Package ‘PAA’

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Title PAA (Protein Array Analyzer)
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Description PAA imports single color (protein) microarray data that has been saved in gpr file format - esp. ProtoArray data. After preprocessing (background correction, batch filtering, normalization) univariate feature preselection is performed (e.g., using the ”minimum M statistic” approach - hereinafter referred to as ”mMs”). Subsequently, a multivariate feature selection is conducted to discover biomarker candidates. Therefore, either a frequency-based backwards elimination approach or ensemble feature selection can be used. PAA provides a complete toolbox of analysis tools including several different plots for results examination and evaluation.
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URL http://www.ruhr-uni-bochum.de/mpc/software/PAA/
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batchAdjust

Adjust microarray data for batch effects.

Usage

batchAdjust(elist=NULL, log=NULL)

Arguments

elist
EList or EListRaw object containing the data to be adjusted (mandatory).

log
logical indicating whether the data is in log scale (mandatory; note: if TRUE
log2 scale is expected).

Details

This is a wrapper to sva’s function ComBat() for batch adjustment using the empirical Bayes
approach. To use batchAdjust the targets information of the EList or EListRaw object must contain
the columns “Batch” (containing batch/lot information for each particular array) and “Group” (con-
taining experimental group information for each particular array).

Value

An EListRaw or EList object with the adjusted data in log scale is returned.

Note

The targets information of the EListRaw or EList object must contain the columns “Batch” and
“Group”.
Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

References

The package sva by Jeffrey T. Leek et al. can be downloaded from Bioconductor (http://www.bioconductor.org/).


Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
elist <- batchAdjust(elist=elist, log=FALSE)

batchFilter

Remove differential features regarding array batches/lots.

Description

Finds differential features regarding array batches/lots and removes them.

Usage

batchFilter(elist=NULL, lot1=NULL, lot2=NULL, log=NULL, p.thresh=0.05, fold.thresh=1.5, output.path=NULL)

Arguments

- elist: EList or EListRaw object (mandatory).
- lot1: vector of column names for group 1 (mandatory).
- lot2: vector of column names for group 2 (mandatory).
- log: logical indicating whether the data is in log scale (mandatory; note: if TRUE log2 scale is expected).
- p.thresh: positive float number between 0 and 1 indicating the maximum Student’s t-test p-value for features to be considered as differential (e.g., "0.5").
- fold.thresh: float number indicating the minimum fold change for features to be considered as differential (e.g., "1.5").
- output.path: string indicating a path for saving results (optional).

Details

This function takes an EList or EListRaw object (see limma documentation) and the batch-specific column name vectors lot1 and lot2 to find differential features regarding batches/lots. For this purpose, thresholds for p-values (Student’s t-test) and fold changes can be defined. To visualize the differential features a volcano plot is drawn. Then, differential features are removed and the remaining data are returned. When an output path is defined (via output.path) volcano plots and result files are saved on the hard disk.
Value
An EList or EListRaw object without differential features regarding array batches/lots.

Author(s)
Michael Turewicz, <michael.turewicz@rub.de>

Examples
```r
cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
lot1 <- elist$targets[elist$targets$Batch=='Batch1', 'ArrayID']
lot2 <- elist$targets[elist$targets$Batch=='Batch2', 'ArrayID']
elist <- batchFilter(elist=elist, lot1=lot1, lot2=lot2, log=FALSE,
p.thresh=0.001, fold.thresh=3)
```

Description
Finds features which are differential regarding at least two microarray batches / lots in a multi-batch scenario (i.e., more than two batches) via one-way analysis of variance (ANOVA) and removes them.

Usage
`batchFilter.anova(elist=NULL, log=NULL, p.thresh=0.05, fold.thresh=1.5, output.path=NULL)`

Arguments
- `elist` EList or EListRaw object (mandatory).
- `log` logical indicating whether the data is in log scale (mandatory; note: if TRUE log2 scale is expected).
- `p.thresh` positive float number between 0 and 1 indicating the maximum Student’s t-test p-value for features to be considered as differential (e.g., "0.5").
- `fold.thresh` float number indicating the minimum fold change for features to be considered as differential (e.g., "1.5").
- `output.path` string indicating a path for saving results (optional).

Details
This function takes an EList or EListRaw object (see limma documentation) to find features which are differential regarding at least two microarray batches / lots in a multi-batch scenario (i.e., more than two batches). For this purpose, thresholds for p-values obtained from an one-way analysis of variance (ANOVA) and fold changes can be defined. To visualize the differential features a volcano plot is drawn. Then, differential features are removed and the remaining data are returned. When an output path is defined (via `output.path`) volcano plots and result files are saved on the hard disk.
**diffAnalysis**

**Value**

An EList or EListRaw object without differential features regarding at least two microarray batches / lots.

**Author(s)**

Ivan Grishagin (Rancho BioSciences LLC, San Diego, CA, USA), John Obenauer (Rancho BioSciences LLC, San Diego, CA, USA) and Michael Turewicz (Ruhr-University Bochum, Bochum, Germany), <michael.turewicz@rub.de>

**Examples**

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist$eList$genes$Block < 10,]
elist <- batchFilter.anova(elist=elist, log=FALSE, p.thresh=0.001,
fold.thresh=3)

diffAnalysis  **Differential analysis.**

**Description**

Performs a univariate differential analysis.

