# Stock assessment of blue shark (*Prionace glauca)* in the Indian Ocean using Stock Synthesis.

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## Executive summary

This paper presents a stock assessment of blue shark in the Indian Ocean using Stock Synthesis (version 3.30.23.2 https://nmfs-ost.github.io/ss3-website/). The blue shark assessment model is an age structured (25 years), spatially aggregated (1 region) and two sex model. The catch, effort, and size composition of catch, are grouped into 8 fisheries covering the time period from 1950 through 2023. Six indices of abundance, all from longline fisheries were considered for this analysis. This assessment considered two alternative time series of total catch. The diagnostic case model is parameterized using indices of abundance all indices of abundance with the exception of the index from South Africa which showed a divergent trend from the other indices of abundance. The historical catch series used is considered to be one of the key sources of uncertainty and the Working Party requested that participants develop approaches to reconstructing historical catches to account for non reporting and reporting to an aggregate level (i.e. '*sharks-nei')* to be used as potential input for this assessment. Nominal reported catch of blue shark was revised in 2025 by some CPCs and this has altered the historical reported catch, which forms the basis for any estimation of any blue shark catch that is unreported or reported to an aggregate level. Estimates of catch generated via a generalized additive model were used based on the reported data as of 2024 with data for 2023 supplied by the 2025 nominal catch, as well as the 2025 nominal catch data. The revision of reported

Blue sharks are most often caught as bycatch in the Indian Ocean tuna fisheries, though some directed mixed species (sharks and tunas/billfish) fisheries do exist. Commercial reporting of landings has been minimal, as has information regarding the targeting and fate of blue sharks encountered in the fisheries. Useful data on catch and effort is mostly limited to recent years, and time series of historical catches are highly uncertain, and recently revised.

This analysis was developed as an assessment model that included the Portuguese, EU-France (Reunion) and Spain, and Japanese CPUE series, with the estimates of total catch based on generalized additive model based GAM series as the diagnostic case, from the estimates based on the revised 2025 nominal catch, as it is referred to in the main text when presenting the model parametrization and diagnostics. The upcoming 21st meeting of the Indian Ocean Tuna

Commission Working Party on Ecosystems and Bycatch (WPEB21) will recommend the final parameterization as a base case model for the provision of stock status. Initial analysis based on the sensitivity analysis done with SS3 indicated that the stock is not over fished nor experiencing overfishing. Though it should be noted that the historical catch series remains highly uncertain.

# Introduction

Blue shark (*Prionace glauca*) are a large pelagic species, broadly distributed throughout the Indian Ocean to a southern limit of ~50° S (Figure 1). Indian Ocean blue shark have been incidentally caught by the Japanese longline fleet since the early 1950s. The population was not heavily exploited before targeted fisheries (or bycatch rates increased) in the early 1990s. At this time the Taiwanese long line vessels began taking large numbers, initially in the SW region, followed by the other areas (Figure 1). The European longline fleet (predominantly Spanish vessels) also started a targeted fishery in the 1990s, while only small numbers are reported in the driftnet fisheries, and purse seine catches are very rare.

# 1 Methods

### Data

There are many different fleets catching blue shark in the Indian Ocean, with vastly different gear types and levels of data quality (Martin et. al. 2015). This model uses the same fishing fleet structure previously used (Rice 2021, Rice 2017, Rice and Sharma 2015), 8 fleets representing a wide variety of gears, some of which have been aggregated (e.g. F1 Miscellaneous). The number of CPUE series recommended by the WPEB data prep meeting is 6, all of which are based on longline fisheries. There is enough uncertainty about the selectivity assumptions with respect to time, and the low numbers of size composition data, that the size composition data are not expected to be very informative about year-class strength. Hence, in the assessment presented here, the length-composition data are down weighted so as to inform the selectivity but not alter the model fit to the abundance trend.

### Total catch

Reported catch has recently been revised and total catch estimates in both scale and trend are highly uncertain (Rice 2025, IOTC-2025-WPEB21(AS)-28). Estimates used for the diagnostic case by year and fishery, are in Figure 2. In the previous assessment (Rice 2021), estimates of total catch were produced based on generalized additive models (GAM) and the ratio of blue shark

(BSH) to total target catch. While the total catch data are estimates, they are derived in large part from the industrial fleets in the Indian Ocean and are thought to be more reasonable for blue shark than for the other shark species. The reader is cautioned that the basis for these catch estimates is the reported nominal catch, which was revised just prior to this assessment, which included the removal of some significant catch histories as well as the downscaling of others.

The major concern identified with respect to the catch time series are that catch-and-effort for BSH are highly incomplete. Reliable data are thought to be available for a limited number of years (i.e., from the late-1990s onwards) and for a very limited number of fisheries. In the 2015 assessment an alternative catch series was used based on trade based estimates using the proportion of tuna caught (Clarke, 2011). This series extends from 1981-2011, and was previously extended (both earlier and later) using a ratio based approach. This method used the average ratio of the nominal to trade based estimates from the years previous to 2011 to estimate the values for the years prior to 1981 and post 2011. Because of the uncertainty in the reported nominal catches introduced by using the average ratio, this method was not repeated for this analysis.

### 1.1 Relative abundance indices

Newly estimated CPUE series by Japan, Taiwan, Portugal, Spain, South Africa and EU France (Reunion) were used in this analysis (Figure 3). The standardized CPUE series from Portugal, Reunion and Spain in 2025 were similar to those from those previously submitted to the WPEB Figure 3 ( bottom panel). All of these are based on catch /bycatch in the longline fisheries. For further information consult the working papers.

### 1.2 Size composition data

As with the previous analysis sex based length-composition data collected by observers and from logsheets for the main fleets (Japan, Taiwan and Portugal) were used (Coelho et al 2017) along with additional length composition data submitted to the IOTC. In all, between 10 and 20 years of length composition data from the LL fleets were organized and used in the analysis. Some size and sex composition data of catch were available, but in many cases the data were in aggregated form covering several years, or size sampling was incomplete across fisheries. Many of the time series suffered from low sample sizes and inconsistencies across years. For this reason and because of the evidence that there was a conflict between the CPUE and the size data (see results below) lower weight was given to the size data in the model. This allowed the model to estimate selectivity, but did not allow the size data to dominate the estimates of abundance in the model. We assumed an annual effective sample size calculated as the square root of the overall (male and female) sample size. The annual sample size was then weighted (once) by the Francis (2011 and 2014) likelihood weighting method.

### 1.3 Software

The analysis was undertaken with Stock synthesis SS V3.30.23.02, Methot 2000, 2009, (executable available from https://nmfs-ost.github.io/ss3-website/). Typical function minimization of the fully disaggregated model on a 3.0 GHz personal computer required about 10 minutes. Additional simplifications and aggregations could probably reduce the minimization time further, without significant loss to the stock status inferences.

### 1.4 Model Assumptions

The most important model assumptions are described in the following sections. Standard population dynamics and statistical terms are described verbally, while equations can be found in Methot (2000, 2009). Attachment 1 is the template specification file for all of the models, and includes additional information on secondary elements of model formulation which may be omitted in the description below. All of the specification files are archived with the IOTC Secretariat. Table 2 lists the assumptions for the sensitivity runs.

### 1.5 Time Period

The model was iterated from 1950-2023 using an annual time-step, however, further analysis of seasonal processes is encouraged.

## 1.6 Biological inputs and assumptions

Blue sharks have an Indian Ocean wide distribution, and genetic evidence of distinct population structure within other oceans (e.g. Pacific) has not been found (Taguchi and Yokawa 2013), and hence was assumed to be homogenous here as well. Conventional tagging studies need to be examined in the Indian Ocean, but currently limited data exist, though some tagging effort in the Pacific shows limited movement to the western Australian EEZ. In addition to assumptions regarding stock structure, the other critical information on the biology of blue shark necessary for the stock synthesis assessment relates to sex-specific growth, natural mortality, maturity and fecundity.

## 1.7 Growth

The standard assumptions made concerning age and growth in the SS model are (i) the lengths-at-age are assumed to be normally distributed for each age-class; (ii) the mean lengths-at-age are assumed to follow a von Bertalanffy growth curve. For any specific model, it is necessary to assume the number of significant age-classes in the exploited population, with the last age-class being defined as a “plus group”, i.e. all fish of the designated age and older. For the results presented here, 30 yearly age-classes have been assumed, as age 30 approximates to the age at the theoretical maximum length of an average fish.

No attempt was made to estimate growth within the model due to the uninformative nature of the size data to track cohorts through time. This assessment uses sex specific growth curves based on data from the Indian Ocean (Jolly et al. 2013). A CV of 0.22 was used to model variation in length-at-age. All lengths reported from the assessment relate to fork length (FL).

## 1.8 Natural mortality

Sets of age and sex-specific natural mortality ogives were considered in the assessment based on the Peterson and Wroblewski (1984) method (Rice 2021) (Table2).

## 1.9 Maturity and fecundity

For the purpose of computing the spawning biomass, we assume a logistic maturity schedule based on length with the age-at-50% maturity for females equal to 145cm (Nakano and Seki

2003). There is no information which indicates that sex ratio differs from parity throughout the lifecycle of blue shark. Fecundity was fixed to an average of 25 pups per annual gestation period.

### 1.10 Population and fishery dynamics

The model partitions the population into 30 yearly age-classes in one region (Figure 1). The last age-class comprises a "plus group" in which mortality and other characteristics are assumed to be constant. The population is "monitored" in the model at yearly time steps, extending through a time window of 1950-2023. The main population dynamics processes are as follows: In this model "recruitment" is the appearance of age-class 1 fish (i.e. fish averaging approximately 50 cm in the population). The results presented in this report were derived using one recruitment episode per year, which is assumed to occur at the start of each year. Annual recruitment deviates from the recruitment relationship were estimated, but constrained reflecting the limited scope for compensation given estimates of fecundity. Deviations from the SRR were estimated in two parts (i) the early recruitment deviates for the 10 years prior to the model period which has the bulk of the length composition information (1960 -1970) and (ii) the main recruitment deviates that covered the model period (1971 - 2023).

There is no information which indicates that sex ratio differs from parity throughout the lifecycle of blue shark. In this assessment the term spawning biomass (SB) is a relative measure of spawning potential (the mature female population) and is a dimensionless term. It is not comparable to total biomass.

### 1.11 Initial population state

In the previous model it was assumed that the blue shark population was at an unfished state of equilibrium at the start of the model (1950) with the beginning of longline fishing occurring in the following years (at least from the 1950s onwards).

The population age structure and overall size in the first year is determined as a function of the estimate of the first years recruitment ($R_1$) offset from virgin recruitment ($R_0$), the initial 'equilibrium' fishing mortality discussed above, and the initial recruitment deviations.

### 1.12 Selectivity Curves

Selectivity is fishery-specific and was assumed to be time-invariant. A double-half normal functional form was assumed for all selectivity curves except the miscellaneous fishery which was set to a logistic. An offset on the peak and scale was estimated for sex-specific differences in selectivity that were evident in the data. The selectivity function location and scale were estimated for fleets 2, 3, 4, 6, 7 and 8 and the ascending and descending functions were fixed to a best fit when estimated independently. Only the location parameter was estimated for fleet 5 as the model failed to converge if the scale was also estimated.

### 1.13 Parameter estimation and uncertainty

Model parameters were estimated by maximizing the log-likelihoods of the data plus the log of the probability density functions of the priors, and the normalized sum of the recruitment deviates estimated in the model. For the catch and the CPUE series we assumed lognormal likelihood functions while a multinomial was assumed for the size data. The maximization was performed by an efficient optimization using exact numerical derivatives with respect to the model parameters (Fournier et al. 2012). Estimation was conducted in a series of phases, the first of which used arbitrary starting values for most parameters. The Hessian matrix computed at the mode of the posterior distribution was used to obtain estimates of the covariance matrix. This was used in combination with the Delta method to compute approximate confidence intervals for parameters of interest.

### 1.14 Profile Likelihood

An investigation of the information content in the data components was undertaken via the use of profile likelihood on the global scaling parameter (R0) (Lee et al 2014). The negative log likelihood of a specific parameter or data component should, in theory, decline to an obvious minimum. In situations where this does not happen, at least from one side, there may be insufficient information within the data to estimate other parameters. Virgin recruitment (R0) is an ideal scaling parameter because it is proportional to the unfished biomass. Profiles were run with the natural log of virgin recruitment, ln(R0), fixed at various values above and below the model estimated value; the corresponding likelihood profile quantified how much loss of fit was contributed by each data source. One of the primary uses of the likelihood profile is to identify conflicting data and provide a rationale for down weighting or excluding any data.

### 1.15 Hierarchical cluster analysis

A hierarchical cluster analysis (HCA) was used to identify groupings of CPUE series that represented similar, or same states of nature. The goal of this analysis was to develop a framework for identifying groupings of CPUE series that were similar, so that the model did not include trends that implied conflicting states of nature (i.e. increasing and decreasing). The methods were adapted from those recently implemented in an Atlantic shortfin mako assessment conducted by the International Commission for the Conservation of Atlantic Tunas (ICCAT 2017). As noted in the Atlantic shortfin mako assessment (ICCAT 2017), "it is not uncommon for CPUE indices to contain conflicting information. However, when CPUE indices are conflicting, including them in a single assessment (either explicitly or after combining them into a single index) tends to result in parameter estimates intermediate to what would be obtained from the data sets individually. Schnute and Hilborn (1993) showed the most likely parameter values are usually not intermediate but occur at one of the apparent extremes. Including conflicting indices in a stock assessment scenario may also result in residuals not being identically and independently distributed (IID) and so procedures such as the bootstrap cannot be used to estimate parameter uncertainty. Consequently, when CPUEs with conflicting information are identified, an alternative is to assume that indices reflect hypotheses about states of nature and to run scenarios for single or sets of indices that represent a common hypothesis."

The HCA used methods conducted in R using FLR (http://www.flr-project.org/). and the *diags* package. FLR provides a set of common methods for reading these data into R, plotting and summarizing them to assess the consistency in the CPUE trends. The CPUE time series along with a lowess smoother fitted to CPUE each year using a general additive model (GAM) to compare trends for the CPUEs. Hierarchical cluster analysis identified two groupings of time-series neither of which matched exactly the pervious groupings.

The first group was characterized by time-series which were lightly positively correlated with each other, EU-Reunion and EU Portugal. The second group was characterized by time-series which were less correlated with each other or were slightly negatively correlated with the CPUE series in other (positively correlated) group. This group was made up of Taiwan, South Africa, Japan and EU Spain. EU Spain was positively correlated with all of the other CPUE series except South Africa (see paper IOTC-2025-WPEB21(AS)-29 for further details). Because CPUEs with conflicting information were identified, it may be reasonable to assume that the indices reflect alternative hypotheses about states of nature and to run separate scenarios for each group. For this analysis it is recommended that we utilize the previous base case grouping that was defined by expert opinion as well as the groupings defined through the HCA.

### 1.16 Selection of a diagnostic case.

During the data prep meeting the WPEB noted that there are conflicting trends among some CPUE series and that the inclusion of conflicting data would result in a mis-specified model. This assessment follows uses all of the CPUE series with the exception of the South African series as a diagnostic case. With respect to the estimated catch history the WPEB data prep meeting noted that the available nominal catch data currently held in the IOTC database is likely a gross underestimate of the true catch, has recently been revised and would benefit from additional research regarding the catches of blue shark. Given that approximately one third of the total reported sharks in the IOTC database are non species specific reports (i.e. reported as “sharks”) it is reasonable to assume that some of these reports represent blue shark given that blue shark are among most commonly caught pelagic shark. Therefore the diagnostic case assumes that the GAM estimated catches from Data Set 3 (IOTC-2025-WPEB21(AS)-28 ) are appropriate catch estimates, however additional research is needed with respect to the catches, as IOTC members are currently revising their catch history.

Sensitivity trials were run using the other CPUE time series and combinations of CPUE. Sensitivities to the base case CPUE series groupings were run for those groups identified in Table 3. Groupings of CPUE series will be chosen by the WPEB which will seek to use the results of the HCA as well as expert opinion to extend the spatial extent and the temporal coverage of the CPUE series groupings. Initial groupings of CPUE series used in this report are

- All Indices_ZAF_ALT
- Indx_PRT_REU
- Indx_PRT_REU_ZAF
- Indx_TWN_SPN_JPN
- Indx_TWN_SPN_JPN_ZAF

In addition to the CPUE series groupings additional parametrizations of steepness (values of 0.75 and 0.8) and along with weight at age based on Zhu et al 2023, and the growth equation from Andrade et al 2019.

## 1.17 Benchmark and Reference Point Methods

Benchmarks included estimates of absolute population levels and fishing mortality for the terminal year, 2019 ($F_{2023}$, $SSB_{2023}$, $B_{2023}$). These values are reported against reference points relative to MSY levels.

## 1.18 Other Model Considerations

As explained above the length composition annual sample sizes were re-weighted by the Francis (2011) likelihood weighting method. The minimum average CV associated with the indices of abundance length likelihoods were re-weighting based on the Francis (2014) method. The life history and biology in the model are treated as constants, these parameters, along with the catch inputs influence the plausible range of population dynamics in the model.

### 1.19 Diagnostics and additional model runs

Additional model diagnostics which were carried out include expanded analysis on the residual and hierarchal cluster analysis, runs tests and joint residual plots, likelihood profiles, and hindcasting cross-validation.

## 2 Results

In this section we focus on the results from the diagnostic case model and the key results and diagnostics for this model. We then comment on any important differences in both outputs and model diagnostics for the sensitivity analyses, and present all results. The assessment model was implemented in Stock Synthesis version 3.30.23.02 (SS3 Methot 2013). A newer version of the model is available (version 3.30.24) but due to time constraints and the overall similarity of the model versions for the features implemented in this assessment the executable was not updated. Stock Synthesis 3 was implemented here as a length-based age-structured stock assessment model (Methot and Wetzel 2013; e.g., Wetzel and Punt 2011a, 2011b). Stock synthesis utilizes an integrated modeling approach (Maunder and Punt 2013) to take advantage of the many data sources available for the Indian Ocean stock of blue shark (*Prionace glauca*). An advantage of the integrated modeling approach is that the development of statistical methods that combine several sources of information into a single analysis allows for consistency in assumptions and permits the uncertainty associated with each data source to be propagated to final model outputs (Maunder and Punt 2013).

### 2.1 Diagnostic case model

The diagnostic case model choice is described in above. The choice of model parameters and data inputs reflected the input of the WPEB 21 data prep meeting and the available updated data for biology and life history. This will be further refined by input at the WPEB assessment meeting.

***Model Fits to Abundance Indices***

The model was able to fit the general trends of the indices of abundance (Figure 10). Although the CPUE series S1 and S3 had periodic increases in the CPUE that the model was unable to fit, especially S1, which had a high terminal year estimate. As a result, the model fitted the central tendency of each series, which for S2 the Japanese series was a slight increase in the early 1990 until 1999, after which a slight decline and levelling off is evident. The fits to S3 the Portuguese series and S7 Reunion show a modest and slight decline, respectively, throughout. The model interpreted these trends by predicting a decreasing total biomass through time. The spawning output was estimated to increase slightly in the late 1990s to the early 2000s followed by a period of decline coincident with the increase in catch (Figure 2) and decline in the CPUE series.

### Fits to the Length composition

The differences estimated in the sex-specific selectivity curves for many of the fisheries reinforce the observations of biologists for areas of sex-segregation during the life history of blue sharks (Figure 12). With the exception of the Japanese longline fishery; all fisheries where sex specific selectivity could be estimated resulted in a lower peak selectivity (therefore catchability) for females.

The overall fit to the length data was generally good (Figure 13). Fleet specific annual length samples were often quite different, i.e. left skewed one year and bimodal the next, which accounts for the small amount of misfit in the aggregated samples. When attempting to estimate selectivity curves for fisheries with sex specific patterns the model often did not converge, therefore the sex specific offsets were fixed. Pearson residuals of the fit to the length compositions were small – on the order of 2 to -2 and did not show any temporal trend (Figures 14-15).

### *Stock-recruitment Parameters*

The predicted virgin recruitment (R0; number of age 0 pups) was approximately 2,014,000 animals and the number of estimated pups was relatively constant from the early 1960 through the early 1980s, after which estimated recruitment slowly declined, and then experienced large fluctuations from 1990-2019 (Figure 16). The bias correction estimated in the model is shown in Figure 17. The corresponding estimated stock recruitment relationship and annual deviations are also shown in Figure 18.

### *Fishing Mortality*

Estimated $F/F_{MSY}$ and fleet-specific instantaneous fishing mortality rates are presented in Figures 19 and 20 respectively. Fishing mortality was relatively low from the 1950 to the mid 1990s, which is in accordance with low catches and effort during that period. In the late 1990s fishing mortality increased with the advent of F1 the Miscellaneous fishery, this fishery is comprised mostly of coastal longline (>98%), with trolling, sport and artisanal fisheries contributing small percentages of the catch. Starting in the late-1990s overall fishing mortality began to increase sharply, with large fluctuations in the individual fisheries contribution to the overall fishing mortality. The overall fishing mortality has been below $F_{MSY}$ (i.e. overfishing is not occurring) for the entire time series, however, in recent years the confidence intervals have included values greater than one.

### *Estimated stock status and other quantities*

The estimated equilibrium yield curve for the diagnostic case model is shown in Figure 21. The estimated MSY is predicted to occur at 34% of the unfished biomass (Figure 21), which is less than the standard Schaefer production model ($0.5B_0$). The diagnostic case model estimates that the total biomass of the stock was at approximately 100% of the unfished level at the start of the model period (Figure 11) and steadily decreased to an estimate of $SB_{2023}/SB_{MSY} = 2.5$ that corresponds with $F_{2023}/F_{MSY} = 0.16$. Recruitment is fairly well estimated throughout the model, though with large standard errors (Figure 8), with recent recruitment estimated to be lower than the implied stock recruitment curve due to deviations implied by the length data. The estimates of recruitment were quite tightly constrained to the stock recruitment curve for the initial period of the model when there was no length information to inform the model. The main trends in the population dynamics can be explained through the estimated fishing mortality which was greatly increased in the 1990s and early 2000s due to the increase in catch (Figures 19 and 20). These changes in fishing mortality correspond to an overall stock status that is headed from a virgin state to the direction of overfished and overfishing (Figure 22).

### Model Uncertainty

Stock status uncertainty was evaluated delta-Multivariate lognormal (MVLN)approximation to generate joint error distributions for $SSB_{2023}/SSB_{MSY}$ and $F_{2023}/F_{MSY}$. Figure 22 shows the estimated stock status based on the MVLN analysis for the base case model and Figure 23 shows the estimated timeseries based on the MVLN approximation. Figure 24 shows the distribution of the MLE estimates of $SSB_{2023}/SSB_{MSY}$ and $F_{2023}/F_{MSY}$.

