R2. Model fitting and evaluation

2020 - 2021 Skagit River steelhead forecast.

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This is version 0.21.01.05.	

Requirements

All analyses require the R software (v3.4.3) for data retrieval, data processing, and summarizing model results, and the JAGS software (v4.2.0) for Markov chain Monte Carlo (MCMC) simulation. Please note that some of the R code below may not work with older versions of JAGS due to some changes in the ways that arrays are handled.

We also need a few packages that are not included with the base installation of R, so we begin by installing them (if necessary) and then loading them.

```
if(!require("here")) {
  install.packages("here")
  library("here")
if(!require("readr")) {
  install.packages("readr")
  library("readr")
}
if(!require("rjags")) {
  install.packages("rjags")
  library("rjags")
}
if(!require("loo")) {
  install.packages("loo")
  library("loo")
if(!require("ggplot2")) {
  install.packages("ggplot2")
  library("ggplot2")
}
if(!require("coda")) {
  install.packages("coda")
  library("coda")
}
if(!require("shinystan")) {
  install.packages("shinystan")
  library("shinystan")
}
if(!require("R2jags")) {
  install.packages("R2jags")
  library("R2jags")
if(!require("dclone")) {
  install.packages("dclone")
  library("dclone")
if(!require("snow")) {
  install.packages("snow")
  library("snow")
if(!require("rstan")) {
  install.packages("rstan")
  library("rstan")
if(!require("RColorBrewer")) {
  install.packages("RColorBrewer")
  library("RColorBrewer")
}
## set directory locations
datadir <- here("data")</pre>
```

```
jagsdir <- here("jags")
analdir <- here("analysis")
savedir <- here("analysis/cache")</pre>
```

We also need a couple of helper functions.

```
## better round
Re2prec <- function(x, map = "round", prec = 1) {</pre>
  ## 'map' can be "round", "floor", or "ceiling"
 ## 'prec' is nearest value (eg, 0.1 means to nearest tenth; 1 gives normal behavior)
 if(prec<=0) { stop("\"prec\" cannot be less than or equal to 0") }</pre>
 do.call(map,list(x/prec))*prec
## wrapper function to fit JAGS models & rearrange output
fit_jags <- function(model, data, params, inits, ctrl, dir = jagsdir) {</pre>
  jm <- jags.model(file.path(jagsdir, model),</pre>
                    data,
                    inits,
                    ctrl$chains,
                    ctrl$burn,
                    quiet = TRUE)
 return(coda.samples(jm, params, ctrl$length, ctrl$thin))
}
#alternative wrapper to fit model in parallel; one chain per core
fit_jags2<-function(model,data,params,inits,ctrl,dir=jagsdir){</pre>
  cl <- makeCluster(3, type = "SOCK")</pre>
  inits2 <- jags.fit(data=data,</pre>
                      params=params,
                      model=file.path(jagsdir, model),
                      inits=inits,
                      n.chains=ctrl$chains,
                      n.adapt = 0,
                      n.update = 0,
                      n.iter = 0)$state(internal = TRUE)
  jm <- jags.parfit(cl=cl,</pre>
                     data = data,
                     params = params,
                     model = file.path(jagsdir, model),
                     inits = inits2,
                     n.adapt = ctrl$burn*0.5,
                     n.update = ctrl$burn*0.5,
                     n.iter = ctrl$length-ctrl$burn,
                     thin = ctrl$thin,
                     n.chains = ctrl$chains
  stopCluster(cl)
 return(jm)
}
#generate summary stats file from MCMC object
sum_stats<-function(mcmclist){</pre>
```

```
ESS<-apply(as.matrix(mcmclist),2,ess_bulk)</pre>
  Rhat<-apply(as.matrix(mcmclist),2,Rhat)</pre>
  summary_stats<-summary(mcmclist)</pre>
  summary_stats<-data.frame(summary_stats$statistics,summary_stats$quantiles,ESS,Rhat)
}
# functions for approximate LFO
# many functions modified from:
# https://github.com/paul-buerkner/LFO-CV-paper/blob/master/case-study-LFO-CV.Rmd
#load complete model fits & model refits with subset data
loadmodfits<-function(modelnames){</pre>
  mod_fits<-list(NULL)</pre>
  for(i in 1:length(modelnames)){
    mod_fits[[i]] <- readRDS(file.path(savedir,paste0(modelnames[i],"_y",n_forecasts+1,".rds")))</pre>
    \#mod_fits[[i]] \leftarrow readRDS(file.path(savedir,pasteO("fit_",modelnames[i],".rds")))
  }
  return(mod_fits)
}
#refits
loadrefits<-function(refitname,N,L){</pre>
  numrefits < -N-L+1
  re_fits<-list()
  for(i in 1:numrefits){
     re_fits[[i]] <- readRDS(file.path(savedir,paste0(refitname,"_y",i,".rds")))</pre>
  }
  return(re_fits)
# more stable than log(sum(exp(x)))
log_sum_exp <- function(x) {</pre>
 max_x \leftarrow max(x)
  \max_{x} + \log(\sup(\exp(x - \max_{x})))
}
# more stable than log(mean(exp(x)))
log_mean_exp <- function(x) {</pre>
  log_sum_exp(x) - log(length(x))
# compute log of raw importance ratios
# sums over observations *not* over posterior samples
sum_log_ratios <- function(ll, ids = NULL) {</pre>
  if (!is.null(ids)) ll <- ll[, ids, drop = FALSE]</pre>
  - rowSums(11)
}
# for printing comparisons later
rbind_print <- function(...) {</pre>
  round(rbind(...), digits = 2)
}
#function to extract log likelihood from fitted model
```

```
extract_log_lik<-function(m,esc_only,N,mod_fits){</pre>
  #extract pontwise log likelihoods
  tmp_lp <- as.matrix(mod_fits[[m]])</pre>
  ## extract pointwise likelihoods
  tmp_lp <- tmp_lp[,grepl("lp_", colnames(tmp_lp))]</pre>
  ## if numerical underflows, convert -Inf to 5% less than min(likelihood)
  if(any(is.infinite(tmp_lp))) {
    tmp lp[is.infinite(tmp lp)] <- NA</pre>
    tmp_min <- min(tmp_lp, na.rm = TRUE)</pre>
    tmp_lp[is.na(tmp_lp)] \leftarrow tmp_min * 1.05
  if(esc_only =="Yes"){
    tmp_lp<-tmp_lp[,grepl("esc", colnames(tmp_lp))]</pre>
  #qet yrs assoc
  names_loglik<-data.frame(strsplit(colnames(tmp_lp),"\\[|\\]"))</pre>
  yrnames<-as.numeric(names_loglik[2,])</pre>
  loglik <- matrix(NA,ncol=N,nrow=dim(tmp_lp)[1])</pre>
  for(i in 1:N){
    if(!is.null(ncol(tmp_lp[,yrnames==i]))){
      loglik[,i] = apply(tmp_lp[,yrnames==i],1,sum)
    }else(loglik[,i] = tmp_lp[,yrnames==i])
  }
  return(loglik)
}
approx_LFO<-function(N=N,L,m=m,esc_only,mod_fits,userefits,refitname,thres){
  loglik = extract_log_lik(m=m, esc_only = esc_only, N=N, mod_fits = mod_fits)
  ## look at Pareto k's
  k_LOOIC<-pareto_k_values(loo(loglik))[(L+1):N]</pre>
  if(userefits=="Yes"){
    re_fits =loadrefits(refitname=refitname, N=N, L=L)
  i_refit <- L
  refits <- L
  ks <- NULL
  approx_elpds_1sap <- rep(NA, N)
  for (i in (N - 1):L) {
    logratio <- sum_log_ratios(loglik, (i + 1):N)</pre>
    psis_obj <- suppressWarnings(psis(logratio))</pre>
    k<-pareto_k_values(psis_obj)
    ks \leftarrow c(ks, k)
    if(k>thres & userefits=="Yes"){
    #use_refit of model based on the first[i] observations
      i_refit <- i
      refits <- c(refits, i)
      loglik = extract_log_lik(m=(i+1)-L+1, esc_only = esc_only, N=N, mod_fits = re_fits)
      approx_elpds_1sap[i + 1] <- log_mean_exp(loglik[, i + 1])</pre>
    }else{
      lw <- weights(psis_obj, normalize = TRUE)[, 1]</pre>
      approx_elpds_1sap[i + 1] <- log_sum_exp(lw + loglik[, i + 1])</pre>
```

```
}
  results<-list(approx_elpds_1sap,ks,k_L00IC)</pre>
  names(results)<-c("LFO","ks","k_LOOIC")</pre>
  return(results)
plot_ks <- function(ks, thres = 0.7,N,L) {</pre>
  ids = N:(L + 1)
  dat_ks <- data.frame(ks = ks, ids = ids)</pre>
  ggplot(dat_ks, aes(x = ids, y = ks)) +
    geom_point(aes(color = ks > thres), shape = 3, show.legend = FALSE) +
    geom_hline(yintercept = thres, linetype = 2, color = "red2") +
    scale_color_manual(values = c("cornflowerblue", "darkblue")) +
    labs(x = "Data point", y = "Pareto k") +
    ylim(-0.5, max(dat_ks$ks))
}
#function for printing out a read text file
processFile = function(filepath) {
  con = file(filepath, "r")
  while ( TRUE ) {
    line = readLines(con, n = 1)
    if ( length(line) == 0 ) {
      break
    }
    cat(paste0(noquote(line)),"\n")
  }
  close(con)
```

