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Wildlife Research

Supplementary Material

Monitoring and habitat inferences change with population metric: a case study with mesocarnivores

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JAGS MODEL CODE

Occupancy model

```
sink("occ_.txt")
cat("
  model {

#####
### PRIORS ###
#####
psi0 ~ dlogis(0,1)
beta_shdi ~ dlogis(0,1)
beta_fw ~ dlogis(0,1)
beta_road ~ dlogis(0,1)

p0 ~ dlogis(0,1)

#####
### LIKELIHOOD ###
#####

# OCCUPANCY SUBMODEL - ECOLOGICAL PROCESS
for(i in 1:nsite){
z[i] ~ dbern(psi[i])

logit(psi[i]) <- psi0 +
beta_shdi * shdi[i] +
beta_road * road[i] +
beta_fw * fw[i]

# DETECTION SUBMODEL - OBSERVATION PROCESS
for(j in 1:nsurvey){
y[i,j] ~ dbern(z[i]*p[i,j])

logit(p[i,j]) <- p0

#####
# Goodness of fit #
#####

# Replicated data
y_rep[i,j] ~ dbern(z[i]*p[i,j]) # replicated data

# Squared error for observed data
```

```

D_obs[i,j] <- (y[i,j] - z[i]*p[i,j])^2

# Squared error for replicated data
D_rep[i,j] <- (y_rep[i,j] - z[i]*p[i,j])^2

} # j survey

} # i site

#DERIVED PARAMETERS
sites.occ <- sum(z[])/74
p_overall <- mean(p[,])

# Sum of squared errors
total_D_obs <- sum(D_obs[,])
total_D_rep <- sum(D_rep[,])

# Bayesian p-value
bp_value <- step(total_D_rep - total_D_obs)

} # end of model
",fill = TRUE)
sink()

```

Royle-Nichols model

```

sink("RN.txt")
cat("
  model {
#####
### PRIORS ###
#####
beta0 ~ dnorm(0,0.001)
beta_shdi ~ dnorm(0,0.001)
beta_fw ~ dnorm(0,0.001)
beta_road ~ dnorm(0,0.001)

p0 ~ dlogis(0,1)

#####
### LIKELIHOOD ###
#####

for(i in 1:nsite){
  N[i] ~ dpois(lambda[i])

```

```

log(lambda[i]) <- beta0 +
  beta_shdi * shdi[i] +
  beta_road * road[i] +
  beta_fw * fw[i]

for (j in 1:nweek){
  y[i,j] ~ dbern(p[i,j]) # observed data
  p[i,j] <- 1 - (1 - r[i,j])^(N[i])
  logit(r[i,j]) <- p0

#####
# Goodness of fit #
#####

  # Generate replicated data
  y_rep[i,j] ~ dbern(p[i,j]) # replicated data

  # Squared error for observed data
  D_obs[i,j] <- (y[i,j] - p[i,j])^2

  # Squared error for replicated data
  D_rep[i,j] <- (y_rep[i,j] - p[i,j])^2
}
}

#####
### DERIVED PARAMETERS ###
#####

# Abundance: average across sites
abun <- sum(N[])/nsite

# Sum of squared errors
total_D_obs <- sum(D_obs[,j])
total_D_rep <- sum(D_rep[,j])

# Bayesian p-value
bp_value <- step(total_D_rep - total_D_obs)

} # end of model
",fill = TRUE)
sink()

```

Poisson regression model

```

sink("count.txt")
cat("
  model {

#####
### PRIORS ###
#####

beta0 ~ dnorm(0, 0.001)
beta_shdi ~ dnorm(0, 0.001)
beta_fw ~ dnorm(0, 0.001)
beta_road ~ dnorm(0, 0.001)

tau <- 1/sigma^2
sigma ~ dunif(0,20)

#####
### LIKELIHOOD ###
#####

for (i in 1:nsite) {
y[i] ~ dpois(lambda[i])

log(lambda[i]) <- beta0 +
beta_shdi * shdi[i] +
beta_road * road[i] +
beta_fw * fw[i] +
log(effort[i]) +
eps[i]

eps[i] ~ dnorm(0,tau)

#####
# Goodness of fit #
#####

pr[i] <- (y[i] - lambda[i])/sqrt(lambda[i])
pr2[i] <- pr[i]^2

y.new[i] ~ dpois(lambda[i])

pr.new[i] <- (y.new[i] - lambda[i])/sqrt(lambda[i])
pr.new2[i] <- pr.new[i]^2

} #i