Stock synthesis provides estimates of the MSY-related quantities and these and other quantities of interest for management are provided in Table 4. We note that the IOTC has not yet adopted target or limit reference points for any shark species, so a suite of MSY-related quantities are presented.

### *Retrospective Analysis*

As part of an analysis of model structure, retrospective analysis (sequentially deleting 1 year of data from the end of the model and re-running) was run using the base case formulation (the Portuguese, Japanese late and Reunion series and the GAM estimated catches). The estimates of spawning depletion remain very similar across all the retrospective model runs considered (Figure 25) indicating that the changes in estimates of virgin spawning biomass are based on the total catch (Figure 25 right panel). The last retrospective run (-5 years) estimated a more depleted stock that corresponds to a slightly smaller virgin recruitment (Figure 25 right panel), this is associated with higher estimated total fishing mortalities in the last 4 years. In general the retrospective analysis shows no large departures from the estimated scale, depletion, or overall trend based on the sequential deletion of the last 5 years of data.

## 2.2 Other model diagnostics

Annex 1 shows the results of the expanded analysis on the residuals runs tests joint residual plots, likelihood profiles, age structured production model and hindcasting cross-validation are presented in Annex 1. Select details from Annex 1 are repeated here, the reader is encouraged to read Annex 1 in its entirety. Additionally the control file used for the diagnostic case model is shown in Annex 2.

The runs test indicated that the Japanese CPUE and length data did contain some patterns in the residuals, indicating a trend in the departure from the expected values the (Figures A7 and A8) the cause of this was the early time period in which the index had high contrast and little data. The joint residual plots (Figure A6) shows that in the latter part of the time series the model fits the Japanese data fairly well.

An age structured production model (ASPM) can help evaluate whether the catch and CPUE data give evidence for a production function within the model (Carvalho 2017). Overall the ASPM evaluates whether the effect of surplus production and observed catches alone could explain trends in the CPUE, in contrast to a more complex model (i.e. SS3) that incorporates annual recruitment deviations to improve the fit (Carvalho et al 2021). Maunder and Piner (2017) note that if the ASPM fits well to the indices of abundance with contrast the production function is likely to drive the stock dynamics and the indices will provide information about absolute abundance (Minte-Vera et al., 2017). Figure A13 shows that the biomass trajectories for both models (ASPM and the diagnostic) follow the same trend and that the estimates of *LN(R0)* are comparable. The fits to the indices are shown in Figure A14 and indicate an overall good fit, indicating that the information content in the data is sufficient.

# 3 Conclusion

Although most pelagic sharks can be considered data poor when compared to targeted tuna and other teleosts, the information for blue shark in the Indian Ocean is relatively abundant because they one of are the most commonly caught pelagic shark. Although blue shark lack the traditional fisheries statistics such as landings and historic catch rates (CPUE series), blue shark have been caught in mixed target fisheries for at least the last two decades. The resulting CPUE series from these fisheries are concentrated in the most recent decade, and all come from fishery dependent longline sources. An issue of concern regarding the indices of relative abundance, is that many of them show inter-annual variability that is not compatible with the life history of the species, suggesting that the methods used to standardize the indices did not include all factors to help track relative abundance or that the spatial scope of sampling is too limited to allow for precise inference about stock-wide trends. In addition, the changes in the CPUE series from the previous assessment to this assessment have resulted in series with lower contrast which may be less informative than the previous CPUE trends.

Recent work has led to similar estimates with respect to age, growth, reproduction and the associated life history characteristics. As such the range of variation investigated in the previous assessment was not undertaken for this study. The parameterization of the model reflected the best available estimates. Changes to the biology and life history inputs were minor with respect to the last assessment.

The results of the assessment are compared across different groupings of CPUE series and show the diagnostic case parameterization resulting in estimates of $SB_{2023}/SB_{MSY}=2.6$ and $F_{2023}/F_{MSY} = 0.16$ Stock status is reported in relation to MSY based reference points however the authors note that the IOTC has not yet adopted reference points for sharks.

The main conclusions of this assessment are:

- The estimates of catch are highly influential in the model, but mostly in terms of scale, as the current depletion and fishing mortality indicators are approximately equal across almost all alternative catch estimates for a given CPUE series.
- The scale of the assessment is influenced by the CPUE series chosen, and the catch.
- The reported nominal catch, which is the basis of the estimated total catch has recently been revised, and is currently under revision – this means that the results of this assessment will likely change

The main drivers of this assessment are the trend in the catch and CPUE series. In particular the large increase in recent years of catch has different interpretations (within the model), based on whether the CPUE series is variable or decreasing. Recommended studies that would improve future analyses are:

- Develop appropriate length inputs for all fleet.
- Further investigation of CPUE series and their representativeness.
- Develop region specific biological inputs.
- Further work on developing catch histories.

- Undertake collaborative study of blue shark CPUE from multiple Indian Ocean longline fleets

## 4 Acknowledgements

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# 6 Tables

**Table 1. Fishery definitions for the Indian Ocean Assessment**

| Fleet/ Survey Number and Short Name | Gear(s) | Selectivity |
|---|---|---|
| F1 MISC | Costal longline, trolling, sport and artisanal fisheries | Fixed logistic |
| F2 GILL | Gillnet Fisheries | Estimated double normal |
| F3 OTHER_LL | All longline fishery other than Japan, TWN, China, Korea, Portugal and Spain. | Estimated double normal |
| F4 JPN_LL | Japanese longline fishery | Estimated double normal |
| F5 KOR_LL | Korean longline fishery | Estimated double normal |
| F6 PRT_LL | Taiwanese longline fishery | Estimated double normal |
| F7 TWN_LL | Portuguese longline fishery | Estimated double normal |
| F8 ESP_LL | Spanish longline fishery | Estimated double normal |
| S2 JPN_LATE | Japan late years longline CPUE | NA |
| S3 POR | Portugal longline CPUE | NA |
| S4 ESP | Spain longline CPUE | NA |
| S5 TWN | Taiwanese longline CPUE | NA |
| S7 REU | EU-Reunion longline CPUE | NA |
| S8 ZAF | South African EEZ Longline | NA |

**Table 2: Estimates of age-specific natural mortality used in the assessment. The diagnostic case used those based on the approach of Peterson and Wroblewski (1984) method and estimates of growth from Andrade et al 2019.**

| Age | Female | Male |
|---|---|---|
| 0 | 0.453 | 0.453 |
| 1 | 0.288 | 0.277 |
| 2 | 0.222 | 0.212 |
| 3 | 0.187 | 0.179 |
| 4 | 0.165 | 0.158 |
| 5 | 0.15 | 0.144 |
| 6 | 0.139 | 0.134 |
| 7 | 0.131 | 0.126 |
| 8 | 0.124 | 0.121 |
| 9 | 0.119 | 0.116 |
| 10 | 0.115 | 0.113 |
| 11 | 0.112 | 0.11 |
| 12 | 0.109 | 0.107 |
| 13 | 0.107 | 0.105 |
| 14 | 0.105 | 0.104 |
| 15 | 0.103 | 0.102 |
| 16 | 0.102 | 0.101 |
| 17 | 0.101 | 0.1 |
| 18 | 0.1 | 0.1 |
| 19 | 0.099 | 0.099 |
| 20 | 0.098 | 0.098 |
| 21 | 0.098 | 0.098 |
| 22 | 0.097 | 0.097 |
| 23 | 0.097 | 0.097 |
| 24 | 0.096 | 0.097 |
| 25 | 0.096 | 0.097 |
| 26 | 0.095 | 0.096 |
| 27 | 0.095 | 0.096 |
| 28 | 0.095 | 0.096 |
| 29 | 0.095 | 0.096 |
| 30 | 0.095 | 0.096 |

**Table 3. Summary of SS3 specification options for the Indian Ocean blue shark assessment models. Other assumptions were constant for all models the bold text indicates the diagnostic case configuration.**

- **CPUE Groupings**
  - PrevCPUE_JPN_POR_REU,
  - All Indices,
  - LOO_JPN,
  - LOO_POR,
  - LOO_ESP,
  - LOO_TWN,
  - **LOO_ZAF**,
  - LOO_REU,
  - All Indices_ZAF_ALT,
  - Indx_PRT_REU
  - Indx_PRT_REU_ZAF,
  - Indx_TWN_SPN_JPN,
  - Indx_TWN_SPN_JPN_ZAF

- **Steepness**
  - H=0.75
  - **H=0.8**
  - H=0.85

- **Length at Maturity**
  - **Jolly et al. 2013**
  - Zhu et al. 2023

- **Growth**
  - **Jolly et al. 2013**
  - Andrade et al. 2019
- **Catch Estimates**
  - Data Set 1 GAM
  - **Data Set 3 GAM**

**Table 4: Management related quantities for the diagnostic model (in the grey shaded rows) and sensitivity runs.**

| | Quantitiy | | | |
|---|---|---|---|---|
| Model Run | F/Fmsy | SSB/SSBmsy | SSB_2023 | Recr_2023 |
| LOO_ZAF | 0.160 | 2.546 | 74,353 | 1,626 |
| PrevCPUE_JPN_POR_REU | 0.166 | 2.526 | 66,309 | 1,426 |
| All Indices | 0.265 | 2.469 | 41,196 | 894 |
| LOO_JPN | 0.309 | 2.294 | 37,662 | 888 |
| LOO_POR | 0.281 | 2.368 | 41,271 | 947 |
| LOO_ESP | 0.284 | 2.359 | 40,820 | 940 |
| LOO_TWN | 0.293 | 2.323 | 39,520 | 922 |
| LOO_REU | 0.287 | 2.344 | 40,227 | 931 |
| All Indices_ZAF_ALT | 14.704 | 0.200 | 1,624 | 225 |
| Indx_PRT_REU | 0.340 | 1.864 | 34,881 | 1,006 |
| Indx_PRT_REU_ZAF | 0.321 | 2.262 | 36,229 | 865 |
| Indx_TWN_SPN_JPN | 0.155 | 2.593 | 76,293 | 1,640 |
| Indx_TWN_SPN_JPN_ZAF | 0.265 | 2.475 | 41,171 | 891 |
| H=0.75 | 0.142 | 2.566 | 86,713 | 1,802 |
| H=0.85 | 0.124 | 2.834 | 80,612 | 1,704 |
| Mturity_Zhu_2023 | 0.144 | 2.848 | 58,733 | 1,778 |
| Andrade_2019 | 0.088 | 2.880 | 130,839 | 2,575 |
| Catch Data Set 1 GAM | 0.142 | 2.566 | 86,713 | 1,802 |

# 7 Figures

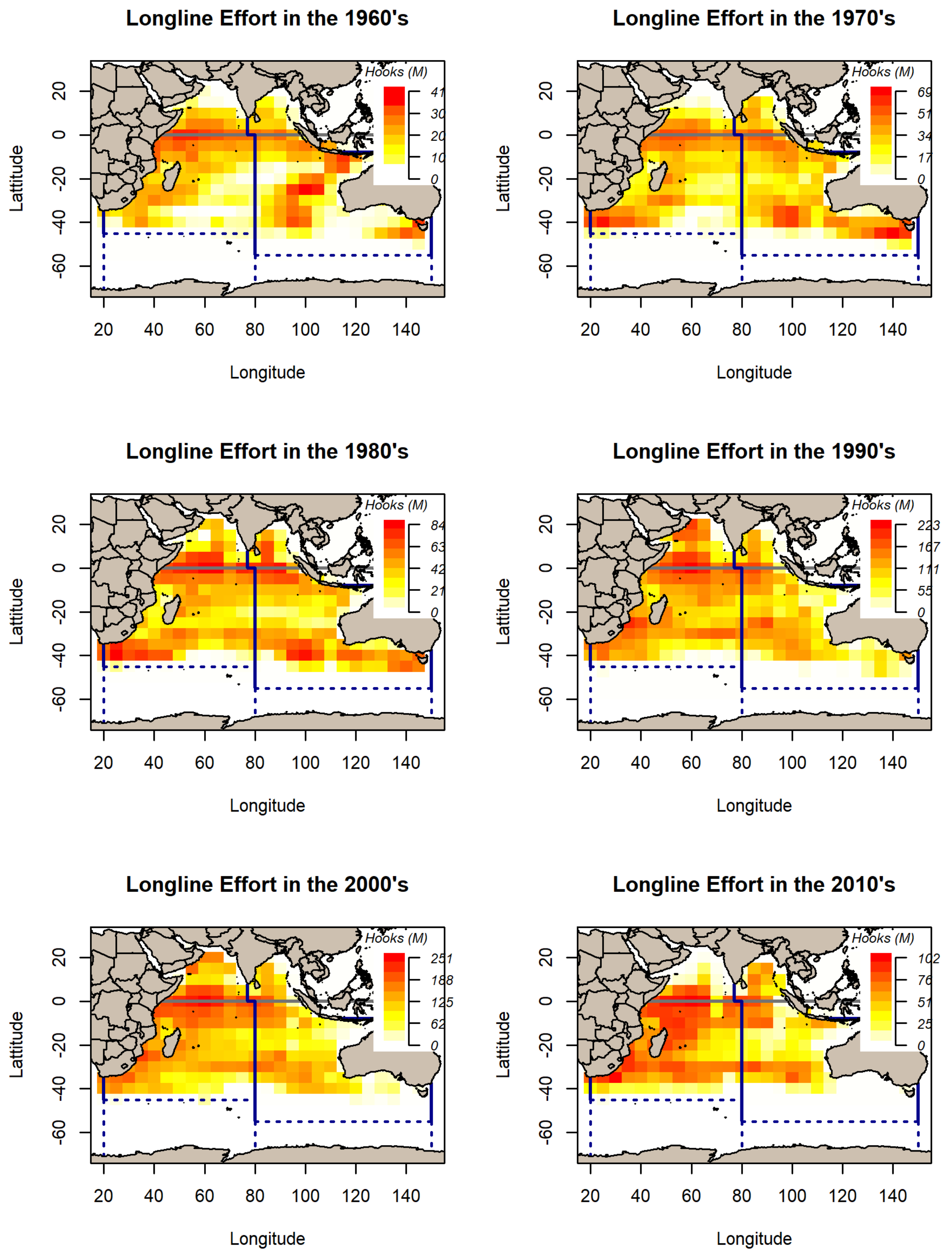


**Figure 1. Study area and reported longline effort by decade 1960s-2010s. The darker colors indicate higher effort (in millions of hooks), note the scale varies by decade.**

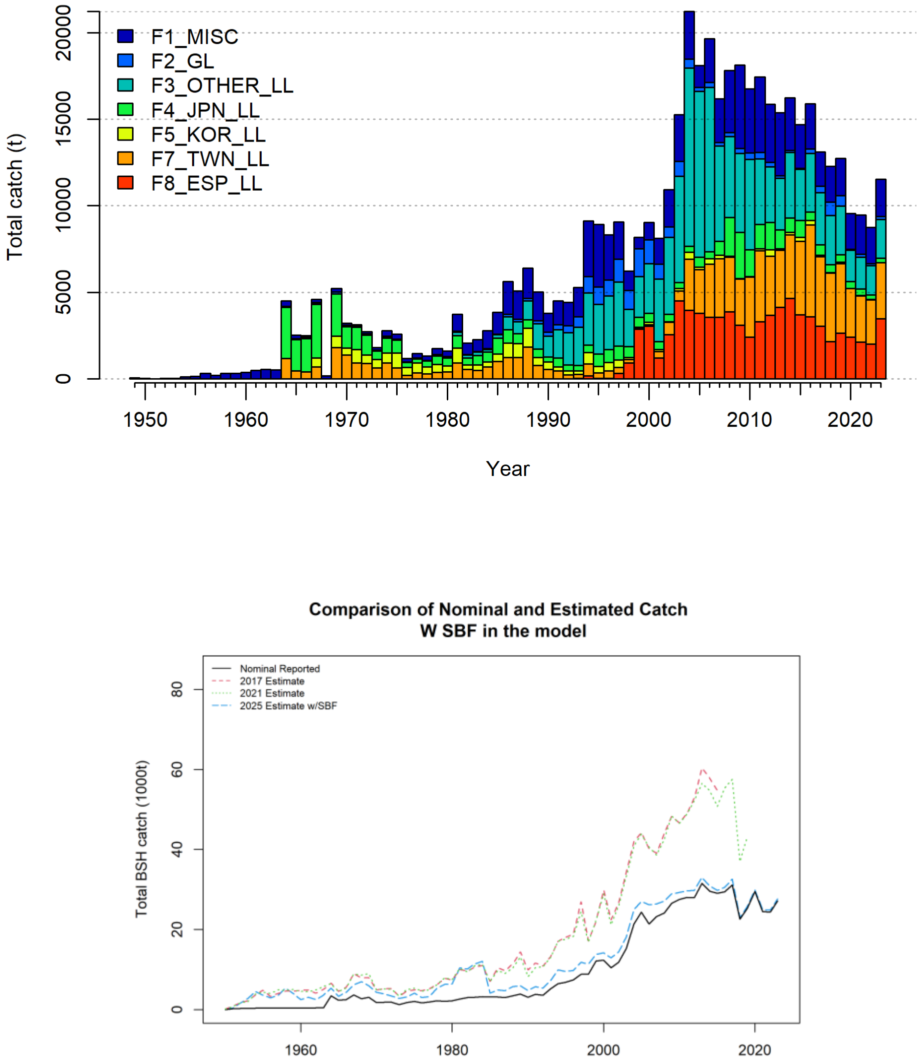


**Figure 2 Estimated total blue shark catch in mass by fishery over time for the Indian Ocean based on the GAM estimates of catch (top panel). Comparison of the 2017, 2021 and 2025 estimated catch, and the nominal catch(bottom panel).**

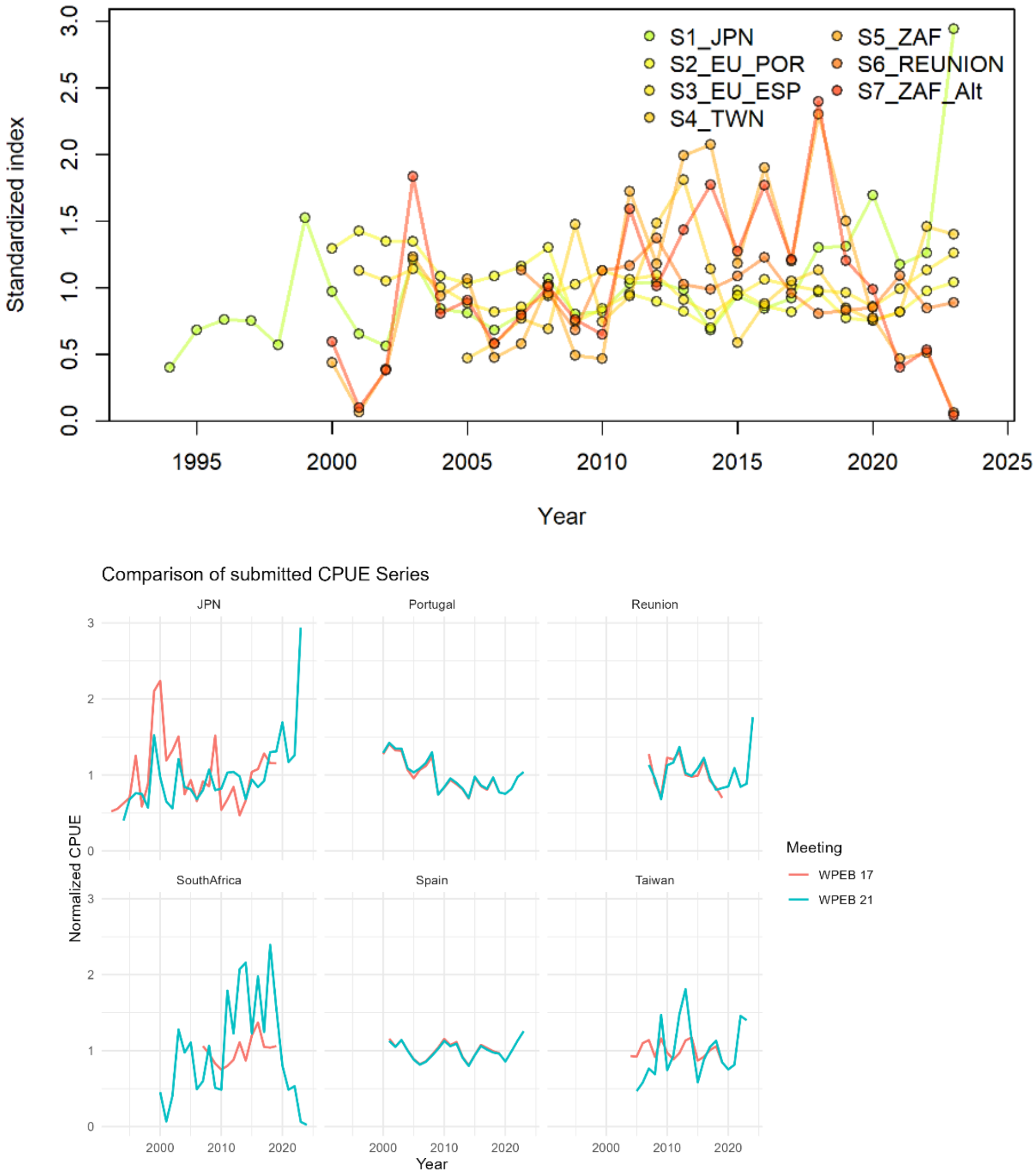


**Figure 3. Standardized CPUE for Japanese, Portuguese, Taiwanese ,Spanish, South African, and EU Reunion longline fleets based on papers submitted to WPEB-21. All series have been rescaled by their mean so that they are visually comparable for relevant periods of overlap(top panel. Comparison of the previous and current CPUE Series (bottom panel) .**

