Appendix S2. Summarize S/R model results and compute management reference points

2021 Skagit River Summer/Fall escapement goal estimation

Contents

This is version 0.24.09.03.

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 delimter
fig_cap <- captioner(infix = ".")

management_unit <- "summer_fall"

## 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("\"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_new",".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       1.00
## beta               1       1.00
## sigma_r            1       1.00
## sigma_s            1       1.00
## pi_tau             1       1.00
## pi_eta[1]          1       1.01
## pi_eta[2]          1       1.00
## pi_eta[3]          1       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%   2.32   0.907 2.34e-05
## 50%    4.10   1.483 7.22e-05
## 97.5%  7.22   2.068 1.24e-04
```

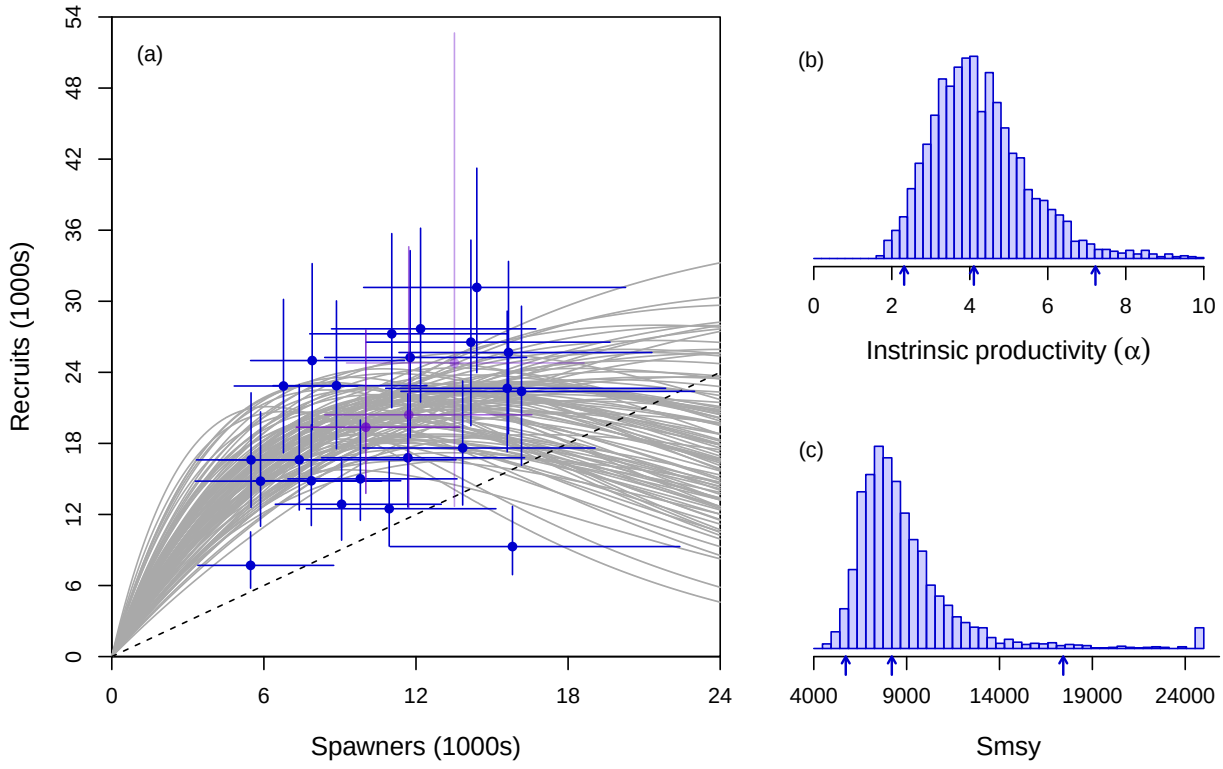
2.2.1 Spawner-recruit relationship

Here is the relatonship 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 2.5^{th}, 50^{th}, and 97.5^{th} percentiles.

