xps

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`AffyRNAdeg` *Functions to assess RNA Degradation.*

Description

Functions to detect possible RNA degradation.

Usage

```
AffyRNAdeg(xps.data, treename = "*", qualopt = "raw", log.it = TRUE)

summaryAffyRNAdeg(rna.deg, signif.digits=3)

plotAffyRNAdeg(rna.deg, transform = "shift.scale", col = NULL, summary = FALSE,

xpsRNAdeg(object, ...)
```

Arguments

`xps.data`	object of class `QualTreeSet`.
`treename`	vector of tree names to export.
`qualopt`	option determining the data to which to apply qualification, one of ‘raw’, ‘adjusted’, ‘normalized’.
`log.it`	logical, if TRUE, then probe data is log2 transformed.
`rna.deg`	`list`, output from `AffyRNAdeg`.
`signif.digits`	number of significant digits to show.
`transform`	transform data before plotting, one of "shift.scale", "shift.only", "none".
`col`	vector of colors for plot, length is number of samples.
`summary`	logical, if TRUE then the slope of `summaryAffyRNAdeg` will be plotted.
`add.legend`	logical or integer, if TRUE or larger than zero then a legend with the tree names will be drawn.
`object`	object of class `QualTreeSet`.
`...`	optional arguments to be passed to `plotAffyRNAdeg`.

Details

Since probes within a probeset are ordered directionally from the 5' end to the 3' end, it is possible to estimate the quality (degradation status) of the RNA.

Function `AffyRNAdeg` averages the probe intensities by location in the probeset, with the average taken over all probesets with identical number of probes.

Function `summaryAffyRNAdeg` produces a single summary statistic for each array.

Function `plotAffyRNAdeg` produces a side-by-side plot of the averaged intensities. Option `transform = "none"` shows the averaged intensities for each array while option "shift" staggers the plots for individual arrays vertically to make the display easier to read, and option "scale" normalizes the averaged intensities so that the standard deviation is equal to one.

Setting parameter `add.legend = TRUE` will add a legend containing all tree names to the plot, while setting e.g. `add.legend = 6` will only show the first 6 tree names.

Value

`AffyRNAdeg` returns a `list` with following components:

`N`	number of probesets with identical number of probes
`sample.names`	names of samples, derived from affy batch object
`mns`	average intensity by probe position
`ses`	standard errors for probe position averages
`slope`	from linear regression of means.by.number
`pvalue`	from linear regression of means.by.number

Author(s)

Christian Stratowa, adapted from package affy

Examples

```
## Not run:
rnadeg <- xpsRNAdeg(rlm.all, treename="*", qualopt="raw")
plotAffyRNAdeg(rnadeg)

rnadeg <- AffyRNAdeg(rlm.all)
result <- summaryAffyRNAdeg(rnadeg)

## plot RNA degradation
plotAffyRNAdeg(rnadeg)

## plot slope of RNA degradation
plotAffyRNAdeg(rnadeg, summary = TRUE)

## End(Not run)
```

`AnalysisTreeSet-class`

Class AnalysisTreeSet

Description

This class provides the link to the `ROOT` analysis file and the `ROOT` trees contained therein. It extends class `ProcesSet`.

Objects from the Class

Objects are currently created using function `unifilter`.

Slots

`fltrset`**:** Object of class `"FilterTreeSet"` providing indirect access to the `ExprTreeSet` used and the `UniFilter` settings.

`scheme`**:** Object of class `"SchemeTreeSet"` providing access to `ROOT` scheme file.

`data`**:** Object of class `"data.frame"`. The data.frame contains the data of the unitest stored in `ROOT` data trees.

`params`**:** Object of class `"list"` representing relevant parameters.

`setname`**:** Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` trees are stored, currently 'UniFilterSet'.

`settype`**:** Object of class `"character"` describing the type of treeset stored in `setname`, currently 'unifilter'.

`rootfile`**:** Object of class `"character"` representing the name of the `ROOT` file, including full path.

`filedir`**:** Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`**:** Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`**:** Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"ProcesSet"`, directly. Class `"TreeSet"`, by class "ProcesSet", distance 2.

Methods

filterTreeset `signature(object = "AnalysisTreeSet")`: extracts slot `fltrset`.

getTreeData `signature(object = "AnalysisTreeSet")`: exports tree data and returns a data.frame.

validData `signature(object = "AnalysisTreeSet")`: extracts data.frame `data`.

validFilter `signature(object = "AnalysisTreeSet")`: extracts data.frame `data` from `fltrset`.

volcanoplot `signature(x = "AnalysisTreeSet")`: creates a volcano-plot.

Author(s)

Christian Stratowa

See Also

related classes `FilterTreeSet`.

Examples

```
showClass("AnalysisTreeSet")
```

`CallTreeSet-class` *Class CallTreeSet*

Description

This class provides the link to the `ROOT` call file and the `ROOT` trees contained therein. It extends class `ProcesSet`.

Objects from the Class

Objects are created using functions `mas5.call` or `dabg.call`, respectively.

Slots

`calltype`: Object of class `"character"` representing the call type, i.e. ‘mas5’ or ‘dabg’.

`detcall`: Object of class `"data.frame"`. The data.frame can contain the detection calls stored in `ROOT` call trees.

`scheme`: Object of class `"SchemeTreeSet"` providing access to `ROOT` scheme file.

`data`: Object of class `"data.frame"`. The data.frame can contain the data (i.e. p-values) stored in `ROOT` call trees.

`params`: Object of class `"list"` representing relevant parameters.

`setname`: Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` call trees are stored, usually ‘CallTreeSet’.

`settype`: Object of class `"character"` describing the type of treeset stored in `setname`, usually ‘preprocess’.

`rootfile`: Object of class `"character"` representing the name of the `ROOT` call file, including full path.

`filedir`: Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`: Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"ProcesSet"`, directly. Class `"TreeSet"`, by class "ProcesSet", distance 2.

Methods

attachCall `signature(object = "CallTreeSet")`: exports detection call data from `ROOT` call file and and saves as data.frame `detcall`.

attachPVal `signature(object = "CallTreeSet")`: exports call p-values from `ROOT` call file and and saves as data.frame `data`.

callplot `signature(x = "CallTreeSet")`: creates a barplot of percent present and absent calls.

presCall `signature(object = "CallTreeSet")`: extracts the detection call data.frame.

presCall<- `signature(object = "CallTreeSet", value = "data.frame")`: replaces the detection call data.frame.

pvalData `signature(object = "CallTreeSet")`: extracts the detection p-value data.frame.

pvalData<- `signature(object = "CallTreeSet", value = "data.frame")`: replaces the detection p-value data.frame.

removeCall `signature(object = "CallTreeSet")`: replaces data.frame `detcall` with an empty data.frame of dim(0,0).

removePVal `signature(object = "CallTreeSet")`: replaces data.frame `data` with an empty data.frame of dim(0,0).

validCall `signature(object = "CallTreeSet")`: extracts a subset of columns from data.frame `detcall`.

validPVal `signature(object = "CallTreeSet")`: extracts a subset of columns from data.frame `data`.

Author(s)

Christian Stratowa

See Also

related classes `DataTreeSet`, `ExprTreeSet`.

Examples

```
showClass("CallTreeSet")
```

`DataTreeSet-class` *Class DataTreeSet*

Description

This class provides the link to the `ROOT` data file and the `ROOT` trees contained therein. It extends class `ProcesSet`.

Objects from the Class

Objects can be created using the functions `import.data` or `root.data`.

Slots

`bgtreenames`: Object of class `"list"` representing the names of optional `ROOT` background trees.

`bgrd`: Object of class `"data.frame"`. The data.frame can contain background intensities stored in `ROOT` background trees.

`projectinfo`: Object of class `"ProjectInfo"` containing information about the project.

`scheme`: Object of class `"SchemeTreeSet"` providing access to `ROOT` scheme file.

`data`: Object of class `"data.frame"`. The data.frame can contain the data (e.g. intensities) stored in `ROOT` data trees.

`params`: Object of class `"list"` representing relevant parameters.

`setname`: Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` data trees are stored, usually 'DataTreeSet'.

`settype`: Object of class `"character"` describing the type of treeset stored in `setname`, usually 'rawdata'.

`rootfile`: Object of class `"character"` representing the name of the `ROOT` data file, including full path.

`filedir`: Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`: Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"ProcesSet"`, directly. Class `"TreeSet"`, by class "ProcesSet", distance 2.

Methods

addData `signature(object = "DataTreeSet")`: import additional CEL-files and update `ROOT` data file `rootfile`.

attachBgrd `signature(object = "DataTreeSet")`: exports background trees from `ROOT` data file and and saves as data.frame `bgrd`.

attachInten `signature(object = "DataTreeSet")`: exports intensity trees from `ROOT` data file and and saves as data.frame `data`.

attachMask `signature(object = "DataTreeSet")`: exports scheme tree from `ROOT` scheme file and and saves as data.frame `mask` of slot `scheme`.

background `signature(object = "DataTreeSet")`: extracts slot `bgrd`.

background<- `signature(object = "DataTreeSet", value = "data.frame")`: replaces slot `bgrd`.

bgtreeNames `signature(object = "DataTreeSet")`: extracts slot `bgtreenames`.

intensity `signature(object = "DataTreeSet")`: extracts slot `data`.

intensity<- `signature(object = "DataTreeSet", value = "data.frame")`: replaces slot `data`.

mm `signature(object = "DataTreeSet")`: extracts the mismatch intensities.

ncols `signature(object = "DataTreeSet")`: extracts the physical number of array columns from slot `scheme`.

nrows `signature(object = "DataTreeSet")`: extracts the physical number of array rows from slot `scheme`.

pm `signature(object = "DataTreeSet")`: extracts the perfect match intensities.

pmplot `signature(x = "DataTreeSet")`: creates a barplot of mean perfect match and mismatch intensities.

projectInfo `signature(object = "DataTreeSet")`: extracts slot `projectinfo`.

projectInfo<- `signature(object = "DataTreeSet", value = "ProjectInfo")`: replaces slot `projectinfo`.

rawCELName `signature(object = "DataTreeSet")`: returns the name(s) of the imported raw CEL-files.

removeBgrd `signature(object = "DataTreeSet")`: replaces data.frame `bgrd` with an empty data.frame of dim(0,0).

removeInten `signature(object = "DataTreeSet")`: replaces data.frame `data` with an empty data.frame of dim(0,0).

removeMask `signature(object = "DataTreeSet")`: replaces data.frame `mask` from slot `scheme` with an empty data.frame of dim(0,0).

validBgrd `signature(object = "DataTreeSet")`: extracts the valid data from data.frame `bgrd`.

validData `signature(object = "DataTreeSet")`: extracts a subset of valid data from data.frame `data`.

xpsBgCorrect `signature(object = "DataTreeSet")`: applies background correction methods. See `bgcorrect`.

xpsDABGCall `signature(object = "DataTreeSet")`: computes DABG call.

xpsFIRMA `signature(object = "DataTreeSet")`: computes FIRMA expression level and splice score.

xpsINICall `signature(object = "DataTreeSet")`: computes I/NI call.

xpsMAS4 `signature(object = "DataTreeSet")`: computes MAS4 expression levels.

xpsMAS5 `signature(object = "DataTreeSet")`: computes MAS5 expression levels.

xpsMAS5Call `signature(object = "DataTreeSet")`: computes MAS5 detection call.

xpsNormalize `signature(object = "DataTreeSet")`: applies normalization methods.

xpsPreprocess `signature(object = "DataTreeSet")`: applies normalization methods.

xpsQualify `signature(object = "DataTreeSet")`: applies quality control methods.

xpsQualityControl `signature(object = "DataTreeSet")`: applies quality control methods.

xpsRMA `signature(object = "DataTreeSet")`: computes RMA expression levels.

xpsSummarize `signature(object = "DataTreeSet")`: applies summarization methods.

Author(s)

Christian Stratowa

See Also

related classes `ExprTreeSet`, `CallTreeSet`.

Examples

```
showClass("DataTreeSet")
```

ExprTreeSet-class *Class ExprTreeSet*

Description

This class provides the link to the ROOT expression file and the ROOT trees contained therein. It extends class ProcesSet.

Objects from the Class

Objects are created using functions express, summarize or normalize, or the specialized functions rma, mas5 or mas4.

Slots

`exprtype`: Object of class "character" representing the exression type, i.e. ‘rma’, ‘mas5’, ‘mas4’ or ‘custom’.

`normtype`: Object of class "character" representing the normalization type, i.e. ‘mean’, ‘median’, ‘lowess’,‘supsmu’.

`scheme`: Object of class "SchemeTreeSet" providing access to ROOT scheme file.

`data`: Object of class "data.frame". The data.frame can contain the data (e.g. expression levels) stored in ROOT data trees.

`params`: Object of class "list" representing relevant parameters.

`setname`: Object of class "character" representing the name to the ROOT file subdirectoy where the ROOT data trees are stored, usually ‘PreprocesSet’.

`settype`: Object of class "character" describing the type of treeset stored in `setname`, usually ‘preprocess’.

`rootfile`: Object of class "character" representing the name of the ROOT data file, including full path.

`filedir`: Object of class "character" describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class "numeric" representing the number of ROOT trees stored in subdirectoy `setname`.

`treenames`: Object of class "list" representing the names of the ROOT trees stored in subdirectoy `setname`.

Extends

Class "ProcesSet", directly. Class "TreeSet", by class "ProcesSet", distance 2.

Methods

attachExpr `signature(object = "ExprTreeSet")`: exports expression trees from `ROOT` expression file and and saves as data.frame `data`.

corplot `signature(x = "ExprTreeSet")`: creates a correlation heat map.

exprType `signature(object = "ExprTreeSet")`: extracts slot `exprtype`.

exprType<- `signature(object = "ExprTreeSet", value = "character")`: replaces slot `exprtype`.

exprs `signature(object = "ExprTreeSet")`: extracts the expression data.frame.

exprs<- `signature(object = "ExprTreeSet", value = "data.frame")`: replaces the expression data.frame.

madplot `signature(x = "ExprTreeSet")`: creates a false color display of between arrays distances.

mvaplot `signature(x = "ExprTreeSet")`: creates an MvA-plot.

normType `signature(object = "ExprTreeSet")`: extracts slot `normtype`.

normType<- `signature(object = "ExprTreeSet", value = "character")`: replaces slot `normtype`.

nuseplot `signature(x = "ExprTreeSet")`: creates a NUSE-plot.

pcaplot `signature(x = "ExprTreeSet")`: plots first two principal components of PCA.

rleplot `signature(x = "ExprTreeSet")`: creates a RLE-plot.

removeExpr `signature(object = "ExprTreeSet")`: replaces data.frame `data` with an empty data.frame of dim(0,0).

se.exprs `signature(object = "ExprTreeSet")`: extracts the standard deviation data.frame.

validExpr `signature(object = "ExprTreeSet")`: extracts a subset of columns from data.frame `data`.

validSE `signature(object = "ExprTreeSet")`: extracts data columns from data.frame `se.exprs`.

xpsNormalize `signature(object = "ExprTreeSet")`: applies normalization methods.

xpsPreFilter `signature(object = "ExprTreeSet")`: applies prefiltering methods.

xpsUniFilter `signature(object = "ExprTreeSet")`: applies unifiltering methods.

Author(s)

Christian Stratowa

See Also

related classes `DataTreeSet`, `CallTreeSet`, `QualTreeSet`.

Examples

```
showClass("ExprTreeSet")
```

`Filter-class` *Base Class Filter*

Description

Base class for classes `PreFilter` and `UniFilter`.

Slots

`numfilters`: Object of class `"numeric"` giving the number of filters applied.

Methods

numberFilters `signature(object = "Filter")`: number of filters applied.

Author(s)

Christian Stratowa

See Also

related classes `PreFilter`, `UniFilter`.

Examples

```
showClass("Filter")
```

`FilterTreeSet-class` *Class FilterTreeSet*

Description

This class provides the link to the `ROOT` filter file and the `ROOT` trees contained therein. It extends class `ProcesSet`.

Objects from the Class

Objects are currently created using function `prefilter`.

Slots

`filter`: Object of class `"Filter"` currently providing access to the `PreFilter` settings.

`exprset`: Object of class `"ExprTreeSet"` providing direct access to the `ExprTreeSet` used for filtering.

`callset`: Object of class `"CallTreeSet"` providing direct access to the optional `CallTreeSet` used for filtering.

`scheme`: Object of class `"SchemeTreeSet"` providing access to `ROOT` scheme file.

`data`: Object of class `"data.frame"`. The data.frame contains the data of the filter stored in `ROOT` filter trees.

`params`: Object of class `"list"` representing relevant parameters.

`setname`: Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` trees are stored, currently 'PreFilterSet'.

`settype`: Object of class `"character"` describing the type of treeset stored in `setname`, currently 'prefilter'.

`rootfile`: Object of class `"character"` representing the name of the `ROOT` file, including full path.

`filedir`: Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`: Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"ProcessSet"`, directly. Class `"TreeSet"`, by class "ProcesSet", distance 2.

Methods

callTreeset `signature(object = "FilterTreeSet")`: extracts slot `callset`.

exprTreeset `signature(object = "FilterTreeSet")`: extracts slot `exprset`.

getTreeData `signature(object = "FilterTreeSet")`: exports tree data and returns a data.frame.

validData `signature(object = "FilterTreeSet")`: extracts data.frame `data`.

Author(s)

Christian Stratowa

See Also

related classes `AnalysisTreeSet`.

Examples

```
showClass("FilterTreeSet")
```

`PreFilter-class` *Class PreFilter*

Description

Class PreFilter allows to apply different filters to class `ExprTreeSet`, i.e. to the expression level data.frame `data`.

Objects from the Class

Objects can be created by calls of the form `new("PreFilter", ...)`.
Alternatively, the contructor `PreFilter` can be used.

Slots

- `mad`: Object of class `"list"` describing parameters for `madFilter`.
- `cv`: Object of class `"list"` describing parameters for `cvFilter`.
- `variance`: Object of class `"list"` describing parameters for `varFilter`.
- `difference`: Object of class `"list"` describing parameters for `diffFilter`.
- `ratio`: Object of class `"list"` describing parameters for `ratioFilter`.
- `gap`: Object of class `"list"` describing parameters for `gapFilter`.
- `hithreshold`: Object of class `"list"` describing parameters for `highFilter`.
- `lothreshold`: Object of class `"list"` describing parameters for `lowFilter`.
- `quantile`: Object of class `"list"` describing parameters for `quantileFilter`.
- `prescall`: Object of class `"list"` describing parameters for `callFilter`.
- `numfilters`: Object of class `"numeric"` giving the number of filters applied.

Extends

Class `"Filter"`, directly.

Methods

- **callFilter** `signature(object = "PreFilter")`: extracts slot `prescall`.
- **callFilter<-** `signature(object = "PreFilter", value = "character")`: replaces slot `prescall` with character vector c(cutoff, samples, condition).
- **cvFilter** `signature(object = "PreFilter")`: extracts slot `cv`.
- **cvFilter<-** `signature(object = "PreFilter", value = "numeric")`: replaces slot `cv` with numeric vector c(cutoff, trim, epsilon).
- **diffFilter** `signature(object = "PreFilter")`: extracts slot `difference`.
- **diffFilter<-** `signature(object = "PreFilter", value = "numeric")`: replaces slot `difference` with numeric vector c(cutoff, trim, epsilon).
- **gapFilter** `signature(object = "PreFilter")`: extracts slot `gap`.
- **gapFilter<-** `signature(object = "PreFilter", value = "numeric")`: replaces slot `gap` with numeric vector c(cutoff, window, trim, epsilon).
- **highFilter** `signature(object = "PreFilter")`: extracts slot `hithreshold`.
- **highFilter<-** `signature(object = "PreFilter", value = "character")`: replaces slot `hithreshold` with character vector c(cutoff, parameter, condition).
- **lowFilter** `signature(object = "PreFilter")`: extracts slot `lothreshold`.
- **lowFilter<-** `signature(object = "PreFilter", value = "character")`: replaces slot `lothreshold` with character vector c(cutoff, parameter, condition).
- **madFilter** `signature(object = "PreFilter")`: extracts slot `mad`.
- **madFilter<-** `signature(object = "PreFilter", value = "numeric")`: replaces slot `mad` with numeric vector c(cutoff, epsilon).
- **quantileFilter** `signature(object = "PreFilter")`: extracts slot `quantile`.
- **quantileFilter<-** `signature(object = "PreFilter", value = "numeric")`: replaces slot `quantile` with numeric vector c(cutoff, loquantile, hiquantile).
- **ratioFilter** `signature(object = "PreFilter")`: extracts slot `ratio`.

ratioFilter<- `signature(object = "PreFilter", value = "numeric")`: replaces slot `ratio` with numeric vector c(cutoff).

varFilter `signature(object = "PreFilter")`: extracts slot `variance`.

varFilter<- `signature(object = "PreFilter", value = "numeric")`: replaces slot `variance` with numeric vector c(cutoff, trim, epsilon).

Author(s)

Christian Stratowa

See Also

related classes `Filter`, `UniFilter`.

Examples

```
## for demonstration purposes only:  initialize all pre-filters
prefltr <- new("PreFilter")
madFilter(prefltr) <- c(0.5,0.01)
cvFilter(prefltr) <- c(0.3,0.0,0.01)
varFilter(prefltr) <- c(0.6,0.02,0.01)
diffFilter(prefltr) <- c(2.2,0.0,0.01)
ratioFilter(prefltr) <- c(1.5)
gapFilter(prefltr) <- c(0.3,0.05,0.0,0.01)
lowFilter(prefltr) <- c(4.0,3,"samples")
highFilter(prefltr) <- c(14.5,75.0,"percent")
quantileFilter(prefltr) <- c(3.0, 0.05, 0.95)
callFilter(prefltr) <- c(0.02,80.0,"percent")
str(prefltr)
```

`PreFilter-constructor` *Constructor for Class PreFilter*

Description

Constructor for class PreFilter allows to apply different filters to class `ExprTreeSet`, i.e. to the expression level data.frame `data`.

Usage

```
PreFilter(mad          = character(),
          cv           = character(),
          variance     = character(),
          difference   = character(),
          ratio        = character(),
          gap          = character(),
          lothreshold  = character(),
          hithreshold  = character(),
          quantile     = character(),
          prescall     = character())
```

Arguments

`mad`	`"character"` vector describing parameters for `madFilter`.
`cv`	`"character"` vector describing parameters for `cvFilter`.
`variance`	`"character"` vector describing parameters for `varFilter`.
`difference`	`"character"` vector describing parameters for `diffFilter`.
`ratio`	`"character"` vector describing parameters for `ratioFilter`.
`gap`	`"character"` vector describing parameters for `gapFilter`.
`lothreshold`	`"character"` vector describing parameters for `lowFilter`.
`hithreshold`	`"character"` vector describing parameters for `highFilter`.
`quantile`	`"character"` vector describing parameters for `quantileFilter`.
`prescall`	`"character"` vector describing parameters for `callFilter`.

Details

The PreFilter constructor allows to apply the following filters to class `ExprTreeSet`:

`mad`:	character vector c(cutoff,epsilon).
`cv`:	character vector c(cutoff,trim,epsilon).
`variance`:	character vector c(cutoff,trim,epsilon).
`difference`:	character vector c(cutoff,trim,epsilon).
`ratio`:	character vector c(cutoff).
`gap`:	character vector c(cutoff,window,trim,epsilon).
`lothreshold`:	character vector c(cutoff,parameter,condition).
`hithreshold`:	character vector c(cutoff,parameter,condition).
`quantile`:	character vector c(cutoff,loquantile,hiquantile).
`prescall`:	character vector c(cutoff,samples,condition).

Value

An object of type `"PreFilter"`

Note

Function `PreFilter` is used as constructor for class `PreFilter` so that the user need not know details for creating S4 classes.

Author(s)

Christian Stratowa

See Also

`Filter`, `UniFilter`

Examples

```
## fill character vectors within constructor
prefltr <- PreFilter(mad=c(0.5,0.01), prescall=c(0.002, 6,"samples"),
                     lothreshold=c(6.0,0.02,"mean"), hithreshold=c(10.5,80.0,"percent"))
str(prefltr)
```

```
## alternatively add character vectors as methods after creation of constructor
prefltr <- PreFilter()
madFilter(prefltr) <- c(0.5,0.01)
gapFilter(prefltr) <- c(0.3,0.05,0.0,0.01)
lowFilter(prefltr) <- c(4.0,3,"samples")
highFilter(prefltr) <- c(14.5,75.0,"percent")
str(prefltr)
```

`ProcesSet-class` *Class ProcesSet*

Description

This class provides access to class `SchemeTreeSet` for the derived classes `DataTreeSet`, `ExprTreeSet` and `CallTreeSet`. It extends class `TreeSet`.

Objects from the Class

Usually, no objects are created from it.

Slots

`scheme`: Object of class `"SchemeTreeSet"` providing access to `ROOT` scheme file.

`data`: Object of class `"data.frame"`. The data.frame can contain the data stored in `ROOT` data trees.

`params`: Object of class `"list"` representing relevant parameters.

`setname`: Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` trees are stored, usually one of ‘DataTreeSet’, ‘PreprocesSet’, ‘CallTreeSet’.

`settype`: Object of class `"character"` describing the type of treeset stored in `setname`, usually one of ‘rawdata’, ‘preprocess’.

`rootfile`: Object of class `"character"` representing the name of the `ROOT` file, including full path.

`filedir`: Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`: Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"TreeSet"`, directly.

Methods

boxplot `signature(x = "ProcessSet")`: creates a `boxplot` of the data from data.frame `data`.

chipName `signature(object = "ProcessSet")`: extracts slot `chipname` from slot `scheme`.

chipType `signature(object = "ProcessSet")`: extracts slot `chiptype` from slot `scheme`.

export `signature(object = "ProcessSet")`: exports `ROOT` trees as text file, see `export-methods`.

getTreeData `signature(object = "ProcessSet")`: exports tree data from `ROOT` file `rootfile`, and saves as data.frame `data`.

hist `signature(x = "ProcessSet")`: creates a plot showing the histograms for data.frame `data`.

image `signature(x = "ProcessSet")`: creates an image for each column from data.frame `data` or `bgrd`, respectively.

mboxplot `signature(x = "ProcessSet")`: creates an M-boxplot of the data from data.frame `data`.

schemeFile `signature(object = "ProcessSet")`: extracts the `ROOT` scheme file from slot `scheme`.

schemeFile<- `signature(object = "ProcessSet"), value = "character")`: replaces the `ROOT` scheme file from slot `scheme`.

schemeSet `signature(object = "ProcessSet")`: extracts slot `scheme`.

schemeSet<- `signature(object = "ProcessSet"), value = "SchemeTreeSet")`: replaces slot `scheme` with a different `SchemeTreeSet`.

validData `signature(object = "ProcessSet")`: extracts a subset of columns from data.frame `data`.

Author(s)

Christian Stratowa

See Also

derived classes `DataTreeSet`, `ExprTreeSet`, `CallTreeSet`, `QualTreeSet`.

Examples

```
showClass("ProcessSet")
```

`ProjectInfo-class` *Class ProjectInfo*

Description

This class allows to save the relevant project information in the `ROOT` data file and in class `DataTreeSet`.

Objects from the Class

Objects can be created by calls of the form
`new("ProjectInfo", submitter=[character], laboratory=[character], contact=[chara`
`...)`.
Alternatively, the constructor `ProjectInfo` can be used.

Slots

`submitter`: Object of class `"character"` representing the name of the submitter.

`laboratory`: Object of class `"character"` representing the laboratory of the submitter.

`contact`: Object of class `"character"` representing the contact address of the submitter.

`project`: Object of class `"list"` representing the project information.

`author`: Object of class `"list"` representing the author information.

`dataset`: Object of class `"list"` representing the dataset information.

`source`: Object of class `"list"` representing the sample source information.

`sample`: Object of class `"list"` representing the sample information.

`celline`: Object of class `"list"` representing the sample information for cell lines.

`primarycell`: Object of class `"list"` representing the sample information for primary cells.

`tissue`: Object of class `"list"` representing the sample information for tissues.

`biopsy`: Object of class `"list"` representing the sample information for biopsies.

`arraytype`: Object of class `"list"` representing the array information.

`hybridizations`: Object of class `"data.frame"` representing the hybridization information for each hybridization.

`treatments`: Object of class `"data.frame"` representing the treatment information for each hybridization.

