Package: RepViz (via r-universe)

November 25, 2026

Type Package

Title Replicate oriented Visualization of a genomic region

Version 1.30.0

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

Config/pak/sysreqs
libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:42:37 UTC

RemoteUrl https://github.com/bioc/RepViz

RemoteRef RELEASE_3_24

RemoteSha 0f1a490319e3820978579e78a3794374659ac9df

Contents

RepViz 2

Index **4**

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)
```

Index

RepViz, 2