**Usage**

diffAnalysis(input=NULL, label1=NULL, label2=NULL, class1=NULL, class2=NULL,
output.path=NULL, mMs.matrix1=NULL, mMs.matrix2=NULL, above=1500,
between=400, features=NULL, feature.names=NULL)

**Arguments**

input  
EList$E- or EListRaw$E-matrix extended by row names comprising BRC-IDs of the corresponding features (mandatory; note: it is expected that this matrix is in original scale and not in log2 scale).

label1  
vector of column names for group 1 (mandatory).

label2  
vector of column names for group 2 (mandatory).

class1  
label of group 1 (mandatory).

class2  
label of group 2 (mandatory).

output.path  
string indicating a path for saving the results (optionally).

mMs.matrix1  
precomputed mMs reference matrix (see mMsMatrix()) for group 1 (mandatory).

mMs.matrix2  
precomputed mMs reference matrix (see mMsMatrix()) for group 2 (mandatory).

above  
mMs above parameter (integer). Default is "1500".

between  
mMs between parameter (integer). Default is "400".

features  
vector of row indices (optional).

feature.names  
vector of corresponding feature names (additionally to features).
Details

This function takes an EList$E- or EListRaw$E-matrix (e.g., temp <-elist$E) extended by row names comprising BRC-IDs of the corresponding features. The BRC-IDs can be created via: brc <- paste(elist$genes[,1], elist$genes[,3], elist$genes[,2]). The BRC-row names can be defined as follows: rownames(temp) <- brc. Furthermore, the corresponding column name vectors, group labels and mMs-parameters are needed to perform the univariate differential analysis. This analysis covers inter alia p-value computation, p-value adjustment (method: Benjamini & Hochberg, 1995), and fold change computation. Since the results table is usually large, a path for saving the results can be defined via output.path. Optionally, a vector of row indices (features) and additionally (not mandatory for subset analysis) a vector of corresponding feature names (feature.names) can be forwarded to perform the analysis for a feature subset.

Value

A matrix containing the analysis results is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
c1 <- paste(rep("AD",20), 1:20, sep="")
c2 <- paste(rep("NDC",20), 1:20, sep="")
mMs.matrix1 <- mMs.matrix2 <- mMsMatrix(x=20, y=20)
temp <- elist$E
rownames(temp) <- paste(elist$genes[,1], elist$genes[,2], elist$genes[,2])
diffAnalysis(input=temp, label1=c1, label2=c2, class1="AD", class2="NDC",
mMs.matrix1=mMs.matrix1, mMs.matrix2=mMs.matrix2, above=1500,
between=400)

loadGPR

Importing raw data from gpr files.

Description

Constructs an EListRaw object from a set of gpr files containing ProtoArray data or other protein microarray data.

Usage

loadGPR(gpr.path = NULL, targets.path = NULL, array.type = NULL, aggregation = "none", array.columns = list(E = "F635 Median", Eb = "B635 Median"), array.annotation = c("Block", "Column", "Row", "Description", "Name", "ID"), description = NULL, description.features = NULL, description.discard = NULL)
Arguments

gpr.path string indicating the path to a folder containing gpr files (mandatory).

targets.path string indicating the path to targets file (see limma, mandatory).

array.type string indicating the microarray type of the imported gpr files. Only for ProtoArray duplicate aggregation will be performed. The possible options are: "ProtoArray", "HuProt" and "other" (mandatory).

aggregation string indicating which type of ProtoArray spot duplicate aggregation should be performed. If "min" is chosen, the value for the corresponding feature will be the minimum of both duplicate values. If "mean" is chosen, the arithmetic mean will be computed. Alternatively, no aggregation will be performed, if "none" is chosen. The default is "min" (optional).

array.columns list containing the column names for foreground intensities (E) and background intensities (Eb) in the gpr files that is passed to limma’s "read.maimages" function (optional).

array.annotation string vector containing further mandatory column names that are passed to limma (optional).

description string indicating the column name of an alternative column containing the information which spot is a feature, control or to be discarded for gpr files not providing the column "Description" (optional).

description.features string containing a regular expression identifying feature spots. Mandatory when description has been defined.

description.discard string containing a regular expression identifying spots to be discarded (e.g., empty spots). Mandatory when description has been defined.

Details

This function is partially a wrapper to limma’s function read.maimages() featuring optional duplicate aggregation for ProtoArray data. Paths to a targets file and to a folder containing gpr files (all gpr files in that folder that are listed in the targets file will be read) are mandatory. The folder "R_HOME/library/PAA/extdata" contains an exemplary targets file that can be used as a template. If array.type (also mandatory) is set to "ProtoArray", duplicate spots can be aggregated. The corresponding method ("min", "mean" or "none") can be specified via the argument aggregation. As another ProtoArray-specific feature, control spot data and information will be stored in additional components of the returned object (see below). Arguments array.columns and array.annotation define the columns where read.maimages() will find foreground and background intensity values as well as other important columns. For array.annotation the default columns "Block", "Column", "Row", "Description", "Name" and "ID" are mandatory.

If the column "Description" is not provided by the gpr files for ProtoArrays a makeshift column will be constructed from the column "Name" automatically. For other microarrays the arguments description, description.features and description.discard can be used to provide the mandatory information (see the example below).

Value

An extended object of class EListRaw (see the documentation of limma for details) is returned. If array.type is set to "ProtoArray" (default), the object provides additional components for control spot data: C, Cb and cgenes which are analogous to the probe spot data E, Eb and genes. Moreover,
the returned object always provides the additional component `array.type` indicating the type of the imported protein microarray data (e.g., "ProtoArray").

**Note**

Don’t forget to check column names in your gpr files. They may differ from the default settings of `loadGPR()` and should be renamed to the default column names (see also the exemplary gpr files accompanying PAA as a reference for the default column names). At worst, important columns in your gpr files may be completely missing and should be added in order to provide all information needed by PAA.

Note that if `array.type` is not "ProtoArray", neither aggregation will be done nor controls components will be added to the returned object of class `EListRaw`.

**Author(s)**

Michael Turewicz, <michael.turewicz@rub.de>

**References**

The package `limma` by Gordon Smyth et al. can be downloaded from Bioconductor (http://www.bioconductor.org/).


