**Notes S1** R code for hierarchical Bayesian models estimating the effects of functional traits on extinction risk, fit via JAGS using the R2jags library.

#Inputs (all standardized) for binary and ordinal models

#specified in BUGS syntax:

#functional traits

size #(log) female body size

mean.flight.month #average month of flight activity

duration.of.activity #average duration of flight activity

pollen.specialisation #vector of 1=oligolectic 0=polylectic/mesolectic/cuckoo

nest.location #vector of 1=ground-nesting; 0=air nesting/cuckoo

sociality #vector of 1=solitary; 0=social/cuckoo

#habitat preferences

altitude #(log) mean altitudinal distribution

habitat.breadth #habitat breadth (number of occupied habitat types [1–6])

urban.areas #vector of 1=occurrence in urban areas; 0=no occurrence

hedgerows #vector of 1=occurrence in hedgerows and field edges; 0=no occurrence

wasteland #vector of 1=occurrence in wasteland and ruderal sites; 0=no occurrence

meadows #vector of 1=occurrence in meadows; 0=no occurrence

raw.soil #vector of 1=occurrence in raw-soil sites; 0=no occurrence

forest #vector of 1=occurrence in forests; 0=no occurrence

#taxonomic information

N.spp = 428 #number of species with information on Red List status

N.spp = 445 #number of species with information on abundance status

N.spp = 404 #number of species with information on population trends

N.genus = 37 #number of genera

N.family = 6 #number of families

genus #genus categories

family #family categories

#Binary model

#Additional input

response

#either extinction risk (Red List status) vector of 1=threatened; 0=not threatened

#population trend vector of 1=decrease; 0=no change or increase

#or abundance vector of 1=rare (occasional to extinct); 0=abundant to frequent

mod <- "model

{

#fixed effect components from Fig. S2, with corresponding betas (b)

for(i in 1:N.spp) { #loop over observations (species)

response[i] ~ dbern(p.binary[i])

logit(p.binary[i]) <- b0 #intercept term

+ b3\*size[i] + b2\*mean.flight.month[i]

+ b1\*duration.of.activity[i] + b4\*pollen.specialisation[i]

+ b6\*nest.location[i] + b5\*sociality[i] + b10\*altitude[i]

+ b7\*habitat.breadth[i] + b8\*urban.areas[i]

+ b9\*hedgerows[i] + b11\*wasteland[i] + b12\*meadows[i]

+ b13\*raw.soil[i] + b14\*forest[i] #fixed effects

+ b.genus[genus[i]] #genus random effect

+ b.family[family[i]] } #family random effect

#Genus random effect

for(i in 1:N.genus) {

b.genus[i] ~ dnorm(0, genus.tau)}

#Family random effect

for(i in 1:N.family) {

b.family[i] ~ dnorm(0, family.tau)}

##Priors

#Genus random effect priors

genus.tau <- genus.sigma^-2

genus.sigma ~ dunif(0, 100)

#Family random effect priors

family.tau <- family.sigma^-2

family.sigma ~ dunif(0, 100)

#prior for overall intercept

b0 ~ dnorm(0,0.0001)

#non-informative priors for fixed effects (mean=0, var=1000)

for(i in 1:14) {b[i] ~ dnorm(0,0.0001)}

}" #end model

#Ordinal model

#Additional input:

response

#either ordinal vector of Red List status: 1=not threatened; 2=near-threatened;

#3=threatened; 4=highly threatened; 5=almost extinct; 6=extinct

#ordinal vector of population trend: 1=increase; 2=no change; 3=small decline;

#4=decline; 5=large decline; 6=extinct

#or ordinal vector of abundance: 1=abundant; 2=common; 3=frequent;

#4=occasional; 5=rare; 6=extremely rare; 7=extinct

M=6 #maximum value of ordinal classes for extinction risk and population trend

M=7 #maximum value of ordinal classes for abundance

mod <- "model

{

#fixed effect components from Figs. 2a and S4, with corresponding betas (b)

for(i in 1:N.spp) { #loop over observations (species)

mu[i] <- b3\*size[i] + b2\*mean.flight.month[i] + b1\*duration.of.activity[i]

+ b4\*pollen.specialisation[i] + b6\*nest.location[i] + b5\*sociality[i]

+ b10\*altitude[i] + b7\*habitat.breadth[i] + b8\*urban.areas[i]

+ b9\*hedgerows[i] + b11\*wasteland[i] + b12\*meadows[i] + b13\*raw.soil[i]

+ b14\*forest[i] #fixed effects

+ b.genus[genus[i]] + b.family[family[i]] #genus + family random effects

## cumulative logistic probabilities: ordinal logit part from Jackman 2009

#M is the maximum value of classes(M=6)

logit(Q[i,1]) <- tau[1]-mu[i]

p[i,1] <- Q[i,1]

for(j in 2:M){

logit(Q[i,j]) <- tau[j]-mu[i]

p[i,j] <- Q[i,j] - Q[i,j-1]

}

p[i,(M+1)] <- 1 - Q[i,M]

response[i] ~ dcat(p[i,1:(M+1)]) ## p[i,] sums to 1 for each i

}

#genus random effect

for(i in 1:N.genus) {

b.genus[i] ~ dnorm(0, genus.tau)}

#family random effect

for(i in 1:N.family) {

b.family[i] ~ dnorm(0, family.tau)}

## ordinal logit thresholds

for(j in 1:M){

tau0[j] ~ dnorm(0, .01)

}

tau[1:M] <- sort(tau0)

##Priors

#genus random effect priors

genus.tau <- genus.sigma^-2

genus.sigma ~ dunif(0, 100)

#family random effect priors

family.tau <- family.sigma^-2

family.sigma ~ dunif(0, 100)

#non-informative priors for fixed effects (mean=0, var=1000)

for(i in 1:14) {b[i] ~ dnorm(0,0.0001)}

}" #end model