Package 'chromVAR'

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Type Package

Title Chromatin Variation Across Regions

Version 1.30.1

Description Determine variation in chromatin accessibility across sets of annotations or peaks. Designed primarily for single-cell or sparse chromatin accessibility data, e.g. from scATAC-seq or sparse bulk ATAC or DNAse-seq experiments.

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Imports IRanges, GenomeInfoDb, GenomicRanges, ggplot2, nabor, BiocParallel, BiocGenerics, Biostrings, TFBSTools, Rsamtools, S4Vectors, methods, Rcpp, grid, plotly, shiny, miniUI, stats, utils, graphics, DT, Rtsne, Matrix, SummarizedExperiment, RColorBrewer, BSgenome

Depends R (>= 3.4)

Suggests JASPAR2016, BSgenome.Hsapiens.UCSC.hg19, readr, testthat, knitr, rmarkdown, pheatmap, motifmatchr

biocViews SingleCell, Sequencing, GeneRegulation, ImmunoOncology

LazyData TRUE

LinkingTo Rcpp, RcppArmadillo

SystemRequirements C++11

VignetteBuilder knitr

RoxygenNote 6.0.1

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Contents

`addGCBias` *addGCBias*

Description

Computes GC content for peaks

Usage

```
addGCBias(object, ...)

## S4 method for signature 'RangedSummarizedExperiment'
addGCBias(object,
  genome = GenomeInfoDb::genome(object))

## S4 method for signature 'SummarizedExperiment'
addGCBias(object, peaks,
  genome = GenomeInfoDb::genome(peaks))
```

Arguments

`object`	(Ranged)SummarizedExperiment
`...`	additional arguments
`genome`	BSgenome object, by defualt hg19
`peaks`	GenomicRanges with peaks, needed if object is SummarizedExperiment and not RangedSummarizedExperiment

Value

(Ranged)SummarizedExperiment object with new column in row metadata with the gc content of the peak in question

Methods (by class)

- RangedSummarizedExperiment: method for RangedSummarizedExperiment
- SummarizedExperiment: method for SummarizedExperiment

Examples

```
data(example_counts, package = "chromVAR")
# show example on small part of data
subset_counts <- example_counts[1:500,]
library(BSgenome.Hsapiens.UCSC.hg19)
example_counts <- addGCBias(subset_counts,
                            genome = BSgenome.Hsapiens.UCSC.hg19)
```

---

annotationMatches *annotationMatches*

Description

annotationMatches

Usage

```
annotationMatches(object)

annotationMatches(object) <- value

## S4 method for signature 'SummarizedExperiment'
annotationMatches(object)

## S4 replacement method for signature 'SummarizedExperiment'
annotationMatches(object) <- value
```

Arguments

object	SummarizedExperiment with matches slot, see details
value	logical Matrix with annotation matches

Details

Will extract matrix from the "matches", "annotationMatches", or "motif_matches" assay of a SummarizedExperiment

Value

logical matrix of annotation matches

Author(s)

Alicia Schep

Examples

```
# load annotation matrix; result from matchMotifs
data(mini_ix, package = "chromVAR")
matches <- annotationMatches(mini_ix)
```

`assembleKmers` *assembleKmers*

Description

function to create de novo motifs from kmers based on deviations

Usage

```
assembleKmers(object, threshold = 1.5, p = 0.01, progress = TRUE)
```

Arguments

`object`	kmer chromVARDeviations object
`threshold`	variability threshold
`p`	p value threshold for inclusion of kmer
`progress`	show progress bar?

Details

function for assembling de novo kmers from kmer deviations

Value

list with (1) motifs: de novo motif matrices, (2) seed: seed kmer for de novo motif

cbind,chromVARDeviations-method

cbind method for chromVARDeviations

Description

cbind returns an error when applied to chromVARDeviations because results for all cells or samples should originate from same computeDeviations computation

Usage

```
## S4 method for signature 'chromVARDeviations'
cbind(..., deparse.level = 1)
```

Arguments

...	chromVARDeviations object to be combined
deparse.level	See ?base::rbind for a description of this argument.

Value

chromVARDeviations object

Author(s)

Alicia Schep

See Also

chromVARDeviations-class

chromVAR

chromVAR: A package for computing variability across sets of peaks.

Description

Determine variation in chromatin accessibility across sets of annotations or peaks. Designed primarily for single-cell or sparse chromatin accessibility, e.g. from scATAC-seq or sparse ATAC or DNAse-seq experiments.

`chromVARDeviations-class` *chromVARDeviations*

Description

Class for storing results from `computeDeviations` function.

Details

This class inherits from `SummarizedExperiment`, and most methods for that class should work for objects of this class as well. Additionally, two accessor functions are defined for extracting bias corrected deviations (`deviations`) and deviation Z-scores (`deviationScores`)

`chromVAR_theme` *chromVAR_theme*

Description

theme for use with ggplot2, used by chromVAR plotting functions

Usage

```
chromVAR_theme(base_size = 12, base_family = "Helvetica")
```

Arguments

`base_size`	base font size
`base_family`	base font family

Value

ggplot2 theme

Author(s)

Alicia Schep

Examples

```
p <- ggplot2::qplot(1:3,1:3) + chromVAR_theme(18)
```

computeDeviations *computeDeviations*

Description

Computes deviations in chromatin accessibility across sets of annotations

Usage

```
computeDeviations(object, annotations, ...)

## S4 method for signature 'SummarizedExperiment,SummarizedExperiment'
computeDeviations(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object))

## S4 method for signature 'SummarizedExperiment,MatrixOrmatrix'
computeDeviations(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object))

## S4 method for signature 'SummarizedExperiment,list'
computeDeviations(object, annotations,
  background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object))

## S4 method for signature 'SummarizedExperiment,missingOrNULL'
computeDeviations(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object))

## S4 method for signature 'MatrixOrmatrix,SummarizedExperiment'
computeDeviations(object,
  annotations, background_peaks, expectation = computeExpectations(object))

## S4 method for signature 'MatrixOrmatrix,MatrixOrmatrix'
computeDeviations(object, annotations,
  background_peaks, expectation = computeExpectations(object))

## S4 method for signature 'MatrixOrmatrix,list'
computeDeviations(object, annotations,
  background_peaks, expectation = computeExpectations(object))

## S4 method for signature 'MatrixOrmatrix,missingOrNULL'
computeDeviations(object, annotations,
  background_peaks, expectation = computeExpectations(object))
```

