Package ‘hSDM’

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Description hSDM is an R package for estimating parameters of hierarchical Bayesian species distribution models. Such models allow interpreting the observations (occurrence and abundance of a species) as a result of several hierarchical processes including ecological processes (habitat suitability, spatial dependence and anthropogenic disturbance) and observation processes (species detectability). Hierarchical species distribution models are essential for accurately characterizing the environmental response of species, predicting their probability of occurrence, and assessing uncertainty in the model results.
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hSDM-package ......................................................... 2
altitude ................................................................. 3
cfr.env ................................................................. 3
data.Kery2010 .......................................................... 4
**Description**

hSDM is an R package for estimating parameters of hierarchical Bayesian species distribution models. Such models allow interpreting the observations (occurrence and abundance of a species) as a result of several hierarchical processes including ecological processes (habitat suitability, spatial dependence and anthropogenic disturbance) and observation processes (species detectability). Hierarchical species distribution models are essential for accurately characterizing the environmental response of species, predicting their probability of occurrence, and assessing uncertainty in the model results.

**Details**

- **Package:** hSDM
- **Type:** Package
- **Version:** 1.3
- **Date:** 2013-10-15
- **License:** GPL-3
- **LazyLoad:** yes
altitude

**Description**

Data frame with virtual altitudinal data. The data frame is used in the examples of the hSDM package vignette to derive an altitude raster determining species habitat suitability.

**Usage**

```r
altitude
```

**Format**

- `altitude` is a data frame with 2500 observations (50 x 50 cells) and 3 variables:
  - `x` coordinates of the center of the cell on the x axis
  - `y` coordinates of the center of the cell on the y axis
  - `altitude` altitude (m)

---

cfr.env

**Description**

Data include environmental variables for 36909 one minute by one minute grid cells on the whole South Africa’s Cap Floristic Region.

**Usage**

```r
cfr.env
```
Format
cfr.env is a data frame with 36909 observations (cells) on the following six environmental variables.

lon longitude
lat latitude
min07 minimum temperature of the coldest month (July)
smdwin winter soil moisture days
fert3 moderately high fertility (percent of grid cell)
ph1 acidic soil (percent of grid cell)
text1 fine soil texture (percent of grid cell)
text2 moderately fine soil texture (percent of grid cell)

Source
Cory Merow's personal data

References

data.Kery2010 NA

Description

Usage
data.Kery2010

Format
data.Kery2010 is a data frame with 264 observations (1 km² quadrats) and the following 10 variables.

coordx quadrat x coordinate
coordy quadrat y coordinate
elevation mean quadrat elevation (m)
forest quadrat forest cover (in %)
datacells.Latimer2006

count1  count for survey 1
count2  count for survey 2
count3  count for survey 3
juldate1  Julian date of survey 1
juldate2  Julian date of survey 2
juldate3  Julian date of survey 3

Source

References

Description
Data come from a small region including 476 one minute by one minute grid cells. This region is a small corner of South Africa's Cape Floristic Region, and includes very high plant species diversity and a World Biosphere Reserve. The data frame can be used as an example for several functions in the hSDM package.

Usage
datacells.Latimer2006

Format
datacells.Latimer2006 is a data frame with 476 observations (cells) on the following 9 variables.
y  the number of times the species was observed to be present in each cell
n  the number of visits or sample locations in each cell (which can be zero)
rough  elevational range or "roughness"
julmint  July minimum temperature
pptcv  interannual variation in precipitation
smdsum  summer soil moisture days
evi  enhanced vegetation or "greenness" index
ph1  percent acidic soil
num  number of neighbors of each cell, this is a sparse representation of the adjacency matrix for the subregion.
**Source**

Latimer et al. (2006) *Ecological Applications*, Appendix B

**References**


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**hSDM.binomial**

*Binomial logistic regression model*

**Description**

The `hSDM.binomial` function performs a Binomial logistic regression in a Bayesian framework. The function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of model’s parameters.

**Usage**

```r
hSDM.binomial(presences, trials, suitability, data, suitability.pred = NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, mubeta = 0, Vbeta = 1e+06, seed = 1234, verbose = 1, save.p = 0)
```

**Arguments**

- **presences**: A vector indicating the number of successes (or presences) for each observation.
- **trials**: A vector indicating the number of trials for each observation. \( t_n \) should be superior or equal to \( y_n \), the number of successes for observation \( n \). If \( t_n = 0 \), then \( y_n = 0 \).
- **suitability**: A one-sided formula of the form ‘~x1+...+xp’ with \( p \) terms specifying the explicative variables for the suitability process of the model.
- **data**: A data frame containing the model’s explicative variables.
- **suitability.pred**: An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
- **burnin**: The number of burnin iterations for the sampler.
- **mcmc**: The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to \( \text{burnin} + \text{mcmc} \). \( \text{burnin} + \text{mcmc} \) must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
- **thin**: The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.
- **beta.start**: Starting values for beta parameters of the suitability process. If beta.start takes a scalar value, then that value will serve for all of the betas.
Means of the priors for the $\beta$ parameters of the suitability process. $\text{mubeta}$ must be either a scalar or a p-length vector. If $\text{mubeta}$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Variances of the Normal priors for the $\beta$ parameters of the suitability process. $\text{vbeta}$ must be either a scalar or a p-length vector. If $\text{vbeta}$ takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to $1.0\times 10^6$ for an uninformative flat prior.

The seed for the random number generator. Default to 1234.

A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the $\text{thetaNpred}$ vector. Be careful, setting $\text{save.p}$ to 1 might require a large amount of memory.

We model an ecological process where the presence or absence of the species is explained by habitat suitability.

**Ecological process:**

$$y_i \sim \text{Binomial}(\theta_i, t_i)$$

$$\logit(\theta_i) = X_i \beta$$

An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod P(y_i|\beta, t_i))$, is also provided.

If $\text{save.p}$ is set to 0 (default), $\text{thetaNpred}$ is the predictive posterior mean of the probability associated to the suitability process for each prediction. If $\text{save.p}$ is set to 1, $\text{thetaNpred}$ is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

Predictive posterior mean of the probability associated to the suitability process for each observation.

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See Also

plot.mcmc, summary.mcmc

Examples

```r
## Not run:

#============================================================
# hSDM.binomial()
# Example with simulated data
#============================================================

#==========
#== Load libraries
library(hSDM)

#==========
#== Data simulation

#= Number of sites
nsite <- 200

#= Set seed for repeatability
seed <- 1234

#= Number of visits associated to each site
set.seed(seed)
visits <- rpois(nsite,3)
visits[visits==0] <- 1

#= Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1)
logit.theta <- X %*% beta.target
theta <- inv.logit(logit.theta)
set.seed(seed)
Y <- rbinom(nsite,visits,theta)

#= Data-sets
data.obs <- data.frame(Y,visits,x1,x2)

#============================================================
#== Site-occupancy model

mod.hSDM.binomial <- hSDM.binomial(presences=data.obs$Y,
trials=data.obs$visits,
suitability=~x1+x2,
```
**hSDM.binomial.iCAR**

**Binomial logistic regression model with CAR process**

**Description**

The `hSDM.binomial.iCAR` function performs a Binomial logistic regression model in a hierarchical Bayesian framework. The suitability process includes a spatial correlation process. The spatial correlation is modelled using an intrinsic CAR model. The `hSDM.binomial.iCAR` function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

**Usage**

```R
hSDM.binomial.iCAR(presences, trials, suitability,
spatial.entity, data, n.neighbors, neighbors, suitability.pred=NULL,
spatial.entity.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10,
beta.start, Vrho.start, mubeta = 0, Vbeta = 1e+06, priorVrho =
```

```R
data=data.obs,
suitability.pred=NULL,
burnin=1000, mcmc=1000, thin=1,
beta.start=0,
mubeta=0, Vbeta=1.0E6,
seed=1234, verbose=1,
save.p=0)
```

```R
#========
#== Outputs

#= Parameter estimates
summary(mod.hSDM.binomial$mcmc)
pdf(file="Posteriors_hSDM.binomial.pdf")
plot(mod.hSDM.binomial$mcmc)
dev.off()

#== glm resolution to compare
mod.glm <- glm(cbind(Y,visits~Y)-x1+x2,family="binomial",data=data.obs)
summary(mod.glm)

#= Predictions
summary(mod.hSDM.binomial$theta.latent)
summary(mod.hSDM.binomial$theta.pred)
pdf(file="Pred-Init.pdf")
plot(theta,mod.hSDM.binomial$theta.pred)
abline(a=0,b=1,col="red")
dev.off()

## End(Not run)
```
Arguments

presences: A vector indicating the number of successes (or presences) for each observation.

trials: A vector indicating the number of trials for each observation. $t_i$ should be superior to zero and superior or equal to $y_i$, the number of successes for observation $i$.

suitability: A one-sided formula of the form $\sim x_1 + \ldots + x_p$ with $p$ terms specifying the explicative variables for the suitability process.

spatial.entity: A vector indicating the spatial entity identifier (from one to the total number of entities) for each observation. Several observations can occur in one spatial entity. A spatial entity can be a raster cell for example.

data: A data frame containing the model’s variables.

n.neighbors: A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. $\text{length}(\text{n.neighbors})$ indicates the total number of spatial entities.

neighbors: A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form $c(\text{neighbors of entity 1}, \text{neighbors of entity 2}, \ldots, \text{neighbors of the last entity})$. Length of the neighbors vector should be equal to $\text{sum}(\text{n.neighbors})$.

suitability.pred: An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

spatial.entity.pred: An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.

burnin: The number of burnin iterations for the sampler.

mcmc: The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to $\text{burnin} + \text{mcmc}$. $\text{burnin} + \text{mcmc}$ must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

thin: The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start: Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a $p$-length vector.

Vrho.start: Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta: Means of the priors for the $\beta$ parameters of the suitability process. $\text{mubeta}$ must be either a scalar or a $p$-length vector. If $\text{mubeta}$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.
Vbeta | Variances of the Normal priors for the $\beta$ parameters of the suitability process. Vbeta must be either a scalar or a p-length vector. If Vbeta takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

priorVrho | Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval [0,Vrho.max]. Default set to "1/Gamma".

shape | The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is shape=0.05 for uninformative prior.

rate | The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.

Vrho.max | Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed | The seed for the random number generator. Default set to 1234.

verbose | A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho | A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p | A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the theta.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

We model an ecological process where the presence or absence of the species is explained by habitat suitability. The ecological process includes an intrinsic conditional autoregressive (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

Ecological process:

$$y_i \sim \text{Binomial}(\theta_i, t_i)$$

$$\logit(\theta_i) = X_i\beta + \rho_{j(i)}$$

$\rho_{j}$: spatial random effect

$j(i)$: index of the spatial entity for observation $i$.

Spatial autocorrelation:

An intrinsic conditional autoregressive model (iCAR) is assumed:

$$\rho_j \sim \text{Normal}(\mu_j, V_p/n_j)$$

$\mu_j$: mean of $\rho_{j'}$ in the neighborhood of $j$.

$V_p$: variance of the spatial random effects.

$n_j$: number of neighbors for spatial entity $j$. 
Value

mcmc  An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod P(y_i|\ldots))$, is also provided.

rho.pred  If save.rho is set to 0 (default), rho.pred is the predictive posterior mean of the spatial random effect associated to each spatial entity. If save.rho is set to 1, rho.pred is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

theta.pred  If save.p is set to 0 (default), theta.pred is the predictive posterior mean of the probability associated to the suitability process for each prediction. If save.p is set to 1, theta.pred is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

theta.latent  Predictive posterior mean of the probability associated to the suitability process for each observation.

Author(s)

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References


See Also

plot.mcmc, summary.mcmc

Examples

```r
## Not run:

# hSDM.binomial.iCAR()
# Example with simulated data

# Load libraries
library(hSDM)
```
library(raster)
library(sp)

# Multivariate normal distribution
rmvn <- function(n, mu = 0, V = matrix(1), seed=1234) {
  p <- length(mu)
  if (any(is.na(match(dim(V), p)))) {
    stop("Dimension problem!")
  }
  D <- chol(V)
  set.seed(seed)
  t(matrix(rnorm(n*p),ncol=p)%*%D+rep(mu,rep(n,p)))
}

# Set seed for repeatability
seed <- 1234

# Landscape
xLand <- 30
yLand <- 30
Landscape <- raster(ncol=xLand,nrow=yLand,crs='+proj=utm +zone=1')
Landscape[] <- 0
extent(Landscape) <- c(0,xLand,0,yLand)
cords <- coordinates(Landscape)
cells <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncells), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0,ncells,ncells)
index.start <- 1
for (i in 1:ncells) {
  index.end <- index.start+n.neighbors[i]-1
  A[i,adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial effects
Vrho.target <- 5
d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors)-d*A + diag(.0001,ncells) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
rho <- c(rmvn(1,mu=rep(0,ncells),V=V*carho,seed=seed)) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero
# Raster and plot spatial effects
r.rho <- rasterFromXYZ(cbind(coords, rho))
plot(r.rho)

# Sample the observation sites in the landscape
nsite <- 250
set.seed(seed)
x.coord <- runif(nsite, 0, xLand)
set.seed(2 * seed)
y.coord <- runif(nsite, 0, yLand)
sites.sp <- SpatialPoints(coords = cbind(x.coord, y.coord))
cells <- extract(Landscape, sites.sp, cell = TRUE)[, 1]

# Number of visits associated to each observation point
set.seed(seed)
visits <- rpois(nsite, 3)
visits[visits == 0] <- 1

# Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite, 0, 1)
set.seed(2 * seed)
x2 <- rnorm(nsite, 0, 1)
X <- cbind(rep(1, nsite), x1, x2)
beta.target <- c(-1, 1, -1)
logit.theta <- X %*% beta.target + rho[cells]
theta <- inv.logit(logit.theta)
set.seed(seed)
Y <- rbinom(nsite, visits, theta)

# Relative importance of spatial random effects
RImp <- mean(abs(rho[cells]) / abs(X %*% beta.target))
RImp

# Data-sets
data.obs <- data.frame(Y, visits, x1, x2, cell = cells)

# Site-occupancy model

Start <- Sys.time()  # Start the clock
mod.hSDM.binomial.iCAR <- hSDM.binomial.iCAR(presences = data.obs$Y,
                                          trials = data.obs$visits,
                                          suitability = ~ x1 + x2,
                                          spatial.entity = data.obs$cell,
                                          data = data.obs,
                                          n.neighbors = n.neighbors,
                                          neighbors = adj,
                                          suitability.pred = NULL,
                                          spatial.entity.pred = NULL,
                                          burnin = 5000, mcmc = 5000, thin = 5,
                                          beta.start = 0,
                                          Vrho.start = 1,
                                          )
hSDM.binomial.iCAR

mubeta=0, Vbeta=1.0E6,
priorVrho="1/Gamma",
shape=0.5, rate=0.0005,
seed=1234, verbose=1,
save.rho=1, save.p=0)

Time.hSDM <- difftime(Sys.time(), Start, units="sec")  # Time difference

#= Computation time
Time.hSDM

#======
#== Outputs

#= Parameter estimates
summary(mod.hSDM.binomial.iCAR$mcmc)
pdf("Posterior_hSDM.binomial.iCAR.pdf")
plot(mod.hSDM.binomial.iCAR$mcmc)
dev.off()

#= Predictions
summary(mod.hSDM.binomial.iCAR$theta.latent)
save_theta <- summary(mod.hSDM.binomial.iCAR$theta.pred)
pdf(file="Pred-Init.pdf")
plot(theta, mod.hSDM.binomial.iCAR$theta.pred)
abline(a=0, b=1, col="red")
dev.off()

#= Summary plots for spatial random effects

# rho.pd
rho.prd <- apply(mod.hSDM.binomial.iCAR$rho.prd, 2, mean)
r.rho.prd <- rasterFromXYZ(cbind(coords, rho.prd))

# plot
pdf(file="Summary_hSDM.binomial.iCAR.pdf")
par(mfrow=c(2,2))
# rho target
plot(r.rho, main="rho target")
plot(sites.sp, add=TRUE)
# rho estimated
plot(r.rho.prd, main="rho estimated")
# correlation and "shrinkage"
Levels.cells <- sort(unique(cells))
plot(rho[-Levels.cells], rho.prd[-Levels.cells],
     xlim=range(rho), ylim=range(rho),
     xlab="rho target",
     ylab="rho estimated")
points(rho[Levels.cells], rho.prd[Levels.cells], pch=16, col="blue")
legend(x=-3, y=4, legend="Visited cells", col="blue", pch=16, bty="n")
abline(a=0, b=1, col="red")
dev.off()
hSDM.Nmixture

