**Co-occurrence of snow leopard *Panthera uncia*, Siberian ibex *Capra sibirica* and livestock: potential relationships and effects**

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Supplementary Material 1 Model formulation and parameter constraints applied to fit the two scenarios, and model fitting procedures

The latent binary variable , with *i* = {LI,IB,SL} for livestock, ibex, and snow leopard, respectively, and probability of occurrence , indicates whether species *i* was present () or absent () from site *j* (with *j* = 1, …, *J* = 49 camera trap stations). Livestock occurrence probability was modelled as a function of elevation (‘elev’):

where the average occurrence probability is , where expit is the inverse-logit function. Ibex occurrence was assumed to depend on the occurrence of livestock, with an additional effect of distance of site *j* to herders’ houses and camps, as a proxy of anthropic disturbance (‘dist’):

logit() = + (1 - ) + dist*j*

where is the conditional average probability of ibex occurrence given that livestock is present, and is the conditional average probability of ibex occurrence given that livestock is absent. The full linear predictor for snow leopard occurrence, i.e. the one that explicitly account for co-occurrence with both livestock and ibex, in addition to the effect of previous mentioned covariates, was as follows:

logit() = + (1 - ) +

(1 - ) + (1 - ) (1 - ) +

elev*j* + dist*j*

where is the conditional average probability of snow leopard occurrence given that livestock and ibex are present, is the conditional average probability of snow leopard occurrence given that livestock is absent and ibex is present, is the conditional average probability of snow leopard occurrence given that livestock is present and ibex is absent, and is the conditional average probability of snow leopard occurrence given that livestock and ibex are absent. The two scenarios where expressed by specifying the following constraints: (scenario 1) snow leopard occurrence depends on livestock occurrence only, =

= and = = ; (scenario 2) snow leopard occurrence depends on ibex occurrence only, = = and = = .

In the encounter model, the observations were , for species *i*, site *j* and sampling occasion (day) *k*, with *k* = 1, …, *K* and *K* ranging from 25 to 68 days (median 46) between sites, where if species *i* was detected at site *j* in sampling occasion *k*, and if the species was not encountered. The site totals were modeled as , where encounter probability was modeled differently for each species. Livestock encounter probability was assumed to be constant and independent of occurrence of other species, , with average encounter probability . Ibex encounter probability was tested for an effect of distance to herders’ houses and camps (‘dist’):

logit() = + (1 - ) + dist*j*

where is the conditional probability that ibex is encountered given that livestock is present, and is the conditional probability that ibex is encountered given that livestock is absent. In our case, due to data paucity, we fixed average ibex encounter probability independent of livestock presence, i.e. . The full linear predictor for snow leopard encounter probability was as follows:

logit() = + (1 - ) +

(1 - ) + (1 - ) (1 - ) + dist*j*

where average encounter probability was differently constrained under the two scenarios: (scenario 1) snow leopard encounter probability depended on whether livestock was present, =

= and = = ; (scenario 2) snow leopard encounter probability was independent of whether livestock and ibex were present, i.e. = = = = . Note that snow leopard encounter probability was a function of distance to herders’ houses and camps.

Models were fitted using the Markov chain Monte Carlo (MCMC) framework We used Normal (0,100) prior distributions for , , and parameters and Uniform(0,1) prior distributions for all parameters. Summaries of the posterior distribution generated from a three Markov chains initialized with random starting values, run for 15,000 iterations after a 2,000 burn-in, and without thinning. The diagnostics (Brooks 1998) used to assess convergence was <1.006 for all parameters.

**Reference**

Brooks, S.P. & Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics* 7, 434–455.

Supplementary Material 2 R and JAGS model code to fit the co-occurrence occupancy models for the two scenarios.

