Package 'RepViz'

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Type Package

Title Replicate oriented Visualization of a genomic region

Version 1.23.0

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Description RepViz enables the view of a genomic region in a simple and
efficient way. RepViz allows simultaneous viewing of both
intra- and intergroup variation in sequencing counts of the
studied conditions, as well as their comparison to the output
features (e.g. identified peaks) from user selected data analysis
methods.The RepViz tool is primarily designed for chromatin data
such as ChIP-seq and ATAC-seq, but can also be used with other
sequencing data such as RNA-seq, or combinations of different
types of genomic data.

License GPL-3

Encoding UTF-8

RoxygenNote 6.1.1

VignetteBuilder knitr

Depends R (>= 3.5.1), GenomicRanges (>= 1.30.0), Rsamtools (>=
1.34.1), IRanges (>= 2.14.0), biomaRt (>= 2.36.0), S4Vectors
(>= 0.18.0), graphics, grDevices, utils

Suggests rmarkdown, knitr, testthat

biocViews WorkflowStep, Visualization, Sequencing, ChIPSeq, ATACSeq,
Software, Coverage, GenomicVariation

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RepViz   *Plot a genomic region*

Description

Plot a genomic region

Usage

```
RepViz(region, genome = c("hg19", "hg38", "mm10"), BAM = NULL,
  BED = NULL, avgTrack = TRUE, geneTrack = TRUE, max = NULL,
  verbose = TRUE, cex = 1)
```

Arguments

region	a GRange object with chr, start, end
genome	a character vector 'hg19','hg38' or 'mm10'
BAM	a path to the BAM related csv input file
BED	a path to the BED related csv input file
avgTrack	a logical indicating if the average track should be included or not
geneTrack	a logical indicating if the gene track should be included or not
max	a numerical vector containing the yaxis maximum value of each BAM track
verbose	a logical indicating whether the progress of the plotting is shown
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
col	vector of character user can set color of the different BED tracks.

Value

displays the region specified by the user

Examples

```
region <- GRanges('chr12:110938000-110940000')
setwd(tempdir())
#Copying the files to the user working directory
file.copy(from = list.files(system.file('extdata', package = 'RepViz'), full.names = TRUE),
    to = tempdir())
#Generate the visualization of the given region
RepViz::RepViz(region = region,
    genome = 'hg19',
```

```
BAM = 'BAM_input.csv',
BED = 'BED_input.csv',
avgTrack = TRUE,
geneTrack = TRUE)
```

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