Package ‘a4Base’

April 25, 2017

Type Package
Title Automated Affymetrix Array Analysis Base Package
Version 1.24.0
Date 2013-10-02
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Description Automated Affymetrix Array Analysis
Depends methods, graphics, grid, Biobase, AnnotationDbi, annaffy, mpm, genefilter, limma, multtest, glmnet, a4Preproc, a4Core, gplots
Suggests Cairo, ALL
Enhances gridSVG, JavaGD
License GPL-3
biocViews Microarray
NeedsCompilation no

R topics documented:

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Utility function that defines a color palette for use in a4.

**Usage**

```r
a4palette(n, alpha = 1, Janssen = FALSE)
```

**Arguments**

- `n`: Number of color levels the palette should provide
- `alpha`: alpha transparency level of the colors
- `Janssen`: logical. If TRUE, Janssen Pharmaceutical colors are used (with a maximum of 6 possible colors).

**Details**

For n = 1, "blue" is returned; for n = 2 c("red", "blue") is returned; for n = 3 c("red", "green", "blue") is returned; for n = 4 c("red", "green", "blue", "purple") is returned and for n > 2, the output of `rainbow(n)` is returned.

**Value**

- a character vector of colors

**Author(s)**

Steven Osselaer, Tobias Verbeke
addQuantilesColors

See Also

rainbow

Examples

op <- par(mfrow = c(2, 3))
for (nGroups in 1:6)
  pie(rep(1, nGroups), a4palette(nGroups))
par(op)

addQuantilesColors  Compute quantiles for plotGeneDE function

Description

Compute quantiles on mean expression level for plotGeneDE function. Colors of bars in the plot could then be allocated using buckets defined by those quantiles.

Usage

addQuantilesColors(e, ngroups = 3)

Arguments

e  ExpressionSet object to use for computation
ngroups  Number of groups to be created

Details

Number of computed quantiles is equal to (ngroups - 1).

Value

The ExpressionSet object e is returned, with a new column called colorsQuantilesVector in its slot featureData

Author(s)

Eric Lecoutre

See Also

plotLogRatio

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALLQ <- addQuantilesColors(ALL)
  fData(ALLQ)
}
boxPlot

Create a boxplot for a given gene.

Description

Create a boxplot for a given gene. The boxplot displays the expression values (y-axis) by groups (x-axis). The raw data are superimposed as dots, jittered for readability of the plot. Optionally, the dots can be colored by another variable.

Usage

boxPlot(probesetId = NULL, geneSymbol = NULL, object, groups, main = NULL, colvec = NULL, colgroups = NULL, probe2gene = TRUE, addLegend = TRUE, legendPos = "topleft", ...)

Arguments

- **probesetId**: The probeset ID. These should be stored in the `featureNames` of the `expressionSet` object.
- **geneSymbol**: The gene symbol. These should be stored in the column `Gene Symbol` in the `featureData` of the `expressionSet` object.
- **object**: ExpressionSet object for the experiment.
- **groups**: String containing the name of the grouping variable. This should be a name of a column in the `pData` of the `expressionSet` object.
- **main**: Main title on top of the graph.
- **colvec**: Vector of colors to be used for the groups. If not specified, the default colors of `a4palette` are used.
- **colgroups**: String containing the name of the variable to color the superimposed dots. This should be a name of a column in the `pData` of the `expressionSet` object.
- **probe2gene**: Boolean indicating whether the probeset should be translated to a gene symbol (used for the default title of the plot).
- **addLegend**: Boolean indicating whether a legend for the colors of the dots should be added.
- **legendPos**: Specify where the legend should be placed. Typically either `topright`, `bottomright`, `topleft` (the default) or `bottomleft`.
- **...**: Possibility to add extra plot options. See `par`.

Author(s)

Willem Talloen

See Also

`plot1gene`
combineTwoExpressionSet

Combine two ExpressionSet objects

Examples

# simulated data set
esSim <- simulateData()
boxPlot(probesetId = 'Gene.1', object = esSim, groups = 'type', addLegend = FALSE)

# ALL data set
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  boxPlot(geneSymbol = 'HLA-DPB1', object = ALL, boxwex = 0.3,
     groups = 'BTtype', colgroups = 'BT', legendPos='topright')
}

combienTwoExpressionSet

Description

Merge two ExpressionSet objects, checking their attributes.

Usage

combineTwoExpressionSet(x, y)

Arguments

x An object of class ExpressionSet

y An object of class ExpressionSet

Details

exprs and pData are merged. Other data (such as MIAME or annotation) are those of x.

Value

An object of class ExpressionSet

Author(s)

Eric Lecoutre

See Also

ExpressionSet
### Examples

```r
## Not run:
# prepare and combine two ExpressionSet
data(data.H2009); data(phenodata.H2009)
data(data.SKOV3); data(phenodata.SKOV3)
eH2009 <- prepareExpressionSet(exprs = data.H2009, phenodata = phenodata.H2009, changeColumnsNames = TRUE)
eSKOV3 <- prepareExpressionSet(exprs = data.SKOV3, phenodata = phenodata.SKOV3, changeColumnsNames = TRUE)
newE <- combineTwoExpressionSet(eH2009, eSKOV3)
## End(Not run)
```

---

### computeLogRatio

#### Summary statistics for gene expression

#### Description

Compute summary statistics per gene of expression data in a `ExpressionSet` object.

#### Usage

```r
computeLogRatio(e, reference, within = NULL, across = NULL, nReplicatesVar = 3, ...)
```

#### Arguments

- **e**: An object of class `ExpressionSet`
- **reference**: A list with two items: `var` and `level` - See details
- **within**: Character vector - names of `pData` columns - See details
- **across**: Character vector - names of `pData` columns - See details
- **nReplicatesVar**: Integer - Minimum number of replicates to compute variances
- **...**

#### Details

Summary statistics (mean, variances and difference to reference or control) will be computed on the `exprs` slot of the `ExpressionSet` object. The parameters of the computation are specified by the parameters 'reference', 'within' and 'across'.

The design of the computations is such that the differences and pooled variances are calculated against the sample(s) that was(were) chosen as reference. The reference is specified by the level of a certain variable in the `pData` slot (e.g.: column 'control' and level 'WT' of the `pData` slot or a boolean ('ref') variable with 0 or 1) – the list object of `var` and `level` together determine the reference group.

All groups determined by combining the `reference$var` and across variables will be compared to the reference group. Two different approaches to obtain necessary computations:

- Prepare a boolean variable that reflects only the reference group and specify all groupings in the across arguments. E.g.: `reference=list(var = 'boolean', level = 1),` across = c('compound',...)
```
createExpressionSet

- Add an extra column to the phenoData slot that contains all combinations, with a specific one for the reference group; for example, `pData(e)["refvar"] <- paste(pData(e)["compound"], pData(e)["dose"], sep=".")` so as to use `reference = list(var = 'refvar', level = 'comp1.dose1')` as argument for reference.

Sometimes computations need to be conducted within groups, and are thus nested. For example, when comparing treatment values of different cell lines, each will have gene expression values for its own reference. The parameter 'within' allows to define such subgroups, for which computations will be done separately and combined afterwards. Both parameters 'within' and 'across' can be a vector of column names, whose unique combinations will be used for groupings.

**Value**

Returns an object of class ExpressionSet with pData inherited from the submitted ExpressionSet object, supplemented by the computed statistics in the 'exprs' slot and info thereof in the 'phenoData' slot.

**Author(s)**

Eric Lecoutre

**See Also**

plotLogRatio

**Examples**

