

Appendix S3. Code to recreate figures from main text.

Contents

1	Background	1
2	Load the information	2
3	Extract posterior values	3
4	Figures	4
4.1	Deterministic Ricker model	4
4.2	Total population size	6
4.3	Spawner-recruit relationship	7
4.4	Covariate effects	10
4.5	Process errors	12

This is version 0.19.03.21.

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 (v3.4.3 or later), as well as a few packages that are not included with the base installation of R.

```
## for dir management
if(!require("here")) {
  install.packages("here")
  library("here")
}
## set directory locations
datadir <- here("data")
jagsdir <- here("jags")
## for reading csv
if(!require("readr")) {
  install.packages("readr")
  library("readr")
}
## for Lambert function
if(!require("gsl")) {
  install.packages("gsl")
  library("gsl")
}
## for figure captions
if(!require("captioner")) {
  devtools::install_github("adletaw/captioner")
}
```

```

  library("captioner")
}
## set default caption options
fig_cap <- captioner(suffix = ".", style = "b", style_prefix = TRUE)

```

We also need the following helper function.

```

Re2prec <- function(x, map = "round", prec = 1) {
  ## 'map' can be "round", "floor", or "ceiling"
  ## 'prec' is nearest value
  ## (eg, 0.1 is to nearest tenth; 1 is to nearest integer)
  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 model fits, covariates, and harvest data.

```

best_fit <- readRDS(file.path(jagsdir, paste0("fit_ricker_cov_", best_i, ".rds")))

## covariate(s)
dat_cvrs <- read_csv(file.path(datadir, "Willamette_Chin_SR_mainstem_flow_covariates.csv"))
t_idx <- seq(yr_frst, length.out = n_yrs-age_min)
dat_cvrs <- as.matrix(dat_cvrs[seq(length(t_idx)),])

## escapement
dat_esc <- read_csv(file.path(datadir, "chin_esc.csv"))
## use total counts
dat_esc <- dat_esc[dat_esc$group=="total",-1]
## log of escapement
ln_dat_esc <- log(dat_esc[,-1])

## harvest
dat_harv <- read_csv(file.path(datadir, "chin_harv.csv"))
## trim to correct years & drop year col
dat_harv <- dat_harv[dat_harv$year>=yr_frst & dat_harv$year<=yr_last,-1]

```

3 Extract posterior values

```
## convert the `mcmc.list` output into a more user-friendly form
mod_res <- do.call("rbind", best_fit)

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

## total run size
run_size <- s_pst + matrix(as.matrix(dat_harv), length(CI_vec), n_yrs, byrow = TRUE)

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

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

## alpha w/ effect of median flow
alpha_est <- mod_res[, "alpha"] * exp(mod_res[, "gamma"] * median(dat_cvrs[,best_i+1]))
alphaCI <- quantile(alpha_est, CI_vec)

## carrying capacity in 1000s
K_est <- log(alpha_est) / mod_res[, "beta"] / 1000
K_est <- K_est[K_est > 0]
K_est_CI <- quantile(K_est, CI_vec)
## pile into last bin for plotting
K_est[K_est > 24] <- 24
```

4 Figures

4.1 Deterministic Ricker model