Arguments

object	chromVARCounts object
annotations	chromVARAnnotations object
...	additional arguments
background_peaks	(optional) background peaks matrix computed using getBackgroundPeaks, computed internally with default paramaters if not provided
expectation	(optional) expectations computed using computeExpectations, computed automatically if not provided

Details

multiprocessing using bplapply

Value

chromVARDeviations-class, which inherits from SummarizedExperiment, and has two assays: deviations and deviation scores.

Methods (by class)

- object = SummarizedExperiment,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = SummarizedExperiment,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = SummarizedExperiment,annotations = list: object is SummarizedExperiment, annotations are list
- object = SummarizedExperiment,annotations = missingOrNULL: object is SummarizedExperiment, annotations are missing
- object = MatrixOrmatrix,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = MatrixOrmatrix,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = MatrixOrmatrix,annotations = list: object is SummarizedExperiment, annotations are list
- object = MatrixOrmatrix,annotations = missingOrNULL: object is SummarizedExperiment, annotations are missing

Author(s)

Alicia Schep

See Also

computeVariability, plotVariability

Examples

```
# Register BiocParallel
BiocParallel::register(BiocParallel::SerialParam())
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
# load annotation matrix; result from matchMotifs
data(mini_ix, package = "chromVAR")

# computing deviations
dev <- computeDeviations(object = mini_counts,
                         annotations = mini_ix)
```

`computeExpectations` *computeExpectations*

Description

computeExpectations

Usage

```
computeExpectations(object, ...)

## S4 method for signature 'MatrixOrmatrix'
computeExpectations(object, norm = FALSE,
  group = NULL)

## S4 method for signature 'SummarizedExperiment'
computeExpectations(object, norm = FALSE,
  group = NULL)
```

Arguments

`object`	SummarizedExperiment
`...`	additional arguments
`norm`	weight all samples equally?
`group`	an group vector, optional

Details

By default, this function will compute the expected fraction of reads per peak as the the total fragments per peak across all samples divided by total reads in peaks in all samples. Optionally, norm can be set to TRUE and then the expectation will be the average fraction of reads in a peak across the cells. This is not recommended for single cell applications as cells with very few reads will have a large impact. Another option is to give a vector of groups, in which case the expectation will be the average fraction of reads per peak within each group. If group vector is provided and norm is set to TRUE then within each group the fraction of reads per peak is the average fraction of reads per

peak in each sample. Otherwise, the within group fraction of reads per peak is based on the reads per peak within the sample divided by the total reads within each sample. The group can also be given by a length 1 character vector representing the name of a column in the colData of the input object if the input is a SummarizedExperiment

Value

vector with expected fraction of reads per peak.

Methods (by class)

- `MatrixOrmatrix`: method for Matrix or matrix
- `SummarizedExperiment`: method for SummarizedExperiment with counts slot

Author(s)

Alicia Schep

Examples

```
# First get some data
data(mini_counts, package = "chromVAR")

# Compute expectations
expectations <- computeExpectations(mini_counts)
```

`computeVariability` *computeVariability*

Description

function to compute overall variability of motif sets across samples

Usage

```
computeVariability(object, bootstrap_error = TRUE, bootstrap_samples = 1000,
  bootstrap_quantiles = c(0.025, 0.975), na.rm = TRUE)
```

Arguments

`object`	output from `computeDeviations`
`bootstrap_error`	compute bootstrap confidence interval
`bootstrap_samples`	number of bootstrap samples to take
`bootstrap_quantiles`	quantiles for bootstrap
`na.rm`	remove NAs? default is true

Value

data.frame with columns for name, variability, bootstrap lower bound, bootstrap upper bound, raw p value, adjust p value.

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
variability <- computeVariability(mini_dev)
```

---

counts,SummarizedExperiment-method

Accessors for the 'counts' slot of a SummarizedExperiment

Description

Accessors for the 'counts' slot of a SummarizedExperiment

Usage

```
## S4 method for signature 'SummarizedExperiment'
counts(object)

## S4 replacement method for signature 'SummarizedExperiment,MatrixOrmatrix'
counts(object) <- value
```

Arguments

object	SummarizedExperiment object
value	matrix of counts

Value

Matrix of counts

Examples

```
data(mini_counts, package = "chromVAR")
fragment_counts <- counts(mini_counts)
```

deviations *deviations*

Description

Accessor for bias corrected deviations from chromVARDeviations-class object

Usage

```
deviations(object)

## S4 method for signature 'chromVARDeviations'
deviations(object)
```

Arguments

object	chromVARDeviations object

Value

matrix of bias corrected deviations

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
bias_corrected_deviations <- deviations(mini_dev)
```

deviationScores *deviationScores*

Description

Accessor for deviation Z-scores from chromVARDeviations-class object

Usage

```
deviationScores(object)

## S4 method for signature 'chromVARDeviations'
deviationScores(object)
```

Arguments

object	chromVARDeviations object

Value

The deviationScores and deviations accessors both return matrices.

matrix of deviation Z-scores

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
scores <- deviationScores(mini_dev)
```

---

deviationsCovariability
deviationsCovariability

Description

deviationsCovariability

Usage

```
deviationsCovariability(object)
```

Arguments

object	deviations result

Details

Returns the 'covariability' between motifs/kmers/peaksets. Covariability' is defined as covariance between Z-scores divided by variance of Z-scores for one motif/kmer/peakset (the row).

Value

'covariability' matrix

Examples