```r
if (require(ALL)){
data(ALL, package = "ALL")
ALL <- addGeneInfo(ALL)
ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
ALL2 <- ALL[,ALL$BT != 'T1'] # omit subtype T1 as it only contains one sample
ALL2$BTtype <- as.factor(substr(ALL2$BT,0,1)) # create a vector with only T and B

# Test for differential expression between B and T cells
tTestResult <- tTest(ALL, "BTtype", probe2gene = FALSE)
topGenes <- rownames(tTestResult)[1:20]

# plot the log ratios versus subtype B of the top genes
LogRatioALL <- computeLogRatio(ALL2, reference=list(var='BT', level='B'))
a <- plotLogRatio(e=LogRatioALL[topGenes,],openFile=FALSE, tooltipvalues=FALSE, device='X11', colorsColumnsBy=c('BTtype'), main = 'Top 20 genes most differentially between T- and B-cells', orderBy = list(rows = "hclust"), probe2gene = TRUE)
}
```

---

createExpressionSet

*combine gene expression and phenotype data onto a ExpressionSet object*
createExpressionSet

Description

Basically a wrapper for new('ExpressionSet', ...), this function gathers gene expression and phenotype data, after having checked their compatibility.

Usage

createExpressionSet(exprs = new("matrix"), phenoData = new("AnnotatedDataFrame"), varMetadata = NULL, dimLabels = c("rowNames", "colNames"), featureData = NULL, experimentData = new("MIAME"), annotation = character(0), changeColumnsNames = TRUE, ...)

Arguments

exprs    gene expression matrix
phenoData phenotype data associated with exprs columns, as a matrix or data.frame
varMetadata optional metadata on phenotype data
dimLabels see 'ExpressionSet'
featureData see 'ExpressionSet'
experimentData see 'ExpressionSet'
annotation see 'ExpressionSet'
changeColumnsNames Change exprs columns names – see details
... ...

Details

If changeColumnsNames is TRUE, then the procedure is the following: first one checks if phenoData contains a column named 'colNames'. If so, content will be used to rename exprs columns. On the other case, one uses combinations of phenoData columns to create new names. In any case, old columns names are stored within a column named 'oldcolnames' in the pData.

Value

An object of class ExpressionSet

Author(s)

Eric Lecoutre

See Also

ExpressionSet

Examples

# simulate expression data of 10 features (genes) measured in 4 samples
x <- matrix(rnorm(40), ncol = 4)
colnames(x) <- paste("sample", 1:4, sep = ".")
rownames(x) <- paste("feature", 1:10, sep = ".")

# simulate a phenodata with two variables
ToBePheno <- data.frame(Gender = rep(c('Male', 'Female'), 2),
Treatment = rep(c('Trt', 'Control'), each=2))
rownames(ToBePheno) <- paste("sample", 1:4, sep = ".")

eset <- createExpressionSet(exprs = x, phenoData = ToBePheno)
ExpressionSetWithComputation-class

Class "ExpressionSetWithComputation"

Description

This class adds statistical information to the exprs of the ExpressionSet as well as descriptive information to the pData of the ExpressionSet.

Objects from the Class

Objects can be created by calls of the form new("ExpressionSetWithComputation", assayData, phenoData, featureData, experimentData, annotation, exprs, ...).

Slots

assayData: Object of class "AssayData"
phenoData: Object of class "AnnotatedDataFrame"
featureData: Object of class "AnnotatedDataFrame"
experimentData: Object of class "MIAME"
annotation: Object of class "character"
__classVersion__: Object of class "Versions"

Extends


Methods

No methods defined with class "ExpressionSetWithComputation" in the signature.

Author(s)

Tobias Verbeke

See Also

ExpressionSet, computeLogRatio
filterVarInt  
*Filter Features On Intensity and Variance*

**Description**

Function to filter on intensity and variance as typically used in gene expression studies.

**Usage**

```r
filterVarInt(object, IntCutOff = log2(100), IntPropSamples = 0.25, VarCutOff = 0.5)
```

**Arguments**

- `object`: ExpressionSet object
- `IntCutOff`: cut-off value used for the intensity filter
- `IntPropSamples`: proportion of samples used by the intensity filter; by default `IntPropSamples` is set to 0.25
- `VarCutOff`: cut-off value used for the variance filter

**Details**

The intensity filter implies that (by default) the intensity levels must be greater than `log2(100)` in at least 25 percent of the samples.

The variance filter requires that the features have an interquartile range (IQR) greater than 0.5. Note that the IQR is quite insensitive to outliers such that genes with outlying expression values in a few samples are excluded as long as their overall variation is small.

**Value**

Object of class ExpressionSet containing only the features that pass the variance and intensity filter.

**Author(s)**

Willem Talloen

**References**


**See Also**

`pOverA`, `filterfun`
**Examples**

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  fALL <- filterVarInt(ALL)
  fALL
}
```

**heatmap.expressionSet**  
*Image plot of an expressionSet*

**Description**

Grid version of heatmap function adapted to expressionSet objects with some specific requirements such as the possibility to display subgroups, define colors, adapt text graphical parameters (sizes...). The function also suggests a size appropriate for a device to generate a complete plot with all elements.

