# Supplementary Material 1

R and JAGS code.

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###\*\* R code as supplemental material for Gonçalves et al. 2022

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###\*\* Amphibian roadkill estimation for EGR project

#

### Dail-Madsen open population model for unmarked individuals

### with a dependent double observer protocol

### to estimate road mortality at multiple sites

#

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#\* 50 sites (road stretches)

#\* double dependent observers in (up to) 6 visits

#\* Data are available at the repository: https://figshare.com/s/0cebdfcedb591dea6fed

library(jagsUI)

library(ggplot2)

devtools::source\_url("https://github.com/ismaelvbrack/predictJAGS\_func/blob/main/func\_predictJAGS.R?raw=TRUE") # predictJAGS function

# Import data -------------------------------------------------------------

#\* Count data

counts1 <- read.table("counts\_camp1.txt",header=F)

#\* Site covars

siteCovars <- read.table("siteCovs\_2021.txt",header=T)

siteCovars$Trafego <- factor(siteCovars$Trafego, levels=c("baixo","medio","alto"))

#\* Intervals covars

turnos1 <- read.table("turnos\_camp1.txt",header=T)

rain1 <- read.table("pluv\_camp1.txt",header=T)

intervals1 <- ifelse(turnos1[,2:(ncol(turnos1)-1)]=="tarde","night","day")

# Arranging data ----------------------------------------------------------

#\* Arranging data

S <- nrow(counts1) # number of sites

J <- ncol(counts1)/2 # number of visits

#\* Count data

Y1 <- array(as.matrix(counts1),dim=c(S,2,J),

 dimnames=list(siteCovars$Trecho,c("obs1","obs2"),1:J))

# counts by both obs

ncap1 <- array(dim=c(S,J))

for (j in 1:J) {

 for (i in 1:nrow(Y1[,,j])) {

 ncap1[i,j] <- sum(Y1[i,,j])

 }}

#\* Gathering data

data1 <- list(Y=Y1,ncap=ncap1, # counts

 night=ifelse(intervals1=="night",1,0),day=ifelse(intervals1=="day",1,0), # visits covs

 rain=ifelse(rain1[,2:ncol(rain1)]=="chuva",1,0),

 urban=siteCovars$urban,wetland=siteCovars$wetland,traffic=as.numeric(siteCovars$Trafego), # site covs

 new.wet=new.wet, # data to predict entries for non-sampled sites

 S=S,J=J) # sampling design

#\* Define initial values

# Initial values session 1

inity1 <- ncap1+3

inity1[which(is.na(inity1), arr.ind=T)] <- inity1[which(is.na(inity1),arr.ind=T)[,1],2]

N1.1 <- inity1

N1.1[,2:J] <- NA

Pers.in1 <- Entrs.in1 <- array(,c(S,J))

for (i in 1:S){

 for(j in 2:J){

 Pers.in1[i,j] <- rbinom(1,inity1[i,j-1],.5) # keep ~half individuals

 Entrs.in1[i,j] <- ifelse((inity1[i,j]-Pers.in1[i,j])>0, (inity1[i,j]-Pers.in1[i,j]), 0)

 }}

inits1 <- function(){list(alpha.lam=rnorm(1),betaUrb.lam=rnorm(1),betaWet.lam=rnorm(1), # lambda

 alpha.gam=rnorm(1),betaWet.gam=rnorm(1),betaRain.gam=rnorm(1), # gamma

 alpha.phi=rnorm(3),betaDay.phi=rnorm(1), # phi

 p0=runif(1,0,1), # p

 Persists=Pers.in1,Entries=Entrs.in1,N=N1.1,z=rep(1,S))}

#\* Parameters monitored

params <- c("alpha.lam","betaUrb.lam","betaWet.lam",

 "alpha.gam","betaWet.gam","betaRain.gam",

 "alpha.phi","betaDay.phi",

 "p0",

 #"Entries",

 "siteFatals",#"new.siteFatals",

 "AllFatals")#,"new.AllFatas")

# Writing JAGS model ------------------------------------------------------

sink("DM-depObs\_fullCovs.txt")

cat("

 model{

##\* Priors -------------

# Initial abundance

alpha.lam ~ dnorm(0,0.1) # intercept for lambda

betaUrb.lam ~ dnorm(0,0.1) # effect of urban

betaWet.lam ~ dnorm(0,0.1) # effect of wetland

# Entries

alpha.gam ~ dnorm(0,0.1) # intercept for gamma

betaWet.gam ~ dnorm(0,0.1) # effect of wetland

betaRain.gam ~ dnorm(0,0.1) # effect of rain/no-rain (binary)