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### Co-occurrence model for scenario 1

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# Legend:

#DOM = livestock

#UNG = ibex

#LEO = snow leopard

# BUGS model

modelFileName = 'model\_LEO\_covs.txt'

cat("

model {

### PRIORS FOR OCCUPANCY PARAMETERS

# Livestock

mean.psi.DOM ~ dunif(0,1)

mu.psi.DOM <- log(mean.psi.DOM) - log(1-mean.psi.DOM)

# Ibex

psi.UNG\_withDOM ~ dunif(0,1)

psi.UNG\_withoutDOM ~ dunif(0,1)

mu.psi.UNG\_withDOM <- log(psi.UNG\_withDOM) - log(1-psi.UNG\_withDOM)

mu.psi.UNG\_withoutDOM <- log(psi.UNG\_withoutDOM) - log(1-psi.UNG\_withoutDOM)

# Snow leopard

psi.LEO\_withDOM\_withUNG <- equal.psi.LEO\_withDOM

psi.LEO\_withoutDOM\_withUNG <- equal.psi.LEO\_withoutDOM

psi.LEO\_withDOM\_withoutUNG <- equal.psi.LEO\_withDOM

psi.LEO\_withoutDOM\_withoutUNG <- equal.psi.LEO\_withoutDOM

equal.psi.LEO\_withDOM ~ dunif(0,1)

equal.psi.LEO\_withoutDOM ~ dunif(0,1)

mu.psi.LEO\_withDOM\_withUNG <- log(psi.LEO\_withDOM\_withUNG) - log(1-psi.LEO\_withDOM\_withUNG)

mu.psi.LEO\_withoutDOM\_withUNG <- log(psi.LEO\_withoutDOM\_withUNG) - log(1-psi.LEO\_withoutDOM\_withUNG)

mu.psi.LEO\_withDOM\_withoutUNG <- log(psi.LEO\_withDOM\_withoutUNG) - log(1-psi.LEO\_withDOM\_withoutUNG)

mu.psi.LEO\_withoutDOM\_withoutUNG <- log(psi.LEO\_withoutDOM\_withoutUNG) - log(1-psi.LEO\_withoutDOM\_withoutUNG)

### PRIORS FOR DETECTION PARAMETERS

# Livestock

mean.p.DOM ~ dunif(0,1)

mu.p.DOM <- log(mean.p.DOM) - log(1-mean.p.DOM)

# Ibex

mean.p.UNG\_withDOM <- equal.p.UNG

mean.p.UNG\_withoutDOM <- equal.p.UNG

equal.p.UNG ~ dunif(0,1)

mu.p.UNG\_withDOM <- log(mean.p.UNG\_withDOM) - log(1-mean.p.UNG\_withDOM)

mu.p.UNG\_withoutDOM <- log(mean.p.UNG\_withoutDOM) - log(1-mean.p.UNG\_withoutDOM)

# Snow leopard

mean.p.LEO\_withDOM\_withUNG <- equal.p.LEO\_withDOM

mean.p.LEO\_withoutDOM\_withUNG <- equal.p.LEO\_withoutDOM

mean.p.LEO\_withDOM\_withoutUNG <- equal.p.LEO\_withDOM

mean.p.LEO\_withoutDOM\_withoutUNG <- equal.p.LEO\_withoutDOM

equal.p.LEO\_withDOM ~ dunif(0,1)

equal.p.LEO\_withoutDOM ~ dunif(0,1)

mu.p.LEO\_withDOM\_withUNG <- log(mean.p.LEO\_withDOM\_withUNG) - log(1-mean.p.LEO\_withDOM\_withUNG)

mu.p.LEO\_withoutDOM\_withUNG <- log(mean.p.LEO\_withoutDOM\_withUNG) - log(1-mean.p.LEO\_withoutDOM\_withUNG)

mu.p.LEO\_withDOM\_withoutUNG <- log(mean.p.LEO\_withDOM\_withoutUNG) - log(1-mean.p.LEO\_withDOM\_withoutUNG)

mu.p.LEO\_withoutDOM\_withoutUNG <- log(mean.p.LEO\_withoutDOM\_withoutUNG) - log(1-mean.p.LEO\_withoutDOM\_withoutUNG)

### PRIORS FOR SLOPES

# occurrence

beta.psi.DOM.elev ~ dnorm(0,0.01)

beta.psi.DOM.dist ~ dnorm(0,0.01)

beta.psi.UNG.dist ~ dnorm(0,0.01)

beta.psi.LEO.elev ~ dnorm(0,0.01)

beta.psi.LEO.dist ~ dnorm(0,0.01)