**Usage**

```r
heatmap.expressionSet(eset, col.groups = pData(phenoData(eset))[, "subGroup"], col.orderBy = order(data(phenoData(eset))[, "subGroup"])
  hclust(d, method = "ward")
), values.min = 0, values.max = 16, title.gpar = gpar(cex = 1.4), title.main = "This is the title possibly being very long and not suitable for a figure..."

Arguments

- **eset**: expressionSet object
- **col.groups**: Vector specifying sub-groups for individual. Sub-groups are treated separately and can thus on plot have different colors.
- **col.orderBy**: Vector specifying ordering for individual. In case there are sub-groups, individual must first be ordered by sub-groups, but an additional variable gives a way to sort individual within sub-groups.
- **col.groups.sep.width**: Object of class unit (grid package). Width used to visually separate sub-groups of individuals. This can be unit(0,"points") for example for no separation.
- **col.labels**: Character vector for columns labels (individuals), by default taken from phenoData.
- **col.labels.sep.width**: Object of class unit (grid package). Space between image matrix zone and columns labels.
- **col.labels.gpar**: Object of class gpar (grid package). Parameters to be used for labels (cex,...).
- **col.labels.max.nchar**: Integer. Number of maximum characters to be used for labels truncation.
- **colors.pergroup**: Boolean. If TRUE, separate colors are used to color image matrix. Colors defined for groups are used.
- **colors.groups**: Vector. Colors to be used for each group of individual. If NULL (default), colors are taken from column "sampleColor" of expressionSet phenodata.
colors.groups.min
- Character vector of length 1 corresponding to a valid color. If colors.groups are provided, a shading is done between color.group and this color (default: white).

colors.max
- Character vector of length 1 corresponding to a valid color. See colors details.

colors.min
- Character vector of length 1 corresponding to a valid color. See colors details.

colors.nbreaks
- Integer. Number of cutpoints used to split the color palette/shading.

colors.palette
- Character vector of valid color names.

cell.gpar
- Object of class gpar (grid package). Parameters used to format cells, for example to add border (gpar(lty=1)).

row.groups.sep.height
- Object of class unit (grid package). Height between rows sub-groups.

row.labels.sep.height
- Object of class unit (grid package). Height between image plot zone and rows labels.

row.col.groups.display
- Boolean. Display or not colored band for subgroups of individuals.

row.col.groups.display.height
- Object of class unit (grid package). If row.col.groups.display is TRUE then height used for the displayed band.

row.labels.gpar
- Object of class gpar (grid package). Parameters to be used for labels (cex,...).

row.labels.max.nchar
- Integer. Number of maximum characters to be used for labels truncation.

row.labels
- Character vector or list. If vector, direct labels to be used. If list, elements of the list will be taken from featureData and collapsed using row.labels.sep.

row.labels.sep
- In case labels are taken from featureData (list for row.labels), separator used to paste the provided columns.

row.groups
- Boolean specifying whether rows are split into sub-groups.

row.order
- Either a vector of indices to be used to reorder features (rows) or "none" or "hclust" to use clustering.

row.groups.hclust
- Boolean. If row.order equals "hclust", one can ask to split features into sub-groups based on a cut of the clustering dendogram.

row.groups.hclust.n
- Integer. If row.order equals "hclust" and row.groups.hclust is TRUE, number of sub-groups.

distfun
- Function. For row.order equals "hclust", metric function.

hclustfun
- Function. For row.order equals "hclust", clustering function.

values.min
- Minimum value for the data range. Values that are inferior are assigned to that value. That ensures a maximal cutpoint for the coloring scale.

values.max
- Maximum value for the data range. Values that are superior are assigned to that value. That ensures a maximal cutpoint for the coloring scale.

title.gpar
- Object of class gpar (grid package). Parameters to be used for the main title (cex,...).

title.main
- Character vector. Main title to be displayed.

title.just
- Title justification, one of "center","left","right" (first letter of the word can also be used).
heatmap.expressionSet

**Value**

The function suggests a size (width, height) for the graphic returned as a vector. A typical usage will be to call the function a first time to get those values and call it again with an output device.

**Colors**

There are several ways to specify colors used for the image zone. The usual way is to have a shading from colors.groups.min to a color per group (typically the same). By default, a shading is indeed proposed between white (for colors.groups.min) and a same color shared by groups (red for colors.groups.max). The number of possible colors in the shading is determined by colors.nbreaks. In case one asks for distinct colors for groups, only a single value for colors.groups.min is allowed. By default, subgroups colors are taken from phenoData ("sampleColor" column), consequence of colors.groups being NULL. Colors for groups are overided by providing a vector of valid colors for this colors.groups argument. An additional and flexible way to determine colors is to provide a complete palette of possible colors, as a character vector of valid colors (argument colors.palette). Note that in this case the argument colors.nbreaks has no effect as the number of possible values is the length of the palette.
Author(s)

Eric Lecoutre <eric.lecoutre@gmail.com>

Examples

```r
## Not run:
library(RColorBrewer)
library(dichromat)
library(Biobase)
library(grid)
pdf.directory=getwd()

load(file.path(getwd(),"expressionSetRma.Rda")) #expressionSetRma

eset <- expressionSetRma[100:130,pData(phenoData(expressionSetRma))[,"sample"]

exprs(eset)[1,5] <- 13.8
exprs(eset)[10,7] <- 0.5

eset2 <- expressionSetRma[200:250,] # ARG
eset3 <- expressionSetRma[1000:1009,pData(phenoData(expressionSetRma))[,"sample"]
eset4 <- expressionSetRma[100:230,pData(phenoData(expressionSetRma))[,"sample"]
eset5 <- expressionSetRma[1:400,] # ARG

# eset <- eset2
pdf(file.path(pdf.directory,"eset.pdf"))
size <- heatmap.expressionSet(eset,subtitle.main=" ")
dev.off()
pdf(file.path(pdf.directory,"eset.pdf"),width=size[1],height=size[2])
heatmap.expressionSet(eset,subtitle.main=" ")
dev.off()

pdf(file.path(pdf.directory,"eset2.pdf"))
size <- heatmap.expressionSet(eset2,
  colors.nbreaks = 20,
  colors.pergroup=TRUE,
  legend.range="data",
  row.col.groups.display=FALSE,
  cell.gpar=gpar(lwd=0.5),
  legend.height=unit(50,"points"),
  title.just=c("center","center"),
  title.maxlines=2,
  col.groups.sep.width=unit(0,"points"),
  row.labels=featureNames(eset),
  subtitle.main="This is subtitle",
  row.order="hclust",row.groups.hclust=FALSE,
  title.gpar=gpar(cex=2),
  subtitle.gpar=gpar(cex=1.5)
)
dev.off()
```
pdf(file.path(pdf.directory, "eset2.pdf"), width=size[1], height=size[2])
size <- heatmap.expressionSet(
eset2,
colors.nbreaks = 20,
colors.pergroup=TRUE,
legend.range="data",
row.col.groups.display=FALSE,
cell.gpar=gpar(lwd=0.5),
legend.height=unit(50,"points"),
title.just=c("center","center"),
title.maxlines=2,
col.groups.sep.width=unit(0,"points"),
row.labels=featureNames(eset),
subtitle.main="This is subtitle",
row.order="hclust",row.groups.hclust=FALSE,
title.gpar=gpar(cex=2),
subtitle.gpar=gpar(cex=1.5)
)
devoff()

pdf(file.path(pdf.directory, "eset3.pdf"))
size <- heatmap.expressionSet(
eset3,
row.labels.gpar=gpar(cex=0.4,col=c(rep("red",2),rep("black",49)) ), # col will correctly be a vector only if
col.labels.gpar=gpar(cex=0.6),
colors.nbreaks = 20,
colors.pergroup=TRUE,
legend.range="data",
row.col.groups.display=FALSE,
cell.gpar=gpar(lwd=0.5),
legend.height=unit(50,"points"),
title.just=c("center","center"),
title.maxlines=2,
col.groups.sep.width=unit(0,"points"),
row.labels=featureNames(eset),
subtitle.main="Essai subtitle",
row.order="hclust",row.groups.hclust=FALSE,
interactive=FALSE
)
devoff()

pdf(file.path(pdf.directory, "eset3.pdf"), width=size[1], height=size[2])
size <- heatmap.expressionSet(
eset3,
row.labels.gpar=gpar(cex=0.4,col=c(rep("red",2),rep("black",49)) ), # col will correctly be a vector only if
col.labels.gpar=gpar(cex=0.6),
colors.nbreaks = 20,
colors.pergroup=TRUE,
legend.range="data",
row.col.groups.display=FALSE,
cell.gpar=gpar(lwd=0.5),
legend.height=unit(50,"points"),
plot the distribution of P values
**histPvalue**

**Description**

This function displays the distribution of the p values using a histogram; the horizontal line represents a uniform distribution based on the p value distribution between 0.5 and 1. This represents the hypothetical p value distribution arising just by chance. This uniform distribution is used to estimate the proportion of differentially expressed genes.

**Usage**

```r
histPvalue(object, ...)  
## S4 method for signature 'MArrayLM'  
histPvalue(object, coef, ...)
```

**Arguments**

- `object` either a numeric vector of p-values, or an object of class `tTest`, `limma` or `MArrayLM`
- `coef` index of the coefficient for which the p values should be plotted; only applies to the `MArrayLM` method
- `...` further arguments passed to the method

**Value**

The histogram is displayed on the current device.

**Author(s)**

Willem Talloen and Tobias Verbeke

**References**


**See Also**

`hist`, `histpvalueplotter`

**Examples**

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  tTestResult <- tTest(ALL, "BTtype")
  histPvalue(tTestResult[,"p"], addLegend = TRUE)
  propDEgenesRes <- propDEgenes(tTestResult[,"p"])
}
```
histpvalueplotter  Workhorse function for the histPvalue function

Description

Workhorse function for the histPvalue function. This function displays the distribution of the p values using a histogram; the horizontal line represents a uniform distribution based on the p value distribution between 0.5 and 1. This represents the hypothetical p value distribution arising just by chance. This uniform distribution is used to estimate the proportion of differentially expressed genes.

