Appendix S3. Steps to recreate figures from main text.

Supporting information for Scheuerell et al.

Contents

This is version 0.19.12.02.

1 Background

This appendix shows how to recreate the figures in the main text based on the results from the best of the fitted models. 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("gtools")) {
  install.packages("gtools")
  library("gtools")
}


## set default caption delimter
fig_cap <- captioner(suffix = ".")

## set directory locations
datadir <- here("data")
analdir <- here("analysis")
savedir <- here("analysis/cache")

## 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
}
```

The last thing we'll need is the following function for trimming real numbers to a desired precision when plotting output.

```
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.

```
best_fit <- readRDS(file.path(savedir,"fit_bh_cov_flow_wtr+flow_spr+NPGO+whidbey_basin_pink_esc
```

```
## covariate(s)
dat_cvrs <- read_csv(file.path(datadir, "skagit_chum_covars.csv"))
## total number of covariates
n_cov <- dim(dat_cvrs)[2] - 1
```

```
## escapement
dat_esc <- read_csv(file.path(datadir, "skagit_chum_esc.csv"))
dat_esc <- dat_esc[which(dat_esc$year %in% seq(yr_frst,yr_last,1)),]

## log of escapement
ln_dat_esc <- c(log(dat_esc$escapement), rep(NA, n_fore))
```

```
## harvest
dat_harv <- read_csv(file.path(datadir, "skagit_chum_catch.csv"))
dat_harv <- dat_harv[which(dat_harv$year %in% seq(yr_frst,yr_last,1) ),]

## drop year col & first age_max rows
dat_harv <- c(dat_harv$catch, rep(0, n_fore))
```

3 Model forms

Here are the model parameters we used for the schematics of the deterministic forms for the Ricker and Beverton-Holt models.

```
## params
## Ricker
ra <- 3
rb <- 1.2e-4
## B-H
ba <- 3
bb <- 3/1.4e4

## ref pts
## Ricker
rmr <- ra/rb*exp(-1)
rsy <- (1 - lambert_W0(exp(1)/ra)) / rb
ruy <- 1 - lambert_W0(exp(1)/ra)
## B-H
bmr <- ba/bb
bsy <- (ba/bb)*sqrt(1/ba)-(1/bb)
bsy <- (sqrt(ba)-1)/bb
buy <- 1 - sqrt(1/ba)

## S-R curves
## spawners
ss <- seq(0,1.2e4,10)
```

```
## recuits (Ricker)
rr <- ra*ss/exp(rb*ss)
## recruits (B-H)
br <- ba*ss/(1 + bb*ss)
```

Here is the code to recreate the schematics in Figure 1.

```
layout(matrix(c(1,0,2),3,1),
       heights=lcm(c(3,0.3,3)*2.54),
       widths=lcm(3*2.54))

par(mai=c(0.4,0.4,0.2,0.2), omi=c(0,0,0,0.25))

## Ricker
plot(ss, rr, type="n", xlim=range(ss), ylim=range(ss), xaxs="i", yaxs="i",
     xlab="", ylab="", xaxt="n", yaxt="n", bty="L")
mtext(expression(italic(S[t])), 1, line=1, cex=1.1, at=max(ss))
mtext(expression(italic(R[t])), 2, line=0.5, cex=1.1, at=max(ss), las=1)
rttl <- "(a) Ricker"
text(400, max(ss), rttl, cex=1.1, adj=c(0,1), xpd=NA)
## 1:1
abline(a=0, b=1, col="gray")
#text(1.2e4, 1.2e4, "1:1", adj=c(1,0))
## R-S
lines(ss, rr, lwd=2)
rmod <- expression(frac(italic(alpha * S[t]),italic(e^{beta * S[t]})))
text(12300, ra*max(ss)/exp(rb*max(ss)), rmod, adj=c(0,0.5), xpd=NA)
## alpha
segments(0, 0, 1900, ra*1900, lty="dashed")
text(2000, ra*2000, expression(alpha), adj=c(0.5,0.5))
## MSY
segments(rsy,0,rsy,ra*rsy/exp(rb*rsy), lty="dashed")
text(rsy, 0, expression(frac(1-italic(W)~bgroup("(",frac(italic(e),alpha),")"),beta)), adj=c(0
segments(par()$usr[1],ra*rsy/exp(rb*rsy),rsy,ra*rsy/exp(rb*rsy), lty="dashed")
text(0, ra*rsy/exp(rb*rsy), expression(italic(R)[MSY]), pos=2, xpd=NA)
## K
segments(0, log(ra)/rb, log(ra)/rb, log(ra)/rb, lty="dashed")
segments(log(ra)/rb, 0, log(ra)/rb, log(ra)/rb, lty="dashed")
text(log(ra)/rb, 0, expression(frac(log(alpha),beta)), adj=c(0.5,1.2), xpd=NA)
text(0, log(ra)/rb, expression(italic(K)), pos=2, xpd=NA)

## B-H
plot(ss, br, type="n", xlim=range(ss), ylim=range(ss), xaxs="i", yaxs="i",
     xlab="", ylab="", xaxt="n", yaxt="n", bty="L")
mtext(expression(italic(S[t])), 1, line=1, cex=1.1, at=max(ss))
mtext(expression(italic(R[t])), 2, line=0.5, cex=1.1, at=max(ss), las=1)
bttl <- "(b) Beverton-Holt"
text(400, max(ss), bttl, cex=1.1, adj=c(0,1), xpd=NA)
## 1:1
```

```
abline(a=0, b=1, col="gray")
## R-S
lines(ss, br, lwd=2)
bmod <- expression(frac(italic(alpha * S[t]),1+italic(beta * S[t])))
text(max(ss)+300, ba*max(ss)/(1 + bb*max(ss)), bmod, adj=c(0,0.5), xpd=NA)
## alpha
segments(0, 0, 1500, ba*1500, lty="dashed")
text(1600, ba*1600, expression(alpha), adj=c(0.5,0.5))
## MSY
segments(bsy,0,bsy,ba*bsy/(1 + bb*bsy), lty="dashed")
text(bsy, 0, expression(frac(root(alpha)-1,beta)), adj=c(0.5,1.2), xpd=NA)
segments(par()$usr[1],ba*bsy/(1 + bb*bsy),bsy,ba*bsy/(1 + bb*bsy), lty="dashed")
text(0, ba*bsy/(1 + bb*bsy), expression(italic(R)[MSY]), pos=2, xpd=NA)
## K
segments(0, (ba-1)/bb, (ba-1)/bb, (ba-1)/bb, lty="dashed")
segments((ba-1)/bb, 0, (ba-1)/bb, (ba-1)/bb, lty="dashed")
text((ba-1)/bb, 0, expression(frac(alpha-1,beta)), adj=c(0.5,1.2), xpd=NA)
text(0, (ba-1)/bb, expression(italic(K)), pos=2, xpd=NA)
```

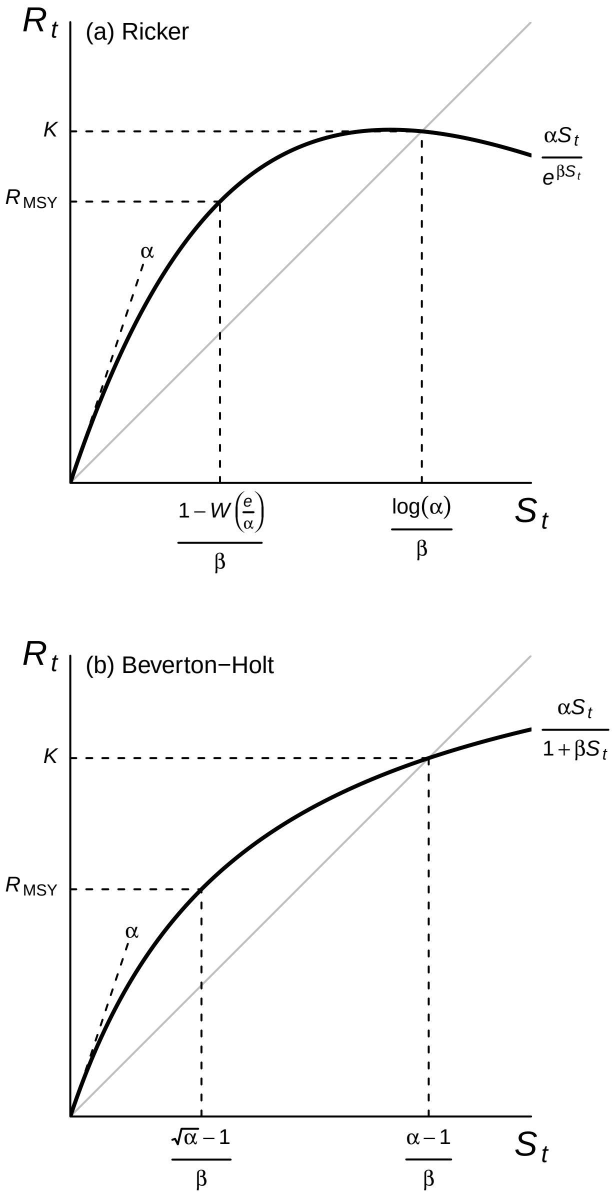

R_t
(a) Ricker
K
R_{MSY}
α
$\frac{\alpha S_t}{e^{\beta S_t}}$
$\frac{1 - W\left(\frac{e}{\alpha}\right)}{\beta}$
$\frac{\log(\alpha)}{\beta}$
S_t
R_t
(b) Beverton−Holt
$\frac{\alpha S_t}{1 + \beta S_t}$
K
R_{MSY}
α
$\frac{\sqrt{\alpha} - 1}{\beta}$
$\frac{\alpha - 1}{\beta}$
S_t

Figure 1. Deterministic forms of the (a) Ricker and (b) Beverton-Holt models used in the analyses (thick lines), including equations for carrying capacity (K) and the number of recruits corresponding to the maximum sustained yield (R_{MSY}). The parameter α defines the slope at the origin, the constant e is Eulers number, and W is the Lambert function (see Scheuerell 2016 for details). The gray line is where $R_t = S_t$.

