Package ‘DEScan2’

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binnedCoverage

Description

This function computes the coverage over a binned chromosome, starting from a per base computed coverage.

Usage

binnedCoverage(
  bins,
  numvar,
  mcolname,
  covMethod = c("max", "mean", "sum", "min"),
  roundingMethod = c("none", "floor", "ceiling", "round")
)

Arguments

- `bins`: A GRanges object representing a chromosome binned.
- `numvar`: An RleList representing the per base coverage over the chr.
- `mcolname`: The name of column where the sum have to be stored.
- `covMethod`: A method to apply for the computing of the coverage. It can be one of "max", "mean", "sum", "min". ("max" is default)
- `roundingMethod`: A method to apply to round the computations. It can be one of "none", "floor", "ceiling", "round". It's useful only when using `covMethod="mean"`. ("none" is default)

Value

The bins GRanges with the mcolname attached

Examples

```r
## dividing one chromosome in bins of 50 bp each
seqinfo <- GenomeInfoDb::Seqinfo(genome="mm9")
bins <- GenomicRanges::tileGenome(
  seqlengths=GenomeInfoDb::seqlengths(seqinfo)[1],
  tilewidth=50,
  cut.last.tile.in.chrom=TRUE)
gr <- GenomicRanges::GRanges(seqnames = S4Vectors::Rle("chr1", 100),
  ranges=IRanges::IRanges(start = seq(from=10, to=1000, by=10),
  end=seq(from=20, to=1010, by = 10)))
cov <- GenomicRanges::coverage(x=gr)
(binnedMaxCovGR <- binnedCoverage(bins, cov, "binned_cov"))
(binnedMeanCovGR <- binnedCoverage(bins, cov, "binned_cov", covMethod="mean", roundingMethod="ceiling")
```
binnedCovOnly

Description

it's useful just to coerce the bin coverage to an Rle object

Usage

binnedCovOnly(bins, numvar, mcolname)

Arguments

bins a GRanges object representing a chromosome binned
numvar an RleList representing the per base coverage over the chr
mcolname the name of column where the sum have to be stored

Value

an Rle within the per bin computed coverage

binToChrCoordMatRowNames

Description

computes the starting range of the bins for the binMatrix, taking in input the length of the chromosome of the matrix.

Usage

binToChrCoordMatRowNames(binMatrix, chrLength, binWidth = 50)

Arguments

binMatrix a matrix where each row represents a bin.
chrLength the length of the chromosome of the binMatrix.
binWidth the width of the bin.

Value

the binMatrix with start range as rownames.
computeCoverageMovingWindowOnChr

**Description**

computes the coverage on a chromosome with a set of moving windows of dimensions minWinWidth:maxWinWidth

**Usage**

```r
computeCoverageMovingWindowOnChr(
  chrBedGRanges,
  minWinWidth = 50,
  maxWinWidth = 1000,
  binWidth = 50,
  verbose = TRUE
)
```

**Arguments**

- `chrBedGRanges` a GRanges to compute the coverage
- `minWinWidth` the minimum width of the window to use for the coverage
- `maxWinWidth` the maximum width of the window to use for the coverage
- `binWidth` the dimension of the bin in base number

**Value**

RleList where each element is a window within the Rle of its coverage

computeLambdaOnChr

**Description**

computes the lambdas on a chromosome for the winVector windows and other two windows (min/maxCompWinWidth) to compare with
Usage

computeLambdaOnChr(
  chrGRanges,
  winVector = seq_len(20),
  minChrRleWComp,
  minCompWinWidth = 5000,
  maxChrRleWComp,
  maxCompWinWidth = 10000,
  verbose = TRUE
)

Arguments

chrGRanges  the GRanges representing the reads of the chromosome.
winVector   the of width of the windows used to compute the coverage.
minChrRleWComp  and Rle object within coverage of window of width minCompWinWidth.
minCompWinWidth  the width of the window used for the coverage of minChrRleWComp in bases.
maxChrRleWComp  and Rle object within coverage of window of width minCompWinWidth.
maxCompWinWidth  the width of the window used for the coverage of maxChrRleWComp in bases.
verbose      verbose flag.
binSize      the size of the bin in bases.

