Package ‘crisprViz’

March 3, 2024

Title Visualization Functions for CRISPR gRNAs
Version 1.4.0
Description Provides functionalities to visualize and contextualize CRISPR guide RNAs (gRNAs) on genomic tracks across nuclease 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
Suggests AnnotationHub, BiocStyle, BSgenome.Hsapiens.UCSC.hg38, knitr, rmarkdown, rtracklayer, testthat, utils
biocViews CRISPR, FunctionalGenomics, GeneTarget
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\begin{verbatim}
cage  \hfill \textit{CAGE peak annotation from AnnotationHub}
\end{verbatim}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
data(cage, package="crisprViz")
\end{verbatim}

\textbf{Format}

A \texttt{GRanges} object.

\begin{verbatim}
cas12aGuideSet  \hfill \textit{Example GuideSet targeting the human LTN1 gene.}
\end{verbatim}

\textbf{Description}

An example \texttt{GuideSet} object targeting the CDS of the human LTN1 gene. Generated using the AaCas12a CRISPR nuclease, the genome sequence from the B5genome.Hsapiens.UCSC.hg38 package, and the gene model from txdb_human in the crisprDesignData package (Ensembl release 104).
**cas9GuideSet**

**Usage**

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

**Format**

A `GuideSet` object.

---

**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**

```r
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**

```r
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**

```r
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**

```r
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**

```r
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**

```r
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**

```r
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**

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

**Format**

A *CompressedGRangesList* object.
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**

```r
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**

```r
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,
includeSNP Track = 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.
includeSNP Track
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.
**plotMultipleGuideSets**

**Value**

A Gviz plot; see `plotTracks`.

**Author(s)**

Luke Hoberecht

**See Also**

`plotMultipleGuideSets` for plotting multiple GuideSet objects together.

**Examples**

```r
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**

```r
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 BSeqnome object; used to generate SequenceTrack and GC content Data-
Track.
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
repeats

See Also

plotGuideSet

Examples

```r
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

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

Format

A GRanges object.
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