4 Main results

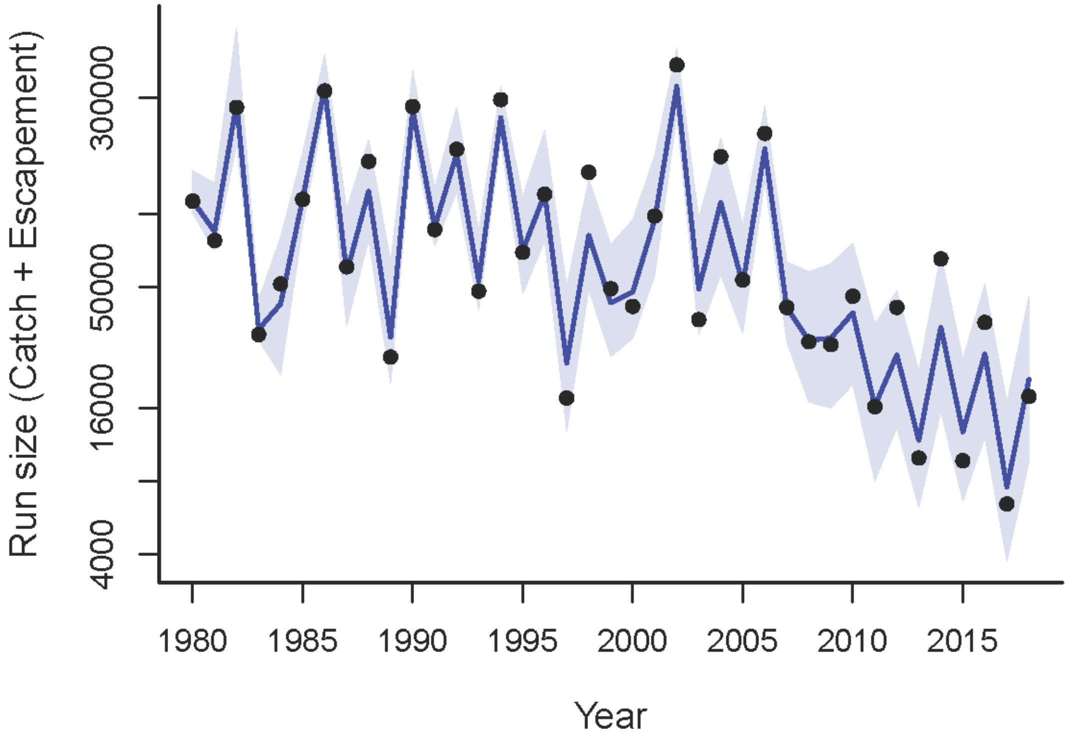
We need to convert the mcmc.list output into a more user-friendly form for plotting, etc.

```
## results
mod_res <- do.call("rbind", best_fit)
```

4.1 Total population size

Here is our estimate of the total run size (i.e., catch + escapement) over time. 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.

```r
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
## estimated spawner data for plotting
p_dat <- mod_res[,grep("Sp", colnames(mod_res))]
p_dat <- apply(p_dat, 2, quantile, CI_vec)
p_dat <- p_dat + matrix(dat_harv, length(CI_vec), n_yrs+n_fore, byrow = TRUE)
## time seq
t_idx_f <- seq(yr_frst, length.out = n_yrs+n_fore)
## plot
yp_min <- min(p_dat)
yp_max <- max(p_dat)
par(mai = c(0.8,0.8,0.1,0.1), omi = c(0.5,0.2,0.1,0.2))
plot(t_idx_f, p_dat[3,], ylim = c(yp_min,yp_max), type = "n",
     log = "y", xaxt = "n", yaxt = "n", bty = "L",
     xlab = "Year", ylab = "Run size (Catch + Escapement)", main = "", cex.lab = 1.2)
polygon(c(t_idx_f, rev(t_idx_f)), c(p_dat[3,], rev(p_dat[1,])),
        col = clr, border = NA)
lines(t_idx_f, p_dat[2,], col = "blue3", lwd = 2)
points(t_idx_f, exp(ln_dat_esc) + dat_harv, pch = 16, cex = 1)
axis(1, at = seq(1980, 2015, 5))
axis(2, at = c(4000, 8000, 16000,50000,100000,300000))
```



```
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
## estimated spawner data for plotting
p_dat <- mod_res[,grep("Sp", colnames(mod_res))]
p_dat <- apply(p_dat, 2, quantile, CI_vec)
## time seq
t_idx_f <- seq(yr_frst, length.out = n_yrs+n_fore)
## plot
yp_min <- min(p_dat)
yp_max <- max(p_dat)
par(mai = c(0.8,0.8,0.1,0.1), omi = c(0.5,0.2,0.1,0.2))
plot(t_idx_f, p_dat[3,], ylim = c(yp_min,yp_max), type = "n",
     log = "y", xaxt = "n", yaxt = "n", bty = "L",
     xlab = "Year", ylab = "Escapement", main = "", cex.lab = 1.2)
polygon(c(t_idx_f, rev(t_idx_f)), c(p_dat[3,], rev(p_dat[1,])),
        col = clr, border = NA)
lines(t_idx_f, p_dat[2,], col = "blue3", lwd = 2)
points(t_idx_f, exp(ln_dat_esc), pch = 16, cex = 1)
abline(h = 46000,lty = 2)
axis(1, at = seq(1980, 2015, 5))
axis(2, at = c(4000, 8000, 16000,50000,100000,300000))
```

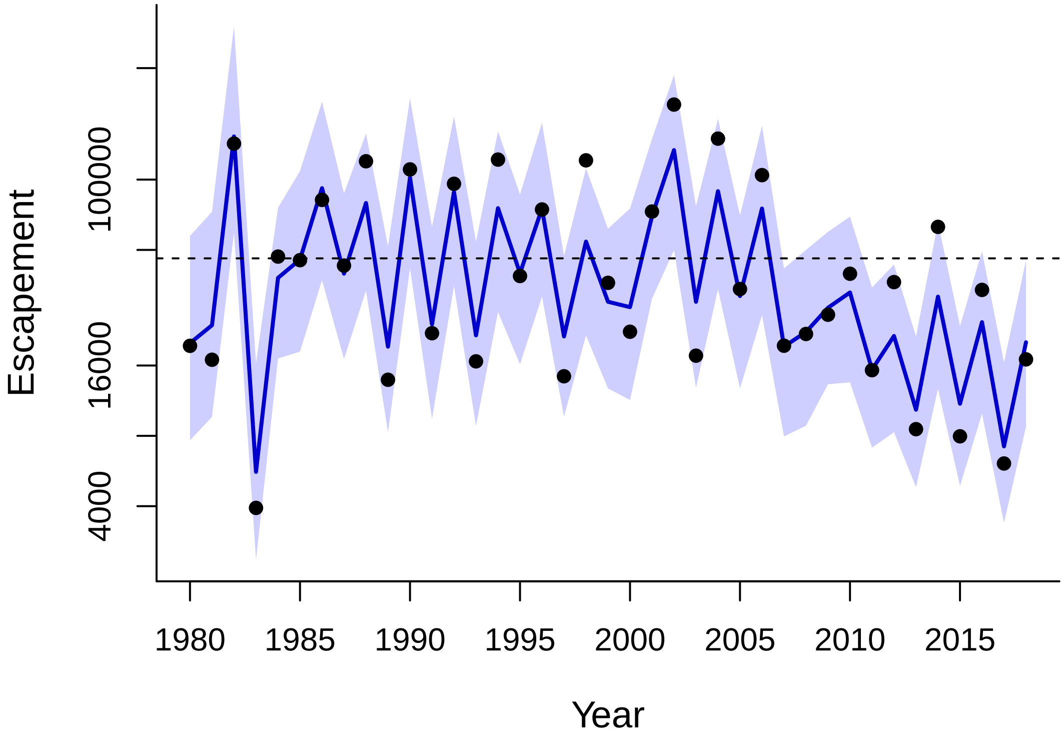


Figure 2. Time series of the estimated total population size (catch plus the adults that escaped to spawn). The observed data are the points; the solid line is the median estimate and the shaded region indicates the 95% credible interval.