```
# load very small example data
data(mini_counts, package = "chromVAR")
motifs <- getJasparMotifs()
library(motifmatchr)
motif_ix <- matchMotifs(motifs, mini_counts,
  genome = BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19)

# computing deviations
dev <- computeDeviations(object = mini_counts,
                         annotations = motif_ix)

# get covariability for just first three motifs
devcov <- deviationsCovariability(dev[1:3,])
```

`deviationsTsne` *deviationsTsne*

Description

Perform tsne using bias corrected deviations to visualize either cell/sample similarity or motif/kmer/annotation similarity

Usage

```
deviationsTsne(object, threshold = 1.5, perplexity = if (what == "samples")
  30 else 8, max_iter = 1000, theta = 0.5, what = c("samples",
  "annotations"), shiny = FALSE)
```

Arguments

`object`	deviations result
`threshold`	variability threshold – use only deviations with variability greater than threshold
`perplexity`	perplexity parameter for tsne
`max_iter`	max iterations parameter for tsne
`theta`	theta parameter for tsne
`what`	tsne for similarity of samples or annotations?
`shiny`	load a shiny widget that enable you to explore perplexity and variability threshold parameter?

Value

data.frame with two columns for the two dimensions of tSNE output

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")

tsne_res <- deviationsTsne(mini_dev, threshold = 0.8, shiny = FALSE)
# setting very low variabilitiy threshold because this is mini data set
# threshold should generally be above 1
# Use plotVariability to get a sense of an appropriate threshold
```

---

differentialDeviations *differentialDeviations*

Description

Function to see whether deviations differ between groups

Usage

```
differentialDeviations(object, groups, alternative = c("two.sided", "less",
  "greater"), parametric = TRUE)
```

Arguments

object	chromVARDeviations object
groups	either vector of groups or name of column in colData of object with group information
alternative	only used if there are two groups – two.sided or one sided test
parametric	use parametric test. alternatively will use kruskal wallace

Value

data.frame with p value and adjusted p value

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
difdev <- differentialDeviations(mini_dev, "Cell_Type")
```

differentialVariability *differentialVariability*

Description

Function to determine whether groups differ in variability

Usage

```
differentialVariability(object, groups, parametric = TRUE)
```

Arguments

object	chromVARDeviations object
groups	either vector of groups or name of column in colData of object with grouop information
parametric	use parametric test. alternatively will use kruskal wallace

Value

data.frame with p value and adjusted p value

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
difvar <- differentialVariability(mini_dev, "Cell_Type")
```

example_counts *example_counts*

Description

Very small sample data set for trying out chromVAR

Usage

```
data(example_counts)
```

Value

RangedSummarizedExperiment

Examples

```
data(example_counts)
```

---

filterPeaks *filterPeaks*

Description

function to get indices of peaks that pass filters

Usage

```
filterPeaks(object, min_fragments_per_peak = 1, non_overlapping = TRUE,
  ix_return = FALSE)
```

Arguments

object	SummarizedExperiment with matrix of fragment counts per peak per sample, as computed by getCounts
min_fragments_per_peak	minimum number of fragmints in peaks across all samples
non_overlapping	reduce peak set to non-overlapping peaks, see details
ix_return	return indices of peaks to keep instead of subsetted counts object

Details

if non_overlapping is set to true, when peaks overlap the overlapping peak with lower counts is removed

Value

vector of indices, representing peaks that should be kept

Author(s)

Alicia Schep

See Also

getPeaks, filterSamples, getCounts

Examples

```
data(example_counts, package = "chromVAR")

counts_filtered <- filterSamples(example_counts, min_depth = 1500,
                                 min_in_peaks = 0.15, shiny = FALSE)
counts_filtered <- filterPeaks(example_counts)
```

`filterSamples` *filterSamples*

Description

function to get indices of samples that pass filtters

Usage

```
filterSamples(object, min_in_peaks = NULL, min_depth = NULL,
  shiny = interactive(), ix_return = FALSE)
```

Arguments

`object`	SummarizedExperiment with matrix of fragment counts per peak per sample, as computed by `getCounts`
`min_in_peaks`	minimum fraction of samples within peaks
`min_depth`	minimum library size
`shiny`	make shiny gadget?
`ix_return`	return indices of sample to keep instead of subsetted counts object

Details

If unspecified, min_in_peaks and min_depth cutoffs will be estimated based on data. min_in_peaks is set to 0.5 times the median proportion of fragments in peaks. min_depth is set to the maximum of 500 or 10 median library size.

Value

indices of samples to keep

See Also

`getCounts`, `getPeaks`, `filterPeaks`

Examples

```
data(example_counts, package = "chromVAR")

counts_filtered <- filterSamples(example_counts, min_depth = 1500,
                                 min_in_peaks = 0.15, shiny = FALSE)
```

filterSamplesPlot *filterSamplesPlot*

Description

plot filtering of samples

Usage

```
filterSamplesPlot(object, min_in_peaks = NULL, min_depth = NULL,
  use_plotly = interactive())
```

Arguments

object	SummarizedExperiment with matrix of fragment counts per peak per sample, as computed by getCounts
min_in_peaks	minimum fraction of samples within peaks
min_depth	minimum library size
use_plotly	make interactive plot?

Details

If unspecified, min_in_peaks and min_depth cutoffs will be estimated based on data. min_in_peaks is set to 0.5 times the median proportion of fragments in peaks. min_depth is set to the maximum of 500 or 10 median library size.

