Namibian hake model update, 2024

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Contents

```r
library(knitr)
hook_output = knit_hooks$get('output')
knit_hooks$set(output = function(x, options) {
  # this hook is used only when the linewidth option is not NULL
  if (!is.null(n <- options$linewidth)) {
    x = knitr:::split_lines(x)
    # any lines wider than n should be wrapped
    if (any(nchar(x) > n)) x = strwrap(x, width = n)
    x = paste(x, collapse = '\n')
  }
  hook_output(x, options)
})

knitr::opts_chunk$set(collapse = TRUE, comment = "  " ,fig.align = 'center', cache=FALSE,tid
knitr::opts_knit$set(root.dir=here::here())
#knitr::opts_chunk$set(warning=F, message=F, echo=F, results=F,fig.width=6, fig.height=5)
```

Project overview

The following reflects my interpretation of the Marine Stewardship Council's certification request. There is a need to catch up on missed milestones and outlines the necessary steps for the upcoming Year 4 milestone.

Key Points

1. Year 3 Milestone Missed: The milestone required revised stock assessments for *M. paradoxus*, which was not met.
2. Year 4 Milestone: By February 2025, the MFMR must use the Harvest Control Rule (HCR) systematically to verify the TAC for *M. paradoxus*. This needs to be applied in the August/September 2024 management meetings.
3. Namibian Stock Assessment: There's a recommendation to review and re-evaluate the assumptions and parameter values of assessment models, particularly the pessimistic base case model.
4. Implementation Issues: MFMR has Dr. Ianelli's report but not the code to run the model, and training is required for the Namibian team.

Draft agenda

The following draft agenda outlines the steps to address the missed milestones and prepare for the upcoming Year 4 milestone.

Week 1:

1. Day 1-2: Review and Planning

   - Review the Year 3 milestone requirements and current progress.
   - Plan steps to implement the HCR for *M. paradoxus*.

2. Day 3-4: Data Preparation

   - Gather and prepare Namibia stock assessment data.
   - Coordinate with MFMR to understand current data handling and management practices.

3. Day 5: Meeting Preparation

   - Prepare documentation and a presentation for the MFMR management meeting.
   - Outline the steps needed for the August/September 2024 meeting to include HCR in TAC setting.

Week 2:

4. Day 1-2: Model Review

   - Review Dr. Ianelli's report and identify key elements for implementation.
   - Develop a preliminary implementation plan for the HCR model.

5. Day 3-4: Training Coordination

- Arrange a training session with Dr. Ianelli or another suitable individual for MFMR.
- Coordinate with the training provider and MFMR to schedule the session.

6. Day 5: Reporting

- Compile a progress report summarizing activities, challenges, and next steps.
- Send the report to Hugh and relevant stakeholders for feedback.

This agenda ensures a systematic approach to address the milestones and prepare for the upcoming management meeting, focusing on implementing the HCR and providing necessary training to MFMR.

Below are two main sections, first on model developments and second on application of a control rule that accounts for the signals in the data on the different species.

Assessment model runs

The original base-case model was evaluated for a number of features and extensions. These included focus on what data components were fit well and how improvements in consistency can be made. For the latter part, we found that the fits to the index and CPUE data were particularly poor and could be improved.

Below are examples which show how models can be run based on the directory location.

Model descriptions

The following table was developed based on testing the model with different assumptions and data sources. Key differences from the 2023 assessment configuration was the assumption that model estimation of variance terms was appropriate. This feature resulted in unacceptable residual patterns and essentially a complete down weighting of the index data. We used the assumed variance terms (CVs) for the indices in all of the following model configurations:

Model	Description
Previous base case	As specified in past assessments, estimated steepness and all variance terms
Base case (m0)	Model with survey "minus group" to be ages 0, and 1 instead of 0, 1, and 2 as done in the past, steepness fixed at 0.7, q estimated, and time-varying fishery asymptotic selectivity specified.
m1	As base case but with survey catchability fixed at 1.0
m2	As base case but with survey catchability fixed at 0.5