Value

an RleList where each element is a window of winVector, within an Rle representing the lambda computed for that window.

computeZ  computeZ

Description

Computes Z-Scores returning the z matrix.

Usage

computeZ(
  lambdaChrRleList,
  runWinRleList,
  chrLength,
  minCount = 0.1,
  binSize = 50,
  verbose = FALSE
)
constructBedRanges

**Arguments**

lambdaChrRleList
an RleList of lambda values computed by computeLambdaOnChr function each element of the list is an Rle representing the lambda for the moving window in the list position.

runWinRleList
an RleList of coverage values computed by computeCoverageMovingWindowOnChr function each element of the list is an Rle representing the coverage for the moving window in the list position.

chrLength
the length of the chr in analysis.

minCount
A small constant (usually no larger than one) to be added to the counts prior to the log transformation to avoid problems with log(0).

binSize
the size of the bin.

verbose
verbose output.

**Value**

z a matrix of z scores for each window (column) and bin (row). where the rownames represent the starting base of each bin.

**Description**

Constructs a GRanges object from a bam/bed/bed.zip file in a consistent way.

**Usage**

constructBedRanges(
  filename,
  filetype = c("bam", "bed", "bed.zip", "narrow", "broad"),
  genomeName = NULL,
  onlyStdChrs = FALSE,
  arePeaks = FALSE,
  verbose = FALSE
)

**Arguments**

filename
the complete file path of a bam?bed file.

filetype
the file type bam/bed/bed.zip/narrow/broad.

genomeName
the name of the genome used to map the reads (i.e. "mm9"). N.B. if NOT NULL the GRanges Seqinfo will be forced to genomeName Seqinfo (needs Internet access, but strongly suggested!)

onlyStdChrs
flag to keep only standard chromosome.

arePeaks
flag indicating if the file contains peaks.

verbose
flag to obtain verbose output.
Value

a GRanges object.

Examples

```r
files <- list.files(system.file("extdata/bam/", package="DEScan2"), pattern="bam$", full.names=TRUE)
bgr <- constructBedRanges(files[1], filetype="bam", genomeName="mm9", onlyStdChrs=TRUE)
bgr
```

countFinalRegions

description

count reads falling within the final regions.

Usage

```r
countFinalRegions(
  regionsGRanges, 
  readsFilePath = NULL, 
  fileType = c("bam", "bed"), 
  minCarriers = 2, 
  genomeName = NULL, 
  onlyStdChrs = FALSE, 
  carrierscolname = "k-carriers", 
  ignStrandSO = TRUE, 
  modeSO = "Union", 
  saveFlag = FALSE, 
  savePath = "finalRegions", 
  verbose = TRUE 
)
```

Arguments

- `regionsGRanges`: a GRanges objects representing the peaks to compute the coverage, with a "k-carriers" mcols. (tipically generated by finalRegions function).
- `readsFilePath`: the filepath of bam or bed files necessary to compute the coverage.
- `fileType`: the file type of the input files.
- `minCarriers`: minimum number of carriers (samples).
- `genomeName`: code name of the genome of reads files (i.e. "mm9").
- `onlyStdChrs`: a flag indicating if to keep only the standard chromosomes.
createGranges

```r
createGranges
```  

**Description**

A simplified wrapper function to create a GRanges object.

**Usage**

```r
createGranges(chrSeqInfo, starts, widths, mcolname = NULL, mcolvalues = NULL)
```  

**Arguments**

- `chrSeqInfo`: a seqinfo object.
- `starts`: the start ranges.
- `widths`: the width of each range.
- `mcolname`: the name for the mcol attribute.
- `mcolvalues`: the values for the mcol attribute.
cutGRangesPerChromosome

Value

a GRanges object.

Examples

```r
chrSeqInfo <- GenomeInfoDb::Seqinfo(genome="mm9")["chr1"]
starts=sample(seq_len(100), 10)
widths=starts+10;
mcolname <- "z-score";
mcolvalues <- sample(seq_len(100), 10)
chrGR <- createGranges(chrSeqInfo=chrSeqInfo, starts=starts, widths=widths,
mcolname=mcolname, mcolvalues=mcolvalues)
```

cutGRangesPerChromosome

```r
cutGRangesPerChromosome(GRanges)
```

Description

takes in input a GRanges object, producing a LIST of GRanges, one for each chromosome.

