Package ‘Ringo’

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Description The package Ringo facilitates the primary analysis of ChIP-chip data. The main functionalities of the package are data read-in, quality assessment, data visualisation and identification of genomic regions showing enrichment in ChIP-chip. The package has functions to deal with two-color oligonucleotide microarrays from NimbleGen used in ChIP-chip projects, but also contains more general functions for ChIP-chip data analysis, given that the data is supplied as RGLList (raw) or ExpressionSet (pre-processed). The package employs functions from various other packages of the Bioconductor project and provides additional ChIP-chip-specific and NimbleGen-specific functionalities.
License Artistic-2.0
biocViews Microarray,TwoChannel,DataImport,QualityControl,Preprocessing
LazyLoad yes
NeedsCompilation yes

R topics documented:

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asExprSet

converts a Ringo MAList into an ExpressionSet

Description

Function to convert an object of class MAList into an object of class ExpressionSet. Note that the otherwise optional targets component is required in this case to generate the phenoData of the new ExpressionSet.

Usage

asExprSet(from, idColumn="PROBE_ID")

Arguments

from object of class MAList to convert into an ExpressionSet
idColumn string; indicating which column of the genes data.frame of the MAList holds the identifier for reporters on the microarray. This column, after calling make.names on it, will make up the unique featureNames of the resulting ExpressionSet.
Function to compute auto-correlation of probe intensities

**Description**

Function to compute auto-correlation of probe intensities at specified offsets from the original positions.

**Usage**

```r
autocor(x, probeAnno, chrom, samples = NULL, lag.max = 2000, 
lag.step = 100, cor.method = "pearson", 
channel = c("red","green","logratio"), 
idColumn = "ID", verbose = TRUE)
```

**Arguments**

- `x`: an object either of class `ExpressionSet` containing the normalized probe intensities or of class `RGList` containing the raw intensities.
- `probeAnno`: Object of class `probeAnno` holding chromosomal match positions and indices of reporters in data matrix.
- `chrom`: character; chromosome to compute the autocorrelation for.
- `samples`: which samples of the data to use; if more than 1 for each probe the mean intensity over these samples is taken.
- `lag.max`: integer; maximal offset from the original position, the auto-correlation is to be computed for.
- `lag.step`: integer; step size of lags between 0 and maximal lag.
cor.method character; which type of correlation to compute, translates to argument method of function cor
channel character; in case x is an RGList, which channel to plot, either red, green or the logratio \log_2(\text{red}) - \log_2(\text{green})
idColumn string; indicating which column of the genes data.frame of the RGList holds the identifier for reporters on the microarray. Character entries of the index elements of the probeAnno will be matched against these identifiers. If the index elements of the probeAnno are numeric or x is of class ExpressionSet, this argument will be ignored.
verbose logical; extended output to STDOUT

Details
the lags, i.e. the offsets from the original position, the auto-correlation is to be computed for, are constructed from the given arguments as seq(0, lag.max, by=lag.step).

Value
Object of class autocor.result, a numeric vector of auto-correlation values at the offsets specified in argument lags. The lag values are stored as the names of the vector. Argument chrom is stored as attribute chromosome of the result.

Author(s)
Joern Toedling

See Also
cor, plot.autocor.result

Examples
exDir <- system.file("exData", package="Ringo")
load(file.path(exDir,"exampleProbeAnno.rda"))
load(file.path(exDir,"exampleX.rda"))
exAc <- autocor(exampleX, probeAnno=exProbeAnno,
                chrom="9", lag.max=1000)
plot(exAc)
cher-class

Slots

name: character vector of length 1 unequivocally describing the cher, e.g. "Suz12.Nudt2.upstream.cher"

chromosome: character vector of length one, naming the chromosome of the region, e.g. "9"

start: integer, region start position on the chromosome, e.g. 34318900

dend: integer, region end position on the chromosome, e.g. 34320100

cellType: character vector describing the cell type the ChIP chip experiment has been done on, e.g. "HeLa" or "human"

antibody: character vector describing the antibody or characteristic for which fragments were supposedly enriched in immuno-precipitation step, e.g. "Suz12" for the protein Suz12

maxLevel: numeric, maximal (smoothed) probe level in the cher, e.g. 2.00

score: numeric of a cher score, currently we use the sum of smoothed probe levels (log fold changes), e.g. 69.16

probes: vector of probe identifiers of all probes with match positions in the cher

extras: list of further elements used to annotate the cher; examples of such that are used in Ringo are:

  typeUpstream optional character vector of features that this cher is located upstream of, e.g. the transcriptional start site of "ENST00000379158". See relateChers for details.

  typeInside optional character vector of features that this cher is located inside of

  distMid2TSS optional named numeric vector of distances of the cher’s middle position to features, e.g. TSSs of features upstream and inside; names are the features to which the distances are given; only meaningful in combination with typeUpstream and typeInside; e.g. 55 with name "ENST00000379158"

  upSymbol optional character vector of gene symbols of features the cher is located upstream of; supplements typeUpstream; e.g. "Nudt2"

  inSymbol optional character vector of gene symbols of features the cher is located upstream of; supplements typeInside.

  ... further list elements can be added using the update method.

Methods

initialize create a new cher; see section examples below

plot calls chipAlongChrom to plot the cher; see plot.cher for more details

update signature(cher, ...); updates elements of the cher object; The further arguments in `...` are interpreted. Arguments corresponding to defined slot names of the cher result in the value by that slot being replaced by the specified value for the argument; argument names that do not correspond to slot names of the object result in list elements of the extras list of the cher being replaced by the given values for these arguments or the values are appended to the current extras list and the argument names make up the list names of the appended arguments. See section examples below for an example how to use this method.

cellType obtain or replace the description of the cell type, the ChIP-enriched regions was found in with this antibody

probes obtain the vector of probes involved in a ChIP-enriched region

cherList

A list in which each element is of class cher, is called a cherList. This class, however, is rarely used (yet).
Note

The **cher** class used to be an S3 list before.

The term 'cher' is shorthand for 'ChIP-enriched region'. We think this term is more appropriate than the term 'peak' commonly used in ChIP-chip context. Within such regions the actual signal could show two or more actual signal peaks or none at all (long plateau).

Author(s)

Joern Toedling, Tammo Krueger

See Also

plot.cher, findChersOnSmoothed, relateChers

Examples

```r
## how to create a cher object from scratch
cherNudt2 <- new("cher", name="nudt2.cher", chromosome=9,
                start=34318954, end=34319944, antibody="Suz12",
                maxLevel=2.00, score=69.2, upSymbol="NUDT2")
                #extras=list(upSymbol="NUDT2"))
cherNudt2
str(cherNudt2)

## use the update method (note:this update is biologically meaningless)
cher2 <- update(cherNudt2, cellType="HeLa", downSymbol="P53",
                probes=c("probe1","probe2"))
cher2; str(cher2)

## plot a cher object
exDir <- system.file("exData",package="Ringo")
load(file.path(exDir,"exampleProbeAnno.rda"))
load(file.path(exDir,"exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno,
                modColumn = "Cy5", allChr = "9", winHalfSize = 400)
plot(cherNudt2, smoothX, probeAnno=exProbeAnno, gff=exGFF, extent=5000)
```

cherByThreshold

*Function to identify chers based on thresholds*

Description

Given a vector of probe positions on the chromosome, a vector of smoothed intensities on these positions, and a threshold for intensities to indicated enrichment, this function identifies **Chers** (ChIP-enriched regions) on this chromosome.

