

Package ‘phcfM’

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Type Package

Title A package for modelling anthropogenic deforestation

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Description A package for modelling anthropogenic deforestation

License GPL (>= 2)

URL <http://phcfm.sourceforge.net>

LazyLoad yes

R topics documented:

phcfM-package	2
deforestation	2
demography	6
InvGamma	10
InvWishart	11
logit	12
Wishart	13
Index	15

phcfM-package	<i>phcfM: A R package for modelling anthropogenic deforestation in tropical forest</i>
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Description

The phcfM R package aims at modelling anthropogenic deforestation in tropical forest. It has first been developed and used through the "holistic program for forest conservation in Madagascar" (phcfM in French).

Details

Package:	phcfM
Type:	Package
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LazyLoad:	yes

Author(s)

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deforestation	<i>MCMC for logistic regression with variable time-interval between censuses</i>
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Description

This function generates a sample from the posterior distribution of a logistic regression model with variable time-interval between censuses using a random walk Metropolis algorithm. The user supplies data and priors, and a sample from the posterior distribution is returned as an mcmc object, which can be subsequently analyzed with functions provided in the coda package.

Usage

```
deforestation(formula, interval=1, data, burnin=1000, mcmc=1000,
  thin=1, verbose=1, seed=NA, tune=1, beta.start=NA, mubeta=0,
  Vbeta=1.0E6)
```

Arguments

formula	A two-sided linear formula of the form 'y~x1+...+xp' describing the fixed-effects part of the model, with the response on the left of a '~' operator and the p fixed terms, separated by '+' operators, on the right. Response variable y must be 0 or 1 (Binomial process).
interval	A numeric scalar or vector of length equal to the number of observations. interval specifies the time interval between censuses for the observation of mortality. Default to 1.
data	A data frame containing the variables of the model.
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.
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.
seed	The seed for the random number generator. If NA, the Mersenne Twister generator is used with default seed 12345; if an integer is passed it is used to seed the Mersenne twister.
tune	Metropolis tuning parameter. Must be a positive scalar. The tuning parameter is updated during the burning period to approach an acceptance rate of 0.44.
beta.start	The starting values for the β vector. This can either be a scalar or a p-length vector. The default value of NA will use the OLS β estimate of the corresponding Gaussian Linear Regression without random effects. If this is a scalar, that value will serve as the starting value mean for all of the betas.
mubeta	The prior mean of β . This can either be a scalar or a p-length vector. If this takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value of 0 will use a vector of zeros for an uninformative prior.
Vbeta	The prior variance of β . This can either be a scalar or a square p-dimension matrix. If this takes a scalar value, then that value times an identity matrix serves as the prior variance of beta. Default value of 1.0E6 will use a diagonal matrix with very large variance for an uninformative flat prior.

Details

The `deforestation()` function estimates the parameters of a logistic regression model with a variable time-interval between observations. The estimation is done in a hierarchical Bayesian framework using an adaptive Metropolis algorithm. Function is developped in C++ code using the Scythe statistical library (Pemstein et al. 2007) to maximize efficiency.

The model takes the following form:

$$y_i \sim \text{Bernoulli}(\theta'_i)$$

With $\theta'_i = 1 - (1 - \theta_i)^{I_i}$, where I_i stands for the time-interval for observation i . Thus, θ_i is a probability by unit of time (an annual rate for example if the unit of the time-interval is in year).

Using the logit link function denoted ϕ , we set:

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

By default, we assume a multivariate Normal prior on β :

$$\beta \sim \mathcal{N}(\mu_\beta, V_\beta)$$

For the Metropolis algorithm, the proposal distribution is centered at the current value of β and has variance-covariance $V = T(V_\beta^{-1} + C^{-1})^{-1}T$, where T is a the diagonal positive definite matrix formed from the tune, V_β is the prior variance, and C is the large sample variance-covariance matrix of the MLEs without considering the variation of the time-interval between observations. This last calculation is done via an initial call to `glm`.