Model	Description
m3	As base case but with natural mortality estimated
m4	As base case but with fishery selectivity allowed to be dome-shaped
m5	As base case but with stock-recruit steepness fixed at 0.43
m6	As base case but with stock-recruit steepness fixed at 0.9

```r
# Run names
mod_ref <- c("old_bc", "m0", "m1", "m2", "m3", "m4", "m5", "m6")
mod_dir <- c("old_bc", "m0", "m1", "m2", "m3", "m4", "m5", "m6")
mod_label <- c("2023 base case", "2024 base case", "Model 1", "Model 2", "Model 3",
    "Model 4", "Model 5", "Model 6")
res <- get_results(mod_names. = mod_label, moddir = mod_dir)
modlst <- res$modlst
old_bc <- modlst[[1]]
m0 <- modlst[[2]]
moddiag <- res$moddiag
dfsrr <- data.frame()
for (i in 1:length(mod_ref)) {
    # assign(modlst[[i]], run_nh(mod_dir[i] ,runit=FALSE) )
    dfsrr <- rbind(dfsrr, data.frame(Model = mod_label[i], SSB = modlst[[i]]$SSB,
        R = modlst[[i]]$Pred_Rec))
}
mods <- data.frame()
for (i in 1:length(mod_ref)) {
    mods <- rbind(mods, data.frame(moddiag[[i]], Model = names(moddiag[i])))
}
# head(mods)
```

Fits to index data
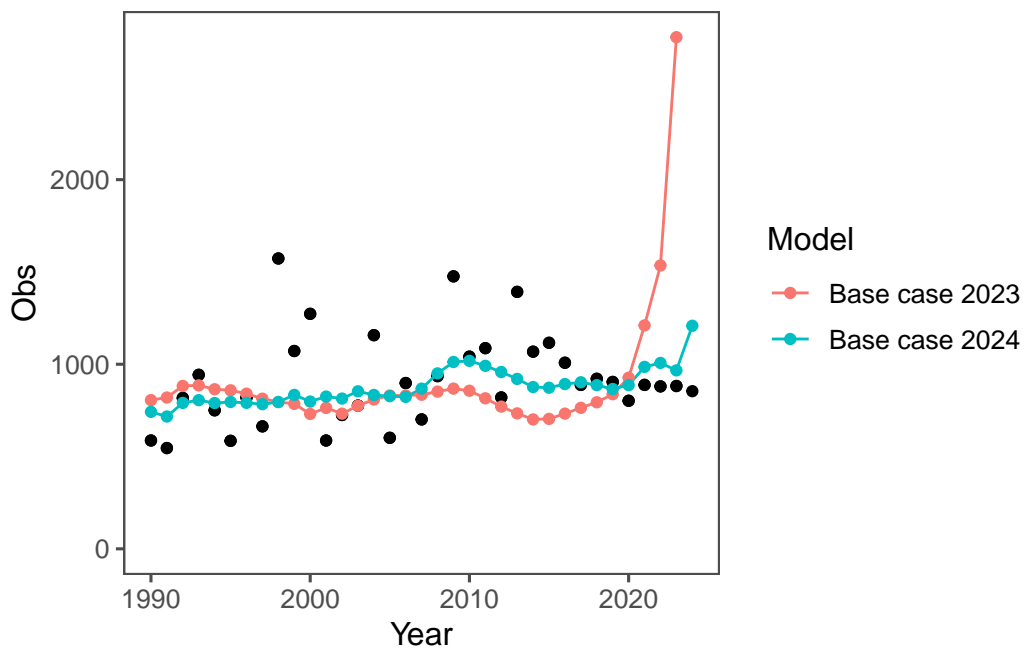
Figure 1: Base case model fits to main survey data compared to the previous assessment.
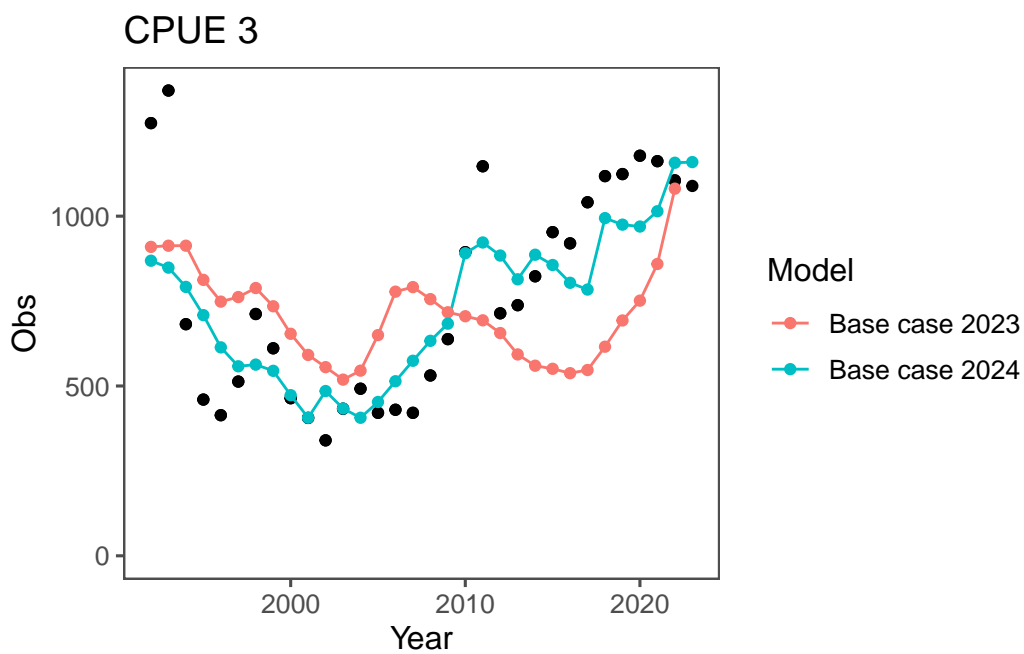

