Package ‘MGFR’

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Type Package

Title Marker Gene Finder in RNA-seq data

Version 1.35.0

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

Depends R (>= 3.5)

Imports biomaRt, annotate

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License GPL-3

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Contents

`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
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=FAL
```

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=TRU
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.i
```

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="ens
```

`grid-internal` *Internal MGFR Functions*

Description

Internal MGFR functions

Details

These are not intended to be called by the user.

`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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