Methods

projectInfo `signature(object = "ProjectInfo")`: extracts slot `project`.

projectInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `project` with character vector c(name,date,type,description,comments).

authorInfo `signature(object = "ProjectInfo")`: extracts slot `author`.

authorInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `author` with character vector c(lastname,firstname,type,company,department,email, phone,comments).

datasetInfo `signature(object = "ProjectInfo")`: extracts slot `dataset`.

datasetInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `dataset` with character vector c(name,type,sample,submitter,date,description,comments).

sourceInfo `signature(object = "ProjectInfo")`: extracts slot `source`.

sourceInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `source` with character vector c(name,type,species,subspecies,description,comments).

sampleInfo `signature(object = "ProjectInfo")`: extracts slot `sample`.

sampleInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `sample` with character vector c(name,type,sex,phenotype,genotype,extraction, isxenograft,xenostrain,xenosex,xenoage,xenoageunit,comments).

cellineInfo `signature(object = "ProjectInfo")`: extracts slot `celline`.

cellineInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `celline` with character vector c(name,type,parent,atcc,modification,sex,phenotype, genotype,extraction,isxenograft,xenostrain,xenosex,xenoage,xenoageunit,comments).

primcellInfo `signature(object = "ProjectInfo")`: extracts slot `primarycell`.

primcellInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `primarycell` with character vector c(name,type,date,description,sex,phenotype, genotype,extraction,isxenograft,xenostrain,xenosex,xenoage,xenoageunit,comments).

tissueInfo `signature(object = "ProjectInfo")`: extracts slot `tissue`.

tissueInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `tissue` with character vector c(name,type,development,morphology,disease,stage, donorage,ageunit,status,sex,phenotype,genotype,extraction,isxenograft,xenostrain,xenosex, xenoage,xenoageunit,c

biopsyInfo `signature(object = "ProjectInfo")`: extracts slot `biopsy`.

biopsyInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `biopsy` with character vector c(name,type,morphology,disease,stage,donorage,ageunit, status,sex,phenotype,genotype,extraction,isxenograft,xenostrain,xenosex,xenoage,xenoageunit,comments).

arrayInfo `signature(object = "ProjectInfo")`: extracts slot `arraytype`.

arrayInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `arraytype` with character vector c(chipname,chiptype,description,comments).

hybridizInfo `signature(object = "ProjectInfo")`: extracts slot `hybridizations`.

hybridizInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `hybridizations` with vector of character vectors with each containing c(name,type,inputname,date,p

treatmentInfo `signature(object = "ProjectInfo")`: extracts slot `treatments`.

treatmentInfo<- `signature(object = "ProjectInfo", value = "character")`: replaces slot `treatments` with vector of character vectors with each containing c(name,type,concentration,concen

show `signature(object = "ProjectInfo")`: shows the content of `ProjectInfo`.

Author(s)

Christian Stratowa

Examples

```
project <- new("ProjectInfo",submitter="Christian", laboratory="home",contact="email")
projectInfo(project)    <- c("TestProject","20060106","Project Type","use Test3 data for
authorInfo(project)     <- c("Stratowa","Christian","Project Leader","Company","Dept","cs
datasetInfo(project)    <- c("Test3Set","MC","Tissue","Stratowa","20060106","description"
sourceInfo(project)     <- c("Unknown","source type","Homo sapiens","caucasian","descript
primcellInfo(project)   <- c("Mel31","primary cell",20071123,"extracted from patient","ma
arrayInfo(project)      <- c("Test3","GeneChip","description","my comment")
hybridizInfo(project)   <- c(c("TestA1","hyb type","TestA1.CEL",20071117,"my prep1","star
                             c("TestA2","hyb type","TestA2.CEL",20071117,"my prep2","star
                             c("TestB1","hyb type","TestB1.CEL",20071117,"my prep1","star
                             c("TestB2","hyb type","TestB2.CEL",20071117,"my prep2","star
treatmentInfo(project)  <- c(c("TestA1","DMSO",4.3,"mM",1.0,"hours","intravenous","my com
                             c("TestA2","DMSO",4.3,"mM",8.0,"hours","intravenous","my com
                             c("TestB1","DrugA2",4.3,"mM",1.0,"hours","intravenous","my c
                             c("TestB2","DrugA2",4.3,"mM",8.0,"hours","intravenous","my c
show(project)
```

ProjectInfo-constructor
Constructor for Class ProjectInfo

Description

Constructor for class ProjectInfo class allows to save the relevant project information in the ROOT data file and in class DataTreeSet.

Usage

```
ProjectInfo(submitter      = character(),
            laboratory     = character(),
            contact        = character(),
            project        = character(),
            author         = character(),
            dataset        = character(),
            source         = character(),
            sample         = character(),
            celline        = character(),
            primarycell    = character(),
            tissue         = character(),
            biopsy         = character(),
            arraytype      = character(),
            hybridizations = character(),
            treatments     = character())
```

Arguments

submitter	"character" representing the name of the submitter.
laboratory	"character" representing the laboratory of the submitter.
contact	"character" representing the contact address of the submitter.
project	"character" vector representing the project information.
author	"character" vector representing the author information.
dataset	"character" vector representing the dataset information.
source	"character" vector representing the sample source information.
sample	"character" vector representing the sample information.
celline	"character" vector representing the sample information for cell lines.
primarycell	"character" vector representing the sample information for primary cells.
tissue	"character" vector representing the sample information for tissues.
biopsy	"character" vector representing the sample information for biopsies.
arraytype	"character" vector representing the array information.
hybridizations	"character" vector representing the hybridization information for each hybridization.
treatments	"character" vector representing the treatment information for each hybridization.

Details

The ProjectInfo constructor allows to save the following project information in the `ROOT` data file and in class `DataTreeSet`:

`submitter:`	name of the submitter.
`laboratory:`	laboratory of the submitter.
`contact:`	contact address of the submitter.
`project:`	character vector c(name,date,type,description,comments).
`author:`	character vector c(lastname,firstname,type,company,department,email, phone,comments)..
`dataset:`	character vector c(name,type,sample,submitter,date,description,comments).
`source:`	character vector c(name,type,species,subspecies,description,comments).
`sample:`	character vector c(name,type,sex,phenotype,genotype,extraction, isxenograft,xenostrain,xenose
`celline:`	character vector c(name,type,parent,atcc,modification,sex,phenotype, genotype,extraction,isxer
`primarycell:`	character vector c(name,type,date,description,sex,phenotype, genotype,extraction,isxenograft,x
`tissue:`	character vector c(name,type,development,morphology,disease,stage, donorage,ageunit,status,s
`biopsy:`	character vector c(name,type,morphology,disease,stage,donorage,ageunit, status,sex,phenotype
`arraytype:`	character vector c(chipname,chiptype,description,comments).
`hybridizations:`	vector of character vectors with each containing c(name,type,inputname,date,preparation,protoc
`treatments:`	vector of character vectors with each containing c(name,type,concentration,concentrationunit,ti

Value

An object of type "`ProjectInfo`"

Note

Function `ProjectInfo` is used as constructor for class `ProjectInfo` so that the user need not know details for creating S4 classes.

Author(s)

Christian Stratowa

See Also

`ProjectInfo`

Examples

```
## fill character vectors within constructor
project <- ProjectInfo(submitter="Christian", laboratory="home",contact="email",
                       project=c("TestProject","20060106","Project Type","use Test3 data
                       hybridizations=c(c("TestA1","hyb type","TestA1.CEL",20071117,"my p
                                        c("TestA2","hyb type","TestA2.CEL",20071117,"my p
                                        c("TestB1","hyb type","TestB1.CEL",20071117,"my p
                                        c("TestB2","hyb type","TestB2.CEL",20071117,"my p
str(project)

## alternatively add character vectors as methods after creation of constructor
authorInfo(project)    <- c("Stratowa","Christian","Project Leader","Company","Dept","cst
datasetInfo(project)   <- c("Test3Set","MC","Tissue","Stratowa","20060106","description",
treatmentInfo(project) <- c(c("TestA1","DMSO",4.3,"mM",1.0,"hours","intravenous","my comm
                            c("TestA2","DMSO",4.3,"mM",8.0,"hours","intravenous","my comm
                            c("TestB1","DrugA2",4.3,"mM",1.0,"hours","intravenous","my co
                                c("TestB2","DrugA2",4.3,"mM",8.0,"hours","intravenous","my co
str(project)
```

QualTreeSet-class *Class QualTreeSet*

Description

This class provides the link to the ROOT quality control file and the ROOT trees contained therein. It extends class ProcesSet.

Objects from the Class

Objects are created using functions qualify, fitQC, or the specialized functions qualify.rlm, fitRLM or rmaPLM.

Slots

qualopt: Object of class "character" representing the quality control option, i.e. 'raw', 'adjusted', 'normalized' or 'all'.

qualtype: Object of class "character" representing the quality control type, i.e. 'rlm'.

scheme: Object of class "SchemeTreeSet" providing access to ROOT scheme file.

data: Object of class "data.frame". The data.frame can contain the data (e.g. expression levels) stored in ROOT data trees.

params: Object of class "list" representing relevant parameters.

setname: Object of class "character" representing the name to the ROOT file subdirectoy where the ROOT data trees are stored, usually 'PreprocesSet'.

settype: Object of class "character" describing the type of treeset stored in setname, usually 'preprocess'.

rootfile: Object of class "character" representing the name of the ROOT data file, including full path.

filedir: Object of class "character" describing the full path to the system directory where rootfile is stored.

numtrees: Object of class "numeric" representing the number of ROOT trees stored in subdirectoy setname.

treenames: Object of class "list" representing the names of the ROOT trees stored in subdirectoy setname.

Extends

Class "ProcesSet", directly. Class "TreeSet", by class "ProcesSet", distance 2.

Methods

borderplot `signature(x = "QualTreeSet")`: creates a boxplot of positive and negative border elements.

borders `signature(object = "QualTreeSet")`: exports border trees from `ROOT` quality control file as data.frame `data`.

coiplot `signature(x = "QualTreeSet")`: creates a Center-of-Intensity-plot for positive and negative feature intensities.

image `signature(x = "QualTreeSet")`: creates a pseudo image for each quality control tree, i.e. residual images.

nuseplot `signature(x = "QualTreeSet")`: creates a NUSE-plot.

qualOption `signature(object = "QualTreeSet")`: extracts slot `qualopt`.

qualOption<- `signature(object = "QualTreeSet", value = "character")`: replaces slot `qualopt`.

qualType `signature(object = "QualTreeSet")`: extracts slot `qualtype`.

qualType<- `signature(object = "QualTreeSet", value = "character")`: replaces slot `qualtype`.

residuals `signature(object = "QualTreeSet")`: exports residuals from the residuals trees of the `ROOT` quality control file as data.frame `data`.

rleplot `signature(x = "QualTreeSet")`: creates a RLE-plot.

weights `signature(object = "QualTreeSet")`: exports weights from the residuals trees of the `ROOT` quality control file as data.frame `data`.

xpsRNAdeg `signature(x = "QualTreeSet")`: list with parameters for RNA degradation.

Author(s)

Christian Stratowa

See Also

related classes `DataTreeSet`, `CallTreeSet`, `ExprTreeSet`.

Examples

```
showClass("QualTreeSet")
```

`ROOT` *ROOT An Object-Oriented Data Analysis Framework*

Description

ROOT system overview

Details

ROOT is a modular object-oriented framework aimed at solving the data analysis challenges of high-energy physics. The relevant features of ROOT are as follows:

Architecture: The ROOT architecture is a layered class hierarchy with over 500 classes divided into different categories. Most of the classes inherit from a common base class TObject, which provides the default behavior and protocol for all objects.

ROOT Files: Object input/output is handled by class TFile, which has a UNIX-like directory structure and provides a hierarchical sequential and direct access persistent object store. ROOT files store information in a machine independent format and support on-the-fly data compression. Furthermore, ROOT files are self-describing: for every object stored in TFile, a dictionary describing the corresponding class is written to the file. A dictionary generator, called ROOTCINT, parses the class header files and generates a dictionary. Note: TFile can be considered to be the ROOT analogon to an R environment.

Data Trees: Any object derived from TObject can be written to a file with an associated key TKey. However, each key has an overhead in the directory structure in memory. To reduce this overhead, a novel concept, called Trees (class TTree) has been developed. Trees are designed to support very large numbers of complex objects in a large number of files. A Tree consists of branches (TBranch) with each branch described by its leaves (TLeaf). Trees allow direct and random access to any entry of a selected subset of branches. Thus, Trees extend and replace the usual data tables. The concept of Tree friends allows the joining of many trees as one virtual tree. However, unlike table joins in an RDBMS, the processing time is independent of the number of tree friends. Note: TTree can be considered to be the ROOT analogon to an R data.frame.

CINT: CINT is an interactive C/C++ interpreter, which is aimed at processing C/C++ scripts, called macros. Currently, CINT covers 99% of ANSI C and 95% of ANSI C++. CINT offers a gdb-like debugger for interpreted programs and allows the automatic compilation of scripts using ACLiC, the automatic compiler of libraries for CINT. Although available as independent program, CINT is embedded in ROOT as command line interpreter and macro processor, as well as dictionary generator.

User interaction: The ROOT system can be accessed from the command line, by writing macros, or via a graphic user interface (e.g. RootBrowser). Furthermore, it is possible to write libraries and applications. The ROOT GUI classes allow the development of full-featured standalone applications. Note: A macro can be considered to be the ROOT analogon of an R script. The RootBrowser can be opened using function `root.browser`

Platform independence: The ROOT system is available for most platforms and operating systems, including Linux, MacOS X, and the major flavors of UNIX and Windows. ROOT and ROOT-derived applications can be compiled for any supported platform.

Author(s)

The ROOT team `http://root.cern.ch/root/Authors.html`

References

ROOT User Guide `http://root.cern.ch/root/doc/RootDoc.html`

ROOT publications `http://root.cern.ch/root/Publications.html`

Christian Stratowa (2003), Distributed Storage and Analysis of Microarray Data in the Terabyte Range: An Alternative to BioConductor `http://www.ci.tuwien.ac.at/Conferences/DSC-2003/Proceedings/Stratowa.pdf`

`SchemeTreeSet-class` *Class SchemeTreeSet*

Description

This class provides the link to the `ROOT` scheme file and the `ROOT` trees contained therein. It extends class `TreeSet`.

Objects from the Class

Objects can be created using the functions `import.expr.scheme`, `import.exon.scheme`, `import.genome.scheme` or `root.scheme`.

Slots

`chipname`**:** Object of class `"character"` representing the Affymetrix chip name.

`chiptype`**:** Object of class `"character"` representing the chip tpye, either 'GeneChip', 'GenomeChip' or 'ExonChip'.

`probeinfo`**:** Object of class `"list"` representing chip information, including nrows, ncols, number of probes, etc.

`mask`**:** Object of class `"data.frame"`. The data.frame can contain the mask used to identify the probes as e.g. PM, MM or control probes.

`setname`**:** Object of class `"character"` representing the name to the `ROOT` file subdirectoy where the `ROOT` scheme trees are stored; it is identical to `chipname`.

`settype`**:** Object of class `"character"` describing the type of treeset stored in `setname`, i.e. 'scheme'.

`rootfile`**:** Object of class `"character"` representing the name of the `ROOT` scheme file, including full path.

`filedir`**:** Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`**:** Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`**:** Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Extends

Class `"TreeSet"`, directly.

Methods

attachMask `signature(object = "SchemeTreeSet")`: exports scheme tree from `ROOT` scheme file and and saves as data.frame `mask`.

chipMask `signature(object = "SchemeTreeSet")`: extracts data.frame `mask`.

chipMask<- `signature(object = "SchemeTreeSet", value = "data.frame")`: replaces data.frame `mask`.

chipName `signature(object = "SchemeTreeSet")`: extracts slot `chipname`.

chipType `signature(object = "SchemeTreeSet")`: extracts slot `chiptype`.

chipType<- `signature(object = "SchemeTreeSet", value = "character")`: replaces slot `chiptype`.

export `signature(object = "SchemeTreeSet")`: exports `ROOT` trees as text file, see `export-methods`.

ncols `signature(object = "SchemeTreeSet")`: extracts the physical number of array columns from slot `probeinfo`.

nrows `signature(object = "SchemeTreeSet")`: extracts the physical number of array rows from slot `probeinfo`.

probeInfo `signature(object = "SchemeTreeSet")`: extracts slot `probeinfo`.

removeMask `signature(object = "SchemeTreeSet")`: replaces data.frame `mask` with an empty data.frame of dim(0,0).

Author(s)

Christian Stratowa

Examples

```
showClass("SchemeTreeSet")
```

`TreeSet-class` *Class TreeSet*

Description

This is the virtual base class for all other classes providing the link to a `ROOT` file and the `ROOT` trees contained therein.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`setname`: Object of class `"character"` representing the name to the `ROOT` file subdirectory where the `ROOT` trees are stored, usually one of ‘DataTreeSet’, ‘PreprocesSet’, ‘CallTreeSet’.

`settype`: Object of class `"character"` describing the type of treeset stored in `setname`, usually one of ‘scheme’, ‘rawdata’, ‘preprocess’.

`rootfile`: Object of class `"character"` representing the name of the `ROOT` file, including full path.

`filedir`: Object of class `"character"` describing the full path to the system directory where `rootfile` is stored.

`numtrees`: Object of class `"numeric"` representing the number of `ROOT` trees stored in subdirectoy `setname`.

`treenames`: Object of class `"list"` representing the names of the `ROOT` trees stored in subdirectoy `setname`.

Methods

export `signature(object = "TreeSet")`: exports `ROOT` trees as text file, see `export-methods`.

fileDir `signature(object = "TreeSet")`: extracts slot `filedir`.

fileDir<- `signature(object = "TreeSet", value = "character")`: replaces slot `filedir`.

root.browser `signature(object = "TreeSet")`: opens the `ROOT` file browser.

rootFile `signature(object = "TreeSet")`: extracts slot `rootfile`.

rootFile<- `signature(object = "TreeSet", value = "character")`: replaces slot `rootfile`.

setName `signature(object = "TreeSet")`: extracts slot `setname`.

setName<- `signature(object = "TreeSet", value = "character")`: replaces slot `setname`.

setType `signature(object = "TreeSet")`: extracts slot `settype`.

setType<- `signature(object = "TreeSet", value = "character")`: replaces slot `settype`.

treeInfo `signature(object = "TreeSet")`: extracts UserInfo from `ROOT` trees.

treeNames `signature(object = "TreeSet")`: extracts slot `treenames`.

Author(s)

Christian Stratowa

See Also

derived classes `SchemeTreeSet`, `DataTreeSet`, `ExprTreeSet`, `CallTreeSet`.

Examples

```
showClass("TreeSet")
```

UniFilter-class *Class UniFilter*

Description

Class UniFilter allows to apply different unitest filters to class `ExprTreeSet`, i.e. to the expression level data.frame `data`.

Objects from the Class

Objects can be created by calls of the form `new("UniFilter", ...)`.
Alternatively, the contructor `UniFilter` can be used.

Slots

`foldchange`**:** Object of class `"list"` describing parameters for `fcFilter`.

`prescall`**:** Object of class `"list"` describing parameters for `callFilter`.

`unifilter`**:** Object of class `"list"` describing parameters for `unitestFilter`.

`unitest`**:** Object of class `"list"` describing parameters for `uniTest`.

`numfilters`**:** Object of class `"numeric"` giving the number of filters applied.

Extends

Class `"Filter"`, directly.

Methods

callFilter `signature(object = "UniFilter")`: extracts slot `prescall`.

callFilter<- `signature(object = "UniFilter", value = "character")`: replaces slot `prescall` with character vector c(cutoff, samples, condition).

fcFilter `signature(object = "UniFilter")`: extracts slot `foldchange`.

fcFilter<- `signature(object = "UniFilter", value = "numeric")`: replaces slot `foldchange` with numeric vector c(cutoff, direction).

uniTest `signature(object = "UniFilter")`: extracts slot `unitest`.

uniTest<- `signature(object = "UniFilter", value = "character")`: replaces slot `unitest` with character vector c(type, alternative, correction, numperm, mu, paired, conflevel, varequ).

unitestFilter `signature(object = "UniFilter")`: extracts slot `unifilter`.

unitestFilter<- `signature(object = "UniFilter", value = "character")`: replaces slot `unifilter` with character vector c(cutoff, variable).

Author(s)

Christian Stratowa

See Also

related classes `Filter`, `PreFilter`.

Examples

```
unifltr <- new("UniFilter", unitest=list("t.test"))
fcFilter(unifltr) <- c(1.5,"both")
unitestFilter(unifltr) <- c(0.01,"pval")
str(unifltr)
```

UniFilter-constructor *Constructor for Class UniFilter*

Description

Constructor for class UniFilter allows to apply different unitest filters to class `ExprTreeSet`, i.e. to the expression level data.frame `data`.

Usage

```
UniFilter(unitest    = "t.test",
          foldchange = character(),
          prescall   = character(),
          unifilter  = character())
```

Arguments

`unitest`	`"character"` vector describing parameters for `uniTest`.
`foldchange`	`"character"` vector describing parameters for `fcFilter`.
`prescall`	`"character"` vector describing parameters for `callFilter`.
`unifilter`	`"character"` vector describing parameters for `unitestFilter`.

Details

The UniFilter constructor allows to apply the following unitest filters to class `ExprTreeSet`:

`unitest:`	character vector c(type,alternative,correction.numperm,mu,paired,conflevel,varequ).
`foldchange:`	character vector c(cutoff,direction).
`prescall:`	character vector c(cutoff,samples,condition).
`unifilter:`	character vector c(cutoff,variable).

Value

An object of type `"UniFilter"`

Note

Function `UniFilter` is used as constructor for class `UniFilter` so that the user need not know details for creating S4 classes.

Author(s)

Christian Stratowa

See Also

`UniFilter`, `PreFilter`

Examples

```
## fill character vectors within constructor
unifltr <- UniFilter(unitest=c("t.test","two.sided","none",0,0.0,FALSE,0.95,TRUE),
                     foldchange=c(1.3,"both"),unifilter=c(0.1,"pval"))
str(unifltr)

## alternatively add character vectors as methods after creation of constructor
unifltr <- UniFilter()
fcFilter(unifltr) <- c(1.5,"both")
unitestFilter(unifltr) <- c(0.01,"pval")
str(unifltr)
```

`addData-methods` *Import additional CEL files into a DataTreeSet*

Description

Import additional CEL files into a DataTreeSet and update `ROOT` data file.

Usage

`addData(object, celdir = NULL, celfiles = "", celnames = NULL, project = NULL, verbose = TRUE)`

Arguments

`object`	object of class `DataTreeSet`.
`celdir`	system directory containing the CEL-files for corresponding scheme.
`celfiles`	optional vector of CEL-files to be imported.
`celnames`	optional vector of names which should replace the CEL-file names.
`project`	optional class `ProjectInfo`.
`verbose`	logical, if `TRUE` print status information.

Details

Import additional CEL-files and update `ROOT` data file `rootfile`.

To import CEL-files from different directories, vector `celfiles` must contain the full path for each CEL-file and `celdir` must be `celdir=NULL`.

Value

A `DataTreeSet` object.

Author(s)

Christian Stratowa

See Also

`import.data`, `root.data`

Examples

```
## get scheme and import subset of CEL-files from package
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- import.data(scheme.test3,"tmp_test3",celdir=paste(.path.package("xps"),"raw
                          celfiles=c("TestA1.CEL","TestB2.CEL"),verbose=FALSE)

unlist(treeNames(data.test3))

## add further subset of CEL-files
data.test3 <- addData(data.test3,celdir=paste(.path.package("xps"),"raw",sep="/"),
                          celfiles=c("TestA2.CEL","TestB1.CEL"),verbose=FALSE)

unlist(treeNames(data.test3))
```

`attachBgrd-methods` *Attach/Remove Background Intensities*

Description

Attach/remove background intensities to/from `DataTreeSet`.

Usage

`attachBgrd(object, treenames = "*")`

`removeBgrd(object)`

Arguments

`object`	Object of class `"DataTreeSet"`.
`treenames`	Object of class `"list"` representing the names of the `ROOT` background trees.

Details

Whenever one of the `bgcorrect` methods will be applied to raw CEL intensities, the background intensities will be stored in `ROOT` background trees. However, the background intensities will not be saved as data.frame `bgrd`, thus avoiding memory problems. Function `attachBgrd` allows to fill slot `bgrd` on demand.

`attachBgrd` exports intensities from background trees from `ROOT` data file and saves as data.frame `bgrd`. `treenames` is a vector of tree names to attach; for `treenames="*"` all trees from slot `treenames` will be exported and background intensities attached as data.frame `bgrd`.

`removeBgrd` removes background intensities from `DataTreeSet` and replaces data.frame `bgrd` with an empty data.frame of dim(0,0).

Value

A `DataTreeSet` object.

Note

Do not use `attachBgrd` unless you know that your computer has sufficient RAM, especially when using exon arrays. It may be advisible to use a subset of `treenames` only.

Author(s)

Christian Stratowa

See Also

`attachInten`, `removeInten`

`attachCall-methods` *Attach/Remove Detecion Call Measures*

Description

Attach/remove detection call and detection p-value to/from `CallTreeSet`.

Usage

```
attachCall(object, treenames = "*")
attachPVal(object, treenames = "*")
removeCall(object)
removePVal(object)
```

Arguments

`object`	Object of class `"CallTreeSet"`.
`treenames`	Object of class `"list"` representing the names of the `ROOT` call trees.

Details

By default detection calls will be saved in class `CallTreeSet` in slots `data` and `detcall`, respectively, since usually the `data.frames` obtained as result of e.g. `mas5.call` are of reasonable size. However, when computing many arrays, especially exon arrays at probeset levels, it may be better to compute detection calls with slot `add.data=FALSE` thus avoiding memory problems. In this case, functions `attachCall` and `attachPVal` allow to fill slots `detcall` and `data`, respectively, on demand.

`attachCall` exports detection calls from call trees from `ROOT` call file and and saves as data.frame `detcall`. `treenames` is a vector of tree names to attach; for `treenames="*"` all trees from slot `treenames` will be exported and detection calls attached as data.frame `detcall`.

`attachPVal` exports detection p-values from call trees from `ROOT` call file and and saves as data.frame `data`. `treenames` is a vector of tree names to attach; for `treenames="*"` all trees from slot `treenames` will be exported and detection p-values attached as data.frame `data`.

`removeCall` removes detection calls from `CallTreeSet` and replaces data.frame `detcall` with an empty data.frame of dim(0,0).

`removePVal` removes detection p-values from `CallTreeSet` and replaces data.frame `data` with an empty data.frame of dim(0,0).

Value

A `CallTreeSet` object.

Note

Do not use `attachCall` and `attachPVal` unless you know that your computer has sufficient RAM, especially when using exon arrays. It may be advisible to use a subset of `treenames` only.

Author(s)

Christian Stratowa

See Also

`attachExpr`, `removeExpr`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## MAS5 detection call
call.mas5 <- mas5.call(data.test3,"tmp_Test3Call0",tmpdir="",add.data=FALSE,verbose=FALSE

## attach data
call.mas5 <- attachPVal(call.mas5)
call.mas5 <- attachCall(call.mas5)

## get data.frames
pval.mas5 <- pvalData(call.mas5)
pres.mas5 <- presCall(call.mas5)
head(pval.mas5)
head(pres.mas5)

## remove data
call.mas5 <- removePVal(call.mas5)
call.mas5 <- removeCall(call.mas5)

rm(scheme.test3, data.test3)
gc()
```

`attachExpr-methods` *Attach/Remove Expression Measures*

Description

Attach/remove expression levels to/from `ExprTreeSet`.

Usage

`attachExpr(object, treenames = "*")`

`removeExpr(object)`

Arguments

`object`	Object of class `"ExprTreeSet"`.
`treenames`	Object of class `"list"` representing the names of the `ROOT` expression trees.

Details

By default expression levels will be saved in class ExprTreeSet as slot data, since usually the data.frame obtained as result of e.g. rma normalization is of reasonable size. However, when normalizing many arrays, especially exon arrays at probeset levels, it may be better to compute rma with slot add.data=FALSE thus avoiding memory problems. In this case, function attachExpr allows to fill slot data on demand.

attachExpr exports expression levels from expression trees from ROOT expression file and and saves as data.frame data. treenames is a vector of tree names to attach; for treenames="*" all trees from slot treenames will be exported and expression levels attached as data.frame data.

removeExpr removes expression levels from ExprTreeSet and replaces data.frame data with an empty data.frame of dim(0,0).

Value

A ExprTreeSet object.

Note

Do not use attachExpr unless you know that your computer has sufficient RAM, especially when using exon arrays. It may be advisible to use a subset of treenames only.

Author(s)

Christian Stratowa

See Also

attachCall, removeCall

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.rma <- rma(data.test3,"tmp_Test3RMA0",tmpdir="",background="pmonly",normalize=TRUE,a

## attach data
data.rma <- attachExpr(data.rma)

## get data.frame
expr.rma <- validData(data.rma)
head(expr.rma)

## remove data
data.rma <- removeExpr(data.rma)

rm(scheme.test3, data.test3)
gc()
```

`attachInten-methods` *Attach/Remove Intensities*

Description

Attach/remove raw CEL intensities to/from `DataTreeSet`.

Usage

```
attachInten(object, treenames = "*")
```

```
removeInten(object)
```

Arguments

`object`	Object of class `"DataTreeSet"`.
`treenames`	Object of class `"list"` representing the names of the `ROOT` data trees.

Details

When CEL files will be imported using function `import.data`, the raw intensities will be stored in `ROOT` data trees. However, the intensities will not be saved in class `DataTreeSet` as slot `data`, thus avoiding memory problems. Function `attachInten` allows to fill slot `data` on demand.

`attachInten` exports intensities from data trees from `ROOT` data file and and saves as data.frame `data`. `treenames` is a vector of tree names to attach; for `treenames="*"` all trees from slot `treenames` will be exported and intensities attached as data.frame `data`.

`removeInten` removes intensities from `DataTreeSet` and replaces data.frame `data` with an empty data.frame of dim(0,0).

Value

A `DataTreeSet` object.

Note

Do not use `attachInten` unless you know that your computer has sufficient RAM, especially when using exon arrays. It may be advisible to use a subset of `treenames` only.