Figure 2: Base case model fits to the CPUE index 3 data compared to the previous assessment.

```
dfcpue <- rbind(data.frame(Year = 1964:2023, Obs = old_bc$Obs_CPUE_1, predicted = old_bc$e_CI
    Model = "Base case 2023"), data.frame(Year = 1964:2024, Obs = m0$Obs_CPUE_1,
    predicted = m0$e_CPUE_1, Model = "Base case 2024"))
dfcpue |>
    filter(Obs > 0) |>
    ggplot(aes(x = Year, y = Obs, color = Model)) + geom_point(color = "black") +
    geom_line(aes(y = predicted)) + geom_point(aes(y = predicted)) + ggtitle("CPUE 1") +
    ylim(0, NA)
```
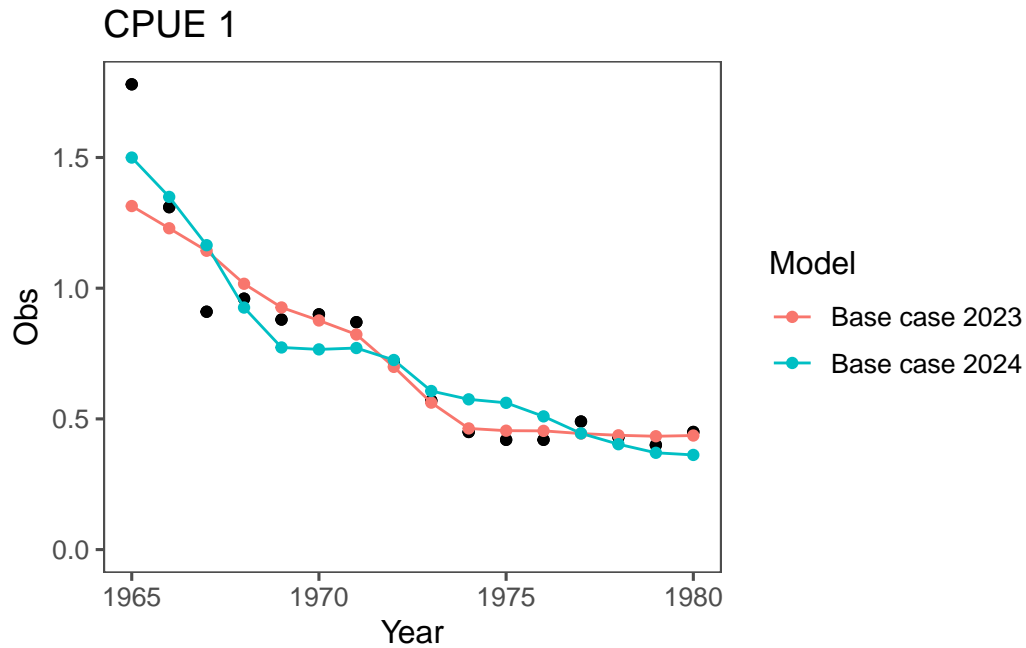

Figure 3: Base case model fits to the CPUE index 1 data compared to the previous assessment.