**Examples**

```r
  gpr <- system.file("extdata", package="PAA")
  targets <- list.files(system.file("extdata", package="PAA"),
                        pattern = "dummy_targets", full.names=TRUE)
  elist <- loadGPR(gpr.path=gpr, targets.path=targets, array.type="ProtoArray")

  # Example showing how to use the arguments description, description.features and
  # description.discard in order to construct a makeshift column 'Description'
  # for gpr files without this column. Please see also the exemplary gpr files
  # coming with PAA.
  targets2 <- list.files(system.file("extdata", package="PAA"),
                         pattern = "dummy_no_descr_targets", full.names=TRUE)
  elist2 <- loadGPR(gpr.path=gpr, targets.path=targets2, array.type="other",
                    description="Name", description.features="^Hs~", description.discard="Empty")
```

---

**mMsMatrix**

*Compute a reference minimum M statistic (n1 x n2)-matrix.*

**Description**

Computes a reference minimum M statistic (n1 x n2)-matrix (mMs matrix).

**Usage**

```r
  mMsMatrix(x, y)
```
Arguments

\( x \) integer, first dimension (i.e., number of samples in group 1) of the mMs matrix to be computed (mandatory).

\( y \) integer, second dimension (i.e., number of samples in group 2) of the mMs matrix to be computed (mandatory).

Details

For feature preselection the "minimum M Statistic" (mMs) proposed by Love B. can be used. The mMs is a univariate measure that is sensitive to population subgroups. To avoid redundant mMs computations for a large number of features (e.g., ca. 9500 features on ProtAarray v5) a reference matrix containing all relevant mMs values can be precomputed. For this purpose, only two parameters are needed: the number of samples in group 1 \( (n1) \) and the number of samples in group 2 \( (n2) \). According to mMs definition for each matrix element \( (i,m) \) a mMs value (= the probability of) for having \( m \) values in group 1 larger than the \( i \)-th largest value in group 2 is computed.

Value

A \((n1 \times n2)\)-matrix containing all mMs values for group 1 and group 2.

Note

To check whether a feature is more prevalent in group 1 or in group 2, PAA needs both the mMs for having \( m \) values in group 1 larger than the \( i \)-th largest element in group 2 as well as the mMs for having \( m \) values in group 2 larger than the \( i \)-th largest element in group 1. Hence, always both must be computed: \( \text{mMsMatrix}(n1,n2) \) and \( \text{mMsMatrix}(n2,n1) \).

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

References


Examples

```r
#exemplary computation for a group 1 comprising 10 arrays and a group 2
#comprising 12 arrays
mMs.matrix1 <- mMsMatrix(x=10, y=12)
mMs.matrix2 <- mMsMatrix(x=12, y=10)
```

normalizeArrays

Normalize microarray data.

Description

Normalizes \texttt{EListRaw} data and returns an \texttt{EList} object containing normalized data in \texttt{log2} scale.
normalizeArrays

normalizeArrays(elist = NULL, method = "quantile", cyclicloess.method = "pairs", controls="internal", group1 = NULL, group2 = NULL, output.path=NULL)

Arguments

elist EListRaw object containing raw data to be normalized (mandatory).
method string indicating the normalization method ("cyclicloess", "quantile", "vsn" or "rlm") to be used (mandatory).
cyclicloess.method string indicating which type of cyclicloess normalization ("pairs", "fast", "affy") should be performed (optional).
controls string indicating the ProtoArray controls for rlm normalization (optional). Valid options are "internal" (default), "external", "both" or a regular expression defining a specific control or a specific set of controls.
group1 vector of integers (column indices) indicating all group 1 samples (optional).
group2 vector of integers (column indices) indicating all group 2 samples (optional).
output.path output.path for ProtoArray rlm normalization (optional).

Details

This function is partially a wrapper to limma’s function normalizeBetweenArrays() for inter-array normalization featuring optional groupwise normalization when the arguments group1 AND group2 are assigned. For more information on "cyclicloess", "quantile" or "vsn" see the documentation of the limma package. Furthermore, for ProtoArrays robust linear normalization ("rlm", see Sboner A. et al.) is provided.

For rlm normalization (method = "rlm") the additional argument controls needs to be specified in order to select a set of controls used for normalization. Valid options are "internal" (default), "external" and "both" which refer to the following sets of ProtoArray controls:

- internal: The set of all internal controls spotted on the ProtoArray. The human-IgG series and anti-human-IgG series, which respond to serum and secondary antibodies.
- external: The V5-CMK1 series spotted on the ProtoArray which responds to exogenously added anti-V5 antibody (external control).
- both: The combined set of both the internal and the external controls (i.e., the human-IgG and anti-human-IgG series and the V5-CMK1 series).

Moreover, via controls a regular expression can be passed in order to select a more specific group of controls. Please check the column "Name" in your gpr files in order to obtain the complete list of names of all controls spotted on the ProtoArray. In the following some examples of valid regular expressions are given:

- "^HumanIg" Only human IgGs and IgAs are selected (esp., no anti-human Igs).
- "Anti-HumanIgA" Only anti-human-IgAs are selected (esp., no human IgGs and IgAs).
- "(Anti-HumanIg|^V5control|BSA|ERa)" Only anti-human IgGs and anti-human IgAs, the V5-CMK1 series, BSA and ERa are selected.
- "HumanIgG" Only human IgGs and anti-human IgGs are selected.
- "V5control" Only the V5-CMK1 series is selected.
plotArray

Value

An EList object with the normalized data in log2 scale is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

References

The package limma by Gordon Smyth et al. can be downloaded from Bioconductor (http://www.bioconductor.org/).


Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
normalized.elist <- normalizeArrays(elist=elist, method="quantile")

plotArray

Plot ProtoArray expression intensities in the original arrangement mimicking the original scan image.

