

Appendix S2. Summarize S/R model results and compute management reference points 2021 Skagit River Spring Chinook RER.

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This is version 0.21.10.06.

1 Background

This appendix shows how generate model averaged parameter estimates and generate figures relevant to the 2020-2021 wild Skagit River steelhead forecast. All analyses require the R software (v3.5 or later), as well as a few packages that are not included with the base installation of R.

```
if(!require("readr")) {  
  install.packages("readr")  
  library("readr")  
}  
if(!require("captioner")) {  
  devtools::install_github("adletaw/captioner")  
  library("captioner")  
}  
if(!require("coda")) {  
  install.packages("coda")  
}
```

```

  library("coda")
}
if(!require("here")) {
  install.packages("here")
  library("here")
}
if(!require("gsl")) {
  install.packages("gsl")
  library("gsl")
}
if(!require("loo")) {
  install.packages("loo")
  library("loo")
}

## set default caption delimiter
fig_cap <- captioner(infix = ".")

management_unit <- "spring"

## set directory locations
datadir <- here(paste(management_unit, "/", "data", sep = ""))
jagsdir <- here(paste(management_unit, "/", "jags", sep = ""))
analdir <- here(paste(management_unit, "/", "analysis", sep = ""))
savedir <- here(paste(management_unit, "/", "analysis/cache", sep = ""))

## better round/floor/ceiling
around <- function(x, func = "round", prec = 1) {
  ## 'func' can be "round", "floor", or "ceiling"
  ## 'prec' is desired precision (eg, 0.1 is to nearest tenth)
  if(!is.double(x)) {
    stop("'x' must be a real number")
  }
  if(!(func %in% c("round", "floor", "ceiling"))) {
    stop("'func' must be \"round\", \"floor\", or \"ceiling\"")
  }
  if(prec <= 0) {
    stop("'prec' cannot be less than or equal to 0")
  }
  do.call(func, list(x / prec)) * prec
}

#load complete model fits & model refits with subset data
loadmodfits<-function(modelnames){
  mod_fits<-list(NULL)
  for(i in 1:length(modelnames)){
    mod_fits[[i]] <- readRDS(file.path(savedir,paste0(modelnames[i], "_y", n_forecasts+1, "_", run
    #mod_fits[[i]] <- readRDS(file.path(savedir,paste0("fit_", modelnames[i], ".rds"))))
  }

```

```

    }
    return(mod_fits)
}

Re2prec <- function(x,map="round",prec=1) {
  ## 'map' can be round, floor, or ceiling
  ## 'prec' is nearest value (eg, 0.1 means to nearest tenth); default 1 gives normal behavior
  if(prec<=0) { stop("\n\"prec\" cannot be less than or equal to 0") }
  do.call(map,list(x/prec))*prec
}

```

2 Load the information

Here we load in the estimated parameters and states from the selected model, as well as the covariates and harvest data and escapement data.

```

## fit or load models
models=c("IPM_RK")
n_mods<-length(models)
mod_fits <- loadmodfits(models)
model <- as.matrix(mod_fits[[1]])

## covariate(s)
#dat_cvrs <- read_csv(file.path(datadir, paste("skagit","_",run,"_", "covars",".csv",sep = "")))
## total number of covariates
#n_cov <- dim(dat_cvrs)[2] - 1

## escapement
dat_esc <- read_csv(file.path(datadir, paste("skagit","_",run,"_", "esc",".csv",sep = "")))
## log of escapement
ln_dat_esc <- c(log(dat_esc$escapement), rep(NA, n_fore))

## harvest
dat_harv <- read_csv(file.path(datadir, paste("skagit","_",run,"_", "catch",".csv",sep = "")))
## drop year col & first age_max rows
dat_harv <- c(dat_harv$catch, rep(0, n_fore))

```

2.1 Model diagnostics

Here is a histogram of the Gelman & Rubin statistics (R_{hat}) for the estimated parameters.

```

mod_fit <- mod_fits[[1]]

par_conv <- c("alpha","beta",
"sigma_r","sigma_s","pi_tau",paste0("pi_eta[",seq(A-1),"]"))
gelman.diag(mod_fit[,par_conv])

```

```
## Potential scale reduction factors:
##
##          Point est. Upper C.I.
## alpha          1.00      1.01
## beta           1.00      1.00
## sigma_r        1.00      1.00
## sigma_s        1.00      1.00
## pi_tau         1.01      1.01
## pi_eta[1]      1.00      1.01
## pi_eta[2]      1.00      1.00
## pi_eta[3]      1.00      1.00
##
## Multivariate psrf
##
## 1
```

The convergence statistics show that Rhat for all parameters « 1.1 which indicates model achieved full convergence.

2.2 Main results

Here is a table of summary statistics for some of the model parameters.

```
tbl_smry <- apply(model[,c("alpha", "E_Rkr_a", "beta")], 2, quantile, CI_vec)
```

```
print(tbl_smry, digits=3, quote=FALSE, justify="right")
```

```
##      alpha E_Rkr_a      beta
## 2.5%   1.46   0.498 3.68e-05
## 50%    2.48   1.053 4.35e-04
## 97.5%  6.20   2.022 1.22e-03
```

