Package ‘SIS’

February 14, 2018

Version 0.8-6
Date 2018-02-13
Title Sure Independence Screening
Author Jianqing Fan, Yang Feng, Diego Franco Saldana, Richard Samworth, Yichao Wu
Maintainer Yang Feng <yang.feng@columbia.edu>
Depends R (>= 3.2.4)
Imports glmnet, ncvreg, survival
Description Variable selection techniques are essential tools for model selection and estimation in high-dimensional statistical models. Through this publicly available package, we provide a unified environment to carry out variable selection using iterative sure independence screening (SIS) and all of its variants in generalized linear models and the Cox proportional hazards model.
License GPL-2
RoxygenNote 6.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2018-02-13 23:52:33 UTC

R topics documented:

leukemia.test ......................................................... 2
leukemia.train ....................................................... 2
predict.SIS ............................................................ 3
prostate.test .......................................................... 5
prostate.train ......................................................... 6
SIS .......................................................... 6
standardize .......................................................... 10
tune.fit ......................................................... 11

Index 14
leukemia.test

*Gene expression Leukemia testing data set from Golub et al. (1999)*

**Description**

Gene expression testing data of 7129 genes from 34 patients with acute leukemias (20 in class Acute Lymphoblastic Leukemia and 14 in class Acute Myeloid Leukemia) from the microarray study of Golub et al. (1999).

**Usage**

data(leukemia.test)

**Format**

A data frame with 34 observations on 7129 variables.

**Source**

http://wwwprod.broadinstitute.org/cgi-bin/cancer/datasets.cgi

**References**


---

leukemia.train

*Gene expression Leukemia training data set from Golub et al. (1999)*

**Description**

Gene expression training data of 7129 genes from 38 patients with acute leukemias (27 in class Acute Lymphoblastic Leukemia and 11 in class Acute Myeloid Leukemia) from the microarray study of Golub et al. (1999).

**Usage**

data(leukemia.train)

**Format**

A data frame with 38 observations on 7129 variables.

**Source**

http://wwwprod.broadinstitute.org/cgi-bin/cancer/datasets.cgi
predict.SIS

References


predict.SIS  
*Model prediction based on a fitted SIS object.*

Description

Similar to the usual predict methods, this function returns predictions from a fitted 'SIS' object.

Usage

```r
## S3 method for class 'SIS'
predict(object, newx, lambda = object$lambda, which = NULL, type = c("response", "link", "class"), ...)
```

Arguments

- **object**  
  Fitted 'SIS' model object.
- **newx**  
  Matrix of new values for x at which predictions are to be made, without the intercept term.
- **lambda**  
  Penalty parameter lambda of the final fitted model by (I)SIS at which predictions are required. By default, only the lambda minimizing the criterion `tune` is returned.
- **which**  
  Indices of the penalty parameter lambda of the final fitted model by (I)SIS at which predictions are required. If supplied, will overwrite the default lambda value.
- **type**  
  Type of prediction required. Type 'response' gives the fitted values for 'gaussian', fitted probabilities for 'binomial', fitted mean for 'poisson', and the fitted relative risk for 'cox'. Type 'link' returns the linear predictors for 'binomial', 'poisson' and 'cox' models; for 'gaussian' models it is equivalent to type 'response'. Type 'class' applies only to 'binomial' models, and produces the class label corresponding to the maximum probability (0-1 labels).
- **...**  
  Not used. Other arguments to predict.

Value

The object returned depends on type.

