

# 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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---

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

|                                     |  |
|-------------------------------------|--|
| <code>obj</code>                    | An object of class <code>GWASTrack</code>                        |
| <code>session</code>                | a Shiny session object   |
| <code>id</code>                     | character the identifier of the target igv object in the browser |
| <code>deleteTracksOfSameName</code> | 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

|                  |   |
|------------------|---|
| <code>obj</code> | An object of class <code>GWASTrack</code> |
|------------------|---|

### 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 | <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)
```

---

|                             |   |
|-----------------------------|---|
| <code>get_tracks_dir</code> | <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

|                      |  |
|----------------------|--|
| <code>env_var</code> | 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")
```

---

|                              |                                  |
|------------------------------|----------------------------------|
| <code>GWASTrack-class</code> | <i>Constructor for GWASTrack</i> |
|------------------------------|----------------------------------|

---

### 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 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

|                        |  |
|------------------------|--|
| 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 | <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

*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 | <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**

|                      |   |
|----------------------|---|
| <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>region</code>  | 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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