# Departures / Persistence

for(i in 1:3){

 alpha.phi[i] ~ dnorm(0,0.1) # intercepts for phi

} # one for each traffic category (low, medium, high)

betaDay.phi ~ dnorm(0,0.1) # effect of day/night

# Detection

p0 ~ dunif(0,1)

##\* Likelihood -------------

for (i in 1:S){ #each site

 ### State variable process

 #\* initial abundance j=1

 N[i,1] ~ dpois(lambda[i])

 log(lambda[i]) <- alpha.lam + betaUrb.lam\*urban[i] + betaWet.lam\*wetland[i]

 # dynamics j>1

 for(j in 2:J){

 # Persistence

 Persists[i,j] ~ dbin(phi[i,j],N[i,j-1])

 logit(phi[i,j]) <- alpha.phi[traffic[i]] + betaDay.phi\*day[i,j-1]

 # Entries

 Entries[i,j] ~ dpois(gamma[i,j])

 log(gamma[i,j]) <- alpha.gam + betaWet.gam\*wetland[i] + betaRain.gam\*rain[i,j-1]

 # Abundance

 N[i,j] <- Persists[i,j] + Entries[i,j]

 }#j

 ## Conditional multinomial cell probabilities

 for(j in 1:J){

 p[i,j] <- p0 # detection prob.

 pi[i,1,j] <- p[i,j] # 1st observer

 pi[i,2,j] <- (1-p[i,j]) \* p[i,j] # 2nd observer

 pi0[i,j] <- 1 - pi[i,1,j] - pi[i,2,j] # prob. of non-detection

 pcap[i,j] <- 1 - pi0[i,j] # prob. of at least one observer to detect

 pic[i,1,j] <- pi[i,1,j] / pcap[i,j] # conditional prob.1

 pic[i,2,j] <- pi[i,2,j] / pcap[i,j] # conditional prob.2

 ## Observation process

 ncap[i,j] ~ dbin(pcap[i,j] , N[i,j])

 Y[i,1:2,j] ~ dmulti(pic[i,1:2,j] , ncap[i,j])

 }#j

#\* Derived -------------

 # All entries/fatalities per site

 siteFatals[i] <- sum(Entries[i,2:J])

}#i

 # All fatalities in sampled sites

 AllFatals <- sum(siteFatals[])

}",fill=TRUE)

sink()

# Running... --------------------------------------------------------------

#\* MCMC settings

na <- 10000

ni <- 100000

nt <- 1

nb <- 20000

nc <- 3

# Run!

out1 <- jags(data1, inits1, params, "DM-depObs\_fullCovs.txt",

 n.chains=nc,n.thin=nt, n.iter=ni, n.burnin=nb, n.adapt=na, parallel=T)

# See results -------------------------------------------------------------

site.length <- 0.1 # in km

time.int <- 0.5 # in days

#\* Parameter estimates

print(out1, digits=2)

#\* Traceplots

traceplot(out1, param="AllFatals")

traceplot(out1, param="alpha.phi")

# Roadkills per day for each site

siteFatalsDay <- as.data.frame(t(apply(out1$sims.list$siteFatals / (time.int\*(J-1)), 2,

 function(x) c(mean(x),quantile(x,probs=c(0.025,0.5,0.975))))))

names(siteFatalsDay) <- c("mean","lower","median","upper")

siteFatalsDay <- cbind(Trecho=siteCovars$Trecho,siteFatalsDay)

siteFatalsDay <- cbind(siteFatalsDay,

 t(apply(ncap1,1,function(x) c(c.mean=mean(x,na.rm=T),c.max=max(x,na.rm=T)))))

# Roadkills per km per day for all sites (average)

c(mean=mean(out1$sims.list$AllFatals / (time.int\*(J-1)) / (S\*site.length)),

 quantile(out1$sims.list$AllFatals / (time.int\*(J-1)) / (S\*site.length),probs=c(0.025,0.5,0.975)))

# Relationship predictions ------------------------------------------------

# Initial abundance (lambda)

# ~ wetland

# wetland values to predict

new.wet <- cbind(urban=median(siteCovars$urban),

 wetland=seq(min(siteCovars$wetland),max(siteCovars$wetland),,100)

