# Package 'RepViz'

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**Type** Package

**Title** Replicate oriented Visualization of a genomic region

**Version** 1.28.0

**Author** Thomas Faux, Kalle Rytkönen, Asta Laiho, Laura L. Elo

**Maintainer** Thomas Faux, Asta Laiho <faux.thomas1@gmail.com> <asta.laiho@utu.fi>

**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*

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## 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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