```r
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 <- 1000

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)
write.csv(t((sDat)),file.path(savedir,"sf_adults_spawners.csv"))

sDat <- sDat[,1:(n_yrs-age_min)]

## posterior of recruits
rDat <- exp(apply(model[,grep("tot_ln_Rec",colnames(model))],2,quantile,CI_vec))
write.csv(t((rDat)),file.path(savedir,"sf_adults_recruits.csv"))

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 <- 3000
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=
```

```
segments(sDat[1,(nCB+1):nTB],rDat[2,(nCB+1):nTB],sDat[3,(nCB+1):nTB],rDat[2,(nCB+1):nTB], col=c
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(Instrinsic~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 beta
# 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>1e5] <- 1e5
# brks <- seq(Re2prec(min(R_b_est),"floor",2000),1e5,length.out=length(seq(0,9,0.2)))
# hist(R_b_est, freq=FALSE, breaks=brks, col=clr, border="blue3",
#    xlab="", xaxt="n", yaxt="n",
#    main="", ylab="", cex.lab=1.2)
# axis(1, at=seq(Re2prec(min(R_b_est),"floor",2000),1e5,20000))
# 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)")

## 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 <- (1 - lambert_W0(exp(1-aa))) / bb
#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>2.5e4] <- 2.5e4
brks <- seq(Re2prec(min(R_b_est),"floor",2000),2.5e4,length.out=length(seq(0,9,0.2)))
hist(R_b_est, freq=FALSE, breaks=brks, col=clr, border="blue3",
     xlab="", xaxt="n", yaxt="n",
     main="", ylab="", cex.lab=1.2)
axis(1, at=seq(Re2prec(min(R_b_est),"floor",2000),3e4,by = 5000))
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("Smsy", 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 Smsy 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.

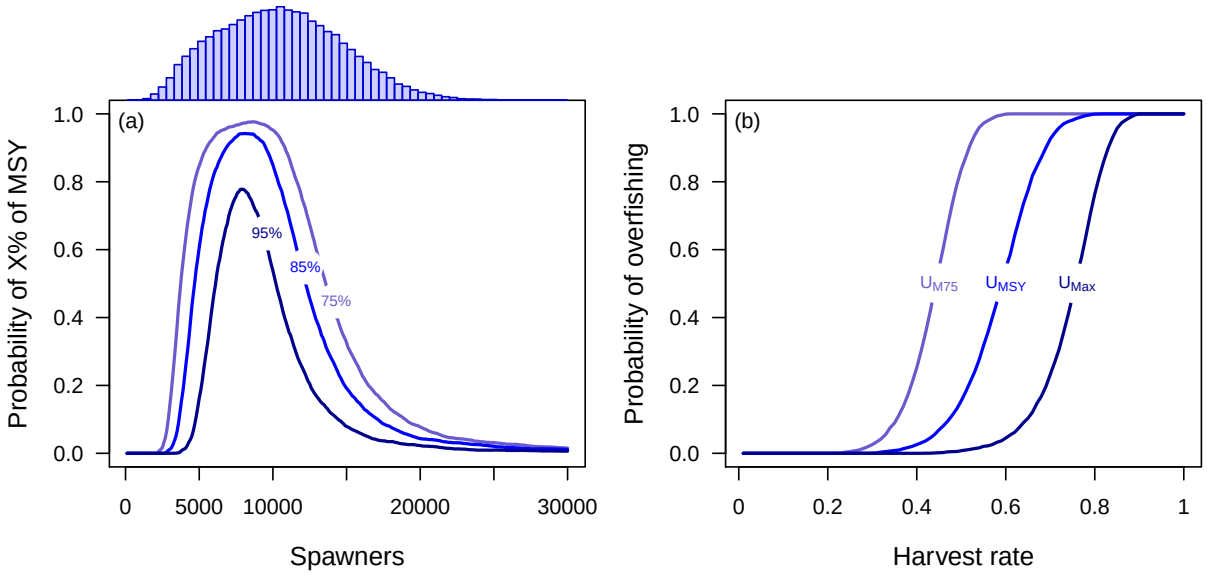
```
# abbreviations for ref points
ref_names <- c("MSY","Smsy","Umsy","Umax","Seq","Scrit")
# proportions of MSY to consider
yld_prop <- c(0.75,0.85,0.95)
aa <- matrix(model[,"E_Rkr_a"],ncol=1)
alpha <- matrix(model[,"alpha"],ncol=1)
mcmc <- length(aa)
# empty matrix for ref pts
ref.pts <- matrix(NA,mcmc,length(ref_names))
colnames(ref.pts) <- ref_names
# spawner series for optimal yield profile
SS <- seq(100,3e4,100)
# 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
  Pr_over[i,"Umsy"] <- sum(ref.pts[,"Umsy"] < i/100)/mcmc
  Pr_over[i,"Umax"] <- sum(ref.pts[,"Umax"] < i/100)/mcmc
```

```
}

## 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 probabilty 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")
```

