Package ‘MGFM’

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Type Package

Title Marker Gene Finder in Microarray gene expression data

Version 1.4.0

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Description The package is designed to detect marker genes from Microarray gene expression data sets

Depends AnnotationDbi,annotate

Suggests hgu133a.db

biocViews Genetics, GeneExpression, Microarray

License GPL-3

LazyData yes

NeedsCompilation no

R topics documented:

`MGFM-package` *Marker Gene Finder in Microarray gene expression data*

Description

The package is designed to detect marker genes from microarray gene expression data sets

Details

Package:	MGFM
Type:	Package
Version:	1.2.0
Date:	2014-08-13
License:	GPL-3

Author(s)

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`ds2.mat` *Microarray gene expression data set*

Description

microarray expression data set derived from 5 tissue types (lung, liver, heart, kidney, and brain) from two GEO Series GSE1133 and GSE2361. Each tissue type is represented by 3 replicates.

Usage

```
data(ds2.mat)
```

Format

A `matrix` with 22283 probe sets and 15 samples.

Details

The data consist of the following samples: GSM44702, GSM18953, GSM18954, GSM44704, GSM18949, GSM18950, GSM44690, GSM18921, GSM18922, GSM44675, GSM18955, GSM18956, GSM44671, GSM18951, GSM18952

Value

microarray data matrix

Examples

```
data(ds2.mat)
```

`getHtmlpage` *Function to build HTML pages to show marker genes*

Description

Function to build HTML pages to show marker genes

Usage

```
getHtmlpage(markers.list,chip, directory=getwd())
```

Arguments

`markers.list`	List of marker genes, returned by the function `getMarkerGenes`.
`chip`	Chip name.
`directory`	Path to the directory where to save the html pages.

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)

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Examples

```
data("ds2.mat")
res.list <- getMarkerGenes(ds2.mat, samples2compare="all", annotate=TRUE, chip="hgu133a",
score.cutoff=1)
getHtmlpage(res.list, chip="hgu133a",directory=getwd())
```

`getMarkerGenes` *Marker Gene Detection*

Description

Function to detect marker genes using microarray gene expression data sets

Usage

```
    getMarkerGenes(data.mat, samples2compare="all", annotate=TRUE, chip=NULL,
score.cutoff=1)
```

Arguments

`data.mat`	The microarray data matrix with probe sets corresponding to rows and samples corresponding to columns.
`samples2compare`	A character vector with the sample names to be compared (e.g. c("liver", "lung", "brain")). By default all samples are used.
`annotate`	A boolean value. If TRUE the gene symbol and the entrez gene id are shown.
`chip`	Chip name.
`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 probe set 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. The score values range from 0 to 1. Values near 0 would indicate high specificity and large values closer to 1 would indicate low specificity.

Value

A list with marker genes associated with each sample type.

Author(s)

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

Examples

```
data("ds2.mat")
res.list <- getMarkerGenes(ds2.mat, samples2compare="all", annotate=TRUE,
chip="hgu133a", score.cutoff=1)
names(res.list)
## show the first 20 markers of liver
res.list[["liver_markers"]][1:20]
```

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