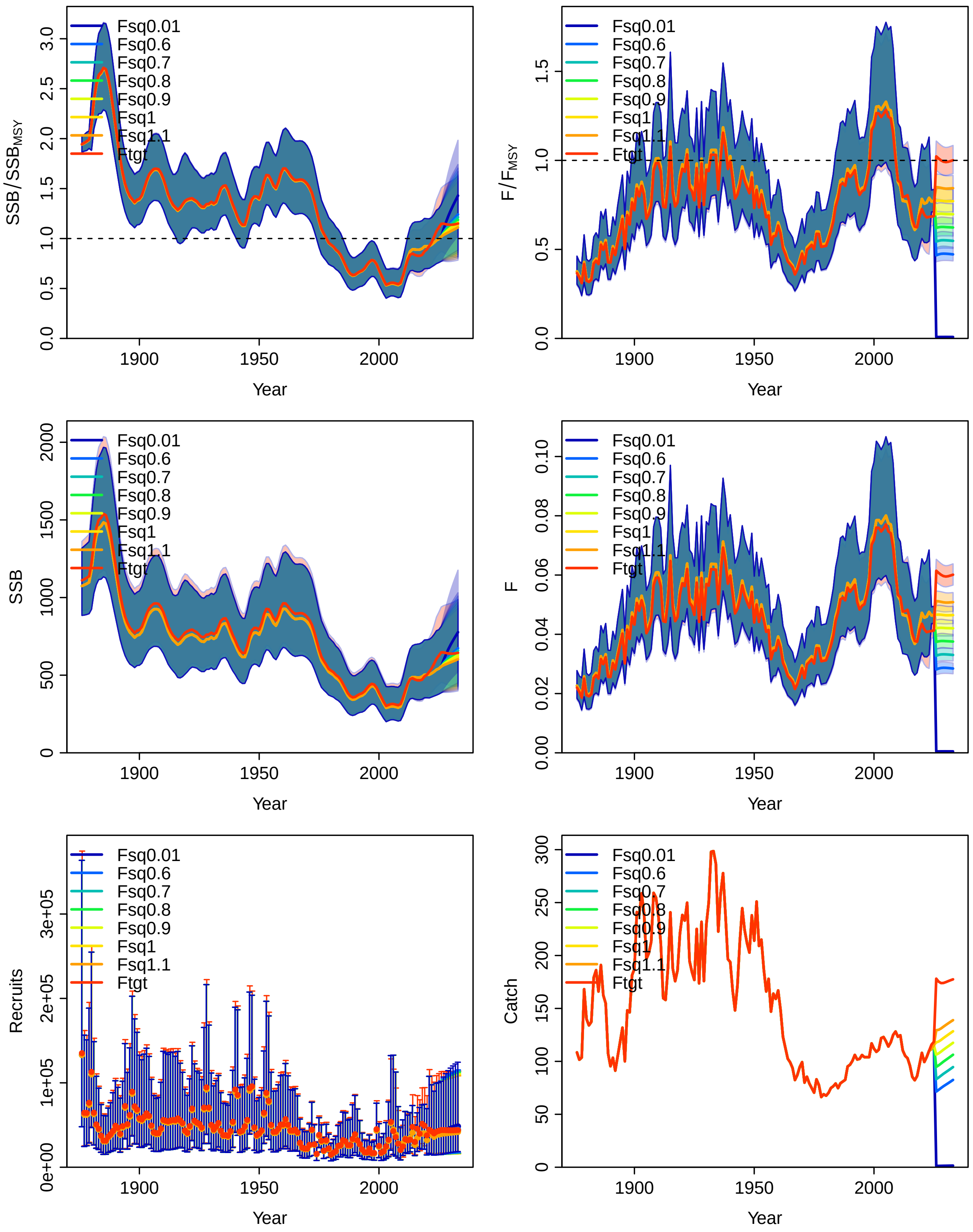


Figure 28: Stock trajectories with 95% CIs for basecase run and forecast scenarios relative F_{sq} and for F_{tgt}

Convert to `FLR` format

```
fstks = FLStocks(Map(function(x, y) {
    out = FLRef::ssmvln(x, Fref = "MSY", verbose = F, run = y,
        addprj = T)
    out = ss2FLStockR(out)
    out@refpts = stkf@refpts[-4]  # Remove B0
    return(out)
}, x = fcs, y = as.list(c(paste0("Fsq", Ffrac), "Ftgt"))))
names(fstks) = c(paste0("Fsq", Ffrac), "Ftgt")
```

```
plotAdvice(window(fstks, start = 2013)) + geom_vline(xintercept = c(2022,
    2024), linetype = 28)
```

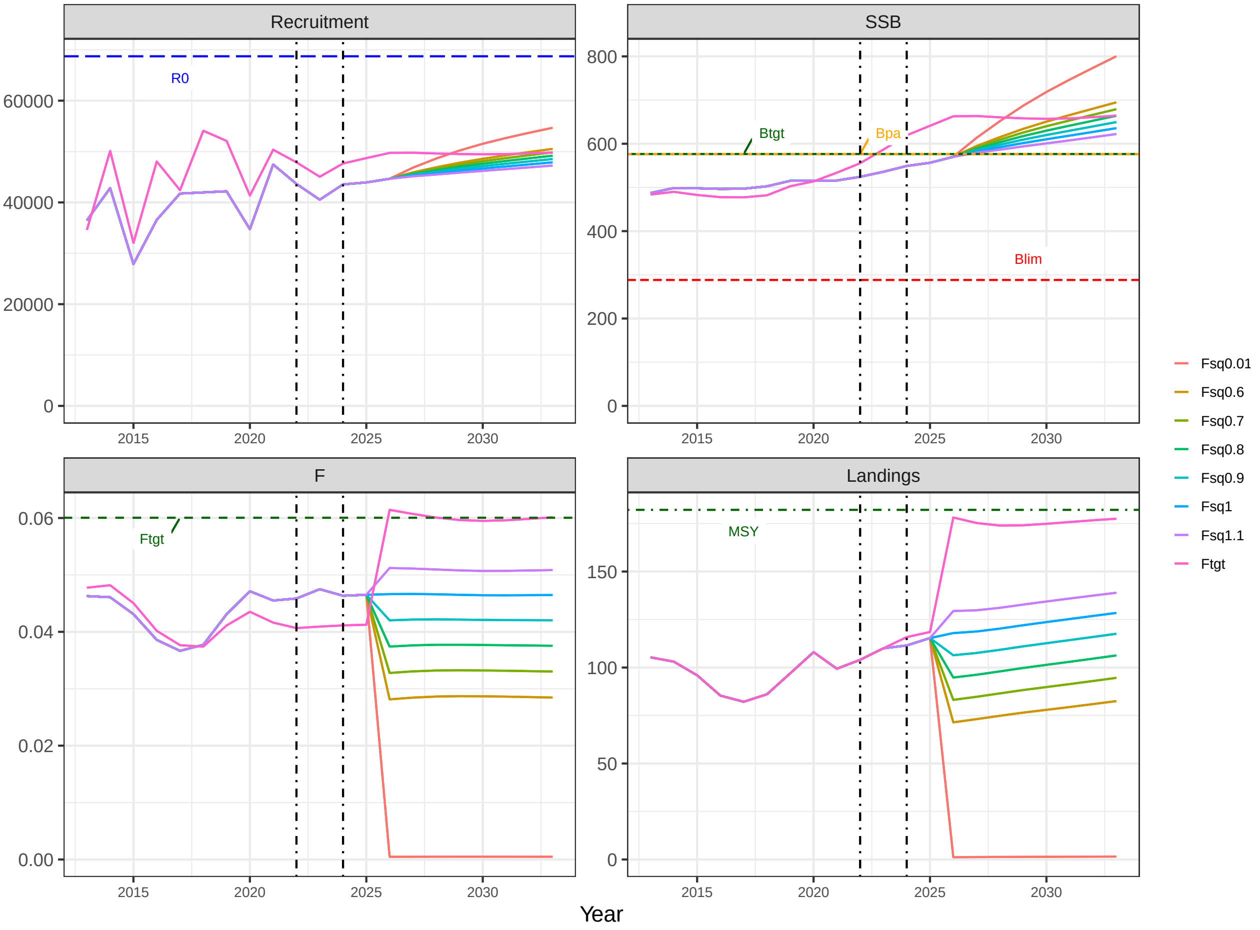


Figure 29: Trajectories for the basecase run and forecast scenarios relative F_{sq} and for F_{tgt}

```
out = cbind(FLRef::fwd2stars(fstks, eval.yrs = 2026), FLRef::fwd2stars(fstks,
    eval.yrs = 2026, rel = T)[, 3:4])

out[, 2:3] = round(out[, 2:3], 1)
out[, 4:6] = round(out[, 4:6], 3)
knitr::kable(out, "pipe", align = "lccccc", caption = "Summary of short-term forecast
      scenario results for 2026")
```

Table 2: Summary of short-term forecast scenario results for 2026

scenario	C2026	B2026	F2026	B2026/Btgt	F2026/Ftgt
Fsq0.01	1.2	570.1	0.000	0.989	0.008
Fsq0.6	71.4	570.1	0.028	0.989	0.469
Fsq0.7	83.1	570.1	0.033	0.989	0.546
Fsq0.8	94.8	570.1	0.037	0.989	0.623
Fsq0.9	106.4	570.1	0.042	0.989	0.700
Fsq1	117.9	570.1	0.047	0.989	0.776
Fsq1.1	129.4	570.1	0.051	0.989	0.853
Ftgt	178.1	662.8	0.061	1.150	1.023

Save forecast table to STAR format

```
write.csv(out, file = "Lobster3a.fwd.stars.csv", row.names = F)
```

5 Supplement: R code to run diagnostics and summary

```r
# ><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>
# > Stock Synthesis reference model summary and diagnostic
# for Lobsters 3a > @author Henning Winker (GFCM), modified
# by Max Cardinale (SLU) > henning.winker@fao.org

# ><>><>><>><>><>><> Load packages
library("r4ss")
library("ss3diags")

# First set working directory to the R file location with
# ss3 subfolders

# Define run name of folder
run = "Run2"

# Load the model run
ss3rep = SS_output(run)

# Plot the model run
r4ss::SS_plots(ss3rep)

# Save the r4ss object as rdata
dir.create("rdata")
save(ss3rep, file = file.path("rdata", paste0("Lobster3a_", run,
    ".rdata")))

# approximate uncertainty and produce Kobe Plot
sspar(mfrow = c(1, 1))
mvn = SSdeltaMVLN(ss3rep, Fref = "MSY", run = "ref", catch.type = "Exp")

# Plot trajectories with CIs
sspar(mfrow = c(3, 2))
SSplotEnsemble(list(mvn), add = T)

# ><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>
# DO RETRO
# ><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>
start.retro <- 0  # end year of reference year
end.retro <- 5  # number of years for retrospective e.g.,
dirname.base = run
model.run <- file.path(dirname.base)
model.run

### Step 3: DAT and CONTROL files
DAT = "Lobster_dat.dat"
CTL = "Lobster_ctl.ss"
dir.retro = file.path(dirname.base, "Retrospective")
dir.create(path = dir.retro, showWarnings = F)

# Copy files
file.copy(file.path(model.run, "starter.ss_new"), file.path(dir.retro,
    "starter.ss"))
```

```r
file.copy(file.path(model.run, "control.ss_new"), file.path(dir.retro,
    CTL))
file.copy(file.path(model.run, DAT), file.path(dir.retro, DAT))
file.copy(file.path(model.run, "forecast.ss"), file.path(dir.retro,
    "forecast.ss"))
file.copy(file.path(model.run, "ss3.exe"), file.path(dir.retro,
    "ss3.exe"))

# Automatically ignored for models without wtatage.ss
file.copy(file.path(model.run, "wtatage.ss"), file.path(dir.retro,
    "wtatage.ss"))
starter <- readLines(paste0(dir.retro, "/starter.ss"))

# [8] '2 # run display detail (0,1,2)'
linen <- grep("# run display detail", starter)
starter[linen] <- paste0(1, " # run display detail (0,1,2)")

# write modified starter.ss
write(starter, file.path(dir.retro, "starter.ss"))

### Step 6: Execute retrospective runs r4ss::retro(dir =
### dir.retro, oldsubdir = '', newsubdir = '', years =
### start.retro:-end.retro)
r4ss::retro(dir = dir.retro, oldsubdir = "", newsubdir = "",
    years = start.retro:-end.retro, verbose = T)

retro <- r4ss::SSgetoutput(dirvec = file.path(dir.retro, paste0("retro",
    start.retro:-end.retro)))
save(retro, file = paste0("retro_", run, ".rdata"))

# Reload
load(file = paste0("retro_", run, ".rdata"))
retro.idx = r4ss::SSsummarize(retro)
retro.len = ss3diags::SSretroComps(retro)

# ><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>
# Compile results summary
# ><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>

# Make output PDF
pdf(paste0("Lobster3a_", run, ".pdf"))
sspar(mfrow = c(2, 2), plot.cex = 0.7)
SSplotBiology(ss3rep, mainTitle = F, subplots = c(1))
SSplotBiology(ss3rep, mainTitle = F, subplots = c(21))
SSplotBiology(ss3rep, mainTitle = F, subplots = c(6))
SSplotBiology(ss3rep, mainTitle = F, subplots = c(9))

sspar(mfrow = c(2, 2), plot.cex = 0.7)
SSplotBiology(ss3rep, mainTitle = F, subplots = c(4))

# Recruitment
sspar(mfrow = c(2, 2), plot.cex = 0.7)
SSplotRecdevs(ss3rep, subplots = 1)
```

```r
SSplotRecdevs(ss3rep, subplots = 2)
SSplotSpawnrecruit(ss3rep, subplots = 1)
SSplotSpawnrecruit(ss3rep, subplots = 3)

par(mfrow = c(1, 1))
SSplotDynamicB0(ss3rep)

sspar(mfrow = c(1, 3), plot.cex = 0.7)
SSplotIndices(ss3rep, subplots = 2)

sspar(mfrow = c(1, 1), plot.cex = 0.7)
SSplotIndices(ss3rep, subplots = 9)

sspar(mfrow = c(2, 3), plot.cex = 0.9)
SSplotHCxval(retro.idx, xmin = 2006, add = T, legendcex = 0.6,
    Season = 1)
SSplotHCxval(retro.len, add = T, subplots = "len", legendloc = "topleft",
    indexUncertainty = TRUE, legendcex = 0.6)

par(mfrow = c(1, 1))
SSplotSelex(ss3rep, subplots = 1)

SSplotComps(ss3rep, subplots = 21)

SSplotComps(ss3rep, subplots = 1)

SSplotSexRatio(ss3rep, kind = "LEN")

# Bubble
SSplotComps(ss3rep, subplots = 24)

# ALK
SSplotComps(ss3rep, kind = "cond", subplots = 3)

# Runs Fleets
sspar(mfrow = c(3, 3), plot.cex = 0.5)
SSplotRunstest(ss3rep, subplots = "len", add = T)

# HC Fleets
sspar(mfrow = c(3, 2), plot.cex = 0.5)
for (i in 1:2) {
    SSplotHCxval(retro.len, subplots = "len", add = T, legendloc = "topleft",
        indexselect = i)
}

# Retro
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(retro.idx, add = T, legend = F, forecast = F)
SSplotRetro(retro.idx, add = T, forecastrho = T, legend = F)
SSplotRetro(retro.idx, subplots = "F", add = T, legend = F, forecast = F)
SSplotRetro(retro.idx, subplots = "F", add = T, forecastrho = T,
    legend = F)
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3,
```

```
    0.8), cex = 0.8)

par(mfrow = c(1, 1))
SSplotYield(ss3rep, subplots = 2)

sspar(mfrow = c(1, 1))
mvn = SSdeltaMVLN(ss3rep, Fref = "MSY", catch.type = "Exp", run = "ref")

sspar(mfrow = c(3, 2))
SSplotEnsemble(list(mvn), add = T)

dev.off()
```

```
#><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>
### PROFILING STEEPNESS
#><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>><>

# Create subdirectory for profile runs
dir.create(file.path(getwd(),run, "profile"))

# specify directory
dir_prof <- file.path(getwd(),run, "profile")

# Copy/Paste ss3 files for running profiles
copy_SS_inputs(
  dir.old = file.path(getwd(),run),
  dir.new = dir_prof,
  copy_exe = TRUE,
  create.dir = TRUE,
  overwrite = TRUE,
  copy_par = TRUE,
  verbose = TRUE
)

# Manipulate starter file
starter <- SS_readstarter(file.path(dir_prof, "starter.ss"))

# change control file name in the starter file
starter[["ctlfile"]] <- "control_modified.ss"

# make sure the prior likelihood is calculated
# for non-estimated quantities
starter[["prior_like"]] <- 1

# write modified starter file
SS_writestarter(starter, dir = dir_prof, overwrite = TRUE)

# define steepness range
h.vec <- seq(0.45, 0.95, .05)

# Specify dat and control files
DAT = "Lobster_dat.dat"
CTL = "Lobster_ctl.ss"
Nprofile <- length(h.vec)
```

```r
# run profile command
ncores <- parallelly::availableCores(omit = 1)
future::plan(future::multisession, workers = ncores)
profile <- r4ss::profile(
  dir = dir_prof,
  oldctlfile = paste(CTL),
  newctlfile = "control_modified.ss",
  string = "Ricker_beta", # subset of parameter label
  exe = "ss3.exe",
  profilevec = h.vec, skipfinished=T,
)

future::plan(future::sequential)

# compile model runs (exclude 6 and 7 because the Hessian did not invert)
profilemodels <- SSgetoutput(dirvec = dir_prof, keyvec = c(1:7,8:Nprofile))

# Save as rdata
save(profilemodels,file=paste0(dir_prof,"/profile_h.ref.rdata"))

# summarize output
profilesummary <- SSsummarize(profilemodels)

# Make log-likelihood profile plot
results <- SSplotProfile(profilesummary,
                         profile.string = "Ricker_beta",
                         profile.label = "Stock-recruit steepness (h)"
)

# check results
results
```

