Appendix S1. The R and WinBUGS codes for the integrated population model where immigration is constrained to be a function of vole abundance v ($\phi_{age2+T+sex}$, p_{t+sex}, b_t, imm_v)


```
#**********************************************************************
# 1  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)
#**********************************************************************

#**********************************************************************
# 2 LOAD THE REQUIRED PACKAGES
#**********************************************************************
        library(lattice)
        library(coda)
        library(R2WinBUGS)

#**********************************************************************
# 3 SPECIFY THE DIRECTORY WHERE WinBUGS IS LOCATED
#**********************************************************************
        bugs.dir <- c("P:/WinBUGS14")   # Change to the correct directory


#**********************************************************************
# 4 SPECIFY WORKING DIRECTORY
#**********************************************************************
        # setwd("c:/imm")         # This is optional and can be changed to any other
                                  #  directory
                                 # Keep the data files in this directory


#**********************************************************************
# 5 READ DATA
#**********************************************************************
        # Number of years (Number of sample occasion in year)  (1978-2003)
                ti <- 26

        # Capture recapture data for females and males

            mfem <- matrix(c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,13,
            0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9,
            0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
            0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,12,
            0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,22,
            0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,22,
```

0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,12,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,8,
0,0,0,0,0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9,
0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,15,
0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,0,0,14,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,17,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,17,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,8,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,4,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,14,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,13,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,15,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,15,
1,2,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,6,
0,3,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,7,
0,0,0,6,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,3,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9,
0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,7,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,3,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,4,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,1,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,4,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3),nrow=50,ncol=26,byrow=T)

```
mmal<-matrix(c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,13,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9,
0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,23,
0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,22,
0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,7,
0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,10,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,15,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,16,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,16,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,17,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,4,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,8,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,5,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,11,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,13,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,14,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,15,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,14,
1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,2,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,5,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,2,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,
```

```
        0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,
        0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3,
        0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,
        0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),nrow=50,ncol=26,byrow=T)


    # 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

    vole <- 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)

#****************************************************************************
# 5  WinBUGS CODES TO FIT THE INTEGRATED POPULATION MODEL
      # The file is called "IPM_IMM.bug"
#****************************************************************************
      sink("IPM_IMM.bug")

      cat("

      model
      {

          #*******************************************
          # 5.1 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)

                # standardize the variable
```

```
          stdT[i] <- (time[i]-mean(time[]))/sd(time[])

     # 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)

    } #i

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

    for (i in 1:7)
       {
           v[i] ~ dnorm(0,0.0001)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
    N1[1] ~ dnorm(100,0.0001)I(0,)                # 1-year

    NadSurv[1] ~ dnorm(100,0.0001)I(0,)           # Adults

    Nadimm[1] ~ dnorm(100,0.0001)I(0,)            # Immigrants

#**********************************
# 5.3 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])

   } #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
#*****************************************
# 5.4 The Integrated population model
#*****************************************

   #***************************************************
    # 5.4.1 Likelihood for reproductive data
    #***************************************************

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

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

      } #i


  #**********************************************
   # 5.4.2 Likelihood for population survey data
  #**********************************************

  #**************************
  # System process
  #**************************

  for (tt in 2:ti)
     {

        mean1[tt] <- 0.5*fec[tt-1]*phij[tt-1]*Ntot[tt-1]

        N1[tt] ~ dpois(mean1[tt])

        mpo[tt] <- Ntot[tt-1]*im[tt-1]

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

        Nadimm[tt] ~ dpois(mpo[tt])

     } # tt

#**************************
# Observation process
#**************************

 for(tt in 1:ti)
```

```
   {

     Ntot[tt] <- NadSurv[tt] + Nadimm[tt] + N1[tt]

     popcount[tt] ~ dpois(Ntot[tt])

   } # tt

    #**********************************************************
    # 5.4.3 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])

        } # i

     # No. of released individuals

     for(i in 1:2*(ti-1))
        {
           r[i] <- sum(m[i,])

        } # i

     # m-array cell probabilities for juveniles

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

          # Main diagonal

           pr[i,i]<-phij[i]*p[i]

          # above main diagonal

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

             } # j
```

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

          } # j
     # Last column

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

} # i

 # 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)])

    } # i
```

```
#*********************************
 # Male capture recapture data
#*********************************

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

    } # i
  # No. of released individuals

  for(i in 1:(ti-1))
      {
        rM[i] <- sum(mM[i,])

      } # 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]

          } # j

    # below main diagonal

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

        } # j
```

```
      # last column

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

    } # i

    # 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]

         } # j

       # below main diagonal

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

         } # j

        # last column

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

    } # i

} # End Model

",fill=TRUE)

sink()
```

```
#**********************************************************
# 6  PREPARE INPUT DATA FOR WinBUGS
#**********************************************************
        data.athene <-list(ti=ti,m=mfem,mM=mmal,popcount=popcount,
                     nestlings=nestlings[1:(ti-1)], sample.size=sample.size[1:(ti-1)],
                   time=time,voleH=voleH[2:ti])
                 # m and mM are capture-recapture data for female and male


#**********************************************************
# 7  CREATE INITIAL VALUES TO START THE MCMC CHAINS
#**********************************************************
        init.nt <- function(){list(v=rnorm(7),bp=rnorm((ti-1)),fec=runif((ti-1),0,5),
                  N1=round(runif(ti,1,50),0),NadSurv=round(runif(ti,5,10),0),
                  Nadimm=round(runif(ti,5,10),0))}


#***************************************
# 8  PARAMETERS TO BE MONITORED
#***************************************
        parameters <- c("phij","phia","phijM","phiaM","fec","im","lambda",
                   "p","pM","NadSurv","Nadimm","Ntot","MEPHJUF",
                   "MEPHADF","MEFE","MEIM_H","MEIM_L","MEPHJUM",
                   "MEPHADM","v","bp")


#*********************************************
# 9  RUN THE MODEL FROM R USING R2WinBUGS
#*********************************************
    # The WinBUGS code "IPM_IMM.bug" is needed to specify in model.file
    # Save the file in the current working directory (i.e. c:/imm)
    # Here we run a single 200000 iterations, 100000 burnin and and retained every
    #100th observation
    # The posterior summary was computed based on 1000 samples
    # Specify the correct path (directory) where the WinBUGS program located
    #*********************************
      # MCMC SPECIFICATIONS
     #*********************************
        chain <- 1
        iter <- 200000
        burn  <- 100000
        thin <- 100

    out.athene <- bugs(data.athene,inits=init.nt,model.file = "IPM_IMM.bug",
                  parameters=parameters, n.chains =chain, n.iter =iter,
                  n.burnin=burn,n.thin=thin,debug=F, bugs.directory =bugs.dir,
                 clearWD=TRUE)


 #****************** END*****************************************
```