**Description**

The hSDM.Nmixture function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a *Poisson* suitability process (referring to environmental suitability explaining abundance) and a *Binomial* observability process (referring to various ecological and methodological issues explaining species detection). The hSDM.Nmixture function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

**Usage**

```r
hSDM.Nmixture(counts, observability, site, data.observability,
   habitat, data.suitability, predictions = NULL,
   chains = 2000, burnin = 5000, mcmc = 10000, thin = 10,
   starting values = beta.start, gamma.start,
   priors = mubeta = 0, vbeta = 1.0E6,
   mugamma = 0, vgamma = 1.0E6,
   various = seed = 1234, verbose = 1,
   save.p = 0, save.N = 0)
```

**Arguments**

- `counts` A vector indicating the count (or abundance) for each observation.
- `observability` A one-sided formula of the form ~ $w_1 + \ldots + w_q$ with $q$ terms specifying the explicative variables for the observability process.
- `site` A vector indicating the site identifier (from one to the total number of sites) for each observation. Several observations can occur at one site. A site can be a raster cell for example.
- `data.observability` A data frame containing the model’s variables for the observability process.
suitability  A one-sided formula of the form $x_1 + \ldots + x_p$ with $p$ terms specifying the explicative variables for the suitability process.

data.suitability  A data frame containing the model’s variables for the suitability process.
suitability.pred  An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
burnin  The number of burnin iterations for the sampler.
mcmc  The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to burnin+mcmc. burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
thin  The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.
beta.start  Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a $p$-length vector.
gamma.start  Starting values for $\beta$ parameters of the observability process. This can either be a scalar or a $q$-length vector.
mubeta  Means of the priors for the $\beta$ parameters of the suitability process. $\mubeta$ must be either a scalar or a $p$-length vector. If $\mubeta$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.
Vbeta  Variances of the Normal priors for the $\beta$ parameters of the suitability process. $\Vbeta$ must be either a scalar or a $p$-length vector. If $\Vbeta$ takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.
mugamma  Means of the Normal priors for the $\gamma$ parameters of the observability process. $\mugamma$ must be either a scalar or a $p$-length vector. If $\mugamma$ takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.
Vgamma  Variances of the Normal priors for the $\gamma$ parameters of the observability process. $\Vgamma$ must be either a scalar or a $p$-length vector. If $\Vgamma$ takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.
seed  The seed for the random number generator. Default set to 1234.
verbose  A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.
save.p  A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the $\lambda_{\text{pred}}$ vector. Be careful, setting save.p to 1 might require a large amount of memory.
save.N  A switch (0,1) which determines whether or not the sampled values for the latent count variable $N$ for each observed cells are saved. Default is 0: the mean (rounded to the closest integer) is computed and returned in the $N_{\text{pred}}$ vector. Be careful, setting save.N to 1 might require a large amount of memory.
Details

The model integrates two processes, an ecological process associated to the abundance of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one.

**Ecological process:**

\[ N_i \sim \text{Poisson}(\lambda_i) \]
\[ \log(\lambda_i) = X_i \beta \]

**Observation process:**

\[ y_{it} \sim \text{Binomial}(N_i, \delta_{it}) \]
\[ \logit(\delta_{it}) = W_{it} \gamma \]

Value

- **mcmc**
  An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod_{it} P(y_{it}, N_i | \ldots)) \), is also provided.

- **lambda.pred**
  If `save.p` is set to 0 (default), `lambda.pred` is the predictive posterior mean of the abundance associated to the suitability process for each prediction. If `save.p` is set to 1, `lambda.pred` is an mcmc object with sampled values of the abundance associated to the suitability process for each prediction.

- **N.pred**
  If `save.N` is set to 0 (default), `N.pred` is the posterior mean (rounded to the closest integer) of the latent count variable \( N \) for each observed cell. If `save.N` is set to 1, `N.pred` is an mcmc object with sampled values of the latent count variable \( N \) for each observed cell.

- **lambda.latent**
  Predictive posterior mean of the abundance associated to the suitability process for each observation.

- **delta.latent**
  Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References


See Also

plot.mcmc, summary.mcmc

Examples

## Not run:

#----------------------------------------------------------------------
# hSDM.Nmixture()
# Example with simulated data
#----------------------------------------------------------------------

#------------------
## Load libraries
library(hSDM)

#------------------
## Data simulation

# Number of observation sites
nsite <- 200

## Set seed for repeatability
seed <- 4321

## Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1) # Target parameters
log.lambda <- X %*% beta.target
lambda <- exp(log.lambda)
set.seed(seed)
N <- rpois(nsite,lambda)

## Number of visits associated to each observation point
set.seed(seed)
visits <- rpois(nsite,3)
visits[visits==0] <- 1
## Vector of observation points
sites <- vector()
for (i in 1:nsite) {
  sites <- c(sites,rep(i,visits[i]))
}

## Observation process (detectability)
nobs <- sum(visits)
set.seed(seed)
w1 <- rnorm(nobs,0,1)
```r
set.seed(2*seed)
w2 <- rnorm(nobs,0,1)
W <- cbind(rep(1,nobs),w1,w2)
gamma.target <- c(-1,1,-1) # Target parameters
logit.delta <- W %*% gamma.target
delta <- inv.logit(logit.delta)
set.seed(seed)
Y <- rbinom(nobs,N[sites],delta)

# Data-sets
data.obs <- data.frame(Y,w1,w2,site=sites)
data.suit <- data.frame(x1,x2)

# Parameter inference with hSDM
Start <- Sys.time() # Start the clock
mod.hSDM.Nmixture <- hSDM.Nmixture(# Observations
counts=data.obs$Y,
observability=-w1+w2,
site=data.obs$sites,
data.observability=data.obs,
# Habitat
suitability=-x1+x2,
data.suitability=data.suit,
# Predictions
suitability.pred=NULL,
# Chains
burnin=5000, mcmc=5000, thin=5,
# Starting values
beta.start=0,
gamma.start=0,
# Priors
mubeta=0, Vbeta=1.0E6,
mugamma=0, Vgamma=1.0E6,
# Various
seed=1234, verbose=1,
save.p=0, save.N=1)
Time.hSDM <- difftime(Sys.time(),Start,units="sec") # Time difference

# Computation time
Time.hSDM

# Outputs

# Parameter estimates
summary(mod.hSDM.Nmixture$mcmc)
pdf(file="Posteriors_hSDM.Nmixture.pdf")
plot(mod.hSDM.Nmixture$mcmc)
dev.off()

# Predictions
```
hSDM.Nmixture.iCAR

N-mixture model with CAR process

Description

The hSDM.Nmixture.iCAR function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Poisson suitability process (refering to environmental suitability explaining abundance) which takes into account the spatial dependence of the observations, and a Binomial observability process (refering to various ecological and methodological issues explaining the species detection). The hSDM.Nmixture.iCAR function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model's parameters.

Usage

hSDM.Nmixture.iCAR(
  # Observations
counts, observability, site, data.observability,
  # Habitat
  habitat, data.suitability,
)
# Spatial structure
spatial.entity, n.neighbors, neighbors,
# Predictions
suitability.pred = NULL, spatial.entity.pred = NULL,
# Chains
burnin = 5000, mcmc = 10000, thin = 10,
# Starting values
beta.start, gamma.start, Vrho.start,
# Priors
mubeta = 0, Vbeta = 1.0E6, mugamma = 0, Vgamma = 1.0E6,
priorVrho = "1/Gamma", shape = 0.5, rate = 0.0005,
Vrho.max = 1000,
# Various
seed = 1234, verbose = 1,
save.rho = 0, save.p = 0, save.N = 0)

Arguments

- **counts**
  A vector indicating the count (or abundance) for each observation.

- **observability**
  A one-sided formula of the form $\sim w_1 + ... + w_q$ with $q$ terms specifying the explicative variables for the observability process.

- **site**
  A vector indicating the site identifier (from one to the total number of sites) for each observation. Several observations can occur at one site. A site can be a raster cell for example.

- **data.observability**
  A data frame containing the model's variables for the observability process.

- **suitability**
  A one-sided formula of the form $\sim x_1 + ... + x_p$ with $p$ terms specifying the explicative variables for the suitability process.

- **data.suitability**
  A data frame containing the model's variables for the suitability process. The number of rows of the data frame should be equal to the total number of spatial entities.

- **spatial.entity**
  A vector (of length 'site') indicating the spatial entity identifier for each site. Values must be between 1 and the total number of spatial entities. Several sites can be found in one spatial entity. A spatial entity can be a raster cell for example.

- **n.neighbors**
  A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. length(n.neighbors) indicates the total number of spatial entities.

- **neighbors**
  A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, ... ,
neighbors of the last entity). Length of the neighbors vector should be equal to \(\text{sum(n.neighbors)}\).

**suitability.pred**

An optional data frame in which to look for variables with which to predict. If NULL, the data frame data.suitability for observations is used.

**spatial.entity.pred**

An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.

**burnin**

The number of burnin iterations for the sampler.

**mcmc**

The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to \(\text{burnin+mcmc}\). burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

**thin**

The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

**beta.start**

Starting values for \(\beta\) parameters of the suitability process. This can either be a scalar or a \(p\)-length vector.

**gamma.start**

Starting values for \(\beta\) parameters of the observability process. This can either be a scalar or a \(q\)-length vector.

**vrho.start**

Positive scalar indicating the starting value for the variance of the spatial random effects.

**mubeta**

Means of the priors for the \(\beta\) parameters of the suitability process. \(\text{mubeta}\) must be either a scalar or a \(p\)-length vector. If \(\text{mubeta}\) takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

**vbeta**

Variances of the Normal priors for the \(\beta\) parameters of the suitability process. \(\text{vbeta}\) must be either a scalar or a \(p\)-length vector. If \(\text{vbeta}\) takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

**mugamma**

Means of the Normal priors for the \(\gamma\) parameters of the observability process. \(\text{mugamma}\) must be either a scalar or a \(p\)-length vector. If \(\text{mugamma}\) takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

**vgamma**

Variances of the Normal priors for the \(\gamma\) parameters of the observability process. \(\text{vgamma}\) must be either a scalar or a \(p\)-length vector. If \(\text{vgamma}\) takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

**priorvrho**

Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters \(\text{shape}\) and \(\text{rate}\), or to a uniform distribution ("Uniform") on the interval \([0,\text{vrho.max}]\). Default set to "1/Gamma".

**shape**

The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is \(\text{shape}=0.05\) for uninformative prior.

**rate**

The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is \(\text{rate}=0.0005\) for uninformative prior.
\textbf{Vrho.max} Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

\textbf{seed} The seed for the random number generator. Default set to 1234.

\textbf{verbose} A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in \%) reached by the Gibbs sampler.

\textbf{save.rho} A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

\textbf{save.p} A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the lambda.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

\textbf{save.N} A switch (0,1) which determines whether or not the sampled values for the latent count variable N for each observed cells are saved. Default is 0: the mean (rounded to the closest integer) is computed and returned in the N.pred vector. Be careful, setting save.N to 1 might require a large amount of memory.

\textbf{Details}

The model integrates two processes, an ecological process associated to the abundance of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one. The ecological process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the abundance of the species at one site depends on the abundance of the species on neighboring sites.

\textbf{Ecological process:}
\[ N_i \sim \text{Poisson}(\lambda_i) \]
\[ \log(\lambda_i) = X_i \beta + \rho_i \]
\[ \rho_i: \text{spatial random effect} \]

\textbf{Spatial autocorrelation:}
An intrinsic conditional autoregressive model (iCAR) is assumed:
\[ \rho_i \sim \text{Normal}(\mu_i, V_{\rho}/n_i) \]
\[ \mu_i: \text{mean of } \rho_{ij} \text{ in the neighborhood of } i. \]
\[ V_{\rho}: \text{variance of the spatial random effects.} \]
\[ n_i: \text{number of neighbors for spatial entity } i. \]

\textbf{Observation process:}
\[ y_{it} \sim \text{Binomial}(N_i, \delta_{it}) \]
\[ \logit(\delta_{it}) = W_{it} \gamma \]
Value

mcmc
An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod_{it} P(y_{it}, \lambda_{it}|...))$, is also provided.

rho.pred
If save.rho is set to 0 (default), rho.pred is the predictive posterior mean of the spatial random effect associated to each spatial entity. If save.rho is set to 1, rho.pred is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

lambda.pred
If save.p is set to 0 (default), lambda.pred is the predictive posterior mean of the abundance associated to the suitability process for each prediction. If save.p is set to 1, lambda.pred is an mcmc object with sampled values of the abundance associated to the suitability process for each prediction.

N.pred
If save.N is set to 0 (default), N.pred is the posterior mean (rounded to the closest integer) of the latent count variable N for each observed cell. If save.N is set to 1, N.pred is an mcmc object with sampled values of the latent count variable N for each observed cell.

lambda.latent
Predictive posterior mean of the abundance associated to the suitability process for each observation.

delta.latent
Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References


See Also

plot.mcmc, summary.mcmc

Examples

```
## Not run:

# Example with simulated data
```

```
```
```r
# Load libraries
library(hSDM)
library(raster)
library(sp)

# Multivariate normal distribution
rmvn <- function(n, mu = 0, V = matrix(1), seed=1234) {
  p <- length(mu)
  if (any(is.na(match(dim(V), p)))) {
    stop("Dimension problem!")
  }
  D <- chol(V)
  set.seed(seed)
  t(matrix(rnorm(n*p),ncol=p)%*%D+rep(mu,rep(n,p)))
}

# Data simulation
# Set seed for repeatability
seed <- 4321

# Landscape
xland <- 20
yland <- 20
Landscape <- raster(ncol=xLand,nrow=yLand,crs='+proj=utm +zone=1')
Landscape[] <- 0
extent(Landscape) <- c(0,xLand,0,yLand)
coords <- coordinates(Landscape)
ncells <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncells), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0,ncells,ncells)
index.start <- 1
for (i in 1:ncells) {
  index.end <- index.start+n.neighbors[i]-1
  A[i,adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial effects
vrho.target <- 5
d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
```
Q <- diag(n.neighbors)-d*A + diag(.0001,n.cells) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
rho <- c(rmvn(1, mu=rep(0,n.cells), V=covrho, seed=seed)) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

#= Raster and plot spatial effects
r.rho <- rasterFromXYZ(cbind(coords,rho))
plot(r.rho)

#= Sample the observation sites in the landscape
nsite <- 150
set.seed(seed)
x.coord <- runif(nsite,0,x.Land)
set.seed(2*seed)
y.coord <- runif(nsite,0,y.Land)
sites.sp <- SpatialPoints(coords=cbind(x.coord,y.coord))
cells <- extract(Landscape,sites.sp,cell=TRUE)[,1]

#= Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1)
log.lambda <- X %*% beta.target + rho[cells]
lambda <- exp(log.lambda)
set.seed(seed)
N <- rpois(nsite,lambda)

#= Relative importance of spatial random effects
RImp <- mean(abs(rho[cells])/abs(X %*% beta.target))

#= Number of visits associated to each observation point
set.seed(seed)
visits <- rpois(nsite,3)
visits[visits==0] <- 1
# Vector of observation points
sites <- vector()
for (i in 1:nsite) {
  sites <- c(sites,rep(i,visits[i]))
}

#= Observation process (detectability)
nobs <- sum(visits)
set.seed(seed)
w1 <- rnorm(nobs,0,1)
set.seed(2*seed)
w2 <- rnorm(nobs,0,1)
W <- cbind(rep(1,nobs),w1,w2)
gamma.target <- c(-1,1,-1)
logit.delta <- W %% gamma.target
delta <- inv.logit(logit.delta)
set.seed(seed)
Y <- rbinom(n.obs,N[sites],delta)