Author(s)

Christian Stratowa

See Also

`attachBgrd`, `removeBgrd`

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.
dim(intensity(data.test3))

data.test3 <- attachInten(data.test3)
dim(intensity(data.test3))
head(intensity(data.test3))

data.test3 <- removeInten(data.test3)
dim(intensity(data.test3))
```

`attachMask-methods` *Attach/Remove Scheme Mask*

Description

Attach/remove scheme mask to/from `SchemeTreeSet` or to slot `scheme` of `DataTreeSet`.

Usage

```
attachMask(object)

removeMask(object)
```

Arguments

`object`	Object of class `"SchemeTreeSet"` or `"DataTreeSet"`.

Details

`attachMask` exports mask from scheme tree from `ROOT` scheme file and and saves mask as data.frame `mask` of slot `scheme`.

`removeMask` removes mask from `SchemeTreeSet` or from slot `scheme` of `DataTreeSet` and replaces data.frame `mask` with an empty data.frame of dim(0,0).

Value

A `DataTreeSet` object or `SchemeTreeSet`.

Note

Do not use `attachMask` unless you know that your computer has sufficient RAM, especially for exon array schemes.

Author(s)

Christian Stratowa

See Also

`import.expr.scheme`, `import.exon.scheme`

Examples

```
## load existing ROOT scheme file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
dim(chipMask(scheme.test3))

scheme.test3 <- attachMask(scheme.test3)
dim(chipMask(scheme.test3))
head(chipMask(scheme.test3))

scheme.test3 <- removeMask(scheme.test3)
dim(chipMask(scheme.test3))
```

`bgcorrect` *Background Correction*

Description

Background corrects probe intensities in an object of class `DataTreeSet`.

Usage

```
bgcorrect(xps.data, filename = character(0), filedir = getwd(), tmpdir = "", upd

bgcorrect.gc(xps.data, filename = character(0), filedir = getwd(), tmpdir = "",

bgcorrect.mas4(xps.data, filename = character(0), filedir = getwd(), tmpdir = ""

bgcorrect.mas5(xps.data, filename = character(0), filedir = getwd(), tmpdir = ""

bgcorrect.rma(xps.data, filename = character(0), filedir = getwd(), tmpdir = "",

xpsBgCorrect(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`select`	type of probes to select for background correction.
`method`	background method to use.
`option`	type of background correction to use.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	vector of parameters for background method.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataSet`.
`...`	the arguments described above.

Details

Background corrects probe intensities in an object of class `DataTreeSet`.

`xpsBgCorrect` is the `DataSet` method called by function `bgcorrect`, containing the same parameters.

Value

An `DataTreeSet`

Author(s)

Christian Stratowa

See Also

`express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## MAS4 sector background
data.bg.mas4 <- bgcorrect.mas4(data.test3,"tmp_Test3MAS4Bgrd",filedir=getwd(),tmpdir="",v

## need to attach background intensities
data.bg.mas4 <- attachBgrd(data.bg.mas4)

## get data.frame
bg.mas4 <- validBgrd(data.bg.mas4)
head(bg.mas4)

## plot images
if (interactive()) {
image.dev(data.bg.mas4,bg=TRUE,col=rainbow(32))
image(matrix(bg.mas4[,1], ncol=ncols(schemeSet(data.bg.mas4)), nrow=nrows(schemeSet(data.
}

## Not run:
## examples using Affymetrix human tissue dataset (see also xps/examples/script4exon.R)

## example - exon array, e.g. HuEx-1_0-st-v2:
scmdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Schemes"
datdir <- "/Volumes/GigaDrive/CRAN/Workspaces/ROOTData"
scheme.exon <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na25.root",sep="/"))
data.exon   <- root.data(scheme.exon, paste(datdir,"HuTissuesExon_cel.root",sep="/"))

## compute rma background
workdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Exon/hutissues/exon"
data.bg.rma <- bgcorrect(data.exon, "HuExonRMABgrd", filedir=workdir, tmpdir="",
               method="rma", select="antigenomic", option="pmonly:epanechnikov",
               params=c(16384), exonlevel="metacore+affx")

# or alternatively:
data.bg.rma <- bgcorrect.rma(data.exon, "HuExonRMABgrd", filedir=workdir, tmpdir="",
                 select="antigenomic", exonlevel="metacore+affx")

## End(Not run)
```

---

borderplot-methods *Plots of Border Elements*

Description

Produce box-and-whisker plot(s) of the positive and negative feature intensities.

Usage

```
 borderplot(x, type = c("pos", "neg"), qualopt = "raw", transfo = log2,
range = 0, names = "namepart", ylim = NULL, bmar = NULL, las = 2, ...)
```

Arguments

`x`	object of class `QualTreeSet`.
`type`	type of border elements to be used, one of "pos", "neg", or both.
`qualopt`	character string specifying whether to draw boxplots for "raw", "adjusted", or "normalized" border intensities.
`transfo`	a valid function to transform the data, usually "log2", or "0".
`range`	determines how far the plot whiskers extend out from the box.
`names`	optional vector of sample names.
`ylim`	the y limits of the plot.
`bmar`	optional `list` for bottom margin and axis label magnification `cex.axis`.
`las`	the style of axis labels.
`...`	optional arguments to be passed to `borderplot`.

Details

Creates a boxplot of the positive and negative feature intensities for an object of class `QualTreeSet`.

For `names=NULL` full tree names will be displayed while for `names="namepart"` tree names will be displayed without name extension. If `names` is a vector of tree names, only these columns will displayed as boxplot.

For `bmar=NULL` the default list `bmar = list(b=6, cex.axis=1.0)` will be used initially. However, both bottom margin `b` and axis label magnification `cex.axis` will be adjusted depending on the number of label characters and the number of samples.

Author(s)

Christian Stratowa

See Also

`coiplot`, `boxplot`

Examples

```
## Not run:
## border intensities, created by e.g. rmaPLM()
getTreeNames(rootFile(rlm.all), treetype="brd")
borderplot(rlm.all)
borderplot(rlm.all, type="pos")
borderplot(rlm.all, type="neg")

## End(Not run)
```

`boxplot-methods` *Box Plots*

Description

Produce box-and-whisker plot(s) of the samples.

Usage

```
 boxplot(x, which = "", size = 0, transfo = log2, range = 0, names
= "namepart", bmar = NULL, ...)
```

Arguments

`x`	object of class `DataTreeSet`, `ExprTreeSet` or `QualTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`transfo`	a valid function to transform the data, usually "log2", or "0".
`range`	determines how far the plot whiskers extend out from the box.
`names`	optional vector of sample names.
`bmar`	optional `list` for bottom margin and axis label magnification `cex.axis`.
`...`	optional arguments to be passed to `boxplot`.

Details

Creates a boxplot for slot `data` for an object of class `DataTreeSet`, `ExprTreeSet` or `QualTreeSet`.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as boxplot.

For `bmar=NULL` the default list `bmar = list(b=6, cex.axis=1.0)` will be used initially. However, both bottom margin and axis label magnification will be adjusted depending on the number of label characters and the number of smaples.

Note

For a `DataTreeSet` object, data must first be attached using method `attachInten`.

Alternatively it is possible to use the pre-calculated quantiles stored in the `userinfo` of the data trees by calling `which="userinfo:varlist"`, where the `varlist` to call is described in method `treeInfo`.

Author(s)

Christian Stratowa

See Also

`boxplot.dev`, `boxplot`

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## need to attach scheme mask and probe intensities only if "userinfo" is not used
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)

if (interactive()) {
boxplot(data.test3)
}

## optionally remove mask and data to free memory
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)

## alternatively use the quantiles stored in userinfo of trees
if (interactive()) {
boxplot(data.test3, which="userinfo:fIntenQuant")
}

rm(scheme.test3, data.test3)
gc()
```

`callFilter-methods` *Detection Call Filter*

Description

Detection Call Filter.
The `cutoff` value defines the upper threshold for allowed detection call p-values. If e.g. the number of samples exceeding this cutoff value is greater than `samples` then the corresponding expression dataframe row is flagged, i.e. `flag = 0`.
The Detection Call Filter flags all rows with: `flag = (sum(call[i] >= cutoff) >= samples)`

Usage

```
callFilter(object)
callFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter` or `UniFilter`.
`value`	character vector `c(cutoff, samples, condition)`.

Details

The method `callFilter` initializes the following parameters:

`cutoff`:	the cutoff value for the filter:
	`cutoff = 1.0`: present/absent call is used.
	`cutoff < 1.0`: detection p-value is used as cutoff.
`samples`:	this value depends on the `condition` used:
`condition`:	`condition="samples"`: number of samples (default):
	`condition="percent"`: percent of samples.

Value

An initialized `PreFilter` or `UniFilter` object.

Author(s)

Christian Stratowa

Examples

```
## initialize PreFilter
prefltr <- PreFilter()
callFilter(prefltr) <- c(0.02,80.0,"percent")
str(prefltr)

## initialize UniFilter
unifltr <- UniFilter()
callFilter(unifltr) <- c(0.02,80.0,"percent")
str(unifltr)
```

`callplot-methods` *Barplot of Percent Present and Absent Calls.*

Description

Creates a barplot of percent Present/Marginal/Absent calls.

Usage

```
 callplot(x, beside = TRUE, names = "namepart", col = c("red","green","blue"),
legend = c("P","M","A"), ylim = c(0,100), ylab = "detection call [%]",
las = 2, ...)
```

Arguments

`x`	object of class `CallTreeSet`.
`beside`	logical. If `FALSE`, the columns of height are portrayed as stacked bars, and if `TRUE` the columns are portrayed as juxtaposed bars.
`names`	optional vector of sample names.
`col`	color for P/M/A bars
`legend`	legend for the plot, defaults to P/M/A.
`ylim`	the y limits of the plot.

`ylab`	a label for the y axis.
`las`	the style of axis labels.
`...`	optional arguments to be passed to `barplot`.

Details

Creates a barplot of percent Present/Marginal/Absent calls.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as callplot.

Author(s)

Christian Stratowa

See Also

`pmplot`

`coiplot-methods` *Center-Of-Intensity QC Plots*

Description

Produce Center-Of-Intensity plot(s) of the positive and negative feature intensities.

Usage

```
 coiplot(x, type = c("pos", "neg"), qualopt = "raw", radius = 0.5,
linecol = "gray70", visible = TRUE, ...)
```

Arguments

`x`	object of class `QualTreeSet`.
`type`	type of border elements to be used, one of “pos”, “neg”, or both.
`qualopt`	character string specifying whether to draw boxplots for “raw”, “adjusted”, or “normalized” border intensities.
`radius`	determines the radius within which the COI for each array should be located.
`linecol`	the color of the ablines and the circle to be drawn.
`visible`	logical, if TRUE then arrays outside the circle with `radius` will be flagged by labeling the data point with the array name.
`...`	optional arguments to be passed to `coiplot`.

Details

Produces Center-Of-Intensity (COI) plot(s) of the positive and negative feature intensities for an object of class `QualTreeSet`. This plot is useful for detecting spatial biases in intensities on an array.

Mean intensities for the left, right, top and bottom border elements are calculated, separated into positive and negative controls, and the “center of intensity” is calculated on a relative scale [-1,1]. Arrays with a COI outside a range with `radius` are considered to be outliers. If `visible = TRUE` then outlier arrays will be flagged by labeling the data point(s) with the array name(s).

Value

The names ot the outlier arrays, otherwise `NULL`.

Author(s)

Christian Stratowa

See Also

`borderplot`

Examples

```
## Not run:
## border intensities, created by e.g. rmaPLM()
coiplot(rlm.all)
coiplot(rlm.all, type="pos")
coiplot(rlm.all, type="neg", radius=0.1)

## End(Not run)
```

`corplot-methods` *Array-Array Expression Level Correlation Plot*

Description

A heat map of the array-array Spearman rank correlation coefficients.

Usage

```
 corplot(x, which = "UnitName", transfo = log2, method = "spearman",
col = NULL, names = "namepart", sort = FALSE, reverse = TRUE, bmar
= NULL, add.legend = FALSE, ...)
```

Arguments

`x`	object of class `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`transfo`	a valid function to transform the data, usually "log2", or "0".
`method`	a character string indicating which correlation coefficient is to be computed.
`col`	vector of colors for plot, length is number of samples.
`names`	optional vector of sample names.
`sort`	logical, if TRUE the correlation matrix will be sorted decreasingly.
`reverse`	logical, if TRUE the correlation matrix will be replaced by `1 - cor()`.
`bmar`	optional `list` for bottom margin and axis label magnification `cex.axis`.
`add.legend`	logical, if TRUE then a color bar will be drawn.
`...`	optional arguments to be passed to `plot`.

Details

Produces a heat map of the array-array Spearman rank correlation coefficients for slot `data` for an object of class `ExprTreeSet`.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as `corplot`.

For `bmar=NULL` the default list `bmar = list(b=6, cex.axis=1.0)` will be used initially. However, both bottom margin and axis label magnification will be adjusted depending on the number of label characters and the number of smaples.

Note

Setting `reverse = FALSE` displays the correlation heat map as in package `affyQCReport`.

Author(s)

Christian Stratowa

See Also

`madplot`

`cvFilter-methods` *Coefficient of Variation Filter*

Description

This method initializes the Coefficient of Variation Filter.
The coefficient of variation is the standard deviation divided by the absolute value of the mean.
The CV Filter flags all rows with: `flag = (cv >= cutoff)`

Usage

```
cvFilter(object)
cvFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric vector `c(cutoff, trim, epsilon)`.

Details

The method `cvFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`trim`:	the trim value for trimmed mean (default is `trim=0`).
`epsilon`:	value to replace mean (default is `epsilon=0.01`):
	`epsilon > 0`: replace mean=0 with epsilon.
	`epsilon = 0`: always set mean=1.

Note, that for `epsilon = 0` the filter flags all rows with: stdev >= cutoff

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
cvFilter(prefltr) <- c(0.3,0.0,0.01)
str(prefltr)
```

`dabg.call` *Detection Above Background Call*

Description

Computes the Detection Above Background Call first implemented for the Exon arrays.

Usage

```
dabg.call(xps.data, filename = character(0), filedir = getwd(),
          alpha1 = 0.04, alpha2 = 0.06,
          option = "transcript", exonlevel = "", xps.scheme = NULL, add.data = T

xpsDABGCall(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`alpha1`	a significance threshold in (0,alpha2).
`alpha2`	a significance threshold in (alpha1,0.5).
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` call data will be added to slots `data` and `detcall`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

This function generates a detection p-value based on comparing the perfect match probe intensity to the intensity distribution provided by background probes sharing the same GC-content as the PM probe under consideration. For exon/genome arrays special 'antigenomic' background probes of defined GC-content are used, while for expression arrays the Mismatch probes will be grouped by their GC-content.

For exon/genome arrays it is necessary to supply `option` and `exonlevel`.

Following `options` are valid for exon arrays only:

`transcript`:	expression levels are computed for transcript clusters, i.e. probe sets containing the same 'transcript_clu
`exon`:	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where e
`probeset`:	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.

Following `exonlevel` annotations are valid for exon arrays:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`ambiguous`:	ambiguous probesets only.
`affx`:	standard AFFX controls.
`all`:	combination of above.

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	probesets with category 'unique' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above.

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affx"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper 'exon_probeset_trans_clust_whitepaper.pdf'.

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeTreeSet `xps.scheme`.

`xpsDABGCall` is the `DataTreeSet` method called by function `dabg.call`, containing the same parameters.

Value

A `CallTreeSet`

Note

Yes, it is possible to compute DABG detection call for expression arrays, but it is very slow and thus not recommended.

Author(s)

Christian Stratowa

References

Affymetrix (2005) Exon Probeset Annotations and Transcript Cluster Groupings, Affymetrix Inc., Santa Clara, CA, exon_probeset_trans_clust_whitepaper.pdf.

See Also

mas5.call

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## DABG detection call
call.dabg <- dabg.call(data.test3,"tmp_Test3DABG",verbose=FALSE)

## get data.frames
pval.dabg <- pvalData(call.dabg)
pres.dabg <- presCall(call.dabg)
head(pval.dabg)
head(pres.dabg)

## plot results
if (interactive()) {
callplot(call.dabg)
}

rm(scheme.test3, data.test3)
gc()
```

---

dfw *Distribution Free Weighted Expression Measure*

Description

This function converts a DataTreeSet into an ExprTreeSet using the Distribution Free Weighted Fold Change (DFW) method.

Usage

```
dfw(xps.data,
    filename   = character(0),
    filedir    = getwd(),
    tmpdir     = "",
    normalize  = TRUE,
    m          = 3,
    n          = 1,
    c          = 0.01,
    option     = "transcript",
    exonlevel  = "",
    xps.scheme = NULL,
    add.data   = TRUE,
    verbose    = TRUE)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`m`	positive number as exponent of the weighted range WR.
`n`	positive number as exponent of the weighted standard deviation WSD.
`c`	scaling parameter.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.

Details

This function computes the DFW (Distribution Free Weighted Fold Change) expression measure described in Chen et al. for both expression arrays and exon arrays. For exon arrays it is necessary to supply the requested `option` and `exonlevel`.

Following `options` are valid for exon arrays:

`transcript:`	expression levels are computed for transcript clusters, i.e. probe sets containing the same 'transcript_clu
`exon:`	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where ea
`probeset:`	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.

Following `exonlevel` annotations are valid for exon arrays:

`core:`	probesets supported by RefSeq and full-length GenBank transcripts.

`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	probesets with category 'unique', 'similar' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affy"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper exon_probeset_trans_clust_whitepaper.pdf: "Exon Probeset Annotations and Transcript Cluster Groupings".

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeSet `xps.scheme`.

Value

An `ExprTreeSet`

Note

The expression measure obtained with DFW is given in linear scale, analogously to the expression measures computed with `mas5` and `rma`.

For the analysis of many exon arrays it may be better to define a `tmpdir`, since this will store only the results in the main file and not e.g. background and normalized intensities, and thus will reduce the file size of the main file. For quantile normalization memory should not be an issue, however DFW depends on RAM unless you are using a temporary file.

Author(s)

Christian Stratowa

References

Chen, Z., McGee M., Liu Q., and Scheuermann, R.H. (2007), A distribution free summarization method for Affymetrix GeneChip arrays. Bioinformatics 23(3):321-327

See Also

`express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.dfw <- dfw(data.test3,"tmp_Test3DFW",verbose=FALSE)

## get data.frame
expr.dfw <- validData(data.dfw)
head(expr.dfw)
```

`diffFilter-methods` *Difference Filter*

Description

This method initializes the Difference Filter.
The difference is the maximum value minus minimum value for each row of the expression dataframe divided by the mean value of each row.
The Difference Filter flags all rows with: `flag = ((max - min)/mean >= cutoff)`

Usage

```
diffFilter(object)
diffFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric vector `c(cutoff, trim, epsilon)`.

Details

The method `diffFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`trim`:	the trim value for trimmed mean (default is `trim=0`).
`epsilon`:	value to replace mean (default is `epsilon=0.01`):
	`epsilon > 0`: replace mean=0 with epsilon.
	`epsilon = 0`: always set mean=1.

Note, that for `epsilon = 0` the filter flags all rows with: (max - min) >= cutoff

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
diffFilter(prefltr) <- c(2.2,0.0,0.01)
str(prefltr)
```

`existsROOTFile` *Test for Existing ROOT File*

Description

Test if a ROOT file does already exist.

Usage

```
existsROOTFile(filename, tmp.rm = TRUE)
```

Arguments

`filename`	name of ROOT file, including full path.
`tmp.rm`	logical, if `TRUE` then exlude filenames beginning with dQuote(tmp_).

Value

Return `TRUE` if file `filename` is an already existing `ROOT` file.

Note

It is possible to create temporary `ROOT` files called “tmp” or with `filename` starting with “tmp_” which can be overwritten. Thus by default temporary files will not be recognized by `existsROOTFile`. If you want to recognize temporary files, set `tmp.rm = TRUE`.

Author(s)

Christian Stratowa

See Also

`isROOTFile`

Examples

```
existsROOTFile(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
```

exonLevel *Conversion of Parameter exonlevel to Integer*

Description

Conversion of parameter `exonlevel` to an integer vector.

Usage

```
exonLevel(exonlevel = "", chiptype = "GeneChip", as.sum = TRUE)
```

Arguments

`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`chiptype`	chip tpye, one of 'GeneChip', 'GenomeChip', 'ExonChip'.
`as.sum`	logical, if `TRUE` an integer vector of size three will be returned, if `FALSE` then the levels will be split into the basic integer representations.

Details

Conversion of parameter `exonlevel` to an integer; this function is a utility function, which is usually only used internally.

Following `exonlevel` annotations are valid for exon arrays:

`core`:	`(=8192+1024)` probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	`(=8192)` core meta-probesets.
`extended`:	`(=4096+512)` probesets with other cDNA support.
`metaextended`:	`(=4096)` extended meta-probesets.
`full`:	`(=2048+256)` probesets supported by gene predictions only.
`metafull`:	`(=2048)` full meta-probesets.
`ambiguous`:	`(=128)` probesets that fall within multiple genes.
`affx`:	`(=60)` standard AFFX controls.
`all`:	`(=16316)` combination of above (including affx).

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	`(=8192+1024)` probesets with category 'unique', 'similar' and 'mixed'.
`metacore`:	`(=8192)` probesets with category 'unique' only.
`affx`:	`(=60)` standard AFFX controls.
`all`:	`(=9276)` combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affx"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper exon_probeset_trans_clust_whitepaper.pdf: “Exon Probeset Annotations and Transcript Cluster Groupings”.

Parameter `exonlevel` determines not only which probes are used for medianpolish, but also the probes used for background calculation and for quantile normalization. If you want to use seperate probes for background calculation, quantile normalization and medianpolish summarization, you can pass a numeric vector containing three integer values corresponding to the respective `exonlevel`. These integers must be the sum of the integers shown above, e.g. you can use `exonlevel=c(16316,8252,8252)`, where `8252=8192+60` for `"metacore+affx"`.

Value

an `integer` vector.

Note

The following `exonlevels` are unsupported:

`control->bgp->genomic:`	`(=32768)`	genomic background probes.
`control->bgp->antigenomic:`	`(=65536)`	antigenomic background probes.
`normgene->intron:`	`(=131072)`	intronic controls.
`normgene->exon:`	`(=262144)`	exronic controls.
`rescue->FLmRNA->unmapped:`	`(=524288)`	unmapped mRNAs.

For whole genome arrays it is possible (but not recommended) to use all probesets by using `exonlevel=c(992316,9`
For exon arrays it is possible to use e.g. `exonlevel=c(1032124,1032124,631868)`.
However, please note that these settings are not recommended and not supported.

Author(s)

Christian Stratowa

See Also

`rma`, `mas5`

Examples

```
exonLevel("core", "GenomeChip")
exonLevel("all", "GenomeChip")
exonLevel("core+extended+full", "ExonChip")
exonLevel("core+extended+full", "ExonChip", as.sum=FALSE)
exonLevel(c(16316,8252,8252), "ExonChip")
```

`export` *Export data as text files*

Description

Export data from classes `SchemeTreeSet`, `DataTreeSet`, `ExprTreeSet`, or `CallTreeSet` to `outfile`.

Usage

```
export.scheme(xps.scheme, treetype = character(0), varlist = "*", outfile = char

export.data(xps.data, treename = "*", treetype = "cel", varlist = "*", outfile =

export.expr(xps.expr, treename = "*", treetype = character(0), varlist = "*", ou

export.call(xps.call, treename = "*", treetype = character(0), varlist = "*", ou

export(object, ...)
```

Arguments

`xps.scheme`	an object of type `SchemeTreeSet`.
`xps.data`	an object of type `DataTreeSet`.
`xps.expr`	an object of type `ExprTreeSet`.
`xps.call`	an object of type `CallTreeSet`.
`treename`	vector of tree names to export.
`treetype`	type of tree(s) to export, see `validTreetype`
`varlist`	names of tree leaves to export
`outfile`	name of output file.
`sep`	column separator
`as.dataframe`	if `TRUE` a data.frame will be returned.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	arguments `treenames`,`treetype`,`varlist`,`outfile`,`sep`,`as.dataframe`.

Details

Export data from classes `SchemeTreeSet`, `DataTreeSet`, `ExprTreeSet`, or `CallTreeSet` to `outfile`.

Parameter `varlist` lists the parameters to export:
- parameters are separated by ":", e.g. `varlist="fInten:fStdev"`.
- for `varlist="*"` all valid parameters will be exported.

For class `DataTreeSet` the following `varlist` parameters are valid:

`fInten`:	intensities from e.g. tree.cel.
`fStdev`:	standard deviation from e.g. tree.cel.
`fNPixels`:	number of pixels from e.g. tree.cel.
`fBg`:	background values (background trees only).

For classes `ExprTreeSet` and `CallTreeSet` `varlist` can contain annotation parameters and parameters of the resulting data.
Following `varlist` annotation parameters are valid:

`fUnitName`:	unit name (probeset ID).
`fTranscriptID`:	transcript_id (probeset ID).
`fName`:	gene name.

fSymbol:	gene symbol.
fAccession:	mRNA accession such as Refseq ID.
fEntrezID:	entrez ID.
fChromosome:	chromosome.
fStart:	start position.
fStop:	stop position.
fStrand:	strand on chromosome.
fCytoBand:	cytoband.

Following varlist parameters are valid for ExprTreeSet:

fLevel:	expression level.
fStdev:	standard deviation.
fNPairs:	number of pairs.

Following varlist parameters are valid for CallTreeSet:

fCall:	detection call.
fPValue:	detection p-value.

An example: varlist="fUnitName:fName:fSymbol:fLevel:fStdev:fEntrezID"

export is a generic method to export data from ROOT trees as text file.

Value

If as.dataframe is TRUE, the data will be imported into the current R session as data.frame. Otherwise, NULL will be returned.

Author(s)

Christian Stratowa

See Also

export-methods

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## export as table only
export(scheme.test3, treetype="idx", outfile="Test3_idx.txt",verbose=FALSE)

## export as table and import as data.frame
ann <- export.scheme(scheme.test3, treetype="ann", outfile="Test3_ann.txt",as.dataframe=T
head(ann)
data <- export.data(data.test3, outfile="Test3_cel.txt",as.dataframe=TRUE,verbose=FALSE)
head(data)
```

`export.filter` *Export filter data as text files*

Description

Export data from classes `FilterTreeSet` or `AnalysisTreeSet` to `outfile`.

Usage

```
export.filter(xps.fltr, treename = "*", treetype = character(0), varlist = "*",
```

Arguments

`xps.fltr`	an object of type `FilterTreeSet` or `AnalysisTreeSet`.
`treename`	tree name to export.
`treetype`	type of tree(s) to export, 'pfr', 'ufr' or 'stt'.
`varlist`	names of tree leaves to export.
`outfile`	name of output file.
`sep`	column separator
`as.dataframe`	if `TRUE` a data.frame will be returned.
`verbose`	logical, if `TRUE` print status information.

Details

Export data from classes `FilterTreeSet`, or `AnalysisTreeSet` to `outfile`.

Parameter `varlist` lists the parameters to export:
- parameters are separated by ":", e.g. `varlist="fUnitName:fFlag"`.
- for `varlist="*"` all valid parameters will be exported.

For class `FilterTreeSet` the following `varlist` parameters are valid:

`fUnitName`:	unit name (probeset ID).
`fFlag`:	mask.

For class `AnalysisTreeSet` `varlist` can contain annotation parameters and parameters of the resulting data.
Following `varlist` annotation parameters are valid:

`fUnitName`:	unit name (probeset ID).
`fTranscriptID`:	transcript_id (probeset ID).
`fName`:	gene name.
`fSymbol`:	gene symbol.
`fAccession`:	mRNA accession such as Refseq ID.
`fEntrezID`:	entrez ID.
`fChromosome`:	chromosome.
`fStart`:	start position.
`fStop`:	stop position.
`fStrand`:	strand on chromosome.
`fCytoBand`:	cytoband.

For class `AnalysisTreeSet` the following `varlist` parameters are valid:

`mn1:`	mean of group 1.
`mn2:`	mean of group 2.
`fc:`	fold-change fc=mn2/mn1.
`se:`	standard error.
`df:`	degree of freedom.
`stat:`	t-statistic.
`pval:`	p-value.
`nper:`	number of permutations.
`pcha:`	p-chance.
`padj:`	adjusted p-value.
`flag:`	flag.
`mask:`	only rows with `flag=1` will be exported.

Value

If `as.dataframe` is `TRUE`, the data will be imported into the current R session as `data.frame`. Otherwise, `NULL` will be returned.

Author(s)

Christian Stratowa

See Also

`export-methods`

`export.root` *Export data from ROOT file*

Description

Export data as text files directly from a `ROOT` file.

Usage

```
export.root(datafile = character(0), schemefile = character(0), treeset = charac
```

Arguments

`datafile`	name of ROOT data file including full path
`schemefile`	name of ROOT scheme file including full path
`treeset`	name of subdirectory in ROOT file where trees are stored
`treename`	name of ROOT tree to export.
`treetype`	type of tree(s) to export, see `validTreetype`.
`varlist`	names of tree leaves to export.
`outfile`	name of output file.
`sep`	column separator
`as.dataframe`	if `TRUE` a data.frame will be returned.
`verbose`	logical, if `TRUE` print status information.

Details

Export data as text files directly from a `ROOT` file.

Value

If `as.dataframe` is `TRUE`, the data will be imported into the current R session as `data.frame`. Otherwise, `NULL` will be returned.