# detectability

beta.p.UNG.dist ~ dnorm(0,0.01)

beta.p.LEO.dist ~ dnorm(0,0.01)

# MODEL OF OCCURRENCES

for (i in 1:nsites) {

# Livestock

psi.DOM.def[i] <- ifelse(DOM.limits[i]==1,psi.DOM[i],0)

z.DOM[i] ~ dbern(psi.DOM.def[i])

logit(psi.DOM[i]) <- mu.psi.DOM + beta.psi.DOM.elev \* elev[i] + beta.psi.DOM.dist \* dist[i]

# Ibex

z.UNG[i] ~ dbern(psi.UNG.def[i])

logit(psi.UNG.def[i]) <- z.DOM[i] \* mu.psi.UNG\_withDOM + (1-z.DOM[i]) \* mu.psi.UNG\_withoutDOM +

beta.psi.UNG.dist \* dist[i]

# Snow leopard

z.LEO[i] ~ dbern(psi.LEO.def[i])

logit(psi.LEO.def[i]) <- z.DOM[i] \* z.UNG[i] \* mu.psi.LEO\_withDOM\_withUNG +

(1-z.DOM[i]) \* z.UNG[i] \* mu.psi.LEO\_withoutDOM\_withUNG +

z.DOM[i] \* (1-z.UNG[i]) \* mu.psi.LEO\_withDOM\_withoutUNG +

(1-z.DOM[i]) \* (1-z.UNG[i]) \* mu.psi.LEO\_withoutDOM\_withoutUNG +

beta.psi.LEO.elev \* elev[i] + beta.psi.LEO.dist \* dist[i]

}

# MODEL OF DETECTIONS

for (i in 1:nsites) {

# Livestock

y\_DOM[i] ~ dbinom(p.DOM.def[i],K[i])

p.DOM.def[i] <- z.DOM[i] \* p.DOM[i]

logit(p.DOM[i]) <- mu.p.DOM

# Ibex

y\_UNG[i] ~ dbinom(p.UNG.def[i],K[i])

p.UNG.def[i] <- z.UNG[i] \* p.UNG[i]

logit(p.UNG[i]) <- mu.p.UNG\_withDOM \* z.DOM[i] + mu.p.UNG\_withoutDOM \* (1-z.DOM[i]) +

beta.p.UNG.dist \* dist[i]

# Snow leopard

y\_LEO[i] ~ dbinom(p.LEO.def[i],K[i])

p.LEO.def[i] <- z.LEO[i] \* p.LEO[i]

logit(p.LEO[i]) <- mu.p.LEO\_withDOM\_withUNG \* z.DOM[i] \* z.UNG[i] +

mu.p.LEO\_withoutDOM\_withUNG \* (1-z.DOM[i]) \* z.UNG[i] +

mu.p.LEO\_withDOM\_withoutUNG \* z.DOM[i] \* (1-z.UNG[i]) +

mu.p.LEO\_withoutDOM\_withoutUNG \* (1-z.DOM[i]) \* (1-z.UNG[i]) +

beta.p.LEO.dist \* dist[i]

}

}", fill=TRUE, file=modelFileName)

# data

bugs.data <- list(nsites=nsites,y\_DOM=y\_DOM,y\_UNG=y\_UNG,y\_LEO=y\_LEO,K=K,DOM.limits=DOM.limits,

elev=covs\_st$El,dist=covs\_st$Dis

)

# data structure

#str(bugs.data)

#List of 8

# $ nsites : int 49

# $ y\_DOM : num [1:49] 13 11 1 31 1 15 6 1 14 0 ...

# $ y\_UNG : num [1:49] 0 0 0 0 0 0 0 0 0 0 ...

# $ y\_LEO : num [1:49] 0 3 0 25 0 5 0 0 5 0 ...

# $ K : int [1:49] 44 43 43 44 44 44 43 43 42 47 ...

# $ DOM.limits: num [1:49] 1 1 1 1 1 1 1 1 1 0 ...

# $ elev : num [1:49] -1.3941 -0.7505 0.0895 -1.07 -0.5587 ...

# $ dist : num [1:49] -1.0264 -0.6178 -0.1643 -0.3798 0.0871 ...

# Legend:

#nsites = number of sites

#y\_DOM, y\_UNG, y\_LEO = species-specific detection frequences

#K = site-specific number of sampling occasions (days)