This function is called by the function findChersOnSmoothed.

Usage

```r
cherByThreshold(positions, scores, threshold, distCutOff, 
        minProbesInRow = 3)
```
Arguments

positions numeric vector of genomic positions of probes
scores scores (intensities) of probes on those positions
threshold threshold for scores to be called a cher
distCutOff maximal positional distance between two probes to be part of the same cher
minProbesInRow integer; minimum number of enriched probes required for a cher; see details for further explanation.

Details

Specifying a minimum number of probes for a cher (argument minProbesInRow) guarantees that a cher is supported by a reasonable number of measurements in probe-sparse regions. For example, if there’s only one enriched probe within a certain genomic 1kb region and no other probes can be mapped to that region, this single probe does arguably not provide enough evidence for calling this genomic region enriched.

Value

A LIST with n components, where the first n components are the cher clusters, each one holding the scores and, as their names, the genomic positions of probes in that cluster.

Author(s)

Joern Toedling

See Also

findChersOnSmoothed

Examples

## example with random generated data:
rpos <- cumsum(round(runif(200)*5))
rsc <- rnorm(200)+0.2
plot(rpos, rsc, type="l", col="seagreen3", lwd=2)
rug(rpos, side=1, lwd=2); abline(h=0, lty=2)
rchers <- cherByThreshold(rpos, rsc, threshold=0, distCutOff=2)
sapply(rchers[-length(rchers)], function(thisClust){
  points(x=as.numeric(names(thisClust)), y=thisClust, type="h", lwd=2, col="gold")})

chipAlongChrom

Visualize ChIP intensities along the chromosome

Description

This function can visualize the array intensities from a ChIP chip experiment for a chromosomal region or the whole chromosome. It’s based on the plotAlongChrom function from the package tilingArray, but provides a different visualization.
Usage

```r
## S4 method for signature 'ExpressionSet,probeAnno'
plot(x, y, ...)

chipAlongChrom(eSet, probeAnno, chrom, xlim, ylim,
  samples = NULL, paletteName = "Set2", colPal = NULL,
  ylab = "Fold change [log]", ipch = 16, ilwd = 3, ilty = 1,
  icex = 3, gff = NULL,
  featureExclude=c("chromosome", "nucleotide_match","insertion"),
  zeroLine = TRUE, sampleLegend = TRUE, sampleLegendPos = "topleft",
  featureLegend = FALSE, maxInterDistance = 200, coord = NULL,
  highlight, main, ...)```

Arguments

- `eSet` An expression set containing the (normalized) ChIP intensities, e.g. the result objects from functions preprocess and computeRunningMedians.
- `x` Corresponds to argument `eSet` when calling the S4 method
- `probeAnno` An object of class `probeAnno` holding genomic position, index and gene association of probes on array.
- `y` Corresponds to argument `probeAnno` when calling the S4 method
- `chrom` character; the chromosome to visualize
- `xlim` start and end genomic coordinates on the chromosome to visualize
- `ylim` minimum and maximum probe intensities for the plot, if missing (default) set to `range(exprs(eSet))`
- `samples` numeric; which samples from the `eSet` are to be shown. Default is to show all samples in the `eSet`.
- `paletteName` character; Name of the RColorBrewer palette to use for sample colors. If the number of samples is greater than the palette size, random colors are taken.
- `colPal` vector of colors to use for the sample intensities. This is alternative to the argument `paletteName` for specifying which colors to use.
- `ylab` character; label for the y-axis, passed on to the plotting function as `ylab`
- `ipch` plot character to use
- `icex` character expansion to use for plotting symbol
- `ilwd` line width of plotted data lines
- `ilty` line type of plotted data lines; passed on to `par(1ty)`.
- `gff` data frame containing annotation for genomic feature to be used to further annotate the plot.
- `featureExclude` character vector specifying the feature types in the data.frame `gff` that should not be shown in the plot.
- `zeroLine` logical; should a dashed horizontal line at y=0 be put into the plot?
- `sampleLegend` logical; should a sample legend be put into the plot?
- `sampleLegendPos` character; where to put the sample legend; one of 'topleft' (default), 'bottom-left', 'topright', or 'bottomright'
- `featureLegend` logical; should a feature legend be put beneath the plot?
chipAlongChrom

maxInterDistance numeric; only used when itype is either "r" or "u"; specifies the maximal distance up to which adjacent probe positions should be connected by a line.

coord optional integer of length 2; can be used instead of xlim to specify the start and end coordinates of the genomic region to plot

highlight optional list specifying a genomic region to be highlighted in the shown plot

main optional main title for the plot; if not specified: the default is ‘Chromosome coordinate [bp]’

... further parameters passed on to grid.polyline and grid.points

Value

invisible list of probe positions (element x) and probe levels (element y) in the selected genomic region.

Note

The S4 method is provided as a mere convenience wrapper.

When plotting a new ‘grid’ plot in an active x11 window that already contains a plot, remember to call grid.newpage() before.

Author(s)

Joern Toedling

See Also

ExpressionSet-class, probeAnno-class, grid.points, plotAlongChrom in package tilingArray

Examples

```r
### load data
ringoExampleDir <- system.file("exData",package="Ringo")
load(file.path(ringoExampleDir,"exampleProbeAnno.rda"))
load(file.path(ringoExampleDir,"exampleX.rda"))

### show a gene that is well represented on this microarray
plot(exampleX, exProbeAnno, chrom="9",
     xlim=c(34318000,34321000), ylim=c(-2,4), gff=exGFF)