# Data-sets
data.obs <- data.frame(Y,w1,w2,site=sites)
data.suit <- data.frame(x1,x2,cell=cells)

# Parameter inference with hSDM
Start <- Sys.time() # Start the clock
mod.hSDM.Nmixture.iCAR <- hSDM.Nmixture.iCAR(# Observations
counts=data.obs$Y,
observability=w1+w2,
site=data.obs$site,
data.observability=data.obs,
# Habitat
suitability=-x1+x2, data.suitability=data.suit,
# Spatial structure
spatial.entity=data.suit$cell,
n.neighbors=n.neighbors, neighbors=adj,
# Predictions
suitability.pred=NULL,
spatial.entity.pred=NULL,
# Chains
burnin=5000, mcmc=5000, thin=5,
# Starting values
beta.start=0,
gamma.start=0,
Vrho.start=1,
# Priors
mubeta=0, Vbeta=1.0E6,
mugamma=0, Vgamma=1.0E6,
priorVrho="1/Gamma",
shape=0.5, rate=0.005,
Vrho.max=10,
# Various
seed=1234, verbose=1,
save.rho=1, save.p=0, save.N=1)
Time.hSDM <- difftime(Sys.time(),Start,units="sec") # Time difference

# Computation time
Time.hSDM

# Outputs

# Parameter estimates
summary(mod.hSDM.Nmixture.iCAR$mcmc)
pdf(file="Posteriors_hSDM.Nmixture.iCAR.pdf")
plot(mod.hSDM.Nmixture.iCAR$mcmc)
dev.off()

# Predictions
summary(mod.hSDM.Nmixture.iCAR$lambda.latent)
summary(mod.hSDM.Nmixture.iCAR$delta.latent)
summary(mod.hSDM.Nmixture.iCAR$lambda.pred)
pdf(file="Pred-Init.pdf")
plot(lambda(mod.hSDM.Nmixture.iCAR$lambda.pred))
abline(a=0,b=1,col="red")
dev.off()

# MCMC for latent variable N
pdf(file="MCMC_N.pdf")
plot(mod.hSDM.Nmixture.iCAR$N.pred)
dev.off()

# Check that Ns are correctly estimated
M <- as.matrix(mod.hSDM.Nmixture.iCAR$N.pred)
N.est <- apply(M,2,mean)
Y.by.site <- tapply(data.obs$Y,data.obs$site,mean) # Mean by site
pdf(file="Check_N.pdf",width=10,height=5)
par(mfrow=c(1,2))
plot(Y.by.site, N.est) ## More individuals are expected (N > Y) due to detection process
abline(a=0,b=1,col="red")
plot(N, N.est) ## N are well estimated
abline(a=0,b=1,col="red")
cor(N, N.est) ## Very close to 1
dev.off()

# Summary plots for spatial random effects
# rho.pred
rho.pred <- apply(mod.hSDM.Nmixture.iCAR$rho.pred,2,mean)
r.rho.pred <- rasterFromXYZ(cbind(coords,rho.pred))

# plot
pdf(file="Summary_hSDM.Nmixture.iCAR.pdf")
par(mfrow=c(2,2))
# rho target
plot(r.rho, main="rho target")
plot(sites.sp,add=TRUE)
# rho estimated
plot(r.rho.pred, main="rho estimated")
# correlation and "shrinkage"
Levels.cells <- sort(unique(cells))
plot(rho[-Levels.cells],rho.pred[-Levels.cells],
     xlim=range(rho),
     ylim=range(rho),
     xlab="rho target",
     ylab="rho estimated")
points(rho[Levels.cells],rho.pred[Levels.cells],pch=16,col="blue")
legend(x=3,y=4,legend="Visited cells",col="blue",pch=16,bty="n")
abline(a=0,b=1,col="red")
**hSDM.poisson**

**Poisson log regression model**

### Description

The `hSDM.poisson` function performs a Poisson log regression in a Bayesian framework. The function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of model’s parameters.

### Usage

```
hsdm.poisson(counts, suitability, data, suitability.pred = NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, mubeta = 0, Vbeta = 1e+06, seed = 1234, verbose = 1, save.p = 0)
```

### Arguments

- **counts**
  A vector indicating the count (or abundance) for each observation.

- **suitability**
  A one-sided formula of the form `'~x1+...+xp'` with `p` terms specifying the explicative covariates for the suitability process of the model.

- **data**
  A data frame containing the model’s explicative variables.

- **suitability.pred**
  An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

- **burnin**
  The number of burnin iterations for the sampler.

- **mcmc**
  The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to `burnin+mcmc`. `burnin+mcmc` must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

- **thin**
  The thinning interval used in the simulation. The number of `mcmc` iterations must be divisible by this value.

- **beta.start**
  Starting values for beta parameters of the suitability process. If `beta.start` takes a scalar value, then that value will serve for all of the betas.

- **mubeta**
  Means of the priors for the $\beta$ parameters of the suitability process. `mubeta` must be either a scalar or a `p`-length vector. If `mubeta` takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

- **Vbeta**
  Variances of the Normal priors for the $\beta$ parameters of the suitability process. `Vbeta` must be either a scalar or a `p`-length vector. If `Vbeta` takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.
seed The seed for the random number generator. Default to 1234.

verbose A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.p A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the lambda.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

We model the abundance of the species as a function of environmental variables.

Ecological process:

\[ y_i \sim P_{\text{Poisson}}(\lambda_i) \]

\[ \log(\lambda_i) = X_i \beta \]

Value

mcmc An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod P(y_i, n_i|\beta)) \), is also provided.

lambda.pred If save.p is set to 0 (default), lambda.pred is the predictive posterior mean of the abundance associated to the suitability process for each prediction. If save.p is set to 1, lambda.pred is an mcmc object with sampled values of the abundance associated to the suitability process for each prediction.

lambda.latent Predictive posterior mean of the abundance associated to the suitability process for each observation.

Author(s)

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References


See Also

plot.mcmc, summary.mcmc
Examples

```r
## Not run:

#---------------------------------------------
# hSDM.poisson()
# Example with simulated data
#---------------------------------------------

#------------------
#== Load libraries
library(hSDM)
#------------------

#== Data simulation

# Number of sites
nsite <- 200

# Set seed for repeatability
seed <- 1234

# Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1)
log.lambda <- X %*% beta.target
lambda <- exp(log.lambda)
set.seed(seed)
y <- rpois(nsite,lambda)

# Data-sets
data.obs <- data.frame(Y,x1,x2)

#------------------
#== Site-occupancy model

mod.hSDM.poisson <- hSDM.poisson(counts=data.obs$Y,
suitability=x1+x2,
data=data.obs,
suitability.pred=NULL,
burnin=1000, mcmc=1000, thin=1,
beta.start=0,
mubeta=0, Vbeta=1.0E6,
seed=1234, verbose=1,
save.p=0)
```

#== Outputs
hSDM.poisson.iCAR

Poisson log regression model with CAR process

Description
The hSDM.poisson.iCAR function performs a Poisson log regression in a hierarchical Bayesian framework. The suitability process includes a spatial correlation process. The spatial correlation is modelled using an intrinsic CAR model. The hSDM.poisson.iCAR function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

Usage
hSDM.poisson.iCAR(counts, suitability, spatial.entity, data, n.neighbors, neighbors, suitability.pred=NULL, spatial.entity.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, Vrho.start, mubeta = 0, Vbeta = 1e+06, priorVrho = "1/Gamma", shape = 0.5, rate = 0.0005, Vrho.max=1000, seed = 1234, verbose = 1, save.rho = 0, save.p = 0)

Arguments
counts A vector indicating the count (or abundance) for each observation.
suitability A one-sided formula of the form $\sim x_1 + ... + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
spatial.entity A vector indicating the spatial entity identifier (from one to the total number of entities) for each observation. Several observations can occur in one spatial entity. A spatial entity can be a raster cell for example.

data A data frame containing the model's variables.
n.neighbors A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. length(n.neighbors) indicates the total number of spatial entities.

neighbors A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, ..., neighbors of the last entity). Length of the neighbors vector should be equal to sum(n.neighbors).
suitability.pred An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

spatial.entity.pred An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.
burnin The number of burnin iterations for the sampler.
mcmc The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to burnin+mcmc. burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

thin The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start Starting values for \( \beta \) parameters of the suitability process. This can either be a scalar or a \( p \)-length vector.

Vrho.start Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta Means of the priors for the \( \beta \) parameters of the suitability process. \( \text{mubeta} \) must be either a scalar or a \( p \)-length vector. If \( \text{mubeta} \) takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta Variances of the Normal priors for the \( \beta \) parameters of the suitability process. \( \text{Vbeta} \) must be either a scalar or a \( p \)-length vector. If \( \text{Vbeta} \) takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

priorVrho Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval [0, Vrho.max]. Default set to "1/Gamma".

shape The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is shape=0.05 for uninformative prior.

rate The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.
Vrho.Nmax \quad \text{Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.}

seed \quad \text{The seed for the random number generator. Default set to 1234.}

verbose \quad \text{A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in \%) reached by the Gibbs sampler.}

save.rho \quad \text{A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.}

save.p \quad \text{A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the lambda.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.}

Details

We model an ecological process where the abundance of the species is explained by habitat suitability. The ecological process includes an intrinsic conditional autoregressive (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

Ecological process:

\[ y_i \sim Poisson(\lambda_i, t_i) \]

\[ \log(\lambda_i) = X_i \beta + \rho_j(i) \]

\[ \rho_j: \text{ spatial random effect} \]

\[ j(i): \text{ index of the spatial entity for observation } i. \]

Spatial autocorrelation:

An intrinsic conditional autoregressive model (iCAR) is assumed:

\[ \rho_j \sim Normal(\mu_j, V_\rho/n_j) \]

\[ \mu_j: \text{ mean of } \rho_{j'} \text{ in the neighborhood of } j. \]

\[ V_\rho: \text{ variance of the spatial random effects.} \]

\[ n_j: \text{ number of neighbors for spatial entity } j. \]

Value

mcmc \quad \text{An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance } D, \text{ with } D = -2 \log(\prod_i P(y_i|...)), \text{ is also provided.}

rho.pred \quad \text{If save.rho is set to 0 (default), rho.pred is the predictive posterior mean of the spatial random effect associated to each spatial entity. If save.rho is set to 1, rho.pred is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.}
If `saveNp` is set to 0 (default), `lambda.pred` is the predictive posterior mean of the abundance associated to the suitability process for each prediction. If `saveNp` is set to 1, `lambda.pred` is an `mcmc` object with sampled values of the abundance associated to the suitability process for each prediction.

`lambda.latent` Predictive posterior mean of the abundance associated to the suitability process for each observation.

**Author(s)**

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

**References**


**See Also**

`plot.mcmc`, `summary.mcmc`

**Examples**

```r
## Not run:

#---------------------------------------------------------------
# hSDM.poisson.iCAR()
# Example with simulated data
#---------------------------------------------------------------

#-----------------
# Load libraries
library(hSDM)
library(raster)
library(sp)

#-----------------
# Multivariate normal distribution
rmvn <- function(n, mu = 0, V = matrix(1), seed=1234) {
  p <- length(mu)
  if (any(is.na(match(dim(V), p)))) {
    stop("Dimension problem!")
  }
```

```
D <- chol(V)
set.seed(seed)
t(matrix(rnorm(n*p),ncol=p)%*%rep(mu,rep(n,p)))
}

# Data simulation

# Set seed for repeatability
seed <- 1234

# Landscape
xLand <- 30
yLand <- 30
Landscape <- raster(ncol=xLand,nrow=yLand,crs='+proj=utm +zone=1')
Landscape[] <- 0
extent(Landscape) <- c(0,xLand,0,yLand)
coords <- coordinates(Landscape)
ncells <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncells), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0,ncells,ncells)
index.start <- 1
for (i in 1:ncells) {
  index.end <- index.start+n.neighbors[i]-1
  A[i,adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial effects
Vrho.target <- 5
d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors)-d*A + diag(.0001,ncells) # Add small constant to make Q non-singular
covrho <- Vrho.target+solve(Q) # Covariance of rhos
set.seed(seed)
rho <- crmvn(1,mu=rep(0,ncells),V=covrho,seed=seed) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

# Raster and plot spatial effects
r.rho <- rasterFromXYZ(cbind(coords,rho))
plot(r.rho)

# Sample the observation sites in the landscape
nsite <- 250
set.seed(seed)
x.coord <- runif(nsite,0,xLand)
set.seed(2*seed)
y.coord <- runif(nsite,0,yLand)
```r
sites.sp <- SpatialPoints(coords=cbind(x.coord,y.coord))
cells <- extract(Landscape,sites.sp,cell=TRUE)[,1]

# Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1)
log.lambda <- X %*% beta.target + rho[cells]
lambda <- exp(log.lambda)
set.seed(seed)
Y <- rpois(nsite,lamba)

# Relative importance of spatial random effects
Rlmp <- mean(abs(rho[cells]))/abs(X %*% beta.target)
Rlmp

# Data-sets
data.obs <- data.frame(Y,x1,x2,cell=cells)

# Site-occupancy model
Start <- Sys.time() # Start the clock
mod.hSDM.poisson.iCAR <- hSDM.poisson.iCAR(counts=data.obs$Y,
suitability=x1+x2,
spatial.entity=data.obs$cell,
data=data.obs,
n.neighbors=n.neighbors,
neighbours=adj,
suitability.pred=NULL,
spatial.entity.pred=NULL,
burnin=5000, mcmc=5000, thin=5,
beta.start=0,
Vrho.start=1,
mubeta=0, Vbeta=1.0E6,
priorVrho="1/Gamma",
shape=0.5, rate=0.0005,
seed=1234, verbose=1,
save.rho=1, save.p=0)

Time.hSDM <- difftime(Sys.time(),Start,units="sec") # Time difference

# Computation time
Time.hSDM

# Outputs

# Parameter estimates
summary(mod.hSDM.poisson.iCAR$mcmc)
pdf("Posteriors_hSDM.poisson.iCAR.pdf")
```
The `hSDM.siteocc` function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (refering to environmental suitability) and a Bernoulli observability process (refering to various ecological and methodological issues explaining the species detection). The `hSDM.siteocc` function calls a Gibbs sampler.
written in C code which uses a Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

Usage

```r
hSDM.siteocc(# Observations
  presence, observability, site, data.observability,
  # Habitat
  suitability, data.suitability,
  # Predictions
  suitability.pred = NULL,
  # Chains
  burnin = 1000, mcmc = 1000, thin = 1,
  # Starting values
  beta.start,
  gamma.start,
  # Priors
  mubeta = 0, Vbeta = 1.0E6,
  mugamma = 0, Vgamma = 1.0E6,
  # Various
  seed = 1234, verbose = 1,
  save.p = 0)
```

Arguments

- **presence**: A vector indicating the presence/absence for each observation.
- **observability**: A one-sided formula of the form $\sim w_1 + \ldots + w_q$ with $q$ terms specifying the explicative variables for the observability process.
- **site**: A vector indicating the site identifier (from one to the total number of sites) for each observation. Several observations can occur at one site. A site can be a raster cell for example.
- **data.observability**: A data frame containing the model’s variables for the observability process.
- **suitability**: A one-sided formula of the form $\sim x_1 + \ldots + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
- **data.suitability**: A data frame containing the model’s variables for the suitability process.
- **suitability.pred**: An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
- **burnin**: The number of burnin iterations for the sampler.
- **mcmc**: The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to $\text{burnin} + \text{mcmc}$. $\text{burnin} + \text{mcmc}$ must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
- **thin**: The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.
beta.start  Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a $p$-length vector.
gamma.start  Starting values for $\beta$ parameters of the observability process. This can either be a scalar or a $q$-length vector.
mubeta     Means of the priors for the $\beta$ parameters of the suitability process. $\mu_{\beta}$ must be either a scalar or a $p$-length vector. If $\mu_{\beta}$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

$\Sigma_{\beta}$  Variances of the Normal priors for the $\beta$ parameters of the suitability process. $\Sigma_{\beta}$ must be either a scalar or a $p$-length vector. If $\Sigma_{\beta}$ takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to $1.0E6$ for an uninformative flat prior.

$mugamma$  Means of the Normal priors for the $\gamma$ parameters of the observability process. $mugamma$ must be either a scalar or a $p$-length vector. If $mugamma$ takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.
$vgamma$  Variances of the Normal priors for the $\gamma$ parameters of the observability process. $vgamma$ must be either a scalar or a $p$-length vector. If $vgamma$ takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to $1.0E6$ for an uninformative flat prior.

seed  The seed for the random number generator. Default set to 1234.
verbose  A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.
save.p  A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the $\lambda_{\text{pred}}$ vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one.

**Ecological process:**

$$z_i \sim Bernoulli(\theta_i)$$

$$\logit(\theta_i) = X_i \beta$$

**Observation process:**

$$y_{it} \sim Bernoulli(z_i * \delta_{it})$$

$$\logit(\delta_{it}) = W_{it} \gamma$$
Value

**mcmc**
An `mcmc` object that contains the posterior sample. This object can be summarized by functions provided by the `coda` package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod_{it} P(y_{it}, N_i|\ldots)) \), is also provided.

**theta.pred**
If `save.p` is set to 0 (default), `theta.pred` is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, `theta.pred` is an `mcmc` object with sampled values of the probability associated to the suitability process for each prediction.

**theta.latent**
Predictive posterior mean of the probability associated to the suitability process for each site.

**delta.latent**
Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References


See Also

`plot.mcmc`, `summary.mcmc`

Examples