7.11 Appendix XI - Diagnostics and Sensitivity of Stock Synthesis model for European lobster

Separate page numbering: 1 - 41

Diagnostics and Sensitivity of Stock Synthesis model for European lobster in 3a

Max Cardinale (SLU)

30 September, 2024

0.1 Load packages

```
# Load
library(r4ss)
library(ss3diags)
library(mvtnorm)
library(FLCore)
library(ggplotFL)
library(kobe)
require(plyr)
require(dplyr)
require(reshape2)
library(grid)
library(png)
library(parallel)
library(doParallel)
cl <- makeCluster(10, type = "PSOCK")
registerDoParallel(cl)
```

1 Lobster 3a benchmark

All models are annual, two sex, two fleets and with several surveys

The B_{MSY} proxy is used as reference point with a corresponding F_{MSY}

- *Reference_run* Reference run, average catches, steepness 0.80
- *Run1* Low catches
- *Run2* High catches
- *Run3* Reference run, low steepness (0.65)
- *Run4* Reference run, high steepness (0.90)
- *Run5* Reference run, time varying selectivity of the commercial fleet since 2018
- *Run6* Reference run, high catches, low steepness

```
scenarios = c("Reference_run", "Run1", "Run2", "Run3", "Run4", "Run5", "Run6")
```

1.1 Load runs

Define folder with R data files

```
rdata = "rdata_runs"
runs = list.files(rdata)
```

Get list of rdata files

```
mods = list()
for (i in 1:length(runs)) {
    load(file.path(rdata, runs[i]))
    mods[[i]] = ss3rep
}
mods = mods[c(1, 2, 3, 4, 5, 6, 7)]
names(mods) = scenarios
```

2 Selected Model Diagnostics

More computational intense model diagnostic were run for 7 selected runs:

- *Reference_run* Reference run, average catches
- *Run1* Low catches
- *Run2* High catches
- *Run3* Reference run, low steepness
- *Run4* Reference run, high steepness
- *Run5* Reference run, time varying selectivity of the commercial fleet since 2018
- *Run6* Reference run, high catches, low steepness

Select the runs used for diagnostics

```
dm = mods[c(1, 2, 3, 4, 5, 6, 7)]
```

Load retro data

```
rdata = "rdata_retros"
runs = list.files(rdata)
retros = list()
for (i in 1:length(runs)) {
    load(file.path(rdata, runs[i]))
    retros[[i]] = retroModels
}

hcs = retros[c(1, 2, 3, 4, 5, 6, 7)]
names(hcs) = names(dm)
```

Make list of hindcast trends form retrospective runs

```

hc = lapply(hcs, function(x) {
    hci = r4ss::SSsummarize(x, verbose = F)
    hci
})
```

Compile length comps from retrospective runs

```

hc.age = lapply(hcs, function(x) {
    hcl = ss3diags::SSretroComps(x)
    hcl
})
```

2.1 Goodness of Fits

2.1.1 Indices

```
sspar(mfrow = c(2, 4), plot.cex = 0.9)
SSplotJABBAres(dm[[1]], add = T, verbose = F)
        indices RMSE.perc nobs
  1      Safari      36.3   10
  2       SREAS       9.6   74
  3    VCD_2017      29.7    7
  4    VCD_1938      15.4   70
  5 Halland_com      35.4   24
  6    Lobserve      10.4    3
  7    Combined      19.7  188
legend("topleft", "Reference run", cex = 1.3)
SSplotJABBAres(dm[[2]], add = T, verbose = F)
        indices RMSE.perc nobs
  1      Safari      35.5   10
  2       SREAS       9.5   74
  3    VCD_2017      29.3    7
  4    VCD_1938      15.4   70
  5 Halland_com      35.2   24
  6    Lobserve      10.5    3
  7    Combined      19.6  188
legend("topleft", "Run1", cex = 1.3)
SSplotJABBAres(dm[[3]], add = T, verbose = F)
        indices RMSE.perc nobs
  1      Safari      37.0   10
  2       SREAS       9.7   74
  3    VCD_2017      30.1    7
  4    VCD_1938      15.5   70
  5 Halland_com      35.6   24
  6    Lobserve      10.3    3
  7    Combined      19.9  188
legend("topleft", "Run2", cex = 1.3)
SSplotJABBAres(dm[[4]], add = T, verbose = F)
        indices RMSE.perc nobs
  1      Safari      38.4   10
  2       SREAS       9.5   74
  3    VCD_2017      31.0    7
  4    VCD_1938      15.2   70
  5 Halland_com      35.1   24
  6    Lobserve      10.0    3
  7    Combined      19.9  188
legend("topleft", "Run3", cex = 1.3)
SSplotJABBAres(dm[[5]], add = T, verbose = F)
        indices RMSE.perc nobs
  1      Safari      35.4   10
  2       SREAS       9.7   74
  3    VCD_2017      29.3    7
  4    VCD_1938      15.6   70
  5 Halland_com      35.9   24
  6    Lobserve      10.5    3
  7    Combined      19.8  188
```

```
legend("topleft", "Run4", cex = 1.3)
SSplotJABBAres(dm[[6]], add = T, verbose = F)
         indices RMSE.perc nobs
   1      Safari      32.1   10
   2       SREAS       9.6   74
   3    VCD_2017      29.3    7
   4    VCD_1938      15.6   70
   5 Halland_com      34.4   24
   6    Lobserve      11.5    3
   7    Combined      19.1  188
legend("topleft", "Run5", cex = 1.3)
SSplotJABBAres(dm[[7]], add = T, verbose = F)
         indices RMSE.perc nobs
   1      Safari      39.2   10
   2       SREAS       9.6   74
   3    VCD_2017      31.4    7
   4    VCD_1938      15.2   70
   5 Halland_com      35.6   24
   6    Lobserve       9.9    3
   7    Combined      20.1  188
legend("topleft", "Run6", cex = 1.3)
```

```
sspar(mfrow = c(3, 5), plot.cex = 0.9)
SSplotRunstest(dm[[1]], add = T, verbose = F)
           Index runs.p     test  sigma3.lo sigma3.hi type
   1      Safari  0.004   Failed -0.6428083 0.6428083 cpue
   2       SREAS  0.322   Passed -0.2814719 0.2814719 cpue
   3    VCD_2017  0.024   Failed -0.5992328 0.5992328 cpue
   4    VCD_1938  0.016   Failed -0.3889467 0.3889467 cpue
   5 Halland_com  0.006   Failed -0.4669317 0.4669317 cpue
   6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Reference run", cex = 1.2)
SSplotRunstest(dm[[2]], add = T, verbose = F)
           Index runs.p     test  sigma3.lo sigma3.hi type
   1      Safari  0.004   Failed -0.6393968 0.6393968 cpue
   2       SREAS  0.322   Passed -0.2804605 0.2804605 cpue
   3    VCD_2017  0.024   Failed -0.5957325 0.5957325 cpue
   4    VCD_1938  0.017   Failed -0.3892941 0.3892941 cpue
   5 Halland_com  0.006   Failed -0.5227946 0.5227946 cpue
   6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run1", cex = 1.2)
SSplotRunstest(dm[[3]], add = T, verbose = F)
           Index runs.p     test  sigma3.lo sigma3.hi type
   1      Safari  0.004   Failed -0.6459705 0.6459705 cpue
   2       SREAS  0.322   Passed -0.2824468 0.2824468 cpue
   3    VCD_2017  0.024   Failed -0.6024173 0.6024173 cpue
   4    VCD_1938  0.016   Failed -0.3887542 0.3887542 cpue
   5 Halland_com  0.006   Failed -0.4647152 0.4647152 cpue
   6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run2", cex = 1.3)
```

```
sspar(mfrow = c(4, 5), plot.cex = 0.9)
SSplotRunstest(dm[[4]], add = T, verbose = F)
           Index runs.p     test  sigma3.lo sigma3.hi type
```

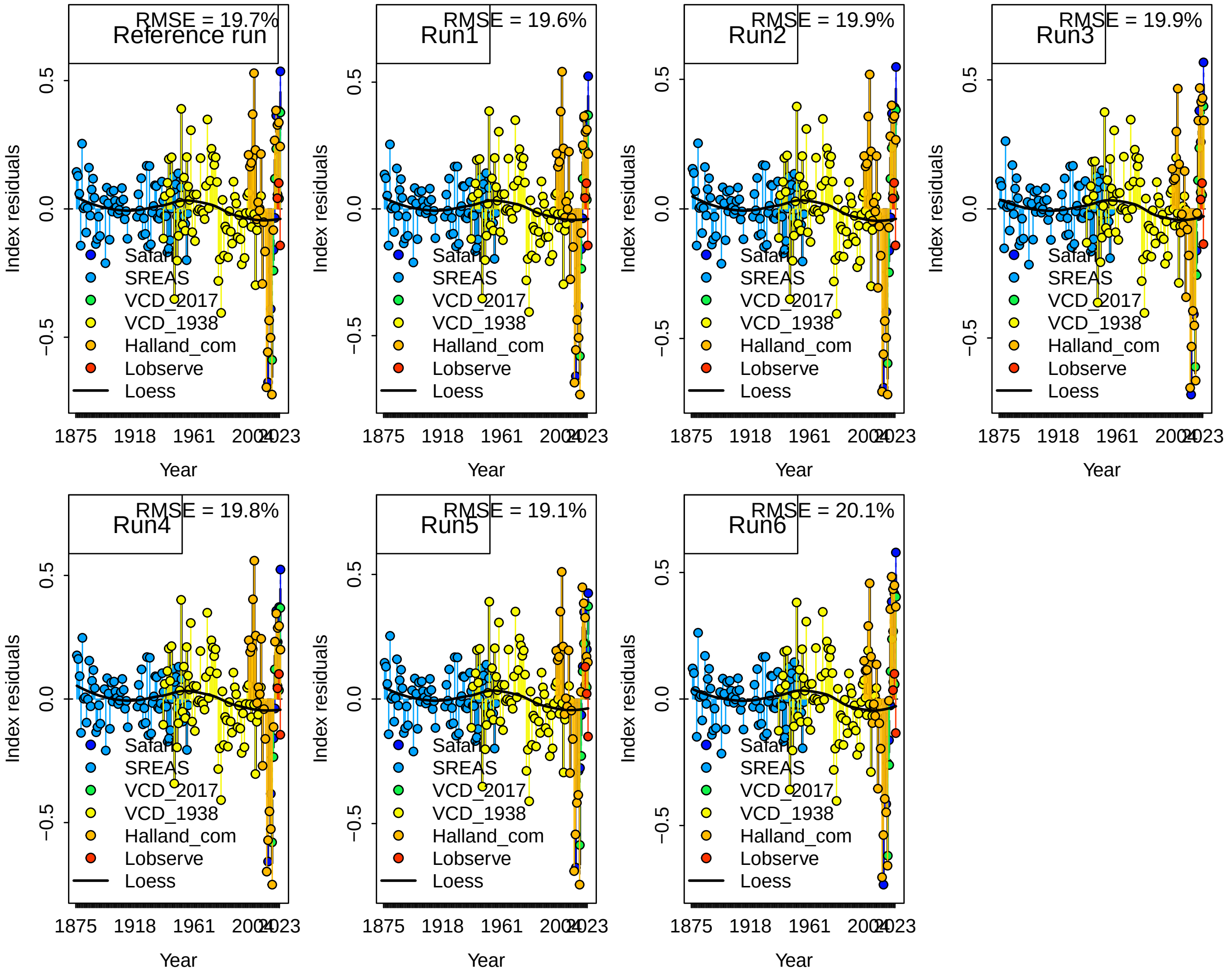


Figure 1: Index residual plots for the surveys index with trends for seven scenarios

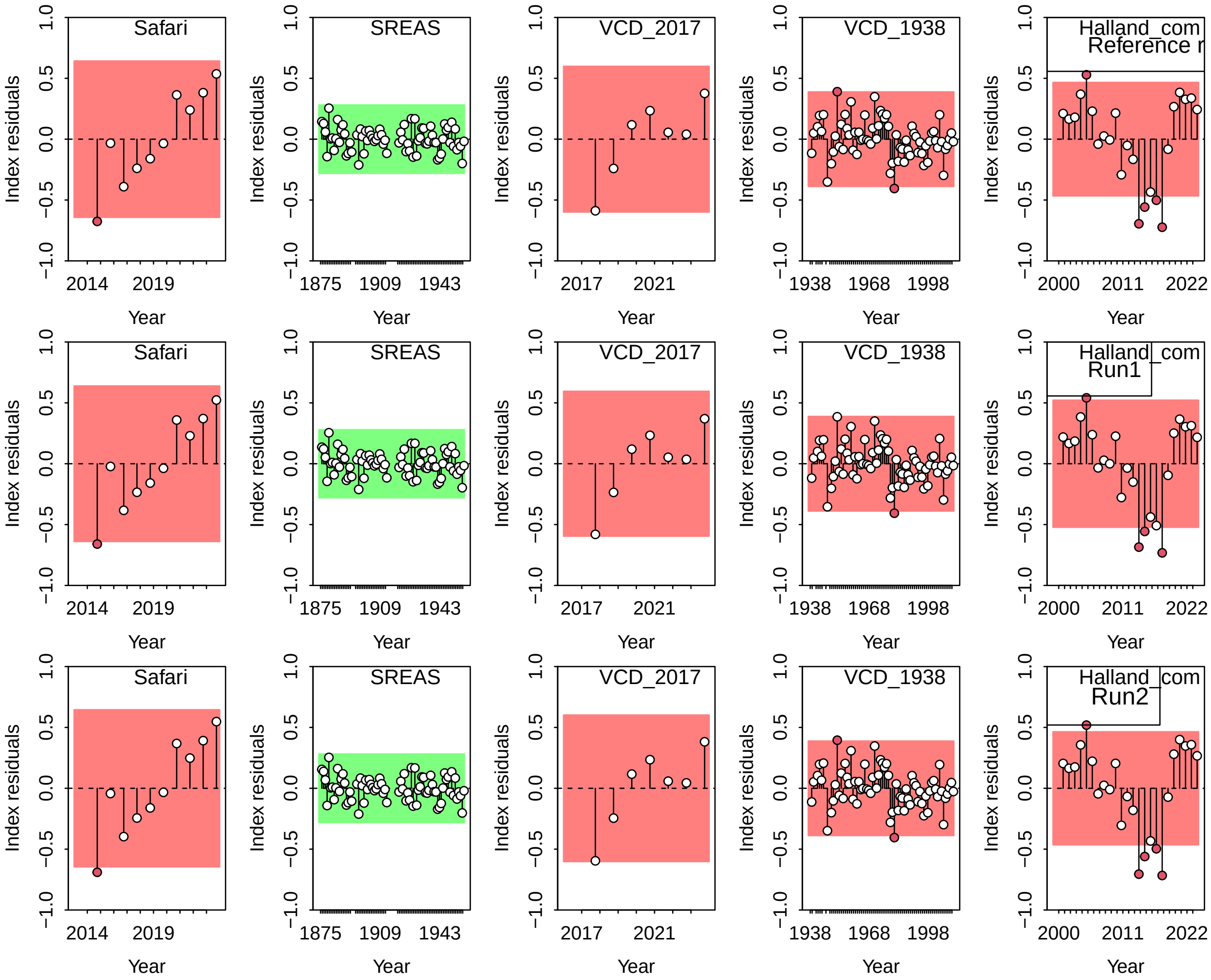


Figure 2: Index residual runs tests for the survey indeces for Reference run, Run1 and Run2

```
  1      Safari  0.004   Failed -0.6564131 0.6564131 cpue
  2       SREAS  0.322   Passed -0.2797275 0.2797275 cpue
  3    VCD_2017  0.024   Failed -0.6086843 0.6086843 cpue
  4    VCD_1938  0.048   Failed -0.3861595 0.3861595 cpue
  5 Halland_com  0.000   Failed -0.4654041 0.4654041 cpue
  6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run3", cex = 1.2)
SSplotRunstest(dm[[5]], add = T, verbose = F)
          Index runs.p     test  sigma3.lo sigma3.hi type
  1      Safari  0.004   Failed -0.6375889 0.6375889 cpue
  2       SREAS  0.339   Passed -0.2824150 0.2824150 cpue
  3    VCD_2017  0.024   Failed -0.5954087 0.5954087 cpue
  4    VCD_1938  0.017   Failed -0.3903560 0.3903560 cpue
  5 Halland_com  0.000   Failed -0.5214147 0.5214147 cpue
  6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run4", cex = 1.2)
SSplotRunstest(dm[[6]], add = T, verbose = F)
          Index runs.p     test  sigma3.lo sigma3.hi type
  1      Safari  0.004   Failed -0.5663857 0.5663857 cpue
  2       SREAS  0.322   Passed -0.2808420 0.2808420 cpue
  3    VCD_2017  0.024   Failed -0.5804599 0.5804599 cpue
  4    VCD_1938  0.017   Failed -0.3886723 0.3886723 cpue
  5 Halland_com  0.007   Failed -0.4908392 0.4908392 cpue
  6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run5", cex = 1.2)
SSplotRunstest(dm[[7]], add = T, verbose = F)
          Index runs.p     test  sigma3.lo sigma3.hi type
  1      Safari  0.004   Failed -0.6598543 0.6598543 cpue
  2       SREAS  0.322   Passed -0.2807736 0.2807736 cpue
  3    VCD_2017  0.024   Failed -0.6117915 0.6117915 cpue
  4    VCD_1938  0.046   Failed -0.3859203 0.3859203 cpue
  5 Halland_com  0.000   Failed -0.4631637 0.4631637 cpue
  6    Lobserve     NA Excluded         NA        NA cpue
legend("topleft", "Run6", cex = 1.2)
```