### this should give you the same result as:
chipAlongChrom(exampleX, chrom="9", xlim=c(34318000,34321000),
               ylim=c(-2,4), probeAnno=exProbeAnno, gff=exGFF)
```
compute.gc

Compute the GC content of DNA and probe sequences

Description
Simple auxiliary function to compute the GC content of a given set of DNA sequences, such as microarray probe sequences.

Usage
compute.gc(probe.sequences, digits = 2)

Arguments
- probe.sequences: character vector of DNA or probe sequences of which the GC content is to be computed
- digits: integer specifying the desired precision

Value
a numeric vector with sequence-wise GC contents; the names of this vector are the names of the supplied probe.sequences.

Author(s)
Joern Toedling

See Also
Function basecontent in package matchprobes for a more general function to compute base occurrence in sequences

Examples
ex.seqs <- c("gattaca", "GGGNTT", "ggAtT", "tata","gcccg")
names(ex.seqs) <- paste("sequence",1:5,sep="")
compute.gc(ex.seqs)

computeRunningMedians

Function to compute running medians on a tiling expression set

Description
Function to compute running medians (or other quantiles) on a tiling expression set.

Usage
computeRunningMedians(xSet, probeAnno, modColumn = "Cy5", allChr, winHalfSize = 400, min.probes = 5, quant = 0.5, combineReplicates = FALSE, nameSuffix = ".sm", checkUnique=TRUE, uniqueCodes=c(0), verbose = TRUE)
computeRunningMedians

Arguments

xSet Object of class ExpressionSet holding the normalized probe intensity data
probeAnno Environment holding the genomic positions of probes in the ExpressionSet
modColumn Column of the ExpressionSet’s phenoData holding the samples’ difference of interest
allChr Character vector of all chromosomes in genome; if not specified (default) all chromosomes annotated in the supplied probeAnno are used.
winHalfSize Half the size of the window centered at a probe position, in which all other probes contribute to the calculation of the median.
min.probes integer; if less probes are in the sliding window, NA instead of the median is returned. This meant to avoid to computing non-meaningful medians. If unwanted, set this to 1 or less
quant numeric; which quantile to use for the smoothing. The default 0.5 means compute the median over the values in the sliding window.
combineReplicates logical; should the median not be computed over individual samples in the ExpressionSet, but should samples be combined according to the column modColumn of the phenoData. The median is then computed across all probe levels and samples of the same type in the window. The resulting ExpressionSet has so many columns as are there different entries in the column modColumn
nameSuffix character; suffix attached to the sample labels of the supplied ExpressionSet xSet for the sample names of the resulting ExpressionSet.
checkUnique logical; indicates whether the uniqueness indicator of probe matches from the probeAnno environment should be used.
uniqueCodes numeric; which numeric codes in the chromosome-wise match-uniqueness elements of the probeAnno environment indicate uniqueness?
verbose logical; detailed progress output to STDOUT?

Value

An object of class ExpressionSet, holding smoothed intensity values for the probes of the supplied ExpressionSet. The number of results samples is either the number of levels in the supplied modColumn of the supplied ExpressionSet’s phenoData if combineReplicates is set to TRUE or equal to the number of samples in the supplied ExpressionSet xSet otherwise.

Author(s)

Joern Toedling

See Also

ExpressionSet, sliding.quantile, probeAnno-class

Examples

exDir <- system.file("exData", package="Ringo")
load(file.path(exDir, "exampleProbeAnno.rda"))
load(file.path(exDir, "exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno,
winHalfSize = 400)
computeSlidingT

Function to compute sliding T statistics on a tiling expression set

Description

Function to compute sliding (regularized) one- or two-sample T statistics on a tiling expression set.

Usage

computeSlidingT(xSet, probeAnno, allChr = c(1:19, "X", "Y"), test = "one.sample", grouping = NULL, winHalfSize = 400, min.probes = 5, checkUnique = TRUE, uniqueCodes = c(0), verbose = TRUE)

Arguments

xSet Object of class ExpressionSet holding the normalized probe intensity data
probeAnno Environment holding the genomic positions of probes in the ExpressionSet
allChr Character vector of all chromosomes in genome
test character; one of one.sample or two.sample
grouping factor vector of length equal to number of samples, not required if test=one.sample
winHalfSize Half the size of the window centered at a probe position, in which all other probes contribute to the calculation of the mean and standard deviation.
min.probes integer; if less probes are in the sliding window, NA instead of the mean and sd is returned. This is meant to avoid to computing non-meaningful means and standard deviations. If unwanted, set this to 1 or less
checkUnique logical; indicates whether the uniqueness indicator of probe matches from the probeAnno environment should be used.
uniqueCodes numeric; which numeric codes in the chromosome-wise match-uniqueness elements of the probeAnno environment indicate uniqueness?
verbose logical; detailed progress output to STDOUT?

Value

An object of class ExpressionSet, holding the T statistics values for the probes of the supplied ExpressionSet. The number of results samples is the number of levels in the supplied factor grouping.

Author(s)

Joern Toedling

See Also

sliding.meansd
Examples

```r
exDir <- system.file("exData",package="Ringo")
load(file.path(exDir,"exampleProbeAnno.rda"))
load(file.path(exDir,"exampleX.rda"))
tX <- computeSlidingT(exampleX, probeAnno=exProbeAnno,
allChr=c("9"), winHalfSize=400)
sampleNames(tX) <- "t-Stat_Suz12vsTotal"
if (interactive()){
  grid.newpage()
  plot(cbind2(exampleX, tX), exProbeAnno, chrom="9",
xlim=c(34318000,34321000), ylim=c(-2,8.5), gff=exGFF,
paletteName="Paired")
}
```

---

**corPlot**

*Function to plot correlation of different samples*

**Description**

This function can be used to visualise the (rank) correlation in expression data between different samples or sample groups.

**Usage**

```r
corPlot(eset, samples = NULL, grouping = NULL, ref = NULL,
useSmoothScatter = TRUE, 
...)
```

**Arguments**

- `eset` object of class `ExpressionSet` holding the array data, or a numeric matrix instead
- `samples` which samples’ expression shall be correlated to each other; either a numeric vector of sample numbers in the `ExpressionSet` or a character vector that must be contained in the `sampleNames` of the `ExpressionSet`, default NULL means take all samples in the `ExpressionSet`
- `grouping` an optional factor vector defining if the correlation should be assessed between groups of samples, rather than individual samples. If two or more samples are assigned into the same group, the mean over these samples’ expression values is taken before computing correlation. Default NULL means assess correlation between individual samples only.
- `ref` reference than only applies if argument `grouping` is given; see `relevel`
- `useSmoothScatter` logical; should the function `smoothScatter` be used?
- `...` additional arguments, not used yet

**Value**

The function only returns NULL (invisible). The function is called for its side-effect producing the pairs plot.
exportCherList

Author(s)
Joern Toedling

See Also
ExpressionSet, relevel, pairs, smoothScatter

Examples

data(sample.ExpressionSet)
if (interactive())
corPlot(sample.ExpressionSet,
grouping=paste(sample.ExpressionSet$sex,
sample.ExpressionSet$type, sep="."))

exportCherList

Function to export cherList into a file

Description

Function to export cherList into a file of gff or BED format. This files can be imported as tracks into genome browsers.

Usage

exportCherList(object, filename = "chers.gff", format = "gff3",
genome="hg18", ...)

Arguments

object     an object of class cherList
filename   character; path to file to be written
format     Format of exported file; currently only "gff3" and "bed" are supported
genome     character; which genome the ChIP-enriched regions were found in denoting species and assembly, e.g. ‘hg18’ or ‘mm9’
...         further arguments to be passed on to the trackSet method

Details

First converts the cherList into an object of class trackSet from package rtracklayer and then calls the export method as defined for a trackSet.

Value

returns invisible NULL; called for the side effect of writing the file filename.

Author(s)
Joern Toedling
See Also

Class trackset in package rtracklayer

Examples

## Not run:
exDir <- system.file("exData", package="Ringo")
load(file.path(exDir, "exampleProbeAnno.rda"))
load(file.path(exDir, "exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno, modColumn = "Cy5", allChr = "9", winHalfSize = 400)
chersX <- findChersOnSmoothed(smoothX, probeAnno=exProbeAnno, thresholds=0.45, allChr="9", distCutOff=600, cellType="human")
exportCherList(chersX, file="chers.gff")
## End(Not run)
features2Probes

Author(s)
Joern Toedling

See Also
posToProbeAnno, probeAnno-class

features2Probes  Function for mapping genomic features to probes

Description
This function creates a mapping between annotated genomic features and probes on the array whose
matching genomic positions are stored in a probeAnno environment.

Usage
features2Probes(gff, probeAnno, upstream = 5000, checkUnique = TRUE, uniqueCodes = c(0), mem.limit, verbose = TRUE)

Arguments
gff  data.frame holding genomic feature annotation
probeAnno  Object of class environment holding the genomic positions of probes in the ExpressionSet
upstream  up to how many bases upstream of annotated genomic features should probes be counted as related to that feature (see details)
checkUnique  logical; indicates whether the uniqueness indicator of probe matches from the probeAnno environment should be used.
uniqueCodes  numeric; which numeric codes in the chromosome-wise match-uniqueness elements of the probeAnno environment indicate uniqueness?
mem.limit  integer value; what is the maximal allowed size of matrices during the computation; see regionOverlap
verbose  logical; detailed progress output to STDOUT?

Value
The results is a list of length equal to the number of rows in the provided gff, the data.frame of
genomic features. The names of the list are the names specified in the gff. Each element of the
list is specified by the probes mapping into the genomic region from upstream bases upstream
of the feature’s start site to the feature’s end site. The entries itself are either NULL, if no probe
was mapped into this region, or a named numeric vector, with its values being the distances of the
probes’ middle positions to the feature’s start site (which depends on the strand the feature is on)
and its names being the identifiers of these probes.

Note
This resulting mapping is not used excessively by other Ringo functions, so creating this mapping
is optional at this time, but it may simplify subsequent gene/transcript-based analyses.
Here, the term feature describes a genomic entity such as a gene, transcript, non-coding RNA or a
similar feature annotated to a genome. It does NOT refer to oligo-nucleotide or cDNA probes on
the microarray.
findChersOnSmoothed

Author(s)
Joern Toedling

See Also
regionOverlap

Examples