Author(s)

Jianqing Fan, Yang Feng, Diego Franco Saldana, Richard Samworth, and Yichao Wu
References


See Also

SIS

Examples

```r
set.seed(0)
n = 400; p = 50; rho = 0.5
corrmat = diag(rep(1-rho, p)) + matrix(rho, p, p)
corrmat[,4] = sqrt(rho)
corrmat[4,] = sqrt(rho)
corrmat[4,4] = 1
corrmat[,5] = 0
corrmat[5,] = 0
corrmat[5,5] = 1
cholmat = chol(corrmat)
x = matrix(rnorm(n*p, mean=0, sd=1), n, p)
x = x %*% cholmat
testX = matrix(rnorm(10*p, mean=0, sd=1), nrow=10, ncol=p)

# gaussian response
set.seed(1)
b = c(4,4,4,-6*sqrt(2),4/3)
y=x[, 1:5]%*%b + rnorm(n)
model1=SIS(x, y, family='gaussian', tune='bic', varISIS='aggr', seed=11)
predict(model1, testX, type='response')
predict(model1, testX, which=1:10, type='response')
```

## Not run:
prostate.test

# binary response
set.seed(2)
feta = x[, 1:5]*x*b; fprob = exp(feta)/(1+exp(feta))
y = rbinom(n, 1, fprob)
model2=SIS(x, y, family='binomial', tune='bic', varISIS='aggr', seed=21)
predict(model2, testX, type='response')
predict(model2, testX, type='link')
predict(model2, testX, type='class')
predict(model2, testX, which=1:10, type='response')
predict(model2, testX, which=1:10, type='link')
predict(model2, testX, which=1:10, type='class')

# poisson response
set.seed(3)
b = c(0.6, 0.6, 0.6, -0.9*sqrt(2))
myrates = exp(x[, 1:4]*x*b)
y = rpois(n, myrates)
model3=SIS(x, y, family='poisson', penalty = 'lasso', tune='bic', varISIS='aggr', seed=31)
predict(model3, testX, type='response')
predict(model3, testX, type='link')

## End(Not run)

---

**prostate.test**

**Gene expression Prostate Cancer testing data set from Singh et al. (2002)**

Description

Gene expression testing data of 12600 genes from 25 patients with prostate tumors and 9 normal specimens from the microarray study of Singh et al. (2002).

Usage

data(prostate.test)

Format

A data frame with 34 observations on 12600 variables.

Source

http://wwwprod.broadinstitute.org/cgi-bin/cancer/datasets.cgi
**References**


---

**prostate.train**

*Gene expression Prostate Cancer training data set from Singh et al. (2002)*

---

**Description**

Gene expression training data of 12600 genes from 52 patients with prostate tumors and 50 normal specimens from the microarray study of Singh et al. (2002).

**Usage**

```r
data(prostate.train)
```

**Format**

A data frame with 102 observations on 12600 variables.

**Source**

http://wwwprod.broadinstitute.org/cgi-bin/cancer/datasets.cgi

**References**


---

**SIS**

*(Iterative) Sure Independence Screening ((I)SIS) and Fitting in Generalized Linear Models and Cox’s Proportional Hazards Models*

---

**Description**

This function first implements the Iterative Sure Independence Screening for different variants of (I)SIS, and then fits the final regression model using the R packages `ncvreg` and `glmnet` for the SCAD/MCP/LASSO regularized loglikelihood for the variables picked by (I)SIS.
Usage

SIS(x, y, family = c("gaussian", "binomial", "poisson", "cox"),
penalty = c("SCAD", "MCP", "lasso"), concavity.parameter = switch(penalty,
SCAD = 3.7, 3), tune = c("bic", "ebic", "aic", "cv"), nfolds = 10,
type.measure = c("deviance", "class", "auc", "mse", "mae"),
gamma.ebic = 1, nsis = NULL, iter = TRUE, iter.max = ifelse(greedy ==
FALSE, 10, floor(nrow(x)/log(nrow(x)))), var1sis = c("vanilla", "aggr",
"cons"), perm = FALSE, q = 1, greedy = FALSE, greedy.size = 1,
seed = 0, standardize = TRUE)

Arguments

x The design matrix, of dimensions n * p, without an intercept. Each row is an observation vector. SIS standardizes the data and includes an intercept by default.

y The response vector of dimension n * 1. Quantitative for family='gaussian', non-negative counts for family='poisson', binary (0-1) for family='binomial'. For family='cox', y should be an object of class Surv, as provided by the function Surv() in the package survival.