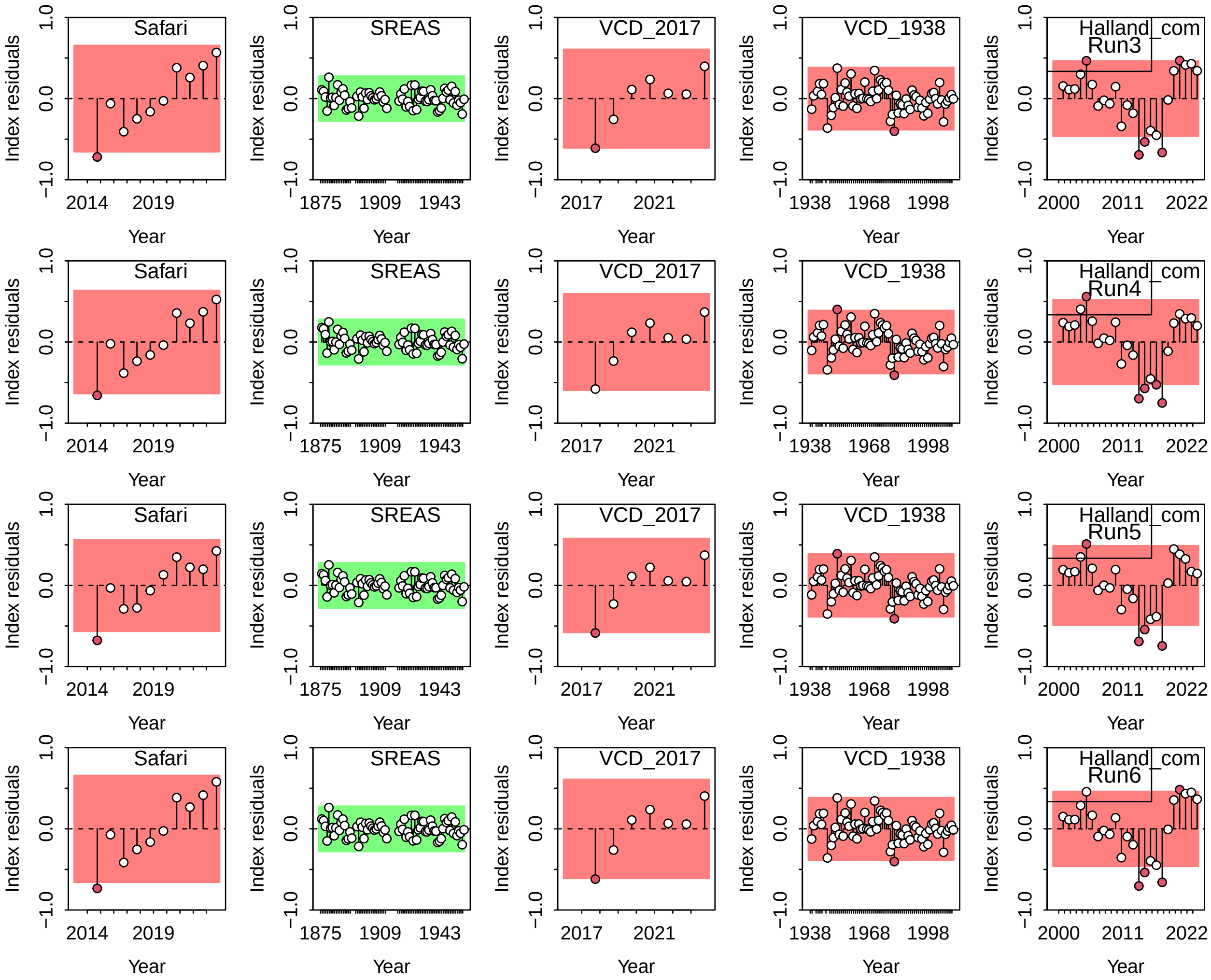


Figure 3: Index residual runs tests for the survey indeces for Run3 to Run6

2.1.2 Size Composition Data

```
sspar(mfrow = c(2, 4), plot.cex = 0.9)
SSplotJABBAres(dm[[1]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.3    7
   3            Combined       3.1   18
legend("topleft", "Reference run", cex = 1.3)
SSplotJABBAres(dm[[2]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.3    7
   3            Combined       3.1   18
legend("topleft", "Run1", cex = 1.3)
SSplotJABBAres(dm[[3]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.3    7
   3            Combined       3.1   18
legend("topleft", "Run2", cex = 1.3)
SSplotJABBAres(dm[[4]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.7   11
   2            VCD_2017       1.2    7
   3            Combined       3.0   18
legend("topleft", "Run3", cex = 1.3)
SSplotJABBAres(dm[[5]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.3    7
   3            Combined       3.1   18
legend("topleft", "Run4", cex = 1.3)
SSplotJABBAres(dm[[6]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       2.8   11
   2            VCD_2017       1.3    7
   3            Combined       2.3   18
legend("topleft", "Run5", cex = 1.3)
SSplotJABBAres(dm[[7]], add = T, subplots = "len", verbose = F)
                 indices RMSE.perc nobs
   1 Commercial_official       3.8   11
   2            VCD_2017       1.2    7
   3            Combined       3.0   18
legend("topleft", "Run6", cex = 1.3)
```

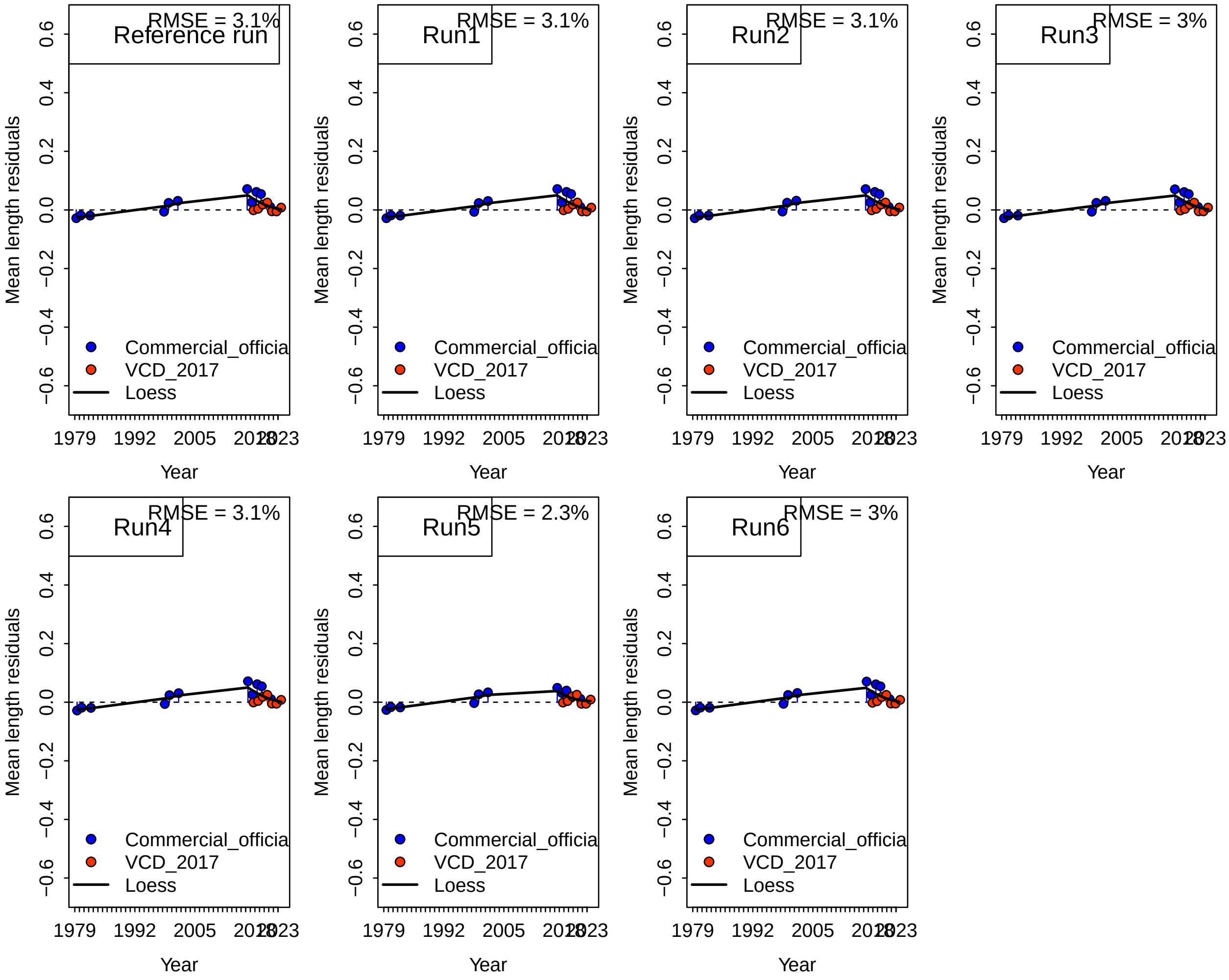


Figure 4: Index residual plots for the mean length with trends for seven scenarios

2.1.3 Reference run

```
i = 1
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                   Index runs.p   test   sigma3.lo  sigma3.hi type
   1 Commercial_official  0.002 Failed -0.06183628 0.06183628  len
   2            VCD_2017  0.358 Passed -0.03094218 0.03094218  len
```

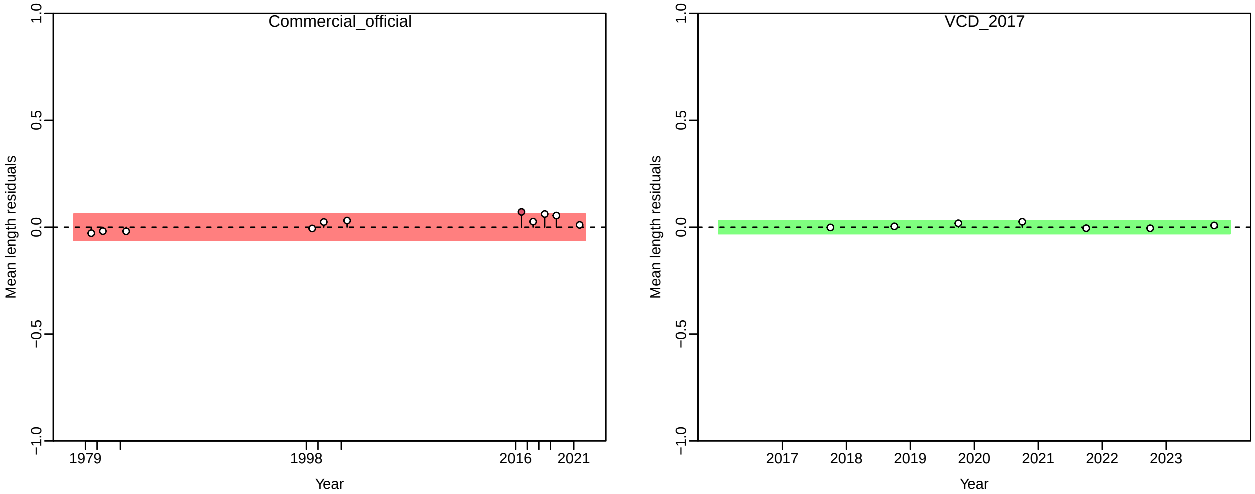


Figure 5: Residual runs tests on mean length for the Reference run

2.1.4 Run1

```
# Retro
i = 2
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                  Index runs.p   test   sigma3.lo  sigma3.hi type
  1 Commercial_official  0.002 Failed -0.06202354 0.06202354  len
  2            VCD_2017  0.358 Passed -0.03096474 0.03096474  len
```

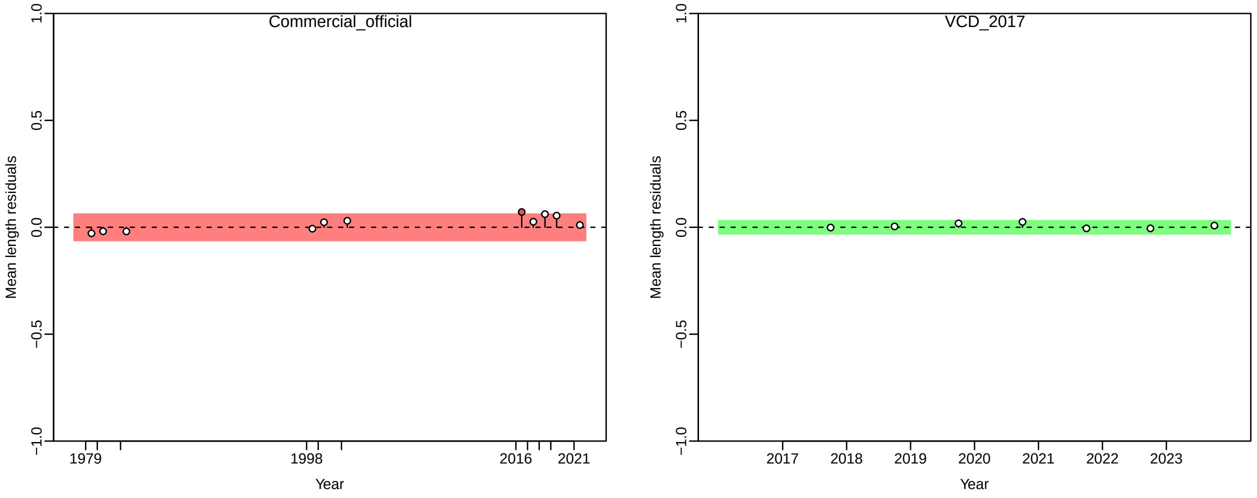


Figure 6: Residual runs tests on mean length for the Run1

2.1.5 Run2

```
i = 3
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                    Index runs.p   test   sigma3.lo  sigma3.hi type
   1 Commercial_official  0.002 Failed -0.06166386 0.06166386  len
   2            VCD_2017  0.358 Passed -0.03092499 0.03092499  len
```

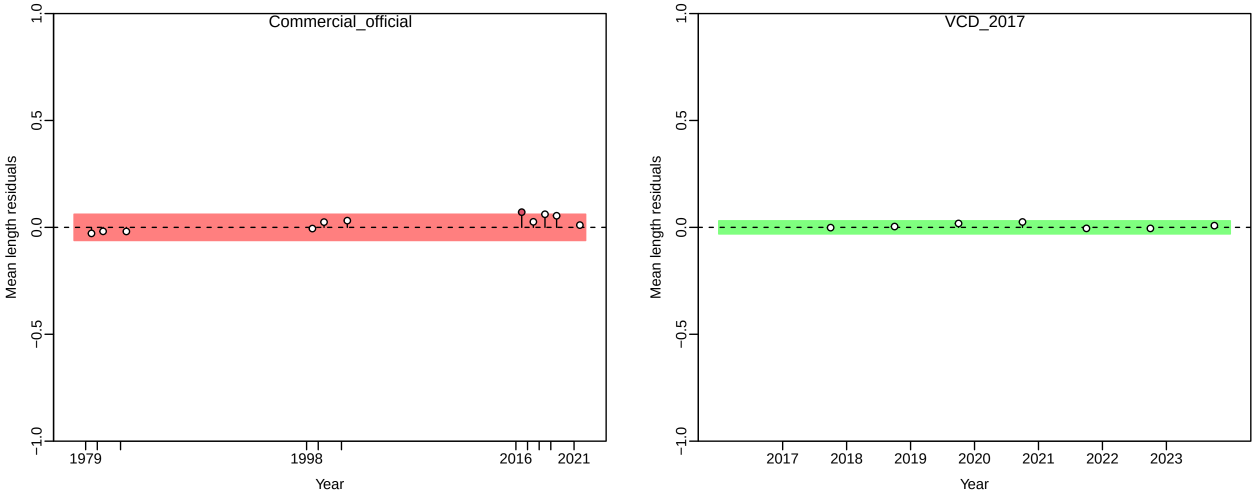


Figure 7: Residual runs tests on mean length for the Run2

2.1.6 Run3

```
i = 4
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                  Index runs.p   test   sigma3.lo  sigma3.hi type
  1 Commercial_official  0.002 Failed -0.06143299 0.06143299  len
  2            VCD_2017  0.358 Passed -0.03092336 0.03092336  len
```