SSB results
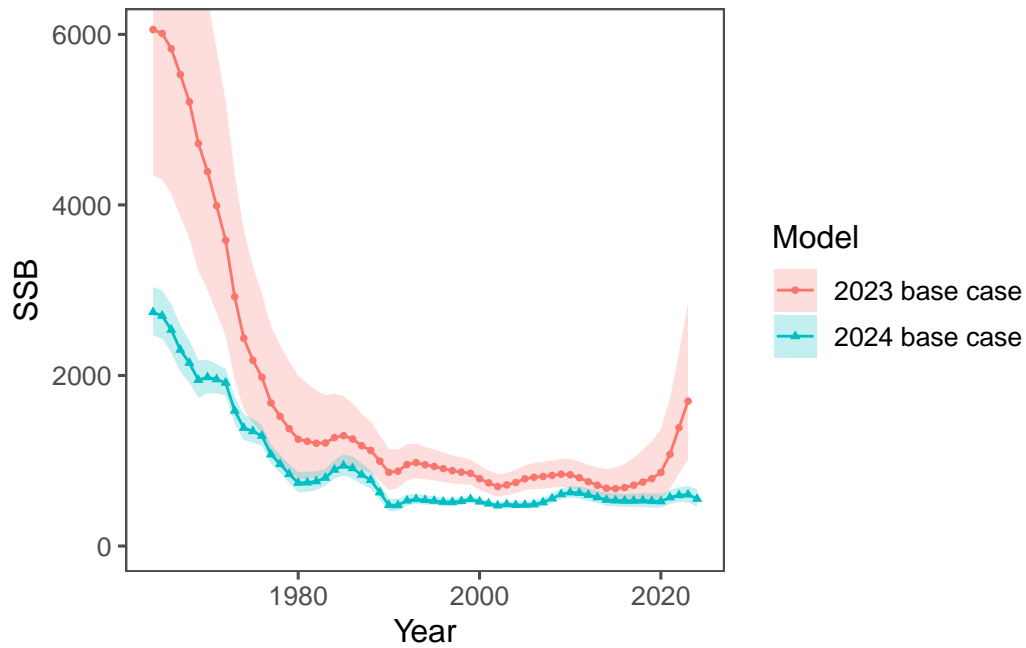
Figure 4: Base case model showing the SSB estimates compared to the previous assessment.

```
mods |>
    filter(Model %in% mod_label[1:2], Year > 1960, Variable == "Depletion") |>
    ggplot(aes(x = Year, y = value, ymin = ymin, ymax = ymax, type = Model, fill = Model)) +
    geom_ribbon(alpha = 0.24) + ggthemes::theme_few() + geom_line(aes(color = Model)) +
    geom_point(aes(color = Model, shape = Model), size = 1) + ylab("Relative SSB") +
