Package ‘MGFM’

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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
**getHtmlpage**

**Value**

microarray data matrix

**Examples**

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

**Description**

Function to build HTML pages to show marker genes

**Usage**

```r
cgetHtmlpage(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())
```
**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)
```

**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]
```
Internal MGFM Functions

**Description**

Internal MGFM functions

**Details**

These are not intended to be called by the user.
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