**Appendix S2.** Multi-Species, dynamic hierarchical model: R and BUGS code used to fit the model. R script with the JAGS model specification for multi-species hierarchical occupancy model with effect of grass height and grass cover on occupancy (Ψ), persistence (φ) and colonisation (γ) probabilities with additional effect of environment (cloud cover and wind) on detection probability (p).

###########################################################################

# Define model and write text file into R working directory

##################################################################################

sink (‘MultiSpeciesDynoccRandCovs3.txt’)

# this code writes the model text file for a multi-species model with random effects

# observability as a covariate on p; and avh and cover as covariates on psi, phi, and gamma

# psi, p, phi, and gamma are all time dependent

cat("

model {

# Specify priors and constraints

for (s in 1:nspecies){

for (i in 1:nsite) {

for (k in 1:(nyear)){

for (j in 1:nrep){

logit(p[i,j,k,s]) <- mu.p + betaobs \* obs[i,j,k] + eps.s[s]

} # j

} # k

logit(psi1[i,s]) <- max(-100, min(100, psi.temp[i,s]))

psi.temp[i,s] <- mu.psi[s] + betapsiavh[s] \* avh[i,1] + betapsicov[s] \* cover[i,1]

for (k in 1:(nyear-1)){

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logit(phi[i,k,s]) <- max(-100, min(100, phi.temp[i,k,s]))

# persistence depends on grass at t=k+1

phi.temp[i,k,s] <- mu.phi[s] + betaphiavh[s] \* avh[i,k+1] + betaphicov[s] \* cover[i,k+1]

logit(gamma[i,k,s]) <- max(-100, min(100, gamma.temp[i,k,s]))

gamma.temp[i,k,s] <- mu.gam[s] + betagamavh[s] \* avh[i,k+1] + betagamcov[s] \* cover[i,k+1] # colonisation depends on grass at t=k+1

} # k

} # i

} # s

for (s in 1:nspecies){

eps.s[s] ~ dnorm(0, tau.p)

mu.psi[s] ~ dnorm(mpsi, tau.psi)

mu.phi[s] ~ dnorm(mphi, tau.phi)

mu.gam[s] ~ dnorm(mgam, tau.gam)

betapsiavh[s] ~ dnorm(bpsiavh, tau.bpsiavh)

betaphiavh[s] ~ dnorm(bphiavh, tau.bphiavh)

betagamavh[s] ~ dnorm(bgamavh, tau.bgamavh)

betaphicov[s] ~ dnorm(bphicov, tau.bphicov)

betapsicov[s] ~ dnorm(bpsicov, tau.bpsicov)

betagamcov[s] ~ dnorm(bgamcov, tau.bgamcov)

}

# hyperpriors

mpsi ~ dnorm(0,0.01)

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tau.psi ~ dgamma(0.01,0.01) #<- pow(sd.psi, -2)

sig.psi <- pow(tau.psi, -1) #~ dunif(0,15)

mphi ~ dnorm(0,0.01)

tau.phi ~ dgamma(0.01,0.01) # <- pow(sd.phi, -2)

sig.phi <- pow(tau.phi, -1) # ~ dunif(0,15)

mgam ~ dnorm(0,0.01)

tau.gam ~ dgamma(0.01,0.01) # <- pow(sd.gam, -2)

sig.gam <- pow(tau.gam, -1) # ~ dunif(0,15)

bpsiavh ~ dnorm(0,0.01)

tau.bpsiavh ~ dgamma(0.01,0.01) # <- pow(sd.bpsiavh, -2)

sig.bpsiavh <- pow(tau.bpsiavh, -1) # ~ dunif(0,15)

bphiavh ~ dnorm(0,0.01)

tau.bphiavh ~ dgamma(0.01,0.01) # <- pow(sd.bphiavh, -2)

sig.bphiavh <- pow(tau.bphiavh, -1) # ~ dunif(0,15)

bgamavh ~ dnorm(0,0.01)

tau.bgamavh ~ dgamma(0.01,0.01) # <- pow(sd.bgamavh, -2)

sig.bgamavh <- pow(tau.bgamavh, -1) # ~ dunif(0,15)

bpsicov ~ dnorm(0,0.01)

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tau.bpsicov ~ dgamma(0.01,0.01) # <- pow(sd.bpsicov, -2)

sig.bpsicov <- pow(tau.bpsicov, -1) # ~ dunif(0,15)

bphicov ~ dnorm(0,0.01)

tau.bphicov ~ dgamma(0.01,0.01) # <- pow(sd.bphicov, -2)

sig.bphicov <- pow(tau.bphicov, -1) # ~ dunif(0,15)

bgamcov ~ dnorm(0,0.01)

tau.bgamcov ~ dgamma(0.01,0.01) # <- pow(sd.bgamcov, -2)

sig.bgamcov <- pow(tau.bgamcov, -1) # ~ dunif(0,15)

# let detection probability vary among species

mean.p ~ dunif(0, 1) # Prior for mean detection probability

mu.p <- log(mean.p / (1-mean.p)) # Logit transformation

sig.p <- pow(tau.p, -1) # ~ dunif(0, 10) # Prior for standard deviation

tau.p ~ dgamma(0.01,0.01) # <- pow(sigma.p, -2)

betaobs ~ dunif(-10,10)

# Ecological submodel: Define state conditional on parameters

for (s in 1:nspecies){

for (i in 1:nsite){

z[i,1,s] ~ dbern(psi1[i,s])

for (k in 2:nyear){

muZ[i,k,s]<- z[i,k-1,s]\*phi[i,k-1,s] + (1-z[i,k-1,s])\*gamma[i,k-1,s]

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z[i,k,s] ~ dbern(muZ[i,k,s])

} # k

} # i

} #s

# Observation model

for (s in 1:nspecies){

for (i in 1:nsite){

for (j in 1:nrep){

for (k in 1:nyear){

muy[i,j,k,s] <- z[i,k,s]\*p[i,j,k,s]

y[i,j,k,s] ~ dbern(muy[i,j,k,s])

} # k

} # j

} # i

} #s

# Derived parameters: Sample and population occupancy, growth rate and turnover

for (s in 1:nspecies){

# psi[1,s] <- psi1[s]

n.occ[1,s]<-sum(z[1:nsite,1,s])

for (k in 2:nyear){

# psi[k,s] <- psi[k-1,s]\*phi[k-1,s] + (1-psi[k-1,s])\*gamma[k-1,s]

n.occ[k,s] <- sum(z[1:nsite,k,s])

# growthr[k,s] <- psi[k,s]/psi[k-1,s]

# turnover[k-1,s] <- (1 - psi[k-1,s]) \* gamma[k-1,s]/psi[k,s]

} # k

} # s

for (i in 1:nsite) {

for (k in 1:nyear) {

srichness[k,i] <- sum(z[i,k,1:nspecies]) # species richness per site and season

} # k

for (s in 1:nspecies) {

sppres[i,s] <- min(sum(z[i,1:nyear,s]),1)

} # s

siterichness[i] <- sum(sppres[i, 1:nspecies]) # species richness per site

} # i

} # end of model

",fill = TRUE)

sink()