    xlab("Year")
```
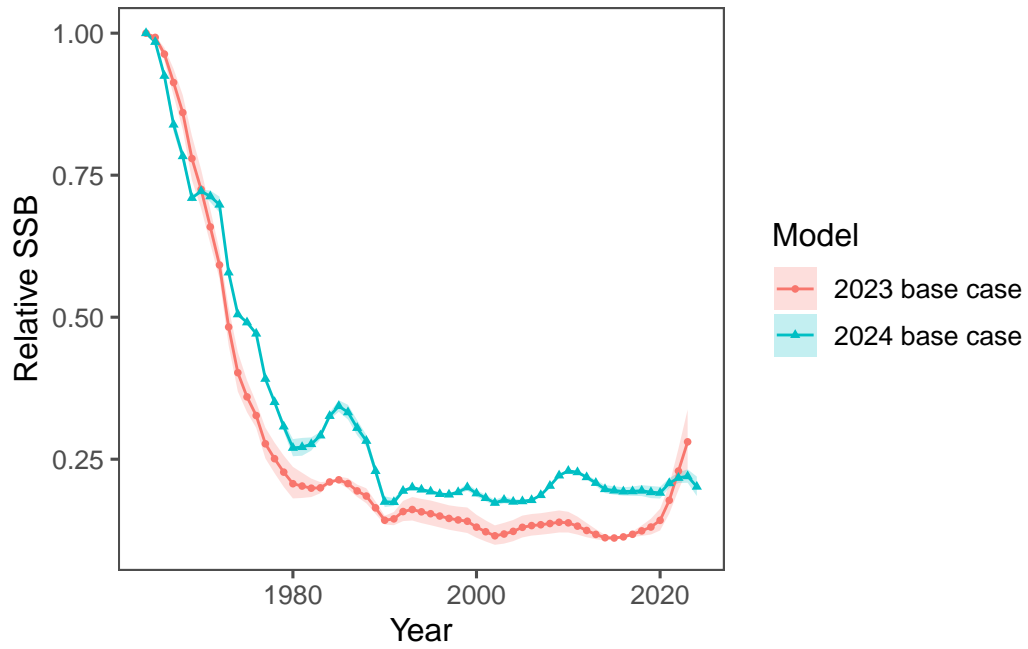
Figure 5: Base case model showing the relative SSB estimates compared to the previous assessment.
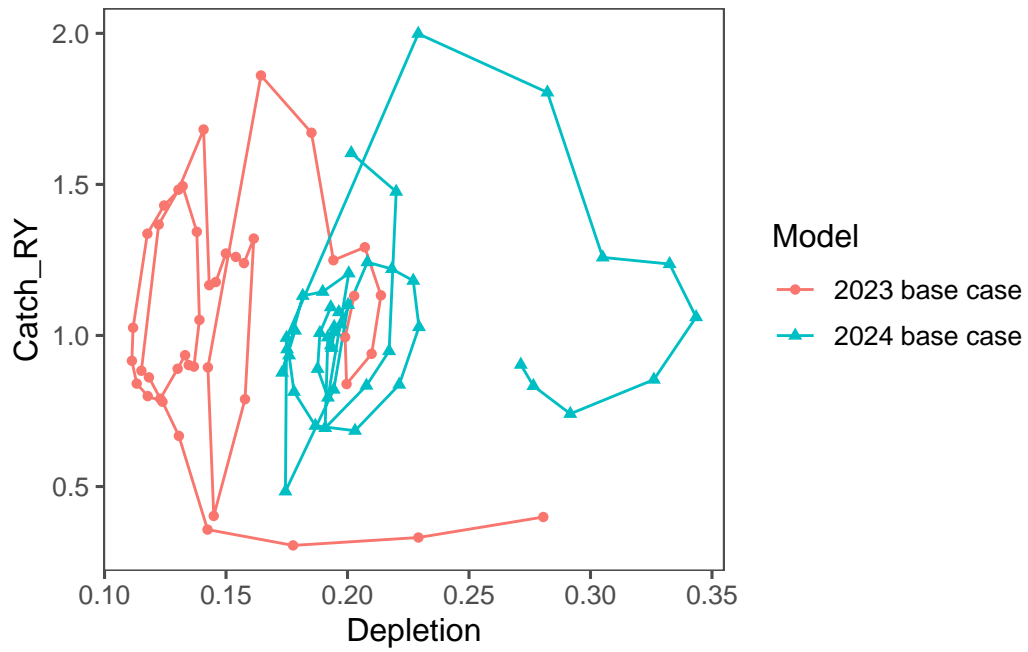
Figure 6: Base case model showing the relative SSB estimates compared to the previous assessment.
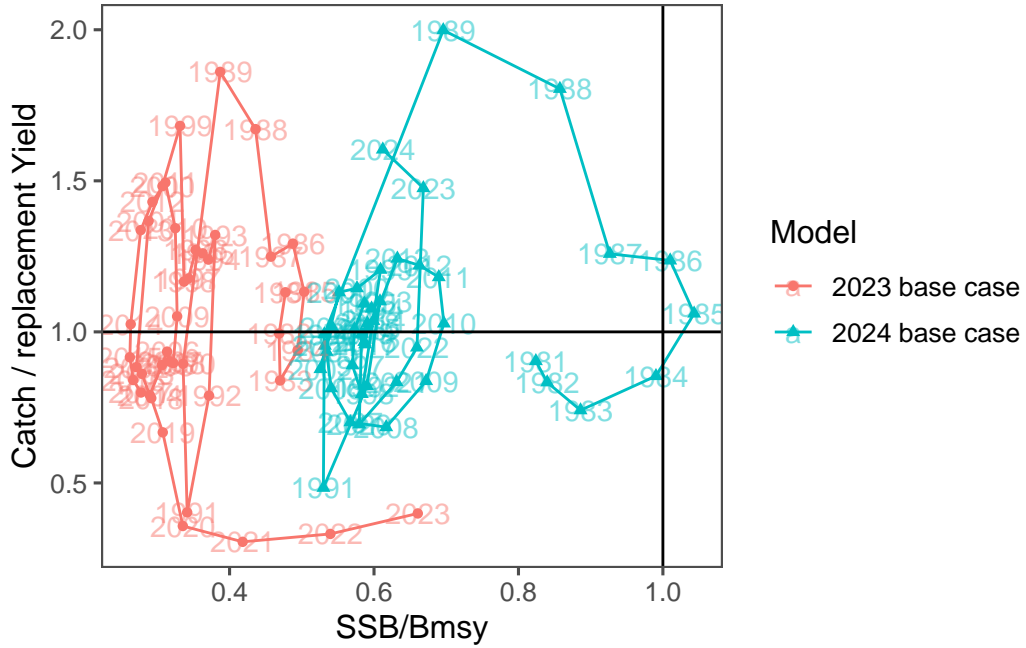
Figure 7: Base case model showing the relative SSB estimates compared to the previous assessment.
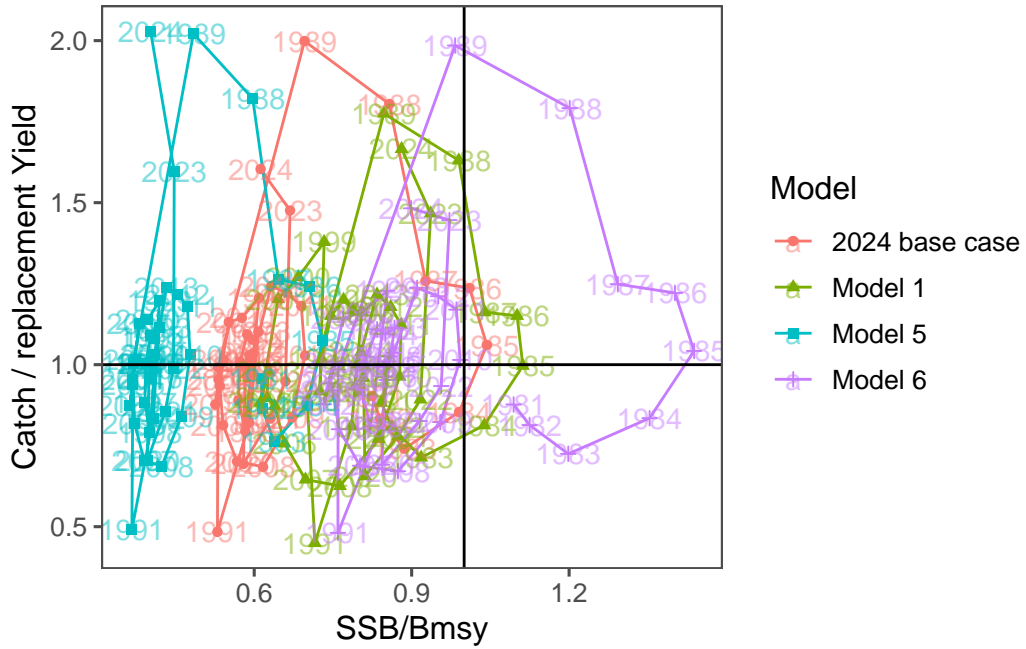

