Package ‘HCmodelSets’

December 16, 2019

Type Package
Title Regression with a Large Number of Potential Explanatory Variables
Version 1.1
Author H. H. Hoeltgebaum
Maintainer H. H. Hoeltgebaum <hh3015@ic.ac.uk>
BugReports https://github.com/hhhello/HmodelSets/issues
Description Software for performing the reduction, exploratory and model selection phases of the procedure proposed by Cox, D.R. and Battey, H.S. (2017) <doi:10.1073/pnas.1703764114> for sparse regression when the number of potential explanatory variables far exceeds the sample size. The software supports linear regression, likelihood-based fitting of generalized linear regression models and the proportional hazards model fitted by partial likelihood.
License MIT + file LICENSE
Encoding UTF-8
LazyData true
Depends R (>= 2.10), mvtnorm, ggplot2, survival,
RoxygenNote 6.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2019-12-16 20:20:06 UTC

R topics documented:

DGP ................................................................. 2
Exploratory.Phase .................................................. 3
LymphomaData ...................................................... 5
ModelSelection.Phase ............................................... 6
Reduction.Phase .................................................... 8

Index 10
Description

This function generates realizations of random variables as described in the simple example of Battey, H. S. & Cox, D. R. (2018).

Usage

DGP(s,a,sigStrength,rho,n,noise=NULL,var,d,intercept,type.response="N",DGP.seed=NULL, scale=NULL,shape=NULL,rate=NULL)

Arguments

s  Number of signal variables.
a  Number of noise variables correlated with signal variables.
sigStrength  Signal strength.
rho  Correlation among signal variables and noise variables correlated with signal variables.
n  Sample size.
noise  Variance of the observations around the true regression line.
var  Variance of the potential explanatory variables.
d  Number of potential explanatory variables.
intercept  Expected value of the response variable when all potential explanatory variables are at zero. It is only considered when type.response="N".
type.response  Generates gaussian ("N") or survival ("S") data from a proportional hazards model with Weibull baseline hazard.
DGP.seed  Seed for the random number generator.
scale  scale parameter of the proportional hazards model with Weibull baseline hazard.
shape  shape parameter of the proportional hazards model with Weibull baseline hazard.
rate  rate parameter of the exponential distribution of censoring times. If not provided, uncensored data are generated.

Value

X  The simulated design matrix.
Y  The simulated response variable.
TRUE.idx  Indices of the variables in the true model.
status  If type.response="S", provides the status from survival data.
Acknowledgement

The work was supported by the UK Engineering and Physical Sciences Research Council under grant number EP/P002757/1.

Author(s)

Hoeltgebaum, H. H.

References


Examples

```r
## Generates DGP

## Generates a random DGP
dgp = DGP(s=5, a=3, sigStrength=1, rho=0.9, n=100, intercept=5, noise=1, var=1, d=1000, DGP.seed = 2018)
```

Exploratory.Phase

*Perform the Exploratory phase on the hypercube dimension reduction proposed by Cox, D. R. & Battey, H. S. (2017)*

Description

This function performs the exploratory phase on the variables retained through the reduction phase, returning any significant squared and interaction terms.

Usage

```r
Exploratory.Phase(X, Y, list.reduction, family=gaussian, signif=0.01, silent=TRUE, Cox.Hazard = FALSE)
```
Arguments

X  Design matrix.
Y  Response vector.
list.reduction  Indices of retained variables from the reduction phase.
family  A description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function. See family for more details.
signif  Significance level for the assessment of squared and interaction terms. The default is 0.01.
silent  By default, silent=TRUE. If silent=FALSE the user can decide upon the exclusion of individual interaction terms.
Cox.Hazard  If TRUE fits proportional hazards regression model. The family argument will be ignored if Cox.Hazard=TRUE.

Value

mat.select.SQ  Indices of variables with significant squared terms.
mat.select.INTER  Indices of the pairs of variables with significant interaction terms.

Acknowledgement

The work was supported by the UK Engineering and Physical Sciences Research Council under grant number EP/P002757/1.

Author(s)

Hoeltgebaum, H. H.

References


See Also

Reduction.Phase
Examples

```r
## Generates a random DGP
dgp = DGP(s=5, a=3, sigStrength=1, rho=0.9, n=100, intercept=5, noise=1, var=1, d=1000, DGP.seed = 2018)

#Reduction Phase using only the first 70 observations
outcome.Reduction.Phase = Reduction.Phase(X=dgp$X[1:70,],Y=dgp$Y[1:70],
                                           family=gaussian, seed.HC = 1012)

# Exploratory Phase using only the first 70 observations, choosing the variables which # were selected at least two times in the third dimension reduction
idxs = outcome.Reduction.Phase$List.Selection$`Hypercube with dim 2`$numSelected1
outcome.Exploratory.Phase = Exploratory.Phase(X=dgp$X[1:70,],Y=dgp$Y[1:70],
                                           list.reduction = idxs,
                                           family=gaussian, signif=0.01)
```

LymphomaData

Lymphoma patients data set.

Description

Data set of lymphoma patients used in the study of Alizadeh et al. (2000) and also Simon et al. (2011).

Usage

data(LymphomaData)

Format

patient.data A list with survival times, status and covariates from patients.

Value

- **x** Covariates from patients.
- **time** Survival times.
- **status** Patient status.

References


Examples

```r
data(LymphomaData)
x <- t(patient.data$x)
y <- patient.data$time
```

Description

This function tests low dimensional subsets of the set of retained variables from the reduction phase and any squared or interaction terms suggested at the exploratory phase. Lists of well-fitting models of each dimension are returned.