2.2.1 Spawner-recruit relationship

Here is the relationship between spawner and subsequent recruits (a), assuming mean values for all covariates. Gray lines show 100 plausible spawner recruit relationships derived from posterior distributions for a and b parameters. Note that for plotting purposes only in (b) and (c), the density in the largest bin for each parameter contains counts for all values greater or equal to that. Vertical arrows under the x-axes in (b) and (c) indicate the 2.5th, 50th, and 97.5th percentiles.

```
layout(matrix(c(1,1,2,3), 2,2), c(3,2), c(1,1))
CI_vec <- c(0.025, 0.5, 0.975)
offSet <- 0.06

mcmc_samp <- 4000
```

```

MC <- 100
set.seed(123)
idx <- sample(seq(mcmc_samp),MC)

## posterior of spawners

sDat <- apply(model[,grep("Sp",colnames(model))],2,quantile,CI_vec)
sDat <- sDat[,1:(n_yrs-age_min)]
## posterior of recruits
rDat <- exp(apply(model[,grep("tot_ln_Rec",colnames(model))],2,quantile,CI_vec))

aa <- model[,grep("mu_Rkr_a",colnames(model))]
bb <- model[,grep("beta",colnames(model))]
# aa <- median(mod_fit$BUGSoutput$sims.list$alpha)
## empty plot space for spawner-recruit relationships
dd <- 500
yM <- Re2prec(max(rDat),"ceiling",dd)
#yM <- 30000
xM <- Re2prec(max(sDat),"ceiling",dd)
par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0,0,0))
plot(sDat[2,],rDat[2,], xlim=c(0,xM),ylim = c(0,yM), pch=16, col="blue3", type="n",
     xaxs="i", yaxs="i", ylab="Recruits (1000s)", xlab="Spawners (1000s)", cex.lab=1.2,
     xaxt="n", yaxt="n")
axis(1, at=seq(0,xM,dd*2), labels=seq(0,xM,dd*2)/1000)
axis(2, at=seq(0,yM,dd*2), labels=seq(0,yM,dd*2)/1000)
for(i in 1:MC) { lines((seq(xM)*exp(aa[idx[i]]-bb[idx[i]]*seq(xM))), col="darkgray") }
# lines(aa*seq(0,xM)/(1+bb*seq(0,xM)), col="darkgray")
## add S-R estimates and medians
abline(a=0,b=1,lty="dashed")
nCB <- n_yrs-age_max
points(sDat[2,1:nCB],rDat[2,1:nCB], xlim=c(0,xM), ylim=c(0,yM), pch=16, col="blue3")
segments(sDat[2,1:nCB],rDat[1,1:nCB],sDat[2,1:nCB],rDat[3,1:nCB], col="blue3")
segments(sDat[1,1:nCB],rDat[2,1:nCB],sDat[3,1:nCB],rDat[2,1:nCB], col="blue3")
nTB <- dim(sDat)[2]
clr <- rgb(100, 0, 200, alpha=seq(200,100,length.out=age_max-age_min), maxColorValue=255)
segments(sDat[2,(nCB+1):nTB],rDat[1,(nCB+1):nTB],sDat[2,(nCB+1):nTB],rDat[3,(nCB+1):nTB], col=clr)
segments(sDat[1,(nCB+1):nTB],rDat[2,(nCB+1):nTB],sDat[3,(nCB+1):nTB],rDat[2,(nCB+1):nTB], col=clr)
points(sDat[2,(nCB+1):nTB],rDat[2,(nCB+1):nTB],
       xlim=c(0,xM), ylim=c(0,yM), pch=16, col=clr)
text(x=par()$usr[1]+par()$pin[2]/par()$pin[1]*offset*diff(par()$usr[1:2]),
     y=par()$usr[4]-offset*diff(par()$usr[3:4]),"(a)")

## posterior for alpha
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
a_thresh <- 99
par(mai=c(0.8,0.4,0.3,0.1))

```

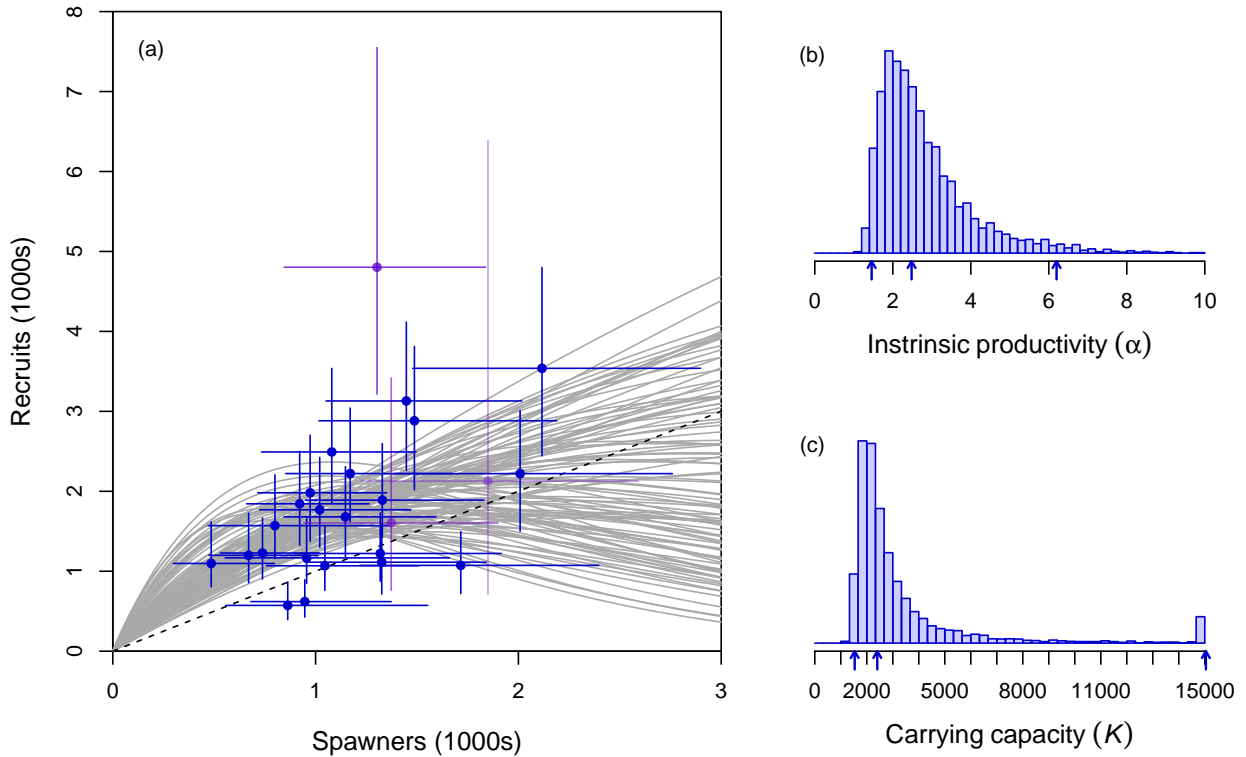
```

## Ricker alpha
R_alpha_est <- mod_fit$BUGSoutput$sims.list$alpha
R_alpha_est <- model[, "alpha"]

alphaCI <- quantile(R_alpha_est, c(0.025, 0.5, 0.975))
R_alpha_est[R_alpha_est > a_thresh] <- a_thresh
hist(R_alpha_est, freq=FALSE, xlab="", main="", breaks=seq(0, 10, 0.2),
      col=clr, border="blue3", ylab="", cex.lab=1.2, yaxt="n")
aHt <- (par()$usr[4] - par()$usr[3]) / 12
arrows(alphaCI, par()$usr[3], alphaCI, par()$usr[3] - aHt,
        code=1, length=0.05, xpd=NA, col="blue3", lwd=1.5)
mtext(expression(Intrinsic~productivity~(alpha)), 1, line=3, cex=1)
text(x=par()$usr[1] + par()$pin[2] / par()$pin[1] * offSet * diff(par()$usr[1:2]),
      y=par()$usr[4] - offSet * diff(par()$usr[3:4]), "(b)")

## posterior for K
par(mai=c(0.8, 0.4, 0.3, 0.1))
aa <- matrix(model[, "E_Rkr_a"], ncol=1)
bb <- matrix(model[, "beta"], ncol=1)
R_b_est <- (aa) / bb
R_b_est <- R_b_est[R_b_est > 0]
R_b_CI <- quantile(R_b_est, c(0.025, 0.5, 0.975))
R_b_est[R_b_est > 1.5e4] <- 1.5e4
brks <- seq(Re2prec(min(R_b_est), "floor", 2000), 1.5e4, length.out=length(seq(0, 9, 0.2)))
hist(R_b_est, freq=FALSE, breaks=brks, col=clr, border="blue3",
      xlab="", yaxt="n", ylab="", cex.lab=1.2)
axis(1, at=seq(Re2prec(min(R_b_est), "floor", 2000), 15000, 1000))
aHt <- (par()$usr[4] - par()$usr[3]) / 12
arrows(R_b_CI, par()$usr[3], R_b_CI, par()$usr[3] - aHt,
        code=1, length=0.05, xpd=NA, col="blue3", lwd=1.5)
mtext(expression(Carrying~capacity~(italic(K))), 1, line=3, cex=1)
text(x=par()$usr[1] + par()$pin[2] / par()$pin[1] * offSet * diff(par()$usr[1:2]),
      y=par()$usr[4] - offSet * diff(par()$usr[3:4]), "(c)")

