Package ‘genArise’
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Imports graphics, grDevices, methods, stats, tcltk, utils, xtable

Description genArise is an easy to use tool for dual color microarray data. Its GUI-Tk based environment let any non-experienced user performs a basic, but not simple, data analysis just following a wizard. In addition it provides some tools for the developer.

biocViews Microarray, TwoChannel, Preprocessing

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R topics documented:

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**Description**

Extract **A values** from a Spot.
Usage

a.arise(mySpot)

Arguments

mySpot Spot object for one microarray.

Value

List of A-values. \((\log(cy3, 2) + \log(cy5, 2))/2\)

See Also

m.arise.

Examples

```r
## read the spot from a file and save it in spot
data(Simon)
## Extract A from spot and save in a
a <- a.arise(mySpot = Simon)
```

---

alter.unique Remove Duplicates

Description

This function allows to remove from the spot repeated Id’s. Before moving one of the repeated Id’s the function compute the log ratio of both values with the same Id and delete the least absolute value if both of them are positive or negative. In other case delete both observations.

Usage

alter.unique(mySpot)

Arguments

mySpot Spot object for one microarray.

Value

Spot object without duplicates.

Examples

```r
data(Simon)
## filter the spot and save it in f.spot
f.spot <- filter.spot(Simon)
## remove duplicates and save it in u.spot
u.spot <- alter.unique(f.spot)
```
### analysis.window

**Description**

Auxiliar function of genArise GUI, in this window you can apply operations to original data.

**Usage**

```
analysis.window(texto, follow.wizard = FALSE, envir, swap)
```

**Arguments**

- `texto`: Historical project string
- `follow.wizard`: Boolean value, if this argument is TRUE, an analysis are performed
- `envir`: Environment where are the project variables
- `swap`: Is this a swap analysis or an individual analysis

**Value**

tkwidget

---

### annotations

**Description**

Performed an HTML file

**Usage**

```
annotations(specie.data, specie, column, symbol,
output.file = "annotations.html")
```

**Arguments**

- `specie.data`: A data frame
- `specie`: Name of specie
- `column`: Number of column where are the gene name in the data frame
- `symbol`: An optional symbol besides GenBank ID
- `output.file`: Name of output file

**Value**

HTML file with link for each spot in data frame
back.gui

Return to the last window

Description

Auxiliar function of genArise GUI.

Usage

back/gui(envir)

Arguments

envir  Environment where are the project variables

Value

tkwidget

bg.correct  Background Correction

Description

This function use the background data to eliminate unwanted effects in signal. The background correction establish the new Cy3 signal as Cy3 - BgCy3 and the new Cy5 as Cy5 - BgCy5.

Usage

bg.correct(mySpot)

Arguments

mySpot  Spot object for one microarray.

Value

Spot object with the background correction done.

Examples

data(Simon)
## background correction and save it in c.spot
c.spot <- bg.correct(Simon)
Classes Defined by this Package

Description

This package defines the following data classes.

**Spot**  A class used to store spot data with the following attributes: Cy3, Cy5, BgCy3, BgCy5, Ids as they are read by `read.spot` or obtained from a function that return a spot object.

**DataSet**  A class used to store spot data with the following attributes: Cy3, Cy5, Ids, Z-score.

create.project  

Create directory for the project and its results and graphics

Description

Auxiliar function for genAriseGUI. Create the directory’s hierarchy of the project.

Usage

```r
create.project(project.name, results.file = "Results",
               graphics.file = "Graphics")
```

Arguments

- **project.name**  Project directory name.
- **results.file**  Filename of the project result.
- **graphics.file**  Filename of the project graphics.

cys.plot  

Data Visualization: log2(Cy3) vs log2(Cy5)

Description

This function shows the plot of the values from the log Cy3 against log Cy5 intensities that belongs to an object of the Spot class.

Usage

```r
cys.plot(mySpot, col = "green")
```

Arguments

- **mySpot**  An Spot object
- **col**  Color in which the points of the plot will be shown. This argument must be quoted and the possible values it can take are the same from the color funcion in the R base.
**Examples**

```r
data(Simon)
cys.plot(Simon)
```

**DataSet-class**

*DataSet-class*

**Description**

A simple list-based class for storing red and green channel foreground, z-scores and the Ids.