Usage

```r
ModelSelection.Phase(X, Y, list.reduction, family=gaussian,
  signif=0.01, sq.terms=NULL, in.terms=NULL,
  modelSize=NULL, Cox.Hazard = FALSE)
```

Arguments

- `X`: Design matrix.
- `Y`: Response vector.
- `list.reduction`: Indices of variables that where chosen at the reduction phase.
- `family`: A description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function. See `family` for more details.
- `signif`: Significance level of the likelihood ratio test against the comprehensive model. The default is 0.01.
- `sq.terms`: Indices of squared terms suggested at the exploratory phase (See `Exploratory.Phase`).
- `in.terms`: Indices of pairs of variables suggested at the exploratory phase (See `Exploratory.Phase`).
- `modelSize`: Maximum size of the models to be tested. Currently the maximum is 7. If not provided a default is used.
- `Cox.Hazard`: If TRUE fits proportional hazards regression model. The family argument will be ignored if Cox.Hazard=TRUE.

Value

- `goodModels`: List of models that are in the confidence set of size 1 to modelSize. An interaction term between, say, variables x_1 and x_2 is displayed as “x_1 * x_2”; a squared term in, say, variable x_1 is displayed as “x_1 ^2”. If an interaction term is present without the corresponding main effects, the main effects should be added.
Acknowledgement

The work was supported by the UK Engineering and Physical Sciences Research Council under grant number EP/P002757/1.

Author(s)

Hoeltgebaum, H. H.

References


See Also

Reduction.Phase, Exploratory.Phase

Examples

```r
## Generates a random DGP
dgp = DGP(s=5, a=3, sigStrength=1, rho=0.9, n=100, intercept=5, noise=1, var=1, d=1000, DGP.seed = 2018)

#Reduction Phase using only the first 70 observations
outcome.Reduction.Phase = Reduction.Phase(X=dgp$X[1:70,],Y=dgp$Y[1:70],
family=gaussian, seed.HC = 1012)

# Exploratory Phase using only the first 70 observations, choosing the variables which # were selected at least two times in the third dimension reduction
idxs = outcome.Reduction.Phase$List.Selection$`Hypercube with dim 2`$numSelected1
outcome.Exploratory.Phase = Exploratory.Phase(X=dgp$X[1:70,],Y=dgp$Y[1:70],
list.reduction = idxs,
family=gaussian, signif=0.01)

# Model Selection Phase using only the remainder observations
sq.terms = outcome.Exploratory.Phase$mat.select.SQ
in.terms = outcome.Exploratory.Phase$mat.select.INTER

MS = ModelSelection.Phase(X=dgp$X[71:100,],Y=dgp$Y[71:100], list.reduction = idxs,
sq.terms = sq.terms,in.terms = in.terms, signif=0.01)
```
Reduction.Phase


Description

This function traverses successively lower dimensional hypercubes, discarding variables according to the appropriate decision rules. It provides the number and indices of variables selected at each stage.

Usage

```r
Reduction.Phase(X, Y, family = gaussian, 
                  dmHC = NULL, vector.signif = NULL, seed.HC = NULL, Cox.Hazard = FALSE)
```

Arguments

- `X` Design matrix.
- `Y` Response vector.
- `family` A description of the error distribution and link function to be used in the model. For `glm` this can be a character string naming a family function, a family function or the result of a call to a family function. See `family` for more details.
- `dmHC` Dimension of the hypercube to be used in the first-stage reduction. This version supports dimensions 2, 3, 4 and 5. If not specified a sensible value is calculated and used.
- `vector.signif` Vector of decision rules to be used at each stage of the reduction. The first value makes reference to the decision rule for the highest dimensional hypercube and so on. If values are less than 1, this specifies a significance level of a test. All variables significant at this level in at least half the analyses in which they appear will be retained. If the value is 1 or 2, variables are retained if they are among the 1 or 2 most significant in at least half the analyses in which they appear. If unspecified a default rule is used.
- `seed.HC` Seed for randomization of the variable indices in the hypercube. If not provided, the variables are arranged according to their original order.
- `Cox.Hazard` If TRUE fits proportional hazards regression model. The family argument will be ignored if Cox.Hazard=TRUE.

Value

- `Matrix.Selection` The number of variables selected at each reduction of the hypercube.
- `List.Selection` The indices of the variables retained through each stage of the reduction phase.

Acknowledgement

The work was supported by the UK Engineering and Physical Sciences Research Council under grant number EP/P002757/1.
**Author(s)**

Hoeltgebaum, H. H.

**References**


**Examples**

```r
## Generates a random DGP
dgp = DGP(s=5, a=3, sigStrength=1, rho=0.9, n=100, intercept=5, noise=1, var=1, d=1000, DGP.seed = 2018)

#Reduction Phase using only the first 70 observations
outcome.Reduction.Phase = Reduction.Phase(X=dgp$X[1:70,], Y=dgp$Y[1:70],
                                           family=gaussian, seed.HC = 1012)

# Not run, using vector.signif argument
# Fixing a decision rule of getting the 2 most significant in the first reduction
# and in the subsequent reduction, only those variables significant at 0.001 level
# outcome.Reduction.Phase = Reduction.Phase(X=dgp$X[1:70,], Y=dgp$Y[1:70],
#                                           vector.signif = c(2,0.001), family=gaussian, dmHC = 3)
```
Index

*Topic datasets
  LymphomaData, 5

DGP, 2
Exploratory.Phase, 3, 6, 7
family, 4, 6, 8
LymphomaData, 5
ModelSelection.Phase, 6
patient.data(LymphomaData), 5
Reduction.Phase, 4, 7, 8