Package ‘chromVAR’

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Type Package

Title Chromatin Variation Across Regions

Version 1.26.0

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

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LinkingTo Rcpp, RcppArmadillo

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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 default 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

addGCBias
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

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 Sum-
marizedExperiment

Value

logical matrix of annotation matches
assembleKmers

Author(s)
Alicia Schep

Examples

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

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>kmer chromVARDeviations object</td>
</tr>
<tr>
<td>threshold</td>
<td>variability threshold</td>
</tr>
<tr>
<td>p</td>
<td>p value threshold for inclusion of kmer</td>
</tr>
<tr>
<td>progress</td>
<td>show progress bar?</td>
</tr>
</tbody>
</table>

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

```r
## 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

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

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

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))
computeDeviations

Arguments

- **object**: chromVARCounts object
- **annotations**: chromVARAnnotations object
- **background_peaks** (optional): background peaks matrix computed using `getBackgroundPeaks`, computed internally with default parameters 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`
## computeExpectations

**Examples**

```r
# 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)
```

### Description

This function computes the expected fraction of reads per peak as 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

### Usage

```r
computeExpectations(object, ...)
```

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

### 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 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(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)
Description
Accessor for bias corrected deviations from 
\texttt{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)

Description
Accessor for deviation Z-scores from \texttt{chromVARDeviations-class} object

Usage
deviationScores(object)

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

Arguments
object deviationScores object

Value

Author(s)
Alicia Schep

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

```r
# 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,])
```

Description

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

Usage

```r
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

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 group 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")

data(example_counts)

Description

Very small sample data set for trying out chromVAR

Usage

data(example_counts)
filterPeaks

Value

RangedSummarizedExperiment

Examples

data(example_counts)

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 fragments 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

ggetPeaks, filterSamples, getCounts
Examples

```r
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)
```

Description

function to get indices of samples that pass filters

Usage

```r
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

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

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

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 = getBackgroundPeaks(object),
  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)
getAnnotations

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`
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
getAnnotationSynergy

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))

describe(getAnnotationSynergy)
Usage

getAnnotationSynergy(object, annotations, ...)

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

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

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

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

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

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

```r
## 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
- `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

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
...
  additional 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 parameter 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
getCisGroups

Methods (by class)

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

Examples

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

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

Description

Function for grouping peaks based on proximity along chromosomes

Usage

```r
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 group
- `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)

description

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

Usage

gETCHNUMTS(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

gETCHSampleDepths, gETCHPeaks, filterSamples
Examples

```r
# 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")
```

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
getFragmentsPerSample

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)

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
getJasparMotifs

See Also

getFragmentsPerPeak, getTotalFragments

Examples

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

getJasparMotifs

Description

Function to get motifs from JASPAR database

Usage

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

Arguments

species Which species? use either 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

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)
Description

Function to get permuted data while maintaining biases

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>SummarizedExperiment</td>
</tr>
<tr>
<td>niterations</td>
<td>number of background peaks to sample</td>
</tr>
<tr>
<td>w</td>
<td>parameter controlling similarity of background peaks</td>
</tr>
<tr>
<td>bs</td>
<td>bin size parameter</td>
</tr>
</tbody>
</table>

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)
Description

Get correlation between samples based on bias corrected deviations

Usage

generateFunction(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

generateFunction

Examples

# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
sample_cor <- generateFunction(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

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

g 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

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 dimensions 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

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)
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
...
        additional 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
**makePermutedSets**

**Author(s)**
Alicia Schep

**Examples**

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

**Description**

Makes annotations sets with similar bias to input sets

**Usage**

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

## S4 method for signature 'SummarizedExperiment,SummarizedExperiment'

```r
makePermutedSets(object,
  annotations, bias = rowData(object)$bias, window = 10)
```

## S4 method for signature 'RangedSummarizedExperiment,SummarizedExperiment'

```r
makePermutedSets(object,
  annotations, bias = rowRanges(object)$bias, window = 10)
```

## S4 method for signature 'MatrixOrmatrix,SummarizedExperiment'

```r
makePermutedSets(object,
  annotations, bias, window = 10)
```

## S4 method for signature 'SummarizedExperiment,MatrixOrmatrix'

```r
makePermutedSets(object,
  annotations, bias = rowData(object)$bias, window = 10)
```

## S4 method for signature 'RangedSummarizedExperiment,MatrixOrmatrix'

```r
makePermutedSets(object,
  annotations, bias = rowRanges(object)$bias, window = 10)
```

## S4 method for signature 'MatrixOrmatrix,MatrixOrmatrix'

```r
makePermutedSets(object, annotations,
  bias, window = 10)
```

## S4 method for signature 'SummarizedExperiment,list'

```r
makePermutedSets(object, annotations,
  window = 10)
```
makePermutedSets

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)

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**: 
  - numeric, subject = DNAStringSet: For DNAStringSet Objects
  - numeric, subject = ANY: Catch-all for other un-documented types
  - DNAStringSet, subject = ANY: Catch-all for other un-documented types with DNAStringSet
  - DNAString, subject = ANY: Catch-all for other un-documented types with DNAString

- **subject**: 
  - either GenomicRanges, DNAStringSet, DNAString, or character vector
  - DNAStringSet, subject = ANY: Catch-all for other un-documented types with DNAStringSet
  - DNAString, subject = ANY: Catch-all for other un-documented types with DNAString

- **...**: 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 subject 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)

Description

Tiny sample data set for chromVAR function examples

Usage

data(mini_counts)

Value

RangedSummarizedExperiment

See Also

mini_dev, mini_ix

Examples

data(mini_counts)

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
plotDeviationsTsne

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())
plotKmerMismatch

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

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

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

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

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

---

**Description**

Concatenates chromVARDeviations results for different sets of annotations

**Usage**

```r
## 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

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

```
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

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

Arguments

- `filename`: filename
- `width`: desired width of peaks
- `non_overlapping`: remove overlapping peaks

Value

- `GRanges-class`
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