**Creating Objects from the Class**

Objects can be created by calls of the form `new("DataSet", sets, type)` where *sets* is a list containing Cy3, Cy5, Id and Zscore and *type* is "ri" or "ma". Objects are normally created by `read.spot`.

**Slots/List Components**

This class contains no slots (other than `.Data`), but objects should contain the following list components:

- **Cy5**: numeric matrix containing the red (cy5) foreground intensities. Rows correspond to spots and columns to arrays.
- **Cy3**: numeric matrix containing the green (cy3) foreground intensities.
- **Id**: Ids from all the observations.
- **Zscore**: The result of `(R - mean) / sd` that define an intensity-dependent Z-score threshold to identify differential expression.

All of these matrices should have the same dimensions.

**Methods**

This class inherits directly from class `list` so any operation appropriate for lists will work on objects of this class.

**filter.spot**

*Intensity-based filtering of array elements*

**Description**

This function keep only array elements with intensities that are 2 standard deviation above background.

**Usage**

```r
filter.spot(mySpot)
```

**Arguments**

- **mySpot**: Spot object for one microarray.
Value

Array elements with intensities that are 2 standard deviation above background.

References


Examples

data(Simon)
## background correction and save it in c.spot
c.spot <- bg.correct(Simon)
## normalize spot
n.spot <- grid.norm(c.spot, nr = 23, nc = 24)
## filtering the spot
filter.spot(n.spot)


genaRise

GUI: Graphical User Interface

Description

This is the main function and display the GUI of genAri.se.

Usage

genaRise()

genaRise.init

Description

Auxiliar function of genAri.se GUI, this function show a principal menu of genAri.seGUI

Usage

genaRise.init(envir)

Arguments

envir Environment where are the project variables

Value

tkwidget
Description

After we finished our slice analysis we get a up-regulated and down-regulated set. This will be the set of study genes for genMege. Given this set, genMerge retrieves functional genomic data for each gene and provides statistical rank scores for over-representation of particular functions in the dataset.

Usage

geneMerge(gene.association, description, population.genes, study.genes, output.file = "GenMerge.txt")

Arguments

gene.association
  The gene-association file links gene names with a particular datum of information using a shorthand of gene-association IDS
description
  The description file contains human-readable description of gene-association IDS
population.genes
  Set of all genes detected on a array
study.genes
  Set of genes may be those that are up-regulated or down-regulated or both of them.
output.file
  The name of output file that includes all results obtained after this analysis.

Note

This function is completely based on GeneMerge from Cristian I. Castillo-Davis and Daniel L. Hartl

References

Cristian I. Castillo-Davis Department of Statistics Harvard University http://www.oeb.harvard.edu/hartl/lab/publications/GeneMerge

Auxiliary function for post-analysis

description

This function get values from an DataSet object.
This is just a function for the GUI, and can not be used in the command line.

Usage

geneMerge(list.values, genes.values, up.down, min.val, max.val)
**get.Zscore**

**Arguments**

- `list.values`: Zscore values from DataSet object
- `genes.values`: Ids values from DataSet object
- `up.down`: If the analysis will be done with "up" or "down" regulated
- `min.val`: Minimal value of the range
- `max.val`: Maximal value of the range

**Value**

An Ids list

---

**get.Zscore** | **Swap from Files**

**Description**

Read both files, but only extract the interested columns and create a Spot object.

**Usage**

```
get.Zscore( spot, name, Zscore.min=NULL, Zscore.max=NULL, all=FALSE, envir)
```

**Arguments**

- `spot`: a connection or a character string giving the name of the file to read where each column represent the spot components.
- `name`: a connection or a character string giving the name of the file to read where each column represent the spot components.
- `Zscore.min`: column that represent Cy3.
- `Zscore.max`: column that represent Cy5.
- `all`: column that represent BgCy3.
- `envir`: Environment where are the genArise variables.

**See Also**

`write.spot`
**global.norm**  

*Global Normalization of Spot*

**Description**

This function normalize R and I values and fit the value of Cy5 from his argument. In this function the normalize algorithm will be applied to all observations to get the lowess factor and then fit Cy5 with this factor. The observations. The observations with values \( R = 0 \) are deleted because they have no change in their expression levels.

**Usage**

```r
global.norm(mySpot)
```

**Arguments**

- **mySpot**  
  A spot object

**Value**

A new spot object but normalized, it means with a different Cy5 that is the result of the fit with the lowess factor.