Author(s)

Christian Stratowa

See Also

`export`, `export-methods`

Examples

```
## export data directly from root file
schemefile <- paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/")
datafile   <- paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/")
data <- export.root(datafile, schemefile, "DataSet", "*", "cel", "*", "DataOutFile.txt",
head(data)
```

`express` *Compute expression levels from raw data*

Description

This function allows to combine different algorithms to compute expression levels, or to return the result for different algorithms only.

Usage

```
express(xps.data,
        filename = character(),
        filedir = getwd(),
        tmpdir = "",
        update = FALSE,
      # background correction
        bgcorrect.method = NULL,
        bgcorrect.select = character(),
        bgcorrect.option = character(),
        bgcorrect.params = list(),
      # normalization
        normalize.method = NULL,
        normalize.select = character(),
        normalize.option = character(),
        normalize.logbase = character(),
        normalize.params = list(),
      # expression values
        summarize.method = NULL,
        summarize.select = character(),
        summarize.option = character(),
        summarize.logbase = character(),
        summarize.params = list(),
      # reference values
        reference.index  = 0,
        reference.method = "mean",
        reference.params = list(0),
      # misc.
        exonlevel  = "",
        xps.scheme = NULL,
        add.data   = TRUE,
        bufsize    = 32000,
        verbose    = TRUE)

xpsPreprocess(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`bgcorrect.method`	background method to use.
`bgcorrect.select`	type of probes to select for background correction.
`bgcorrect.option`	type of background correction to use.
`bgcorrect.params`	vector of parameters for background method.
`normalize.method`	normalization method to use.
`normalize.select`	type of probes to select for normalization.
`normalize.option`	normalization option.
`normalize.logbase`	logarithm base as character, one of ‘0’, ‘log’, ‘log2’, ‘log10’.
`normalize.params`	vector of parameters for normalization method.
`summarize.method`	summarization method to use.
`summarize.select`	type of probes to select for summarization.
`summarize.option`	option determining the grouping of probes for summarization, one of ‘transcript’, ‘exon’, ‘probeset’; exon arrays only.

summarize.logbase	logarithm base as character, one of '0', 'log', 'log2', 'log10'.
summarize.params	vector of parameters for summarization method.
reference.index	index of reference tree to use, or 0.
reference.method	for refindex=0, either trimmed mean or median of trees.
reference.params	vector of parameters for reference method.
exonlevel	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
xps.scheme	optional alternative SchemeSet.
add.data	logical. If TRUE expression data will be included as slot data.
bufsize	integer which sets the buffer size of the tree branch baskets (default is 32000).
verbose	logical, if TRUE print status information.
object	object of class DataTreeSet.
...	the arguments described above.

Details

This function allows to combine different algorithms to compute expression levels, or to return the result for different algorithms only.

Please have a look at vignette "xpsPreprocess.pdf" for details on how to use function express.

xpsPreprocess is the DataTreeSet method called by function express, containing the same parameters.

Value

An object of type DataTreeSet or ExprTreeSet.

Author(s)

Christian Stratowa

See Also

bgcorrect, normalize, summarize

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## compute rma with a single call to express()
expr.rma <- express(data.test3,"tmp_Test3Exprs",filedir=getwd(),tmpdir="",update=FALSE,
            bgcorrect.method="rma",bgcorrect.select="none",bgcorrect.option="pmonly:epane
            normalize.method="quantile",normalize.select="pmonly",normalize.option="trans
            summarize.method="medianpolish",summarize.select="pmonly",summarize.option="t
            verbose=FALSE)
```

```
## get expression data.frame
expr <- exprs(expr.rma)
head(expr)

## plot expression levels
if (interactive()) {
boxplot(expr.rma)
boxplot(log2(expr[,3:6]))
}

## Not run:
## examples using Affymetrix human tissue dataset (see also xps/examples/script4exon.R)

## example - exon array, e.g. HuEx-1_0-st-v2:
scmdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Schemes"
datdir <- "/Volumes/GigaDrive/CRAN/Workspaces/ROOTData"
scheme.exon <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na25.root",sep="/"))
data.exon   <- root.data(scheme.exon, paste(datdir,"HuTissuesExon_cel.root",sep="/"))

workdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Exon/hutissues/exon"
expr.rma <- express(data.exon,"HuExonExprs",filedir=workdir,tmpdir="",update=F,
            bgcorrect.method="rma",bgcorrect.select="antigenomic",bgcorrect.option="pmonl
            normalize.method="quantile",normalize.select="pmonly",normalize.option="trans
            summarize.method="medianpolish",summarize.select="pmonly",summarize.option="t
            exonlevel="metacore+affx")

## End(Not run)
```

`exprs-methods` *Get/Set Expression Values*

Description

Get/set expression values from/for class `ExprTreeSet`.

Usage

```
exprs(object)
exprs(object, treenames = NULL) <- value
```

Arguments

`object`	object of class `ExprTreeSet`.
`treenames`	`character` vector containing optional tree names to be used as subset.
`value`	`data.frame` containing expression values.

Details

Get the expression values from slot `data` or set slot `data` to `value`.

Method `exprs` returns the expression values from slot `data` as `data.frame`, while replacement method `exprs<-` allows to replace slot `data` with a `data.frame`.

In order to create an `ExprTreeSet` containing only a subset of slot `data`, first export slot `data` using method `exprs`, create a `character` vector containing only `treenames` to be used in the subset, and then use replacement method `exprs<-` to replace slot `data` with the subset. Slots `treenames` and `numtrees` will be updated automatically.

Note: When creating `character` vector `treenames` it is sufficient to use the name part of the tree name w/o the extension.

Note: If you do not want to replace your current object, create first a copy of type `ExprTreeSet` by simply writing `newobj <- oldobj`, and use `newobj` for replacement. This is important since `exprs<-` does also update slots `treenames` and `numtrees` as already mentioned.

Author(s)

Christian Stratowa

See Also

`pvalData`, `presCall`

Examples

```
## Not run:
## load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## create an ExprTreeSet
data.rma <- rma(data.test3,"tmp_TestRMA",tmpdir="",background="pmonly",normalize=TRUE,ver

## get expression values
value <- exprs(data.rma)

## selected treenames only
treenames <- c("TestA2", "TestB1")

## make a copy of your object if you do not want to replace it
subset.rma <- data.rma

## replace slot data with subset
exprs(subset.rma, treenames) <- value
str(subset.rma)

## End(Not run)
```

`extenPart` *Get Extension of Tree Names*

Description

Get the extension(s) of (tree) names.

Usage

```
extenPart(names, as.unique=TRUE)
```

Arguments

`names`	vector of names.
`as.unique`	if TRUE return only unique extensions.

Details

Extracts the extension part of `names`, e.g.of tree names of `treename.treetype` stored in a `ROOT` file.

Value

A `vector` of (unique) extensions.

Author(s)

Christian Stratowa

See Also

`namePart`

Examples

```
names <- c("TestA1.int", "TestA2.int")
extenPart(names)
extenPart(names, as.unique=FALSE)
```

`farms` *Factor Analysis for Robust Microarray Summarization Expression Measure*

Description

This function converts a `DataTreeSet` into an `ExprTreeSet` using the Factor Analysis for Robust Microarray Summarization (FARMS) method.

Usage

```
farms(xps.data,
      filename   = character(0),
      filedir    = getwd(),
      tmpdir     = "",
      normalize  = TRUE,
      weight     = 0.5,
      mu         = 0.0,
      scale      = 1.0,
      tol        = 0.00001,
      cyc        = 100,
      weighted   = TRUE,
      version    = "1.3.1",
      option     = "transcript",
      exonlevel  = "",
      xps.scheme = NULL,
      add.data   = TRUE,
      verbose    = TRUE)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`weight`	hyperparameter, usually set to 0.5 for `version="1.3.1"` and to 8.0 for `version="1.3.0"`.
`mu`	hyperparameter allowing to correct for potential bias.
`scale`	scaling parameter, usually set to 1.0 for `version="1.3.1"` and to 2.0 for `version="1.3.0"`.
`tol`	termination tolerance for EM algorithm.
`cyc`	maximum number of cycles of EM algorithm.
`weighted`	logical, used only with `version="1.3.1"`. Default is TRUE.
`version`	version of original farms package. Currently, `version="1.3.1"` and `version="1.3.0"` are implemented. Default is `version="1.3.1"`.
`option`	option determining the grouping of probes for summarization, one of ‘transcript’, ‘exon’, ‘probeset’; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.

Details

This function computes the FARMS (Factor Analysis for Robust Microarray Summarization) expression measure described in Hochreiter et al. for both expression arrays and exon arrays.

Parameter `version` currently allows the user to choose between the original implementation of FARMS as implemented in package ‘farms_1.3.0’ or enhanced FARMS as implemented in package ‘farms_1.3.1’. By default `version="1.3.1"` is used.

Parameter `weight` is a hyperparameter which determines the influence of the prior. For `version="1.3.1"` the value in the range of [0,1].

Parameter `mu` is a hyperparameter which allows to quantify different aspects of potential prior knowledge. Values near zero assume that most genes do not contain a signal and introduce a bias for loading matrix elements near zero.

Parameter `weighted` is a logical and indicates whether a weighted mean or a least square fit is used to summarize the loading matrix. It is applicable only to `version="1.3.1"`.

For exon arrays it is necessary to supply the requested `option` and `exonlevel`.

Following `options` are valid for exon arrays:

`transcript`:	expression levels are computed for transcript clusters, i.e. probe sets containing the same ‘transcript_clu
`exon`:	expression levels are computed for exon clusters, i.e. probe sets containing the same ‘exon_id’, where ea
`probeset`:	expression levels are computed for individual probe sets, i.e. for each ‘probeset_id’.

Following `exonlevel` annotations are valid for exon arrays:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	probesets with category 'unique', 'similar' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affy"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper exon_probeset_trans_clust_whitepaper.pdf: "Exon Probeset Annotations and Transcript Cluster Groupings".

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeSet `xps.scheme`.

Value

An `ExprTreeSet`

Note

The expression measure obtained with FARMS is given in linear scale, analogously to the expression measures computed with `mas5` and `rma`.

For the analysis of many exon arrays it may be better to define a `tmpdir`, since this will store only the results in the main file and not e.g. background and normalized intensities, and thus will reduce the file size of the main file. For quantile normalization memory should not be an issue, however DFW depends on RAM unless you are using a temporary file.

Author(s)

Christian Stratowa

References

Hochreiter, S., Clevert D.-A., and Obermayer, K. (2006), A new summarization method for Affymetrix probe level data. Bioinformatics 22(8):943-949

See Also

express

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.farms <- farms(data.test3,"tmp_Test3FARMS",verbose=FALSE)

## get data.frame
expr.farms <- validData(data.farms)
head(expr.farms)
```

`fcFilter-methods` *Fold-Change Filter*

Description

This method initializes the Fold-Change Filter.
The fold-change is determined by the mean value of group 2 divided by the mean value of group 1.
The Fold-Change Filter flags all rows with: `flag = (fc >= cutoff)`

Usage

```
fcFilter(object)
fcFilter(object, value)<-
```

Arguments

`object`	object of class `UniFilter`.
`value`	numeric vector `c(cutoff, direction)`

Details

The method `fcFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`direction`:	`direction="both"` (default): select up and downregulated genes.
	`direction="up"`: select upregulated genes only.
	`direction="down"`: select downregulated genes only.

Value

An initialized `UniFilter` object.

Author(s)

Christian Stratowa

Examples

```
unifltr <- UniFilter()
fcFilter(unifltr) <- c(1.5,"both")
str(unifltr)
```

`firma` *Finding Isoforms using Robust Multichip Analysis*

Description

This function converts a `DataTreeSet` for exon arrays into an `ExprTreeSet` using the Finding Isoforms using Robust Multichip Analysis (FIRMA).

Usage

```
firma(xps.data,
      filename   = character(0),
      filedir    = getwd(),
      tmpdir     = "",
      background = "antigenomic",
      normalize  = TRUE,
      option     = "probeset",
      exonlevel  = "metacore",
      method     = "mdp",
      params     = list(16384, 0.0, 1.0, 10, 0.01, 1.0),
      xps.scheme = NULL,
      add.data   = TRUE,
      verbose    = TRUE)

xpsFIRMA(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`background`	probes used to compute background, one of ‘genomic’, ‘antigenomic’
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`option`	option determining the grouping of probes for summarization, one of ‘exon’, ‘probeset’.
`exonlevel`	exon annotation level determining which probes should be used for summarization.
`method`	method to be used for summarization, currently ‘mdp’.
`params`	list of (default) parameters for `rma`.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

This function computes FIRMA (Finding Isoforms using Robust Multichip Analysis) for detecting differential alternative splicing for exon arrays, as described in Purdom et al.

Following `options` are valid for exon arrays:

`probeset`:	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.
`exon`:	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where each

Following `exonlevel` annotations are valid for exon arrays:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`ambiguous`:	ambiguous probesets only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affx"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper exon_probeset_trans_clust_whitepaper.pdf: "Exon Probeset Annotations and Transcript Cluster Groupings".

Method `xpsFIRMA` is the `DataTreeSet` method called by function `firma`, containing the same parameters.

Value

An `ExprTreeSet`

Note

In contrary to other implementations of (FI)RMA the expression measure of FIRMA is given in linear scale, analogously to the expression measures computed with `mas5` and `mas4`.

Please note that the current implementation of FIRMA is based on median-polish only, see: `http://www.aroma-project.org/node/81`

Please note that the default settings of `params` gives results which are identical to the results obtained with APT (Affymetrix Power Tools) and with package `affy_1.14.2` or earlier. If you want to obtain results which are identical to the results obtained with `affy_1.16.0` or later then you need to set `params = list(16384, 0.0, 0.4, 10, 0.01, 1.0)`.

By setting parameter `background="none"` it is possible to skip background correction .

For the analysis of many exon arrays it may be better to define a `tmpdir`, since this will store only the results in the main file and not e.g. background and normalized intensities, and thus will reduce the file size of the main file. For quantile normalization memory should not be an issue, however medianpolish depends on RAM unless you are using a temporary file.

Parameter `exonlevel` determines not only which probes are used for medianpolish, but also the probes used for background calculation and for quantile normalization. If you want to use seperate probes for background calculation, quantile normalization and medianpolish summarization, you can pass a numeric vector containing three integer values corresponding to the respective `exonlevel`, e.g. you can use `exonlevel=c(16316,8252,8252)`, see function `exonLevel` for more details.

Author(s)

Christian Stratowa

References

Purdom, E., Simpson K.M., Robinson M.D., Conboy J.G., Lapuk A.V. and Speed, T.P. (2008), FIRMA: a method for detection of alternative splicing from exon array data. Bioinformatics 24(15):1707-1714

Examples

```
## Not run:
## load ROOT scheme file
scmdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Schemes"
scheme.exon <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na27.root",sep="/"))

## load subset of ROOT data file
datdir <- "/Volumes/GigaDrive/CRAN/Workspaces/ROOTData"
subnames <- c("HeartA","HeartB","HeartC", "MuscleA","MuscleB","MuscleC")
sub.exon <- root.data(scheme.exon, rootFile(data.exon), celnames=subnames)

## firma
outdir <- getwd()
sub.firma.ps <- firma(sub.exon,"HeartMuscleFIRMAcorePS",filedir=outdir,tmpdir="",backgrou
                      normalize=TRUE,option="probeset",exonlevel="core")

## get transcript expression levels for all transcripts or transcript=2429277
expr.firma <- firma.expr(sub.firma.ps, probeset=NULL, option="transcript")
expr.firma <- firma.expr(sub.firma.ps, probeset=2429277, option="transcript")

## get probeset expression levels for all probeset or probeset=2429278 or transcript=2429
expr.firma <- firma.expr(sub.firma.ps, probeset=NULL, option="probeset")
expr.firma <- firma.expr(sub.firma.ps, probeset=2429278, option="probeset")
expr.firma <- firma.expr(sub.firma.ps, probeset=2429277, option="probeset")

## get probeset splice scores for all probeset or probeset=2429278 or transcript=2429277
score.firma <- firma.score(sub.firma.ps, probeset=NULL, option="probeset")
score.firma <- firma.score(sub.firma.ps, probeset=2429278, option="probeset")
score.firma <- firma.score(sub.firma.ps, probeset=2429277, option="probeset")

## different plots
boxplot(sub.firma.ps, which="UnitName:LEVEL_PS")
boxplot(sub.firma.ps, which="UnitName:LEVEL_TS")

hist(sub.firma.ps, which="UnitName:LEVEL_PS")
hist(sub.firma.ps, which="UnitName:LEVEL_TS")
```

```
rleplot(sub.firma.ps, which="UnitName:LEVEL_PS")
rleplot(sub.firma.ps, which="UnitName:LEVEL_TS")

nuseplot(sub.firma.ps, which="UnitName:STDEV_PS")
nuseplot(sub.firma.ps, which="UnitName:STDEV_TS")

## End(Not run)
```

firma.expr *Get Expression Levels from FIRMA*

Description

Extracts FIRMA expression levels from data.frame `data`.

Usage

```
firma.expr(xps.data,
           probeset = NULL,
           option   = "probeset")
```

Arguments

`xps.data`	object of class `ExprTreeSet`.
`probeset`	transcriptID or probesetID or NULL.
`option`	option determining the `probeset` type for which to extract expression levels, one of 'transcript', 'probeset', 'exon'.

Details

Function `firma.expr` returns the expression levels from slot `data` for a given `probeset`, or for all probesets or transcripts in case of `probeset=NULL`. Row names will be the Affymetrix transcriptIDs, probesetIDs or exonIDs, respectively, dependent on the selected `option`.

Value

A `data.frame`.

Note

For `option="probeset"` parameter `probeset` should usually be the transcriptID in order to get the expression levels for all probesetIDs of the corresponding transcriptID.

Author(s)

Christian Stratowa

See Also

`firma`

Examples

```
## Not run:
## get transcript expression levels for all transcripts or for transcript=2429277
expr.firma <- firma.expr(sub.firma.ps, probeset=NULL, option="transcript")
expr.firma <- firma.expr(sub.firma.ps, probeset=2429277, option="transcript")

## get probeset expression levels for all probeset or for probeset=2429278
expr.firma <- firma.expr(sub.firma.ps, probeset=NULL, option="probeset")
expr.firma <- firma.expr(sub.firma.ps, probeset=2429278, option="probeset")

## get probeset expression levels for all probesets corresponding to transcript=2429277
expr.firma <- firma.expr(sub.firma.ps, probeset=2429277, option="probeset")

## End(Not run)
```

`firma.score` *Get Splice Score from FIRMA*

Description

Extracts the FIRMA splice score from data.frame `data`.

Usage

```
firma.score(xps.data,
            probeset = NULL,
            option   = "probeset")
```

Arguments

`xps.data`	object of class `ExprTreeSet`.
`probeset`	probesetID or NULL.
`option`	option determining the `probeset` type for which to extract expression levels, one of 'probeset', 'exon'.

Details

Function `firma.score` returns the FIRMA splice score described in Purdom et al. from slot `data` for a given `probeset`, or for all probesets in case of `probeset=NULL`. Row names will be the Affymetrix probesetIDs or exonIDs, respectively, dependent on the selected `option`.

Value

A `data.frame`.

Note

For `option="probeset"` parameter `probeset` should usually be the transcriptID in order to get the splice scores for all probesetIDs of the corresponding transcriptID.

Author(s)

Christian Stratowa

References

Purdom, E., Simpson K.M., Robinson M.D., Conboy J.G., Lapuk A.V. and Speed, T.P. (2008), FIRMA: a method for detection of alternative splicing from exon array data. Bioinformatics 24(15):1707-1714

See Also

firma

Examples

```
## Not run:
## get probeset splice scores for all probeset or for probeset=2429278
score.firma <- firma.score(sub.firma.ps, probeset=NULL, option="probeset")
score.firma <- firma.score(sub.firma.ps, probeset=2429278, option="probeset")

## get probeset splice scores for all probesets corresponding to transcript=2429277
score.firma <- firma.score(sub.firma.ps, probeset=2429277, option="probeset")

## End(Not run)
```

---

fitQC *Functions for fitting probe-level models*

Description

This function allows to combine different algorithms to compute background correction, normalization and fit a multichip model for summarization.

Usage

```
fitQC(xps.data,
      filename = character(),
      filedir = getwd(),
      tmpdir = "",
      update = FALSE,
    # background correction
      bgcorrect.method  = "rma",
      bgcorrect.select  = "none",
      bgcorrect.option  = "pmonly:epanechnikov",
      bgcorrect.params  = c(16384),
    # normalization
      normalize.method  = "quantile",
      normalize.select  = "pmonly",
      normalize.option  = "transcript:together:none",
      normalize.logbase = "0",
      normalize.params  = c(0.0),
    # quality control
      qualify.method    = "rlm",
      qualify.select    = "pmonly",
      qualify.qualopt   = "all",
      qualify.option    = "transcript",
      qualify.estimator = "huber",
      qualify.logbase   = "log2",
      qualify.params    = list(10, 0.01, 1.0),
    # reference values
      reference.index   = 0,
      reference.method  = "mean",
      reference.params  = list(0.0),
    # misc.
      exonlevel  = "",
      xps.scheme = NULL,
      add.data   = FALSE,
      bufsize    = 32000,
      verbose    = TRUE)

xpsQualityControl(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`bgcorrect.method`	background method to use.
`bgcorrect.select`	type of probes to select for background correction.
`bgcorrect.option`	type of background correction to use.
`bgcorrect.params`	vector of parameters for background method.
`normalize.method`	normalization method to use.
`normalize.select`	type of probes to select for normalization.
`normalize.option`	normalization option.
`normalize.logbase`	logarithm base as character, one of ‘0’, ‘log’, ‘log2’, ‘log10’.
`normalize.params`	vector of parameters for normalization method.
`qualify.method`	qualification method to use, currently `rlm`.
`qualify.select`	type of probes to select for qualification.
`qualify.qualopt`	option determining the data to which to apply qualification, one of ‘raw’, ‘adjusted’, ‘normalized’, ‘all’.

`qualify.option`	option determining the grouping of probes for qualification, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`qualify.estimator`	option determining the M-estimator to use, one of 'huber', 'fair', 'cauchy', 'gemanmcclure', 'welsch', 'tukey', 'andrew'.
`qualify.logbase`	logarithm base as character, one of '0', 'log', 'log2', 'log10'.
`qualify.params`	vector of parameters for qualification method.
`reference.index`	index of reference tree to use, or 0.
`reference.method`	for `refindex=0`, either trimmed mean or median of trees.
`reference.params`	vector of parameters for reference method.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`xps.scheme`	optional alternative `SchemeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`bufsize`	integer which sets the buffer size of the tree branch baskets (default is 32000).
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

This function allows to combine different algorithms to compute background correction, normalization and fit a multichip model for summarization.

`xpsQualityControl` is the `DataTreeSet` method called by function `fitQC`, containing the same parameters.

Value

An object of type `QualTreeSet`.

Author(s)

Christian Stratowa

See Also

`fitRLM`, `qualify`, `express`

Examples

```
## Not run:
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.
## qualification - rlm
rlm.all <- fitQC(data.test3, "tmp_Test3RLMall", filedir=getwd(), tmpdir="",
                 qualify.method="rlm", qualify.qualopt="all", qualify.option="transcript"

## get expression data.frame
expr.rlm.all <- validData(rlm.all)

## get borders
brd.rlm.all <- borders(rlm.all)

## get residuals
res.rlm.all <- residuals(rlm.all)

## get weights
w.rlm.all <- weights(rlm.all)

## plot expression levels
if (interactive()) {
coiplot(rlm.all)
borderplot(rlm.all)
nuseplot(rlm.all)
rleplot(rlm.all)
image(rlm.all, type="resids")
}

## End(Not run)
```

`fitRLM` *Functions for fitting RMA as probe-level model*

Description

Convert Affymetrix probe level data to expression levels by fitting RMA as multichip model.

Usage

```
fitRLM(xps.data,
       filename   = character(),
       filedir    = getwd(),
       tmpdir     = "",
       background = "pmonly",
       normalize  = TRUE,
       qualopt    = "all",
       option     = "transcript",
       exonlevel  = "",
       params     = list(16384, 0.0, 1.0, 10, 0.01, 1),
       xps.scheme = NULL,
       add.data   = FALSE,
       bufsize    = 32000,
       verbose    = TRUE)

rmaPLM(xps.data,
       filename   = character(),
       filedir    = getwd(),
       tmpdir     = "",
       background = "pmonly",
       normalize  = TRUE,
       qualopt    = "all",
       option     = "transcript",
       exonlevel  = "",
       params     = list(16384, 0.0, 1.0, 10, 0.01, 1),
       xps.scheme = NULL,
       add.data   = FALSE,
       bufsize    = 32000,
       verbose    = TRUE)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`background`	probes used to compute background, one of 'pmonly', 'mmonly', 'both'; for genome/exon arrays one of 'genomic', 'antigenomic'
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`qualopt`	option determining the data to which to apply qualification, one of 'raw', 'adjusted', 'normalized', 'all'.
`option`	option determining the grouping of probes for qualification, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	list of (default) parameters for `rma`.
`xps.scheme`	optional alternative `SchemeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`bufsize`	integer which sets the buffer size of the tree branch baskets (default is 32000).
`verbose`	logical, if `TRUE` print status information.

Details

Convert Affymetrix probe level data to expression levels by fitting RMA as multichip model.

Value

An object of type `QualTreeSet`.

Author(s)

Christian Stratowa

See Also

`fitQC`, `qualify`, `express`

Examples

```
## Not run:
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## qualification - rlm
rlm.all <- rmaPLM(data.test3, "tmp_Test3RLMall", filedir=getwd(), tmpdir="", qualopt="all

## get borders
brd.rlm.all <- borders(rlm.all)

## get residuals
res.rlm.all <- residuals(rlm.all)

## get weights
w.rlm.all <- weights(rlm.all)

## plot expression levels
if (interactive()) {
coiplot(rlm.all)
borderplot(rlm.all)
nuseplot(rlm.all)
rleplot(rlm.all)
image(rlm.all, type="resids")
}

## End(Not run)
```

`gapFilter-methods` *Gap Filter*

Description

This method initializes the Gap Filter.
The `gapFilter` looks for genes that might usefully discriminate between two groups. To do this we look for a gap in the ordered expression values. The gap should come in the central portion, thus a parameter `window` is defined to exclude jumps in the initial `window` values and the final `window` values.
The Gap Filter flags all rows with: `flag = ((gap[i+1] - gap[i])/mean >= cutoff)`

```
gapFilter(object)
gapFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric vector `c(cutoff, window, trim, epsilon)`.

Details

The method `gapFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.

`window`:	trim value for the ordered expression levels (default is `window=0.05`).
`trim`:	the trim value for trimmed mean (default is `trim=0`).
`epsilon`:	value to replace mean (default is `epsilon=0.01`):
	`epsilon > 0`: replace mean=0 with epsilon.
	`epsilon = 0`: always set mean=1.

