Package ‘bglm’

February 19, 2015

Type Package

Title Bayesian Estimation in Generalized Linear Models

Version 1.0

Date 2014-10-29

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Description Implementation of Bayesian estimation in generalized linear models following Gamerman (1997).

License GPL-2

Depends R (>= 3.0.2), mvtnorm, methods

Suggests car, coda, faraway

 NeedsCompilation no

Repository CRAN

Date/Publication 2014-11-20 18:16:40

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Bayesian estimation in glm is implemented via Metropolis Hastings algorithm following the proposal kernel defined by Gamerman (1997).

Description

The package provides functions which perform Bayesian estimation via Metropolis-Hastings algorithm in generalized linear models.

Details

Package: bglm
Type: Package
Version: 1.0
Date: 2014-10-29
License: GPL-2
Depends: mvtnorm

Author(s)

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References


Examples

```r
library(faraway)
data(babyfood)
summary(babyfood)
g2<- glm(cbind(disease, nondisease) ~ sex+food,family=binomial,babyfood)
#####use N > 8000 for more accurate results
bmen<-binommh(disease~ sex+food,babyfood$disease+babyfood$nondisease,N=1000,
data=babyfood)
data.frame(R.coef=coef(g2),R.sd=sqrt(diag(summary(g2)$cov.unscaled)),
          mh.mean=apply(bmen$chain,2,mean),mh.sd=apply(bmen$chain,2,sd))
```
Function for Bayesian Estimation in Binomial Models

Description

In this function the transition kernel proposed by Gamerman (1997) is implemented for a Metropolis Hastings algorithm, in order to sample the posterior distribution of the regression parameters given the data in a binomial distribution model. A normal Prior is assumed for the regression parameters. For now only the logit link is implemented.

Usage

```r
## Default S3 method:
binommh(y, m, X, b = rep(0, dim(X)[2]),
B = diag(rep(10000, dim(X)[2])), N = 3000, flag = F,...)
## S3 method for class 'formula'
binommh(formula, data = list(), weights, ...)
```

Arguments

- `formula`: an object of class formula: a symbolic description of the model to be fitted.
- `data`: A data frame containing the variables in the model.
- `weights`: Vector indicating the total number of experiments in each observation. Note: it is not searched in the data environment.
- `y`: Response variable, a vector coding for counts of success in a given number of trials, where m is a vector indicating the total number of experiments in each observation.
- `m`: Vector indicating the total number of experiments in each observation.
- `X`: Design matrix.
- `b`: Mean of the normal prior distribution of the regression parameters.
- `B`: Covariance matrix of the normal prior distribution of the regression parameters.
- `N`: Number mcmc simulations of the posterior distributions of the regression parameters given de data.
- `flag`: Logical, if TRUE iterations and acceptance ratio of the samples is printed to monitor the mcmc progress.
- `...`: When using binommh.formula, the formula object encapsulates the arguments y and X of binommh.default, thus ... represents all other arguments needed in binommh.default to be passed to binommh.formula

Details

See Gamerman (1997) for the details.
Value

A list with the following objects:

- **chain**: A matrix where mcmc simulations of the posterior distributions of the regression parameters given the data is stored. Rows correspond to mcmc simulation and columns correspond to the regression parameters.
- **Deviance**: A vector with -2*l(y,chain[i,]), where l(... is the log-likelihood of the model.
- **Accepted_samples**: An integer with the number of samples accepted by the M-H algorithm.

Author(s)

Nicolas Molano-Gonzalez, Edilberto Cepeda-Cuervo

References


Examples

```
library(faraway)
data(babyfood)
summary(babyfood)
g2<- glm(cbind(disease, nondisease) ~ sex+food,family=binomial,babyfood)
use N > 8000 for more accurate results
bmen<- binommh(disease~ sex+food,babyfood$disease+babyfood$nondisease,N=1000, data=babyfood)
compare Bayesian estimation vs classical
data.frame(R.coef=coef(g2),R.sd=sqrt(diag(summary(g2)$cov.unscaled)), mh.mean=apply(bmen$chain,2,mean),mh.sd=apply(bmen$chain,2,sd))
```

Description

In this function the transition kernel proposed by Gamerman (1997) is implemented for a Metropolis Hastings algorithm, in order to sample the posterior distribution of the regression parameters given data in an exponential distribution model. A normal Prior is assumed for the regression parameters. For now only the log link is implemented.

Usage

```
# Default S3 method:
expmh(y, X, b = rep(0, dim(X)[2]), B = diag(rep(100, dim(X)[2])), N = 3000, flag = F,...)
# S3 method for class 'formula'
expmh(formula, data = list(), ...)
```
Arguments

formula: an object of class formula: a symbolic description of the model to be fitted.
data: A data frame containing the variables in the model.
... When using expmh.formula, the formula object encapsulates the arguments y
and X of expmh.default, thus ... represents all other arguments needed in expmh.default
to be passed to expmh.formula

y: Response variable, vector of positive numbers.
x: Design matrix
b: Mean of the normal prior distribution of the regression parameters.
B: Covariance matrix of the normal prior distribution of the regression parameters.
N: Number mcmc simulations of the posterior distributions of the regression pa-
rameters given de data.
flag: Logical, if TRUE iterations and acceptance ratio of the samples is printed to
monitor the mcmc progress.