**Examples**

```r
data(Simon)  
# Background Correction  
c.spot <- bg.correct(Simon)  
#Normalized data  
n.spot <- global.norm(c.spot)
```

---

**graphic.choose**  

*Graphic choose*

**Description**

This function show the plot of an spot object. This plot are identify with the graphic.type.value

**Usage**

```r
graphic.choose(spot.object, graphic.type)
```

**Arguments**

- **spot.object**  
  An object ob Spot class
- **graphic.type**  
  representative integer of type graphic will be plot

**Value**

Plot device
**grid.norm**

**Normalization by grid of Spot**

**Description**

This function normalize R and I values and fit the value of Cy5 for each grid in the spot that it receives as argument. In this function the dimension of grid is (meta-row * meta-column).

**Usage**

```
grid.norm(mySpot, nr, nc)
```

**Arguments**

- `mySpot`: Spot object for one microarray.
- `nr`: Total of meta-row.
- `nc`: Total of meta-column.

**Value**

Spot object with the grid normalization done.

**Examples**

```r
data(Simon)
nn ## background correction and save it in c.spot
c.spot <- bg.correct(Simon)
nn ## normalization and save it in n.spot
n.spot <- grid.norm(c.spot, 23, 24)
```

---

**help**

**Help of genArise**

**Description**

Display the help of genArise in the GUI. This is just a function for the GUI, and can not be used in the command line.

**Usage**

```
help()
```
**i.arise**

**I Arise**

**Description**
Extract I from a Spot.

**Usage**

```r
i.arise(mySpot)
```

**Arguments**

- `mySpot` Spot object for one microarray.

**Value**
List of I-values

**See Also**

`r.arise`

**Examples**

```r
data(Simon)
## Extract I from spot and save in i
i.arise(Simon)
```

---

**imageLimma**

**Image Plot of Microarray**

**Description**
Plot an image of colours representing the log intensity ratio for each spot on the array. This function can be used to explore whether there are any spatial effects in the data.

**Usage**

```r
imageLimma(z, row, column, meta.row, meta.column, low = NULL, high = NULL)
```
Arguments

z numeric vector or array. This vector can contain any spot statistics, such as log intensity ratios, spot sizes or shapes, or t-statistics. Missing values are allowed and will result in blank spots on the image

row rows in the microarray

column columns in the microarray

meta.row metarows in the microarray

meta.column metacolumns in the microarray

low color associated with low values of 'z'. May be specified as a character string such as "green", "white" etc, or as a rgb vector in which 'c(1,0,0)' is red, 'c(0,1,0)' is green and 'c(0,0,1)' is blue. The default value is "green" if 'zerocenter=T' or "white" if 'zerocenter=F'.

high color associated with high values of 'z'. The default value is "red" if 'zerocenter=T' or "blue" if 'zerocenter=F'.

Note

This function is based in the imageplot function from limma package.

References


Examples

data(Simon)
spot.data <- attr(Simon, "spotData")
M <- log(spot.data$Cy5, 2) - log(spot.data$Cy3, 2)
imageLimma(z = M, row = 23, column = 24, meta.row = 2, meta.column = 2,
low = NULL, high = NULL)

Description

Extract M values from a Spot.

Usage

m.arise(mySpot)

Arguments

mySpot Spot object for one microarray.

Value

List of M-values
**ma.plot**

*Data Visualization: M vs. A plot*

**Description**

This function allows to plot M -vs- A in spot.

**Usage**

```r
ma.plot(mySpot, col = "green")
```

**Arguments**

- `mySpot`: Spot for one microarray.
- `col`: color of points in graphic

**Examples**

```r
data(Simon)
## Extract M from spot and save in m
m <- m.arise(Simon)
ma.plot(m)
```

---

**make.swap**

*Swap analysis*

**Description**

Read both files, but only extract the interested columns and create a Spot object.

**Usage**

```r
make.swap(spot1, spot2, Cy3, Cy5, BgCy3, BgCy5, Id, Symdesc, header = FALSE, is.ifc = FALSE, envir, nr, nc)
```
meanUnique

Arguments

spot1 a connection or a character string giving the name of the file to read where each column represent the spot components.

spot2 a connection or a character string giving the name of the file to read where each column represent the spot components.