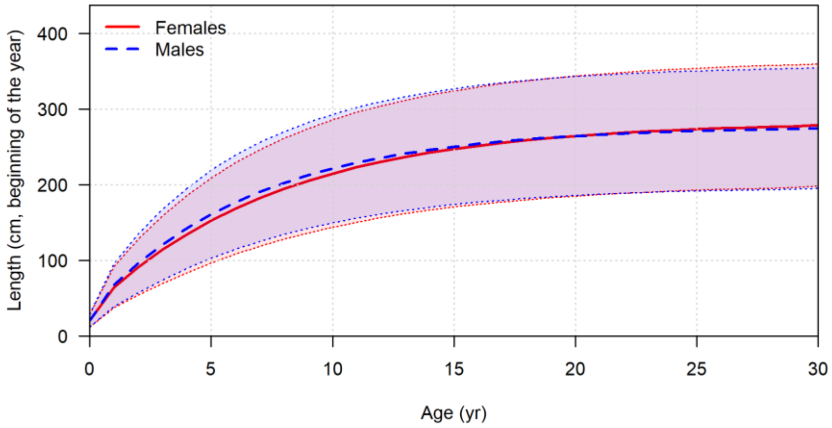


**Figure 4. Sex-specific growth curves (from Coelho et al 2017) calculated based on blue sharks in the Indian Ocean.**

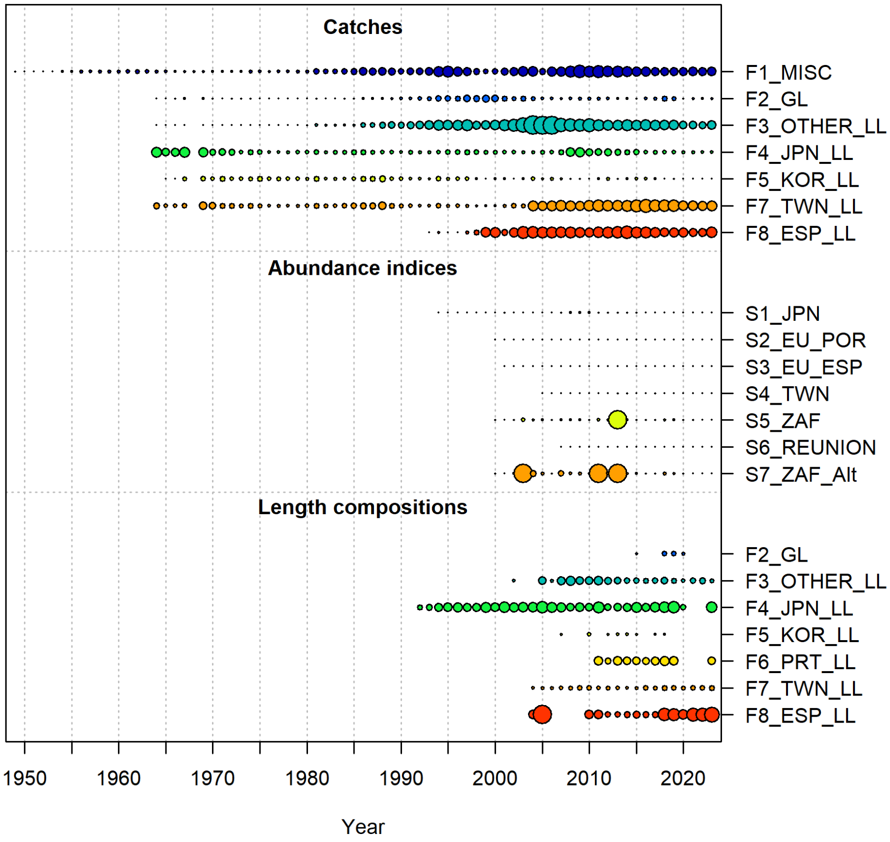


**Figure 5: Temporal data coverage for the diagnostic case model for the assessment of blue sharks in the Indian Ocean.**

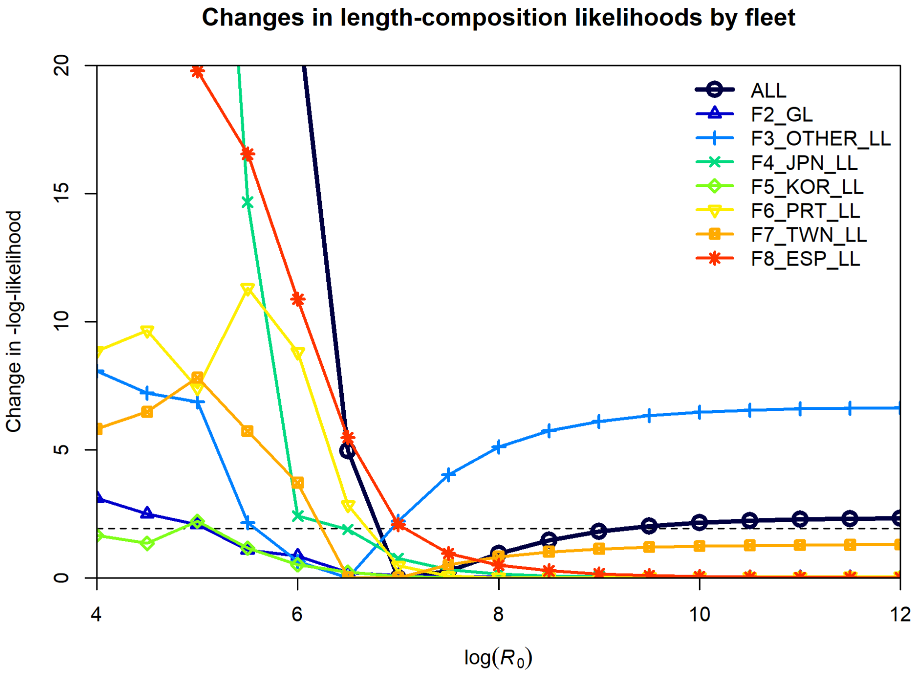


**Figure 6: Likelihood profiles for length composition, the bottom panel is a close up version of the top..**

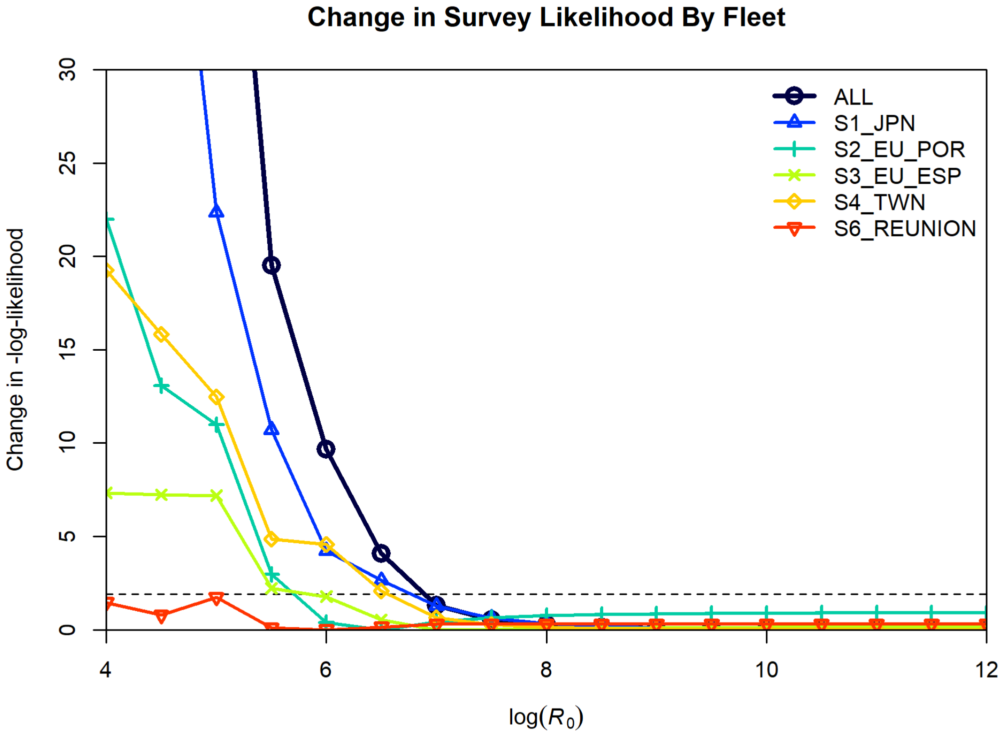


**Figure 7**: Likelihood profiles for the CPUE components for the reference run.

**Figure 8** Likelihood profile for the total likelihood, based on the diagnostic run.

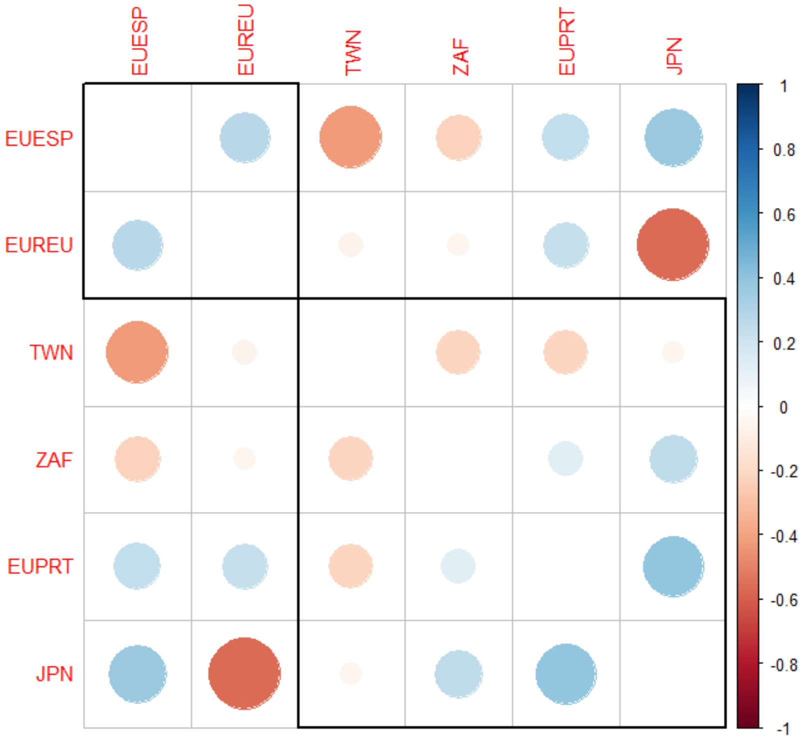


**Figure 9.** Correlation matrix for CPUE indices available for the Indian Ocean blue shark. Blue indicates positive and red negative correlations. The order of the indices and the rectangular boxes are chosen based on a hierarchical cluster analysis using a set of dissimilarities.

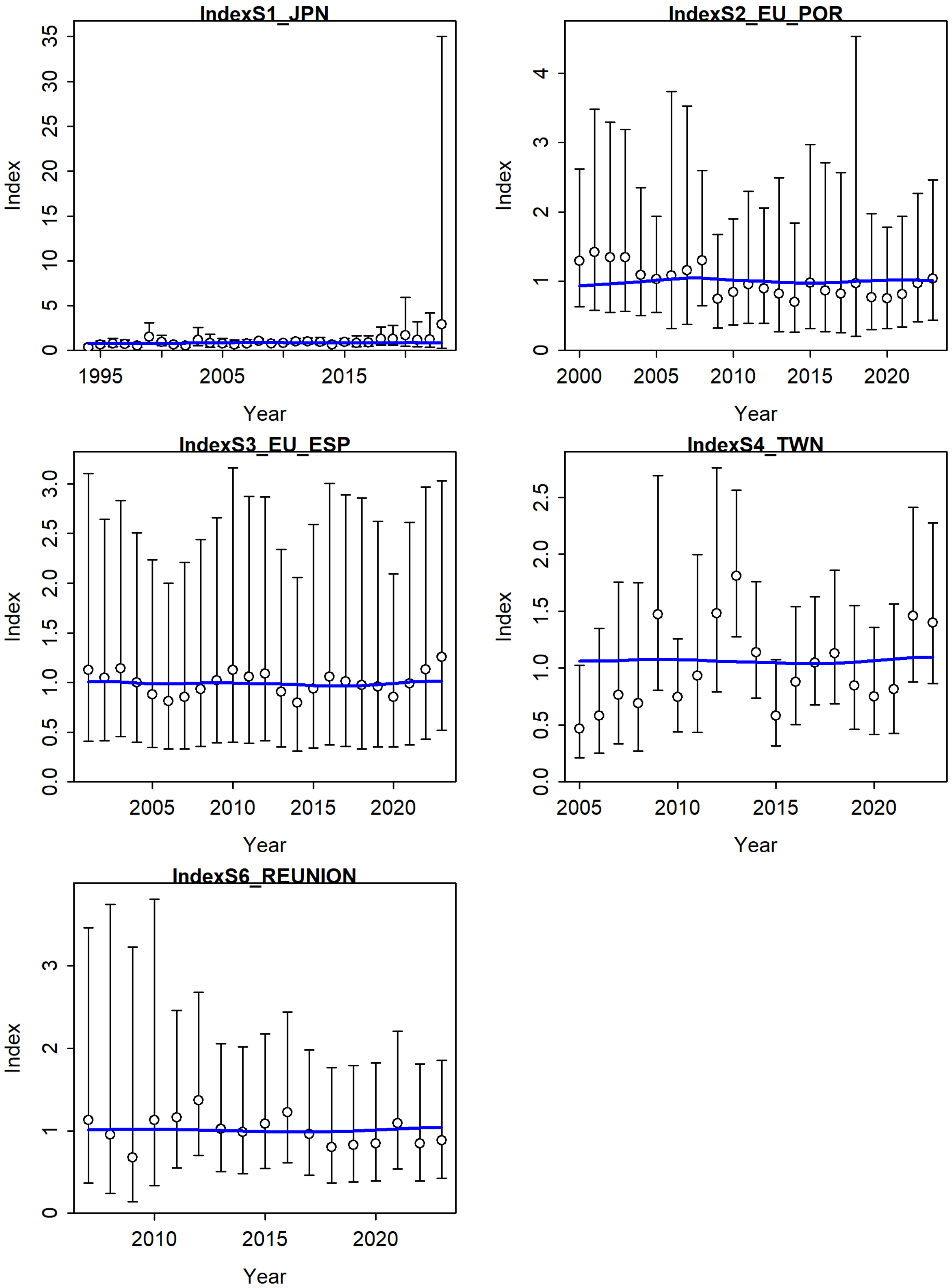


**Figure 10: Diagnostic case fit to the CPUE series, presented on a log scale. The top left panel is the Japanese late series (S2) the top right is the Portuguese series (S3) and the bottom is S7 Reunion.**

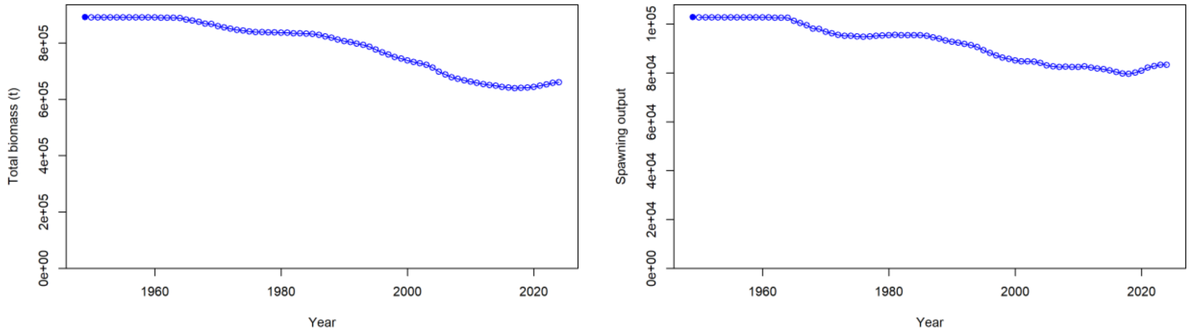


**Figure 11: Total biomass (left) and spawning potential (output) for the diagnostic case parameterization model. The filled dot represents the pre-model estimate of unfished biomass.**

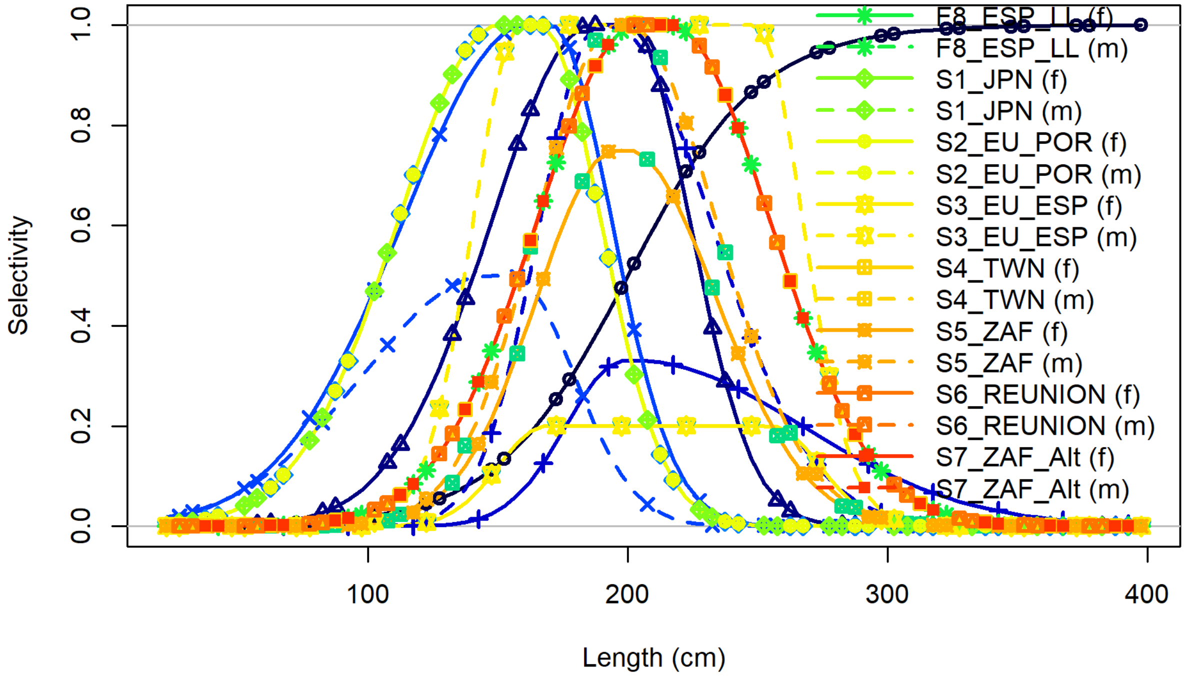


**Figure 12: Selectivity curves estimated for female and male from the diagnostic case model for the assessment of blue sharks in the Indian Ocean.**

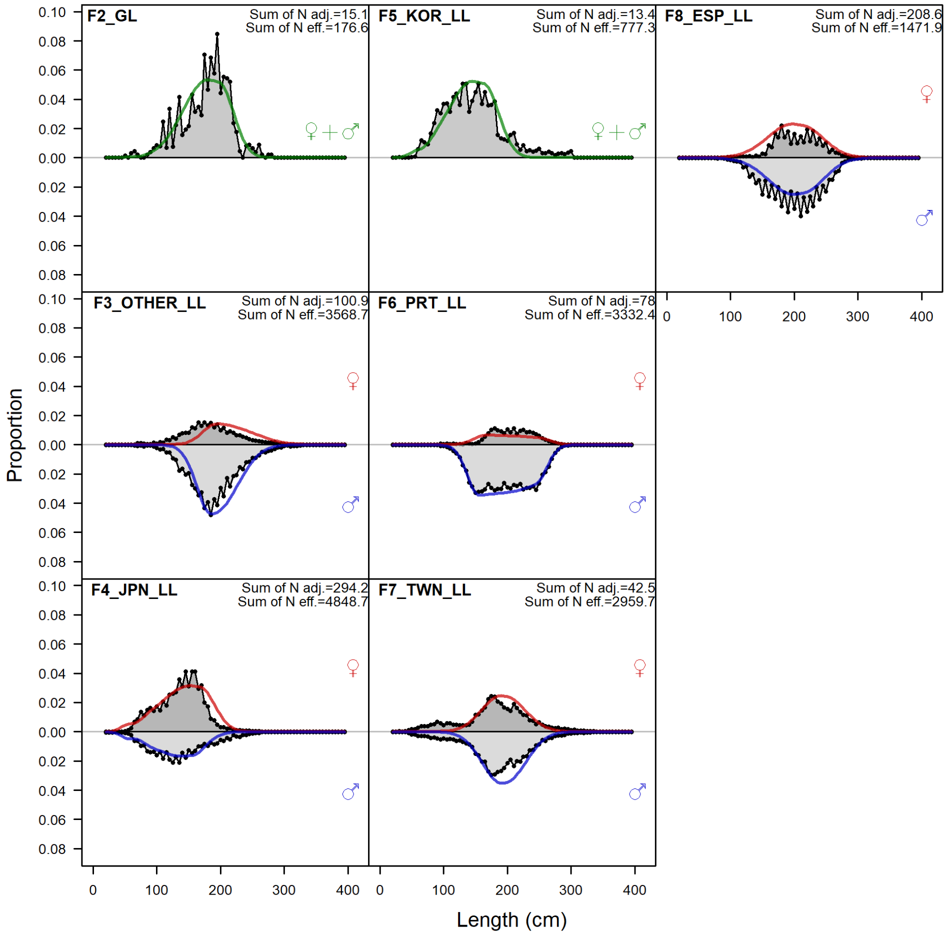


**Figure 13. Fits to the length frequency data for the diagnostic case model for the assessment of blue sharks in the Indian Ocean.**