Usage

cutGRangesPerChromosome(GRanges)

Arguments

- `GRanges` a GRanges object.

Value

a named list of GRanges, one for each chromosome.

Examples

```r
library("GenomicRanges")
gr <- GRanges(
  seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
ranges=IRanges(1:10, end=10),
strand=Rle(strand(c("-", "*", "*", "+", "-")), c(1, 2, 2, 3, 2)),
seqlengths=c(chr1=11, chr2=12, chr3=13))
(grchrlist <- cutGRangesPerChromosome(gr))
```
**c_get_disjoint_max_win**

**Description**

just a wrapper for the C function. Useful to modify indexes and colnames.

**Usage**

```r
C Get_disjoint_max_win(
  z0,
  sigwin = 10,
  nmax = 9999999,
  zthresh = 10,
  verbose = FALSE
)
```

**Arguments**

- `z0`: the z matrix.
- `sigwin`: the sigwin.
- `nmax`: the nmax.
- `zthresh`: peaks lower than this value will not be kept.
- `verbose`: verbose flag.

**Value**

a matrix

---

**DEScan2**

**Description**

integrated peak and differential caller, specifically designed for broad epigenomic signals.

**Author(s)**

some authors
divideEachSampleByChromosomes

Description

taken in input a grangeslist of samples, generate a list of samples where each element has a GRanges-
List each element of the GRangesList represents a single chromosome.

Usage

divideEachSampleByChromosomes(samplesGRangesList)

Arguments

samplesGRangesList
    a GRangesList of samples.

Value

list of samples where each element is a list of chromosomes and each of these elements is a
GRanges.

Examples

library("GenomicRanges")
gr1 <- GRanges(
    seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
    ranges=IRanges(1:10, end=10),
    strand=Rle(strand(c("-", "+", "+", "+", "-")), c(1, 2, 2, 3, 2)),
    seqlengths=c(chr1=11, chr2=12, chr3=13))
gr2 <- GRanges(
    seqnames=Rle(c("chr1", "chr4", "chr1", "chr3"), c(1, 3, 2, 4)),
    ranges=IRanges(1:10, end=10),
    strand=Rle(strand(c("-", "+", "+", "+", "-")), c(1, 2, 2, 3, 2)),
    seqlengths=c(chr1=11, chr4=12, chr3=13))
sgrl <- GRangesList(gr1, gr2)
names(sgrl) <- c("samp1", "samp2")
(sampChrGrl <- divideEachSampleByChromosomes(sgrl))
**Description**

this function computes a running mean over x with a window width k (modified from S4Vectors package to work on even k, see evenRunSum).

**Usage**
evenRunMean(x, k, endrule = c("drop", "constant"), na.rm = FALSE)

**Arguments**
- **x**: an Rle object, typically a coverage object.
- **k**: window dimension for the running sum over x.
- **endrule**: refer to S4Vectors::runMean.
- **na.rm**: refer to S4Vectors::runMean.

**Value**
an Rle within the running mean over x with a win of length k.

---

**Description**

this function computes a running sum over x with a window width k (modified from S4Vectors package to work on even k, in such a case it adds a length at the end of the output Rle).

**Usage**
evenRunSum(x, k, endrule = c("drop", "constant"), na.rm = FALSE)

**Arguments**
- **x**: an Rle object, typically a coverage object.
- **k**: window dimension for the running sum over x.
- **endrule**: refer to S4Vectors::runSum.
- **na.rm**: refer to S4Vectors::runSum.

**Value**
an Rle within the running sum over x with a win of length k.
finalRegions

Description

Align peaks to form common regions then filter regions for presence in multiple replicates taking in input a GRangesList where each element is a sample of called peaks.