```



2.2.2 Management Reference Points

Here are a number of management reference points. We make use of the Lambert W function, $W(z)$, which allows for an explicit solution of S_{msy} that depends only on parameters a and b (see Scheuerell, 2016).

Scheuerell, M. D. 2016. An explicit solution for calculating optimum spawning stock size from Ricker's stock recruitment model. PeerJ, 4: e1623.

```
# abbreviations for ref points
ref_names <- c("MSY","Smsy","Umsy","Umax","Seq","Scrit")
# proportions of MSY to consider
yld_prop <- c(0.75,0.85,0.95)
aa <- matrix(model[, "E_Rkr_a"], ncol=1)
alpha <- matrix(model[, "alpha"], ncol=1)
mcmc <- length(aa)
# empty matrix for ref pts
ref.pts <- matrix(NA, mcmc, length(ref_names))
colnames(ref.pts) <- ref_names
# spawner series for optimal yield profile
SS <- seq(100, 5e3, 100)
# empty matrix for optimal yield profiles
OYP <- matrix(0, length(SS), length(yld_prop))
for(i in 1:mcmc) {
  # spawners at MSY
```

```

ref.pts[i,"Smsy"] <- (1 - lambert_W0(exp(1-aa[i]))) / bb[i]
# MSY
ref.pts[i,"MSY"] <- ref.pts[i,"Smsy"]*((exp(aa[i]-bb[i]*ref.pts[i,"Smsy"])) - 1)
# harvest rate at MSY
ref.pts[i,"Umsy"] <- (1 - lambert_W0(exp(1-aa[i])))
# max harvest rate
ref.pts[i,"Umax"] <- 1 - 1/alpha[i]
# equilibrium escapement
ref.pts[i,"Seq"] <- aa[i]/bb[i]
# critical escapement
ref.pts[i,"Scrit"] <- .05*ref.pts[i,"Seq"]

# yield over varying S
yield <- SS*(exp(aa[i]-bb[i]*SS) - 1)
for(j in 1:length(yld_prop)) {
  OYP[,j] <- OYP[,j] + 1*(yield > yld_prop[j]*ref.pts[i,"MSY"])
}
}
OYP <- OYP/mcmc

## Prob of overfishing
hh <- seq(100)
Pr_over <- cbind(hh,hh,hh)
colnames(Pr_over) <- c("Umsy75","Umsy","Umax")
for(i in hh) {
  Pr_over[i,"Umsy75"] <- sum(ref.pts[, "Umsy"]*0.75 < i/100)/mcmc_samp
  Pr_over[i,"Umsy"] <- sum(ref.pts[, "Umsy"] < i/100)/mcmc_samp
  Pr_over[i,"Umax"] <- sum(ref.pts[, "Umax"] < i/100)/mcmc_samp
}

## observed exploitation rate & posterior spawner abundance
Sp_ts <- model[,grep("Sp",colnames(model))]

