Package ‘EMA’

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Title Easy Microarray Data Analysis
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Description We propose both a clear analysis strategy and a selection of tools to investigate microarray gene expression data. The most usual and relevant existing R functions were discussed, validated and gathered in an easy-to-use R package (EMA) devoted to gene expression microarray analysis. These functions were improved for ease of use, enhanced visualisation and better interpretation of results.
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EMA-package

Description

Numerous analysis methods and tools have been developed to study microarray, many of them being implemented as free R and/or Bioconductor packages. This abundance of methods makes choosing the best approach difficult for newcomers and non-specialist users. Based on the experience of the biostatisticians of Institut Curie, we propose a clear analysis strategy combining a large variety of standard methodologies. The most usual and relevant R functions needed to perform these analyses were selected and gathered in the R package EMA (Easy Microarray data Analysis). EMA covers an entire analysis process including quality control, normalisation, exploratory analysis, supervised
and supervised classification, functional analysis andensored data exploration. The package can be used for both one or two colours gene expression micrarrays and for exon expression experiments.

Details

Package: EMA
Type: Package
Version: 1.3.1
Date: 2011-06-09
License: GPL
LazyLoad: yes

For details, see vignette.

Author(s)

References
EMA - A R package for Easy Microarray data Analysis

---

### as.colors

*Convert labels to colors*

#### Description
This function returns a object a colors values according to a palette function

#### Usage

```r
as.colors(x, col.na="#E6E6E6",palette="rainbow", ...)
```

#### Arguments

- `x` A object (vector or matrix) to convert in colors.
- `col.na` Colors to use for missing values.
- `palette` The palette function to use
- `...` Additional argument for the palette function. The ‘n’ parameters must exist in the palette function

#### Value
A vector or matrix of color label.
Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

Examples
```
lab1<-c(rep("a",5), rep("b",5))
lab2<-c(rep("c",5), rep("a",5))
as.colors(lab1)
as.colors(rbind(lab1, lab2))
as.colors(lab2, palette="heat.colors", alpha=0.8)
```

Description
Annot input IDs using the biomaRt package.

Usage
```
bioMartAnnot(data, inputTypeId, outputTypeId =c("entrezgene","hgnc_symbol", "ensembl_gene_id", "description", "chromosome_name", "start_position", "end_position", "band", "strand"), dataset= c("hsapiens_gene_ensembl"), database = "ensembl", sort.by = NULL, outfile = NA)
```

Arguments
- data: A data.frame with the input names as rownames or a vector of probesets
- inputTypeId: Input Ids type. see details
- outputTypeId: Output Ids type. if NULL the description of some genes names are returned. see details
- dataset: The dataset used for the annotation
- database: The database used for the annotation
- sort.by: optional. Allow to sort the output data.frame
- outfile: optional. Write an html file with the results

Details
This function is based on the biomaRt package. First, you have to define the database and the dataset you want to use for the annotation (default dataset=c("hsapiens_gene_ensembl"), database = "ensembl"). The input IDs type have to be defined as in the biomaRt package. The listFilters() functions of the biomaRt package lists the available input type. If the inputs are probe names, use the microarray name: affy_hg_u95a,affy_hg_u95av2,affy_hg_u133a_2,affy_hg_u133a, affy_hg_u133b,affy_hg_u133_plus_2, illumina_humanwg_6_v2, ... Use the biomaRt function 'listAttributes()', to select your output. By default, the function returns "description", "chromosome_name", "start_position", "end_position", "band", "strand", and "ensembl_gene_id".
clustering

Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also
useMart

Examples

```r
## Not run:
## load data
data(marty)

##Annotations example
bioMartAnnot(rownames(marty)[1:50], inputTypeId = "affy.hg.u133_plus_2",
outputTypeId = c("entrezgene", "hgnc_symbol"),
dataset=c("hsapiens_gene_ensembl"),database = "ensembl")

## End(Not run)
```

clustering     Agglomerative hierarchical clustering

Description
Computes agglomerative hierarchical clustering of the dataset.

Usage
```
clustering(data, metric="euclidean", method="ward", nb)
```

Arguments

- **data**: Expression matrix, genes on rows and samples on columns
- **metric**: Character string specifying the metric to be used for calculating dissimilarities between the columns of the matrix. This must be one of 'euclidean', 'manhattan', 'pearson', 'pearsonabs', 'spearman', 'spearmanabs', 'jaccard', 'dice'
- **method**: Character string defining the clustering method. This must be one of 'average', 'single', 'complete', 'ward'
- **nb**: The number of classes for kmeans and PAM clustering (kcentroids)
Details

Available metrics are (written for two vectors x and y):

- **euclidean**: Usual square distance between the two vectors.
- **manhattan**: Absolute distance between the two vectors.
- **pearson**: Pearson correlation distance. \((1 - r)/2\)
- **pearsonabs**: Absolute Pearson correlation distance. \(1 - |r|\)
- **spearman**: Spearman rank correlation distance. \((1 - r)/2\)
- **spearmanabs**: Absolute Spearman rank correlation distance. \(1 - |r|\)
- **jaccard**: Jaccard distance on 0-1 matrix
- **dice**: Dice distance on 0-1 matrix

Available agglomerative methods are:

- **average**: The distance between two clusters is the average of the dissimilarities between the points in one cluster and the points in the other cluster.
- **single**: We use the smallest dissimilarity between a point in the first cluster and a point in the second cluster (nearest neighbor method).
- **complete**: We use the largest dissimilarity between a point in the first cluster and a point in the second cluster.
- **ward**: Ward’s agglomerative method
- **weighted**: The weighted distance from the agnes package
- **diana**: Computes a divisive clustering
- **kcentroids**: Perform either kmeans clustering if the distance is euclidean or PAM clustering. The number of classes nb has to be done.

Value

An object of class ‘agnes’ representing the clustering. See ‘agnes.object’ for details.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cécile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

References


See Also

agnes.clust.dist
Example:
   data(marty)
   c <- clustering(marty, metric = "pearson", method = "ward")
   clustering.plot(c, title = "Hierarchical Clustering\nPearson\nWard")

---

**clustering.kmeans**

*Kmeans and hierarchical clustering*

**Description**

Kmeans clustering to summarize the genes information and hierarchical clustering on the kmeans’ groups.

**Usage**

```r
clustering.kmeans(data, N = 100, iter.max = 20,
title = "Kmeans - Hierarchical Clustering",
dist.s = "pearson", dist.g = "pearsonabs", method = "ward")
```

**Arguments**

- **data**: Expression matrix, genes on rows and samples on columns.
- **N**: The number of a priori clusters for the kmeans.
- **iter.max**: The maximum number of iterations allowed for the kmeans clustering.
- **title**: The plot title.
- **dist.s**: The distance used for the sample clustering.
- **dist.g**: The distance used for the genes clustering.
- **method**: The linkage used for both clusterings.

**Details**

The goal of this analysis is to first summarizes the genes information using the kmeans clustering. Then, a two-ways clustering is performed using the center of each kmean groups, and all the samples.

**Value**

A list with the kmeans object and the two hierarchical clusterings.