Usage

histpvalueplotter(pValue, addLegend = FALSE, xlab = NULL, ylab = NULL, main = NULL, ...)

Arguments

- pValue: numeric vector of p values
- addLegend: logical; should a legend be added (TRUE) or not (FALSE; default)
- xlab: label for the x axis; defaults to NULL (no label)
- ylab: label for the y axis; defaults to NULL (no label)
- main: main title for the plot; if NULL (default) no main title is displayed
- ...: further arguments for the hist call; currently none are used

Author(s)

Willem Talloen and Tobias Verbeke

See Also

histPvalue, propdegenescalculation

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  tTestResult <- tTest(ALL, "BTtype")
  histPvalue(tTestResult[,"p"], addLegend = TRUE, xlab = "Adjusted P Value")
  histPvalue(tTestResult[,"p"], addLegend = TRUE, main = "Histogram of Adjusted P Values")
  propDEgenesRes <- propDEgenes(tTestResult[,"p"])
}

lassoReg

Multiple regression using the Lasso algorithm as implemented in the glmnet package

Description

Multiple regression using the Lasso algorithm as implemented in the glmnet package. This is a theoretically nice approach to see which combination of genes predict best a continuous response. Empirical evidence that this actually works with high-dimensional data is however scarce.

Usage

lassoReg(object, covariate)

Arguments

object object containing the expression measurements; currently the only method supported is one for ExpressionSet objects
covariate character string indicating the column containing the continuous covariate.

Value

object of class glmnet

Author(s)

Willem Talloen

References


See Also

lassoClass

Examples

if (require(ALL)){
data(ALL, package = "ALL")
ALL <- addGeneInfo(ALL)
ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

resultLasso <- lassoReg(object = ALL[1:100,], covariate = "age")
plot(resultLasso, label = TRUE,
main = "Lasso coefficients in relation to degree of penalization.
featResultLasso <- topTable(resultLasso, n = 15)
}
}
limmaTwoLevels  

*Wrapper function for the comparison of two groups using limma*

**Description**

Wrapper function for the comparison of two groups using limma

**Usage**

```r
limmaTwoLevels(object, group, probe2gene = TRUE)
```

**Arguments**

- `object`: object of class ExpressionSet
- `group`: string indicating the variable defining the two groups to be compared, i.e. the name of a factor with two levels
- `probe2gene`: logical; if `TRUE` Affymetrix probeset IDs are translated into gene symbols; if `FALSE` no such translation is done

**Value**

S4 object of class 'limma' with the following two components:

- `MArrayLM`: S4 object of class MArrayLM as returned by the limma function of the limma package
- `geneSymbols`: character vector of gene symbols; this slot is only populated if `probe2gene=TRUE` (and if the ExpressionSet object is appropriately annotated by `addGeneInfo` for gene symbols to be extracted)

**Note**

A 'topTable' method is defined for 'limma' objects.

**Author(s)**

Tobias Verbeke and Willem Talloen

---

logReg  

*Logistic regression for predicting the probability to belong to a certain class in binary classification problems.*

**Description**

Logistic regression for predicting the probability to belong to a certain class in binary classification problems.

**Usage**

```r
logReg(object, groups, probesetId = NULL, geneSymbol = NULL, main = NULL, probe2gene = TRUE, ...)
```
logReg

Arguments

- **object**
  ExpressionSet object for the experiment

- **groups**
  String containing the name of the grouping variable. This should be a the name of a column in the pData of the expressionSet object.

- **probesetId**
  The probeset ID. These should be stored in the featureNames of the expressionSet object.

- **geneSymbol**
  The gene symbol. These should be stored in the column `Gene Symbol` in the featureData of the expressionSet object.

- **main**
  Main title on top of the graph

- **probe2gene**
  Boolean indicating whether the probeset should be translated to a gene symbol (used for the default title of the plot)

... Possibility to add extra plot options. See par

Details

It will always estimate probability scores to belong to the second level of the factor variable. If a probability score to other level is preferred, then you need to change the order of the levels of the factor.

Value

A data.frame object with three columns and rownames

- **rownames**
  The `sampleNames` of the expressionSet object

- **x**
  The expression values for the specified gene for all samples

- **y**
  The labels of the samples

- **fit**
  The fitted probability score to belong to one of the two classes.

Author(s)

Willem Talloen

References

~put references to the literature/web site here ~

See Also

ROCcurve, probabilitiesPlot

Examples

```r
## Not run:
if (require(ALL)){
data(ALL, package = "ALL")
ALL <- addGeneInfo(ALL)
ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

logRegRes <- logReg(geneSymbol = "HLA-DPB1", object = ALL, groups = "BTtype")

# scoresplot
probabilitiesPlot(proportions = logRegRes$fit, classVar = logRegRes$y,
```
Data to Demonstrate nlcv and Co Functions

Description

Simulated data set used to demonstrate nlcv and accompanying plot functions to study classification problems.

Usage

data(nlcvTT)

Format

The object is of class "nlcv", an object as produced by the nlcv function.

Source

data simulated using nlcvTT <- nlcv(selBcrAb10rNeg, classVar = 'mol.biol', classdist = "unbalanced")

See Also

nlcv

Examples

## Not run:
data(nlcvTT)
if (require(nlcv)) # on R-Forge
  scoresPlot(nlcvTT, tech = 'svm', nfeat = 25)

## End(Not run)
plot1gene

Description

Create a profile plot for a given gene. A profile plot displays the expression values (y-axis) by samples (x-axis), sorted by group. This is a useful working graph as samples can be directly identified. For presentation purposes, a boxPlot can also be considered. with jittered for readability of the plot.

Usage

plot1gene(probesetId = NULL, geneSymbol = NULL, object, groups, main = NULL, colvec = NULL, colgroups = NULL, probe2gene = TRUE, sampleIDs = TRUE, addLegend = TRUE, legendPos = "topleft", cex = 1.5, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>probesetId</td>
<td>The probeset ID. These should be stored in the featureNames of the expressionSet object.</td>
</tr>
<tr>
<td>geneSymbol</td>
<td>The gene symbol. These should be stored in the column <code>Gene Symbol</code> in the featureData of the expressionSet object.</td>
</tr>
<tr>
<td>object</td>
<td>ExpressionSet object for the experiment</td>
</tr>
<tr>
<td>groups</td>
<td>String containing the name of the grouping variable. This should be a name of a column in the pData of the expressionSet object.</td>
</tr>
<tr>
<td>colgroups</td>
<td>String containing the name of the variable to color the superimposed dots. This should be a name of a column in the pData of the expressionSet object.</td>
</tr>
<tr>
<td>main</td>
<td>Main title on top of the graph</td>
</tr>
<tr>
<td>colvec</td>
<td>Vector of colors to be used for the groups. If not specified, the default colors of a4palette are used.</td>
</tr>
<tr>
<td>probe2gene</td>
<td>Boolean indicating whether the probeset should be translated to a gene symbol (used for the default title of the plot)</td>
</tr>
<tr>
<td>sampleIDs</td>
<td>A boolean or a string to determine the labels on the x-axis. Setting it to FALSE results in no labels (interesting when the labels are unreadable due to large sample sizes). Setting it to a string will put the values of that particular pData column as labels. The string should be a name of a column in the pData of the expressionSet object.”</td>
</tr>
<tr>
<td>addLegend</td>
<td>Boolean indicating whether a legend for the colors of the dots should be added.</td>
</tr>
<tr>
<td>legendPos</td>
<td>Specify where the legend should be placed. Typically either topright, bottomright, topleft (the default) or bottomleft</td>
</tr>
<tr>
<td>cex</td>
<td>character expansion used for the plot symbols; defaults to 1.5</td>
</tr>
<tr>
<td>...</td>
<td>Further arguments, e.g. to add extra plot options. See par</td>
</tr>
</tbody>
</table>