Description

Uses the “Block”, “Row” and “Column” information of an EList or EListRaw object to resemble the original positions on the array(s). The resulting plot is similar to the original scan image of the considered array(s). Thus, this function is a visualization tool that can be used to visualize protein microarrays for which the original scan image is not available. Visual inspection of the spatial expression pattern can then identify possible local tendencies and strong spatial biases. Moreover, the array can be inspected at all stages of the preprocessing workflow in order to check the impact of the particular methods that have been applied.

Usage

plotArray(elist=NULL, idx=NULL, data.type="fg", log=NULL, normalized=NULL, aggregation=NULL, colpal="heat.colors", graphics.device="tiff", output.path=NULL)

Arguments

elist EList or EListRaw object (mandatory).
idx integer, vector of integers or the string "all" indicating the column indices of the sample(s) for drawing the plot(s) (mandatory).
data.type string indicating whether the foreground ("fg") or background ("bg") data should be plotted. The default is "fg" (optional).
plotArray

log logical indicating whether the input data is logarithmized. If TRUE the log2 scale is expected. If FALSE a log2-transformation will be performed (mandatory).

normalized logical indicating whether elist was normalized (mandatory).

aggregation string indicating whether the data stored in elist has been aggregated and, if this is the case, which method has been used by the function loadGPR(). Possible values are "min", "mean" and "none" (mandatory).

colpal string indicating the color palette for the plot(s). The default is "heat.colors" (optional).

graphics.device string indicating the file format for the plot(s) saved in output.path. Accepted values are "tiff" and "png". The default is "tiff" (optional).

output.path string indicating the output path for the plots (optional).

Details

This function allows plotting of protein microarray data using the gplots function heatmap.2() for visual quality control. The data obtained from an EList or ELiStRaw object is re-ordered and represented in the same way the spots are ordered on the actual microarray. Consequently, the resulting plot is similar to the original scan image of the considered array. This allows for visual control and assessment of possible patterns in spatial distribution.

Mandatory arguments are elist, idx, log, normalized and aggregation. While elist specifies the EList or ELiStRaw object to be used, idx designates the array column index in elist to plot a single array from the EList object. Alternatively, a vector (e.g., 1:5) or the string "all" can be designated to include multiple, respectively, all arrays that were imported.

Furthermore, data.type allows for plotting of "fg", foreground data (i.e., elist$E and elist$C), which is the default or "bg", background data (i.e., elist$Eb and elist$Cb).

The normalization approaches of PAA which comprise also data logarithmization do not include control data. With normalized=TRUE it is indicated that the input data was normalized, so the control data will be logarithmized (log2) before plotting as well. However, since the complete data (foreground and background values of protein features and control spots) can be logarithmized regardless of normalization the argument log states whether the designated data is already logarithmized (note: log2 scale is always expected).

The parameter aggregation indicates whether the protein microarray data has been aggregated by loadGPR() and, if so, which method has been used.

Moreover, the parameter colpal defines the color palette that will be used for the plot. Some exemplary values are "heat.colors" (default), "terrain.colors", "topo.colors", "greenred" and "bluered".

Finally, the output path optionally can be specified with the argument output.path to save the plot(s). Then, one or more tiff or png file(s) containing the corresponding plot(s) are saved into the subfolder "array_plots".

Value

No value is returned.

Note

Please note the instructions of the PAA function loadGPR(). Note that the data has to be imported including controls to avoid annoying gaps in the plot (for ProtoArrays this is done automatically and for other types of arrays the arguments description, description.features and
**plotFeatures**

description. discard must be defined). Note that the data can be imported without aggregation by loadGPR() (when aggregation="none") in order to inspect the array visually with plotArray() before duplicate aggregation.

**Author(s)**

Daniel Bemmerl and Michael Turewicz <michael.turewicz@rub.de>

**References**

The package gplots by Gregory R. Warnes et al. can be downloaded from CRAN (http://CRAN.R-project.org/package=gplots).


**Examples**

```r
wd <- system.file(package="PAA")
load(paste(cwd, "/extdata/BadData.RData", sep=""))
plotArray(elist=bad.elist, idx=1, data.type="bg", log=FALSE, normalized=FALSE,
aggregation="none")
```

**plotFeatures**  
*Plot intensities of features.*

**Description**

Plots intensities of all given features (one sub-plot per feature) in group- specific colors.

**Usage**

```r
plotFeatures(features = NULL, elist = NULL, n1 = NULL, n2 = NULL,
             group1 = "group1", group2 = "group2", output.path = NULL)
```

**Arguments**

- `features` vector containing "BRC"-IDs (mandatory).
- `elist` EListRaw or EList object containing all intensity data in log2 scale (mandatory).
- `n1` integer indicating the sample size of group 1 (mandatory).
- `n2` integer indicating the sample size of group 2 (mandatory).
- `group1` class label of group 1.
- `group2` class label of group 2.
- `output.path` string indicating the folder where the figure will be saved (optional).
plotFeaturesHeatmap

Plot feature intensities as a heatmap.

Description

Plots intensities of given features as a heatmap.

Usage

plotFeaturesHeatmap(features = NULL, elist = NULL, n1 = NULL, n2 = NULL, output.path = NULL, description=FALSE)
Arguments

- **features**: vector containing "BRC"-IDs (mandatory).
- **elist**: ELList or ELList object containing all intensity data in log2 scale (mandatory).
- **n1**: integer indicating the sample size of group 1 (mandatory).
- **n2**: integer indicating the sample size of group 2 (mandatory).
- **output.path**: path for saving the heatmap as a tiff file (default: NULL).
- **description**: if TRUE, features will be described via protein names instead of UniProtKB accessions (default: FALSE).

Details

Plots intensities of all features given in the vector `features` via their corresponding "BRC"-IDs as a heatmap. If `description` is TRUE (default: FALSE), features will be described via protein names instead of UniProtKB accessions. Furthermore, if `output.path` is not NULL, the heatmap will be saved as a tiff file in `output.path`. This function can be used to check whether the selected features are differential.

