# Supplementary Information for Blanc et al.

# Improving abundance estimation by combining capture-recapture and occupancy data:

# example with a large carnivore

# Load packages

library(coda)

library(rjags)

# Setup directory

setwd(“your-directory”)

#---------------------- patch occupancy data ----------------------------#

# Presence-absence data structure: rows = sites; columns = occasions

y <- read.csv ('your-presence-absence-data.csv') # load presence-absence data

nsites <- dim(y)[1]

nsurvs <- dim(y)[2]

#--------------------- capture-recapture data -----------------------------#

# Capture-recapture data structure : rows = individuals; columns = capture occasions

mydata <- read.table('your-capture-recapture-data.txt') # load capture-recapture data

mydata <- matrix(mydata)

extra = 250 # define large number of extra individual capture histories

n = nrow(mydata) # number of observed individuals

M = extra + n

xn = rowSums(mydata)

x = c(xn,rep(0,extra))

k = ncol(mydata)

zerouse <- 0

#-------------------- specify model ------------------------------#

sink("CRandPO\_HET.txt")

cat("

model{

# Patch-occupancy (PO) likelihood

for (i in 1:nsites){

truocc[i] ~ dbern(psi[i]) # true occupancy for site i

logit(psi[i]) <- mupsi + betapsi[i] # occupancy probability as a function of μψ anda site random effect βs

betapsi[i] ~ dnorm(0,sigmabeta)

logit(ppo[i]) <- logitppo[i] # pOs = site-dependant detection probability from PO model

logitppo[i] ~ dnorm(mean.p0,sigmaeps)

# observation model

for (t in 1:nsurvs) {

y[i,t] ~ dbern(effp[i,t])

effp[i,t] <- truocc[i]\*ppo[i]

}

}

# Capture-recapture (CR) likelihood

for(i in 1:M){

x[i] ~ dbin(pee[i],k)

pee[i] <- pcr[i]\*step(N-i) # pcr = individual detection probability pi from CR model

logit(pcr[i]) <- mumup + xi\*etap[i] # integration of an individual random effect ηi

etap[i] ~ dnorm(0,sigmeta)

}

N ~ dpois(lamn)T(0,M)

psi0 <- 1/(1+exp(-mupsi)) # μψ back transformed

log(lamn) <- log(-log(1-psi0)) # definition of λ as a function of ψ

mumup0 <- 1/(1+exp(-mumup)) # μp back transformed

zerouse ~ dpois(comb)

comb <- logfact(M)-logfact(N)+logfact((N-n)\*step(N-n))

# priors for occupancy probability

mupsi ~ dnorm(0,0.2)

sigmabeta <- 1/(sdbeta\*sdbeta)

sdbeta~ dunif(0,5)

# priors for detection probability in PO likelihood

mean.p0 ~ dnorm(0,0.1)

sigmaeps <- 1/(sdeps\*sdeps)

sdeps ~ dunif(0,10)

# priors for detection probability in CR likelihood

mumup ~ dlogis(0,1)

sigmeta ~ dgamma(1.5,37.5)

xi ~ dnorm(0,1)

}

",fill=TRUE)

sink()

#-------------------- Jags stuff -----------------------#

# List of data

mydatax <- list (x=x,M=M,n=n,k=k,zerouse=zerouse,y=y,nsites=nsites,nsurvs=nsurvs)

# Parameters monitored

parameters = c ('N', 'ppo', 'mumup0', 'psi0', 'mupsi', 'mean.p0', 'sdeps', 'taueps', 'betapsi', 'etap')

# Initial values

init1 <- list(mupsi=runif(1),truocc=as.numeric(apply(y,1,sum)>0),xi = rnorm(1,sd=2), N = sample(n:M,1),mumup = rnorm(1), taup = rlnorm(1))

init2 <- list(mupsi=runif(1),truocc=as.numeric(apply(y,1,sum)>0),xi = rnorm(1,sd=2), N = sample(n:M,1),mumup = rnorm(1), taup = rlnorm(1))

init3 <- list(mupsi=runif(1),truocc=as.numeric(apply(y,1,sum)>0),xi = rnorm(1,sd=2), N = sample(n:M,1),mumup = rnorm(1), taup = rlnorm(1))

inits <- list(init1,init2,init3)

#-------------------- Call jags from R -----------------------#

jmodel <- jags.model("CRandPO\_HET.txt", mydatax, inits, n.chains = 3,n.adapt = 2500)

jsample <- coda.samples(jmodel, parameters, n.iter=15000, thin = 1)