Package 'metaSVM'

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Type Package

Title Meta-analytic Framework Based on Support Vector Machine

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Description This package contains functions for metaSVM.

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LazyData TRUE

Imports foreach, MCMCpack, glmnet, penalized, e1071

URL https://sites.google.com/site/sunghwanshome/

NeedsCompilation no

R topics documented:

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iSVM   *Integrated Support Vector Machine*

Description

This function develops an estimation and variable selection algorithm for meta-analytic framework based on the meta-analytic support vector machine (Meta-SVM).

Usage

```
iSVM(sm, is.constant=TRUE)
```

Arguments

sm	A list generated from SETUP
is.constant	if TRUE, an intercept is included in the model.

Format

Dlist_lung_svm.Rdata consists of three microarray profiles of the idiopathic pulmonary fibrosis (IPF) gathered from KangA (Kang et al., 2012), Konishi (Konishi et al., 2009), and Pardo (Pardo et al., 2005), each containing 63, 38, and 24 samples, respectively. For pre-processing, we performed unbiased filtering via standard deviation such that it remains 39 features.

Details

The proposed Meta-SVM is motivated by the recent meta-analytic method exploiting the logistic regression. We develop a novel implementation strategy in spirit of Newton's method in the Meta-SVM. For the most part, the objective function of SVM is formed with the hinge loss and a range of penalty terms (e.g., L1-lasso, group lasso and etcs). We particularly adopts the sparse group lasso enabling to capture both common and study specific genetic signals among all studies.

Value

A list contains information on the final model

Author(s)

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Source

The time required to fit the metaSVM model was measured on R version 3.3.1 (2016-06-21) running on macOS Sierra, in a laptop with an Intel Core i7 CPU (2.60 GHz) and 16.0 GB RAM.

References

Kang, D., Sibille, E., Kaminski, N., Tseng, G. MetaQC: objective quality control and inclusion/exclusion criteria for genomic meta-analysis. Nucleic Acids Res., 40, e15, 2012.

Konishi K., Gibson K., Lindell K., Richards T., Zhang Y., et al. Gene expression profiles of acute exacerbations of idiopathic pulmonary fibrosis Am J Respir Crit Care Med, 180(2):167–75, 2009.

Pardo A., Selman M. Role of matrix metaloproteases in idiopathic pulmonary fibrosis Fibrogenesis Tissue Repair, 5(Suppl 1):S9, 2012.

See Also

SETUP

Examples

```
library(metaSVM)
fpath = system.file("extdata", "DList_lung_svm.Rdata", package = "metaSVM")
DList = get(load(fpath))

#==============#
# The following stage proceeds to rename the binary outcome variable (1:IPF/0:control)
# and gene features.
#==============#
Y = list()
for (k in 1:length(DList))
{
   tmp = as.numeric(rownames(DList[[k]]) == "1")
```

```
    tmp[tmp == 0] = -1
    Y[[k]] = tmp
}
for(i in 1:length(DList))
    rownames(DList[[i]]) = 1:dim(DList[[i]])[1]

#==============#
# As a part of preprocessing, SETUP undertakes tasks to collect all required data
# and to put them into the list form.
#==============#
sm = SETUP(X = DList, Y = Y, lambda1 = 0.1, lambda2 = 0.1)
# Fit the meta-SVM model using the example data set
# The following process takes about 25 minutes on average.
# Res = iSVM(sm, is.constant = TRUE)
```

SETUP   *Setup a basic list*

Description

This function generates a list containing all relevant objects to perform the meta-SVM.

Usage

```
SETUP(X, Y, lambda1, lambda2)
```

Arguments

X	The predictor variable
Y	The response variable
lambda1	A tuning parameter controls the first penalty term (group lasso)
lambda2	A tuning parameter controls the second penalty term (L1-lasso)

Value

sm	A list contains all related objects to implement the Meta-SVM.

Author(s)

SungHwan Kim, Jae-Hwan Jhong, JungJun Lee, Ja-Yong Koo

See Also

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