```

These are plots of (a) the probability that a given number of spawners produce average yields exceeding X% of MSY (i.e, optimal yield profiles); and (b) the cumulative probability of overfishing the population, based on harvest rates equal to those at 75% of MSY (U_{M75}), MSY (U_{MSY}), and the maximum (U_{Max}). The probability of exceeding U_{Max} indicates the risk that offspring will not replace their parents, which, if sustained, will lead to eventual extinction. The histograms above (a) and (b) are distributions of the posterior estimates for the number of spawners and harvest rates, respectively

```

layout(matrix(c(2,1,4,3),2,2),heights=c(1,5))

## OYP
par(mai=c(0.9,0.9,0,0), omi=c(0,0,0.1,0.1))
x_lp <- yld_prop

```

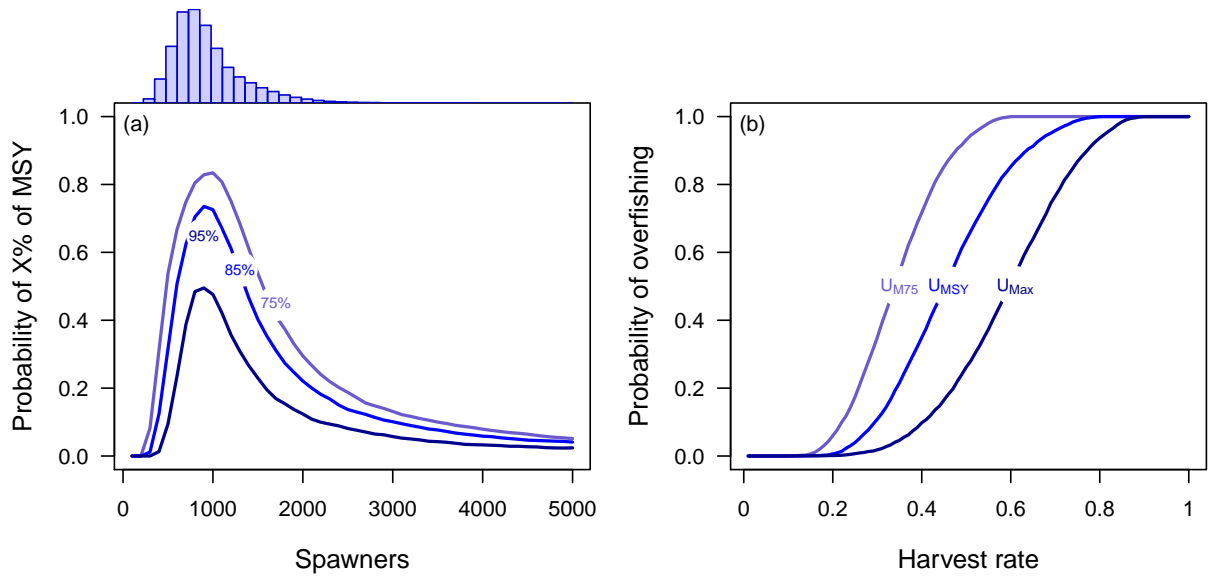


```

for(i in 1:length(x_lp)) {
  x_lp[i] <- SS[max(which(OYP[,i] == max(OYP[,i]) | abs(OYP[,i] - (yld_prop[i]-0.3)) <= 0.05))]
}
matplot(SS, OYP, type="l", lty="solid", las=1, col=c("slateblue","blue","darkblue"), lwd=2,
        xlab="Spawners", ylab="Probability of X% of MSY", cex.lab=1.2,
        main="", ylim=c(0,1))
points(x=x_lp, y=yld_prop-0.3, pch=21, cex=3.5, col="white", bg="white")
text(x=x_lp, y=yld_prop-0.3, paste0(yld_prop*100,"%"),
     col=c("slateblue","blue","darkblue"), cex=0.7)
text(x=par()$usr[1]+par()$pin[2]/par()$pin[1]*offset*diff(par()$usr[1:2]),
     y=par()$usr[4]-offset*diff(par()$usr[3:4]), "(a)")
## posterior spawner abundance over all years
par(mai=c(0,0.9,0.05,0))
hist(Sp_ts[Sp_ts<3e4], col=clr, border="blue3", breaks=40,
     main="", yaxs="i", xaxt="n", yaxt="n", ylab="")

## prob of overfishing
par(mai=c(0.9,0.9,0,0))
matplot(Pr_over, type="l", las=1, lwd=2, lty="solid", col=c("slateblue","blue","darkblue"),
        ylab="Probability of overfishing", cex.lab=1.2,
        xlab="Harvest rate", xaxt="n")
axis(1,seq(0,100,20),seq(0,100,20)/100)
x_lp <- c(0,0,0)
for(i in 1:length(x_lp)) {
  x_lp[i] <- max(which(abs(Pr_over[,i] - 0.5) <= 0.05))
}
points(x=x_lp, y=rep(0.5,3), pch=21, cex=4, col="white", bg="white")
text(x=x_lp, y=0.5, expression(U[M75], U[MSY], U[Max]),
     col=c("slateblue","blue","darkblue"), cex=0.8)
text(x=par()$usr[1]+par()$pin[2]/par()$pin[1]*offset*diff(par()$usr[1:2]),
     y=par()$usr[4]-offset*diff(par()$usr[3:4]), "(b)")

```



Here is a summary of estimated reference points

```
tbl_refpt_smry <- apply(ref.pts,2,quantile,CI_vec)
print(tbl_refpt_smry,digits=3,quote=FALSE,justify="right")
```