Cy3 column that represent Cy3.

Cy5 column that represent Cy5.

BgCy3 column that represent BgCy3.

BgCy5 column that represent BgCy5.

Id column that represent Id.

Symdesc optional identifier besides the Id column.

header the logical value of the header input file

is.ifc If is.ifc = TRUE this experiment was done in the Unit of Microarray from Cellular Physiology Institute.

envir Environment where are the genArise variables.

nr Total of meta-row.

nc Total of meta-column.

See Also

write.spot.

meanUnique Remove Duplicates

Description

This function allows to remove from the spot repeated Id's. Before moving one of the repeated Id's the function compute the average of Cy3 intensity and Cy5 intensity.

Usage

meanUnique(mySpot)

Arguments

mySpot Spot object for one microarray.

Value

Spot object without duplicates

Examples

data(Simon)
c.spot <- bg.correct(Simon)
n.spot <- global.norm(c.spot)
f.spot <- filter.spot(n.spot)
meanUnique(f.spot)
Description

Call a editor for note about actual experiment

Usage

`note(envir)`

Arguments

- `envir` Environment where are the experiment variables

---

`old.project` *Open previous project*

Description

Show the information that was obtained from the analysis of a previous project. This is just an auxiliar function for genAriseGUI, and can not be used in the command line.

Usage

`old.project(project.name, envir, parent)`

Arguments

- `project.name` path of project file (PRJ)
- `envir` Environment where are the genArise variables
- `parent` The parent widget

Value

`tkwidget`
post.analysis  
Set-combinatorial analysis

Description
This function allows you to perform a set combinatorial analysis between the results previously obtained in different projects. This function is called post.analysis and it is mandatory that you have done the Zscore operation in all the selected projects. It is important to clarify that this function receives a list of files with extension prj as argument and for this reason you can’t use it if the results to compare was not obtained by the genArise GUI.

Usage
post.analysis(values, min.val, max.val, up.down, output)

Arguments
values  
A list of projects to compare
min.val  
The minimal value of the range
max.val  
The maximal value of the range
up.down  
If the analysis will be done with "up" or ''down'' regulated
output  
The directory that will contain all the output files

Value
Once obtained the ids list for each project a number of files with extension set are created in a directory. The name of this files consists in a sequence of 0 and 1. The number of digits in the file names is the same to the number of projects in the list passed as argument to the function. There is then, a relation between the number of digits in the file names and the projects. This relation is defined by the position specified in the file order.txt in the same directory you have passed as another argument in the function.

principal  
Principal window of genAriseGUI

Description
This function show a window with the information of experiment like name and dimensions, too plot an image of colours representing the log intensity ratio for each spot on the array. This is just an auxiliar function for genAriseGUI, and can not be used in the command line.

Usage
principal(envir, swap)

Arguments
envir  
Environment where are the genArise variables
swap  
Is this a swap analysis or an individual analysis
**project.select**

**Value**

tkwidget

---

**project.select**  
*File selector*

**Description**

Previous window to post-analysis. In this window you can select one or several files (projects) and arguments to be used by post analysis function.

This is just an auxiliary function for genAriseGUI, and can not be used in the command line.

**Usage**

`projects.select(envir, nombre)`

**Arguments**

- `envir`  
  Environment where are the genArise variables

- `nombre`  
  Name of directory where the post-analysis results will be placed.

**Value**

tkwidget

---

**r.arise**  
*Get R value*

**Description**

Get the **R values** from an object of the Spot class.

**Usage**

`r.arise(mySpot)`

**Arguments**

- `mySpot`  
  An object of the Spot class

**Value**

A vector containing the R value (log(Cy5/Cy3)) for each observation of the spot object.

**See Also**

`i.arise`
Examples

```r
data(Simon)
#Get R-value from an object of the Spot class and save the result
R <- r.arise(Simon)
#Show the R-values
```

---

**read.dataset**  
*Read Dataset from File*

**Description**

Read all file and extract the interested columns to create a DataSet object (this file contain the zscore with all the genes after the duplicates filtering and makes not distinction between up-regulated and down-regulated. If you want to make this distinction you must write the data with the function `write.dataSet`, but there is no way to read this files with this function).