Value

<code>mcmc</code>	An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package.
<code>deviance</code>	The posterior mean of the deviance D , with $D = -2 \log(\prod_i P(y_i \theta_i))$.
<code>tune</code>	The optimized value for the tuning parameter. This value can be used for potential future runs.

Author(s)

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References

- Daniel Pemstein, Kevin M. Quinn, and Andrew D. Martin. 2007. *Scythe Statistical Library 1.0*. <http://scythe.wustl.edu>.
- Martyn Plummer, Nicky Best, Kate Cowles, and Karen Vines. 2002. *Output Analysis and Diagnostics for MCMC (CODA)*. <http://www-fis.iarc.fr/coda/>.

See Also

[plot.mcmc](#), [summary.mcmc](#)

Examples

```
## Not run:
#####
# Logistic regression with variable time-interval between observations
#####

#= Library
library(phcfM)
```

```

#== Generating data

# Random seed
set.seed(1234)

# Constants
nobs <- 3000

# Covariates
X1 <- runif(n=nobs,min=-10,max=10)
X2 <- runif(n=nobs,min=-10,max=10)
X <- cbind(rep(1,nobs),X1,X2)
I <- runif(n=nobs,min=1,max=5) # Time-interval

# Target beta parameters
beta.target <- matrix(c(0.3,0.2,0.1),ncol=1)

# Response
theta <- vector()
theta_prim <- vector()
Y <- vector()
for (n in 1:nobs) {
  theta[n] <- inv.logit(X[n,]%*%beta.target)
  theta_prim[n] <- 1-(1-theta[n])^I[n]
  Y[n] <- rbinom(n=1,size=1,prob=theta_prim[n])
}

# Data-set
Data <- as.data.frame(cbind(Y,I,theta_prim,theta,X1,X2))
plot(Data$X1,Data$theta)
plot(Data$X2,Data$theta)

#== Call to deforestation()
model <- deforestation(formula=Y~X1+X2, interval=Data$I, data=Data, burnin=1000, mcmc=1000,
  thin=1, verbose=1, seed=NA, tune=1, beta.start=NA, mubeta=0,
  Vbeta=1.0E6)

#== MCMC analysis

# Graphics
plot(model$mcmc)

# Parameter estimates
str(model)
summary(model$mcmc)
model$deviance
model$tune

## We obtain good parameter estimates
##
##           Mean          SD Naive SE Time-series SE
## beta.(Intercept) 0.3362 0.054534 0.0017245      0.006589

```

```
## beta.X1      0.2027 0.009345 0.0002955      0.001154
## beta.X2      0.1037 0.007269 0.0002299      0.000838

##== GLM resolution if time-interval is not taken into account

model.glm <- glm(Y~X1+X2,data=Data,family="binomial")
summary(model.glm)

## In this case, the parameter estimates are biased
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) 2.000761   0.072069   27.76  <2e-16 ***
## X1          0.247514   0.012060   20.52  <2e-16 ***
## X2          0.123137   0.009803   12.56  <2e-16 ***

## End(Not run)
```

demography	<i>Markov Chain Monte Carlo for the Hierarchical Gaussian Linear Regression Model</i>
------------	---

Description

The 'demography' function generates a sample from the posterior distribution of a Hierarchical Gaussian Linear Regression Model using Algorithm 2 of Chib and Carlin (1999). This model uses a multivariate Normal prior for the fixed effects parameters, an Inverse-Wishart prior on the random effects variance matrix, and an Inverse-Gamma prior on the residual error variance. The user supplies data and priors, and a sample from the posterior distribution is returned as an mcmc object, which can be subsequently analyzed with functions provided in the coda package.