Value

indices of samples to keep

See Also

getCounts, getPeaks, filterPeaks

Examples

```
data(example_counts, package = "chromVAR")

counts_filtered <- filterSamples(example_counts, min_depth = 1500,
                                 min_in_peaks = 0.15, shiny = FALSE)
counts_filtered_plot <- filterSamplesPlot(counts_filtered,
                                          min_in_peaks = 0.15,
                                          min_depth = 1500,
                                          use_plotly = FALSE)
```

getAnnotationCorrelation
getAnnotationCorrelation

Description

getAnnotationCorrelation

Usage

```
getAnnotationCorrelation(object, annotations, ...)


  ## S4 method for signature 'SummarizedExperiment,SummarizedExperiment'
getAnnotationCorrelation(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL)


  ## S4 method for signature 'SummarizedExperiment,MatrixOrmatrix'
getAnnotationCorrelation(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL)

## S4 method for signature 'SummarizedExperiment,list'
getAnnotationCorrelation(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL)


  ## S4 method for signature 'MatrixOrmatrix,SummarizedExperiment'
getAnnotationCorrelation(object,
  annotations, background_peaks, expectation = computeExpectations(object),
  variabilities = NULL)

## S4 method for signature 'MatrixOrmatrix,MatrixOrmatrix'
getAnnotationCorrelation(object,
  annotations, background_peaks, expectation = computeExpectations(object),
  variabilities = NULL)

## S4 method for signature 'MatrixOrmatrix,list'
getAnnotationCorrelation(object, annotations,
  background_peaks, expectation = computeExpectations(object),
  variabilities = NULL)
```

Arguments

object	result from computeDeviations
annotations	SummarizedExperiment of annotation matches
...	additional arguments
background_peaks	optional, matrix of background peaks
expectation	optional, expected fraction of reads per peak, as computed by computeExpectations
variabilities	optional, variabilities computed from computeVariability

Details

should only be run on small number of motifs/kmers/peaksets (very slow!)

Value

correlation matrix

Methods (by class)

- object = SummarizedExperiment,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = SummarizedExperiment,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = SummarizedExperiment,annotations = list: object is SummarizedExperiment, annotations are list
- object = MatrixOrmatrix,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = MatrixOrmatrix,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = MatrixOrmatrix,annotations = list: object is SummarizedExperiment, annotations are list

---

getAnnotations *getAnnotations*

Description

getAnnotations

Usage

```
getAnnotations(annotations, ...)

## S4 method for signature 'GRangesList'
getAnnotations(annotations, rowRanges, ...)

## S4 method for signature 'MatrixOrmatrix'
getAnnotations(annotations, ...)

## S4 method for signature 'data.frame'
getAnnotations(annotations, ...)

## S4 method for signature 'list'
getAnnotations(annotations, npeaks = NULL, ...)

## S4 method for signature 'character'
getAnnotations(annotations, rowRanges, column = NULL,
  ...)
```

Arguments

annotations	matrix, Matrix, or data.frame of fragment counts, or SummarizedExperiment with counts assays, see details
...	additional arguments to pass to SummarizedExperiment
rowRanges	GenomicRanges or GenomicRangesList or RangedSummarizedExperiment
npeaks	number of peaks
column	column of bed file with annotation names, see details

Value

SummarizedExperiment object with 'matches' assay

Methods (by class)

- GRangesList: get annotation matrix from GRangesList
- MatrixOrmatrix: get annotation matrix from Matrix or matrix
- data.frame: get annotation matrix from data.frame
- list: get annotation matrix from list
- character: get annotations from bed files

Author(s)

Alicia Schep

Examples

```
# First get example counts
data(mini_counts, package = "chromVAR")

# Get annotations from genomic ranges list
library(GenomicRanges)
library(SummarizedExperiment)
my_annotation_granges <- GRangesList(GRanges("chr1",
                                             ranges = IRanges(start =
                                             c(566763,805090), width = 8)),
                                     GRanges("chr1", ranges = IRanges(start =
                                               c(566792,895798), width = 8)))
anno_ix <- getAnnotations(my_annotation_granges,
                          rowRanges = rowRanges(mini_counts))
```

---

getAnnotationSynergy *getAnnotationSynergy*

Description

getAnnotationSynergy

Usage

```
getAnnotationSynergy(object, annotations, ...)


  ## S4 method for signature 'SummarizedExperiment,SummarizedExperiment'
getAnnotationSynergy(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL,
  nbg = 25)

## S4 method for signature 'SummarizedExperiment,MatrixOrmatrix'
getAnnotationSynergy(object,
  annotations, background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL,
  nbg = 25)

## S4 method for signature 'SummarizedExperiment,list'
getAnnotationSynergy(object, annotations,
  background_peaks = getBackgroundPeaks(object),
  expectation = computeExpectations(object), variabilities = NULL,
  nbg = 25)

## S4 method for signature 'MatrixOrmatrix,SummarizedExperiment'
getAnnotationSynergy(object,
```

```
  annotations, background_peaks, expectation = computeExpectations(object),
  variabilities = NULL, nbg = 25)

## S4 method for signature 'MatrixOrmatrix,MatrixOrmatrix'
getAnnotationSynergy(object,
  annotations, background_peaks, expectation = computeExpectations(object),
  variabilities = NULL, nbg = 25)

## S4 method for signature 'MatrixOrmatrix,list'
getAnnotationSynergy(object, annotations,
  background_peaks, expectation = computeExpectations(object),
  variabilities = NULL, nbg = 25)
```

Arguments

object	result from computeDeviations
annotations	SummarizedExperiment of annotation matches
...	additional arguments
background_peaks	optional, matrix of background peaks
expectation	optional, expected fraction of reads per peak, as computed by computeExpectations
variabilities	optional, variabilities computed from computeVariability
nbg	number of background iterations

Details

should only be run on small number of motifs/kmers/peaksets (very slow!)

