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.
License MIT + file LICENSE
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
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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
annotationMatches

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)

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
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 the 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`

---

**Description**

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

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

*chromVARDeviations*

**Description**

Class for storing results from `computeDeviations` function.

**Details**

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

**chromVAR_theme**

*chromVAR_theme*

**Description**

theme for use with ggplot2, used by chromVAR plotting functions

**Usage**

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

**Arguments**

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

**Value**

ggplot2 theme

**Author(s)**

Alicia Schep

**Examples**

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

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
- **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)

dev

dev <- computeDeviations(object = mini_counts,
                           annotations = mini_ix)

dev

dev <- computeDeviations(object = mini_counts,
                           annotations = mini_ix)

computeExpectations

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

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

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

Description

function to compute overall variability of motif sets across samples

Usage

```r
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)

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

Accessor for bias corrected deviations from `chromVARDeviations-class` object

**Usage**

```r
deviations(object)
```

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

**Arguments**

- `object` chromVARDeviations object

**Value**

matrix of bias corrected deviations

**Author(s)**

Alicia Schep

**Examples**

```r
# 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 `chromVARDeviations-class` object

**Usage**

```r
deviationScores(object)
```

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

**Examples**

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

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(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 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")

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

getPeaks, 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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>SummarizedExperiment with matrix of fragment counts per peak per sample, as</td>
</tr>
<tr>
<td></td>
<td>computed by <code>getCounts</code></td>
</tr>
<tr>
<td>min_in_peaks</td>
<td>minimum fraction of samples within peaks</td>
</tr>
<tr>
<td>min_depth</td>
<td>minimum library size</td>
</tr>
<tr>
<td>shiny</td>
<td>make shiny gadget?</td>
</tr>
<tr>
<td>ix_return</td>
<td>return indices of sample to keep instead of subsetted counts object</td>
</tr>
</tbody>
</table>

**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, 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

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

```r
# 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))
```

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,
getAnnotationSynergy

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
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

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

# get background peaks
gbpeaks <- getBackgroundPeaks(mini_counts)

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)

Description

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

Usage

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

Arguments

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

Value

RangedSummarizedExperiment-class object

See Also

gtc, getSampleDepths, getPeaks, filterSamples
getFragmentsPerPeak

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")

description

getFragmentsPerPeak

Usage

getFragmentsPerPeak(object)

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

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

Arguments

object SummarizedExperiment, matrix, or Matrix object
Value

vector with sum across rows of counts assay within chromVARCounts

Methods (by class)

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

See Also

getFragmentsPerSample, getTotalFragments

Examples

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

frags_per_peak <- getFragmentsPerPeak(mini_counts)

getFragmentsPerSample  getFragmentsPerSample  

Description

getFragmentsPerSample

Usage

getFragmentsPerSample(object)

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

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

Arguments

object SummarizedExperiment, matrix, or Matrix object

Value

vector with sum across columns of counts assay within chromVARCounts

Methods (by class)

• SummarizedExperiment: method for SummarizedExperiment object with counts assay
• MatrixOrmatrix: method for Matrix or matrix object
See Also

getFragmentsPerPeak, getTotalFragments

Examples

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

getJasparMotifs

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()
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

```r
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

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

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

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)
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 dimention 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

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
Author(s)
Alicia Schep

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

makePermutedSets

Description
Makes annotations sets with similar bias to input sets

Usage
makePermutedSets(object, annotations, ...)

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

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

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

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

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

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

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

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

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

Arguments

object  
fragment counts stored as RangedSummarizedExperiment, SummarizedExperiment, matrix, or Matrix

annotations  
annotations as SummarizedExperiment, matrix, or list

...  
additional arguments

bias  
vector of some bias signal (usually gc content) for each row of object

window  
number of nearest neighbors to consider

Details

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

Value

SummarizedExperiment storing bias bins annotation

Methods (by class)

- object = SummarizedExperiment, annotations = SummarizedExperiment: method for SummarizedExperiment and SummarizedExperiment
- object = RangedSummarizedExperiment, annotations = SummarizedExperiment: method for RangedSummarizedExperiment and SummarizedExperiment
- object = MatrixOrmatrix, annotations = SummarizedExperiment: method for Matrix or matrix and SummarizedExperiment
- object = SummarizedExperiment, annotations = MatrixOrmatrix: method for SummarizedExperiment and MatrixOrmatrix
- object = RangedSummarizedExperiment, annotations = MatrixOrmatrix: method for Ranged-SummarizedExperiment 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
matchKmers

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

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,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, ...)
## matchKmers

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

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

### Arguments

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

```r
# 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

```r
data(mini_counts)
```

Value

`RangedSummarizedExperiment`

See Also

`mini_dev, mini_ix`

Examples

```r
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

```r
data(mini_dev)
```

Value

`chromVARDeviations-class`
See Also

computeDeviations, mini_counts, mini_ix

Examples

data(mini_dev)

---

**Description**

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

**Usage**

```r
data(mini_ix)
```

**Value**

*RangedSummarizedExperiment*

**See Also**

mini_counts, mini_dev

**Examples**

```r
data(mini_ix)
```

---

**Description**

plots sample similarity tsne

**Usage**

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

**Arguments**

- `object` deviation 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

---

**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 to other
```

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>filename</td>
<td>filename</td>
</tr>
<tr>
<td>width</td>
<td>desired width of peaks</td>
</tr>
<tr>
<td>non_overlapping</td>
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Value

`GRanges-class`
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