

Package ‘RobSAOD’

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Type Package

Title Robust Significance Analysis of Omics Data: A Weighted Approach
for Biomarkers and Drug Discovery in Omics Data

Version 1.0

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Description Performs weighted significance analysis for identifying the differentially expressed genes (e.g.,microarray) from noisy data.It is an extension of classical significance analysis of omics dataset. It is achieved by adding a weight function.

License GPL (>= 2.10)

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RobSAOD-package	<i>Robust Significance Analysis of Omics Data: A Weighted Approach for Biomarkers and Drug Discovery in Omics Data</i> <i>Robust Significance Analysis of Omics Data: A Weighted Approach for Biomarkers and Drug Discovery in Omics Data</i>
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Description

This package implements a weight based significance analysis for identifying differentially expressed (DE) genes from noisy gene expression dataset (e.g.,microarray). This method is outlier-robust because a weight function is used to produce very smaller weight for outlying cell of the data matrix.

Details

Package: RobSAOD
 Type: Package
 Version: 1.0
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 License: GPL
 Depends: R (>=2.10)

Package RobSAOD has the following functions:

wmean(): This function calculates the weighted mean function.
 wVarSs(): This function calculates the weighted sum of squares function.
 RobSAOD(): This function calculates the weighted significance analysis of Omics Data

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dummyData

Artificially generated gene expression (e.g., microarray) data

Description

This dataset is a matrix containing measurements of gene expression of different subjects.

Usage

```
data("dummyData")
```

Format

A data matrix (e.g., microarray) with 2000 rows and 120 columns. Each row is a gene. The columns are the measurements of gene expression from different subjects.

Details

This data set contains three groups. The first group contains 50 subjects, the second group includes 40 subjects, and the third group contains 30 subjects. of 2000 genes, the first 300 are differentially expressed (DE) genes, and the rest are equally expressed (DE) genes. This data also contain outliers.

Examples

```

data(dummyData)
## str(dummyData)
heatmap(dummyData)

```

RobSAOD	<i>Weighted significance analysis for identifying differentially expressed(DE) genes.</i>
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Description

This is a function of weighted significance analysis for identifying differentially expressed (DE) genes.

Usage

```
RobSAOD(x, ngroup = 3, noGrpMem = c(50,40,30))
```

Arguments

x	a data matrix of gene expression (e.g.,microarray), whose row contains genes and column contains subjects
ngroup	number of group in the dataset
noGrpMem	a vector that contains the number of subjects of each group.

Value

calculate the p-value

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Examples

```
data(dummyData)
pvalue<-RobSAOD(dummyData,ngroup = 3, noGrpMem = c(50,40,30))
```

wmean	<i>Calculation of Weighted Mean</i>
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Description

This function calculates the weighted mean. The user must put the weight in this function; otherwise, it will calculate the classical mean.

Usage

```
wmean(x, w = c(rep(1, length(x))))
```

Arguments

x	a numerical vector
w	value of the weight of the vector. The default weight is 1 for each observation of the vector.

Value

Computed the weighted mean.

Author(s)

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Examples

```
set.seed(1234)
x<-c(rnorm(10,3,0.25))
x1<-c(rnorm(7,3,0.25),rnorm(3,20,2)) #contain 20 outliers#
wmean(x,w= c(rep(1,10)))
mean(x)
wmean(x1,w= c(c(rep(1,7),c(rep(0,3)))))
mean(x1)
```

wVarSs

Weighted sum of square calculation

Description

This function calculates the weighted sum of the square. The user must put the weight in this function, otherwise, it will calculate the classical sum of the square.

Usage

```
wVarSs(x, w = c(rep(1, length(x))), center = 0)
```

Arguments

x	a numerical vector
w	value of the weight of the vector. The default weight is 1 for each observation of the vector.
center	Put the center value.Default is 0.

Value

Computed the weighted sum of square.

Author(s)

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Examples

```
set.seed(1234)
x<-c(rnorm(10,3,0.25))
x1<-c(rnorm(7,3,0.25),rnorm(3,20,2)) #contain 20 outliers#
wVarSs(x,w= c(rep(1,10)),center=3)
wVarSs(x1,w= c(c(rep(1,7),c(rep(0.15,3)))),center=3)
```

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