Package 'DEScan2'

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binnedCoverage *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 coverate 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

```
## dividing one chromosome in bins of 50 bp each
seqinfo <- Seqinfo::Seqinfo(genome="mm9")
bins <- GenomicRanges::tileGenome(
            seqlengths=Seqinfo::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="floor"))
(binnedSumCovGR <- binnedCoverage(bins, cov, "binned_cov", covMethod="sum"))
```

`binnedCovOnly` *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` *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 *computeCoverageMovingWindowOnChr*

Description

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

Usage

```
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 *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
)
```

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.

---

constructBedRanges *constructBedRanges*

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

```
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 *countFinalRegions*

Description

count reads falling within the final regions.

Usage

```
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

carrierscolname	character describing the name of the column within the carriers number (default is "k-carriers").
ignStrandSO	a flag indicating if to ignore the reads strand. (see GenomicAlignments::summarizeOverlaps).
modeSO	the mode to use, default is "Union". (see GenomicAlignments::summarizeOverlaps).
saveFlag	a flag indicating if to save the results.
savePath	the path where to store the results.
verbose	verbose output.

Value

A SummarizedExperiment object containing as assays the read counts matrix with regions as rows and samples as columns, and as rowRanges the GRanges object representing the peaks used as rows in the matrix.

Examples

```
filename <- system.file("extdata/regions/regions.rds", package="DEScan2")
regionsGR <- readRDS(file=filename)
reads.path <- system.file("extdata/bam", package="DEScan2")
finalRegionsSE <- countFinalRegions(regionsGRanges=regionsGR,
    readsFilePath=reads.path, fileType="bam", minCarriers=1,
    genomeName="mm9", onlyStdChrs=TRUE, ignStrandSO=TRUE, saveFlag=FALSE,
    verbose=TRUE)
library("SummarizedExperiment")
assay(finalRegionsSE) ## matrix of counts
rowRanges(finalRegionsSE) ## the GRanges of the input regions
```

---

createGranges *createGranges*

Description

a simplified wrapper function to create a GRanges object.

Usage

```
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.

Value

a GRanges object.

Examples

```
chrSeqInfo <- Seqinfo::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`

cutGRangesPerChromosome

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

```
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 *c_get_disjoint_max_win*

Description

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

Usage

```
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 *DEScan2*

Description

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

Author(s)

Dario Righelli

divideEachSampleByChromosomes
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))
```

evenRunMean *evenRunMean*

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.

evenRunSum *evenRunSum*

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 *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

```
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.

Examples

```
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` *findOverlapsOverSamples*

Description

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

Usage

```
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)

Value

a GRanges of peaks overlapped and unique between samples.

Examples

```
(peaks.file <- system.file("extdata/peaks/RData/peaksGRL_all_files.rds",
                           package="DEScan2"))
peaksGRLFiles <- readRDS(peaks.file)
(overlPeaks <- findOverlapsOverSamples(peaksGRLFiles))
```

`findPeaks` *findPeaks*

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

```
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)

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	Cuttoff 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` *fromSamplesToChrsGRangesList*

Description

converts a GRangesList orgnized 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. Tipically generaed 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("-", "+", "*", "+", "-")), 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")
(chrGrlSampGr <- 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).

Usage

```
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 *get_disjoint_max_win*

Description

find significant z score windows keeping the max value without intersections

Usage

```
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

giveUniqueNamesToPeaksOverSamples *giveUniqueNamesToPeaksOverSamples*

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.

initMergedPeaksNames *initMergedPeaksNames*

Description

given a GRanges of merged peaks assigns them new names.

Usage

```
initMergedPeaksNames(mergedGRanges)
```

Arguments

mergedGRanges	A GRanges object. (Tipically Generated in findOverlapsOverSamples function)

Value

a granges of renamed peaks.

keepRelevantChrs *keepRelevantChrs*

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, tipically created with cutGRangesPerChromosome.
chr	a character vector of chromosomes names of the form "chr#".

Value

the input chrGRangesList with only the relevat chromosomes.

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))
grlc <- cutGRangesPerChromosome(gr1)
(grlChr <- 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

```
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.

---

readBamAsBed *readBamAsBed*

Description

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

Usage

```
readBamAsBed(file)
```

Arguments

file	Character indicating path to bam file.

Value

GRanges object.

Examples

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

readBedFile *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 *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 *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

```
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))
```

---

saveGRangesAsBed *saveGRangesAsBed*

Description

save a GRanges object as bed file.

Usage

```
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

```
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))

saveGRangesAsBed(GRanges=gr, filepath=tempdir(), filename=tempfile(),
                    verbose=TRUE)
```

`saveGRangesAsTsv` *saveGRangesAsTsv*

Description

save a GRanges object as tsv file.

Usage

```
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", "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))
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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