```r
## Not run:

#---------------------------------------------
# hSDM.siteocc()
# Example with simulated data
#---------------------------------------------

#-------------
## Load libraries
library(hSDM)

#-------------
## Data simulation

## Number of observation sites
nsite <- 200

## Set seed for repeatability
seed <- 4321
```
### Ecological process (suitability)

```r
set.seed(seed)
set.seed(2*seed)
x1 <- rnorm(nsite, 0, 1)
x2 <- rnorm(nsite, 0, 1)
X <- cbind(rep(1, nsite), x1, x2)
beta.target <- c(-1, 1, -1)  # Target parameters
logit.theta <- X %*% beta.target
theta <- inv.logit(logit.theta)
set.seed(seed)
Z <- rbinom(nsite, 1, theta)
```

### Number of visits associated to each observation point

```r
set.seed(seed)
visits <- rpois(nsite, 3)
visits[visits==0] <- 1
# Vector of observation points
sites <- vector()
for (i in 1:nsite) {
  sites <- c(sites, rep(i, visits[i]))
}
```

### Observation process (detectability)

```r
set.seed(seed)
set.seed(2*seed)
w1 <- rnorm(nobs, 0, 1)
w2 <- rnorm(nobs, 0, 1)
W <- cbind(rep(1, nobs), w1, w2)
gamma.target <- c(-1, 1, -1)  # Target parameters
logit.delta <- W %*% gamma.target
delta <- inv.logit(logit.delta)
set.seed(seed)
Y <- rbinom(nobs, 1, delta*Z[sites])
```

### Data-sets

```r
data.obs <- data.frame(Y, w1, w2, site=sites)
data.suit <- data.frame(x1, x2)
```

```r
# Parameter inference with hSDM
```

Start <- Sys.time()  # Start the clock
mod.hSDM.siteocc <- hSDM.siteocc(# Observations
  presence=data.obs$Y,
  observability=-w1+w2,
  site=data.obs$site,
  data.observability=data.obs,
  # Habitat
  suitability=-x1+x2,
  data.suitability=data.suit,
  # Predictions
)
The `hsdm_siteocc.iCAR` function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (referred to environmental suitability) which takes into account the spatial dependence of the observations, and a Bernoulli observability process (referring to various ecological and methodological issues explaining the species detection). The `hsdm_siteocc.iCAR` function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.
Usage

hSDM.siteocc.iCAR(
  presence, observability, site, data.observability,
  # Habitat
  suitability, data.suitability,
  # Spatial structure
  spatial.entity,
  n.neighbors, neighbors,
  # Predictions
  suitability.pred = NULL, spatial.entity.pred = NULL,
  # Chains
  burnin = 1000, mcmc = 1000, thin = 1,
  # Starting values
  beta.start, gamma.start, Vrho.start,
  # Priors
  mubeta = 0, Vbeta = 1.0E6,
  mugamma = 0, Vgamma = 1.0E6,
  priorVrho = "1/Gamma",
  shape = 0.5, rate = 0.0005,
  Vrho.max = 1000,
  # Various
  seed = 1234, verbose = 1,
  save.rho = 0, save.p = 0)

Arguments

presence A vector indicating the presence/absence for each observation.
observability A one-sided formula of the form $w_1 + \ldots + w_q$ with $q$ terms specifying the explicative variables for the observability process.
site A vector indicating the site identifier (from one to the total number of sites) for each observation. Several observations can occur at one site. A site can be a raster cell for example.
data.observability A data frame containing the model's variables for the observability process.
suitability A one-sided formula of the form $x_1 + \ldots + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
data.suitability A data frame containing the model's variables for the suitability process.
spatial.entity A vector (of length 'nsite') indicating the spatial entity identifier for each site. Values must be between 1 and the total number of spatial entities. Several sites can be found in one spatial entity. A spatial entity can be a raster cell for example.
n.neighbors A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. length(n.neighbors) indicates the total number of spatial entities.
neighbors A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, ..., neighbors of the last entity). Length of the neighbors vector should be equal to \(\text{sum(n.neighbors)}\).

suitability.pred An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

spatial.entity.pred An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.

burnin The number of burnin iterations for the sampler.

mcmc The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to \(\text{burnin+mcmc}\). \(\text{burnin+mcmc}\) must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

thin The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start Starting values for \(\beta\) parameters of the suitability process. This can either be a scalar or a \(p\)-length vector.

gamma.start Starting values for \(\gamma\) parameters of the observability process. This can either be a scalar or a \(q\)-length vector.

Vrho.start Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta Means of the priors for the \(\beta\) parameters of the suitability process. \(\text{mubeta}\) must be either a scalar or a \(p\)-length vector. If \(\text{mubeta}\) takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta Variances of the Normal priors for the \(\beta\) parameters of the suitability process. \(\text{Vbeta}\) must be either a scalar or a \(p\)-length vector. If \(\text{Vbeta}\) takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

mugamma Means of the Normal priors for the \(\gamma\) parameters of the observability process. \(\text{mugamma}\) must be either a scalar or a \(p\)-length vector. If \(\text{mugamma}\) takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

Vgamma Variances of the Normal priors for the \(\gamma\) parameters of the observability process. \(\text{Vgamma}\) must be either a scalar or a \(p\)-length vector. If \(\text{Vgamma}\) takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

priorVrho Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval \([0, \text{Vrho}.\text{max}]\). Default set to "1/Gamma".

shape The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is \(\text{shape}=0.05\) for uninformative prior.
rate

The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.

vrho.max

Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed

The seed for the random number generator. Default set to 1234.

verbose

A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho

A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p

A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the theta.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one. The ecological process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

**Ecological process:**

\[ z_i \sim Bernoulli(\theta_i) \]

\[ \text{logit}(\theta_i) = X_i \beta + \rho_j(i) \]

\( \rho_j: \) spatial random effect

\( j(i): \) index of the spatial entity for observation \( i. \)

**Spatial autocorrelation:**

An intrinsic conditional autoregressive model (iCAR) is assumed:

\[ \rho_j \sim \text{Normal}(\mu_j, V_\rho/n_j) \]

\( \mu_j: \) mean of \( \rho_j \) in the neighborhood of \( j. \)

\( V_\rho: \) variance of the spatial random effects.

\( n_j: \) number of neighbors for spatial entity \( j. \)

**Observation process:**

\[ y_{it} \sim Bernoulli(z_i \delta_{it}) \]

\[ \text{logit}(\delta_{it}) = W_{it} \gamma \]
Value

mcmc
An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod_i P(y_i, z_i|...))$, is also provided.

rho.pred
If `save.rho` is set to 0 (default), `rho.pred` is the predictive posterior mean of the spatial random effect associated to each spatial entity. If `save.rho` is set to 1, `rho.pred` is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

theta.pred
If `save.p` is set to 0 (default), `theta.pred` is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, `theta.pred` is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

theta.latent
Predictive posterior mean of the probability associated to the suitability process for each site.

delta.latent
Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References


See Also

plot.mcmc, summary.mcmc

Examples

```r
## Not run:

#==============================
# hSDM.siteocc.iCAR()
```
# Example with simulated data
#=================================

# Load libraries
library(hSDM)
library(raster)
library(sp)

# Multivariate normal distribution
rmvn <- function(n, mu = 0, V = matrix(1), seed=1234) {
  p <- length(mu)
  if (any(is.na(match(dim(V), p)))) {
    stop("Dimension problem!")
  }
  D <- chol(V)
  set.seed(seed)
  t(matrix(rnorm(n*p),ncol=p)*D+rep(mu,rep(n,p))
}

# Data simulation
# Set seed for repeatability
seed <- 1234

# Landscape
xLand <- 30
yLand <- 30
Landscape <- raster(ncol=xLand,nrow=yLand,crs=’+proj=utm +zone=1’)
Landscape[] <- 0
extent(Landscape) <- c(0,xLand,0,yLand)
coords <- coordinates(Landscape)
ncells <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncells), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0,ncells,ncells)
index.start <- 1
for (i in 1:ncells) {
  index.end <- index.start+n.neighbors[i]-1
  A[i,adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial effects
vrho.target <- 5
d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors)-d*A + diag(.0001,ncells) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
rho <- c(rmvn(1,mu=rep(0,ncells),V=covrho,seed=seed)) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

# Raster and plot spatial effects
r.rho <- rasterFromXYZ(cbind(coords,rho))
plot(r.rho)

# Sample the observation sites in the landscape
nsite <- 250
set.seed(seed)
x.coord <- runif(nsite,0,xLand)
set.seed(2*seed)
y.coord <- runif(nsite,0,yLand)
sites.sp <- SpatialPoints(coords=cbind(x.coord,y.coord))
cells <- extract(Landscape,sites.sp,cell=TRUE)[,1]

# Ecological process (suitability)
set.seed(seed)
x1 <- rnorm(nsite,0,1)
set.seed(2*seed)
x2 <- rnorm(nsite,0,1)
X <- cbind(rep(1,nsite),x1,x2)
beta.target <- c(-1,1,-1)
logit.theta <- X * beta.target + rho[cells]
theta <- inv.logit(logit.theta)
set.seed(seed)
Z <- rbinom(nsite,1,theta)

# Relative importance of spatial random effects
RImp <- mean(abs(rho[cells])/abs(X * beta.target))

# Number of visits associated to each observation point
set.seed(seed)
visits <- rpois(nsite,3)
visits[visits==0] <- 1
# Vector of observation points
sites <- vector()
for (i in 1:nsite) {
  sites <- c(sites,rep(i,visits[i]))
}

# Observation process (detectability)
nobs <- sum(visits)
set.seed(seed)
w1 <- rnorm(nobs,0,1)
set.seed(2*seed)
w2 <- rnorm(nobs,0,1)
W <- cbind(rep(1,nobs),w1,w2)
gamma.target <- c(-1,1,-1)
logit.delta <- \$\gamma \%\% \gamma.\text{target}
delta <- inv.logit(logit.delta)
set.seed(seed)
Y <- rbinom(nobs, 1, delta*Z[sites])

### Data-sets
data.obs <- data.frame(Y, w1, w2, site=sites)
data.suit <- data.frame(x1, x2, cell=cells)

### Parameter inference with hSDM

Start <- Sys.time() # Start the clock
mod.hSDM.siteocc.iCAR <- hSDM.siteocc.iCAR(
  # Observations
presence=data.obs$Y,
  observability=w1+w2,
  site=data.obs$site,
  data.observability=data.obs,
  # Habitat
  suitability=-x1+x2, data.suitability=data.suit,
  # Spatial structure
  spatial.entity=data.suit$cell,
  n.neighbors=n.neighbors, neighbors=adj,
  # Predictions
  suitability.pred=NULL,
  spatial.entity.pred=NULL,
  # Chains
  burnin=10000, mcmc=5000, thin=5,
  # Starting values
  beta.start=0,
  gamma.start=0,
  Vrho.start=1,
  # Priors
  mubeta=0, Vbeta=1.0E6,
  mugamma=0, Vgamma=1.0E6,
  priorVrho="Uniform",
  Vrho.max=10,
  # Various
  seed=1234, verbose=1,
  save.rho=1, save.p=0)

Time.hSDM <- difftime(Sys.time(), Start, units="sec") # Time difference

### Computation time
Time.hSDM

### Outputs

### Parameter estimates
summary(mod.hSDM.siteocc.iCAR$mcmc)
pdf("Posteriors_hSDM.siteocc.iCAR.pdf")
plot(mod.hSDM.siteocc.iCAR$mcmc)
dev.off()
# Predictions
summary(mod.hSDM.siteocc.iCAR$theta.latent)
summary(mod.hSDM.siteocc.iCAR$delta.latent)
summary(mod.hSDM.siteocc.iCAR$theta.pred)
pdf(file="Pred-Init.pdf")
plot(theta,mod.hSDM.siteocc.iCAR$theta.pred)
abline(a=0,b=1,col="red")
dev.off()

# Summary plots for spatial random effects

# rho.pred
rho.pred <- apply(mod.hSDM.siteocc.iCAR$rho.pred,2,mean)
r.rho.pred <- rasterFromXYZ(cbind(coords,rho.pred))

# plot
pdf(file="Summary_hSDM.siteocc.iCAR.pdf")
par(mfrow=c(2,2))
# rho target
plot(r.rho, main="rho target")
plot(sites.sp,add=TRUE)
# rho estimated
plot(r.rho.pred, main="rho estimated")
# correlation and "shrinkage"
Levels.cells <- sort(unique(cells))
plot(rho[-Levels.cells],rho.pred[-Levels.cells],
     xlim=range(rho),
     ylim=range(rho),
     xlab="rho target",
     ylab="rho estimated")
points(rho[Levels.cells],rho.pred[Levels.cells],pch=16,col="blue")
legend(x=-3,y=4,legend="Visited cells",col="blue",pch=16,bty="n")
abline(a=0,b=1,col="red")
dev.off()

## End(Not run)

---

**hSDM.ZIB**

**ZIB (Zero-Inflated Binomial) model**

### Description

The hSDM.ZIB function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (refering to environmental suitability) and a Binomial observability process (refering to various ecological and methodological issues explaining the species detection). The hSDM.ZIB function calls a Gibbs sampler written in C code which uses a Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.
Usage

hSDM.ZIB(presences, trials, suitability, observability, data, suitability.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, gamma.start, mubeta = 0, Vbeta = 1e+06, mugamma = 0, Vgamma = 1e+06, seed = 1234, verbose = 1, save.p = 0)

Arguments

presences A vector indicating the number of successes (or presences) for each observation.

trials A vector indicating the number of trials for each observation. \( t_i \) should be superior to zero and superior or equal to \( y_i \), the number of successes for observation \( i \).

suitability A one-sided formula of the form \( \sim x_1 + \ldots + x_p \) with \( p \) terms specifying the explicative variables for the suitability process.

observability A one-sided formula of the form \( \sim w_1 + \ldots + w_q \) with \( q \) terms specifying the explicative variables for the observability process.

data A data frame containing the model’s variables.

suitability.pred An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

burnin The number of burnin iterations for the sampler.

mcmc The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to \( \text{burnin} + \text{mcmc} \). \( \text{burnin} + \text{mcmc} \) must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

thin The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start Starting values for \( \beta \) parameters of the suitability process. This can either be a scalar or a \( p \)-length vector.

gamma.start Starting values for \( \beta \) parameters of the observability process. This can either be a scalar or a \( q \)-length vector.

mubeta Means of the priors for the \( \beta \) parameters of the suitability process. \( \text{mubeta} \) must be either a scalar or a \( p \)-length vector. If \( \text{mubeta} \) takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta Variances of the Normal priors for the \( \beta \) parameters of the suitability process. \( \text{Vbeta} \) must be either a scalar or a \( p \)-length vector. If \( \text{Vbeta} \) takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

mugamma Means of the Normal priors for the \( \gamma \) parameters of the observability process. \( \text{mugamma} \) must be either a scalar or a \( p \)-length vector. If \( \text{mugamma} \) takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.
Vgamma
Variances of the Normal priors for the $\gamma$ parameters of the observability process. $\text{Vgamma}$ must be either a scalar or a $p$-length vector. If $\text{Vgamma}$ takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

seed
The seed for the random number generator. Default set to 1234.

verbose
A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.p
A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the $\text{prob.p.pred}$ vector. Be careful, setting $\text{save.p}$ to 1 might require a large amount of memory.

Details
The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one.

Ecological process:
$$z_i \sim \text{Bernoulli}(\theta_i)$$
$$\text{logit}(\theta_i) = X_i \beta$$

Observation process:
$$y_i \sim \text{Binomial}(z_i * \delta_i, t_i)$$
$$\text{logit}(\delta_i) = W_i \gamma$$

Value

mcmc
An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod_i P(y_i, z_i | ...))$, is also provided.

prob.p.pred
If $\text{save.p}$ is set to 0 (default), $\text{prob.p.pred}$ is the predictive posterior mean of the probability associated to the suitability process for each prediction. If $\text{save.p}$ is set to 1, $\text{prob.p.pred}$ is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

prob.p.latent
Predictive posterior mean of the probability associated to the suitability process for each observation.

prob.q.latent
Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)
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References


See Also

`plot.mcmc`, `summary.mcmc`

Examples