```r
ingoExampleDir <- system.file("exData", package="Ringo")
load(file.path(ringoExampleDir, "exampleProbeAnno.rda"))
trans2Probe <- features2Probes(exGFF, exProbeAnno)
trans2Probe[exGFF$name[match("NUDT2", exGFF$symbol)]]
exGFF[match(names(trans2Probe)[listLen(trans2Probe)>0], exGFF$name),]
trans2Probe[hasProbes(listLen(trans2Probe)==1)]
```

Description

Given an ExpressionSet of smoothed probe intensities, an environment with the mapping of probes to chromosomes, and a vector of thresholds for calling genomic sites enriched, this function finds the ‘chers’ (ChIP-enriched regions) consisting of enriched genomic positions, with probes mapped to them. ‘Adjacent’ enriched positions are condensed into a single Cher.

Usage

```r
findChersOnSmoothed(smoothedX, probeAnno, thresholds, allChr = NULL,
                     distCutOff = 600, minProbesInRow = 3, cellType = NULL,
                     antibodyColumn=NULL, checkUnique = TRUE, uniqueCodes = c(0),
                     verbose = TRUE)
```

Arguments

- `smoothedX`: Object of class ExpressionSet holding the smoothed probe intensities, e.g. the result of function `computeRunningMedians`.
- `probeAnno`: environment containing the probe to genome mapping.
- `thresholds`: numeric vector of threshold above which smoothed probe intensities are considered to correspond to enriched probes. The vector has to be of length equal the number of samples in `smoothedX`, with a single threshold for each sample.
- `allChr`: character vector of all chromosomes on which enriched regions are sought. Every chromosome here has to have probes mapped to it in the `probeAnno` environment. By default (NULL) the chromosomeNames of the `probeAnno` object are used.
- `distCutOff`: integer; maximum amount of base pairs at which enriched probes are condensed into one Cher.
- `minProbesInRow`: integer; minimum number of enriched probes required for a Cher; see details for further explanation.

findChersOnSmoothed  Find ChIP-enriched regions on smoothed ExpressionSet
**findChersOnSmoothed**

**cellType**  
character; name of cell type the data comes from, is either a. of length one indicating the column of pData(smoothedX) that holds the cell type OR b. of length one indicating the common cell type for all samples in the ExpressionSet OR c. of length equal to ncol(smoothedX) specifying the cell type of each sample individually.

**antibodyColumn**  
the name or number of the column of the pData(smoothedX) that holds the description of the antibody used for each sample. This information is used to annotate found ChIP-enriched regions accordingly. If NULL (default), the sampleNames of smoothedX are used.

**checkUnique**  
logical; indicates whether the uniqueness indicator of probe matches from the probeAnno environment should be used.

**uniqueCodes**  
numeric; which numeric codes in the chromosome-wise match-uniqueness elements of the probeAnno environment indicate uniqueness?

**verbose**  
logical; extended output to STDOUT?

**Details**

Specifying a minimum number of probes for a Cher (argument `minProbesInRow`) guarantees that a Cher is supported by a reasonable number of measurements in probe-sparse regions. For example, if there’s only one enriched probe within a certain genomic 1kb region and no other probes can been mapped to that region, this single probe does arguably not provide enough evidence for calling this genomic region enriched.

**Value**

A list of class `cherList`, holding objects of class `cher` that were found on the supplied data.

**Author(s)**

Joern Toedling

**See Also**

`cherByThreshold`, `computeRunningMedians`, `relateChers`

**Examples**

