Package ‘crisprShiny’

April 8, 2025

Title Exploring curated CRISPR gRNAs via Shiny

Version 1.3.0

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Description Provides means to interactively visualize guide RNAs (gRNAs) in GuideSet objects via Shiny application. This GUI can be self-contained or as a module within a larger Shiny app. The content of the app reflects the annotations present in the passed GuideSet object, and includes intuitive tools to examine, filter, and export gRNAs, thereby making gRNA design more user-friendly.

Depends R (>= 4.4.0), shiny

Imports BiocGenerics, Biostrings, BSgenome, crisprBase, crisprDesign, crisprScore, crisprViz, DT, GenomeInfoDb, htmlwidgets, methods, pwalign, S4Vectors, shinyBS, shinyjs, utils, waiter

Suggests BiocStyle, knitr, rmarkdown, shinyFeedback, testthat (>= 3.0.0), BSgenome.Hsapiens.UCSC.hg38

biocViews CRISPR, FunctionalGenomics, GeneTarget, GUI

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

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Contents

`crisprServer` *Server component for crisprShiny App*

Description

Server component for crisprShiny App. Not intended for direct use. (intended to be passed as server component of module in shinyApp function)

Usage

```
crisprServer(id, guideSet, geneModel, title = NULL, useFilterPresets = TRUE)
```

Arguments

`id`	Module ID.
`guideSet`	A GuideSet object.
`geneModel`	A GRangesList object obtained using `crisprDesign::TxDb2GRangesList`.
`title`	Optional title to display at head of app.
`useFilterPresets`	Whether to use preset filter values on app launch. See details section for `?crisprShiny`.

Value

Shiny module server component.

Examples

```
library(crisprShiny)
ui <- function(id){
    fluidPage(
        crisprUI(id)
    )
}

server <- function(id, gs){
    function(input, output, session){
        observeEvent(gs, {
            crisprServer(
                id,
                guideSet=gs,
                geneModel=NULL,
                useFilterPresets=TRUE
            )
        })
    }
}

myApp <- function(gs){
    shinyApp(ui=ui("id"), server=server("id", gs))
}

if (interactive()){
    data("guideSetExample_basic", package="crisprShiny")
    myApp(guideSetExample_basic)
}
```

`crisprShiny` *Interactive visualization of GuideSets via Shiny applications*

Description

Means to interactively visualize gRNAs within a `GuideSet` object via a Shiny application. Contents of the Shiny app reflect annotations contained within the `GuideSet` object, and provide intuitive controls to examine, filter, and export `.csv` tables of gRNAs.

Usage

```
crisprShiny(guideSet, geneModel = NULL, useFilterPresets = TRUE)
```

Arguments

`guideSet`	A GuideSet object.
`geneModel`	A GRangesList object obtained using `crisprDesign::TxDb2GRangesList`.
`useFilterPresets`	Whether to use preset filter values on app launch. See details.

Details

Preset filter values

Using sensible, preset filters can conveniently remove many poorer-quality gRNAs from view upon app launch. This can be done by setting `useFilterPresets=TRUE`, while passing `FALSE` will retain all gRNAs in `guideSet`. Of course, filters can still be adjusted within the app to either further refine or broaden the list of gRNAs to view. Setting `useFilterPresets=TRUE` (default) will impose the following filter criteria, as appropriate to the `guideSet`, upon app launch:

- spacers with polyT are excluded
- permissible spacer percent GC range set to [20, 80]
- spacers missing values for any score method (`NA`) are excluded
- (SpCas9 nuclease only) minimum permissible DeepHF and DeepSpCas9 scores set to 0.5
- spacers targeting repeat elements are excluded
- spacers overlapping SNPs are excluded
- (for GuideSets having gene annotation) spacers targeting the final 15% of the gene CDS (i.e., 3' end) are excluded

Filters will not be applied if the `guideSet` lacks the necessary annotation. For example, a `guideSet` lacking SNP annotation will not be filtered on the SNP criterium.

Value

A Shiny app object.

Examples

```
library(crisprShiny)
data("guideSetExample_kras", package="crisprShiny")
app <- crisprShiny(guideSetExample_kras)

if (interactive()) {
    shiny::runApp(app)
}
```

`crisprUI` *UI component for crisprShiny App*

Description

UI component for crisprShiny App. Not intended for direct use.

Usage

```
crisprUI(id, cssFile = NULL)
```

Arguments

`id`	Module ID.
`cssFile`	Optional path of CSS file to be included in rendering app. `NULL` gives default styling, found in `inst/www/styling.css`.