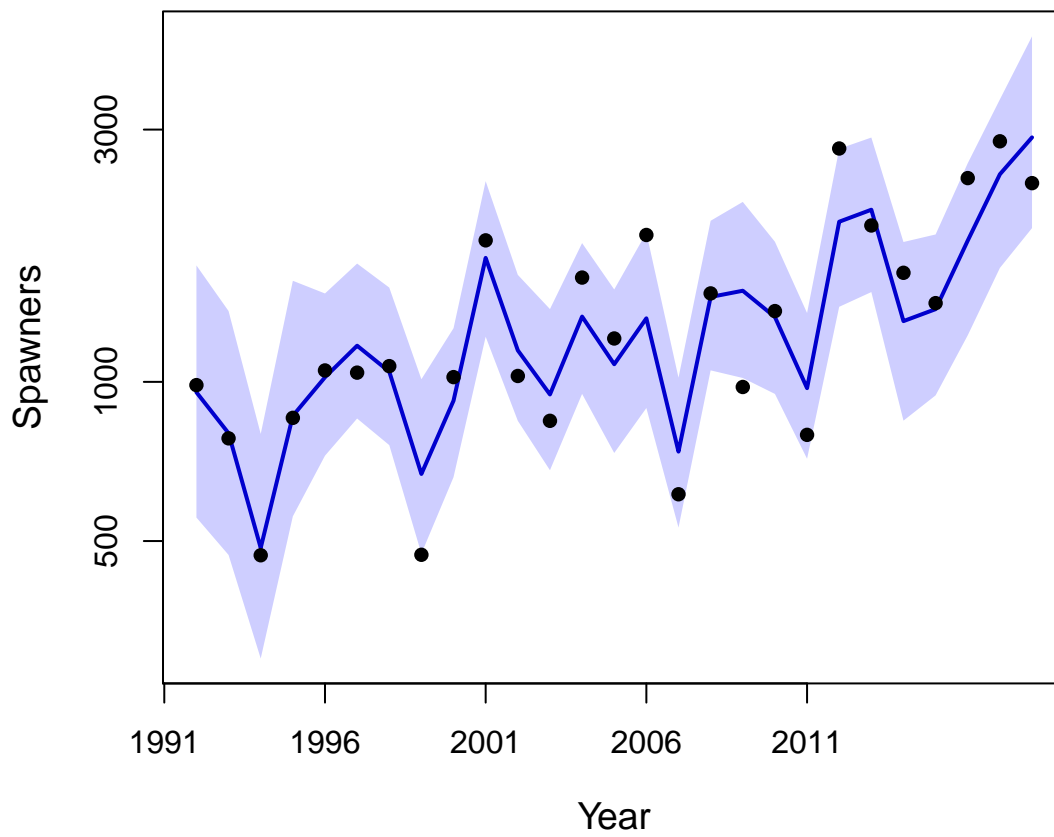
##	MSY	Smsy	Umsy	Umax	Seq	Scrit
## 2.5%	496	576	0.233	0.314	1534	76.7
## 50%	960	1024	0.452	0.597	2403	120.2
## 97.5%	2828	6987	0.726	0.839	15042	752.1

2.2.3 Total population size

Here is our estimate of the escapement over time through return year 2014. The black points are the data, the blue line is the median posterior estimate, and the shaded region is the 95% credible interval. Note that the y-axis is on a log scale.

```
pDat <- apply(model[,grep("Sp",colnames(model))],2,quantile,CI_vec)

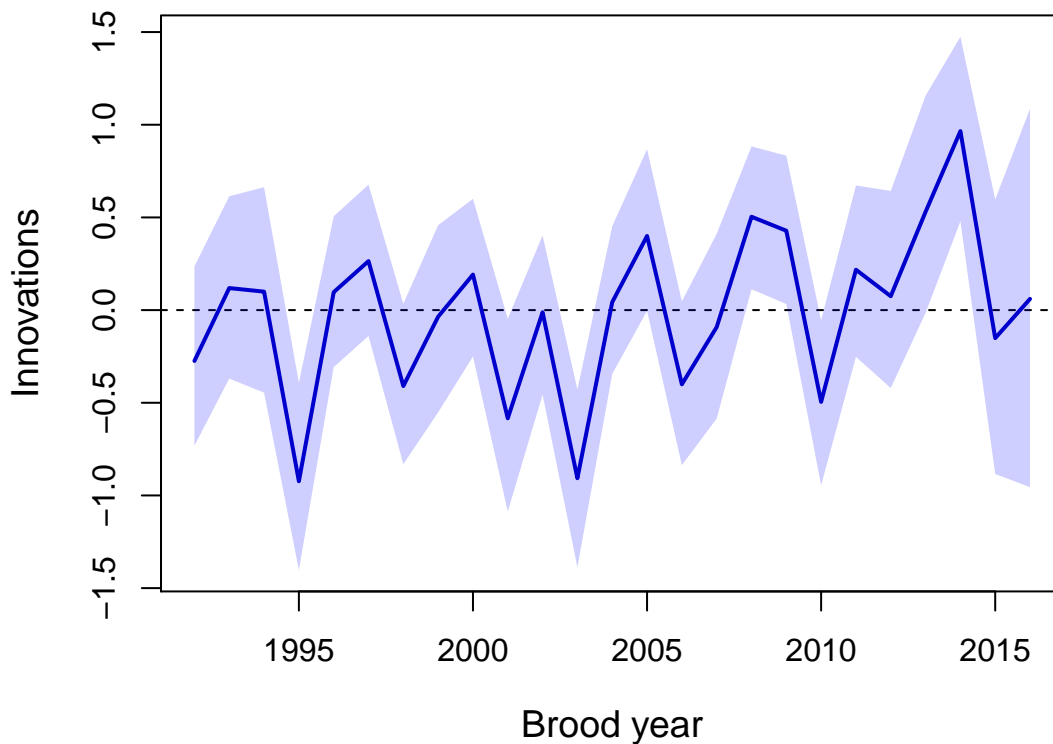
ypMin <- min(pDat[,1:n_yrs])
ypMax <- max(pDat[,1:n_yrs])
t_idx_T <- seq(yr_frst,length.out=n_yrs)
par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0.2,0.1,0.2))
plot(t_idx_T,pDat[3,1:n_yrs], ylim=c(ypMin,ypMax), type="n", log="y", xaxt="n", yaxt="n",
     xlab="Year", ylab="Spawners", main="", cex.lab=1.2)
polygon(c(t_idx_T,rev(t_idx_T)),c(pDat[3,1:n_yrs],rev(pDat[1,1:n_yrs])), col=clr, border=NA)
lines(t_idx_T, pDat[2,1:n_yrs], col="blue3", lwd=2)
points(seq(yr_frst,length.out=n_yrs), exp(ln_dat_esc), pch=16, cex=1)
axis(1,at=seq(1986,2015,5))
axis(2,at=c(500,1000,3000))
```