Value

synergy matrix

Methods (by class)

- object = SummarizedExperiment,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = SummarizedExperiment,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = SummarizedExperiment,annotations = list: object is SummarizedExperiment, annotations are list
- object = MatrixOrmatrix,annotations = SummarizedExperiment: object and annotations are SummarizedExperiment
- object = MatrixOrmatrix,annotations = MatrixOrmatrix: object is SummarizedExperiment, annotations are Matrix
- object = MatrixOrmatrix,annotations = list: object is SummarizedExperiment, annotations are list

getBackgroundPeaks *getBackgroundPeaks*

Description

Function to get a set of background peaks for each peak based on GC content and # of fragments across all samples

Usage

```
getBackgroundPeaks(object, ...)

## S4 method for signature 'SummarizedExperiment'
getBackgroundPeaks(object,
  bias = rowData(object)$bias, niterations = 50, w = 0.1, bs = 50)

## S4 method for signature 'RangedSummarizedExperiment'
getBackgroundPeaks(object,
  bias = rowRanges(object)$bias, niterations = 50, w = 0.1, bs = 50)

## S4 method for signature 'MatrixOrmatrix'
getBackgroundPeaks(object, bias, niterations = 50,
  w = 0.1, bs = 50)
```

Arguments

object	fragment counts as SummarizedExperiment, RangedSummarized, Matrix, or matrix
...	addtional arguments
bias	vector of values for some bias signal for each row of object
niterations	number of background peaks to sample
w	parameter controlling similarity of background peaks
bs	bin size parameter

Details

Background peaks are chosen by sampling peaks based on similarity in GC content and # of fragments across samples using the Mahalanobis distance. The w paramter controls how similar background peaks should be. The bs parameter controls the precision with which the similarity is computed; increasing bs will make the function run slower. Sensible default parameters are chosen for both.

Value

matrix with one row per peak and one column per iteration. values in a row represent indices of background peaks for the peak with that index

Methods (by class)

- SummarizedExperiment: method for SummarizedExperiment
- RangedSummarizedExperiment: method for RangedSummarizedExperiment
- MatrixOrmatrix: method for Matrix or matrix

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")

# get background peaks
bgpeaks <- getBackgroundPeaks(mini_counts)
```

---

getCisGroups *getCisGroups*

Description

Function for grouping peaks based on proximity along chromosomes

Usage

```
getCisGroups(object, ...)

## S4 method for signature 'RangedSummarizedExperiment'
getCisGroups(object, grpsize = 25,
  stepsize = 10)

## S4 method for signature 'GenomicRanges'
getCisGroups(object, grpsize = 25, stepsize = 10)
```

Arguments

object	GenomicRanges or RangedSummarizedExperiment
...	additional arguments
grpsize	number of peaks to include in each grouop
stepsize	number of peaks between each new set of groups

Value

SummarizedExperiment with annotationMatches assay storing which peaks belong to which groups

Methods (by class)

- RangedSummarizedExperiment: method for RangedSummarizedExperiment
- GenomicRanges: method for GenomicRanges

Author(s)

Alicia Schep

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
mini_counts <- sort(mini_counts)
cisg <- getCisGroups(mini_counts)
```

`getCounts` *getCounts*

Description

makes matrix of fragment counts in peaks using one or multiple bam or bed files

Usage

```
getCounts(alignment_files, peaks, paired, by_rg = FALSE, format = c("bam",
  "bed"), colData = NULL)
```

Arguments

`alignment_files`	filenames for bam or bed files with aligned reads
`peaks`	GRanges object with peaks
`paired`	paired end data?
`by_rg`	use RG tags in bam to separate groups?
`format`	bam or bed? default is bam
`colData`	sample annotation DataFrame

Value

`RangedSummarizedExperiment-class` object

See Also

`getSampleDepths`, `getPeaks`, `filterSamples`

Examples

```
# First we'll read in some peaks
peaks_file <- system.file("extdata", "test_bed.txt", package = "chromVAR")
test_peaks <- getPeaks(peaks_file, sort = TRUE)

# With single bam with RG tags (can also give multiple bams with RG)
test_rg <- system.file("extdata", "test_RG.bam", package = "chromVAR")
test_counts <- getCounts(test_rg, peaks = test_peaks, by_rg = TRUE,
                         paired = TRUE,
                         colData = S4Vectors::DataFrame(condition ="A"))


# Multiple bams without RG tags
test_bam1 <- system.file("extdata", "test_single1.bam", package = "chromVAR")
test_bam2 <- system.file("extdata", "test_single2.bam", package = "chromVAR")
test_bam3 <- system.file("extdata", "test_single3.bam", package = "chromVAR")
test_counts2 <- getCounts(c(test_bam1, test_bam2,test_bam3),
                          peaks = test_peaks, by_rg = FALSE,
                          paired = TRUE,
                          colData = S4Vectors::DataFrame(celltype =
                                                  c("A","B","C")))

# Bed file with reads (can give multiple bed files, here we will just read 1)
test_bed <- system.file("extdata", "test_reads.bed", package = "chromVAR")
test_counts3 <- getCounts(test_bed, test_peaks, by_rg = FALSE,
                          paired = FALSE,
                          format = "bed")
```

`getFragmentsPerPeak` *getFragmentsPerPeak*

Description

getFragmentsPerPeak

Usage

```
getFragmentsPerPeak(object)

## S4 method for signature 'SummarizedExperiment'
getFragmentsPerPeak(object)

## S4 method for signature 'MatrixOrmatrix'
getFragmentsPerPeak(object)
```

Arguments

`object`	SummarizedExperiment, matrix, or Matrix object

Value

vector with sum across rows of counts assay within chromVARCounts

Methods (by class)

- `SummarizedExperiment`: method for SummarizedExperiment object with counts assay
- `MatrixOrmatrix`: method for Matrix or matrix object

See Also

`getFragmentsPerSample`, `getTotalFragments`

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")

frags_per_peak <- getFragmentsPerPeak(mini_counts)
```

`getFragmentsPerSample` *getFragmentsPerSample*

Description

getFragmentsPerSample

Usage

```
getFragmentsPerSample(object)

## S4 method for signature 'SummarizedExperiment'
getFragmentsPerSample(object)

## S4 method for signature 'MatrixOrmatrix'
getFragmentsPerSample(object)
```

Arguments

`object`	SummarizedExperiment, matrix, or Matrix object

Value

vector with sum across columns of counts assay within chromVARCounts

Methods (by class)

- `SummarizedExperiment`: method for SummarizedExperiment object with counts assay
- `MatrixOrmatrix`: method for Matrix or matrix object

See Also

getFragmentsPerPeak, getTotalFragments

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
frags_per_sample <- getFragmentsPerSample(mini_counts)
```

---

getJasparMotifs *getJasparMotifs*

Description

Function to get motifs from JASPAR database

Usage

```
getJasparMotifs(species = "Homo sapiens", collection = "CORE", ...)
```

Arguments

species	Which species? use eithe jaspar code or latin name. default is 'Homo sapiens'
collection	Which collection to use? default is 'CORE'
...	additional arguments to opts for getMatrixSet

Details

Simply a wrapper function for getMatrixSet that calls JASPAR2016 database using JASPAR2016

Value

PFMatrixList

Examples

```
motifs <- getJasparMotifs()
```

getPeaks *getPeaks*

Description

Read in peaks from a bed file.