```
## params
ra <- 3
rb <- 1.2e-4

## ref pts
rmr <- ra/rb*exp(-1)
rsy <- (1 - lambert_W0(exp(1)/ra)) / rb
ruy <- 1 - lambert_W0(exp(1)/ra)

## S-R curve
## spawners
ss <- seq(0,1.2e4,10)
## recruits
rr <- ra*ss/exp(rb*ss)

par(mai=c(0.8,0.6,0.2,0.2), omi=c(0,0,0,0.25))
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)
## 1:1
abline(a=0, b=1, col="gray")
## 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(0.5,1.1), xpd=NA)
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)
```

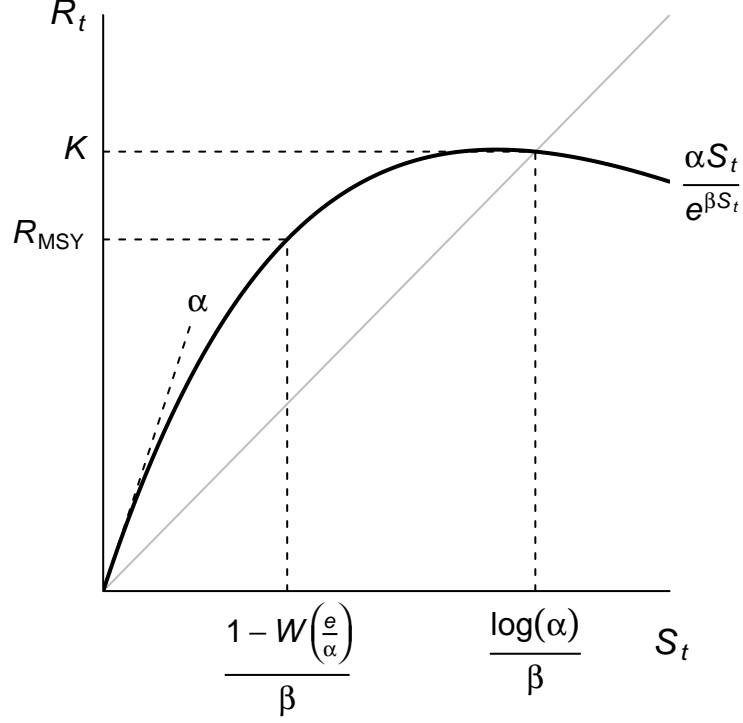


Figure 1. Deterministic form of the Ricker model used in the analysis, including equations for carrying capacity (K) and the number of recruits corresponding to the maximum sustained yield (R_{MSY}). The parameter α defines the slope at the origin, the constant e is Euler's number, and W is the Lambert function (see Scheuerell 2016 for details). The gray line is where $R_t = S_t$.

4.2 Total population size