User inputs

We begin by supplying values for the following parameters, which we need for model fitting and evaluation.

```
## first & last years of fish data
yr_frst <- 1978
yr_last <- 2020

## min & max adult age classes
age_min <- 3
age_max <- 8

## years (if any) of age-comp to skip; see below
age_skip <- 0

## number of years ahead for run forecasts from the most recent year of data
n_fore <- 1

## number of recent year forecasts
n_forecasts <- 10</pre>
```

```
## first year of 1 step ahead forecast
yr_begin <- 2011

## last year of 1 step ahead forecast
yr_end <- 2020

## upper threshold for Gelman & Rubin's potential scale reduction factor (Rhat).
Rhat_thresh <- 1.1</pre>
```

Next we specify the names of three necessary data files containing the following information:

- 1. observed total number of adult spawners (escapement) by year;
- 2. observed age composition of adult spawners by year;
- 3. observed total harvest by year;

```
## 1. file with escapement data
## [n_yrs x 2] matrix of obs counts; 1st col is calendar yr
fn_esc <- "skagit_sthd_esc.csv"

## 2. file with age comp data
## [n_yrs x (1+A)]; 1st col is calendar yr
fn_age <- "skagit_sthd_age.csv"

## 3. file with harvest data
## [n_yrs x 2] matrix of obs catch; 1st col is calendar yr
fn_harv <- "skagit_sthd_catch.csv"</pre>
```

Loading the fish data

Here we load in the first three data files and do some simple calculations and manipulations. First the spawner data:

```
## escapement
dat_esc <- read_csv(file.path(datadir, fn_esc))
## years of data
dat_yrs <- dat_esc$year

## number of years of data
n_yrs <- length(dat_yrs)

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

Next the age composition data:

```
## age comp data
dat_age <- read_csv(file.path(datadir, fn_age))
## num of age classes
A <- age_max - age_min + 1</pre>
```

```
# ## drop year col & first age_min+age_skip rows
# dat_age <- dat_age[-(1:(age_min+age_skip)),-1]
# ## add row(s) of NA's for forecast years
# if(n fore > 0) {
   dat_age <- rbind(dat_age,</pre>
                      matrix(0, n_fore, A,
#
                              dimnames = list(n_yrs+seq(n_fore),
#
                                             colnames(dat age))))
# }
# ## total num of age obs by cal yr
# dat_aqe[,"sum"] <- apply(dat_aqe, 1, sum)</pre>
# ## row indices for any years with no obs age comp
# idx_NA_yrs <- which(dat_age$sum<A, TRUE)</pre>
# ## replace 0's in yrs w/o any obs with NA's
\# dat_aqe[idx_NA_yrs,(1:A)] \leftarrow NA
# ## change total in yrs w/o any obs from 0 to A to help dmulti()
# dat_age[idx_NA_yrs,"sum"] <- A</pre>
# ## convert class
# dat_age <- as.matrix(dat_age)</pre>
```

And then the harvest data:

```
## harvest
dat_harv <- read_csv(file.path(datadir, fn_harv))
## drop year col & first age_max rows
#dat_harv <- c(dat_harv$catch,rep(NA,n_fore))</pre>
```

Loading the covariates

Our analysis investigates 5 covariates as possible drivers of the population's instrinic growth rate:

- 1. Maximum river discharge in winter;
- 2. Minimum river discharge in summer;
- 3. North Pacific Gyre Oscillation;

All of the covariates are contained in the file <code>/data/skagit_sthd_covars.csv</code>. We will load and then standardize them to have zero-mean and unit-variance.

```
dat_cvrs <- read_csv(file.path(datadir, "skagit_sthd_covars.csv"))
## drop year col
# dat_cvrs <- dat_cvrs[,-1]
# ## transform the covariates to z-scores
# scl_cvrs <- as.matrix(scale(dat_cvrs))
# ## total number of covariates
# n_cov <- dim(dat_cvrs)[2]</pre>
```

Specifying models in JAGS

Now we can specify the model in JAGS. We fit a total one model, which we outline below, based on a beverton holt process model with covariates.

Beverton-Holt with covars and AR1 process errors (MA1 recruitment residuals). Here we will print out the model (contained in a separate text file)

```
processFile(file.path(jagsdir, "IPM_BH_cov_AR.txt"))
```

```
##
##
       model {
##
##
       ##----
##
       ## PRIORS
       ##----
##
       ## alpha = intrinsic productivity
##
##
       alpha ~ dnorm(0,0.001) T(0,);
##
       mu_BH_a <- log(alpha);</pre>
##
       E_BH_a \leftarrow mu_BH_a + sigma_r/(2 - 2*phi^2);
##
       ## strength of dens depend
##
       beta_inv ~ dnorm(0, 1e-9) T(0,);
##
##
       beta <- 1/beta_inv;</pre>
##
##
       ## covariate effects
##
       for(i in 1:n_cov) { gamma[i] ~ dnorm(0,0.01) }
##
##
       ## AR(1) coef for proc errors
##
       #phi ~ dunif(-0.999,0.999);
##
       #phi <- 0;
##
       phi_prior ~ dbeta(2,2);
##
       phi <- phi_prior*2-1;</pre>
       #phi ~ dunif(0,0.999);
##
##
##
       ## innovation in first year
       innov_1 ~ dnorm(0,tau_r*(1-phi*phi));
##
##
       ## process variance for recruits model
##
##
       sigma_r ~ dnorm(0, 2e-2) T(0,);
##
       tau_r <- 1/sigma_r;</pre>
##
##
       ## obs variance for spawners
##
       tau_s <- 1/sigma_s;</pre>
       sigma_s ~ dnorm(0, 0.001) T(0,);
##
##
##
       ## unprojectable early recruits;
##
       ## hyper mean across all popns
       Rec_mu ~ dnorm(0,0.001);
##
       ## hyper SD across all popns
##
##
       Rec_sig ~ dunif(0,100);
       ## precision across all popns
##
##
       Rec_tau <- pow(Rec_sig,-2);</pre>
       ## multipliers for unobservable total runs
##
       ttl_run_mu ~ dunif(1,5);
##
       ttl_run_tau ~ dunif(1,20);
##
##
```

