

Package ‘chromVAR’

February 19, 2025

Type Package

Title Chromatin Variation Across Regions

Version 1.29.0

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

LazyData TRUE

LinkingTo Rcpp, RcppArmadillo

SystemRequirements C++11

VignetteBuilder knitr

RoxygenNote 6.0.1

git_url <https://git.bioconductor.org/packages/chromVAR>

git_branch devel

git_last_commit 261e3b9

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-02-19

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|-----------|------------------|
| addGCBias | <i>addGCBias</i> |
|-----------|------------------|

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

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 | <i>assembleKmers</i> |
|---------------|----------------------|

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

| | |
|--------------------------|------------------|
| <code>base_size</code> | base font size |
| <code>base_family</code> | 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 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](#)

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 | <i>deviations</i> |
|------------|-------------------|

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 | <i>deviationScores</i> |
|-----------------|------------------------|

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 variability 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 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")
```

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 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

[getPeaks](#), [filterSamples](#), [getCounts](#)

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 |
| ... | 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

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 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)
```

`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

| | |
|------------------------------|---|
| <code>alignment_files</code> | filenames for bam or bed files with aligned reads |
| <code>peaks</code> | GRanges object with peaks |
| <code>paired</code> | paired end data? |
| <code>by_rg</code> | use RG tags in bam to separate groups? |
| <code>format</code> | bam or bed? default is bam |
| <code>colData</code> | 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)
```

| | |
|------------------------------|------------------------|
| <code>getJasparMotifs</code> | <i>getJasparMotifs</i> |
|------------------------------|------------------------|

Description

Function to get motifs from JASPAR database

Usage

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

Arguments

| | |
|-------------------------|--|
| <code>species</code> | Which species? use either jaspar code or latin name. default is 'Homo sapiens' |
| <code>collection</code> | Which collection to use? default is 'CORE' |
| <code>...</code> | 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 | <i>getPeaks</i> |
|----------|-----------------|

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 | <i>getPermutedData</i> |
|-----------------|------------------------|

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 variability 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 | <i>getSampleDepths</i> |
|-----------------|------------------------|

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 variability 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_fragments <- getTotalFragments(mini_counts)
```

| | |
|--------------|---------------------|
| makeBiasBins | <i>makeBiasBins</i> |
|--------------|---------------------|

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

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 $\text{nbins} * 3$ 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 'DNAStrngSet,ANY'
matchKmers(k, subject, ...)
```

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

Arguments

| | |
|---------|---|
| k | k |
| subject | either GenomicRanges , DNAStrngSet , DNAStrng , 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 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 = [DNAStrngSet](#): For [DNAStrngSet](#) Objects
- k = character, subject = character: For character strings
- k = character, subject = [DNAStrng](#): 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 = [DNAStrngSet](#), subject = ANY: Catch-all for other un-documented types with [DNAStrngSet](#)
- k = [DNAStrng](#), subject = ANY: Catch-all for other un-documented types with [DNAStrng](#)

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 | <i>mini_counts</i> |
|-------------|--------------------|

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)
```

| | |
|----------|-----------------|
| mini_dev | <i>mini_dev</i> |
|----------|-----------------|

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)
```

| | |
|----------------------|----------------|
| <code>mini_ix</code> | <i>mini_ix</i> |
|----------------------|----------------|

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)
```

| | |
|---------------------------------|---------------------------|
| <code>plotDeviationsTsne</code> | <i>plotDeviationsTsne</i> |
|---------------------------------|---------------------------|

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 [PWMMatrixList](#) 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 | <i>readNarrowpeaks</i> |
|-----------------|------------------------|

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](#)

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