4.2 Spawner-recruit relationship

Here is the relationship between spawner and subsequent recruits (a), assuming mean values for all covariates. Gray lines show the median relationship for each of the 39 years based on a_t. 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))
xoffSet <- 0.05
yoffSet <- 0.03

## colors for plotting
clr <- rgb(100, 0, 200,
           alpha = seq(200, 100,
                       length.out = age_max-age_min+n_fore),
           maxColorValue = 255)

## posterior of spawners
```

```
s_dat <- mod_res[,grep("Sp", colnames(mod_res))]
s_dat <- apply(s_dat, 2, quantile, CI_vec)
s_dat <- s_dat[, 1:(n_yrs-age_min+n_fore)]

## posterior of recruits
r_dat <- mod_res[, grep("tot_ln_Rec", colnames(mod_res))]
r_dat <- exp(apply(r_dat, 2, quantile, CI_vec))

r_s_dat <- data.frame(years = dat_yrs[1:(n_yrs-age_min+n_fore)],escapement = (s_dat[2,]),adult_

# ## write model time series of recruits and spawners to a file
# write_csv(r_s_dat, file.path(datadir, "skagit_chum_rec_sp.csv"))


## median values for a & b
aa <- apply(mod_res[, grep("ln_BH_a", colnames(mod_res))], 2, median)
bb <- median(mod_res[, "beta"])



## empty plot space for spawner-recruit relationships
dd <- 50000
yM <- around(max(r_dat), "ceiling", dd)
xM <- around(max(s_dat), "ceiling", dd)
par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0,0,0))
plot(s_dat[2,], r_dat[2,], xlim = c(0,xM), ylim = c(0,yM), type = "n",
     xaxs = "i", yaxs = "i", cex.lab = 1.2,
     xlab = expression(Spawners~(10^3)),
     ylab = expression(Recruits~(10^3)),
     xaxt = "n", yaxt = "n", bty="L")
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, las=1)

samples <- sample(seq(1,5000,1),100)
aa_sample <- aa[samples]
b_sample <- bb[samples]

for(i in 1:length(aa)) {
  lines(exp(aa[i]) * seq(0,xM) / (1 + bb * seq(0,xM)),
      col = "darkgray")
}
abline(a = 0,b = 1,lty = "dashed")

## add S-R estimates and medians
nCB <- n_yrs-age_max
## years with complete returns
points(s_dat[2, 1:nCB], r_dat[2, 1:nCB],
       xlim = c(0,xM), ylim = c(0,yM),
       pch = 16, col = "blue3")
segments(s_dat[2, 1:nCB], r_dat[1, 1:nCB],
         s_dat[2, 1:nCB], r_dat[3, 1:nCB],
         col = "blue3")
segments(s_dat[1, 1:nCB], r_dat[2, 1:nCB],
         s_dat[3, 1:nCB], r_dat[2, 1:nCB],
         col = "blue3")
nTB <- dim(s_dat)[2]
## years with incomplete returns
segments(s_dat[2, (nCB+1):nTB], r_dat[1, (nCB+1):nTB],
         s_dat[2, (nCB+1):nTB], r_dat[3, (nCB+1):nTB],
         col = clr)
segments(s_dat[1, (nCB+1):nTB], r_dat[2, (nCB+1):nTB],
         s_dat[3, (nCB+1):nTB], r_dat[2, (nCB+1):nTB],
         col = clr)
points(s_dat[2, (nCB+1):nTB],r_dat[2, (nCB+1):nTB],
       xlim = c(0,xM), ylim = c(0,yM),
       pch = 16, col = clr)
text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
     y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
     "(a)")

## posterior for alpha
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
a_thresh <- 15
par(mai = c(0.8,0.4,0.3,0.1))
## B-H alpha
R_alpha_est <- mod_res[, "alpha"]
alphaCI <- quantile(R_alpha_est, CI_vec)
R_alpha_est[R_alpha_est > a_thresh] <- a_thresh
hist(R_alpha_est, freq = FALSE, breaks = seq(0, a_thresh, 0.5),
    col = clr, border = "blue3",
    xlab = "", ylab = "", main = "", 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()$usr[1],
     y = par()$usr[4] * 1.05,
     "(b)", xpd=NA)


## posterior for K
par(mai = c(0.8,0.4,0.3,0.1))
aa <- mod_res[, "alpha"]
bb <- mod_res[, "beta"]
## K in 1000s
R_b_est <- (aa-1) / bb / 1000
R_b_est <- R_b_est[R_b_est > 0]
R_b_CI <- quantile(R_b_est, CI_vec)
## pile into last ban for plotting
R_b_est[R_b_est > 150] <- 150
brks <- seq(around(min(R_b_est), "floor"),
            150,
            length.out=length(seq(0,15,0.5)))
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(around(min(R_b_est), "floor"),
                 around(max(R_b_est), "ceiling"),
                 50))
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(paste("Carrying capacity (",italic(K),", ",10^3,")")),
      side = 1, line = 3, cex = 1)
text(x = par()$usr[1],
     y = par()$usr[4] * 1.05,
     "(c)", xpd=NA)
```

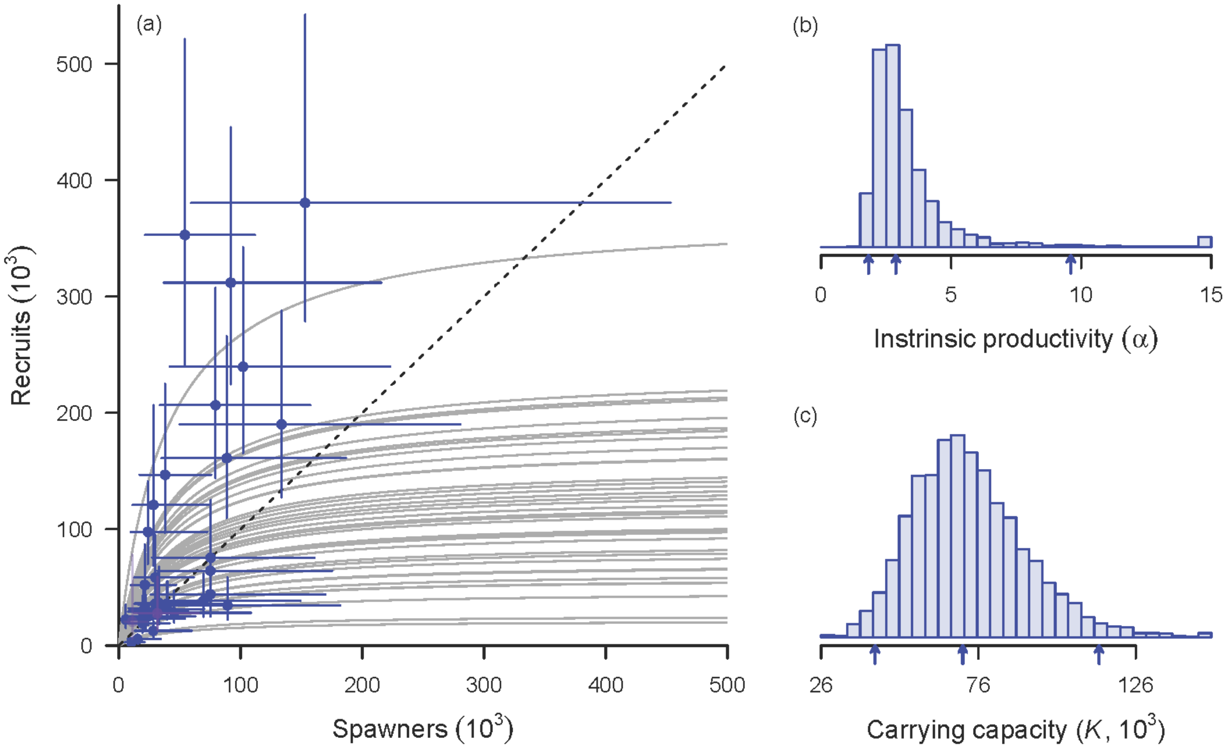


Figure 3. Relationship between the number of spawning adults and their subsequent surviving offspring (recruits), assuming mean values for all covariates (a); and the estimated posterior distributions for the intrinsic productivity (b) and carrying capacity (c). Points in (a) are medians of the posterior estimates; error bars indicate the 95% credible intervals. Blue points are for estimates

with complete broods; purple points are for the most recent years with incomplete broods. Gray lines show the median relationship for each of the 41 years in the time series based on annual model estimates of productivity. 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 than or equal to it. Vertical arrows under the x-axes in (b) and (c) indicate the 2.5$^{\text{th}}$, 50$^{\text{th}}$, and 97.5$^{\text{th}}$ percentiles.

Here are summaries of the posterior distributions for α and K.