```
##
       ## get total cal yr returns for first age_min yrs
##
       for(i in 1:(age_min+age_skip)) {
       ln_tot_Run[i] ~ dnorm(ttl_run_mu*Rec_mu,Rec_tau/ttl_run_tau);
##
       tot_Run[i] <- exp(ln_tot_Run[i]);</pre>
##
##
##
##
       ## maturity schedule
       ## unif vec for Dirch prior
##
##
       theta <-c(1,10,10,5,1,1)
##
       ## hyper-mean for maturity
##
       pi_eta ~ ddirch(theta);
       ## hyper-prec for maturity
##
       pi_tau ~ dnorm(0, 0.01) T(0,);
##
##
       for(t in 1:(n_yrs-age_min+n_fore)) { pi_vec[t,1:A] ~ ddirch(pi_eta*pi_tau) }
##
##
       ## estimated harvest rate
##
       for(t in 1:(n_yrs+n_fore)) { h_rate[t] ~ dunif(0,1) }
##
##
       ## LIKELIHOOD
       ##-----
##
##
       ## predicted recruits in BY t
##
       covar[1] <- inprod(gamma,mod_cvrs[1,]);</pre>
##
       ln_BH_a[1] <- mu_BH_a + covar[1];</pre>
##
       E_{n_{ec}[1]} < n_{BH_a[1]} + n_{Sp[1]} - \log(1 + \beta_{Sp[1]}) + \beta_{Sp[1]}
       tot_ln_Rec[1] ~ dnorm(E_ln_Rec[1],tau_r);
##
##
       res_ln_Rec[1] <- tot_ln_Rec[1] - E_ln_Rec[1];
##
       w[1] <- phi * innov_1 + res_ln_Rec[1];
##
##
       ## median of total recruits
       tot_Rec[1] <- exp(tot_ln_Rec[1]);</pre>
##
##
       ## R/S
##
       ln_RS[1] <- tot_ln_Rec[1] - ln_Sp[1];</pre>
##
##
##
       ## brood-yr recruits by age
##
       for(a in 1:A) {
##
       Rec[1,a] <- tot_Rec[1] * pi_vec[1,a];</pre>
##
##
##
       ## brood years 2:(n_yrs-age_min)
##
       for(t in 2:(n_yrs-age_min+n_fore)) {
##
       ## predicted recruits in BY t
       covar[t] <- inprod(gamma, mod_cvrs[t,]);</pre>
##
##
       ln_BH_a[t] <- mu_BH_a + covar[t];</pre>
##
       tot_ln_Rec[t] ~ dnorm(E_ln_Rec[t],tau_r);
##
       res_ln_Rec[t] <- tot_ln_Rec[t] - E_ln_Rec[t];</pre>
##
##
       w[t] <- phi * res_ln_Rec[t-1] + res_ln_Rec[t];</pre>
##
       ## median of total recruits
##
##
       tot_Rec[t] <- exp(tot_ln_Rec[t]);</pre>
##
##
       ## R/S
##
       ln_RS[t] <- tot_ln_Rec[t] - ln_Sp[t];</pre>
```

```
##
##
       ## brood-yr recruits by age
       for(a in 1:A) {
##
##
       Rec[t,a] <- tot_Rec[t] * pi_vec[t,a];</pre>
##
##
       } ## end t loop over year
##
##
       ## get predicted calendar year returns by age
##
       ## matrix Run has dim [(n_yrs-age_min) x A]
##
       ## step 1: incomplete early broods
##
       ## first cal yr of this grp is first brood yr + age_min + age_skip
##
       for(i in 1:(age_max-age_min-age_skip)) {
##
##
       ## projected recruits
##
       for(a in 1:(i+age_skip)) {
##
       Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
       }
##
##
       ## imputed recruits
       for(a in (i+1+age_skip):A) {
##
##
       lnRec[i,a] ~ dnorm(Rec_mu,Rec_tau);
##
       Run[i,a] <- exp(lnRec[i,a]);</pre>
##
       }
##
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
       ## predicted age-prop vec for multinom
##
##
       for(a in 1:A) {
       age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
##
##
##
       ## multinomial for age comp
##
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
##
       lp_age[i] <- logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]);</pre>
##
##
##
       ## step 2: info from complete broods
##
       ## first cal yr of this grp is first brood yr + age_max
##
       for(i in (A-age_skip):(n_yrs-age_min-age_skip+n_fore)) {
##
       for(a in 1:A) {
##
       Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
##
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
##
       ## predicted age-prop vec for multinom
##
       for(a in 1:A) {
       age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
##
##
##
       ## multinomial for age comp
##
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
```

```
##
       lp_age[i] <- ifelse(i < n_yrs-age_min-age_skip+n_fore, logdensity.multi(dat_age[i,1:A],age_v[i,1</pre>
##
##
##
       ## get predicted calendar year spawners
##
       ## first cal yr is first brood yr
       for(t in 1:(n_yrs+n_fore)) {
##
       ## obs model for spawners
##
       #Sp[t] <- max(10,tot_Run[t] - dat_harv[t]);
##
##
       est_harv[t] = ifelse(t > n_yrs,1,h_rate[t] * tot_Run[t]);
       dat_harv[t] ~ dlnorm(log(est_harv[t]), 20);
##
##
       Sp[t] = tot_Run[t] - est_harv[t];
       ln_Sp[t] <- log(Sp[t]);</pre>
##
       ln_dat_esc[t] ~ dnorm(ln_Sp[t], tau_s);
##
##
##
       lp_{-}esc[t] \leftarrow ifelse(t < n\_yrs + 1, logdensity.norm(ln\_dat\_esc[t], ln\_Sp[t], tau\_s), 0);
##
##
     } ## end model description
##
## Warning in readLines(con, n = 1): incomplete final line found on 'C:/Users/buehrtwb/OneDrive -
## Washington State Executive Branch Agencies/Documents/Scripts/Skagit-River-Steelhead-Forecast-Laptop/
## jags/IPM_BH_cov_AR.txt'
```

Beverton-Holt with covars and AR1MA1 recruitment residuals

```
processFile(file.path(jagsdir, "IPM_BH_cov_MA1_AR1.txt"))
```

```
##
## model {
##
     ##----
##
     ## PRIORS
##
     ##----
##
     ## alpha = intrinsic productivity
##
##
     alpha ~ dnorm(0,0.001) T(0,);
##
     mu_BH_a <- log(alpha);</pre>
##
     E_BH_a \leftarrow mu_BH_a + sigma_r/(2 - 2*phi^2);
##
##
     ## strength of dens depend
     beta_inv ~ dnorm(0, 1e-9) T(0,);
##
##
     beta <- 1/beta_inv;</pre>
##
##
     ## covariate effects
     for(i in 1:n_cov) { gamma[i] ~ dnorm(0,0.01) }
##
##
     ## AR(1) coef for recruitment residual
##
     #phi ~ dunif(-0.999,0.999);
##
##
     #phi <- 0;</pre>
##
     phi_prior ~ dbeta(2,2);
##
     phi <- phi_prior*2-1;</pre>
     #phi ~ dunif(0,0.999);
##
```

```
##
##
     ## MA(1) coef recruitment residual
##
     theta res prior ~ dbeta(2,2);
##
     theta_res <- theta_res_prior*2-1;</pre>
##
     #theta_res ~ dunif(0,0.999);
##
##
     ## innovation in first year
##
     #innov_1 ~ dnorm(0,tau_r*(1-phi*phi));#AR1
##
     innov_1 \sim dnorm(0,(1-phi^2)/((1+2*phi*theta_res+theta_res^2)*sigma_r^2));#AR1MA1
##
##
     ## process variance for recruits model
     sigma_r ~ dnorm(0, 2e-2) T(0,);
##
     tau_r <- 1/sigma_r;</pre>
##
##
##
     ## obs variance for spawners
##
     tau_s <- 1/sigma_s;</pre>
##
     sigma_s ~ dnorm(0, 0.001) T(0,);
##
##
     ## unprojectable early recruits;
##
     ## hyper mean across all popns
##
    Rec_mu ~ dnorm(0,0.001);
##
    ## hyper SD across all popns
##
    Rec_sig ~ dunif(0,100);
    ## precision across all popns
##
##
    Rec_tau <- pow(Rec_sig,-2);</pre>
    ## multipliers for unobservable total runs
## ttl_run_mu ~ dunif(1,5);
## ttl_run_tau ~ dunif(1,20);
##
     ## get total cal yr returns for first age_min yrs
##
##
     for(i in 1:(age_min+age_skip)) {
##
        ln_tot_Run[i] ~ dnorm(ttl_run_mu*Rec_mu,Rec_tau/ttl_run_tau);
        tot_Run[i] <- exp(ln_tot_Run[i]);</pre>
##
##
     }
##
##
    ## maturity schedule
##
     ## unif vec for Dirch prior
##
    theta \leftarrow c(1,10,10,5,1,1)
##
    ## hyper-mean for maturity
##
    pi_eta ~ ddirch(theta);
    ## hyper-prec for maturity
##
     pi_tau ~ dnorm(0, 0.01) T(0,);
     for(t in 1:(n_yrs-age_min+n_fore)) { pi_vec[t,1:A] ~ ddirch(pi_eta*pi_tau) }
##
##
     ## estimated harvest rate
##
     for(t in 1:(n_yrs+n_fore)) { h_rate[t] ~ dunif(0,1) }
##
##
     ##-----
##
##
     ## LIKELIHOOD
     ##----
##
##
     ## predicted recruits in BY t
##
     covar[1] <- inprod(gamma,mod_cvrs[1,]);</pre>
##
     ln_BH_a[1] <- mu_BH_a + covar[1];</pre>
    E_{\ln Rec[1]} \leftarrow \ln_BH_a[1] + \ln_Sp[1] - \log(1 + beta*Sp[1]) + phi * innov_1 + theta_res * 0;
```