- **c.km**: An object of class 'kmeans'.
- **c.sample**: An object of class 'agnes'. The hierarchical clustering on samples.
- **c.kcenters**: An object of class 'agnes'. The hierarchical clustering on the kmeans centers.
Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton,
Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also
kmeans, agnes

Examples

data(marty)
# Example on 100 genes for 5 classes
clustering.kmeans(marty[1:100,], N=5)

declustering.plot Clustering plots for one or two ways representation

Description
Creates plots for a clustering analysis.

Usage

clustering.plot(tree, tree.sup, data, lab, lab.sup,
dendro=TRUE, dendro.sup=TRUE, title=", scale="row", heatcol,
names=TRUE, names.sup=TRUE, names.dist=TRUE,
trim.heatmap=1, palette="rainbow", legend=TRUE, legend.pos="topright", ...)

Arguments

tree an object of class ‘agnes’ representing the first clustering.
tree.sup optional - an object of class ‘agnes’ representing the second clustering.
data optional - expression data for the heatmap plot
lab optional - a matrix or data.frame of labels for ‘tree’ (by columns)
lab.sup optional - a matrix or data.frame of labels for ‘tree.sup’ (by columns)
dendro display dendrogram of tree object - The default is TRUE
dendro.sup display dendrogram of tree.sup object - The default is TRUE
title optional - title of the graphic
scale optional - character indicating if the values should be centered and scaled in
either the row direction (gene) or the column direction (sample), or none. The
default is ‘’row’’
heatcol colors for the heatmap generated by myPalette
names optional - if names=FALSE, the labels for ‘tree’ are not written - The default is TRUE
clustering.plot

names.sup  optional - if names.sup=FALSE, the labels for 'tree.sup' are not written - The default is TRUE
names.dist  Display the distance used for the Hierachical Clustering - The default is TRUE
trim.heatmap Percentile of the data to be trimmed. This helps to keep an informative color scale in the heatmap
palette  Palette used for color selection. see as.colors()
legend  Draw legend of the labels. Default is TRUE
legend.pos  Position of the legend (topright, topleft, bottomright, bottomleft). Default is topright
... Arguments to be passed to methods, such as graphical parameters (see 'par').

Details

If the data matrix is specified, the function draws a clustering using the heatmap representation. If tree.sup is specified the function draws a two-ways clustering using the heatmap representation. Otherwise, a classical dendrogram is displayed. If a labels matrix is specified, each column of the matrix is represented under the dendrogram. If a pdfname is specified, the output is a pdf file. Setting 'trim.heatmap' to a number between 0 and 1 uses equidistant classes between the (trim.heatmap)- and (1-trim.heatmap)-quantile, and lumps the values below and above this range into separate open-ended classes. If the data comes from a heavy-tailed distribution, this can save the display from putting too many values into to few classes.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

clustering, heatmap.plus

Examples

data(marty)

#Clustering on 50 most variant genes amongst 500 first
mv.genes<-genes.selection(marty[1:500,], thres.num=50)
c.sample<-clustering(marty[mv.genes,], metric="pearson", method="ward")
clustering.plot(c.sample, lab=marty.type.cl, title="H.Clustering\nPearson-Ward")

c.gene<-clustering(data=t(marty[mv.genes,]), metric="pearson",method="ward")

#Two-ways clustering
clustering.plot(tree=c.sample, tree.sup=c.gene, data=marty[mv.genes,], trim.heatmap=0.99)
distrib.plot  Distribution plots of genes expression level

Description
Plot the distribution of the expression level of each gene of interest.

Usage
distrib.plot(data, labels = NULL, plot = TRUE, ...)

Arguments
data  Expression matrix, genes on rows and samples on columns
labels  A character string or numeric vector of label
plot  If true, plots are displayed
...  Arguments to be passed to methods, such as graphical parameters (see 'par').

Details
For each gene (row of the matrix), the distribution of the expression level for all the samples is
plotted. The colors are chosen according to the label information.

Value
A list of objects of class 'histogram':
mids  The n cell midpoints
counts  n integers; for each cell, the number of 'x[]' inside.

Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton,
Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also
hist

Examples

data(marty)
distrib.plot(marty[1:5,], labels=marty.type.cl)
eval.stability.clustering

Compares several clustering methods by means of its stability.

Description

This function compares several clustering methods (link functions and distances) by means of its stability.

Usage

```r
eval.stability.clustering(X, nb=c(2:4), f=0.8, nsub=100, s=0.98,
list_DIS=c("euclidean","pearson"),
list_ALGO=c("average","complete","ward"), pdfname = NULL,
verbose = TRUE)
```

Arguments

- `X`: a data frame with p rows and n columns; if clustering on genes - samples by row and genes by column; if clustering on samples genes by row and samples by column
- `nb`: number of classes for partition; it must start at 2 and be sequential(by default 2,3 and 4)
- `f`: part of the data set which is randomly picked for each subsample in the resampling procedure (by default 0.8)
- `nsub`: half of the number of times the perturbation procedure is applied in the resampling procedure (by default 100)
- `list_DIS`: the list of distances to test
- `list_ALGO`: the list of linkage method to test
- `s`: similarity threshold, must lie between 0 and 1 (by default 0.98)
- `pdfname`: pdf file name for saving graphic, by default = NULL
- `verbose`: print results if verbose = TRUE, by default = TRUE

Details

Resampling is done by randomly picking without replacement f of the data set; similarity threshold is the value which is pertinent to decide that two partitions are similar; see references

Value

- `stab.methods`: a list containing methods declared stable for each partition

Returns a graphic containing the frequencies of methods declared stable
expFilter

Filter expression data

Description

This function takes an expression matrix and filtered out non detected genes.

Usage

expFilter(data, threshold = 3.5, p=0.01, graph = TRUE)

Arguments

data expression matrix, genes on rows and samples on columns.
threshold minimal value of expression to be reached
p keep probes with at least p*ncol(data) samples higher than threshold
graph boolean indicating if an histogram of the data should be plotted.
... Arguments to be passed to methods, such as graphical parameters (see 'par').

Details

The non variant genes are defined by the threshold value. A gene is kept if at least p*ncol(data) of its values is higher than threshold.

The graph represents the distribution of all the genes in data. A line shows the threshold value used.
Value
An expression matrix.

Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

Examples

data(marty)
exppFilter(marty, threshold = 3.5, graph = TRUE)

foldchange    Compute foldchange

Description
Caculates the foldchange for each genes.

Usage
foldchange(data, labels, unlog = TRUE)

Arguments
data      A matrix or a data frame of expression data. Each row of 'data' must correspond to a gene, and each column to a sample.
labels    A vector of length 'ncol(data)' containing the class labels of the samples. 'labels' should be a numeric vector 0 / 1. 0 specifying the samples of, e.g., the control group and 1 specifying, e.g., the case group.
unlog     'TRUE' if the data have to be unlog before the foldchange calculation.

Value
A vector of length 'n genes' with the foldchange for each genes.

Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe
genes.selection

Examples

```r
# load data
data(marty)

# Not run:
# filtering data
marty <- expFilter(marty, threshold=3.5, graph=FALSE)

# End (Not run)

# Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)

# run foldchange on 50 genes
fcOUT <- foldchange(marty[1:50,], marty.type.num)
```

Description

Selects the most variant genes of a expression dataset. For each gene, the difference between the quantile with probability \((1 - \text{probs})\) and the quantile with probability \(\text{probs}\) is computed. Default for \(\text{probs}\) value is set to 0.25 such that the difference corresponds to the Inter Quartile Range (IQR).

Usage

```r
genes.selection(data, thres.diff, thres.num, probs=0.25)
```

Arguments

- **data**: A expression matrix, genes on rows and samples on columns
- **thres.diff**: Difference threshold - Genes are selected based on the difference threshold
- **thres.num**: Genes number threshold - Selects the \(N\) genes with the highest difference value
- **probs**: probability value used to compute both quantiles

Details

The difference is computed for each genes. If the \(\text{thres.diff}\) option is chosen, the most variant genes are selected according to the difference threshold. If the \(\text{thres.num}\) option is chosen, the genes are ordered according to their difference value level, and the \(N\) first genes are selected.

Value

The name of the selected genes.
**intersectg**

**Author(s)**
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

**See Also**
`iqr`, `quantile`

**Examples**
```r
data(marty)
data.f<-expFilter(marty, graph=FALSE)

# Select the 50 most variant genes amongst the 1000 first genes
sel<-genes.selection(data.f[1:1000,], thres.num=50)
```

---

**intersectg**

*Generalized version of intersect for n objects*

**Description**
This function returns the intersection for the n objects in argument

**Usage**

`intersectg(...)`

**Arguments**

`...`  
The objects to compare

**Value**

A vector of intersection between the n objects

**Author(s)**
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

**Examples**
```r
a<-1:10
b<-2:7
c<-5:8
intersectg(a,b,c)
```
km

Compute survival curves and test difference between the curves

Description

Computes and draws estimates of survival curves for censored data using Kaplan-Meier’s method. In case of >=2 survival curves, use logrank test to assess the difference between the survival curves. Missing values are removed.

Usage

km(time, status, group = NULL, xlab="Time (years)", ylab="", ...)

Arguments

time numeric, this is the follow up time (used with right censored data)
status The status indicator, normally 0=alive, 1=dead (numeric). Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death)
group indicates the group to which is assigned each observation (factor). For one groupe only (no comparison), group is set to null (default)
xlab (optional): a character string, xlabel of the Kaplan Meier’s plot
ylab (optional): a character string, ylabel of the Kaplan Meier’s plot
... (optional): Additional graphical parameters

Value

A list with

fit.km results provided by Kaplan Meier analysis. See the R help on survfit for details
lr results provided by logrank analysis. See the R help on survdiff for details
p.lr pvalue of the logrank test

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

survfit, survdiff
Examples

```r
require(survival)
data(leukemia)
time<-leukemia$time
status<-leukemia$status
# One group
res<-km(time,status)
res$fit.km

# Two groups
group<-leukemia$x
res<-km(time,status,group)
res$km(time,status,group,title="Kaplan Meier curve")
res$km(time,status,group,title="Kaplan Meier curve",pdfname="My survival curve")
res$km(time,status,group,pdfname="My survival curve",pdfwidth=11.69, pdfheight=8.27)
res$fit.km
names(res$fit.km)
res$lr
names(res$lr)
res$p.lr
```

Description

Create the matrix of all pairwise contrasts between parameters for the test.LC function

Usage

```r
makeAllContrasts(X, annot)
```

Arguments

- `X` the design matrix
- `annot` the annotation table of the individuals with the columns corresponding to the model variables

Details

This function create a contrasts matrix that can be used with the test.LC function. All pairwise comparisons for each variable stratified into all other variables are returned.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe
Examples

data(marty)

#Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)

#Annotation of the grade of tumor
grade <- factor(sample(c(1:3),23,rep=TRUE),labels=c("I","II","III"))

annot <- data.frame(type=marty.type.num, grade=grade)
rownames(annot) <- colnames(marty)

marty.lm <- lm(marty[1,]~ annot$grade * annot$type)
X <- model.matrix(marty.lm)

LC <- makeAllContrasts(X, annot)

Description

marty data

Usage

data(marty)

Format

A matrix with 54613 rows and 23 columns. Each row represents the expression level of a probeset for the 23 samples. The original .CEL files (hgu133plus2) were normalized using GCRMA and the AFFX probesets were discarded from the dataset.

Details

The data are available on the ArrayExpress website (E-GEOD-13787) or in the NCBI-GEO website (GEO - GSE13787).

Source


References

marty.type.cl

Examples

data(marty)
dim(marty)
class(marty)

marty.type.cl  martyr class data for Basal vs HER2 cancer type

Description

marty class data for Basal vs HER2 cancer type

Usage

data(marty)

Format

A vector of 0/1 according to the sample type. The HER2+ samples are labeled as 0 and the Basal-like samples as 1.

Details

The clinical data are available on the ArrayExpress website (E-GEOD-13787) or in the NCBI-GEO website (GEO - GSE13787).

Source


References


Examples

data(marty)
## maybe str(marty) ; plot(marty) ...
multiple.correction  

Multiple testing correction

Description

Given a set of p-values, returns p-values adjusted using one of several methods.

Usage

multiple.correction(pval, typeFDR, q)

Arguments

- **pval**  
  Vector of p-values.
- **typeFDR**  
  The correction method.
- **q**  
  The error rate to use for the Two-stages procedure (FDR-TST).

Details

The multiple correction methods include Bonferroni correction ("FWER"), Benjamini-Hochberg standard false discovery rate correction ("FDR-BH"), Benjamini-Hochberg Adaptive Procedure ("FDR-TST") and the Qvalue procedure (Storey).

Value

A vector of adjusted pvalues.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

References


See Also

- p.adjust
### myPalette

#### Microarray color palette

**Description**
This function returns a vector of color names corresponding to a range of colors specified in the arguments.

**Usage**

```r
myPalette(low = "white", high = c("green", "red"), mid=NULL, k = 50)
```

**Arguments**

- **low**
  Color for the lower end of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of 'colors'), a hexadecimal string of the form `"#rrggbb"`, or an integer 'i' meaning `palette()[i]`.

- **high**
  Color for the upper end of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of 'colors'), a hexadecimal string of the form `"#rrggbb"`, or an integer 'i' meaning `palette()[i]`.

- **mid**
  Color for the middle portion of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of 'colors'), a hexadecimal string of the form `"#rrggbb"`, or an integer 'i' meaning `palette()[i]`.

- **k**
  Number of colors in the palette.
Value

A "character" vector of color names. This can be used to create a user-defined color palette for subsequent graphics by 'palette', in a 'col=' specification in graphics functions, or in 'par'.

Author(s)

Sandrine Dudoit, Yee Hwa (Jean) Yang.

Examples

par(mfrow=c(1,4))
pal <- myPalette(low="red", high="green", mid="yellow")
image(x=1, y=1:21, z=matrix(seq(-2,2, 0.2),nrow=1),
     axes=FALSE, ylab="", xlab="", col=pal)

---

normAffy

Normalisation of Affymetrix expression arrays

Description

This function converts .CEL files into a matrix of normalised data using GCRMA, RMA or MAS5 normalisation.