```
## intrinsic productivity
round(alphaCI, 2)
```

```
##  2.5%   50% 97.5%
##  1.83  2.87  9.60
```

```
## carrying capacity
round(R_b_CI, 2)
```

```
##   2.5%    50%  97.5%
##  43.13  71.02 114.32
```

4.3 Covariate effects

Here are time series plots of the covariates (a-c) and histograms of their effects on productivity (d-f).

```
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
xoffSet <- 0.04
yoffSet <- 0.03


par(mfrow=c(4,2), mai=c(0.4,0.3,0.05,0.1), omi=c(0.2,0.5,0,0))

c_est <- mod_res[,grep("gamma", colnames(mod_res))]
ylN <- floor(min(c_est)*10)/10
ylM <- ceiling(max(c_est)*10)/10
brks <- seq(ylN,ylM,length.out=diff(c(ylN,ylM))*40+1)
t_idx <- seq(yr_frst,length.out=n_yrs-age_min+n_fore)
dat_cvrs <- as.matrix(dat_cvrs[seq(length(t_idx)),])

whichCov <- c(1,2,3,4)
c <- 1
for(i in whichCov) {
  if(i==4) {
    dat_cvrs[,i+1] <- dat_cvrs[,i+1]/1000
  }
  ## plot covar ts
  plot(dat_cvrs[, "year"], dat_cvrs[, i+1],
       pch = 16, col = "blue3", type = "o",
       xlab = "", ylab = "", main = "", bty = "L",
       cex.axis = 1.2)
  text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
       y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
       paste0("(",letters[c],")"),
       cex = 1.2)
  mtext(side = 2, cov_names[c], line = 3, cex = 1.2)
  if(i == n_cov) {
    mtext(side = 1, "Brood year", line = 3)
  }
  ## plot covar effect
  hist(c_est[,c],
       freq = FALSE, breaks = brks, col = clr, border =" blue3",
       xlab = "", yaxt = "n", main = "", ylab = "", cex.axis = 1.2)
  c_CI <- quantile(c_est[,c],CI_vec)
  aHt <- (par()$usr[4]-par()$usr[3])/20
  arrows(c_CI, par()$usr[3]-0.005, c_CI, par()$usr[3] - aHt,
         code = 1,length = 0.05, xpd = NA, col = "blue3", lwd = 1.5)
  abline(v = 0, lty = "dashed")
  text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
       y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
       paste0("(",letters[c+length(whichCov)],")"),
       cex = 1.2)
  if(i == n_cov) { mtext(side = 1,"Effect size", line = 3) }
  c <- c+1
}
```

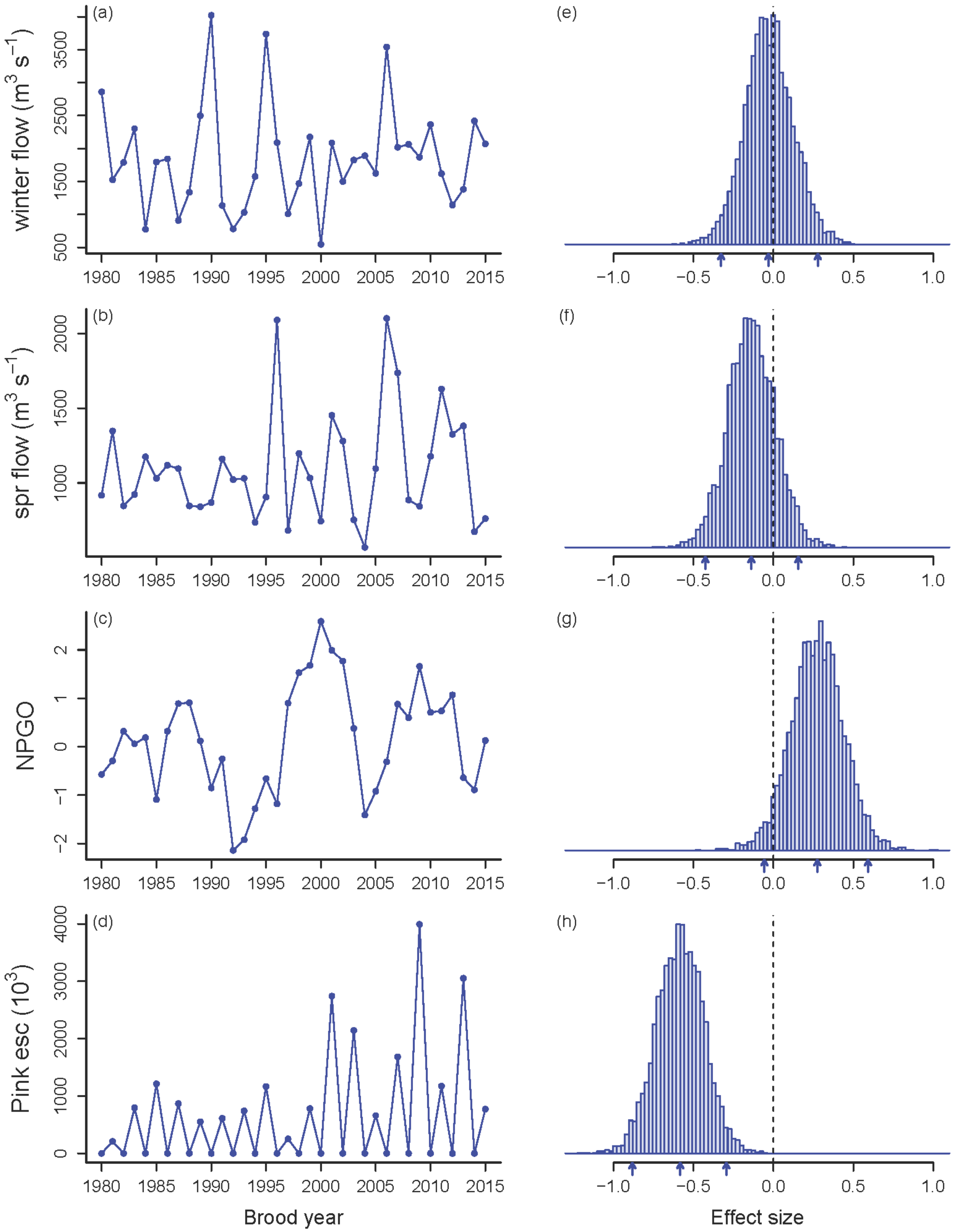


Figure 4. Time series of the environmental covariates used in the model (a-b), and their estimated effects on population productivity (c-d). Small arrows under histograms denote 2.5th, 50th, and 97.5th percentiles of the posterior distribution.

Here is a summary of the covariate effect sizes

```
gamma_CI <- apply(c_est, 2, quantile, c(2.5, 5, 50, 95, 97.5)/100)
t(round(gamma_CI, 2))
```

```
##           2.5%    5%   50%   95% 97.5%
## gamma[1] -0.33 -0.27 -0.03  0.23  0.28
## gamma[2] -0.43 -0.38 -0.14  0.11  0.16
## gamma[3] -0.06  0.01  0.27  0.54  0.59
## gamma[4] -0.88 -0.83 -0.58 -0.34 -0.29
```

4.4 Time-varying productivity

Here is the time series of the time-varying productivity (a_t), which includes the cumulative effects of the 4 covariates.

