

daMA

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analyseMA

ANALYSIS OF FACTORIAL MICROARRAY EXPERIMENTS

Description

analyseMA is used for the analysis of factorial two-colour microarray experiments based on the experimental design, a user-defined matrix containing the experimental question in contrast form and a vector to discern vectorial contrasts from contrasts given in matrix form.

Usage

```
analyseMA( data, design, id, cmat, cinfo, padj=c("none","bonferroni","fdr"), tol
```

Arguments

data	a matrix of size $G \times N$ containing the normalized and/or standardized data to be analyzed, where G is the number of spots under investigation and N is the number of arrays used in the experiment. The matrix should contain one row for each spot. The matrix should contain as many columns as arrays involved in the experiment, such that each column contains the data for one single array. The matrix should not contain any ID variables, which are entered separately. Missing values should be entered as NA.
design	the design matrix of size $N \times (K + 2)$, where K is the number of experimental conditions. This is the design matrix X known from linear model theory and its elements are typically 0, 1, or -1. A 0 means that the associated parameter does not apply for the corresponding observation (i.e., row). The first two columns are reserved for the two dyes and are usually filled up with 1 and -1, respectively.
id	an ID vector of length G for the identification of the spots.
cmat	a matrix describing the p experimental questions (contrasts) to be analysed in the experiment. The matrix can be composed of vectorial contrasts (a single row of the matrix) and of contrasts in matrix form (several rows of the matrix), e.g. an $A \times B$ interaction effect in a 3×2 design. All contrasts have to be combined into one matrix (using rbind for instance).
cinfo	a vector of length p describing the grouping of the contrast matrix rows in vector or matrix form. E.g. if the design matrix contains three contrasts in vector form, cinfo = rep(1,3), if it contains two vectorial contrast and one as matrix with three rows, cinfo=c(1,1,3).

`cinfo`*Vector indexing the matrix cmat*

Description

This vector is used to describe the structure of the rows of the contrast matrix `cmat`. The number of entries in `cinfo` mirrors the number of experimental questions. "1" indicates a contrast in vectorial form, integers $n > 1$ indicate n contrasts given in matrix form.

References

Bretz, F and Landgrebe J and Brunner E (2003): "Design and analysis of two colour factorial microarray experiments", submitted.

Examples

```
data(cinfo)
```

`cinfoB.AB`*Vector indexing the matrix cmatB.AB*

Description

This vector is used to describe the structure of the rows of the contrast matrix `cmatB.AB`. Its first element (1) indicates that the first experimental question (main effect B) is described by a single contrast in vectorial form. The second element (2) indicates that the second experimental question (interaction between A and B) is given by a contrast in matrix form.

References

Bretz, F and Landgrebe J and Brunner E (2003): "Design and analysis of two colour factorial microarray experiments", submitted.

Examples

```
data(cinfoB.AB)
```

 cmat

Contrast matrix describing the experimental questions

Description

This matrix of numerical constants describes the experimental question, p say. Each experimental question is described by a single contrast vector (a single row in cmat) or by a contrast matrix (several rows in cmat). The ordering of the columns corresponds to that of the associated design matrix X . Thus, typically the first two elements in a row of cmat are reserved for for the two dyes. E.g. to compare the two dyes, we set $(-1, 1, 0, \dots, 0)$.

Usage

```
data(cmat)
```

References

Bretz, F and Landgrebe J and Brunner E (2003):"Design and analysis of two colour factorial microarray experiments", submitted.

Examples

```
data(cmat)
## maybe str(cmat) ; plot(cmat) ...
```

 cmatB.AB

Contrast matrix describing the experimental questions

Description

This matrix of numerical constants describes the experimental question, say p . Each experimental question is described by a single contrast vector (a single row in cmat) or by a contrast matrix (several rows in cmat). The ordering of the columns corresponds to that of the associated design matrix X . Thus, typically the first two elements in a row of cmat are reserved for for the two dyes. E.g. the first line of the matrix cmatB.AB describes the main effect B.

Usage

```
data(cmatB.AB)
```

References

Bretz, F and Landgrebe J and Brunner E (2003):"Design and analysis of two colour factorial microarray experiments", submitted.

Examples

```
data(cmatB.AB)
```

`core`*Internal function of analyseMA*

Description

This internal function of analyseMA computes the statistics and estimators that are organised and given out by the main function analyseMA.