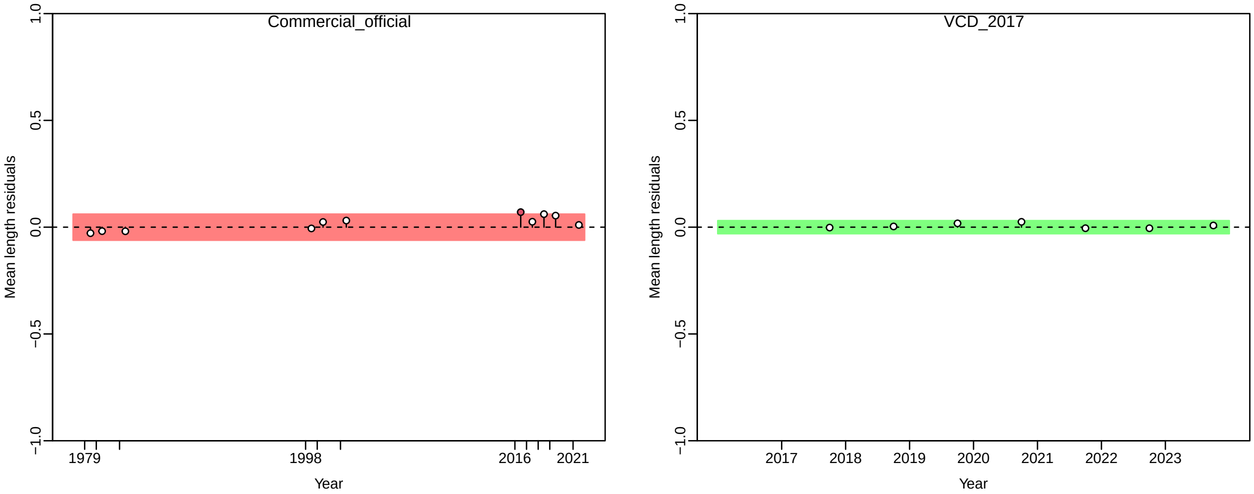


Figure 8: Residual runs tests on mean length for the Run3

2.1.7 Run4

```
i = 5
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                  Index runs.p   test   sigma3.lo  sigma3.hi type
  1 Commercial_official  0.002 Failed -0.06201207 0.06201207  len
  2            VCD_2017  0.358 Passed -0.03093980 0.03093980  len
```

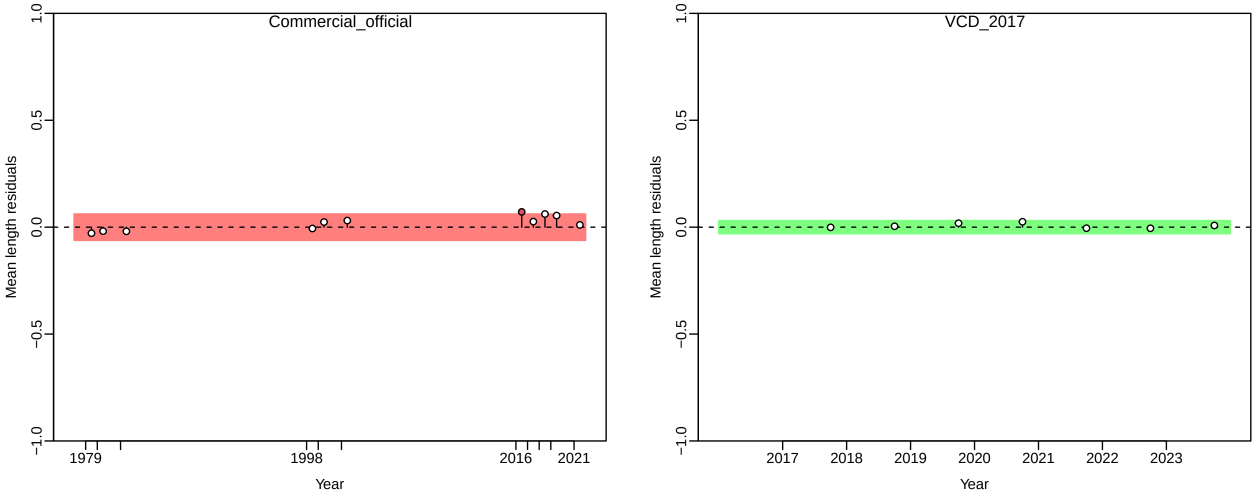


Figure 9: Residual runs tests on mean length for the Run4

2.1.8 Run5

```
i = 5
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                  Index runs.p   test   sigma3.lo  sigma3.hi type
   1 Commercial_official  0.002 Failed -0.06201207 0.06201207  len
   2            VCD_2017  0.358 Passed -0.03093980 0.03093980  len
```

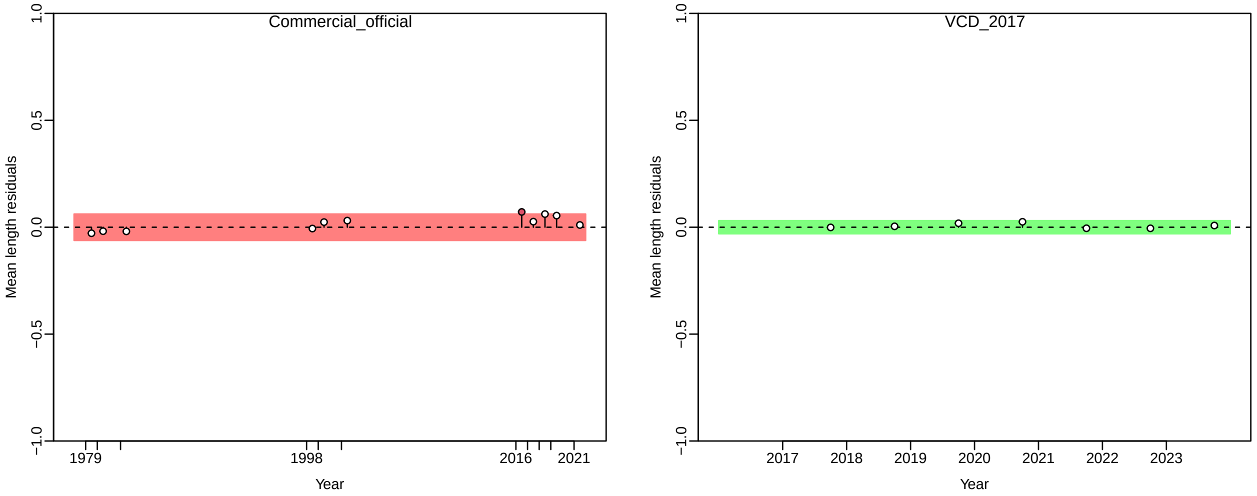


Figure 10: Residual runs tests on mean length for the Run5

2.1.9 Run6

```
i = 6
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRunstest(dm[[i]], add = T, subplots = "len", verbose = F)
                  Index runs.p   test   sigma3.lo  sigma3.hi type
   1 Commercial_official  0.002 Failed -0.03481926 0.03481926  len
```

```
  2          VCD_2017  0.358 Passed -0.03214353 0.03214353  len
```

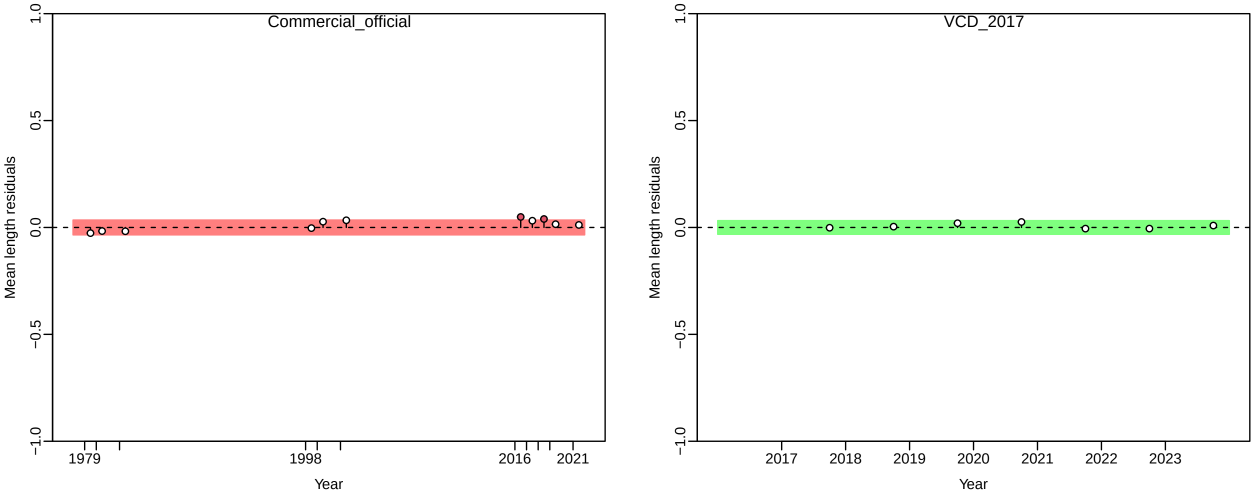


Figure 11: Residual runs tests on mean length for the Run6

2.2 Retrospective Analysis

2.2.1 Reference run

```
# Retro
i = 1
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F, verbose = F)
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02281115 -0.03535847
   2  SSB     2021 -0.06052096 -0.07498143
   3  SSB     2020 -0.16568139 -0.14036269
   4  SSB     2019 -0.22876252 -0.22121913
   5  SSB     2018 -0.29681483 -0.30968865
   6  SSB Combined -0.15491817 -0.15632207
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F, verbose = F)
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02281115 -0.03535847
   2  SSB     2021 -0.06052096 -0.07498143
   3  SSB     2020 -0.16568139 -0.14036269
   4  SSB     2019 -0.22876252 -0.22121913
   5  SSB     2018 -0.29681483 -0.30968865
   6  SSB Combined -0.15491817 -0.15632207
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F, verbose = F)
     type     peel        Rho ForecastRho
   1    F     2022 0.05163841  0.04705691
   2    F     2021 0.10593070  0.13328807
   3    F     2020 0.08863853  0.08737569
   4    F     2019 0.20531882  0.14106748
   5    F     2018 0.38952101  0.28029045
   6    F Combined 0.16820949  0.13781572
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F, verbose = F)
     type     peel        Rho ForecastRho
   1    F     2022 0.05163841  0.04705691
   2    F     2021 0.10593070  0.13328807
   3    F     2020 0.08863853  0.08737569
   4    F     2019 0.20531882  0.14106748
   5    F     2018 0.38952101  0.28029045
   6    F Combined 0.16820949  0.13781572
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

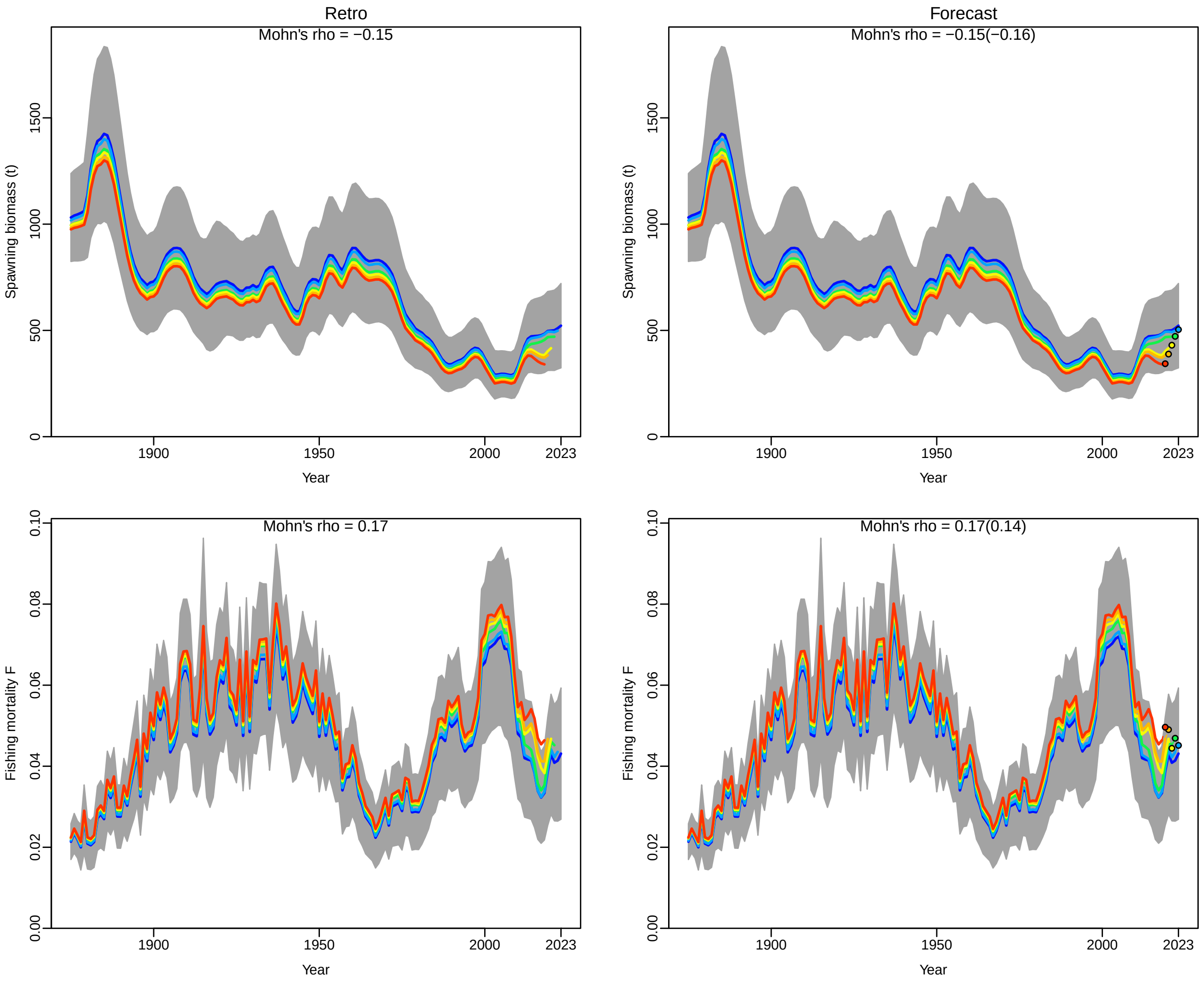


Figure 12: Retrospective analysis and retrospective forecasts for the Reference run

2.2.2 Run1

```
# Retro
i = 2
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F, verbose = F)
     type      peel         Rho ForecastRho
   1  SSB      2022 -0.01544425 -0.02713530
   2  SSB      2021 -0.04609378 -0.05954398
   3  SSB      2020 -0.15242782 -0.12707108
   4  SSB      2019 -0.21327484 -0.20641126
   5  SSB      2018 -0.28393494 -0.29689119
   6  SSB Combined -0.14223512 -0.14341056
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F, verbose = F)
     type      peel         Rho ForecastRho
   1  SSB      2022 -0.01544425 -0.02713530
   2  SSB      2021 -0.04609378 -0.05954398
   3  SSB      2020 -0.15242782 -0.12707108
   4  SSB      2019 -0.21327484 -0.20641126
   5  SSB      2018 -0.28393494 -0.29689119
   6  SSB Combined -0.14223512 -0.14341056
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F, verbose = F)
     type      peel        Rho ForecastRho
   1    F      2022 0.04300870  0.03765159
   2    F      2021 0.08828711  0.11384705
   3    F      2020 0.06917258  0.06085709
   4    F      2019 0.18674502  0.11565549
   5    F      2018 0.37641248  0.26326568
   6    F Combined 0.15272518  0.11825538
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F, verbose = F)
     type      peel        Rho ForecastRho
   1    F      2022 0.04300870  0.03765159
   2    F      2021 0.08828711  0.11384705
   3    F      2020 0.06917258  0.06085709
   4    F      2019 0.18674502  0.11565549
   5    F      2018 0.37641248  0.26326568
   6    F Combined 0.15272518  0.11825538
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

