

# Package: fdrame (via r-universe)

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**Title** FDR adjustments of Microarray Experiments (FDR-AME)

**Version** 1.84.0

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**Description** This package contains two main functions. The first is `fdr.ma` which takes normalized expression data array, experimental design and computes adjusted p-values. It returns the `fdr` adjusted p-values and plots, according to the methods described in (Reiner, Yekutieli and Benjamini 2002). The second, is `fdr.gui()` which creates a simple graphic user interface to access `fdr.ma`

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**License** GPL (>= 2)

**Imports** tcltk, graphics, grDevices, stats, utils

**biocViews** Microarray, DifferentialExpression, MultipleComparison

**Repository** <https://bioc-release.r-universe.dev>

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design	<i>Experimental design</i>
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**Description**

A vector of integers specifying for each column(sample) to which group number it belongs.

**Usage**

```
data(design)
```

**Format**

The format is: num [1:16] 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1

**Details**

In the example above there are two groups. Each group contains 8 samples

**Examples**

```
data(design)
```

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exp.arr	<i>Normalized Expression Array</i>
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**Description**

The source of this Data is a lipid metabolism study described and analyzed in Dudoit,S., Yang,Y.H, Callow,M.J. and Speed,T.P. (2002) Statistical Methods for Identifying Differentially Expressed Genes in Replicated cDNA Microarray Experiments. Stat Sinica, 12, 111-139.

**Usage**

```
data(exp.arr)
```

**Format**

The format is: num [1:6384, 1:16] -0.2500 0.0329 -0.2065 -0.2240 -0.8542 ... - attr(\*, "dim-names")=List of 2 Each row represents a gene: chr [1:6384] "1" "2" "3" "4" ... Each column represents a sample : chr [1:16] "X1" "X2" "X3" "X4" ...

**Details**

The data is normalized.

**Source**

<http://www.stat.berkeley.edu/users/terry/zarray/Html/matt.html>

**References**

Reiner A, Yekutieli D, Benjamini Y: Identifying differentially expressed genes using false discovery rate controlling procedures. *Bioinformatics* 19:368-375, 2003

**Examples**

```
data(exp.arr)
```

---

`fdr.gui`

*fdr.gui*

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**Description**

This function runs the `fdr.gui` Graphic User Interface.

**Usage**

```
fdr.gui()
```

**Author(s)**

Yoav Benjamini, Effi Kenigsberg, Anat Reiner, Daniel Yekutieli

**References**

Reiner A, Yekutieli D, Benjamini Y: Identifying differentially expressed genes using false discovery rate controlling procedures. *Bioinformatics* 19:368-375, 2003 Benjamini, Y., Krieger, A.M., Yekutieli, D. (2001) "Two Staged Linear Step Up FDR Controlling Procedure", Technical Report Department of Statistics and O.R., Tel Aviv University.

**Examples**

```
fdr.gui()
```

fdr.ma

*fdr.ma***Description**

This function takes normalized expression data array, experimental design and computes adjusted p-values. It returns the fdr adjusted p-values and plots, according to the methods described in (Reiner, Yekutieli and Benjamini 2002)

**Usage**

```
fdr.ma(exp.arr, design, p.method="resampling", fdr.adj="BH-LSU", equal.var=TRUE, plot=c("pv1VSrank", "adj
```

**Arguments**

exp.arr	A data frame or matrix, with m rows corresponding to the gene expression level of an observation and n columns to the observations. In the case of gene expression data, rows correspond to genes and columns to mRNA samples. The data can be read using 'read.table'. The matrix is as the X matrix in multtest package.
design	A vector of characters corresponding to observation (column) class labels. For k classes, the labels must be k different characters. The vector is similar to classlabel vector in multtest package.
p.method	A character string specifying whether resampling method may be used. If 'p.method="resampling"', resampling method is used. If 'p.method="theoretic"', statistic is computed without resampling.
fdr.adj	A character string specifying which type of p-value adjustment method may be used. If 'fdr.adj="BH-LSU"', Benjamini-Hochberg Linear Step Up procedure is used. If 'fdr.adj="point.est"', point estimation procedure is used.(p.method value must be "resampling") If 'fdr.adj="upper.est"', upper estimation procedure is used.(p.method value must be "resampling") If 'fdr.adj="adaptive"', two-stage adaptive procedure is used.
equal.var	A boolean variable specifying whether equal variance assumption may be taken. If TRUE, an equal group variances is assumed. If FALSE, welch approximation is used, for the unequal group variances
plot	A vector of character strings specifying the plots that may be drawn. If the vector contains "pv1VSrank", a plot of p-values vs rank is drawn. If the vector contains "adjVSrank", a plot of adjusted p-values vs rank is drawn. If the vector contains "adjVSstat", a plot of adjusted p-values vs computed statistic (f or t, depends depends on the number of groups on the design) is drawn.
perms.num	An integer specifying the number of permutations that would be used.

**Value**

A data frame with components

adj                    adjusted p-values.

`dif` When there are only two groups `dif` contains the differences between the means of the two groups. when there are more than two groups `dif` contains the multiple R-Squared values.

`res.pvalues` resampling p-values. (in case resampling was requested)

**Author(s)**

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**References**

Reiner A, Yekutieli D, Benjamini Y: Identifying differentially expressed genes using false discovery rate controlling procedures. *Bioinformatics* 19:368-375, 2003 Benjamini, Y., Krieger, A.M., Yekutieli, D. (2001) "Two Staged Linear Step Up FDR Controlling Procedure", Technical Report Department of Statistics and O.R., Tel Aviv University.

**Examples**

```
data(exp.arr, design)
output<-fdr.ma(exp.arr, design, p.method="theoretic", fdr.adj="BH-LSU", equal.var=TRUE, plot=c("pv1VSrank", "adjVSra
```

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