family Response type (see above).

penalty The penalty to be applied in the regularized likelihood subproblems. 'SCAD' (the default), 'MCP', or 'lasso' are provided.

concavity.parameter The tuning parameter used to adjust the concavity of the SCAD/MCP penalty. Default is 3.7 for SCAD and 3 for MCP.

tune Method for tuning the regularization parameter of the penalized likelihood subproblems and of the final model selected by (I)SIS. Options include tune='bic', tune='ebic', tune='aic', and tune='cv'.

nfolds Number of folds used in cross-validation. The default is 10.

type.measure Loss to use for cross-validation. Currently five options, not all available for all models. The default is type.measure='deviance', which uses squared-error for gaussian models (also equivalent to type.measure='mse' in this case), deviance for logistic and poisson regression, and partial-likelihood for the Cox model. Both type.measure='class' and type.measure='auc' apply only to logistic regression and give misclassification error and area under the ROC curve, respectively. type.measure='mse' or type.measure='mae' (mean absolute error) can be used by all models except the 'cox'; they measure the deviation from the fitted mean to the response. For penalty='SCAD' and penalty='MCP', only type.measure='deviance' is available.

gamma.ebic Specifies the parameter in the Extended BIC criterion penalizing the size of the corresponding model space. The default is gamma.ebic=1. See references at the end for details.

nsis Number of predictors recruited by (I)SIS.

iter Specifies whether to perform iterative SIS. The default is iter=TRUE.

iter.max Maximum number of iterations for (I)SIS and its variants.
varISIS Specifies whether to perform any of the two ISIS variants based on randomly splitting the sample into two groups. The variant varISIS='aggr' is an aggressive variable screening procedure, while varISIS='cons' is a more conservative approach. The default is varISIS='vanilla', which performs the traditional vanilla version of ISIS. See references at the end for details.

perm Specifies whether to impose a data-driven threshold in the size of the active sets calculated during the ISIS procedures. The threshold is calculated by first decoupling the predictors $x_i$ and response $y_i$ through a random permutation $\pi$ of $(1,...,n)$ to form a null model. For this newly permuted data, marginal regression coefficients for each predictor are recalculated. As the marginal regression coefficients of the original data should be larger than most recalculated coefficients in the null model, the data-driven threshold is given by the $q$th quantile of the null coefficients. This data-driven threshold only allows a $1-q$ proportion of inactive variables to enter the model when $x_i$ and $y_i$ are not related (in the null model). The default is here is perm=FALSE. See references at the end for details.

q Quantile for calculating the data-driven threshold in the permutation-based ISIS. The default is $q=1$ (i.e., the maximum absolute value of the permuted estimates).

greedy Specifies whether to run the greedy modification of the permutation-based ISIS. The default is greedy=FALSE.

greedy.size Maximum size of the active sets in the greedy modification of the permutation-based ISIS. The default is greedy.size=1.

seed Random seed used for sample splitting, random permutation, and cross-validation sampling of training and test sets.

standardize Logical flag for x variable standardization, prior to performing (iterative) variable screening. The resulting coefficients are always returned on the original scale. Default is standardize=TRUE. If variables are in the same units already, you might not wish to standardize.

Value

Returns an object with

- **ix** The vector of indices selected by (I)ISIS.
- **coef.est** The vector of coefficients of the final model selected by (I)ISIS.
- **fit** A fitted object of type ncvreg, cv.ncvreg, glmnet, or cv.glmnet for the final model selected by the (I)ISIS procedure. If tune='cv', the returned fitted object is of type cv.ncvreg if penalty='SCAD' or penalty='MCP'; otherwise, the returned fitted object is of type cv.glmnet. For the remaining options of tune, the returned object is of type glmnet if penalty='lasso', and ncvreg otherwise.
- **path.index** The index along the solution path of fit for which the criterion specified in tune is minimized.