```
##
     tot_ln_Rec[1] ~ dnorm(E_ln_Rec[1], tau_r);
##
     res_ln_Rec[1] <- tot_ln_Rec[1] - E_ln_Rec[1];
     w[1] <- phi * innov_1 + theta_res * 0 + res_ln_Rec[1]</pre>
##
##
##
     ## median of total recruits
##
     tot_Rec[1] <- exp(tot_ln_Rec[1]);</pre>
##
##
     ## R/S
##
     ln_RS[1] <- tot_ln_Rec[1] - ln_Sp[1];</pre>
##
##
     ## brood-yr recruits by age
     for(a in 1:A) {
##
       Rec[1,a] <- tot_Rec[1] * pi_vec[1,a];</pre>
##
##
##
##
     ## brood years 2:(n_yrs-age_min)
##
     for(t in 2:(n_yrs-age_min+n_fore)) {
       ## predicted recruits in BY t
##
##
       covar[t] <- inprod(gamma, mod_cvrs[t,]);</pre>
       ln_BH_a[t] <- mu_BH_a + covar[t];</pre>
##
##
##
       #-----
##
       #version 4; more similar to AR1 original model
       #-----
##
##
       E_{n_Rec[t]} \leftarrow n_BH_a[t] + n_Sp[t] - \log(1 + beta*Sp[t]) + phi * w[t-1] + theta_res * res_ln_Rec[t]
##
       tot_ln_Rec[t] ~ dnorm(E_ln_Rec[t], tau_r);
##
       res_ln_Rec[t] <- tot_ln_Rec[t] - E_ln_Rec[t];</pre>
##
       w[t] \leftarrow phi * w[t-1] + theta_res * res_ln_Rec[t-1] + res_ln_Rec[t];
##
##
##
       ## median of total recruits
##
       tot_Rec[t] <- exp(tot_ln_Rec[t]);</pre>
##
##
       ln_RS[t] <- tot_ln_Rec[t] - ln_Sp[t];</pre>
##
       ## brood-yr recruits by age
##
       for(a in 1:A) {
##
         Rec[t,a] <- tot_Rec[t] * pi_vec[t,a];</pre>
##
       }
##
     } ## end t loop over year
##
##
     ## get predicted calendar year returns by age
##
     ## matrix Run has dim [(n_yrs-age_min) x A]
     ## step 1: incomplete early broods
##
##
     ## first cal yr of this grp is first brood yr + age_min + age_skip
     for(i in 1:(age_max-age_min-age_skip)) {
##
       ## projected recruits
##
       for(a in 1:(i+age_skip)) {
##
##
         Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
       }
##
       ## imputed recruits
##
       for(a in (i+1+age_skip):A) {
##
         lnRec[i,a] ~ dnorm(Rec_mu,Rec_tau);
##
         Run[i,a] <- exp(lnRec[i,a]);</pre>
##
       }
```

```
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
       ## predicted age-prop vec for multinom
##
       for(a in 1:A) {
##
         age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
##
       ## multinomial for age comp
##
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
##
       lp_age[i] <- logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]);</pre>
##
##
     ## step 2: info from complete broods
##
     ## first cal yr of this grp is first brood yr + age_max
##
##
     for(i in (A-age_skip):(n_yrs-age_min-age_skip+n_fore)) {
##
       for(a in 1:A) {
##
         Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
       ## predicted age-prop vec for multinom
##
       for(a in 1:A) {
##
         age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
       }
##
       ## multinomial for age comp
##
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
##
       #lp_age[i] <- logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]);</pre>
##
       lp_age[i] <- ifelse(i < n_yrs-age_min-age_skip+n_fore,</pre>
##
       logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]),0)
##
##
##
     ## get predicted calendar year spawners
##
     ## first cal yr is first brood yr
     for(t in 1:(n_yrs+n_fore)) {
##
##
       ## obs model for spawners
       # Sp[t] <- max(10,tot_Run[t] - dat_harv[t]);
##
##
       est_harv[t] = ifelse(t > n_yrs,1,h_rate[t] * tot_Run[t]);
##
       dat_harv[t] ~ dlnorm(log(est_harv[t]), 20);
##
       Sp[t] = tot_Run[t] - est_harv[t];
##
       ln_Sp[t] \leftarrow log(Sp[t]);
##
       ln_dat_esc[t] ~ dnorm(ln_Sp[t], tau_s);
##
       lp_esc[t] <- ifelse(t < n_yrs + 1,logdensity.norm(ln_dat_esc[t],ln_Sp[t], tau_s),0);</pre>
##
     }
##
## } ## end model description
## Warning in readLines(con, n = 1): incomplete final line found on 'C:/Users/buehrtwb/OneDrive -
## Washington State Executive Branch Agencies/Documents/Scripts/Skagit-River-Steelhead-Forecast-Laptop/
## jags/IPM_BH_cov_MA1_AR1.txt'
```

Beverton-Holt with covars and AR1 recruitment residuals

```
processFile(file.path(jagsdir, "IPM_BH_cov_AR_resid.txt"))
##
## model {
##
     ##----
##
##
     ## PRIORS
     ##----
##
##
     ## alpha = intrinsic productivity
     alpha ~ dnorm(0,0.001) T(0,);
##
##
     mu_BH_a <- log(alpha);</pre>
##
     E_BH_a \leftarrow mu_BH_a + sigma_r/(2 - 2*phi^2);
##
##
     ## strength of dens depend
     beta_inv ~ dnorm(0, 1e-9) T(0,);
##
##
     beta <- 1/beta inv;</pre>
##
##
     ## covariate effects
##
     for(i in 1:n_cov) { gamma[i] ~ dnorm(0,0.01) }
##
     ## AR(1) coef for recruitment residual
##
     #phi ~ dunif(-0.999,0.999);
##
##
     #phi <- 0;
##
     phi_prior ~ dbeta(2,2);
##
     phi <- phi_prior*2-1;</pre>
##
     #phi ~ dunif(0,0.999);
##
##
     ## innovation in first year
##
     innov_1 ~ dnorm(0,tau_r*(1-phi*phi));#AR1
##
##
     ## process variance for recruits model
     sigma_r ~ dnorm(0, 2e-2) T(0,);
##
##
     tau_r <- 1/sigma_r;</pre>
##
##
     ## obs variance for spawners
##
     tau_s <- 1/sigma_s;</pre>
     sigma_s ~ dnorm(0, 0.001) T(0,);
##
##
##
     ## unprojectable early recruits;
     ## hyper mean across all popns
##
```

Rec_mu ~ dnorm(0,0.001);

Rec_sig ~ dunif(0,100);

ttl_run_mu ~ dunif(1,5);
ttl_run_tau ~ dunif(1,20);

hyper SD across all popns

precision across all popns
Rec_tau <- pow(Rec_sig,-2);</pre>

for(i in 1:(age_min+age_skip)) {

multipliers for unobservable total runs

get total cal yr returns for first age_min yrs

##

##

##

##

##

##