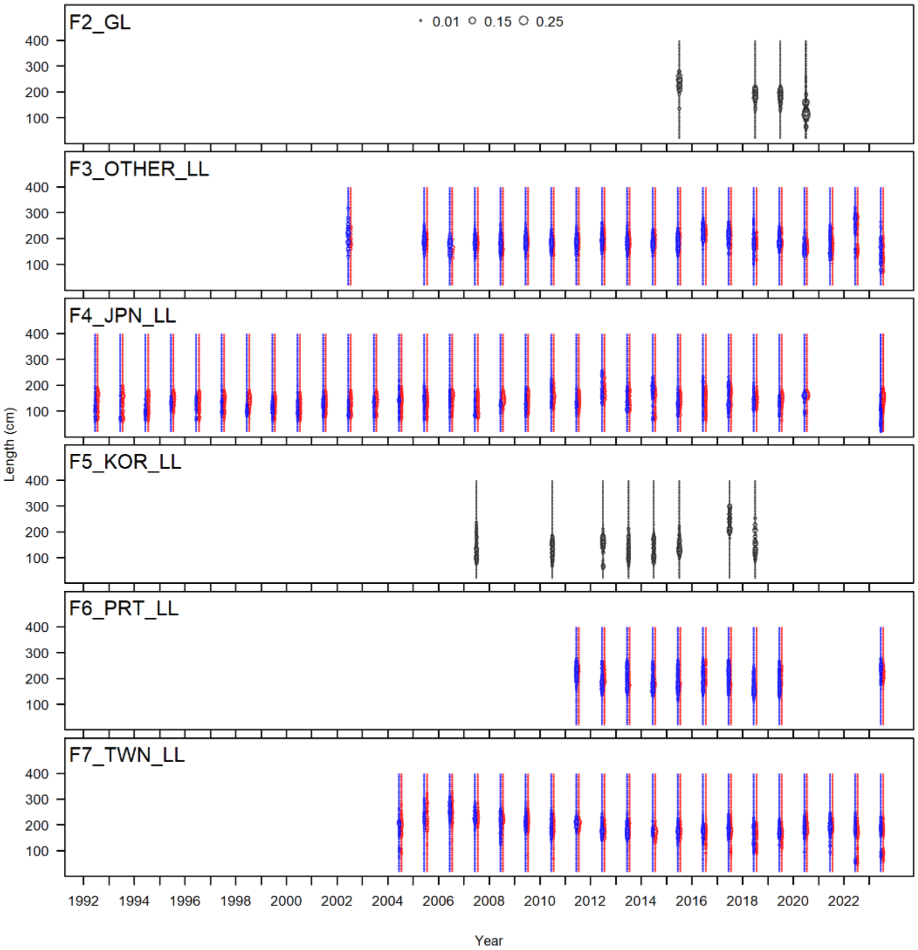


**Figure 14. Residuals from the fits to the length frequency data for the diagnostic case model for the assessment of blue sharks in the Indian Ocean, Fleets 2-5. combined sex length data is shown in black, female length data in red and male length data in blue. Closed bubbles are positive residuals and open bubbles are negative residuals, bubble sizes are scaled to maximum within each panel. Thus, comparisons across panels should focus on patterns, not bubble sizes**

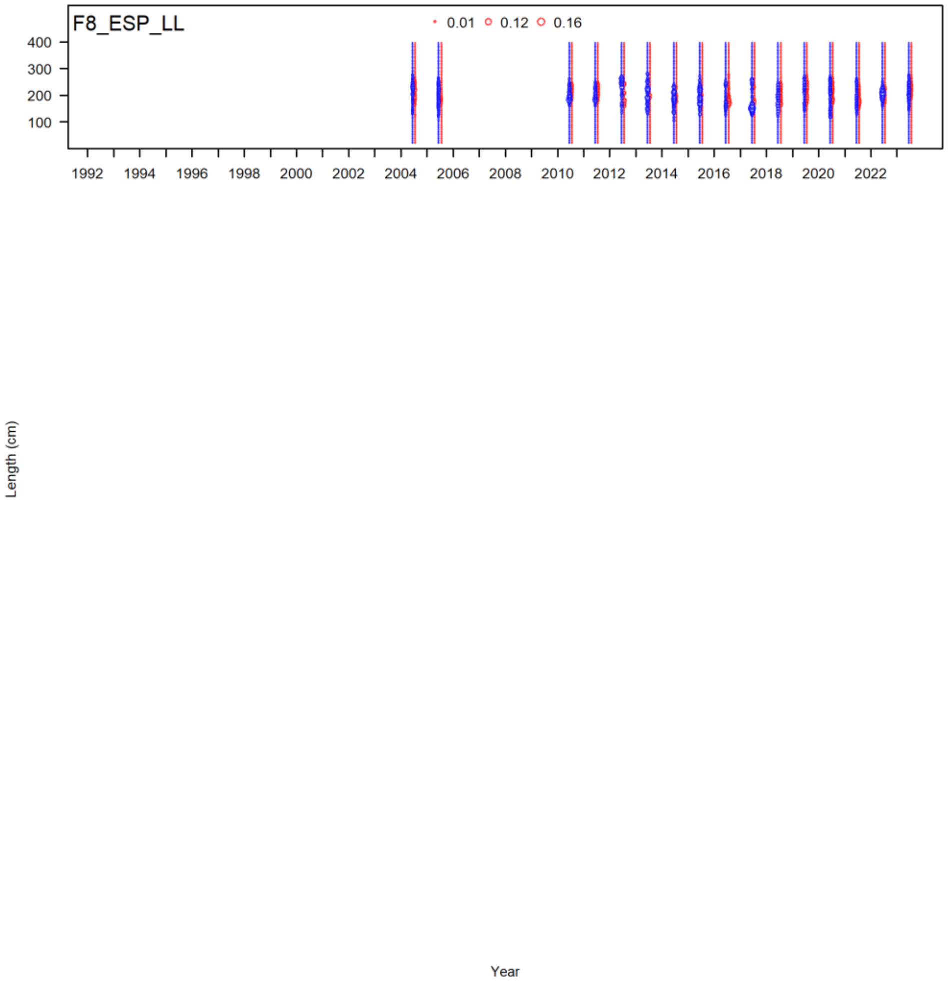


**Figure 15 Residuals from the fit to the length frequency data for the diagnostic case model for the assessment of blue sharks in the Indian Ocean, Fleets. Combined sex length data is shown in black, female length data in red and male length data in blue. Closed bubbles are positive residuals and open bubbles are negative residuals, bubble sizes are scaled to maximum within each panel. Thus, comparisons across panels should focus on patterns, not bubble sizes.**

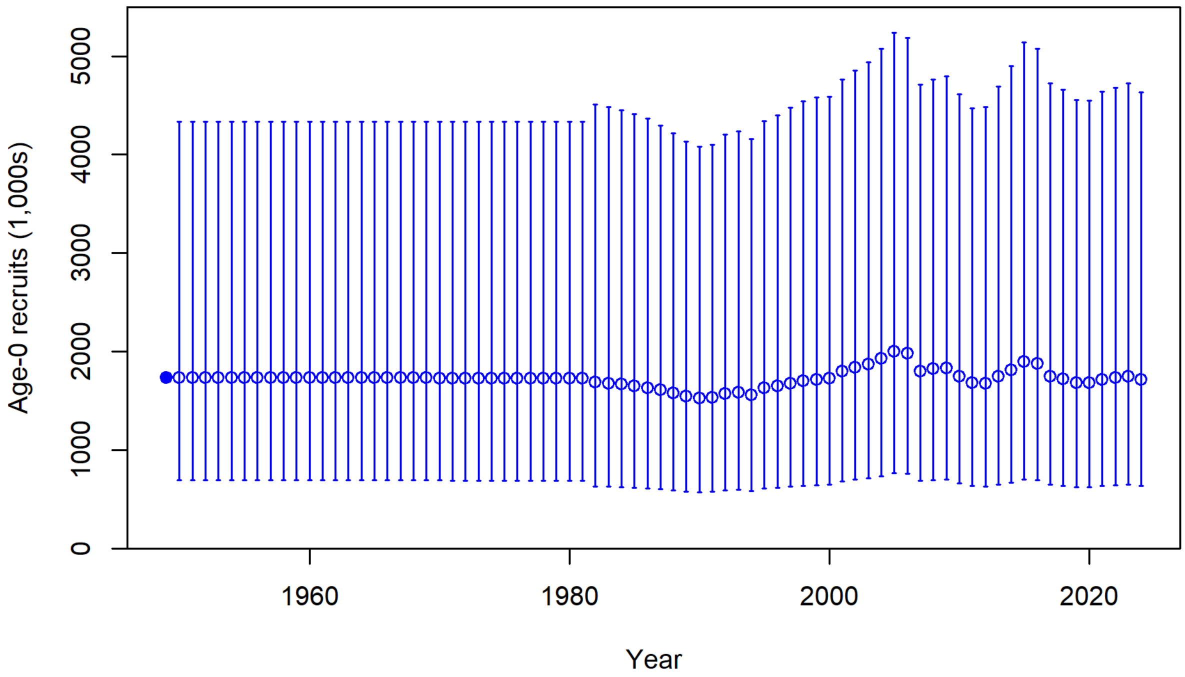


**Figure 16 .Estimated recruitment including the estimate of virgin recruitment (filled circle at the start of the time series) for the diagnostic case model for the assessment of blue sharks in the Indian Ocean.**

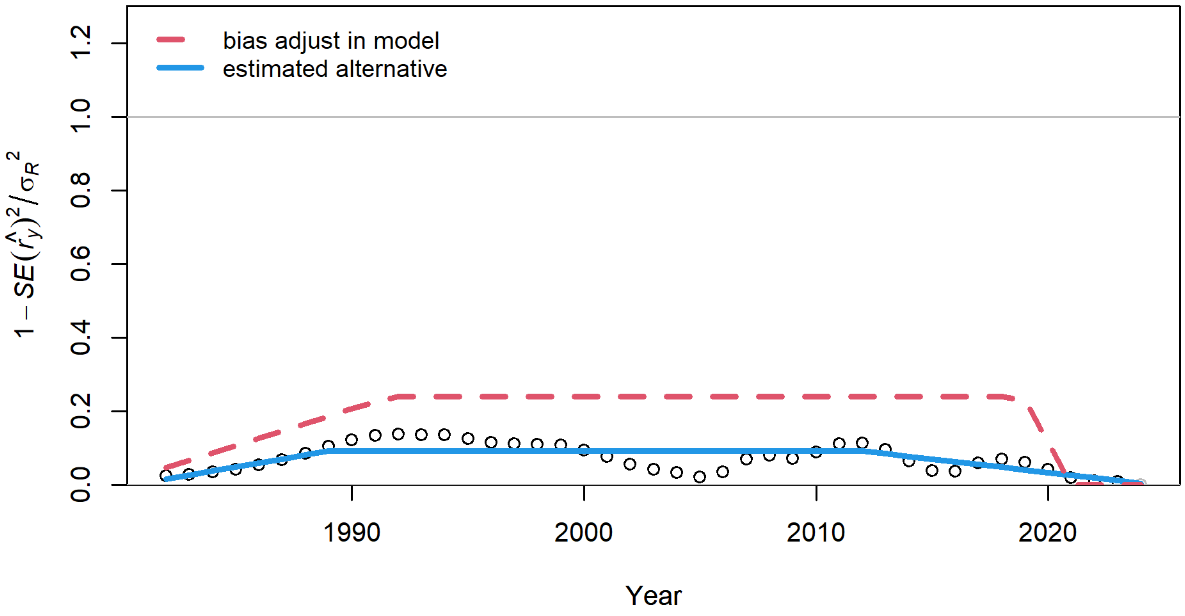


**Figure 17 .Estimated bias adjustment in the model.**

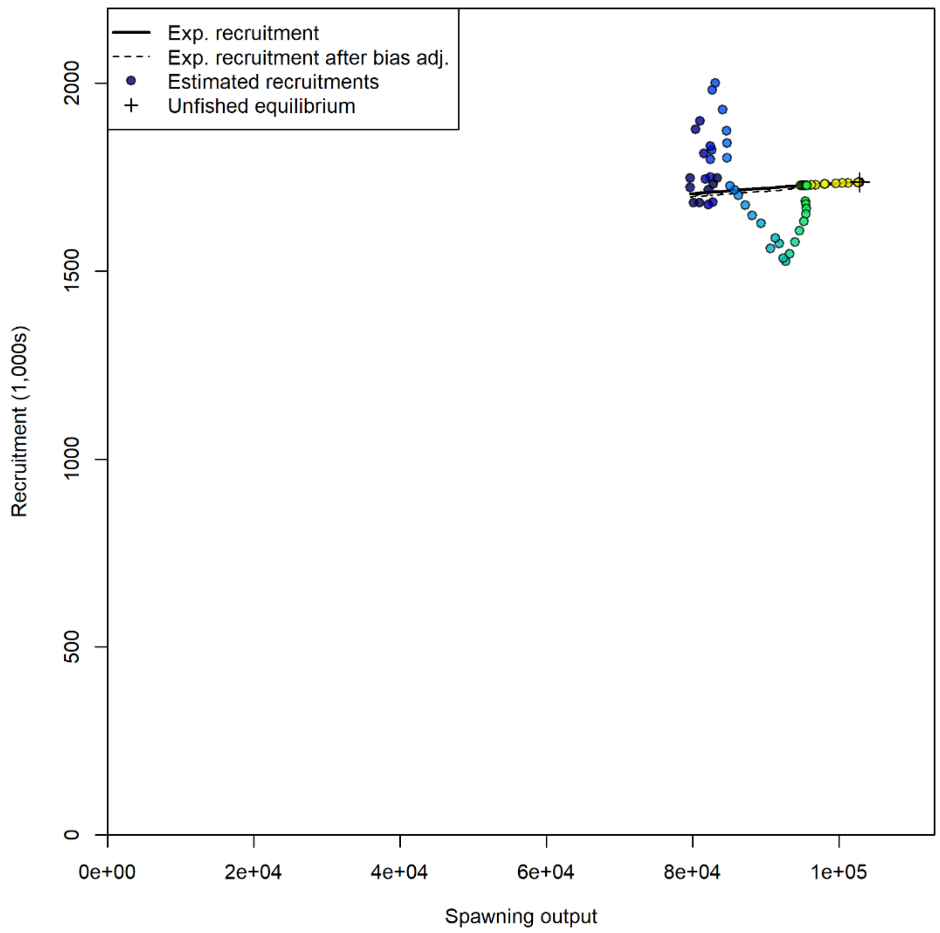


**Figure 18 Stock recruitment curve used in the assessment and time series of estimates of recruitment deviations (colored points).**

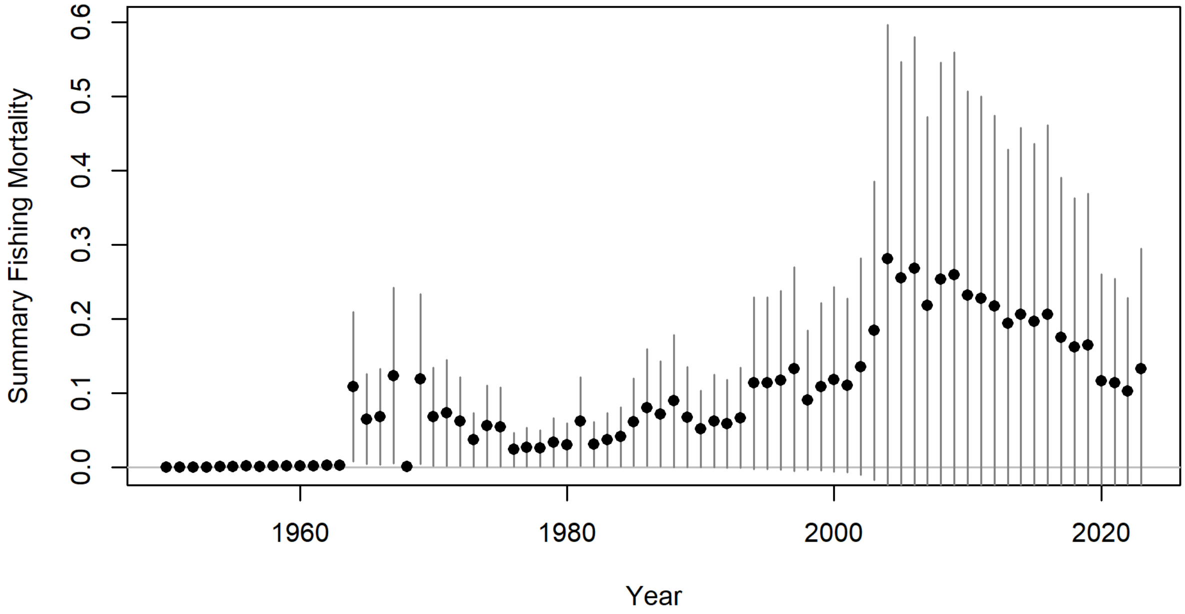


**Figure 19 Estimated total fishing mortality/FMSY**.

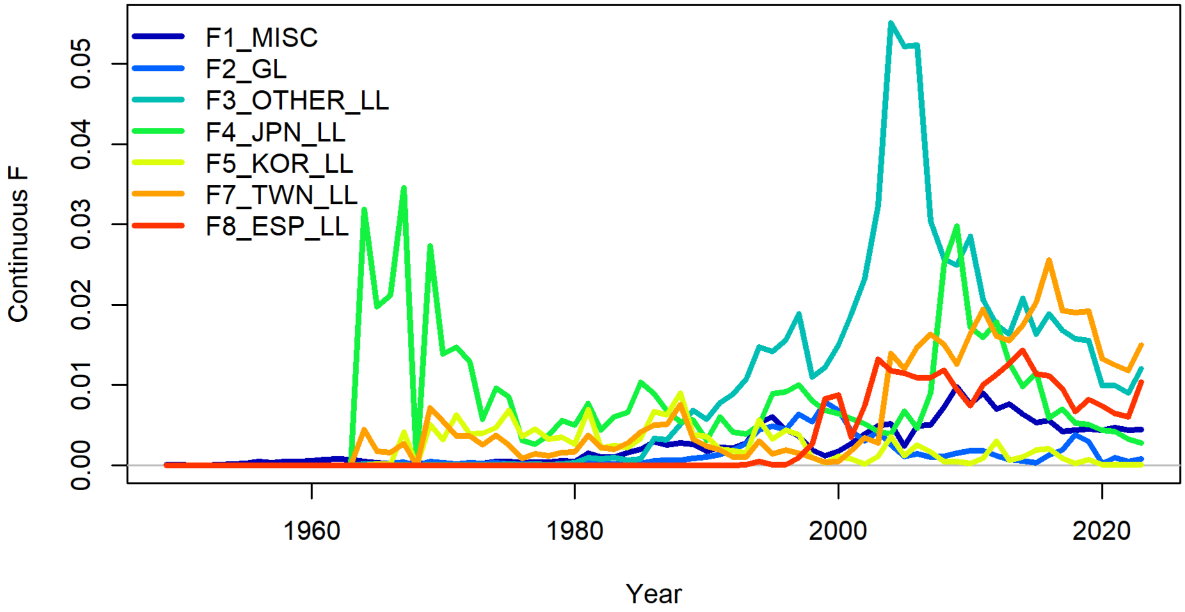


**Figure 20. Estimated fleet specific fishing mortality by year for the base case model configuration.**

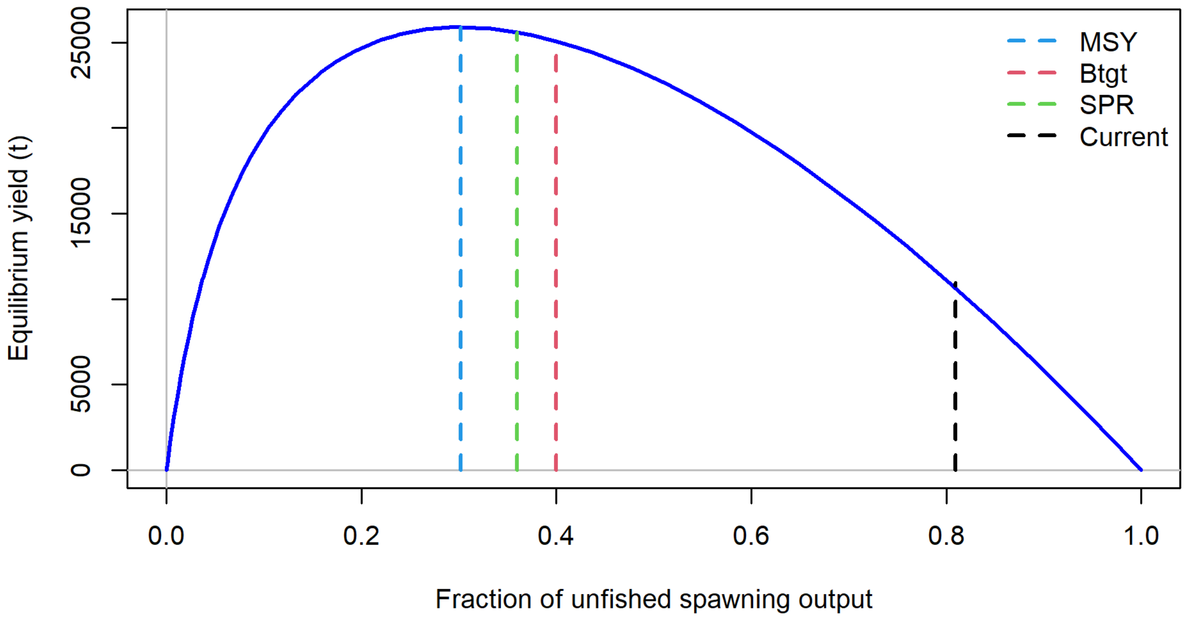


**Figure 21. Equilibrium yield curve for the diagnostic case model for the assessment of blue sharks in the Indian Ocean.**

