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Casal2 Stock Assessment for Antarctic krill in CCAMLR Subarea 48.1

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Abstract

The Casal2 model for Antarctic krill initially reported in Kinzey and Watters (2023) now incorporates MCMC estimation of parameter uncertainty in addition to the MPD estimates described in the earlier paper. Four model configurations are explored employing two different methods of estimating annual recruitment multipliers - simplex transformation and non-simplex - and two alternative approaches to modeling future projected catches, either with all model years combined into a single '@process Instantaneous_Mortality' block, or with future catch years separated from past catch years into a second '@project future_catch' block. Differences in AIC scores between the simplex and non-simplex approaches indicated the two non-simplex configurations were much better descriptors of the data than the two configurations using the simplex transformation. The two configurations that combined past and future catches into the same block produced MPD and MCMC outputs that could be processed by the 'extract.mcmc()', 'extract.mpd()' and 'extract.tabular()' functions in the r4Casal2 package so that the CCAMLR decision rules could be applied to the projections. As implemented here, in the two configurations that separated future catches into a '@project future_catch' block the spawning stock biomasses (SSBs) for the projected years 2022-2041 were not extracted by the r4Casal2 'extract()' functions so the CCAMLR decision rules could not be applied to those. One of these configurations, the non-simplex model configuration using a separate block for future catches, had the best AIC score of the four configurations. The configuration with the second-best AIC (ΔAIC = 1.2) was able to be read by the 'extract()' functions so those results are reported here. The Casal2 input files, 'estimation.csl2', 'observation.csl2', 'population.csl2', 'reports.csl2' and 'config.csl2' for the models described in this paper are available at 'https://github.com/us-amlr/Casal2-krill-model-mcmc'.

Introduction

The intent of this note is to show how an integrated model for the krill fishery in Subarea 48.1 could be developed from data that are currently available and future data that will become available. The model configurations described in this paper are examples of how such a model could be applied in estimating precautionary yields that meet the CCAMLR decision rules. The Casal2 krill model described in this paper is not ready to provide management advice but could be developed further. Issues that remain to be addressed are discussed in the paper.

Methods

The basic model for Antarctic krill in Subarea 48.1 was described in Kinzey and Watters (2023) with code and data documented at 'https://github.com/us-amlr/Casal2-krill-model'. The more recent model configurations with MCMC sampling are documented at 'https://github.com/us-amlr/Casal2-krill-model-mcmc'.

The model uses all available summer survey data (January-February) from the U.S. AMLR ship surveys (1991-2011) (acoustics and length-frequencies), German ship surveys (1981, 1982, 1984-1987)(length-frequencies), catches from commercial fisheries (1976, 1977, 1980-2021) and length-frequencies from fishery observers (2011-2016, 2018-2020). The data values obtained from these sources is reported in the 'observations.csl2' files available on the two U.S. AMLR GitHub repositories for the Casal2 krill model.

The last year of data used in the model was 2021. Model configurations were projected forward for 20 years (2022 to 2041) without fishing, and with fishing, to discriminate between variability expected due to natural population dynamics and variability due to increases in fishing.

A sequence of models was constructed for the two model configurations with output files that were readable using the r4Casal2 'extract()' functions. First, a model with no future catches and all recruitment multipliers equal to 1.0 was run in both MPD and MCMC modes. Second, the estimated recruitment multipliers for 1992-2011 from the first model were applied to the future projected years 2022-2041 and this model was run again with no future catches. This represents how the population could be expected to look without fishing in the future if the same recruitments estimated from the time period with the most survey data were repeated going forward. Third, the model was run with 600,000 tonnes of future catches with the future recruitment multipliers assigned from 1992-2011.

MCMC sampling of the parameter distributions was initially conducted for 110,000 samples, saving every 1,000th sample. A single run of 110,000 samples required about 25 to 30 minutes. Twelve runs could be completed simultaneously on a multicore workstation. MCMC sampling was increased to 2,100,000 samples for two configurations, saving every 10,000 for selected configurations to evaluate the effect of longer MCMC runs. These longer runs required 7-8 hours.

The first of the four configurations of the Casal2 krill model to be developed, the 'combined non-simplex' model, merged past and future projected catches into the '@process Instantaneous_Mortality' block. The second configuration, the 'combined simplex' model, was configured the same as the first configuration except it used the simplex transformation to estimate the recruitment multipliers. The mode in which these models were run (-r for no estimation, -e for MPD estimation, -m for MCMC estimation, -t for tabular output) was selected using simple combinations of these arguments (Table 1).

A possible issue with these first two configurations is that merging past and future catches in '@process Instantaneous_Mortality' will include the future years with no data in the estimation process. In theory years without data shouldn't affect the likelihood but this might cause issues in practice.