Value

Shiny module UI component.

Examples

```
library(crisprShiny)
ui <- function(id){
    fluidPage(
        crisprUI(id)
    )
}

server <- function(id, gs){
    function(input, output, session){
        observeEvent(gs, {
            crisprServer(
                id,
                guideSet=gs,
                geneModel=NULL,
                useFilterPresets=TRUE
            )
        })
    }
}

myApp <- function(gs){
    shinyApp(ui=ui("id"), server=server("id", gs))
}

if (interactive()){
    data("guideSetExample_basic", package="crisprShiny")
    myApp(guideSetExample_basic)
}
```

`guideSetExample_basic` *Example of a GuideSet object storing gRNA sequences targeting the CDS of the human gene KRAS*

Description

Example of a GuideSet object (with no additional annotation) storing gRNA sequences targeting the coding sequence of human gene KRAS (ENSG00000133703) for SpCas9 nuclease.

Usage

```
data(guideSetExample_basic, package="crisprShiny")
```

Format

A GuideSet object.

Details

The object was obtained by using `crisprDesign::findSpacers` on a GRanges of the CDS region of human gene KRAS. See code in `inst/scripts/generateKrasData.R`.

`guideSetExample_kras` *Example of a GuideSet object storing gRNA sequences targeting the CDS of the human gene KRAS*

Description

Example of a fully annotated GuideSet object storing gRNA sequences targeting the coding sequence of human gene KRAS (ENSG00000133703) for SpCas9 nuclease.

Usage

```
data(guideSetExample_kras, package="crisprShiny")
```

Format

A GuideSet object.

Details

The object was obtained by applying all available `add*` annotation functions in `crisprDesign` on a GuideSet storing gRNAs targeting the CDS region of human gene KRAS. See code in `inst/scripts/generateKrasData.R`.

`guideSetExample_kras_be` *Example of a GuideSet object storing gRNA sequences targeting the CDS of the human gene KRAS*

Description

Example of a GuideSet object storing gRNA sequences targeting the coding sequence of human gene KRAS (ENSG00000133703) for BE4max nuclease.

Usage

```
data(guideSetExample_kras_be, package="crisprShiny")
```

Format

A GuideSet object.

Details

The object was obtained by applying all base-editor-specific annotation functions in `crisprDesign` on the CDS region of human gene KRAS. See code in `inst/scripts/generateKrasData.R`.

`guideSetExample_ntcs` *Example of a GuideSet object storing gRNA sequences targeting the CDS of the human gene KRAS and NTCs*

Description

Example of a fully annotated GuideSet object storing gRNA sequences targeting the coding sequence of human gene KRAS (ENSG00000133703) and some non-targeting controls (NTCs) for SpCas9 nuclease.

Usage

```
data(guideSetExample_kras, package="crisprShiny")
```

Format

A GuideSet object.

Details

The object was obtained by applying all available `add*` annotation functions in `crisprDesign` on a GuideSet storing gRNAs targeting the CDS region of human gene KRAS and some NTCs. See code in `inst/scripts/generateKrasData.R`.

`tooltipAnnotation` *List of tooltip annotations*

Description

Tooltip messages for crisprShiny app stored in a `list` object.

Usage

```
data(tooltipAnnotation, package="crisprShiny")
```

Format

A `list` object.

Details

See code in `inst/scripts/generateKrasData.R` for tooltip annotations.

`tss_kras` *Example of a* `GenomicRanges` *object storing annotated TSS ranges for the human gene KRAS*

Description

Example of a `GenomicRanges` object storing annotated TSS ranges for the human gene KRAS (ENSG00000133703).

Usage

```
data(tss_kras, package="crisprShiny")
```

Format

A `GenomicRanges` object.

Details

The object was obtained by subsetting genomic ranges in `tss_human` from the `crisprDesignData` package for the KRAS gene (Ensembl ID: ENSG00000133703). See code in `inst/scripts/generateKrasData.R`.

`txdb_kras` *Example of a* `CompressedGenomicRangesList` *object storing annotated ranges for the human gene KRAS*

Description

Example of a `CompressedGenomicRangesList` object storing annotated genomic ranges for the human gene KRAS (ENSG00000133703).

Usage

```
data(txdb_kras, package="crisprShiny")
```

Format

A `CompressedGenomicRangesList` object.

Details

The object was obtained by subsetting all genomic ranges annotations in `txdb_human` from the `crisprDesignData` package for the KRAS gene (Ensembl ID: ENSG00000133703). See code in `inst/scripts/generateKrasData.R`.

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