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# MODEL DESCRIPTION
# Age structured model ( 2 age classes: 1-year and 2 years or older)
# Age at first breeding =1 year
# Pre-breeding census
# Little owl data (1978-2003)
#*****
# Model

model{

  #*****
  # Define the regression equations
  #*****

  for (i in 1:(ti-1))
  {

    # Best model structure (phi(a2+sex+T),p(sex+t),b(t)) for little owl
    # data from Schaub et al.(2006)

    # Juvenile survival rate

    logit(phiJM[i]) <- v[1] + v[3] + v[4]*stdT[i] # Male

    logit(phiJ[i]) <- v[1] + v[4]*stdT[i] # Female

    # Adult survival

    logit(phiaM[i]) <- v[1] + v[2] + v[3] + v[4]*stdT[i] # Male

    logit(phia[i]) <- v[1] + v[2] + v[4]*stdT[i] # Female

    # Recapture rate

    logit(pM[i]) <- v[5] + bp[i] # Male

    logit(p[i]) <- bp[i] # Female

    # Immigration

    log(im[i]) <- v[6] + v[7]*voleH[i] # Immigration rate as a function of
                                     # vole abundance
                                     # voleH is a categorical variable
                                     # with 2 levels (high,low)

  }

  #*****
  # Define the priors for the parameters
  #*****

  for (i in 1:7)
  {
    v[i] ~ dnorm(0,0.01)#I(-10,10)
  } #i

  for (i in 1:(ti-1))
  {
    bp[i] ~ dnorm(0,0.0001)I(-10,10)

    fec[i] ~ dunif(0,10)
  } #i

  probl <- rep(1/101,101)

  Nlprior ~ dcat(probl) # 1-year

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Nl[1] <- Nlprior-1

NadSurvprior ~ dcat(probl)      # Adults
NadSurv[1] <- NadSurvprior-1

Nadimmprior ~ dcat(probl)      # Immigrants
Nadimm[1] <- Nadimmprior-1

#####
# Derived parameters
#####
# Population growth rate r[t], Mean population growth rate using
# geometric mean

for(tt in 1:(ti-1))
{
  lambda[tt] <- Ntot[tt+1]/Ntot[tt]

  logla[tt] <- log(lambda[tt])
}

MELAM <- exp((1/(ti-1))*sum(logla[1:(ti-1)]))      # Mean population
                                                    # growth rate
# Mean survival rates for females

MEPHJUF <- exp(v[1] + v[4]*0*mean(time[ ])) /(1+exp(v[1] + v[4]*0*mean(time[ ])))

MEPHADF <- exp(v[1] + v[2] + v[4]*0*mean(time[ ])) /(1+exp(v[1] + v[2] + v[4]*0*mean(time
[ ])))

# Mean survival rates for males

MEPHJUM <- exp(v[1] + v[3] + v[4]*0*mean(time[ ])) /(1+exp(v[1] + v[3] + v[4]*0*mean(time
[ ])))

MEPHADM <- exp(v[1] + v[2] + v[3] + v[4]*0*mean(time[ ]))/ (1+exp(v[1] + v[2] + v[3] + v[4
]*0*mean(time[ ])))

# Mean fecundity rate

MEFE <- mean(fec[ ])

# Mean immigration rate

MEIM_H <- exp(v[6] + v[7])      # High vole abundance

MEIM_L <- exp(v[6])            # Low vole abundance

#####
# The Integrated population model
#####

#####
# Likelihood for reproductive data
#####

for (i in 1:(ti-1))
{
  nestlings[i] ~ dpois(rho[i])

  rho[i] <- sample.size[i]*fec[i]
}

#####
# Likelihood for population survey data
#####

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#####
# Observation process
#####

for(tt in 1:ti)
{
  Ntot[tt] <- NadSurv[tt] + Nadimm[tt] + N1[tt]
  popcount[tt] ~ dpois(NadSurv[tt] + Nadimm[tt] + N1[tt])
}

#####
# System process
#####

for (tt in 2:ti)
{

  mean1[tt] <- 0.5*fec[tt-1]*phi[j][tt-1]*Ntot[tt-1]
  N1[tt] ~ dpois(mean1[tt])

  mpo[tt] <- Ntot[tt-1]*im[tt-1]
  Nadimm[tt] ~ dpois(mpo[tt])

  NadSurv[tt] ~ dbin(phia[tt-1],Ntot[tt-1])

}

#####
# Likelihood for capture-recapture data : CJS models (2 age classes)
#####

#####
# Female capture recapture data
#####

for( i in 1:(2*(ti-1))){
  m[i,1:ti] ~ dmulti(pr[i,],r[i])
}

# m-array cell probabilities for juveniles

for(i in 1:(ti-1))
{
  q[i] <- 1-p[i]

  # Main diagonal

  pr[i,i]<-phi[j][i]*p[i]

  # above main diagonal

  for(j in (i+1):(ti-1))
  {
    pr[i,j] <- phi[j][i]*prod(phia[(i+1):j])*prod(q[i:(j-1)])*p[j]
  }

  # Below main diagonal
  for( j in 1:(i-1))
  {
    pr[i,j] <- 0
  }

  # Last column

  pr[i,ti] <- 1-sum(pr[i,1:(ti-1)])

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}

# m-array cell probabilities for adults

for(i in 1:(ti-1))
{
  # main diagonal

  pr[i+ti-1,i] <- phia[i]*p[i]

  # above main diagonal

  for(j in (i+1):(ti-1))
  {
    pr[i+ti-1,j] <- prod(phia[i:j])*prod(q[i:(j-1)])*p[j]

  } # j

  # below main diagonal

  for(j in 1:(i-1))
  {
    pr[i+ti-1,j] <- 0

  } # j

  # last column

  pr[i+ti-1,ti] <- 1-sum(pr[i+ti-1,1:(ti-1)])
}

#####
# Male capture recapture data
#####

for(i in 1:(2*(ti-1)))
{
  mM[i,1:ti] ~ dmulti(prM[i,],rM[i])
}

# m-array cell probabilities for juveniles

for(i in 1:(ti-1)) {
  qM[i] <- 1-pM[i]

  # main diagonal

  prM[i,i] <- phiJM[i]*pM[i]

  # above main diagonal

  for(j in (i+1):(ti-1)) {
    prM[i,j] <- phiJM[i]*prod(phiaM[(i+1):j])*prod(qM[i:(j-1)])*pM[j]

  }

  # below main diagonal

  for(j in 1:(i-1)) {
    prM[i,j] <- 0

  }

  # last column

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    prM[i,ti] <- 1-sum(prM[i,1:(ti-1)])
  }

# m-array cell probabilities for adults

for(i in 1:(ti-1)) {
  # main diagonal

  prM[i+ti-1,i] <- phiaM[i]*pM[i]

  # above main diagonal

  for(j in (i+1):(ti-1)) {
    prM[i+ti-1,j] <- prod(phiaM[(i+1):j])*prod(qM[i:(j-1)])*pM[j]
  }

  # below main diagonal

  for(j in 1:(i-1)) {
    prM[i+ti-1,j] <- 0
  }

  # last column

  prM[i+ti-1,ti] <- 1-sum(prM[i+ti-1,1:(ti-1)])
}
}

```