Package

March 5, 2019

Type Package

Title Replicate oriented Visualization of a genomic region

Version 0.1.14

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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 RepView 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

LazyData true

RoxygenNote 6.1.1

VignetteBuilder knitr

Depends R (>= 3.4.0),
GenomicRanges (>= 1.30.0),
rbamtools (>= 2.16.11),
IRanges (>= 2.14.0),
biomaRt (>= 2.36.0),
S4Vectors (>= 0.18.0)

Suggests knitr,
testthat

R topics documented:

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RepViz *Plot a genomic region*

Description

Plot a genomic region

Usage

```
RepViz(region, genome, BAM = NULL, BED = NULL, avgTrack = TRUE,
  geneTrack = TRUE, max = NULL, verbose = TRUE)
```

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 present or not
geneTrack	a logical indicating if the gene track should be present or not
max	a vector of numbers containing the yaxis maximum value of each BAM track
verbose	prompt the progress of the plotting

Examples

```
region <- GRanges("chr12:110938000-110940000")

#Copying the files in the curent user working directory for the purpose of the example
file.copy(from = list.files(system.file("extdata", package = "RepViz"), full.names = TRUE),
          to = getwd())
RepViz::RepViz(region = region,
               genome = "hg19",
               BAM = "BAM_input.csv",
               BED = "BED_input.csv",
               avgTrack = TRUE,
               geneTrack = TRUE)
```

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