Package 'igvShiny'

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Description This package is a wrapper of Integrative Genomics Viewer (IGV). It comprises an htmlwidget version of IGV. It can be used as a module in Shiny apps.

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Author Paul Shannon [aut], Arkadiusz Gladki [aut, cre] (ORCID: <https://orcid.org/0000-0002-7059-6378>), Karolina Scigocka [aut]

Maintainer Arkadiusz Gladki <gladki.arkadiusz@gmail.com>

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`display,GWASTrack-method`
display the already constructed and configured track

Description

display the already constructed and configured track

Usage

```
## S4 method for signature 'GWASTrack'
display(obj, session, id, deleteTracksOfSameName = TRUE)
```

Arguments

`obj`	An object of class GWASTrack
`session`	a Shiny session object
`id`	character the identifier of the target igv object in the browser
`deleteTracksOfSameName`	logical to avoid duplications in track names

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

---

getUrl,GWASTrack-method

the url of the gwas table

Description

the url of the gwas table

Usage

```
## S4 method for signature 'GWASTrack'
getUrl(obj)
```

Arguments

obj	An object of class GWASTrack

Value

character

Examples

```
file <-
  # a local gwas file
  system.file(package = "igvShiny", "extdata", "gwas-5k.tsv.gz")
tbl.gwas <- read.table(file,
                       sep = "\t",
                       header = TRUE,
                       quote = "")
track <-
  GWASTrack(
    "gwas 5k",
    tbl.gwas,
    chrom.col = 12,
    pos.col = 13,
    pval.col = 28
  )
getUrl(track)
```

get_basic_genomes *get_basic_genomes*

Description

a helper function for basic genomes, obtains the genome codes (e.g. 'hg38')

Usage

```
get_basic_genomes()
```

Value

an list of short genome codes, e.g., "hg38", "dm6"

Examples

```
bs <- get_basic_genomes()
```

get_cas_genomes *get_cas_genomes*

Description

a helper function for common always available stock genomes, obtains the genome codes (e.g. 'hg38')

Usage

```
get_cas_genomes()
```

Value

an list of short genome codes, e.g., "hg38", "dm6"

Examples

```
cas <- get_cas_genomes()
```

get_css_genomes *get_css_genomes*

Description

a helper function for mostly internal use, obtains the genome codes (e.g. 'hg38') supported by igv.js

Usage

```
get_css_genomes(test = FALSE)
```

Arguments

test	logical(1) defaults to FALSE

Value

an list of short genome codes, e.g., "hg38", "dm6", "tair10"

Examples

```
css <- get_css_genomes(test = TRUE)
```

get_tracks_dir *get_tracks_dir Get the directory where tracks are stored. The directory can be defined with environmental variable. If not defined the default is a directory called "tracks" in the temp directory. We need a local directory to write files - for instance, a vcf file representing a genomic region of interest. We then tell shiny about that directory, so that shiny's built-in http server can serve up files we write there, ultimately consumed by igv.js*

Description

get_tracks_dir Get the directory where tracks are stored. The directory can be defined with environmental variable. If not defined the default is a directory called "tracks" in the temp directory. We need a local directory to write files - for instance, a vcf file representing a genomic region of interest. We then tell shiny about that directory, so that shiny's built-in http server can serve up files we write there, ultimately consumed by igv.js

Usage

```
get_tracks_dir(env_var = "TRACKS_DIR")
```

Arguments

env_var	The name of the environmental variable to use.

Value

string with the path to the tracks directory.

Examples

```
gtd <- get_tracks_dir(env_var = "TRACKS_DIR")
```

GWASTrack-class *Constructor for GWASTrack*

Description

GWASTrack creates an IGV manhattan track from GWAS data

Usage

```
GWASTrack(
  trackName,
  data,
  chrom.col,
  pos.col,
  pval.col,
  trackHeight = 50,
  autoscale = TRUE,
  minY = 0,
  maxY = 30
)
```

Arguments

trackName	A character string, used as track label by igv, we recommend unique names per track.
data	a data.frame or a url pointing to one, whose structure is described by chrom.col, pos.col, pval.col
chrom.col	numeric, the column number of the chromosome column
pos.col	numeric, the column number of the position column
pval.col	numeric, the column number of the GWAS pvalue column
trackHeight	numeric in pixels
autoscale	logical
minY	numeric for explicit (non-auto) scaling
maxY	numeric for explicit (non-auto) scaling