Value

No value is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

```r
cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
#elist <- elist[elist$genes$Block < 10,]

#c1 <- paste(rep("AD",20), 1:20, sep="")
#c2 <- paste(rep("NDC",20), 1:20, sep="")

#pre.sel.results <- preselect(elist=elist, columns1=c1, columns2=c2, label1="AD", label2="NDC", discard.threshold=0.1, fold.thresh=1.9, discard.features=TRUE, method="tTest")
#elist <- elist[-pre.sel.results$discard,]

#selectFeatures.results <- selectFeatures(elist,n1=20,n2=20,label1="AD", label2="NDC", selection.method="rf.rfe",preselection.method="none",subruns=2, k=2,candidate.number=20,method="frequency")

load(paste(cwd, "/extdata/selectFeaturesResultsFreq.RData", sep=""))
plotFeaturesHeatmap(features=selectFeatures.results$features, elist=elist, n1=20, n2=20, description=TRUE)
```
plotFeaturesHeatmap.2  Alternative function to plot feature intensities as a heatmap.

Description

This function is an alternative to `plotFeaturesHeatmap()` and is based on the function `heatmap.2()` provided by the package `gplots`.

Usage

```r
plotFeaturesHeatmap.2(features = NULL, elist = NULL, n1 = NULL, n2 = NULL, output.path = NULL, description=FALSE)
```

Arguments

- `features`  vector containing the selected features as "BRC"-IDs (mandatory).
- `elist`  `ELlistRaw` or `ELlist` object containing all intensity data in log2 scale (mandatory).
- `n1`  integer indicating the sample size of group 1 (mandatory).
- `n2`  integer indicating the sample size of group 2 (mandatory).
- `output.path`  path for saving the heatmap as a png file (default: NULL).
- `description`  if TRUE, features will be described via protein names instead of UniProtKB accessions (default: FALSE).

Details

Plots intensities of all features given in the vector `features` via their corresponding "BRC"-IDs as a heatmap. If `description` is TRUE (default: FALSE), features will be described via protein names instead of UniProtKB accessions. Furthermore, if `output.path` is not NULL, the heatmap will be saved as a png file in `output.path`. This function can be used to check whether the selected features are differential.

`plotFeaturesHeatmap.2()` is an alternative to `plotFeaturesHeatmap()` and is based on the function `heatmap.2()` provided by the package `gplots`.

Value

No value is returned.

Author(s)

Ivan Grishagin (Rancho BioSciences LLC, San Diego, CA, USA), John Obenauer (Rancho BioSciences LLC, San Diego, CA, USA) and Michael Turewicz (Ruhr-University Bochum, Bochum, Germany), <michael.turewicz@rub.de>
References
The package gplots by Gregory R. Warnes et al. can be downloaded from CRAN (http://CRAN.R-project.org/package=gplots).

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
#elist <- elist[elist$genes$Block < 10,]

#c1 <- paste(rep("AD",20), 1:20, sep="")
#c2 <- paste(rep("NDC",20), 1:20, sep="")

#pre.sel.results <- preselect(elist=elist, columns1=c1, columns2=c2, label1="AD", label2="NDC", discard.threshold=0.1, fold.thresh=1.9, discard.features=TRUE, method="tTest")
#elist <- elist[-pre.sel.results$discard,]

#selectFeatures.results <- selectFeatures(elist, n1=20, n2=20, label1="AD", label2="NDC", selection.method="rf.rfe", preselection.method="none", subruns=2, k=2, candidate.number=20, method="frequency")

load(paste(cwd, "/extdata/selectFeaturesResultsFreq.RData", sep=""))
plotFeaturesHeatmap.2(features=selectFeatures.results$features, elist=elist, n1=20, n2=20, description=TRUE)

plotMAPlots

Check normalization results with MA plots.

Description
Draws MA plots of raw data and data after all kinds of normalization provided by PAA.

Usage
plotMAPlots(elist = NULL, idx="all", include.rlm=FALSE, controls="internal", output.path = NULL)

Arguments
elist EListRaw object containing raw data (mandatory).
idx integer indicating the column index of the sample for drawing MA plots or the string 'all' for drawing MA plots for all samples (default: all).
include.rlm logical indicating whether RLM normalization should be included (for ProtoArrays only; deafult: FALSE).
controls string indicating the ProtoArray controls for rlm normalization (optional). Valid options are "internal" (default), "external", "both" or a regular expression defining a specific control or a specific set of controls.
output.path string indicating the folder where the tiff files will be saved (mandatory when idx="all").

Details

When idx="all" (default) for each microarray a tiff file containing MA plots for raw data, cyclecoess normalized data, quantile normalized data and vsn normalized data (and, optionally, for ProtoArrays, rlm normalized data) will be created. When idx is an integer indicating the column index of a particular sample, MA plots only for this sample will be created. For A and M value computation the artificial median array is used as reference signal. All figures can be saved in output.path (mandatory when idx="all"). The resulting MA plots can be used to compare the results of the different normalization methods.

Value

No value is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block == 1,]
plotMAPlots(elist=elist, idx=1)

Description

Checks normalization results with boxplots.

Usage

plotNormMethods(elist = NULL, include.rlm=FALSE, controls="internal", output.path = NULL)

Arguments

eлист EListRaw object containing raw data (mandatory).
include.rlm logical indicating whether RLM normalization should be included (for ProtoArrays only, deafult: FALSE).
controls string indicating the ProtoArray controls for rlm normalization (optional). Valid options are “internal” (default), “external”, “both” or a regular expression defining a specific control or a specific set of controls.
output.path string indicating a folder for saving the boxplots as tiff files (optional).
Details

For each normalization approach sample-wise boxplots are created. All boxplots can be saved as high-quality tiff files (when an output path has been specified via the argument `output.path`). The resulting boxplots can be used to compare the results of different normalization methods.