Usage

```r
finalRegions(
  peakSamplesGRangesList,
  zThreshold = 20,
  minCarriers = 2,
  saveFlag = TRUE,
  outputFolder = "overlappedPeaks",
  verbose = FALSE,
  scorecolname = "z-score",
  coverageFlag = FALSE,
  BPPARAM = BiocParallel::bpparam()
)
```

Arguments

- `peakSamplesGRangesList` named GRangesList where each element is a sample of called peaks. A score mcols values is needed for each GRanges. The scorecolname param can be used as reference name for the score. (tipically returned by findPeaks function).
- `zThreshold` a minimum threshold for the z score. All peaks lesser than this value will be ignored.
- `minCarriers` a threshold of minimum samples (carriers) for overlapped regions.
- `saveFlag` a flag for saving results in a tsv file.
- `outputFolder` the directory name to store the bed file.
- `verbose` verbose output.
- `scorecolname` character describing the name of the column within the peaks score.
- `coverageFlag` boolean indicating if to compute the scores in a coverage mode (sum of the reads of merged peak) or in a score mode (a normalized score across the merged peaks)
- `BPPARAM` object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

Value

a GRanges of selected overlapping peaks with z-score, n-peaks, k-carriers as mcols object.
**findOverlapsOverSamples**

**Examples**

```r
peak.path <- system.file("extdata/peaks/RData/peaksGRL_all_files.rds",
                        package="DEScan2")
grl <- readRDS(peak.path)
grl

regionsGR <- finalRegions(peakSamplesGRangesList=grl, zThreshold=1,
                          minCarriers=3, saveFlag=FALSE, verbose=TRUE)
```

---

**findOverlapsOverSamples**

**Description**

given in input a GRangesList where each element is a sample computes the coverage extending a both direction window of prefixed length.

**Usage**

```r
findOverlapsOverSamples(
  samplePeaksGRangelist,
  extendRegions = 200,
  minOverlap = 0L,
  maxGap = -1L,
  zThresh = 10,
  verbose = FALSE,
  scorecolname = "z-score",
  coverageFlag = FALSE
)
```

**Arguments**

- **samplePeaksGRangelist**
  
given a granges list of samples finds the overlapping regions between them.

- **extendRegions**
  
  the number of bases to extend each region at its start and end.

- **minOverlap**
  
  the minimum overlap each peak needs to have. (see ChipPeakAnno::findOverlapsOfPeaks)

- **maxGap**
  
  the maximum gap admissible between the peaks. (see ChipPeakAnno::findOverlapsOfPeaks)

- **zThresh**
  
  a threshold value on z-score/scorecolname

- **verbose**
  
  verbose flag

- **scorecolname**
  
  character describing the name of the column within the peaks score.

- **coverageFlag**
  
  boolean indicating if to compute the scores in a coverage mode (sum of the reads of merged peak) or in a score mode (a normalized score across the merged peaks)
findPeaks

Value

a GRanges of peaks overlapped and unique between samples.

Examples

```r
(peaks.file <- system.file("extdata/peaks/RData/peaksGRL_all_files.rds", 
package="DEScan2"))

peaksGRLFiles <- readRDS(peaks.file)
(overlPeaks <- findOverlapsOverSamples(peaksGRLFiles))
```

Description

This function calls peaks from bed or bam inputs using a variable window scan with a poisson model using the surrounding maxCompWinWidth (10kb) as background.