Value

A GWASTrack object

Examples

```
file <-
  # a local gwas file
  system.file(package = "igvShiny", "extdata", "gwas-5k.tsv.gz")
tbl.gwas <- read.table(file,
                       sep = "\t",
                       header = TRUE,
                       quote = "")
dim(tbl.gwas)
track <-
  GWASTrack(
    "gwas 5k",
    tbl.gwas,
    chrom.col = 12,
    pos.col = 13,
    pval.col = 28
  )
getUrl(track)

url <- "https://gladki.pl/igvShiny/gwas_sample.tsv.gz"
track <- GWASTrack(
  "remote url gwas",
  url,
  chrom.col = 3,
  pos.col = 4,
  pval.col = 10,
  autoscale = FALSE,
  minY = 0,
  maxY = 300,
  trackHeight = 100
)
getUrl(track)
```

`igvShiny` *Create an igvShiny instance*

Description

This function is called in the server function of your shiny app

Usage

```
igvShiny(
  genomeOptions,
  width = NULL,
  height = NULL,
  elementId = NULL,
  displayMode = "squished",
  tracks = list()
)
```

Arguments

genomeOptions	a list with these fields: genomeName, initialLocus, annotation, dataMode, fasta, fastaIndex, stockGenome, validated
width	a character string, standard css notations, either e.g., "1000px" or "95%"
height	a character string, needs to be an explicit pixel measure, e.g., "800px"
elementId	a character string, the html element id within which igv is created
displayMode	a character string, default "SQUISHED".
tracks	a list of track specifications to be created and displayed at startup

Value

the created widget

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

---

igvShinyOutput *create the UI for the widget*

Description

This function is called in the ui function of your shiny app

Usage

```
igvShinyOutput(outputId, width = "100%", height = NULL)
```

Arguments

outputId	a character string, specifies the html element id
width	a character string, standard css notations, either e.g., "1000px" or "95%", "100%" by default
height	a character string, needs to be an explicit pixel measure, e.g., "800px", "400px" by default

Value

the created widget's html

Examples

```
io <- igvShinyOutput("igvOut")
```

`loadBamTrackFromLocalData` *load GenomicAlignments data as an igv.js alignment track*

Description

load GenomicAlignments data as an igv.js alignment track

Usage

```
loadBamTrackFromLocalData(
  session,
  id,
  trackName,
  data,
  deleteTracksOfSameName = TRUE,
  displayMode = "EXPANDED"
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`data`	GenomicAlignments object
`deleteTracksOfSameName`	logical, default TRUE
`displayMode`	character string, possible values are "EXPANDED"(default), "SQUISHED" or "COLLAPSED"

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadBamTrackFromURL` *load a bam track which, with index, is served up by http*

Description

load a remote bam track

Usage

```
loadBamTrackFromURL(
  session,
  id,
  trackName,
  bamURL,
  indexURL,
  deleteTracksOfSameName = TRUE,
  displayMode = "EXPANDED",
  showAllBases = FALSE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`bamURL`	character string http url for the bam file, typically very large
`indexURL`	character string http url for the bam file index, typically small
`deleteTracksOfSameName`	logical, default TRUE
`displayMode`	character string, possible values are "EXPANDED"(default), "SQUISHED" or "COLLAPSED"
`showAllBases`	logical, show all bases in the alignment, default FALSE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadBedGraphTrack` *load a scored genome annotation track provided as a data.frame*

Description

load a genome annotation track provided as a data.frame

Usage

```
loadBedGraphTrack(
  session,
  id,
  trackName,
  tbl,
  color = "gray",
  trackHeight = 30,
  autoscale,
  autoscaleGroup = -1,
  min = NA_real_,
  max = NA_real_,
  deleteTracksOfSameName = TRUE,
  quiet = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`tbl`	data.frame, with at least "chrom" "start" "end" "score" columns
`color`	character string, a legal CSS color, or "random", "gray" by default
`trackHeight`	an integer, 30 (pixels) by default
`autoscale`	logical
`autoscaleGroup`	numeric(1) defaults to -1
`min`	numeric, consulted when autoscale is FALSE
`max`	numeric, consulted when autoscale is FALSE
`deleteTracksOfSameName`	logical, default TRUE
`quiet`	logical, default TRUE, controls verbosity

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadBedGraphTrackFromURL` *load a bedgraph track from a URL*

Description

load a bedgraph track provided as a data.frame

Usage

```
loadBedGraphTrackFromURL(
  session,
  id,
  trackName,
  url,
  color = "gray",
  trackHeight = 30,
  autoscale = TRUE,
  min = 0,
  max = 1,
  autoscaleGroup = -1,
  deleteTracksOfSameName = TRUE,
  quiet = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`url`	character
`color`	character string, a legal CSS color, or "random", "gray" by default
`trackHeight`	an integer, 30 (pixels) by default
`autoscale`	logical
`min`	numeric, consulted when autoscale is FALSE
`max`	numeric, consulted when autoscale is FALSE
`autoscaleGroup`	numeric(1) defaults to -1
`deleteTracksOfSameName`	logical(1) defaults to TRUE
`quiet`	logical, default TRUE, controls verbosity