Value

No value is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block == 1,]
plotNormMethods(elist=elist)

---

**preselect**

Score and preselect features.

Description

Iterates all features to score them via mMs, Student's t-test, or mRMR. Optionally, a list of not informative features can be obtained (for discarding them).

Usage

```r
preselect(elist=NULL, columns1=NULL, columns2=NULL, label1="A", label2="B",
log=NULL, discard.threshold=0.5, fold.thresh=1.5, discard.features=TRUE,
mMs.above=1500, mMs.between=400, mMs.matrix1=NULL,
mMs.matrix2=NULL, method=NULL)
```

Arguments

- **elist** EListRaw or EList object (mandatory).
- **columns1** column name vector (string vector) of group 1 (mandatory).
- **columns2** column name vector (string vector) of group 2 (mandatory).
- **label1** class label of group 1.
- **label2** class label of group 2.
- **log** indicates whether the data is in log scale (mandatory; note: if TRUE log2 scale is expected).
- **discard.threshold** positive numeric between 0 and 1 indicating the maximum mMs or, respectively, the maximum t-test p-value for features to be included for further analysis. Default is "0.5".
- **fold.thresh** numeric indicating the minimum fold change for features to be included for further analysis. Default is "1.5".
discard.features

boolean indicating whether merely feature scores (i.e., mMs or t-test p-values) (="FALSE") or feature scores and a discard list (="TRUE") should be returned. Default is "TRUE".

mMs.above

mMs above parameter (integer). Default is "1500".

mMs.between

mMs between parameter (integer). Default is "400".

mMs.matrix1

precomputed mMs reference matrix (see mMsMatrix()) for group 1 (mandatory).

mMs.matrix2

precomputed mMs reference matrix (see mMsMatrix()) for group 2 (mandatory).

method

preselection method ("mMs", "tTest", "mrmr"). Default is "mMs".

Details

This function takes an EListRaw or EList object and group-specific column vectors. Furthermore, the class labels of group 1 and group 2 are needed. If discard.features is "TRUE" (default), all features that are considered as not differential will be collected and returned for discarding.

If method = "mMs", additionally precomputed mMs reference matrices (see mMsMatrix()) for group 1 and group 2 will be needed to compute mMs values (see Love B.) as scoring method. All mMs parameters (mMs.above and mMs.between) can be set. The defaults are "1500" for mMs.above and "400" for mMs.between. Features having an mMs value larger than discard.threshold (here: numeric between 0.0 and 1.0) or do not satisfy the minimal absolute fold change fold.thresh are considered as not differential.

If method = "tTest", Student’s t-test will be used as scoring method. Features having a p-value larger than discard.threshold (here: numeric between 0.0 and 1.0) or do not satisfy the minimal absolute fold change fold.thresh are considered as not differential.

If method = "mrmr", mRMR scores for all features will be computed as scoring method (using the function mRMR.classic() of the CRAN R package mRMRe). Features that are not the discard.threshold (here: integer indicating a number of features) best features regarding their mRMR score are considered as not differential.

Value

If discard.features is "FALSE": matrix containing metadata, feature scores and intensity values for the whole data set.

If discard.features is "TRUE": a list containing:

results

matrix containing metadata, feature scores and intensity values for the whole data set.

discard

vector containing row indices (= features) for discarding features considered as not differential.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

References

The software "Prospector" for ProtoArray analysis can be downloaded from the Thermo Fisher Scientific web page (https://www.thermofisher.com).


The package limma by Gordon Smyth et al. can be downloaded from Bioconductor (https://www.bioconductor.org).


Examples

```r
cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
c1 <- paste(rep("AD",20), 1:20, sep="")
c2 <- paste(rep("NDC",20), 1:20, sep="")
preselect(elist, columns1=c1, columns2=c2, label1="AD", label2="NDC", log=FALSE,
discard.threshold=0.5, fold.thresh=1.5, discard.features=TRUE, method="tTest")
```

`printFeatures`  
`Print features into a table.`

**Description**

Creates a table containing the given features (e.g., the selected biomarker candidate panel).

**Usage**

```r
printFeatures(features = NULL, elist = NULL, output.path = NULL)
```

**Arguments**

- `features`  
  vector containing "BRC"-IDs (mandatory).
- `elist`  
  EListRaw or EList object containing all intensity data (mandatory).
- `output.path`  
  string indicating the folder where the table will be saved as a txt file (optional).

**Details**

Creates a table containing the given features (e.g., the selected biomarker candidate panel) as well as additional information. When `output.path` is defined this table will be saved in a txt file ("candidates.txt").

**Value**

Table containing the given features.

**Author(s)**

Michael Turewicz, <michael.turewicz@rub.de>
pvaluePlot

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
#elist <- elist[elist$genes$Block < 10,]
#c1 <- paste(rep("AD",20), 1:20, sep="")
#c2 <- paste(rep("NDC",20), 1:20, sep="")
#pre.sel.results <- preselect(elist=elist, columns1=c1, columns2=c2, label1="AD", # label2="NDC", discard.threshold=0.1, fold.thresh=1.9, discard.features=TRUE, # method="tTest")
#elist <- elist[-pre.sel.results$discard,]
#selectFeatures.results <- selectFeatures(elist,n1=20,n2=20,label1="AD", # label2="NDC",selection.method="rf.rfe",preselection.method="none",subruns=2, # k=2,candidate.number=20,method="frequency")
load(paste(cwd, "/extdata/selectFeaturesResultsFreq.RData", sep=""))
printFeatures(features=selectFeatures.results$features, elist=elist)

pvaluePlot

Description

Draws a p-value plot to visualize the p-values for all features stored in an \texttt{EList} or \texttt{EListRaw} object.