```

clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
## time seq
t_idx_f <- seq(yr_frst, length.out = n_yrs+n_fore)
## plot
yp_min <- min(run_size)
yp_max <- max(run_size)
par(mai = c(1,1,0.1,0.1), omi = c(0.5,0.5,0.1,0.2))
plot(t_idx_f, run_size[3,], ylim = c(yp_min,yp_max), type = "n",
     log = "y", xaxt = "n", yaxt = "n", bty = "L",
     xlab = "Year", ylab = expression(Catch~+~Escapement~(10^3)), main = "", cex.lab = 1.2)
polygon(c(t_idx_f, rev(t_idx_f)), c(run_size[3,], rev(run_size[1,])),
       col = clr, border = NA)
lines(t_idx_f, run_size[2,], col = "blue3", lwd = 2)
points(cbind(t_idx_f, exp(ln_dat_esc) + dat_harv), pch = 16, cex = 1)
axis(1, at = seq(2000, 2015, 3))
axis(2, at = c(5000, 10000, 20000, 40000),
      labels = c(c(5, 10, 20, 40)), las = 1)

```

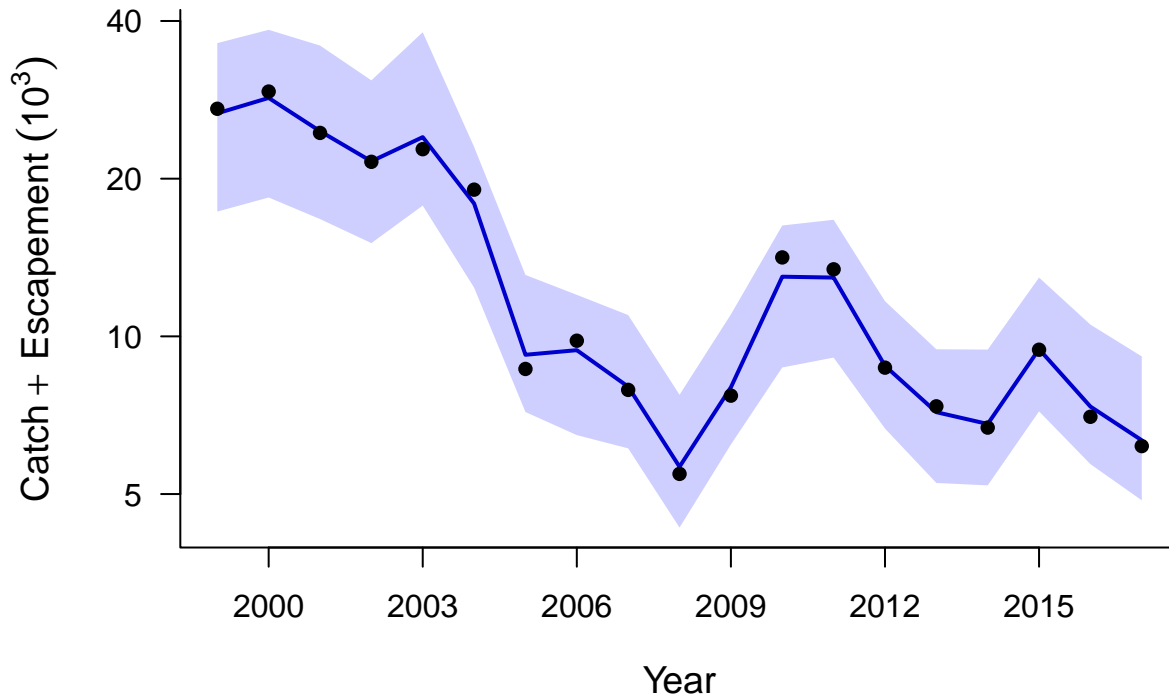


Figure 2. Time series of the estimated total population size (catch plus escapement). The observed data are the points; the solid line is the median estimate of the true number of spawners and the shaded region indicates the 95% credible interval.

4.3 Spawner-recruit relationship

```
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)