Separating the future projection years from the data years using '@project future_catch' in the third and fourth (non-simplex, and simplex, respectively) configurations completely removes the projection

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years from the parameter estimation so that only years with data are used for the estimates. The third and fourth configurations that separate past and future catches into different blocks were called the 'separate non-simplex' and 'separate simplex', respectively. They were first initiated using different mode arguments (Table 2) to make the output files similar to toothfish Casal2 outputs, but then reinitiated using the arguments in Table 1 for plotting the figures in this paper.

All four configurations were assigned lognormal recruitment multipliers with a mean of 1.0 and CV of 0.8. All configurations completed all MCMC samples with these recruitment inputs. Other CV values for the recruitment multipliers often created a 'std::bad_alloc' error before completing all MCMC samples for at least one of the configurations.

The 'extract.mcmc()', extract.mpd()' and 'extract.tabular()' functions in the r4Casal2 package were applied to the output files from each run and those that were extractable were processed using 'r4Casal2_krill.r' (see attached appendix for the R code) to produce the figures and assessments of future catches using the CCAMLR decision rules as reported here.

The Rhat function from the Rstan library was applied to these configurations as a diagnostic for parameter identifiability. It uses the outputs of multiple MCMC chains to assess the reliability of the estimates for each parameter. Ideally, no parameter should have a rhat score > 1.10. The Rhat function was applied to sets of 3 chains with identical input values but different random seeds.

Results

The configurations with recruitment multipliers estimated using the simplex transform were over 300 AIC units worse than those with non-simplex recruitment multipliers (Table 3), indicating the non-simplex versions were a much better representation of the data. For the non-simplex configurations, the 'separate non-simplex' configuration was 1.2 AIC units better than the 'combined non-simplex'. Models within 2 or 3 AIC units of one another are considered to have good support in the data (Burnham and Anderson, 1998).

The output files from the 'combined non-simplex' and 'combined simplex' configurations were supplied to 'r4Casal2_krill.r' as extract.mcmc('samples.1'), extract.tabular('krill_samples.txt') and extract.mpd('krill.e.txt') to produce Figures 1-3. For these two configurations the first run represented the population without fishing or recruitment variability in the future (Figure 1), the second run represented no fishing with future recruitment variability (Figure 2) and the third run represented 600,000 tonnes of annual catches in future years with recruitment variability (Figure 3).

The output files from the 'separate non-simplex' and 'separate simplex' configurations obtained using the arguments in Table 2 produced errors when supplied to r4Casal2 functions as extract.tabular('projections.log') and extract.mpd('MPD.dat'). When the two configurations were reinitiated using the arguments in Table 1 to obtain output files the extract.tabular('krill_samples.txt') and extract.mpd('krill.e.txt') produced files that were readable in R, but the extract.tabular('krill_samples.txt') function did not produce the derived SSB values from the future projections even though they were reported in 'krill_samples.txt'. Only the 1976-2021 estimates were extracted (Figure 4). This did not allow the CCAMLR decision rules to be calculated for the future projections. Time limitations prevented the development of alternative R code to extract the 2022-2041

SSB values from the Casal2 projection file, so no calculation of the CCAMLR decision rules using the 'separate' configurations was made at this time. This included the best configuration selected by AIC, the 'separate non-simplex' configuration. Future work should include developing R code to extract the SSB values for the projection years from the 'separate' configurations.

The simplex and non-simplex configurations of the combined model produced substantially different calculated values for the decisions rules Gamma 1 (depletion) and Gamma 2 (escapement) (Table 4). 600,000 tonne catches from Subarea 48.1 would not be considered precautionary using the 'combined non-simplex' configuration. Annual catches of this magnitude fail both decision rules, with a 60% chance of SSB falling below 20% of B0 (the depletion rule) and the median SSB in 2041 being 60% of median B0 (less than the 75% permitted by the escapement rule).

Alternatively, in the 'combined simplex' configuration 600,000 tonne catches pass both rules and would allow catches greater than this (Table 4). This configuration calculates a 0% probability of depletion less than 20% of B0 and median SSB in 2041 to be 94% of median B0. This wide difference between different configurations using the same data highlights the importance of using a model selection tool like AIC in making statistical inference. In this case, the much lower AIC score of the 'combined simplex' configuration does not support catches of 600,000 tonnes from Subarea 48.1.

The configurations had 53 to 55 estimated parameters (Table 3). The rhat diagnostic indicated that 1 to 3 parameters failed the diagnostic with scores > 1.10 (Figures 5-9). These were usually selectivity parameters. Increasing the MCMC sampling for the 'combined non-simplex' and 'combined simplex' from 110,000 to 2,100,000 reduced the rhat scores but some parameters remained above 1.10.

A feature apparent in all of Figures 1-4 is that the model estimated less variability in SSBs for the years 2012-2021 when the data were supplied by fisheries acoustic surveys and length-frequencies from fisheries observers than during 1992-2011 when these data were from research surveys. The 2012-2021 time period showed a declining trend in estimated SSB in all models. Differences between the AMLR survey length-frequencies and the fishery length-frequencies noted in Kinzey et al. (in press) could be responsible for these differences in population dynamics in the model and could be explored further.