)

pred.lamWet <- predictJAGS(fm=out1,params=c("alpha.lam","betaUrb.lam","betaWet.lam"),

 newdata=new.wet,link="log",quants=c(0.025,0.5,0.975),appendData=T)

names(pred.lamWet)[2:4] <- c("lower","median","upper")

#\* Figure! lambda ~ wetland

fig.lamWet <- ggplot(pred.lamWet, aes(x=wetland,y=median,ymax=upper,ymin=lower)) +

 geom\_line(size=1.4, color="darkgreen") + geom\_ribbon(alpha=0.4, fill="darkgreen") +

 theme\_classic() + #coord\_cartesian(ylim=c(0,100)) +

 labs(x="% of wetlands (200m buffer)",y="Initial number of carcasses") +

 scale\_x\_continuous(breaks=seq(.1,.9,0.2),labels=seq(10,90,20)) +

 scale\_y\_continuous(limits=c(0,12),breaks=seq(0,12,2)) +

 annotate("text",label="a",x=0,y=12,size=7) +

 theme(axis.title=element\_text(size=14),axis.text=element\_text(size=12))

# Initial abundance (lambda)

# ~ urban

# urban values to predict

new.urb <- cbind(urban=seq(min(siteCovars$urban),max(siteCovars$urban),,100),

 wetland=median(siteCovars$wetland))

# predict

pred.lamUrb <- predictJAGS(fm=out1,params=c("alpha.lam","betaUrb.lam","betaWet.lam"),

 newdata=new.urb,link="log")

names(pred.lamUrb)[2:4] <- c("lower","median","upper")

#\* Figure! lambda ~ urban

fig.lamUrb <- ggplot(pred.lamUrb, aes(x=urban,y=median,ymax=upper,ymin=lower)) +

 geom\_line(size=1.4, color="black") + geom\_ribbon(alpha=0.4, fill="gray30") +

 theme\_classic() + #coord\_cartesian(ylim=c(0,100)) +

 labs(x="% of urban areas (200m buffer)",y="Initial number of carcasses") +

 scale\_x\_continuous(breaks=seq(0,.3,0.1),labels=seq(0,30,10)) +

 annotate("text",label="b",x=0,y=8,size=7) +

 theme(axis.title=element\_text(size=14),axis.text=element\_text(size=12))

# Entries (gamma)

# ~ wetland + rain

# wetland values to predict

new.wet2 <- data.frame(wetland=rep(seq(min(siteCovars$wetland),max(siteCovars$wetland),,100),2),

 rain=rep(c(0,1),each=100))

pred.gamWet <- predictJAGS(fm=out1,params=c("alpha.gam","betaWet.gam","betaRain.gam"),

 newdata=new.wet2,link="log",quants=c(0.025,0.5,0.975),appendData=T)

names(pred.gamWet)[2:4] <- c("lower","median","upper")

pred.gamWet$rain <- factor(pred.gamWet$rain,labels=c("no-rain","rain"))

#\* Figure! lambda ~ wetland

fig.gamWet <- ggplot(pred.gamWet, aes(x=wetland,y=median,ymax=upper,ymin=lower)) +

 geom\_line(aes(color=rain),size=1.4) + geom\_ribbon(aes(fill=rain),alpha=0.4) +

 theme\_classic() + #ylim(0,16) +

 scale\_color\_manual(values=c("tan4","blue4")) +

 scale\_fill\_manual(values=c("tan3","blue")) +

 labs(x="% of wetlands (200m buffer)",y="Entrant carcasses / 12h") +

 scale\_x\_continuous(breaks=seq(.1,.9,0.2),labels=seq(10,90,20)) +

 scale\_y\_continuous(limits=c(0,16),breaks=seq(0,16,4)) +

 annotate("text",label="c",x=0,y=16,size=7) +

 theme(axis.title=element\_text(size=14),axis.text=element\_text(size=12),

 legend.title=element\_blank(),legend.text=element\_text(size=12),

 legend.position="top")

