Package: sampleClassifier (via r-universe)

November 5, 2026

Type Package

Title Sample Classifier

Version 1.36.0

Description The package is designed to classify microarray RNA-seq gene expression profiles.

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Imports e1071, ggplot2, stats, utils

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License Artistic-2.0

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sampleClassifier-package *Sample Classifier*

Description

The package is designed to classify samples from microarray and RNA-seq gene expression datasets.

Details

Package:	sampleClassifier
Type:	Package
Version:	1.0.0
License:	GPL-3

Author(s)

Khadija El Amrani Maintainer: Khadija El Amrani <khadija.el-amrani@charite.de>

Examples

```
## Not run:
library(sampleClassifierData)
data("se_micro_refmat")
micro_refmat <- assay(se_micro_refmat)
data("se_micro_testmat")
micro_testmat <- assay(se_micro_testmat)
res1.list <- classifyProfile(ref_matrix=micro_refmat, query_mat=micro_testmat,
chip1="hgu133plus2",chip2="hgu133a", write2File=FALSE)
res1.list

## End(Not run)
```

classifyProfile *Expression profile classification*

Description

Function to classify microarray gene expression profiles

Usage

```
classifyProfile(ref_matrix, query_mat, chip1 = "hgu133plus2", chip2 = "hgu133a", fun1 = median, fun2 = m
```

Arguments

ref_matrix	Normalized microarray data matrix to be used as reference, with probe sets corresponding to rows and samples corresponding to columns.
query_mat	Normalized microarray query matrix to be classified, with probe sets corresponding to rows and samples corresponding to columns.
chip1	Chip name of the reference matrix.
chip2	Chip name of the query matrix. This parameter can be ignored if the reference and query matrix are from the same chip.
fun1	mean or median. This will specify the number of marker genes that will be used for classification. Default is median.
fun2	mean or median. This will be used to summarize the expression values of probe sets that belong to the same gene. This parameter can be ignored if the reference and query matrix are from the same chip. Default is mean.
write2File	If TRUE, the classification results for each query profile will be written to a file.
out.dir	Path to a directory to write the classification results, default is the current working directory.

Details

Each query profile is compared to all sample types in the reference matrix and a similarity score is calculated. The similarity score is based on the number of marker genes that are shared between the query and the reference. These marker genes are given in a file if write2File is TRUE.

Value

A list with top hits for each query profile, sorted according to a similarity score.

Author(s)

Khadija El Amrani <khadija.el-amrani@charite.de>

See Also

see also getMarkerGenes.

Examples

```
library(sampleClassifierData)
data("se_micro_refmat")
micro_refmat <- assay(se_micro_refmat)
data("se_micro_testmat")
micro_testmat <- assay(se_micro_testmat)
res1.list <- classifyProfile(ref_matrix=micro_refmat, query_mat=micro_testmat,
chip1="hgu133plus2",chip2="hgu133a", write2File=FALSE)
res1.list
```

`classifyProfile.rnaseq` *Expression profile classification*

Description

Function to classify RNA-seq gene expression profiles

Usage

```
classifyProfile.rnaseq(ref_matrix, query_mat, gene.ids.type="ensembl", fun1 = median, write2File=FALS
```

Arguments

`ref_matrix`	RNA-seq data matrix to be used as reference, with genes corresponding to rows and samples corresponding to columns.
`query_mat`	RNA-seq query matrix to be classified, with genes corresponding to rows and samples corresponding to columns.
`gene.ids.type`	Type of the used gene identifiers, the following gene identifiers are supported: ensembl, refseq and ucsc gene ids. Default is ensembl.
`fun1`	mean or median. This will specify the number of marker genes that will be used for classification. Default is median.
`write2File`	A logical value. If TRUE the classification results will be written to a file.
`out.dir`	Path to the directory, in which to write the results. Default is the actual working directory.

Details

Each query profile is compared to all sample types in the reference matrix and a similarity score is calculated. The similarity score is based on the number of marker genes that are shared between the query and the reference. These marker genes are given in a file if write2File is TRUE.

Value

A list with top hits for each query profile, sorted according to a similarity score.