Figure 8: Base case model showing the relative SSB estimates compared to the previous assessment.

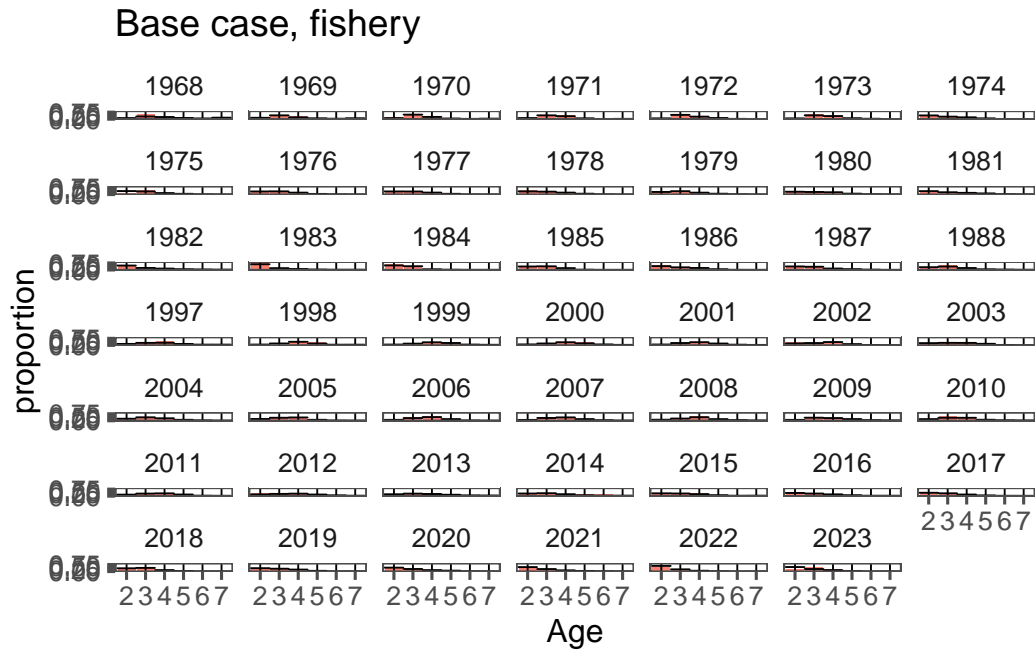**Age composition fits**

Base case, fishery

Figure 9: Base case model fits to survey and fishery age composition data. Note that the base case model uses a 'minus group' equal to '1' for the survey data.