**Usage**

```r
read.dataset(file.name, cy3 = 1, cy5 = 2, ids = 3, symdesc = NULL, zscore = 4, type = 6, header = FALSE, sep = "\t")
```

**Arguments**

- `file.name` a connection or a character string giving the name of the file to read where each column represent the dataset components.
- `cy3` column that represent Cy3.
- `cy5` column that represent Cy5.
- `ids` column that represent Id.
- `symdesc` optional identifier besides Id column.
- `zscore` column that represent the zscore value.
- `type` column that represent if the experiment was performed as R vs I or M vs A.
- `header` the logical value of the header input file
- `sep` the separator in the inputfile

**See Also**

*write.zscore.*
**read.spot**

*Read Spot from File*

**Description**

Read all file, but only extract the interested columns and create a Spot object.

**Usage**

```r
read.spot(file.name, cy3, cy5, bg.cy3, bg.cy5, ids, symdesc, header = FALSE, sep = "\t", is.ifc = FALSE, envir)
```

**Arguments**

- **file.name** a connection or a character string giving the name of the file to read where each column represent the spot components.
- **cy3** column that represent Cy3.
- **cy5** column that represent Cy5.
- **bg.cy3** column that represent BgCy3.
- **bg.cy5** column that represent BgCy5.
- **ids** column that represent Id.
- **symdesc** (optional) identifier besides Id column.
- **header** the logical value of the header input file.
- **sep** the separator in the input file.
- **is.ifc** If is.ifc = TRUE this experiment was done in the Unit of Microarray from Cellular Phisiology Institute.
- **envir** Environment where are the genArise variables. You don’t need to specify this argument.

**See Also**

- `write.spot`

---

**reset.history**

*Reset the prj history file*

**Description**

Clean all the operations saved in the prj history file.

**Usage**

```r
reset.history(history.file, text)
```

**Arguments**

- **history.file** The name of the prj history file.
- **text** The new content of the prj history file.
Value
The history file without operations.

\[
\text{ri.plot} \quad \text{Data Visualization: R vs I}
\]

Description
This function allows to plot **R-values vs I-values** from a Spot object.

Usage
\[
\text{ri.plot(mySpot, col = "green")}
\]

Arguments
- **mySpot**: Spot Object
- **col**: Color in which the points of the plot will be shown. This argument must be quoted and the possible values it can take are the same from the `colors()` function in the R base package.

See Also
colors()

Examples
\[
\text{data(Simon)} \\
\text{ri.plot(Simon)}
\]
**set.history.project**  
Save the history of a project

**Description**
Save in the history file each operation performed while the analysis. This is just to get the open this particular project in the future. This is just an auxiliary function for the GUI, and can not be used in the command line.

**Usage**
```r
set.history.project(history.file, id.name, data.file)
```

**Arguments**
- `history.file`: The name of the prj history file.
- `id.name`: The name of the operation.
- `data.file`: The file with the results of the operation.

**Value**
The history file with the new performed operation.

---

**set.path.project**

**Description**
Auxiliar function for genAriseGUI

**Usage**
```r
set.path.project(path, results.file, graphics.file, envir)
```

**Arguments**
- `path`: Project path value
- `results.file`: Name of directory where results file will be
- `graphics.file`: Name of directory where pdf graphics will be
- `envir`: Environment where are the experiment variables
set.project.properties

Description

Auxiliar function for genAriseGUI

Usage

set.project.properties(envir)

Arguments

envir Environment where are the experiment variables

Simon

Dataset: Little fragment of a microarray from IFC UNAM

Description

This structure is a data fragment of a yeast microarray from the Microarrays Unit in IFC UNAM. The original microarray contains 6 meta-rows and 4 meta-columns, however this data just belongs to the first meta-row order in a way of 2 meta-rows and 2 meta-columns.

Usage

data(Simon)

Format

A list that contains 1104 observations, because the dimensions of this example are: 2 meta-rows, 2 meta-columns, 23 rows, 24 columns.

Examples

data(Simon)
#A preview from the chip
datos <- attr(Simon, "spotData")
M <- log(datos$Cy3, 2) - log(datos$Cy5, 2)
extremLimma(M, 23, 24, 2, 2)
**Description**

Read both files, but only extract the interested columns and create a Spot object.

**Usage**

```r
single.norm(envir)
```

**Arguments**

- `envir` Environment where are the genArise variables.

