Package: crisprViz (via r-universe)

May 26, 2026

Title Visualization Functions for CRISPR gRNAs

Version 1.14.0

Description Provides functionalities to visualize and contextualize CRISPR guide RNAs (gRNAs) on genomic tracks across nucleases and applications. Works in conjunction with the crisprBase and crisprDesign Bioconductor packages. Plots are produced using the Gviz framework.

Depends R (>= 4.2.0), crisprBase (>= 0.99.15), crisprDesign (>= 0.99.77)

Imports BiocGenerics, Biostrings, BSgenome, Seqinfo, GenomicFeatures, GenomicRanges, grDevices, Gviz, IRanges, methods, S4Vectors, txdbmaker

Suggests AnnotationHub, BiocStyle, BSgenome.Hsapiens.UCSC.hg38, knitr, rmarkdown, rtracklayer, testthat, utils

biocViews CRISPR, FunctionalGenomics, GeneTarget

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

VignetteBuilder knitr

BugReports `https://github.com/crisprVerse/crisprViz/issues`

URL `https://github.com/crisprVerse/crisprViz`

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev python3 libx11-dev xz-utils zlib1g-dev

Repository https://bioc-release.r-universe.dev

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Contents

`cage` *CAGE peak annotation from AnnotationHub*

Description

A sample of CAGE peak annotation from AnnotationHub (ascension number AH5084), lifted over to hg38.

Usage

```
data(cage, package="crisprViz")
```

Format

A GRanges object.

`cas12aGuideSet` *Example GuideSet targeting the human LTN1 gene.*

Description

An example GuideSet object targeting the CDS of the human LTN1 gene. Generated using the AsCas12a CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(cas12aGuideSet, package="crisprViz")
```

Format

A GuideSet object.

`cas9GuideSet` *Example GuideSet targeting the human LTN1 gene.*

Description

An example GuideSet object targeting the CDS of the human LTN1 gene. Generated using the SpCas9 CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(cas9GuideSet, package="crisprViz")
```

Format

A GuideSet object.

`dnase` *DNase I hypersensitive site annotation from AnnotationHub*

Description

A sample of DNase I hypersensitive site annotation from AnnotationHub (ascension number AH30743), lifted over to hg38.

Usage

```
data(dnase, package="crisprViz")
```

Format

A GRanges object.

`gpr21GeneModel` *CompressedGRangesList describing the human GPR21 gene.*

Description

A CompressedGRangesList object describing the gene model of the human GPR21 gene. Coordinates were subset from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(gpr21GeneModel, package="crisprViz")
```

Format

A CompressedGRangesList object.

`gpr21GuideSet` *Example GuideSet targeting the human GPR21 gene.*

Description

An example GuideSet object targeting a section of the CDS of the human GPR21 gene. Generated using the BE4max CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(gpr21GuideSet, package="crisprViz")
```

Format

A GuideSet object.

`krasGeneModel` *CompressedGRangesList describing the human KRAS gene.*

Description

A CompressedGRangesList object describing the gene model of the human KRAS gene. Coordinates were subset from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(krasGeneModel, package="crisprViz")
```

Format

A CompressedGRangesList object.

`krasGuideSet` *Example GuideSet targeting the human KRAS gene.*

Description

An example GuideSet object targeting the CDS of the human KRAS gene. Generated using the SpCas9 CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(krasGuideSet, package="crisprViz")
```

Format

A GuideSet object.

`ltn1GeneModel` *CompressedGRangesList describing the human LTN1 gene.*

Description

A CompressedGRangesList object describing the gene model of the human LTN1 gene. Coordinates were subset from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(ltn1GeneModel, package="crisprViz")
```

Format

A CompressedGRangesList object.

`mmp7GeneModel` *CompressedGRangesList describing the human MMP7 gene.*

Description

A CompressedGRangesList object describing the gene model of the human MMP7 gene. Coordinates were subset from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(mmp7GeneModel, package="crisprViz")
```

Format

A CompressedGRangesList object.

`mmp7GuideSet` *Example GuideSet targeting the human MMP7 gene.*

Description

An example GuideSet object targeting the promoter region of the human MMP7 gene. Generated using the SpCas9 CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `tss_human` in the `crisprDesignData` package (Ensembl release 104).

Usage

```
data(mmp7GuideSet, package="crisprViz")
```

Format

A GuideSet object.

`plotGuideSet` *Plotting a GuideSet and other genomic annotations*

Description

Function to plot guide targets stored in a GuideSet object in a gene browser view supported by `Gviz`. Target gene isoforms and other genomic annotation, along with the target chromosome ideogram and sequence, may also be added, permitting a comprehensive visualization of the genomic context around the target protospacer sequences.

Usage

```
plotGuideSet(
  x,
  geneModel = NULL,
  targetGene = NULL,
  annotations = list(),
  from = NULL,
  to = NULL,
  extend.left = 0,
  extend.right = 0,
  margin = 1,
  includeIdeogram = TRUE,
  bands = NULL,
  guideStacking = "squish",
  bsgenome = NULL,
  pamSiteOnly = FALSE,
```

```
  showGuideLabels = TRUE,
  onTargetScore = NULL,
  includeSNPTrack = TRUE,
  gcWindow = NULL
)
```