Usage

```
demography(fixed, random, group, data, burnin=1000, mcmc=10000,
thin=10, verbose=1, seed=NA, beta.start=NA, sigma2.start=NA,
Vb.start=NA, mubeta=0, Vbeta=1.0E6, r, R, nu=0.001, delta=0.001)
```

Arguments

fixed	A two-sided linear formula of the form 'y~x1+...+xp' describing the fixed-effects part of the model, with the response on the left of a '~' operator and the p fixed terms, separated by '+' operators, on the right.
random	A one-sided formula of the form '~x1+...+xq' specifying the model for the random effects part of the model, with the q random terms, separated by '+' operators. If random=NULL, a fixed effect model is fitted.
group	String indicating the name of the grouping variable in data, defining the hierarchical structure of the model.
data	A data frame containing the variables in the model.
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.
seed	The seed for the random number generator. If NA, the Mersenne Twister generator is used with default seed 12345; if an integer is passed it is used to seed the Mersenne twister.
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.
beta.start	The starting values for the β vector. This can either be a scalar or a p-length vector. The default value of NA will use the OLS β estimate of the corresponding Gaussian Linear Regression without random effects. If this is a scalar, that value will serve as the starting value mean for all of the betas.
sigma2.start	Scalar for the starting value of the residual error variance. The default value of NA will use the OLS estimates of the corresponding Gaussian Linear Regression without random effects.
Vb.start	The starting value for variance matrix of the random effects. This must be a square q-dimension matrix. Default value of NA uses an identity matrix.
mubeta	The prior mean of β . This can either be a scalar or a p-length vector. If this takes a scalar value, then that value will serve as the prior mean for all of the betas. The default value of 0 will use a vector of zeros for an uninformative prior.
Vbeta	The prior variance of β . This can either be a scalar or a square p-dimension matrix. If this takes a scalar value, then that value times an identity matrix serves as the prior variance of beta. Default value of 1.0E6 will use a diagonal matrix with very large variance for an uninformative flat prior.
r	The shape parameter for the Inverse-Wishart prior on variance matrix for the random effects. r must be superior or equal to q . Set $r=q$ for an uninformative prior. See the NOTE for more details
R	The scale matrix for the Inverse-Wishart prior on variance matrix for the random effects. This must be a square q-dimension matrix. Use plausible variance regarding random effects for the diagonal of R. See the NOTE for more details
nu	The shape parameter for the Inverse-Gamma prior on the residual error variance. Default value is $\text{nu}=\text{delta}=0.001$ for uninformative prior.
delta	The rate (1/scale) parameter for the Inverse-Gamma prior on the residual error variance. Default value is $\text{nu}=\text{delta}=0.001$ for uninformative prior.
...	further arguments to be passed

Details

demography simulates from the posterior distribution sample using the blocked Gibbs sampler of Chib and Carlin (1999), Algorithm 2. The simulation is done in compiled C++ code to maximize efficiency. Please consult the coda documentation for a comprehensive list of functions that can be used to analyze the posterior sample.

The model takes the following form:

$$y_i = X_i\beta + W_ib_i + \varepsilon_i$$

Where each group i have k_i observations.

Where the random effects:

$$b_i \sim \mathcal{N}_q(0, V_b)$$

And the errors:

$$\varepsilon_i \sim \mathcal{N}(0, \sigma^2 I_{k_i})$$

We assume standard, conjugate priors:

$$\beta \sim \mathcal{N}_p(\mu_\beta, V_\beta)$$

And:

$$\sigma^2 \sim \mathcal{IGamma}(\nu, 1/\delta)$$

And:

$$V_b \sim \mathcal{IWishart}(r, rR)$$

See Chib and Carlin (1999) for more details.

NOTE: We do not provide default parameters for the priors on the variance matrix for the random effects. When fitting one of these models, it is of utmost importance to choose a prior that reflects your prior beliefs about the random effects. Using the `dwish` and `rwish` functions might be useful in choosing these values.

Value

mcmc	An mcmc object that contains the posterior sample. This object can be summarized by functions provided by the coda package.
deviance	The posterior mean of the deviance D , with $D = -2 \log(\prod_i P(y_i \beta, b_i, \sigma^2))$, is also provided.
Y.pred	Predictive posterior mean for each observation.