Usage

pvaluePlot(elist=NULL, group1=NULL, group2=NULL, log=NULL, method="tTest", output.path=NULL, tag="", mMs.matrix1=NULL, mMs.matrix2=NULL, above=1500, between=400, adjust=FALSE)

Arguments

elist \hspace{1cm} \text{EList or EListRaw object (mandatory).}

group1 \hspace{1cm} \text{vector of column names for group 1 (mandatory).}

group2 \hspace{1cm} \text{vector of column names for group 2 (mandatory).}

log \hspace{1cm} \text{indicates whether the data is in log scale (mandatory; note: if TRUE log2 scale is expected).}

method \hspace{1cm} \text{method for p-value computation: "tTest" or "mMs". Default is "tTest".}

output.path \hspace{1cm} \text{string indicating a path for saving the plot (optional).}

tag \hspace{1cm} \text{string that can be used for tagging the saved plot (optional).}

mMs.matrix1 \hspace{1cm} \text{precomputed M score reference matrix (see \texttt{mMsMatrix()}) for group 1 (mandatory when method = "mMs").}

mMs.matrix2 \hspace{1cm} \text{precomputed M score reference matrix (see \texttt{mMsMatrix()}) for group 2 (mandatory when method = "mMs").}

above \hspace{1cm} \text{M score above parameter (integer). Default is "1500".}

between \hspace{1cm} \text{M score between parameter (integer). Default is "400".}

adjust \hspace{1cm} \text{logical indicating whether p-values should be adjusted. Default is FALSE.}
Details

This function takes an EList or EListRaw object and the corresponding column name vectors to draw a plot of p-values for all features stored in elist (sorted in increasing order and in log2 scale). The p-value computation method ("tTest" or "mMs") can be set via the argument method. Furthermore, when adjust=TRUE adjusted p-values (method: Benjamini & Hochberg, 1995, computed via p.adjust()) will be used. When an output path is defined (via output.path) the plot will be saved as a tiff file.

Value

No value is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
c1 <- paste(rep("AD",20), 1:20, sep="")
c2 <- paste(rep("NDC",20), 1:20, sep="")
pvaluePlot(elist=elist, group1=c1, group2=c2, log=FALSE, method="tTest",
tag="_tTest", adjust=FALSE)

selectFeatures

Select features using frequency-based or ensemble feature selection.

Description

Performs a multivariate feature selection using frequency-based feature selection (based on RF-RFE, RJ-RFE or SVM-RFE) or ensemble feature selection (based on SVM-RFE).

Usage

selectFeatures(elist = NULL, n1 = NULL, n2 = NULL, label1 = "A", label2 = "B",
log=NULL, cutoff = 10, selection.method = "rf.rfe",
preselection.method = "mMs", subruns = 100, k = 10, subsamples = 10,
bootstraps = 10, candidate.number = 300, above=1500, between=400,
panel.selection.criterion="accuracy", importance.measure="MDA", ntree = 500,
method = "frequency")

Arguments

elist EListRaw or EList object containing all microarray data (mandatory).
n1 integer indicating the sample number in group 1 (mandatory).
n2 integer indicating the sample number in group 2 (mandatory).
label1 class label of group 1 (default: "A").
label2 class label of group 2 (default: "B").
selectFeatures

log indicates whether the data is in log scale (mandatory; note: if TRUE log2 scale is expected).
cutoff integer indicating how many features will be selected (default: 10).
selection.method string indicating the feature selection method: "rf.rfe" (default), "svm.rfe" or "rj.rfe". Has no effect when method="ensemble".
preselection.method string indicating the feature preselection method: "mMs" (default), "tTest", "mrmr" or "none". Has no effect when method="ensemble".
cutoff integer indicating how many features will be selected (default: 10). Has no effect when method="ensemble".
k integer indicating the number of k-fold cross validation subsets (default: 10, i.e., 10-fold CV).
subsamples integer indicating the number of subsamples for ensemble feature selection (default: 10). Has no effect when method="frequency".
bootstraps integer indicating the number of bootstrap samples for ensemble feature selection (default: 10). Has no effect when method="frequency" only.
candidate.number integer indicating how many features shall be preselected. Default is "300". Has no effect when method="ensemble".
above mMs above parameter (integer). Default is "1500". There will be no effect when method="ensemble".
between mMs between parameter (integer). Default is "400". There will be no effect when method="ensemble".
panel.selection.criterion indicating the panel selection criterion: "accuracy" (default), "sensitivity" or "specificity". No effect for method="ensemble".
importance.measure string indicating the random forest importance measure: "MDA" (default) or "MDG". Has no effect when method="ensemble".
ntree random forest parameter ntree (default: "500"). There will be no effect when method="ensemble".
mtry random forest parameter mtry (default: $\sqrt{p}$ where p is the number of predictors). Has no effect when method="ensemble".
plot logical indicating whether performance plots shall be plotted (default: FALSE).
output.path string indicating whether performance plots shall be plotted (default: FALSE).
verbose logical indicating whether additional information shall be printed to the console (default: FALSE).
method the feature selection method: "frequency" (default) for frequency-based or "ensemble" for ensemble feature selection.

Details

This function takes an EListRaw or EList object, group-specific sample numbers, group labels and parameters choosing and configuring a multivariate feature selection method (frequency-based or ensemble feature selection) to select a panel of differential features. When an output path is defined (via output.path) results will be saved on the hard disk and when verbose is TRUE additional information will be printed to the console.
Frequency-based feature selection (method="frequency"): The whole data is split into k cross validation training and test set pairs. For each training set a multivariate feature selection procedure is performed. The resulting k feature subsets are tested using the corresponding test sets (via classification). As a result, selectFeatures() returns the average k-fold cross validation classification accuracy as well as the selected feature panel (i.e., the union set of the k particular feature subsets). As multivariate feature selection methods random forest recursive feature elimination (RF-RFE), random jungle recursive feature elimination (RJ-RFE) and support vector machine recursive feature elimination (SVM-RFE) are supported. To reduce running times, optionally, univariate feature preselection can be performed (control via preselection.method). As univariate preselection methods mMs ("mMs"), Student’s t-test ("tTest") and mRMR ("mrmr") are supported. Alternatively, no preselection can be chosen ("none"). This approach is similar to the method proposed in Baek et al.