```
pDat <- apply(mod_res[, grep("ln_BH_a", colnames(mod_res))],2,quantile,CI_vec)
ypMin <- min(pDat)
ypMax <- max(pDat)
t_idx_a <- seq(yr_frst, length.out = n_yrs-age_min+n_fore)

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="Productivity", main="", cex.lab=1.2)
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)
```

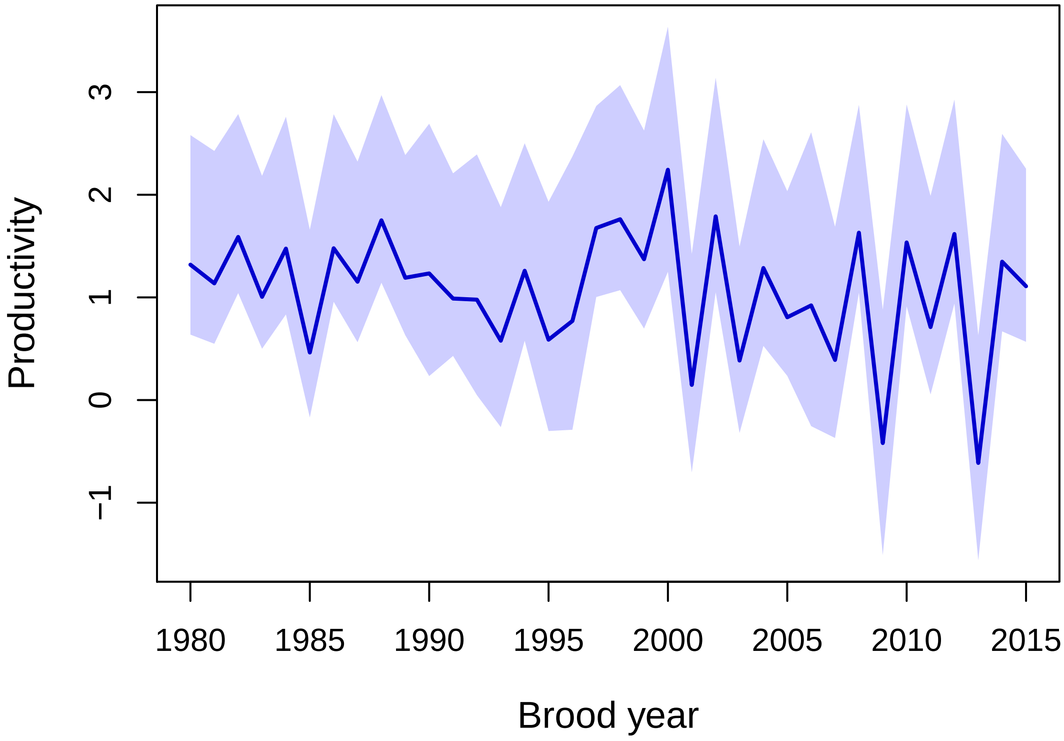


Figure 5. Time series of the time-varying productivity, which includes the cumulative effects of the 2 covariates.

4.5 Process errors

Here is the time series of the residuals from the process model. They represent the population's productivity after accounting for the effects of density dependence and environmental covariates.

```
dat_SAR <- read_csv(file.path(datadir,"ps_hatchery_chum_return_rates.csv"))

dat_SAR <- dat_SAR[which(dat_SAR$year >= yr_frst),]
dat_SAR <- data.frame(dat_SAR)
## time sequence
t_idx_a <- seq(yr_frst, length.out = n_yrs-age_min+n_fore)
## plot data
p_dat <- mod_res[, grep("res_ln_Rec", colnames(mod_res))]
p_dat <- apply(p_dat, 2, quantile, CI_vec)
yp_min <- min(p_dat)
yp_max <- max(p_dat)

## plot

#par(mfrow = c(2,2),mai = c(0.8,0.8,0.3,0.1), omi = c(0,0,0,0))
#par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0.2,0.1,0.2))
layout(matrix(c(1,2,3,0),2,2),c(3,3),c(3,3))
xoffSet <- 0.05
yoffSet <- 0.03
par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0,0,0))
plot(t_idx_a, p_dat[3,],
     type = "n",  bty = "L",
     ylim = c(yp_min,yp_max),
     xlab = "", ylab = "Process error", main = "",
     cex.lab = 1.2)
abline(h = 0, lty = "dashed")
polygon(c(t_idx_a, rev(t_idx_a)), c(p_dat[3,], rev(p_dat[1,])),
        col = clr, border = NA)
lines(t_idx_a, p_dat[2,], col = "blue3", lwd = 2)
text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
paste0("(",letters[1],")"),
cex = 1.2)

plot(dat_SAR[,"Tulalip"]~dat_SAR[,"year"],
     xlim = c(1980,2015),type = "n",bty = "L"
     ,xlab = "Brood year",ylab = "Tulalip hatchery chum SAR",
     cex.lab = 1.2)
  lines(dat_SAR[,"Tulalip"]~dat_SAR[,"year"],col = "blue3",lwd = 2)
```

```
text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
paste0("(",letters[2],")"),
cex = 1.2)


## get SAR data

dat_SAR <- read_csv(file.path(datadir,"ps_hatchery_chum_return_rates.csv"))

dat_SAR <- dat_SAR[which(dat_SAR$year >= yr_frst),]

## get innov
innov <- t(mod_res[, grep("res_ln_Rec", colnames(mod_res))])
## trim to same brood yrs as SAR data
innov_1 <- innov[t_idx_a %in% dat_SAR$year,]

## compute correlation over all mcmc samples
cor_vec_SAR <- apply(innov_1,2,function(x) { cor((dat_SAR$Tulalip),x) })
cor_SAR_CI <- print(quantile(cor_vec_SAR,CI_vec),digits = 2)
```

```
##  2.5%   50% 97.5%
##  0.34  0.53  0.68
```

```
##compute innov_CI <- apply(p_dat, 2, quantile, CI_vec)
innov_CI <- apply(innov_1, 1, quantile, CI_vec)


y <- innov_CI
a <- dat_SAR$Tulalip
pred_a<- seq(min(a),max(a),0.1)


model_SAR_median <- lm(y[2,]~a)


pred_SAR <- predict(model_SAR_median,newdata = list(a = pred_a))

#layout(matrix(c(1,2,3,0),2,2),c(3,3),c(3,3))
#xoffSet <- 0.05
#yoffSet <- 0.03
#par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0,0,0))
plot(pred_a, pred_SAR,
     type = "n",  bty = "L",
     ylim = c(yp_min,yp_max),
     xlab = "Hatchery Chum SAR", ylab = "Process error", main = "",
     cex.lab = 1.2)
abline(h = 0, lty = "dashed")
lines(pred_a, pred_SAR, col = "blue3", lwd = 2)
```

```
points(innov_CI[2,]~a,pch = 16, col = "black")
text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
paste0("(",letters[3],")"),
cex = 1.2)
```

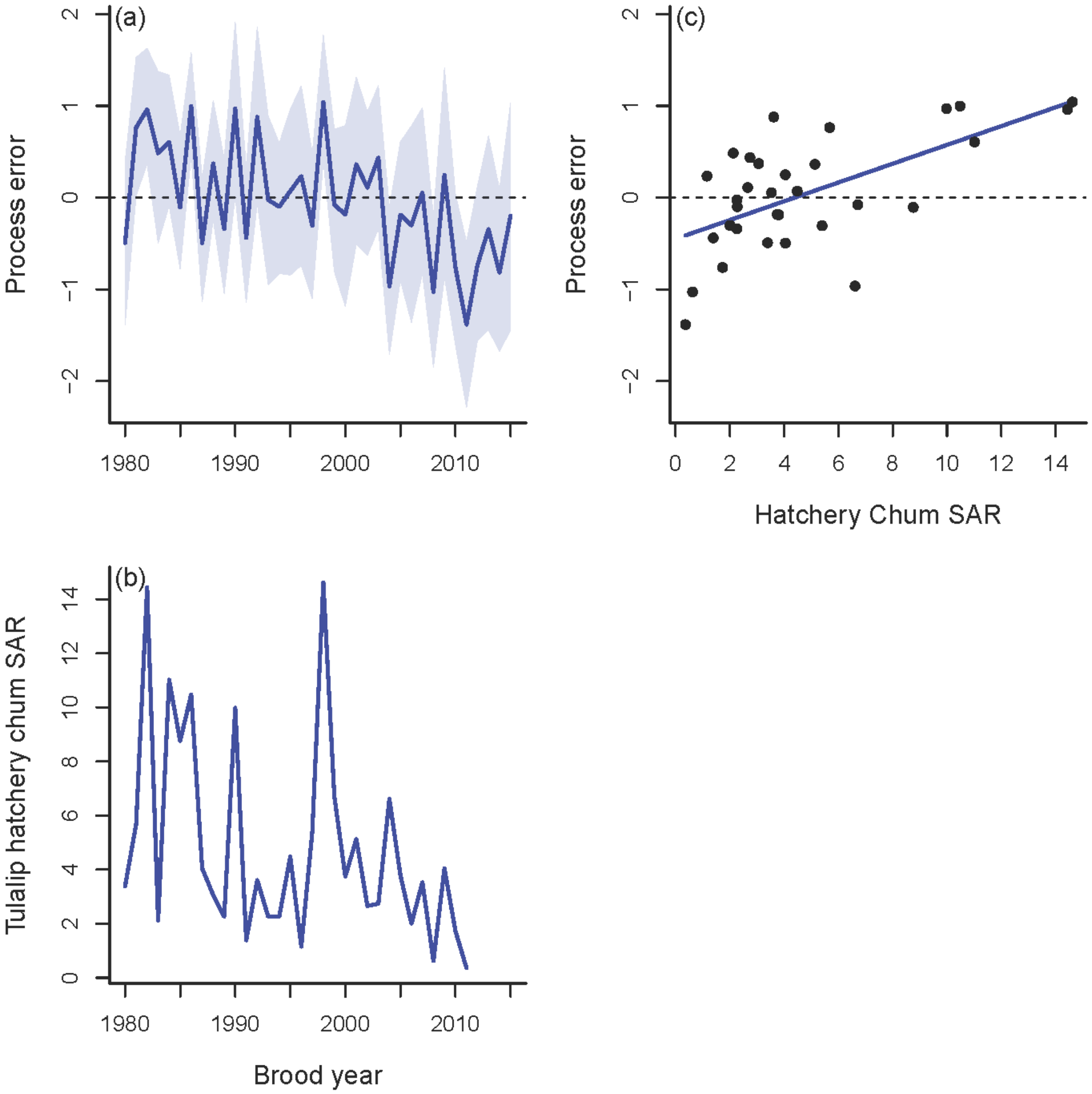


Figure 6. (a) Time series of the estimated process errors, which represent the population's productivity after accounting for the effects of density dependence and environmental covariates. The solid line is the median estimate and the shaded region indicates the 95% credible interval. (b) Time series of marine survival index for Tulalip hatchery chum salmon in units of adult recruits per pounds of fry released

4.5.1 Correlation of process errors & hatchery SAR

Here is our estimate of the correlation between the model innovations (i.e, process residuals) and other potential explanetory variables not included in our model: 1. smolt-to-adult return rate (i.e., logit transformed proportion of smolts that survive to adulthood) of hatchery chum from the Tulalip hatchery. This gives an indication as to whether the unexplained variance in the productivity of wild fish might be related to the marine environment; 2. Skagit pink escapement;