The configurations varied in the level of correspondence between the MPD estimates (red points) and MCMC estimates (black lines). In the best model selected by AIC, the 'separate non-simplex' configuration (Figure 4 left) the median MCMC estimates were larger than the MPD estimates. Longer MCMC samples for this model could be used to investigate this difference between the MPD and MCMC estimates.

Literature cited

Burnham, K.P. and Anderson, D.R. 1998. Model Selection and Inference: A Practical Information-Theoretic Approach, Springer-Verlag New York Inc. 353 pp.

Kinzey, D. and G.M. Watters. 2023. Casal2 assessment for Antarctic krill in Subarea 48.1: a pilot model. CCAMLR WG-SAM-2023/25

Kinzey, D., J.T. Hinke, C.S. Reiss, G.M. Watters. (in press). Recruitment variability of Antarctic krill in Subarea 48.1 expressed as 'proportional recruitment': length threshold effects. CCAMLR Science Special Issue on Krill Management.

Table 1. Casal2 arguments and output filenames used for the first two 'combined' model configurations.

casal2 -r >> krill.r.txt
casal2 -e >> krill.e.txt
casal2 -m >> krill_mcmc.m.txt
casal2 -r -i samples.1 -t >> krill_samples.txt
casal2 -f 1 -i samples.1 -t >> projection.out.txt

Table 2. Casal2 arguments and output filenames used for the third and fourth 'separate' model configurations.

casal2 -r > run.log 2> run.err
casal2 -E MPD.dat -o free.dat > estimate.log 2> estimate.err
casal2 -M MPD.dat -g 0 > MCMC.log 2> MCMC.err
casal2 -f 1 -I samples.1 -t > projections.log 2> projections.err

Table 3. Negative log-likelihoods (NLL), number of parameters (k) and Akaike Information Criterion (AIC) for four configurations of the Casal2 krill model. AIC = 2k-2(LL).

Configuration	NLL	k	AIC
combined non-simplex	-261.413	55	-412.826
combined simplex	-76.2836	53	-46.5672
separate non-simplex	-269.588	55	-429.176
separate simplex	-75.0953	54	-42.1906

Table 4. CCAMLR decision rules for 'combined non-simplex' and 'combined simplex' configurations.

	Gamma 1 - Depletion	Gamma 2 - Escapement
combined non-simplex	0.70	0.60
combined simplex	0.0	0.94

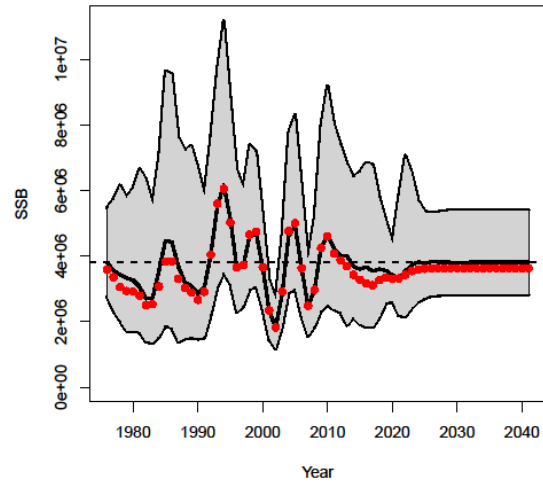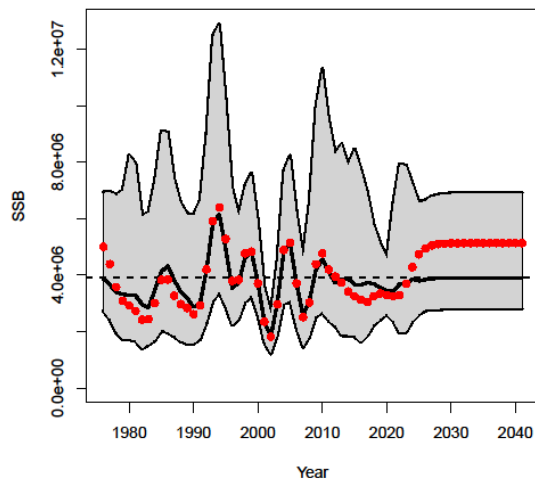non-simplex   simplex

Figure 1. No future catches, future (2022-2041) recruitment multipliers = 1.0 for 'combined' non-simplex and simplex. Red dots are MPD estimates of annual spawning biomasses, black lines and grey areas indicate the median and 95% CIs from the MCMC sampling.