Author(s)

Ghislain Vieilledent <ghislain.vieilledent@cirad.fr>

References

- Siddhartha Chib and Bradley P. Carlin. 1999. “On MCMC Sampling in Hierarchical Longitudinal Models.” *Statistics and Computing*. 9: 17-26.
- Daniel Pemstein, Kevin M. Quinn, and Andrew D. Martin. 2007. *Scythe Statistical Library 1.0*. <http://scythe.wustl.edu>.
- Andrew D. Martin and Kyle L. Saunders. 2002. “Bayesian Inference for Political Science Panel Data.” Paper presented at the 2002 Annual Meeting of the American Political Science Association.
- Martyn Plummer, Nicky Best, Kate Cowles, and Karen Vines. 2002. *Output Analysis and Diagnostics for MCMC (CODA)*. <http://www-fis.iarc.fr/coda/>.

See Also

[plot.mcmc](#), [summary.mcmc](#)

Examples

```
## Not run:
#=====
# Hierarchical Gaussian Linear Regression
#=====

##== Generating data

# Constants
nobs <- 1000
ntown <- 20
town <- c(1:ntown,sample(c(1:ntown),(nobs-ntown),replace=TRUE))

# Covariates
X1 <- runif(n=nobs,min=0,max=10)
X2 <- runif(n=nobs,min=0,max=10)
X <- cbind(rep(1,nobs),X1,X2)
W <- X

# Target parameters
# beta
beta.target <- matrix(c(0.1,0.3,0.2),ncol=1)
# Vb
Vb.target <- c(0.5,0.2,0.1)
# b
b.target <- cbind(rnorm(ntown,mean=0,sd=sqrt(Vb.target[1])),
                  rnorm(ntown,mean=0,sd=sqrt(Vb.target[2])),
                  rnorm(ntown,mean=0,sd=sqrt(Vb.target[3])))
# sigma2
sigma2.target <- 0.02

# Response
Y <- vector()
for (n in 1:nobs) {
  Y[n] <- rnorm(n=1,
               mean=X[n,]%*%beta.target+W[n,]%*%b.target[town[n],],
               sd=sqrt(sigma2.target))
}

# Data-set
Data <- as.data.frame(cbind(Y,X1,X2,town))
plot(Data$X1,Data$Y)

##== Call to demography
model <- demography(fixed=Y~X1+X2, random=~X1+X2, group="town",
                   data=Data, burnin=1000, mcmc=1000, thin=1,verbose=1,
                   seed=NA, beta.start=0, sigma2.start=1,
```

```

Vb.start=1, mubeta=0, Vbeta=1.0E6,
r=3, R=diag(c(1,0.1,0.1)), nu=0.001, delta=0.001)

##== MCMC analysis

# Graphics
pdf("Posteriors-demography.pdf")
plot(model$mcmc)
dev.off()

# Summary
summary(model$mcmc)

# Predictive posterior mean for each observation
model$Y.pred

# Predicted-Observed
plot(Data$Y,model$Y.pred)
abline(a=0,b=1)

## End(Not run)

```

InvGamma

The Inverse Gamma Distribution

Description

Density function and random generation from the inverse gamma distribution.

Usage

```

rinvgamma(n, shape, scale = 1)
dinvgamma(x, shape, scale = 1)

```

Arguments

x	Scalar location to evaluate density.
n	Number of draws from the distribution.
shape	Scalar shape parameter.
scale	Scalar scale parameter (default value one).

Details

An inverse gamma random variable with shape a and scale b has mean $\frac{b}{a-1}$ (assuming $a > 1$) and variance $\frac{b^2}{(a-1)^2(a-2)}$ (assuming $a > 2$).

Value

dinvgamma evaluates the density at x . rinvgamma takes n draws from the inverse Gamma distribution. The parameterization is consistent with the Gamma Distribution in the stats package.

Author(s)

Andrew D. Martin <admartin@wustl.edu>, Kevin M. Quinn <kquinn@law.berkeley.edu>, and Jong Hee Park <jhp@uchicago.edu>

References

Andrew Gelman, John B. Carlin, Hal S. Stern, and Donald B. Rubin. 2004. *Bayesian Data Analysis*. 2nd Edition. Boca Raton: Chapman & Hall.