Usage

```
getPeaks(filename, extra_cols = c(), sort_peaks = FALSE)
```

Arguments

filename	filename of bed file
extra_cols	extra columns to read in beyond first three
sort_peaks	sort the peaks?

Details

As in standard definition of bed file, first column is assumed to be chromosome, second is assumed to be start of peak (0-based), and third is assumed to be end of peak (1-based). Note that in output GenomicRanges output, start and end indices are both 1-based. Extra columns can be added as metadata or strand information if provided, but the user must indicate column index and name using named vector for extra_cols.

Value

GenomicRanges containing peaks from file

See Also

getCounts, filterPeaks, readNarrowpeaks

Examples

```
peaks_file <- system.file("extdata", "test_bed.txt", package = "chromVAR")
peaks <- getPeaks(peaks_file, sort = TRUE)
```

getPermutedData *getPermutedData*

Description

Function to get permuted data while maintaining biases

Usage

```
getPermutedData(object, niterations = 10, w = 0.1, bs = 50)
```

Arguments

object	SummarizedExperiment
niterations	number of background peaks to sample
w	parameter controlling similarity of background peaks
bs	bin size parameter

Details

Replaces the counts at a given peak with the count from another peak with similar GC content and average accessibility

Value

new SummarizedExperiment with addition assays representing permuted version of counts

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")

# get background peaks
perm_counts <- getPermutedData(mini_counts, niterations = 2)
```

getSampleCorrelation *getSampleCorrelation*

Description

Get correlation between samples based on bias corrected deviations

Usage

```
getSampleCorrelation(object, threshold = 1.5)
```

Arguments

object	deviations result
threshold	threshold for variability

Details

This function will compute the correlation between samples based on the normalized deviations. It will first remove correlated motifs/peak sets. Then the pearson correlation coefficient will be computed and returned.

Value

correlation matrix between samples

Author(s)

Alicia Schep

See Also

getSampleDistance

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
sample_cor <- getSampleCorrelation(mini_dev, threshold = 0.8)
# setting very low variabilitiy threshold because this is mini data set
# threshold should generally be above 1
# Use plotVariability to get a sense of an appropriate threshold
# As this is mini data set, results probably not meaningful!
```

getSampleDepths *getSampleDepths*

Description

makes vector of read depths in bam files or RG groups within bam files

Usage

```
getSampleDepths(alignment_files, paired = TRUE, by_rg = FALSE,
  format = c("bam", "bed"))
```

Arguments

alignment_files	filenames for bam or bed file(s) with aligned reads
paired	paired end data?
by_rg	use RG tags to separate groups?
format	bam or bed format? default is bam

Value

numeric vector

See Also

getCounts, filterSamples

Examples

```
# With single bam with RG tags (can also give multiple bams with RG)
test_rg <- system.file("extdata", "test_RG.bam", package = "chromVAR")
test_counts <- getSampleDepths(test_rg,  by_rg = TRUE,
                          paired = TRUE)


# Multiple bams without RG tags
test_bam1 <- system.file("extdata", "test_single1.bam", package = "chromVAR")
test_bam2 <- system.file("extdata", "test_single2.bam", package = "chromVAR")
test_bam3 <- system.file("extdata", "test_single3.bam", package = "chromVAR")
test_counts2 <- getSampleDepths(c(test_bam1, test_bam2,test_bam3),
                           by_rg = FALSE,
                           paired = TRUE)
```

getSampleDistance *getSampleDistance*

Description

Get distance between samples based on bias corrected deviations

Usage

```
getSampleDistance(object, threshold = 1.5, initial_dims = 50,
  distance_function = dist)
```

Arguments

object	deviations result
threshold	threshold for variability
initial_dims	initial dimentions for preliminary dimensionality reduction via pca
distance_function	distance function to use

Details

This function will compute the distance between samples based on the normalized deviations. It will first remove correlated motifs / peak sets. Then the dimensionality will be further reduced via PCA if the number of dimensions exceeds initial_dims. Then the supplied distance_function will be used.

Value

dist object for distance between samples

Author(s)

Alicia Schep

See Also

getSampleCorrelation

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
sample_dist <- getSampleDistance(mini_dev, threshold = 0.8)
# setting very low variabilitiy threshold because this is mini data set
# threshold should generally be above 1
# Use plotVariability to get a sense of an appropriate threshold
# As this is mini data set, results  not meaningful!
```

getTotalFragments *getTotalFragments*

Description

getTotalFragments

Usage

```
getTotalFragments(object)

## S4 method for signature 'SummarizedExperiment'
getTotalFragments(object)

## S4 method for signature 'MatrixOrmatrix'
getTotalFragments(object)
```

Arguments

object	SummarizedExperiment, matrix, or Matrix object

Value

sum of all counts within object

Methods (by class)

- SummarizedExperiment: method for SummarizedExperiment object with counts assay
- MatrixOrmatrix: method for Matrix or matrix object

See Also

getFragmentsPerSample, getFragmentsPerPeak

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
total_frags <- getTotalFragments(mini_counts)
```

makeBiasBins *makeBiasBins*

Description

Makes bins based on fragment counts

Usage

```
makeBiasBins(object, ...)

## S4 method for signature 'SummarizedExperiment'
makeBiasBins(object,
  bias = rowData(object)$bias, nbins = 25, frac = 0.3)

## S4 method for signature 'RangedSummarizedExperiment'
makeBiasBins(object,
  bias = rowRanges(object)$bias, nbins = 25, frac = 0.3)

## S4 method for signature 'MatrixOrmatrix'
makeBiasBins(object, bias, nbins = 25,
  frac = 0.3)
```

