**Supplemental information to submitted article: Density and population viability of coastal marten: a rare and geographically isolated small carnivore**

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Supplemental File 1. Bayesian modeling and example code

We used JAGS (Plummer, 2003), accessed with the jagsUI package (Kellner, 2014) in R v. 3.2.3 (R Core Team 2016), to run the spatial mark-recapture analysis. Estimates were calculated from 4,500 MCMC samples, taken from 3 chains run for 5,000 iterations, thinned by 3, following a burn-in of 500. Below is the code we used to fit our spatial mark-recapture model with telemetry data to a population of coastal martens in central Oregon.

model {

*# Definitions*

*# nG = number of grid cells in the state space*

*# M = number of augmented individuals (unmarked)*

*# m = number of marked individuals*

*# sm = activity centers for marked individuals*

*# x0g = x coordinate of grid cell center*

*# y0g = y coordinate of grid cell center*

*# locs = matrix of x/y coordinates of telemetry locations*

*# off = matrix indicating which rows of telemetry locations are assigned to each individual*

*# trapmat = 2 column matrix of x/y coordinates of camera trap locations*

*# nU = the number of unmarked individuals seen on camera j on day k*

*# Priors and constraints*

alpha0 ~ dunif(-10, 10) # Intercept of forest cover effect

alpha1 ~ dnorm(0, 0.01) # Effect of forest cover

alpha2 ~ dnorm(0, 0.01) # Effect of forest cover2

beta0 ~ dunif(-10, 10) # Intercept for capture probability (beta0)

beta1 ~ dnorm(0, 0.01) # Effect of sex on capture probability (beta1)

psi.sex ~ dunif(0, 1) # Prior for sex

for(s in 1:2){

sigma[s] ~ dunif(0, 5000) # Movement parameter

}

*# Intensity function for discrete state space with habitat covariates*

for(g in 1:nG){

mu[g] <- exp(alpha0 + alpha1\*cancov[g] + alpha2\*pow(cancov[g],2))\*pixArea

probs[g] <- mu[g]/EN # Probability of an activity center being in a grid cell in a year

} #g

EN <- sum(mu[])

psi <- EN/(M+m)

*# Likelihood for marked individuals*

for (i in 1:m){

Sex[i] ~ dbern(psi.sex)

Sex2[i] <- Sex[i] + 1

sm[i] ~ dcat(probs[])

x0g[i] <- S[sm[i],1]

y0g[i] <- S[sm[i],2]

*# Telemetry model*

for (r in off1[i]:off2[i]){

locs[r,1] ~ dnorm(x0g[i], 1/(sigma[Sex2[i]]^2))

locs[r,2] ~ dnorm(y0g[i], 1/(sigma[Sex2[i]]^2))

}

for (j in 1:J){

Dist2[i,j] <- sqrt((x0g[i] - trapmat[j,1])^2 + (y0g[i] - trapmat[j,2])^2)

y[i,j] ~ dpois(lambdam[i,j]\*K)

lambdam[i,j] <- p0[i,j]\*exp(-Dist2[i,j]^2/(2\*sigma[Sex2[i]]^2))

logit(p0[i,j]) <- beta0 + beta1\*Sex[i]

} #j

} #i

*# Likelihood for unmarked individuals*

for(i in 1:M) {

z[i] ~ dbern(psi) # probability of inclusion

s[i] ~ dcat(probs[])

Sexu[i] ~ dbern(psi.sex)

Sexu2[i] <- Sexu[i] + 1

x0gu[i] <- S[s[i],1]

y0gu[i] <- S[s[i],2]

for(j in 1:J){

dist[i,j] <- sqrt((x0gu[i] - trapmat[j,1])^2 + (y0gu[i] - trapmat[j,2])^2)

logit(p0u[i,j]) <- beta0 + beta1\*Sexu[i]

lambda[i,j] <- p0u[i,j]\*exp(-dist[i,j]^2/(2\*sigma[Sexu2[i]]^2))

for(k in 1:K) {

yu[i,j,k] ~ dpois(lambda[i,j]\*z[i])

}

}

}

for(j in 1:J){

for(k in 1:K){

nU[j,k] ~ dsum(yu[1,j,k], yu[2,j,k], yu[3,j,k], yu[4,j,k], yu[5,j,k], yu[6,j,k], yu[7,j,k], yu[8,j,k], yu[9,j,k], yu[10,j,k], yu[11,j,k], yu[12,j,k], yu[13,j,k], yu[14,j,k], yu[15,j,k], yu[16,j,k], yu[17,j,k], yu[18,j,k], yu[19,j,k], yu[20,j,k])

}

}

}