Usage

```
core(vector, design, cmat, cinfo, tol)
```

Arguments

<code>vector</code>	a simple help variable for the apply call
<code>design</code>	the design matrix of size $N \times (K + 2)$, where K is the number of experimental conditions. This is the design matrix X known from linear model theory and its elements are typically 0, 1, or -1. A 0 means that the associated parameter does not apply for the corresponding observation (i.e., row). The first two columns are reserved for the two dyes and are usually filled up with 1 and -1, respectively.
<code>cmat</code>	a matrix describing the p experimental questions (contrasts) to be analysed in the experiment. The matrix can be composed of vectorial contrasts (a single row of the matrix) and of contrasts in matrix form (several rows of the matrix), e.g. an $A \times B$ interaction effect in a 3×2 design. All contrasts have to be combined into one matrix (using <code>rbind</code> for instance).
<code>cinfo</code>	a vector of length p describing the grouping of the contrast matrix rows in vector or matrix form. E.g. if the design matrix contains three contrasts in vector form, <code>cinfo = rep(1,3)</code> , if it contains two vectorial contrast and one as matrix with three rows, <code>cinfo=c(1,1,3)</code> .
<code>tol</code>	A value indicating the tolerance for contrast estimability check

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References

Bretz, F and Landgrebe J and Brunner E (2003):"Design and analysis of two colour factorial microarray experiments", submitted. <http://www.microarrays.med.uni-goettingen.de/>

`data.3x2`*3x2 microarray data*

Description

These are data from a microarray experiment in which the expression profiles of three cell lines were analysed with and without drug treatment using cDNA microarrays spotted with 30012 human cDNAs. The data matrix consists of 30012 rows and 18 columns. Each row represents one spot, each column corresponds to one microarray.

Usage

```
data(data.3x2)
```

Format

The format is: matrix of size 30012 x 18.

Source

cDNA microarray lab of the University of Goettingen, Germany. <http://www.microarrays.med.uni-goettingen.de>

Examples

```
data(data.3x2)
## maybe str(data.3x2) ; plot(data.3x2) ...
```

`designMA`*DESIGN OF FACTORIAL MICROARRAY EXPERIMENTS*

Description

designMA computes efficient factorial microarray experimental designs for two-colour microarrays based on a list of user-defined design matrices, a matrix describing the experimental questions (contrasts), a vector to discern vectorial contrasts from contrasts given in matrix form and a design optimality criterion.

Usage

```
designMA(design.list, cmat, cinfo, type = c("d", "e", "t"), tol = 1e-06)
```

Arguments

`design.list` a named list of design matrices. Each design matrix should have `nrow` = number of arrays and `ncol` = number of experimental conditions. With `p` columns, the first two columns describe the dye labeling (green and red), the remaining columns describe the experimental conditions.


```
## End(Not run)
## Not run:
t.eff.3x2.all <- designMA(designs.composite,
                          cmat,cinfo,type="t")

## End(Not run)
#compute design effi
# a \eqn{3 \times
# experiment usin
# microarrays and
# the the simple
# effects, the ma
# A, B and the in
# effect \eqn{A
```

designs.basic

Basic designs for two-colour factorial 3 x 2 microarray data

Description

A list of matrices describing basic designs for two-colour factorial microarray data of size 3 x 2. Matrix rows represent microarrays, matrix columns represent parameters.

Usage

```
data(designs.basic)
```

Format

List of matrices of size 6 x 9.

Details

The designs are abbreviated as in the paper (cf. source and references): BS - swap over B, AL - A loop, XL - crossed loop, CL - circle loop, RS - star swap, TL - triangular loop, CR - common reference.

Source

cDNA microarray lab of the University of Goettingen, Germany. <http://www.microarrays.med.uni-goettingen.de>

designs.composite *Composite designs for two-colour factorial 3 x 2 microarray data*

Description

A list of matrices describing composite designs for two-colour factorial microarray data of size 3 x 2 using 18 microarrays each. The design matrices are made up of basic designs. Matrix rows represent microarrays, matrix columns represent parameters.

Usage

```
data(designs.composite)
```

Format

List of 10 matrices of size 18 x 9.

Details

The matrix names reflect the basic designs they are made up from. The first two digits of the names abbreviated the first basic design, the second two the second design etc. The basic design abbreviations are: BS - swap over B, AL - A loop, XL - crossed loop, CL - circle loop, RS - star swap, TL - triangular loop, CR - common reference. BSBSBS is a tripled basic BS design, CLCLTL is a double circle loop design combined with a triangular design and so on.

Source

cDNA microarray lab of the University of Goettingen, Germany. <http://www.microarrays.med.uni-goettingen.de>

Examples

```
data(designs.composite)
```

id.3x2 *A vector of length 30012 containing numeric identifiers of the genes from the microarray dataset data.3x2.*

Description

Cf. data.3x2

Usage

```
data(id.3x2)
```

Format

The format is: num [1:30012] 12 24 108 120 204 216 300 312 396 408 ...

Examples

```
data(id.3x2)
```

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