2.2.4 Innovations

Here is the time series of the so-called “innovations”, which are the residuals from the process model. They give some indication of population productivity after accounting for the effects of density dependence.

```
t_idx_a <- seq(yr_frst,length.out=n_yrs-age_min)
#pDat <- apply(mod_fit$BUGSoutput$sims.list$res_ln_Rec,2,quantile,CI_vec)
pDat <- apply(model[,grep("res_ln_Rec",colnames(model))],2,quantile,CI_vec)
ypMin <- min(pDat)
ypMax <- max(pDat)
par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0.2,0.1,0.2))
plot(t_idx_a,pDat[3,], ylim=c(ypMin,ypMax), type="n", #log="y",
      xlab="Brood year", ylab="Innovations", main="", cex.lab=1.2)
abline(h=0, lty="dashed")
polygon(c(t_idx_a,rev(t_idx_a)),c(pDat[3,],rev(pDat[1,])), col=clr, border=NA)
lines(t_idx_a, pDat[2,], col="blue3", lwd=2)
```



2.2.5 VRAP Simulation

Here is a simulation fram work to assess risk. In this case, we are assessing the maximum harvest rate that results inlp_age 1) less than 5% probability of simulated escapements falling below the lower escapement threshold (Ecrit) relative to a baseline scenario of no fishing, and 2) at least an 80% probability of simulated escapements being above the upper threshold. To do this, we run 1000 25 simulations accross a range in target exploitation rates form 0% - 80% with 100 random samples drawn from the paired retained posterior distributions of a and b from the MCMC.

```
## ----VRAP_sim-----

## posterior S/R parameters
aa <- model[,grep("E_Rkr_a",colnames(model))]
bb <- model[,grep("beta",colnames(model))]

## management error mean and std dev. (FRAM post season ER/pre- season ER)
me_mean <- 1.07
me_sd <- 0.19

## bound observed ER by a minimum and maximum to avoid unrealistic harvest scenarios
ER_max <- 0.95
ER_min <- 0.15

##select whether to apply management error or not (1 = include, 0 = exclude)
me <- 0
```

```

## number of years for each simulation: starting with 25 since this is what NOAA requires
numYears <- 25

## number of simulations
numSim <- 1000

## range of target harvest rates to explore
ER_range <- seq(0,0.8,.01)

## start with most recent five spawner years in time series

#S_start <- apply(mod_fit$BUGSoutput$sims.list$Sp,2,quantile,probs=CI_vec)[2,(n_yrs - 4):n_yrs]
S_start <- apply(model[,grep("Sp",colnames(model))],2,quantile,probs=CI_vec)[2,(n_yrs - 4):n_yrs]

## SMSY under average conditions
Smsy <- quantile(ref.pts[,"Smsy"],CI_vec)
#Scrit <- quantile(ref.pts[,"Scrit"],CI_vec)

Scrit <- 470

## maturation schedule
matSched_2 <- apply(model[,grep("pi_vec",colnames(model))][,1:25],2,quantile,CI_vec)
matSched_3 <- apply(model[,grep("pi_vec",colnames(model))][,26:50],2,quantile,CI_vec)
matSched_4 <- apply(model[,grep("pi_vec",colnames(model))][,51:75],2,quantile,CI_vec)
matSched_5 <- apply(model[,grep("pi_vec",colnames(model))][,76:100],2,quantile,CI_vec)

matSched <- rbind(matSched_2[2,],matSched_3[2,],matSched_4[2,],matSched_5[2,])

## take 100 random samples of S/R parameters from posterior distribution
sample <- 100
samplePosterior <- sample(1:mcmc,sample,replace = TRUE)

## these are the posterior samples that will be used. Note that for each paired sample,
## 1000 25 year simulations will be conducted for each target exploitation rate
a <- aa[samplePosterior]
b <- bb[samplePosterior]

## median posterior process standard deviation
median_sd_r <- median(model[, "sigma_r"])^0.5

## output arrays for RER criteria
p_UET <- array(data = NA,dim = c(length(ER_range),(sample + 1)))
p_UET_10pct <- array(data = NA,dim = c(length(ER_range),(sample + 1)))
p_Crit_5pct <- array(data = NA,dim = c(length(ER_range),(sample + 1)))

```

```

if(file.exists(file.path(savedir,paste("p_UET", ".csv", sep = ""))) &
  file.exists(file.path(savedir,paste("p_UET_10pct", ".csv", sep = ""))) &
  file.exists(file.path(savedir,paste("p_Crit_5pct", ".csv", sep = "")))){

  p_UET <- read.csv(file.path(savedir,paste("p_UET", ".csv", sep = "")))
  p_UET_10pct <- read.csv(file.path(savedir,paste("p_UET_10pct", ".csv", sep = "")))
  p_Crit_5pct <- read.csv(file.path(savedir,paste("p_Crit_5pct", ".csv", sep = "")))

  p_UET <- read.csv(file.path(savedir,paste("p_UET", ".csv", sep = "")))
  p_UET <- p_UET[,-1]

  p_UET_10pct <- read.csv(file.path(savedir,paste("p_UET_10pct", ".csv", sep = "")))
  p_UET_10pct <- p_UET_10pct[,-1]

  p_Crit_5pct <- read.csv(file.path(savedir,paste("p_Crit_5pct", ".csv", sep = "")))
  p_Crit_5pct <- p_Crit_5pct[,-1]

  ## compute median RER based on criterion
  RER_UET_median <- ER_range[length(which(p_UET[,1] >= 0.80))]
  RER_UET_10pct_median <- ER_range[length(which(p_UET_10pct[,1] <= 0.10))]
  RER_Crit_5pct_median <- ER_range[length(which(p_Crit_5pct[,1] <= 0.05))]

}else{## run risk assessment procedure and save output

  for(i in 1:(sample + 1)){

    ## set up arrays for keeping track of abundance
    sp<-array(data = NA, dim = c(numSim,(numYears+5),length(ER_range)))
    catch<-array(data = NA, dim = c(numSim,(numYears+5),length(ER_range)))
    mature_Run<-array(data = NA, dim = c(numSim,(numYears+5),length(ER_range)))

    ## SR parameters used for this set of simulations.Median is evaluated first.
    if(i == 1){a_Sim <- median(aa);b_Sim <- median(bb)}else{
      a_Sim <- a[i-1];b_Sim <- b[i-1]
    }

    ## reset counter for each round of simulations
    c <- 1
    for (ER_target in ER_range){
      for (sim in 1:numSim){
        #sim <- 2
        ## output vector for total age specific recruitment
        age2Rec <- NULL
        age3Rec <- NULL
        age4Rec <- NULL

