

## S1 Code

In this supporting information we provide the R-code and JAGS-code used to run the models in the main text. R-packages on which the analysis depends, are included at the start. The code used two pieces of data as provided in S1 Dataset and S2 dataset, being the biomass data and covariate data respectively.

```
# required libraries
library(R2jags)
# Function to standardize variables
standardize <- function(x,mu=mean(x),sig=sd(x)) (x-mu)/sig
# read the data
data <- read.table("S1_Dataset.csv",header=TRUE,sep=",")
model.frame<- read.table("S2_Dataset.csv",header=TRUE,sep=",")
summary(data)
summary(model.frame)
```

Below, for each of the seven models in Table 3 in the main text, we first create a dataset based on the two loaded datasets, write a JAGS model file, and run the model through JAGS.

## Null model

Setup the data for running the JAGS model:

```
jagsdataNull<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot))  
)
```

Write JAGS model file:

```
sink("NullModel.jag")  
cat("  
model{  
  for( i in 1:n){  
    m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
    tau[i] <- 1/Var[i]  
    Var[i] <- sum( vr[index1[i]:index2[i]] )  
  }  
  for(i in 1:ndaily){  
    y[i] <- exp(z[i])  
    z[i] <- int +  
    c[1]*daynr[i] + c[2]*daynr2[i]+  
    b[loctype[i]] +  
    eps[plot[i]]  
    vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )  
  }  
  int ~ dnorm(0,.01)  
  b[1]<-0  
  for( i in 2:3) { b[i] ~ dnorm(0,.01) }  
  for( i in 1:2) { c[i] ~ dnorm(0,.01) }  
  sdhat ~ dunif(0,5)  
  lvar <- pow(sdhat,2)  
  for(i in 1:nrandom){  
    eps[i] ~ dnorm(0,tau.re)  
  }  
  tau.re<- pow(sd.re,-2)  
  sd.re ~ dunif(0,1)  
}  
")  
sink(NULL)
```

Run the model:

```
# Model NULL  
parametersNull=c("int","b","c","eps","sdhat","sd.re")  
jagsmod0<- jags(jagsdataNull,init=NULL,parametersNull,  
  "NullModel.jag",n.chains=3,n.iter=12000,n.burnin=2000,n.thin=10)  
jagsmod0
```

## Basic model

Setup the data for running the JAGS model:

```
# prepare a list with data elements for JAGS
jagsdataBasic<-list(
  m = data$biomass,
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],
  plot= as.numeric(model.frame$plot),
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,
  year=model.frame$year-1988,
  ndaily= nrow(model.frame),
  n=nrow(data),
  nrandom=max( as.numeric(model.frame$plot))
)
```

Write JAGS model file:

```
sink("BasicModel.jag")
cat("
model{
for( i in 1:n){
m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])
tau[i] <- 1/Var[i]
Var[i] <- sum( vr[index1[i]:index2[i]] )
}
for(i in 1:ndaily){
y[i] <- exp(z[i])
z[i] <- int + log.lambda*year[i] +
c[1]*daynr[i] + c[2]*daynr2[i]+
c[3]*daynr[i]*year[i]+c[4]*daynr2[i]*year[i]+
b[loctype[i]] + eps[plot[i]]
vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )
}
int~ dnorm(0,.01)
log.lambda~ dnorm(0,.01)
b[1]<-0
for( i in 2:3) { b[i] ~ dnorm(0,.01) }
for( i in 1:4) { c[i] ~ dnorm(0,.01) }
sdhat ~ dunif(0,5)
lvar <- pow(sdhat,2)
for(i in 1:nrandom){
eps[i] ~ dnorm(0,tau.re)
}
tau.re<- pow(sd.re,-2)
sd.re ~ dunif(0,1)
}
" )
sink(NULL)
```

Run the model:

```
parametersBasic=c("int","log.lambda","b","c","eps","sdhat","sd.re")
jagsmodBasic<- jags(jagsdataBasic,inits=NULL,parameters=parametersBasic,
  "BasicModel.jag", n.chains=3,n.iter=24000,n.burnin=4000,n.thin=10)
```