```
##
                     ln_tot_Run[i] ~ dnorm(ttl_run_mu*Rec_mu,Rec_tau/ttl_run_tau);
##
                     tot_Run[i] <- exp(ln_tot_Run[i]);</pre>
             }
##
##
##
            ## maturity schedule
            ## unif vec for Dirch prior
##
            theta \leftarrow c(1,10,10,5,1,1)
##
             ## hyper-mean for maturity
##
##
             pi_eta ~ ddirch(theta);
##
             ## hyper-prec for maturity
            pi_tau ~ dnorm(0, 0.01) T(0,);
##
             for(t in 1:(n_yrs-age_min+n_fore)) { pi_vec[t,1:A] ~ ddirch(pi_eta*pi_tau) }
##
##
             ## estimated harvest rate
##
             for(t in 1:(n_yrs+n_fore)) { h_rate[t] ~ dunif(0,1) }
##
##
##
             ## LIKELIHOOD
##
            ##-----
##
             ## predicted recruits in BY t
##
             covar[1] <- inprod(gamma,mod_cvrs[1,]);</pre>
##
             ln_BH_a[1] <- mu_BH_a + covar[1];</pre>
            E_{\ln_{e}} = \ln_{e} = 
##
             tot_ln_Rec[1] ~ dnorm(E_ln_Rec[1], tau_r);
##
##
             res_ln_Rec[1] <- tot_ln_Rec[1] - E_ln_Rec[1];</pre>
##
             w[1] <- phi * innov_1 + res_ln_Rec[1];
##
             ## median of total recruits
##
##
             tot_Rec[1] <- exp(tot_ln_Rec[1]);</pre>
##
##
             ## R/S
##
             ln_RS[1] <- tot_ln_Rec[1] - ln_Sp[1];</pre>
##
##
             ## brood-yr recruits by age
##
             for(a in 1:A) {
##
                  Rec[1,a] <- tot_Rec[1] * pi_vec[1,a];</pre>
##
             }
##
##
             ## brood years 2:(n_yrs-age_min)
##
             for(t in 2:(n_yrs-age_min+n_fore)) {
##
                  ## predicted recruits in BY t
##
                  covar[t] <- inprod(gamma, mod_cvrs[t,]);</pre>
                  ln_BH_a[t] <- mu_BH_a + covar[t];</pre>
##
##
                  E_{n_{ec}[t]} < n_{BH_a[t]} + n_{Sp[t]} - \log(1 + beta*Sp[t]) + phi * w[t-1];
##
                  tot_ln_Rec[t] ~ dnorm(E_ln_Rec[t], tau_r);
##
                  res_ln_Rec[t] <- tot_ln_Rec[t] - E_ln_Rec[t];</pre>
##
                  w[t] <- phi * w[t-1] + res_ln_Rec[t];
##
##
                  ## median of total recruits
##
                  tot_Rec[t] <- exp(tot_ln_Rec[t]);</pre>
##
                  ## R/S
                  ln_RS[t] <- tot_ln_Rec[t] - ln_Sp[t];</pre>
##
##
                  ## brood-yr recruits by age
                  for(a in 1:A) {
##
```

```
##
         Rec[t,a] <- tot_Rec[t] * pi_vec[t,a];</pre>
##
##
     } ## end t loop over year
##
##
     ## get predicted calendar year returns by age
##
     ## matrix Run has dim [(n yrs-age min) x A]
     ## step 1: incomplete early broods
##
     ## first cal yr of this grp is first brood yr + age_min + age_skip
##
##
     for(i in 1:(age_max-age_min-age_skip)) {
##
       ## projected recruits
##
       for(a in 1:(i+age_skip)) {
         Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
##
##
       ## imputed recruits
##
       for(a in (i+1+age_skip):A) {
##
         lnRec[i,a] ~ dnorm(Rec_mu,Rec_tau);
##
         Run[i,a] <- exp(lnRec[i,a]);</pre>
##
       }
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
       ## predicted age-prop vec for multinom
##
       for(a in 1:A) {
##
         age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
##
       ## multinomial for age comp
##
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
##
       lp_age[i] <- logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]);</pre>
##
##
##
     ## step 2: info from complete broods
##
     ## first cal yr of this grp is first brood yr + age_max
##
     for(i in (A-age_skip):(n_yrs-age_min-age_skip+n_fore)) {
##
       for(a in 1:A) {
##
         Run[i,a] <- Rec[(age_skip+i)-a+1,a];</pre>
##
##
       ## total run size
##
       tot_Run[i+age_min+age_skip] <- sum(Run[i,1:A]);</pre>
##
       ## predicted age-prop vec for multinom
##
       for(a in 1:A) {
##
         age_v[i,a] <- Run[i,a] / tot_Run[i+age_min];</pre>
##
##
       ## multinomial for age comp
       dat_age[i,1:A] ~ dmulti(age_v[i,1:A],dat_age[i,A+1]);
##
##
       #lp_age[i] <- logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]);</pre>
##
       lp_age[i] <- ifelse(i < n_yrs-age_min-age_skip+n_fore,</pre>
##
       logdensity.multi(dat_age[i,1:A],age_v[i,1:A],dat_age[i,A+1]),0)
##
##
##
     ## get predicted calendar year spawners
##
     ## first cal yr is first brood yr
##
     for(t in 1:(n_yrs+n_fore)) {
       ## obs model for spawners
##
##
       # Sp[t] <- max(10,tot_Run[t] - dat_harv[t]);
##
       est_harv[t] = ifelse(t > n_yrs,1,h_rate[t] * tot_Run[t]);
```

```
##
       dat_harv[t] ~ dlnorm(log(est_harv[t]), 20);
##
       Sp[t] = tot_Run[t] - est_harv[t];
##
       ln_{Sp}[t] \leftarrow log(Sp[t]);
##
       ln_dat_esc[t] ~ dnorm(ln_Sp[t], tau_s);
##
       lp_esc[t] <- ifelse(t < n_yrs + 1,logdensity.norm(ln_dat_esc[t],ln_Sp[t], tau_s),0);</pre>
##
##
## } ## end model description
##
## Warning in readLines(con, n = 1): incomplete final line found on 'C:/Users/buehrtwb/OneDrive -
## Washington State Executive Branch Agencies/Documents/Scripts/Skagit-River-Steelhead-Forecast-Laptop/
## jags/IPM_BH_cov_AR_resid.txt'
```

Fitting the models and generating the one year ahead forecasts

Before fitting the model in JAGS, we need to specify the MCMC control parameters.

```
## 1. MCMC control params
mcmc_ctrl <- list(
  chains = 4,
  length = 200000, #5e5,
  burn = 100000, #2e5,
  thin = 100#400
)

## total number of MCMC samples after burnin
mcmc_samp <- mcmc_ctrl$length*mcmc_ctrl$chains/mcmc_ctrl$thin</pre>
```

```
## models
models <- c("IPM BH cov MA1 AR1",
            "IPM_BH_cov_AR",
            "IPM BH cov AR resid",
            "IPM_BH_cov_MA1_AR1_age",
            "IPM_BH_cov_AR_age",
            "IPM_BH_cov_AR_resid_age"
## empty list for fits
n_mods <- length(models)</pre>
## empty list for fits
mod_fits <- vector("list", n_mods*(n_forecasts+1))</pre>
## counter to index fitted jags models (33 in total: 3 models x 11 1 year ahead forecasts including upc
## return year)
t <- 1
for(n in 1:n_mods){
  ## counter to index data to feed model for year specific forecasts
  ## first forecast will be for 10 years prior to the most recent return year;
  ## last forecast will be current forecast for the upcoming return year
c <- 0
```

```
#n <-2
model <- models[n]</pre>
for(i in 1:(n forecasts+1)){
  if(file.exists(file.path(savedir,paste(model,"_","y",i,".rds",sep = "")))) {
    mod_fits[[t]] <- readRDS(file.path(savedir,paste(model,"_","y",i,".rds",sep = "")))</pre>
    c < - c + 1
    t < -t + 1
} else { ## else, fit & save
      ## cnt & time stamp
      cat("Count =", t, "; Time =", round(((proc.time()-timer_start)/60)["elapsed"], 1), "\n",
          file="cnt_time.txt", append=TRUE)
      #range of years. Last year in range
      dat_yrs <- seq(yr_frst,(yr_last - n_forecasts + c),1)</pre>
      ## number of years of data
      n_yrs <- length(dat_yrs)</pre>
      ## get first & last years
      yr_frst_forecast <- min(dat_yrs)</pre>
      yr_last_forecast <- max(dat_yrs)</pre>
      ## get escapement data
      dat_esc_forecast <- dat_esc[which(dat_esc$year %in% dat_yrs),]</pre>
      ## log of escapement
      ln_dat_esc <- c(log(dat_esc_forecast$escapement),rep(NA,n_fore))</pre>
      ## get age data
      dat_age_forecast <- dat_age[which(dat_age$year %in% dat_yrs),]</pre>
      ## drop year col & first age_min+age_skip rows
      dat_age_forecast <- dat_age_forecast[-(1:(age_min+age_skip)),-1]</pre>
      ## add row(s) of NA's for forecast years
      if(n fore > 0) {
        dat_age_forecast <- rbind(dat_age_forecast,</pre>
                                    matrix(0, n_fore, A,
                                           dimnames = list(n_yrs+seq(n_fore),colnames(dat_age_forecast)
      }
      ## total num of age obs by cal yr
      dat_age_forecast[,"sum"] <- apply(dat_age_forecast, 1, sum)</pre>
      ## row indices for any years with no obs age comp
      idx_NA_yrs <- which(dat_age_forecast$sum<A, TRUE)</pre>
      ## replace 0's in yrs w/o any obs with NA's
      dat_age_forecast[idx_NA_yrs,(1:A)] <- NA</pre>
      ## change total in yrs w/o any obs from 0 to A to help dmulti()
      dat_age_forecast[idx_NA_yrs,"sum"] <- A</pre>
      ## convert class
      dat_age_forecast <- as.matrix(dat_age_forecast)</pre>
```

