

Package ‘DEScan2’

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R topics documented:

| | |
|---|-----------|
| binnedCoverage | 2 |
| computeZ | 3 |
| constructBedRanges | 4 |
| countFinalRegions | 5 |
| createGranges | 6 |
| cutGRangesPerChromosome | 7 |
| DEScan2 | 8 |
| divideEachSampleByChromosomes | 8 |
| finalRegions | 9 |
| findOverlapsOverSamples | 10 |
| findPeaks | 11 |
| fromSamplesToChrsGRangesList | 13 |
| keepRelevantChrs | 14 |
| readBamAsBed | 14 |
| readBedFile | 15 |
| readFilesAsGRangesList | 16 |
| RleListToRleMatrix | 17 |
| saveGRangesAsBed | 17 |
| saveGRangesAsTsv | 18 |
| setGRGenomeInfo | 19 |
| Index | 20 |

| | |
|----------------|-----------------------|
| binnedCoverage | <i>binnedCoverage</i> |
|----------------|-----------------------|

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 <- 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="floor"))
(binnedSumCovGR <- binnedCoverage(bins, cov, "binned_cov", covMethod="sum"))

```

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 | <i>constructBedRanges</i> |
|--------------------|---------------------------|

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 | <i>countFinalRegions</i> |
|-------------------|--------------------------|

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. (typically 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 <- 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

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))
```

DEScan2

DEScan2

Description

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

Author(s)

some authors

divideEachSampleByChromosomes

divideEachSampleByChromosomes

Description

taken in input a grangeslist of samples, generate a list of samples where each element has a GRangesList 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))
sgr1 <- GRangesList(gr1, gr2)
names(sgr1) <- c("samp1", "samp2")
(sampChrGr1 <- divideEachSampleByChromosomes(sgr1))

```

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",
  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. (typically 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. |
| BPPARAM | object of class <code>bpparamClass</code> that specifies the back-end to be used for computations. See <code>bpparam</code> 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")
gr1 <- readRDS(peak.path)
gr1

regionsGR <- finalRegions(peakSamplesGRangesList=gr1, 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"
)
```

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.

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 | <i>findPeaks</i> |
|-----------|------------------|

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 | 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
```

```
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. Typically 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))
sgr1 <- GRangesList(gr1, gr2)
names(sgr1) <- c("samp1", "samp2")
(chrGr1SampGr <- fromSamplesToChrsGRangesList(sgr1))

```

| | |
|------------------|-------------------------|
| keepRelevantChrs | <i>keepRelevantChrs</i> |
|------------------|-------------------------|

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(
  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")))
```

| | |
|--------------|---------------------|
| readBamAsBed | <i>readBamAsBed</i> |
|--------------|---------------------|

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 | <i>readBedFile</i> |
|-------------|--------------------|

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")  
gr1 <- readFilesAsGRangesList(filePath=files.path, fileType="bam",  
                             genomeName="mm9", onlyStdChrs=TRUE,  
                             verbose=TRUE)  
  
class(gr1)  
names(gr1)  
gr1
```

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)
e11 <- S4Vectors::Rle(values=values, lengths=lengths)

e12 <- S4Vectors::Rle(values=sort(values), lengths=lengths)

rleList <- IRanges::RleList(e11, e12)
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(),
  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

```
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 | <i>setGRGenomeInfo</i> 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)
```

Index

* **internal.**

computeZ, [3](#)

binnedCoverage, [2](#)

bpparam, [10](#), [12](#)

computeZ, [3](#)

constructBedRanges, [4](#)

countFinalRegions, [5](#)

createGranges, [6](#)

cutGRangesPerChromosome, [7](#)

DEScan2, [8](#)

divideEachSampleByChromosomes, [8](#)

finalRegions, [9](#)

findOverlapsOverSamples, [10](#)

findPeaks, [11](#)

fromSamplesToChrsGRangesList, [13](#)

keepRelevantChrs, [14](#)

readBamAsBed, [14](#)

readBedFile, [15](#)

readFilesAsGRangesList, [16](#)

RleListToRleMatrix, [17](#)

saveGRangesAsBed, [17](#)

saveGRangesAsTsv, [18](#)

setGRGenomeInfo, [19](#)