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[illegible][illegible]

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# No. of released individuals (2 age classes)
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# Females:
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rfem <- array(0, 2*(ti-1))
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for(i in 1:(2*(ti-1))) {
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rfem[i] <- sum(mfem[i,])
}

# Males:

rmal <- array(0,2*(ti-1))

for(i in 1:(2*(ti-1))){
  rmal[i] <- sum(mmal[i,])
}

# Population count data
popcount <- c(14,9,8,15,17,15,13,9,8,9,9,10,12,11,10,
             11,10,7,5,5,8,12,14,15,18,21) # number of occupied nest boxes

# Data on reproductive success
nestlings <- c(27,19,25,25,47,46,26,29,23,24,20,21,33,
              32,35,35,8,7,17,10,24,31,28,30,33,25) # number of offspring produced

sample.size <- c(15,9,8,17,18,16,13,9,8,9,9,11,13,11,11,
                11,10,7,5,5,8,12,14,15,20,24) # number of breeding females counted

# Vole abundance

voleH <- c(1,0,0,1,1,0,0,1,0,0,0,1,0,0,1,0,0,0,1,0,1,1,0,0,1,0)

# Time

time <- seq(1,25,1)

# standardize the variable

stdT <- array(0,ti)

for (i in 1:ti) {
  stdT[i] <- (time[i]-mean(time))/sd(time)
}

# Place all data into list:

data <-list(ti=ti,m=mfem,mM=mmal,r=rfem,rM=rmal,popcount=popcount,nestlings=nestlings[1:(ti-1)],
           sample.size=sample.size[1:(ti-1)],time=time,stdT=stdT,voleH=voleH[2:ti])

# Set initial parameter values:

# Simulate values for population sizes from the model:

#Nlinit <- rep(2,ti)
#Nadimmininit <- rep(2,ti)
#NadSurvinit <- rep(10,ti)
#Ntotinit <- Nlinit+Nadimmininit+NadSurvinit

#for (i in 2:ti){
#  Nlinit[i] <- rpois(1,0.1*Ntotinit[i-1])
#  Nadimmininit[i] <- rpois(1,Ntotinit[i-1]*0.1)
#  NadSurvinit[i] <- rbinom(1,Ntotinit[i-1],0.75)
#  Ntotinit[i] <- Nlinit[i] + Nadimmininit[i] + NadSurvinit[i]
#}

#Nlinit[1] <- NA
#Nadimmininit[1] <- NA
#NadSurvinit[1] <- NA

inits <- function(){list(v=rnorm(7),bp=rnorm((ti-1)),fec=runif((ti-1),0,5),
                        Nl=c(NA,round(runif(ti-1,1,50),0)),
                        NadSurv=c(NA,round(runif(ti-1,5,10),0)),
                        Nadimm=c(NA,round(runif(ti-1,5,10),0)),

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Nlprior=5,NadSurvprior=20,Nadimmprior=5)}

#inits <- function(){list(v=rep(0,7),bp=rep(0,ti-1),fec=rep(1,(ti-1)),
#                          Nl=Nlinit,NadSurv=NadSurvinit,
#                          Nadimm=Nadimminit)}

#inits <- function(){list(v=rep(0,7),bp=rep(0,ti-1),fec=rep(1,(ti-1)),
#                          Nl=c(NA,rep(2,ti-1)),NadSurv=c(NA,rep(10,ti-1)),
#                          Nadimm=c(NA,rep(2,ti-1)),Nlprior=2,NadSurvprior=10,Nadimmprior=2)}

# Set the parameters:

#params <- c('phij','phia','phijM','phiaM','fec','im','lambda',
#            'p','pM','NadSurv','Nadimm','Ntot','MEPHJUF',
#            'MEPHADF','MEFE','MEIM_H','MEIM_L','MEPHJUM',
#            'MEPHADM','v','bp')

params <- c('Nl','Ntot','MEPHJUF',
            'MEPHADF','MEFE','MEIM_H','MEIM_L','MEPHJUM',
            'MEPHADM','v','bp','fec')

# Run the MCMC:

tstart=proc.time()
mod <- jags.model('AbadiJPE.jag.R',data,inits,n.chains=cha,n.adapt=ada)
temp=proc.time()-tstart

tend <- temp

# output1 <- coda.samples(mod,params,n.iter=iter,thin=th)

```