Usage

```r
findPeaks(
  files,
  filetype = c("bam", "bed"),
  genomeName = NULL,
  binSize = 50,
  minWin = 50,
  maxWin = 1000,
  zthresh = 10,
  minCount = 0.1,
  minCompWinWidth = 5000,
  maxCompWinWidth = 10000,
  outputFolder = "Peaks",
  save = TRUE,
  force = TRUE,
  verbose = FALSE,
  sigwin = 10,
  onlyStdChrs = TRUE,
  chr = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```

Arguments

- `files` Character vector containing paths of files to be analyzed.
- `filetype` Character, either "bam" or "bed" indicating format of input file.
- `genomeName` the code of the genome to use as reference for the input files. (cfr. constructBedRanges function parameters)
findPeaks

binSize Integer size in bases of the minimum window for scanning, 50 is the default.

minWin Integer indicating the minimum window size in bases notation.

maxWin Integer indicating the maximum window size in bases notation.

zthresh Cutoff value for z-scores. Only windows with greater z-scores will be kept, default is 10.

minCount A small constant (usually no larger than one) to be added to the counts prior to the log transformation to avoid problems with log(0).

minCompWinWidth minimum bases width of a comparing window for Z-score.

maxCompWinWidth maximum bases width of a comparing window for Z-score.

outputFolder A string. Name of the folder to save the Peaks (optional) if the directory doesn’t exist, it will be created. (Default is "Peaks")

save Boolean. if TRUE files will be saved in a "./Peaks/chr*" directory created (if not already present) in the current working directory.

force a boolean flag indicating if to force output overwriting.

verbose if to show additional messages

sigwin an integer value used to compute the length of the signal of a peak (default value is 10).

onlyStdChrs a flag to work only with standard chromosomes. (cfr. constructBedRanges function parameters).

chr if not NULL, a character like "chr#" indicating the chromosomes to use.

BPPARAM object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

Value

A GRangesList where each element is a sample. Each GRanges represents the founded peaks and attached the z-score of the peak as mcols.

Examples

bam.files <- list.files(system.file("extdata/bam", package = "DEScan2"), full.names = TRUE)

peaks <- findPeaks(files=bam.files[1], filetype="bam",
  genomeName="mm9",
  binSize=50, minWin=50, maxWin=1000,
  zthresh=5, minCount=0.1, sigwin=10,
  minCompWinWidth=5000, maxCompWinWidth=10000,
  save=FALSE,
  onlyStdChrs=TRUE,
  chr=NULL,
  verbose=FALSE)

head(peaks)
fromSamplesToChrsGRangesList

Description

converts a GRangesList organized per samples to a GRangesList organized per Chromosomes where each element is a GRangesList of samples.

Usage

fromSamplesToChrsGRangesList(samplesGRangesList)

Arguments

samplesGRangesList

a GRangesList of samples. Typically generated by findPeaks function.

Value

A GRangesList of chromosomes where each element is a GRanges list of samples.

Examples

library("GenomicRanges")
gr1 <- GRanges(
  seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
  ranges=IRanges(1:10, end=10),
  strand=Rle(strand(c("-", "+", "x", "+", "-")), c(1, 2, 2, 3, 2)),
  seqlengths=c(chr1=11, chr2=12, chr3=13))
gr2 <- GRanges(
  seqnames=Rle(c("chr1", "chr4", "chr1", "chr3"), c(1, 3, 2, 4)),
  ranges=IRanges(1:10, end=10),
  strand=Rle(strand(c("-", "+", "x", "+", "-")), c(1, 2, 2, 3, 2)),
  seqlengths=c(chr1=11, chr4=12, chr3=13))
sgrl <- GRangesList(gr1, gr2)
(names(sgrl) <- c("samp1", "samp2")
(chrGr1SampGr <- fromSamplesToChrsGRangesList(sgrl))

generateDFofSamplesPerChromosomes
generateDFofSamplesPerChromosomes

Description

generates a dataframe where each row is a sample (1st col) and a string with its chromosomes separated by ";" (2nd col) (useful to fromSamplesToChromosomesGRangesList function).
**get_disjoint_max_win**

**Usage**

```r
generateDFofSamplesPerChromosomes(samplesChrGRList)
```

**Arguments**

- `samplesChrGRList`  
  a GRangesList of samples each divided by chromosome.

**Value**

a dataframe where each row is a sample (1st col) and a string with its chromosomes separated by ";" (2nd col).

**get_disjoint_max_win**

find significant z score windows keeping the max value without intersections

**Usage**