Usage

`normAffy(filenames, celfile.path, method = c("GCRMA","RMA","MAS5"),
cdfname = NULL, rmaffx = TRUE, fast=TRUE)`

Arguments

- `filenames`: The .CEL files to normalize separated by comma, if empty the celfile.path.
- `celfile.path`: Path to the directory containing the cel files
- `method`: Normalisation method to use
- `cdfname`: Used to specify the name of an alternative cdf package. If set to NULL, the usual cdf package based on Affymetrix’ mappings will be used. Note that the name should not include the ‘cdf’ on the end, and that the corresponding probe package is also required to be installed. If either package is missing an error will result.
- `rmaffx`: boolean, indicating wether the probe control should be removed
- `fast`: logical, option of GCRMA normalisation. see details
Details

This function allows to use several normalisation methods. It is a wrapper for functions \texttt{justRMA}, \texttt{justGCRMA} and \texttt{mas5} from packages \texttt{affy} and \texttt{gcrma}. The \texttt{fast} parameter of the \texttt{justRMA} can lead to different results. If \texttt{fast} is true, the Lim et al. correction is applied. All expression values smaller than a threshold are put to the same values, leading to a sharp pick on the left of the distribution. Set \texttt{fast} to false to obtain a standard GCRMA distribution.

If the filenames parameter is missing, then all the files of the celfile.path are used.

Value

A matrix containing the normalised data, genes on rows and samples on columns.

Examples

```r
## Not run:
## GCRMA normalisation
normData <- normAffy(celfile.path="PathToCelFiles", method="GCRMA")

## End(Not run)
```

---

\code{ordinal.chisq} \hspace{1cm} \textit{Chisq test for ordinal values}

Description

This function computes a chisq test for ordinal values

Usage

\code{ordinal.chisq(x)}

Arguments

\texttt{x} \hspace{1cm} a contingency table with ordinal values in column

Details

This function applies a ordinal chisq test as described in http://www.uvm.edu/~dhowell/StatPages/More_Stuff/OrdinalChiSq/Chi-Sq-Tests-For-Ordinal-Values.html. The results are identical to those returned by SPSS

Value

\texttt{Chisq statistics and pvalues}

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe
Examples

## General hypothesis: was that participants who had experienced more traumatic events 
## during childhood would be more likely to drop out of treatment.

```r
trau = matrix(c(25, 13, 9, 10, 6, 31, 21, 6, 2, 3), byrow = TRUE, nrow = 2)
colnames(trau) <- c("0", "1", "2", "3", "4+)
rownames(trau) <- c("dropout", "remain")
ordinal.chisq(trau)
```

## Association between grade and local breast cancer relapse

```r
grade <- matrix(c(16, 42, 71, 4, 27, 49), ncol = 3, byrow = TRUE)
colnames(grade) <- c("low", "intermediate", "high")
rownames(grade) <- c("0", "1")
ordinal.chisq(grade)
```

---

**plotBiplot**

**Sample and variable representation on a same graph for PCA**

### Description

Sample and variable representation on a same graph for Principal Component Analysis (PCA)

### Usage

```r
plotBiplot(acp, ...)
```

### Arguments

- **acp**
  - result from PCA or do.pca function
- **...**
  - Arguments to be passed to methods, such as graphical parameters (see `par`).

### Value

Plot of samples and variables on a same graph

### Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

### See Also

runPCA, PCA
plotInertia

Examples

```r
## Not run:
data(marty)

## PCA on sample
## example dataset
eexample subset <- martyr[1:100, 1:100]
pca <- runPCA(t(example subset), verbose = FALSE, plotSample = FALSE,
plotInertia = FALSE)

## Biplot of PCA object
plotBiplot(pca)

## End(Not run)
```

plotInertia Barplot of component inertia percentage for PCA

Description

Barplot of component inertia percentage for Principal Component Analysis (PCA)

Usage

```r
plotInertia(acp, ncp = 5, ...)
```

Arguments

- `acp` result from do.pca or PCA function
- `ncp` number of components displayed, by default 5
- `...` Arguments to be passed to methods, such as graphical parameters (see 'par').

Value

Barplot of component inertia percentage

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

runPCA,PCA
Examples

```r
data(marty)

## PCA on sample - example set
example.subset <- marty[1:100,]
pca <- runPCA(t(example.subset), verbose = FALSE, plotInertia = FALSE, plotSample = FALSE)

## Inertia plot of PCA object
plotInertia(pca)
```

---

**plotSample**  
*Sample representation for Principal Component Analysis*

**Description**

Sample representation for Principal Component Analysis (PCA)

**Usage**

```r
plotSample(acp, axes = c(1, 2), new.plot = FALSE, lab = "quality",
palette="rainbow", lim.cos2.sample = 0, text = TRUE,
lab.title = NULL, ellipse=FALSE, ...)
```

**Arguments**

- `acp`: result from PCA or do.pca function
- `axes`: axes for sample representation, by default 1 and 2
- `new.plot`: if TRUE, a new graphical device is created, by default = FALSE
- `lab`: character. Sample label, by default = quality (points are labelled by quality index). If lab=NULL, no label is displayed.
- `lim.cos2.sample`: keep samples with cos2 >= lim.cos2.sample, by default = 0
- `palette`: characters. Name of a palette, By default, "rainbow" palette
- `text`: add sample name or not, by default = TRUE
- `lab.title`: title for the legend, by default = NULL
- `ellipse`: if TRUE and lab provided, draw 95% confidence ellipse around barycentre of each group
- `...`: Arguments to be passed to methods, such as graphical parameters (see 'par').

**Value**

Sample representation on axes `axes[1]` and `axes[2]` colored by quality index (= cos2 of samples) or colored by `lab`
plotVariable

Author(s)
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton,
Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also
runPCA, PCA

Examples

data(marty)

## PCA on sample - example set
example.subset <- martyr[1:100,]
pca <- runPCA(t(example.subset), verbose = FALSE, plotInertia = FALSE, plotSample = FALSE)

## Sample plot of PCA object colored by tumour type
perso.colors <- colorRampPalette(c("red", "green"))
plotSample(pca, lab = marty.type.cl, palette="perso.colors", ellipse=TRUE)

plotVariable

Variable representation for Principal Component Analysis

Description
Variable representation for Principal Component Analysis (PCA)

Usage

plotVariable(acp, axes = c(1, 2), new.plot = FALSE, lab, lim.cos2.var = 0, palette="rainbow", ...)

Arguments

acp result from PCA or do.pca function
axes axes for variable representation, by default 1 and 2
new.plot if TRUE, a new graphical device is created, by default = FALSE
lab variable label
palette character, name of color palette, by default = "rainbow"
lim.cos2.var keep variables with cos2 >= lim.cos2.var
... Arguments to be passed to methods, such as graphical parameters (see 'par').

Value
Variable representation on axes axes[1] and axes[2]

If PCA is normed, the correlation circle is plotted colored by lab
Partial Least Squares

PLS

Description

Partial Least Squares

Usage

PLS(E, F, n = 1, scale = TRUE)

Arguments

E  Matrix which correspond to the predictor variables.
F  Matrix which corresponds to the outcome variables.
n  Number of components to compute.
scale  If TRUE, each variable is scaled to have a unit variance.