Author(s)

Jianqing Fan, Yang Feng, Diego Franco Saldana, Richard Samworth, and Yichao Wu
References

See Also
predict.SIS

Examples

dat <- data.frame(x = rnorm(n*p, mean=0, sd=1), y)
dat$x <- x[cholmat]
dat$y <- dat$y[cholmat]
dat$y[cholmat] = rnorm(n-p, mean=0, sd=1)
set.seed(1)
b = c(4,4,4,-6*sqrt(2),4/3)
y=x[1:5]%*%b + rnorm(n)
model11=SIS(x, y, family='gaussian', tune='bic')
model12=SIS(x, y, family='gaussian', tune='bic', varISIS='aggr', seed=1)
model11$data
model12$data

# binary response
set.seed(1)
model11b=SIS(x, y, family='gaussian', tune='bic')
model12b=SIS(x, y, family='gaussian', tune='bic', varISIS='aggr', seed=1)
model11b$data
model12b$data
set.seed(2)
fe = x[, 1:5] %*% b; fprob = exp(feta)/(1+exp(feta))
y = rbinom(n, 1, fprob)
model1 = SIS(x, y, family = 'binomial', tune = 'bic')
model2 = SIS(x, y, family = 'binomial', tune = 'bic', varISIS = 'aggr', seed = 21)
model1$ix
model2$ix

# poisson response
set.seed(3)
b = c(0.6, 0.6, 0.6, -0.9 * sqrt(2))
myrates = exp(x[, 1:4] %*% b)
y = rpois(n, myrates)
model1 = SIS(x, y, family = 'poisson', penalty = 'lasso', tune = 'bic', perm = TRUE, q = 0.9,
            greedy = TRUE, seed = 31)
model2 = SIS(x, y, family = 'poisson', penalty = 'lasso', tune = 'bic', varISIS = 'aggr',
            perm = TRUE, q = 0.9, seed = 32)
model1$ix
model2$ix

# Cox model
set.seed(4)
b = c(4.4, 4.4, -6 * sqrt(2), 4/3)
myrates = exp(x[, 1:5] %*% b)
Sur = rexp(n, myrates); CT = rexp(n, 0.1)
Z = pmin(Sur, CT); ind = as.numeric(Sur <= CT)
y = survival::Surv(Z, ind)
model1 = SIS(x, y, family = 'cox', penalty = 'lasso', tune = 'bic',
            varISIS = 'aggr', seed = 41)
model2 = SIS(x, y, family = 'cox', penalty = 'lasso', tune = 'bic',
            varISIS = 'cons', seed = 41)
model1$ix
model2$ix

## End(Not run)

---

**standardize**

**Standardization of High-Dimensional Design Matrices**

**Description**

Standardizes the columns of a high-dimensional design matrix to mean zero and unit Euclidean norm.

**Usage**

standardize(X)
Arguments

\( X \)  
A design matrix to be standardized.

Details

Performs a location and scale transform to the columns of the original design matrix, so that the resulting design matrix with \( p \)-dimensional observations \( \{x_i : i = 1, ..., n\} \) of the form \( x_i = (x_{i1}, x_{i2}, ..., x_{ip}) \) satisfies \( \sum_{i=1}^{n} x_{ij} = 0 \) and \( \sum_{i=1}^{n} x_{ij}^2 = 1 \) for \( j = 1, ..., p \).

Value

A design matrix with standardized predictors or columns.

Author(s)

Jianqing Fan, Yang Feng, Diego Franco Saldana, Richard Samworth, and Yichao Wu

References


Examples

```r
set.seed(0)
n = 400; p = 50; rho = 0.5
corrmat = diag(rep(1-rho, p)) + matrix(rho, p, p)
corrmat[,4] = sqrt(rho)
corrmat[4, ] = sqrt(rho)
corrmat[4,4] = 1
corrmat[,5] = 0
corrmat[5, ] = 0
corrmat[5,5] = 1
cholmat = chol(corrmat)
x = matrix(rnorm(n*p, mean=15, sd=9), n, p)
x = x%*%cholmat

x.standard = standardize(x)
```

Using the `glmnet` and `ncvreg` packages, fits a Generalized Linear Model or Cox Proportional Hazards Model using various methods for choosing the regularization parameter \( \lambda \).
Description

This function fits a generalized linear model or a Cox proportional hazards model via penalized maximum likelihood, with available penalties as indicated in the `glmnet` and `ncvreg` packages. Instead of providing the whole regularization solution path, the function returns the solution at a unique value of $\lambda$, the one optimizing the criterion specified in `tune`.

