

# Package ‘RepViz’

February 25, 2021

**Type** Package

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

**Version** 1.7.0

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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** knitr, testthat

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

**git\_url** <https://git.bioconductor.org/packages/RepViz>

**git\_branch** master

**git\_last\_commit** 3035195

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-02-24

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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)
```

**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

**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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