```
## get harvest data
dat_harv_forecast <- dat_harv[which(dat_harv$year %in% dat_yrs),]</pre>
## drop year col & first age max rows
dat_harv_forecast <- c(dat_harv_forecast$catch,rep(NA,n_fore))</pre>
## get covariate data
dat_cvrs_forecast <- dat_cvrs[which(dat_cvrs$year <= yr_last + n_fore - age_min),1:4]</pre>
## drop year col
dat_cvrs_forecast <- dat_cvrs_forecast[,-1]</pre>
## transform the covariates to z-scores
scl_cvrs_forecast <- scale(dat_cvrs_forecast)</pre>
## total number of covariates
n_cov <- dim(dat_cvrs_forecast)[2]</pre>
## ----jags_setup-----
## 1. Data to pass to JAGS
dat_jags <- list(dat_age = dat_age_forecast,</pre>
                  ln_dat_esc = ln_dat_esc,
                  dat_harv = dat_harv_forecast,
                  A = A
                  age_min = age_min,
                  age_max = age_max,
                  age_skip = age_skip,
                  n_yrs = n_yrs,
                  n_fore = n_fore)
## 2. Model params/states for JAGS to return
##
      These are specific to the process model,
      so we define them in 'par_jags' below.
if(model == "IPM_BH_cov_AR" | model == "IPM_BH_cov_AR_resid"){
  init_vals_cov <- function() {</pre>
  list(alpha = 5,
       beta_inv = exp(mean(ln_dat_esc, na.rm = TRUE)),
       gamma = rep(0, 3),
       pi_tau = 10,
       pi_eta = rep(1,A),
       pi vec = matrix(c(0.01, 0.35, 0.47, 0.15, 0.01, 0.01),
                        n_yrs-age_min+n_fore, A,
                        byrow = TRUE),
       Rec_mu = log(1000),
       Rec_sig = 0.1,
       tot_ln_Rec = rep(log(1000), n_yrs - age_min + n_fore),
       phi_prior = 0.5,
       innov_1 = 0
  }
  ## params/states to return
  par_jags<- c("alpha", "E_BH_a", "ln_BH_a",</pre>
                 "beta",
                 "gamma",
                 "Sp", "Rec", "tot_ln_Rec", "ln_RS",
                 "pi_eta", "pi_tau",
```

```
"sigma_r", "sigma_s", "w", "res_ln_Rec",
                 "lp_age","lp_esc","phi","Run"
}else{
  init_vals_cov <- function() {</pre>
    list(alpha = 5,
         beta_inv = exp(mean(ln_dat_esc, na.rm = TRUE)),
         gamma = rep(0, 3),
         pi_tau = 10,
         pi_eta = rep(1,A),
          \# pi_vec = matrix(c(0.01, 0.35, 0.47, 0.15, 0.01, 0.01),
                             n_yrs-age_min+n_fore, A,
                             byrow = TRUE),
         Rec_mu = log(1000),
         Rec_sig = 0.1,
         tot_ln_Rec = rep(log(1000), n_yrs - age_min + n_fore),
         phi_prior = 0.5,theta_res_prior = 0.5,
         innov_1 = 0)
    }
  ## params/states to return
  par_jags <- c("alpha", "E_BH_a", "ln_BH_a",</pre>
                 "beta",
                 "gamma".
                 "Sp", "Rec", "tot_ln_Rec", "ln_RS", "tot_Run",
                 "pi_eta", "pi_tau",
                 "sigma_r", "sigma_s", "res_ln_Rec", "w", "theta_res", "phi",
                 "lp_age", "lp_esc", "Run"
}#endif
## set of multi-covariate models
cset <- colnames(scl_cvrs_forecast)</pre>
dat jags$n cov <- length(cset)</pre>
dat_jags$mod_cvrs <- scl_cvrs_forecast[1:(n_yrs-age_min+1), cset]</pre>
## fit model & save it
 \# \ mod\_fits[[t]] \ <- \ fit\_jags(paste(model,".txt",sep = ""), \ dat\_jags, \ par\_jags, \\
                              init_vals_cov, mcmc_ctrl)
mod_fits[[t]]<-fit_jags2(model=paste(model,".txt",sep = ""),</pre>
                    data=dat_jags,
                    params=par_jags,
                    inits=init_vals_cov,
                    ctrl=mcmc ctrl
saveRDS(mod_fits[[t]], file.path(savedir,paste(model,"_","y",i,".rds",sep = "")))
summary_stats<-NULL</pre>
```

```
summary_stats<-sum_stats(mcmclist= mod_fits[[t]])</pre>
        write.csv(summary_stats,file.path(savedir, paste(model,"_","y",i,"_summary_stats.csv",sep = "")
        c < -c + 1
        t < -t + 1
   }## end if
  }##next forecast year(i)
}## next model(n)
## Compiling model graph
##
      Resolving undeclared variables
      Allocating nodes
##
## Graph information:
      Observed stochastic nodes: 89
      Unobserved stochastic nodes: 143
##
##
      Total graph size: 2356
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 92
##
      Unobserved stochastic nodes: 146
##
      Total graph size: 2428
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 95
##
      Unobserved stochastic nodes: 149
##
      Total graph size: 2500
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
      Observed stochastic nodes: 98
##
##
      Unobserved stochastic nodes: 152
##
      Total graph size: 2572
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
```

```
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
     Resolving undeclared variables
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 101
##
      Unobserved stochastic nodes: 155
      Total graph size: 2644
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
## Initializing model
##
## Parallel computation in progress
##
## Compiling model graph
     Resolving undeclared variables
##
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 104
##
      Unobserved stochastic nodes: 158
##
      Total graph size: 2716
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
```

```
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
     Resolving undeclared variables
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 107
##
      Unobserved stochastic nodes: 161
      Total graph size: 2788
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
## Initializing model
##
## Parallel computation in progress
##
## Compiling model graph
     Resolving undeclared variables
##
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 110
##
      Unobserved stochastic nodes: 164
##
      Total graph size: 2860
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
```

```
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
     Resolving undeclared variables
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 113
##
      Unobserved stochastic nodes: 167
      Total graph size: 2932
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
## Initializing model
##
## Parallel computation in progress
##
## Compiling model graph
     Resolving undeclared variables
##
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 116
##
      Unobserved stochastic nodes: 170
##
      Total graph size: 3004
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
```

```
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
      Resolving undeclared variables
      Allocating nodes
##
## Graph information:
      Observed stochastic nodes: 119
##
##
      Unobserved stochastic nodes: 173
##
      Total graph size: 3076
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 89
##
      Unobserved stochastic nodes: 142
##
      Total graph size: 2318
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 3
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
      Observed stochastic nodes: 92
      Unobserved stochastic nodes: 145
##
##
      Total graph size: 2389
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
## Parallel computation in progress
##
```

```
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 95
      Unobserved stochastic nodes: 148
##
      Total graph size: 2460
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta res prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
##
     Resolving undeclared variables
      Allocating nodes
##
## Graph information:
      Observed stochastic nodes: 98
##
##
      Unobserved stochastic nodes: 151
##
      Total graph size: 2531
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 101
      Unobserved stochastic nodes: 154
##
##
      Total graph size: 2602
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta res prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 4
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 104
##
      Unobserved stochastic nodes: 157
##
      Total graph size: 2673
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
      Resolving undeclared variables
      Allocating nodes
##
## Graph information:
      Observed stochastic nodes: 107
##
##
      Unobserved stochastic nodes: 160
##
      Total graph size: 2744
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
      Resolving undeclared variables
      Allocating nodes
##
## Graph information:
##
      Observed stochastic nodes: 110
##
      Unobserved stochastic nodes: 163
      Total graph size: 2815
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta res prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 3
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
      Observed stochastic nodes: 113
      Unobserved stochastic nodes: 166
##
##
      Total graph size: 2886
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 4
## Initializing model
##
## Parallel computation in progress
##
```