Usage

tune.fit(x, y, family = c("gaussian", "binomial", "poisson", "cox"),
penalty = c("SCAD", "MCP", "lasso"), concavity.parameter = switch(penalty,
  SCAD = 3.7, 3), tune = c("cv", "aic", "bic", "ebic"), nfolds = 10,
type.measure = c("deviance", "class", "auc", "mse", "mae"),
gamma.ebic = 1)

Arguments

x The design matrix, of dimensions n * p, without an intercept. Each row is an observation vector.
y The response vector of dimension n * 1. Quantitative for family='gaussian', non-negative counts for family='poisson', binary (0-1) for family='binomial'. For family='cox', y should be an object of class Surv, as provided by the function Surv() in the package survival.
family Response type (see above).
penalty The penalty to be applied in the regularized likelihood subproblems. 'SCAD' (the default), 'MCP', or 'lasso' are provided.
concavity.parameter The tuning parameter used to adjust the concavity of the SCAD/MCP penalty. Default is 3.7 for SCAD and 3 for MCP.
tune Method for selecting the regularization parameter along the solution path of the penalized likelihood problem. Options to provide a final model include tune='cv', tune='aic', tune='bic', and tune='ebic'. See references at the end for details.
nfolds Number of folds used in cross-validation. The default is 10.
type.measure Loss to use for cross-validation. Currently five options, not all available for all models. The default is type.measure='deviance', which uses squared-error for gaussian models (also equivalent to type.measure='mse' in this case), deviance for logistic and poisson regression, and partial-likelihood for the Cox model. Both type.measure='class' and type.measure='auc' apply only to logistic regression and give misclassification error and area under the ROC curve, respectively. type.measure='mse' or type.measure='mae' (mean absolute error) can be used by all models except the 'cox'; they measure the deviation from the fitted mean to the response. For penalty='SCAD' and penalty='MCP', only type.measure='deviance' is available.
gamma.ebic Specifies the parameter in the Extended BIC criterion penalizing the size of the corresponding model space. The default is gamma.ebic=1. See references at the end for details.
Value

Returns an object with

- `ix` The vector of indices of the nonzero coefficients selected by the maximum penalized likelihood procedure with `tune` as the method for choosing the regularization parameter.
- `a0` The intercept of the final model selected by `tune`.
- `beta` The vector of coefficients of the final model selected by `tune`.
- `fit` The fitted penalized regression object.
- `lambda` The corresponding lambda in the final model.
- `lambda.ind` The index on the solution path for the final model.

Author(s)

Jianqing Fan, Yang Feng, Diego Franco Saldana, Richard Samworth, and Yichao Wu

References


Examples

```r
set.seed(0)
data('leukemia.train', package = 'SIS')
y.train = leukemia.train[,dim(leukemia.train)[2]]
x.train = as.matrix(leukemia.train[,-dim(leukemia.train)[2]])
x.train = standardize(x.train)
model = tune.fit(x.train[,1:3500], y.train, family='binomial', tune='bic')
model$ix
model$a0
model$beta
```
Index

*Topic datasets
  leukemia.test, 2
  leukemia.train, 2
  prostate.test, 5
  prostate.train, 6

*Topic models
  predict.SIS, 3
  SIS, 6
  standardize, 10
  tune.fit, 11

leukemia.test, 2
leukemia.train, 2

predict.SIS, 3, 9
prostate.test, 5
prostate.train, 6

SIS, 4, 6
standardize, 10

tune.fit, 11