

# Camera trap surveys reveal high diversity of mammals and pheasants in Medog, Tibet

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SUPPLEMENTARY MATERIAL 1 Multi-species variant of Royle-Nichols (RN) occupancy model JAGS code adapted from Li et al. (2018). For goodness-of-fit, see Supplementary Fig. 1.

```
#The 7-day pooled observation data are 3-dimensional, i.e. Station × Species ×
Count.
#The camera trap station data are 7-dimensional, i.e. Station × Days × Elevation
× HumanDisturbance
#y= a 2-D Station × Species matrix of detection counts
#N= number of observed species
#J= number of camera stations
#k= number of occasions each camera was operating (round(Station$Days/7))
#human=scale(Station$HumanDisturbance)
#elevation=scale(Station$Elevation)

#Specify the data
occ.data = list(N=N, J=J, k=as.numeric(k),
y=y,human=as.numeric(human),elev=as.numeric(elevation))
#Specify the parameters to be monitored
occ.params =
c("a", "b", 'u', 'v', "mu.human", 'mu.elev', 'mu.p.human', 'beta1', 'beta2', 'eta',
'fit', 'fit.new')
# initial values
inits <- function() { list(
                                psi.mean=runif(1), p.mean=runif(1),
mu.a=matrix(rbinom(nspecies*J,size=1,prob=1),nrow=J,ncol=nspecies))
}
#Specify the number of chains, number of iterations...
nc=3
ni=100000
nb=80000
nthin=20

# BUGS model
modelFilename = "smsom.txt"          #Static multi-species occupancy models

cat("
model {
# Priors for community-level parameters
psi.mean ~ dunif(0,1)
a <- log(psi.mean) - log(1-psi.mean)
p.mean ~ dunif(0,1)
b <- log(p.mean) - log(1-p.mean)
mu.human~dnorm(0,0.001)
mu.elev~dnorm(0,0.001)
mu.p.human~dnorm(0,0.001)
tau.a~dgamma(0.1,0.1)
tau.b~dgamma(0.1,0.1)
tau.human~dgamma(0.1,0.1)
tau.p.human~dgamma(0.1,0.1)