Value

If a geneSymbol is given that has more than one probeSet, the plots for only the first probeSet is displayed. A character vector of corresponding probeset IDs is returned invisibly, so that one can check the profiles of the other related probeset IDs with an extra plot1gene statement

If a probesetId is given, one single profile plot for the probeset is displayed.
plotComb2Samples

Plots the correlation in gene expression between two samples

**Description**

Plots the correlation in gene expression between two samples. Each dot represents a gene, and the dots have a density-dependent coloring. Genes with exceptional behavior can be highlighted by showing their gene symbol.

**Usage**

```r
plotComb2Samples(object, x, y, trsholdX = NULL, trsholdY = NULL, probe2gene = TRUE, ...)
```

**Arguments**

- `object` ExpressionSet object for the experiment
- `x` String containing the name of the first sample. This should be a the name of a column in the `exprs` data of the expressionSet object.
- `y` String containing the name of the second sample. See `x`
- `trsholdX` Vector of two values specifying the X-axis thresholds within which genes should be highlighted by their gene symbol.
- `trsholdY` Vector of two values specifying the Y-axis thresholds within which genes should be highlighted by their gene symbol.

**Examples**

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)

  # one variable (specified by groups)
  aa <- plot1gene(geneSymbol = 'HLA-DPB1', object = ALL, groups = "BT",
                  addLegend = TRUE, legendPos = 'topright')
  aa

  # two variables (specified by groups and colGroups)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
  plot1gene(probeset = "1636.g_at", object = ALL, groups = "BT",
            colgroups = 'mol.biol', legendPos='topright', sampleIDs = "BT")
}
```

plotComb2Samples

Plots the correlation in gene expression between two samples

**Author(s)**

S. Osselaer, W. Talloen, T. Verbeke

**References**

~put references to the literature/web site here~

**See Also**

`plotCombination2genes`, `boxPlot`
plotCombination2genes

plotCombination2genes

Plot a Combination of Two Genes

Description

Plot a Combination of Two Genes

Usage

plotCombination2genes(probesetId1 = NULL, probesetId2 = NULL, geneSymbol1 = NULL, geneSymbol2 = NULL, object, groups, addLegend = TRUE, legendPos = "topleft", probe2gene = TRUE, colvec = NULL, ...)
probe2gene should the probeset be translated to a gene symbol (used for the default title of the plot)
colvec a character vector of colors. If not specified it will be automatically generated by a4palette
... This allows to specify typical arguments in the plot function

Value

If a gene id is given, the plots for only the first probeset is displayed and a character vector of corresponding probeset IDs is returned invisibly.

It is a list containing

```
probeset1 Probeset ids measuring 'gene1'
probeset1 Probeset ids measuring 'gene1'
```

If a probeset id is given, one single profile plot for the probeset is displayed.

Author(s)

W. Talloen, T. Verbeke

See Also

plot1gene

Examples

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  aa <- plotCombination2genes(geneSymbol1 = "HLA-DPB1", geneSymbol2 = "CD3D",
                             object = ALL, groups = "BT",
                             addLegend = TRUE, legendPos = "topright")
  aa
}
```

```
plotCombMultSamples Plots the correlation in gene expression between more than 2 samples
```

Description

Plots a correlation matrix in gene expression between two samples. Each dot represents a gene, and the dots have a density-dependent coloring.

Usage

```
plotCombMultSamples(exprsMatrix, ...)
```
plotLogRatio

Arguments

exprsMatrix ExpressionSet object to plot. For larger datasets, this will typically be a subset of the data.

... Further arguments, e.g. to add extra plot options. See par

Author(s)

Willem Talloen

See Also

plotComb2Samples

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)

  plotCombMultSamples(exprs(ALL)[,c("84004", "11002", "01003")])
}

plotLogRatio

Plot a summary gene expression graph

Description

Plot ratios of expression values observed in a treatment versus those of a reference. First the ratios and variances are computed on the gene expression data.

Usage

plotLogRatio(e, reference, within = NULL, across = NULL, nReplicatesVar = 3,
  filename = "Rplots", device = "svg", orderBy = list(rows = "hclust", cols = NULL),
  colorsColumns = NULL, colorsColumnsBy = NULL, colorsColumnsByPalette = c("#1B9E77", 
  "#D95F02", 
  "#7570B3", 
  "#E7298A", 
  "#66A61E", 
  "#A6761D", 
  "#666666"), colorsMeanQuantilesPalette = c("orange", "red", "darkred"),
  colorsBarsMatrix = NULL, colorsGenesNames = c("black"), main = paste("log2 ratio ",
  "Var"), shortvarnames = NULL,
  longvarnames = NULL, gene.length = 50, gene.fontsize = 6, main.fontsize = 9,
  columnhead.fontsize = 8, mx = 1.5,
  exp.width = 1.8, exp.height = 0.2, log2l.show = TRUE, log4l.show = FALSE, quantiles.show = FALSE, quantiles.compute = c(0.9),
  error.show = TRUE, view.psid = FALSE,
  errorLabel = "Error bars show the pooled standard deviation",
  closeX11 = FALSE, openFile = FALSE, tooltipvalues = FALSE, probe2gene = TRUE, ...)

Arguments

e ExpressionSet object to use
reference List with components 'var' and 'level' – see computeLogRatio help
within Vector of characters for pData column – see computeLogRatio help
Across Vector of characters for pData column – see computeLogRatio help

nReplicatesVar Minimum number of replicates to compute variances and pooled standard errors – see computeLogRatio help

filename Name of the filename to use. No need to specify extension which will be added according to device.

device One of ‘pdf’, ’X11’, ’png’, ’svg’. For svg device, one X11 device is also opened.

orderBy See details

colorsColumns A vector of colors to be used for plotting columns; default value is NULL which ends up with red – see Colors section

colorsColumnsBy A vector of pData columns which combinations specify different colors to be used – see Colors section

colorsColumnsByPalette If colorsColumns is NULL, vector of colors to be used for coloring columns potentially splitted by colorsColumnsBy

colorsUseMeanQuantiles Boolean to indicate if the quantile groups computed on averages over all treatments should be used for coloring – see Colors section

colorsMeanQuantilesPalette if colorsUseMeanQuantiles is TRUE, these colors will be used for the different groups – see Colors section

colorsBarsMatrix Matrix of colors to be used for each individual bar; colors are provided for genes in data order and thus are possibly reordered according to orderBy – see Colors section

colorsGenesNames Vector of colors to be used for gene names; will be recycled if necessary; colors are provided for genes in data order and thus are possibly reordered according to orderBy

main Main title

shortvarnames Vector or pData column to be used to display in graph columns. If NULL, those names will be used from the coded names added to pData during computations (list of columns values pasted with a dot). Warning: shortvarnames must be defined in the order columns are present in the ExpressionSet object so that they will be reordered if one asks to order columns.