Note, that for `epsilon = 0` the filter flags all rows with: (gap[i+1] - gap[i]) >= cutoff

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
gapFilter(prefltr) <- c(0.3,0.05,0.0,0.01)
str(prefltr)
```

`getChipName` *Get Chip Name*

Description

Get chip name from ROOT scheme file.

Usage

```
getChipName(rootfile)
```

Arguments

`rootfile`	name of ROOT scheme file, including full path.

Details

Extracts the chip name directly from `ROOT` scheme file `rootfile`.

Value

a `character` with the chip name.

Author(s)

Christian Stratowa

See Also

`getChipType`, `getNameType`

Examples

```
## correct usage
getChipName(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
## incorrect usage
getChipName(paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/"))
```

`getChipType` *Get Chip Type*

Description

Get chip type from ROOT scheme file.

Usage

```
getChipType(rootfile)
```

Arguments

`rootfile`	name of ROOT scheme file, including full path.

Details

Extracts the chip type directly from `ROOT` scheme file `rootfile`.

Value

a `character` with the chip type, either ‘GeneChip’ or ‘ExonChip’.

Author(s)

Christian Stratowa

See Also

`getChipName`, `getNameType`

Examples

```
## correct usage
getChipType(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
## incorrect usage
getChipType(paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/"))
```

`getDatatype` *Get Data Type*

Description

Get data type corresponding to tree type.

Usage

```
getDatatype(treetype)
```

Arguments

`treetype`	tree type.

Details

Get data type corresponding to tree type. Valid tree types are described in `validTreetype`.

Value

a `character` with the correct data type, i.e. 'rawdata', 'preprocess' or 'normation'.

Author(s)

Christian Stratowa

See Also

`type2Exten`, `validTreetype`

Examples

```
getDatatype("cel")
getDatatype("tbw")
```

`getNameType` *Get Chip Name and Type*

Description

Get chip name and type from ROOT scheme file.

Usage

```
getNameType(rootfile)
```

Arguments

`rootfile`	name of ROOT scheme file, including full path.

Details

Extracts the chip name and type directly from ROOT scheme file rootfile.

Value

a list with parameters:

chipname	chip name.
chiptype	chip type, either ‘GeneChip’ or ‘ExonChip’.

Author(s)

Christian Stratowa

See Also

getChipName, getChipType

Examples

```
## correct usage
getNameType(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
## incorrect usage
getNameType(paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/"))
```

---

getNumberTrees *Get Number of Trees*

Description

Get number of trees stored in a ROOT file.

Usage

```
getNumberTrees(rootfile, treetype = "*", setname = NULL)
```

Arguments

rootfile	name of ROOT file, including full path.
treetype	tree type.
setname	name of ROOT subdirectory containing trees.

Details

Extracts the number of trees of treetype stored in ROOT file rootfile.
Valid tree types are listed in validTreetype. For treetype="*" the total number of trees in rootfile are returned.
If setname is provided, only trees in subdirectory setname are counted.

Value

Number of trees.

Author(s)

Christian Stratowa

Examples

```
getNumberTrees(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
getNumberTrees(paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/"))
```

---

getProbeInfo *Get Probe Information*

Description

Get GeneChip probe information from root scheme file.

Usage

```
getProbeInfo(rootfile)
```

Arguments

`rootfile`	name of ROOT scheme file, including full path.

Details

Extracts GeneChip probe information directly from ROOT scheme file `rootfile`.

Value

a `list` with parameters:

`nrows`	physical number of rows in the array.
`ncols`	physical number of columns in the array.
`nprobes`	number of probes on the array.
`ncontrols`	number of controls on the array.
`ngenes`	number of genes on the array.
`nunits`	number of units on the array.
`nprobesets`	umber of probesets on the array.
`naffx`	number of AFFX controls on the array.

Author(s)

Christian Stratowa

Examples

```
getProbeInfo(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
```

`getTreeData-methods` *Export Tree Data*

Description

Exports tree data from `ROOT` data file and and saves as `data.frame`.

Usage

```
getTreeData(object, treetype = "cel", varlist = "fInten")
```

Arguments

`object`	Object of class `"ProcessSet"`.
`treetype`	type of tree to export, see `validTreetype`
`varlist`	names of tree leaves to export.

Details

Exports tree leaves from `ROOT` data file and and saves as `data.frame`.

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`export`

`getTreeNames` *Get Tree Names*

Description

Get tree names stored in a ROOT file.

Usage

```
getTreeNames(rootfile, treetype = "*", setname = NULL, gettitle = FALSE)
```

Arguments

`rootfile`	name of ROOT file, including full path.
`treetype`	tree type.
`setname`	name of ROOT subdirectory containing trees.
`gettitle`	If `TRUE` the titles of the trees will be returned.

Details

Extracts the tree names of `treetype` stored in ROOT file `rootfile`.
Valid tree types are listed in `validTreetype`. For `treetype="*"` names for all trees in `rootfile` are returned.
If `setname` is provided, only tree names in subdirectory `setname` are returned.

Value

A `vector` of tree names. For `gettitle=TRUE` a `vector` of tree titles.

Author(s)

Christian Stratowa

Examples

```
getTreeNames(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
getTreeNames(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"), "scm")
getTreeNames(paste(.path.package("xps"),"rootdata/DataTest3_cel.root",sep="/"))
```

`highFilter-methods` *Upper Threshold Filter*

Description

This method initializes the Upper Threshold Filter.
The `cutoff` value defines the upper threshold for allowed expression levels. If e.g. the number of samples exceeding this cutoff value is greater than `parameter` then the corresponding dataframe row is flagged, i.e. `flag = 0`.
The Upper Threshold Filter flags all rows with: `flag = (sum(expression[i] <= cutoff) >= parameter)`

Usage

```
highFilter(object)
highFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	character vector `c(cutoff, parameter, condition)`.

Details

The method `highFilter` initializes the following parameters:

`cutoff`:	the upper threshold level for the filter.
`parameter`:	this value depends on the `condition` used:
`condition`:	`condition="samples"`: number of samples (default):
	`condition="percent"`: percent of samples.
	`condition="mean"`: mean value of samples.
	`condition="percentile"`: percentile of samples.

Value

An initialized PreFilter object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
highFilter(prefltr) <- c(14.5,75.0,"percent")
str(prefltr)
```

`hist-methods` *Density Estimate*

Description

Plot the density estimates for each sample.

Usage

```
 hist(x, which = "", size = 0, transfo = log2, ylab = "density", xlab
= "log intensity", type = "l", col = 1:6, ...)
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`ylab`	a title for the y axis.
`xlab`	a title for the x axis.
`type`	type for the plot.
`col`	colors to use for the different arrays.
`...`	optional arguments to be passed to `plot`.

Details

Plots the non-parametric density estimates using values contained in the columns of slot `data`.

For a `DataTreeSet` object, data must first be attached using method `attachInten`.

Note

For exon array raw data only a limited number of samples can be displayed as density plot due to memory limitations. To display all samples it is proposed to use function `root.density` instead.

Author(s)

Christian Stratowa

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## need to attach scheme mask and probe intensities
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)

if (interactive()) {
hist(data.test3)
}

## optionally remove mask and data to free memory
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)
```

`image-methods` *Display an Image*

Description

Creates an image of intensities or residuals, respectively, for each sample.

Usage

```
image(x, bg = FALSE, transfo = log2, col = NULL, names = "namepart",
xlab = "", ylab = "", add.legend = FALSE, ...)
```

```
image(x, type = c("resids", "pos.resids", "neg.resids", "sign.resids",
"weights"), qualopt = c("raw", "adjusted", "normalized"), transfo =
log2, col = NULL, names = "namepart", xlab = "", ylab = "", add.legend
= FALSE, ...)
```

Arguments

`x`	object of class `ProcessSet`.
`bg`	logical. If `FALSE`, intensities from slot `data` will be used; if `TRUE`, background intensities from slot `bgrd` will be used.
`type`	character string specifying the type of residual image.
`qualopt`	character string specifying whether to draw residual image for “raw”, “adjusted”, or “normalized” intensities.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`col`	color range for intensities.
`names`	optional vector of sample names.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.
`add.legend`	logical, if TRUE then a color bar will be drawn.
`...`	optional arguments to be passed to `image`.

Details

Creates an image of intensities or residuals, respectively, for each array, i.e. 'pseudo chip images'.

If x belongs to class DataTreeSet then images of raw intensities will be drawn.

If x belongs to class ExprTreeSet and bg=FALSE then images of background corrected intensities will be drawn.

If x belongs to class ExprTreeSet and bg=TRUE the distribution of the background intensities will be shown; this can be useful to see potential density gradients caused by hybridization conditions. For the computation of background intensities see function bgcorrect; it is suggested to use bgcorrect.mas4 to identify density gradients.

If x belongs to class QualTreeSet then images of the residuals or the probe weights, respectively, will be drawn. For col=NULL the same colors will be used as described in vignette "QualityAssess.pdf" of package affyPLM, using internally function pseudoPalette described in affyPLM.

For names=NULL full tree names will be displayed while for names="namepart" column names will be displayed without name extension. If names is a vector of tree names then data from these trees only will displayed as image(s).

Author(s)

Christian Stratowa

See Also

plotImage

Examples

```
## Not run:
## images of raw intensities as imported using import.data()
unlist(treeNames(data.test3)) # show available tree names
image(data.test3, names="TestA2.cel")
image(data.test3)

## images of background adjusted or background intensities, created by e.g. rma()
getTreeNames(rootFile(data.rma))
image(data.rma, names="TestA2.int")
image(data.rma, names="TestA2.rbg", bg=TRUE)

## residual images, created by e.g. rmaPLM()
getTreeNames(rootFile(rlm.all), treetype="res")
image(rlm.all, type="resids")
image(rlm.all, type="resids", names="TestA2_raw.res", add.legend=TRUE)
image(rlm.all, type="pos.resids", names="TestA2_raw.res", add.legend=TRUE)
image(rlm.all, type="neg.resids", names="TestA2_raw.res", add.legend=TRUE)
image(rlm.all, type="sign.resids", names="TestA2_raw.res", add.legend=TRUE)
image(rlm.all, type="weights", names="TestA2_raw.res", add.legend=TRUE)
image(rlm.all, type="resids", qualopt="adjusted", names="TestA2_adjusted.res", add.legenc

## End(Not run)
```

import.data — *Import CEL files into a DataTreeSet*

Description

Import the Affymetrix CEL files into a ROOT file and create S4 class DataTreeSet

Usage

```
import.data(xps.scheme,
            filename = character(0),
            filedir  = getwd(),
            celdir   = NULL,
            celfiles = "*",
            celnames = NULL,
            project  = NULL,
            verbose  = TRUE)
```

Arguments

`xps.scheme`	a `SchemeTreeSet` containing the correct scheme for the CEL-files
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`celdir`	system directory containing the CEL-files for corresponding scheme.
`celfiles`	optional vector of CEL-files to be imported.
`celnames`	optional vector of names which should replace the CEL-file names.
`project`	optional class `ProjectInfo`.
`verbose`	logical, if `TRUE` print status information.

Details

`import.data` is used to import CEL-files from directory `celdir` into a `ROOT` data file. To import only a subset of CEL-files, list these CEL-files as vector `celfiles`.

To import CEL-files from different directories, vector `celfiles` must contain the full path for each CEL-file and `celdir` must be `celdir=NULL`.

The optional parameter `celnames` allows you to replace the original CEL-file names with names of your choice, otherwise the names of the CEL-files will be used as `celnames`.

Currently, the following types of Affymetrix CEL-files can be imported: text (version 3), xml, binary (xda), generic (agcc,calvin)

An S4 class `DataTreeSet` will be created, serving as R wrapper to the `ROOT` data file `filename`.

Use function `root.data` to access the `ROOT` data file from new R sessions to avoid creating a new `ROOT` data file for every session.

Value

A `DataTreeSet` object.

Note

As mentioned above, use function `root.data` to access the ROOT data file from new R sessions to avoid creating a new `ROOT` data file for every R session.

Do not separate `filename` of ROOT files with dots, use underscores, e.g. do not use `filename="Data.Test3"` but use `filename="Data_Test3"` or `filename="DataTest3"` instead.

To every ROOT data file the extension "_cel" is attached to `filename` to easily recognize ROOT data files containing the raw CEL data, e.g. for `filename="Data_Test3"` the final name is "Data_Test3_cel.root". Extension "root" is added automatically, so that ROOT is able to recognize the file as ROOT file.

Once a `ROOT` file is created it can not be overwritten, it must be deleted manually first. Only `ROOT` files called "tmp" or with `filename` starting with "tmp_" will be re-created automatically.

If CEL-file names contain dots, colons, parenthesis, etc. as characters, these characters will be replaced by underscores. It is recommended to use parameter `celnames` to create shorter CEL names and to replace special characters.

Author(s)

Christian Stratowa

See Also

`root.data`, `DataTreeSet`

Examples

```
## get scheme and import CEL-files from package
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- import.data(scheme.test3,"tmp_data_test3",celdir=paste(.path.package("xps")
unlist(treeNames(data.test3))

## import only subset of CEL-files
subdata.test3 <- import.data(scheme.test3,"tmpdt_data_test3",celdir=paste(.path.package("
                 celfiles=c("TestA1.CEL","TestB2.CEL"),verbose=FALSE)
unlist(treeNames(subdata.test3))
```

`import.exon.scheme` *Import CLF, PGF and annotation files into a SchemeTreeSet*

Description

Import the Affymetrix CLF, PGF, and probeset and transcript annotation files into a ROOT file and create S4 class SchemeTreeSet

Usage

```
import.exon.scheme(filename   = character(0),
                   filedir    = getwd(),
                   layoutfile = character(0),
                   schemefile = character(0),
                   probeset   = character(0),
                   transcript = character(0),
                   control    = "",
                   add.mask   = FALSE,
                   verbose    = TRUE)
```

Arguments

`filename`	file name of ROOT scheme file.
`filedir`	system directory where ROOT scheme file should be stored.
`layoutfile`	name of CLF-file, including full path.
`schemefile`	name of PGF-file, including full path.
`probeset`	name of probeset annotation-file, including full path.
`transcript`	name of transcript annotation-file, including full path.
`control`	optional name of controls.ps-file, including full path.
`add.mask`	logical. If `TRUE` mask information will be included as slot `mask`.
`verbose`	logical, if `TRUE` print status information.

Details

`import.exon.scheme` is used to import all information for an Affymetrix exon array into a `ROOT` scheme file, including CLF and PGF-files, and the current Afymetrix probeset and transcript annotation files.

An S4 class `SchemeTreeSet` will be created, serving as R wrapper to the `ROOT` scheme file `filename`.

Since a new `ROOT` scheme file needs only to be created when new annotation files are available from the Affymetrix website, it is recommended to store all `ROOT` scheme files in a commonly accessible system directory `filedir`.

Use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every session.

Value

A `SchemeTreeSet` object.

Warning

The current version of 'xps' should be able to import all Affymetrix exon array annotation files up to November 2008. However, since Affymetrix is still changing the headers and/or columns of the annotation files, future annotation files may require adaptation of the source code, thus the current version of 'xps' may not be able to read these files.

Note

As mentioned above, use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every R session.

Do not separate `filename` of ROOT files with dots, use underscores, e.g. do not use `filename="Scheme.HuEx10s` but use `filename="Scheme_HuEx10stv2r2_na27"` instead. Extension "root" is added automatically, so that ROOT is able to recognize the file as ROOT file.

Do not set `add.mask=TRUE` unless you know that your computer has sufficient RAM.

Do not add item `control` unless you want to use one of the old annotation files where the probeset annotation file does not contain the AFFX controls.

Author(s)

Christian Stratowa

See Also

`import.expr.scheme`, `root.scheme`, `SchemeTreeSet`

Examples

```
## Not run:
## define paths
scmdir <- "/common/path/schemes"
libdir <- "/my/path/Affy/libraryfiles"
anndir <- "/my/path/Affy/Annotation"

## create scheme for HuEx-1_0-st-v2.r2 Exon array
scheme.huex10stv2r2.na27 <- import.exon.scheme("Scheme_HuEx10stv2r2_na27",filedir=scmdir,
                            layoutfile=paste(libdir,"HuEx-1_0-st-v2_libraryfile/HuEx-1_0-
                            schemefile=paste(libdir,"HuEx-1_0-st-v2_libraryfile/HuEx-1_0-
                            probeset=paste(anndir,"HuEx-1_0-st-v2.na27.hg18.probeset.csv"
                            transcript=paste(anndir,"HuEx-1_0-st-v2.na27.hg18.transcript.

## access ROOT scheme file from new R session
scheme.huex10stv2r2 <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na27.root",sep="/"))

## create scheme for HuGene-1_0-st-v1.r4 as exon array
scheme.hugene10stv1r4.na27 <- import.exon.scheme("Scheme_HuGene10stv1r4_na27_2",filedir=s
                              layoutfile=paste(libdir,"HuGene-1_0-st-v1.r4.analysis-lib-f
                              schemefile=paste(libdir,"HuGene-1_0-st-v1.r4.analysis-lib-f
                              probeset=paste(anndir,"HuGene-1_0-st-v1.na27.2.hg18.probese
                              transcript=paste(anndir,"HuGene-1_0-st-v1.na27.hg18.transcr

## access ROOT scheme file from new R session
scheme.hugene10stv1r4 <- root.scheme(paste(scmdir,"Scheme_HuGene10stv1r4_na27_2.root",sep

## create scheme for HuEx-1_0-st-v2.r2 Exon array with the old annotation file
scheme.huex10stv2r2.old <- import.exon.scheme("Scheme_HuEx10stv2r2_old",filedir=scmdir,
                           layoutfile=paste(libdir,"HuEx-1_0-st-v2_libraryfile/HuEx-1_0-s
                           schemefile=paste(libdir,"HuEx-1_0-st-v2_libraryfile/HuEx-1_0-s
                           probeset=paste(anndir,"HuEx-1_0-st-probeset-annot.csv",sep="/"
                           transcript=paste(anndir,"HuEx-1_0-st-transcript-annot.csv",sep
                           control=paste(libdir,"HuEx-1_0-st-v2_libraryfile/HuEx-1_0-st-r

## End(Not run)
```

`import.expr.scheme` *Import CDF, probe and annotation files into a SchemeTreeSet*

Description

Import the Affymetrix CDF, probe and annotation files into a ROOT file and create S4 class SchemeTreeSet

Usage

```
import.expr.scheme(filename   = character(0),
                   filedir    = getwd(),
                   schemefile = character(0),
                   probefile  = character(0),
                   annotfile  = character(0),
                   chipname   = NULL,
                   add.mask   = FALSE,
                   verbose    = TRUE)
```

Arguments

`filename`	file name of ROOT scheme file.
`filedir`	system directory where ROOT scheme file should be stored.
`schemefile`	name of CDF-file, including full path.
`probefile`	name of probe-file, including full path.
`annotfile`	name of annotation-file, including full path.
`chipname`	optional chip name when using an alternative CDF-file.
`add.mask`	logical. If `TRUE` mask information will be included as slot `mask`.
`verbose`	logical, if `TRUE` print status information.

Details

`import.expr.scheme` is used to import all information for an Affymetrix expression array into a `ROOT` scheme file, including CDF-file, the corresponding probe file, and the current Afymetrix annotation file.

Usually, `chipname` is extracted from the name of the CDF-file, however, when using an alternative CDF-file, e.g. from BrainArray or AffyProbeMiner, a `chipname` must be supplied which starts with (or contains) the exact Affymetrix chip name.

An S4 class `SchemeTreeSet` will be created, serving as R wrapper to the `ROOT` scheme file `filename`.

Since a new `ROOT` scheme file needs only to be created when a new annotation file is available from the Affymetrix website, it is recommended to store all `ROOT` scheme files in a commonly accessible system directory `filedir`.

Use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every session.

Value

A `SchemeTreeSet` object.

Note

As mentioned above, use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every R session.

Do not separate `filename` of ROOT files with dots, use underscores, e.g. do not use `filename="Scheme.Test3.r` but use `filename="Scheme_Test3_na27"` or simply `filename="SchemeTest3na27"` instead. Extension “root” is added automatically, so that ROOT is able to recognize the file as ROOT file.

For a few probesets, parsing the Affymetrix annotation files will provide ambiguous results. Setting `verbose=11` will list these probesets.

Author(s)

Christian Stratowa

See Also

`import.exon.scheme`, `import.genome.scheme`, `root.scheme`, `SchemeTreeSet`

Examples

```
## Not run:
## define paths
scmdir <- "/common/path/schemes"
libdir <- "/my/path/Affy/libraryfiles"
anndir <- "/my/path/Affy/Annotation"

## create scheme for Test3 GeneChip
scheme.test3.na27 <- import.expr.scheme("Scheme_Test3_na27",filedir=scmdir,
                     schemefile=paste(libdir,"Test3.CDF",sep="/"),
                     probefile=paste(libdir,"Test3_probe.tab",sep="/"),
                     annotfile=paste(anndir,"Test3.na27.annot.csv",sep="/"))

## access ROOT scheme file from new R session
scheme.test3 <- root.scheme(paste(scmdir,"Scheme_Test3_na27.root",sep="/"))

## create scheme for HG-U133_Plus_2 GeneChip
scheme.hgu133p2.na27 <- import.expr.scheme("Scheme_HGU133p2_na27",filedir=scmdir,
                        schemefile=paste(libdir,"HG-U133_Plus_2.cdf",sep="/"),
                        probefile=paste(libdir,"HG-U133-PLUS_probe.tab",sep="/"),
                        annotfile=paste(anndir,"HG-U133_Plus_2.na27.annot.csv",sep="/"))
## access ROOT scheme file from new R session
scheme.hgu133p2 <- root.scheme(paste(scmdir,"Scheme_HGU133p2_na27.root",sep="/"))

## End(Not run)
```

`import.genome.scheme` *Import CLF, PGF and annotation files into a SchemeTreeSet*

Description

Import the Affymetrix CLF, PGF and transcript annotation files into a ROOT file and create S4 class SchemeTreeSet

Usage

```
import.genome.scheme(filename   = character(0),
                     filedir    = getwd(),
                     layoutfile = character(0),
                     schemefile = character(0),
                     transcript = character(0),
                     add.mask   = FALSE,
                     verbose    = TRUE)
```

Arguments

`filename`	file name of ROOT scheme file.
`filedir`	system directory where ROOT scheme file should be stored.
`layoutfile`	name of CLF-file, including full path.
`schemefile`	name of PGF-file, including full path.
`transcript`	name of transcript annotation-file, including full path.
`add.mask`	logical. If `TRUE` mask information will be included as slot `mask`.
`verbose`	logical, if `TRUE` print status information.

Details

`import.genome.scheme` is used to import all information for an Affymetrix whole genome array into a `ROOT` scheme file, including CLF and PGF-files, and the current Afymetrix transcript annotation files.

An S4 class `SchemeTreeSet` will be created, serving as R wrapper to the `ROOT` scheme file `filename`.

Since a new `ROOT` scheme file needs only to be created when new annotation files are available from the Affymetrix website, it is recommended to store all `ROOT` scheme files in a commonly accessible system directory `filedir`.

Use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every session.

Value

A `SchemeTreeSet` object.

Warning

The current version of 'xps' is able to import all Affymetrix genome array annotation files up to November 2008, i.e. all files of release 3 (r3) and earlier. However, in January 2009 Affymetrix has updated all CLF, PGF and annotation files to release 4 (r4) and added a new probeset annotation file, thus in effect changing the whole genome arrays to exon arrays!

Thus, for release 4 (r4) files, function `import.genome.scheme` can no longer be used, but you must use function `import.exon.scheme` instead (see examples).

Note

As mentioned above, use function `root.scheme` to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every R session.

Do not separate `filename` of ROOT files with dots, use underscores, e.g. do not use `filename="Scheme.HuGene1` but use `filename="Scheme_HuGene10stv1_na27"` instead. Extension "root" is added automatically, so that ROOT is able to recognize the file as ROOT file.

Do not set `add.mask=TRUE` unless you know that your computer has sufficient RAM.

Do not add item `control` unless you want to use one of the old annotation files where the probeset annotation file does not contain the AFFX controls.

Author(s)

Christian Stratowa

See Also

`import.exon.scheme`, `root.scheme`, `SchemeTreeSet`

Examples

```
## Not run:
## define paths
scmdir <- "/common/path/schemes"
libdir <- "/my/path/Affy/libraryfiles"
anndir <- "/my/path/Affy/Annotation"

## create scheme for HuGene-1_0-st-v1 whole genome array
scheme.hugene10stv1r3.na27 <- import.genome.scheme("Scheme_HuEx10stv1r3_na27",filedir=scm
                              layoutfile=paste(libdir,"HuGene-1_0-st-v1.r3.analysis_libra
                              schemefile=paste(libdir,"HuGene-1_0-st-v1.r3.analysis_libra
                              transcript=paste(anndir,"HuGene-1_0-st-v1.na27.hg18.transcr

## access ROOT scheme file from new R session
scheme.hugene10stv1r3 <- root.scheme(paste(scmdir,"Scheme_HuEx10stv1r3_na27.root",sep="/"

## End(Not run)
```

`ini.call` *Informative/Non-Informative Call*

Description

Computes the Informative/Non-Informative Call for the exclusion of non-informative probe sets.

Usage

```
ini.call(xps.data,
         filename   = character(0),
         filedir    = getwd(),
         tmpdir     = "",
         weight     = 0.5,
         mu         = 0.0,
         scale      = 1.0,
         tol        = 0.00001,
         cyc        = 100,
         alpha1     = 0.4,
         alpha2     = 0.6,
         version    = "1.3.1",
         option     = "transcript",
         exonlevel  = "",
         xps.scheme = NULL,
         add.data   = TRUE,
         verbose    = TRUE)
```

```
xpsINICall(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`weight`	hyperparameter, usually set to 0.5 for `version="1.3.1"` and to 8.0 for `version="1.3.0"`.
`mu`	hyperparameter allowing to correct for potential bias.
`scale`	scaling parameter, usually set to 1.0 for `version="1.3.1"` and to 2.0 for `version="1.3.0"`.
`tol`	termination tolerance for EM algorithm.
`cyc`	maximum number of cycles of EM algorithm.
`alpha1`	a significance threshold in (0,alpha2).
`alpha2`	a significance threshold in (alpha1,1.0).
`version`	version of original farms package. Currently, `version="1.3.1"` and `version="1.3.0"` are implemented. Default is `version="1.3.1"`.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` call data will be added to slots `data` and `detcall`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

In contrast to `mas5.call` this function quantifies the signal-to-noise ratio for each probe set, as described in Talloen et al. Thus, the returned p-values and detection calls have a different meaning:

The p-value that is returned estimates the signal-to-noise ratio (SNR):
P-values (SNR) of less than 0.5 indicate that there is more signal than noise and the corresponding genes are considered to be 'informative' for further analysis. In contrast, values greater than 0.5 indicate 'non-informative' genes.

The informative call is computed by thresholding the p-value as in:

call "P" if p-value < alpha1
call "M" if alpha1 <= p-value < alpha2
call "A" if alpha2 <= p-value

Here "P" should be considered as informative "I", "M" as marginally informative, and "A" as non-informative "NI".

The defaults for `alpha1=0.4` and `alpha2=0.6` are set to allow "M" calls. In order to get the same results as package 'farms_1.3.1', you need to set `alpha1=0.5` and `alpha2=0.5`.

For exon/genome arrays it is necessary to supply `option` and `exonlevel`.

Following `options` are valid for exon arrays only:

`transcript`:	expression levels are computed for transcript clusters, i.e. probe sets containing the same 'transcript_clu
`exon`:	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where e
`probeset`:	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.

Following `exonlevel` annotations are valid for exon arrays:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`ambiguous`:	ambiguous probesets only.
`affx`:	standard AFFX controls.
`all`:	combination of above.

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	probesets with category 'unique' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above.

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affy"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper 'exon_probeset_trans_clust_whitepaper.pdf'.

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeTreeSet `xps.scheme`.

`xpsINICall` is the `DataTreeSet` method called by function `ini.call`, containing the same parameters.

Value

A `CallTreeSet`

Note

Since I/NI-calls distinguish only between informative and non-informative genes, the calls are identical for all samples.

Author(s)

Christian Stratowa

References

Talloen, W., Clevert D.-A., Hochreiter, S., Amaratunga, D., Bijnens, J., Kass, S., and Gohlmann, H.W.H. (2006), I/NI-calls for the exclusion of non-informative genes: a highly effective filtering tool for microarray data. Bioinformatics 23(21):2897-2902

See Also

farms, mas5.call

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## I/NI call
call.ini <- ini.call(data.test3,"tmp_Test3INI",verbose=FALSE)

## get data.frames
snr.ini <- pvalData(call.ini)
inf.ini <- presCall(call.ini)
head(snr.ini)
head(inf.ini)

## plot results
if (interactive()) {
callplot(call.ini)
}

rm(scheme.test3, data.test3)
gc()
```

---

initialize-methods *Initialize Classes*

Description

Initialize S4 classes.

Methods

Internal method to initialize S4 classes.

`intensity-methods` *Get/Set Data Values*

Description

Get/set data values from/for class `DataTreeSet`.

Usage

```
intensity(object)
intensity(object, filename = NULL, verbose = FALSE) <- value
```

Arguments

`object`	object of class `DataTreeSet`.
`filename`	`character` vector containing optional ROOT file name.
`verbose`	logical, if `TRUE` print status information.
`value`	`data.frame` containing expression values.

Details

Get the intensity values from slot `data` or set slot `data` to `value`.

Method `intensity` returns the data values from slot `data` as `data.frame`, while replacement method `intensity<-` allows to replace slot `data` with a `data.frame`.

Using replacement method `intensity<-` with default settings will not change the data stored in the ROOT data file, and thus will not have any effect on subsequent processing methods. If you really want to use the replacement data for further processing you must supply a new ROOT `filename`. This will export each intensity column of `value` as CEL-file (version 3), which will then be imported into the new ROOT data file `filename`.

Warning: Do not use replacement method `intensity<-` until you really know what you are doing!

Note: The first two columns of replacement `data.frame value` must be the (X,Y) coordinates, followed by the intensities whereby the number of intensity columns must be identical to the columns to be replaced.

Note: If you do not want to replace your current object, create first a copy of type `DataTreeSet` by simply writing `newobj <- oldobj`, and use `newobj` for replacement. This is important since `intensity<-` does also update slots `rootfile`, `filedir` and `treenames` when a new `filename` was chosen.

Note: The CEL-files created are fully functional CEL-files (version 3), however some header rows such as GridCornerUL, AlgorithmParameters, and some of the data in DatHeader are placeholders only.

Warning: The CEL-files created WILL REPLACE THE ORIGINAL CEL-files, if they have identical names to the original CEL-files and the original CEL-files are located in the working directory. Thus the original CEL-files should preferable be located in directory `celdir` of function `import.data`.

Author(s)

Christian Stratowa

See Also

validData

Examples

```
## Not run:
## load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## get intensity values
value <- intensity(data.test3)

## make a copy of your object if you do not want to replace it
newdata.test3 <- data.test3

## replace slot data with value
intensity(newdata.test3, "ReplacementData", FALSE) <- value
str(newdata.test3)

## now you can create an ExprTreeSet using the new intensity data
data.rma <- rma(newdata.test3,"ReplacementRMA",tmpdir="",background="none",normalize=TRUE

## End(Not run)
```

`isROOTFile` *Test for ROOT File*

Description

Test if a file is a valid ROOT file.

Usage

```
isROOTFile(filename)
```

Arguments

filename	name of ROOT file, including full path.

Value

Return TRUE if file filename is a valid ROOT file.

Author(s)

Christian Stratowa

See Also

existsROOTFile

Examples

```
isROOTFile(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"))
```

`lowFilter-methods` *Lower Threshold Filter*

Description

This method initializes the Lower Threshold Filter. The `cutoff` value defines the lower threshold for allowed expression levels. If e.g. the number of samples lower than this cutoff value is greater than `parameter` then the corresponding dataframe row is flagged, i.e. `flag = 0`.
The Lower Threshold Filter flags all rows with: `flag = (sum(expression[i] >= cutoff) >= parameter)`

Usage

```
lowFilter(object)
lowFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	character vector `c(cutoff, parameter, condition)`.