```

```

age5Rec <- NULL

## sample from yearly estimates of maturation schedule
matSchedule_sim <- matSched[,sample(1:dim(matSched)[2],numYears + 5, replace = TRUE)]

if(me == 1){

  ## apply management error to target exploitation rates within bounds of
  ## 15% - 95% total ER
  mgmtError <- rnorm(numYears + 5,me_mean,me_sd)
  ER_Obs <- ER_target*mgmtError
  ER_Obs[which(ER_Obs > ER_max)] <- ER_max
  ER_Obs[which(ER_Obs < ER_min)] <- ER_min

}else{ER_Obs <- rep(ER_target,numYears + 5)}

for(year in 1:(numYears + 5)){

  if(year <= 5){

    lnRec <- (log(S_start[year]) + a_Sim- b_Sim*S_start[year])

    totRec <- exp(rnorm(1,lnRec,median_sd_r))

    ## apply maturation schedule to project recruits forward
    totRec <- totRec * matSchedule_sim[,year]
    age2Rec[year+2]<-totRec[1]
    age3Rec[year+3]<-totRec[2]
    age4Rec[year+4]<-totRec[3]
    age5Rec[year+5]<-totRec[4]

  }

  if(year > 5){
    #year <- 6
    mature_Run[sim,year,c] <- age2Rec[year] + age3Rec[year] + age4Rec[year] + age5Rec[year]
    catch[sim,year,c]<-ER_Obs[year]*(mature_Run[sim,year,c])
    sp[sim,year,c] <- mature_Run[sim,year,c] - catch[sim,year,c]

    lnRec <- (log(sp[sim,year,c]) + a_Sim - b_Sim*sp[sim,year,c])

    totRec <- exp(rnorm(1,lnRec,median_sd_r))

    ## apply maturation schedule to project recruits forward
    totRec <- totRec * matSchedule_sim[,year]
    age2Rec[year+2]<-totRec[1]
    age3Rec[year+3]<-totRec[2]

```

```

        age4Rec[year+4]<-totRec[3]
        age5Rec[year+5]<-totRec[4]

    }

    }#next time step
  }# next sim
  c <- c+1
}#next Er

p_UET[,i] <- apply(sp[,27:30,],3,function(x){length(which(x > Smsy[2]))/length(x)})
p_UET_10pct[,i] <- p_UET[1,i] - p_UET[,i]

p_Crit_temp <- apply(sp[,5:30,],3,function(x){length(which(x < Scrit))/length(x)})
p_Crit_5pct[,i] <- p_Crit_temp - p_Crit_temp[1]

}## next sample

## compute median RER based on criterion
RER_UET_median <- ER_range[length(which(p_UET[,1] >= 0.80))]
RER_UET_10pct_median <- ER_range[length(which(p_UET_10pct[,1] <= 0.10))]
RER_Crit_5pct_median <- ER_range[length(which(p_Crit_5pct[,1] <= 0.05))]

## save results
write.csv(p_UET,file.path(savedir, paste("p_UET",".csv",sep = "")))
write.csv(p_UET_10pct,file.path(savedir, paste("p_UET_10pct",".csv",sep = "")))
write.csv(p_Crit_5pct,file.path(savedir, paste("p_Crit_5pct",".csv",sep = "")))
}

```

Here are probability profiles for the three criteria assessed across the range of target exploitation rates from 0% - 80%

```

## plot RER profiles for each criterion
layout(matrix(seq(1,3,1),1,3),heights = 4,widths = c(4,4,4,4))
par(mai=c(0.15,0.15,0.15,0.15), omi=c(0.5,0.5,0.5,0.5))

plot(p_Crit_5pct[,1]~ER_range,xlab = "",ylab = "",type = "l", bty = "n",lwd = 2,main = "% > LE")
points(RER_Crit_5pct_median,0.05,pch = 16,col = "red",cex = 1.5)
abline(h = 0.05,v =RER_Crit_5pct_median,lty = 2, col = "grey" )

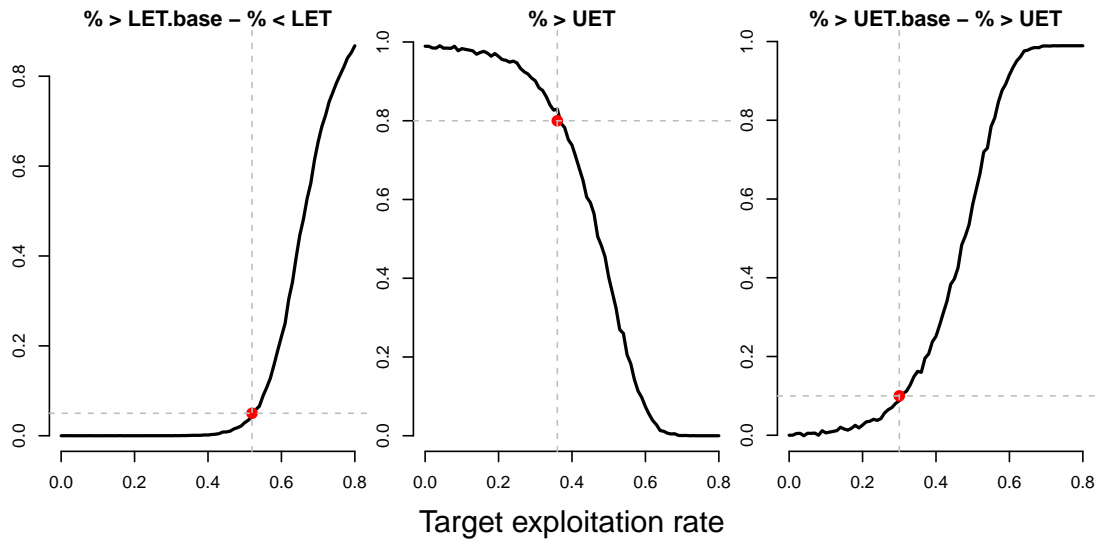
plot(p_UET[,1]~ER_range,xlab = "",ylab = "",type = "l",bty = "n",lwd = 2, main = "% > UET")
points(RER_UET_median,0.80,pch = 16,col = "red",cex = 1.5)
abline(h = 0.80,v = RER_UET_median,lty = 2, col = "grey")

plot(p_UET_10pct[,1]~ER_range,xlab = "",ylab = "",type = "l",bty = "n", lwd = 2, main = "% > U")
points(RER_UET_10pct_median,0.10,pch = 16,col = "red",cex = 1.5)
abline(h = 0.10,v = RER_UET_10pct_median,lty = 2, col = "grey")