Details

The function implements the PLS1 algorithm (Wold, 1966; Wold et al., 1982) (details about this algorithm and other implementations can be found in Tenenhaus (1998)).
Value

A list with the following elements:

- \( T \) PLS components. \( T = EW(P'W)^{-1} \)
- \( E^0 \) The input \( E \) matrix. If \( \text{scale}=\text{TRUE} \), then \( E \) is scaled.
- \( F^0 \) The input \( F \) matrix. If \( \text{scale}=\text{TRUE} \), then \( F \) is scaled.
- \( C \) Covariance between the PLS components and the outcome variables \( F \).
- \( \hat{W}^\text{star} \) \( EW(P'W)^{-1} \)
- \( P \) Regression vectors.
- \( \text{param.center} \) Means of \( E \) columns.
- \( \text{param.scaled} \) Standard-deviation of \( E \) columns.

References


Examples

```r
X <- matrix(rnorm(100), 20, 5)
Y <- matrix(c(rep(0,10), rep(1,10)))
res <- PLS(X,Y)
```

```r
probePlots
```

Plot the expression profiles of the probes corresponding to given probesets

Description

Performs expression plots of probes for given probesets. This function is interesting to show which probes are responsible of intensity signal.

Usage

```r
probePlots(abatch, path, pbsList, labAxisProbes=TRUE, labAxisArrays=TRUE, legendArrays=TRUE, legendProbes=TRUE, cex.axis=0.9, cex.legend=0.8, pdfName)
```
Arguments

- **abatch**: An affybatch object.
- **path**: A character. If no affyBatch object, the path where are .CEL files.
- **pbsList**: A character. A vector of character listing the interesting probesets.
- **labAxisProbes**: A logical. TRUE if probes names have to be plotted in the x axis, FALSE otherwise.
- **labAxisArrays**: A logical. TRUE if arrays names have to be plotted in the x axis, FALSE otherwise.
- **legendArrays**: A logical. TRUE if legend corresponding to the arrays names have to be plotted, FALSE otherwise.
- **legendProbes**: A logical. TRUE if legend corresponding to the probes names have to be plotted, FALSE otherwise.
- **cex.axis**: A numeric. The magnification to be used for x axis relative to the current setting of ‘cex’.
- **cex.legend**: A numeric. The magnification to be used for legend relative to the current setting of ‘cex’.
- **pdfName**: A character. Name for a pdf file if needed.

Value

Three plots for each probesets are generated. The first one is an inter chips plot. For each arrays in the AffyBatch, the perfect match intensity of probesets’ probes are plotted. The second one is an inter probes plot on the perfect match. For each probes in the probeset, the perfect match intensity in each arrays are plotted. The third one is an inter probes plot on the mis match. For each probes in the probeset, the mis match intensity in each arrays are plotted.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

Examples

```r
## Not run:
if (require(affydata)) {
  ## load example
data(Dilution)
probePlots(Dilution, pbsList=geneNames(Dilution)[1:2])
}

## End(Not run)
```
runGSA

GSA analysis

Description

Determines the significance of pre-defined sets of genes with respect to an outcome variable, such as a group indicator, a quantitative variable or a survival time.

Usage

runGSA(nData, labels, gmtfile, chip = "hgu133plus2", np = 1000, minsize = 10, maxsize = 800, resp.type = "Two class unpaired", fdr = 0.25)

Arguments

nData: a matrix or a data frame of expression data. Each row of 'data' must correspond to a gene, and each column to a sample.

labels: a vector of length 'nrow(data)' containing the class labels of the samples. In "Two class unpaired", 'labels' should be a vector containing 0's (specifying the samples of, e.g., the control group) and 1's (specifying, e.g., the case group) or more if multiclass (0,1,2...) In "Two class paired" for paired outcomes, coded -1,1 (first pair), -2,2 (second pair), etc..

gmtfile: a character string corresponding to the path file of a gmt file, corresponding to a gene set collection (a list).

chip: a character string corresponding to the chip type of the data.

np: a numerical value corresponding to the number of permutations.

minsize: a numerical value corresponding to the minimum number of genes in genesets to be considered.

maxsize: a numerical value corresponding to the minimum number of genes in genesets to be considered.

resp.type: Problem type: "quantitative" for a continuous parameter; "Two class unpaired" ; "Survival" for censored survival outcome; "Multiclass" : more than 2 groups. "Two class paired" for paired outcomes.

fdr: a numerical value corresponding to the fdr threshold.

Details

The GSA package is presented as an improvement of the GSEA approach. It differs from a GSEA in its use of the "maxmean" statistic: this is the mean of the positive or negative part of gene scores in the gene set, whichever is large in absolute values. Efron and Tibshirani shows that this is often more powerful than the modified KS statistic used in GSEA. GSA also does "restandardization" of the genes (rows), on top of the permutation of columns (done in GSEA).
Value

A list of geneset found If it is a LIST, use

FDRcut a numerical value corresponding to the threshold FDR.
negative a character matrix corresponding to the downexpressed gene sets found.
positive a character matrix corresponding to the upexpressed gene sets found.
nsets.neg a numerical value corresponding to the number of downexpressed gene sets found.
nsets.pos a numerical value corresponding to the number of upexpressed gene sets found.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

References


See Also

GSA

Examples

## Not run:
require(hgu133plus2.db)

## Two class unpaired comparison
## load data
data(marty)

## filtering data
marty <- expFilter(marty, threshold=3.5, graph=FALSE)

## Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)

## run sam analysis
gsaOUT <- runGSA(marty, marty.type.num ,
gmtfile="./c2.kegg.v2.5.symbols.gmt", chip="hgu133plus2")

## End(Not run)
runHyperGO

Run Gene Ontology analysis based on hypergeometric test from a probeset list

Description

Run Gene Ontology analysis based on hypergeometric test from a probeset list

Usage

runHyperGO(list, pack.annot, categorySize = 1, verbose = TRUE, name = "hyperGO", htmlreport = TRUE, txtreport = TRUE, tabResult = FALSE, pvalue = 0.05)

Arguments

- **list**: vector of character with probeset names
- **pack.annot**: annotation package to use
- **categorySize**: integer, minimum size for category, by default = 1
- **verbose**: logical, if TRUE, results are displayed, by default TRUE
- **name**: character, name for output files, by default "hyperGO"
- **htmlreport**: logical, if TRUE, a html report is created, by default TRUE
- **txtreport**: logical, if TRUE, a txt report is created, by default TRUE
- **tabResult**: logical, if TRUE, a list with the results is created, by default FALSE
- **pvalue**: numeric, a cutoff for the hypergeometric test pvalue, by default 0.05