# Persistence (phi)

# ~ traffic + day

pred.phi <- out1$summary[grep("alpha.phi",rownames(out1$summary)),

 c("mean","2.5%","50%","97.5%")]

pred.phi <- as.data.frame(plogis(rbind(pred.phi,

 pred.phi +

 rep(out1$summary["betaDay.phi",c("mean","2.5%","50%","97.5%")],each=nrow(pred.phi)))))

pred.phi$traffic <- rep(c("baixo","medio","alto"),2)

pred.phi$turno <- rep(c("night","day"),each=3)

names(pred.phi)[2:4] <- c("lower","median","upper")

pred.phi$traffic <- factor(pred.phi$traffic, levels=c("baixo","medio","alto"), labels=c("low","medium","high"))

fig.phi <- ggplot(pred.phi, aes(x=traffic, y=mean,ymin=lower,ymax=upper,color=turno))+

 geom\_point(size=3,position=position\_dodge(0.3)) +

 geom\_errorbar(width=0.3,size=1,position=position\_dodge(0.3)) +

 theme\_classic() + scale\_y\_continuous(breaks=seq(0,1,0.2)) +

 labs(x="Traffic",y="Carcass persistence prob.",color="") +

 scale\_color\_manual(values=c("red3","blue3")) +

 annotate("text",label="d",x=0.6,y=1,size=7) +

 theme(axis.title=element\_text(size=14),axis.text=element\_text(size=12),

 legend.text=element\_text(size=12),legend.position="top")

# Supplementary Material 2

**Table S1.** Records of amphibian carcass with family and species or group identification. NI is not identified Anura carcass.

|  |  |
| --- | --- |
| **Family/***Species*  | **Road**  |
| **ERS-040**  | **ERS-784**  | **Total count**  |
| **Bufonidae**  | **63**  | **41**  | **104**  |
| *Rhinella dorbignyi*  | 13  | 30  | 43  |
| *Rhinella icterica*  |   | 3  | 3  |
| *Rhinella* sp.  | 50  | 8  | 58  |
| **Hylidae**  | **1121**  | **194**  | **1315**  |
| *Boana faber*  |   | 1  | 1  |
| *Boana pulchella*  | 99  | 48  | 147  |
| *Boana* sp.  | 3  |   | 3  |
| *Dendropsophus* gr. *microcephalus*  | 148  | 6  | 154  |
| *Dendropsophus minutus*  | 3  |   | 3  |
| *Dendropsophus* sp.  | 459  | 21  | 480  |
| Hylidae  | 147  | 26  | 173  |
| *Pseudis minuta*  | 136  | 39  | 175  |
| *Scinax* gr. *catharinae*  | 8  | 1  | 9  |
| *Scinax* gr. *ruber*  | 10  | 4  | 14  |
| *Scinax granulatus*  | 3  |   | 3  |
| *Scinax nasicus*  | 1  |   | 1  |
| *Scinax* sp.  | 38  | 23  | 61  |
| *Scinax squalirostris*  | 64  | 24  | 88  |
| *Scinax tymbamirim*  | 1  | 1  | 2  |
| *Trachycephalus mesophaeus*  | 1  |   | 1  |
| **Leptodactylidae**  | **1013**  | **172**  | **1185**  |
| Leptodactylidae  | 156  | 4  | 160  |
| *Leptodactylus gracilis*  | 72  | 19  | 91  |
| *Leptodactylus latinasus*  | 4  | 1  | 5  |
| *Leptodactylus luctator*  | 294  | 41  | 335  |
| *Leptodactylus* sp.  | 212  | 16  | 228  |
| *Physalaemus biligonigerus*  | 59  | 18  | 77  |
| *Physalaemus cuvieri*  | 2  | 3  | 5  |
| *Physalaemus gracilis*  | 30  | 40  | 70  |
| *Physalaemus henselii*  | 5  |   | 5  |
| *Physalaemus lisei*  | 2  |   | 2  |
| *Physalaemus* sp.  | 97  | 30  | 127  |
| *Pseudopaludicola falcipes*  | 80  |   | 80  |
| **Microhylidae**  | **8**  |   | **8**  |
| *Elachistocleis bicolor*  | 8  |   | 8  |
| **Odontophrynidae**  | **7**  | **13**  | **20**  |
| *Odontophrynus* sp.  | 7  | 13  | 20  |
| **Anura NI**  | **596**  | **106**  | **702**  |
| **Total count**  | **2808**  | **526**  | **3334**  |