```r
## Not run:

#==============================================
# hSDM.ZIB()
# Example with simulated data
#==============================================

#========
#== Preambule
library(hSDM)

#========
#== Data simulation

# Set seed for repeatability
seed <- 1234

# Number of observations
nobs <- 1000

# Target parameters
beta.target <- matrix(c(0.2,0.5,0.5),ncol=1)
gamma.target <- matrix(c(1),ncol=1)
## Uncomment if you want covariates on the observability process
## gamma.target <- matrix(c(0.2,0.5,0.5),ncol=1)

# Covariates for "suitability" process
set.seed(seed)
X1 <- rnorm(n=nobs,0,1)
set.seed(2*seed)
X2 <- rnorm(n=nobs,0,1)
X <- cbind(rep(1,nobs),X1,X2)

# Covariates for "observability" process
```

W <- cbind(rep(1,nobs))
## Uncomment if you want covariates on the observability process
## set.seed(3*seed)
## W1 <- rnorm(n=nobs,0,1)
## set.seed(4*seed)
## W2 <- rnorm(n=nobs,0,1)
## W <- cbind(rep(1,nobs),W1,W2)

## Simulating latent variables

# Suitability
logit.theta.1 <- X %% beta.target
theta.1 <- inv.logit(logit.theta.1)
set.seed(seed)
y.1 <- rbinom(nobs,1,theta.1)

# Observability
set.seed(seed)
trials <- rpois(nobs,5) # Number of trial associated to each observation
trials[trials==0] <- 1
logit.theta.2 <- W %% gamma.target
theta.2 <- inv.logit(logit.theta.2)
set.seed(seed)
y.2 <- rbinom(nobs,trials,theta.2)

## Simulating response variable
Y <- y.2*y.1

## Data-set
Data <- data.frame(Y, trials, X1, X2)
## Uncomment if you want covariates on the observability process
## Data <- data.frame(Y, trials, X1, X2, W1, W2)

-----------------------------
## ZIB model

mod.hSDM.ZIB <- hSDM.ZIB(presences=Data$Y, trials=Data$trials,
suitability=X1+X2,
observability=-1, #=-1+W1+W2 if covariates
data=Data,
suitability.pred=NULL,
burnin=1000, mcmc=1000, thin=5,
beta.start=0,
gamma.start=0,
mubeta=0, Vbeta=1.0E6,
mugamma=0, Vgamma=1.0E6,
seed=1234, verbose=1,
save.p=0)

-------------
## Outputs
pdf(file="Posteriors_hSDM.ZIB.pdf")
Description

The hSDM.ZIB.iCAR function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (refering to environmental suitability) which takes into account the spatial dependence of the observations, and a Binomial observability process (refering to various ecological and methodological issues explaining the species detection). The hSDM.ZIB.iCAR function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

Usage

hSDM.ZIB.iCAR(presences, trials, suitability, observability, spatial.entity, data, n.neighbors, neighbors, suitability.pred=NULL, spatial.entity.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, gamma.start, Vrho.start, mubeta = 0, Vbeta = 1e+06, mugamma = 0, Vgamma = 1e+06, priorVrho = "1/Gamma", shape = 0.5, rate = 0.0005, Vrho.max=1000, seed = 1234, verbose = 1, save.rho = 0, save.p = 0)

Arguments

- `presences`: A vector indicating the number of successes (or presences) for each observation.
- `trials`: A vector indicating the number of trials for each observation. $t_i$ should be superior to zero and superior or equal to $y_i$, the number of successes for observation $i$.
- `suitability`: A one-sided formula of the form $\sim x_1 + ... + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
- `observability`: A one-sided formula of the form $\sim w_1 + ... + w_q$ with $q$ terms specifying the explicative variables for the observability process.
- `spatial.entity`: A vector indicating the spatial entity identifier (from one to the total number of entities) for each observation. Several observations can occur in one spatial entity. A spatial entity can be a raster cell for example.
data
A data frame containing the model’s variables.

n.neighbors
A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. length(n.neighbors) indicates the total number of spatial entities.

neighbors
A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, ... , neighbors of the last entity). Length of the neighbors vector should be equal to sum(n.neighbors).

suitability.pred
An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.

spatial.entity.pred
An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.

burnin
The number of burnin iterations for the sampler.

mcmc
The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to burnin+mcmc. burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.

thin
The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start
Starting values for \( \beta \) parameters of the suitability process. This can either be a scalar or a \( p \)-length vector.

gamma.start
Starting values for \( \gamma \) parameters of the observability process. This can either be a scalar or a \( q \)-length vector.

Vrho.start
Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta
Means of the priors for the \( \beta \) parameters of the suitability process. mubeta must be either a scalar or a \( p \)-length vector. If mubeta takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta
Variances of the Normal priors for the \( \beta \) parameters of the suitability process. Vbeta must be either a scalar or a \( p \)-length vector. If Vbeta takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

mugamma
Means of the Normal priors for the \( \gamma \) parameters of the observability process. mugamma must be either a scalar or a \( q \)-length vector. If mugamma takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

Vgamma
Variances of the Normal priors for the \( \gamma \) parameters of the observability process. Vgamma must be either a scalar or a \( q \)-length vector. If Vgamma takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.
priorVrho: Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval [0,Vrho.max]. Default set to "1/Gamma".

shape: The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is shape=0.05 for uninformative prior.

rate: The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.

Vrho.max: Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed: The seed for the random number generator. Default set to 1234.

verbose: A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho: A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p: A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the prob.p.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one. The ecological process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

Ecological process:

$$z_i \sim \text{Bernoulli}(\theta_i)$$

$$\logit(\theta_i) = X_i \beta + \rho_{j(i)}$$

$$\rho_{j(i)}$$: spatial random effect

$$j(i)$$: index of the spatial entity for observation $$i$$.

Spatial autocorrelation:

An intrinsic conditional autoregressive model (iCAR) is assumed:

$$\rho_j \sim \text{Normal}(\mu_j, V_\rho/n_j)$$

$$\mu_j$$: mean of $$\rho_{j'}$$ in the neighborhood of $$j$$.

$$V_\rho$$: variance of the spatial random effects.

$$n_j$$: number of neighbors for spatial entity $$j$$. 

Observation process:

\[ y_i \sim \text{Binomial}(z_i \ast \delta_i, t_i) \]
\[ \logit(\delta_i) = W_i \gamma \]

Value

**mcmc**  
An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod_i P(y_i | ...)) \), is also provided.

**rho.pred**  
If `save.rho` is set to 0 (default), `rho.pred` is the predictive posterior mean of the spatial random effect associated to each spatial entity. If `save.rho` is set to 1, `rho.pred` is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

**prob.p.pred**  
If `save.p` is set to 0 (default), `prob.p.pred` is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, `prob.p.pred` is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

**prob.p.latent**  
Predictive posterior mean of the probability associated to the suitability process for each observation.

**prob.q.latent**  
Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

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References


See Also

`plot.mcmc`, `summary.mcmc`

Examples

```r
## Not run:

#===============================================
# hSDM.ZIB.iCAR()
```
# Example with simulated data
#================================

#=============
#== Preamble
library(hSDM)
library(raster)
library(sp)
library(mvtnorm)

#=================
#== Data simulation

# Set seed for repeatability
seed <- 1234

# Target parameters
beta.target <- matrix(c(0.2,0.5,0.5),ncol=1)
gamma.target <- matrix(c(1),ncol=1)
## Uncomment if you want covariates on the observability process
## gamma.target <- matrix(c(0.2,0.5,0.5),ncol=1)
vrho.target <- 1 # Spatial Variance

# Landscape
Landscape <- raster(ncol=20,nrow=20,crs='+proj=utm +zone=1')
ncell <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncell), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0,ncell,ncell)
index.start <- 1
for (i in 1:ncell) {
  index.end <- index.start+n.neighbors[i]-1
  A[i,adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial dependence parameter = 1 for intrinsic CAR
d <- diag(n.neighbors)-d*A + diag(.0001,ncell) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
rho <- c(rmvnorm(1,sigma=covrho)) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

# Visited cells
n.visited <- 150 # Compare with 400, 350 and 100 for example
set.seed(seed)
visited.cells <- sort(sample(1:ncell,n.visited,replace=FALSE)) # Draw visited cells at random
notvisited.cells <- c(1:ncell)[-visited.cells]

# Number of observations
nobs <- 300

# Cell vector
set.seed(seed)
cells <- c(visited.cells,sample(visited.cells,nobs-n.visited,replace=TRUE))
coords <- xyFromCell(Landscape,cells) # Get coordinates

# Covariates for "suitability" process
set.seed(seed)
X1.cell <- rnorm(n=ncell,0,1)
set.seed(2*seed)
X2.cell <- rnorm(n=ncell,0,1)
X1 <- X1.cell[cells]
X2 <- X2.cell[cells]
X <- cbind(rep(1,nobs),X1,X2)

# Covariates for "observability" process
W <- cbind(rep(1,nobs))
## Uncomment if you want covariates on the observability process
## set.seed(3*seed)
## W1 <- rnorm(n=nobs,0,1)
## set.seed(4*seed)
## W2 <- rnorm(n=nobs,0,1)
## W <- cbind(rep(1,nobs),W1,W2)

## Simulating latent variables

## Suitability
logit.theta.1 <- vector()
for (n in 1:nobs) {
  logit.theta.1[n] <- X[n,]*theta.target+rho[cells[n]]
}
theta.1 <- inv.logit(logit.theta.1)
set.seed(seed)
y.1 <- rbinom(nobs,1,theta.1)

## Observability
set.seed(seed)
trials <- rpois(nobs,5) # Number of trial associated to each observation
trials[trials==0] <- 1
logit.theta.2 <- W*gamma.target
theta.2 <- inv.logit(logit.theta.2)
set.seed(seed)
y.2 <- rbinom(nobs,trials,theta.2)

## Simulating response variable
Y <- y.2*y.1

## Data-set
Data <- data.frame(Y,trials,cells,X1,X2)
```r
## Uncomment if you want covariates on the observability process
## Data <- data.frame(Y, trials, cells, X1, X2, W1, W2)
Data <- SpatialPointsDataFrame(coords=coords, data=data)
plot(Data)

### Data-set for predictions (suitability on each spatial cell)
Data.pred <- data.frame(X1=X1.cell, X2=X2.cell, cells=c(1:ncell))

### Site-occupancy model
mod.hSDM.ZIB.iCAR <- hSDM.ZIB.iCAR(presences=data$Y,
    trials=data$trials,
    suitability=-X1+X2,
    observability=-1,
    spatial.entity=data$cells,
    data=data,
    n.neighbors=n.neighbors,
    neighbors=adj,
    # suitability.pred=NULL,
    # spatial.entity.pred=NULL,
    suitability.pred=Data.pred,
    spatial.entity.pred=Data.pred$cells,
    burnin=5000, mcmc=5000, thin=5,
    beta.start=0,
    gamma.start=0,
    Vrho.start=10,
    priorVrho="1/Gamma",
    #priorVrho="Uniform",
    #priorVrho=10,
    mubeta=0, Vbeta=1.0E6,
    mugamma=0, Vgamma=1.0E6,
    shape=0.5, rate=0.0005,
    #Vrho.max=1000,
    seed=1234, verbose=1,
    save.rho=1, save.p=0)

### Outputs
### Parameter estimates
summary(mod.hSDM.ZIB.iCAR$mcmc)

### MCMC and posteriors
pdf(File="Posteriors_hSDM.ZIB.iCAR.pdf")
plot(mod.hSDM.ZIB.iCAR$mcmc)
dev.off()

pdf(file="Posteriors.rho_hSDM.ZIB.iCAR.pdf")
plot(mod.hSDM.ZIB.iCAR$rho.pred)
dev.off()

