

Package ‘GGRidge’

October 12, 2022

Type Package

Title Graphical Group Ridge

Version 0.1.0

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Description The Graphical Group Ridge 'GGRidge' package package classifies ridge regression predictors in disjoint groups of conditionally correlated variables and derives different penalties (shrinkage parameters) for these groups of predictors. It combines the ridge regression method with the graphical model for high-dimensional data (i.e. the number of predictors exceeds the number of cases) or ill-conditioned data (e.g. in the presence of multicollinearity among predictors). The package reduces the mean square errors and the extent of over-shrinking of predictors as compared to the ridge method.

License GPL-2

Imports gRbase, CVglasso, MASS, graph

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

Date/Publication 2021-03-02 10:10:06 UTC

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GGRidge-package

GGRidge: Graphical Group Ridge

Description

The Graphical Group Ridge 'GGRidge' classifies ridge regression predictors in disjoint groups of conditionally correlated variables and derives different penalties (shrinkage parameters) for these groups of predictors. It combines the ridge regression method with the graphical model for high-dimensional data (i.e. the number of predictors exceeds the number of cases) or ill-conditioned data (e.g. in the presence of multicollinearity among predictors). The package reduces the mean square errors and the extent of over-shrinking of predictors as compared to the ridge method.

Details

Package: GGRidge
Type: Package
Version: 1.0
Date: 2021-1-28
License: GPL-2

Author(s)

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References

Claus Dethlefsen and Soren Hojsgaard (2005): A Common Platform for Graphical Models in R: The gRbase Package, *Journal of Statistical Software*, <https://www.jstatsoft.org/v14/i17/>, 14(17).

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Saeed Aldahmani and Taoufik Zoubeidi (2020): Graphical group ridge, *Journal of Statistical Computation and Simulation*.

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Scheetz, T.E., Kim, K.Y.A., Swiderski, R.E., Philp, A.R., Braun, T.A., Knudtson, K.L., Dorrance, A.M., DiBona, G.F., Huang, J., Casavant, T.L. and Sheffield, V.C. (2006). Regulation of gene expression in the mammalian eye and its relevance to eye disease. *Proceedings of the National Academy of Sciences*.

GGRidge

GGRidge: Graphical group ridge

Description

The function has two main tasks. The first task is to find the graph structure (using GraphicalLasso) which is used to identify the conditionally correlated groups of predictors and then search for the optimal values of the tuning parameters to estimate the GGRidge regression coefficients. For given data, an estimated regression coefficients, mean squared error (MSE) and the shrinkage parameters for the estimated groups of predictors are returned.

Usage

```
GGRidge(data, kg=5, sq=c(0.01,5,0.01), k=5, PE=50)
```

Arguments

data	A matrix of dimension $n \times v$ where $v=(p+1)$ consisting of the values of the predictors and the response variable (last variable).
kg	Number of splits in k-fold cross-validation to find the graph structure. Default value is kg=5.
sq	The starting (maximal) end values and number: increment of the sequence of the tuning parameters for the generated penalty term. Defaults are 0.01, 5 & 0.01 respectively.
k	Number of splits in k-fold cross-validation to find the ridge penalty parameter. Default value is k=5.
PE	The number of iterations used in computing the prediction mean square error for each group of predictors. The default is PE=50.

Value

A list of three values:

Coefficients	The vector of estimated regression parameters.
MSE	Mean square error for the parameters.
lambda.opt	Optimal values of the penalty.

Author(s)

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Claus Dethlefsen and Soren Hojsgaard (2005): A Common Platform for Graphical Models in R: The gRbase Package, *Journal of Statistical Software*, <https://www.jstatsoft.org/v14/i17/>, 14(17).

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Examples

```
#####

# Example

#####
library(gRbase)
library("CVglasso")
library("MASS")
#load the data
data(SampleEyeData)
x <- scale(SampleEyeData[,-51], center = TRUE, scale = TRUE)
y <- scale(SampleEyeData[,51], center = TRUE)

Data<-as.matrix(cbind(x,y))

# Call GGRidge(.) .

results <- GGRidge(data=Data,kg=3,sq=c(0.1,.5,0.1),k=3,PE=30)

# The returned objects are

results$Coefficients
results$MSE
results$lambda.opt
```

*SampleEyeData**SampleEyeData*

Description

The package utilizes a sample of 50 genes from the genes expressions dataset used in Scheetz et al. [2006]. The sampled data set consists of 50 predictors and 40 observations with a continuous response (TRIM32 gene).

Usage

```
data("SampleEyeData")
```

Format

A data frame with 40 observations on 51 variables including the response.

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