```r
exDir <- system.file("exData", package="Ringo")
load(file.path(exDir, "exampleProbeAnno.rda"))
load(file.path(exDir, "exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno,
  modColumn = "Cy5", allChr = "9", winHalfSize = 400)
chersX <- findChersOnSmoothed(smoothX, probeAnno=exProbeAnno,
  thresholds=0.45, allChr="9", distCutOff=600, cellType="human")
if (interactive())
  plot(chersX[[1]], smoothX, probeAnno=exProbeAnno, gff=exGFF)
chersX <- relateChers(chersX, exGFF)
as.data.frame.cherList(chersX)
```
ftr2xys

Convert a NimbleScan ftr-file into a xys-file

Description

Auxiliary function to convert a NimbleScan feature-report file into a xys-file that can be used with the function read.xysfiles of package oligo.

Usage

ftr2xys(ftr.file, path=getwd())

Arguments

ftr.file character; file path of feature report file to convert into an xys file
path file path to directory where the xys-file should be written to; defaults to the current working directory

Details

The output file is names as the input ftr file; with the file extension .ftr replaced by .xys.

Value

Function returns only NULL invisibly and is only called for its side effect to write the xys-file into the current working directory.

Note

This function should only be used with one-color Nimblegen microarrays and when the correct xys-file of the raw data is not available. The output file can be used with the function read.xysfiles of package oligo.

Author(s)

Joern Toedling

Examples

## Not run:
sapply(list.files(pattern=".ftr"),ftr2xys)
library(oligo)
fs = read.xysfiles(list.xysfiles())

## End(Not run)
getFeats  Utility function to extract all features from a cherList

Description

This is a small utility function for extracting all related features from a cherList, a list of ChIP-enriched regions.

Usage

getFeats(cl)

Arguments

cl  object of class cherList, a list of cher objects

Value

a character vector containing the names of all features that were associated to any ChIP-enriched region in the list before, using the function relateChers

Author(s)

Joern Toedling

See Also

relateChers,cher-class

image.RGList  Function to visualize spatial distribution of raw intensities

Description

Function to visualize spatial distribution of raw intensities on NimbleGen Oligoarrays. Requires RGList with component genes complete with genes$X and genes$Y coordinates of probes on array. arrayImage is a synonym of image.RGList.

Usage

## S3 method for class 'RGList'
image(x, arrayno, channel=c("red","green","logratio"),
mycols=NULL, mybreaks=NULL, dim1="X", dim2="Y",
ppch=20, pcex=0.3, verbose=TRUE, ...)

Arguments

- **x**: object of class `RGLlist` containing red and green channel raw intensities; possibly result of `readNimblegen`.
- **arrayno**: integer; which array to plot; one of `1:ncol(x$R)`
- **channel**: character; which channel to plot, either `red`, `green` or the logratio `log2(red)-log2(green)`
- **mycols**: vector of colors to use for image; if NULL defaults to `colorRampPalette(c("White", "Yellow", "Red")(10))`
- **mybreaks**: optional numeric vector of breaks to use as argument `breaks` in `image.default`; default NULL means take `length(mycols)+1` quantiles of the data as breaks.
- **dim1**: string; which column of the 'genes' element of the supplied `RGLlist` indicates the first dimension of the reporter position on the microarray surface; for example this column is called 'X' with some NimbleGen arrays and 'Row' with some Agilent arrays.
- **dim2**: string; which column of the 'genes' element of the supplied `RGLlist` indicates the second dimension of the reporter position on the microarray surface; for example this column is called 'Y' with some NimbleGen arrays and 'Col' with some Agilent arrays.
- **ppch**: which symbol to use for intensities; passed on as `pch` to `points`. default
- **pcex**: enlargement factor for intensity symbols; passed on as `cex` to `points.default`. default
- **verbose**: logical; extended output to STDOUT?
- **...**: further arguments passed on to `plot.default` and `points.default`

Value

invisibly returns NULL; function is called for its side effect, this is producing the plot

Author(s)

Joern Toedling

See Also

`readNimblegen`, `plot.default`, `points`

Examples

```r
exDir <- system.file("exData", package="Ringo")
exRG <- readNimblegen("example_targets.txt","spottypes.txt",path=exDir)
image(exRG, 1, channel="red", mycols=c("black","darkred","red"))
## this example looks strange because the example data files only
## includes the probe intensities of probes mapped to the forward
## strand of chromosome 9.
## you can see these probes are distributed all over the array
```
nonzero-methods  Methods for Function nonzero

Description

Auxiliary functions to retrieve the indices of non-zero elements in sparse matrices.

Value

A two-column matrix. Each row gives the row and column index of a non-zero element in the supplied matrix \( x \).

Methods

- \( x = "\text{dgCMatrix}" \) returns the indices of non-zero elements in matrices of class \( \text{dgCMatrix} \)
- \( x = "\text{matrix.csr}" \) returns the indices of non-zero elements in matrices of class \( \text{matrix.csr} \)
- \( x = "\text{matrix}" \) returns the indices of non-zero elements in matrices of base class \( \text{matrix} \); equivalent to \( \text{which}(x \neq 0, \text{arr.ind}=\text{TRUE}) \)

Note

Originally we used the \( \text{matrix.csr} \) class from SparseM, but we have switched to the class \( \text{dgCMatrix} \) from package Matrix, as that package is part of the R distribution bundle now.

The idea is to have a function similar to \( \text{which}(x \neq 0, \text{arr.ind}=\text{TRUE}) \) if \( x \) is a matrix.

See Also

dgCMatrix-class

Examples

```r
(A <- matrix(c(0,0,0,0,0,1,0,0,0,0,0,0,0,0,-34),
nrow=5, byrow=TRUE))
str(A.dgc <- as(A, "dgCMatrix"))
nonzero(A.dgc)
A2.dgc <- Matrix::cBind(A.dgc, A.dgc)
as.matrix(A2.dgc)
nonzero(A2.dgc)
```

plot.autocor.result  Plots auto-correlation of probe intensities

Description

Function to plot the auto-correlation of probe intensities computed by function autocor.

Usage

```r
## S3 method for class 'autocor.result'
plot(x, plot.title = "ChIP: Autocorrelation of Intensities", ...)```
plot.cher

Arguments

x                  an object of class autocor.result, the result of function autocor
plot.title        main title of the plot
...               further arguments passed on to plot.default, see details

Details

The following arguments to plot.default are already defined in the function and thus cannot be specified by the user as further arguments in ...: type, lwd, xlab, ylab, col. Argument main is specified in plot.title.

Value

invisible NULL

Author(s)

Joern Toedling

See Also

autocor

Examples

## see the help page of 'autocor' for an example

---

plot.cher  
Plot identified Chers

Description

Function for plotting identified Chers (ChIP-enriched regions).

Usage

## S4 method for signature 'cher,ExpressionSet'
plot(x, y, probeAnno, samples=NULL, extent = 1000, gff = NULL, ...)

Arguments

x                  object of class cher
y                  data object of class ExpressionSet that was used for function findChersOnSmoothed
probeAnno          object of class probeAnno holding the reporter/probe to genome mappings
samples            which samples to plot, either a numeric vector of entries in 1 to ncol(dat), or character vector with entries in sampleNames(dat) or NULL meaning plot the levels from all samples in the ExpressionSet
extent             integer; how many base pairs to the left and right should the plotted genomic region be extended
gff                data frame with gene/transcript annotation
...                further arguments passed on to function chipAlongChrom
plotBM

Visualization of a binary matrix

Description
This function produces simple, heatmap-like visualizations of binary matrices.

Usage
plotBM(x, boxCol = "darkblue", reorder = FALSE, frame = TRUE, ...)

Arguments
- **x**: Binary matrix to visualize
- **boxCol**: Color to use for boxes of '1's
- **reorder**: logical; states whether the rows shall be reordered according to the size of the category
- **frame**: logical; states whether a frame should be drawn around the visualization. In contrast to the frame drawn in plot.default, there is no gap between the visualization and this frame.
- **...**: further arguments passed on to plot.default

Details
For reordering, each row is interpreted as a binary matrix, for example a row z=(1,0,0,1) would be interpreted as the binary number 1001 = 9 in the decimal system. Rows are then reordered by the frequency of each binary number with the rows that correspond to the most frequent binary number shown at the top in the visualization.

Value
The function invisibly returns the (reordered) matrix x, but its mainly called for its side effect of producing the visualization.