### Summary plots
```
# rho
r.rho <- r.rho.pred <- r.visited <- Landscape
r.rho[] <- rho
r.rho.pred <- apply(mod:hSDM.ZIB.iCAR$rho.pred,2,mean)
r.rho.pred[] <- rho.pred
r.visited[] <- 0
r.visited[visited.cells] <- 1
# prob.p
r.prob.p <- Landscape
r.prob.p[] <- mod:hSDM.ZIB.iCAR$prob.p.pred

pdf(file="Summary_hSDM.ZIB.iCAR.pdf")
par(mfrow=c(3,2))
plot(r.rho, main="rho target")
plot(r.visited,main="Visited cells and presences")
plot(Data[Y>0,],add=TRUE,pch=16,cex=0.5)
plot(r.rho.pred, main="rho estimated")
plot(rho[visited.cells],r.ho.pred[visited.cells],
  xlab="rho target",
  ylab="rho estimated")
points(rho[notvisited.cells],rho.pred[notvisited.cells],pch=16,col="blue")
legend(x=-4,y=3.5,legend="Unvisited cells",col="blue",pch=16,bty="n")
abline(a=0,b=1,col="red")
plot(r.prob.p,main="Proba of presence")
plot(Data[Y>0,],add=TRUE,pch=16,cex=0.5)
dev.off()

## End(Not run)

---

**hSDM.ZIB.iCAR.alteration**

*ZIB (Zero-Inflated Binomial) model with CAR process taking into account site alteration*

---

**Description**

The `hSDM.ZIB.iCAR.alteration` function can be used to model species distribution including different processes in a hierarchical Bayesian framework: (i) a Bernoulli suitability process (referred to as environmental suitability) which takes into account the spatial dependence of the observations, (ii) an alteration process (referred to as anthropogenic disturbances), and (iii) a Binomial observability process (referred to as various ecological and methodological issues explaining the species detection). The `hSDM.ZIB.iCAR.alteration` function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model's parameters.
Usage

hSDM.ZIB.iCAR.alteration(presences, trials, suitability, observability, spatial.entity, alteration, data, n.neighbors, neighbors, suitability.pred=NULL, spatial.entity.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, gamma.start, Vrho.start, mubeta = 0, Vbeta = 1e+06, mugamma = 0, Vgamma = 1e+06, priorVrho = "1/Gamma", shape = 0.5, rate = 0.0005, Vrho.max=1000, seed = 1234, verbose = 1, save.rho = 0, save.p = 0)

Arguments

presences A vector indicating the number of successes (or presences) for each observation.
trials A vector indicating the number of trials for each observation. \( t_i \) should be superior to zero and superior or equal to \( y_i \), the number of successes for observation \( i \).
suitability A one-sided formula of the form \( \sim x_1 + ... + x_p \) with \( p \) terms specifying the explicative variables for the suitability process.
observability A one-sided formula of the form \( \sim w_1 + ... + w_q \) with \( q \) terms specifying the explicative variables for the observability process.
spatial.entity A vector indicating the spatial entity identifier (from one to the total number of entities) for each observation. Several observations can occur in one spatial entity. A spatial entity can be a raster cell for example.
alteration A vector indicating the proportion of area in the spatial cell which is transformed (by anthropogenic activities for example) for each observation. Must be between 0 and 1.
data A data frame containing the model’s variables.
n.neighbors A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. \( \text{length(n.neighbors)} \) indicates the total number of spatial entities.
neighbors A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form \( c(\text{neighbors of entity 1}, \text{neighbors of entity 2}, ..., \text{neighbors of the last entity}) \). Length of the neighbors vector should be equal to \( \text{sum(n.neighbors)} \).
suitability.pred An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
spatial.entity.pred An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.
burnin The number of burnin iterations for the sampler.
mcmc The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to \( \text{burnin} + \text{mcmc} \). \( \text{burnin} + \text{mcmc} \) must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
thin

The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.

beta.start

Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a p-length vector.

gamma.start

Starting values for $\beta$ parameters of the observability process. This can either be a scalar or a q-length vector.

Vrho.start

Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta

Means of the priors for the $\beta$ parameters of the suitability process. mubeta must be either a scalar or a p-length vector. If mubeta takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta

Variances of the Normal priors for the $\beta$ parameters of the suitability process. Vbeta must be either a scalar or a p-length vector. If Vbeta takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

mugamma

Means of the Normal priors for the $\gamma$ parameters of the observability process. mugamma must be either a scalar or a p-length vector. If mugamma takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

Vgamma

Variances of the Normal priors for the $\gamma$ parameters of the observability process. Vgamma must be either a scalar or a p-length vector. If Vgamma takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

priorVrho

Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval [0, Vrho.max]. Default set to "1/Gamma".

shape

The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is shape=0.05 for uninformative prior.

rate

The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.

Vrho.max

Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed

The seed for the random number generator. Default set to 1234.

verbose

A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho

A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p

A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the prob.p.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.
Details

The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one. The ecological process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

**Ecological process:**

\[ z_i \sim Bernoulli(\theta_i) \]
\[ \logit(\theta_i) = X_i \beta + \rho_{j(i)} \]

\( \rho_{j}: \) spatial random effect

\( j(i): \) index of the spatial entity for observation \( i. \)

**Spatial autocorrelation:**

An intrinsic conditional autoregressive model (iCAR) is assumed:

\[ \rho_j \sim Normal(\mu_j, V_\rho/n_j) \]

\( \mu_j: \) mean of \( \rho_{j'} \) in the neighborhood of \( j. \)

\( V_\rho: \) variance of the spatial random effects.

\( n_j: \) number of neighbors for spatial entity \( j. \)

**Observation process:**

\[ y_i \sim Binomial(z_i \delta_i, t_i) \]
\[ \logit(\delta_i) = W_i \gamma \]

Value

- **mcmc**
  An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod_i P(y_i, z_i|...)) \), is also provided.

- **rho.pred**
  If `save.rho` is set to 0 (default), **rho.pred** is the predictive posterior mean of the spatial random effect associated to each spatial entity. If `save.rho` is set to 1, **rho.pred** is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

- **prob.p.pred**
  If `save.p` is set to 0 (default), **prob.p.pred** is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, **prob.p.pred** is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

- **prob.p.latent**
  Predictive posterior mean of the probability associated to the suitability process for each observation.

- **prob.q.latent**
  Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

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References


See Also

(plot.mcmc, summary.mcmc)

Examples

```r
## Not run:

# hSDM.ZIB.iCAR.alteration()
# Example with simulated data

#== Preambule
library(hSDM)
library(raster)
library(sp)
library(mvtnorm)

# Set seed for repeatability
seed <- 1234

# Target parameters
beta.target <- matrix(c(0.2, 0.5, 0.5), ncol = 1)
gamma.target <- matrix(c(0), ncol = 1)

# Landscape
Landscape <- raster(ncol = 20, nrow = 20, crs = '+proj=utm +zone=1')
ncell <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells = c(1:ncell), directions = 8, pairs = TRUE, sorted = TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[, 1])))[, 2]
```
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0, ncell, ncell)
index.start <- 1
for (i in 1:ncell) {
  index.end <- index.start + n.neighbors[i]-1
  A[i, adj[c(index.start:index.end)]] <- 1
  index.start <- index.end+1
}

# Spatial effects
Q <- diag(n.neighbors) - d*A + diag(.0001, ncell) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
rho <- c(rmvnorm(1, sigma=diag(covrho))) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

# Visited cells
n.visited <- 150 # Compare with 400, 350 and 100 for example
visited.cells <- sort(sample(1:ncell, n.visited, replace=FALSE)) # Draw visited cells at random
notvisited.cells <- c(1:ncell)[-visited.cells]

# Number of observations
nobs <- 300

# Cell vector
cells <- c(visited.cells, sample(visited.cells, nobs-n.visited, replace=TRUE))
coords <- xyFromCell(Landscape, cells) # Get coordinates

# Covariates for "suitability" process
X1.cell <- rnorm(n=ncell, 0, 1)
set.seed(2*seed)
X2.cell <- rnorm(n=ncell, 0, 1)
X1 <- X1.cell[cells]
X2 <- X2.cell[cells]
X <- cbind(rep(1, nobs), X1, X2)

# Alteration
U <- runif(n=nobs, min=0, max=1)

# Covariates for "observability" process
W <- cbind(rep(1, nobs))
## Uncomment if you want covariates on the observability process
## set.seed(3*seed)
## W1 <- rnorm(n=nobs, 0, 1)
## set.seed(4*seed)
## W2 <- rnorm(n=nobs, 0, 1)
## W <- cbind(rep(1, nobs), W1, W2)
```r
### Simulating latent variables

# Suitability
logit.theta.1 <- vector()
for (n in 1:nobs) {
    logit.theta.1[n] <- X[n,] %*% beta.target + rho[cells[n]]
}
theta.1 <- inv.logit(logit.theta.1)
set.seed(seed)
y.1 <- rbinom(nobs, 1, theta.1)

# Alteration
u <- rbinom(nobs, 1, U)

# Observability
set.seed(seed)
trials <- rpois(nobs, 5) # Number of trial associated to each observation
trials[trials==0] <- 1
logit.theta.2 <- W %*% gamma.target
theta.2 <- inv.logit(logit.theta.2)
set.seed(seed)
y.2 <- rbinom(nobs, trials, theta.2)

### Simulating response variable
Y <- y.2*(1-u)*y.1

### Data-set
Data <- data.frame(Y, trials, cells, X1, X2, U)
## Uncomment if you want covariates on the observability process
## Data <- data.frame(Y, trials, cells, X1, X2, W1, W2, U)
Data <- SpatialPointsDataFrame(coords=coords, data=Data)
plot(Data)

### Data-set for predictions (suitability on each spatial cell)
Data.pred <- data.frame(X1=X1.cell, X2=X2.cell, cells=c(1:ncell))

# Site-occupancy model

mod.hSDM.ZIB.iCAR.alteration <- hSDM.ZIB.iCAR.alteration(presences=Data$Y, trials=Data$trials, suitability=X1*X2, observability=1, spatial.entity=Data$cells, alteration=Data$U, data=Data, n.neighbors=n.neighbors, neighbors=adj, ## suitability.pred=NULL, ## spatial.entity.pred=NULL, suitability.pred=Data.pred, spatial.entity.pred=Data.pred$cells,
```
burnin=5000, mcmc=5000, thin=5,
beta.start=0,
gamma.start=0,
Vrho.start=10,
priorVrho="1/Gamma",
#priorVrho="Uniform",
#priorVrho=10,
mubeta=0, Vbeta=1.0E6,
mugamma=0, Vgamma=1.0E6,
shape=0.5, rate=0.0005,
#Vrho.max=1000,
seed=1234, verbose=1,
save.rho=1, save.p=0)

# Output

Parameter estimates
summary(mod.hSDM.ZIB.iCAR.alteration$mcmc)

MCMC and posteriors
pdf(file="Posteriors_hSDM.ZIB.iCAR.alteration.pdf")
plot(mod.hSDM.ZIB.iCAR.alteration$mcmc)
dev.off()

pdf(file="Posteriors.rho_hSDM.ZIB.iCAR.alteration.pdf")
plot(mod.hSDM.ZIB.iCAR.alteration$rho.pred)
dev.off()

Summary plots

rho
r.rho <- r.rho.pred <- r.visited <- Landscape
r.rho[] <- rho
rho.pred[] <- apply(mod.hSDM.ZIB.iCAR.alteration$rho.pred,2,mean)
r.rho.pred[] <- rho.pred
r.visited[] <- 0
r.visited[visited.cells] <- 1
# prob.p
r.prob.p <- Landscape
r.prob.p[] <- mod.hSDM.ZIB.iCAR.alteration$prob.p.pred

pdf(file="Summary_hSDM.ZIB.iCAR.alteration.pdf")
par(mfrow=c(3,2))
plot(r.rho, main="rho target")
plot(r.visited, main="Visited cells and presences")
plot(Data[Y>0,],add=TRUE,pch=16,cex=0.5)
plot(r.rho.pred, main="rho estimated")
plot(rho[visited.cells],rho.pred[visited.cells],
  xlab="rho target",
ylab="rho estimated")
points(rho[notvisited.cells],rho.pred[notvisited.cells],pch=16,col="blue")
legend(x=-4,y=3.5,legend="Unvisited cells",col="blue",pch=16,bty="n")
**hSDM.ZIP**

**ZIP (Zero-Inflated Poisson) model**

**Description**

The hSDM.ZIP function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (refering to various ecological variables explaining environmental suitability or not) and a Poisson abundance process (refering to various ecological variables explaining the species abundance when the habitat is suitable). The hSDM.ZIP function calls a Gibbs sampler written in C code which uses a Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.

**Usage**

```r
hsdm.ZIP(counts, suitability, abundance, data,
suitability.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10,
beta.start, gamma.start, mubeta = 0, Vbeta = 1e+06, mugamma = 0, Vgamma = 1e+06, seed = 1234, verbose = 1, save.p = 0)
```

**Arguments**

- **counts**: A vector indicating the count for each observation.
- **suitability**: A one-sided formula of the form $\sim x_1 + ... + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
- **abundance**: A one-sided formula of the form $\sim w_1 + ... + w_q$ with $q$ terms specifying the explicative variables for the abundance process.
- **data**: A data frame containing the model’s variables.
- **suitability.pred**: An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
- **burnin**: The number of burnin iterations for the sampler.
- **mcmc**: The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to burnin+mcmc. burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
- **thin**: The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.
beta.start
Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a $p$-length vector.

gamma.start
Starting values for $\beta$ parameters of the abundance process. This can either be a scalar or a $q$-length vector.

mubeta
Means of the priors for the $\beta$ parameters of the suitability process. $mubeta$ must be either a scalar or a $p$-length vector. If $mubeta$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

$\beta$ parameters of the suitability process. $mubeta$ must be either a scalar or a $p$-length vector. If $mubeta$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

vbeta
Variances of the Normal priors for the $\beta$ parameters of the suitability process. $vbeta$ must be either a scalar or a $p$-length vector. If $vbeta$ takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

mugamma
Means of the Normal priors for the $\gamma$ parameters of the abundance process. $mugamma$ must be either a scalar or a $p$-length vector. If $mugamma$ takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

vgamma
Variances of the Normal priors for the $\gamma$ parameters of the abundance process. $vgamma$ must be either a scalar or a $p$-length vector. If $vgamma$ takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

seed
The seed for the random number generator. Default set to 1234.

verbose
A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.p
A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the prob.p.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

The model integrates two processes, an ecological process associated to habitat suitability (habitat is suitable or not for the species) and an abundance process that takes into account ecological variables explaining the species abundance when the habitat is suitable.

Suitability process:

$$z_i \sim \text{Bernoulli}(\theta_i)$$

$$\text{logit}(\theta_i) = X_i \beta$$

Abundance process:

$$y_i \sim \text{Poisson}(z_i \cdot \lambda_i)$$

$$\text{log}(\lambda_i) = W_i \gamma$$
Value

**mcmc**  
An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod_{i} P(y_i, z_i|...))$, is also provided.

**prob.p.pred**  
If `save.p` is set to 0 (default), `prob.p.pred` is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, `prob.p.pred` is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

**prob.p.latent**  
Predictive posterior mean of the probability associated to the suitability process for each observation.

**prob.q.latent**  
Predictive posterior mean of the probability associated to the abundance process for each observation.

Author(s)

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References


See Also

`plot.mcmc, summary.mcmc`

Examples

```r
## Not run:

#---------------------------------
# hSDM.ZIP()
# Example with simulated data
#---------------------------------

#-------
#== Preamble
library(hSDM)