```
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 116
##
      Unobserved stochastic nodes: 169
      Total graph size: 2957
##
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 2
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 3
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 4
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta res prior" in chain 4
## Initializing model
##
##
## Parallel computation in progress
##
## Compiling model graph
##
     Resolving undeclared variables
      Allocating nodes
##
## Graph information:
      Observed stochastic nodes: 119
##
##
      Unobserved stochastic nodes: 172
##
      Total graph size: 3028
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "pi_eta" in chain 1
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## initial value for "theta_res_prior" in chain 1
```

```
## Warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::jags.model(model, data, inits, n.chains = n.chains, n.adapt = n.adapt, : Unused
## warning in rjags::
```

Model selection

```
tot_mods <- n_forecasts*n_mods
# get escapement data
dat_esc_forecast <- dat_esc[which(dat_esc$year %in% seq(yr_begin,yr_end,1)),]</pre>
## get harvest data
dat_harv_forecast <- dat_harv[which(dat_harv$year %in% seq(yr_begin,yr_end,1)),]</pre>
## observed terminal run size
obs_trs <- dat_esc_forecast$escapement + dat_harv_forecast$catch
pred_trs <- NULL</pre>
for(n in 1:n_mods){
  #n <- 1
  pred_esc <- NULL</pre>
  for(i in 1:(n_forecasts)){
    #i <- 1
  mod res<-NULL
  mod_res<-as.matrix(readRDS(file.path(savedir,paste0(models[n],"_y",i,".rds"))))</pre>
  p_dat <- mod_res[,grep("Sp", colnames(mod_res))]</pre>
  p_dat <- round(median(p_dat[,dim(p_dat)[2]]))</pre>
  pred_esc[i] <- p_dat</pre>
```

```
pred_trs_mod <- pred_esc + 1#+ dat_harv_forecast$catch #you don't need to add catch in because it is
  pred_trs <- cbind(pred_trs,pred_trs_mod)</pre>
  #names(pred_trs) <- paste(models[n],"_","pred_trs",sep = "")</pre>
}
colnames(pred_trs) <- models</pre>
## compute model performance statistics
Error <- pred_trs - obs_trs</pre>
SE <- Error<sup>2</sup>
PE <- Error/obs_trs
APE <- abs(PE)
LAR <- log(obs_trs/pred_trs)
RMSE <- apply(SE,2,function(x){sqrt(mean(x))})</pre>
MPE <- apply(PE,2,function(x){mean(x)})</pre>
MAPE <- apply(APE,2,function(x){mean(x)})
MSA \leftarrow apply(LAR, 2, function(x) \{100*(exp(mean(abs(x))-1))\})
model_selection <- data.frame(RMSE,MPE,MAPE,MSA)</pre>
weights<-apply(model_selection[,!colnames(model_selection)=="MPE"], 2,function(x) (1/x)/sum(1/x))</pre>
colnames(weights)<-paste0(colnames(weights),"_weight")</pre>
model_selection <- data.frame (model_selection, weights)
```

Model Selection Via Approximate Leave-Future-Out Cross Validation following the methods here: link.

```
N=yr_last-yr_frst+1
L=N-n_forecasts
thres=0.1
esc_only="No"
userefits="Yes"
mod_fits<-loadmodfits(modelnames=models)

LF01<-approx_LF0(N=N,L=L,m=1,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[1]
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.</pre>
```

```
# plot_ks(LF01$ks,N=N,L=L,thres=thres)
# plot_ks(LF01$k_L00IC, N=N, L=L, thres=thres)
LF02<-approx_LF0(N=N,L=L,m=2,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[2]
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
# plot_ks(LF02$ks, N=N,L=L,thres=thres)
# plot_ks(LF02$k_L00IC, N=N,L=L,thres=thres)
LF03<-approx_LF0(N=N,L=L,m=3,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[3]
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
# plot_ks(LF03$ks, N=N,L=L,thres=thres)
# plot_ks(LF03$k_L00IC, N=N,L=L,thres=thres)
LF04<-approx_LF0(N=N,L=L,m=4,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[4]
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
# plot_ks(LF03$ks, N=N,L=L,thres=thres)
# plot_ks(LF03$k_L00IC, N=N,L=L,thres=thres)
LF05<-approx_LF0(N=N,L=L,m=5,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[5]
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
# plot_ks(LF03$ks, N=N,L=L,thres=thres)
# plot_ks(LF03$k_L00IC, N=N,L=L,thres=thres)
LF06<-approx_LF0(N=N,L=L,m=6,esc_only=esc_only,mod_fits=mod_fits,userefits=userefits,refitname=models[6]
```

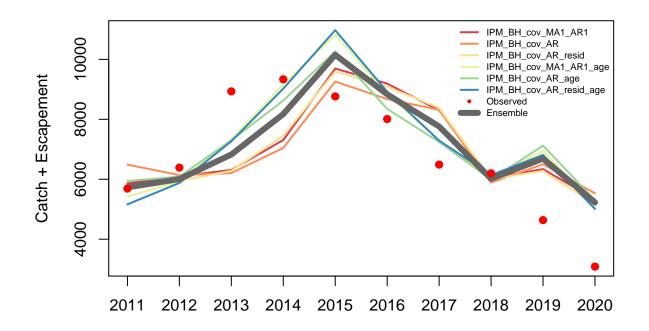
```
## Warning: Relative effective sample sizes ('r_eff' argument) not specified.
## For models fit with MCMC, the reported PSIS effective sample sizes and
## MCSE estimates will be over-optimistic.
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
# plot_ks(LFO3$ks, N=N,L=L,thres=thres)
# plot_ks(LF03$k_L00IC, N=N,L=L,thres=thres)
ELPD < -c(sum(LF01\$LF0,na.rm=T),
        sum(LF02$LF0,na.rm=T),
        sum(LFO3$LFO,na.rm=T),
        sum(LF04$LF0,na.rm=T),
        sum(LF05$LF0,na.rm=T),
        sum(LF06$LF0,na.rm=T)
LFOIC<--2*(ELPD)
delta_LFOIC<-LFOIC-min(LFOIC)</pre>
LFOIC_weight <-exp(ELPD)/sum(exp(ELPD))
LFOIC_results<-data.frame(ELPD, LFOIC, delta_LFOIC, LFOIC_weight)
rownames(LFOIC_results)<-models</pre>
model_selection<-data.frame(model_selection,LFOIC_results)</pre>
```

Model Averaging and 2020 forecast

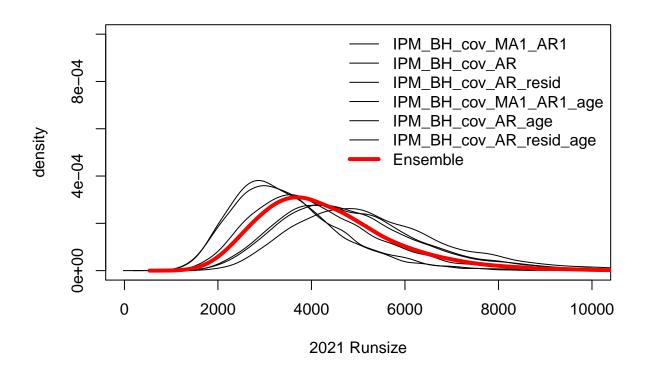
```
## extract median 2020 forecast from each model
f_dat<-data.frame(</pre>
  sort(unlist(mod_fits[[1]][,paste0("Sp","[",n_yrs+n_fore,"]")])),
  sort(unlist(mod_fits[[2]][,paste0("Sp","[",n_yrs+n_fore,"]")])),
  sort(unlist(mod_fits[[3]][,paste0("Sp","[",n_yrs+n_fore,"]")])),
  sort(unlist(mod_fits[[4]][,paste0("Sp","[",n_yrs+n_fore,"]")])),
  sort(unlist(mod_fits[[5]][,paste0("Sp","[",n_yrs+n_fore,"]")])),
  sort(unlist(mod_fits[[6]][,paste0("Sp","[",n_yrs+n_fore,"]")]))
)
colnames(f_dat)<-models</pre>
model_selection[,"2020_forecast"] <- apply(f_dat,2,median)</pre>
weighted forecast dist <-(
  as.matrix(f_dat) %*% (as.vector(model_selection[,"RMSE_weight"]))
weighted_forecast_quantiles<-quantile(weighted_forecast_dist,c(0.025,0.25,0.50,0.75,0.975))</pre>
weighted_forecast<-weighted_forecast_quantiles[3]</pre>
print(model_selection)
```

