

MiPP

April 19, 2009

colon

Gene expression data for colon cancer

Description

This data set consists of gene expression of colon cancer study.

Usage

```
data(colon)
```

Format

A matrix containing 2000 probe sets and 2 classes (T, F)

Source

Alon, U., Barkai, N., Notterman, D.A., Gish, K., Ybarra, S., Mack, D., Levine, A.J. (1999). Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues probed by Oligonucleotide Arrays, PNAS, 96(12), 6745–6750.

cv.mipp.rule

Fitting cross-validation MiPP

Description

Fits cross-validation MiPP

get.mipp

Choosing a rule

Description

Choose a rule to compute MiPP

get.mipp.lda *Fitting LDA to compute MiPP*

Description

Fits LDA to compute MiPP

get.mipp.logistic *Fitting logistic model to compute MiPP*

Description

Fits logistic model to compute MiPP

get.mipp.qda *Fitting QDA to compute MiPP*

Description

Fits QDA to compute MiPP

get.mipp.svm.linear
 Fitting SVM (linear) to compute MiPP

Description

Fits SVM (linear) to compute MiPP

get.mipp.svm.rbf *Fitting SVM (RBF) to compute MiPP*

Description

Fits SVM (RBF) to compute MiPP

leuk1

Gene expression data for leukemia

Description

This data set consists of gene expression of leukemia study.

Usage

```
data(leukemia)
```

Format

A matrix containing 6817 probe sets and 38 samples (2 classes: AML, ALL)

Source

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

leuk2

Gene expression data for leukemia

Description

This data set consists of gene expression of leukemia study.

Usage

```
data(leukemia)
```

Format

A matrix containing 6817 probe sets and 34 samples (2 classes: AML, ALL)

Source

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

leukemia

Gene expression data for leukemia

Description

This data set consists of gene expression of leukemia study.

Usage

```
data(leukemia)
```

Format

A matrix containing 6817 probe sets and 2 classes (AML, ALL)

Source

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

linearkernel.decision.function

SVM (linear) kernel to compute MiPP

Description

SVM (linear) kernel to compute MiPP

mipp

MiPP-based Classification

Description

Finds optimal sets of genes for classification

Usage

```
mipp(x, y, x.test = NULL, y.test = NULL, probe.ID = NULL,
     rule = "lda", method.cut = "t.test", percent.cut = 0.01,
     model.sMiPP.margin = 0.01, min.sMiPP = 0.85, n.drops = 2,
     n.fold = 5, p.test = 1/3, n.split = 20,
     n.split.eval = 100)
```

Arguments

<code>x</code>	data matrix
<code>y</code>	class vector
<code>x.test</code>	test data matrix if available
<code>y.test</code>	test class vector if available
<code>probe.ID</code>	probe set IDs; if NULL, row numbers are assigned.
<code>rule</code>	classification rule: "lda","qda","logistic","svmlin","svmrbf"; the default is "lda".
<code>method.cut</code>	method for pre-selection; t-test is available.
<code>percent.cut</code>	proportion of pre-selected genes; the default is 0.01.
<code>model.sMiPP.margin</code>	smallest set of genes s.t. $sMiPP \leq (\max sMiPP - \text{model.sMiPP.margin})$; the default is 0.01.
<code>min.sMiPP</code>	Adding genes stops if max sMiPP is at least min.sMiPP; the default is 0.85.
<code>n.drops</code>	Adding genes stops if sMiPP decreases (n.drops) times, in addition to min.sMiPP criterion.; the default is 2.
<code>n.fold</code>	number of folds; default is 5.
<code>p.test</code>	partition percent of train and test samples when test samples are not available; the default is 1/3 for test set.
<code>n.split</code>	number of splits; the default is 20.
<code>n.split.eval</code>	numbr of splits for evaluation; the default is 100.

Value

<code>model</code>	candidate genes (for each split if no indep set is available)
<code>model.eval</code>	Optimal sets of genes for each split when no indep set is available

Author(s)

Soukup M, Cho H, and Lee JK

References

Soukup M, Cho H, and Lee JK (2005). Robust classification modeling on microarray data using misclassification penalized posterior, *Bioinformatics*, 21 (Suppl): i423-i430.

Soukup M and Lee JK (2004). Developing optimal prediction models for cancer classification using gene expression data, *Journal of Bioinformatics and Computational Biology*, 1(4) 681-694

Examples

```
#####
#Example 1: When an independent test set is available

data(leukemia)

#Normalize combined data
leukemia <- cbind(leuk1, leuk2)
leukemia <- mipp.preproc(leukemia, data.type="MAS4")
```

```

#Train set
x.train <- leukemia[,1:38]
y.train <- factor(c(rep("ALL",27),rep("AML",11)))

#Test set
x.test <- leukemia[,39:72]
y.test <- factor(c(rep("ALL",20),rep("AML",14)))

#Compute MiPP
out <- mipp(x=x.train, y=y.train, x.test=x.test, y.test=y.test, probe.ID = 1:nrow(x.train))

#Print candidate models
out$model

#####
#Example 2: When an independent test set is not available

data(colon)

#Normalize data
x <- mipp.preproc(colon)
y <- factor(c("T", "N", "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
             "T", "N", "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
             "T", "T", "T", "T", "T", "T", "T", "T", "N", "T",
             "T", "N", "N", "T", "T", "T", "T", "N", "T", "N",
             "N", "T", "T", "N", "N", "T", "T", "T", "T", "N",
             "T", "N"))

#Deleting contaminated chips
x <- x[,-c(51,55,45,49,56)]
y <- y[ -c(51,55,45,49,56)]

#Compute MiPP
out <- mipp(x=x, y=y, probe.ID = 1:nrow(x), n.fold=5, p.test=1/3, n.split=5, n.split.eval=
percent.cut= 0.1, rule="lda")

#Print candidate models for each split
out$model

#Print optimal models and independent evaluation for each split
out$model.eval