#DOM.limits = site accessability for livestock (0=not accessible, 1=accessible)

#elev = standardized site elevation

#dist = standardized distance to herder’s houses and camps

# initial values

inits <- function() {list(mean.psi.DOM=runif(1,0.5,1),

psi.UNG\_withDOM=runif(1,0.5,1),psi.UNG\_withoutDOM=runif(1,0.5,1),

psi.LEO\_withDOM\_withUNG=runif(1,0.5,1),psi.LEO\_withoutDOM\_withUNG=runif(1,0.5,1),

psi.LEO\_withDOM\_withoutUNG=runif(1,0.5,1),psi.LEO\_withoutDOM\_withoutUNG=runif(1,0.5,1),

mean.p.DOM=runif(1,0.5,1),equal.p.UNG=runif(1,0.5,1),

equal.p.LEO\_withDOM=runif(1,0.5,1),equal.p.LEO\_withoutDOM=runif(1,0.5,1),

beta.psi.DOM.elev=runif(1,-1,1),beta.psi.DOM.dist=runif(1,-1,1),

beta.psi.UNG.dist=runif(1,-1,1),

beta.psi.LEO.elev=runif(1,-1,1),beta.psi.LEO.dist=runif(1,-1,1),

beta.p.UNG.dist=runif(1,-1,1),beta.p.LEO.dist=runif(1,-1,1),

z.DOM=DOM.limits,z.UNG=rep(1,length(y\_DOM)),z.LEO=rep(1,length(y\_DOM))

)

}

# parameters to monitor

parameters<-c("mean.psi.DOM","psi.UNG\_withDOM","psi.UNG\_withoutDOM",

"equal.psi.LEO\_withDOM","equal.psi.LEO\_withoutDOM",

"mean.p.DOM","equal.p.UNG",

"equal.p.LEO\_withDOM","equal.p.LEO\_withoutDOM",

"beta.psi.DOM.elev","beta.psi.DOM.dist","beta.psi.UNG.dist","beta.psi.LEO.elev","beta.psi.LEO.dist",

"beta.p.UNG.dist","beta.p.LEO.dist"

)

# MCMC settings

n.adapt <- 1000

n.burnin <- 2000

n.iter <- 15000

thin <- 1

chains <- 3

# run the model for scenario 1

out <- jags(data = bugs.data,

inits = inits,

parameters.to.save = parameters,

model.file = "model\_LEO\_covs.txt",

n.chains = chains,

n.adapt = n.adapt,

n.iter = n.iter,

n.burnin = n.burnin,

n.thin = thin,seed=2446,

parallel=T)

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### Co-occurrence model for scenario 2

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# Legend:

#DOM = livestock

#UNG = ibex

#LEO = snow leopard

# BUGS model

modelFileName = 'model\_LEO\_covs\_sc3a.txt'

cat("

model {

### PRIORS FOR OCCUPANCY PARAMETERS

# Livestock

mean.psi.DOM ~ dunif(0,1)

mu.psi.DOM <- log(mean.psi.DOM) - log(1-mean.psi.DOM)

# Ibex

psi.UNG\_withDOM ~ dunif(0,1)

psi.UNG\_withoutDOM ~ dunif(0,1)

mu.psi.UNG\_withDOM <- log(psi.UNG\_withDOM) - log(1-psi.UNG\_withDOM)

mu.psi.UNG\_withoutDOM <- log(psi.UNG\_withoutDOM) - log(1-psi.UNG\_withoutDOM)