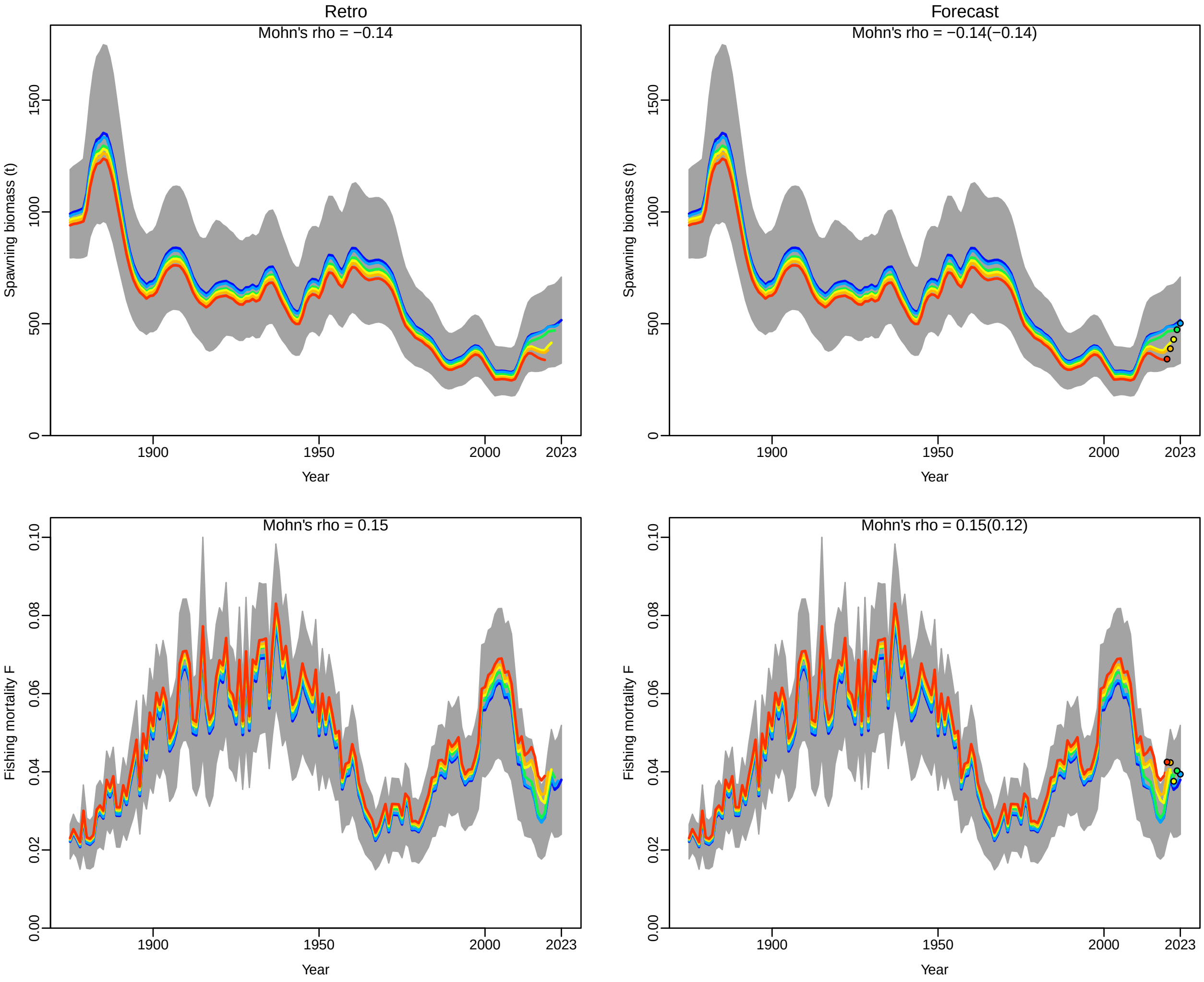


Figure 13: Retrospective analysis and retrospective forecasts for the Run1

2.2.3 Run2

```
# Retro
i = 3
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02628519 -0.03965041
   2  SSB     2021 -0.06772356 -0.08312696
   3  SSB     2020 -0.16545752 -0.13969912
   4  SSB     2019 -0.23085416 -0.22257962
   5  SSB     2018 -0.30509461 -0.31794733
   6  SSB Combined -0.15908301 -0.16060069
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02628519 -0.03965041
   2  SSB     2021 -0.06772356 -0.08312696
   3  SSB     2020 -0.16545752 -0.13969912
   4  SSB     2019 -0.23085416 -0.22257962
   5  SSB     2018 -0.30509461 -0.31794733
   6  SSB Combined -0.15908301 -0.16060069
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05591402  0.05208445
   2    F     2021 0.11483160  0.14370420
   3    F     2020 0.08888969  0.09877999
   4    F     2019 0.20326943  0.14477405
   5    F     2018 0.39511122  0.28950523
   6    F Combined 0.17160319  0.14576958
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05591402  0.05208445
   2    F     2021 0.11483160  0.14370420
   3    F     2020 0.08888969  0.09877999
   4    F     2019 0.20326943  0.14477405
   5    F     2018 0.39511122  0.28950523
   6    F Combined 0.17160319  0.14576958
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

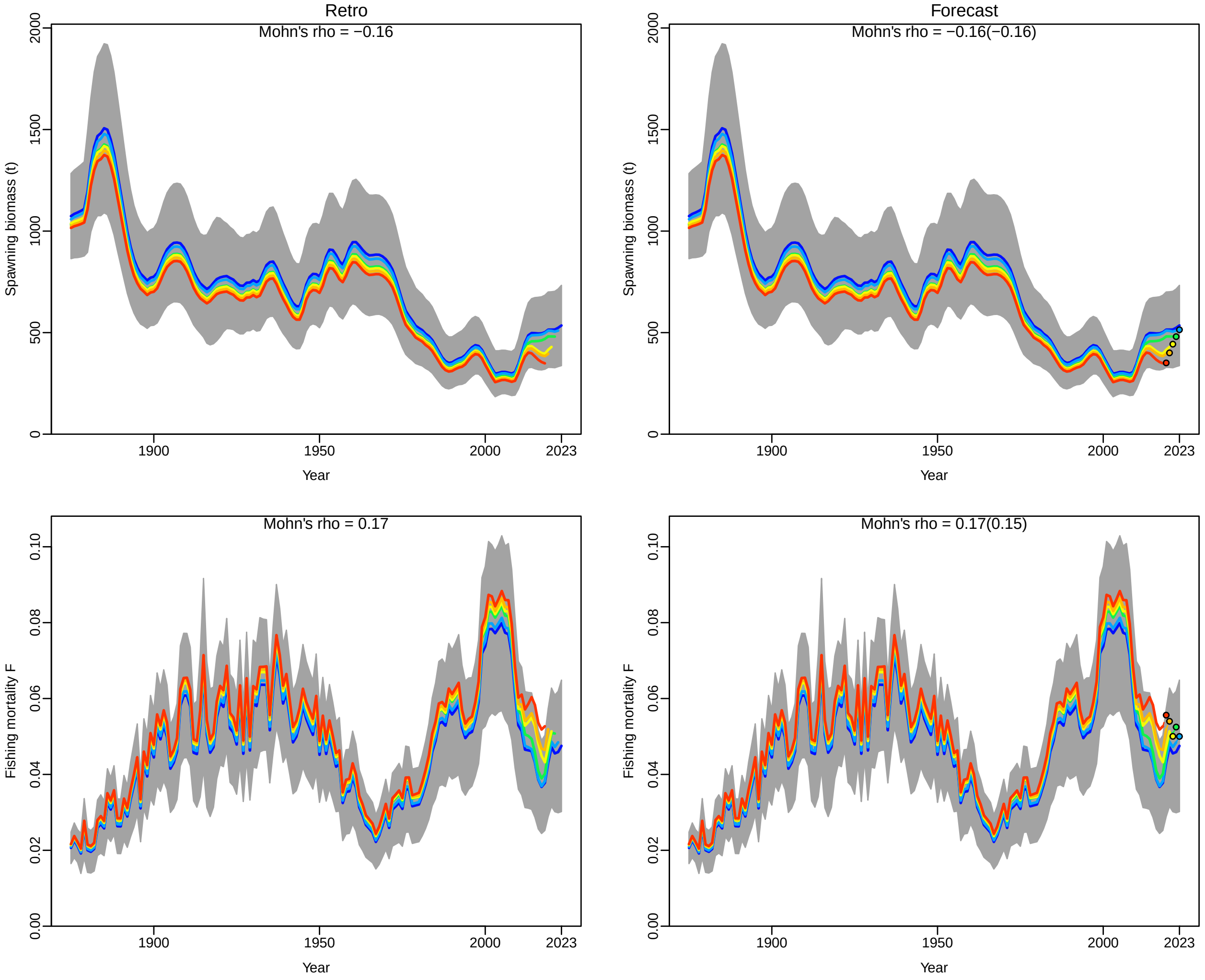


Figure 14: Retrospective analysis and retrospective forecasts for the Run2

2.2.4 Run3

```
# Retro
i = 4
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02336802 -0.03728832
   2  SSB     2021 -0.05124991 -0.06756569
   3  SSB     2020 -0.15461875 -0.13211628
   4  SSB     2019 -0.21747248 -0.21078068
   5  SSB     2018 -0.28853658 -0.30201638
   6  SSB Combined -0.14704915 -0.14995347
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02336802 -0.03728832
   2  SSB     2021 -0.05124991 -0.06756569
   3  SSB     2020 -0.15461875 -0.13211628
   4  SSB     2019 -0.21747248 -0.21078068
   5  SSB     2018 -0.28853658 -0.30201638
   6  SSB Combined -0.14704915 -0.14995347
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05482692  0.05265425
   2    F     2021 0.09880397  0.13012273
   3    F     2020 0.08585618  0.05989588
   4    F     2019 0.19339174  0.14738959
   5    F     2018 0.37848233  0.28703588
   6    F Combined 0.16227223  0.13541967
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05482692  0.05265425
   2    F     2021 0.09880397  0.13012273
   3    F     2020 0.08585618  0.05989588
   4    F     2019 0.19339174  0.14738959
   5    F     2018 0.37848233  0.28703588
   6    F Combined 0.16227223  0.13541967
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

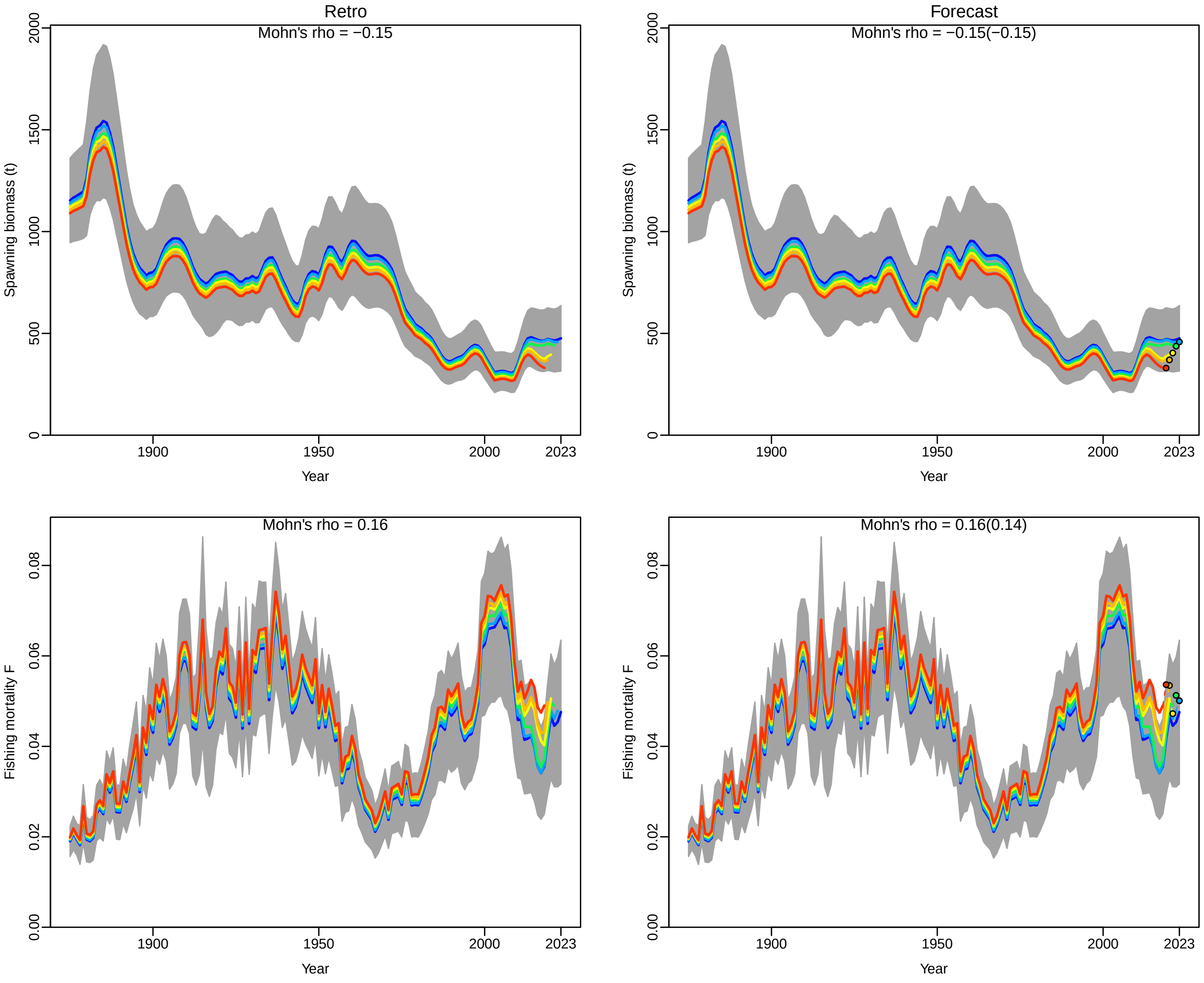


Figure 15: Retrospective analysis and retrospective forecasts for the Run3

2.2.5 Run4

```
# Retro
i = 5
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02138338 -0.03323513
   2  SSB     2021 -0.06510977 -0.07843734
   3  SSB     2020 -0.16466361 -0.13779495
   4  SSB     2019 -0.22862118 -0.22050911
   5  SSB     2018 -0.30066172 -0.31290174
   6  SSB Combined -0.15608793 -0.15657566
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02138338 -0.03323513
   2  SSB     2021 -0.06510977 -0.07843734
   3  SSB     2020 -0.16466361 -0.13779495
   4  SSB     2019 -0.22862118 -0.22050911
   5  SSB     2018 -0.30066172 -0.31290174
   6  SSB Combined -0.15608793 -0.15657566
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.04897344  0.04355844
   2    F     2021 0.10905910  0.13458557
   3    F     2020 0.08030891  0.10147729
   4    F     2019 0.20182024  0.12810912
   5    F     2018 0.39440398  0.27575651
   6    F Combined 0.16691314  0.13669738
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.04897344  0.04355844
   2    F     2021 0.10905910  0.13458557
   3    F     2020 0.08030891  0.10147729
   4    F     2019 0.20182024  0.12810912
   5    F     2018 0.39440398  0.27575651
   6    F Combined 0.16691314  0.13669738
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

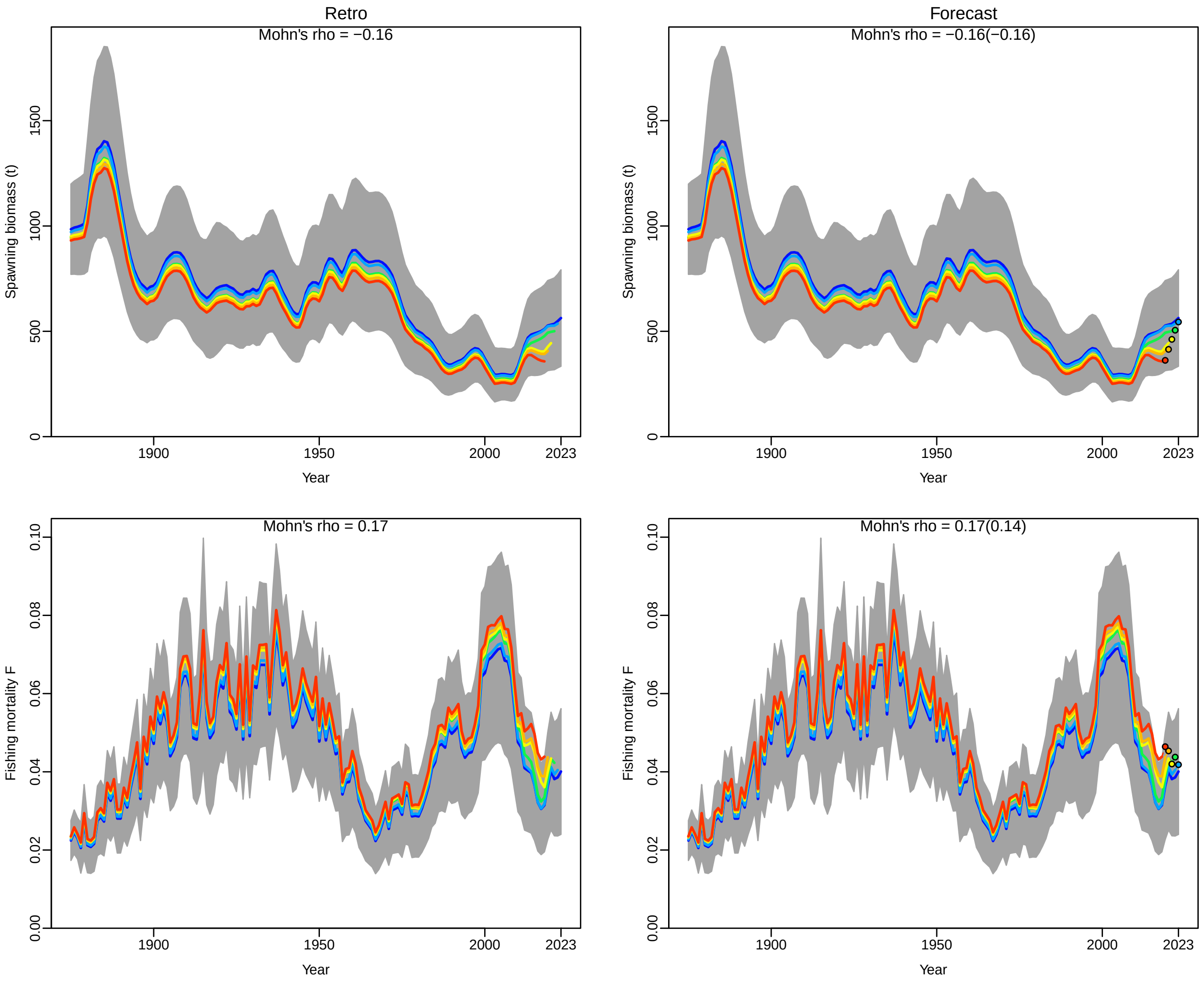


Figure 16: Retrospective analysis and retrospective forecasts for the Run4

2.2.6 Run5