```
## get SAR data

dat_SAR <- read_csv(file.path(datadir,"ps_hatchery_chum_return_rates.csv"))

dat_SAR <- dat_SAR[which(dat_SAR$year >= yr_frst),]

## get innov
innov <- t(mod_res[, grep("res_ln_Rec", colnames(mod_res))])
## trim to same brood yrs as SAR data
innov_1 <- innov[t_idx_a %in% dat_SAR$year,]

## compute correlation over all mcmc samples
cor_vec_SAR <- apply(innov_1,2,function(x) { cor((dat_SAR$Tulalip),x) })
cor_SAR_CI <- print(quantile(cor_vec_SAR,CI_vec),digits = 2)
```

```
##  2.5%   50% 97.5%
##  0.34  0.53  0.68
```

```
##compute innov_CI <- apply(p_dat, 2, quantile, CI_vec)
innov_CI <- apply(innov_1, 1, quantile, CI_vec)


y <- innov_CI
a <- dat_SAR$Tulalip
pred_a<- seq(min(a),max(a),0.1)


model_SAR_median <- lm(y[2,]~a)


pred_SAR <- predict(model_SAR_median,newdata = list(a = pred_a))

#layout(matrix(c(1,2,3,0),2,2),c(3,3),c(3,3))
#xoffSet <- 0.05
#yoffSet <- 0.03
#par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0,0,0))
plot(pred_a, pred_SAR,
     type = "n",  bty = "L",
     ylim = c(yp_min,yp_max),
     xlab = "Hatchery Chum SAR", ylab = "Process error", main = "",
     cex.lab = 1.2)
```

```
abline(h = 0, lty = "dashed")
lines(pred_a, pred_SAR, col = "blue3", lwd = 2)
points(innov_CI[2,]~a,pch = 16, col = "black")
```

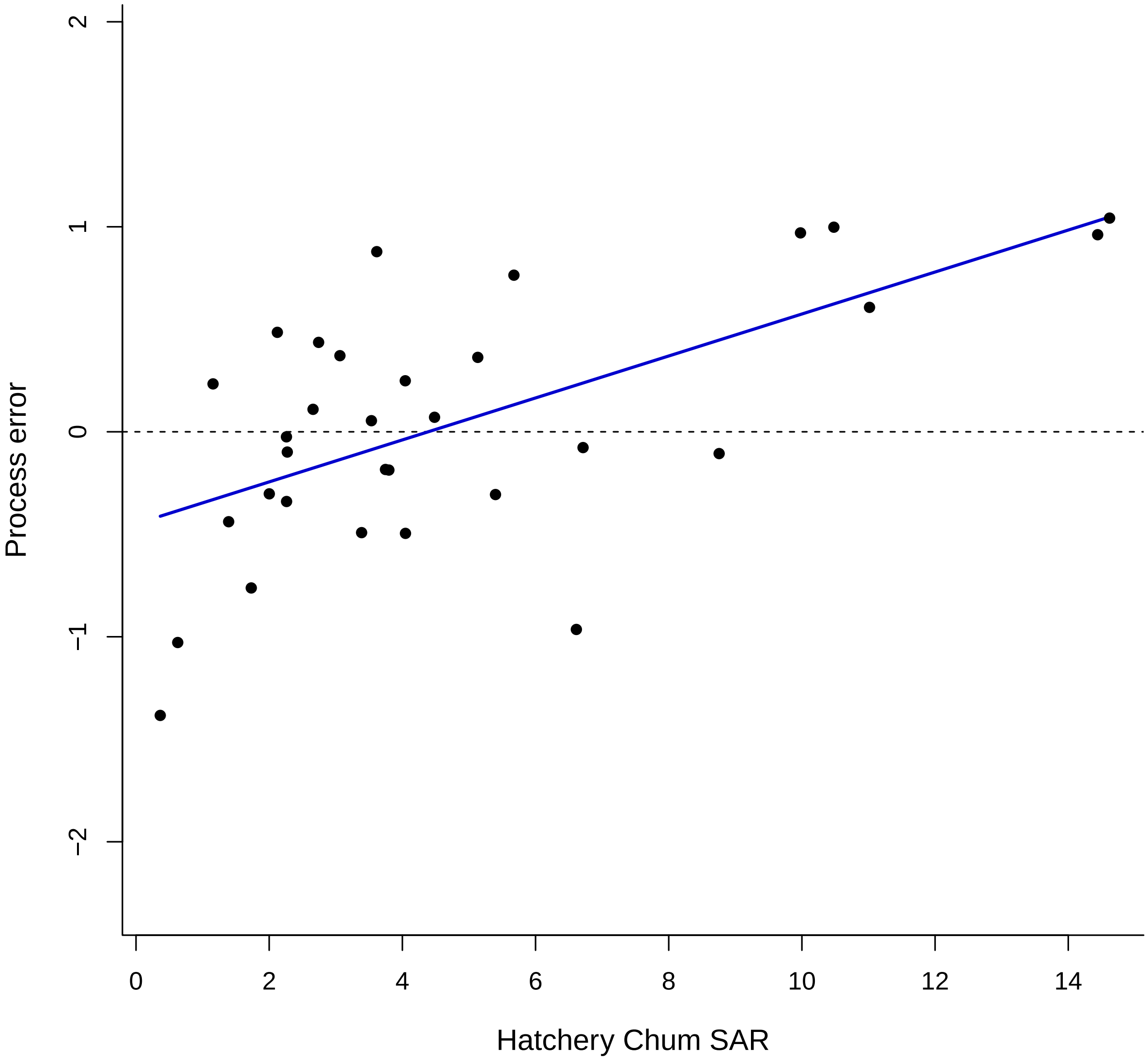


Figure 7. Linear relationships between estimated process errors, which represent the population's productivity after accounting for the effects of density dependence and environmental covariates, and additional potential explanetory variables.

4.6 Time-varying productivity

```
pDat <- apply(mod_res[, grep("ln_RS", colnames(mod_res))],2,quantile,CI_vec)
ypMin <- min(pDat)
```

```
ypMax <- max(pDat)
t_idx_a <- seq(yr_frst, length.out = n_yrs-age_min+n_fore)

