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
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R topics documented:

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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.

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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)
**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)**

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**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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