```
# Retro
i = 6
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel          Rho ForecastRho
   1  SSB     2022 -0.01687914 -0.02973726
   2  SSB     2021 -0.04184190 -0.05662891
   3  SSB     2020 -0.14966469 -0.11386450
   4  SSB     2019 -0.21978482 -0.20629303
   5  SSB     2018 -0.28539216 -0.29484714
   6  SSB Combined -0.14271254 -0.14027417
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel          Rho ForecastRho
   1  SSB     2022 -0.01687914 -0.02973726
   2  SSB     2021 -0.04184190 -0.05662891
   3  SSB     2020 -0.14966469 -0.11386450
   4  SSB     2019 -0.21978482 -0.20629303
   5  SSB     2018 -0.28539216 -0.29484714
   6  SSB Combined -0.14271254 -0.14027417
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1    F     2022 0.08632909  0.05168774
   2    F     2021 0.08527544  0.18244999
   3    F     2020 0.08901621  0.15045737
   4    F     2019 0.17395533  0.20013039
   5    F     2018 0.35660502  0.22375773
   6    F Combined 0.15823622  0.16169664
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1    F     2022 0.08632909  0.05168774
   2    F     2021 0.08527544  0.18244999
   3    F     2020 0.08901621  0.15045737
   4    F     2019 0.17395533  0.20013039
   5    F     2018 0.35660502  0.22375773
   6    F Combined 0.15823622  0.16169664
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

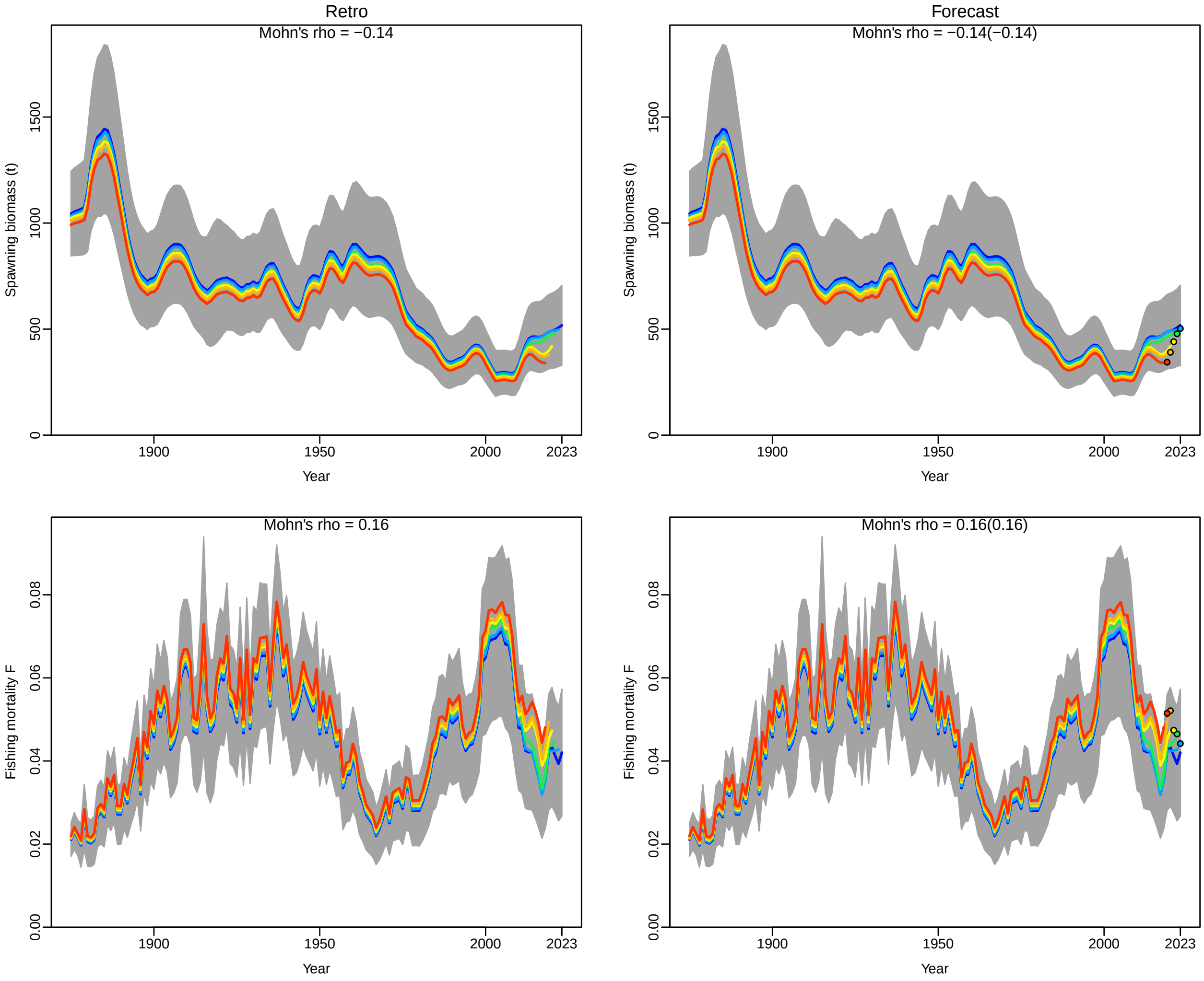


Figure 17: Retrospective analysis and retrospective forecasts for the Run5

2.2.7 Run6

```
# Retro
i = 7
sspar(mfrow = c(2, 2), plot.cex = 0.65)
SSplotRetro(hc[[i]], add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02651623 -0.04128651
   2  SSB     2021 -0.05909101 -0.07636971
   3  SSB     2020 -0.16401458 -0.14166527
   4  SSB     2019 -0.22934625 -0.22219496
   5  SSB     2018 -0.30465535 -0.31810931
   6  SSB Combined -0.15672468 -0.15992515
SSplotRetro(hc[[i]], add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel         Rho ForecastRho
   1  SSB     2022 -0.02651623 -0.04128651
   2  SSB     2021 -0.05909101 -0.07636971
   3  SSB     2020 -0.16401458 -0.14166527
   4  SSB     2019 -0.22934625 -0.22219496
   5  SSB     2018 -0.30465535 -0.31810931
   6  SSB Combined -0.15672468 -0.15992515
SSplotRetro(hc[[i]], subplots = "F", add = T, legend = F, forecast = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05872083  0.05734880
   2    F     2021 0.10819250  0.14119902
   3    F     2020 0.09880181  0.07808045
   4    F     2019 0.20634251  0.16579837
   5    F     2018 0.39895918  0.31024886
   6    F Combined 0.17420337  0.15053510
SSplotRetro(hc[[i]], subplots = "F", add = T, forecastrho = T, legend = F)
   Plotting Retrospective pattern

   Mohn's Rho stats, including one step ahead forecasts:
     type     peel        Rho ForecastRho
   1    F     2022 0.05872083  0.05734880
   2    F     2021 0.10819250  0.14119902
   3    F     2020 0.09880181  0.07808045
   4    F     2019 0.20634251  0.16579837
   5    F     2018 0.39895918  0.31024886
   6    F Combined 0.17420337  0.15053510
mtext(c("Retro", "Forecast"), 3, outer = T, line = -0.5, at = c(0.3, 0.8), cex = 0.8)
```

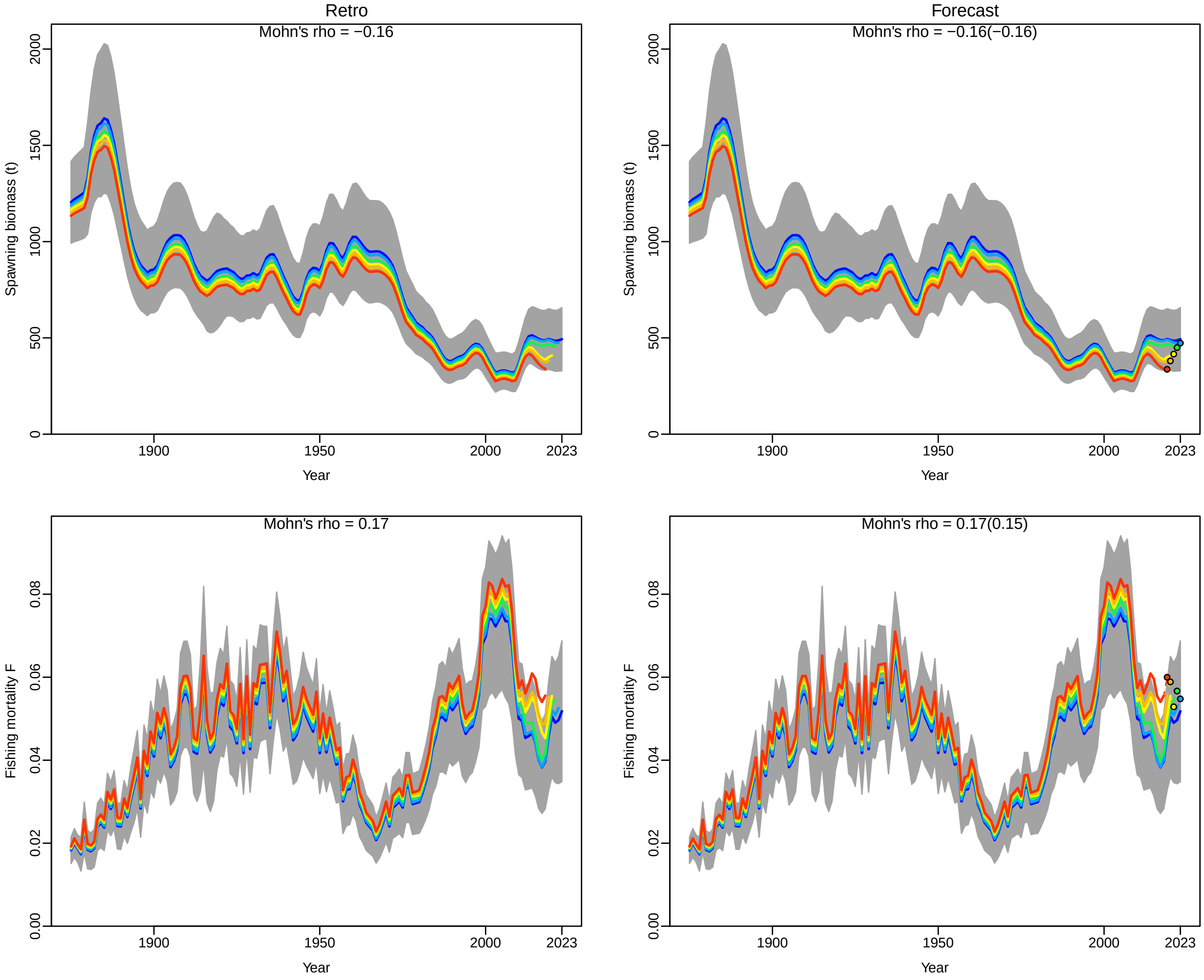


Figure 18: Retrospective analysis and retrospective forecasts for the Run6

2.3 Hindcasting Cross-Validation

2.3.1 Indices

```
sspar(mfrow = c(3, 4), plot.cex = 0.8)
SSplotHCxval(hc[[1]], add = T, verbose = FALSE)
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
           Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
   1      Safari      1  3.006373 0.6990414 0.2325198  3.006373      5
   2       SREAS      1        NA        NA        NA        NA      0
   3    VCD_2017      1  1.504788 0.2982494 0.1982003  1.504788      5
   4    VCD_1938      1        NA        NA        NA        NA      0
   5 Halland_com      1  3.950732 0.6343841 0.1605738  3.950732      5
   6    Lobserve      1 12.775070 2.0464565 0.1601914 12.775070      2
legend("topleft", "Reference run", cex = 0.5)
SSplotHCxval(hc[[2]], add = T, verbose = FALSE)
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in min(x): no non-missing arguments to max; returning -Inf
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
           Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
   1      Safari      1  2.904353 0.6753196 0.2325198  2.904353      5
   2       SREAS      1        NA        NA        NA        NA      0
   3    VCD_2017      1  1.452641 0.2879138 0.1982003  1.452641      5
   4    VCD_1938      1        NA        NA        NA        NA      0
   5 Halland_com      1  3.709036 0.5955741 0.1605738  3.709036      5
   6    Lobserve      1 12.834912 2.0560426 0.1601914 12.834912      2
legend("topleft", "Run1", cex = 0.5)
SSplotHCxval(hc[[3]], add = T, verbose = FALSE)
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in min(x): no non-missing arguments to max; returning -Inf
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
           Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
   1      Safari      1  3.053345 0.7099632 0.2325198  3.053345      5
   2       SREAS      1        NA        NA        NA        NA      0
   3    VCD_2017      1  1.548711 0.3069549 0.1982003  1.548711      5
   4    VCD_1938      1        NA        NA        NA        NA      0
   5 Halland_com      1  4.094495 0.6574687 0.1605738  4.094495      5
   6    Lobserve      1 12.876485 2.0627023 0.1601914 12.876485      2
legend("topleft", "Run2", cex = 0.5)
```

```
sspar(mfrow = c(4, 4), plot.cex = 0.8)
SSplotHCxval(hc[[4]], add = T, verbose = FALSE)
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
   Warning in min(x): no non-missing arguments to min; returning Inf
   Warning in max(x): no non-missing arguments to max; returning -Inf
           Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
   1      Safari      1  3.155996 0.7338316 0.2325198  3.155996      5
   2       SREAS      1        NA        NA        NA        NA      0
```