## empty plot space for spawner-recruit relationships
dd <- 3000
yM <- Re2prec(max(r_dat), "ceiling", dd)
xM <- Re2prec(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)
for(i in 1:length(alphaCI)) {
  lines(alphaCI[i] * seq(0,xM) * exp(-bb * seq(0,xM)),
        col = ifelse(i==2, "black", "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)
par(mai = c(0.8,0.4,0.3,0.1))
hist(alpha_est, freq = FALSE, breaks = seq(0, Re2prec(max(alpha_est), "ceiling", 0.5), 0.2),
      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(Intrinsic~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))
brks <- seq(Re2prec(min(K_est), "floor"),
           Re2prec(max(K_est), "ceiling", 2))
hist(K_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(K_est), "floor"),
                Re2prec(max(K_est), "ceiling"),
                2))
aHt <- (par()$usr[4] - par()$usr[3]) / 12
arrows(K_est_CI, par()$usr[3], K_est_CI,par()$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)

```

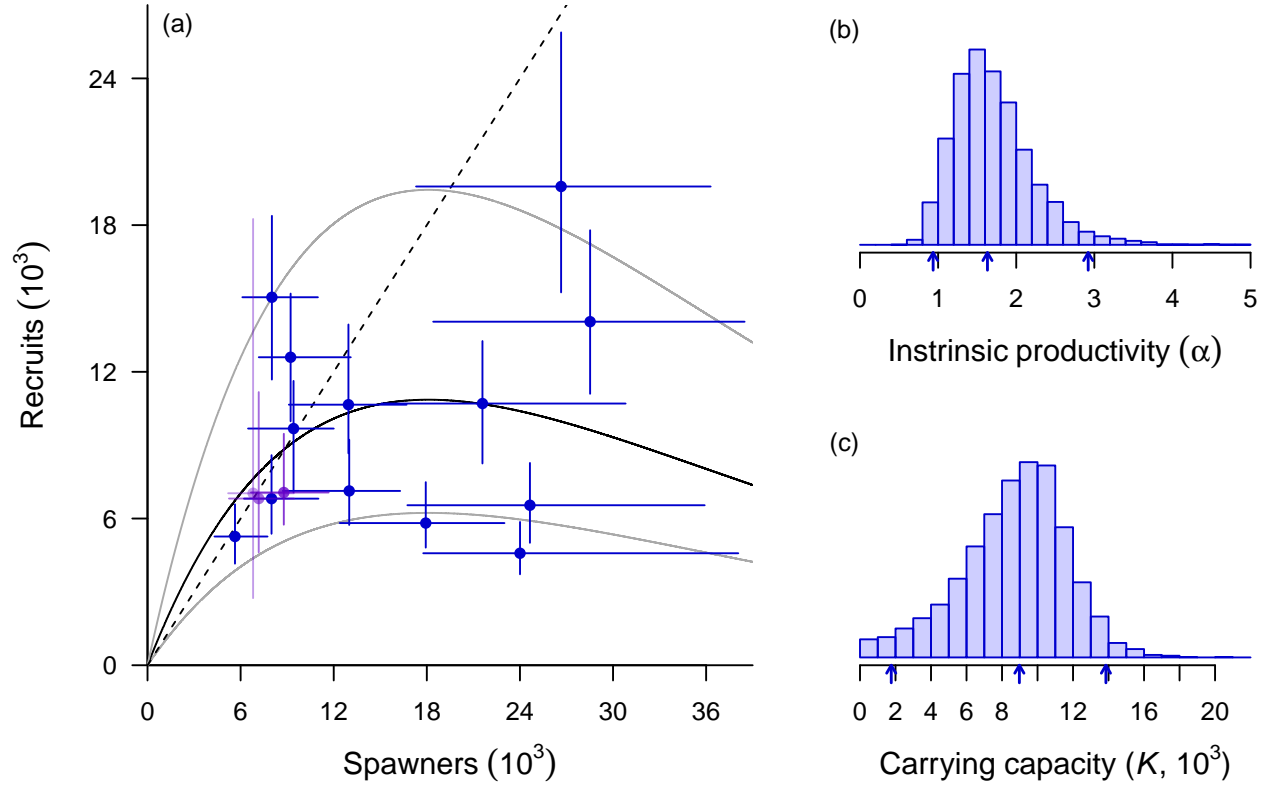



Figure 3. Relationship between the number of spawning adults and their subsequent surviving offspring (recruits), assuming median values for the flow covariate (a); and the estimated posterior distributions for the intrinsic productivity (b) and carrying capacity (c). Points in (a) are medians of the 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. The black line in (a) shows the expected relationship based on the median flow value over all years; gray lines indicate the 2.5th and 97.5th credible intervals. 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 2.5th, 50th, and 97.5th percentiles.

4.4 Covariate effects

```
clr <- rgb(0, 0, 255, alpha = 50, maxColorValue = 255)
xoffSet <- 0.05
yoffSet <- 0.03

c_est <- mod_res[,grep("gamma", colnames(mod_res))] * 1000
ylN <- Re2prec(min(c_est), "floor", 0.02)
ylM <- Re2prec(max(c_est), "ceiling", 0.02)
brks <- seq(ylN,ylM, length.out = diff(c(ylN,ylM))*400+1)

par(mfrow=c(1,2), mai=c(0.4,0.4,0.1,0.1), omi=c(0.5,0.5,0,0))

