

# Package ‘igvShiny’

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**Title** igvShiny: a wrapper of Integrative Genomics Viewer (IGV - an interactive tool for visualization and exploration integrated genomic data)

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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.

**URL** <https://github.com/gladkia/igvShiny>,  
<https://gladkia.github.io/igvShiny/>

**BugReports** <https://github.com/gladkia/igvShiny/issues>

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## Contents

|                                      |           |
|--------------------------------------|-----------|
| display,GWASTrack-method . . . . .   | 2         |
| getUrl,GWASTrack-method . . . . .    | 3         |
| get_basic_genomes . . . . .          | 4         |
| get_cas_genomes . . . . .            | 4         |
| get_css_genomes . . . . .            | 5         |
| get_tracks_dir . . . . .             | 5         |
| GWASTrack-class . . . . .            | 6         |
| igvShiny . . . . .                   | 7         |
| igvShinyOutput . . . . .             | 8         |
| loadBamTrackFromLocalData . . . . .  | 9         |
| loadBamTrackFromURL . . . . .        | 10        |
| loadBedGraphTrack . . . . .          | 11        |
| loadBedGraphTrackFromURL . . . . .   | 12        |
| loadBedTrack . . . . .               | 13        |
| loadCramTrackFromURL . . . . .       | 14        |
| loadGFF3TrackFromLocalData . . . . . | 15        |
| loadGFF3TrackFromURL . . . . .       | 16        |
| loadGwasTrack . . . . .              | 17        |
| loadSegTrack . . . . .               | 18        |
| loadVcfTrack . . . . .               | 19        |
| parseAndValidateGenomeSpec . . . . . | 19        |
| removeTracksByName . . . . .         | 21        |
| removeUserAddedTracks . . . . .      | 21        |
| renderIgvShiny . . . . .             | 22        |
| showGenomicRegion . . . . .          | 23        |
| <b>Index</b>                         | <b>24</b> |

---

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 | <i>get_basic_genomes</i> |
|-------------------|--------------------------|

---

**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 | <i>get_cas_genomes</i> |
|-----------------|------------------------|

---

**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 | <i>get_css_genomes</i> |
|-----------------|------------------------|

---

**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 | <i>get_tracks_dir</i> 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")
```

---

GWAS*Track*-class

*Constructor for GWAS*Track**


---

**Description**

GWAS*Track* 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 GWAS*Track* 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 | <i>create the UI for the widget</i> |
|----------------|-------------------------------------|

---

**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

|                                     |                                                                                      |
|-------------------------------------|--------------------------------------------------------------------------------------|
| <code>session</code>                | an environment or list, provided and managed by shiny                                |
| <code>id</code>                     | character string, the html element id of this widget instance                        |
| <code>trackName</code>              | character string                                                                     |
| <code>data</code>                   | GenomicAlignments object                                                             |
| <code>deleteTracksOfSameName</code> | logical, default TRUE                                                                |
| <code>displayMode</code>            | 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 | <i>load a bam track which, with index, is served up by http</i> |
|---------------------|-----------------------------------------------------------------|

---

### 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 | <i>load a scored genome annotation track provided as a data.frame</i> |
|-------------------|-----------------------------------------------------------------------|

---

## 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 | <i>load a bed track provided as a data.frame</i> |
|--------------|--------------------------------------------------|

---

**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 | <i>load a GWAS (genome-wide association study) track provided as a data.frame</i> |
|---------------|-----------------------------------------------------------------------------------|

---

### 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 | <i>load a VCF (variant) track provided as a Bioconductor VariantAnnotation object</i> |
|--------------|---------------------------------------------------------------------------------------|

---

### 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 | <i>parseAndValidateGenomeSpec</i> |
|----------------------------|-----------------------------------|

---

### 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 | <i>remove tracks from the browser</i> |
|--------------------|---------------------------------------|

---

### 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 | <i>remove only those tracks explicitly added by your app</i> |
|-----------------------|--------------------------------------------------------------|

---

### 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 | <i>draw the igv genome browser element</i> |
|----------------|--------------------------------------------|

---

**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 | <i>focus igv on a region</i> |
|-------------------|------------------------------|

---

**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)
}
```

# Index

- \* **GWASTrack\_class**
  - display, GWASTrack-method, [2](#)
  - getUrl, GWASTrack-method, [3](#)
  - GWASTrack-class, [6](#)
- \* **igvShiny**
  - igvShiny, [7](#)
  - igvShinyOutput, [8](#)
  - parseAndValidateGenomeSpec, [19](#)
  - removeTracksByName, [21](#)
  - removeUserAddedTracks, [21](#)
  - renderIgvShiny, [22](#)
  - showGenomicRegion, [23](#)
- \* **track\_loaders**
  - loadBamTrackFromLocalData, [9](#)
  - loadBamTrackFromURL, [10](#)
  - loadBedGraphTrack, [11](#)
  - loadBedGraphTrackFromURL, [12](#)
  - loadBedTrack, [13](#)
  - loadCramTrackFromURL, [14](#)
  - loadGFF3TrackFromLocalData, [15](#)
  - loadGFF3TrackFromURL, [16](#)
  - loadGwasTrack, [17](#)
  - loadSegTrack, [18](#)
  - loadVcfTrack, [19](#)
- \* **utils**
  - get\_basic\_genomes, [4](#)
  - get\_cas\_genomes, [4](#)
  - get\_css\_genomes, [5](#)
  - get\_tracks\_dir, [5](#)
- .GWASTrack (GWASTrack-class), [6](#)

display (display, GWASTrack-method), [2](#)  
display, GWASTrack-method, [2](#)

get\_basic\_genomes, [4](#)  
get\_cas\_genomes, [4](#)  
get\_css\_genomes, [5](#)  
get\_tracks\_dir, [5](#)  
getGenomicRegion (showGenomicRegion), [23](#)  
getUrl (getUrl, GWASTrack-method), [3](#)  
getUrl, GWASTrack-method, [3](#)  
GWASTrack (GWASTrack-class), [6](#)  
GWASTrack-class, [6](#)

igvShiny, [7](#)  
igvShinyOutput, [8](#)

loadBamTrackFromLocalData, [9](#)  
loadBamTrackFromURL, [10](#)  
loadBedGraphTrack, [11](#)  
loadBedGraphTrackFromURL, [12](#)  
loadBedTrack, [13](#)  
loadCramTrackFromURL, [14](#)  
loadGenomeAnnotationTrack  
    (loadBedGraphTrack), [11](#)  
loadGFF3TrackFromLocalData, [15](#)  
loadGFF3TrackFromURL, [16](#)  
loadGwasTrack, [17](#)  
loadSegTrack (loadSegTrack), [18](#)  
loadSegTrack, [18](#)  
loadVcfTrack, [19](#)

parseAndValidateGenomeSpec, [19](#)

removeTracksByName, [21](#)  
removeUserAddedTracks, [21](#)  
renderIgvShiny, [22](#)

showGenomicRegion, [23](#)