# Package 'GGRidge' 

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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 pre-
dictors in disjoint groups of conditionally correlated variables and derives different penal-
ties (shrinkage parameters) for these groups of predictors. It combines the ridge regres-
sion method with the graphical model for high-dimensional data (i.e. the number of predic-
tors exceeds the number of cases) or ill-conditioned data (e.g. in the presence of multicollinear-
ity among predictors). The package reduces the mean square errors and the extent of over-
shrinking of predictors as compared to the ridge method.
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## 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 highdimensional 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

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## 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).
Gabor Csardi and Tamas Nepusz (2006): The igraph software package for complex network research, Inter Journal, https://igraph .org.
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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.

## 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 coeffcients. For given data, an estimated regression coeffcients, mean squared error (MSE) and the shrinkage parameters for the estimated groups of predictors are returned.

## Usage

GGRidge(data, $\mathrm{kg}=5, \mathrm{sq}=\mathrm{c}(0.01,5,0.01), \mathrm{k}=5, \mathrm{PE}=50)$

## Arguments

data A matrix of dimension $n x v$ ) where $v=(p+1)$ consisting of the values of the predictors and the response variable (last variable).
$\mathrm{kg} \quad$ Number of splits in k-fold cross-validation to find the graph structure. Default value is $\mathrm{kg}=5$.
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.
$\mathrm{k} \quad$ Number of splits in k-fold cross-validation to find the ridge penalty parameter. Default value is $\mathrm{k}=5$.

PE The number of iterations used in computing the prediction mean square error for each group of predictors. The default is $\mathrm{PE}=50$.

## 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.

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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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