

Package ‘BayesH’

April 4, 2016

Type Package

Title Bayesian Regression Model with Mixture of Two Scaled Inverse Chi Square as Hyperprior

Version 1.0

Date 2016-04-03

Author Renato Rodrigues Silva

Maintainer Renato Rodrigues Silva <renato.rrsilva@ufg.br>

Description Functions to performs Bayesian regression model with mixture of two scaled inverse chi square as hyperprior distribution for variance of each regression coefficient.

License GPL-3

Depends R (>= 2.10)

NeedsCompilation yes

Repository CRAN

Date/Publication 2016-04-04 23:58:49

R topics documented:

bayesModel.fit	2
example	3
get.scale.bayesH	3
plot.BayesH	4
predict.BayesH	5
summary.BayesH	6
X	7
y	7
Index	8

bayesModel.fit	<i>Bayesian regression model with mixture of two scaled inverse chi square as hyperprior distribution.</i>
----------------	--

Description

Performs Gibbs Sampling algorithm for fitting the Bayesian regression model with mixture of two scaled inverse chi square as hyperprior distribution for variance of each regression coefficients.

Usage

```
bayesModel.fit(X, y, nu0, s0, niter = 2000, burnin = 500, type="bayesH")
```

Arguments

X	the incidence matrix of model.
y	the vector of response variable of the model.
nu0	the degree of freedom hyperparameter(s) nu0 for all mixture components.
s0	the scale hyperparameter(s) s0 for all mixture components.
niter	the number of iterations of Gibbs Sampling algorithm.
burnin	the number of 'burn in' in a Gibbs Sampling algorithm.
type	it is a string which if were defined as "ridge" the function performs Bayesian ridge regression, otherwise, Bayes H model.

Details

For bayesian ridge regression (type == "ridge"), the prior distribution for the error variance and the hyperprior distribution for variance of the regression coefficients follows scaled inverse chi square with same hyperparameters (nu0[1], s0[1]) and (nu0[2], s0[2]), respectively. On the other hand, for hierarchical regression model (type == "bayesH") is assumed that each the regression coefficient has different variance and each one of them follows a mixture of scaled inverse chi square with hyperparameters (nu0[1]; s0[1]) and (nu0[2]; s0[2]), respectively. In this case, the prior distribution for error variance also follows scaled inverse chi square with hyperparameters nu0[3] and s0[3]. NA's in the incidence matrix are not allowed. All elements of vector s0 must be greater than zero.

Value

The output is an object of class BayesH that contains the posterior distribution of intercept, posterior distribution of variance error, posterior mean of regression coefficients and posterior mean of predicted values.

Author(s)

Renato Rodrigues Silva, <renato.rrsilva@ufg.br>

See Also[get.scale.bayesH](#)**Examples**

```
data(example)

mod = bayesModel.fit(X = X, y = y, nu0 = c(3,30,20),
                    s0 = c(1e-10,0.1, 0.5), niter = 2000,
                    burnin = 300, type = "bayesH" )

summary(mod)
```

`example`*example dataset*

Description

A simulated data set composed by 500 covariables and 150 values of response variable.

Usage

```
data(example)
```

Format

markers is the incidence matrix. yield is the vector of response variable.

`get.scale.bayesH`*Get the vector of the scale hyperparameter*

Description

Get the vector of the scale hyperparameter.

Usage

```
get.scale.bayesH(nu0, R2 = 0.5, X, y, type = "bayesH")
```

Arguments

nu0	the vector with shape parameter(s) of (hyper) prior distribution for variance of each the regression coefficient(s) and error variance.
R2	the expected proportion of the variance of the response variable that can be explained by the model (r squared).
y	the vector of response variable of the model.
X	the incidence matrix.
type	it is a string which if were defined as “ridge” the function performs Bayesian ridge regression, otherwise, Bayes H model.

Details

The user must be provided the vector nu0 and all elements this vector must be greater than zero. The strategy adopted here is based on Perez et. al. (2010).

Value

An object of class vector with values of the scale parameters.

Author(s)

Renato Rodrigues Silva, <renato.rrsilva@ufg.br>

References

Perez. et. al. (2010). Genomic-Enabled Prediction Based on Molecular Markers and Pedigree Using the Bayesian Linear Regression Package in R. Plant Genome. 2010; 3(2): 106-116. doi: 10.3835/plantgenome2010.04.0005.

See Also

[bayesModel.fit](#)

plot.BayesH

Plots observed versus predicted values

Description

Plots observed versus predicted values for objects of class BayesH.

Usage

```
## S3 method for class 'BayesH'
plot(x, ...)
```

Arguments

x An object of class BayesH.
... Further arguments passed to or from other methods.

Details

It is an adaptation of code written by Perez and De Los Campos (2014).

Author(s)

Renato Rodrigues Silva

References

Gustavo de los Campos, Hugo Naya, Daniel Gianola, Jose Crossa, Andre's Legarra, Eduardo Manfredi, Kent Weigel and Jose Miguel Cotes. Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree, 2009. Genetics. doi: 10.1534/genetics.109.101501

`predict.BayesH` *Make Predictions*

Description

Make predictions from the results of bayesModel.fit function.

Usage

```
## S3 method for class 'BayesH'  
predict(object, newdata, ...)
```

Arguments

object An object of class BayesH.
newdata An object of class matrix or data.frame with new data (explanatory variables).
... Further arguments passed to or from other methods.

Author(s)

Renato Rodrigues Silva

References

Gustavo de los Campos, Hugo Naya, Daniel Gianola, Jose Crossa, Andre's Legarra, Eduardo Manfredi, Kent Weigel and Jose Miguel Cotes. Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree, 2009. Genetics. doi: 10.1534/genetics.109.101501

See Also

bayesfit.model.

summary.BayesH

Summary

Description

Provides a summary for a fitted model using bayesModel.fit function.

Usage

```
## S3 method for class 'BayesH'  
summary(object, ...)
```

Arguments

object An object of class BayesH.
... Further arguments passed to or from other methods.

Details

It is an adaptation of code written by Perez and De Los Campos (2014). The output of this function is print the mean of the posterior distribution of the error variance, the variance of reponse observed values (training population). When there are missing values, the correlation between the predicted values and observed values is printed as well.

Author(s)

Renato Rodrigues Silva

References

Gustavo de los Campos, Hugo Naya, Daniel Gianola, Jose Crossa, Andre's Legarra, Eduardo Manfredi, Kent Weigel and Jose Miguel Cotes. Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree, 2009. Genetics. doi: 10.1534/genetics.109.101501

See Also

bayesModel.fit.

x	<i>Incidence Matrix</i>
---	-------------------------

Description

It is a incidence matrix with 150 rows and 500 columns.

y	<i>Vector of observations for the example dataset</i>
---	---

Description

A column vector of observations with 150 rows

Index

*Topic **datasets**

example, [3](#)

X, [7](#)

y, [7](#)

*Topic **plot**

plot.BayesH, [4](#)

bayesModel.fit, [2](#), [4](#)

example, [3](#)

get.scale.bayesH, [3](#), [3](#)

plot.BayesH, [4](#)

predict.BayesH, [5](#)

summary.BayesH, [6](#)

X, [7](#)

y, [7](#)