Details

See Gamerman (1997) for the details.

Value

A list with the following objects:

chain: A matrix where mcmc simulations of the posterior distributions of the regression
parameters given the data is stored. Rows correspond to mcmc simulation and
columns correspond to the regression parameters.

Deviance: a vector with -2*l(y,chain[i,]), where l(...) is the log-likelihood of the model.
Accepted_samples: An integer with the number of samples accepted by the M-H algorithm.

Author(s)

Nicolas Molano-Gonzalez, Edilberto Cepeda-Cuervo

References

Statistics and Computing, 7, 57-68.

Examples

# Simulated data
library(coda)
library(car)
n<-500
(beta<-runif(2,-10,10))
### limits of mu
ld<-c(10,70)
### generate X according to ld
xlm<-c((log(ld[1])-beta[1])/beta[2],(log(ld[2])-beta[1])/beta[2])
### design matrix
X<-as.matrix(data.frame(x0=rep(1,n),x1=runif(n,sort(xlm)[1],sort(xlm)[2])))
mu<-sapply(1:dim(X)[1],function(i){exp(X[i,]%*%beta)})
### generate the data according to the model
y<-rexp(n,1/mu)
### fit the model
bres<-expmh(y~X[,2],N=3000)
### compare with true beta
round(data.frame(true_beta=beta,
    mh_mean=apply(bres$chain,2,mean),
    mh_sd=apply(bres$chain,2,sd)),5)
### examine MCMC chains.
dev.new(width=9,height=6)
par(mfrow=c(2,3))
plot(as.ts(bres$chain[,1]),cex.main=0.9,main=expression(beta[0]),
    ylab="",xlab="iterations")
plot(density(bres$chain[,1]),cex.main=0.9,col="red",lwd=2,
    main=expression(beta[1]))
autocorr.plot(mcmc(bres$chain[,1]),cex.main=0.9,col="red",lwd=2,
    main=expression(beta[0]),auto.layout=FALSE,lag.max=100)
plot(as.ts(bres$chain[,2]),cex.main=0.9,main=expression(beta[1]),
    ylab="",xlab="iterations")
plot(density(bres$chain[,2]),cex.main=0.9,col="red",lwd=2,
    main=expression(beta[0]))
autocorr.plot(mcmc(bres$chain[,2]),cex.main=0.9,col="red",lwd=2,
    main=expression(beta[1]),auto.layout=FALSE,lag.max=100)

---

poissmh

**Function for Bayesian Estimation in Poisson Models**

**Description**

In this function the transition kernel proposed by Gamerman (1997) is implemented for a Metropolis Hastings algorithm, in order to sample the posterior distribution of the regression parameters given the data in a poisson regression. A normal Prior is assumed for the regression parameters. For now only the log link is implemented.

**Usage**

```r
## Default S3 method:
poissmh(y, X, b = rep(0, dim(X)[2]),
B = diag(rep(10000, dim(X)[2])), N = 3000, flag = F, ...)
## S3 method for class 'formula'
poissmh(formula, data = list(), ...)
```
Arguments

- **formula**: an object of class formula: a symbolic description of the model to be fitted.
- **data**: A data frame containing the variables in the model.
- **...**: When using poissmh.formula, the formula object encapsulates the arguments y and X of poissmh.default, thus ... represents all other arguments needed in poissmh.default to be poissmh to binommh.formula
- **y**: Response variable, a vector of counts.
- **X**: Design matrix.
- **b**: Mean of the normal prior distribution of the regression parameters.
- **B**: Covariance matrix of the normal prior distribution of the regression parameters.
- **N**: Number mcmc simulations of the posterior distributions of the regression parameters given de data.
- **flag**: Logical, if TRUE iterations and acceptance ratio of the samples is printed to monitor the mcmc progress.

Details

See Gamerman, 1997 for the details.

Value

A list with the following objects:

- **chain**: A matrix where mcmc simulations of the posterior distributions of the regression parameters given the data is stored. Rows correspond to mcmc simulation and columns correspond to the regression parameters.
- **Deviance**: a vector with -2*l(y,chain[i,]), where l(.,.) is the log-likelihood of the model.
- **Accepted_samples**: An integer with the number of samples accepted by the M-H algorithm.

Author(s)

Nicolas Molano-Gonzalez, Edilberto Cepeda-Cuervo

References


Examples

```r
library(faraway)
data(gala)
g2<-glm(Species ~ .,family=poisson, gala)
####use N > 8000 for more accurate results
bmen<-poissmh(Species ~ .,data=gala,N=1000)
####compare Bayesian estimation vs classical
```
round(data.frame(R.coef=coef(g2),R.sd=sqrt(diag(summary(g2)$cov.unscaled))),
   mh.mean=apply(bmen$chain,2,mean),mh.sd=apply(bmen$chain,2,sd)),4)
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