Author(s)

Khadija El Amrani <khadija.el-amrani@charite.de>

Examples

```
library(sampleClassifierData)
data("se_rnaseq_refmat")
rnaseq_refmat <- assay(se_rnaseq_refmat)
data("se_rnaseq_testmat")
rnaseq_testmat <- assay(se_rnaseq_testmat)
res2.list <- classifyProfile.rnaseq(ref_matrix=rnaseq_refmat, query_mat=rnaseq_testmat,
gene.ids.type="ensembl",write2File=FALSE)
res2.list
```

---

classifyProfile.rnaseq.svm

Expression profile classification

Description

Function to classify RNA-seq gene expression profiles using support vector machines (SVM)

Usage

```
classifyProfile.rnaseq.svm(ref_matrix, query_mat, gene.ids.type="ensembl", fun1 = median)
```

Arguments

`ref_matrix`	RNA-seq data matrix to be used as reference, with genes corresponding to rows and samples corresponding to columns.
`query_mat`	RNA-seq query matrix to be classified, with genes corresponding to rows and samples corresponding to columns.
`gene.ids.type`	Type of the used gene identifiers, the following gene identifiers are supported: ensembl, refseq and ucsc gene ids. Default is ensembl.
`fun1`	mean or median. This will specify the number of marker genes that will be used for classification. Default is median.

Details

This function is based on the function svm from the R-package 'e1071'.

Value

A data frame with the predicted classes for each query profile.

Author(s)

Khadija El Amrani <khadija.el-amrani@charite.de>

Examples

```
library(sampleClassifierData)
data("se_rnaseq_refmat")
rnaseq_refmat <- assay(se_rnaseq_refmat)
data("se_rnaseq_testmat")
rnaseq_testmat <- assay(se_rnaseq_testmat)
res2.svm.df <- classifyProfile.rnaseq.svm(ref_matrix=rnaseq_refmat, query_mat=rnaseq_testmat,
gene.ids.type="ensembl")
res2.svm.df
```

---

classifyProfile.svm *Expression profile classification*

Description

Function to classify microarray gene expression profiles using support vector machines (SVM)

Usage

```
classifyProfile.svm(ref_matrix, query_mat, chip1 = "hgu133plus2", chip2 = "hgu133a", fun1 = median, fun
```

Arguments

ref_matrix	Normalized microarray data matrix to be used as reference, with probe sets corresponding to rows and samples corresponding to columns.
query_mat	Normalized microarray query matrix to be classified, with probe sets corresponding to rows and samples corresponding to columns.
chip1	Chip name of the reference matrix.
chip2	Chip name of the query matrix. This parameter can be ignored if the reference and query matrix are from the same chip.
fun1	mean or median. This will specify the number of marker genes that will be used for classification. Default is median.
fun2	mean or median. This will be used to summarize the expression values of probe sets that belong to the same gene. This parameter can be ignored if the reference and query matrix are from the same chip. Default is mean.

Details

This function is based on the function svm from the R-package 'e1071'.

Value

A data frame with the predicted classes for each query profile.

Author(s)

Khadija El Amrani <khadija.el-amrani@charite.de>

See Also

see also `getMarkerGenes`.

Examples

```
library(sampleClassifierData)
data("se_micro_refmat")
micro_refmat <- assay(se_micro_refmat)
data("se_micro_testmat")
micro_testmat <- assay(se_micro_testmat)
res1.svm.df <- classifyProfile.svm(ref_matrix=micro_refmat, query_mat=micro_testmat,
chip1="hgu133plus2",chip2="hgu133a")
res1.svm.df
```

---

get.heatmap *display classification results as heatmap*

Description

Function to display the classification predictions as a heatmap

Usage

```
get.heatmap(res.list)
```

Arguments

`res.list`	the result list returned by the function `classifyProfile` or `classifyProfile.rnaseq`

Details

This function is based on the function ggplot from the R-package 'ggplot2'.

Value

This function is used only for the side effect of creating a heatmap.

Author(s)

Khadija El Amrani <khadija.el-amrani@charite.de>

Examples

```
library(sampleClassifierData)
data("se_micro_refmat")
micro_refmat <- assay(se_micro_refmat)
data("se_micro_testmat")
micro_testmat <- assay(se_micro_testmat)
res1.list <- classifyProfile(ref_matrix=micro_refmat, query_mat=micro_testmat,
chip1="hgu133plus2",chip2="hgu133a", write2File=FALSE)
get.heatmap(res1.list)
```

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