Details

The method `lowFilter` initializes the following parameters:

`cutoff`:	the lower threshold level for the filter.
`parameter`:	this value depends on the `condition` used:
`condition`:	`condition="samples"`: number of samples (default):
	`condition="percent"`: percent of samples.
	`condition="mean"`: mean value of samples.
	`condition="percentile"`: percentile of samples.

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
lowFilter(prefltr) <- c(4.0,3,"samples")
str(prefltr)
```

`madFilter-methods` *Median Absolute Deviation Filter*

Description

This method initializes the Median Absolute Deviation Filter.
The MAD Filter flags all rows with: `flag = (mad >= cutoff)`

Usage

```
madFilter(object)
madFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric vector `c(cutoff, epsilon)`.

Details

The method `madFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`epsilon`:	value to replace mean (default is `epsilon=0.01`).

Note, that `epsilon` has no effect on `mad`.

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
madFilter(prefltr) <- c(0.5,0.01)
str(prefltr)
```

`madplot-methods` *Array-Array Expression Level Distance Plot*

Description

A false color display of between arrays distances, computed as the MAD of the M-values of each pair of arrays.

Usage

```
 madplot(x, which = "UnitName", transfo = log2, col = NULL, names =
"namepart", sort = FALSE, bmar = NULL, add.legend = FALSE, ...)
```

Arguments

`x`	object of class `ExprTreeSet`.
`transfo`	a valid function to transform the data, usually "log2", or "0".
`col`	vector of colors for plot, length is number of samples.
`names`	optional vector of sample names.
`sort`	logical, if TRUE the correlation matrix will be sorted decreasingly.
`bmar`	optional `list` for bottom margin and axis label magnification `cex.axis`.
`add.legend`	logical, if TRUE then a color bar will be drawn.
`...`	optional arguments to be passed to `plot`.

Details

Produces a false color display, i.e. heatmap, of between arrays distances for slot `data` for an object of class `ExprTreeSet`, computed as the MAD of the M-values of each pair of arrays.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as mdaplot.

For `bmar=NULL` the default list `bmar = list(b=6, cex.axis=1.0)` will be used initially. However, both bottom margin and axis label magnification will be adjusted depending on the number of label characters and the number of smaples.

Author(s)

Christian Stratowa

See Also

`corplot`

`mas4` *MAS 4.0 Expression Measure*

Description

This function converts a `DataTreeSet` into an `ExprTreeSet` using the XPS implementation of Affymetrix's MAS 4.0 expression measure.

Usage

```
mas4(xps.data,
     filename   = character(0),
     filedir    = getwd(),
     tmpdir     = "",
     normalize  = FALSE,
     sc         = 500,
     option     = "transcript",
     exonlevel  = "",
     update     = FALSE,
     xps.scheme = NULL,
     add.data   = TRUE,
     verbose    = TRUE)

xpsMAS4(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`normalize`	logical. If `TRUE` scale normalization is used after an `ExprTreeSet` is obtained.
`sc`	value at which all arrays will be scaled to.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	arguments `filename`,`filedir`,`tmpdir`,`option`,`exonlevel`,`xps.scheme`.

Details

This function computes the Affymetrix MAS 4.0 expression measure, i.e. the 'Average Difference' expression level, as implemented in XPS.

If `normalize=TRUE` then the expression levels will be scaled to `sc`. For `sc=0` the expression levels will be scaled to the mean expression level.

`xpsMAS4` is the `DataTreeSet` method called by function `mas4`, however, expression levels will not be scaled to a common mean expression level.

For further details see `mas5`.

Value

An `ExprTreeSet`

Note

In contrast to function `mas4`, expression levels computed with `xpsMAS4` will not be scaled to a common mean expression level.

Author(s)

Christian Stratowa

References

Affymetrix (1999) GeneChip Expression Analysis Algorithm Tutorial, Affymetrix Inc., Santa Clara, CA.

See Also

`xpsMAS4`, `express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.mas4 <- mas4(data.test3,"tmp_Test3MAS4",tmpdir="",normalize=TRUE,sc=500, update=TRUE

## get data.frame
expr.mas4 <- validData(data.mas4)
head(expr.mas4)

## plot results (negative expression values!)
if (interactive()) {
boxplot(expr.mas4)
}

rm(scheme.test3, data.test3)
gc()
```

---

mas5 *MAS 5.0 Expression Measure*

Description

This function converts a `DataTreeSet` into an `ExprTreeSet` using the XPS implementation of Affymetrix's MAS 5.0 expression measure.

Usage

```
mas5(xps.data,
     filename   = character(0),
     filedir    = getwd(),
     tmpdir     = "",
     normalize  = FALSE,
     sc         = 500,
     option     = "transcript",
     exonlevel  = "",
     update     = FALSE,
     xps.scheme = NULL,
     add.data   = TRUE,
     verbose    = TRUE)


xpsMAS5(object, ...)
```

Arguments

xps.data	object of class DataTreeSet.
filename	file name of ROOT data file.
filedir	system directory where ROOT data file should be stored.
tmpdir	optional temporary directory where temporary ROOT files should be stored.
normalize	logical. If TRUE scale normalization is used after an ExprTreeSet is obtained.
sc	value at which all arrays will be scaled to.
option	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
exonlevel	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
update	logical. If TRUE the existing ROOT data file filename will be updated.
xps.scheme	optional alternative SchemeTreeSet.
add.data	logical. If TRUE expression data will be included as slot data.
verbose	logical, if TRUE print status information.
object	object of class DataTreeSet.
...	arguments filename,filedir,tmpdir,option,exonlevel,xps.scheme.

Details

This function computes the Affymetrix MAS 5.0 expression measure as implemented in XPS. Although this implementation is based on the Affymetrix 'sadd_whitepaper.pdf', it can be used to compute an expression level for both expression arrays and exon arrays. For exon arrays it is necessary to supply the requested option and exonlevel.

Following options are valid for exon arrays:

transcript:	expression levels are computed for transcript clusters, i.e. probe sets containing the same 'transcript_clu
exon:	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where ea
probeset:	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.

Following exonlevel annotations are valid for exon arrays:

core:	probesets supported by RefSeq and full-length GenBank transcripts.
metacore:	core meta-probesets.
extended:	probesets with other cDNA support.
metaextended:	extended meta-probesets.
full:	probesets supported by gene predictions only.
metafull:	full meta-probesets.
ambiguous:	ambiguous probesets only.
affx:	standard AFFX controls.
all:	combination of above (including affx).

Following exonlevel annotations are valid for whole genome arrays:

core:	probesets with category 'unique', 'similar' and 'mixed'.

`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affx"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper 'exon_probeset_trans_clust_whitepaper.pdf'.

If `normalize=TRUE` then the expression levels will be scaled to `sc`. For `sc=0` the expression levels will be scaled to the mean expression level.

If `update=TRUE` then the existing `ROOT` file `filename` will be updated, however, this is usually only recommended as option for function `express`.

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeTreeSet `xps.scheme`.

`xpsMAS5` is the `DataTreeSet` method called by function `mas5`, however, expression levels will not be scaled to a common mean expression level.

Value

An `ExprTreeSet`

Note

In contrast to function `mas5`, expression levels computed with `xpsMAS5` will not be scaled to a common mean expression level.

Author(s)

Christian Stratowa

References

Affymetrix (2002) Statistical Algorithms Description Document, Affymetrix Inc., Santa Clara, CA, whitepaper. http://www.affymetrix.com/support/technical/whitepapers/sadd_whitepaper.pdf

Affymetrix (2005) Exon Probeset Annotations and Transcript Cluster Groupings, Affymetrix Inc., Santa Clara, CA, exon_probeset_trans_clust_whitepaper.pdf.

See Also

`express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.mas5 <- mas5(data.test3,"tmp_Test3MAS5",tmpdir="",normalize=TRUE,sc=500,update=TRUE,
## get data.frame
expr.mas5 <- validData(data.mas5)
head(expr.mas5)

## plot results
if (interactive()) {
boxplot(data.mas5)
boxplot(log2(expr.mas5))
}

rm(scheme.test3, data.test3)
gc()
```

`mas5.call` *MAS 5.0 Absolute Detection Call*

Description

Performs the Wilcoxon signed rank-based gene expression presence/absence detection algorithm first implemented in the Affymetrix Microarray Suite version 5.

Usage

```
mas5.call(xps.data,
          filename = character(0), filedir = getwd(), tmpdir = "",
          tau = 0.015, alpha1 = 0.04, alpha2 = 0.06, ignore.saturated = TRUE, bg
          option = "transcript", exonlevel = "", xps.scheme = NULL, add.data = T

xpsMAS5Call(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`tau`	a small positive constant.
`alpha1`	a significance threshold in (0,alpha2).
`alpha2`	a significance threshold in (alpha1,0.5).
`ignore.saturated`	logical. If `TRUE` do the saturation correction described in the paper, with a saturation level of 46000.
`bgcorrect.option`	bgcorrect option determining wether to subtract background first, one of 'none' or 'correctbg'.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.

`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` call data will be added to slots `data` and `detcall`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

This function performs the hypothesis test:

H0: median(Ri) = tau, corresponding to absence of transcript H1: median(Ri) > tau, corresponding to presence of transcript

where Ri = (PMi - MMi) / (PMi + MMi) for each i a probe-pair in the probe-set represented by data.

The p-value that is returned estimates the usual quantity:

Pr(observing a more "present looking" probe-set than data | data is absent)

Small p-values imply presence while large ones imply absence of transcript. The detection call is computed by thresholding the p-value as in:

call “P” if p-value < alpha1
call “M” if alpha1 <= p-value < alpha2
call “A” if alpha2 <= p-value

The defaults for `tau`, `alpha1` and `alpha2` correspond to those in MAS5.0 for expression arrays. However, when using this function for exon or whole genome arrays, new values for `alpha1` and `alpha2` must be determined. The recommended function for exon/genome arrays is `dabg.call`.

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeTreeSet `xps.scheme`.

`xpsMAS5Call` is the `DataTreeSet` method called by function `mas5.call`, containing the same parameters.

Value

A `CallTreeSet`

Author(s)

Christian Stratowa

References

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Affymetrix (2002) Statistical Algorithms Description Document, Affymetrix Inc., Santa Clara, CA, whitepaper. `http://www.affymetrix.com/support/technical/whitepapers/sadd_whitepaper.pdf`

See Also

dabg.call

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## MAS5 detection call
call.mas5 <- mas5.call(data.test3,"tmp_Test3Call",tmpdir="",verbose=FALSE)

## get data.frames
pval.mas5 <- pvalData(call.mas5)
pres.mas5 <- presCall(call.mas5)
head(pval.mas5)
head(pres.mas5)

## plot results
if (interactive()) {
callplot(call.mas5, beside=FALSE, ylim=c(0,125))
}

rm(scheme.test3, data.test3)
gc()
```

---

mboxplot-methods *Box Plots of Relative M Values*

Description

Produce boxplots of relative M values for the set of arrays.

Usage

```
 mboxplot(x, which = "", size = 0, transfo = log2, method = "mean",
range = 0, ylim = c(-1,1), outline = FALSE, names = "namepart", ...)
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`method`	method to create the reference data, “mean” or “median”.
`range`	determines how far the plot whiskers extend out from the box.
`ylim`	range for the plotted y values.
`outline`	if `outline` is not true, the outliers are not drawn.
`names`	optional vector of sample names.
`...`	optional arguments to be passed to `boxplot`.

Details

Create boxplots of M plots, where M is determined relative to a pseudo-mean reference chip.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as boxplot.

Note

For a `DataTreeSet` object, data must first be attached using method `attachInten`.

Author(s)

Christian Stratowa

See Also

`boxplot.dev`, `boxplot`

Examples

```
# load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

# need to attach scheme mask and probe intensities
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)

if (interactive()) {
mboxplot(data.test3, ylim=c(-6,6))
}

# optionally remove mask and data to free memory
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)
```

`metaProbesets` *Create MetaProbeset File for APT*

Description

Create MetaProbeset File for APT function “apt-probeset-summarize”.

Usage

```
metaProbesets(xps.scheme, infile = character(0), outfile = character(0), exonlev
```

Arguments

`xps.scheme`	exon `SchemeTreeSet`.
`infile`	Name of file containing exon transcript_cluster_ids.
`outfile`	Name of resulting file containing meta probeset definitions.
`exonlevel`	exon annotation level determining which probes should be used.

Details

This function allows to create a metaprobeset file for APT function “apt-probeset-summarize” to be used with option “-m”. The `infile` must contain exon transcript_cluster_ids, one per line, e.g. one can export the `rownames(data.rma)`
The resulting file may be useful if you want to compare results created with `xps` to results created with APT function “apt-probeset-summarize”.

Value

None.

Author(s)

Christian Stratowa

Examples

```
## Not run:
## first, load ROOT exon scheme file:
scmdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Schemes"
scheme.exon <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na25.root",sep="/"))

metaProbesets(scheme.exon,"metacore.txt","metacoreList.mps","metacore")

## End(Not run)
```

`mvaplot-methods` *M vs A Plot*

Description

Produce scatter plots of M values vs A values of the samples.

Usage

```
 mvaplot(x, which = "UnitName", transfo = log2, method = "median",
names = "namepart", ylim = c(-6,6), xlab = "A", ylab = "M", pch = '.',
las = 2, ...)
```

Arguments

`x`	object of class `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`method`	method to compute M, “mean” or “median”.
`names`	optional vector of sample names.
`ylim`	range for the plotted M values.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.
`pch`	an integer specifying a symbol or a character to be used as the default in plotting points.
`las`	the style of axis labels.
`...`	optional arguments to be passed to `plot`.

Details

Produces mvaplots for slot `data` for an object of class `ExprTreeSet`.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as mvaplot.

Author(s)

Christian Stratowa

See Also

`mvaplot.dev`

`mvaplot.dev` *MvA Scatter Plot for Device*

Description

Produce scatter plots of M values vs A values of the samples for the selected device.

Usage

```
mvaplot.dev(x, transfo = log2, method = "median", names = "namepart", ylim = c(-
```

Arguments

`x`	object of class `ExprTreeSet`.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`method`	method to compute M, “mean” or “median”.
`names`	optional vector of sample names.
`ylim`	range for the plotted M values.
`xlab`	a title for the x axis.
`ylab`	a title for the y axis.
`pch`	either an integer specifying a symbol or a single character to be used in plotting points.
`mar`	plot margin.
`dev`	graphics device to plot to, i.e. one of “screen”, “jpeg”,“png”, “pdf” or “ps”.
`outfile`	the name of the output file.
`w`	the width of the device in pixels.
`h`	the height of the device in pixels.
`...`	optional arguments to be passed to `plot`.

Details

Produces mvaplots for slot `data` for an object of class `ExprTreeSet` for the selected graphics device.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as mvaplot.

Author(s)

Christian Stratowa

See Also

`mvaplot`

`namePart` *Get Tree Names w/o Extension*

Description

Get (tree) names w/o their extension.

Usage

```
namePart(names)
```

Arguments

`names`	vector of names.

Details

Extracts the name part of `names`, e.g.of tree names of `treename.treetype` stored in a `ROOT` file.

Value

A `vector` of tree names w/o its extension.

Author(s)

Christian Stratowa

See Also

`extenPart`

Examples

```
names <- c("TestA1.int", "TestA2.int")
namePart(names)
```

`normalize` *Normalization on Affymetrix Probe Level Data or on Expression Levels*

Description

Functions that allow to normalize Affymetrix arrays both at the probe level ("low-level normalization") and/or at the expression level ("high-level normalization").

Usage

```
normalize(xps.data, filename = character(0), filedir = getwd(), tmpdir = "", upd

normalize.constant(xps.data, filename = character(0), filedir = getwd(), tmpdir

normalize.lowess(xps.data, filename = character(0), filedir = getwd(), tmpdir =

normalize.quantiles(xps.data, filename = character(0), filedir = getwd(), tmpdir

normalize.supsmu(xps.data, filename = character(0), filedir = getwd(), tmpdir =

xpsNormalize(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet` or `ExprTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`select`	type of probes to select for normalization.
`method`	normalization method to use.
`option`	option determining the grouping of probes for normalization, and the selection of the probes.
`logbase`	logarithm base as character, one of '0', 'log', 'log2', 'log10'.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`refindex`	index of reference tree to use, or 0.
`refmethod`	for `refindex=0`, either trimmed mean or median of trees.
`params`	vector of parameters for normalization method.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet` or `ExprTreeSet`.
`...`	the arguments described above.

Details

Functions that allow to normalize Affymetrix arrays both at the probe level ("low-level normalization") and/or at the expression level ("high-level normalization").

Please have a look at vignette "xpsPreprocess.pdf" for details on how to use function `normalize`.

`xpsNormalize` are the `DataTreeSet` or `ExprTreeSet` methods, respectively, called by function `normalize`, containing the same parameters.

Value

An object of type `DataTreeSet` or `ExprTreeSet`.

Warning

Functions `normalize.lowess` and `normalize.supsmu` have only be tested for `objects` of type `ExprTreeSet` but not for objects of type `DataTreeSet`, i.e. for probe level intensities.

Author(s)

Christian Stratowa

See Also

`express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## RMA background
data.bg.rma <- bgcorrect.rma(data.test3,"tmp_Test3NormRMA",filedir=getwd(),tmpdir="",verb
## normalize quantiles
data.qu.rma <- normalize.quantiles(data.bg.rma,"tmp_Test3NormRMA",filedir=getwd(),tmpdir=
## summarize medianpolish
data.mp.rma <- summarize.rma(data.qu.rma,"tmp_Test3NormRMA",filedir=getwd(),tmpdir="",upd
```

`nuseplot-methods` *Box Plots of Normalized Unscaled Standard Errors (NUSE)*

Description

Produce boxplot of Normalized Unscaled Standard Errors (NUSE) for the set of arrays.

Usage

```
 nuseplot(x, which = "UnitName", size = 0, range = 0, ylim = c(0.9,1.2),
outline = FALSE, names = "namepart", las = 2, ...)
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`range`	determines how far the plot whiskers extend out from the box.
`ylim`	range for the plotted y values.
`outline`	if `outline` is not true, the outliers are not drawn.
`names`	optional vector of sample names.
`las`	the style of axis labels.
`...`	optional arguments to be passed to `boxplot`.

Details

Create boxplots of Normalized Unscaled Standard Errors (NUSE) for the set of arrays.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as boxplot.

Author(s)

Christian Stratowa

See Also

`rleplot`

Examples

```
# load existing ROOT scheme file and ROOT expression file for rma
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.rma <- root.expr(scheme.test3, paste(.path.package("xps"),"rootdata/tmp_Test3RMA.roo

if (interactive()) {
nuseplot(data.rma)
}
```

`pcaplot-methods` *PCA Plot*

Description

This function produces a PCA plot of the first two principle components.

Usage

```
 pcaplot(x, which = "UnitName", transfo = log2, method = "none", groups
= NULL, screeplot = FALSE, squarepca = FALSE, pcs = c(1,2), add.labels
= FALSE, add.legend = FALSE, col = NULL, names = "namepart", as.list
= FALSE, ...)
```

Arguments

`x`	object of class `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`method`	a character string indicating which correlation coefficient is to be computed. One of “pearson”, “spearman”, “kendall”, or “none”.
`groups`	character `vector` listing the group names in order of the `names`.
`screeplot`	logical, if TRUE plot a `screeplot` instead of a PCA plot.
`squarepca`	logical, if TRUE make the y-axis of the PCA plot comparable to the x-axis.
`pcs`	a character `vector` of length two indicating which principal components to plot.
`add.labels`	logical, if TRUE then name labels will be added to the points.
`add.legend`	logical, if TRUE and `groups` are supplied then a legend indicating the groups will be drawn. Optionally, a character indicating the position of the legend, default is “topleft”.
`col`	vector of colors for plot, length is number of samples.
`names`	optional vector of sample names.
`as.list`	logical, if TRUE then a `list` will be returned in addition to the plot.
`...`	optional arguments to be passed to `plot`.

Details

Function `pcaplot` produces a PCA plot of the first two principle components for slot `data` or the correlations between the columns of slot `data`, respectively, of an object of class `ExprTreeSet`.

For `method="none"` function `[stats]prcomp` will be applied to slot `data` directly, otherwise `prcomp` will be applied to `(1 - cor(data))` with the respective `method`.

For `screeplot=TRUE` a `screeplot` will be plotted instead of a PCA plot.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as mvaplot.

Value

None by default.

Optionally, for `as.list=TRUE` a `list` will be returned with the components `sdev` and `rotation`, see `[stats]prcomp`.

Author(s)

Christian Stratowa, partly adapted from function plotPCA() of package affycoretools

See Also

`corplot`, `madplot`

`plotBoxplot` *Box Plots for Device*

Description

Produce box-and-whisker plot(s) of the samples for the selected device.

Usage

```
plotBoxplot(x,
            which    = "",
            size     = 0,
            transfo  = log2,
            range    = 0,
            names    = "namepart",
            mar      = NULL,
            las      = 2,
            cex      = 1.0,
            dev      = "screen",
            outfile  = "BoxPlot",
            w        = 800,
            h        = 540,
            ...)

boxplot.dev(x, which = "", size = 0, transfo = log2, range = 0, names = "namepar
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`transfo`	a valid function to transform the data, usually `log2`, or 0.
`range`	determines how far the plot whiskers extend out from the box.
`names`	optional vector of sample names.
`mar`	plot margin.
`las`	style of axis labels.
`cex`	amount by which plotting text and symbols should be magnified.
`dev`	graphics device to plot to, i.e. one of “screen”, “jpeg”,“png”, “pdf” or “ps”.
`outfile`	the name of the output file.
`w`	the width of the device in pixels.
`h`	the height of the device in pixels.
`...`	optional arguments to be passed to `boxplot`.

Details

Produces a boxplot for slot `data` for an object of class `DataTreeSet`, `ExprTreeSet` or `QualTreeSet` for the selected graphics device.

Note

Function boxplot.dev() will be deprecated since it needs to attachInten()!!

Author(s)

Christian Stratowa

See Also

`boxplot`

`plotImage` *Plot Image(s) for Device*

Description

Creates an image for each sample for the selected device.

Usage

```
plotImage(x,
          type     = character(),
          qualopt  = c("raw", "adjusted", "normalized"),
          transfo  = log2,
          col      = NULL,
          names    = character(),
          dev      = "screen",
          outfile  = "Image",
          w        = 800,
          h        = 800,
          ...)

image.dev(x, bg = FALSE, transfo = log2, col = gray((0:64)/64), names = "namepar
```

Arguments

`x`	object of class `DataTreeSet` or `QualTreeSet`.
`type`	character string specifying the type of image.
`qualopt`	character string specifying whether to draw residual image for "raw", "adjusted", or "normalized" intensities.
`bg`	logical. If `FALSE`, intensities from slot `data` will be used; if `TRUE`, background intensities from slot `bgrd` will be used.
`transfo`	a valid function to transform the data, usually "log2", or "0".
`col`	color range for intensities.
`names`	vector of sample names.
`xlab`	a title for the x axis.
`ylab`	a title for the y axis.
`mar`	plot margins.

`dev`	graphics device to plot to, i.e. one of “screen”, “jpeg”,“png”, “pdf” or “ps”.
`outfile`	the name of the output file.
`w`	the width of the device in pixels.
`h`	the height of the device in pixels.
`...`	optional arguments to be passed to `image`.

Details

Creates intensity image(s) or residual image(s), respectively, for each array for the selected graphics device.

For intensity image(s) `type` must be one of “intensity”.

For residual image(s) `type` must be one of “resids”,“pos.resids”, “neg.resids”, “sign.resids”, or “weights”. Furthermore, `qualopt` determines if images should be drawn for “raw”, “adjusted”, or “normalized” data.

For `names="*"` names of all samples will be displayed as images. If `names` is a vector of column names, only these samples will displayed as image(s).

Note

Function image.dev() will be deprecated since it needs to attachInten()!!

Author(s)

Christian Stratowa

See Also

`image-methods`, `image`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## qualification - rlm
rlm.all <- rmaPLM(data.test3, "tmp_Test3RLMall", filedir=getwd(), tmpdir="", qualopt="all

if (interactive()) {
## image(s) of raw data
plotImage(data.test3, type="intensity", names="*")
plotImage(data.test3, type="intensity", names="TestA2.cel")

## image(s) of residuals/weights
plotImage(rlm.all, type="weights", names="*")
plotImage(rlm.all, type="weights", qualopt="adjusted", names="*")
plotImage(rlm.all, type="resids", names="TestA2_raw.res")
}

## function image.dev() will be deprecated since it needs attachInten!!
## need to attach scheme mask and data
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)
if (interactive()) {
image.dev(data.test3)
}
## to avoid memory comsumption of R remove data:
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)

## End(Not run)
```

pm-methods *Methods for accessing perfect matches and mismatches*

Description

Methods for accessing perfect match (PM) and mismatch (MM) probes.

Usage

```
pm(object, which = "pm")
mm(object, which = "mm")
```

Arguments

`object`	object of class `DataTreeSet`.
`which`	type of perfect match or mismatch probes to be returned.

Details

For expression arrays all the perfect match (pm) or mismatch (mm) probes on the arrays the object represents are returned as data.frame.

For exon arrays, `pm` returns the probes of the different exon levels as data.frame, i.e. `which` can have one of the following values:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`affx`:	standard AFFX controls.

For whole genome arrays, `pm` returns the probes of the different exon levels as data.frame, i.e. `which` can have one of the following values:

`core`:	probesets with category 'unique' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.

For exon/genome arrays, `mm` returns the background probes as data.frame, i.e. `which` is either "genomic" or "antigenomic".

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`validData`

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## need to attach scheme mask and probe intensities
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)

pm <- pm(data.test3)
mm <- mm(data.test3)
head(pm)
head(mm)

## optionally remove mask and data to free memory
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)
```

---

pmplot-methods *Barplot of PM and MM Intensities.*

Description

Creates a barplot of mean perfect match and mismatch intensities.

Usage

```
 pmplot(x, which = "", size = 0, transfo = NULL, method = "mean", names
= "namepart", beside = TRUE, col = c("red", "blue"), legend = c("PM","MM"),
...)
```

Arguments

`x`	object of class `DataTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`transfo`	a valid function to transform the data, usually “log2”, or “0”.
`method`	method to compute average intensities, “mean” or “median”.
`names`	optional vector of sample names.

beside	logical. If FALSE, mean intensities are portrayed as stacked bars, and if TRUE the columns are portrayed as juxtaposed bars.
col	color of PM, MM bars.
legend	a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included.
...	optional arguments to be passed to barplot.

Details

Produces barplots of mean perfect match and mismatch intensities for slot data for an object of class ExprTreeSet.

For names=NULL full column names of slot data will be displayed while for names="namepart" column names will be displayed without name extension. If names is a vector of column names, only these columns will displayed as pmplot.

Note

Data must first be attached to class DataTreeSet using method attachInten.

Author(s)

Christian Stratowa

See Also

boxplot.dev, boxplot, barplot

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## need to attach scheme mask and probe intensities
data.test3 <- attachMask(data.test3)
data.test3 <- attachInten(data.test3)

if (interactive()) {
pmplot(data.test3)
}

## optionally remove mask and data to free memory
data.test3 <- removeInten(data.test3)
data.test3 <- removeMask(data.test3)
```

`prefilter` *Function for Applying a PreFilter to an ExprTreeSet*

Description

This function applies a `PreFilter` to an `ExprTreeSet`.

Usage

```
prefilter(xps.expr,
          filename   = character(0),
          filedir    = getwd(),
          filter     = NULL,
          minfilters = 999,
          logbase    = "log2",
          treename   = "PreFilter",
          xps.call   = NULL,
          verbose    = TRUE)


xpsPreFilter(object, ...)
```

Arguments

`xps.expr`	object of class `ExprTreeSet`.
`filename`	file name of ROOT filter file.
`filedir`	system directory where ROOT filter file should be stored.
`filter`	object of class `PreFilter`.
`minfilters`	minimum number of initialized filter methods to satisfy (default is all filters).
`logbase`	convert data to logarithm of base: `"0"`, `"log"`, `"log2"` (default), `"log10"`
`treename`	tree name to be used in ROOT filter file.
`xps.call`	optional object of class `CallTreeSet`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `ExprTreeSet`.
`...`	same arguments as function `prefilter`.

Details

This function applies the different filters initialized with constructor `PreFilter` to the `ExprTreeSet` `xps.expr`.

Slot `minfilters` determines the minimum number of initialized filters, which must be satisfied so that the mask is set to `flag=1`. For `minfilters=1` at least one filter must be satisfied, equivalent to logical ‘OR’; for `minfilters=999` all filters must be satisfied, equivalent to logical ‘AND’.

If method `callFilter` was initialized with constructor `PreFilter` then `CallTreeSet` `xps.call` must be supplied, usually created with function `mas5.call`.