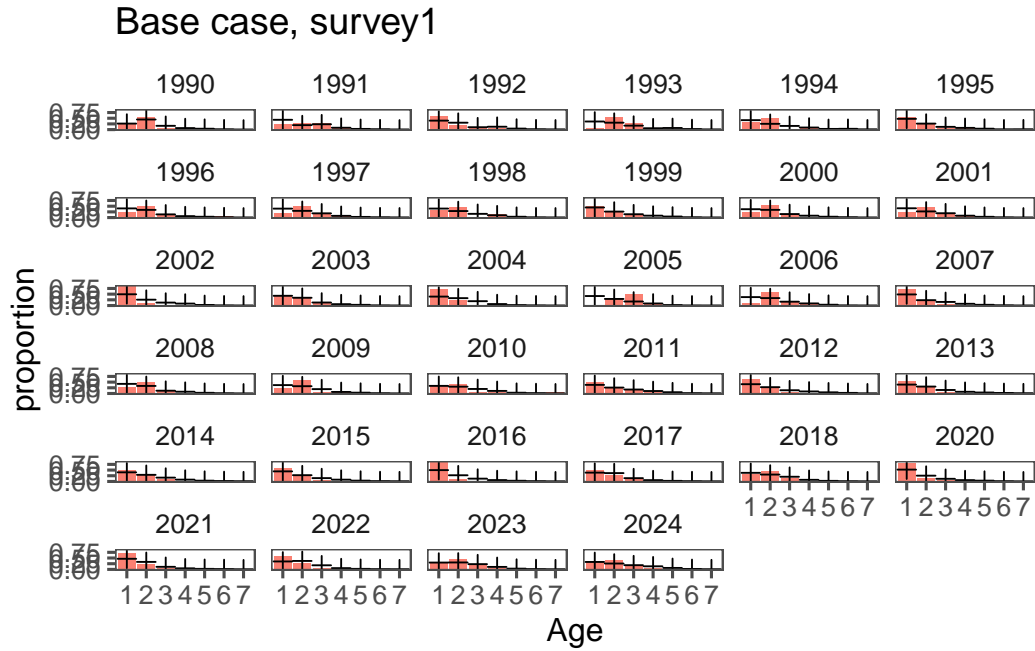
Base case, survey1

Figure 10: Base case model fits to survey and fishery age composition data. Note that the base case model uses a 'minus group' equal to '1' for the survey data.
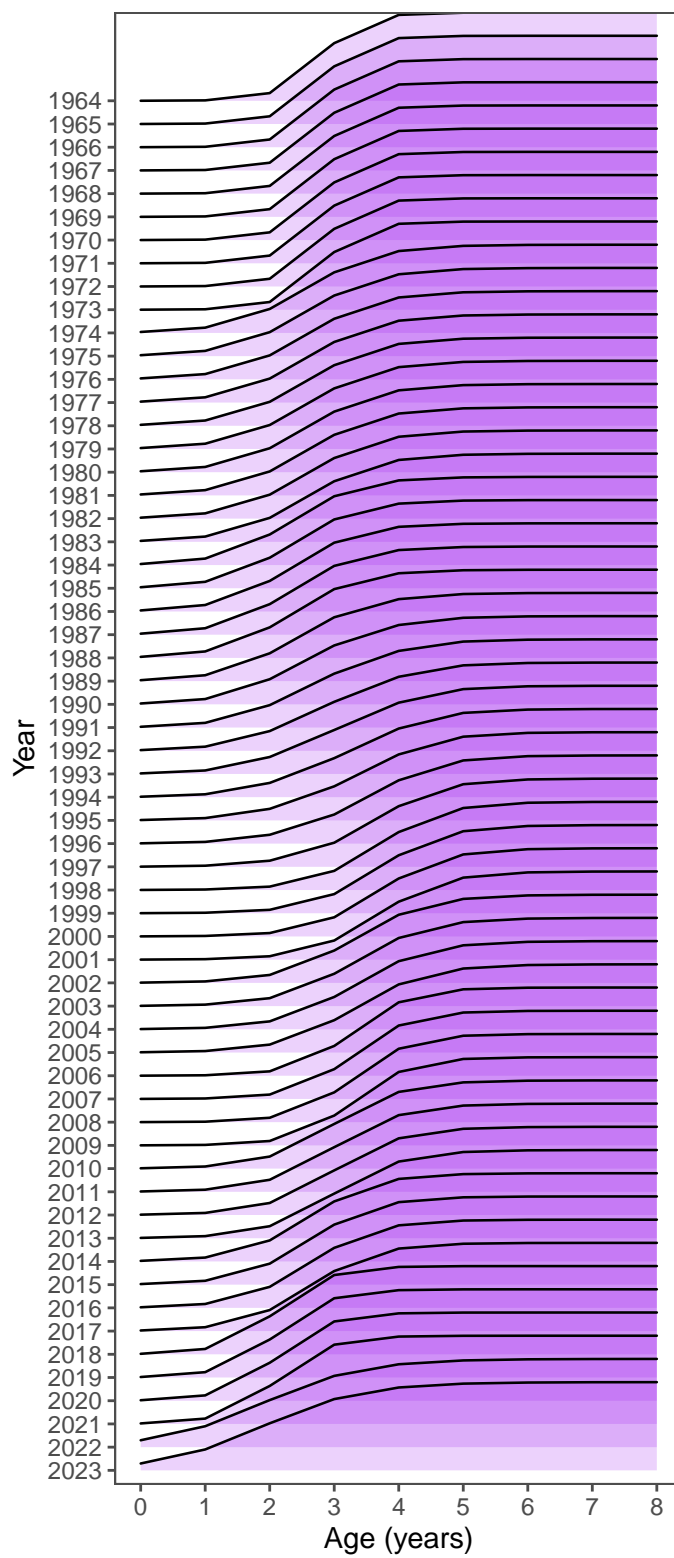
Selectivity