Arguments

`x`	A GuideSet object.
`geneModel`	A TxDb object or a GRangesList object obtained using TxDb2GRangesList.
`targetGene`	String specifying the gene symbol or Ensembl ID of the gene to plot.
`annotations`	A named (optional) list of genomic annotations as GRanges to plot. Provided names are displayed as track titles.
`from`, `to`	Numeric value giving the genomic coordinate range to plot; see plotTracks.
`extend.left`, `extend.right`	Numeric value giving the length in bases to extend the plotting range; see plotTracks.
`margin`	A numeric value that sets the margin of the plotting range with respect to the range of `x`. The value is a ratio of the width of `x` considered as a single range, with a value of `1` (default) extending the plotting window by the same distance as that between `min(start(x))` and `max(end(x))`. Only works for the respective side of the plot if either `from` or `to` are `NULL`.
`includeIdeogram`	Logical; whether to include an IdeogramTrack in the plot.
`bands`	A `data.frame` of cytoband information for the target genome required for ideogram plotting; see IdeogramTrack.
`guideStacking`	Character string specifying how to stack guides. Options are `squish`, `dense`, `hide` (see GeneRegionTrack), or `NA` to have each guide occupy a separate track.
`bsgenome`	A BSgenome object; used to generate SequenceTrack and GC content DataTrack.
`pamSiteOnly`	Whether to plot only the PAM site in representing guides, or plot the full guide and PAM sequence (default).
`showGuideLabels`	Logical; whether to show labels for individual guides.
`onTargetScore`	Optional column name in `mcols(x)` of on-target scores. Applies a color scheme to the guide track based on on-target scores, with light gray corresponding to 0 and dark blue corresponding to 1.
`includeSNPTrack`	Logical; whether to include an AnnotationTrack for SNPs if such annotation exists in `x`.
`gcWindow`	If not `NULL`, a numeric value specifying the distance from a given base for which to establish a window for calculating GC content at that base. These values are then added to the plot in a DataTrack.

Value

A Gviz plot; see plotTracks.

Author(s)

Luke Hoberecht

See Also

plotMultipleGuideSets for plotting multiple GuideSet objects together.

Examples

```
if (interactive()){
data(krasGuideSet, package="crisprViz")
data(krasGeneModel, package="crisprViz")
plotGuideSet(krasGuideSet[1:4],
             geneModel=krasGeneModel,
             targetGene="KRAS")
}
```

`plotMultipleGuideSets` *Plotting a GuideSet and other genomic annotation*

Description

Function to plot guide targets stored in multiple GuideSet objects in a gene browser view supported by `Gviz`. Target gene isoforms and other genomic annotation, along with the target chromosome ideogram and sequence, may also be added, permitting a comprehensive visualization of the genomic context targeted by spacers in GuideSet objects.

Usage

```
plotMultipleGuideSets(
  x,
  geneModel = NULL,
  targetGene = NULL,
  annotations = list(),
  from = NULL,
  to = NULL,
  extend.left = 0,
  extend.right = 0,
  margin = 1,
  includeIdeogram = TRUE,
  bands = NULL,
  bsgenome = NULL,
  onTargetScores = NULL,
```

```
  includeSNPTrack = TRUE,
  gcWindow = NULL
)
```

Arguments

`x`	A named (optional) list of GuideSet objects. List names are displayed as track titles.
`geneModel`	A TxDb object or a GRangesList object obtained using TxDb2GRangesList.
`targetGene`	A character string giving the gene symbol or Ensembl ID of the gene to plot.
`annotations`	A named (optional) list of genomic annotations as GRanges to plot. Provided names are displayed as track titles.
`from`, `to`	Numeric value giving the genomic coordinate range to plot; see plotTracks.
`extend.left`, `extend.right`	Numeric value giving the length in bases to extend the plotting range; see plotTracks.
`margin`	A numeric value that sets the margin of the plotting range with respect to the range of `x`. The value is a ratio of the width of `x` considered as a single range, with a value of `1` (default) extending the plotting window by the same distance as that between `min(start(x))` and `max(end(x))`. Only works for the respective side of the plot if either `from` or `to` are `NULL`.
`includeIdeogram`	Logical; whether to include an IdeogramTrack in the plot.
`bands`	A `data.frame` of cytoband information for the target genome required for ideogram plotting; see IdeogramTrack.
`bsgenome`	A BSgenome object; used to generate SequenceTrack and GC content DataTrack.
`onTargetScores`	Optional list of column names for each element in `x` of on-target scores. Applies a color scheme to the guide track based on on-target scores, with light gray corresponding to 0 and dark blue corresponding to 1.
`includeSNPTrack`	Logical; whether to include an AnnotationTrack for SNPs if such annotation exists in `x`.
`gcWindow`	If not `NULL`, a numeric value specifying the distance from a given base for which to establish a window for calculating GC content at that base. These values are then added to the plot in a DataTrack.

Value

A Gviz plot; see `plotTracks`.

Author(s)

Luke Hoberecht, Jean-Philippe Fortin

See Also

`plotGuideSet`

Examples

```
if (interactive()){
library(BSgenome.Hsapiens.UCSC.hg38)
data(cas9GuideSet, package="crisprViz")
data(cas12aGuideSet, package="crisprViz")
data(ltn1GeneModel, package="crisprViz")
plotMultipleGuideSets(list(SpCas9=cas9GuideSet, AsCas12a=cas12aGuideSet),
                      geneModel=ltn1GeneModel,
                      targetGene="LTN1",
                      bsgenome=BSgenome.Hsapiens.UCSC.hg38,
                      margin=0.2,
                      gcWindow=10)
}
```

`repeats` *Subset of repeat elements for hg38.*

Description

A GRanges object describing a subset of repeat elements for the hg38 genome. Coordinates were subset from `gr.repeats.hg38` in the `crisprDesignData` package.

Usage

```
data(repeats, package="crisprViz")
```

Format

A GRanges object.

Index