```
RMSE
                                                             MSA RMSE_weight MAPE_weight MSA_weight
                                          MPF.
                                                   MAPE
                                                                               0.1565110 0.1641179
## IPM_BH_cov_MA1_AR1
                          1568.000 0.10751942 0.2240939 45.11414
                                                                   0.1536565
                          1642.006 0.11174421 0.2396936 45.71892
## IPM_BH_cov_AR
                                                                   0.1467311
                                                                               0.1463250 0.1619469
                          1525.042 0.09448217 0.2155400 44.83824
                                                                               0.1627223 0.1651277
## IPM_BH_cov_AR_resid
                                                                   0.1579847
```

```
## IPM_BH_cov_MA1_AR1_age 1334.804 0.12616270 0.1951553 43.59182
                                                                   0.1805008
                                                                               0.1797193 0.1698492
## IPM_BH_cov_AR_age
                          1319.431 0.12904289 0.1969258 43.55082
                                                                   0.1826040
                                                                               0.1781034 0.1700091
## IPM_BH_cov_AR_resid_age 1349.594 0.11806776 0.1985809 43.82403
                                                                   0.1785228
                                                                               0.1766190 0.1689492
                                       LFOIC delta_LFOIC LFOIC_weight 2020_forecast
##
                              ELPD
## IPM_BH_cov_MA1_AR1
                          6.974438 -13.94888
                                               1.7034433
                                                            0.1124354
                                                                           4692.778
## IPM_BH_cov_AR
                          7.826160 -15.65232 0.0000000
                                                            0.2635125
                                                                           5094.126
## IPM_BH_cov_AR_resid
                          7.200095 -14.40019 1.2521297
                                                            0.1408980
                                                                           4610.069
## IPM_BH_cov_MA1_AR1_age 7.274766 -14.54953
                                               1.1027870
                                                            0.1518218
                                                                           3380.080
                          7.309776 -14.61955
## IPM_BH_cov_AR_age
                                               1.0327684
                                                            0.1572311
                                                                           3916.261
## IPM_BH_cov_AR_resid_age 7.411696 -14.82339
                                               0.8289274
                                                            0.1741013
                                                                           3297.029
print("The model-averaged forecast is:")
## [1] "The model-averaged forecast is:"
print(weighted_forecast_quantiles)
##
       2.5%
                25%
                         50%
                                  75%
                                         97.5%
## 2176.478 3302.997 4110.690 5121.720 7910.230
ensemble_median<-pred_trs%*%(as.vector(model_selection[,"RMSE_weight"]))</pre>
cols<-brewer.pal(length(models), "Spectral")</pre>
matplot(as.matrix(data.frame(pred_trs,ensemble_median)),type="1",lty=1,col=c(cols,"grey40"),lwd=c(rep(2
axis(1,1:n_forecasts,(yr_last-n_forecasts+1):(yr_last))
points(x=1:n_forecasts,y=obs_trs,cex=1.5,pch=20,col="red")
legend("topright",legend=c(models,"Observed","Ensemble"),lty=c(rep(1,length(models)),NA),col=c(cols,"re
```



```
#density plot for final forecasts and ensemble
res<-apply(f_dat,2,function(x) density(x))
plot(x=1,y=1,ylim=c(0,0.001),xlim=c(0,10000),ylab="density",xlab="2021 Runsize")
lapply(res,function(x) lines(x$y~x$x))
## $IPM_BH_cov_MA1_AR1
## NULL
## $IPM_BH_cov_AR
## NULL
## $IPM_BH_cov_AR_resid
## NULL
##
## $IPM_BH_cov_MA1_AR1_age
## NULL
##
## $IPM_BH_cov_AR_age
## NULL
## $IPM_BH_cov_AR_resid_age
## NULL
lines(density(weighted_forecast_dist)$y~density(weighted_forecast_dist)$x,lwd=4,col="red")
legend("topright",legend=c(models,"Ensemble"),lwd=c(rep(1,length(models)),4),col=c(rep("black",length(models)))
```



Via loo() and compare() with full table of results. Note that elpd_diff will be negative (positive) if the expected predictive accuracy for the first (second) model is higher.

```
LOOIC <- vector("list", n_mods)
## extract log densities from JAGS objects
for(i in 1:n_mods) {
  #i <- 1
  ## convert mcmc.list to matrix
  tmp_lp <- as.matrix(readRDS(file.path(savedir,paste0(models[i],"_y",11,".rds"))))</pre>
  ## extract pointwise likelihoods
  tmp_lp <- tmp_lp[,grepl("lp_", colnames(tmp_lp))]</pre>
  ## if numerical underflows, convert -Inf to 5% less than min(likelihood)
  if(any(is.infinite(tmp_lp))) {
    tmp_lp[is.infinite(tmp_lp)] <- NA</pre>
    tmp_min <- min(tmp_lp, na.rm = TRUE)</pre>
    tmp_lp[is.na(tmp_lp)] <- tmp_min * 1.05</pre>
  ## calculate LOOIC
  LOOIC[[i]] <- loo(tmp_lp)</pre>
}
## compute pseudo weights
model_weights <- loo_model_weights(LOOIC, method = "pseudobma",optim_method = "BFGS", optim_control = 1
## LOOIC for all data
tbl_LOOIC <- round(loo_compare(x = LOOIC), 2)</pre>
```

```
rownames(tbl_L00IC) <- sub("model", "", rownames(tbl_L00IC))</pre>
tbl_LOOIC <- tbl_LOOIC[order(as.numeric(rownames(tbl_LOOIC))), ]</pre>
tbl_LOOIC <- cbind(model = models,</pre>
                    as.data.frame(tbl_LOOIC),pseudo_bma_weight = as.matrix(model_weights))
tbl_L00IC[order(tbl_L00IC[,"looic"]), ]
##
                        model elpd_diff se_diff elpd_loo se_elpd_loo p_loo se_p_loo looic se_looic
## 2
               IPM_BH_cov_AR
                                   0.00
                                            0.00
                                                  -395.32
                                                                 48.96 138.77
                                                                                  10.38 790.64
                                                                                                   97.91
## 1
          IPM_BH_cov_MA1_AR1
                                  -8.91
                                            6.69
                                                  -404.23
                                                                 49.97 147.25
                                                                                  13.57 808.47
                                                                                                   99.94
## 3
         IPM_BH_cov_AR_resid
                                           11.02 -409.64
                                                                 50.51 151.14
                                                                                  16.84 819.28
                                                                                                  101.01
                                 -14.32
                                 -17.41
## 6 IPM_BH_cov_AR_resid_age
                                           11.48 -412.74
                                                                 54.53 140.32
                                                                                  12.61 825.47
                                                                                                  109.06
      IPM_BH_cov_MA1_AR1_age
## 4
                                 -18.02
                                           11.41
                                                 -413.34
                                                                 54.21 142.55
                                                                                  12.00 826.69
                                                                                                  108.42
           IPM_BH_cov_AR_age
## 5
                                 -22.70
                                           12.08 -418.03
                                                                 54.55 140.64
                                                                                  13.02 836.05
                                                                                                  109.10
##
     pseudo_bma_weight
## 2
          0.8735976499
          0.0394495775
## 1
## 3
          0.0270874484
## 6
          0.0366696838
## 4
          0.0225743122
## 5
          0.0006213282
## best model
best_i <- which(tbl_LOOIC[,"looic"] == min(tbl_LOOIC[,"looic"]))</pre>
best_fit <- mod_fits[[best_i]]</pre>
```

These results show that the Beverton-Holt model with AR1 error has the lowest LOOIC value. All results will be derived from model averaging based on pseudo bayesian model average weights.