## Weather model

Setup the data for running the JAGS model:

```
jagsdataWeather<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  year=model.frame$year-1988,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot)),  
  temp=standardize(model.frame$temperature),  
  prec=standardize(model.frame$precipitation),  
  wind=standardize(model.frame$wind.speed),  
  frost=standardize(model.frame$frostdays),  
  w.prec=standardize(model.frame$sum.precW)  
)
```

Write JAGS model file:

```
sink("WeatherModel.jag")  
cat(`  
model{  
  for( i in 1:n){  
    m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
    tau[i] <- 1/Var[i]  
    Var[i] <- sum( vr[index1[i]:index2[i]] )  
  }  
  for(i in 1:ndaily){  
    y[i] <- exp(z[i])  
    z[i] <- int +  
    log.lambda*year[i] +  
    c[1]*daynr[i] + c[2]*daynr2[i]+  
    c[3]*daynr[i]*year[i] + c[4]*daynr2[i]*year[i]+  
    w[1]*temp[i] + w[2]*prec[i] + w[3]*wind[i] +  
    w[4]*frost[i]+ w[5]*w.prec[i]+  
    b[loctype[i]] +  
    eps[plot[i]]  
    vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )  
  }  
  int~ dnorm(0,.01)  
  log.lambda~ dnorm(0,.01)  
  b[1]<-0  
  for( i in 2:3) { b[i] ~ dnorm(0,.01) }  
  for( i in 1:4) { c[i] ~ dnorm(0,.01) }  
  for( i in 1:5) { w[i] ~ dnorm(0,.01) }  
  sdhat ~ dunif(0,5)  
  lvar <- pow(sdhat,2)  
  for(i in 1:nrandom){  
    eps[i] ~ dnorm(0,tau.re)  
  }  
  tau.re<- pow(sd.re,-2)  
  sd.re ~ dunif(0,1)  
}  
)  
sink(NULL)
```

Run the model:

```
parametersWeather=c("int","log.lambda","b","c","w","eps","sdhat","sd.re")  
jagsmodWeather<- jags(jagsdataWeather,NULL,  
  parametersWeather,"WeatherModel.jag",  
  n.chains=3,n.iter=24000,n.burnin=4000,n.thin=10)  
jagsmodWeather
```

## Habitat model

Setup the data for running the JAGS model:

```
jagsdataHabitat<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  year=model.frame$year-1988,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot)),  
  herbs=log(model.frame$nHerbs),  
  Trees=standardize(model.frame$nTrees),  
  nitro=standardize(model.frame$Nitrogen),  
  pH=standardize(model.frame$pH),  
  moist=standardize(model.frame$Moisture),  
  light=standardize(model.frame$Light),  
  etemp=standardize(model.frame$ellenTemperature)  
)
```

Write JAGS model file:

```
sink("HabitatModel.jag")  
cat("  
model{  
  for( i in 1:n){  
    m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
    tau[i] <- 1/Var[i]  
    Var[i] <- sum( vr[index1[i]:index2[i]] )  
  }  
  for(i in 1:ndaily){  
    y[i] <- exp(z[i])  
    z[i] <- int +  
    log.lambda*year[i] +  
    c[1]*daynr[i] + c[2]*daynr2[i]+  
    c[3]*daynr[i]*year[i]+c[4]*daynr2[i]*year[i]+  
    d[1]*herbs[i]+d[2]*Trees[i]+  
    d[3]*nitro[i]+d[4]*pH[i]+d[5]*moist[i]+  
    d[6]*light[i]+d[7]*etemp[i]+  
    b[loctype[i]] +  
    eps[plot[i]]  
    vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )  
  }  
  int~ dnorm(0,.01)  
  log.lambda~ dnorm(0,.01)  
  b[1]<-0  
  for( i in 2:3) { b[i] ~ dnorm(0,.01) }  
  for( i in 1:4) { c[i] ~ dnorm(0,.01) }  
  for( i in 1:7) { d[i] ~ dnorm(0,.01) }  
  sdhat ~ dunif(0,5)  
  lvar <- pow(sdhat,2)  
  for(i in 1:nrandom){  
    eps[i] ~ dnorm(0,tau.re)  
  }  
  tau.re<- pow(sd.re,-2)  
  sd.re ~ dunif(0,1)  
}  
")  
sink(NULL)
```