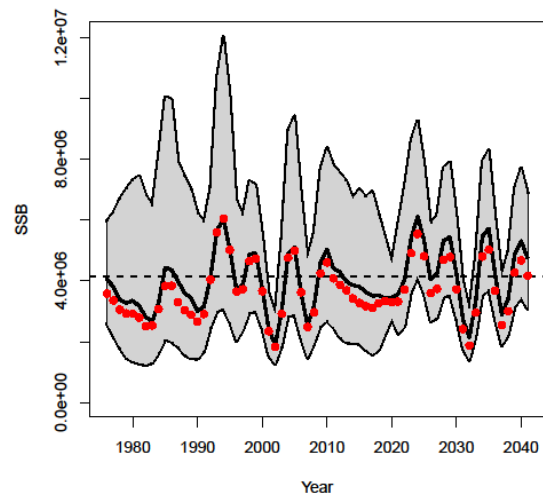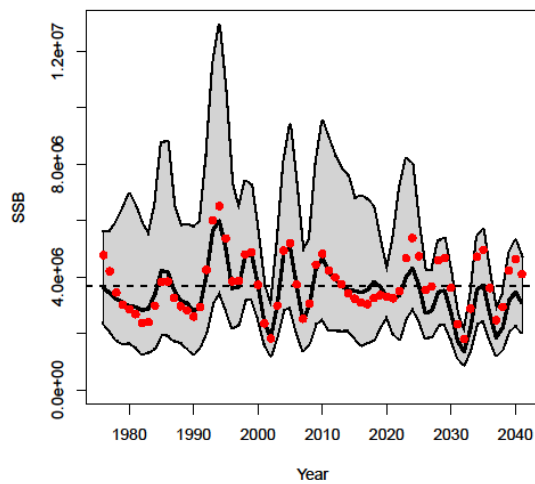non-simplex   simplex

Figure 2. No future catches, future recruitment multipliers for 2022-2041 taken from 1992-2011. Models are 'combined' non-simplex and simplex.

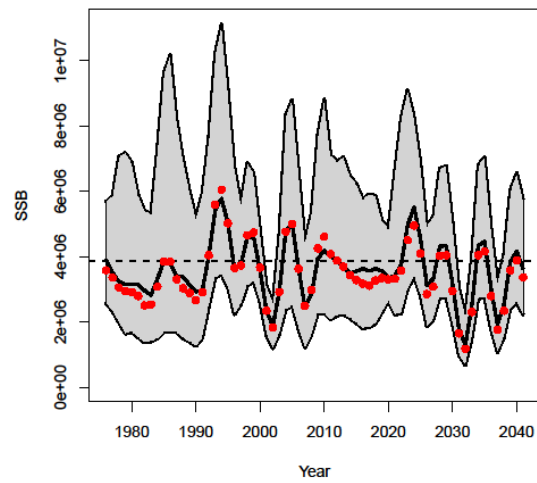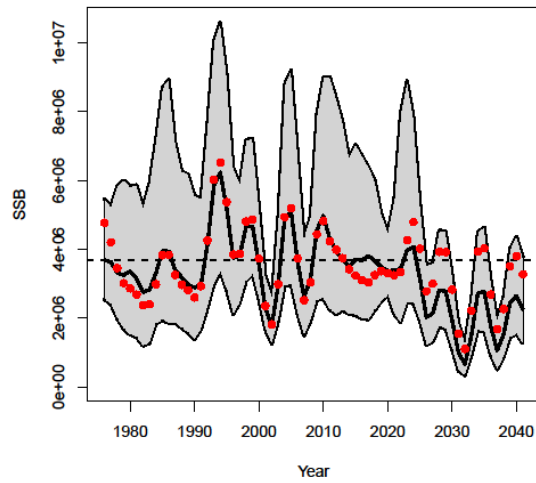non-simplex   simplex

Figure 3. 600 tonnes annual future catches, future recruitment multipliers taken from 1992-2011. Models are 'combined' non-simplex and simplex.

non-simplex   simplex
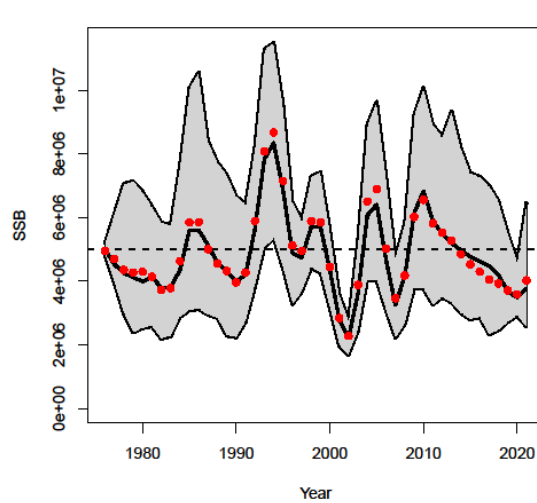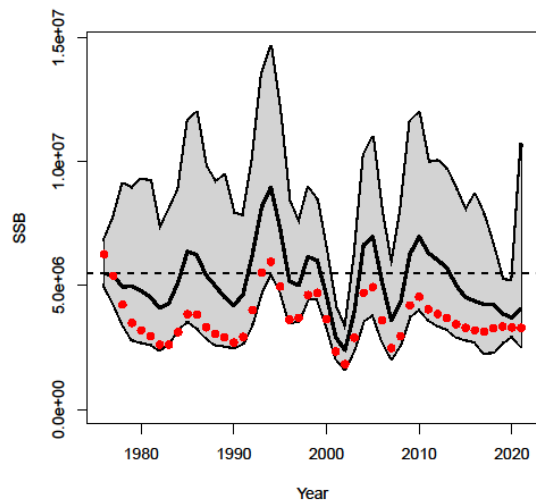

