Package ‘chromVAR’

February 18, 2024

Type  Package
Title  Chromatin Variation Across Regions
Version  1.24.0
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
biocViews  SingleCell, Sequencing, GeneRegulation, ImmunoOncology
LazyData  TRUE
LinkingTo  Rcpp, RcppArmadillo
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VignetteBuilder  knitr
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Author Alicia Schep [aut, cre],
  Jason Buenrostro [ctb],
  Caleb Lareau [ctb],
  William Greenleaf [ths],
  Stanford University [cph]
Maintainer Alicia Schep <aschep@gmail.com>

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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(peak))

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)

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

annotationMatches

Description

annotationMatches

Usage

annotationMatches(object)

annotationMatches(object) <- value

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

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

Arguments

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

Details

Will extract matrix from the "matches", "annotationMatches", or "motif_matches" assay of a Sum-
marizedExperiment

Value

logical matrix of annotation matches
assembleKmers

Author(s)

Alicia Schep

Examples

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

assembleKmers

Description

function to create de novo motifs from kmers based on deviations

Usage

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

Arguments

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
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

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

Description

Class for storing results from `computeDeviations` function.

Details

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

chromVAR_theme

Description

theme for use with ggplot2, used by chromVAR plotting functions

Usage

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

Arguments

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

Value

ggplot2 theme

Author(s)

Alicia Schep

Examples

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

Description
Computes deviations in chromatin accessibility across sets of annotations

Usage

computeDeviations(object, annotations, ...)

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

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

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

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

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

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

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

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

Arguments

object  chromVARCounts object
annotations  chromVARAnnotations object
...  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
computeExpectations

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

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)
```

```r
computeVariability
```

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)
**deviations**

---

### 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)
```

---

**deviationScores**

---

### 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)
```
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

Description

deviationsCovariability

Usage

deviationsCovariability(object)

Arguments

object: deviations result

Details

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

Value

'covariability' matrix
## Examples

```r
# load very small example data
data(mini_counts, package = "chromVAR")
motifs <- getJasparMotifs()
library(motifmatchr)

motif_ix <- matchMotifs(motifs, mini_counts,
    genome = BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19)

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

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

## Description

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

## Usage

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

## Arguments

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

## Value

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

## Author(s)

Alicia Schep
Examples

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

tsne_res <- deviationsTsne(mini_dev, threshold = 0.8, shiny = FALSE)
# setting very low 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

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

genePeaks, filterSamples, getCounts
Examples

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

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

Description

function to get indices of samples that pass filters

Usage

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

Arguments

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

Details

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

Value

indices of samples to keep

See Also

`getCounts`, `getPeaks`, `filterPeaks`

Examples

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

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

plot filtering of samples

Usage

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

Arguments

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

Details

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

Value

indices of samples to keep

See Also

`getCounts`, `getPeaks`, `filterPeaks`

Examples

data(example_counts, package = "chromVAR")

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

Description

getAnnotationCorrelation

Usage

getAnnotationCorrelation(object, annotations, ...)

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

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

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

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

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

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

Arguments

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

Details

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

Value

correlation matrix

Methods (by class)

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

getAnnotations(annotations, ...)

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

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

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

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

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

Arguments

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

Value

SummarizedExperiment object with 'matches' assay

Methods (by class)

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

Author(s)

Alicia Schep
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

description

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

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

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

Description

Function for grouping peaks based on proximity along chromosomes

Usage

```r
getCisGroups(object, ...)
```

## S4 method for signature 'RangedSummarizedExperiment'

```r
cgetCisGroups(object, grpsize = 25,
    stepsize = 10)
```

## S4 method for signature 'GenomicRanges'

```r
cgetCisGroups(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

```r
# 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

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

Arguments

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

Value

*RangedSummarizedExperiment-class* object

See Also

*getSampleDepths, getPeaks, filterSamples*
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")