Run the model:

```
parametersHabitat=c("int","log.lambda","b","c","d","eps","sdhat","sd.re")  
jagsmodHabitat<- jags(jagsdataHabitat,NULL,parametersHabitat,  
  "HabitatModel.jag",n.chains=3,n.iter=24000,n.burnin=4000,n.thin=10)  
jagsmodHabitat
```

## Landuse model

Setup the data for running the JAGS model:

```
jagsdataLandUse<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  year=model.frame$year-1988,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot)),  
  agribuf=(model.frame$Arable.land),  
  forebuf=(model.frame$Forest),  
  grasbuf=(model.frame$Grassland),  
  water=(model.frame$Water)  
)
```

```
sink("LandUseModel.jag")  
cat("  
model{  
for( i in 1:n){  
m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
tau[i] <- 1/Var[i]  
Var[i] <- sum( vr[index1[i]:index2[i]] )  
}  
for(i in 1:ndaily){  
y[i] <- exp(z[i])  
z[i] <- int +  
log.lambda*year[i] +  
c[1]*daynr[i] + c[2]*daynr2[i]+  
c[3]*daynr[i]*year[i] + c[4]*daynr2[i]*year[i] +  
d[1]*agribuf[i]+d[2]*forebuf[i]+  
d[3]*grasbuf[i]+d[4]*water[i]+  
b[loctype[i]]+ eps[plot[i]]  
vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )  
}  
int~ dnorm(0,.01)  
log.lambda~ dnorm(0,.01)  
b[1]<-0  
for( i in 2:3) { b[i] ~ dnorm(0,.01) }  
for( i in 1:4) { c[i] ~ dnorm(0,.01) }  
for( i in 1:4) { d[i] ~ dnorm(0,.01) }  
sdhat ~ dunif(0,5)  
lvar <- pow(sdhat,2)  
for(i in 1:nrandom){  
eps[i] ~ dnorm(0,tau.re)  
}  
tau.re<- pow(sd.re,-2)  
sd.re ~ dunif(0,1)  
}  
")  
sink(NULL)
```

Run the model:

```
parametersLandUse=c("int","log.lambda","b","c","d","eps","sdhat","sd.re")  
jagsmodLandUse<- jags(LandUseModel,NULL,parametersLandUse,"LandUseModel.jag",  
  n.chains=3,n.iter=24000,n.burnin=4000,n.thin=10)  
jagsmodLandUse
```

## Landuse with interactions model

Setup the data for running the JAGS model:

```
jagsdataLandUse<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  year=model.frame$year-1988,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot)),  
  agribuf=(model.frame$Arable.land),  
  forebuf=(model.frame$Forest),  
  grasbuf=(model.frame$Grassland),  
  water=(model.frame$Water)  
)
```

Write JAGS model file:

```
sink("LandUseIntModel.jag")  
cat("  
model{  
  for( i in 1:n){  
    m[i] ~ dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
    tau[i] <- 1/Var[i]  
    Var[i] <- sum( vr[index1[i]:index2[i]] )  
  }  
  for(i in 1:ndaily){  
    y[i] <- exp(z[i])  
    z[i] <- int +  
    log.lambda*year[i] +  
    c[1]*daynr[i] + c[2]*daynr2[i]+  
    c[3]*daynr[i]*year[i] + c[4]*daynr2[i]*year[i] +  
    d[1]*agribuf[i]+d[2]*forebuf[i]+  
    d[3]*grasbuf[i]+d[4]*water[i]+  
    d[5]*agribuf[i]*year[i]+d[6]*forebuf[i]*year[i]+  
    d[7]*grasbuf[i]*year[i]+d[8]*water[i]*year[i]+  
    b[loctype[i]] +  
    eps[plot[i]]  
    vr[i]<- exp( 2* z[i]+ lvar ) * (exp(lvar)-1 )  
  }  
  int~ dnorm(0,.01)  
  log.lambda~ dnorm(0,.01)  
  b[1]<-0  
  for( i in 2:3) { b[i] ~ dnorm(0,.01) }  
  for( i in 1:4) { c[i] ~ dnorm(0,.01) }  
  for( i in 1:8) { d[i] ~ dnorm(0,.01) }  
  sdhat ~ dunif(0,5)  
  lvar <- pow(sdhat,2)  
  for(i in 1:nrandom){  
    eps[i] ~ dnorm(0,tau.re)  
  }  
  tau.re<- pow(sd.re,-2)  
  sd.re ~ dunif(0,1)  
}  
")  
sink(NULL)
```