Note
An alternative way to display such matrices are given by heatmap or, the simpler version thereof, image. However, image files produced with this functions tend to be very large. This function uses plot.default and polygon which results in much smaller file sizes and is sufficient for binary matrices.
posToProbeAnno

Author(s)
Joern Toedling

See Also
polygon.colors

Examples
A <- matrix(round(runif(80)), ncol=4, byrow=TRUE)
dimnames(A)=list(letters[seq(nrow(A))],
               as.character(as.roman(seq(ncol(A)))))
show(A)
plotBM(A, reorder=FALSE)
plotBM(A, reorder=TRUE)

Description
This function allows the user to create a probeAnno environment that holds the mapping between probes on the array and their genomic match position(s). As input, the function takes either a.) one of NimbleGen’s POS file or a similar file that holds the mapping of probes to the genome. OR b.) a data.frame holding this information

Usage
posToProbeAnno(pos, chrNameColumn = "CHROMOSOME",
                probeColumn = "PROBE_ID", chrPositionColumn = "POSITION",
                lengthColumn = "LENGTH", sep="\t", genome="unknown",
                microarrayPlatform="unknown", verbose = TRUE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos</td>
<td>either a file-name that specifies the path to the POS or other mapping file OR a data.frame holding the mapping</td>
</tr>
<tr>
<td>chrNameColumn</td>
<td>name of the column in the file or data.frame that holds the chromosome name of the match</td>
</tr>
<tr>
<td>probeColumn</td>
<td>name of the column that holds the matching probe’s unique identifier</td>
</tr>
<tr>
<td>chrPositionColumn</td>
<td>name of the column that holds the match genomic position/coordinate on the chromosome</td>
</tr>
<tr>
<td>lengthColumn</td>
<td>name of the column that holds the length of the match position, in case of perfect match should correspond to the sequence length of the probe</td>
</tr>
<tr>
<td>sep</td>
<td>string; denotes the separator between elements in the supplied mappings file pos; passed on to function scan; ignored if pos is not a filename.</td>
</tr>
<tr>
<td>genome</td>
<td>string; denotes genome (and assembly) the reporters have been mapped to for this probeAnno object, e.g. &quot;M. musculus (mm9)&quot;</td>
</tr>
</tbody>
</table>
preprocess

microarrayPlatform

string; denotes the commercial or custom microarray platform/design that holds
the reporters whose mapping is stored in this probeAnno object, e.g. "Nimble-
Gen MOD SUZ12"

verbose

logical; should progress be written to STDOUT?

... further arguments passed on to function scan, which is used for reading in the
file pos.

Details

The default column names correspond to the column names in a NimbleGen POS file.
For custom mappings, using the tools Exonerate, BLAT or MUMmer, the scripts directory of this
package holds Perl scripts to generate such a POS file from the respective output files.

Value

The results is an object of class probeAnno.

Author(s)

Joern Toedling

See Also

probeAnno-class, scan

Examples

exPos <- read.delim(file.path(system.file("exData",package="Ringo"),
"MOD_2003-12-05_SUZ12_1in2.pos"),
header=TRUE,as.is=TRUE)
str(exPos)
exProbeAnno <- posToProbeAnno(exPos,
genome="M. musculus (assembly mm8)",
microarrayPlatform="NimbleGen 2005-06-17_Ren_MM5Tiling_Set1")
## is equivalent to
exProbeAnno2 <- posToProbeAnno(file.path(
  system.file("exData",package="Ringo"),"MOD_2003-12-05_SUZ12_1in2.pos"),
genome="M. musculus (assembly mm8)",
microarrayPlatform="NimbleGen 2005-06-17_Ren_MM5Tiling_Set1")
ls(exProbeAnno)
chromosomeNames(exProbeAnno2)

Description

Calls one of various (limma) functions to transform raw probe intensities into (background-corrected)
normalized log ratios (M-values).
Usage

```r
preprocess(myRG, method="vsn", ChIPChannel="R", inputChannel="G",
            returnMAList=FALSE, idColumn="PROBE_ID", verbose=TRUE, ...)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>myRG</td>
<td>object of class <code>RGList</code></td>
</tr>
<tr>
<td>method</td>
<td>string; denoting which normalization method to choose, see below for details</td>
</tr>
<tr>
<td>ChIPChannel</td>
<td>string; which element of the <code>RGList</code> holds the ChIP result, see details</td>
</tr>
<tr>
<td>inputChannel</td>
<td>string; which element of the <code>RGList</code> holds the untreated input sample; see details</td>
</tr>
<tr>
<td>returnMAList</td>
<td>logical; should an <code>MAList</code> object be returned? Default is to return an <code>ExpressionSet</code> object.</td>
</tr>
<tr>
<td>idColumn</td>
<td>string; indicating which column of the <code>genes</code> data.frame of the <code>RGList</code> holds the identifier for reporters on the microarray. This column, after calling <code>make.names</code> on it, will make up the unique featureNames of the resulting <code>ExpressionSet</code>. If argument <code>returnMAList</code> is <code>TRUE</code>, this argument is ignored.</td>
</tr>
<tr>
<td>verbose</td>
<td>logical; progress output to STDOUT?</td>
</tr>
<tr>
<td>...</td>
<td>further arguments to be passed on <code>normalizeWithinArrays</code> and <code>normalizeBetweenArrays</code></td>
</tr>
</tbody>
</table>

Details

The procedure and called `limma` functions depend on the choice of method.

- **loess** Calls `normalizeWithinArrays` with method="loess".
- **vsn** Calls `normalizeBetweenArrays` with method="vsn".
- **Gquantile** Calls `normalizeBetweenArrays` with method="Gquantile".
- **Rquantile** Calls `normalizeBetweenArrays` with method="Rquantile".
- **median** Calls `normalizeWithinArrays` with method="median".
- **nimblegen** Scaling procedure used by Nimblegen. Yields scaled log-ratios by a two step procedure: srat = log2(R) - log2(G) srat = srat - tukey.biweight(srat)
- **Gvsn** Learns vsn model on green channel intensities only and applies that transformation to both channels before computing fold changes.
- **Rvsn** Learns vsn model on red channel intensities only and applies that transformation to both channels before computing fold changes.
- **none** No normalization of probe intensities, takes raw log2(R)-log2(G) as component M and (log2(R)+log2(G))/2 as component A; uses `normalizeWithinArrays` with method="none".

Mostly with two-color ChIP-chip, the ChIP sample is marked with the red Cy5 dye and for the untreated input sample the green Cy3 dye is used. In that case the `RGList`myRG’s element R holds the ChIP data, and element G holds the input data. If this is not the case with your data, use the arguments ChIPChannel and inputChannel to specify the respective elements of `myRG`.

Value

Returns normalized, transformed values as an object of class `ExpressionList` or `MAList`. 
Note

Since Ringo version 1.5.6, this function does not call limma’s function `backgroundCorrect` directly any longer. If wanted by the user, background correction should be indicated as additional arguments passed on to `normalizeWithinArrays` or `normalizeBetweenArrays`, or alternatively call `backgroundCorrect` on the RGList before preprocessing.

Author(s)

Joern Toedling

See Also

`normalizeWithinArrays`, `normalizeBetweenArrays`, `malist`, `ExpressionSet`, `vsnMatrix`

Examples