Figure 4. No future catches, future recruitment multipliers = 1.0 for 'separate' non-simplex and simplex. Although the output file contained derived values for 2022-2041, the 'extract.tabular()' function from r4Casal2 only extracted years 1976-2021.
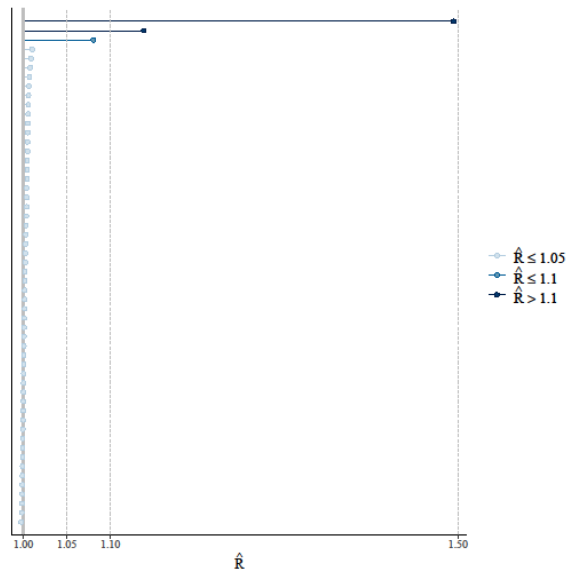
Figure 5. Rhat plot for 'combined non-simplex' configuration with 2,100,000 MCMC samples, saving every 1000th. Two selectivity parameters (selectivity[AMLR_ac_Sel].ato95, selectivity[Fsh_lf_Sel].ato95) had rhat scores > 1.10.
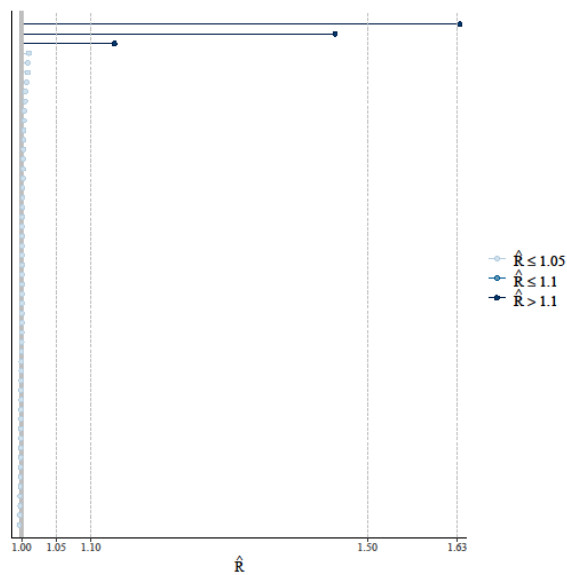

Figure 6. Rhat plot for 'combined simplex' configuration with 2,100,000 MCMC samples, saving every 1000th. Three selectivity parameters (selectivity[AMLR_ac_Sel].a50, selectivity[AMLR_ac_Sel].ato95, selectivity[Fsh_lf_Sel].ato95) had rhat scores > 1.10.
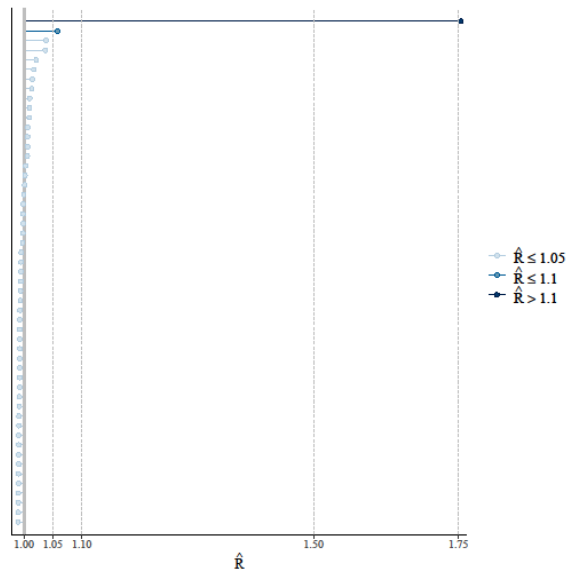
Figure 7. Rhat plot for 'separate non-simplex' configuration with 110,000 MCMC samples, saving every 1000th. One parameter (process[Recruitment].b0) had a rhat score > 1.10.
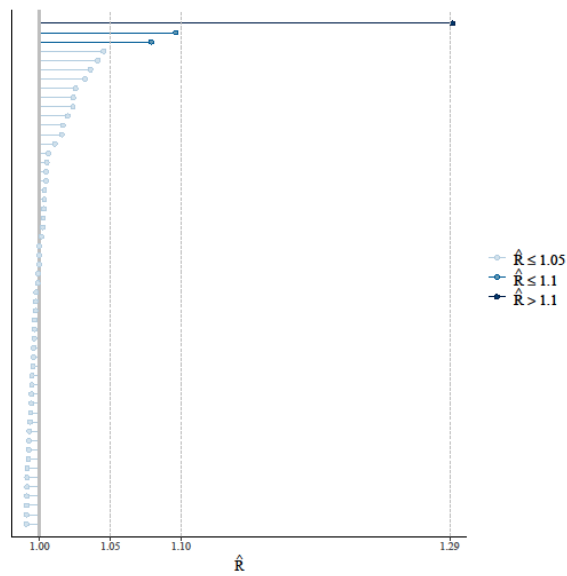