Details

The choice of the universe could have a significant impact on the results. It is well discussed in the vignette of the GOstats package. Here, we decided to apply a non-specific filtering procedure different from the one proposed by Falcon and Gentleman. Since not all genes will be expressed under all conditions in our data, we can ask the question of defining the universe only with the expressed genes or with all the genes of the array. Actually, we are not able to distinguish the genes which are biologically non expressed, from the ones of low quality. That’s why we think that the non-expressed probesets could be biologically relevant, as well as the ones with a little variation accross samples, and we decided to first defined the universe with all the genes of the array. Then, we just remove probe sets that have no Entrez Gene identifier in our annotation data or no GO annotation. Finally, the Hypergeometric test is performed on the unique EntrezId of the gene list, and the unique EntrezId of the universe. The pvalues in output are not corrected from multiple testing. Note that because of the existing dependence structure (between genes, and GO terms) it is difficult to do any multiple testing correction. Moreover the most interesting genesets are not necessarily the ones with the smallest pvalues. Nodes that are interesting are typically those with a reasonable number of genes (10 or more) and small pvalues.

runHyperGO needs packages GOstats and GO.db from Bioconductor.
runHyperKEGG

Value

The R objects or the Txt and html reports

BP
  Data.frame with results for Biological Process with GO Id, pvalue, Odd Ratio, Expected count, Size and GO Term

MF
  Idem for Molecular Function

CC
  Idem for Cellular Component

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

hyperGTest, runHyperKEGG

Examples

```r
## Not run:
require(hgu133plus2.db)
data(marty)

## Probe list
probelist <- rownames(marty)[1:50]

## Hypergeometric test for GO pathway
res <- runHyperKEGO(probelist, htmlreport = FALSE, txtreport = FALSE, tabResult = TRUE, pack.annot = "hgu133plus2.db")

## End(Not run)
```

---

**runHyperKEGG**

Run KEGG pathway analysis based on hypergeometric test from a probeset list

### Description

Run KEGG pathway analysis based on hypergeometric test from a probeset list

### Usage

```r
runHyperKEGG(list, pack.annot, categorySize = 1, name = "hyperKEGG", htmlreport = TRUE, txtreport = TRUE, tabResult = FALSE, pvalue = 0.05)
```
runHyperKEGG

Arguments

- list: vector of character with probeset names
- pack.annot: character string, annotation package to use
- categorySize: integer, minimum size for category, by default = 1
- name: character, name for output files, by default "hyperKEGG"
- htmlreport: logical, if TRUE, a html report is created, by default TRUE
- txtreport: logical, if TRUE, a txt report is created, by default TRUE
- tabResult: logical, if TRUE, a list with the results is created, by default FALSE
- pvalue: numeric, a cutoff for the hypergeometric test pvalue, by default 0.05

Details

runHyperKEGG needs packages G0stats and KEGG.db from Bioconductor.

Value

Txt and html report

Data.frame with KEGG Id, pvalue, Odd Ratio, Expected count, Size and KEGG Term

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

hyperGTest, runHyperGO

Examples

```r
## Not run:
require(hgu133plus2.db)
data(marty)

## Probe list
probelist <- rownames(marty)[1:50]

## Hypergeometric test for KEGG pathway
res <- runHyperKEGG(probelist, htmlreport = FALSE, txtreport = FALSE, tabResult = TRUE, pack.annot = "hgu133plus2.db")

## End(Not run)
```
runIndTest  Computing Differential Analysis for each gene

Description

This function computes test statistics, e.g., two-sample Welch t-statistics, t-statistics, or wilcoxon, independently for each row of a data frame.

Usage

runIndTest(data, labels, gene.names = NULL, plot = TRUE, dirname = NULL, grp.name = c("Group1","Group2"))

Arguments

data  a matrix, a data frame, or an ExpressionSet object. Each row of 'data' (or 'exprs(data)', respectively) must correspond to a gene, and each column to a sample.

labels  A vector of integers corresponding to observation (column) class labels. For 2 classes, the labels must be 0 and 1.

gene.names  A vector of description or name for each gene.

plot  A logical value specifying if drawing plots or not.

dirname  If specified, the .png plots are created in the directory.

grp.name  Vector with the name of the two groups

Details

For each gene independently, the function tests for the normality (Shapiro test) and the variance equality (F test) of each groups. According to the results, a welch test, a student test or a wilcoxon test is performed.

Value

A matrix with the gene names, the statistics, and the p-values.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

shapiro.test, var.test,t.test,wilcoxon.test
Examples

```r
## load data
data(marty)

## random choice of genes - in practice genes of interest
geneOfInterest <- sample(1:ncol(marty), 5)

## Class label 0/1
marty.type.num <- ifelse(marty.type.cl == "Her2+", 0, 1)

## run differential analysis
out <- runIndTest(marty[geneOfInterest, ], labels=marty.type.num)
```

---

runMFA

*Function to perform a Multiple Factor Analysis.*

Description

This function allows to perform a Multiple Factor Analysis and to build a report with the main statistics and the main graphics.

Usage

```r
runMFA(Data, group = NULL, ncp = 5, name.group = NULL, type = NULL, ind.sup = NULL, num.group.sup = NULL, graph = TRUE, report.file = NULL, report.pdf = NULL)
```

Arguments

- **Data**
  A data.frame or a list, see details

- **group**
  A vector indicating the number of variables in each group

- **ncp**
  Number of components to keep

- **name.group**
  Names of the groups of variables, default is NULL

- **type**
  the type of variables in each group; three possibilities: "c" or "s" for quantitative variables (the difference is that for "s" variables are scaled to unit variance), "n" for qualitative variables; by default, all variables are quantitative and scaled to unit variance

- **ind.sup**
  A vector indicating the indexes of the supplementary individuals

- **num.group.sup**
  The indexes of the illustrative groups (by default, NULL and no group are illustrative)

- **graph**
  boolean, if TRUE a graph is displayed

- **report.file**
  Name of the txt file for the text report

- **report.pdf**
  Name of the pdf file for the graphical report
Details

Data can either be a data.frame with all the groups binded or a list containing all the groups such as:
list(group1=group1, group2=group2, ...). In the case of a data.frame, group must be indicated.

The analysis report can also be build later by using function MFReport.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton,
Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

MFA, plot.MFA, MFReport

Examples

data(marty)
## Perform a MFA on splitted data
resMFA <- runMFA(Data=list(group1=t(marty[1:100,]),
group2=t(marty[101:200,])), type=c("c", "c"), graph=FALSE)
## Not run:
## plot global analysis with partial individuals
plot(resMFA, choix="ind", partial="all")

## plot groups link
plot(resMFA, choix="group")

## End(Not run)
Arguments

- **X**: a data frame with n rows (samples) and p columns (variables)
- **ncp**: number of dimensions kept in the results (by default 5)
- **scale**: a boolean, if TRUE (value set by default) then data are scaled to unit variance
- **ind.sup**: a vector indicating the indexes of the supplementary individuals
- **quanti.sup**: a vector indicating the indexes of the quantitative supplementary variables
- **quali.sup**: a vector indicating the indexes of the qualitative supplementary variables
- **sample.qual**: a boolean, if TRUE quality sample is displayed, by default = TRUE
- **variable.qual**: a boolean, if TRUE quality variable is displayed, by default = FALSE
- **sample.cont**: a boolean, if TRUE sample contribution is displayed, by default = TRUE
- **variable.cont**: a boolean, if TRUE variable contribution is displayed, by default = TRUE
- **plotSample**: a boolean, if TRUE samples are displayed, by default = TRUE
- **plotVariable**: a boolean, if TRUE variables are displayed, by default = FALSE
- **plotInertia**: a boolean, if TRUE inertia percentage of components is displayed, by default = TRUE
- **plotBiplot**: a boolean, if TRUE biplot is displayed, by default = FALSE
- **lab.sample**: a vector, sample representation is colored by label.sample, by default = NULL
- **lab.var**: a vector, variable representation is colored by label.var, by default = "quality"
- **palette**: character, name of palette color, by default = "rainbow"
- **lim.cos2.sample**: a numeric, for graphics, keep samples with cos2 >= lim.cos2.sample, by default = 0
- **lim.cos2.var**: a numeric, for graphics, keep variables with cos2 >= lim.cos2.var, by default = 0
- **pdf**: a boolean, if TRUE save all the graphics in a pdf file, by default = FALSE
- **pdfname**: pdf file name for saving graphics
- **verbose**: print results if verbose = TRUE, by default = FALSE
- **...**: Arguments to be passed to methods, such as graphical parameters (see 'par').