```



```
mtext("Target exploitation rate",1,outer = TRUE,cex = 1.2,line = 2)
```



Now we want to calculate the posterior RER based on the 100 random paired samples taken from the posterior distributions for each S/R parameter

```
##calculate posterior RER distribution
RER_UET <- NULL
RER_UET_10pct <- NULL
RER_Crit_5pct <- NULL

for(i in 2:dim(p_UET)[2]){
  #i <- 3

  if(length(which(p_UET[,i] >= 0.80)) == 0){
    RER_UET[i] <- NA
  }else{RER_UET[i] <- ER_range[length(which(p_UET[,i] >= 0.80))]}

  if(length(which(p_UET_10pct[,i] <= 0.10)) == 0){
    RER_UET_10pct[i] <- NA
  }else{RER_UET_10pct[i] <- ER_range[length(which(p_UET_10pct[,i] <= 0.10))]}

  if(length(which(p_Crit_5pct[,i] <= 0.05)) == 0){
    RER_Crit_5pct[i] <- NA
  }else{RER_Crit_5pct[i] <- ER_range[length(which(p_Crit_5pct[,i] <= 0.05))]}

}

## plot posterior RER's
layout(matrix(seq(1,3,1),1,3),heights = 4,widths = c(4,4,4,4))
```

```

par(mai=c(0.15,0.15,0.15,0.15), omi=c(0.5,0.5,0.5,0.5))

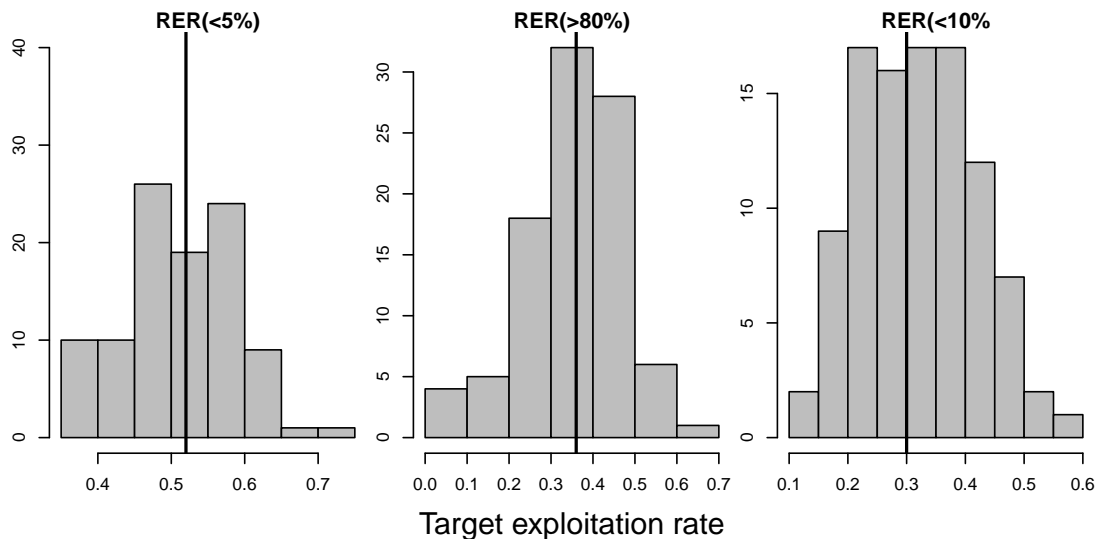
hist(RER_Crit_5pct,col = "grey",main = "RER(<5%)", xlab = "", ylab = "", ylim = c(0,40))
abline(v = RER_Crit_5pct_median,lwd = 2)

hist(RER_UET,col = "grey", main = "RER(>80%)",xlab = "", ylab = "")
abline(v = RER_UET_median,lwd = 2)

hist(RER_UET_10pct,col = "grey", main = "RER(<10%",xlab = "",ylab = "")
abline(v = RER_UET_10pct_median,lwd = 2)

mtext("Target exploitation rate",1,outer = TRUE,cex = 1.2,line = 2)

```



Now we can calculate the 95% credible interval for the RER

```

RER_range <- quantile(RER_UET,c(0.025,0.975),na.rm = TRUE)
RER_range <- c(RER_range[1],RER_UET_median,RER_range[2])
#RER_range <- round(RER_range,2)

## ----summary_tbl
print(rbind(Scrit = round(Scrit),Smsy = round(Smsy),RER_range = RER_range))

##           2.5%      50%      97.5%
## Scrit    470.00000  470.00  470.00000
## Smsy     576.00000 1024.00 6987.00000
## RER_range  0.06625   0.36   0.53675

```