Package 'MGFR'

April 10, 2023

Type Package

Title Marker Gene Finder in RNA-seq data

Version 1.24.0

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Description The package is designed to detect marker genes from
RNA-seq data.

Depends R (>= 3.5)

Imports biomaRt, annotate

biocViews ImmunoOncology, Genetics, GeneExpression, RNASeq

License GPL-3

LazyData yes

NeedsCompilation no

git_url https://git.bioconductor.org/packages/MGFR

git_branch RELEASE_3_16

git_last_commit 2493145

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

R topics documented:

| MGFR-package | *Marker Gene Finder in RNA-seq data* |

Description

The package is designed to detect marker genes from RNA-seq data

Details

Package:	MGFR
Type:	Package
Version:	1.9.2
License:	GPL-3

Author(s)

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Examples

```
data(ref.mat)
res.list <- getMarkerGenes.rnaseq(ref.mat, class.vec=colnames(ref.mat), samples2compare="all", annotate=TRUE, ge
names(res.list)
## show the first 20 markers of liver
res.list[["liver_markers"]][1:20]
```

| getMarkerGenes.rnaseq | *Marker Gene Detection* |

Description

Function to detect marker genes using normalized RNA-seq data

Usage

```
getMarkerGenes.rnaseq(data.mat, class.vec=colnames(data.mat), samples2compare="all", annotate=FALSE,
```

Arguments

`data.mat`	RNA-seq gene expression matrix with genes corresponding to rows and samples corresponding to columns.
`class.vec`	A character vector containing the classes of samples (columns) of data.mat in the same order as provided in the matrix.
`samples2compare`	
	A character vector with the sample names to be compared (e.g. c("liver", "lung", "brain")). By default all samples in the reference matrix are used.
`annotate`	A boolean value. If TRUE the gene symbol and the entrez gene id are shown.
`gene.ids.type`	Type of the used gene identifiers, the following gene identifiers are supported: ensembl, refseq and ucsc gene ids. default is ensembl.
`score.cutoff`	A value in the interval [0,1] to filter the markers according to the specificity score. The default value is 1 (no filtering).

Details

For each marker in the output list, the gene id and the corresponding score are shown. If annotate is TRUE, the gene symbol and the entrez gene id are shown. The score is used to rank the markers according to their specificity. A lower value means a higher specificity.

Value

A list with marker genes associated with each sample type.

Author(s)

Khadija El Amrani <a.khadija@gmx.de>

Examples

```
data(ref.mat)
res.list <- getMarkerGenes.rnaseq(ref.mat, class.vec = colnames(ref.mat), samples2compare="all", annotate=TRUE, g
names(res.list)
## show the first 20 markers of liver
res.list[["liver_markers"]][1:20]
```

`getMarkerGenes.rnaseq.html`

Marker Gene Detection

Description

Function to detect marker genes using normalized RNA-seq data and show the marker genes in HTML tables with links to various online annotation sources (Ensembl, GenBank and EntrezGene repositories)

Usage

```
getMarkerGenes.rnaseq.html(data.mat, class.vec=colnames(data.mat), samples2compare="all", gene.ids.t
```

Arguments

data.mat	RNA-seq gene expression matrix with genes corresponding to rows and samples corresponding to columns.
class.vec	A character vector containing the classes of samples (columns) of data.mat in the same order as provided in the matrix.
samples2compare	
	A character vector with the sample names to be compared (e.g. c("liver", "lung", "brain")). By default all samples in the reference matrix are used.
gene.ids.type	Type of the used gene identifiers, the following gene identifiers are supported: ensembl, refseq and ucsc gene ids. default is ensembl.
score.cutoff	A value in the interval [0,1] to filter the markers according to the specificity score. The default value is 1 (no filtering).
directory	Path to the directory where to save the html pages, default is the current working directory.

Details

This function is based on the function htmlpage from the R-package 'annotate'.

Value

This function is used only for the side effect of creating HTML tables.

Author(s)

Khadija El Amrani <a.khadija@gmx.de>

Examples

```
data(ref.mat)
getMarkerGenes.rnaseq.html(ref.mat, class.vec = colnames(ref.mat), samples2compare="all", gene.ids.type="ensembl
```

---

ref.mat	*RNA-seq gene expression data set*

Description

RNA-seq gene expression data set derived from 5 tissue types (lung, liver, heart, kidney, and brain) from the ArrayExpress database (E-MTAB-1733). Each tissue type is represented by 3 replicates.

Usage

```
data(ref.mat)
```

Format

A [matrix](#) with 32431 genes and 15 samples.

Value

RNA-seq data matrix

Examples

```
data(ref.mat)
```

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