#-------
#== Data simulation

# Set seed for repeatability
```
seed <- 1234

# Number of observations
nobs <- 1000

# Target parameters
beta.target <- matrix(c(0.2,0.5,0.5),ncol=1)
gamma.target <- matrix(c(1),ncol=1)
## Uncomment if you want covariates on the abundance process
## gamma.target <- matrix(c(0.2,0.5,0.5),ncol=1)

# Covariates for "suitability" process
set.seed(seed)
X1 <- rnorm(n=nobs,0,1)
set.seed(2*seed)
X2 <- rnorm(n=nobs,0,1)
X <- cbind(rep(1,nobs),X1,X2)

# Covariates for "abundance" process
W <- cbind(rep(1,nobs))
## Uncomment if you want covariates on the abundance process
## set.seed(3*seed)
## W1 <- rnorm(n=nobs,0,1)
## set.seed(4*seed)
## W2 <- rnorm(n=nobs,0,1)
## W <- cbind(rep(1,nobs),W1,W2)

### Simulating latent variables

# Suitability
logit.theta <- X %*% beta.target
theta <- inv.logit(logit.theta)
set.seed(seed)
y.1 <- rbinom(n=nobs,1,theta)

# Abundance
set.seed(seed)
log.lambda <- W %*% gamma.target
lambda <- exp(log.lambda)
set.seed(seed)
y.2 <- rpois(n=nobs,lambda)

### Simulating response variable
Y <- y.2*y.1

### Data-set
Data <- data.frame(Y,X1,X2)
## Uncomment if you want covariates on the abundance process
## Data <- data.frame(Y,X1,X2,W1,W2)

############################################################
### ZIP model
The hSDM.ZIP.iCAR function can be used to model species distribution including different processes in a hierarchical Bayesian framework: a Bernoulli suitability process (referring to various ecological variables explaining environmental suitability or not) which takes into account the spatial dependence of the observations, and a Poisson abundance process (referring to various ecological variables explaining the species abundance when the habitat is suitable). The hSDM.ZIP.iCAR function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model's parameters.

Usage

hSDM.ZIP.iCAR(counts, suitability, abundance, spatial.entity, data, n.neighbors, neighbors, suitability.pred=NULL, spatial.entity.pred=NULL, burnin = 5000, mcmc = 10000, thin = 10, beta.start, gamma.start, Vrho.start, mubeta = 0, Vbeta = 1e+06, mugamma = 0, Vgamma = 1e+06, priorVrho = "1/Gamma", shape = 0.5, rate = 0.0005, Vrho.max=1000, seed = 1234, verbose = 1, save.rho = 0, save.p = 0)
Arguments

- **counts**: A vector indicating the count for each observation.
- **suitability**: A one-sided formula of the form $\sim x_1 + ... + x_p$ with $p$ terms specifying the explicative variables for the suitability process.
- **abundance**: A one-sided formula of the form $\sim w_1 + ... + w_q$ with $q$ terms specifying the explicative variables for the abundance process.
- **spatial.entity**: A vector indicating the spatial entity identifier (from one to the total number of entities) for each observation. Several observations can occur in one spatial entity. A spatial entity can be a raster cell for example.
- **data**: A data frame containing the model’s variables.
- **n.neighbors**: A vector of integers that indicates the number of neighbors (adjacent entities) of each spatial entity. length(n.neighbors) indicates the total number of spatial entities.
- **neighbors**: A vector of integers indicating the neighbors (adjacent entities) of each spatial entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, ..., neighbors of the last entity). Length of the neighbors vector should be equal to sum(n.neighbors).
- **suitability.pred**: An optional data frame in which to look for variables with which to predict. If NULL, the observations are used.
- **spatial.entity.pred**: An optional vector indicating the spatial entity identifier (from one to the total number of entities) for predictions. If NULL, the vector spatial.entity for observations is used.
- **burnin**: The number of burnin iterations for the sampler.
- **mcmc**: The number of Gibbs iterations for the sampler. Total number of Gibbs iterations is equal to burnin+mcmc. burnin+mcmc must be divisible by 10 and superior or equal to 100 so that the progress bar can be displayed.
- **thin**: The thinning interval used in the simulation. The number of mcmc iterations must be divisible by this value.
- **beta.start**: Starting values for $\beta$ parameters of the suitability process. This can either be a scalar or a $p$-length vector.
- **gamma.start**: Starting values for $\beta$ parameters of the observability process. This can either be a scalar or a $q$-length vector.
- **Vrho.start**: Positive scalar indicating the starting value for the variance of the spatial random effects.
- **mubeta**: Means of the priors for the $\beta$ parameters of the suitability process. mubeta must be either a scalar or a $p$-length vector. If mubeta takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.
- **Vbeta**: Variances of the Normal priors for the $\beta$ parameters of the suitability process. Vbeta must be either a scalar or a $p$-length vector. If Vbeta takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to 1.0E6 for an uninformative flat prior.
mugamma  Means of the Normal priors for the $\gamma$ parameters of the observability process. mugamma must be either a scalar or a p-length vector. If mugamma takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

Vgamma  Variances of the Normal priors for the $\gamma$ parameters of the observability process. Vgamma must be either a scalar or a p-length vector. If Vgamma takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to 1.0E6 for an uninformative flat prior.

priorVrho  Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("1/Gamma") with parameters shape and rate, or to a uniform distribution ("Uniform") on the interval [0, Vrho.max]. Default set to "1/Gamma".

shape  The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is shape=0.05 for uninformative prior.

rate  The rate (1/scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is rate=0.0005 for uninformative prior.

Vrho.max  Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed  The seed for the random number generator. Default set to 1234.

verbose  A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho  A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p  A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the prob.p.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.

Details

The model integrates two processes, an ecological process associated to habitat suitability (habitat is suitable or not for the species) and an abundance process that takes into account ecological variables explaining the species abundance when the habitat is suitable. The suitability process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the suitability at one site depends on the suitability on neighboring sites.

Suitability process:

$$z_i \sim Bernoulli(\theta_i)$$

$$\logit(\theta_i) = X_i \beta + \rho_j(i)$$

$\rho_j$: spatial random effect

$j(i)$: index of the spatial entity for observation $i$. 
Spatial autocorrelation:

An intrinsic conditional autoregressive model (iCAR) is assumed:

$$\rho_j \sim \text{Normal}(\mu_j, V_\rho / n_j)$$

- $\mu_j$: mean of $\rho_j$ in the neighborhood of $j$.
- $V_\rho$: variance of the spatial random effects.
- $n_j$: number of neighbors for spatial entity $j$.

Abundance process:

$$y_i \sim \text{Poisson}(z_i \ast \lambda_i)$$

$$\log(\lambda_i) = W_i \gamma$$

Value

- **mcmc**: An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance $D$, with $D = -2 \log(\prod P(y_i, z_i | ...))$, is also provided.

- **rho.pred**: If `save.rho` is set to 0 (default), `rho.pred` is the predictive posterior mean of the spatial random effect associated to each spatial entity. If `save.rho` is set to 1, `rho.pred` is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

- **prob.p.pred**: If `save.p` is set to 0 (default), `prob.p.pred` is the predictive posterior mean of the probability associated to the suitability process for each prediction. If `save.p` is set to 1, `prob.p.pred` is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

- **prob.p.latent**: Predictive posterior mean of the probability associated to the suitability process for each observation.

- **prob.q.latent**: Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References


See Also

- `plot.mcmc`, `summary.mcmc`
## Examples

```r
## Not run:

# Example with simulated data

### Preamble

library(hSDM)
library(raster)
library(sp)
library(mvtnorm)

### Data simulation

# Set seed for repeatability
seed <- 1234

# Target parameters
beta.target <- matrix(c(0.2, 0.5, 0.5), ncol=1)
gamma.target <- matrix(c(1), ncol=1)
## Uncomment if you want covariates on the observability process
## gamma.target <- matrix(c(0.2, 0.5, 0.5), ncol=1)
vrho.target <- 1 # Spatial Variance

# Landscape
Landscape <- raster(ncol=20, nrow=20, crs='+proj=utm +zone=1')
ncell <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=ncell, directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0, ncell, ncell)
index.start <- 1
for (i in 1:ncell) {
  index.end <- index.start+n.neighbors[i]-1
  A[index.start:index.end,] <- 1
  index.start <- index.end+1
}

# Spatial effects

d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors)-d*A + diag(1, ncell) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
```

---

**Examples**

## Not run:

```r
# Example with simulated data

### Preamble

library(hSDM)
library(raster)
library(sp)
library(mvtnorm)

### Data simulation

# Set seed for repeatability
seed <- 1234

# Target parameters
beta.target <- matrix(c(0.2, 0.5, 0.5), ncol=1)
gamma.target <- matrix(c(1), ncol=1)
## Uncomment if you want covariates on the observability process
## gamma.target <- matrix(c(0.2, 0.5, 0.5), ncol=1)
vrho.target <- 1 # Spatial Variance

# Landscape
Landscape <- raster(ncol=20, nrow=20, crs='+proj=utm +zone=1')
ncell <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=ncell, directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]

# Generate symmetric adjacency matrix, A
A <- matrix(0, ncell, ncell)
index.start <- 1
for (i in 1:ncell) {
  index.end <- index.start+n.neighbors[i]-1
  A[index.start:index.end,] <- 1
  index.start <- index.end+1
}

# Spatial effects

d <- 1 # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors)-d*A + diag(1, ncell) # Add small constant to make Q non-singular
covrho <- Vrho.target*solve(Q) # Covariance of rhos
set.seed(seed)
```
rho <- c(rmvnorm(1, sigma=covrho)) # Spatial Random Effects
rho <- rho-mean(rho) # Centering rhos on zero

# Visited cells
n.visited <- 150 # Compare with 400, 350 and 100 for example
set.seed(seed)
visited.cells <- sort(sample(1:ncell,n.visited,replace=FALSE)) # Draw visited cells at random
notvisited.cells <- c(1:ncell)[-visited.cells]

# Number of observations
nobs <- 300

# Cell vector
set.seed(seed)
cells <- c(visited.cells,sample(visited.cells,nobs-n.visited,replace=TRUE))
coords <- xyFromCell(Landscape,cells) # Get coordinates

# Covariates for "suitability" process
set.seed(seed)
X1.cell <- rnorm(n=ncell,0,1)
set.seed(2*seed)
X2.cell <- rnorm(n=ncell,0,1)
X1 <- X1.cell[cells]
X2 <- X2.cell[cells]
X <- cbind(rep(1,nobs),X1,X2)

# Covariates for "abundance" process
W <- cbind(rep(1,nobs))
## Uncomment if you want covariates on the observability process
## set.seed(3*seed)
## W1 <- rnorm(n=nobs,0,1)
## set.seed(4*seed)
## W2 <- rnorm(n=nobs,0,1)
## W <- cbind(rep(1,nobs),W1,W2)

# Simulating latent variables

# Suitability
logit.theta <- vector()
for (n in 1:nobs) {
  logit.theta[n] <- X[n,]*%*%beta.target+rho[cells[n]]
}
theta <- inv.logit(logit.theta)
set.seed(seed)
y.1 <- rbinom(nobs,1,theta)

# Abundance
set.seed(seed)
log.lambda <- W %*% gamma.target
lambda <- exp(log.lambda)
set.seed(seed)
y.2 <- rpois(nobs,lambda)
## Simulating response variable

Y <- y.2*y.1

## Data-set

Data <- data.frame(Y, cells, X1, X2)

## Uncomment if you want covariates on the observability process

Data <- SpatialPointsDataFrame(coords=coords, data=Data)

plot(Data)

## Data-set for predictions (suitability on each spatial cell)

Data.pred <- data.frame(X1=X1.cell, X2=X2.cell, cells=c(1:ncell))

# Zip model with CAR

mod.hSDM.ZIP.iCAR <- hSDM.ZIP.iCAR(counts=Data$Y, suitability=-X1+X2, abundance=-1, spatial.entity=Data$cells, data=Data, n.neighbors=n.neighbors, neighbors=adj, suitability.pred=Data.pred, spatial.entity.pred=Data.pred$cells, burnin=5000, mcmc=5000, thin=5, beta.start=0, gamma.start=0, Vrho.start=10, priorVrho="1/Gamma", #priorVrho="Uniform", #priorVrho=10, mubeta=0, Vbeta=1.0E6, mugamma=0, Vgamma=1.0E6, shape=0.5, rate=0.0005, #Vrho.max=1000, seed=1234, verbose=1, save.rho=1, save.p=0)

## Outputs

## Parameter estimates

summary(mod.hSDM.ZIP.iCAR$mcmc)

## MCMC and posteriors

pdf(file="Posteriors_hSDM.ZIP.iCAR.pdf")

plot(mod.hSDM.ZIP.iCAR$mcmc)

dev.off()

pdf(file="Posteriors.rho_hSDM.ZIP.iCAR.pdf")

plot(mod.hSDM.ZIP.iCAR$rho.pred)

dev.off()}
ZIP (Zero-Inflated Poisson) model with CAR process taking into account site alteration

Description

The hSDM.ZIP.iCAR.alteration function can be used to model species distribution including different processes in a hierarchical Bayesian framework: (i) a Bernoulli suitability process (referring to various ecological variables explaining environmental suitability or not) which takes into account the spatial dependence of the observations, (ii) an alteration process (referring to anthropogenic disturbances), and (iii) a Poisson abundance process (referring to various ecological variables explaining the species abundance when the habitat is suitable). The hSDM.ZIP.iCAR.alteration function calls a Gibbs sampler written in C code which uses an adaptive Metropolis algorithm to estimate the conditional posterior distribution of hierarchical model’s parameters.
Usage

hSDM.ZIP.iCAR.alteration(counts, suitability, abundance,
spatial.entity, alteration, data, n.neighbors, neighbors,
suitability.pred=NULL, spatial.entity.pred=NULL, burnin = 5000, mcmc =
10000, thin = 10, beta.start, gamma.start, Vrho.start, mubeta = 0, Vbeta
= 1e+06, mugamma = 0, Vgamma = 1e+06, priorVrho = "1/Gamma", shape =
0.5, rate = 0.0005, Vrho.max=1000, seed = 1234, verbose = 1, save.rho =
0, save.p = 0)

Arguments

counts A vector indicating the count for each observation.
suitability A one-sided formula of the form $x_1 + \ldots + x_p$ with $p$ terms specifying the
explicative variables for the suitability process.
abundance A one-sided formula of the form $w_1 + \ldots + w_q$ with $q$ terms specifying the
explicative variables for the abundance process.
spatial.entity A vector indicating the spatial entity identifier (from one to the total number
of entities) for each observation. Several observations can occur in one spatial
ty entity. A spatial entity can be a raster cell for example.
alteration A vector indicating the proportion of area in the spatial cell which is transformed
(by anthropogenic activities for example) for each observation. Must be between
0 and 1.
data A data frame containing the model’s variables.
n.neighbors A vector of integers that indicates the number of neighbors (adjacent entities) of
each spatial entity. length(n.neighbors) indicates the total number of spatial
entities.
n.neighbors A vector of integers indicating the neighbors (adjacent entities) of each spatial
ty entity. Must be of the form c(neighbors of entity 1, neighbors of entity 2, \ldots ,
neighbors of the last entity). Length of the neighbors vector should be equal to
sum(n.neighbors).
suitability.pred An optional data frame in which to look for variables with which to predict. If
NULL, the observations are used.
spatial.entity.pred An optional vector indicating the spatial entity identifier (from one to the total
number of entities) for predictions. If NULL, the vector spatial.entity for
observations is used.
burnin The number of burnin iterations for the sampler.
mcmc The number of Gibbs iterations for the sampler. Total number of Gibbs iterations
is equal to burnin+mc. burnin+mcmc must be divisible by 10 and superior or
equal to 100 so that the progress bar can be displayed.
thin The thinning interval used in the simulation. The number of mcmc iterations
must be divisible by this value.
beta.start Starting values for $\beta$ parameters of the suitability process. This can either be a
scalar or a $p$-length vector.
gamma.start  Starting values for $\beta$ parameters of the observability process. This can either be a scalar or a $q$-length vector.

Vrho.start  Positive scalar indicating the starting value for the variance of the spatial random effects.

mubeta  Means of the priors for the $\beta$ parameters of the suitability process. $\mubeta$ must be either a scalar or a $p$-length vector. If $\mubeta$ takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value is set to 0 for an uninformative prior.

Vbeta  Variances of the Normal priors for the $\beta$ parameters of the suitability process. $\Vbeta$ must be either a scalar or a $p$-length vector. If $\Vbeta$ takes a scalar value, then that value will serve as the prior variance for all of the betas. The default variance is large and set to $1.0\times10^6$ for an uninformative flat prior.

mugamma  Means of the Normal priors for the $\gamma$ parameters of the observability process. $\mugamma$ must be either a scalar or a $p$-length vector. If $\mugamma$ takes a scalar value, then that value will serve as the prior mean for all of the gammas. The default value is set to 0 for an uninformative prior.

Vgamma  Variances of the Normal priors for the $\gamma$ parameters of the observability process. $\Vgamma$ must be either a scalar or a $p$-length vector. If $\Vgamma$ takes a scalar value, then that value will serve as the prior variance for all of the gammas. The default variance is large and set to $1.0\times10^6$ for an uninformative flat prior.

priorVrho  Type of prior for the variance of the spatial random effects. Can be set to a fixed positive scalar, or to an inverse-gamma distribution ("$1/$Gamma") with parameters $\text{shape}$ and $\text{rate}$, or to a uniform distribution ("Uniform") on the interval $[0, \text{Vrho.max}]$. Default set to "$1/$Gamma$".

shape  The shape parameter for the Gamma prior on the precision of the spatial random effects. Default value is $\text{shape}=0.05$ for uninformative prior.

rate  The rate ($1/$scale) parameter for the Gamma prior on the precision of the spatial random effects. Default value is $\text{rate}=0.0005$ for uninformative prior.

Vrho.max  Upper bound for the uniform prior of the spatial random effect variance. Default set to 1000.

seed  The seed for the random number generator. Default set to 1234.

verbose  A switch (0,1) which determines whether or not the progress of the sampler is printed to the screen. Default is 1: a progress bar is printed, indicating the step (in %) reached by the Gibbs sampler.

save.rho  A switch (0,1) which determines whether or not the sampled values for rhos are saved. Default is 0: the posterior mean is computed and returned in the rho.pred vector. Be careful, setting save.rho to 1 might require a large amount of memory.

save.p  A switch (0,1) which determines whether or not the sampled values for predictions are saved. Default is 0: the posterior mean is computed and returned in the prob.p.pred vector. Be careful, setting save.p to 1 might require a large amount of memory.
Details

The model integrates two processes, an ecological process associated to the presence or absence of the species due to habitat suitability and an observation process that takes into account the fact that the probability of detection of the species is inferior to one. The ecological process includes an intrinsic conditional autoregressive model (iCAR) model for spatial autocorrelation between observations, assuming that the probability of presence of the species at one site depends on the probability of presence of the species on neighboring sites.

**Ecological process:**

\[ z_i \sim \text{Bernoulli}(\theta_i) \]

\[ \text{logit}(\theta_i) = X_i \beta + \rho_{j(i)} \]

\( \rho_j \): spatial random effect

\( j(i) \): index of the spatial entity for observation \( i \).

**Spatial autocorrelation:**

An intrinsic conditional autoregressive model (iCAR) is assumed:

\[ \rho_j \sim \text{Normal}(\mu_j, V_\rho / n_j) \]

\( \mu_j \): mean of \( \rho_j \) in the neighborhood of \( j \).

\( V_\rho \): variance of the spatial random effects.

\( n_j \): number of neighbors for spatial entity \( j \).

**Observation process:**

\[ y_i \sim \text{Binomial}(z_i \ast \delta_i, t_i) \]

\[ \text{logit}(\delta_i) = W_i \gamma \]

Value

**mcmc**

An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package. The posterior sample of the deviance \( D \), with \( D = -2 \log(\prod_i P(y_i, z_i | ...)) \), is also provided.

**rho.p.pred**

If save.rho is set to 0 (default), rho.p.pred is the predictive posterior mean of the spatial random effect associated to each spatial entity. If save.rho is set to 1, rho.p.pred is an mcmc object with sampled values for each spatial random effect associated to each spatial entity.

**prob.p.pred**

If save.p is set to 0 (default), prob.p.pred is the predictive posterior mean of the probability associated to the suitability process for each prediction. If save.p is set to 1, prob.p.pred is an mcmc object with sampled values of the probability associated to the suitability process for each prediction.

**prob.p.latent**

Predictive posterior mean of the probability associated to the suitability process for each observation.

**prob.q.latent**

Predictive posterior mean of the probability associated to the observability process for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>
**References**


**See Also**

`plot.mcmc`, `summary.mcmc`

**Examples**