**See Also**

- `write.spot`

---

**Spot-class**

**Description**

A simple list-based class for storing red and green channel foreground and background intensities for a batch of spotted microarrays and the Ids.

**Creating Objects from the Class**

Objects can be created by calls of the form `new("Spot", spot)` where `spot` is a list. Objects are normally created by `read.spot`.

**Slots/List Components**

This class contains no slots (other than `.Data`), but objects should contain the following list components:

- `Cy5`:
  - numeric matrix containing the red (cy5) foreground intensities. Rows correspond to spots and columns to arrays.
- `Cy3`:
  - numeric matrix containing the green (cy3) foreground intensities.
- `BgCy5`:
  - numeric matrix containing the red (cy5) background intensities.
- `BgCy3`:
  - numeric matrix containing the green background intensities.
- `Id`:
  - Ids from all the observations.

All of these matrices should have the same dimensions.

**Methods**

This class inherits directly from class `list` so any operation appropriate for lists will work on objects of this class.
spotUnique  

**Replicate filtering**

**Description**
We consider replicate measures of two samples and adjust the log(ratio,2) measures for each gene so that the transformed values are equal. To do this we take the geometric mean. This procedure can be extended to averaging over \( n \) replicates.

**Usage**

```r
spotUnique(mySpot)
```

**Arguments**

- `mySpot`  
  Spot object for one microarray.

**Value**
Spot object without duplicates

**Examples**

```r
data(Simon)
c.spot <- bg.correct(Simon)
f.spot <- filter.spot(c.spot)
spotUnique(mySpot = f.spot)
```

---

swap.select  

**Dye swap files selector**

**Description**
This is just an auxiliary function for genAriseGUI, and can not be used in the command line.

**Usage**

```r
swap.select(envir)
```

**Arguments**

- `envir`  
  Environment where are the genArise variables

**Value**

- `tkwidget`
**trim**

**Description**
Extract white spaces at the beginning or end of a word.

**Usage**
trim(word)

**Arguments**
- **word**
  A string of characters possibly with white spaces at the beginning or end of the string.

**Value**
Returns a string of characters, with leading and trailing whitespace omitted.

**Examples**

```r
trim(" This is a String ")
## return [1] "This is a String"
```

---

**write.dataSet**

**Write dataSet**

**Description**
Write the values for observations of an object of DataSet class in an output file. This values are written in columns with the follow order: Cy3, Cy5, Cy3 Background, Cy5 Background, Ids and finally the Zscore value. By default this output file has no header.

**Usage**
write.dataSet(dataSet.spot, fileName, quote = FALSE, col.names = FALSE, row.names = FALSE,
Zscore.min = NULL, Zscore.max = NULL, sep = "\t")

**Arguments**
- **dataSet.spot**
  An object of DataSet class
- **fileName**
  The name of the output file where the data will be written. This argument must be quoted.
- **quote**
  If quote = TRUE, all values in the file will be quoted.
- **col.names**
  If col.names = TRUE, an integer is written in every column as header. By default col.names = FALSE.
write.spot

row.names

If row.names = TRUE will be an extra column that numerates every rows in the file.

Zscore.min

The lower value in a range, if Zscore.min = NULL then the file will contain all values bellow Zscore.max

Zscore.max

The greater value in a range, if Zscore.max = NULL then file will be contain all values above Zscore.min. Both values, Zscore.min and Zscore.max can not be NULL

sep

Character to separate the columns in file. By default sep = "\t".

Examples

data(WT.dataset)
write.dataSet(dataSet.spot = WT.dataset, fileName = "Example.csv", Zscore.min = 1, Zscore.max = 1.5, sep = "\t")

write.spot

Write Spot

Description

Write the values for observations of an object of Spot class in an output file. This values are written in columns with the follow order: Cy3, Cy5, Cy3 Background, Cy5 Background and finally Ids. By default this file has no header.

Usage

write.spot(spot, fileName, quote = FALSE, sep = "\t", col.names = FALSE, row.names = FALSE)

Arguments

spot

An object of Spot class

fileName

The name of the output file where the data will be written. This argument must be quoted.

quote

If quote = TRUE, all values in the file will be quoted.

sep

Character to separate the columns in file. By default sep = "\t".

col.names

If col.names = TRUE, an integer is written in every column as header. By default col.names = FALSE.

row.names

If row.names = TRUE will be an extra column that numerates every rows in the file. read.spot.

