

# Package ‘MGFM’

November 29, 2024

**Type** Package

**Title** Marker Gene Finder in Microarray gene expression data

**Version** 1.40.0

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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

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MGFM-package

*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

### 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*

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### 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*

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**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)**

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)
getHtmlpage(res.list, chip="hgu133a", directory=getwd())
```

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`getMarkerGenes`*Marker Gene Detection*

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**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]
```

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grid-internal

*Internal MGFM Functions*

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**Description**

Internal MGFM functions

**Details**

These are not intended to be called by the user.

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