## plot covar ts
plot(dat_cvrs[, 1], dat_cvrs[, best_i+1]/1000,
     pch = 16, col = "blue3", type = "o",
     xlab = "", ylab = "", main = "", bty = "L", las = 1)
text(x = par()$usr[1] + diff(par()$usr[1:2]) * xoffSet,
     y = par()$usr[4] - diff(par()$usr[3:4]) * yoffSet,
     "(a)")
mtext(side = 2, expression(Flow~(10^3~cfs)), line = 3, cex = 1.2)
mtext(side = 1, "Brood year", line = 3, cex = 1.2)

## plot covar effect
hist(c_est,
     freq = FALSE, breaks = brks, col = clr, border = "blue3",
     xlab = "", yaxt = "n", main = "", ylab = "")
c_CI <- quantile(c_est,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,
     "(b)")
mtext(side = 1,expression(Effect~size~(10^{-3}~cfs)), line = 3, cex = 1.2)
```

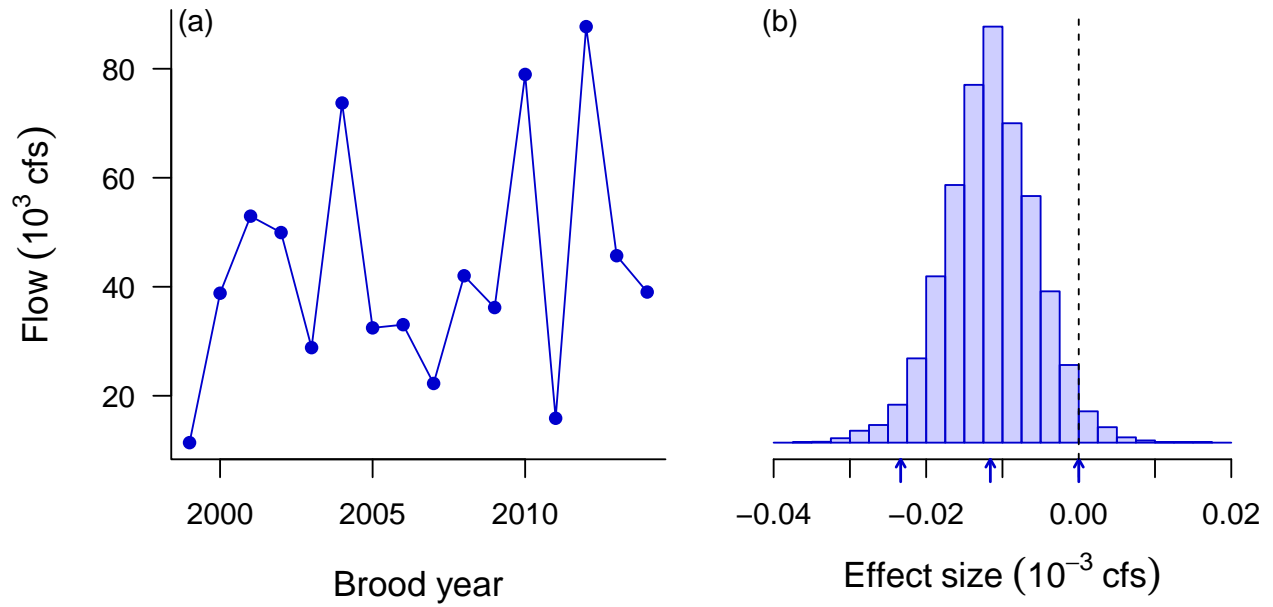


Figure 4. Time series of the range of the 7-day mean flow during the months of February through April (a), and its estimated effect on population productivity (b). Small arrows under the histogram in (b) denote 2.5th, 50th, and 97.5th percentiles of the posterior distribution.

4.5 Process errors