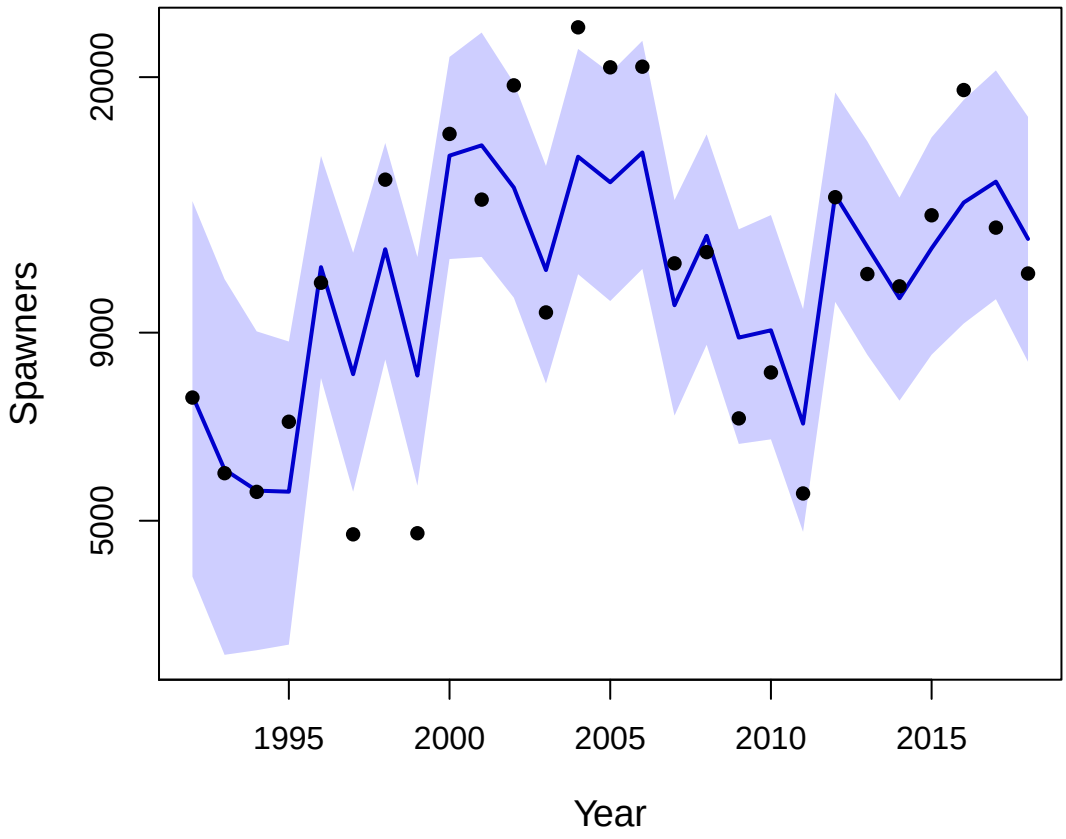
```
##         MSY  Smsy  Umsy  Umax   Seq Scrit
## 2.5%   8139  5721 0.399 0.568 15493   775
## 50%   12193  8201 0.590 0.756 20699  1035
## 97.5% 19270 17433 0.736 0.862 39974  1999
```