```

mipp.preproc

Preprocessing

Description

Performs IQR normalization, thesholding, and log2-transformation

Usage

```
mipp.preproc(x, data.type = "MAS5")
```

Arguments

x data
 data.type data type is MAS5, MAS4, or dChip

See Also

[mipp](#)

Examples

```
library(MiPP)

data(colon)
colon.nor <- mipp.preproc(colon)
```

mipp.rule *Computing MiPP*

Description

Computes MiPP

mipp.seq *MiPP-based Classification*

Description

sequentially finds optimal sets of genes for classification

Usage

```
mipp.seq(x, y, x.test = NULL, y.test = NULL, probe.ID = NULL,
         rule = "lda", method.cut = "t.test", percent.cut = 0.01,
         model.sMiPP.margin = 0.01, min.sMiPP = 0.85, n.drops = 2,
         n.fold = 5, p.test = 1/3, n.split = 20, n.split.eval = 100,
         n.seq=3, cutoff.sMiPP=0.7, remove.gene.each.model="all")
```

Arguments

x data matrix
 y class vector
 x.test test data matrix if available
 y.test test class vector if available
 probe.ID probe set IDs; if NULL, row numbers are assigned.
 rule classification rule: "lda","qda","logistic","svmlin","svmrbf"; the default is "lda".
 method.cut method for pre-selection; t-test is available.

percent.cut proportion of pre-selected genes; the default is 0.01.

model.sMiPP.margin smallest set of genes s.t. sMiPP \leq (max sMiPP-model.sMiPP.margin); the default is 0.01.

min.sMiPP Adding genes stops if max sMiPP is at least min.sMiPP; the default is 0.85.

n.drops Adding genes stops if sMiPP decreases (n.drops) times, in addition to min.sMiPP criterion.; the default is 2.

n.fold number of folds; default is 5.

p.test partition percent of train and test samples when test samples are not available; the default is 1/3 for test set.

n.split number of splits; the default is 20.

n.split.eval numbr of splits for evaluation; the default is 100.

n.seq Number of sequential gene model selection; the default is 3.

cutoff.sMiPP Cutoff point of 5 percent sMiPP to select gene models

remove.gene.each.model Re-run after removing all genes in the selected models if "all" and the first gene for each of the selected models if "first"

Value

model candiadate genes (for each split if no indep set is available)

model.eval Optimal sets of genes for each split when no indep set is available

genes.selected a list of genes selected by sequential selection

Author(s)

Soukup M, Cho H, and Lee JK

References

Soukup M, Cho H, and Lee JK (2005). Robust classification modeling on microarray data using misclassification penalized posterior, *Bioinformatics*, 21 (Suppl): i423-i430.

Soukup M and Lee JK (2004). Developing optimal prediction models for cancer classification using gene expression data, *Journal of Bioinformatics and Computational Biology*, 1(4) 681-694

Examples

```
#####
#Example 1: When an independent test set is available

data(leukemia)

#Normalize combined data
leukemia <- cbind(leuk1, leuk2)
leukemia <- mipp.preproc(leukemia, data.type="MAS4")

#Train set
x.train <- leukemia[,1:38]
y.train <- factor(c(rep("ALL", 27), rep("AML", 11)))
```



```

#Test set
x.test <- leukemia[,39:72]
y.test <- factor(c(rep("ALL",20),rep("AML",14)))

#Compute MiPP
out <- mipp.seq(x=x.train, y=y.train, x.test=x.test, y.test=y.test, n.fold=5, percent.cut

#Print candidate models
out$model

#Print the genes selected
out$genes.selected

#####
#Example 2: When an independent test set is not available

data(colon)

#Normalize data
x <- mipp.preproc(colon)
y <- factor(c("T", "N", "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
             "T", "N", "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
             "T", "T", "T", "T", "T", "T", "T", "T", "N", "T",
             "T", "N", "N", "T", "T", "T", "T", "N", "T", "N",
             "N", "T", "T", "N", "N", "T", "T", "T", "T", "N",
             "T", "N"))

#Deleting contaminated chips
x <- x[,-c(51,55,45,49,56)]
y <- y[ -c(51,55,45,49,56)]

#Compute MiPP
out <- mipp.seq(x=x, y=y, n.fold=5, p.test=1/3, n.split=5, n.split.eval=100,
percent.cut= 0.05, rule="lda", n.seq=2)

#Print candidate models for each split
out$model

#Print optimal models and independent evaluation for each split
out$model.eval

#Print the genes selected
out$genes.selected

```

pre.select

*Pre-selection***Description**

Pre-select genes

`quant.normal` *Quantile normalization*

Description

Performs quantile normalization

`quant.normal2` *Quantile normalization*

Description

Performs quantile normalization

`rbfkernel.decision.function`
SVM (RBF) kernel to compute MiPP

Description

SVM (RBF) kernel to compute MiPP

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