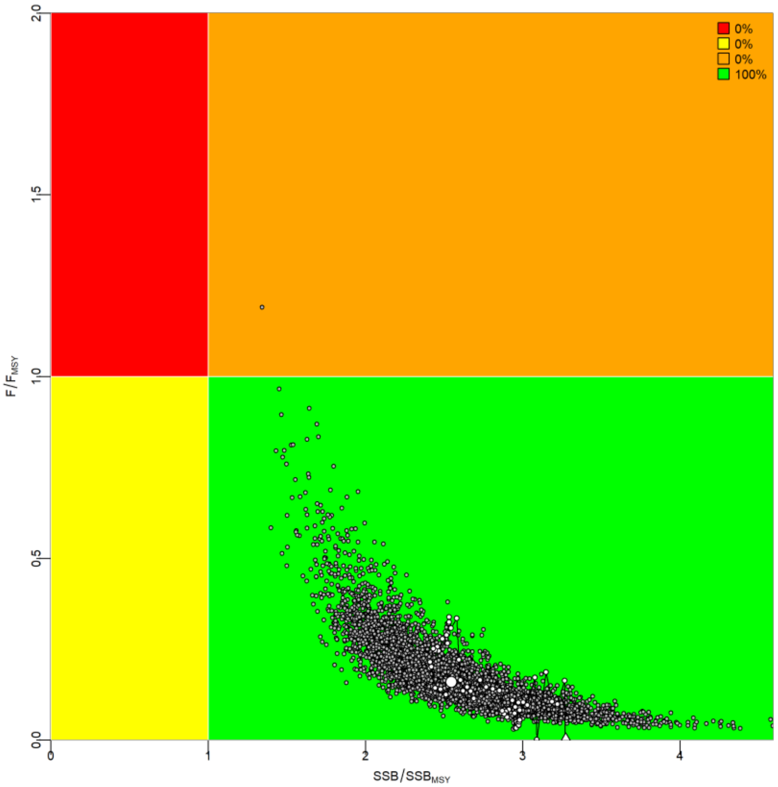


**Figure 22. Kobe plot of the annual stock status**

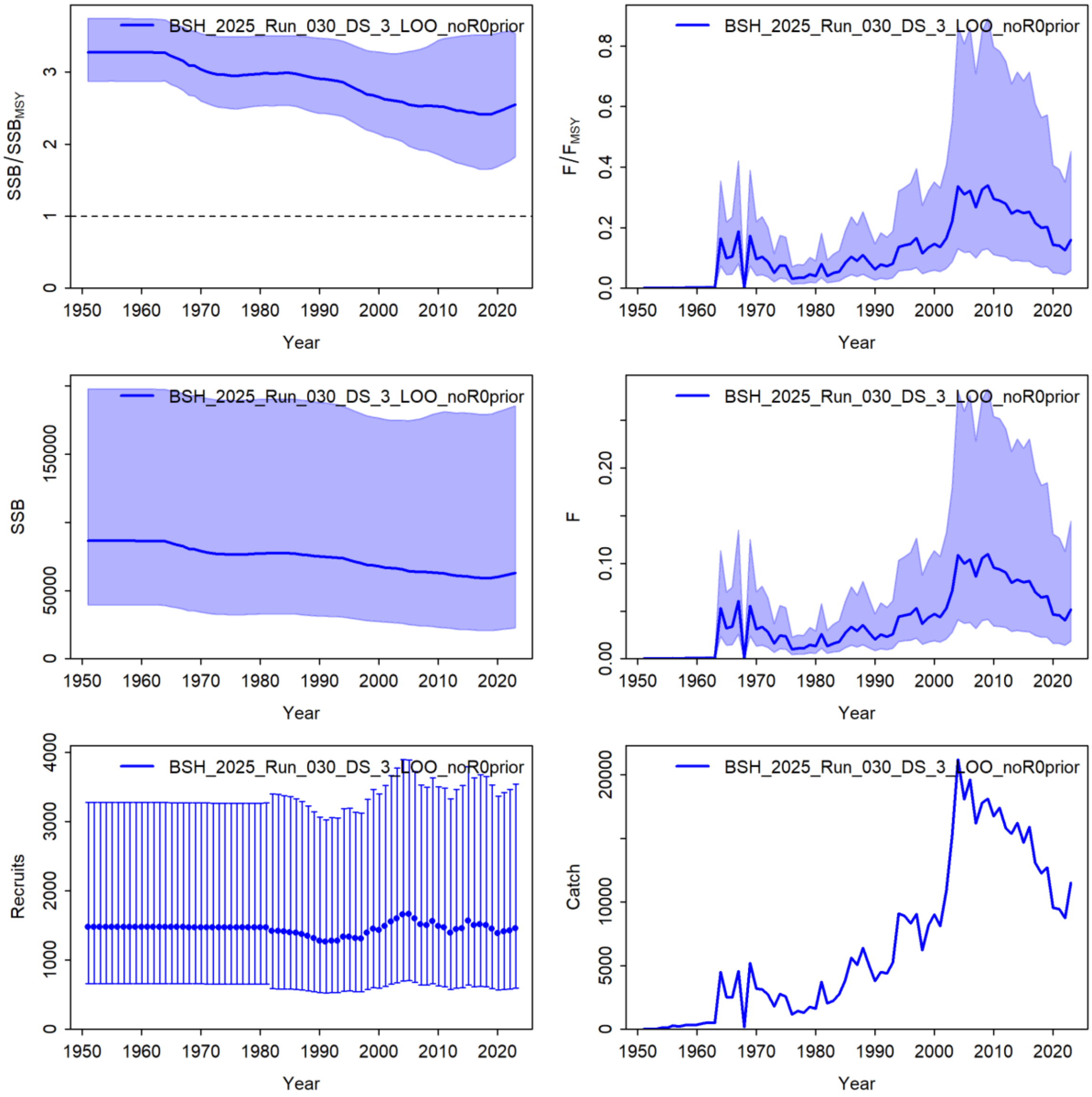


**Figure 23. Estimated timeseries based on the MVLN approximation**

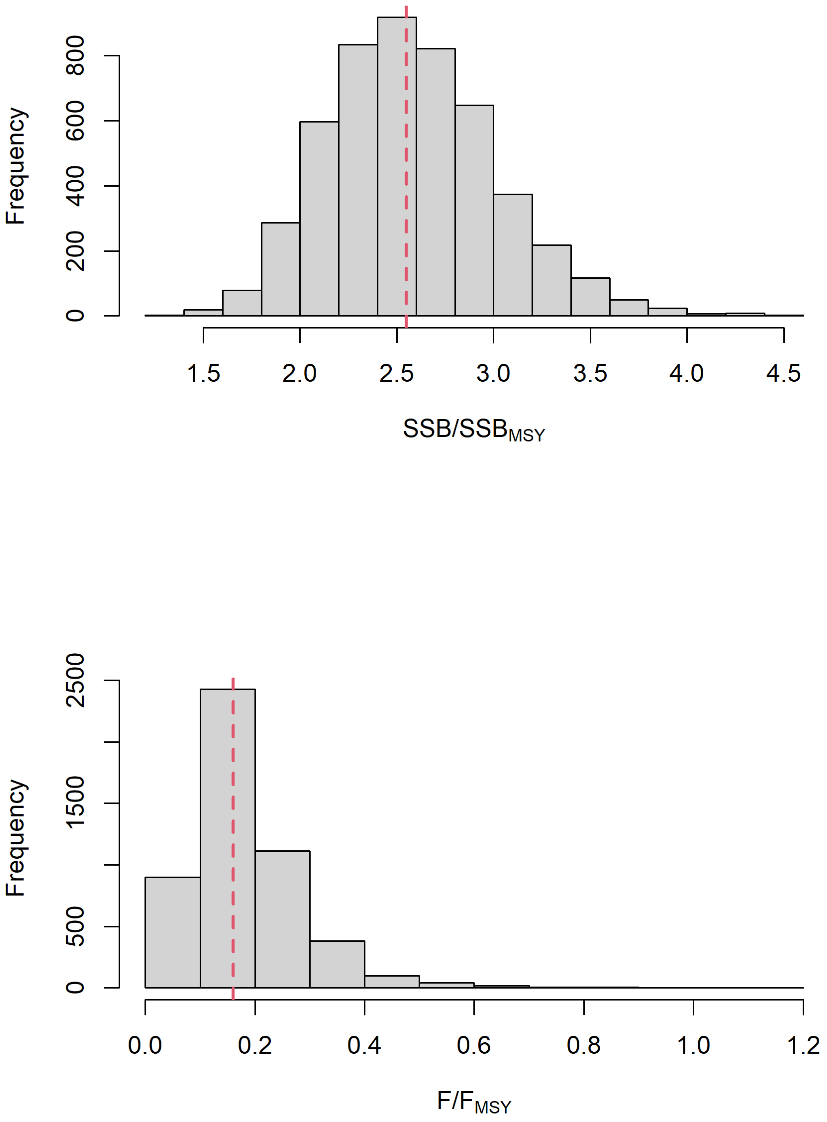


**Figure 24. Estimated spawning biomass in 2023relative to MSY (SSB2023/SSBMSY, top panel) and estimated total fishing mortality in 2023 relative to MSY (F2023/FMSY, bottom panel) for the base case model configuration, dashed lines indicate the 50th quantile.**

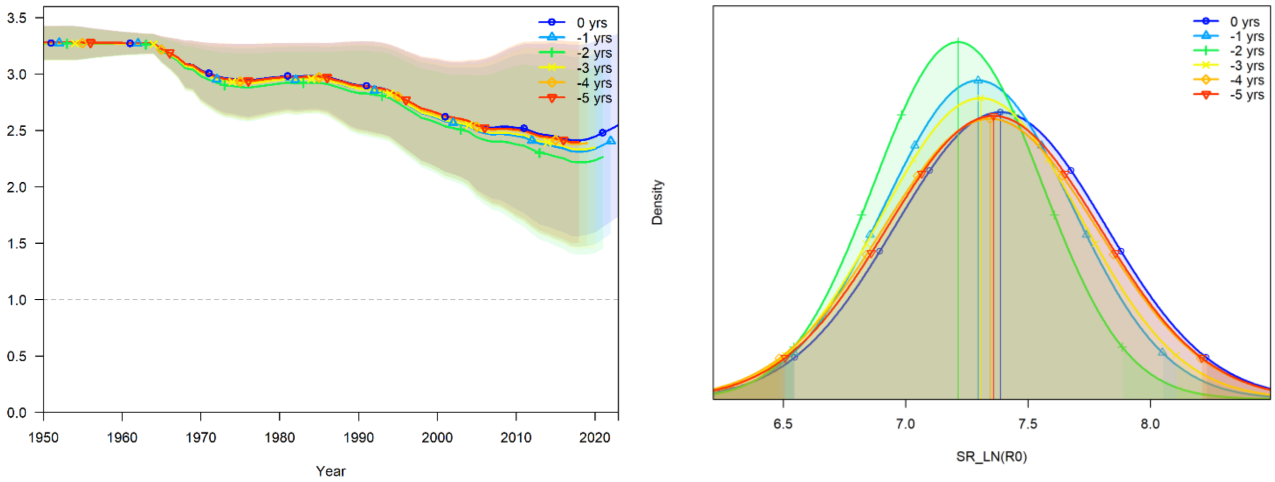
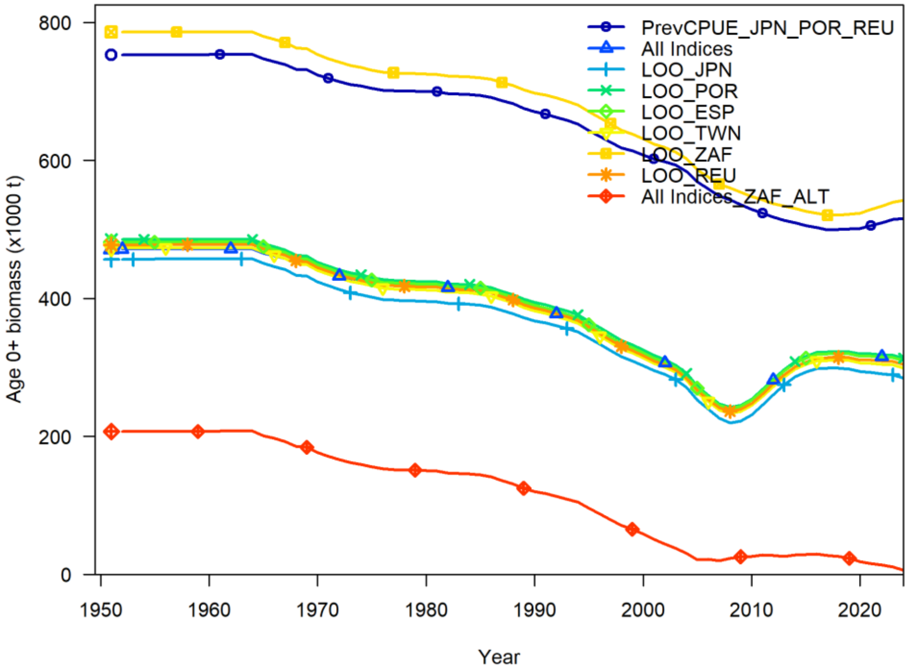


**Figure 25.** Estimated spawning biomass relative to MSY (SB/SB$_{msy}$, left panel) by year along with 95% asymptotic uncertainty (shaded areas) and the maximum likelihood estimate (MLE, vertical lines) and asymptotic uncertainty (bell shaped curves) of the natural log of virgin recruitment size (right panel) for each of the retrospective model runs conducted for the base case model configuration.



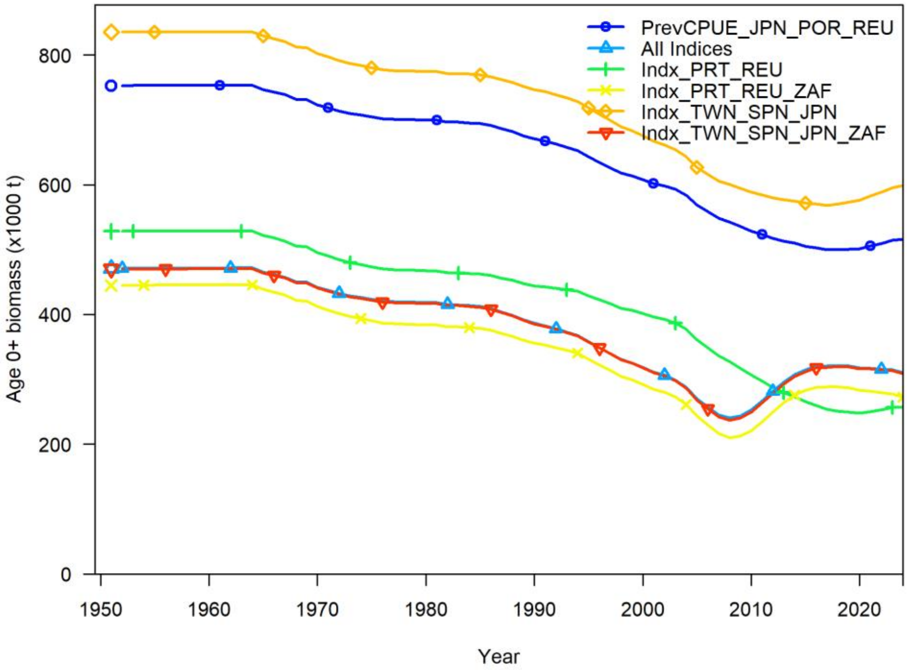


**Figure 26 Total biomass based on the sensitivity runs. The top panel shows the leave-one-out runs and the bottom panel shows the results based on the alternative groupings of CPUE series.**

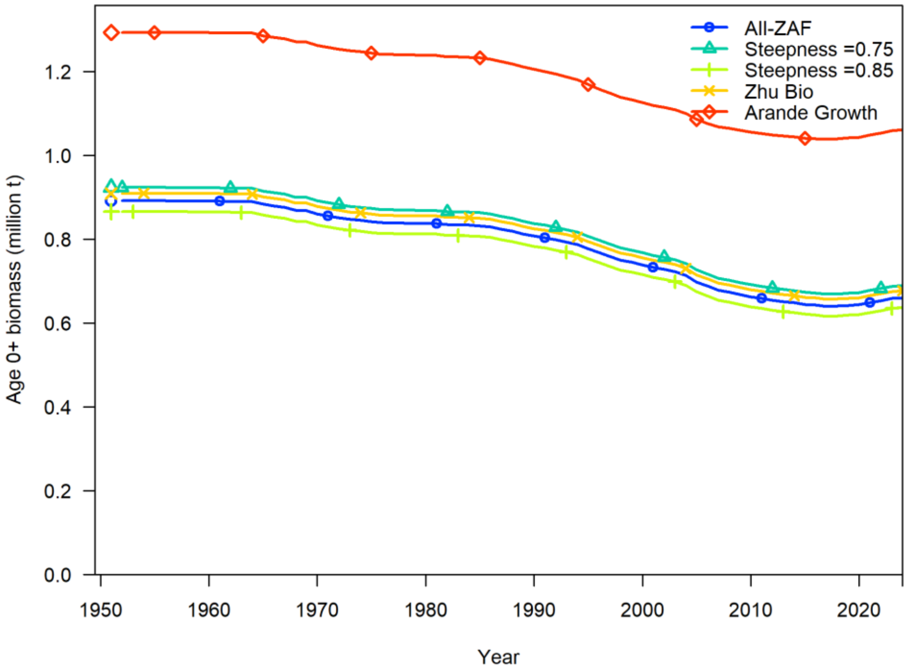


**Figure 27 Estimates of total biomass based on sensitivities from using alternative parameterization for growth, steepness and biology.**

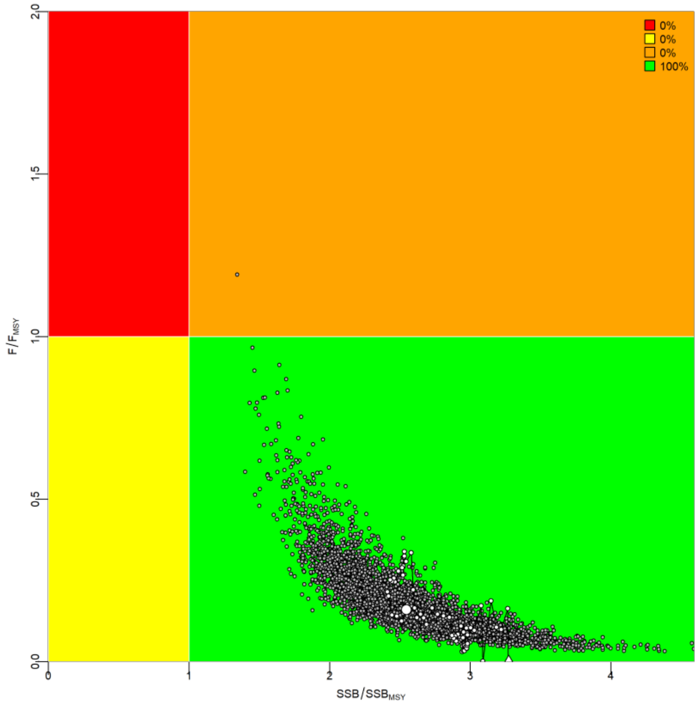


**Figure 28. Kobe plot showing the results the estimation of SB/SB$_{MSY}$ and F/F$_{MSY}$, for the terminal year of the model (2023).**

# ANNEX 1 Model Diagnostics

## Stock assessment of blue shark (*Prionace glauca*) in the Indian Ocean using SS3.

# 8 Annex 1. Diagnostic Tests for the Diagnostic Case SS3 Model

Diagnostic tests are important in determining the robustness of estimates for management advice in integrated stock assessment models. The diagnostics tests included in are based on diagnostics prepared for the previous assessment as well as recently developed methods (Carvallo et al. 2021). Here we present the model diagnostics for the diagnostic model run presented in the main assessment analysis.

## 8.1 Goodness of fit

*Runs test and joint residual plots.*
The goodness of fit of the model can be used as an indication of whether there is presence of significant model misspecification. Models that do not fit the data should be considered suspect, and further investigated. Here we use residual plots to investigate the trends and patterns in the data over time. Temporal correlation (autocorrelation) can drive bias and drift in the model estimates over time. A runs test (Wald and Wolfowitz, 1940) can test for randomness in a data sequence, such as model residuals (Carvalho et al., 2021). Residuals can also be investigated along side the root mean square error (RMSE, Carvalho et al., 2017), and a joint residual plot (Winker et al., 2018), which can highlight the systematically auto-correlated residual patterns.

## 8.2 Model consistency

*R0 Profile*
Use of a likelihood component profile on the a global scaling parameter (or other parameter) has been identified as a key model diagnostic to identify the influence of information sources on model estimates (Carvalho et al. 2017, Ichinokawa et al., 2014; Lee et al., 2014; Wang et al., 2014). Here the equilibrium recruitment parameter, R0, is used because it represents an ideal global scaling parameter given that unfished (virgin) recruitment is proportional to unfished biomass (Carvalho et al 2021, Lee et al., 2014; Maunder and Piner, 2015; Wang et al., 2014).

A relatively large change in negative log-likelihood units along the profile suggests a relatively informative data source for that particular model. Close association in the location of the minimum negative log-likelihood along the profile between data sources suggest that model consistency, and lack of conflict in the data. Figures A9-A11 show the profile likelihoods of R0 for the overall, CPUE and length components of the model. Figure A12 shows the fit to the CPUE series for the range of LN(R0) assumed. The likelihood profiles show that overall the *LN(R0)* parameter is well estimated, led by the length likelihood then the index likelihood and then the recruitment. Interestingly the lower edge of the likelihood is better defined (steeper) for all three components than the upper (Figure AA9). The fleet indices are generally in agreement (Figure AA10), however the length data shows different minimums (Figure A11), which is consistent with the fleets that encounter different components of the stock. The fits to the CPUE series at different values of *LN(R0)* show that values of approximately 7.5 fit the series (Figure A12).

*Age-Structured Production Model (ASPM)*
This diagnostic can help evaluate whether the catch and CPUE data give evidence for a production function within the model (Carvalho 2017). Overall the ASPM evaluates whether the effect of surplus production and observed catches alone could explain trends in the CPUE, in contrast to a more complex model (i.e. SS3) that incorporates annual recruitment deviations to improve the fit (Carvalho et al 2021). Maunder and Piner (2017) note that if the ASPM fits well to the indices of abundance with contrast the production function is likely to drive the stock dynamics and the indices will provide information about absolute abundance (Minte-Vera et al., 2017). Figure A13 shows that the biomass trajectories for both models (ASPM and the diagnostic) follow the same trend and that the estimates of *LN(R0)* are comparable. The fits to the indices are shown in figure Figure A14 and indicate an overall poor fit, indicating that the information content in the data is not sufficient, and perhaps some of the data should be reconsidered.

*Retrospective analysis*
Retrospective analysis is common in fisheries stock assessment to check the consistency of model estimates (Brooks and Legault, 2016; Carvalho et al., 2017; Hurtado-Ferro et al., 2015; Miller and Legault, 2017). A retrospective analysis is carried out by sequentially deleting a number of years of day (i.e. from 0 to 5) and re-running the model. Comparisons of model estimates from the full time-series and the truncated time-series can illuminate the bias and accuracy of the modelled quantities. Statistical analysis in the form of calculating the retrospective bias, rho (ρM, Mohn (1999), is common, with values between -0.15 and 0.2 being considered indicative of no bias. Figure A15 shows the analysis of spawning stock biomass (SSB) and fishing mortality estimates for Indian Ocean blue shark along with the Mohn's rho which indicates no retrospective bias. Forecasting the next year based on the retrospective analysis shows similar analysis (Figure A16).

### 8.3 Prediction Skill

Kell et al. (2016) proposed the hindcasting cross-validation technique (HCXval) where observations are compared to their predicted future values. The key concept behind the HCXval approach is 'prediction skill', which is defined as any measure of the accuracy of a forecasted value to the actual observed that is not known by the model (Kell et al., 2021). The difference, which is referred to as the 'prediction residual' (Michaelsen, 1987) can be evaluated by the mean absolute scaled error (MASE; Hyndman and Koehler, 2006). Carvalho et al note that a MASE score > 1 indicates that the average model forecasts are worse than a random walk. Conversely, a MASE score of 0.5 indicates that the model forecasts twice as accurately as a naïve baseline prediction; i.e. the model has prediction skill. For the CPUE series that constitute the diagnostic case the MASE values are 1.36, 0.93 and 1.09 for the Japanese, Portugal and

Reunion series (respectively, Figure A17), this indicates a mix of poor, good and decent prediction skill.