longvarnames pData column to be used in SVG tooltip title. If NULL, shortvarnames will be used. Same warning than shortvarnames about ordering.

gene.length Maximum number of characters that will be printed of the gene names

gene.fontsize Font size for the gene names, default = 6

main.fontsize Font size for the main, default = 9

columnhead.fontsize Font size for the column headers, default = 8

mx Expansion factor for the width of the bars that represent the expression ratios

exp.width Expansion factor for global graph width, and the space between the plotted columns

exp.height Expansion factor for global graph height, and the space between the plotted rows
plotLogRatio

log2l.show  A logical value. If 'TRUE', the line for log2 values on each column (when max(data) > 2) is drawn

log4l.show  A logical value. If 'TRUE', the line for log4 values on each column (when max(data) > 4) is drawn

quantiles.show  A logical value. If 'TRUE', a line is drawn for quantiles computed separately on each columns

quantiles.compute  A logical value. If 'TRUE', the vector quantiles will be computed and displayed provided that quantile.show is TRUE

error.show  A logical value. If 'TRUE', errors bars are displayed on the graph (only for those columns for which they are available)

view.psid  A logical value. If 'TRUE', the genes psid is displayed on the gene names

errorLabel  A character vector describing the error bars, printed at the bottom of the figure

closeX11  If device is SVG, do we close the required X11 device at the end?

openFile  A logical value. If 'TRUE', the produced output file is opened

tooltipvalues  If device is SVG, one can choose to display each bar separately, with data values as tooltips. Note however that each bar will be considered as a distinct object instead of a column, which will takes much more time to create the graph and produces a much bigger SVG file

probe2gene  Boolean indicating whether the probeset should be translated to a gene symbol (used for the default title of the plot)

...  ...

Value

The ExpressionSet object with the computated variables is returned.

Ordering

orderBy: A list with two components, rows and cols, each one possibly being NULL (no ordering on the specific dimension). Ordering on cols can be done according to (a) pData column(s) (for example: c(‘cellline’, ‘compound’, ‘dose’). Ordering on rows can be done using of the following values:

• NULL no reordering on rows
• numeric vector use the vector values to sort rows
• alphabet genes names alphabetice order
• effect try to assess global gene expression level by taking sum(abs(values)) on specified exprs columns
• hclust use the ordering returned by hclust invoked on specified exprs columns

Colors

The management of colors is very flexible but is a little bit tricky, as a variety of parameters are available to the user. Basically, combinations of arguments allow to set colors for columns headers (text), columns as a whole (different colors for the different columns) or for each of the individual horizontal bars. By default, everything is red. There are four main different arguments that can be used and that are applied in a consecutive order. Each one may override a previous argument value. Below is a list of arguments and their consecutive actions:
• colorsColumns The first way to assign colors is to provide a vector of colors that will be used for each column (headers and its horizontal bars). This vector is recycled so that providing one unique value will color all columns, whereas providing a vector of length 2 will alternate columns colors.

• colorsColumnsBy To be used when the experiment involves groupings for pData, for example dose, cellline or treatment. In order to see the effects of such variables, one can color columns using combinations of those. The argument is a vector of pData columns such as `c('cellline', 'dose')`. Unique combinations will be computed and a color will be assigned for each group of columns. The vector that is provided with the argument colorsColumnsByPalette is used to assign colors. If the argument colorsColumnsBy is not NULL then it overrides the previous argument colorsColumns.

• colorsUseMeanQuantiles A logical value. The default plotGeneDE displays for each gene the expression value difference between treatment and reference, but does not reveal any information about the expression levels in these conditions. Parameter colorsUseMeanQuantiles allows to color the horizontal bars according to expression level that is derived from quantiles computed on averages of the complete ExpressionSet object. As it involves the expression data of all probesets, computations must be done before subsetting the ExpressionSet object and the plotGeneDEting. The function addQuantilesColors computes quantiles and corresponding mean expression level intervals. If colorsUseMeanQuantiles = 'TRUE', previous coloring parameters are overridden. The parameter colorsMeanQuantilesPalette is used to assign colors for average-quantiles-groups. Note that columns headers are still given by previous arguments.

• colorsBarsMatrix The most flexible way to assign colors as the matrix will be used to color each bar of the plot individually. A check is done to ensure that the number of rows and columns are not less than the number of probesets and columns. If not NULL, this parameter overrides the previous ones.

Author(s)
Hinrich Goehlmann and Eric Lecoutre

See Also
computeLogRatio, addQuantilesColors

Examples

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
  ALL2 <- ALL[,ALL$BT != 'T1']  # omit subtype T1 as it only contains one sample
  ALL2$BTtype <- as.factor(substr(ALL2$BT,0,1))  # create a vector with only T and B

  # Test for differential expression between B and T cells
  tTestResult <- tTest(ALL, "BTtype", probe2gene = FALSE)
  topGenes <- rownames(tTestResult)[1:20]

  # plot the log ratios versus subtype B of the top genes
  LogRatioALL <- computeLogRatio(ALL2, reference=list(var='BT', level='B'))
  a <- plotLogRatio(e=LogRatioALL[topGenes,],openFile=FALSE, tooltipvalues=FALSE, device='X11',
                   colorsColumnsBy=c('BTtype'), main = 'Top 20 genes most differentially between T- and B-cells',
                   orderBy = list(rows = "hclust"), probe2gene = TRUE)
}
```
## Not run:
```
a <- plotLogRatio(e=LogRatioALL[topGenes,],openFile=TRUE, tooltipvalues=FALSE, device="pdf", colorsColumnsBy=c("BTtype"), main = "Top 20 genes most differentially between T- and B-cells", orderBy = list(rows = "hclust", cols = "sex"), probe2gene = TRUE)
```
## End(Not run)

probabilitiesPlot

Function to plot the probabilities to belong to a certain class in binary classification problems.

### Description

Function to plot the probabilities to belong to a certain class in binary classification problems. These probabilities are often calculated using a logistic regression model. The class membership of the samples is displayed using a colored strip (with legend below the plot).

### Usage

```
probabilitiesPlot(proportions, classVar, sampleNames, plot = TRUE, barPlot = FALSE, layout = TRUE, main = NULL, sub = NULL, ...)
```

### Arguments

- **proportions**: A vector containing the calculated probabilities to belong to a certain class in binary classification problems. These probabilities are often calculated using a logistic regression model.
- **classVar**: A vector containing the class where the sample belongs to
- **sampleNames**: A vector with the names of the samples
- **plot**: logical. If FALSE, nothing is plotted.
- **barPlot**: Should a barplot be drawn (TRUE) or a scatterplot like MCREstimate-type scores plot (the default, FALSE).
- **layout**: boolean indicating whether mcrPlot should prespecify a layout for a single plot (default, FALSE) or whether the user takes care of the layout (FALSE)
- **main**: Main title for the scores plot; if not supplied, 'Scores Plot' is used as a default
- **sub**: Subtitle for the scores plot; if not supplied, the classification technique and the chosen number of features are displayed
- **...**: Additional graphical parameters to pass to the plot function

### Author(s)

Willem Talloen and Tobias Verbeke

### See Also

- `logReg`
Examples

