Package ‘SubLasso’
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Type Package

Title Lasso-based feature selection for a gene expression profile/matrix, with a user-defined pre-selected feature subset.

Version 1.2

Depends R(>= 2.10), glmnet, psych, gplots

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Description Given a gene expression profile/matrix, this R package SubLasso develops a feature selection and classification algorithm by adding more features into a user-defined seed feature subset. This is per the frequent requests from biomedical researchers whether some well-known disease-biomarkers may work together with some additional features, to form an accurate classifier for a given disease. For example, whether there is a good classifier for breast cancer, by using the patterns of two biomarkers, i.e. BRCA1 and BRCA2, and a few others. The mathematical model is to fix some user-defined features in the finally chosen feature subset, with the optimized classification accuracy.

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URL http://healthinformaticslab.org/ffzhou/

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SubLasso package

Description
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Details

Package: SubLasso
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License: GPL-2

This package implemented a feature selection procedure with the optimized classification accuracy, and the chosen feature subset consists of the user-defined seed features. For the convenience of the users, the k-fold cross validation performance will also be calculated. The other user-friendly assets of this package include the minimum requirement for the parameter tuning, by automatic optimization.

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Colon example dataset
Gene expression data from Alon et al. (1999)

Description
Expression data of 2000 genes for 62 samples, which was generated from the microarray experiments of Colon tissue samples of Alon et al. (1999).

Usage
data(Colon)

Details
This data set contains 62 samples with 2000 genes: 40 tumor tissues, coded 1 and 22 normal tissues, coded 0.
Value

A list with the following elements:

X a (2000 x 62) matrix giving the expression levels of 2000 genes for the 62 Colon tissue samples. Each row corresponds to a gene, and each column to a patient/sample.

y a numeric vector of length 62 giving the type of tissue sample (tumor or normal).

Source

The data are described in Alon et al.(1999) and can be freely downloaded from http://microarray.princeton.edu/oncology/affydata/index.html.

References


Examples

library(SubLasso)

# load data set
data(Colon)

dim(Colon$X)

sum(Colon$y==0)
sum(Colon$y==1)

Golub_Merge example dataset

Combined Training and Test Sets from the Golub Paper

Description

The data are from Golub et al. These are the combined training samples and test samples. There are 47 patients with acute lymphoblastic leukemia (ALL) and 25 patients with acute myeloid leukemia (AML).

Usage

data(Golub_Merge)
Value

X  matrix giving the expression levels.
y  giving the type of tissue sample.

References


Examples

# load SubLasso library
library(SubLasso)

# load data set
data(Golub_Merge)

predict.SubLasso  

Predict method for SubLasso fits.

Description

Similar to other predict methods, this function predicts fitted values, logit, coefficients and more from a fitted "SubLasso" object.

Usage

## S3 method for class 'SubLasso'
predict(object, xpred, type, s, ...)

Arguments

object  Fitted "SubLasso" model object.
xpred  Matrix of new values for x at which predictions are to be made. Must have the same number of rows with x
type  type=c("link","response","class"). Default is "class"; Type of prediction required. Type "link" gives the linear predictors; Type "response" gives the fitted probabilities; Type "class" produces the class label corresponding to the maximum probability.
s  Value(s) of the penalty parameter lambda at which predictions are required. Default is obtained by CV method.
...  not used currently.
**Description**

This package implemented a feature selection procedure with the optimized classification accuracy, and the chosen feature subset consists of the user-defined seed features. For the convenience of the users, the k-fold cross validation performance will also be calculated. The other user-friendly assets of this package include the minimum requirement for the parameter tuning, by automatic optimization.

**Usage**

SubLasso(X, y, subset, nfold)

**Arguments**

- **X**
  The gene expression matrix, row is sample, column is for the expression levels of genes (probe sets).

- **y**
  The category vector, 1 (positive, illness) or 0 (negative, normal).

- **subset**
  The vector of gene names (probe sets) must belong to the genes in the model. Default is null set, meaning no pre-fixed genes.

- **nfold**
  The number of cross-validation. Default is 5.

**Value**

- **selname**
  The vector of features selected by the model.

- **valid**
  The performance measurements sensitivity (Sn), specificity (Sp), Accuracy (Acc), and Matthews correlation coefficient (Mcc).

- **description**
  A descriptive summarization of selected features.

- **correlation**
  The correlations among the selected features.

- **w**
  The coefficient (weight) of each feature in the model.

- **lambda**
  The actual penalty parameter values used or optimized.

- **cv.predp**
  The predict probability in cross-validation.

- **cv.pedy**
  The predict class label in cross-validation.

- **fit**
  The fitted model when doing feature selection.

- **show.boxplot**
  A boxplot produced by the linear prediction function of logistic model. X-axis is the sample group and Y-axis is the prediction function score of each subject. The up and down real line of box is the 0.75 and 0.25 quantile respectively. The bold real line in the middle of box is the median.
show.heatmap  The hierarchical clustering of samples based on expression patterns of the selected features. Each row corresponds to a feature and each column corresponds to a sample. The status of illness or normal for each subject is shown with the above bar. Gene expression value is indicated by different color in the medial matrix.

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References

See Also
glmnet

Examples

```r
### Example 1
library(SubLasso)
data(Golub_Merge)
X <- Golub_Merge$X
y <- Golub_Merge$y
f1=SubLasso(X,y,nfold=1/zero.noslash)
## The linear discriminating function
cat(f1$intercept, " + ", paste(f1$w,f1$selname,collapse=" + ",sep="*"))

## predict.SubLasso(f1,X[1:1/zero.noslash,]) ##error predicted x
predy=predict.SubLasso(f1,X)
predy=predict.SubLasso(f1,X,type="class")
predy=predict.SubLasso(f1,X,type="link")
predy=predict.SubLasso(f1,X,type="response",s=0.05)
subset=f1$selname
f2=SubLasso(X,y,subset,nfold=10)
cat(f2$intercept, " + ", paste(f2$w,f2$selname,collapse=" + ",sep="x"))
f2$show.boxplot()
f2$show.heatmap()

subset=row.names(X)[1:10]
f3=SubLasso(X,y,subset,nfold=10)
predy=predict.SubLasso(f3,X)
predy=predict.SubLasso(f3,X,type="class")
```
predy=predict.SubLasso(f3,X,type="link")
predy=predict.SubLasso(f3,X,type="response")
predy=predict.SubLasso(f3,X,type="response",s=0.05)
cat(f3$intercept, " + ", paste(f3$w,f3$selname,collapse=" + ",sep="*"))
f3$show.heatmap()

###Example 2
library(SubLasso)
data(Colon)
X<-Colon$X
y<-ifelse(Colon$y == 1,1,)
subset=f1$selname
## The linear discriminating function
cat(f1$intercept, " + ", paste(f1$w,f1$selname,collapse=" + ",sep="*"))

f2=SubLasso(X,y,subset,nfold=10)
subset=row.names(X)[30:40]
cat(f2$intercept, " + ", paste(f2$w,f1$selname,collapse=" + ",sep="*"))

f3=SubLasso(X,y,subset,nfold=10)
cat(f3$intercept, " + ", paste(f3$w,f1$selname,collapse=" + ",sep="*"))
f3$show.boxplot()
f3$show.heatmap()
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