Figure 8. Rhat plot for 'separate simplex' configuration with 110,000 MCMC samples, saving every 1000th. One parameter (selectivity[Fsh_ac_Sel].a50) had a rhat score > 1.10.

Appendix: R code to process Casal2 krill output files

```
# Appendix: R code to process Casal2 krill output files
# modified from C. Marsh code at https://niwafisheriesmodelling.github.io/r4Casal2/mcmc.html)
# and from 'https://github.com/NIWAFisheriesModelling/r4Casal2'.
# any future updates can be found at 'https://github.com/us-amlr/Casal2-krill-model-mcmc'


rm(list=ls())
wd <- ''          # working directory for mcmc chains
ch.names <- c('0K.a','0K.b','0K.c')      # directories containing identically configured mcmc chains
n.ch <- length(ch.names)                 # number of chains
current.chain <- '0K.a'                  # chain to be plotted
wd2 <- paste(wd,current.chain,'/biom/',sep='')    # directory for Casal2 outputs to be plotted
setwd(wd)


#lib.path <- 'C:/zot/Casal2/2023/CASAL2_Alistair/R-libraries/'
lib.path <- 'C:/zot/Casal2/2023/R-Libraries_Casal2_Alistair/Casal2_23.09/'
path <- paste(lib.path,'casal2/R/',sep='')
r.scrpts <- dir(path)
for(i in 1:length(r.scrpts))
   source(paste(path,r.scrpts[i],sep=''))
library(knitr)
library(ggplot2)
library(dplyr)
library(reshape2)
library(tidyr)
library(r4Casal2)


mcmc.nm <- mcmc_post <- list()
for(i.ch in 1:(length(ch.names))){
  mcmc.nm[[i.ch]] = extract.mcmc(path = paste(wd,ch.names[i.ch],'/biom',sep=''),
```

```
     samples.file = "samples.1", objectives.file = "objectives.1")

  mcmc.nm[[i.ch]]$chain = as.character(i.ch)

  mcmc_post[[i.ch]] = mcmc.nm[[i.ch]] %>% filter(state == "mcmc")

  }


# script below assumes three mcmc chains were run

mcmc_all <- rbind(mcmc_post[[1]],mcmc_post[[2]],mcmc_post[[3]])

mcmc_non_burn_in = mcmc_all %>% filter(state == "mcmc")

n_posterior_samples =  nrow(mcmc_post[[1]])+nrow(mcmc_post[[2]])+nrow(mcmc_post[[3]])

pars = colnames(mcmc_post[[1]][,12:(ncol(mcmc_non_burn_in) - 1)])

iters = max(nrow(mcmc_post[[1]]),nrow(mcmc_post[[2]]),nrow(mcmc_post[[3]]))

bayes_array = array(dim = c(iters, 3, length(pars)), dimnames = list(1:iters, 1:3, pars))

bayes_array[1:nrow(mcmc_post[[1]]),1,] = as.matrix(mcmc_post[[1]][,12:(ncol(mcmc_non_burn_in) -
1)])

bayes_array[1:nrow(mcmc_post[[2]]),2,] = as.matrix(mcmc_post[[2]][,12:(ncol(mcmc_non_burn_in) -
1)])

bayes_array[1:nrow(mcmc_post[[3]]),3,] = as.matrix(mcmc_post[[3]][,12:(ncol(mcmc_non_burn_in) -
1)])

min_cutoff = min(nrow(mcmc_post[[1]]),nrow(mcmc_post[[2]]),nrow(mcmc_post[[3]]))

bayes_array = bayes_array[1:min_cutoff, ]


library(purrr)

library(bayesplot)

# library(posterior)

library(rstan) # required for function Rhat


rhats = apply(bayes_array, MARGIN = 3, Rhat)