```r
## Not run:
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  logRegRes <- logReg(geneSymbol = "HLA-DPB1", object = ALL, groups = "BTtype")
  # scoresplot
  probabilitiesPlot(proportions = logRegRes$fit, classVar = logRegRes$y, sampleNames = rownames(logRegRes), main = 'Probability of being a T-cell type ALL')
  # barplot
  probabilitiesPlot(proportions = logRegRes$fit, classVar = logRegRes$y, barPlot=TRUE, sampleNames = rownames(logRegRes), main = 'Probability of being a T-cell type ALL')
}
## End(Not run)
```

---

**probe2gene**

*Translate Affymetrix probeset IDs into gene symbols*

**Description**

Translate Affymetrix probeset IDs into gene symbols

**Usage**

```r
probe2gene(probesetIds, chipPkg)
```

**Arguments**

- `probesetIds`: Affymetrix probeset IDs
- `chipPkg`: string indicating the annotation package for the chip

**Value**

Vector containing the respective gene symbols

**Author(s)**

Tobias Verbeke

**See Also**

`spectralMap`, `lassoClass`, ...
**profilesPlot**

Plot expression profiles of multiple genes or probesets

**Description**

Plot expression profiles of multiple genes or probesets. Each line depicts a gene, and the color legend can be used to identify the gene.

**Usage**

```r
profilesPlot(object, probesetIds, sampleIDs = TRUE, addLegend = TRUE, legendPos = "topleft", colvec = NULL, orderGroups = NULL, ...)```

**Arguments**

- **object**
  - ExpressionSet object for the experiment

- **probesetIds**
  - The probeset ID. These should be stored in the `featureNames` of the `expressionSet` object.

- **colvec**
  - Vector of colors to be used for the groups. If not specified, the default colors of `a4palette` are used.

- **sampleIDs**
  - A boolean or a string to determine the labels on the x-axis. Setting it to FALSE results in no labels (interesting when the labels are unreadable due to large sample sizes). Setting it to a string will put the values of that particular `pData` column as labels. The string should be a name of a column in the `pData` of the `expressionSet` object.

- **addLegend**
  - Boolean indicating whether a legend for the colors of the dots should be added.

- **legendPos**
  - Specify where the legend should be placed. Typically either `topright`, `bottomright`, `topleft` (the default) or `bottomleft`

- **orderGroups**
  - String containing the name of the grouping variable to order the samples in the x-axis accordingly. This should be a name of a column in the `pData` of the `expressionSet` object.

- **...**
  - Possibility to add extra plot options. See `par`

**Author(s)**

W. Talloen

**See Also**

- `plot1gene`, `boxPlot`
Examples

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  myGeneSymbol <- c("LCK") # a gene
  probesetPos <- which(myGeneSymbol == featureData(ALL)$SYMBOL)
  myProbesetIds <- featureNames(ALL)[probesetPos]

  profilesPlot(object = ALL, probesetIds = myProbesetIds,
               orderGroups = "BT", sampleIDs = "BT")
}
```

---

**propDEgenes**  
*Generic function to compute the proportion of differentially expressed genes that are present*

**Description**

Generic function to compute the proportion of differentially expressed genes that are present. Methods are available for objects of class `"tTest"`.

**Usage**

```r
propDEgenes(object, ...)
```

**Arguments**

- `object`  
  object of class

- `...`  
  further arguments for the method (currently none implemented)

**Value**

numeric of length one giving the proportion of differentially expressed genes

**Author(s)**

Willem Talloen and Tobias Verbeke

**See Also**

`propDEgenes-methods`
propDEgenes-methods

Methods for propDEgenes

Description

Methods for propDEgenes

Arguments

object object of class
... further arguments for the method (currently none implemented)

Value

numeric of length one giving the proportion of differentially expressed genes

Methods

limma

propDEgenes method for a limma object
numeric

object = "limma", object = "numeric" propDEgenes method for a numeric vector, i.e. a vector of P

Values

Author(s)

Willem Talloen and Tobias Verbeke

See Also

propDEgenes-methods

propdegenescalculation

Estimation of proportion of differentially expressed genes

Description

Estimation of proportion of differentially expressed genes. This estimation is based on a histogram of the p-values. More specifically, based on the horizontal line representing a uniform distribution based on the p value distribution between 0.5 and 1. This represents the hypothetical p value distribution arising just by chance. All genes with small p-values above this line reflect the expected number of differentially expressed genes not by chance.

Usage

propdegenescalculation(pValue)
replicates

Arguments

pValue a vector of p-values

Author(s)

Willem Talloen and Tobias Verbeke

See Also

histPvalue

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  tTestResult <- tTest(ALL, "BTtype")
  histPvalue(tTestResult[,"p"], addLegend = TRUE)
  propDEgenesRes <- propDEgenes(tTestResult[,"p"])
}

replicates computes replicates across a vector

Description

Given a vector, returns the replicates in order

Usage

replicates(x)

Arguments

x character or numeric vector

Value

numeric vector

Author(s)

Henrique Dallazuanna

References

R-help mailing list

See Also

rlie
spectralMap

Examples

```r
x <- c('a','b','a','a','b','a','c','c','c')
data.frame(val=x,rep=replicates(x))
```

spectralMap Draw a Spectral Map

Description

Generic function to draw a spectral map.

Usage

```r
spectralMap(object, groups, ...)
```

Arguments

- `object`: object of class ExpressionSet
- `groups`: string indicating the name of the column in the phenoData that defines the groups
- `...`: further arguments to be passed to the methods

Value

Object of class `plot.mpm`, i.e. the S3 output object of the `plot.mpm` function of the `mpm` package

Note

Coloring of groups on the spectralMap uses the `a4` palette as produced by `a4palette`

Author(s)

Tobias Verbeke

References


See Also

`spectralMap-methods, plot.mpm`
Examples

```r
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)

  spectralMap(object = ALL, groups = "BT", legendPos = 'bottomright')

  spectralMap(object = ALL, groups = "BT",
              plot.mpm.args = list(label.tol = 10, rot = c(-1, 1), sub = "", lab.size = 0.65,
                              dim = c(1,2), sampleNames = FALSE, zoom = c(1,5), col.size = 2,
                              do.smoothScatter = TRUE))