# Snow leopard

psi.LEO\_withDOM\_withUNG <- equal.psi.LEO\_withUNG

psi.LEO\_withoutDOM\_withUNG <- equal.psi.LEO\_withUNG

psi.LEO\_withDOM\_withoutUNG <- equal.psi.LEO\_withoutUNG

psi.LEO\_withoutDOM\_withoutUNG <- equal.psi.LEO\_withoutUNG

equal.psi.LEO\_withUNG ~ dunif(0,1)

equal.psi.LEO\_withoutUNG ~ dunif(0,1)

mu.psi.LEO\_withDOM\_withUNG <- log(psi.LEO\_withDOM\_withUNG) - log(1-psi.LEO\_withDOM\_withUNG)

mu.psi.LEO\_withoutDOM\_withUNG <- log(psi.LEO\_withoutDOM\_withUNG) - log(1-psi.LEO\_withoutDOM\_withUNG)

mu.psi.LEO\_withDOM\_withoutUNG <- log(psi.LEO\_withDOM\_withoutUNG) - log(1-psi.LEO\_withDOM\_withoutUNG)

mu.psi.LEO\_withoutDOM\_withoutUNG <- log(psi.LEO\_withoutDOM\_withoutUNG) - log(1-psi.LEO\_withoutDOM\_withoutUNG)

### PRIORS FOR DETECTION PARAMETERS

# Livestock

mean.p.DOM ~ dunif(0,1)

mu.p.DOM <- log(mean.p.DOM) - log(1-mean.p.DOM)

# Ibex

mean.p.UNG\_withDOM <- equal.p.UNG

mean.p.UNG\_withoutDOM <- equal.p.UNG

equal.p.UNG ~ dunif(0,1)

mu.p.UNG\_withDOM <- log(mean.p.UNG\_withDOM) - log(1-mean.p.UNG\_withDOM)

mu.p.UNG\_withoutDOM <- log(mean.p.UNG\_withoutDOM) - log(1-mean.p.UNG\_withoutDOM)

# Snow leopard

mean.p.LEO\_withDOM\_withUNG <- equal.p.LEO

mean.p.LEO\_withoutDOM\_withUNG <- equal.p.LEO

mean.p.LEO\_withDOM\_withoutUNG <- equal.p.LEO

mean.p.LEO\_withoutDOM\_withoutUNG <- equal.p.LEO

equal.p.LEO ~ dunif(0,1)

mu.p.LEO\_withDOM\_withUNG <- log(mean.p.LEO\_withDOM\_withUNG) - log(1-mean.p.LEO\_withDOM\_withUNG)

mu.p.LEO\_withoutDOM\_withUNG <- log(mean.p.LEO\_withoutDOM\_withUNG) - log(1-mean.p.LEO\_withoutDOM\_withUNG)

mu.p.LEO\_withDOM\_withoutUNG <- log(mean.p.LEO\_withDOM\_withoutUNG) - log(1-mean.p.LEO\_withDOM\_withoutUNG)

mu.p.LEO\_withoutDOM\_withoutUNG <- log(mean.p.LEO\_withoutDOM\_withoutUNG) - log(1-mean.p.LEO\_withoutDOM\_withoutUNG)

### PRIORS FOR SLOPES

beta.psi.DOM.elev ~ dnorm(0,0.01)

beta.psi.DOM.dist ~ dnorm(0,0.01)

beta.psi.UNG.dist ~ dnorm(0,0.01)

beta.psi.LEO.elev ~ dnorm(0,0.01)

beta.psi.LEO.dist ~ dnorm(0,0.01)

beta.p.UNG.dist ~ dnorm(0,0.01)

beta.p.LEO.dist ~ dnorm(0,0.01)

# MODEL OF OCCURRENCES

for (i in 1:nsites) {

# Livestock

psi.DOM.def[i] <- ifelse(DOM.limits[i]==1,psi.DOM[i],0)

z.DOM[i] ~ dbern(psi.DOM.def[i])

logit(psi.DOM[i]) <- mu.psi.DOM + beta.psi.DOM.elev \* elev[i] + beta.psi.DOM.dist \* dist[i]