2.2.3 Total population size

Here is our estimate of the escapement over time through return year 2018. 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)
```

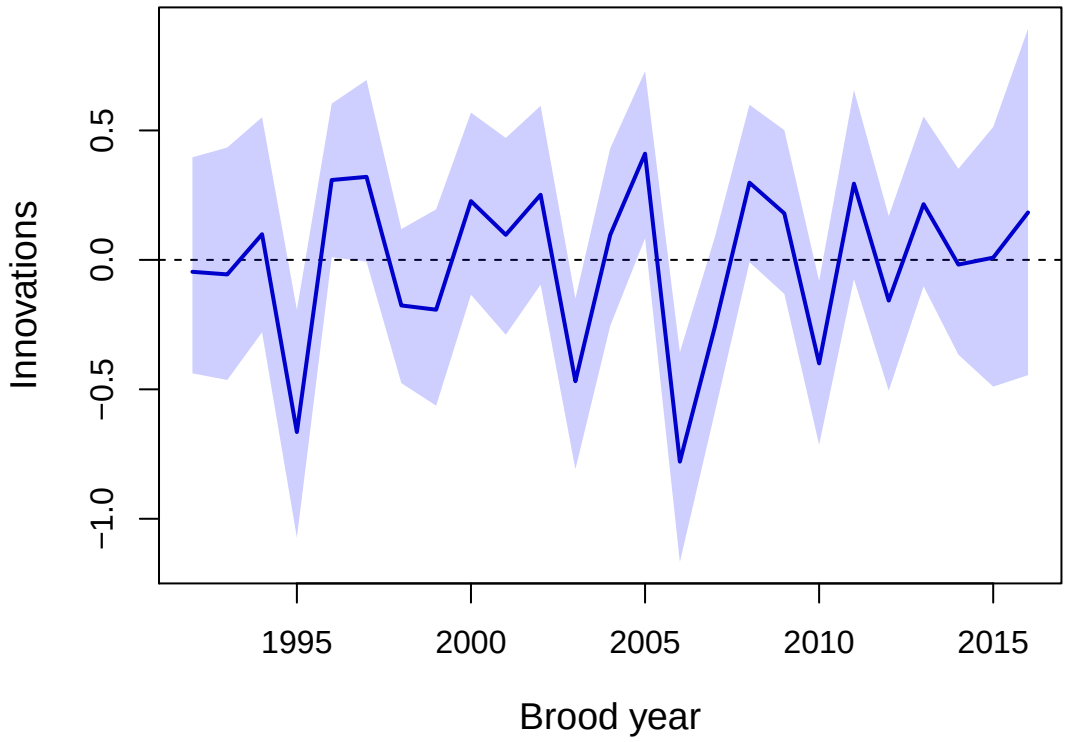
```
lines(t_idx_T, pDat[2,1:n_yrs], col="blue3", lwd=2)
points(seq(yr_frst,length.out=n_yrs), exp(ln_dat_esc), pch=16, cex=1)
axis(1,at=seq(1980,2015,5))
axis(2,at=c(5000,9000,20000))
```



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.

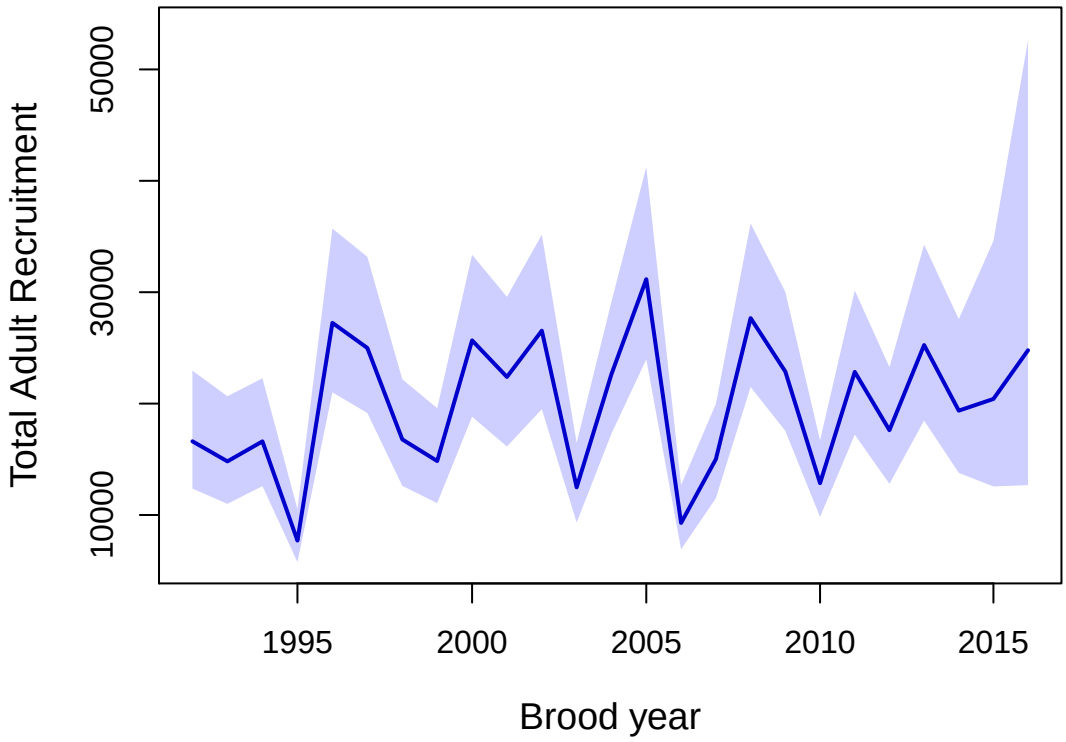
```
t_idx_a <- seq(yr_frst,length.out=n_yrs-age_min)
#pDat <- apply(mod_fit$BUGSoutput$sims.list$res_ln_Rec,2,quantile,CI_vec)
pDat <- apply(model[,grep("res_ln_Rec",colnames(model))],2,quantile,CI_vec)
ypMin <- min(pDat)
ypMax <- max(pDat)
par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0.2,0.1,0.2))
plot(t_idx_a,pDat[3,], 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 Recruitment