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
getFragmentsPerSample

Value

vector with sum across rows of counts assay within chromVARCounts

Methods (by class)

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

See Also

getFragmentsPerSample, getTotalFragments

Examples

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

frags_per_peak <- getFragmentsPerPeak(mini_counts)

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
getJasparMotifs

See Also

getFragmentsPerPeak, getTotalFragments

Examples

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

getJasparMotifs

Description

Function to get motifs from JASPAR database

Usage

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

Arguments

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

Details

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

Value

PFMatrixList

Examples

motifs <- getJasparMotifs()
getPeaks

description

Read in peaks from a bed file.

Usage

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

Arguments

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

details

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

Value

GenomicRanges containing peaks from file

see also

getCounts, filterPeaks, readNarrowpeaks

examples

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

Function to get permuted data while maintaining biases

Usage

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

Arguments

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)
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!
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

**Description**

Get distance between samples based on bias corrected deviations

**Usage**

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

**Arguments**

- `object`: deviations result
- `threshold`: threshold for variability
- `initial_dims`: initial dimensions for preliminary dimensionality reduction via pca
- `distance_function`: distance function to use

**Details**

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

**Value**

- `dist` object for distance between samples

**Author(s)**

Alicia Schep

**See Also**

- `getSampleCorrelation`

**Examples**

```
# Load very small example results from computeDeviations
data(mini_dev, package = "chromVAR")
sample_dist <- getSampleDistance(mini_dev, threshold = 0.8)
# setting very low 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
**makePermutatedSets**

**Author(s)**

Alicia Schep

**Examples**

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

**Description**

Makes annotations sets with similar bias to input sets

**Usage**

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

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

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

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

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

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

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

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

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

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

Arguments

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

Details

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

Value

SummarizedExperiment storing bias bins annotation

Methods (by class)

- object = SummarizedExperiment, annotations = SummarizedExperiment: method for SummarizedExperiment and SummarizedExperiment
- object = RangedSummarizedExperiment, annotations = SummarizedExperiment: method for RangedSummarizedExperiment and SummarizedExperiment
- object = MatrixOrmatrix, annotations = SummarizedExperiment: method for Matrix or matrix and SummarizedExperiment
- object = SummarizedExperiment, annotations = MatrixOrmatrix: method for SummarizedExperiment and MatrixOrmatrix
- object = RangedSummarizedExperiment, annotations = MatrixOrmatrix: method for RangedSummarizedExperiment and MatrixOrmatrix
- object = MatrixOrmatrix, annotations = MatrixOrmatrix: method for Matrix/matrix and Matrix/matrix
- object = SummarizedExperiment, annotations = list: method for SummarizedExperiment and list
- object = RangedSummarizedExperiment, annotations = list: method for RangedSummarizedExperiment and list
- object = MatrixOrmatrix, annotations = list: method for Matrix or matrix and list
**Author(s)**

Alicia Schep

**Examples**

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

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

**Description**

Find kmer matches in the DNA string-based subject

**Usage**

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

## S4 method for signature 'character,DNAStringSet'

```r
matchKmers(k, subject, out = c("matches", "positions"), ranges = NULL)
```

## S4 method for signature 'character,character'

```r
matchKmers(k, subject, out = c("matches", "positions"), ranges = NULL)
```

## S4 method for signature 'character,DNAString'

```r
matchKmers(k, subject, out = c("matches", "positions"), ranges = NULL)
```

## S4 method for signature 'character,GenomicRanges'

```r
matchKmers(k, subject, genome = GenomeInfoDb::genome(subject), out = c("matches", "positions"))
```

## S4 method for signature 'character,RangedSummarizedExperiment'

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

## S4 method for signature 'numeric,ANY'

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

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

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

Arguments

- **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`
mini_counts

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

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

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)

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)

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

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 `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

```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 tother
```

Description

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

Usage

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

Arguments

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

Value

- GRanges-class
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