Package 'crisprViz'

July 16, 2025

Title Visualization Functions for CRISPR gRNAs

Version 1.10.0

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, GenomeInfoDb,
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

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Contents

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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 As-Cas12a 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 Sp-Cas9 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 Sp-Cas9 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