```
## time sequence
t_idx_a <- seq(yr_frst, length.out = n_yrs-age_min+n_fore)
## plot data
proc_err <- mod_res[, grep("res_ln_Rec", colnames(mod_res))]
proc_err <- apply(proc_err, 2, quantile, CI_vec)
yp_min <- min(proc_err)
yp_max <- max(proc_err)
## plot
par(mai = c(0.8,0.8,0.1,0.1), omi = c(0,0.2,0.1,0.2))
plot(t_idx_a, proc_err[3,],
     type = "n", bty = "L", xaxt = "n",
     ylim = c(yp_min,yp_max),
     xlab = "Brood year", ylab = "Process error", main = "",
     cex.lab = 1.2)
abline(h = 0, lty = "dashed")
polygon(c(t_idx_a, rev(t_idx_a)), c(proc_err[3,], rev(proc_err[1,])),
       col = clr, border = NA)
lines(t_idx_a, proc_err[2,], col = "blue3", lwd = 2)
axis(1, at = seq(2000, 2015, 3))
```

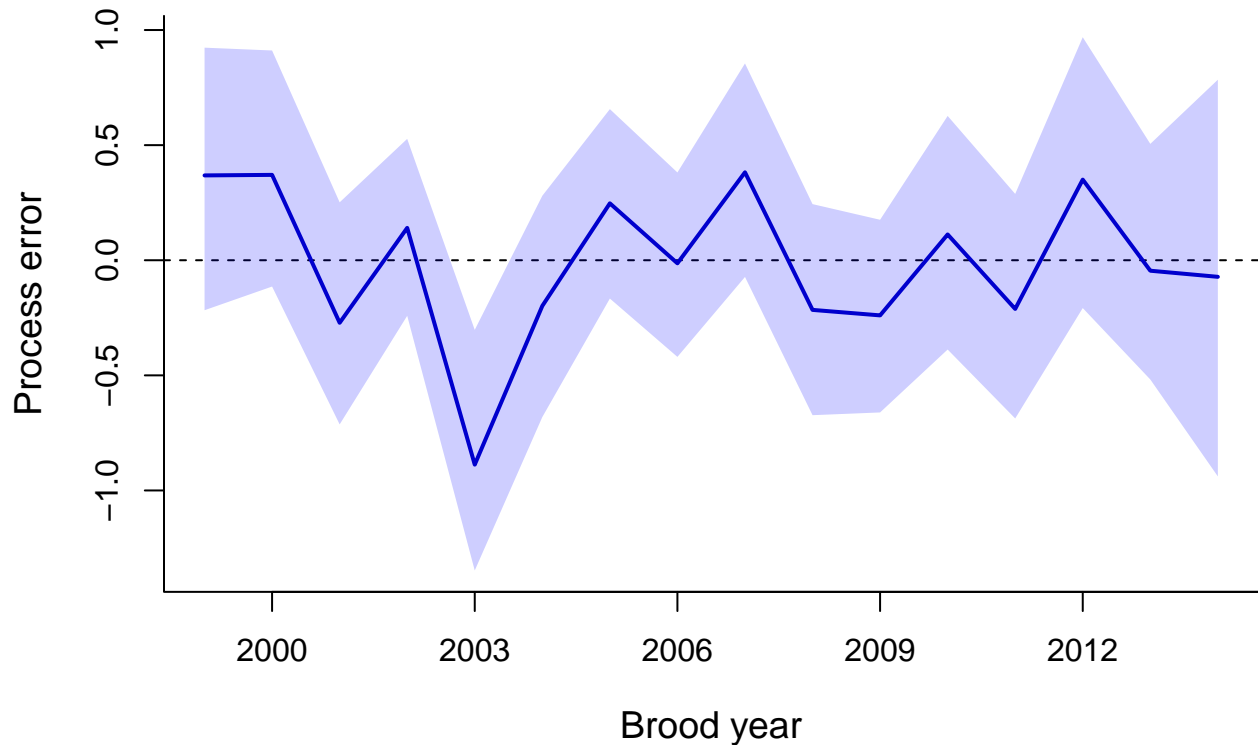


Figure 5. Time series of the estimated process errors, which represent the population's productivity after accounting for the effects of density dependence and environmental covariates. The solid line is the median estimate and the shaded region indicates the 95% credible interval.