See Also

[GammaDist](#)

Examples

```
## Not run:
density <- dinvgamma(4.2, 1.1)
draws <- rinvgamma(10, 3.2)

## End(Not run)
```

InvWishart

The Inverse Wishart Distribution

Description

Density function and random generation from the Inverse Wishart distribution.

Usage

```
diwish(W, v, S)
riwish(v, S)
```

Arguments

W	Positive definite matrix W ($p \times p$).
v	Degrees of freedom (scalar).
S	Scale matrix ($p \times p$).

Details

The mean of an inverse Wishart random variable with v degrees of freedom and scale matrix S is $(v - p - 1)^{-1}S$.

Value

diwish evaluates the density at positive definite matrix W . riwish generates one random draw from the distribution.

Author(s)

Andrew D. Martin <admartin@wustl.edu>, Kevin M. Quinn <kquinn@law.berkeley.edu>, and Jong Hee Park <jhp@uchicago.edu>

Examples

```
## Not run:
density <- diwish(matrix(c(2,-.3,-.3,4),2,2), 3, matrix(c(1,.3,.3,1),2,2))
draw <- riwish(3, matrix(c(1,.3,.3,1),2,2))

## End(Not run)
```

logit

Generalized logit and inverse logit function

Description

Compute generalized logit and generalized inverse logit functions.

Usage

```
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 $[-\text{Inf}, \text{Inf}]$ 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

```
## 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)
```

Wishart

The Wishart Distribution

Description

Density function and random generation from the Wishart distribution.

Usage

```
dwish(W, v, S)
rwish(v, S)
```

Arguments

W	Positive definite matrix W ($p \times p$).
v	Degrees of freedom (scalar).
S	Inverse scale matrix ($p \times p$).

Details

The mean of a Wishart random variable with v degrees of freedom and inverse scale matrix S is vS .

Value

`dwish` evaluates the density at positive definite matrix W . `rwish` generates one random draw from the distribution.

Author(s)

Andrew D. Martin <admartin@wustl.edu>, Kevin M. Quinn <kquinn@law.berkeley.edu>, and Jong Hee Park <jhp@uchicago.edu>

Examples

```
## Not run:
density <- dwish(matrix(c(2,-.3,-.3,4),2,2), 3, matrix(c(1,.3,.3,1),2,2))
draw <- rwish(3, matrix(c(1,.3,.3,1),2,2))

## End(Not run)
```

Index

- *Topic **Binomial**
 - deforestation, [2](#)
 - *Topic **Gaussian**
 - demography, [6](#)
 - *Topic **MCMC**
 - deforestation, [2](#)
 - demography, [6](#)
 - *Topic **anthropogenic pressure**
 - phcfM-package, [2](#)
 - *Topic **bayesian**
 - deforestation, [2](#)
 - demography, [6](#)
 - *Topic **deforestation**
 - phcfM-package, [2](#)
 - *Topic **distribution**
 - InvGamma, [10](#)
 - InvWishart, [11](#)
 - Wishart, [13](#)
 - *Topic **glm**
 - deforestation, [2](#)
 - *Topic **hierarchical models**
 - deforestation, [2](#)
 - demography, [6](#)
 - *Topic **logit**
 - deforestation, [2](#)
 - *Topic **math**
 - logit, [12](#)
 - *Topic **mixed models**
 - demography, [6](#)
 - *Topic **models**
 - deforestation, [2](#)
 - demography, [6](#)
 - *Topic **tropical forest**
 - phcfM-package, [2](#)
- deforestation, [2](#)
demography, [6](#)
dinvgamma (InvGamma), [10](#)
diwish (InvWishart), [11](#)
dwish (Wishart), [13](#)
- GammaDist, [11](#)
- inv.logit (logit), [12](#)
InvGamma, [10](#)
InvWishart, [11](#)
- logit, [12](#)
- phcfM (phcfM-package), [2](#)
phcfM-package, [2](#)
plot.mcmc, [4](#), [9](#)
- rinvgamma (InvGamma), [10](#)
riwish (InvWishart), [11](#)
rwish (Wishart), [13](#)
- summary.mcmc, [4](#), [9](#)
- Wishart, [13](#)