Arguments

object	fragment counts stored as RangedSummarizedExperiment, SummarizedExperiment, matrix, or Matrix
...	addtional arguments
bias	vector of some bias signal (usually gc content) for each row of object
nbins	number of bins for each category, see Details
frac	fraction of peaks within given bin to select randomly

Details

Will create nbins * 3 annotations based on sampling from peaks with a certain fragment count, fragment count, or fragment count & bias.

Value

SummarizedExperiment storing bias bins annotation

Methods (by class)

- `SummarizedExperiment`: method for SummarizedExperiment
- `RangedSummarizedExperiment`: method for RangedSummarizedExperiment
- `MatrixOrmatrix`: method for Matrix or matrix

Author(s)

Alicia Schep

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
bb <- makeBiasBins(mini_counts)
```

---

makePermutedSets *makePermutedSets*

Description

Makes annotations sets with similar bias to input sets

Usage

```
makePermutedSets(object, annotations, ...)

## S4 method for signature 'SummarizedExperiment,SummarizedExperiment'
makePermutedSets(object,
  annotations, bias = rowData(object)$bias, window = 10)


  ## S4 method for signature 'RangedSummarizedExperiment,SummarizedExperiment'
makePermutedSets(object,
  annotations, bias = rowRanges(object)$bias, window = 10)

## S4 method for signature 'MatrixOrmatrix,SummarizedExperiment'
makePermutedSets(object,
  annotations, bias, window = 10)

## S4 method for signature 'SummarizedExperiment,MatrixOrmatrix'
makePermutedSets(object,
  annotations, bias = rowData(object)$bias, window = 10)

## S4 method for signature 'RangedSummarizedExperiment,MatrixOrmatrix'
makePermutedSets(object,
  annotations, bias = rowRanges(object)$bias, window = 10)

## S4 method for signature 'MatrixOrmatrix,MatrixOrmatrix'
makePermutedSets(object, annotations,
  bias, window = 10)

## S4 method for signature 'SummarizedExperiment,list'
makePermutedSets(object, annotations,
```

```
  bias = rowData(object)$bias, window = 10)

## S4 method for signature 'RangedSummarizedExperiment,list'
makePermutedSets(object,
  annotations, bias = rowRanges(object)$bias, window = 10)

## S4 method for signature 'MatrixOrmatrix,list'
makePermutedSets(object, annotations, bias,
  window = 10)
```

Arguments

object	fragment counts stored as RangedSummarizedExperiment, SummarizedExperiment, matrix, or Matrix
annotations	annotations as SummarizedExperiment, matrix, or list
...	additional arguments
bias	vector of some bias signal (usually gc content) for each row of object
window	number of nearest neighbors to consider

Details

Will create nbins * 3 annotations based on sampling from peaks with a certain fragment count, fragment count, or fragment count & bias.

Value

SummarizedExperiment storing bias bins annotation

Methods (by class)

- object = SummarizedExperiment,annotations = SummarizedExperiment: method for SummarizedExperiment and SummarizedExperiment
- object = RangedSummarizedExperiment,annotations = SummarizedExperiment: method for RangedSummarizedExperiment and SummarizedExperiment
- object = MatrixOrmatrix,annotations = SummarizedExperiment: method for Matrix or matrix and SummarizedExperiment
- object = SummarizedExperiment,annotations = MatrixOrmatrix: method for SummarizedExperiment and MatrixOrmatrix
- object = RangedSummarizedExperiment,annotations = MatrixOrmatrix: method for RangedSummarizedExperiment and MatrixOrmatrix
- object = MatrixOrmatrix,annotations = MatrixOrmatrix: method for Matrix/matrix and Matrix/matrix
- object = SummarizedExperiment,annotations = list: method for SummarizedExperiment and list
- object = RangedSummarizedExperiment,annotations = list: method for RangedSummarizedExperiment and list
- object = MatrixOrmatrix,annotations = list: method for Matrix or matrix and list

Author(s)

Alicia Schep

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")
data(example_motifs, package = "motifmatchr")
library(motifmatchr)
library(BSgenome.Hsapiens.UCSC.hg19)
motif_ix <- matchMotifs(example_motifs, mini_counts,
                        genome = BSgenome.Hsapiens.UCSC.hg19)

perm_sets <- makePermutedSets(mini_counts, motif_ix)
```

---

matchKmers *matchKmers*

Description

Find kmer matches in the DNA string-based subject

Usage

```
matchKmers(k, subject, ...)

## S4 method for signature 'character,DNAStringSet'
matchKmers(k, subject, out = c("matches",
  "positions"), ranges = NULL)

## S4 method for signature 'character,character'
matchKmers(k, subject, out = c("matches",
  "positions"), ranges = NULL)

## S4 method for signature 'character,DNAString'
matchKmers(k, subject, out = c("matches",
  "positions"), ranges = NULL)

## S4 method for signature 'character,GenomicRanges'
matchKmers(k, subject,
  genome = GenomeInfoDb::genome(subject), out = c("matches", "positions"))

## S4 method for signature 'character,RangedSummarizedExperiment'
matchKmers(k, subject, ...)

## S4 method for signature 'numeric,ANY'
matchKmers(k, subject, ...)
```

```
## S4 method for signature 'DNAStringSet,ANY'
matchKmers(k, subject, ...)

## S4 method for signature 'DNAString,ANY'
matchKmers(k, subject, ...)
```