```r
## Not run:

# hSDM.ZIP.iCAR.alteration()
# Example with simulated data

# Preamble
library(hSDM)
library(raster)
library(sp)
library(mvtnorm)

# Data simulation

# Set seed for repeatability
seed <- 1234

# Target parameters
beta.target <- matrix(c(0.2,0.5,0.5),ncol=1)
gamma.target <- matrix(c(1),ncol=1)
## Uncomment if you want covariates on the observability process
## gamma.target <- matrix(c(0.2,0.5,0.5),ncol=1)
vrho.target <- 1 # Spatial Variance

# Landscape
Landscape <- raster(ncol=20,nrow=20,crs='+proj=utm +zone=1')
ncell <- ncell(Landscape)

# Neighbors
neighbors.mat <- adjacent(Landscape, cells=c(1:ncell), directions=8, pairs=TRUE, sorted=TRUE)
n.neighbors <- as.data.frame(table(as.factor(neighbors.mat[,1])))[,2]
adj <- neighbors.mat[,2]
```
# Generate symmetric adjacency matrix, A
A <- matrix(0, ncell, ncell)
index.start <- 1
for (i in 1:ncell) {
    index.end <- index.start + n.neighbors[i] - 1
    A[i, adj[c(index.start:index.end)]] <- 1
    index.start <- index.end + 1
}

# Spatial effects
d <- 1  # Spatial dependence parameter = 1 for intrinsic CAR
Q <- diag(n.neighbors) - d * A + diag(.0001, ncell)  # Add small constant to make Q non-singular
covrho <- Vrho.target * solve(Q)  # Covariance of rhos
set.seed(seed)
rho <- c(rmvnorm(1, sigma = covrho))  # Spatial Random Effects
rho <- rho - mean(rho)  # Centering rhos on zero

# Visited cells
n.visited <- 150  # Compare with 400, 350 and 100 for example
set.seed(seed)
visited.cells <- sort(sample(1:ncell, n.visited, replace = FALSE))  # Draw visited cells at random
notvisited.cells <- c(1:ncell)[-visited.cells]

# Number of observations
nobs <- 300

# Cell vector
set.seed(seed)
cells <- c(visited.cells, sample(visited.cells, nobs - n.visited, replace = TRUE))
coords <- xyFromCell(Landscape, cells)  # Get coordinates

# Covariates for "suitability" process
set.seed(seed)
X1.cell <- rnorm(n = ncell, 0, 1)
set.seed(2 * seed)
X2.cell <- rnorm(n = ncell, 0, 1)
X1 <- X1.cell[cells]
X2 <- X2.cell[cells]
X <- cbind(rep(1, nobs), X1, X2)

# Alteration
U <- runif(n = nobs, min = 0, max = 1)

# Covariates for "abundance" process
W <- cbind(rep(1, nobs))
## Uncomment if you want covariates on the observability process
## set.seed(3 * seed)
## W1 <- rnorm(n = nobs, 0, 1)
## set.seed(4 * seed)
## W2 <- rnorm(n = nobs, 0, 1)
## W <- cbind(rep(1, nobs), W1, W2)
# Simulating latent variables

```r
# Suitability
logit.theta <- vector()
for (n in 1:nobs) {
  logit.theta[n] <- X[n,]*%*%beta.target+rho[cells[n]]
}
theta <- inv.logit(logit.theta)
set.seed(seed)
y.1 <- rbinom(nobs,1,theta)

# Alteration
u <- rbinom(nobs,1,U)

# Abundance
set.seed(seed)
log.lambda <- W %*% gamma.target
lambda <- exp(log.lambda)
set.seed(seed)
y.2 <- rpois(nobs,lambda)
```

```r
# Simulating response variable
Y <- y.2*(1-u)*y.1
```

```r
# Data-set
Data <- data.frame(Y,cells,X1,X2,U)
## Uncomment if you want covariates on the observability process
## Data <- data.frame(Y,cells,X1,X2,W1,W2,U)
Data <- SpatialPointsDataFrame(coords=coords,data=Data)
plot(Data)
```

```r
# Data-set for predictions (suitability on each spatial cell)
Data.pred <- data.frame(X1=X1.cell,X2=X2.cell,cells=c(1:ncell))
```

```r
# Site-occupancy model
mod.hSDM.ZIP.iCAR.alteration <- hSDM.ZIP.iCAR.alteration(counts=Data$Y,
suitability=-X1+X2,
abundance=-1,
spatial.entity=Data$cells,
alteration=Data$U,
data=Data,
n.neighbors=n.neighbors,
neighbors=adj,
## suitability.pred=NULL,
## spatial.entity.pred=NULL,
suitability.pred=Data.pred,
spatial.entity.pred=Data.pred$cells,
burnin=5000, mcmc=5000, thin=5,
beta.start=0,
gamma.start=0,
Vrho.start=10,
```

```r
```
# Outputs

### Parameter estimates

```r
summary(mod.hSDM.ZIP.iCAR.alteration$mcmc)
```

### MCMC and posteriors

```r
df(file="Posteriors_hSDM.ZIP.iCAR.alteration.pdf")
plot(mod.hSDM.ZIP.iCAR.alteration$mcmc)
dev.off()
```

```r
df(file="Posteriors.rho_hSDM.ZIP.iCAR.alteration.pdf")
plot(mod.hSDM.ZIP.iCAR.alteration$rho.pred)
dev.off()
```

### Summary plots

```r
# rho
r.rho <- r.rho.pred <- r.visited <- Landscape
r.rho[] <- rho
r.rho.pred[] <- apply(mod.hSDM.ZIP.iCAR.alteration$rho.pred,2,mean)
r.rho.pred[] <- rho.pred
r.visited[] <- 0
r.visited[visited.cells] <- tapply(Data$Y,Data$cells,mean)
# prob.p
r.prob.p <- Landscape
r.prob.p[] <- mod.hSDM.ZIP.iCAR.alteration$prob.p.pred
```

```r
df(file="Summary_hSDM.ZIP.iCAR.alteration.pdf")
par(mfrow=c(3,2))
plot(r.rho, main="rho target")
plot(r.visited,main="Visited cells and counts")
plot(Data,add=TRUE,pch=16,cex=0.5)
plot(r.rho.pred, main="rho estimated")
plot(r.rho,main="rho target")
xlab="rho target",
ylab="rho estimated")
points(rho[notvisited.cells],rho.pred[notvisited.cells],pch=16,col="blue")
legend(x=-4,y=3.5,legend="Unvisited cells",col="blue",pch=16,bty="n")
abline(a=0,b=1,col="red")
plot(r.prob.p,main="Predicted counts")
plot(Data,add=TRUE,pch=16,cex=0.5)
dev.off()
```
Description

Compute generalized logit and generalized inverse logit functions.

Usage

```r
logit(x, min = 0, max = 1)
inv.logit(x, min = 0, max = 1)
```

Arguments

- `x`: value(s) to be transformed
- `min`: Lower end of logit interval
- `max`: Upper end of logit interval

Details

The generalized logit function takes values on \([\min, \max]\) and transforms them to span \([-\infty, \infty]\), it is defined as:

\[
y = \log\left(\frac{p}{1 - p}\right)
\]

where

\[
p = \frac{x - \min}{\max - \min}
\]

The generalized inverse logit function provides the inverse transformation:

\[
x = p' (\max - \min) + \min
\]

where

\[
p' = \frac{\exp(y)}{1 + \exp(y)}
\]

Value

Transformed value(s).
Author(s)
Gregory R. Warnes <greg@warnes.net>

Examples

```r
## Not run:
x <- seq(0,10, by=0.25)
xt <- logit(x, min=0, max=10)
cbind(x,xt)

y <- inv.logit(xt, min=0, max=10)
cbind(x,xt,y)

## End(Not run)
```

Description

Data come from a small region including 476 one minute by one minute grid cells. This region is a small corner of South Africa’s Cape Floristic Region, and includes very high plant species diversity and a World Biosphere Reserve. The data frame can be used as an example for several functions in the `hsdm` package.

Usage

```r
neighbors.Latimer2006
```

Format

`neighbors.Latimer2006` is a vector of 3542 integers indicating the neighbors (adjacent cells) of each spatial cell. The vector is of the form `c(neighbors of cell 1, neighbors of cell 2, ..., neighbors of the last cell).

Source

Latimer et al. (2006) *Ecological Applications*, Appendix B

References

Occurrence data for Protea punctata Meisn. in the Cap Floristic Region

Description

The species data were collected by the Protea Atlas Project of South Africa’s National Botanical Institute.

Usage

punc10

Format

cfr.env is a data frame with 2934 presence-absence observation points.

Occurrence presence (1) or absence (0) of the species
lon longitude
lat latitude

Source

Cory Merow’s personal data

References

Index

*Topic **Binomial logistic regression**
  - hSDM.binomial, 6
  - hSDM.binomial.iCAR, 9

*Topic **MCMC**
  - hSDM-package, 2
  - hSDM.binomial, 6
  - hSDM.binomial.iCAR, 9
  - hSDM.Nmixture, 16
  - hSDM.Nmixture.iCAR, 21
  - hSDM.poisson, 30
  - hSDM.poisson.iCAR, 33
  - hSDM.siteocc, 39
  - hSDM.siteocc.iCAR, 44
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **Markov Chains Monte Carlo**
  - hSDM-package, 2
  - hSDM.binomial, 6
  - hSDM.binomial.iCAR, 9
  - hSDM.Nmixture, 16
  - hSDM.Nmixture.iCAR, 21
  - hSDM.poisson, 30
  - hSDM.poisson.iCAR, 33
  - hSDM.siteocc, 39
  - hSDM.siteocc.iCAR, 44
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **Metropolis algorithm**
  - hSDM-package, 2
  - hSDM.binomial, 6
  - hSDM.binomial.iCAR, 9
  - hSDM.Nmixture, 16
  - hSDM.Nmixture.iCAR, 21
  - hSDM.poisson, 30
  - hSDM.poisson.iCAR, 33
  - hSDM.siteocc, 39
  - hSDM.siteocc.iCAR, 44
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **N-mixture models**
  - hSDM.Nmixture, 16
  - hSDM.Nmixture.iCAR, 21

*Topic **Poisson log regression**
  - hSDM.poisson, 30

*Topic **Poisson regression**
  - hSDM.poisson.iCAR, 33

*Topic **ZIB models**
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **ZIP models**
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **Zero-Inflated Binomial models**
  - hSDM.ZIB, 52
  - hSDM.ZIB.iCAR, 57
  - hSDM.ZIB.iCAR.alteration, 64
  - hSDM.ZIP, 72
  - hSDM.ZIP.iCAR, 76
  - hSDM.ZIP.iCAR.alteration, 83

*Topic **Zero-Inflated Poisson models**
  - hSDM.ZIP, 72

*Topic **biodiversity**
  - hSDM-package, 2
  - hSDM.binomial, 6
  - hSDM.binomial.iCAR, 9
  - hSDM.Nmixture, 16
INDEX

hSDM.Nmixture.iCAR, 21
hSDM.poisson, 30
hSDM.poisson.iCAR, 33
hSDM.siteocc, 39
hSDM.siteocc.iCAR, 44
hSDM.ZIB, 52
hSDM.ZIB.iCAR, 57
hSDM.ZIB.iCAR.alteration, 64
hSDM.ZIP, 72
hSDM.ZIP.iCAR, 76
hSDM.ZIP.iCAR.alteration, 83

*Topic **conditional autoregressive model**
  hSDM-package, 2
  hSDM.binomial.iCAR, 9
  hSDM.Nmixture.iCAR, 21
  hSDM.poisson.iCAR, 33
  hSDM.siteocc.iCAR, 44
  hSDM.ZIB.iCAR, 57
  hSDM.ZIB.iCAR.alteration, 64
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

*Topic **datasets**
  altitude, 3
  cfr.env, 3
  data.Kery2010, 4
  datacells.Latimer2006, 5
  neighbors.Latimer2006, 92
  punc10, 93

*Topic **hierarchical Bayesian models**
  hSDM-package, 2
  hSDM.binomial, 6
  hSDM.binomial.iCAR, 9
  hSDM.Nmixture, 16
  hSDM.Nmixture.iCAR, 21
  hSDM.poisson, 30
  hSDM.poisson.iCAR, 33
  hSDM.siteocc, 39
  hSDM.siteocc.iCAR, 44
  hSDM.ZIB, 52
  hSDM.ZIB.iCAR, 57
  hSDM.ZIB.iCAR.alteration, 64
  hSDM.ZIP, 72
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

*Topic **intrinsic CAR model**
  hSDM-package, 2
  hSDM.binomial.iCAR, 9
  hSDM.Nmixture.iCAR, 21
  hSDM.poisson.iCAR, 33
  hSDM.siteocc.iCAR, 44
  hSDM.ZIB.iCAR, 57
  hSDM.ZIB.iCAR.alteration, 64
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

*Topic **math**
  logit, 91

*Topic **site occupancy models**
  hSDM.siteocc.iCAR, 44
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

*Topic **site-occupancy models**
  hSDM.siteocc, 39

*Topic **spatial correlation**
  hSDM-package, 2
  hSDM.binomial.iCAR, 9
  hSDM.Nmixture.iCAR, 21
  hSDM.poisson.iCAR, 33
  hSDM.siteocc.iCAR, 44
  hSDM.ZIB.iCAR, 57
  hSDM.ZIB.iCAR.alteration, 64
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

*Topic **species distribution models**
  hSDM-package, 2
  hSDM.binomial, 6
  hSDM.binomial.iCAR, 9
  hSDM.Nmixture, 16
  hSDM.Nmixture.iCAR, 21
  hSDM.poisson, 30
  hSDM.poisson.iCAR, 33
  hSDM.siteocc, 39
  hSDM.siteocc.iCAR, 44
  hSDM.ZIB, 52
  hSDM.ZIB.iCAR, 57
  hSDM.ZIB.iCAR.alteration, 64
  hSDM.ZIP, 72
  hSDM.ZIP.iCAR, 76
  hSDM.ZIP.iCAR.alteration, 83

altitude, 3

cfr.env, 3

data.Kery2010, 4

datacells.Latimer2006, 5

hSDM (hSDM-package), 2
hSDM-package, 2
hSDM.binomial, 6
hSDM.binomial.iCAR, 9
hSDM.Nmixture, 16
hSDM.Nmixture.iCAR, 21
hSDM.poisson, 30
hSDM.poisson.iCAR, 33
hSDM.siteocc, 39
hSDM.siteocc.iCAR, 44
hSDM.ZIB, 52
hSDM.ZIB.iCAR, 57
hSDM.ZIB.iCAR.alteration, 64
hSDM.ZIP, 72
hSDM.ZIP.iCAR, 76
hSDM.ZIP.iCAR.alteration, 83

inv.logit (logit), 91

logit, 91

neighbors.Latimer2006, 92

plot.mcmc, 8, 12, 19, 25, 31, 36, 42, 48, 55, 60, 68, 74, 79, 87
punc10, 93

summary.mcmc, 8, 12, 19, 25, 31, 36, 42, 48, 55, 60, 68, 74, 79, 87