# Ibex

z.UNG[i] ~ dbern(psi.UNG.def[i])

logit(psi.UNG.def[i]) <- z.DOM[i] \* mu.psi.UNG\_withDOM + (1-z.DOM[i]) \* mu.psi.UNG\_withoutDOM +

beta.psi.UNG.dist \* dist[i]

# Snow leopard

z.LEO[i] ~ dbern(psi.LEO.def[i])

logit(psi.LEO.def[i]) <- z.DOM[i] \* z.UNG[i] \* mu.psi.LEO\_withDOM\_withUNG +

(1-z.DOM[i]) \* z.UNG[i] \* mu.psi.LEO\_withoutDOM\_withUNG +

z.DOM[i] \* (1-z.UNG[i]) \* mu.psi.LEO\_withDOM\_withoutUNG +

(1-z.DOM[i]) \* (1-z.UNG[i]) \* mu.psi.LEO\_withoutDOM\_withoutUNG +

beta.psi.LEO.elev \* elev[i] + beta.psi.LEO.dist \* dist[i]

}

# MODEL OF DETECTIONS

for (i in 1:nsites) {

# Livestock

y\_DOM[i] ~ dbinom(p.DOM.def[i],K[i])

p.DOM.def[i] <- z.DOM[i] \* p.DOM[i]

logit(p.DOM[i]) <- mu.p.DOM

# Ibex

y\_UNG[i] ~ dbinom(p.UNG.def[i],K[i])

p.UNG.def[i] <- z.UNG[i] \* p.UNG[i]

logit(p.UNG[i]) <- mu.p.UNG\_withDOM \* z.DOM[i] + mu.p.UNG\_withoutDOM \* (1-z.DOM[i]) +

beta.p.UNG.dist \* dist[i]

# Snow leopard

y\_LEO[i] ~ dbinom(p.LEO.def[i],K[i])

p.LEO.def[i] <- z.LEO[i] \* p.LEO[i]

logit(p.LEO[i]) <- mu.p.LEO\_withDOM\_withUNG \* z.DOM[i] \* z.UNG[i] +

mu.p.LEO\_withoutDOM\_withUNG \* (1-z.DOM[i]) \* z.UNG[i] +

mu.p.LEO\_withDOM\_withoutUNG \* z.DOM[i] \* (1-z.UNG[i]) +

mu.p.LEO\_withoutDOM\_withoutUNG \* (1-z.DOM[i]) \* (1-z.UNG[i]) +

beta.p.LEO.dist \* dist[i]

}

}", fill=TRUE, file=modelFileName)

# data

bugs.data <- list(nsites=nsites,y\_DOM=y\_DOM,y\_UNG=y\_UNG,y\_LEO=y\_LEO,K=K,DOM.limits=DOM.limits,

elev=covs\_st$El,dist=covs\_st$Dis

)

# data structure

#str(bugs.data)

#List of 8

# $ nsites : int 49

# $ y\_DOM : num [1:49] 13 11 1 31 1 15 6 1 14 0 ...

# $ y\_UNG : num [1:49] 0 0 0 0 0 0 0 0 0 0 ...

# $ y\_LEO : num [1:49] 0 3 0 25 0 5 0 0 5 0 ...

# $ K : int [1:49] 44 43 43 44 44 44 43 43 42 47 ...

# $ DOM.limits: num [1:49] 1 1 1 1 1 1 1 1 1 0 ...

# $ elev : num [1:49] -1.3941 -0.7505 0.0895 -1.07 -0.5587 ...

# $ dist : num [1:49] -1.0264 -0.6178 -0.1643 -0.3798 0.0871 ...

# Legend:

#nsites = number of sites

#y\_DOM, y\_UNG, y\_LEO = species-specific detection frequences

#K = site-specific number of sampling occasions (days)

#DOM.limits = site accessability for livestock (0=not accessible, 1=accessible)