# 9 Figures

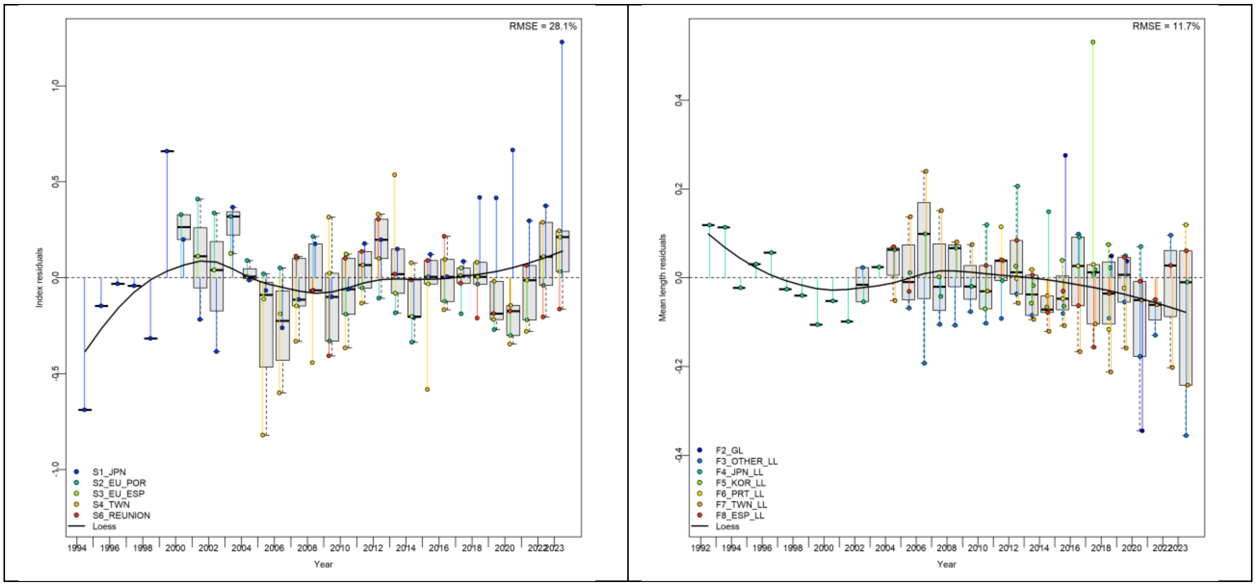


**Figure A1**. Joint residual plots for CPUE fits (left) from the Indian Ocean blue shark Assessment,. and annual mean length estimates for multiple fishing fleets. Vertical lines with points show the residuals (in colors by index), and solid black lines show loess smoother through all residuals. Boxplots indicate the median and quantiles in cases where residuals from the multiple indices are available for any given year. Root-mean squared errors (RMSE) are included in the upper right-hand corner of each plot.

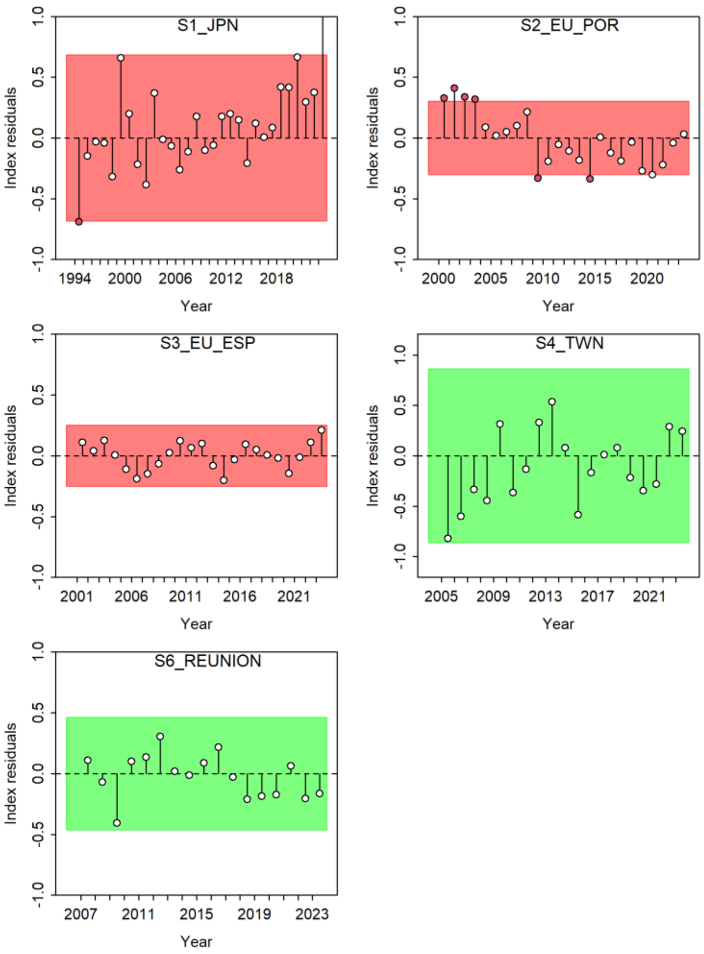


**Figure A2**. Runs tests results illustrated for catch-per-unit-effort (CPUE) fits ( from the Indian Ocean SS3 blue shark (BSH). Green shading indicates no evidence ($p \geq 0.05$) and red shading evidence ($p < 0.05$) to reject the hypothesis of a randomly distributed time-series of residuals, respectively. The shaded (green/red) area spans three residual standard deviations to either side from zero, and the red points outside of the shading violate the ‘three-sigma limit’ for that series.

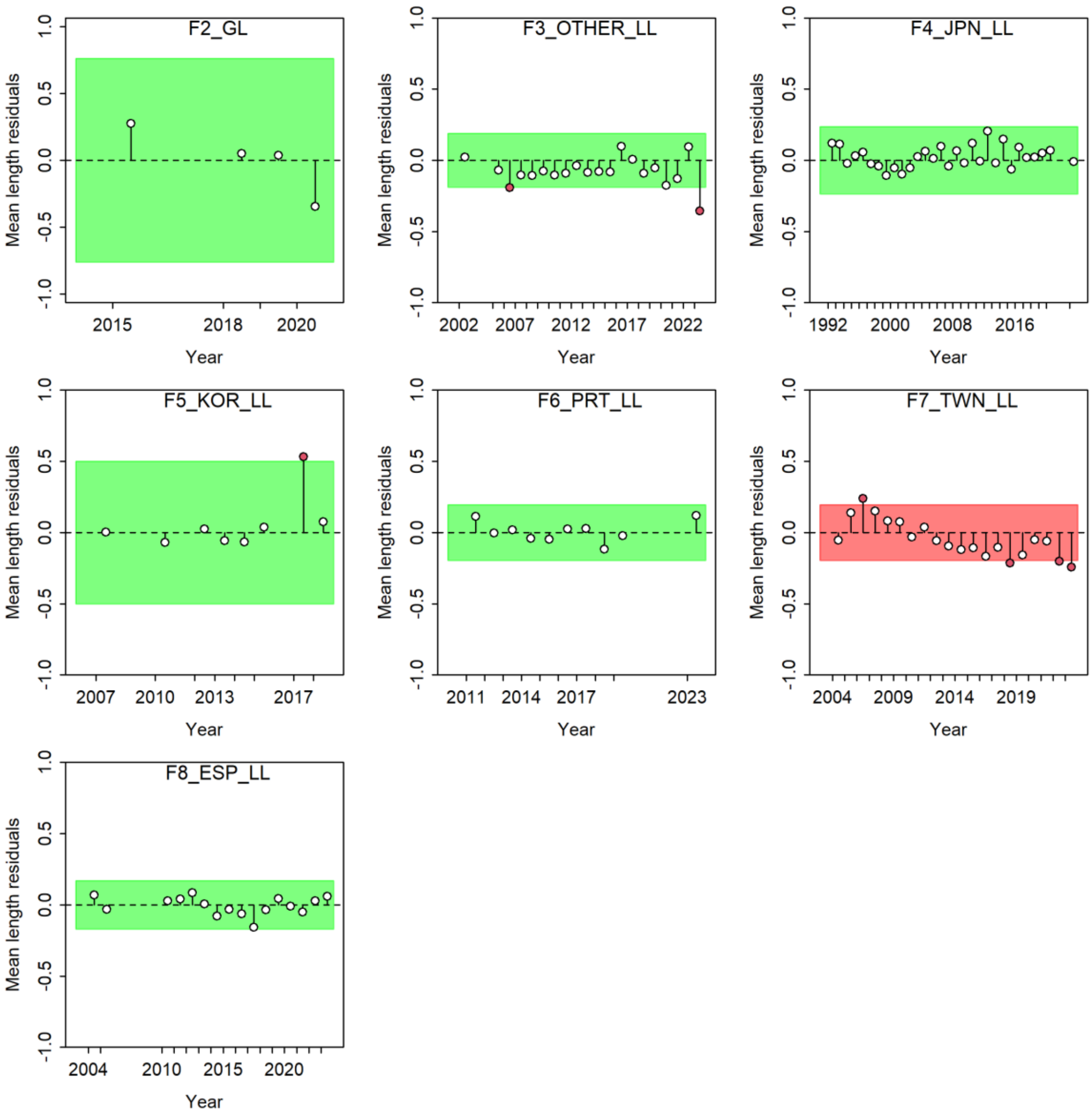


**Figure A3**. Runs tests results illustrated for the length composition fits (with names and fleet numbers on top) from the Indian Ocean SS3 blue shark (BSH). Green shading indicates no evidence ($p \geq 0.05$) and red shading evidence ($p < 0.05$) to reject the hypothesis of a randomly distributed time-series of residuals, respectively. The shaded (green/red) area spans three residual standard deviations to either side from zero, and the red points outside of the shading violate the 'three-sigma limit' for that series.

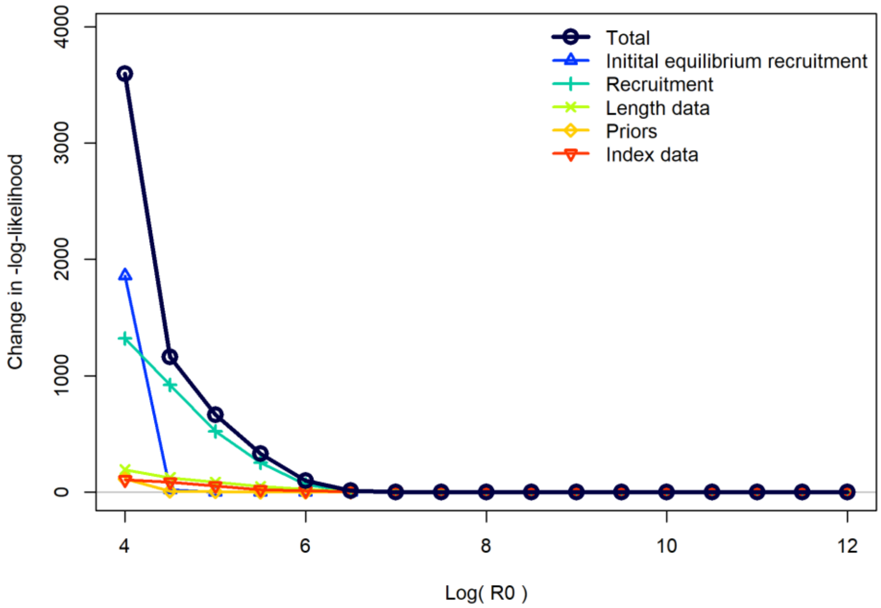


**Figure A4**. Total likelihood and component profiles (recruitment, length and index (CPUE) components).

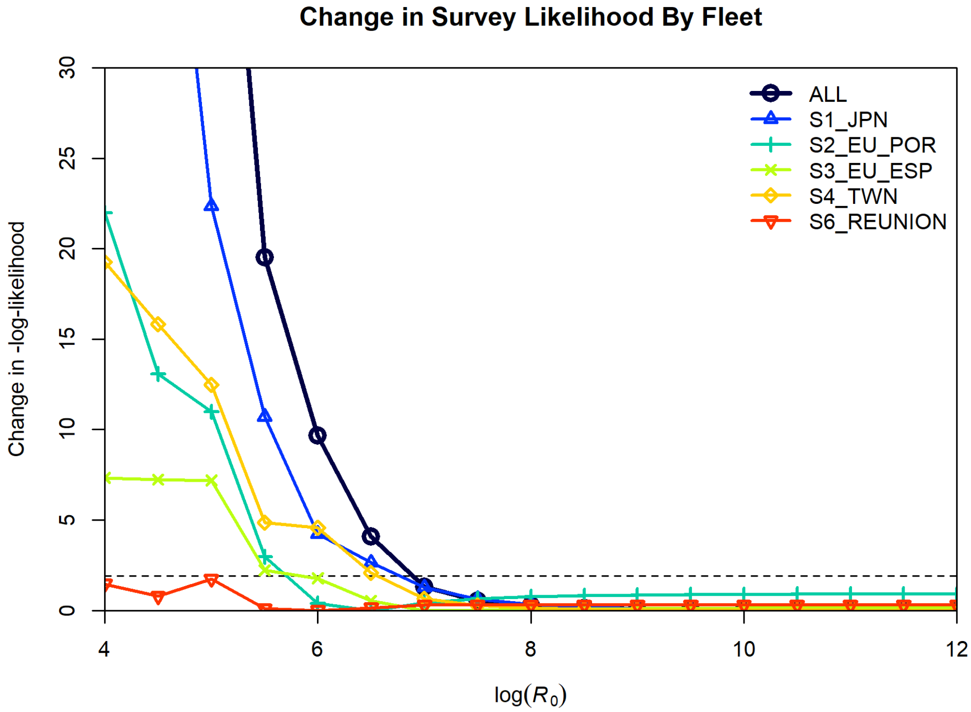


**Figure A5**. CPUE likelihoods for the diagnostic model.

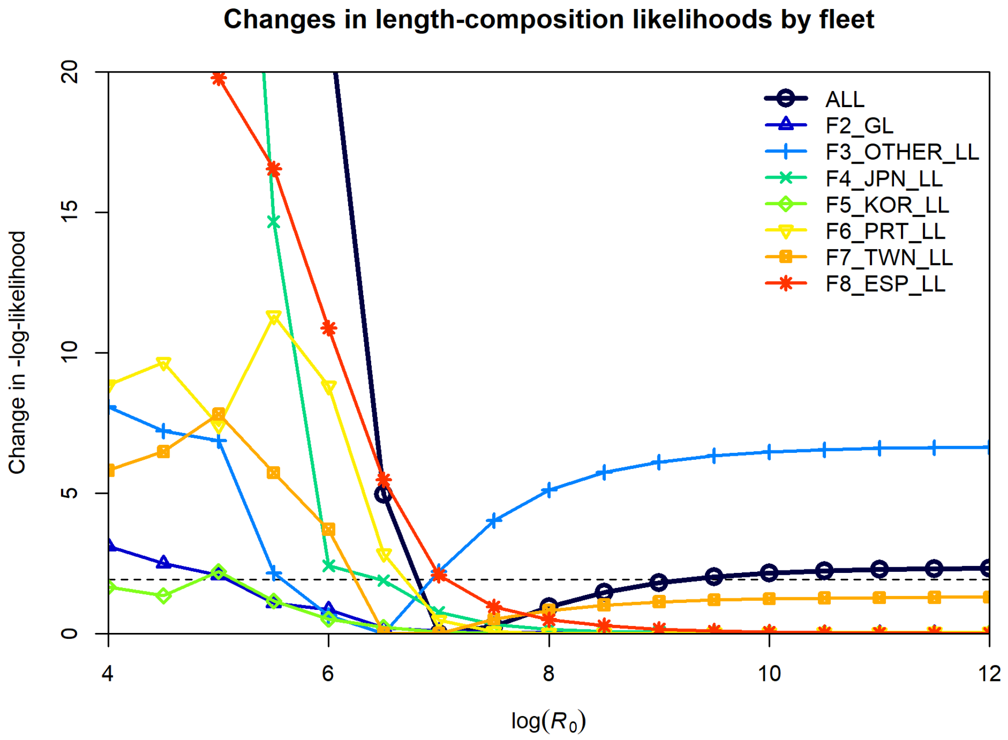


**Figure A6**.R0 profiles likelihoods for the fit to the length data.

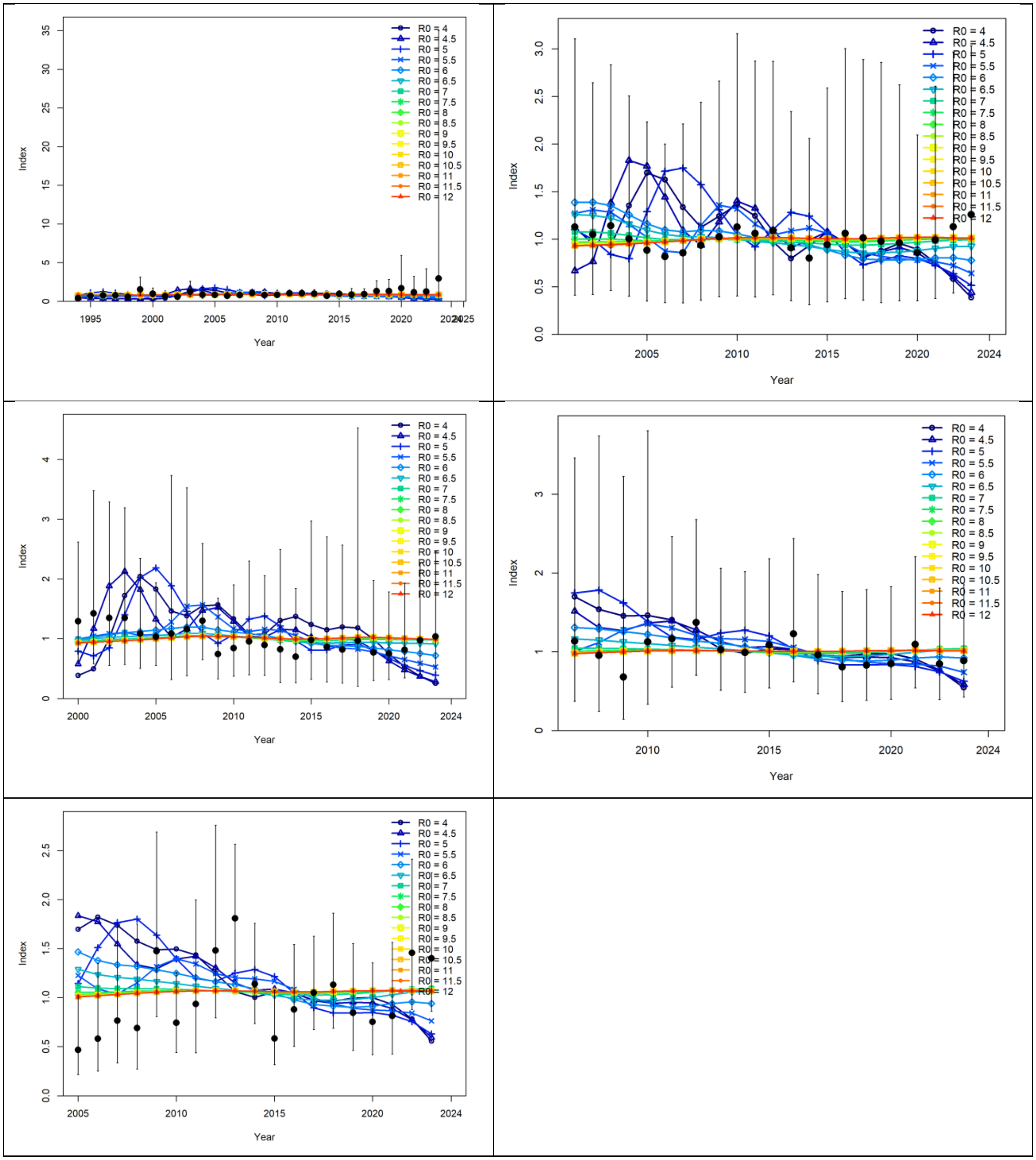


**Figure A7**. Fits to the component CPUE series (black dots and lines) for various profile likelihood values colored lines. Only the CPUE series that were fit in the diagnostic case are presented. The left column is panel is the fit to the Japanese, Portugese and Spanish CPUE (top to bottom), the right hand side is the Tawianese and Reunio (top to middle).

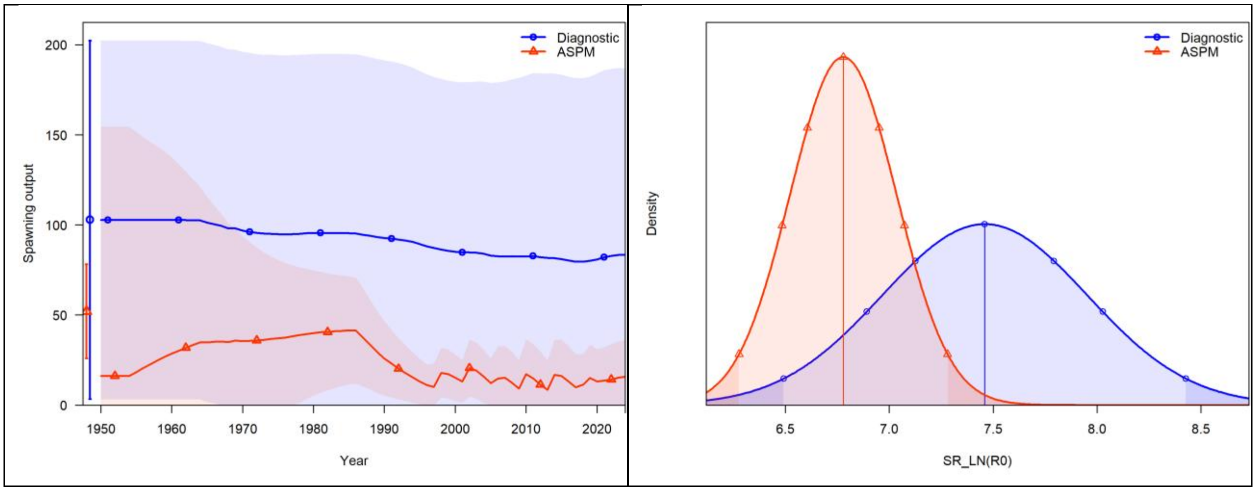


**Figure A8.** Comparison of spawning biomass trajectories for the ASPM and the diagnostic case of the assessment model carried out in stock synthesis (left panel), and the estimation of the densities for the stock recruitment parameter *LN(R0)* on the right hand side.