# Supplementary Material 3

**Table S2.** Data used to segment prioritization to receive mitigation actions (in red are the segments indicated as priority). Estimated fatality rate with credibility intervals for each segment and landscape transition rate.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID**  | **Estimated Fatality Rate (individuals/segment\*day)**  | **Lower Credibility Intervals**  | **Upper Credibility Intervals**  | **Landscape Transition Rate** **(%)** | **Priority segment**  |
| 6 | 52.7 | 48.4 | 57.6 | 2.32 | Yes  |
| 5 | 43.47 | 39.6 | 47.6 | 2.06 | Yes  |
| 4 | 35.99 | 32.4 | 39.6 | 1.15 | Yes  |
| 49 | 19.98 | 16.8 | 23.2 | 3.68 | Yes  |
| 48 | 14.94 | 12 | 18 | 3.13 | Yes  |
| 3 | 14.55 | 12 | 17.2 | 0.00 | Yes  |
| 1 | 12.88 | 10.4 | 15.6 | 0.00 | Yes  |
| 47 | 10.56 | 8.4 | 12.8 | 0.97 | Yes  |
| 2 | 10.47 | 8.4 | 12.4 | 0.00 | Yes  |
| 42 | 10.05 | 8 | 12.4 | 1.61 | Yes  |
| 7 | 27.2 | 24 | 30.4 | 29.41 | No  |
| 13 | 26.19 | 22.4 | 30 | 98.33 | No  |
| 15 | 23.68 | 20 | 27.6 | 94.69 | No  |
| 10 | 23.45 | 19.6 | 27.2 | 51.47 | No  |
| 31 | 22.68 | 21.2 | 24.4 | 35.34 | No  |
| 9 | 22.46 | 19.2 | 26 | 43.56 | No  |
| 11 | 22.12 | 18.4 | 26 | 73.81 | No  |
| 14 | 21.27 | 17.6 | 25.2 | 97.86 | No  |
| 8 | 19.84 | 17.2 | 22.8 | 40.00 | No  |
| 30 | 19.49 | 18 | 21.2 | 11.06 | No  |
| 23 | 18.37 | 16.8 | 20 | 10.00 | No  |
| 12 | 18.31 | 15.2 | 21.6 | 93.33 | No  |
| 32 | 18.26 | 16.8 | 20 | 32.28 | No  |
| 16 | 13.98 | 11.2 | 16.8 | 90.81 | No  |
| 17 | 12.38 | 11.2 | 14 | 6.34 | No  |
| 50 | 9.92 | 8 | 12 | 4.60 | No  |
| 21 | 9.91 | 8.4 | 11.6 | 7.69 | No  |
| 33 | 9.62 | 8.4 | 11.2 | 9.24 | No  |
| 45 | 9.48 | 7.2 | 11.6 | 0.00 | No  |
| 40 | 9.46 | 7.6 | 11.6 | 3.16 | No  |
| 34 | 8.81 | 7.6 | 10.4 | 3.45 | No  |
| 22 | 8.7 | 7.2 | 10.4 | 8.82 | No  |
| 46 | 8.49 | 6.8 | 10.4 | 0.00 | No  |
| 35 | 8.41 | 7.2 | 10 | 0.00 | No  |
| 38 | 7.35 | 5.6 | 9.2 | 3.94 | No  |
| 36 | 7.09 | 5.6 | 8.8 | 1.65 | No  |
| 44 | 6.75 | 4.8 | 8.8 | 0.00 | No  |
| 39 | 6.32 | 4.8 | 8 | 3.94 | No  |
| 41 | 5.51 | 4 | 7.2 | 1.61 | No  |
| 26 | 4.36 | 3.2 | 6 | 6.93 | No  |
| 43 | 4.06 | 2.8 | 5.6 | 0.72 | No  |
| 37 | 3.76 | 2.4 | 5.2 | 3.94 | No  |
| 18 | 3.69 | 2.4 | 5.2 | 2.84 | No  |
| 24 | 2.36 | 1.2 | 4 | 9.52 | No  |
| 29 | 2.31 | 0.8 | 4 | 5.59 | No  |
| 20 | 2.18 | 0.8 | 4 | 8.29 | No  |
| 19 | 2.15 | 0.8 | 3.6 | 5.26 | No  |
| 25 | 1.97 | 0.8 | 3.6 | 8.17 | No  |
| 28 | 1.95 | 0.8 | 3.6 | 6.31 | No  |
| 27 | 1.56 | 0.4 | 3.2 | 7.66 | No  |