Arguments

k	k
subject	either GenomicRanges, DNAStringSet, DNAString, or character vector
...	additional arguments
out	what to return? see details
ranges	if subject is not GenomicRanges, ranges to use when out is positions
genome	BSgenome object, only used if subect is GenomicRanges

Details

Can either return a SummarizedExperiment with just sparse matrix with values set to 1 for a match (if return == 'matches'), or a GenomicRanges object with all the positions of matches

Value

SummarizedExperiment with matches assay storing which peaks contain which kmers

Methods (by class)

- k = character, subject = DNAStringSet: For DNAStringSet Objects
- k = character, subject = character: For character strings
- k = character, subject = DNAString: For DNA String objects
- k = character, subject = GenomicRanges: For GenomicRanges
- k = character, subject = RangedSummarizedExperiment: For RangedSummarizedExperiment (containing GRanges in rowRanges)
- k = numeric, subject = ANY: Catch-all for other un-documented types
- k = DNAStringSet, subject = ANY: Catch-all for other un-documented types with DNAStringSet
- k = DNAString, subject = ANY: Catch-all for other un-documented types with DNAString

See Also

getAnnotations, computeDeviations

Examples

```
# Load very small example counts (already filtered)
data(mini_counts, package = "chromVAR")

# Get peak-kmer annotation matrix for 6mers
library(BSgenome.Hsapiens.UCSC.hg19)
kmer_ix <- matchKmers(6, mini_counts,
                      genome = BSgenome.Hsapiens.UCSC.hg19)
```

`mini_counts` *mini_counts*

Description

Tiny sample data set for chromVAR funtion examples

Usage

```
data(mini_counts)
```

Value

RangedSummarizedExperiment

See Also

mini_dev, mini_ix

Examples

```
data(mini_counts)
```

`mini_dev` *mini_dev*

Description

Tiny sample chromVARDeviations object resulting from computeDeviations Result from running computeDeviations(mini_counts, mini_ix) on mini_ix and mini_counts data from this package

Usage

```
data(mini_dev)
```

Value

chromVARDeviations-class

See Also

computeDeviations, mini_counts, mini_ix

Examples

```
data(mini_dev)
```

---

mini_ix *mini_ix*

Description

Tiny sample annotation object for use in chromVAR examples Result from running matchMotifs(example_motifs,mini_counts,"hg19) on example_motifs from motifmatchr package and mini_counts from this package

Usage

```
data(mini_ix)
```

Value

RangedSummarizedExperiment

See Also

mini_counts, mini_dev

Examples

```
data(mini_ix)
```

---

plotDeviationsTsne *plotDeviationsTsne*

Description

plots sample similarity tsne

Usage

```
plotDeviationsTsne(object, tsne, var_df = NULL, sample_column = NULL,
  annotation_name = NULL, shiny = interactive())
```

Arguments

object	deviations result object
tsne	result from deviationsTsne
var_df	variability result
sample_column	column name for sample data – colData(object) – to be used for coloring points
annotation_name	name of chromVAR annotation for coloring points
shiny	return shiny app? otherwise return static plots

Value

shiny app or plots

Author(s)

Alicia Schep

---

plotKmerMismatch *plotKmerMismatch*

Description

plotKmerMismatch

Usage

```
plotKmerMismatch(kmer, cov_mat, pval = 0.01)
```

Arguments

kmer	kmer, e.g. 'AAAAAAA'
cov_mat	result from deviationsCovariability
pval	p value threshold

Value

A plot

plotVariability *plotVariability*

Description

plot variability of motifs/etc

Usage

```
plotVariability(variability, xlab = "Sorted TFs", n = 3,
  labels = variability$name, use_plotly = interactive())
```

Arguments

variability	output from computeVariability
xlab	label for x-axis (default is 'Sorted TFs')
n	number of toppoints to label?
labels	names of sets. if not given, uses rownames of variability
use_plotly	make plot interactive (using plotly)

Value

ggplot or plotly object, depending on whether use_plotly is TRUE

Author(s)

Alicia Schep

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
variability <- computeVariability(mini_dev)
var_plot <- plotVariability(variability, use_plotly = FALSE)
```

pwmDistance *pwmDistance*

Description

computes distance between every pwm in a list or between pwms in one list with pwms in another

Usage

```
pwmDistance(x, y = NULL, min_overlap = 5)
```

Arguments

x	list of pwms or pfms, see Details
y	list of pwms or pfms, see Details
min_overlap	minimum number of basepairs overlapping between motifs

Details

The format of x and y should be a PWMatrixList or PFMatrixList or a list of matrices with rows corresponding to "A","C","G","T" and columns summing to 1.

Value

a list with three matrices- 'dist' has the distance between each pair of motifs, 'strand' has the strand of the motif for the match, and 'offset' has the offset between the motifs.

Examples

```
motifs <- getJasparMotifs()
library(TFBSTools)
pwm_dists <- pwmDistance(toPWM(motifs[[1]]), toPWM(motifs[[2]]))
```

---

rbind,chromVARDeviations-method

rbind method chromVARDeviations

Description

Concatenates chromVARDeviations results for different sets of annotations

Usage

```
## S4 method for signature 'chromVARDeviations'
rbind(..., deparse.level = 1)
```

Arguments

...	chromVARDeviations object to be combined
deparse.level	See ?base::rbind for a description of this argument.

Value

chromVARDeviations object

Author(s)

Alicia Schep

See Also

chromVARDeviations-class

Examples

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
doubledev <- rbind(mini_dev, mini_dev) #concatenate two of the same tother
```

---

readNarrowpeaks *readNarrowpeaks*

Description

Reads in peaks in narrowpeaks format, as output by macs2. Uses summit as center of peak, and makes peak the given 'width'. By default removes overlapping peaks to get set of peaks with no overlaps

Usage

```
readNarrowpeaks(filename, width = 500, non_overlapping = TRUE)
```

Arguments

filename	filename
width	desired width of peaks
non_overlapping	remove overlapping peaks

Value

GRanges-class

Index