Package ‘MGFM’

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Type Package
Title Marker Gene Finder in Microarray gene expression data
Version 1.8.0
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Description The package is designed to detect marker genes from Microarray gene expression data sets
Depends AnnotationDbi,annotate
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biocViews Genetics, GeneExpression, Microarray
License GPL-3
LazyData yes
NeedsCompilation no

R topics documented:

MGFM-package
 ds2.mat
 getHtmlpage
 getMarkerGenes

Index

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

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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**

```r
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**

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

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**getMarkerGenes**

*Marker Gene Detection*

**Description**

Function to detect marker genes using microarray gene expression data sets

**Usage**

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

**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**

```r
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]
```
Index

*Topic dataset
   ds2.mat, 2

*Topic marker genes
   getHtmlPage, 3
   getMarkerGenes, 3

*Topic microarray data
   getHtmlPage, 3
   getMarkerGenes, 3

*Topic package
   MGFM-package, 1
   ds2.mat, 2
   getHtmlPage, 3
   getMarkerGenes, 3, 3
   htmlPage, 3
   matrix, 2
   MGFM (MGFM-package), 1
   MGFM-package, 1