

Supplementary material

Appendix 1

Joint likelihood and prior probabilities of the integrated population models

Joint likelihood function

The joint likelihood of our female-based IPMs was the product of the individual likelihoods of each of our model components, which were informed by a population census, fecundity estimates, and Cormack-Jolly-Seber models of our marked adults and nestlings. We treated our data sets as independent although many of the same adult females were represented in multiple data sets, because a simulation study examining the impacts of violation of the assumption of independence suggested minor impacts on the accuracy of parameter estimates. Therefore, under the assumption of independence between the four data sources, the joint likelihood is

$$\begin{aligned} L_{joint}(m, J, R, y|N, \Phi_{juv}, \Phi_{ad}, f, imm, p_{juv}, p_{ad}) \\ = L_{cr}(m|\Phi_{juv}, \Phi_{ad}, p_{juv}, p_{ad}) \times L_{rp}(J, R|f) \\ \times L_{ob}(y|N) \times L_{sy}(N|\Phi_{juv}, \Phi_{ad}, f, imm) \end{aligned}$$

where L_{cr} is the likelihood for the Cormack-Jolly-Seber mark-recapture model, L_{rp} is the likelihood for the fecundity model, and L_{ob} and L_{sy} are the likelihoods for the observation and state process components of the state-space model.

Prior probabilities

All prior probabilities were selected to be vague and uninformative, except for initial population numbers in 2008, and are presented in WinBUGS format. We assumed our raw population count in 2008 was less than, but not by much, the latent number of individuals present. We adopted Normal(50, 0.001) priors for the initial population sizes per age class in 2008 for the model without immigration (normal distribution with a mean of 50 and precision, or 1/variance, of 0.001). For the model with immigration, we examined whether the final estimated distribution of kestrels amongst age-classes was dependent on the numbers specified in the priors for 2008 by varying these priors in separate model runs. Therefore, we ran a model with Normal(33, 0.01) for local yearlings, Normal(34, 0.01) for local adults, and Normal(33, 0.01) for immigrants, and another with Normal(10, 0.01), for yearlings, Normal(55, 0.01) for local adults, and Normal(35, 0.01) for immigrants; all truncated to 0. Model results were very similar regardless of priors chosen, so we performed the remaining analyses with the model with the roughly balanced priors, i.e. specifying the age-class distribution as 33, 34, and 33. The priors for the other model parameters were as follows (parameters of the uniform distribution specifies the upper and lower limits; parameters specified in the beta distribution are the α and β shape parameters):

$$f_t \sim \text{Uniform}(0, 10)$$

$$\text{imm}_t \sim \text{Uniform}(0, 20)$$

$$\Phi_{i,t} \sim \text{Beta}(1, 1)$$

$$p_{i,t} \sim \text{Beta}(1, 1)$$

Appendix 2

Example WinBUGS code for integrated population model (IPM) with immigration

```
#####
```

```
# integrated population assessment of American kestrels in Florida
```

```
# uses CJS model of adult kestrels and nestling kestrels
```

```
# observed nest box attendance as index of population size
```

```
# and observed fecundity in nest boxes
```

```
# code written to import and prepare data in R 2.12.1
```

```
# and call WinBUGS 1.4.3 using the package R2WinBUGS
```

```
#####
```

```
library("R2WinBUGS")
```

```
# making a stacked m-array of mark-recapture data with top two rows marked as
```

```
# juveniles and bottom two rows mixture of previous juveniles (first enter
```

```
# after first capture as adults) and marked as adults
```

```
mfem <- matrix(c(2, 1, 180, 0, 6, 196, 32, 0, 35, 0, 14, 34), nrow=4, ncol=3, byrow=T)
```

```
# temporal specs
```

```
ni <- 2 # number of release occasions
```

```
nj <- 2 # number of recapture occasions
```

```
nyear<-3
```

```
T <- nyear
```

```
# census data, which is observed females
```

```
# making sure not to duplicate nests in territories
```

```
yC3 <- c(88,83,85)
```

```
# number of breeding females
```

```
Nb <- c(80,77,74)
```

```
# nestlings, half of observed nestlings
```

```
nestlings3 <-c(113, 107, 122)
```

```
#####
```

```
# integrated population model with immigration
```

```
#####
```

```
sink("IPM_ImmCJS.txt")
```

```
cat(")
```

```
model {
```

```
#defining recapture and survival parameters
```

```
for (i in 1:nj) {
```

```
  pn[i] <- param[1]
```

```

p[i] <- param[2]
Sn[i] <- param[2+i]
S[i] <- param[4+i]
}

# define priors on beta scale
for (i in 1:6) {
param[i] ~ dbeta(1,1)
}

# define CJS model likelihood
for (i in 1:2*ni) {
mfem[i, 1:(nj+1)] ~ dmulti(pr[i, ], r[i])
}

# Calculate number of birds released each year, or row total
for (i in 1:2*ni) {
r[i] <- sum(mfem[i, ])
}

# Calculate multinomial cell probabilities
# Calculate diagonal, above diagonal, and below for juveniles
for (i in 1:ni) {