```r
get_disjoint_max_win(
  z0,
  sigwin = 20,
  nmax = Inf,
  zthresh = -Inf,
  two_sided = FALSE,
  verbose = FALSE
)
```

**Arguments**

- `z0`  
  Matrix containing z scores with bins as rows and windows size as columns.
- `sigwin`  
  Integer indicating how many bins per fragment.
- `nmax`  
  Integer indicating the maximum number of windows to return.
- `zthresh`  
  Integer indicating the minimum z-score considered significant.
- `two_sided`  
  not used argument.
- `verbose`  
  verbose flag.

**Value**

a matrix of integer containing founded peaks
Description

given a GRangesList of samples assigns unique names to the peaks of each sample.

Usage

giveUniqueNamesToPeaksOverSamples(samplePeaksGRangelist)

Arguments

samplePeaksGRangelist

A GRangeList of peaks, one GRanges for each sample.

Value

a GRangesList of samples within renamed peaks for each element.

Description

given a GRanges of merged peaks assigns them new names.

Usage

initMergedPeaksNames(mergedGRanges)

Arguments

mergedGRanges

A GRanges object. (Typically Generated in findOverlapsOverSamples function)

Value

a granges of renamed peaks.
Description

subselect a list of GRanges created with cutGRangesPerChromosome returning only the relevant chromosomes GRanges.

Usage

keepRelevantChrs(chrGRangesList, chr = NULL)

Arguments

chrGRangesList where each element is a chromosome, typically created with cutGRangesPerChromosome.

chr a character vector of chromosomes names of the form "chr#".

Value

the input chrGRangesList with only the relevant chromosomes.

Examples

library("GenomicRanges")
gr1 <- GRanges(
    segnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
    ranges=IRanges(1:10, end=10),
    strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
    seqlengths=c(chr1=11, chr2=12, chr3=13))
grlc <- cutGRangesPerChromosome(gr1)
(gr1Chr <- keepRelevantChrs(grlc, c("chr1", "chr3")))

rcpparma_get_disjoint_max_win

rcpparma_get_disjoint_max_win Computes the disjoint max_win matrix.

Description

rcpparma_get_disjoint_max_win Computes the disjoint max_win matrix.
**Usage**

```r
rcpparma_get_disjoint_max_win(
    z0,
    sigwin = 10L,
    zthresh = 10,
    nmax = 9999999L,
    verbose = TRUE
)
```

**Arguments**

- `z0`: a matrix.
- `sigwin`: sigwin.
- `zthresh`: zthresh.
- `nmax`: nmax.
- `verbose`: verbose.

**Value**

A matrix of three columns (bin_idx, win_idx, z_val) idxs in C style.

---

**Description**

Read a bam file into a bed like format. Forcing UCSC format for chromosomes names.

**Usage**

```r
readBamAsBed(file)
```

**Arguments**

- `file`: Character indicating path to bam file.

**Value**

GRanges object.

**Examples**

```r
files <- list.files(system.file("extdata/bam", package="DEScan2"),
    full.names=TRUE)
gr <- readBamAsBed(files[1])
```
readBedFile

Description

read a bed file into a GenomicRanges like format. forcing UCSC format for chromosomes names.

Usage

readBedFile(filename, arePeaks = FALSE)

Arguments

filename the bed filename.
arePeaks a flag indicating if the the bed file represents peaks.

Value

GRanges object

Examples

bedFile <- list.files(system.file("extdata/bed",package="DEScan2"),
full.names=TRUE)
gr <- readBedFile(bedFile)

readFilesAsGRangesList

Description

Takes in input the path of bam/bed files to process and stores them in a GRangesList object, named with filePath/filenames. (for lazy people)

Usage

readFilesAsGRangesList(
filePath,
fileType = c("bam", "bed", "bed.zip", "narrow", "broad"),
genomeName = NULL,
onlyStdChrs = TRUE,
arePeaks = TRUE,
verbose = TRUE
)

Arguments

filePath  the path of input files.
fileType  the type of the files (bam/bed/bed.zip/narrow/broad).
genomeName  the genome code to associate to the files. (recommended) (i.e. "mm9", "hg17")
onlyStdChrs  a flag to keep only standard chromosomes.
arePeaks  a flag indicating if the files contain peaks.
verbose  verbose output flag.

Value

a GRangesList object

Examples

files.path <- system.file("extdata/bam", package="DEScan2")
grl <- readFilesAsGRangesList(filePath=files.path, fileType="bam",
genomeName="mm9", onlyStdChrs=TRUE,
verbose=TRUE)
class(grl)
names(grl)
grl

RleListToRleMatrix

Description

a wrapper to create a RleMatrix from a RleList object.

Usage

RleListToRleMatrix(RleList, dimnames = NULL)

Arguments

RleList  an RleList object with all elements of the same length.
dimnames  the names for dimensions of RleMatrix (see DelayedArray pkg).

Value

a RleMatrix from DelayedArray package.
Examples