Value

A FilterTreeSet

Author(s)

Christian Stratowa

See Also

PreFilter, unifilter

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## second, create an ExprTreeSet
data.rma <- rma(data.test3,"tmp_TestRMA",tmpdir="",background="pmonly",normalize=TRUE,ver
## note: do not copy/paste this code, it is necessary only because R CMD check fails sinc
data.rma@rootfile <- paste(.path.package("xps"),"rootdata/tmp_Test3RMA.root",sep="/")
data.rma@filedir  <- paste(.path.package("xps"),"rootdata",sep="/")

## third, construct a PreFilter
prefltr <- PreFilter(mad=c(0.5,0.01),lothreshold=c(6.0,0.02,"mean"),hithreshold=c(10.5,80

## finally, create a FilterTreeSet
rma.pfr <- prefilter(data.rma,"tmp_Test3Prefilter",getwd(),prefltr,2,verbose=FALSE)
str(rma.pfr)

## End(Not run)
```

---

presCall-methods *Get/Set Present Call Values*

Description

Get/set present call values from/for class CallTreeSet.

Usage

```
presCall(object)
presCall(object, treenames = NULL) <- value

pvalData(object)
pvalData(object, treenames = NULL) <- value
```

Arguments

object	object of class CallTreeSet.
treenames	character vector containing optional tree names to be used as subset.
value	data.frame containing present call values.

Details

Get the p-values from slot `data` or present calls from slot `detcall`, or set slot `data` or `detcall`, respectively, to `value`.

Method `presCall` returns the present calls from slot `detcall` as `data.frame`, while replacement method `presCall<-` allows to replace slot `detcall` with a `data.frame`.

Method `pvalData` returns the p-values from slot `data` as `data.frame`, while replacement method `pvalData<-` allows to replace slot `data` with a `data.frame`.

In order to create an `CallTreeSet` containing only a subset of e.g. slot `data`, first export slot `data` using method `pvalData`, create a `character` vector containing only `treenames` to be used in the subset, and then use replacement method `pvalData<-` to replace slot `data` with the subset. Slots `treenames` and `numtrees` will be updated automatically for `pvalData<-` but not for `presCall<-`.

Note: When creating `character` vector `treenames` it is sufficient to use the name part of the tree name w/o the extension.

Note: If you do not want to replace your current object, create first a copy of type `CallTreeSet` by simply writing `newobj <- oldobj`, and use `newobj` for replacement.

Author(s)

Christian Stratowa

See Also

`exprs`

Examples

```
## Not run:
## load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## create an CallTreeSet
call.mas5 <- mas5.call(data.test3,"tmp_TestMAS5Call",tmpdir="",verbose=FALSE)

## get p-values
value <- pvalData(call.mas5)

## selected treenames only
treenames <- c("TestA2", "TestB1")

## make a copy of your object if you do not want to replace it
subset.call <- call.mas5

## replace slot data with subset
exprs(subset.call, treenames) <- value
str(subset.call)

## End(Not run)
```

`qualify` *Probe Set Quality Control Functions*

Description

Converts Affymetrix probe level data to expression levels by fitting a multichip model.

Usage

```
qualify(xps.data,
        filename   = character(0),
        filedir    = getwd(),
        tmpdir     = "",
        update     = FALSE,
        select     = "none",
        method     = character(),
        option     = "transcript",
        logbase    = "log2",
        exonlevel  = "",
        params     = list(),
        xps.scheme = NULL,
        add.data   = TRUE,
        verbose    = TRUE)

qualify.rlm(xps.data,
            filename   = character(0),
            filedir    = getwd(),
            tmpdir     = "",
            update     = FALSE,
            option     = "transcript",
            exonlevel  = "",
            xps.scheme = NULL,
            add.data   = TRUE,
            verbose    = TRUE)

xpsQualify(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`select`	type of probes to select for summarization.
`method`	qualification method to use, currently `rlm`.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon/genome arrays only.
`logbase`	logarithm base as character, one of '0', 'log', 'log2', 'log10'.

`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	vector of parameters for summarization method.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

Converts Affymetrix probe level data to expression levels by fitting a multichip model.

This function stores three types of ROOT trees in `filename`:
- quality trees containing expression levels, normalized unscaled standard errors (NUSE), relative log expressions (RLE)
- residual trees containing the residual SE and the model fit weights
- border trees containing the border intensities, mean border intensities and center of intensities (COI)

`xpsQualify` is the `DataTreeSet` method called by function `qualify`, containing the same parameters.

Value

An `QualTreeSet`.

Note

This function takes any `DataTreeSet` and computes expression levels by summarizing the probe set values into one expression measure. It does NOT do any further preprocessing such as background correction or (quantile) normalization. If you want to do background correction and/or normalization first then you need to use function `fitQC`.

Author(s)

Christian Stratowa

See Also

`fitQC`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## compute RMA stepwise

## background correction
data.bg.rma <- bgcorrect.rma(data.test3,"tmp_Test3RMABgrd",filedir=getwd())
```

```
## normalize quantiles
data.qu.rma <- normalize.quantiles(data.bg.rma,"tmp_Test3RMANorm",filedir=getwd())

## summarize medianpolish
data.mp.rma <- summarize.rma(data.qu.rma,"tmp_Test3RMAExpr",filedir=getwd(),tmpdir="")

## qualification - rlm

## fit model on raw data
data.raw.rlm <- qualify.rlm(data.test3, "tmp_Test3RawQual", filedir=getwd(), tmpdir="", c

## fit model on background adjusted data
data.adj.rlm <- qualify.rlm(data.bg.rma, "tmp_Test3AdjQual", filedir=getwd(), tmpdir="",

## fit model on normalized data
data.nrm.rlm <- qualify.rlm(data.qu.rma, "tmp_Test3NormQual", filedir=getwd(), tmpdir="",

## get expression levels
expr.raw.rlm <- validData(data.raw.rlm)
expr.adj.rlm <- validData(data.adj.rlm)
expr.nrm.rlm <- validData(data.nrm.rlm)

## get borders
brd.raw <- borders(data.raw.rlm)
brd.adj <- borders(data.adj.rlm)

## get residuals
res.raw <- residuals(data.raw.rlm)
res.adj <- residuals(data.adj.rlm)

## get weights
w.raw <- weights(data.raw.rlm)
w.adj <- weights(data.adj.rlm)

## End(Not run)
```

---

quantileFilter-methods

Quantile Filter

Description

This method initializes the Quantile Filter.
The Quantile Filter flags all rows with: `flag = (quantile[high]/quantile[low] >= cutoff)`

Usage

```
quantileFilter(object)
quantileFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric vector `c(cutoff, loquantile, hiquantile)`.

Details

The method `quantileFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`loquantile`:	value for low quantile (default is `loquantile=0.05`).
`hiquantile`:	value for high quantile (default is `hiquantile=0.95`).

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
quantileFilter(prefltr) <- c(3.0, 0.05, 0.95)
str(prefltr)
```

`ratioFilter-methods` *Ratio Filter*

Description

This method initializes the Ratio Filter. The ratio is the maximum value divided by minimum value for each row of the expression dataframe.
The Ratio Filter flags all rows with: `flag = (max/min >= cutoff)`

Usage

```
ratioFilter(object)
ratioFilter(object, value)<-
```

Arguments

`object`	object of class `PreFilter`.
`value`	numeric value `c(cutoff).`

Details

The method `ratioFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
ratioFilter(prefltr) <- c(1.5)
str(prefltr)
```

`rawCELName-methods` *Method for getting names of the raw CEL-files*

Description

Method for getting names (and full path) of the original CEL-files.

Usage

```
rawCELName(object, treename = "*", fullpath = TRUE)
```

Arguments

`object`	object of class `DataTreeSet`.
`treename`	treename, for which the name of the original CEL-file should be returned.
`fullpath`	logical, if TRUE return full path.

Details

Since CEL-files can be imported with `import.data` using alternative `celnames`, method `rawCELName` allows to return the original name and optionally the full path for each CEL-file.

Value

A character vector.

Author(s)

Christian Stratowa

See Also

`import.data`

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

rawCELName(data.test3)
rawCELName(data.test3, treename = "TestA2.cel", fullpath = FALSE)
```

`rleplot-methods` *Box Plots of Relative Log Expression (RLE)*

Description

Produce boxplots of Relative Log Expression (RLE) values for the set of arrays.

Usage

```
 rleplot(x, which = "UnitName", size = 0, range = 0, ylim = c(-0.75,0.75),
outline = FALSE, names = "namepart", las = 2, ...)
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`which`	type of probes to be used, for details see `validData`.
`size`	length of sequence to be generated as subset.
`range`	determines how far the plot whiskers extend out from the box.
`ylim`	range for the plotted y values.
`outline`	if `outline` is not true, the outliers are not drawn.
`names`	optional vector of sample names.
`las`	the style of axis labels.
`...`	optional arguments to be passed to `boxplot`.

Details

Create boxplots of Relative Log Expression (RLE) values for the set of arrays, i.e. of M plots, where M is determined relative to a pseudo-median reference chip.

For `names=NULL` full column names of slot `data` will be displayed while for `names="namepart"` column names will be displayed without name extension. If `names` is a vector of column names, only these columns will displayed as boxplot.

Author(s)

Christian Stratowa

See Also

`mboxplot`, `nuseplot`

Examples

```
# load existing ROOT scheme file and ROOT expression file for rma
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.rma <- root.expr(scheme.test3, paste(.path.package("xps"),"rootdata/tmp_Test3RMA.roo

if (interactive()) {
rleplot(data.rma)
}
```

rma *Robust Multi-Array Average Expression Measure*

Description

This function converts a DataTreeSet into an ExprTreeSet using the robust multi-array average (RMA) expression measure.

Usage

```
rma(xps.data,
    filename   = character(0),
    filedir    = getwd(),
    tmpdir     = "",
    background = "pmonly",
    normalize  = TRUE,
    option     = "transcript",
    exonlevel  = "",
    params     = list(16384, 0.0, 1.0, 10, 0.01, 1),
    xps.scheme = NULL,
    add.data   = TRUE,
    verbose    = TRUE)

xpsRMA(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`background`	probes used to compute background, one of 'pmonly', 'mmonly', 'both'; for genome/exon arrays one of 'genomic', 'antigenomic'
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	list of (default) parameters for `rma`.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

This function computes the RMA (Robust Multichip Average) expression measure described in Irizarry et al. for both expression arrays and exon arrays. For exon arrays it is necessary to supply the requested `option` and `exonlevel`.

Following `options` are valid for exon arrays:

`transcript`:	expression levels are computed for transcript clusters, i.e. probe sets containing the same 'transcript_clu
`exon`:	expression levels are computed for exon clusters, i.e. probe sets containing the same 'exon_id', where ea
`probeset`:	expression levels are computed for individual probe sets, i.e. for each 'probeset_id'.

Following `exonlevel` annotations are valid for exon arrays:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`ambiguous`:	ambiguous probesets only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Following `exonlevel` annotations are valid for whole genome arrays:

`core`:	probesets with category 'unique', 'similar' and 'mixed'.
`metacore`:	probesets with category 'unique' only.
`affx`:	standard AFFX controls.
`all`:	combination of above (including affx).

Exon levels can also be combined, with following combinations being most useful:

`exonlevel="metacore+affx"`:	core meta-probesets plus AFFX controls
`exonlevel="core+extended"`:	probesets with cDNA support
`exonlevel="core+extended+full"`:	supported plus predicted probesets

Exon level annotations are described in the Affymetrix whitepaper exon_probeset_trans_clust_whitepaper.pdf: "Exon Probeset Annotations and Transcript Cluster Groupings".

In order to use an alternative `SchemeTreeSet` set the corresponding SchemeSet `xps.scheme`.

`xpsRMA` is the `DataTreeSet` method called by function `rma`, containing the same parameters.

Value

An `ExprTreeSet`

Note

In contrary to other implementations of RMA the expression measure is given to you in linear scale, analogously to the expression measures computed with `mas5` and `mas4`.

Please note that the default settings of `params` gives results which are identical to the results obtained with APT (Affymetrix Power Tools) and with package `affy_1.14.2` or earlier. If you want to obtain results which are identical to the results obtained with `affy_1.16.0` or later then you need to set `params = list(16384, 0.0, 0.4, 10, 0.01, 1)`.

By setting parameter `background="none"` it is possible to skip background correction .

For the analysis of many exon arrays it may be better to define a `tmpdir`, since this will store only the results in the main file and not e.g. background and normalized intensities, and thus will reduce the file size of the main file. For quantile normalization memory should not be an issue, however medianpolish depends on RAM unless you are using a temporary file.

Parameter `exonlevel` determines not only which probes are used for medianpolish, but also the probes used for background calculation and for quantile normalization. If you want to use seperate probes for background calculation, quantile normalization and medianpolish summarization, you can pass a numeric vector containing three integer values corresponding to the respective `exonlevel`, e.g. you can use `exonlevel=c(16316,8252,8252)`, see function `exonLevel` for more details.

Author(s)

Christian Stratowa

References

Rafael. A. Irizarry, Benjamin M. Bolstad, Francois Collin, Leslie M. Cope, Bridget Hobbs and Terence P. Speed (2003), Summaries of Affymetrix GeneChip probe level data Nucleic Acids Research 31(4):e15

Bolstad, B.M., Irizarry R. A., Astrand M., and Speed, T.P. (2003), A Comparison of Normalization Methods for High Density Oligonucleotide Array Data Based on Bias and Variance. Bioinformatics 19(2):185-193

Irizarry, RA, Hobbs, B, Collin, F, Beazer-Barclay, YD, Antonellis, KJ, Scherf, U, Speed, TP (2003) Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. Biostatistics .Vol. 4, Number 2: 249-264

See Also

`express`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.rma <- rma(data.test3,"tmp_Test3RMA",tmpdir="",background="pmonly",normalize=TRUE,ve

## get data.frame
expr.rma <- validData(data.rma)
head(expr.rma)

## plot results
if (interactive()) {
boxplot(data.rma)
boxplot(log2(expr.rma))
}
```

```
rm(scheme.test3, data.test3)
gc()

## Not run:
## examples using Affymetrix human tissue dataset (see also xps/examples/script4exon.R)
## first, load ROOT scheme file and ROOT data file from e.g.:
scmdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Schemes"
datdir <- "/Volumes/GigaDrive/CRAN/Workspaces/ROOTData"

## 1. example - expression array, e.g. HG-U133_Plus_2:
scheme.u133p2 <- root.scheme(paste(scmdir,"Scheme_HGU133p2_na25.root",sep="/"))
data.u133p2   <- root.data(scheme.u133p2, paste(datdir,"HuTissuesU133P2_cel.root",sep="/"

workdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Exon/hutissues/u133p2"
data.rma <- rma(data.u133p2,"MixU133P2RMA",filedir=workdir,tmpdir="",
                background="pmonly",normalize=TRUE)

## 2. example - whole genome array, e.g. HuGene-1_0-st-v1:
scheme.genome <- root.scheme(paste(scmdir,"Scheme_HuGene10stv1r3_na25.root",sep="/"))
data.genome   <- root.data(scheme.genome, paste(datdir,"HuTissuesGenome_cel.root",sep="/"

workdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Exon/hutissues/hugene"
data.g.rma <- rma(data.genome,"HuGeneMixRMAMetacore",filedir=workdir,tmpdir="",
                  background="antigenomic",normalize=T,exonlevel="metacore+affx")

## 3. example - exon array, e.g. HuEx-1_0-st-v2:
scheme.exon <- root.scheme(paste(scmdir,"Scheme_HuEx10stv2r2_na25.root",sep="/"))
data.exon   <- root.data(scheme.exon, paste(datdir,"HuTissuesExon_cel.root",sep="/"))

workdir <- "/Volumes/GigaDrive/CRAN/Workspaces/Exon/hutissues/exon"
data.x.rma <- rma(data.exon,"MixRMAMetacore",filedir=workdir,tmpdir="",background="antige
                  normalize=T,option="transcript",exonlevel="metacore")

## End(Not run)
```

`root.browser-methods` *Open the ROOT object browser*

Description

Open the `ROOT` object browser to see all objects stored in a `ROOT` file including `ROOT` trees.

Usage

```
root.browser(object)
```

Arguments

`object`	an object of type `SchemeTreeSet`, `DataTreeSet`, `ExprTreeSet`, or `CallTreeSet`

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT browser, otherwise you are in the CINT C/C++ interpreter from ROOT. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

root.call *Create class CallTreeSet accessing ROOT detection call file*

Description

Create class CallTreeSet accessing ROOT detection call file.

Usage

```
root.call(xps.scheme, rootfile = character(0), treetype = character(0), treename
```

Arguments

`xps.scheme`	A `SchemeTreeSet` containing the correct scheme for the ROOT data file.
`rootfile`	name of ROOT data file, including full path.
`treetype`	tree type.
`treenames`	optional `character` vector of tree names to get only subset of trees.

Details

An S4 class `CallTreeSet` will be created, serving as R wrapper to the existing `ROOT` detection call file `rootfile`.

Parameter `treetype` must be supplied to identify the ROOT trees for slots `data` and `detcall`. Valid tree types are listed in `validTreetype`.

To get the names of all trees with their extensions `treetype`, which are stored in `rootfile`, you can call function `getTreeNames` first.

If the `CallTreeSet` should only handle a subset of the trees stored in `rootfile`, the tree names must be supplied as vector `treenames`.

Value

A `CallTreeSet` object.

Author(s)

Christian Stratowa

See Also

`root.data`, `root.expr`

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## MAS5 detection call
detcall.mas5 <- mas5.call(data.test3,"tmp_Test3CallAll",tmpdir="",verbose=FALSE)

## use subset of trees
sub.call <- root.call(scheme.test3, "tmp_Test3CallAll.root", "dc5", c("TestA2", "TestB1")
```

`root.data` *Create class DataTreeSet accessing ROOT data file*

Description

Create class DataTreeSet accessing ROOT data file.

Usage

```
root.data(xps.scheme, rootfile = character(0), celnames = "*")
```

Arguments

`xps.scheme`	A `SchemeTreeSet` containing the correct scheme for the ROOT data file.
`rootfile`	name of ROOT data file, including full path.
`celnames`	optional `character` vector of tree names to get only subset of trees.

Details

An S4 class `DataTreeSet` will be created, serving as R wrapper to the existing `ROOT` data file `rootfile`.

If the `DataTreeSet` should only handle a subset of the trees stored in `rootfile`, the tree names must be supplied as vector `celnames`.

To get the names of all trees stored in `rootfile` you can call function `getTreeNames` first.

Value

A `DataTreeSet` object.

Note

Use `root.data` to access the ROOT data file from new R sessions to avoid creating a new `ROOT` data file for every R session.

Author(s)

Christian Stratowa

See Also

`import.data`, `DataTreeSet`

Examples

```
## get scheme and import CEL-files from package
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- import.data(scheme.test3,"tmp_datatest3",celdir=paste(.path.package("xps"),

## use subset of CEL-files
subdata.test3 <- root.data(scheme.test3,"tmp_datatest3_cel.root", celnames=c("TestA1.cel"
```

`root.density` *ROOT Density Plot*

Description

Creates a ROOT density plot for one or all ROOT tree(s).

Usage

```
root.density(x, treename = "*", logbase = "log2", canvasname = "DensityPlot", sa
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`treename`	name of tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT density plot for one or all tree(s) present in `rootfile`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.hist1D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.density(data.test3, "*")
root.density(data.test3, "TestA1.cel")
root.density(data.test3, "TestA1.cel", save.as="png")

## End(Not run)
```

`root.expr` *Create class ExprTreeSet accessing ROOT expression file*

Description

Create class ExprTreeSet accessing ROOT expression file.

Usage

```
root.expr(xps.scheme, rootfile = character(0), treetype = character(0), treename
```

Arguments

`xps.scheme`	A `SchemeTreeSet` containing the correct scheme for the ROOT data file.
`rootfile`	name of ROOT data file, including full path.
`treetype`	tree type.
`treenames`	optional `character` vector of tree names to get only subset of trees.

Details

An S4 class `ExprTreeSet` will be created, serving as R wrapper to the existing `ROOT` expression file `rootfile`.

Parameter `treetype` must be supplied to identify the ROOT trees for slot `data`. Valid tree types are listed in `validTreetype`.

To get the names of all trees with their extensions `treetype`, which are stored in `rootfile`, you can call function `getTreeNames` first.

If the `ExprTreeSet` should only handle a subset of the trees stored in `rootfile`, the tree names must be supplied as vector `treenames`.

Value

A `ExprTreeSet` object.

Author(s)

Christian Stratowa

See Also

root.data, root.call

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

# rma
all.rma <- rma(data.test3,"tmp_Test3RMAAll",tmpdir="",background="pmonly",normalize=TRUE,

## use subset of trees
sub.rma <- root.expr(scheme.test3, "tmp_Test3RMAAll.root", "mdp", c("TestA2.mdp", "TestB1
```

---

root.graph1D *ROOT 1D-Graph*

Description

Creates a ROOT 1D-graph for a ROOT tree.

Usage

```
root.graph1D(x, treename = character(0), logbase = "log2", option = "P", canvasn
```

Arguments

x	object of class DataTreeSet or ExprTreeSet.
treename	name of tree, must be present in rootfile of object x.
logbase	usually “log2”, or “0”, determines if leaf data should be converted to log.
option	ROOT TGraph::PaintGraph option, usually one of “P”, “*”, “L”.
canvasname	name of ROOT canvas
save.as	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
w	the width of the canvas in pixels.
h	the height of the canvas in pixels.

Details

Creates a ROOT 1D-graph for tree treename present in rootfile.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting save.as. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from ROOT. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.graph2D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.graph1D(data.test3, "TestA1.cel")

## End(Not run)
```

`root.graph2D` *ROOT 2D-Graph*

Description

Creates a ROOT 2D-graph for a ROOT tree.

Usage

```
root.graph2D(x, treename1 = character(0), treename2 = character(0),logbase = "lc
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`treename1`	name of first tree, must be present in `rootfile` of object `x`.
`treename2`	name of second tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`option`	ROOT TGraph::PaintGraph option, usually one of “P”, “*”, “L”.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT 2D-graph for trees `treename1` and `treename2` present in `rootfile`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from ROOT. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.graph1D`, `root.mvaplot`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.graph2D(data.test3, "TestA1.cel", "TestB1.cel")

## End(Not run)
```

`root.hist1D` *ROOT 1D-Histogram*

Description

Creates a ROOT 1D-histogram for a ROOT tree.

Usage

```
root.hist1D(x, treename = character(0), logbase = "log2", type = "hist", option
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`treename`	name of tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`type`	ROOT 1D-hist or density, i.e. “hist” or “density”.
`option`	ROOT 1D-hist option only, usually one of “HIST”, “B”, “C”, “E”.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT 1D-histogram for tree `treename` present in `rootfile`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.hist2D`, `root.hist3D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.hist1D(data.test3, "TestA1.cel")
root.hist1D(data.test3, "TestA1.cel", type="density")

## End(Not run)
```

`root.hist2D` *ROOT 2D-Histogram*

Description

Creates a ROOT 2D-histogram for a ROOT tree.

Usage

```
root.hist2D(x, treename1 = character(0), treename2 = character(0),logbase = "log
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`treename1`	name of first tree, must be present in `rootfile` of object `x`.
`treename2`	name of second tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`option`	ROOT hist TH2 option, usually one of “SCAT”, “COLZ”, “BOX”, “SURF2”, “SURF3”.

`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT 2D-histogram for trees `treename1` and `treename2` present in `rootfile`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.hist1D`, `root.hist3D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.hist2D(data.test3, "TestA1.cel", "TestB1.cel", option="COLZ")

## End(Not run)
```

`root.hist3D` *ROOT 3D-Histogram*

Description

Creates a ROOT 3D-histogram for a ROOT tree.

Usage

```
root.hist3D(x, treename1 = character(0), treename2 = character(0), treename3 = c
```

Arguments

`x`	object of class `DataTreeSet` or `ExprTreeSet`.
`treename1`	name of first tree, must be present in `rootfile` of object `x`.
`treename2`	name of second tree, must be present in `rootfile` of object `x`.
`treename3`	name of third tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`option`	ROOT hist TH3 option, usually one of “HIST”, “SCAT”, “BOX”.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT 3D-histogram for trees `treename1`, `treename2` and `treename3` present in `rootfile`. By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

By moving the mouse into the middle of the canvas, the cursor changes and you can rotate the 3D-histogram. By selecting menu “View->View With->OpenGL” the OpenGL viewer opens, where you can rotate the 3D-histogram interactively.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.hist1D`, `root.hist2D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.hist3D(data.test3, "TestA1.cel", "TestB2.cel", "TestB1.cel", option="BOX")

## End(Not run)
```

`root.image` *ROOT Image*

Description

Creates a ROOT image for a ROOT tree.

Usage

```
root.image(x, treename = character(0), leafname = "fInten", logbase = "log2", op
```

Arguments

`x`	object of class `DataTreeSet`.
`treename`	name of tree, must be present in `rootfile` of object `x`.
`leafname`	leaf name of tree, usual "fInten" or "fBg".
`logbase`	usually "log2", or "0", determines if leaf data should be converted to log.
`option`	ROOT graph option, usually. one of "COL", "COLZ".
`zlim`	size limits c(min,max) of `leafname`.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of "ps", "eps", "pdf", "jpg", "gif", "png", "tiff"
`w`	the width of the device in pixels.
`h`	the height of the device in pixels.

Details

Creates a ROOT image for tree `treename` present in `rootfile`.

To zoom-in move the mouse cursor to the x-axis (y-axis) until it changes to a hand and click-drag to select an axis-range. To unzoom move the mouse cursor to the x-axis (y-axis) until it changes to a hand and right-click to select "Unzoom".

By selecting menu "File->Save->canvasname.xxx" you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item "Quit ROOT" from menu "File" to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type ".q".

Author(s)

Christian Stratowa

See Also

`image-methods`, `image`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.image(data.test3, "TestA1.cel")
root.image(data.test3, "TestA1.cel", save.as="png")

## End(Not run)
```

`root.merge.data` *Create class DataTreeSet by merging ROOT data files*

Description

Create class DataTreeSet by merging different ROOT data files.

Usage

```
root.merge.data(xps.scheme, rootfiles = list(), celnames = "*")
```

Arguments

`xps.scheme`	A `SchemeTreeSet` containing the correct scheme for the ROOT data file.
`rootfiles`	`list` of ROOT data file(s), including full path.
`celnames`	optional `character` vector of tree names to get only subset of trees.

Details

This function allows to merge data trees from different existing ROOT data files.

An S4 class `DataTreeSet` will be created, serving as R wrapper to the existing `ROOT` data file(s) `rootfiles`.

If the `DataTreeSet` should only handle a subset of the trees stored in `rootfiles`, the tree names must be supplied as vector `celnames`.

To get the names of all trees stored in separate `rootfiles` you can call function `getTreeNames` first.

Value

A `DataTreeSet` object.

Author(s)

Christian Stratowa

See Also

`root.data`, `DataTreeSet`

Examples

```
## get scheme and import CEL-files from package
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- import.data(scheme.test3,"tmp_datatest3",celdir=paste(.path.package("xps"),

## get subset of CEL-files
subdataA <- root.data(scheme.test3,"tmp_datatest3_cel.root", celnames=c("TestA1.cel","Tes
subdataB <- root.data(scheme.test3,"tmp_datatest3_cel.root", celnames=c("TestB1.cel","Tes

## merge data
dataAB <- root.merge.data(scheme.test3,c(rootFile(subdataA),rootFile(subdataB)), celnames
```

`root.mvaplot` *ROOT M vs A Plot*

Description

Creates a ROOT M vs A plot for a ROOT tree.

Usage

```
root.mvaplot(x, treename1 = character(0), treename2 = character(0),logbase = "lo
```

Arguments

`x`	object of class `ExprTreeSet` or `DataTreeSet`.
`treename1`	name of first tree, must be present in `rootfile` of object `x`.
`treename2`	name of second tree, must be present in `rootfile` of object `x`.
`logbase`	usually “log2”, or “0”, determines if leaf data should be converted to log.
`option`	ROOT TGraph::PaintGraph option, usually one of “P”, “*”.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the canvas in pixels.
`h`	the height of the canvas in pixels.

Details

Creates a ROOT M vs A plot for trees `treename1` and `treename2` present in `rootfile`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT canvas, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

See Also

`root.graph1D`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

# compute RMA
data.rma <- rma(data.test3,"Test3RMA",tmpdir="",background="pmonly",normalize=TRUE)

root.mvaplot(data.rma, "TestA1.mdp", "TestB1.mdp")

## End(Not run)
```

`root.profile` *ROOT Profile Plot*

Description

Creates a ROOT profile plot, i.e. a plot of parallel coordinates

Usage

```
root.profile(x, treename = "*", varlist = NULL, as.log = TRUE, globalscale = TRU
```

Arguments

`x`	S4 object, usually of class `DataTreeSet` or `ExprTreeSet`.
`treename`	name of tree, usually all trees present in `rootfile` of object `x`.
`varlist`	leaf name of tree, usual “fInten” or “fLevel”.
`as.log`	logical indicating if `varlist` should be drawn as logarithmic data.
`globalscale`	logical indicating if all axes should be drawn at the same scale.
`boxes`	logical indicating if box-and-whisker plots should be drawn.
`ylim`	size limits c(min,max) of `varlist`.
`canvasname`	name of ROOT canvas
`save.as`	graphics type for saving canvas, one of “ps”, “eps”, “pdf”, “jpg”, “gif”, “png”, “tiff”
`w`	the width of the device in pixels.
`h`	the height of the device in pixels.

Details

Creates a ROOT profile plot for all trees `treename="*"` present in `rootfile`, or for a subset of trees. In this case `varlist` must be the name of one tree leaf only; for `varlist=NULL` leaf "fInten" will be used for class `DataTreeSet` and leaf "fLevel" will be used for class `ExprTreeSet`.

If `treename` is the name of one tree only then `varlist` can contain up to all leaves of the tree, separated by colons, e.g. `varlist="fLevel:fStdev"`.