```

```

qn[i] <- 1-pn[i]
pr[i,i] <- Sn[i]*pn[i]
for (j in (i+1):nj) {
  pr[i,j] <- Sn[i]*prod(S[(i+1):j])*prod(qn[i:(j-1)])*p[j]
}
for (j in 1:(i-1)) {
  pr[i,j] <- 0
}

# probability of juvenile bird not being seen again
pr[i, nj+1] <- 1-sum(pr[i, 1:nj])
}

# Cell probs for adults
# Calculate diagonal, above diagonal, and below for adults
for (i in 1:ni) {
  q[i] <- 1-p[i]
  pr[i+ni,i] <- S[i]*p[i]
  for (j in (i+1):nj) {
    pr[i+ni,j] <- prod(S[i:j])*prod(q[i:(j-1)])*p[j]
  }
  for (j in 1:(i-1)) {
    pr[i+ni,j] <- 0
  }
}

```

```

}

# probability of adult bird not being seen again
pr[i+ni, nj+1] <- 1-sum(pr[i+ni, 1:nj])
}

# define lambda, mean survival, recapture, and pop growth rate
# could do means post hoc, but this method generates CI
for(t in 1:T-1){
  lambda[t] <- Ntot[t+1]/Ntot[t]
  logla[t] <- log(lambda[t])
  logphij[t] <- log(Sn[t])
  logphia[t] <- log(S[t])
}

MELAM <- exp((1/(T-1))*sum(logla[1:(T-1)]))
MEPHIJ <- exp((1/(T-1))*sum(logphij[1:(T-1)]))
MEPHIA <- exp((1/(T-1))*sum(logphia[1:(T-1)]))

# priors for population
N1[1] ~ dnorm(10, 0.01)I(0,)
Nad[1] ~ dnorm(55, 0.01)I(0,)
Nadimm[1] ~ dnorm(35, 0.01)I(0,)

```

```
# system process using binomial and poisson
```

```
for(tt in 2:T){  
  mean1[tt]<-fec[tt-1]*Sn[tt-1]*Ntot[tt-1]  
  mpo[tt] <- Ntot[tt-1]*imm[tt-1]  
  N1[tt]~dpois(mean1[tt])  
  Nad[tt]~dbin(S[tt-1],Ntot[tt-1])  
  Nadimm[tt] ~ dpois(mpo[tt])  
}
```

```
# observation process for above
```

```
for(tt in 1:T){  
  Ntot[tt]<-Nad[tt] + N1[tt] + Nadimm[tt]  
  yC3[tt]~dpois(Ntot[tt])  
}
```

```
# immigration priors
```

```
for(j in 1:nyear-1){  
  imm[j] ~ dunif(0,20)  
}
```

```
# fecundity priors
```

```
for (t in 1:T){  
  fec[t] ~ dunif(0,10)
```

```
}
```

```
# likelihood for reproductive data
```

```
for (t in 1:T){
```

```
  nestlings3[t] ~ dpois(rho[t])
```

```
  rho[t] <- Nb[t]*fec[t]
```

```
}
```

```
}
```

```
", fill=TRUE)
```

```
sink()
```

```
# specifying data for WinBUGS
```

```
data <- list ("ni", "nj", "T", "nyear", "Nb", "yC3", "nestlings3", "mfem")
```

```
# specifying init generation functions
```

```
inits <- function(){
```

```
  list(N1=round(runif(3,5,30),0), Nad=round(runif(3,5,55),0),
```

```
  Nadimm=round(runif(3,5,55),0), fec=runif(3, 0.5, 4), param=runif(6, 0.01, 0.99),
```

```
  imm=runif(2,0,5)
```

```
)
```

```
}
```

```
# specifying which parameters to monitor

parameters <- c("param", "Ntot", "fec", "N1", "Nad", "rho", "lambda",
               "imm", "Nadimm", "MELAM", "MEPHIJ", "MEPHIA")

# calling WinBUGS from within R

IPM_ImmCJS.mod <- bugs (data, inits, parameters, "IPM_ImmCJS.txt",
                      n.thin=12, n.chains=2, n.burnin=5000, n.iter=140000, debug=T, codaPkg=T)

# reading model results into CODA for further analysis

IPM_ImmCJS.coda <- read.bugs(IPM_ImmCJS.mod)

# exporting posterior probability summaries to csv files

IPM_Imm.out <- summary(IPM_Imm.coda, quantiles=c(0.025, 0.25, 0.5, 0.75, 0.975))

IPM_Imm.hpd <- HPDinterval(IPM_Imm.coda, prob=0.95)

write.csv(IPM_Imm.out$statistics, "IPM_ImmStats.csv")

write.csv(IPM_Imm.out$quantiles, "IPM_ImmQs.csv")

write.csv(IPM_Imm.hpd, "IPM_ImmHPD.csv")
```