```r
exDir <- system.file("exData", package="Ringo")
exRG <- readNimblegen("example_targets.txt", "spottypes.txt", path=exDir)
exampleX <- preprocess(exRG)
sampleNames(exampleX) <- make.names(paste(exRG$targets$Cy5,"vs", exRG$targets$Cy3, sep="_"))
print(exampleX)
## compare VSN to NimbleGen’s tukey-biweight scaling
exampleX.NG <- preprocess(exRG, method="nimblegen")
sampleNames(exampleX.NG) <- sampleNames(exampleX)
if (interactive())
corPlot(cbind(exprs(exampleX), exprs(exampleX.NG)),
        grouping=c("VSN normalized", "Tukey-biweight scaled"))
```

---

**probeAnno-class**

Description

A class that holds the mapping between reporters/probes on a microarray and their genomic match position(s) in a chosen genome.

Objects from the Class

Objects can be created by calls of the form `new("probeAnno", map, arrayName, genome).

Slots

- **map**: Object of class "environment" This map consists of four vectors for each chromosome/strand, namely, say for chromosome 1:
  - **1.start**: genomic start coordinates of probe matches on chromosome 1
  - **1.end**: genomic start coordinates of probe matches on chromosome 1
  - **1.index**: identifier of probes matching at these coordinates
  - **1.unique**: vector of the same length as the three before; encoding how many matches the corresponding probe has in the given file or data.frame. An entry of '0' indicates that the probe matching at this position has only this one match.
arrayName: Object of class "character", the name or identifier of the microarray design, e.g. 2005-06-17_Ren_MM5Tiling_Set1

genome: Object of class "character", which genome the reporters have been mapped to

Methods

arrayName obtain the microarray platform name
arrayName<- replace the microarray platform name
[ get elements from the map environment
[<- assign elements to the map environment

chromosomeNames obtain a character vector holding the names of the chromosomes for which the probeAnno objects holds a mapping.

get get elements from the map environment
initialize create new probeAnno object
ls list elements of the map environment
genome obtain the description of the genome the reporters were mapped to
genome<- replace the description of the genome the reporters were mapped to

as signature(from="environment"); function to coerce old-style 'probeAnno' environments to new-style 'probeAnno' objects. Simply creates a new object with the old environment in its map

Note

'probeAnno' objects used to be environments and still are used as such in package tilingArray

Author(s)

Joern Toedling; Wolfgang Huber

See Also

posToProbeAnno

Examples

pa <- new("probeAnno")
pa["X.start"] <- seq(5000,10000,by=1000)
if (interactive()) show(pa)
pa2 <- posToProbeAnno(file.path(system.file("exData",package="Ringo"),
          "MOD_2003-12-05_SUZ12_1in2.pos"))
arrayName(pa2) <- "NimbleGen MOD_2003-12-05_SUZ12_1in2"
genome(pa2) <- "H. sapiens (hg18)"
show(pa2)
head(pa2["9.start"])
quantilesOverPositions

show ChIP-chip data aligned over genome features, e.g. TSSs

Description

Function to show the ChIP-chip data aligned over certain genome features, for example transcription start sites (TSSs).

Usage

quantilesOverPositions(xSet, selGenes, g2p,
positions = seq(-5000, 10000, by = 250),
quantiles = c(0.1, 0.5, 0.9))

Arguments

xSet an ExpressionSet holding the ChIP-chip data
selGenes character; vector of genome features, e.g. transcripts, to use for the plot
g2p A list object containing the mapping between genome positions and probes on the microarray. Created with the function features2Probes.
positions Numeric vector of positions related to the coordinates of the genome features, such as in which distances of the TSS the values should be computed over the aligned data
quantiles numeric; which quantiles to compute over the aligned data

Value

An object of class qop, which can be visualized by its plot method.

Author(s)

Joern Toedling

See Also

features2Probes, qop-class

Examples

ringoExampleDir <- system.file("exData",package="Ringo")
load(file.path(ringoExampleDir,"exampleProbeAnno.rda"))
trans2Probe <- features2Probes(exGFF, exProbeAnno)
load(file.path(ringoExampleDir,"exampleX.rda"))
exampleSX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno,
modColumn = "Cy5", allChr = "9", winHalfSize = 400)
exampleC <- findChersOnSmoothed(exampleSX, probeAnno=exProbeAnno,
thresholds=0.2, allChr="9", distCutOff=600, cellType="human")
exampleC <- relateChers(exampleC, exGFF)
exampleQop <- quantilesOverPositions(exampleSX,
  selGenes=getFeats(exampleC), quantiles=c(0.5, 0.9),
readNimblegen

Function to read in Nimblegen Intensity Text Files

Description

Function to read in Nimblegen Intensity Text Files into an RGList. Calls some other functions for actual reading of data. This function is to be used with two-color NimbleGen array data. Use the function read.xysfiles of the oligo package for single-color data.

Usage

readNimblegen(hybesFile, spotTypesFile, path = getwd(),
    headerPattern="# software=NimbleScan", verbose = TRUE, ...)

Arguments

- **hybesFile**: Name of the file describing the arrays. In limma this file would be called targets file.
- **spotTypesFile**: spot types also used by limma
- **path**: Path to directory that hold the files hybesFile, spotTypesFile and also the intensity files. Set this to NULL if you prefer the arguments hybesFile, spotTypesFile and the file-name entries of the hybes file to be treated as absolute or relative file paths themselves.
- **headerPattern**: string; pattern used to identify explanatory header lines in the supplied pair-format files
- **verbose**: logical; progress output to STDOUT?
- **...**: further arguments passed on the readNgIntensitiesTxt

Value

Returns raw intensity values in form of an RGList.

Author(s)

Joern Toedling

See Also

rglist, readTargets

Examples

```
exDir <- system.file("exData", package="Ringo")
exRG <- readNimblegen("example_targets.txt", "spottypes.txt", path = exDir)
print(exRG)
```
regionOverlap  Function to compute overlap of genomic regions

Description

Given two data frames of genomic regions, this function computes the base-pair overlap, if any, between every pair of regions from the two lists.

Usage

```r
regionOverlap(xdf, ydf, chrColumn = "chr", startColumn = "start", endColumn = "end", mem.limit=1e8)
```

Arguments

- `xdf`: data.frame that holds the first set of genomic regions
- `ydf`: data.frame that holds the first set of genomic regions
- `chrColumn`: character; what is the name of the column that holds the chromosome name of the regions in `xdf` and `ydf`
- `startColumn`: character; what is the name of the column that holds the start position of the regions in `xdf` and `ydf`
- `endColumn`: character; what is the name of the column that holds the start position of the regions in `xdf` and `ydf`
- `mem.limit`: integer value; what is the maximal allowed size of matrices during the computation

Value

Originally, a matrix with `nrow(xdf)` rows and `nrow(ydf)` columns, in which entry `X[i,j]` specifies the length of the overlap between region `i` of the first list (`xdf`) and region `j` of the second list (`ydf`). Since this matrix is very sparse, we use the `dgCMatrix` representation from the `Matrix` package for it.

Note

The function only return the absolute length of overlapping regions in base-pairs. It does not return the position of the overlap or the fraction of region 1 and/or region 2 that overlaps the other regions.

The argument `mem.limit` is not really a limit to used RAM, but rather the maximal size of matrices that should be allowed during the computation. If larger matrices would arise, the second regions list is split into parts and the overlap with the first list is computed for each part. During computation, matrices of size `nrow(xdf)` times `nrow(ydf)` are created.

Author(s)

Joern Toedling

See Also

dgCMatrix-class
## Examples