#elev = standardized site elevation

#dist = standardized distance to herder’s houses and camps

# intial values

inits <- function() {list(mean.psi.DOM=runif(1,0.5,1),

psi.UNG\_withDOM=runif(1,0.5,1),psi.UNG\_withoutDOM=runif(1,0.5,1),

equal.psi.LEO\_withUNG=runif(1,0.1,0.2),equal.psi.LEO\_withoutUNG=runif(1,0.3,0.5),

mean.p.DOM=runif(1,0.5,1),equal.p.UNG=runif(1,0.5,1),

equal.p.LEO=runif(1,0.08,0.1),

beta.psi.DOM.elev=runif(1,-1,1),beta.psi.DOM.dist=runif(1,-1,1),

beta.psi.UNG.dist=runif(1,-1,1),

beta.psi.LEO.elev=runif(1,-1,1),beta.psi.LEO.dist=runif(1,-1,1),

beta.p.UNG.dist=runif(1,-1,1),beta.p.LEO.dist=runif(1,-1,1),

z.DOM=DOM.limits,z.UNG=rep(1,length(y\_DOM)),z.LEO=rep(1,length(y\_DOM))

)

}

# parameters to monitor

parameters<-c("mean.psi.DOM","psi.UNG\_withDOM","psi.UNG\_withoutDOM",

"equal.psi.LEO\_withUNG","equal.psi.LEO\_withoutUNG",

"mean.p.DOM","equal.p.UNG",

"equal.p.LEO",

"beta.psi.DOM.elev","beta.psi.DOM.dist","beta.psi.UNG.dist","beta.psi.LEO.elev","beta.psi.LEO.dist",

"beta.p.UNG.dist","beta.p.LEO.dist"

)

# MCMC settings

n.adapt <- 1000

n.burnin <- 2000

n.iter <- 15000

thin <- 1

chains <- 3

# run the model for scenario 1

out <- jags(data = bugs.data,

inits = inits,

parameters.to.save = parameters,

model.file = "model\_LEO\_covs\_sc3a.txt",

n.chains = chains,

n.adapt = n.adapt,

n.iter = n.iter,

n.burnin = n.burnin,

n.thin = thin,

parallel=T)

## End of code

Supplementary Figure 1 Posterior (solid line) and prior (dashed line) parameter distribution for each parameter estimated under the first scenario.

Supplementary Figure 2 Posterior (solid line) and prior (dashed line) parameter distribution for each parameter estimated under the second scenario.

Supplementary Table 1 Wild mammals and other species detected by camera trapping, with raw indices of capture, ordered by decreasing naïve occupancy

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Species | No. of photographs | No. of events | Relative abundance index | Naïve occupancy |
| **Wild mammals** | | | | |
| Red fox *Vulpes vulpes* | 85 | 81 | 3.64 | 0.69 |
| Siberian marmot *Marmota sibirica* | 354 | 276 | 12.40 | 0.49 |
| Snow leopard *Panthera uncia* | 17 | 14 | 0.63 | 0.27 |
| Siberian ibex *Capra sibirica* | 88 | 33 | 1.48 | 0.18 |
| Pallas' cat *Otocolobus manul* | 11 | 11 | 0.49 | 0.18 |
| Wolf *Canis lupus* | 28 | 10 | 0.45 | 0.16 |
| Beech marten *Martes foina* | 10 | 10 | 0.45 | 0.16 |
| Steppe polecat *Mustela eversmanii* | 27 | 25 | 1.12 | 0.16 |
| Arctic hare *Lepus timidus* | 19 | 18 | 0.81 | 0.12 |
| Wolverine *Gulo gulo* | 6 | 6 | 0.27 | 0.12 |
| Pika *Pika* spp*.* | 14 | 9 | 0.40 | 0.02 |
| Red squirrel *Sciurus vulgaris* | 1 | 1 | 0.04 | 0.02 |
| **Domestic mammals & people** | | | | |
| Goats | 940 | 138 | 6.20 | 0.29 |
| Cattle and yaks | 397 | 163 | 7.33 | 0.27 |
| Sheep | 226 | 50 | 2.25 | 0.24 |
| Horses | 83 | 50 | 2.25 | 0.22 |
| Dogs | 28 | 28 | 1.26 | 0.20 |
| Camels | 11 | 11 | 0.49 | 0.04 |
| All domestic animals | 1685 | 367 | 16.49 | 0.43 |
| People | 195 | 105 | 4.72 | 0.35 |