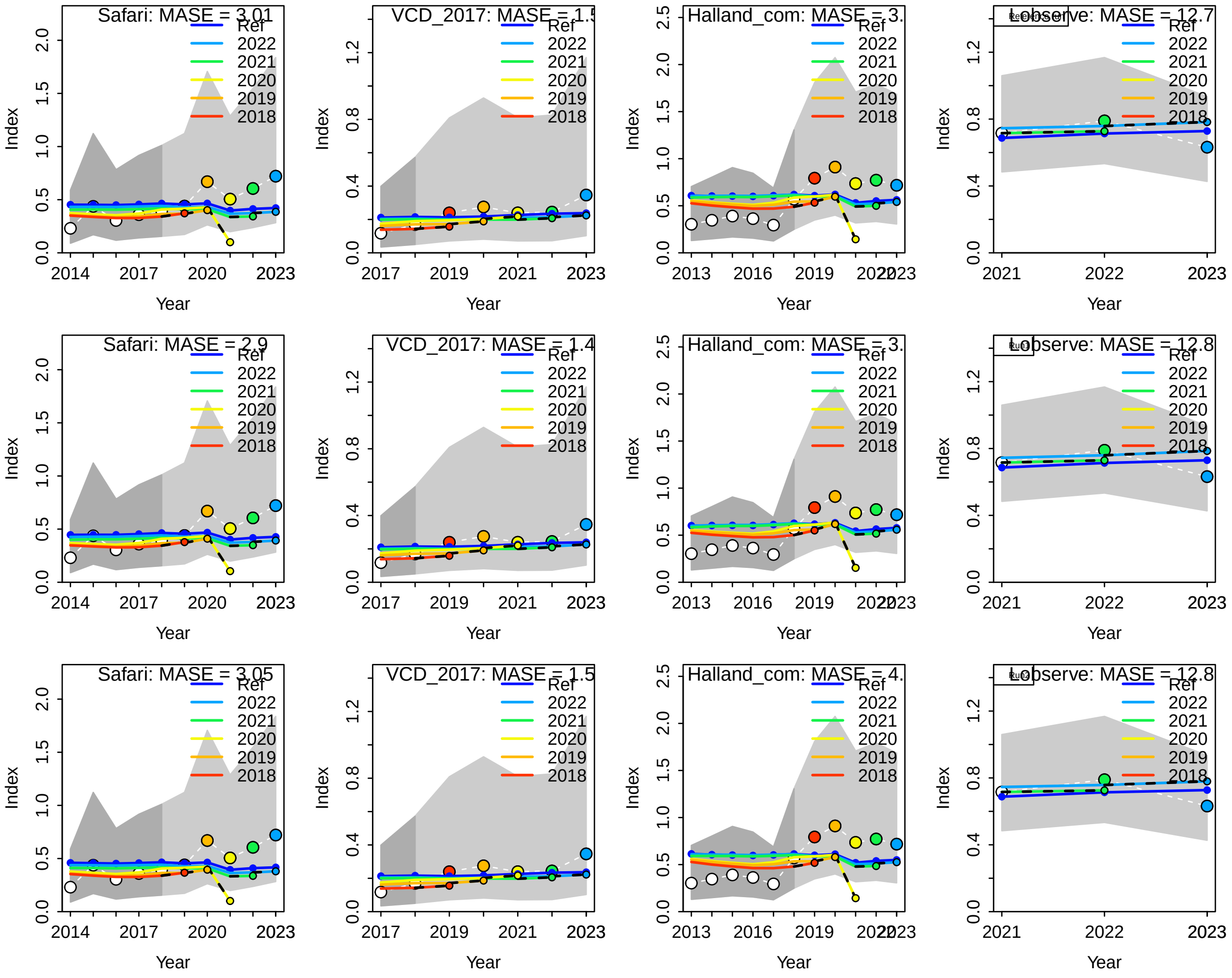


Figure 19: Hindcast cross-validations for the survey indices of the Reference run, Run1 and Run2

```
  3    VCD_2017      1  1.673909 0.3317692 0.1982003  1.673909      5
  4    VCD_1938      1        NA        NA        NA        NA      0
  5 Halland_com      1  4.599185 0.7385087 0.1605738  4.599185      5
  6    Lobserve      1 12.673945 2.0302572 0.1601914 12.673945      2
legend("topleft", "Run3", cex = 0.5)
SSplotHCxval(hc[[5]], add = T, verbose = FALSE)
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in min(x): no non-missing arguments to max; returning -Inf
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in max(x): no non-missing arguments to max; returning -Inf
          Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
  1      Safari      1  2.863866 0.6659057 0.2325198  2.863866      5
  2       SREAS      1        NA        NA        NA        NA      0
  3    VCD_2017      1  1.431015 0.2836276 0.1982003  1.431015      5
  4    VCD_1938      1        NA        NA        NA        NA      0
  5 Halland_com      1  3.535462 0.5677027 0.1605738  3.535462      5
  6    Lobserve      1 13.079162 2.0951694 0.1601914 13.079162      2
legend("topleft", "Run4", cex = 0.5)
SSplotHCxval(hc[[6]], add = T, verbose = FALSE)
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in min(x): no non-missing arguments to max; returning -Inf
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in max(x): no non-missing arguments to max; returning -Inf
          Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
  1      Safari      1  2.311978 0.5375806 0.2325198  2.311978      5
  2       SREAS      1        NA        NA        NA        NA      0
  3    VCD_2017      1  1.470159 0.2913860 0.1982003  1.470159      5
  4    VCD_1938      1        NA        NA        NA        NA      0
  5 Halland_com      1  3.214379 0.5161451 0.1605738  3.214379      5
  6    Lobserve      1 14.430317 2.3116128 0.1601914 14.430317      2
legend("topleft", "Run5", cex = 0.5)
SSplotHCxval(hc[[7]], add = T, verbose = FALSE)
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in min(x): no non-missing arguments to max; returning -Inf
  Warning in min(x): no non-missing arguments to min; returning Inf
  Warning in max(x): no non-missing arguments to max; returning -Inf
          Index Season      MASE    MAE.PR  MAE.base  MASE.adj n.eval
  1      Safari      1  3.236804 0.7526211 0.2325198  3.236804      5
  2       SREAS      1        NA        NA        NA        NA      0
  3    VCD_2017      1  1.721025 0.3411077 0.1982003  1.721025      5
  4    VCD_1938      1        NA        NA        NA        NA      0
  5 Halland_com      1  4.789749 0.7691083 0.1605738  4.789749      5
  6    Lobserve      1 12.699938 2.0344210 0.1601914 12.699938      2
legend("topleft", "Run6", cex = 0.5)
```

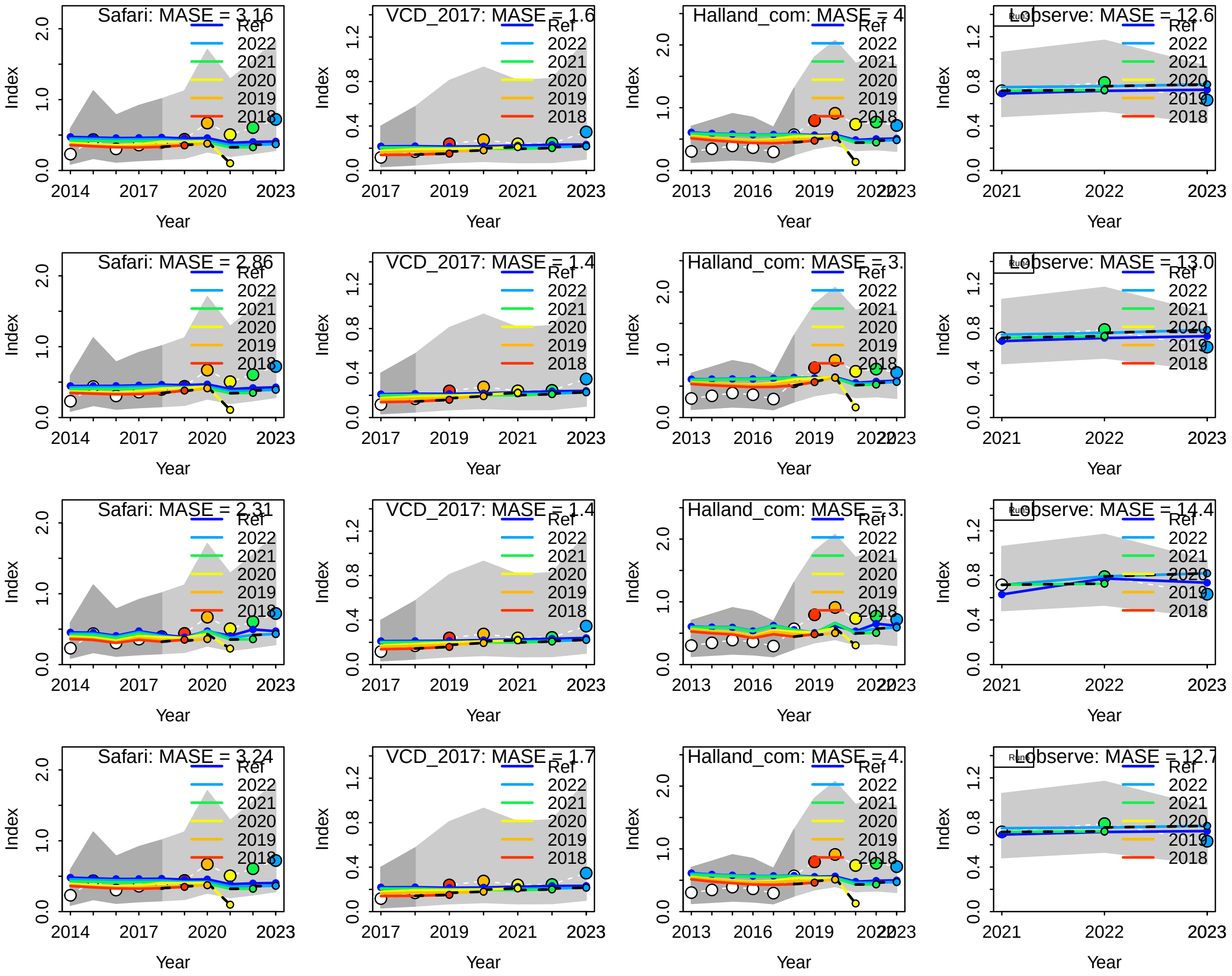


Figure 20: Hindcast cross-validations for the survey indices of Run3 to Run6

3 Sensitivities

Get the labels for the Bratio and Fratio

```
mvn = SSdeltaMVLN(mods[[3]], Fref = "Btgt", mc = 2, plot = F)

    starter.sso with Bratio: SSB/SSBMSY and F: _abs_F

mvn$labels
   expression(SSB/SSB[MSY], "F/F"[SB ~ 40], "SSB", "F", "Recruits",
       "Catch")
```

Create uncertainty with delta-MVLN approximation

```
kbs = NULL
# Compare indices
for (i in 1:length(scenarios)) {
    kbs = rbind(kbs, SSdeltaMVLN(mods[[i]], run = scenarios[i], Fref = "Btgt", plot = F,
        verbose = F, years = 1875:2023)$kb)
}
```

```
sspar(mfrow = c(3, 2), plot.cex = 0.7)
SSplotEnsemble(kbs, uncertainty = F, add = T, ylabs = mvn$labels, legendcex = 0.65,
    legendloc = "topright", verbose = F)
```

```
sspar(mfrow = c(3, 2), plot.cex = 0.7)
SSplotEnsemble(kbs, uncertainty = T, add = T, ylabs = mvn$labels, legendcex = 0.65,
    legendloc = "topright", verbose = F)
```

```
get_plot = "Compare.png"

# By run
Par = list(mfrow = c(1, 1), mar = c(5, 5, 1, 1), mgp = c(3, 1, 0), tck = -0.02, cex = 0.8)
png(file = get_plot, width = 6.5, height = 5.5, res = 200, units = "in")
par(Par)
kbp = kobe:::kobePhaseMar2(transform(kbs[kbs$year == 2023, ], run = paste(run))[,
    c("stock", "harvest", "run")], xlab = expression(B/B[tgt]), ylab = expression(F/F[tgt]),
    ylim = 5, xlim = 3, col = rainbow(9)[3:9], quadcol = c("red", "green", "yellow",
        "orange"))
   Coordinate system already present. Adding new coordinate system, which will
   replace the existing one.
   Coordinate system already present. Adding new coordinate system, which will
   replace the existing one.

dev.off()
   pdf
     2
```

```
# Beautify
DIMs = c(6, 5.5)

# setup plot
par(mar = rep(0, 4), omi = c(0, 0, 0, 0))  # no margins

# layout the plots into a matrix w/ 12 columns, by row
```