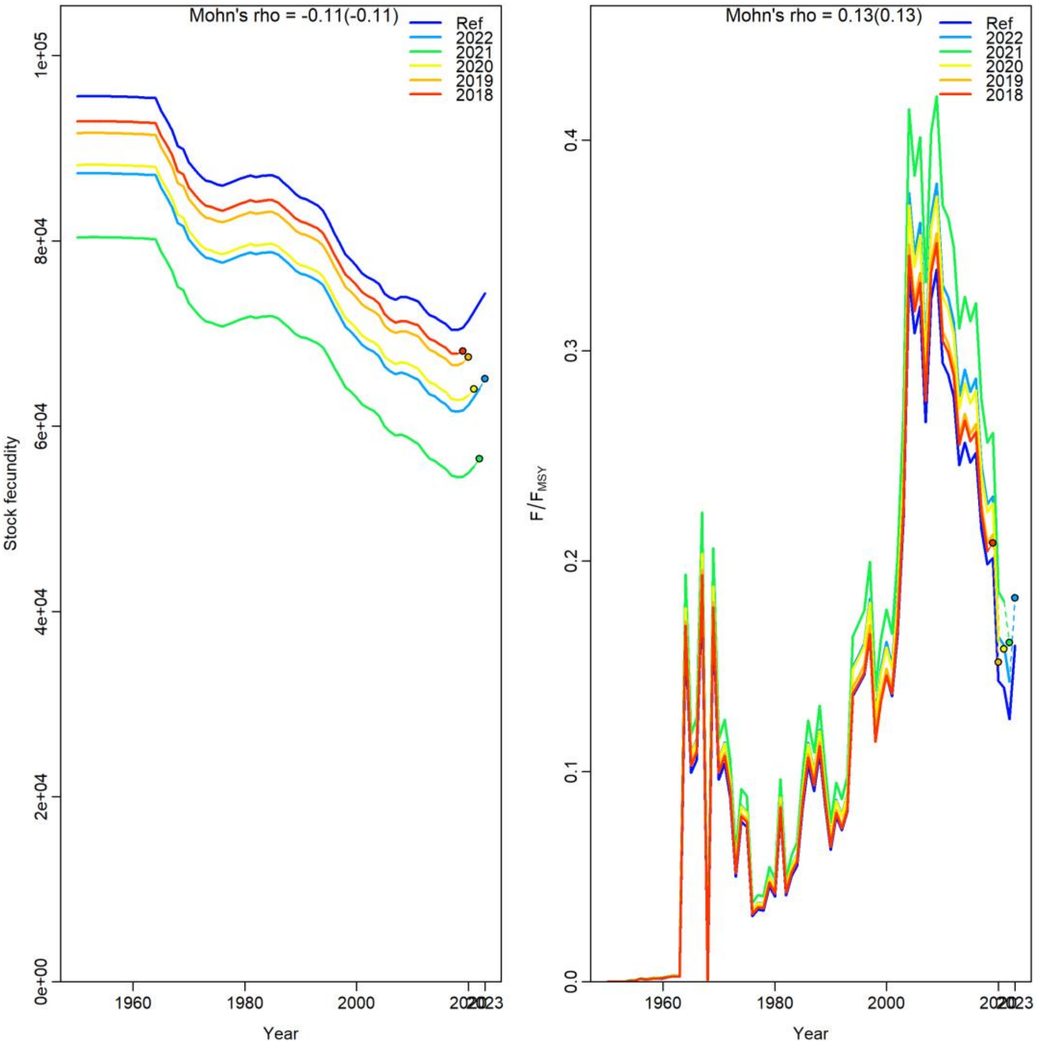


**Figure 9**. Retrospective analysis of spawning stock biomass (SSB) and fishing mortality estimates for Indian Ocean blue shark conducted by re-fitting the reference model (Ref) after seven years, one year at a time sequentially. Mohn's rho statistic are denoted on top of the panels.

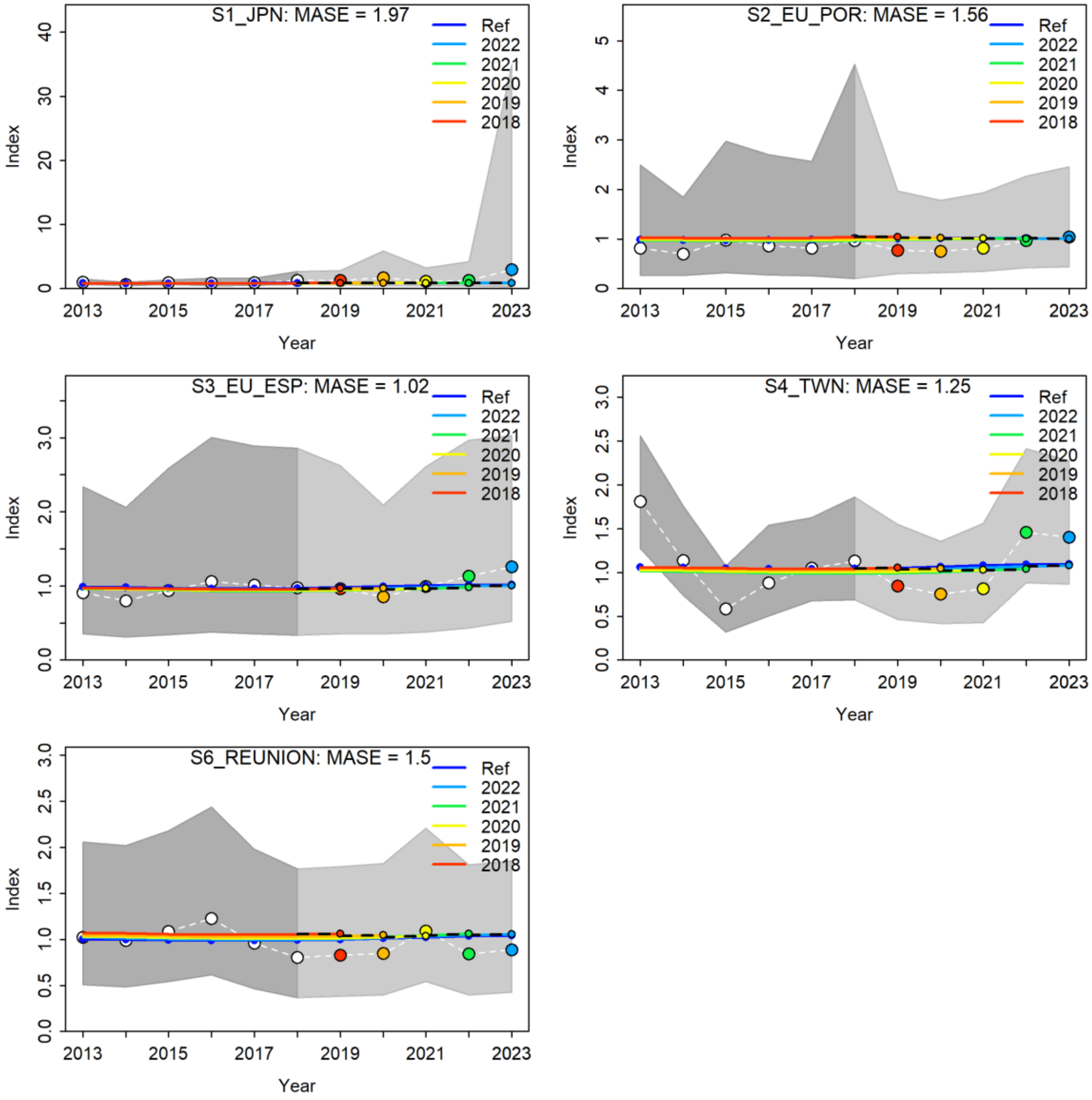


**Figure A10**. Hindcasting cross-validation (HCxval) results from CPUE fits, showing observed (large points connected with dashed line), fitted (solid lines) and one-year ahead forecast values (small terminal points). HCxval was performed using one reference model (Ref) and five hindcast model runs (solid lines) relative to the expected CPUE. The observations used for cross-validation are highlighted as color-coded solid circles with associated 95 % confidence intervals. The model reference year refers to the endpoints of each one-year-ahead forecast and the corresponding observation (i.e., year of retrospective + 1). The mean absolute scaled error (MASE) score associated with each CPUE.