Value

- **eig**: a matrix containing all the eigenvalues, the percentage of variance and the cumulative percentage of variance
- **var**: a list of matrices containing all the results for the active variables (coordinates, correlation between variables and axes, square cosine, contributions)
- **ind**: a list of matrices containing all the results for the active individuals (coordinates, square cosine, contributions)

Returns the individuals factor map for axes 1 and 2, 1 and 3, 2 and 3 Returns the inertia percentage of components By default, print sample coordinates, sample quality and sample contribution
**runSAM**

**Author(s)**
Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

**See Also**
plotsample, plotVariable, plotInertia

**Examples**

data("marty")

## PCA on sample with inertia plot and sample plot colored by tumour type

e.example subset <- marty[1:100,]
 pca <- runPCA(t(example subset), verbose = FALSE, lab.sample = marty.type.cl)

---

**runSAM**

SAM analysis with siggenes package

**Description**

Performs a Significance Analysis of Microarrays (SAM). It is possible to perform one and two class analyses using either a modified t-statistic or a (standardized) Wilcoxon rank statistic, and a multiclass analysis using a modified F-statistic. Moreover, this function provides a SAM procedure for categorical data such as SNP data and the possibility to employ an user-written score function.

**Usage**

runSAM(data, labels, nbpermut = 500, q = 0.05, plot = TRUE, method ="d.stat", var.equal = TRUE, include.zero = FALSE, paired = FALSE, seed=123)

**Arguments**

data A matrix, a data frame, or an ExpressionSet object. Each row of 'data' (or 'exprs(data)', respectively) must correspond to a gene, and each column to a sample.

labels A vector of length 'ncol(data)' containing the class labels of the samples. In the two class unpaired case, 'labels' should be a vector containing 0's (specifying the samples of, e.g., the control group) and 1's (specifying, e.g., the case group). In the two class paired case, 'labels' can be either a numeric vector or a numeric matrix. If it is a vector, then 'labels' has to consist of the integers between -1 and -n/2 (e.g., before treatment group) and between 1 and n/2 (e.g., after treatment group), where n is the length of 'labels' and k is paired with -k, k=1,...,n/2. If 'labels' is a matrix, one column should contain -1's and 1's specifying, e.g., the
runSAM

before and the after treatment samples, respectively, and the other column should contain integer between 1 and n/2 specifying the n/2 pairs of observations.

nbpermut A numeric value specifying the number of permutation.
q A numeric value specifying the FDR threshold. see details.
plot A logical value specifying if drawing plots or not.
method A character string or a name specifying the method/function that should be used in the computation of the expression scores d. If 'method = d.stat', a modified t-statistic or F-statistic, respectively, will be computed as proposed by Tusher et al. (2001). If 'method = wilc.stat', a Wilcoxon rank sum statistic or Wilcoxon signed rank statistic will be used as expression score. For an analysis of categorical data such as SNP data, 'method' can be set to 'chisq.stat'. In this case Pearson’s ChiSquare statistic is computed for each row. If the variables are ordinal and a trend test should be applied (e.g., in the two-class case, the Cochran-Armitage trend test), 'method = trend.stat' can be employed.
var.equal A logical value. If 'method=d.stat', TRUE for student test , FALSE for Welch test.
include.zero A numeric value specifying if sO=0 is possible.
paired A logical value specifying if paired test or not.
seed Seed initialization for results reproducibility.

Details

SAM has it own FDR procedure which allows to find significant genes for a fixed threshold ’q’. The genes’ significance found by SAM is not based on the adjusted p-values (qvalues). That’s why we do not report them.

Value

A matrix with the probes ID, the statistics, the raw p-values, and the significance (according to SAM FDR procedure).

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

References

runTtest

Computing Multiple Student Tests

Description

This function provides a convenient way to compute test statistics, e.g., two-sample Welch t-statistics, t-statistics, paired t-statistics, for each row of a data frame using the multtest package. It returns the raw and adjusted p-values for each gene as well as the significance of the genes and a quantile-quantile plot.

Usage

runTtest(data, labels, typeFDR="FDR-BH", algo="t", q=0.05, plot=TRUE)

Arguments

data A matrix, a data frame, or an ExpressionSet object. Each row of 'data' (or 'exprs(data)'), respectively) must correspond to a gene, and each column to a sample.

labels A vector of integers corresponding to observation (column) class labels. For 2 classes, the labels must be 0 and 1.

typeFDR The method to apply for the multiple testing correction.
runTtest

algo A character string specifying the statistic to be used to test the null hypothesis of no association between the variables and the class labels. If 'test="t"', the tests are based on two-sample Welch t-statistics (unequal variances). The number of ddl is computed using the Satterthwaite approximation. If 'test="t.equalvar"', the tests are based on two-sample t-statistics with equal variance for the two samples. The square of the t-statistic is equal to an F-statistic for k=2. If 'test="pairt"', the tests are based on paired t-statistics. The square of the paired t-statistic is equal to a block F-statistic for k=2.

q A numeric value specifying the pvalue threshold.

plot A logical value specifying if drawing plots or not.

Value

A matrix with the probes ID, the statistics, the raw p-value and the adjust p-value

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

mt.teststat, multiple.correction

Examples

```r
## load data
data(marty)

## Not run:
## filtering data
marty <- expFilter(marty, threshold=3.5, graph=FALSE)

## End(Not run)
##Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)

## run differential analysis on example set
example.subset <- marty[1:100,]
out <- runTtest(example.subset, labels=marty.type.num, typeFDR="FDR-BH", plot=FALSE)
```
Computing Multiple Wilcoxon Tests

Description

This function provides a convenient way to compute the wilcoxon statistics, for each row of a data frame using the multtest package. It returns the raw and adjusted pvalues for each genes as well as the significance of the genes and a quantile-quantile plot.

Usage

runWilcox(data, labels, typeFDR = "FDR-BH", q = 0.05, plot = TRUE)

Arguments

data
A matrix, a data frame, or an ExpressionSet object. Each row of 'data' (or 'exprs(data)', respectively) must correspond to a gene, and each column to a sample.

labels
A vector of integers corresponding to observation (column) class labels. For 2 classes, the labels must be 0 and 1.

typeFDR
The method to apply fo the multiple testing correction.

q
A numeric value specifying the pvalue threshold.

plot
A logical value specifying if drawing plots or not.