tau.elev~dgamma(0.1,0.1)

# Likelihood
for (i in 1:N) {
# occupancy
u[i] ~ dnorm(a, tau.a)
```

```

beta1[i]~dnorm(mu.human,tau.human)
beta2[i]~dnorm(mu.elev,tau.elev)
# detectability
v[i] ~ dnorm(b, tau.b)
eta[i]~dnorm(mu.p.human,tau.p.human)

for (j in 1:J){
#Poisson model for abundance
log(lambda[j,i]) <- u[i]+beta1[i]*human[j]+beta2[i]*elev[j]
mu.a[j,i]~dpois(lambda[j,i]) #Abundance if species is present
Z[j,i]<-step(mu.a[j,i]-1)      #Occupancy

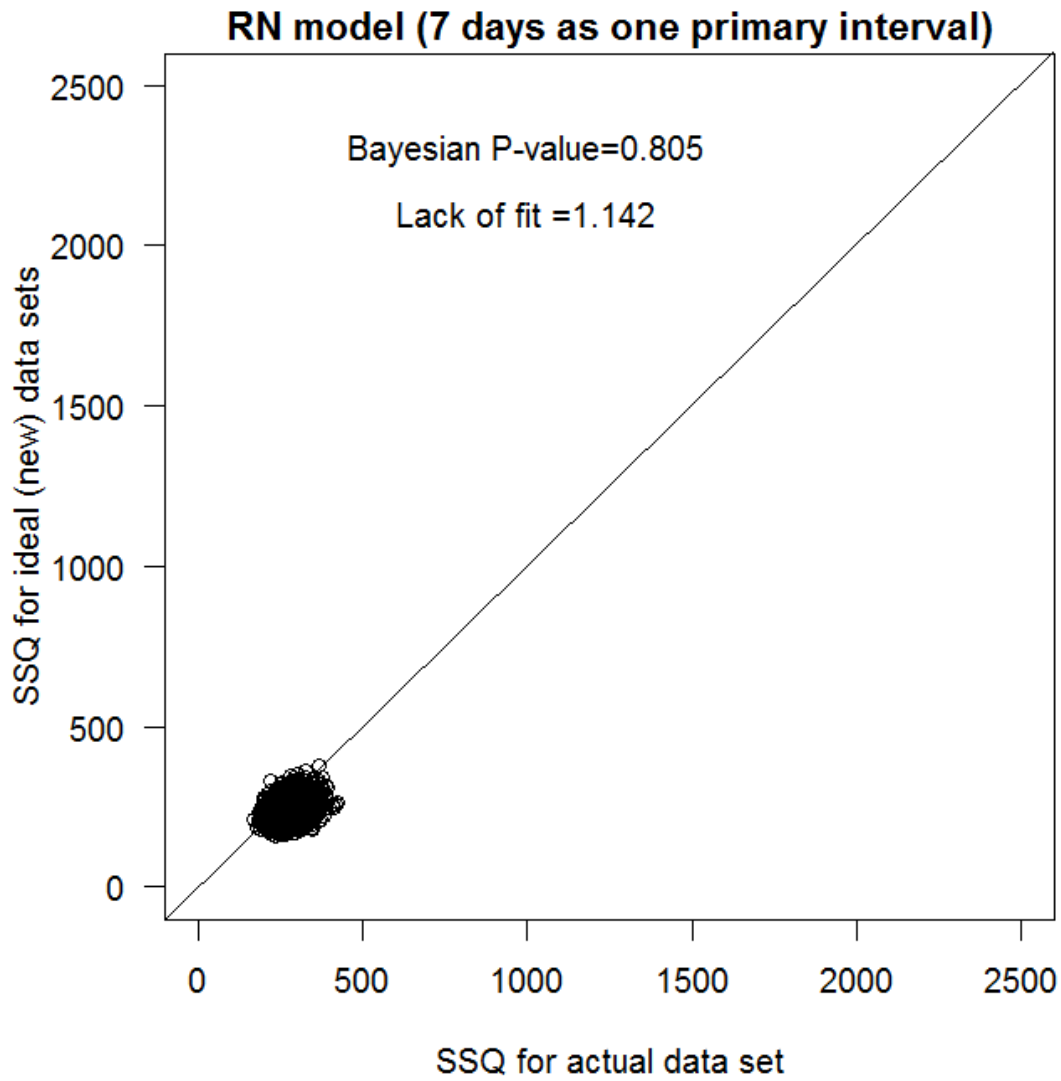
#Logistic model for detection
logit(p[j,i]) <- v[i]+eta[i]*human[j]
mu.p[j,i] <- 1-pow(1-p[j,i],mu.a[j,i])
y[j,i] ~ dbin(mu.p[j,i],k[j])

#Create simulated dataset to calculate the Bayesian p-value
ynew[j,i] ~ dbin(mu.p[j,i],k[j])
#Pearson residuals
d[j,i]<- (y[j,i] - mu.p[j,i]*k[j])/sqrt((mu.p[j,i]+0.001)*k[j]*(1-
mu.p[j,i]-0.001))
dnew[j,i]<- (ynew[j,i]-mu.p[j,i]*k[j])/sqrt((mu.p[j,i]+0.001)*k[j]*(1-
mu.p[j,i]-0.001))
sq[j,i]<- pow(d[j,i],2)
sq.new[j,i]<- pow(dnew[j,i],2)}
fit<-sum(sq[1:J,1:N])
fit.new<-sum(sq.new[1:J,1:N])
test<-step(fit.new-fit)
bpvalue<-mean(test)
}
", fill=TRUE, file=modelFilename)

output<-
jags(data=occ.data,inits=inits,parameters.to.save=occ.params,model.file="smsom.t
xt", n.chains=nc,n.iter=ni,n.burnin=nb,n.thin=nthin)

```

# GOODNESS OF FIT



SUPPLEMENTARY FIG. 1 Graphical posterior predictive check of the model adequacy for the RN model

SUPPLEMENTARY MATERIAL 2 Per individual detection probabilities, occupancy, and IUCN and China Red List status for the species detected with camera-trap surveys in Medog, Tibet. This is a comma separated values file available in the Supplementary materials section at [doi.org/10.1017/S0030605319001467](https://doi.org/10.1017/S0030605319001467).