Ensemble feature selection (method="ensemble"): From the whole data the previously defined number of subsamples is drawn defining pairs of training and test sets. Moreover, for each training set a previously defined number of bootstrap samples is drawn. Then, for each bootstrap sample SVM-RFE is performed and a feature ranking is obtained. To obtain a final ranking for a particular training set, all associated bootstrap rankings are aggregated to a single ranking. To score the cutoff best features, for each subsample a classification of the test set is performed (using a svm trained with the cutoff best features from the training set) and the classification accuracy is determined. Finally, the stability of the subsample-specific panels is assessed (via Kuncheva index, Kuncheva LI, 2007), all subsample-specific rankings are aggregated, the top n features (defined by cutoff) are selected, the average classification accuracy is computed, and all these results are returned in a list. This approach has been proposed in Abeel et al.

Value

If method is "frequency", the results list contains the following elements:

- accuracy: average k-fold cross validation accuracy.
- sensitivity: average k-fold cross validation sensitivity.
- specificity: average k-fold cross validation specificity.
- features: selected feature panel.
- all.results: complete cross validation results.

If method is "ensemble", the results list contains the following elements:

- accuracy: average accuracy regarding all subsamples.
- sensitivity: average sensitivity regarding all subsamples.
- specificity: average specificity regarding all subsamples.
- features: selected feature panel.
- all.results: all feature ranking results.
- stability: stability of the feature panel (i.e., Kuncheva index for the subrun-specific panels).

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>
References


Examples

```r

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]

c1 <- paste(rep("AD",20), 1:20, sep="")
c2 <- paste(rep("NDC",20), 1:20, sep="")

pre.sel.results <- preselect(elist=elist, columns1=c1, columns2=c2, label1="AD", label2="NDC", log=FALSE, discard.threshold=0.1, fold.thresh=1.9, discard.features=TRUE, method="tTest")
elist <- elist[-pre.sel.results$discard,]

selectFeatures.results <- selectFeatures(elist, n1=20, n2=20, label1="AD", label2="NDC", log=FALSE, subsamples=2, bootstraps=1, candidate.number=20, method="ensemble")
```

shuffleData

Shuffles class labels to obtain random groups.

Description

Shuffles class labels of an EList or EListRaw object randomly to obtain two random groups (e.g. "A" and "B").

Usage

```r
shuffleData(elist=NULL, n1=NULL, n2=NULL, label1="A", label2="B")
```

Arguments

- `elist`: EList or EListRaw object (mandatory).
- `n1`: sample size of random group 1 (mandatory).
- `n2`: sample size of random group 2 (mandatory).
- `label1`: class label of random group 1 (default: "A").
- `label2`: class label of random group 2 (default: "B").

Details

Shuffles class labels of an EList or EListRaw object randomly to obtain two random groups (e.g. "A" and "B").
volcanoPlot

Value
EList or EListRaw object with random groups.

Author(s)
Michael Turewicz, <michael.turewicz@rub.de>

Examples
cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
shuffleData(elist=elist, n1=20, n2=20, label1="A", label2="B")

volcanoPlot

Draw a volcano plot.

Description
Draws a volcano plot to visualize differential features.

Usage
volcanoPlot(elist=NULL, group1=NULL, group2=NULL, log=NULL, method="tTest",
p.thresh=NULL, fold.thresh=NULL, output.path=NULL, tag=",", mMs.matrix1=NULL,
mMs.matrix2=NULL, above=1500, between=400)

Arguments
elist EList or EListRaw object (mandatory).
group1 vector of column names for group 1 (mandatory).
group2 vector of column names for group 2 (mandatory).
log indicates whether the data is in log scale (mandatory; note: if TRUE log2 scale
is expected; mandatory).
method method for p-value computation: "tTest" or "mMs". Default is "tTest".
p.thresh positive float number between 0 and 1 indicating the maximum p-value for features
to be considered as differential (e.g., "0.5"). This argument is optional.
fold.thresh float number indicating the minimum fold change for features to be considered
as differential (e.g., "1.5"). This argument is optional.
output.path string indicating a path for saving the plot (optional).
tag string that can be used for tagging the saved plot (optional).
mMs.matrix1 a precomputed M score reference matrix (see mMsMatrix()) for group 1 (mandar-
tory when method = "mMs").
mMs.matrix2 a precomputed M score reference matrix (see mMsMatrix()) for group 2 (mandar-
tory when method = "mMs").
above M score above parameter (integer). Default is "1500".
between M score between parameter (integer). Default is "400".
Details

This function takes an EList or EListRaw object and the corresponding column name vectors to draw a volcano plot. To visualize differential features, thresholds for p-values and fold changes can be defined. Furthermore, the p-value computation method ("mMs" or "tTest") can be set. When an output path is defined (via output.path) the plot will be saved as a tiff file.

Value

No value is returned.

Author(s)

Michael Turewicz, <michael.turewicz@rub.de>

Examples

cwd <- system.file(package="PAA")
load(paste(cwd, "/extdata/Alzheimer.RData", sep=""))
elist <- elist[elist$genes$Block < 10,]
c1 <- paste(rep("AD",20), 1:20, sep="")
c2 <- paste(rep("NDC",20), 1:20, sep="")
volcanoPlot(elist=elist, group1=c1, group2=c2, log=FALSE, method="tTest", p.thresh=0.01, fold.thresh=2)
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