Here is the posterior time series total annual adult recruitment produced from each spawning cohort.

```
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 <- exp(apply(model[,grep("tot_ln_Rec",colnames(model))],2,quantile,CI_vec))
ypMin <- min(pDat)
ypMax <- max(pDat)+1000
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="x",
     xlab="Brood year", ylab="Total Adult Recruitment", 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)
```



2.2.6 Escapement, Recruitment, Innovations

```
layout(matrix(c(1,2,3,4),2,2),c(3,3),c(3,3))


offSet <- 0.06



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

##Escapement
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(0.2,0,0,0))
#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(1980,2015,5))
axis(2,at=c(5000,9000,20000))
text(x=par()$usr[1]+par()$pin[2]/par()$pin[1]*offSet*diff(par()$usr[1:2]),
     y=10^par()$usr[4]-0.14*diff(10^par()$usr[3:4]),"(a)")

##Recruitment
t_idx_a <- seq(yr_frst,length.out=n_yrs-age_min)
#pDat <- apply(mod_fit$BUGSoutput$sims.list$res_ln_Rec,2,quantile,CI_vec)
pDat <- exp(apply(model[,grep("tot_ln_Rec",colnames(model))],2,quantile,CI_vec))
ypMin <- min(pDat)
ypMax <- max(pDat)+1000
#par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0.2,0.1,0.2))
par(mai=c(0.8,0.8,0.1,0.1))
plot(t_idx_a,pDat[3,], ylim=c(ypMin,ypMax), type="n", log="y",
     xlab="Brood year", ylab="Total Adult Recruitment", main="", cex.lab=1.2)
abline(h=0, lty="dashed")
polygon(c(t_idx_a,rev(t_idx_a)),c(pDat[3,],rev(pDat[1,])), col=clr, border=NA)
lines(t_idx_a, pDat[2,], col="blue3", lwd=2)
text(x=par()$usr[1]+par()$pin[2]/par()$pin[1]*offSet*diff(par()$usr[1:2]),
     y=10^par()$usr[4]-0.14*diff(10^par()$usr[3:4]),"(b)")
# ##Innovations
t_idx_a <- seq(yr_frst,length.out=n_yrs-age_min)
#pDat <- apply(mod_fit$BUGSoutput$sims.list$res_ln_Rec,2,quantile,CI_vec)
pDat <- apply(model[,grep("ln_RS",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))
par(mai=c(0.8,0.8,0.1,0.1))
plot(t_idx_a,pDat[3,], ylim=c(ypMin,ypMax), type="n",
     xlab="Brood year", ylab="ln(R/S)", 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)
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)")

###Residuals
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))
par(mai=c(0.8,0.8,0.1,0.1))
plot(t_idx_a,pDat[3,], ylim=c(ypMin,ypMax), type="n",
     xlab="Brood year", ylab="Recruitment Residuals", 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)
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]),"(d)")
```