```r
## toy example:
regionsH3ac <- data.frame(chr=c("chr1","chr7","chr8","chr1","chrX","chr8"), start=c(100,100,100,510,100,60), end=c(200, 200, 200,520,200,80))
regionsH4ac <- data.frame(chr=c("chr1","chr2","chr7","chr8","chr9"), start=c(500,100,50,80,100), end=c(700, 200, 250, 120,200))

## compare the regions first by eye
## which ones do overlap and by what amount?
regionsH3ac
regionsH4ac

## compare it to the result:
as.matrix(regionOverlap(regionsH3ac, regionsH4ac))
nonzero(regionOverlap(regionsH3ac, regionsH4ac))
```

---

## relateChers

**Relate found Chers to genomic features**

### Description

This function relates found 'cher's (ChIP-enriched regions) to annotated genomic features, such as transcripts.

### Usage

```r
relateChers(pl, gff, upstream = 5000, verbose = TRUE)
```

### Arguments

- `pl`: Object of class `cherList`
- `gff`: data.frame holding genomic feature annotation
- `upstream`: up to how many bases upstream of annotated genomic features should chers be counted as related to that feature (see details)
- `verbose`: logical; extended output to STDOUT?

### Details

chers will be counted as related to genomic features, if

- their middle position is located between start and end position of the feature
- their middle position is located not more than argument `upstream` bases upstream of the feature start

One can visualize such cher-feature relations as a graph using the Bioconductor package `Rgraphviz`. See the script 'graphChers2Transcripts.R’ in Ringo’s scripts directory for an example.

### Value

An object of class `cherList` with for each cher the elements `typeUpstream` and `typeInside` filled in with the names of the features that have been related to.
sliding.meansd

Author(s)
Joern Toedling

Examples

# see findChersOnSmoothed for an example

sliding.meansd

Compute mean and standard deviation of scores in a sliding window

Description

This function is used to slide a window of specified size over scores at given positions. Computed is the mean and standard deviation over the scores in the window.

Usage

sliding.meansd(positions, scores, half.width)

Arguments

positions numeric; sorted vector of (genomic) positions of scores
scores numeric; scores to be smoothed associated to the positions
half.width numeric, half the window size of the sliding window

Value

Matrix with three columns:

mean means over scores in running window centered at the positions that were specified in argument positions.
sd standard deviations over scores in running window centered at the positions that were specified in argument positions.
count number of points that were considered for computing the mean and standard deviation at each position

Author(s)
Joern Toedling and Oleg Sklyar

See Also

sliding.quantile
sliding.quantile

Examples

```r
set.seed(123)
sampleSize <- 10
ap <- cumsum(1+round(runif(sampleSize)*10))
as <- c(rnorm(floor(sampleSize/3)),
       rnorm(ceiling(sampleSize/3),mean=1.5),
       rnorm(floor(sampleSize/3)))
sliding.meansd(ap, as, 20)
ap
mean(as[1:3])
sd(as[1:3])
```

Description

This function is used to slide a window of specified size over scores at given positions. Computed is the quantile over the scores in the window.

Usage

```r
sliding.quantile(positions, scores, half.width, prob = 0.5,
                  return.counts = TRUE)
```

Arguments

- `positions`: numeric; sorted vector of (genomic) positions of scores
- `scores`: numeric; scores to be smoothed associated to the positions
- `half.width`: numeric, half the window size of the sliding window
- `prob`: numeric specifying which quantile is to be computed over the scores in the window; default 0.5 means compute the median over the scores.
- `return.counts`: logical; should the number of points, e.g. probes, that were used for computing the median in each sliding window also returned?

Value

Matrix with two columns:

- `quantile`: medians over running window centered at the positions that were specified in argument `positions`.
- `count`: number of points that were considered for computing the median at each position

These positions are given as row names of the resulting vector. If argument `return.counts` is FALSE, only a vector of the medians is returned, with the positions as names.

Author(s)

Oleg Sklyar and Joern Toedling
See Also
quantile

Examples

```r
code for generating example data and performing analyses
```
Note

Please note that the use of the package 'mclust' is only free for strict academic use (see the license of 'mclust' here: http://www.stat.washington.edu/mclust/license.txt). The alternative function upperBoundNull does not have this restriction.

Thanks to Richard Bourgon for pointing out the necessity of providing this method as an alternative way of estimating the threshold.

Author(s)

Joern Toedling, Aleksandra Pekowska

See Also

mclust, p.adjust, upperBoundNull

Examples

```r
exDir <- system.file("exData",package="Ringo")
load(file.path(exDir,"exampleProbeAnno.rda"))
load(file.path(exDir,"exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno,
                                 modColumn = "Cy5", allChr = "9", winHalfSize = 400)

## compare the two different ways of estimating the threshold
y0a <- apply(exprs(smoothX), 2, upperBoundNull)
y0b <- apply(exprs(smoothX), 2, twoGaussiansNull)

hist(exprs(smoothX)[,1], n=10, main=NA,
xlab="Smoothed expression level [log2]"
abline(v=c(y0a, y0b), col=c("blue","orange"), lwd=2)
legend(x="topright", col=c("blue","orange"), lwd=2,
       legend=c(expression(paste(y[0]," Non-parametric")),
               expression(paste(y[0]," Gaussian"))))
```

upperBoundNull function to estimate upper limit of null distribution

Description

The data is assumed to arise from a mixture of two distributions, a symmetric null distribution with its mode close to zero, and an alternative distribution that is stochastically larger than the null. This function tries to pinpoint the minimum of data values that are more likely to arise from the alternative distribution, i.e. an upper bound for values following the null distribution.

Usage

```r
upperBoundNull(x, modeMethod = "shorth", limits = c(-1, 1), prob = 0.99, ...)
```
Arguments

x
numeric vector of data values

modeMethod
character string; which method to use for estimating the mode of the null distribution; see details

limits
numeric of length 2; data values within this range are used for estimating the mode of the null distribution

prob
quantile of the null distribution that will be used as an upper bound

... additional arguments that are passed on to the function for mode estimation

Details

For estimating the mode of the null distribution, current options are

"shorth" the function shorth

"half.range.mode" the function half.range.mode

"null" does not estimate the mode from the data, but sets it to 0

Value

a single numeric value which is the estimated upper bound for the null distribution.

Note

This way of estimating the null distribution is mentioned in the PhD thesis of Richard Bourgon.

Author(s)

Joern Toedling, based on suggestions by Richard Bourgon

See Also

shorth, half.range.mode

Examples

exDir <- system.file("exData", package="Ringo")
load(file.path(exDir,"exampleProbeAnno.rda"))
load(file.path(exDir,"exampleX.rda"))
smoothX <- computeRunningMedians(exampleX, probeAnno=exProbeAnno, modColumn = "Cy5", allChr = "9", winHalfSize = 400)
apply(exprs(smoothX), 2, upperBoundNull)
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