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

**Mark A. Linnell**1a, **Katie M. Moriarty**2a, **David S. Green**3, **Taal Levi**4

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])

 }

 }

 }