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# ANNEX 2

## Model Specifications

## Stock assessment of blue shark (*Prionace glauca)* in the Indian Ocean using SS3.

Control File

```
#V3.30.23.2;_safe;_compile_date:_Apr 17 2025;_Stock_Synthesis_by_Richard_Methot_(NOAA)_using_ADMB_13.2
#_Stock_Synthesis_is_a_work_of_the_U.S._Government_and_is_not_subject_to_copyright_protection_in_the_United_States.
#_Foreign_copyrights_may_apply._See_copyright.txt_for_more_information.
#_User_support_available_at:_https://groups.google.com/g/ss3-forum_and_NMFS.Stock.Synthesis@noaa.gov
#_User_info_available_at:_https://nmfs-ost.github.io/ss3-website/
#_Source_code_at:_https://github.com/nmfs-ost/ss3-source-code

#C file created using an r4ss function
#C file write time: 2025-08-24  19:50:40
#_data_and_control_files: BSH_IO_DAT.SS // BSH_IO_CTL.SS
0  # 0 means do not read wtatage.ss; 1 means read and use wtatage.ss and also read and use growth parameters
1  #_N_Growth_Patterns (Growth Patterns, Morphs, Bio Patterns, GP are terms used interchangeably in SS3)
1 #_N_platoons_Within_GrowthPattern
#_Cond 1 #_Platoon_within/between_stdev_ratio (no read if N_platoons=1)
#_Cond sd_ratio_rd < 0: platoon_sd_ratio parameter required after movement params.
#_Cond  1 #vector_platoon_dist_(-1_in_first_val_gives_normal_approx)
#
2 # recr_dist_method for parameters:  2=main effects for GP, Area, Settle timing; 3=each Settle entity; 4=none (only when N_GP*Nsettle*pop==1)
1 # not yet implemented; Future usage: Spawner-Recruitment: 1=global; 2=by area
1 #  number of recruitment settlement assignments
0 # unused option
#GPattern month  area  age (for each settlement assignment)
 1 1 1 0
#
#_Cond 0 # N_movement_definitions goes here if Nareas > 1
#_Cond 1.0 # first age that moves (real age at begin of season, not integer) also cond on do_migration>0
#_Cond 1 1 1 2 4 10 # example move definition for seas=1, morph=1, source=1 dest=2, age1=4, age2=10
#
1 #_Nblock_Patterns
 1 #_blocks_per_pattern
# begin and end years of blocks
 1949 1949
```

```
#
# controls for all timevary parameters
1 #_time-vary parm bound check (1=warn relative to base parm bounds; 3=no bound check);
Also see env (3) and dev (5) options to constrain with base bounds
#
# AUTOGEN
 1 1 1 1 1 # autogen: 1st element for biology, 2nd for SR, 3rd for Q, 4th reserved, 5th for selex
# where: 0 = autogen time-varying parms of this category; 1 = read each time-varying parm line;
2 = read then autogen if parm min==-12345
#
#_Available timevary codes
#_Block types: 0: P_block=P_base*exp(TVP); 1: P_block=P_base+TVP; 2: P_block=TVP; 3:
P_block=P_block(-1) + TVP
#_Block_trends: -1: trend bounded by base parm min-max and parms in transformed units
(beware); -2: endtrend and infl_year direct values; -3: end and infl as fraction of base range
#_EnvLinks:  1: P(y)=P_base*exp(TVP*env(y));  2: P(y)=P_base+TVP*env(y);  3:
P(y)=f(TVP,env_Zscore) w/ logit to stay in min-max;  4: P(y)=2.0/(1.0+exp(-TVP1*env(y) -
TVP2))
#_DevLinks:  1: P(y)*=exp(dev(y)*dev_se;  2: P(y)+=dev(y)*dev_se;  3: random walk;  4: zero-
reverting random walk with rho;  5: like 4 with logit transform to stay in base min-max
#_DevLinks(more):  21-25 keep last dev for rest of years
#
#_Prior_codes:  0=none; 6=normal; 1=symmetric beta; 2=CASAL's beta; 3=lognormal;
4=lognormal with biascorr; 5=gamma
#
# setup for M, growth, wt-len, maturity, fecundity, (hermaphro), recr_distr, cohort_grow,
(movement), (age error), (catch_mult), sex ratio
#_NATMORT
3 #_natM_type:_0=1Parm;
1=N_breakpoints;_2=Lorenzen;_3=agespecific;_4=agespec_withseasinterpolate;_5=BETA:_Ma
under_link_to_maturity;_6=Lorenzen_range
 #_Age_natmort_by sex x growthpattern (nest GP in sex)
 0.288 0.222 0.187 0.165 0.15 0.139 0.131 0.124 0.119 0.115 0.112 0.109 0.107 0.105 0.103
0.102 0.101 0.1 0.099 0.098 0.098 0.097 0.097 0.096 0.096 0.095 0.095 0.095 0.095 0.095 0.094
 0.277 0.212 0.179 0.158 0.144 0.134 0.126 0.121 0.116 0.113 0.11 0.107 0.105 0.104 0.102
0.101 0.1 0.1 0.099 0.098 0.098 0.097 0.097 0.097 0.097 0.096 0.096 0.096 0.096 0.096 0.096
#
2 # GrowthModel: 1=vonBert with L1&L2; 2=Richards with L1&L2; 3=age_specific_K_incr;
4=age_specific_K_decr; 5=age_specific_K_each; 6=NA; 7=NA; 8=growth cessation
0.5 #_Age(post-settlement) for L1 (aka Amin); first growth parameter is size at this age; linear
growth below this
999 #_Age(post-settlement) for L2 (aka Amax); 999 to treat as Linf
-999 #_exponential decay for growth above maxage (value should approx initial Z; -999
replicates 3.24; -998 to not allow growth above maxage)
0  #_placeholder for future growth feature
#
```

```
0 #_SD_add_to_LAA (set to 0.1 for SS2 V1.x compatibility)
0 #_CV_Growth_Pattern:  0 CV=f(LAA); 1 CV=F(A); 2 SD=F(LAA); 3 SD=F(A); 4
logSD=F(A)
#
1 #_maturity_option:  1=length logistic; 2=age logistic; 3=read age-maturity matrix by
growth_pattern; 4=read age-fecundity; 5=disabled; 6=read length-maturity
5 #_First_Mature_Age
2 #_fecundity_at_length option:(1)eggs=Wt*(a+b*Wt);(2)eggs=a*L^b;(3)eggs=a*Wt^b;
(4)eggs=a+b*L; (5)eggs=a+b*W
0 #_hermaphroditism option:  0=none; 1=female-to-male age-specific fxn; -1=male-to-female
age-specific fxn
3 #_parameter_offset_approach for M, G, CV_G:  1- direct, no offset**; 2-
male=fem_parm*exp(male_parm); 3: male=female*exp(parm) then old=young*exp(parm)
#_** in option 1, any male parameter with value = 0.0 and phase <0 is set equal to female
parameter
#
#_growth_parms
#_ LO HI INIT PRIOR PR_SD PR_type PHASE env_var&link dev_link dev_minyr dev_maxyr
dev_PH Block Block_Fxn
# Sex: 1  BioPattern: 1  NatMort
# Sex: 1  BioPattern: 1  Growth
 10 120 49.8 45 10 6 -4 0 0 0 0 0.5 0 0 # L_at_Amin_Fem_GP_1
 40 410 283.2 400 10 6 -2 0 0 0 0 0.5 0 0 # L_at_Amax_Fem_GP_1
 0.1 0.25 0.129 0.15 0.8 6 -4 0 0 0 0 0.5 0 0 # VonBert_K_Fem_GP_1
 -10 10 1 1 0.8 0 -4 0 0 0 0 0.5 0 0 # Richards_Fem_GP_1
 0.01 1 0.22 0.0834877 0.8 6 -3 0 0 0 0 0.5 0 0 # CV_young_Fem_GP_1
 -3 3 -0.4 0 0.8 6 -3 0 0 0 0 0.5 0 0 # CV_old_Fem_GP_1
# Sex: 1  BioPattern: 1  WtLen
 -3 3 5.388e-06 5.388e-06 0.8 6 -3 0 0 0 0 0.5 0 0 # Wtlen_1_Fem_GP_1
 -3 3.5 3.102 3.102 0.8 6 -3 0 0 0 0 0.5 0 0 # Wtlen_2_Fem_GP_1
# Sex: 1  BioPattern: 1  Maturity&Fecundity
 -3 300 145 55 0.8 6 -3 0 0 0 0 0.5 0 0 # Mat50%_Fem_GP_1
 -3 3 -0.138 -0.138 0.8 6 -3 0 0 0 0 0.5 0 0 # Mat_slope_Fem_GP_1
 -3 46 38 37 0.8 6 -3 0 0 0 0 0.5 0 0 # Eggs_scalar_Fem_GP_1
 -3 3 0 0 0.8 6 -3 0 0 0 0 0.5 0 0 # Eggs_exp_len_Fem_GP_1
# Sex: 2  BioPattern: 1  NatMort
# Sex: 2  BioPattern: 1  Growth
 -3 3 0.0323 0 0.8 0 -3 0 0 0 0 0.5 0 0 # L_at_Amin_Mal_GP_1
 -3 3 -0.0214 0 0.8 0 -2 0 0 0 0 0.5 0 0 # L_at_Amax_Mal_GP_1
 -3 3 0.1306 0 0.8 0 -3 0 0 0 0 0.5 0 0 # VonBert_K_Mal_GP_1
 -3 3 0 0 0.8 6 -3 0 0 0 0 0.5 0 0 # Richards_Mal_GP_1
 -3 3 0 0 0.8 6 -3 0 0 0 0 0.5 0 0 # CV_young_Mal_GP_1
 -3 3 -0.4 0 0.8 6 -3 0 0 0 0 0.5 0 0 # CV_old_Mal_GP_1
# Sex: 2  BioPattern: 1  WtLen
 -3 3 3.293e-06 3.293e-06 0.8 6 -3 0 0 0 0 0.5 0 0 # Wtlen_1_Mal_GP_1
 -3 3.5 3.225 3.225 0.8 6 -3 0 0 0 0 0.5 0 0 # Wtlen_2_Mal_GP_1
```

```
# Hermaphroditism
#  Recruitment Distribution
 -4 4 0 0 99 0 -3 0 0 0 0 0.5 0 0 # RecrDist_GP_1
 -4 4 0 0 99 0 -3 0 0 0 0 0.5 0 0 # RecrDist_Area_1
 -4 4 4 0 99 0 -3 0 0 0 0 0.5 0 0 # RecrDist_month_1
#  Cohort growth dev base
 0.1 10 1 1 1 6 -1 0 0 0 0 0.5 0 0 # CohortGrowDev
#  Movement
#  Platoon StDev Ratio
#  Age Error from parameters
#  catch multiplier
#  fraction female, by GP
 1e-06 0.999999 0.5 0.5 0.5 0 -99 0 0 0 0 0 0 0 # FracFemale_GP_1
#  M2 parameter for each predator fleet
#
#_no timevary MG parameters
#
#_seasonal_effects_on_biology_parms
 0 0 0 0 0 0 0 0 0 0 #_femwtlen1,femwtlen2,mat1,mat2,fec1,fec2,Malewtlen1,malewtlen2,L1,K
#_ LO HI INIT PRIOR PR_SD PR_type PHASE
#_Cond -2 2 0 0 -1 99 -2 #_placeholder when no seasonal MG parameters
#
3 #_Spawner-Recruitment; Options: 1=NA; 2=Ricker; 3=std_B-H; 4=SCAA; 5=Hockey; 6=B-
H_flattop; 7=survival_3Parm; 8=Shepherd_3Parm; 9=RickerPower_3parm
0  # 0/1 to use steepness in initial equ recruitment calculation
0  #  future feature:  0/1 to make realized sigmaR a function of SR curvature
#_       LO        HI       INIT      PRIOR      PR_SD      PR_type     PHASE    env-var
use_dev   dev_mnyr   dev_mxyr    dev_PH      Block    Blk_Fxn #  parm_name
          4        12     7.38718        7         1         0       1        0        0        0        0
0        0        0 # SR_LN(R0)
        0.1        0.9        0.8       0.35        10         6       -2        0        0        0
0        0        0        0 # SR_BH_steep
          0         2        0.2       0.3       0.8         6       -3        0        0        0        0
0        0        0 # SR_sigmaR
         -5         5         0         0         1         6       -1        0        0        0        0
0        1        1 # SR_regime
          0         0         0         0        99         0       -1        0        0        0        0
0        0        0 # SR_autocorr
# timevary SR parameters
 -10 10 -9.0866e-05 0 5 6 1 # SR_regime_BLK1add_1949
2 #do_recdev:  0=none; 1=devvector (R=F(SSB)+dev); 2=deviations (R=F(SSB)+dev);
3=deviations (R=R0*dev; dev2=R-f(SSB)); 4=like 3 with sum(dev2) adding penalty
1992 # first year of main recr_devs; early devs can precede this era
2015 # last year of main recr_devs; forecast devs start in following year
2 #_recdev phase
1 # (0/1) to read 13 advanced options
```

```
 -10 #_recdev_early_start (0=none; neg value makes relative to recdev_start)
 1 #_recdev_early_phase
 0 #_forecast_recruitment phase (incl. late recr) (0 value resets to maxphase+1)
 1 #_lambda for Fcast_recr_like occurring before endyr+1
 1979.7 #_last_yr_nobias_adj_in_MPD; begin of ramp
 1991.7 #_first_yr_fullbias_adj_in_MPD; begin of plateau
 2018.9 #_last_yr_fullbias_adj_in_MPD
 2021 #_end_yr_for_ramp_in_MPD (can be in forecast to shape ramp, but SS3 sets bias_adj to 0.0 for fcast yrs)
 0.2398 #_max_bias_adj_in_MPD (typical ~0.8; -3 sets all years to 0.0; -2 sets all non-forecast yrs w/ estimated recdevs to 1.0; -1 sets biasadj=1.0 for all yrs w/ recdevs)
 0 #_period of cycles in recruitment (N parms read below)
 -10 #min rec_dev
 10 #max rec_dev
 0 #_read_recdevs
#_end of advanced SR options
#
#_placeholder for full parameter lines for recruitment cycles
# read specified recr devs
#_year Input_value

#
#Fishing Mortality info
0.2 # F ballpark value in units of annual_F
-2010 # F ballpark year (neg value to disable)
3 # F_Method:  1=Pope midseason rate; 2=F as parameter; 3=F as hybrid; 4=fleet-specific parm/hybrid (#4 is superset of #2 and #3 and is recommended)
5 # max F (methods 2-4) or harvest fraction (method 1)
4  # N iterations for tuning in hybrid mode; recommend 3 (faster) to 5 (more precise if many fleets)
#
#_initial_F_parms; for each fleet x season that has init_catch; nest season in fleet; count = 1
#_for unconstrained init_F, use an arbitrary initial catch and set lambda=0 for its logL
#_ LO HI INIT PRIOR PR_SD  PR_type  PHASE
 1e-07 0.1 7.75071e-05 0.001 1 6 1 # InitF_seas_1_flt_1F1_MISC
#
#
#_Q_setup for fleets with cpue or survey or deviation data
#_1:  fleet number
#_2:  link type: 1=simple q; 2=mirror; 3=power (+1 parm); 4=mirror with scale (+1p); 5=offset (+1p); 6=offset & power (+2p)
#_    where power is applied as y = q * x ^ (1 + power); so a power value of 0 has null effect
#_    and with the offset included it is y = q * (x + offset) ^ (1 + power)
#_3:  extra input for link, i.e. mirror fleet# or dev index number
#_4:  0/1 to select extra sd parameter
#_5:  0/1 for biasadj or not
```

```
#_6:  0/1 to float
#_   fleet     link link_info  extra_se   biasadj     float  #  fleetname
       9        1       0        0        0        1  #  S1_JPN
      10        1       0        0        0        1  #  S2_EU_POR
      11        1       0        0        0        1  #  S3_EU_ESP
      12        1       0        0        0        1  #  S4_TWN
      13        1       0        0        0        1  #  S5_ZAF
      14        1       0        0        0        1  #  S6_REUNION
      15        1       0        0        0        1  #  S7_ZAF_Alt
-9999 0 0 0 0 0
#
#_Q_parameters
#_          LO          HI         INIT        PRIOR        PR_SD       PR_type      PHASE    env-var
use_dev   dev_mnyr   dev_mxyr    dev_PH      Block     Blk_Fxn  #  parm_name
           -25          25     -8.23622           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S1_JPN(9)
           -25          25     -8.08025           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S2_EU_POR(10)
           -25          25      -7.7913           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S3_EU_ESP(11)
           -25          25     -7.96918           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S4_TWN(12)
           -25          25      -6.9777           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S5_ZAF(13)
           -25          25      -8.0212           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S6_REUNION(14)
           -25          25     -7.56616           0            1            0         -1          0          0          0
0          0          0          0  #  LnQ_base_S7_ZAF_Alt(15)
#_no timevary Q parameters
#
#_size_selex_patterns
#Pattern:_0;  parm=0; selex=1.0 for all sizes
#Pattern:_1;  parm=2; logistic; with 95% width specification
#Pattern:_5;  parm=2; mirror another size selex; PARMS pick the min-max bin to mirror
#Pattern:_11; parm=2; selex=1.0  for specified min-max population length bin range
#Pattern:_15; parm=0; mirror another age or length selex
#Pattern:_6;  parm=2+special; non-parm len selex
#Pattern:_43; parm=2+special+2;  like 6, with 2 additional param for scaling (mean over bin
range)
#Pattern:_8;  parm=8; double_logistic with smooth transitions and constant above Linf option
#Pattern:_9;  parm=6; simple 4-parm double logistic with starting length; parm 5 is first length;
parm 6=1 does desc as offset
#Pattern:_21; parm=2*special; non-parm len selex, read as N break points, then N selex
parameters
#Pattern:_22; parm=4; double_normal as in CASAL
#Pattern:_23; parm=6; double_normal where final value is directly equal to sp(6) so can be >1.0
```

```
#Pattern:_24; parm=6; double_normal with sel(minL) and sel(maxL), using joiners
#Pattern:_2;  parm=6; double_normal with sel(minL) and sel(maxL), using joiners, back
compatibile version of 24 with 3.30.18 and older
#Pattern:_25; parm=3; exponential-logistic in length
#Pattern:_27; parm=special+3; cubic spline in length; parm1==1 resets knots; parm1==2 resets
all
#Pattern:_42; parm=special+3+2; cubic spline; like 27, with 2 additional param for scaling
(mean over bin range)
#_discard_options:_0=none;_1=define_retention;_2=retention&mortality;_3=all_discarded_dead
;_4=define_dome-shaped_retention
#_Pattern Discard Male Special
 1 0 0 0 # 1 F1_MISC
 24 0 0 0 # 2 F2_GL
 24 0 4 0 # 3 F3_OTHER_LL
 24 0 3 0 # 4 F4_JPN_LL
 24 0 0 0 # 5 F5_KOR_LL
 24 0 4 0 # 6 F6_PRT_LL
 24 0 4 0 # 7 F7_TWN_LL
 24 0 0 0 # 8 F8_ESP_LL
 5 0 0 5 # 9 S1_JPN
 5 0 0 5 # 10 S2_EU_POR
 5 0 0 6 # 11 S3_EU_ESP
 5 0 0 8 # 12 S4_TWN
 5 0 0 7 # 13 S5_ZAF
 5 0 0 8 # 14 S6_REUNION
 5 0 0 8 # 15 S7_ZAF_Alt
#
#_age_selex_patterns
#Pattern:_0; parm=0; selex=1.0 for ages 0 to maxage
#Pattern:_10; parm=0; selex=1.0 for ages 1 to maxage
#Pattern:_11; parm=2; selex=1.0  for specified min-max age
#Pattern:_12; parm=2; age logistic
#Pattern:_13; parm=8; age double logistic. Recommend using pattern 18 instead.
#Pattern:_14; parm=nages+1; age empirical
#Pattern:_15; parm=0; mirror another age or length selex
#Pattern:_16; parm=2; Coleraine - Gaussian
#Pattern:_17; parm=nages+1; empirical as random walk  N parameters to read can be overridden
by setting special to non-zero
#Pattern:_41; parm=2+nages+1; // like 17, with 2 additional param for scaling (mean over bin
range)
#Pattern:_18; parm=8; double logistic - smooth transition
#Pattern:_19; parm=6; simple 4-parm double logistic with starting age
#Pattern:_20; parm=6; double_normal,using joiners
#Pattern:_26; parm=3; exponential-logistic in age
#Pattern:_27; parm=3+special; cubic spline in age; parm1==1 resets knots; parm1==2 resets all
```

```
#Pattern:_42; parm=2+special+3; // cubic spline; with 2 additional param for scaling (mean over
bin range)
#Age patterns entered with value >100 create Min_selage from first digit and pattern from
remainder
#_Pattern Discard Male Special
 0 0 0 0 # 1 F1_MISC
 0 0 0 0 # 2 F2_GL
 0 0 0 0 # 3 F3_OTHER_LL
 0 0 0 0 # 4 F4_JPN_LL
 0 0 0 0 # 5 F5_KOR_LL
 0 0 0 0 # 6 F6_PRT_LL
 0 0 0 0 # 7 F7_TWN_LL
 0 0 0 0 # 8 F8_ESP_LL
 0 0 0 0 # 9 S1_JPN
 0 0 0 0 # 10 S2_EU_POR
 0 0 0 0 # 11 S3_EU_ESP
 0 0 0 0 # 12 S4_TWN
 0 0 0 0 # 13 S5_ZAF
 0 0 0 0 # 14 S6_REUNION
 0 0 0 0 # 15 S7_ZAF_Alt
#
#_       LO       HI       INIT      PRIOR      PR_SD     PR_type     PHASE    env-var
use_dev   dev_mnyr   dev_mxyr    dev_PH     Block   Blk_Fxn  #  parm_name
# 1   F1_MISC LenSelex
          1       300       200       100       0.1        6      -2       0       0       0
0      0.5       0       0  #  Size_inflection_F1_MISC(1)
          1       339        75       100       0.1        6      -3       0       0       0
0      0.5       0       0  #  Size_95%width_F1_MISC(1)
# 2   F2_GL LenSelex
         90       215    186.45       180         0        0       1       0       0       0
0      0.5       0       0  #  Size_DblN_peak_F2_GL(2)
        -15        15        -3         0         0        0      -2       0       0       0       0
0.5       0       0  #  Size_DblN_top_logit_F2_GL(2)
        -15        15         8         0         0        0      -4       0       0       0       0
0.5       0       0  #  Size_DblN_ascend_se_F2_GL(2)
        -15        15         7         0         0        0      -5       0       0       0       0
0.5       0       0  #  Size_DblN_descend_se_F2_GL(2)
       -999      -999      -999         0         0        0      -2       0       0       0
0      0.5       0       0  #  Size_DblN_start_logit_F2_GL(2)
       -999      -999      -999         0         5        0      -2       0       0       0
0      0.5       0       0  #  Size_DblN_end_logit_F2_GL(2)
# 3   F3_OTHER_LL LenSelex
        170       200   188.465       190         1        6       2       0       0       0
0      0.5       0       0  #  Size_DblN_peak_F3_OTHER_LL(3)
        -10        -9  -9.69119      -9.5         0        0       2       0       0       0
0      0.5       0       0  #  Size_DblN_top_logit_F3_OTHER_LL(3)
```

```
        -15       15    6.90381        0        0        0     -4      0      0      0
0      0.5      0      0 # Size_DblN_ascend_se_F3_OTHER_LL(3)
        -15       15        8        0        0        0     -5      0      0      0      0
0.5      0      0 # Size_DblN_descend_se_F3_OTHER_LL(3)
       -999     -999     -999        0        0        0     -2      0      0      0
0      0.5      0      0 # Size_DblN_start_logit_F3_OTHER_LL(3)
       -999     -999     -999        0        5        0     -2      0      0      0
0      0.5      0      0 # Size_DblN_end_logit_F3_OTHER_LL(3)
        -20      200       10      125       50        0     -4      0      0      0
0       0      0      0 # SzSel_Fem_Peak_F3_OTHER_LL(3)
        -15       15        0        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Fem_Ascend_F3_OTHER_LL(3)
        -15       15        1        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Fem_Descend_F3_OTHER_LL(3)
        -15       15        0        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Fem_Final_F3_OTHER_LL(3)
        -15       15     0.33        4       50        0     -5      0      0      0      0
0       0      0 # SzSel_Fem_Scale_F3_OTHER_LL(3)
# 4  F4_JPN_LL LenSelex
        145      165  145.002      150        0        0      1      0      0      0
0      0.5      0      0 # Size_DblN_peak_F4_JPN_LL(4)
        -10        9 -3.92263     -9.5        0        0      2      0      0      0
0      0.5      0      0 # Size_DblN_top_logit_F4_JPN_LL(4)
        -15       15  8.42507        0        0        0     -4      0      0      0
0      0.5      0      0 # Size_DblN_ascend_se_F4_JPN_LL(4)
        -15       15        7        0        0        0     -5      0      0      0      0
0.5      0      0 # Size_DblN_descend_se_F4_JPN_LL(4)
       -999     -999     -999        0        0        0     -2      0      0      0
0      0.5      0      0 # Size_DblN_start_logit_F4_JPN_LL(4)
       -999     -999     -999        0        5        0     -2      0      0      0
0      0.5      0      0 # Size_DblN_end_logit_F4_JPN_LL(4)
        -20      200      -15      125       50        0     -4      0      0      0
0       0      0      0 # SzSel_Male_Peak_F4_JPN_LL(4)
        -15       15        0        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Male_Ascend_F4_JPN_LL(4)
        -15       15        0        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Male_Descend_F4_JPN_LL(4)
        -15       15        0        4       50        0     -4      0      0      0      0
0       0      0 # SzSel_Male_Final_F4_JPN_LL(4)
        -15       15      0.5        4       50        0     -5      0      0      0      0
0       0      0 # SzSel_Male_Scale_F4_JPN_LL(4)
# 5  F5_KOR_LL LenSelex
        140      165  149.996      150      0.5        6      1      0      0      0
0      0.5      0      0 # Size_DblN_peak_F5_KOR_LL(5)
        -15       15       -3        0        0        0     -2      0      0      0      0
0.5      0      0 # Size_DblN_top_logit_F5_KOR_LL(5)
```

```
        -15        15        8        0        0        0     -4      0      0      0      0
0.5      0      0  #  Size_DblN_ascend_se_F5_KOR_LL(5)
        -15        15        7        0        0        0     -5      0      0      0      0
0.5      0      0  #  Size_DblN_descend_se_F5_KOR_LL(5)
        -999       -999       -999        0        0        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_start_logit_F5_KOR_LL(5)
        -999       -999       -999        0        5        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_end_logit_F5_KOR_LL(5)
# 6  F6_PRT_LL LenSelex
        155       175    158.891       165        0        0      1      0      0      0
0     0.5      0      0  #  Size_DblN_peak_F6_PRT_LL(6)
        -1         1   -0.520557      -0.4        0        0      3      0      0      0
0     0.5      0      0  #  Size_DblN_top_logit_F6_PRT_LL(6)
        -15        15        6.5        0        0        0     -5      0      0      0      0
0.5      0      0  #  Size_DblN_ascend_se_F6_PRT_LL(6)
        -15        15        6.5        0        0        0     -5      0      0      0      0
0.5      0      0  #  Size_DblN_descend_se_F6_PRT_LL(6)
        -999       -999       -999        0        0        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_start_logit_F6_PRT_LL(6)
        -999       -999       -999        0        5        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_end_logit_F6_PRT_LL(6)
        -20       200        10       125       50        0     -4      0      0      0
0      0      0      0  #  SzSel_Fem_Peak_F6_PRT_LL(6)
        -15        15        0        4       50        0     -4      0      0      0      0
0      0      0  #  SzSel_Fem_Ascend_F6_PRT_LL(6)
        -15        15        0        4       50        0     -4      0      0      0      0
0      0      0  #  SzSel_Fem_Descend_F6_PRT_LL(6)
        -15        15        0        4       50        0     -4      0      0      0      0
0      0      0  #  SzSel_Fem_Final_F6_PRT_LL(6)
        -15        15       0.2        4       50        0     -5      0      0      0      0
0      0      0  #  SzSel_Fem_Scale_F6_PRT_LL(6)
# 7  F7_TWN_LL LenSelex
        195       215    195.004       209        0        0      1      0      0      0
0     0.5      0      0  #  Size_DblN_peak_F7_TWN_LL(7)
        -10        -9   -9.42459      -9.5        0        0      2      0      0      0
0     0.5      0      0  #  Size_DblN_top_logit_F7_TWN_LL(7)
        -15        15        7.5        0        0        0     -4      0      0      0      0
0.5      0      0  #  Size_DblN_ascend_se_F7_TWN_LL(7)
        -15        15        7.75       0        0        0     -5      0      0      0      0
0.5      0      0  #  Size_DblN_descend_se_F7_TWN_LL(7)
        -999       -999       -999        0        0        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_start_logit_F7_TWN_LL(7)
        -999       -999       -999        0        5        0     -2      0      0      0
0     0.5      0      0  #  Size_DblN_end_logit_F7_TWN_LL(7)
        -20       200         0       125       50        0     -4      0      0      0
0      0      0      0  #  SzSel_Fem_Peak_F7_TWN_LL(7)
```

```
        -15        15         0         4        50         0      -4       0       0       0       0
0       0        0 #  SzSel_Fem_Ascend_F7_TWN_LL(7)
        -15        15         0         4        50         0      -4       0       0       0       0
0       0        0 #  SzSel_Fem_Descend_F7_TWN_LL(7)
        -15        15         0         4        50         0      -4       0       0       0       0
0       0        0 #  SzSel_Fem_Final_F7_TWN_LL(7)
        -15        15       0.75        4        50         0      -5       0       0       0       0
0       0        0 #  SzSel_Fem_Scale_F7_TWN_LL(7)
# 8   F8_ESP_LL LenSelex
        200        225    204.057       215         0         0       1       0       0       0
0       0.5       0        0 #  Size_DblN_peak_F8_ESP_LL(8)
         -5         1    -3.12746        -3         1         6       2       0       0       0       0
0.5       0        0 #  Size_DblN_top_logit_F8_ESP_LL(8)
        -15        15         8         0         0         0      -4       0       0       0       0
0.5       0        0 #  Size_DblN_ascend_se_F8_ESP_LL(8)
        -15        15         8         0         0         0      -5       0       0       0       0
0.5       0        0 #  Size_DblN_descend_se_F8_ESP_LL(8)
       -999      -999      -999         0         0         0      -2       0       0       0
0       0.5       0        0 #  Size_DblN_start_logit_F8_ESP_LL(8)
       -999      -999      -999         0         5         0      -2       0       0       0
0       0.5       0        0 #  Size_DblN_end_logit_F8_ESP_LL(8)
# 9   S1_JPN LenSelex
          1       200         1        50        99         0     -99       0       0       0       0
0.5       0        0 #  SizeSel_P1_S1_JPN(9)
          1       239        76        50        99         0     -99       0       0       0
0       0.5       0        0 #  SizeSel_P2_S1_JPN(9)
# 10   S2_EU_POR LenSelex
          1       200         1        50        99         0     -99       0       0       0       0
0.5       0        0 #  SizeSel_P1_S2_EU_POR(10)
          1       239        76        50        99         0     -99       0       0       0
0       0.5       0        0 #  SizeSel_P2_S2_EU_POR(10)
# 11   S3_EU_ESP LenSelex
          1       200         1        50        99         0     -99       0       0       0       0
0.5       0        0 #  SizeSel_P1_S3_EU_ESP(11)
          1       239        76        50        99         0     -99       0       0       0
0       0.5       0        0 #  SizeSel_P2_S3_EU_ESP(11)
# 12   S4_TWN LenSelex
          1       200         1        50        99         0     -99       0       0       0       0
0.5       0        0 #  SizeSel_P1_S4_TWN(12)
          1       239        76        50        99         0     -99       0       0       0
0       0.5       0        0 #  SizeSel_P2_S4_TWN(12)
# 13   S5_ZAF LenSelex
          1       200         1        50        99         0     -99       0       0       0       0
0.5       0        0 #  SizeSel_P1_S5_ZAF(13)
          1       239        76        50        99         0     -99       0       0       0
0       0.5       0        0 #  SizeSel_P2_S5_ZAF(13)
```

```
# 14   S6_REUNION LenSelex
         1        200          1         50         99          0      -99        0        0        0        0
0.5        0        0  #  SizeSel_P1_S6_REUNION(14)
         1        239         76         50         99          0      -99        0        0        0
0      0.5        0        0  #  SizeSel_P2_S6_REUNION(14)
# 15   S7_ZAF_Alt LenSelex
         1        200          1         50         99          0      -99        0        0        0        0
0.5        0        0  #  SizeSel_P1_S7_ZAF_Alt(15)
         1        239         76         50         99          0      -99        0        0        0
0      0.5        0        0  #  SizeSel_P2_S7_ZAF_Alt(15)
# 1   F1_MISC AgeSelex
# 2   F2_GL AgeSelex
# 3   F3_OTHER_LL AgeSelex
# 4   F4_JPN_LL AgeSelex
# 5   F5_KOR_LL AgeSelex
# 6   F6_PRT_LL AgeSelex
# 7   F7_TWN_LL AgeSelex
# 8   F8_ESP_LL AgeSelex
# 9   S1_JPN AgeSelex
# 10   S2_EU_POR AgeSelex
# 11   S3_EU_ESP AgeSelex
# 12   S4_TWN AgeSelex
# 13   S5_ZAF AgeSelex
# 14   S6_REUNION AgeSelex
# 15   S7_ZAF_Alt AgeSelex
#_No_Dirichlet parameters
#_no timevary selex parameters
#
0   #  use 2D_AR1 selectivity? (0/1)
#_no 2D_AR1 selex offset used
#_specs:  fleet, ymin, ymax, amin, amax, sigma_amax, use_rho, len1/age2, devphase,
before_range, after_range
#_sigma_amax>amin means create sigma parm for each bin from min to sigma_amax;
sigma_amax<0 means just one sigma parm is read and used for all bins
#_needed parameters follow each fleet's specifications
# -9999  0 0 0 0 0 0 0 0 0 0 # terminator
#
# Tag loss and Tag reporting parameters go next
0  # TG_custom:  0=no read and autogen if tag data exist; 1=read
#_Cond -6 6 1 1 2 0.01 -4 0 0 0 0 0 0 0  #_placeholder if no parameters
#
# deviation vectors for timevary parameters
#  base   base first block   block  env  env   dev   dev   dev   dev   dev
#  type  index  parm trend pattern link  var  vectr link _mnyr  mxyr phase  dev_vector
#     2    4    1    1    1    0    0    0    0    0    0    0
    #
```

```
# Input variance adjustments factors:
 #_1=add_to_survey_CV
 #_2=add_to_discard_stddev
 #_3=add_to_bodywt_CV
 #_4=mult_by_lencomp_N
 #_5=mult_by_agecomp_N
 #_6=mult_by_size-at-age_N
 #_7=mult_by_generalized_sizecomp
#_factor  fleet  value
     1     9    0.017
     1    10     0.179
     1    11     0.193
     1    12     0.012
     1    13     -0.17
     1    14     0.142
     1    15    -0.197
     4     2  0.194448
     4     3  0.166438
     4     4  0.243305
     4     5  0.058551
     4     6  0.192226
     4     7  0.059066
     4     8  0.535525
 -9999   1    0  # terminator
#
1 #_maxlambdaphase
1 #_sd_offset; must be 1 if any growthCV, sigmaR, or survey extraSD is an estimated parameter
# read 26 changes to default Lambdas (default value is 1.0)
# Like_comp codes:  1=surv; 2=disc; 3=mnwt; 4=length; 5=age; 6=SizeFreq; 7=sizeage;
8=catch; 9=init_equ_catch;
# 10=recrdev; 11=parm_prior; 12=parm_dev; 13=CrashPen; 14=Morphcomp; 15=Tag-comp;
16=Tag-negbin; 17=F_ballpark; 18=initEQregime
#like_comp fleet  phase  value  sizefreq_method
 1 1 1 0 1
 1 2 1 0 1
 1 3 1 0 1
 1 4 1 0 1
 1 5 1 0 1
 1 6 1 0 1
 1 7 1 0 1
 1 8 1 0 1
 1 9 1 1 1
 1 10 1 1 1
 1 11 1 1 1
 1 12 1 1 1
 1 13 1 0 1
```

```
 1 14 1 1 1
 1 15 1 0 1
 4 1 1 0 0
 4 2 1 1 0
 4 3 1 1 0
 4 4 1 1 0
 4 5 1 1 0
 4 6 1 1 0
 4 7 1 1 0
 4 8 1 1 0
 4 9 1 0 0
 4 10 1 0 0
 9 1 1 1 0
-9999  1  1  1  1  #  terminator
#
999
```