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="ln(R/S)", main="", cex.lab=1.2)
polygon(c(t_idx_a,rev(t_idx_a)),c(pDat[3,],rev(pDat[1,])), col=clr, border=NA)
abline(h = 0, lty = 2)
lines(t_idx_a, pDat[2,], col="blue3", lwd=2)
```

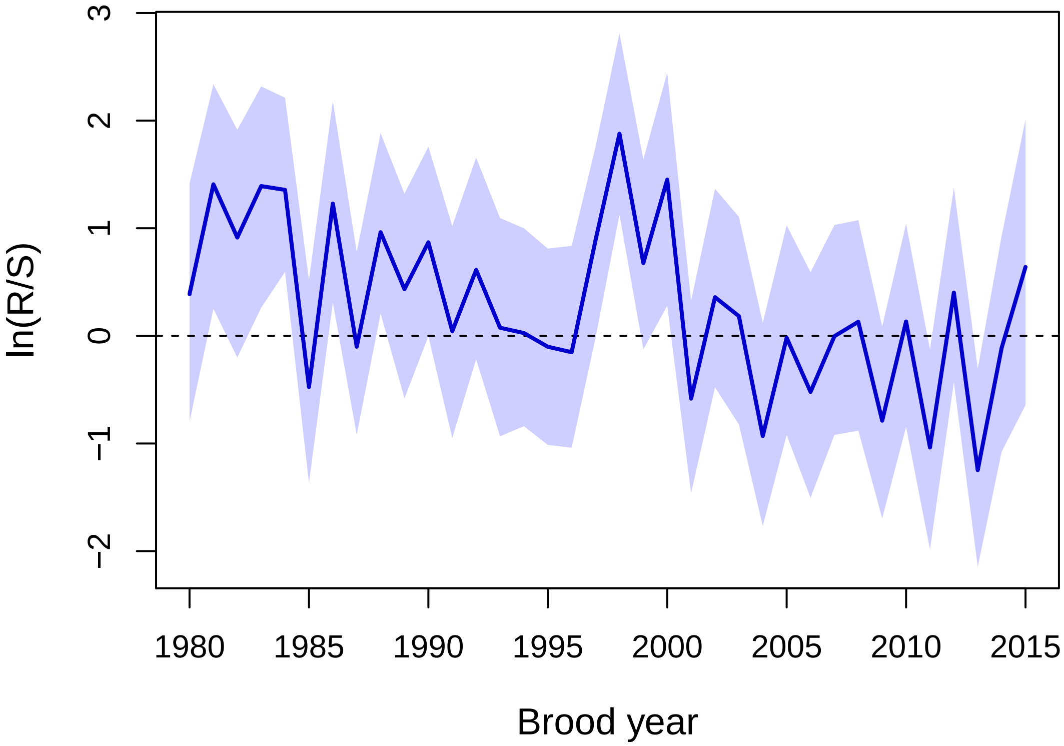


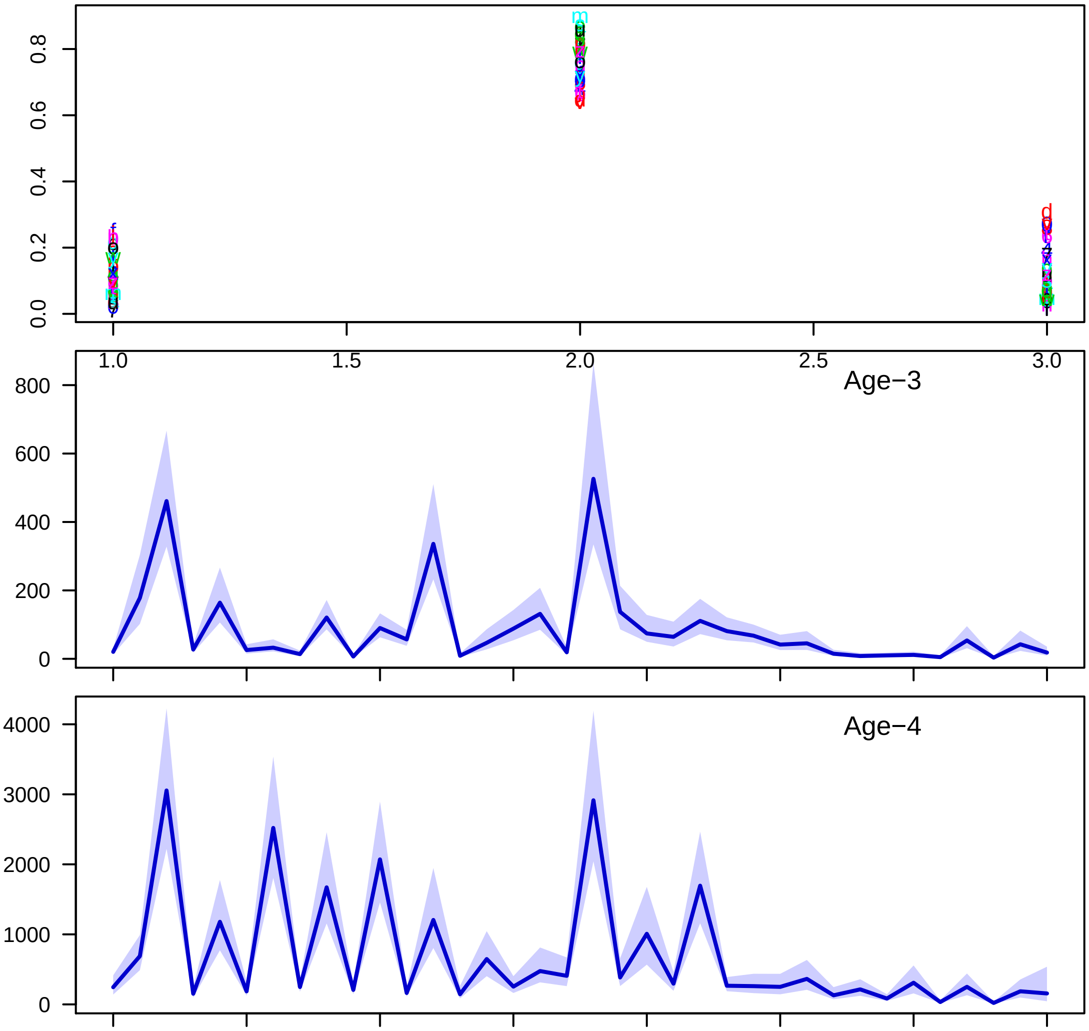
Figure 8. Time series of the time-varying productivity, which includes the cumulative effects of the 2 covariates.

4.6.1 Recruits by age class

Here are the estimated number of recruits by brood year and age. Note that the uncertainty increases in recent years as fewer complete age classes have been observed.

```
CI_vec <- c(0.05,0.5,0.95)
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)

par(mfrow=c(A,1), mai=c(0.1,0.15,0.05,0.1), omi=c(0.5,0.5,0.1,0))
t_idx_R <- seq(yr_frst,length.out= n_yrs-age_min+n_fore)
pltTT <- seq(min(round(t_idx_R/5,0)*5),max(round(t_idx_R/5,0)*5),5)
pDat_1 <- apply(mod_res[,2:37],2,quantile,CI_vec)/100
pDat_2 <- apply(mod_res[,38:73],2,quantile,CI_vec)/100
```

```
pDat_3 <- apply(mod_res[,74:109],2,quantile,CI_vec)/100

rec <- data.frame(age_3 = (pDat_1[2,]),age_4 = (pDat_2[2,]),age_5 = (pDat_3[2,]))


mat_prop <- apply(rec,1,function(x){x/sum(x)})

matplot(mat_prop)

    plot(t_idx_R,pDat_1[3,], #ylim=c(0.001,ypMax),
         type="n", xaxt="n", xlab="", ylab="", main="", las=1)
    polygon(c(t_idx_R,rev(t_idx_R)),c(pDat_1[3,],rev(pDat_1[1,])), col=clr, border=NA)
    lines(t_idx_R, pDat_1[2,], col="blue3", lwd=2)
    aHt <- (par()$usr[4]-par()$usr[3])/7
    ttl <- paste("Age-",3,sep="")
    text(x = par()$usr[1] + diff(par()$usr[1:2]) * .8,
       y = par()$usr[4] - diff(par()$usr[3:4]) * 0.1,
       ttl,
       cex = 1.2)
    axis(1,at=pltTT,labels=FALSE)

    ##
        plot(t_idx_R,pDat_2[3,], #ylim=c(0.001,ypMax),
         type="n", xaxt="n", xlab="", ylab="", main="", las=1)
    polygon(c(t_idx_R,rev(t_idx_R)),c(pDat_2[3,],rev(pDat_2[1,])), col=clr, border=NA)
    lines(t_idx_R, pDat_2[2,], col="blue3", lwd=2)
    aHt <- (par()$usr[4]-par()$usr[3])/7
    ttl <- paste("Age-",4,sep="")
    text(x = par()$usr[1] + diff(par()$usr[1:2]) * .8,
       y = par()$usr[4] - diff(par()$usr[3:4]) * 0.1,
       ttl,
       cex = 1.2)
    axis(1,at=pltTT,labels=FALSE)
```



