Package ‘crisprShiny’

May 15, 2024

Title Exploring curated CRISPR gRNAs via Shiny

Version 1.0.0

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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, markdown, shinyFeedback, testthat (>= 3.0.0), BSgenome.Hsapiens.UCSC.hg38

biocViews CRISPR, FunctionalGenomics, GeneTarget, GUI

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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

```r
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**

```r
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

```r
library(crisprShiny)
u <- function(id){
  fluidPage(
    crisprUI(id)
  )
}
s <- function(id, gs){
  function(input, output, session){
    observeEvent(gs, {
      crisprServer(
        id,
        guideSet=gs,
        geneModel=NULL,
        useFilterPresets=TRUE
      )
    })
  }
}
m <- function(gs){
  shinyApp(ui=u("id"), server=s("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.

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.
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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