  spectralMap(object = ALL, groups = "BT",
              plot.mpm.args = list(label.tol = 10, rot = c(-1, 1), sub = "", lab.size = 0.65,
                              dim = c(1,2), sampleNames = as.character(pData(ALL)$BT),
                              zoom = c(1,5), col.size = 2, do.smoothScatter = TRUE))
}
```

spectralMap-methods

Methods for Function spectralMap

Description

Methods for spectralMap

Arguments

- `makeLognormal` boolean indicating whether one wants to exponentiate the data to make them lognormally shaped (TRUE; the default) or not (FALSE)
- `mpm.args` list of arguments that can be passed to the mpm function
- `plot.mpm.args` list of arguments that can be passed to the plot.mpm function that actually draws the plot
- `probe2gene` boolean indicating whether one wants to display the gene symbols for the labeled points (TRUE) or not (FALSE; the default)
- `addLegend` Boolean indicating whether a legend for the colors of the dots should be added.
- `legendPos` Specify where the legend should be placed. Typically either `topleft`, `bottomright`, `topleft` (the default) or `bottomleft`

Methods

ExpressionSet, character

wrapper around plot.mpm from the mpm package
Methods for topTable. topTable extracts the top n most important features for a given classification or regression procedure.

**Arguments**

- **fit**
  - object resulting from a classification or regression procedure
- **n**
  - number of features that one wants to extract from a table that ranks all features according to their importance in the classification or regression model; defaults to 10 for limma objects

**Methods**

- **glmnet**
  - glmnet objects are produced by lassoClass or lassoReg
- **limma**
  - limma objects are produced by limma2Groups
- **MarrayLM**
  - MarrayLM objects are produced by lmFit of the limma package
- **pamClass**
  - pamClass objects are produced by pamClass
- **rfClass**
  - rfClass objects are produced by rfClass
- **tTest**
  - tTest objects are produced by tTest
- **fTest**
  - fTest objects are produced by fTest

---

**tTest**

*Use t Test to Compare Two Groups*

**Description**

Use a (modified) t test to compare two groups

**Usage**

tTest(object, groups, probe2gene = TRUE)
volcanoPlot

Arguments

object ExpressionSet object
groups string indicating the name of the variable of the phenoData containing the group information
probe2gene logical; if TRUE Affymetrix probeset IDs are translated into gene symbols; if FALSE no such translation is conducted

Details

For multiple testing the mt.rawp2adjp function of package multtest is used.

Value

Object of class "tTest", a data frame with the following columns

gsymbol Gene Symbol
p TODO
logRatio TODO
pBH TODO
tStat TODO

Author(s)

Willem Talloen, Tobias Verbeke

See Also

rowttests

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT, 0, 1))

  tTestRes <- tTest(object = ALL, groups = "BTtype", probe2gene = TRUE)
  volcanoPlot(tTestRes)
}

---

volcanoPlot Draw a Volcano Plot

Description

Generic function to draw a volcano plot. A volcano plot is a graph that allows to simultaneously assess the P values (statistical significance) and log ratios (biological difference) of differential expression for the given genes.
volcanoPlot

Usage

volcanoPlot(x, y, pointLabels, ...)

Arguments

x either an object of class 'tTest', of class 'limma' or a numeric vector of log ratios, i.e. the log of the fold change values; the names of the logRatio vector will be used to display the names of the most interesting genes

y should not be given if an object of class 'tTest' or 'limma' is passed as argument 'x'; if 'x' is a numeric vector of log ratios, 'y' should be given and should be a numeric vector of P-values indicating the statistical significance

pointLabels Labels for points on the volcano plot that are interesting taking into account both the x and y dimensions; typically this is a vector of gene symbols; most methods can access the gene symbols directly from the object passed as 'x' argument; the argument allows for custom labels if needed

... further arguments to specific methods

Value

The volcano plot is drawn to the current device.

Author(s)

Tobias Verbeke, based on code by Willem Talloen

References


See Also

See volcanoPlotter

Examples

if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  tTestRes <- tTest(object = ALL, groups = "BTtype", probe2gene = TRUE)
  volcanoPlot(tTestRes)
}
Draw a Volcano Plot

Description
This function draws a volcano plot, a graph that allows to simultaneously assess the statistical and biological significance of differential expression for the given genes.

Arguments
- **x**: either an object of class 'tTest', or a numeric vector of log ratios, i.e. the log of the fold change values; the names of the logRatio vector will be used to display the names of the most interesting genes
- **y**: should not be given if an object of class 'tTest' is passed as argument 'x'; if 'x' is a numeric vector of log ratios, 'y' should be given and should be a numeric vector of P-values indicating the statistical significance
- **pointLabels**: Labels for points on the volcano plot that are interesting taking into account both the x and y dimensions; typically this is a vector of gene symbols; most methods can access the gene symbols directly from the object passed as 'x' argument; the argument allows for custom labels if needed
- **topPValues**: top n points that will be included in the points to label based on their low P Values
- **topLogRatios**: top n points that will be included in the points to label based on their high absolute values of the log ratio
- **smoothScatter**: use color saturation to indicate dots that are in densely populated regions of the graph; defaults to TRUE
- **xlab**: label for the x axis (string)
- **ylab**: label for the y axis (string)
- **main**: main title for the graph (string)
- **sub**: subtitle for the graph (string)

Details
The set of genes for which labels are displayed is the union of the set of genes that have lowest P-values (topPValues) and the set of genes that display the highest absolute values for the log ratios (topLogRatios).

Value
The volcano plot is drawn to the current device.

Methods
- tTest,missing,missing
  volcanoPlot for an object resulting from tTest
- tTest,missing,character
  x = "tTest", y = "missing", pointLabels = "missing", main = "tTest", ylab = "missing", pointLabels = "character"
  volcanoPlot for an object resulting from tTest
- numeric,numeric,character
volcanoplotter

- \(x = \text{"numeric"}, \ y = \text{"numeric"}, \ pointLabels = \text{"character"}\) volcanoPlot for arbitrary numeric vectors containing log ratio values and p values respectively
- \(x = \text{"numeric"}, \ y = \text{"numeric"}, \ pointLabels = \text{"missing"}\) volcanoPlot for arbitrary numeric vectors containing log ratio values and p values respectively
- \(x = \text{"limma"}, \ y = \text{"missing"}, \ pointLabels = \text{"missing"}\) volcanoPlot for an object resulting from \(\text{limma2Groups}\)
- \(x = \text{"tTest"}, \ y = \text{"missing"}, \ pointLabels = \text{"missing"}\) volcanoPlot for an object resulting from \(\text{limma2Groups}\)

Author(s)

Tobias Verbeke, based on code by Willem Talloen

---

volcanoplotter  
**Workhorse function for the different volcanoPlot methods**

**Description**

Workhorse function for the different volcanoPlot methods. A volcano plot is a graph that allows to simultaneously assess the P values (statistical significance) and log ratios (biological difference) of differential expression for the given genes.

**Usage**

```r
volcanoplotter(logRatio, pValue, pointLabels, topPValues = 10, topLogRatios = 10, logTransformP = TRUE, smoothScatter = TRUE, xlab = NULL, ylab = NULL, main = NULL, sub = NULL, newpage = TRUE, additionalPointsToLabel = NULL, additionalLabelColor = "red")
```

**Arguments**

- `logRatio` numeric vector of log ratios
- `pValue` numeric vector of P values
- `pointLabels` Labels for points on the volcano plot that are interesting taking into account both the x and y dimensions; typically this is a vector of gene symbols; most methods can access the gene symbols directly from the object passed as ’x’ argument; the argument allows for custom labels if needed
- `topPValues` top n points that will be included in the points to label based on their low P Values
- `topLogRatios` top n points that will be included in the points to label based on their high absolute values of the log ratio
- `logTransformP` if \(\text{TRUE}\) (default) \(-\log(10)(pValue)\) is used for the plot instead of the raw P values
- `smoothScatter` use color saturation to indicate dots that are in densely populated regions of the graph; defaults to \(\text{TRUE}\)
- `xlab` label for the x axis (string)
- `ylab` label for the y axis (string)
volcanoplotter

main | main title for the graph (string)
sub | subtitle for the graph (string)
newpage | should the graph be drawn to a new grid page? Defaults to TRUE. This argument is useful for including several volcano plots in one layout.
additionalPointsToLabel | Entrez IDs of genes of interest, that will be highlighted on the plot; the color of highlighting is determined by the `additionalLabelColor` argument.
additionalLabelColor | Color used to highlight the `additionalPointsToLabel`; defaults to "red".

Value

a volcanoplot is drawn to the current device

Author(s)

Tobias Verbeke

See Also

volcanoPlot-methods
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