For `boxes=TRUE` the profile plot draws box-and-whisker plots and can thus be considered the equivalent of the usual `boxplot`.

A ROOT profile plot, i.e. a plot of parallel coordinates, is drawn in a “TreeViewer”, a graphic user interface designed to handle `ROOT` trees. You can activate context menus by right-clicking on items or inside the right panel.

The “TreeViewer” is explained in `http://root.cern.ch/root/html/TTreeViewer.html`.

By selecting menu “File->Save->canvasname.xxx” you can save the figure as e.g. *gif, *.jpg, *.pdf, *.ps or even as C++ macro.

Alternatively, you can save the plot by setting `save.as`. However, this will close the canvas immediately after opening it.

Note

Always select menu item “Quit ROOT” from menu “File” to close the ROOT tree viewer, otherwise you are in the CINT C/C++ interpreter from `ROOT`. To exit CINT, you need to type “.q”.

Author(s)

Christian Stratowa

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

root.profile(data.test3)

## End(Not run)
```

`root.scheme` *Create class SchemeTreeSet accessing ROOT scheme file*

Description

Create class SchemeTreeSet accessing ROOT scheme file.

Usage

```
root.scheme(rootfile = character(0), add.mask = FALSE)
```

Arguments

`rootfile`	name of ROOT scheme file, including full path.
`add.mask`	if `TRUE` mask information will be included as slot `mask`.

Details

An S4 class `SchemeTreeSet` will be created, serving as R wrapper to the `ROOT` scheme file `rootfile`.

Value

A `SchemeTreeSet` object.

Note

Use this function to access the `ROOT` scheme file from new R sessions to avoid creating a new `ROOT` scheme file for every R session.

Do not set `add.mask=TRUE` for exon arrays unless you know that your computer has sufficient RAM.

Author(s)

Christian Stratowa

See Also

`import.expr.scheme`, `import.exon.scheme`, `SchemeTreeSet`

Examples

```
## create class SchemeSet to access the ROOT scheme file for the Test3 GeneChip
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
str(scheme.test3)

## Not run:
## scheme set for existing human root exon scheme file
scheme.huex10stv2r2.na22 <- root.scheme("/my/path/schemes/Scheme_HuEx10stv2r2_na22.root")

## End(Not run)
```

`summarize` *Probe Set Summarizing Functions*

Description

Converts Affymetrix probe level data to expression levels by summarizing the probe set values into one expression measure and a standard error for this summary.

Usage

```
summarize(xps.data, filename = character(0), filedir = getwd(), tmpdir = "", upd

summarize.mas4(xps.data, filename = character(0), filedir = getwd(), tmpdir = ""

summarize.mas5(xps.data, filename = character(0), filedir = getwd(), tmpdir = ""

summarize.rma(xps.data, filename = character(0), filedir = getwd(), tmpdir = "",

xpsSummarize(object, ...)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`update`	logical. If `TRUE` the existing ROOT data file `filename` will be updated.
`select`	type of probes to select for summarization.
`method`	summarization method to use.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`logbase`	logarithm base as character, one of '0', 'log', 'log2', 'log10'.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	vector of parameters for summarization method.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `DataTreeSet`.
`...`	the arguments described above.

Details

Converts Affymetrix probe level data to expression levels by summarizing the probe set values into one expression measure and a standard error for this summary.

`xpsSummarize` is the `DataTreeSet` method called by function `summarize`, containing the same parameters.

Value

An `ExprTreeSet`.

Author(s)

Christian Stratowa

See Also

express

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## RMA background
data.bg.rma <- bgcorrect.rma(data.test3,"tmp_Test3RMA",filedir=getwd(),tmpdir="",verbose=
## normalize quantiles
data.qu.rma <- normalize.quantiles(data.bg.rma,"tmp_Test3RMA",filedir=getwd(),tmpdir="",u
## summarize medianpolish
data.mp.rma <- summarize.rma(data.qu.rma,"tmp_Test3RMA",filedir=getwd(),tmpdir="",update=

## get expression data.frame
expr.rma <- exprs(data.mp.rma)
head(expr.rma)

## plot expression levels
if (interactive()) {
boxplot(data.mp.rma)
boxplot(log2(expr.rma[,3:6]))
}
```

`treeInfo-methods` *Get UserInfo from ROOT Trees*

Description

Extract the UserInfo from ROOT trees, i.e. quality control information.

Usage

```
 treeInfo(object, treenames = "*", treetype = character(0), varlist
= "*", qualopt = NULL, verbose = FALSE, ...)
```

Arguments

`object`	Object of class `"TreeSet"`.
`treenames`	Object of class `"list"` representing the names of the ROOT trees.
`treetype`	type of tree to export, see `validTreetype`
`varlist`	names of tree leaves to export.
`qualopt`	option determining the data to which to apply qualification, one of ‘raw’, ‘adjusted’, ‘normalized’, ‘all’.

Details

ROOT trees have a pointer to a list fUserInfo where it is possible to store data which do not fit into the usual tree structure. Taking advantage of this feature xps stores certain pre-processed results of the tree(s) in this list. For example, data trees store the minimal/maximal intensities and the number of oligos with minimal/maximal intensities of the CEL-files in list fUserInfo, while call trees store the number and percentage of P/M/A calls.

Function treeInfo allows to export this user information as a data.frame, whereby the parameters of varlist depend on the treetype:

Parameters for data trees with extensions "cel", "int", and background trees:
fMinInten: minimal intensity.
fMaxInten: maximal intensity.
fNMinInten: number of probes with minimal intensity.
fNMaxInten: number of probes with maximal intensity.
fMaxNPixels: maximal number of pixels.
fNQuantiles: number of precalculated quantiles.
fQuantiles: quantiles.
fIntenQuant: intensities at quantiles.

Parameters for expression trees:
fNUnits: number of units, i.e. probesets.
fMinLevel: minimal expression level.
fMaxLevel: maximal expression level.
fNQuantiles: number of precalculated quantiles.
fQuantiles: quantiles.
fLevelQuant: expression levels at quantiles.

Parameters for call trees:
fNUnits: number of units, i.e. probesets.
fNAbsent: number of units with absent call.
fNMarginal: number of units with marginal call.
fNPresent: number of units with present call.
fPcAbsent: percentage of units with absent call.
fPcMarginal: percentage of units with marginal call.
fPcPresent: percentage of units with present call.
fMinPValue: minimal p-value.
fMaxPValue: maximal p-value.

Parameters for border trees with extension "brd":
fMeanLeft: mean intensity of left border.
fMeanRight: mean intensity of right border.
fMeanTop: mean intensity of top border.
fMeanBottom: mean intensity of bottom border.
fCOIXhi: x-location of COI for the positive elements.
fCOIYhi: y-location of COI for the positive elements.
fCOIXlo: x-location of COI for the negative elements.
fCOIYlo: y-location of COI for the negative elements.

Parameters for quality trees with extension "rlm":
fNUnits: number of units, i.e. probesets.
fMinLevel: minimal expression level.
fMaxLevel: maximal expression level.
fNQuantiles: number of precalculated quantiles.
fQuantiles: quantiles.
fLevelQuant: expression levels at quantiles.

fNUSEQuant: NUSE at quantiles.
fRLEQuant: RLE at quantiles.
fQualOption: value of qualopt.

Parameters for residual trees with extension "res":
fNQuantiles: number of precalculated quantiles.
fQuantiles: quantiles.
fResiduQuant: residual at quantiles.
fWeightQuant: weight at quantiles.
fQualOption: value of qualopt.

Value

A data.frame.

Note

Taking advantage of function treeInfo plotting methods boxplot, callplot, coiplot, nuseplot and rleplot are able to display their results much faster, which is especially useful for large datasets.

Author(s)

Christian Stratowa

See Also

validTreetype

Examples

```
## load existing ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

userinfo <- treeInfo(data.test3, treetype="cel", varlist="*")
userinfo

userinfo <- treeInfo(data.test3, treename="TestB1", treetype="cel", varlist = "fNQuantile
userinfo

## Not run:
userinfo <- treeInfo(rlm.all, treetype="rlm", varlist = "fNQuantiles:fNUSEQuant:fRLEQuant
userinfo

userinfo <- treeInfo(rlm.all, treetype="brd")
userinfo

userinfo <- treeInfo(rlm.all, treetype="res", qualopt = "raw")
userinfo

userinfo <- treeInfo(rlm.all, treetype="res", varlist = "fResiduQuant", qualopt = "raw")
userinfo

## End(Not run)
```

`trma` *transposed Robust Multi-Array Average Expression Measure*

Description

This function converts a `DataTreeSet` into an `ExprTreeSet` using the transposed robust multi-array average (RMA) expression measure.

Usage

```
trma(xps.data,
     filename   = character(0),
     filedir    = getwd(),
     tmpdir     = "",
     background = "pmonly",
     normalize  = TRUE,
     option     = "transcript",
     exonlevel  = "",
     params     = list(16384, 0.0, 1.0, 10, 0.01, 2),
     xps.scheme = NULL,
     add.data   = TRUE,
     verbose    = TRUE)
```

Arguments

`xps.data`	object of class `DataTreeSet`.
`filename`	file name of ROOT data file.
`filedir`	system directory where ROOT data file should be stored.
`tmpdir`	optional temporary directory where temporary ROOT files should be stored.
`background`	probes used to compute background, one of 'pmonly', 'mmonly', 'both'; for genome/exon arrays one of 'genomic', 'antigenomic'
`normalize`	logical. If `TRUE` normalize data using quantile normalization.
`option`	option determining the grouping of probes for summarization, one of 'transcript', 'exon', 'probeset'; exon arrays only.
`exonlevel`	exon annotation level determining which probes should be used for summarization; exon/genome arrays only.
`params`	list of (default) parameters for `rma`.
`xps.scheme`	optional alternative `SchemeTreeSet`.
`add.data`	logical. If `TRUE` expression data will be included as slot `data`.
`verbose`	logical, if `TRUE` print status information.

Details

This function computes the tRMA (transposed Robust Multichip Average) expression measure described in Giorgi et al. for both expression arrays and exon arrays.

To use method `xpsRMA` or function `express` to compute `trma` you need to set `params = list(16384, 0.0, 1.0, 10, 0.01, 2)`.

For further details please see `rma`

Value

An ExprTreeSet

Author(s)

Christian Stratowa

References

Federico M. Giorgi, Anthony M. Bolger, Marc Lohse and Bjoern Usadel (2010), Algorithm-driven Artifacts in median polish summarization of Microarray data. BMC Bioinformatics 11:553

See Also

rma, xpsRMA, express

Examples

```
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

data.trma <- trma(data.test3,"tmp_Test3tRMA",tmpdir="",background="pmonly",normalize=TRUE

## get data.frame
expr.trma <- validData(data.trma)
head(expr.trma)

rm(scheme.test3, data.test3)
gc()
```

---

type2Exten *Convert Method Type to Tree Extension*

Description

Convert Method Type to Tree Extension.

Usage

```
type2Exten(type, datatype)
```

Arguments

type	method type.
datatype	data type.

Details

For every datatype different methods, i.e. algorithms exist which can be applied. Valid datatypes are ‘preprocess’ and ‘normation’.

For datatype ‘preprocess’ the following methods can be applied:

`mean:`	trimmed mean
`median:`	median
`quantile:`	quantile
`tukeybiweight:`	tukey biweight
`medianpolish:`	median polish

For `datatype` 'normation' the following methods can be applied:

`mean:`	trimmed mean
`median:`	median
`quantile:`	quantile
`lowess:`	lowess
`supsmu:`	supsmu

The tree extensions are described in `validTreetype`.

Value

A `character` with the correct tree extension.

Author(s)

Christian Stratowa

See Also

`getDatatype`, `validTreetype`

Examples

```
type2Exten("quantile","preprocess")
type2Exten("medianpolish","preprocess")
type2Exten("supsmu","normation")
```

`uniTest-methods` *A Two-Group Unitest*

Description

Unitest performs a a two group uni-test such as the `t.test` on each row of the expression dataframe. The Unitest returns a dataframe containing the results of the test.

Usage

```
uniTest(object)
uniTest(object, value)<-
```

Arguments

`object`	object of class `UniFilter`.
`value`	character vector `c(type, alternative, correction, numperm, mu, paired, conflevel, varequ)`

Details

The method `uniTest` initializes the following parameters:

`type`:	a character string specifying the type of test: currently `"t.test"` (default) or `"normal.test".`
`alternative`:	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"`
`correction`:	a correction to adjust p-values for multiple comparisons:
	`correction="none"`: no correction (default).
	`correction="bonferroni"`: Bonferroni correction.
	`correction="BH" or "fdr"`: correction for false discovery rate (Benjamini & Hochberg).
	`correction="BY"`: correction for false discovery rate (Benjamini & Yekutieli).
	`correction="hochberg"`: Hochberg correction.
	`correction="holm"`: Holm correction.
	`correction="wy"`: Westfall-Young step-down adjusted p-chance (E.Manduchi).
`numperm`:	optional number of permutations used to determine p-chance (default is 0).
`mu`:	a number indicating the true value of the difference in means for a two sample test (default is 0).
`paired`:	a logical indicating whether you want a paired uni-test (default is FALSE).
`conflevel`:	confidence level of the interval (default is 0.95).
`varequ`:	a logical variable indicating whether to treat the two variances as being equal. If `TRUE` then the poo

Value

An initialized `UniFilter` object.

Author(s)

Christian Stratowa

References

Benjamini, Y., and Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series* B, **57**, 289–300.

Benjamini, Y., and Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics* **29**, 1165–1188.

Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, **6**, 65–70.

Westfall P.H. and Young S.S. (1993) Resampling-based multiple testing:examples and methods for p-value adjustment. *Wiley series in probability and mathematical statistics*; Wiley.

Dudoit S., Yang Y.H., Callow M.J., Speed T.P. (2000) Statistical methods for identifying differentially expressed genes in replicated cDNA microarray experiments. *Technical report* **578**; UC Berkeley.

Manduchi E. (2000) Software: tpWY, see: `http://www.cbil.upenn.edu/tpWY/`

Examples

```
unifltr <- UniFilter()
uniTest(unifltr) <- c("t.test","two.sided","none",0,0.0,FALSE,0.98,TRUE)
str(unifltr)
```

`unifilter` *Function for Applying an UniFilter to an ExprTreeSet*

Description

This function applies an `UniFilter` to an `ExprTreeSet`.

Usage

```
unifilter(xps.expr,
          filename   = character(0),
          filedir    = getwd(),
          filter     = NULL,
          minfilters = 999,
          logbase    = "log2",
          group      = character(0),
          treename   = "UniTest",
          xps.fltr   = NULL,
          xps.call   = NULL,
          update     = FALSE,
          verbose    = TRUE)


xpsUniFilter(object, ...)
```

Arguments

`xps.expr`	object of class `ExprTreeSet`.
`filename`	file name of ROOT filter file.
`filedir`	system directory where ROOT filter file should be stored.
`filter`	object of class `UniFilter`.
`minfilters`	minimum number of initialized filter methods to satisfy (default is all filters).
`logbase`	convert data to logarithm of base: `"0"`, `"log"`, `"log2"` (default), `"log10"`
`group`	a character vector assigning the trees of `xps.expr` to one of two groups.
`treename`	tree name to be used in ROOT filter file.
`xps.fltr`	optional object of class `FilterTreeSet`.
`xps.call`	optional object of class `CallTreeSet`.
`update`	logical. If `TRUE` the existing ROOT filter file `filename` will be updated.
`verbose`	logical, if `TRUE` print status information.
`object`	object of class `ExprTreeSet`.
`...`	same arguments as function `unifilter`.

Details

This function applies the different filters initialized with constructor `UniFilter` to the `ExprTreeSet` `xps.expr`.

Slot `minfilters` determines the minimum number of initialized filters, which must be satisfied so that the mask is set to `flag=1`. For `minfilters=1` at least one filter must be satisfied, equivalent to logical 'OR'; for `minfilters=999` all filters must be satisfied, equivalent to logical 'AND'.

If pre-filtering should be done before applying function `unifilter` then a `FilterTreeSet` `xps.fltr` must be supplied, created with function `prefilter`.

If method `callFilter` was initialized with constructor `UniFilter` then `CallTreeSet` `xps.call` must be supplied, usually created with function `mas5.call`.

Value

An `AnalysisTreeSet`

Note

Internally, slot `group` will be converted to integer values using `as.integer(as.factor(group))`, thus `group=c("GrpA","GrpA","GrpB","GrpB")` will result in a fold-change of `fc=mean(GrpB)/mean(Gr`

Author(s)

Christian Stratowa

See Also

`UniFilter`, `prefilter`

Examples

```
## Not run:
## first, load ROOT scheme file and ROOT data file
scheme.test3 <- root.scheme(paste(.path.package("xps"),"schemes/SchemeTest3.root",sep="/"
data.test3 <- root.data(scheme.test3, paste(.path.package("xps"),"rootdata/DataTest3_cel.

## second, create an ExprTreeSet
data.rma <- rma(data.test3,"tmp_Test3_RMA",tmpdir="",background="pmonly",normalize=TRUE,v
## note: do not copy/paste this code, it is necessary only because R CMD check fails sinc
data.rma@rootfile <- paste(.path.package("xps"),"rootdata/tmp_Test3RMA.root",sep="/")
data.rma@filedir  <- paste(.path.package("xps"),"rootdata",sep="/")

## third, construct an UniFilter
unifltr <- UniFilter(unitest=c("t.test","two.sided","none",0,0.0,FALSE,0.95,TRUE),foldcha

## finally, create an AnalysisTreeSet
rma.ufr <- unifilter(data.rma,"tmp_Test3Unifilter",getwd(),unifltr,group=c("GrpA","GrpA",
str(rma.ufr)

## End(Not run)
```

`unitestFilter-methods` *Unitest Filter*

Description

This method initializes the Unitest Filter.
Applying an unitest such as the `t.test` to two groups returns the p-value for the test and the value of the t-statistic. The Unitest Filter allows to select only rows satisfying e.g. a certain p-value as cutoff.
The Unitest Filter flags all rows with: `flag = (variable <= cutoff)`

Usage

```
unitestFilter(object)
unitestFilter(object, value)<-
```

Arguments

`object`	object of class `UniFilter`.
`value`	character vector `c(cutoff, variable)`.

Details

The method `unitestFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`variable`:	`variable="pval"` (default): p-value.
	`variable="stat"`: univariate statistic.
	`variable="padj"`: optional adjusted p-value.
	`variable="pcha"`: optional p-value obtained by permutations.

Value

An initialized `UniFilter` object.

Author(s)

Christian Stratowa

Examples

```
unifltr <- UniFilter()
unitestFilter(unifltr) <- c(0.01,"pval")
str(unifltr)
```

`validCall-methods` *Get Valid Detection Call Values*

Description

Extracts valid present call values with unit names as row names.

Usage

```
validCall(object, which = "UnitName")
validPVal(object, which = "UnitName")
```

Arguments

`object`	object of class `CallTreeSet`.
`which`	name of column containing unit name.

Details

Method `validCall` returns the present calls from slot `detcall` as `data.frame` and uses column `which` as row names, usually the probeset IDs stored in column “UnitName”.

Method `validPVal` returns the detection call p-values from slot `data` as `data.frame` and uses column `which` as row names, usually the probeset IDs stored in column “UnitName”.

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`validData`, `validExpr`

`validData-methods` *Extract Subset of Data*

Description

Extracts a subset of valid data from data.frame `data`.

Usage

```
validData(object, which = "")
```

Arguments

`object`	object of class `DataTreeSet`, `ExprTreeSet` or `CallTreeSet`.
`which`	type of probes to be returned for `DataTreeSet`, otherwise name of column containing unit name.

Details

For class `DataTreeSet` and expression arrays, `validData` returns all the perfect match or mismatch probes on the arrays the object represents as data.frame, i.e. `which` can have the following values:

`pm`:	perfect match probes.
`mm`:	mismatch probes.
`both`:	both perfect match and mismatch probes.

For class `DataTreeSet` and exon arrays, `validData` returns the probes of the different exon levels as data.frame, i.e. `which` can have one of the following values:

`core`:	probesets supported by RefSeq and full-length GenBank transcripts.
`metacore`:	core meta-probesets.
`extended`:	probesets with other cDNA support.
`metaextended`:	extended meta-probesets.
`full`:	probesets supported by gene predictions only.
`metafull`:	full meta-probesets.
`affx`:	standard AFFX controls.
`all`:	combination of above.
`genomic`:	genomic background probes.
`antigenomic`:	antigenomic background probes.

For class `ExprTreeSet` `validData` returns the valid expression levels from slot `data` with unit names as row names, usually the probeset IDs stored in column `which="UnitName"`.

For class `CallTreeSet` `validData` returns the valid detection call p-values from slot `data` with unit names as row names, usually the probeset IDs stored in column `which="UnitName"`.

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`pm`, `mm`, `validExpr`, `validCall`

`validExpr-methods` *Get Valid Expression Levels*

Description

Extracts valid expression levels with unit names as row names from data.frame `data`.

Usage

```
validExpr(object, which = "UnitName")
```

Arguments

`object`	object of class `ExprTreeSet`.
`which`	name of column containing unit name.

Details

Method `validExpr` returns the expression levels from slot `data` and uses column `which` as row names, usually the probeset IDs stored in column “UnitName”.

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`validData`, `validCall`

`validSE-methods` *Get Valid Standard Errors*

Description

Extracts valid standard errors with unit names as row names.

Usage

```
validSE(object, which = "UnitName")
```

Arguments

`object`	object of class `ExprTreeSet`.
`which`	name of column containing unit name.

Details

Method `validSE` returns the standard errors (or standard deviations) from the expression trees and uses column `which` as row names, usually the probeset IDs stored in column “UnitName”.

Value

A `data.frame`.

Author(s)

Christian Stratowa

See Also

`validExpr`

`validTreetype` *Validate Tree Type*

Description

Validate tree type for corresponding data type.

Usage

```
validTreetype(treetype, datatype)
```

Arguments

`treetype`	tree type.
`datatype`	data type.

Details

Every `ROOT` tree has an extension, which describes the type of data stored in this tree. For example, 'TestA1.cel' is the tree name that stores the CEL-file data for 'TestA1.CEL'.

Trees with `datatype="scheme"` have the following extensions:
`scm`: scheme tree containing (x,y)-coordinates and mask for UNIT_ID.
`idx`: unit tree containing UnitName (i.e. probeset id), NumCells, NumAtoms, UnitType, for UNIT_ID.
`prb`: probe tree containing probe sequences.
`ann`: transcript annotation tree.
`anx`: exon annotation tree; exon arrays only.
`anp`: probeset annotation tree; exon arrays only.
`cxy`: coordinate tree containing CLF-file information; exon arrays only.
`exn`: exon tree; exon arrays only.
`pbs`: probeset tree; exon arrays only.

Trees with `datatype="rawdata"` have the following extensions:
`cel`: data tree containing CEL-file data.

Trees with `datatype="preprocess"` have the following extensions:
`int`: intensity tree containing background-corrected intensities.
`sbg`: background tree containing MAS4 sector background levels.
`wbg`: background tree containing MAS5 weighted sector background levels.
`rbg`: background tree containing RMA background levels.
`gbg`: background tree containing GC-content background levels.
`cmn`: cell tree containing preprocessed intensities using algorithm 'mean'.
`cmd`: cell tree containing preprocessed intensities using algorithm 'median'.
`clw`: cell tree containing preprocessed intensities using algorithm 'lowess'.
`css`: cell tree containing preprocessed intensities using algorithm 'supsmu'.
`cqu`: cell tree containing preprocessed intensities using algorithm 'quantile'.
`dc5`: detection tree containing MAS5 detection call and p-value.
`dab`: detection tree containing DABG detection call and p-value.
`amn`: expression tree containing expression levels computed with 'arithmetic mean'.
`gmn`: expression tree containing expression levels computed with 'geometric mean'.
`wmn`: expression tree containing expression levels computed with 'weighted mean'.
`wdf`: expression tree containing expression levels computed with 'weighted difference'.

adf: expression tree containing expression levels computed with ‘average difference’.
tbw: expression tree containing expression levels computed with ‘tukey biweight’.
mdp: expression tree containing expression levels computed with ‘median polish’.
rlm: quality tree containing expression levels, NUSE, RLE computed with ‘median polish’.
res: residual tree containing the residual SE and the model fit weights.
brd: border tree containing border intensities, mean border intensities and COI.

Trees with datatype="normation" have the following extensions:
tmn: expression tree after normalization using algorithm ‘trimmed mean’.
med: expression tree after normalization using algorithm ‘median’.
ksm: expression tree after normalization using algorithm ‘kernel smoother’.
low: expression tree after normalization using algorithm ‘lowess’.
sup: expression tree after normalization using algorithm ‘supsmu’.
qua: expression tree after normalization using algorithm ‘quantile’.
mdp: expression tree after normalization using algorithm ‘median polish’.

Value

Returns the valid treetype, otherwise an error message is returned.

Note

Not all tree types are used in the current package.

Author(s)

Christian Stratowa

See Also

getDatatype, type2Exten

Examples

```
validTreetype("prb", "scheme")
validTreetype("cel", "rawdata")
validTreetype("tbw", "preprocess")
```

---

varFilter-methods *Variance Filter*

Description

This method initializes the Variance Filter.
The Variance Filter flags all rows with: flag = (var/mean >= cutoff)

Usage

```
varFilter(object)
varFilter(object, value)<-
```

Arguments

object	object of class PreFilter.
value	numeric vector c(cutoff, trim, epsilon).

Details

The method `varFilter` initializes the following parameters:

`cutoff`:	the cutoff level for the filter.
`trim`:	the trim value for trimmed mean (default is `trim=0`).
`epsilon`:	value to replace mean (default is `epsilon=0.01`):
	`epsilon > 0`: replace mean=0 with epsilon.
	`epsilon = 0`: always set mean=1.

Note, that for `epsilon = 0` the filter flags all rows with: variance >= cutoff

Value

An initialized `PreFilter` object.

Author(s)

Christian Stratowa

Examples

```
prefltr <- PreFilter()
varFilter(prefltr) <- c(0.6,0.02,0.01)
str(prefltr)
```

`volcanoplot-methods` *Volcano Plot*

Description

Produce a scatter plot of fold-change values vs p-values, called volcano plot.

Usage

```
 volcanoplot(x, labels = "", p.value = "pval", mask = FALSE, show.cutoff
= TRUE, cex.text = 0.7, col.text = "blue", col.cutoff = "grey", xlim
= NULL, xlab = "Log2(Fold-Change)", ylab = "-Log10(P-Value)", pch =
'.', ...)
```

Arguments

`x`	object of class `AnalysisTreeSet`.
`labels`	optional transcript labels to be drawn at plotting points.
`p.value`	type of p-value, 'pval' for p-value, 'padj' for adjusted p-value, or 'pcha' for p-chance.
`mask`	logical, if `TRUE` draw only points for transcripts satisfying the univariate test.
`show.cutoff`	logical, if `TRUE` draw lines indicating cutoff.
`cex.text`	magnification to be used for optional `labels`.
`col.text`	color to be used for optional `labels`.

`col.cutoff`	color to be used for lines indicating cutoff, if `show.cutoff=TRUE`.
`xlim`	optional range for the plotted fold-change values.
`xlab`	label of x-axis.
`ylab`	label of y-axis.
`pch`	either an integer specifying a symbol or a single character to be used as the default in plotting points.
`...`	optional arguments to be passed to `plot`.

Details

Produces a volcano plot for slot `data` for an object of class `AnalysisTreeSet`.

It is possible to label the points of the volcano plot, whereby the following `labels` parameters are valid:

`fUnitName`:	unit name (probeset ID).
`fName`:	gene name.
`fSymbol`:	gene symbol.
`fChromosome`:	chromosome.
`fCytoBand`:	cytoband.

Author(s)

Christian Stratowa

`xps-package` *xps Package Overview*

Description

xps Package Overview

Details

Important data classes: `SchemeTreeSet`, `DataTreeSet`, `ExprTreeSet`, `CallTreeSet`, `FilterTreeSet`, `AnalysisTreeSet`. Full help on methods and associated functions is available from within class help pages.

Additional data classes: `ProjectInfo`, `PreFilter`, `UniFilter`.

The package handles pre-processing, normalization, filtering and analysis of Affymetrix GeneChip expression arrays, including exon array systems (Exon 1.0 ST: core, extended, full probesets), gene array systems (Gene 1.0 ST) and plate array systems on computers with 1 GB RAM only. It imports Affymetrix .CDF, .CLF, .PGF and .CEL as well as Affymetrix annotation files, and computes e.g. RMA, MAS5, FARMS, DFW, MAS5-calls, DABG-calls, I/NI-calls. It is an R wrapper to XPS (eXpression Profiling System), which is based on ROOT, an object-oriented framework developed at CERN. Thus, the prior installation of ROOT is a prerequisite for the usage of this package, see the README file. However, no knowledge of ROOT is required. ROOT is licensed under LGPL and can be downloaded from `http://root.cern.ch`.

Author(s)

Christian Stratowa `<cstrato@aon.at>`

`xpsOptions` *xps Options*

Description

Options for xps

Usage

```
xpsOptions(debug=FALSE)
```

Arguments

`debug`	logical, if `TRUE`, print debug information.

Details

Currently only used to set `debug` to `FALSE` or `TRUE`.

Value

A global variable `debug.xps` can be set to `TRUE`.

Author(s)

Christian Stratowa

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