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadBedTrack` *load a bed track provided as a data.frame*

Description

load a bed track provided as a data.frame

Usage

```
loadBedTrack(
  session,
  id,
  trackName,
  tbl,
  color = "",
  trackHeight = 50,
  deleteTracksOfSameName = TRUE,
  quiet = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`tbl`	data.frame, with at least "chrom" "start" "end" columns
`color`	character string, a legal CSS color, or "random", "gray" by default
`trackHeight`	an integer, 50 (pixels) by default
`deleteTracksOfSameName`	logical, default TRUE
`quiet`	logical, default TRUE, controls verbosity

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadCramTrackFromURL` *load a cram track which, with index, is served up by http*

Description

load a remote cram track

Usage

```
loadCramTrackFromURL(
  session,
  id,
  trackName,
  cramURL,
  indexURL,
  deleteTracksOfSameName = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`cramURL`	character string http url for the bam file, typically very large
`indexURL`	character string http url for the bam file index, typically small
`deleteTracksOfSameName`	logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadGFF3TrackFromLocalData` *load a GFF3 track defined by local data*

Description

load a local GFF3 track file

Usage

```
loadGFF3TrackFromLocalData(
  session,
  id,
  trackName,
  tbl.gff3,
  color = "gray",
  colorTable,
  colorByAttribute,
  displayMode,
  trackHeight = 50,
  visibilityWindow,
  deleteTracksOfSameName = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`tbl.gff3`	data.frame in standard 9-column GFF3 format
`color`	character #RGB or a recognized color name. ignored if colorTable and colorByAttribute provided
`colorTable`	list, mapping a gff3 attribute, typically biotype, to a color
`colorByAttribute`	character, name of a gff3 attribute in column 9, typically "biotype"
`displayMode`	character, "EXPANDED", "SQUISHED" or "COLLAPSED"
`trackHeight`	numeric defaults to 50
`visibilityWindow`	numeric, Maximum window size in base pairs for which indexed annotations or variants are displayed
`deleteTracksOfSameName`	logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo-GFF3.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadGFF3TrackFromURL` *load a GFF3 track which, with index, is served up by http*

Description

load a remote GFF3 track

Usage

```
loadGFF3TrackFromURL(
  session,
  id,
  trackName,
  gff3URL,
  indexURL,
  color = "gray",
  colorTable,
  colorByAttribute,
  displayMode,
  trackHeight = 50,
  visibilityWindow,
  deleteTracksOfSameName = TRUE
)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`gff3URL`	character string http url for the bam file, typically very large
`indexURL`	character string http url for the bam file index, typically small
`color`	character #RGB or a recognized color name. ignored if colorTable and colorByAttribute provided
`colorTable`	list, mapping a gff3 attribute, typically biotype, to a color
`colorByAttribute`	character, name of a gff3 attribute in column 9, typically "biotype"
`displayMode`	character, "EXPANDED", "SQUISHED" or "COLLAPSED"
`trackHeight`	numeric defaults to 50

visibilityWindow
: numeric, Maximum window size in base pairs for which indexed annotations or variants are displayed

deleteTracksOfSameName
: logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo-GFF3.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

---

loadGwasTrack *load a GWAS (genome-wide association study) track provided as a data.frame*

Description

load a GWAS (genome-wide association study) track provided as a data.frame

Usage

```
loadGwasTrack(
  session,
  id,
  trackName,
  tbl.gwas,
  ymin = 0,
  ymax = 35,
  deleteTracksOfSameName = TRUE
)
```

Arguments

session
: an environment or list, provided and managed by shiny

id
: character string, the html element id of this widget instance

trackName
: character string

tbl.gwas
: data.frame, with at least "chrom" "start" "end" columns

ymin
: numeric defaults to 0

ymax
: numeric defaults to 35

deleteTracksOfSameName
: logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`loadSegTrack` *load a seg track provided as a data.frame*

Description

load a SEG track provided as a data.frame. igv "displays segmented data as a blue-to-red heatmap where the data range is -1.5 to 1.5... The segmented data file format is the output of the Circular Binary Segmentation algorithm (Olshen et al., 2004)".