```r
library("DelayedArray")
lengths <- c(3, 1, 2)
values <- c(15, 5, 20)
el1 <- S4Vectors::Rle(values=values, lengths=lengths)
el2 <- S4Vectors::Rle(values=sort(values), lengths=lengths)

rleList <- IRanges::RleList(el1, el2)
names(rleList) <- c("one", "two")
(rleMat <- RleListToRleMatrix(rleList))
```

Description

save a GRanges object as bed file.

Usage

```r
saveGRangesAsBed(
  GRanges,
  filepath = tempdir(),
  filename = tempfile(),
  force = FALSE,
  verbose = FALSE
)
```

Arguments

- **GRanges**: the GRanges object.
- **filepath**: the path to store the files.
- **filename**: the name to give to the files.
- **force**: force overwriting.
- **verbose**: verbose output flag.

Value

- **none**
Examples

```r
library("GenomicRanges")
gr <- GRanges(
  seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
  ranges=IRanges(1:10, end=10),
  strand=Rle(strand(c("-", "+", "+", "-")), c(1, 2, 3, 2)),
  seqlengths=c(chr1=11, chr2=12, chr3=13))
saveGRangesAsTsv(GRanges=gr, filepath=tempdir(), filename=tempfile(),
  verbose=TRUE)
```

Description

save a GRanges object as tsv file.

Usage

```r
saveGRangesAsTsv(
  GRanges,
  filepath = tempdir(),
  filename = tempfile(),
  col.names = NA,
  row.names = TRUE,
  sep = "\t",
  force = FALSE,
  verbose = FALSE
)
```

Arguments

- **GRanges** the GRanges object.
- **filepath** the path to store the files.
- **filename** the name to give to the files.
- **col.names** a logical value indicating whether the column names are to be written in the file, or a character vector indicating the column names, or NA for writing column names for writing a TAB for the column name of the row names, default is NA (see write.table).
- **row.names** a logical value indicating whether the row names are to be written in the file, or a character vector indicating the row names (see write.table).
- **sep** the column separator character (default is \"\t\").
- **force** force overwriting.
- **verbose** verbose output flag.
**Value**

none

**Examples**

gr <- GRanges(
  seqnames=Rle(c("chr1", "chr2", "chr3"), c(1, 3, 2, 4)),
  ranges=IRanges(1:10, end=10),
  strand=Rle(strand(c("-", "+", "+", "+", "-")), c(1, 2, 2, 3, 2)),
  seqlengths=c(chr1=11, chr2=12, chr3=13))
saveGRangesAsTsv(gr, verbose=TRUE)

setGRGenomeInfo

*setGRGenomeInfo* given a genome code (i.e. "mm9","mm10","hg19","hg38") retrieve the SeqInfo of that genome and assigns it to the input GRanges. Finally filters out those Infos not necessary to the GRanges.

**Description**

setGRGenomeInfo given a genome code (i.e. "mm9","mm10","hg19","hg38") retrieve the SeqInfo of that genome and assigns it to the input GRanges. Finally filters out those Infos not necessary to the GRanges.

**Usage**

setGRGenomeInfo(GRanges, genomeName = NULL, verbose = FALSE)

**Arguments**

- **GRanges** a GRanges object.
- **genomeName** a genome code (i.e. "mm9")
- **verbose** verbose output

**Value**

a GRanges object with the seqinfo of the genome code

**Examples**

library("GenomicRanges")
gr <- GRanges(
  seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
  ranges=IRanges(1:10, end=10),
  strand=Rle(strand(c("-", "+", "+", "+", "-")), c(1, 2, 2, 3, 2)),
  seqlengths=c(chr1=11, chr2=12, chr3=13))
mm9gr <- setGRGenomeInfo(GRanges=gr, genomeName="mm9", verbose=TRUE)
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