n_eff_bulk = apply(bayes_array, MARGIN = 3, ess_bulk)

n_eff_tail = apply(bayes_array, MARGIN = 3, ess_tail)
```

```
# set probabilities to calculate from mcmc samples

p <- c(0.025, 0.5, 0.975) ## confidence intervals

p_names <- map_chr(p, ~paste0(.x*100, "%"))

p_funs <- map(p, ~partial(quantile, probs = .x, na.rm = TRUE)) %>%

  rlang::set_names(nm = c("low", "mid", "upp"))


# extract derived SSB values from tabular mcmc estimates

cas2_file_name = paste(wd2,'krill_samples.txt',sep='') # this is samples.1 produced from casal2 -m,

                        # casal2 -r -i samples.1 -t >> krill_samples.txt

cas2_tab = extract.tabular(file = cas2_file_name, quiet = T)

## cut off burn-in the first 50 samples

#cas2_tab = burn.in.tabular(cas2_tab, Row = 50)


# get selectivities

selectivity_df = get_selectivities(cas2_tab)

selectivity_df$selectivity_label <- selectivity_df$report_label # dhk hack to get dplyr plotting code to
work

quantile_selectivity_df = selectivity_df %>%

  group_by(bin, selectivity_label) %>%

  summarize_at(vars(selectivity), p_funs)


# get annual spawning stock biomasses

ssbs = get_derived_quanitites(model = cas2_tab)

ssbs$years[ssbs$years == "initialisation_phase_1"] = 1976

#ssbs$years <- as.numeric(ssbs$years)

ssbs <- cbind(ssbs,B0=rep(cas2_tab$summary$values[[1]],47)) # add B0 column to ssbs

                        # (47 years of B0 values*111 mcmc samples)

# calculate mcmc confidence intervals for spawning biomasses

quantile_ssb_df = ssbs %>%
```

```
  group_by(years, dq_label) %>%

  summarize_at(vars(values), p_funs)

quantile_ssb_df$years = as.numeric(quantile_ssb_df$years)


# get annual recruitments

recruits <- cas2_tab$Recruitment[[2]][substr(names(cas2_tab$Recruitment[[2]]),1,8) == 'recruits']

# calculate mcmc confidence intervals for recruitment

quantile_recruits_df <- t(apply(recruits,2,quantile,probs=p))


# calculate mpd estimates of median spawning biomasses

# (note that get_derived_quanitites does not produce uncertainty estimates for mpds)

krill_mpd = extract.mpd(paste(wd2,'krill.e.txt',sep='')) # extract mpd values at this location

ssbs_mpd = get_derived_quanitites(model = krill_mpd)

quantile_ssb_mpd_df = ssbs_mpd %>%

  group_by(years, dq_label) %>%

  summarize_at(vars(values), p_funs)

quantile_ssb_mpd_df$years = as.numeric(quantile_ssb_mpd_df$years)


# Decision Rules

Gamma1 <- ssbs %>% group_by(iteration) %>%

    filter(years > 2021) %>%

        summarize(Dep=min(values/B0)) %>%

        summarize(Pr=mean(Dep < 0.2))

Gamma1


Gamma2 <- ssbs %>%

        filter(years %in% max(years)) %>%

        summarise(ssb=median(values),ssb0=median(B0))

Gamma2$Escapement<-Gamma2$ssb/Gamma2$ssb0
```