Figure 11: Selectivity estimates for the base-case model run.

Stock-recruitment curves

The following plot shows the stock-recruitment curves for the base case and models 1, 2, 3, and 5 and 6.

```
Warning: The shape palette can deal with a maximum of 6 discrete values because more
than 6 becomes difficult to discriminate
i you have requested 8 values. Consider specifying shapes manually if you need
  that many have them.
Warning: Removed 40 rows containing missing values or values outside the scale range
(`geom_point()`).
```
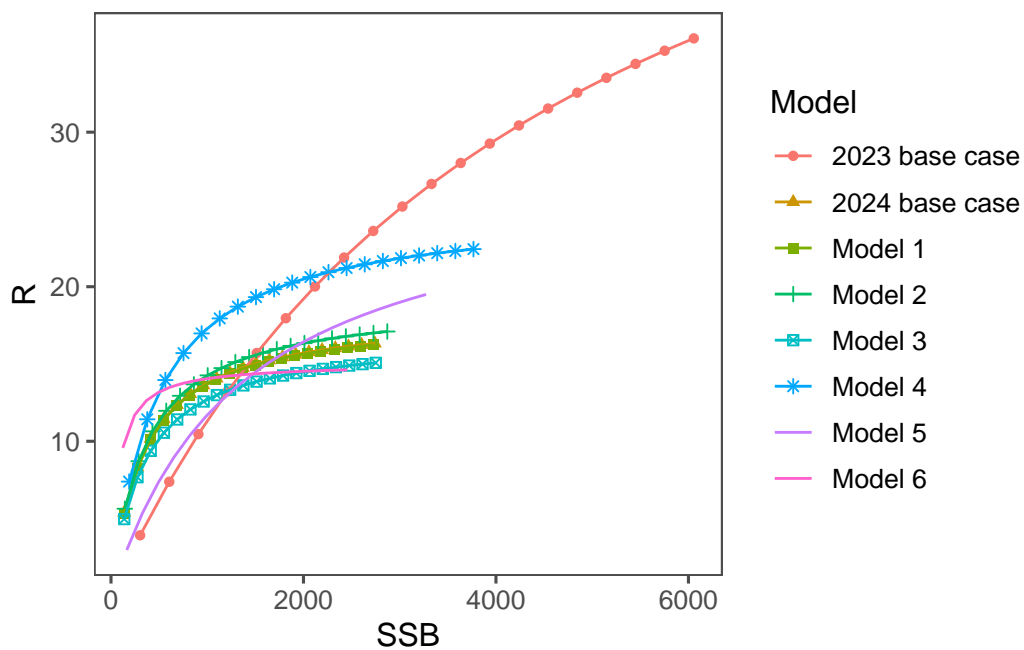

Figure 12: Model runs

Stock status comparisons

Unclear why this table doesn't show up…

```r
dftmp <- NULL
mod_scen <- c(2:5)
for (ii in mod_scen) {
    x <- modlst[[ii]]
```