Examples

data(Simon)
write.spot(spot = Simon, fileName = "Example.csv", quote = FALSE, sep = "\t", col.names = FALSE, row.names = FALSE)
### write.zscore

**Write Z-score data**

**Description**

Write the values for observations of an object of DataSet class in an output file. This values are written in columns tab separated with the follow order: Cy3, Cy5, Cy3 Background, Cy5 Background, Ids and finally the z-score value. The header of the output file is the selected type for the z-score (ri or ma).

**Usage**

```r
write.zscore(dataSet.spot, fileName, sep = "\t")
```

**Arguments**

- **dataSet.spot**: An object of DataSet class
- **fileName**: The name of the output file where the data will be written. This argument must be quoted.
- **sep**: Character to separate the columns in file. By default sep = "\t".

**Examples**

```r
data(WT.dataset)
write.zscore(dataSet.spot = WT.dataset, fileName = "Zscore.csv", sep = "\t")
```

---

### WT.dataset

**Microarray from the IFC**

**Description**

This data set is a Microarray from the IFC.

**Usage**

```r
data(WT.dataset)
```

**Format**

A vector containing 4036 observations.

**Examples**

```r
data(WT.dataset)
Zscore.plot(WT.dataset)
```
Zscore

Z-scores for identifying differential expression

Description
This function identifies differentially expressed genes by calculating an intensity-dependent Z-score. This function uses a sliding window to calculate the mean and standard deviation within a window surrounding each data point, and defines a Z-score where Z measures the number of standard deviations a data point is from the mean.

Usage
Zscore(spot.object, type, window.size)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>spot.object</td>
<td>A spot object</td>
</tr>
<tr>
<td>type</td>
<td>Type of analysis: &quot;ri&quot; is for a R-I analysis and &quot;ma&quot; is for M-A analysis</td>
</tr>
<tr>
<td>window.size</td>
<td>Size of the sliding window</td>
</tr>
</tbody>
</table>

Value
A dataSet object with attributes Cy3, Cy5, Id, Z-score.

Examples

```r
data(Simon)
# Background Correction
c.spot <- bg.correct(Simon)
# Normalized data
n.spot <- grid.norm(c.spot, 23, 24)
# Filter spot
f.spot <- filter.spot(n.spot)
# Replicate filtering
u.spot <- spotUnique(f.spot)
# Z-score analysis
s.spot <- Zscore(u.spot)
```

Zscore.plot

Z-score Data Visualization: R vs I or M vs A

Description
This function allows to plot R-values vs I-values or M-values vs A-values for identifying differential expression.

Usage
Zscore.plot(dataSet.spot, Zscore.min, Zscore.max, all, col)
Zscore.points

Arguments

- **dataSet.spot**: Spot Object
- **Zscore.min**: The lower value in a range, if Zscore.min = NULL then the file will contain all values bellow Zscore.max
- **Zscore.max**: The greater value in a range, if Zscore.max = NULL then file will be contain all values above Zscore.min. Both values, Zscore.min and Zscore.max can not be NULL
- **all**: Plot all the observations in four sets: Z < 1, 1 < Z < 1.5, 1.5 < Z < 2, Z > 2
- **col**: Color in which the points of the plot will be shown where only the points from center are plot. This argument must be quoted and the possible values it can take are the same from the colors function in the R base package.

See Also

colors()

Examples

data(WT.dataset)
Zscore.plot(WT.dataset, Zscore.min = 1, Zscore.max = 2)

Zscore.points

Z-score Window

Description

This function display the window that show the results after the Z-score. This window allow:

1. Show the plots of the up and down generated with the function Zscore.plot regulated spots in: Zscore < 1 sd 1 sd < Zscore < 1.5 sd 1.5 sd < Zscore < 2 sd Zscore > 2 sd and All the points
2. Save the plots in pdf and save the results in an output file

This just a function for the GUI, and can not be used in the command line.

Usage

Zscore.points(type, text, envir, swap)

Arguments

- **type**: Type of analysis done: "ri" is for a R-I analysis and "ma" is for M-A analysis
- **text**: The text for the text area of the history of the project
- **envir**: Environment where the variables are stored
- **swap**: Is this a swap analysis or an individual analysis
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