```

```
#####
#DERIVED PARAMETERS#
#####

sites.count <- sum(lambda[])/74

pr2.sum <- sum(pr2[])
pr.new2.sum <- sum(pr.new2[])

# Bayesian p-value
bp <- pr2.sum > pr.new2.sum

} # end of model
",fill = TRUE)
sink()
```

REST model

```
sink("rho.txt")
cat("model
{
for(i in 1:Nstay){
  is.censored[i] ~ dinterval(stay[i],cens[i])
  stay[i] ~ dlnorm(mean, tau)
}

mean ~ dgamma(0.01, 0.01)
tau ~ dgamma(0.01, 0.01)
tau2 <- 1/sigma^2
sigma ~ dunif(0,20)

for(i in 1:Ncam){
  y[i] ~ dpois(mu[i])

  eps[i] ~ dnorm(0,tau2)

  log(mu[i]) <- log(S) + log(eff[i]) + log(rho[i]) + log(activ) - mean - 1/(2*tau)

  log(rho[i]) <-
    effects[1] +
    effects[2] * shdi[i] +
    effects[3] * fw[i] +
    effects[4] * road[i] +
    eps[i]          # extra site-level variance not captured by the covariates
```

```

# Calculate squared residuals for observed data
D_obs[i] <- ((y[i] - mu[i])/sqrt(mu[i]))^2 # Squared difference for observed data
}

for (v in 1:4) {
  effects[v] ~ dnorm(0, 0.01)
}

# Calculate total squared error for observed data
total_D_obs <- sum(D_obs)

for (i in 1:Ncam) {
  y_rep[i] ~ dpois(mu[i])

  # Calculate squared residuals for replicated data
  D_rep[i] <- ((y_rep[i] - mu[i])/sqrt(mu[i]))^2 # Squared difference for replicated data
}

# Calculate total squared error for replicated data
total_D_rep <- sum(D_rep)

# Bayesian p-value
bp_value <- step(total_D_rep - total_D_obs)

D <- mean(rho[])
}
")
sink()

```

Table S1. Model-estimated means, 95% credible intervals (95% CrI), Gelman-Rubin statistics, and Bayesian p-values of population-level occupancy probability (occupancy), local abundance, relative abundance, and density (individuals/km²) for bobcat, coyote, fisher, gray fox, and red fox from camera trap images collected during summer 2021 in southeastern New Hampshire, USA. Results are based on three MCMC chains of 20,000 iterations each, a burn-in of 2,000 iterations, and a thinning rate of 1.

Metric	Species	Posterior Mean	Lower 95% CrI	Upper 95% CrI	Gelman-Rubin	Bayesian p-value
Occupancy	Bobcat	0.65	0.42	0.95	1.00	0.52
	Coyote	0.70	0.65	0.78	1.00	0.51
	Fisher	0.38	0.24	0.59	1.00	0.53
	Gray fox	0.11	0.07	0.32	1.00	0.55
	Red fox	0.33	0.31	0.38	1.00	0.51
Local abundance	Bobcat	1.16	0.50	3.07	1.00	0.50
	Coyote	1.76	1.16	2.95	1.00	0.66
	Fisher	0.41	0.23	0.95	1.01	0.50
	Gray fox	0.11	0.07	0.28	1.00	0.57
	Red fox	0.47	0.36	0.64	1.00	0.76
Relative abundance	Bobcat	0.61	0.39	0.94	1.00	0.73
	Coyote	2.45	2.10	2.82	1.00	0.57
	Fisher	0.55	0.31	1.00	1.00	0.71
	Gray fox	0.17	0.08	0.29	1.00	0.86
	Red fox	2.14	1.82	2.48	1.00	0.62
Density	Bobcat	0.05	0.03	0.09	1.00	0.36
	Coyote	0.22	0.16	0.28	1.00	0.43
	Fisher	0.02	0.00	0.03	1.00	0.37
	Gray fox	NA	NA	NA	NA	NA
	Red fox	0.28	0.19	0.38	1.02	0.45

Table S2. Model-estimated detection probability and 95% credible intervals (95% CrI) for bobcat, coyote, fisher, gray fox, and red fox from camera trap images collected during summer 2021 in southeastern New Hampshire, USA. Results are based on three MCMC chains of 20,000 iterations each, a burn-in of 2,000 iterations, and a thinning rate of 1.

Species	Posterior Mean	Lower 95% CrI	Upper 95% CrI
Bobcat	0.08	0.04	0.13
Coyote	0.23	0.18	0.27
Fisher	0.09	0.05	0.16
Gray fox	0.16	0.04	0.31
Red fox	0.26	0.20	0.32