Value

A matrix with the probes ID, the statistics, the raw p-value and the adjust p-value

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

See Also

mt.teststat.multiple.correction

Examples

## load data
data(marty)

## filtering data
##marty <- expFilter(marty, threshold=3.5, graph=FALSE)

##Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)
## sample.plot

```r
## run differential analysis
example.subset <- marty[1:100,]
out <- runWilcox(example.subset, labels=marty.type.num, typeFDR="FDR-BH", plot=FALSE)
```

---

**Description**

Plot a barplot of the expression level of each gene of interest.

**Usage**

```r
sample.plot(data, labels=NULL, plot=TRUE, ...)
```

**Arguments**

- `data` Expression matrix, genes on rows and samples on columns
- `labels` A character string or numeric vector of label
- `plot` Display output barplot if TRUE
- `...` Arguments to be passed to methods, such as graphical parameters (see 'par').

**Details**

For each gene (row of the matrix), a barplot of the expression level for all the samples is plotted. The colors are chosen according to the label information.

**Author(s)**

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

**Examples**

```r
data(marty)
sample.plot(marty[1:3,], labels=marty.type.cl)
```
setdiffg | Generalized version of setdiff for n objects

Description

This function returns the difference between the first argument and the (n-1) others

Usage

setdiffg(...)  

Arguments

... | The objects to compare

Value

A vector of differences between the first object and the (n-1) others

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

Examples

a<-1:10  
b<-2:5  
c<-7:8  
setdiffg(a,b,c)

test.LC | Test linear combinations of parameters of a linear model

Description

This function performs either a global significance F-test of one or several linear combinations of the parameters (contrast) of a (generalized) linear model, or tests for the significance of each contrast simultaneously, with or without multiple test correction.

Usage

test.LC(C, X, Y, global=FALSE, cor.multtest=TRUE,typeFDR="FDR-BH")
Arguments

- **C**: Vector or matrix of the linear combinations of factors we want to test.
- **X**: Design matrix of the (generalized) linear model adjusted to the data.
- **Y**: Vector or response matrix (e.g., a gene expression matrix) to which the (generalized) linear model is applied. If a matrix is specified the test(s) will be done on each column of the matrix.
- **global**: logical indicating if one wants to perform a F test of the global hypothesis $H_0=0$, or to test each contrast simultaneously.
- **cor.multtest**: logical. If global=FALSE indicates if one wants to apply a multiple test correction for the computation of the p-values.
- **typeFDR**: If global=FALSE and cor.multtest=TRUE this argument is passed to the function multiple.correction(), it specifies which correction method to apply. See '?multiple.correction' for more details.

Details

The design matrix X can be extracted from a (generalized) linear model with the function `model.matrix`. If Y is a response matrix each column shall be a gene/individual response on which the linear combinations will be tested. If one wishes to test several linear combinations at the same time, C must be a matrix $p \times n$ with $n$ the number of columns in the design matrix X (i.e., the number of parameters in the (generalized) linear model) and $p$ the number of linear combinations, so that each row stands for one linear combination. Else C shall be a vector of length $n$. In case where both C and Y are matrices, each linear combination of the parameters (i.e., each row of C) will be tested for nullity on each gene/individual (i.e., each column of Y).

Value

A list of matrices:

- **Estimate**: A matrix containing the estimated values: $F[i,j]$ is the estimated value of the linear combination $i$ (on gene $j$).
- **F**: A matrix containing the F values: $F[i,j]$ is the F value of the test of linear combination $i$ on gene $j$.
- **pvalue**: A matrix containing the p-values: $pvalue[i,j]$ is the p-value of the test of linear combination $i$ on gene $j$.
- **Y.pred**: A matrix containing the predicted response vectors.
- **resid**: A matrix containing the residuals of the linear model.
- **sigma2**: A matrix with one row containing the residual variance for each gene.
- **theta**: A matrix containing the estimates of the effects of the original model. These estimates are the ones also obtained with `summary.lm()`.

Author(s)

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe
See Also

model.matrix, lm

Examples

data(marty)

#Class label 0/1
marty.type.num <- ifelse(marty.type.cl=="Her2+",0,1)

#Annotation of the grade of tumor
grade=factor(sample(c(1:3),23,rep=TRUE),labels=c("I","II","III"))
typeFfactor=paste(marty.type.num,grade,sep=":")

data for example
normData<-marty[1:100,]

trt<-runTtest(normData, labels=marty.type.num, plot=FALSE)
normData.DE<-normData[which(rtt["AdjpValue"]<0.05),]

marty.lm=lm(t(normData.DE)-as.factor(typeFfactor))
X=model.matrix(marty.lm)

#We want to test Basal vs Her2+ within each grade
LC<-matrix(c(0,0,0,-1,0,0,1,0,0,-1,0,0,0,1,0,0,-1),ncol=6,byrow=TRUE)
#We also want to test grade II vs grade III
LC2=c(0,1,-1,0,1,-1)
LC=cbind(LC,LC2)
marty.LC=test.LC(LC,X,t(normData.DE))
marty.LC$pvalue

#List of the probesets differentially expressed for each of the four tests :
ll=list()
for(i in 1:nrow(marty.LC$pvalue)){
ll[[i]]=as.matrix(marty.LC$pvalue[i,which(marty.LC$pvalue[i,]<0.05)])
rownames(ll[[i]])=names(which(marty.LC$pvalue[i,]<0.05))
}
names(ll)=rownames(marty.LC$pvalue)
print(ll)

test.nested.model Test for nested ANOVA models

Description

The function compute the F-statistic for nested ANOVA model.
**Usage**

test.nested.model(X, X0, Y)

**Arguments**

X  
this is the design matrix corresponding to the full model. X must be of full rank.

X0  
this is the design matrix corresponding to the sub-model. X0 is such that \( \text{span}(X0) \) is a vectorial subspace of \( \text{span}(X) \). X0 must be of full rank.

Y  
this is a matrix corresponding to the dependent variable (samples in row, variables (e.g. genes) in column.

**Details**

The F-statistic is computed and the p-value is returned. The F-statistic has \( r-r0 \) and \( n-r \) degrees of freedom where \( r \) is the rank of matrix X, \( r0 \) is the rank of matrix X0 and \( n \) is the number of observations.

**Value**

A list with the following items:

theta  
The estimation of the parameter of the full model.

F  
Value of the F-statistic.

pvalue  
The p-value.

residuals  
The residuals for the full model.

sigma2  
The estimation of the variance for the full model.

X  
The matrix design X

...  

**Author(s)**

Nicolas Servant, Eleonore Gravier, Pierre Gestraud, Cecile Laurent, Caroline Paccard, Anne Biton, Jonas Mandel, Bernard Asselain, Emmanuel Barillot, Philippe Hupe

**Examples**

```r
Y <- matrix(rnorm(21), 21, 1)
ef <- g1(3,7)
X <- lm(Y ~ ef, x = TRUE)$x
X0 <- lm(Y ~ 1, x = TRUE)$x

res.test <- test.nested.model(X, X0, Y)
```
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