

Package ‘MGFM’

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Type Package

Title Marker Gene Finder in Microarray gene expression data

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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

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License GPL-3

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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

<code>data.mat</code>	The microarray data matrix with probe sets corresponding to rows and samples corresponding to columns.
<code>samples2compare</code>	A character vector with the sample names to be compared (e.g. <code>c("liver", "lung", "brain")</code>). By default all samples are used.
<code>annotate</code>	A boolean value. If TRUE the gene symbol and the entrez gene id are shown.
<code>chip</code>	Chip name.
<code>score.cutoff</code>	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]
```

grid-internal

Internal MGFM Functions

Description

Internal MGFM functions

Details

These are not intended to be called by the user.

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