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Gamma2

```
#The actual Gamma is the smallest of the two gammas:
GammaToUse<-which(c(Gamma1,Gamma2)==min(Gamma1,Gamma2)) #Which gamma is min?
if(length(GammaToUse)==2){GammaToUse=3} #when gamma1 and gamma2 are equal
OUT<-cbind(Gamma1,Gamma2,GammaToUse)
OUT


# Recruitment estimates
krill_mpd$Recruitment$standardised_recruitment_multipliers
krill_mpd$Recruitment$recruitment_multipliers
krill_mpd$Recruitment$true_ycs
krill_mpd$Recruitment$model_year[17:36]      # years 1992-2011
krill_mpd$Recruitment$recruitment_multipliers[17:36]


rhats[order(rhats,decreasing=TRUE)]
median(cas2_tab$summary$values[[1]])  # B0 mcmc median value for the chain


# Plots


##############
# plot rhat diagnostic
pdf(file = paste(wd,'rhat_',current.chain,'.pdf',sep=''))
mcmc_rhat(rhats)
graphics.off()


# plot selectivities
pdf(file = paste(wd,'selectivies_',current.chain,'.pdf',sep=''))
par(cex=1.3)
```

```r
plot(names(krill_mpd$Fsh_lf_Sel$Values),krill_mpd$Fsh_lf_Sel$Values,

  main='Estimate Krill Selectivity',xlab = 'Length (mm)',ylab = 'Length Selectivity',type='l',lwd=3,col='red')

  lines(names(krill_mpd$AMLR_lf_Sel$Values),krill_mpd$AMLR_lf_Sel$Values,col='blue',lwd=3,lty=1)

  lines(names(krill_mpd$AMLR_ac_Sel$Values),krill_mpd$AMLR_ac_Sel$Values,col='blue',lwd=3,lty=2)

  lines(names(krill_mpd$Fsh_ac_Sel$Values),krill_mpd$Fsh_ac_Sel$Values,col='red',lwd=3,lty=2)

  legend(6,0.4,lty=c(1,1,2,2),col=c('red','blue','blue','red'),

    c('Fishery_lfs','AMLR_lfs','AMLRacoustics','FisheryAcoustics'),lwd=3,cex=0.8)

graphics.off()


##############

# plot selectivities

pdf(file = paste(wd,'selectivies_',current.chain,'.pdf',sep=''))

par(cex=1.3)

plot(names(krill_mpd$Fsh_lf_Sel$Values),krill_mpd$Fsh_lf_Sel$Values,

  main='Estimate Krill Selectivity',xlab = 'Length (mm)',ylab = 'Length Selectivity',type='l',lwd=3,col='red')

  lines(names(krill_mpd$AMLR_lf_Sel$Values),krill_mpd$AMLR_lf_Sel$Values,col='blue',lwd=3,lty=1)

  lines(names(krill_mpd$AMLR_ac_Sel$Values),krill_mpd$AMLR_ac_Sel$Values,col='blue',lwd=3,lty=2)

  lines(names(krill_mpd$Fsh_ac_Sel$Values),krill_mpd$Fsh_ac_Sel$Values,col='red',lwd=3,lty=2)

  legend(6,0.4,lty=c(1,1,2,2),col=c('red','blue','blue','red'),

    c('Fishery_lfs','AMLR_lfs','AMLRacoustics','FisheryAcoustics'),lwd=3,cex=0.8)

graphics.off()


##############

# plot median and 95% CIs for mcmc estimates of ssbs, overlay mpd estimates of medians

pdf(file=paste(wd,'SSB_',current.chain,'.pdf',sep=''))

par(cex=1.2)

y.lim <-c(0,max(1,quantile_ssb_df$upp))

plot(quantile_ssb_df$years,quantile_ssb_df$mid,type='l',lwd=3,ylim=y.lim,

  xlab= 'Year',ylab='SSB')
```

```r
lines(quantile_ssb_df$years,quantile_ssb_df$low,lwd=3)

lines(quantile_ssb_df$years,quantile_ssb_df$upp,lwd=3)

polygon(c(quantile_ssb_df$years,rev(quantile_ssb_df$years)),
  c(quantile_ssb_df$mid,rev(quantile_ssb_df$upp)),col='light grey')

polygon(c(quantile_ssb_df$years,rev(quantile_ssb_df$years)),
  c(quantile_ssb_df$mid,rev(quantile_ssb_df$low)),col='light grey')

lines(quantile_ssb_df$years,quantile_ssb_df$mid,lwd=3)

abline(h=median(cas2_tab$summary$values[[1]]),lwd=2,lty=2)

points(quantile_ssb_mpd_df$years,quantile_ssb_mpd_df$mid,col='red',pch=19)

segments(
  quantile_ssb_mpd_df$years,quantile_ssb_mpd_df$low,
  quantile_ssb_mpd_df$years,quantile_ssb_mpd_df$upp,
  lwd=2,col='red')

graphics.off()


##############

# plot median and 95% CIs for mcmc estimates of recruitment

pdf(file=paste(wd,'Recruits_',current.chain,'.pdf',sep=''))

par(cex=1.2)

y.lim <-c(0,max(1,quantile_recruits_df[,3]))

yrs <- as.numeric(c(substr(rownames(quantile_recruits_df),10,13)))

plot(yrs,quantile_recruits_df[,2],type='l',lwd=3,ylim=y.lim,
  xlab= 'Year',ylab='Recruits')

lines(yrs,quantile_recruits_df[,1],lwd=3)

lines(yrs,quantile_recruits_df[,3],lwd=3)

polygon(c(yrs,rev(yrs)),
  c(quantile_recruits_df[,2],rev(quantile_recruits_df[,3])),col='light grey')

polygon(c(yrs,rev(yrs)),
  c(quantile_recruits_df[,2],rev(quantile_recruits_df[,1])),col='light grey')
```

```
lines(yrs,quantile_recruits_df[,2],lwd=3)

#abline(h=median(cas2_tab$summary$values[[1]]),lwd=2,lty=2)

points(yrs,krill_mpd$Recruitment$recruits,col='red',pch=19)

#segments(

#  yrs,quantile_recruit_mpd_df[,1],

#  yrs,,quantile_recruit_mpd_df[,3],

#  lwd=2,col='red')

graphics.off()
```