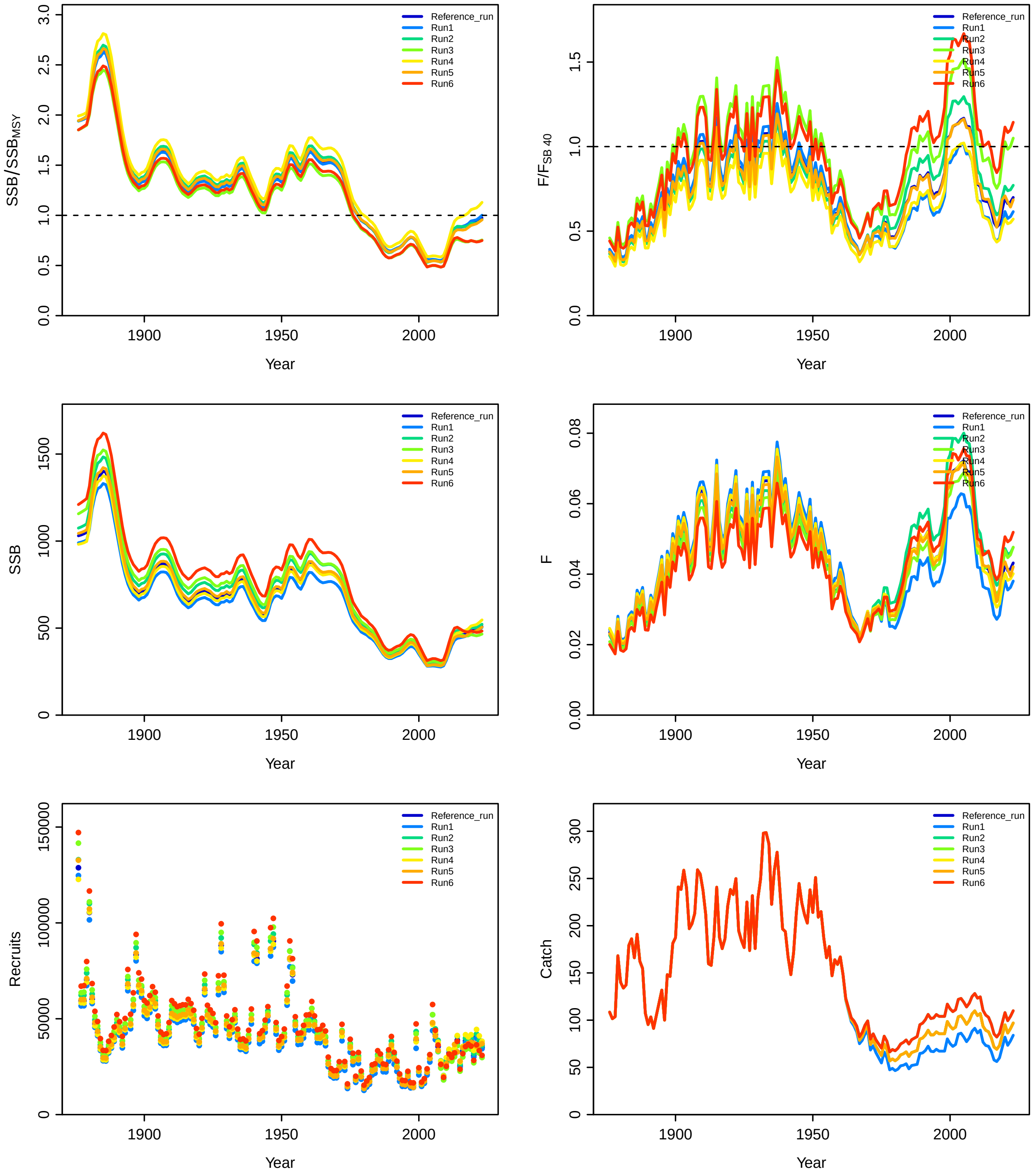


Figure 21: Comparison of stock trajectories

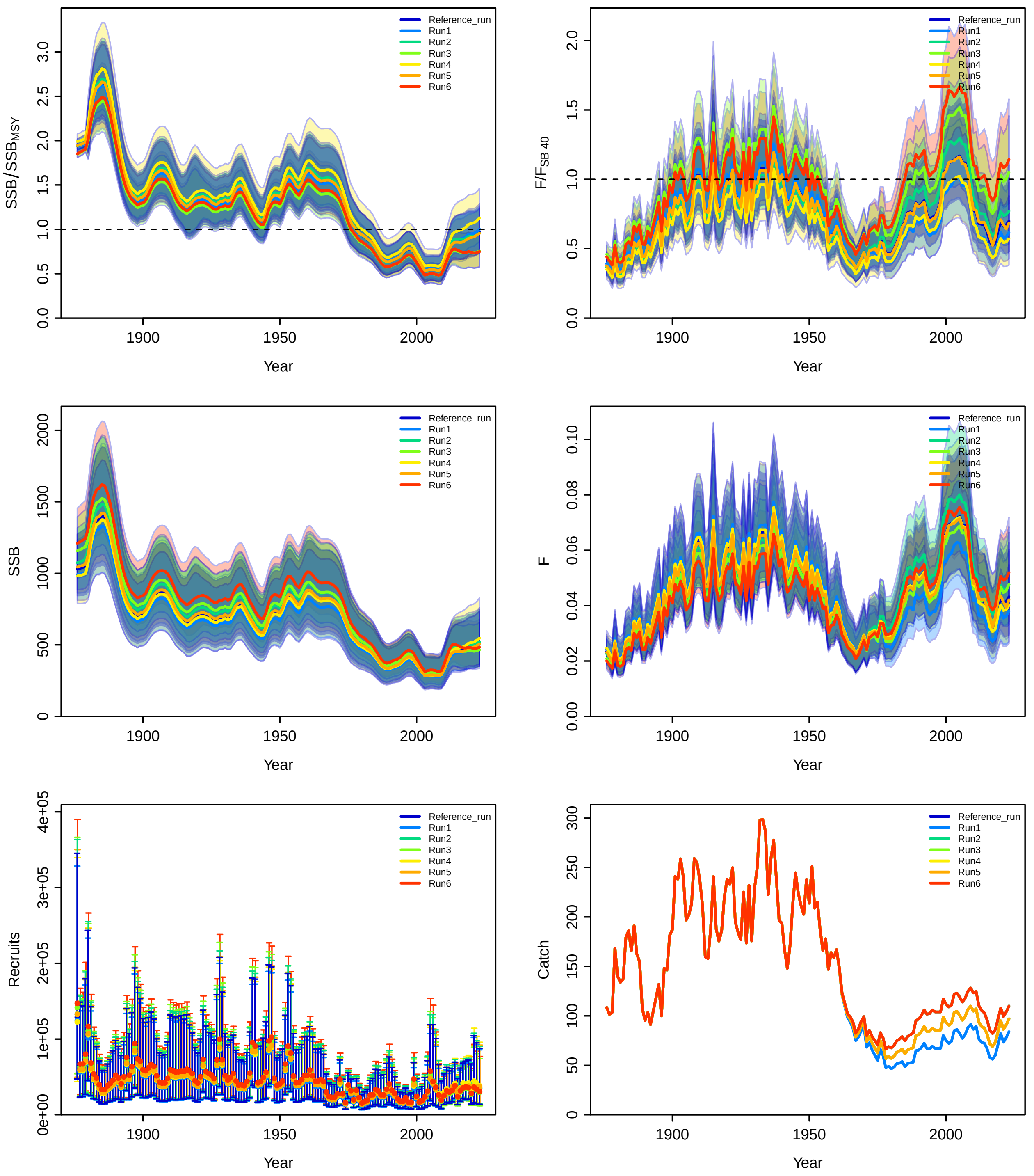


Figure 22: Comparison of stock trajectories with 95% CIs

```
layout(matrix(1:1, ncol = 1, byrow = TRUE))

# example image
img <- readPNG(paste0(get_plot))

# do the plotting
plot(NA, xlim = 0:1, ylim = 0:1, xaxt = "n", yaxt = "n", bty = "n")

rasterImage(img, 0, 0, 1, 1)
legend("topright", scenarios, pch = 22, pt.bg = rainbow(9)[3:9], box.lty = 0, cex = 1.2)
```

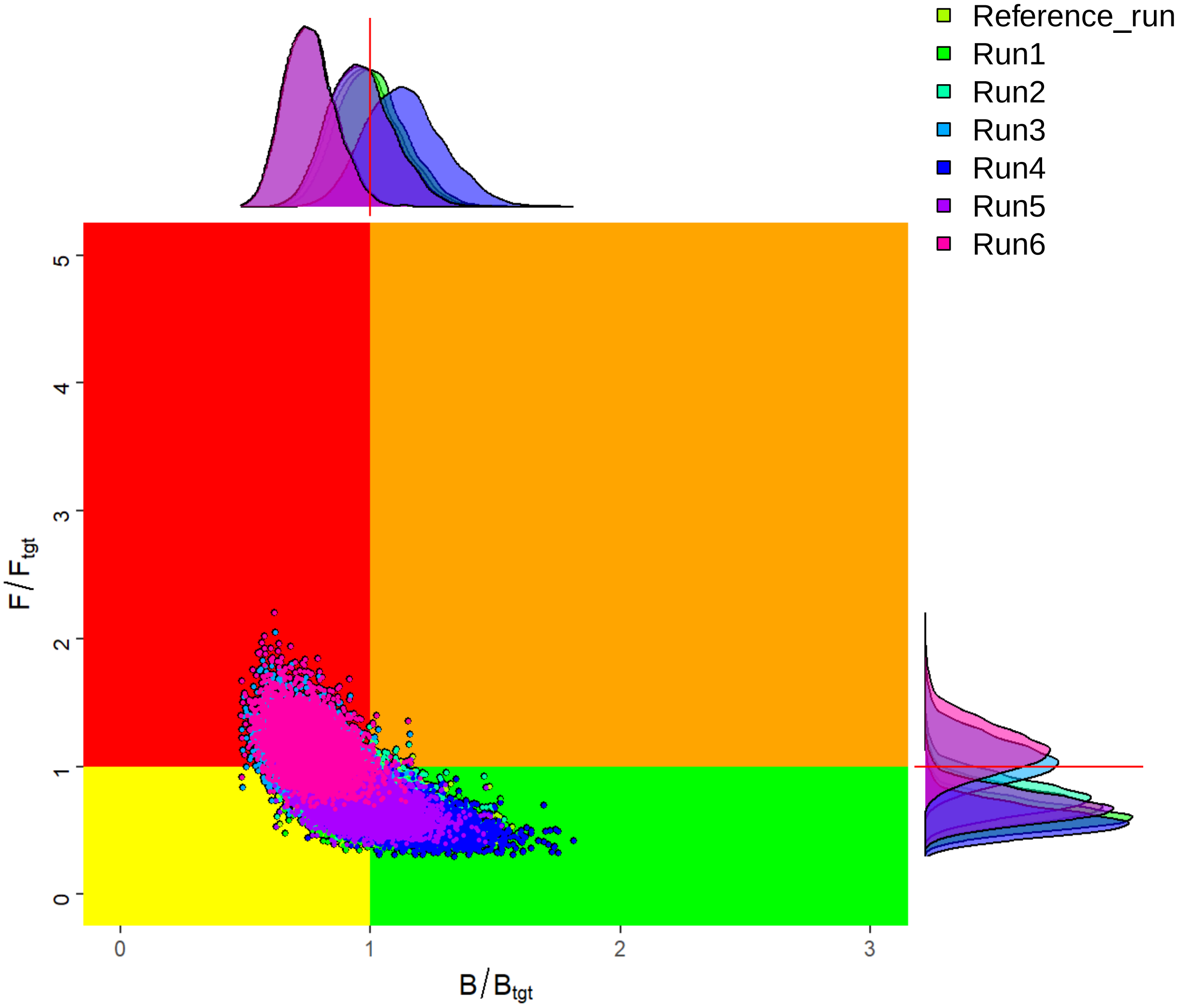


Figure 23: Kobe plot showing the comparison of stock status posteriors for 2023 with marginal posterior distributions

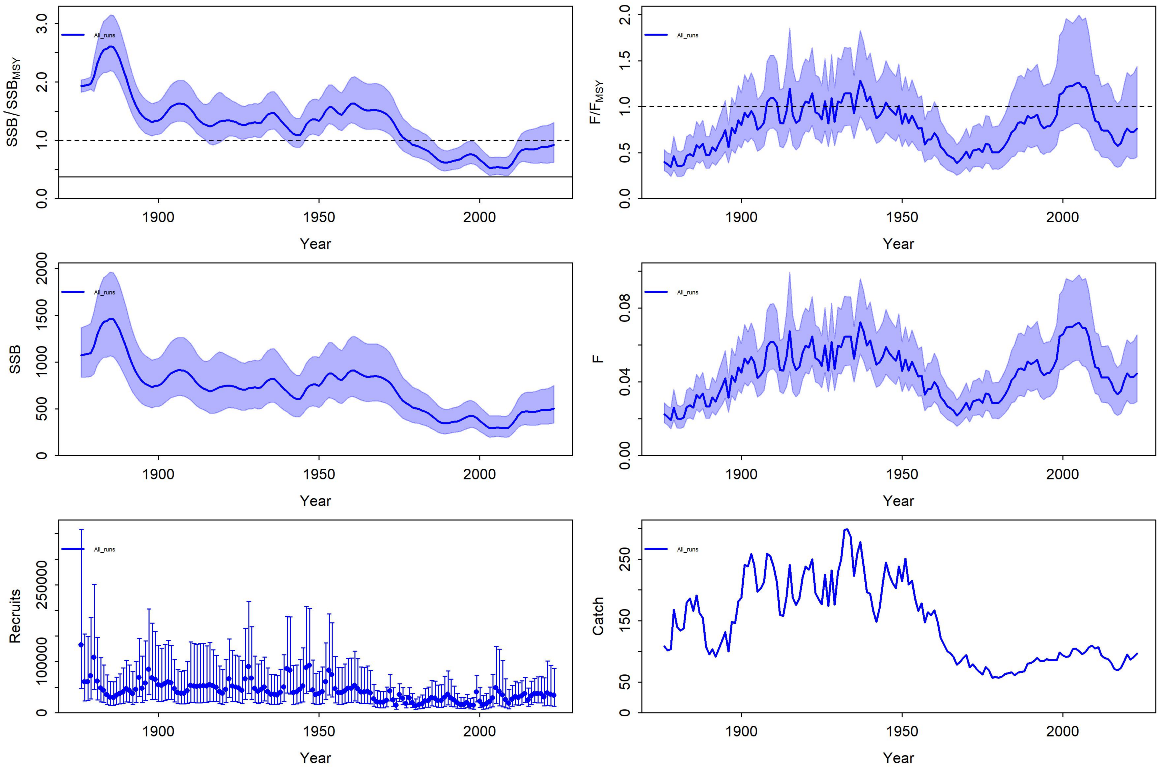


Figure 24: Ensamble time trend plot

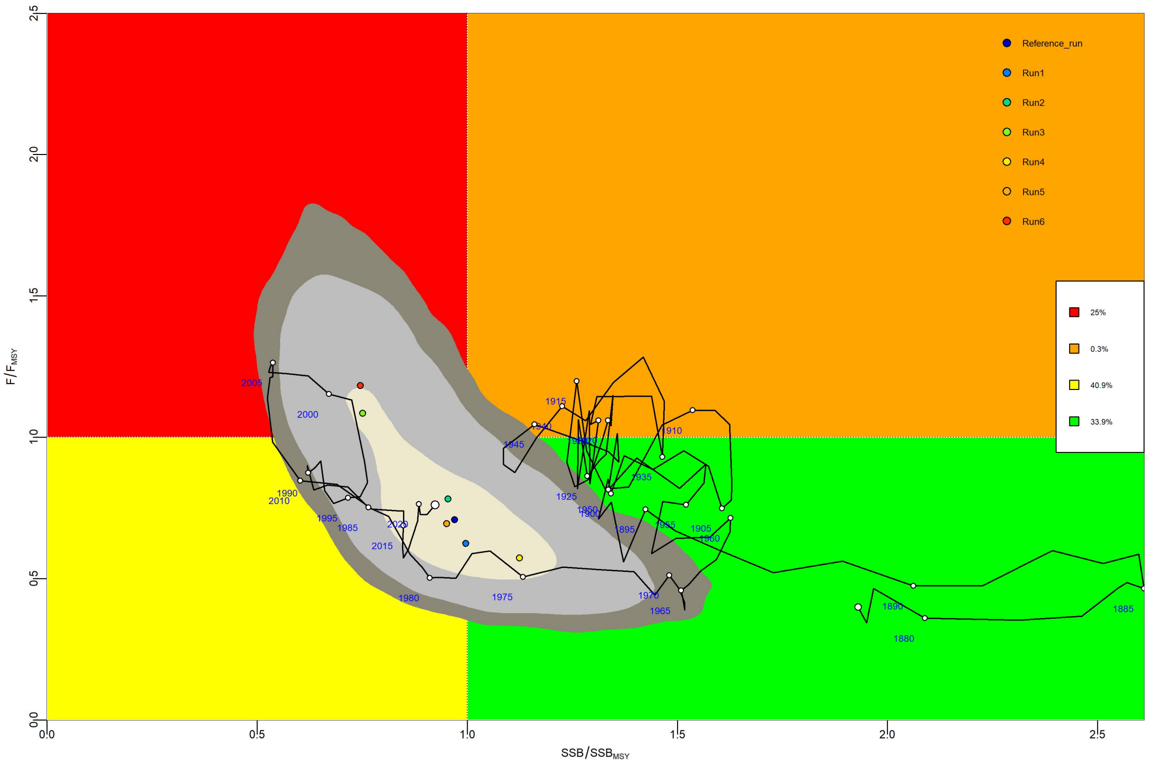


Figure 25: Ensamble kobe plot

```
Reference <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Reference_run",
    covar = T)
sigmaR <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/sigmaR0.6", covar = T)
Run2 <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Run2", covar = T)
Run7 <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Run7", covar = T)
Run8 <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Run8", covar = T)
Run9 <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Run9", covar = T)
Run10 <- SS_output("~/Max/Commitees/National stocks/Lobster 3a/Run10", covar = T)

#### Set the plotting directory
plotdir <- ("~/Max/Commitees/National stocks/Lobster 3a/Figures/")

mymodels <- list(Reference, sigmaR, Run2, Run7, Run8, Run9)
modelnames <- c("Reference", "sigmaR06", "High catches", "Recdev", "TVsel", "M_estimate",
    "ExtraQ_estimated")

# Create a summary of all models
mysummary <- SSsummarize(mymodels)

# Plot the models
SSplotComparisons(mysummary, legendlabels = modelnames, legendloc = "topleft", legendncol = 1,
    endyr = 2023, print = TRUE, plotdir = plotdir, densitynames = "none", uncertainty = TRUE)
```

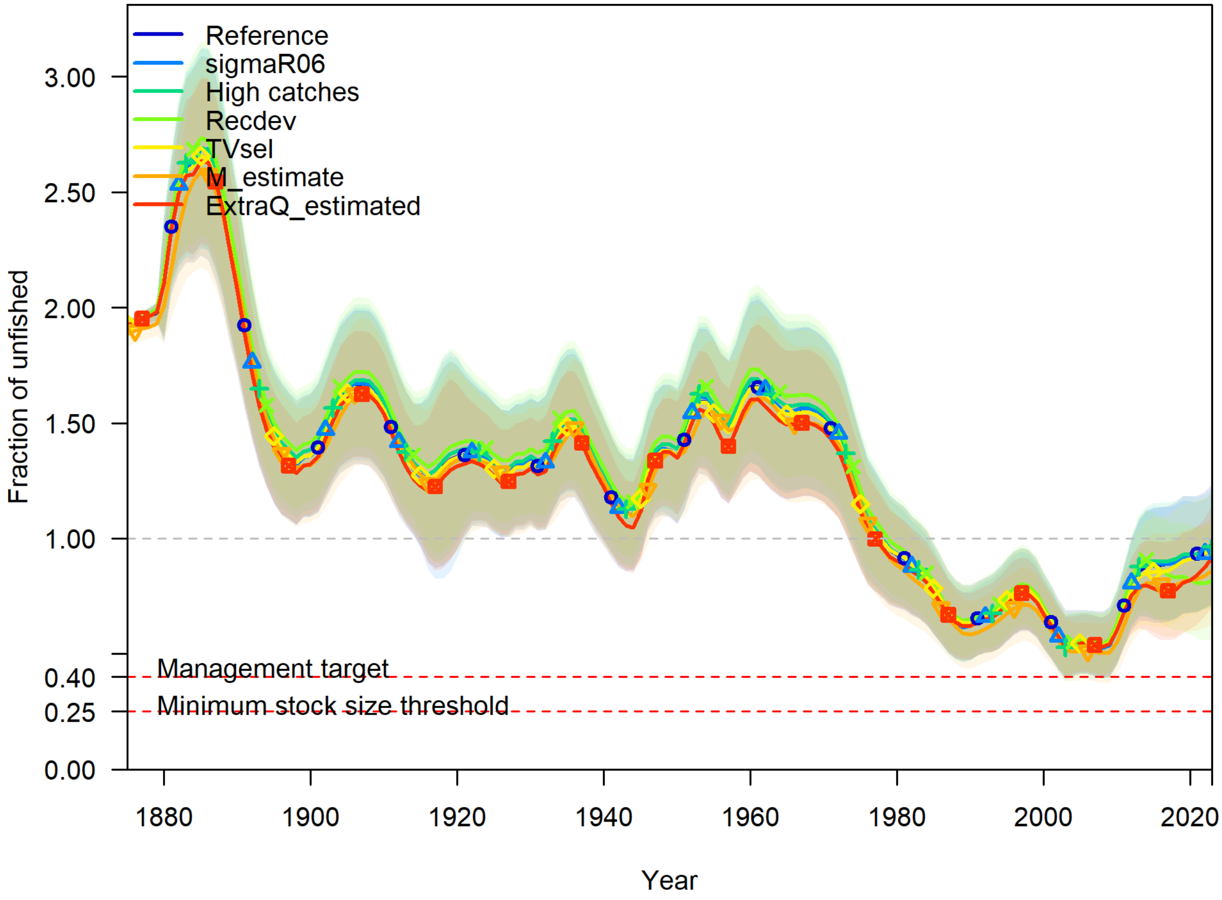


Figure 26: Comparison of alternative models