```
        ##
        plot(t_idx_R,pDat_3[3,], #ylim=c(0.001,ypMax),
         type="n", xaxt="n", xlab="", ylab="", main="", las=1)
    polygon(c(t_idx_R,rev(t_idx_R)),c(pDat_3[3,],rev(pDat_3[1,])), col=clr, border=NA)
    lines(t_idx_R, pDat_3[2,], col="blue3", lwd=2)
    aHt <- (par()$usr[4]-par()$usr[3])/7
    ttl <- paste("Age-",5,sep="")
    text(x = par()$usr[1] + diff(par()$usr[1:2]) * .8,
       y = par()$usr[4] - diff(par()$usr[3:4]) * 0.1,
       ttl,
       cex = 1.2)
    axis(1,at=pltTT)

mtext("Recruits (100s)", 2, line=2.5, outer=TRUE, cex=1.2)
mtext("Year", 1, line=2.5, outer=TRUE, cex=1.2)
```

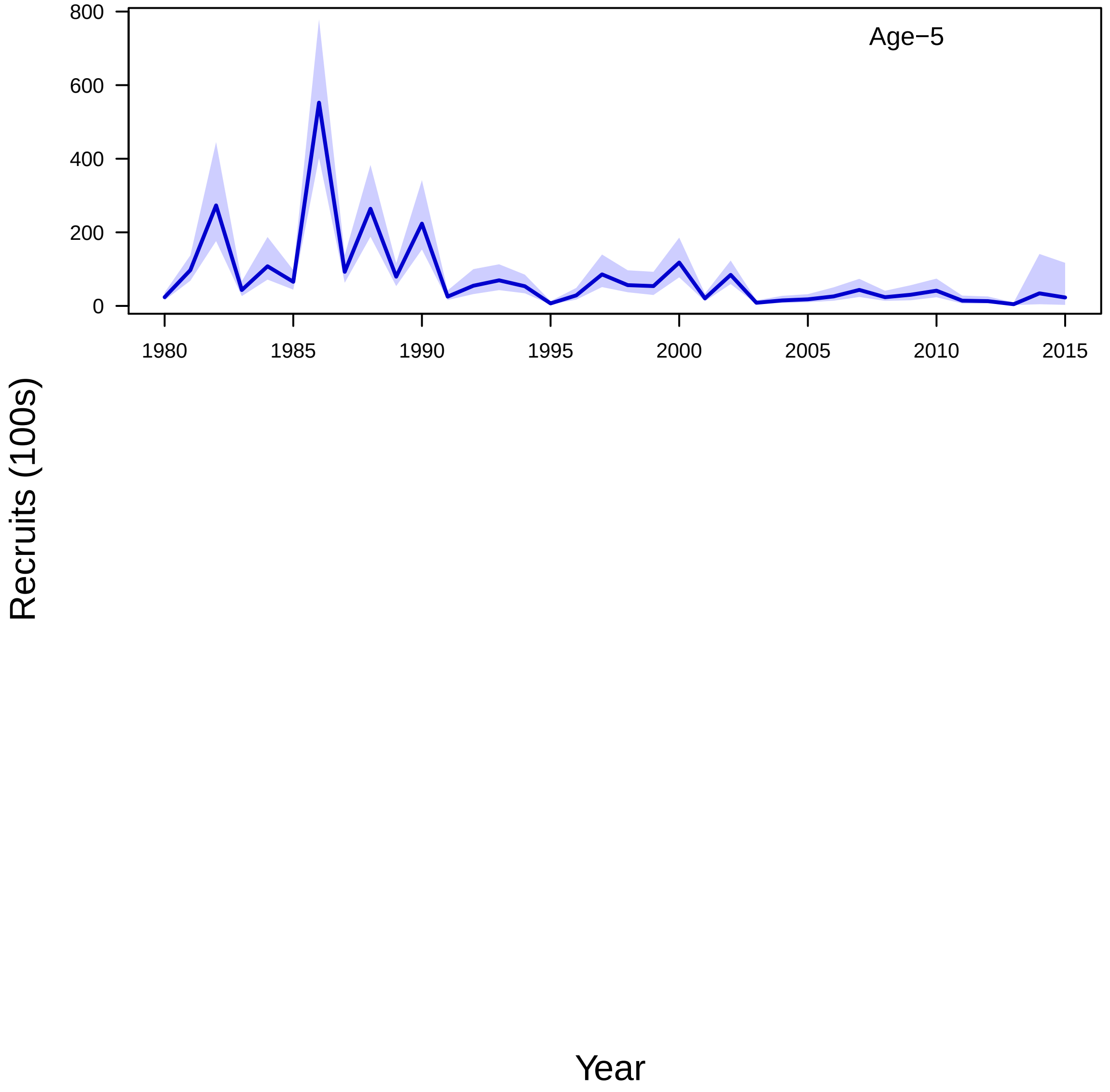
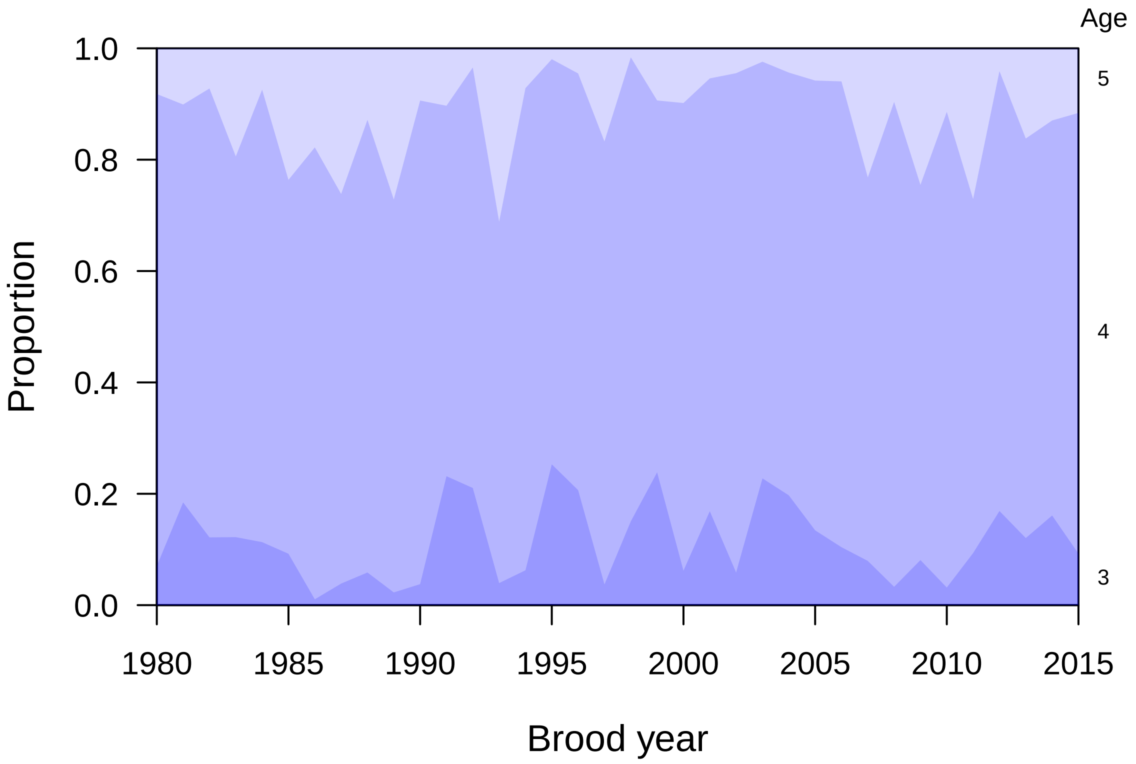


Figure 9. Time series of the estimated number of recruits by brood year and age.

```
par(mai=c(0.8,0.8,0.1,0.1), omi=c(0,0.1,0.2,0.2))
clr <- rgb(0, 0, 255, alpha = 40, maxColorValue = 255)

t_idx_R <- seq(yr_frst,length.out= n_yrs-age_min+n_fore)
pltTT <- seq(min(round(t_idx_R/5,0)*5),max(round(t_idx_R/5,0)*5),5)
pDat_1 <- apply(mod_res[,2:37],2,quantile,CI_vec)/100
pDat_2 <- apply(mod_res[,38:73],2,quantile,CI_vec)/100
pDat_3 <- apply(mod_res[,74:109],2,quantile,CI_vec)/100

rec <- data.frame(age_3 = (pDat_1[2,]),age_4 = (pDat_2[2,]),age_5 = (pDat_3[2,]))


mat_prop <- apply(rec,1,function(x){x/sum(x)})
```

```
age_est <- t(apply(mat_prop,2,cumsum))

nRec <- n_yrs-age_min
plot(t_idx_R, rep(1,nRec+n_fore), ylab="Proportion", xlab="Brood year", ylim=c(0,1), las=1,
     xaxs="i", yaxs="i", type="n", lty="solid", col="blue3", cex.lab=1.2)
for(i in c(1,2,3)) {
    polygon(c(t_idx_R,rev(t_idx_R)),c(age_est[,i],rep(0,nRec+n_fore)), col=clr, border=NA)
    }
lbl <- apply(cbind(c(0,age_est[nRec+n_fore,-A]),age_est[nRec+n_fore,]),1,mean)
text(par()$usr[2],par()$usr[4]*1.05,"Age", xpd=NA, pos=4, offset=0.05, col="black", cex=0.8)
text(par()$usr[2],lbl[1:4],seq(3,5), xpd=NA, pos=4, col="black", cex=0.7)
```


Age
Proportion
Brood year