Run the model:

```
parametersLanduse=c("int","log.lambda","b","c","d","eps","sdhat","sd.re")  
LandUseIntModel<- jags(LandUseData,NULL,parametersLanduse,"LandUseIntModel.jag",  
  n.chains=3,n.iter=24000,n.burnin=4000,n.thin=10)  
LandUseIntModel
```

## Full model

Setup the data for running the JAGS model:

```
jagsdataFull<-list(  
  m = data$biomass,  
  index1= with(model.frame,tapply(1:nrow(model.frame),potID,min))[data$potID],  
  index2=with(model.frame,tapply(1:nrow(model.frame),potID,max))[data$potID],  
  plot= as.numeric(model.frame$plot),  
  loctype = as.numeric(data$location.type[match(model.frame$potID,data$potID)]),  
  daynr= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr)),  
  daynr2= as.numeric((model.frame$daynr-mean(data$mean.daynr))/ sd(data$mean.daynr))^2,  
  year=model.frame$year-1988,  
  ndaily= nrow(model.frame),  
  n=nrow(data),  
  nrandom=max( as.numeric(model.frame$plot)),  
  temp=standardize(model.frame$temperature),  
  prec=standardize(model.frame$precipitation),  
  frost=standardize(model.frame$frostdays),  
  herbs=log(model.frame$nHerbs),  
  Trees=standardize(model.frame$nTrees),  
  nitro=standardize(model.frame$Nitrogen),  
  light=standardize(model.frame$Light),  
  etemp=standardize(model.frame$ellenTemperature),  
  agribuf=(model.frame$Arable.land),  
  forebuf=(model.frame$Forest),  
  grasbuf=(model.frame$Grassland),  
  water=(model.frame$Water)  
)
```

Write JAGS model file:

```
sink("FullModel.jag")  
cat(  
model{  
for(i in 1:n){  
m[i]~dnorm(sum(y[index1[i]:index2[i]]),tau[i])  
tau[i]~1/Var[i]  
Var[i]~sum(vr[index1[i]:index2[i]])  
}  
for(i in 1:ndaily){  
y[i]~exp(z[i])  
z[i]~int+log.lambda*year[i]+  
c[1]*daynr[i]+c[2]*daynr2[i]+  
c[3]*daynr[i]*year[i]+c[4]*daynr2[i]*year[i]+  
w[1]*temp[i]+w[2]*prec[i]+  
w[3]*frost[i]+ b[loctype[i]]+  
d[1]*herbs[i]+d[2]*Trees[i]+  
d[3]*nitro[i]+d[4]*light[i]+d[5]*etemp[i]+  
d[6]*agribuf[i]+d[7]*forebuf[i]+d[8]*grasbuf[i]+d[9]*water[i]+  
d[10]*agribuf[i]*year[i]+d[11]*forebuf[i]*year[i]+d[12]*grasbuf[i]*year[i]+  
eps[plot[i]]  
vr[i]~exp(2*z[i]+lvar)*(exp(lvar)-1)  
}  
int~dnorm(0,.01)  
log.lambda~ dnorm(0,.01)  
b[1]~0  
for(i in 2:3){b[i]~dnorm(0,.01)}  
for(i in 1:4){c[i]~ dnorm(0,.01)}  
for(i in 1:3){w[i]~dnorm(0,.01)}  
for(i in 1:12){d[i]~dnorm(0,.01)}  
sdhat~dunif(0,5)  
lvar<-pow(sdhat,2)  
for(i in 1:nrandom){
```



```
eps[i]~dnorm(0,tau.re)
}
tau.re<-pow(sd.re,-2)
sd.re~dunif(0,1)
}
")
sink(NULL)
```

Run the model:

```
parametersFull<- c("int","log.lambda","b","c","w","d","eps","sdhat","sd.re")
FullModel<- jags(jagsdataFull,NULL,parametersFull,"FullModel.jag",
  n.chains=3,n.iter=24000,n.burnin= 4000,n.thin=10)
FullModel
```