Usage

```
loadSegTrack(session, id, trackName, tbl, deleteTracksOfSameName = TRUE)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackName`	character string
`tbl`	data.frame, with at least "chrom" "start" "end" "score" columns
`deleteTracksOfSameName`	logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

loadVcfTrack *load a VCF (variant) track provided as a Bioconductor VariantAnnotation object*

Description

load a VCF (variant) track provided as a Bioconductor VariantAnnotation object

Usage

```
loadVcfTrack(session, id, trackName, vcfData, deleteTracksOfSameName = TRUE)
```

Arguments

session	an environment or list, provided and managed by shiny
id	character string, the html element id of this widget instance
trackName	character string
vcfData	VariantAnnotation object
deleteTracksOfSameName	logical, default TRUE

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo-withVCF.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

parseAndValidateGenomeSpec *parseAndValidateGenomeSpec*

Description

a helper function for internal use by the igvShiny constructor, but possible also of use to those building an igvShiny app, to test their genome specification for validity

Usage

```
parseAndValidateGenomeSpec(
  genomeName,
  initialLocus = "all",
  stockGenome = TRUE,
  dataMode = NA,
  fasta = NA,
  fastaIndex = NA,
  genomeAnnotation = NA
)
```

Arguments

genomeName	character usually one short code of a supported ("stock") genome (e.g., "hg38") or for a user-supplied custom genome, the name you wish to use
initialLocus	character default "all", otherwise "chrN:start-end" or a recognized gene symbol
stockGenome	logical default TRUE
dataMode	character either "stock", "localFile" or "http"
fasta	character when supplying a custom (non-stock) genome, either a file path or a URL
fastaIndex	character when supplying a custom (non-stock) genome, either a file path or a URL, essential for all but the very small custom genomes.
genomeAnnotation	character when supplying a custom (non-stock) genome, a file path or URL pointing to a genome annotation file in a gff3 format

Value

an options list directly usable by igvApp.js, and thus igv.js

See Also

[get_css_genomes()] for stock genomes we support.

Examples

```
genomeSpec <-
  parseAndValidateGenomeSpec("hg38", "APOE")  # the simplest case
base.url <-
  "https://gladki.pl/igvr/testFiles/sarsGenome"
fasta.file <-
  sprintf("%s/%s", base.url, "Sars_cov_2.ASM985889v3.dna.toplevel.fa")
fastaIndex.file <-
  sprintf("%s/%s",
          base.url,
          "Sars_cov_2.ASM985889v3.dna.toplevel.fa.fai")
annotation.file <-
  sprintf("%s/%s", base.url, "Sars_cov_2.ASM985889v3.101.gff3")
custom.genome.title <- "SARS-CoV-2"
genomeOptions <-
  parseAndValidateGenomeSpec(
    genomeName = custom.genome.title,
```

```
    initialLocus = "all",
    stockGenome = FALSE,
    dataMode = "http",
    fasta = fasta.file,
    fastaIndex = fastaIndex.file,
    genomeAnnotation = annotation.file
  )
```

`removeTracksByName` *remove tracks from the browser*

Description

delete tracks on the browser

Usage

```
removeTracksByName(session, id, trackNames)
```

Arguments

`session`	an environment or list, provided and managed by shiny
`id`	character string, the html element id of this widget instance
`trackNames`	a vector of character strings

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

`removeUserAddedTracks` *remove only those tracks explicitly added by your app*

Description

remove only those tracks explicitly added by your app. stock tracks (i.e., #' Refseq Genes) remain

Usage

```
removeUserAddedTracks(session, id)
```

Arguments

session	an environment or list, provided and managed by shiny
id	character string, the html element id of this widget instance

Value

nothing

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

---

renderIgvShiny *draw the igv genome browser element*

Description

This function is called in the server function of your shiny app

Usage

```
renderIgvShiny(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

expr	an expression that generates an HTML widget
env	the environment in which to evaluate expr
quoted	logical flag indicating if expr a quoted expression

Value

an output or render function that enables the use of the widget within Shiny applications

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

showGenomicRegion *focus igv on a region*

Description

zoom in or out to show the nominated region, by chromosome locus or gene symbol

return the current region displayed by your igv instance

Usage

```
showGenomicRegion(session, id, region)

getGenomicRegion(session, id)
```

Arguments

session	an environment or list, provided and managed by shiny
id	character string, the html element id of this widget instance
region	a character string, either e.g. "chr5:92,221,640-92,236,523" or "MEF2C"

Value

a character string of format "chrom:start-end"

Examples

```
library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}

library(igvShiny)
demo_app_file <-
  system.file(package = "igvShiny", "demos", "igvShinyDemo.R")
if (interactive()) {
  shiny::runApp(demo_app_file)
}
```

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