

# Package ‘igvR’

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**Type** Package

**Title** igvR: integrative genomics viewer

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**Depends** R (>= 3.5.0), GenomicRanges, GenomicAlignments, BrowserViz (>= 2.17.1)

**Imports** methods, BiocGenerics, httpuv, utils, rtracklayer,  
VariantAnnotation, RColorBrewer, httr

**Suggests** RUnit, BiocStyle, knitr, rmarkdown, MotifDb, seqLogo

**Description** Access to igv.js, the Integrative Genomics Viewer running in a web browser.

**URL** <https://gladkia.github.io/igvR/>

**License** MIT + file LICENSE

**LazyLoad** yes

**biocViews** Visualization, ThirdPartyClient, GenomeBrowsers

**Collate** 'Track.R' 'igvAnnotationTrack.R' 'UCSCBedAnnotationTrack.R'  
'DataFrameAnnotationTrack.R' 'VariantTrack.R'  
'QuantitativeTrack.R' 'DataFrameQuantitativeTrack.R'  
'UCSCBedGraphQuantitativeTrack.R' 'GRangesAnnotationTrack.R'  
'GRangesQuantitativeTrack.R' 'GenomicAlignmentTrack.R'  
'BedpeInteractionsTrack.R' 'RemoteAlignmentTrack.R'  
'GWASTrack.R' 'GWASUrlTrack.R' 'GFF3Track.R' 'genomeSpec.R'  
'igvR.R'

**NeedsCompilation** no

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---

BedpeInteractionsTrack-class  
*Constructor for BedpeInteractionsTrack*

---

## Description

BedpeInteractionsTrack creates an IGV track for two-location annotations

## Usage

```
BedpeInteractionsTrack(  
    trackName,  
    table,  
    color = "darkBlue",  
    trackHeight = 50,  
    displayMode = "EXPANDED",  
    visibilityWindow = 1e+05  
)
```

## Arguments

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| table            | data.frame of 6 or more columns   |
| color            | A css color name (e.g., "red" or "#FF0000")   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| displayMode      | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise.   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Value**

A BedpeInteractionsTrack object

**Examples**

```
#-----
# first, from a local file
#-----

file <- system.file(package="igvR", "extdata", "sixColumn-demo1.bedpe")
tbl.bedpe <- read.table(file, sep="\t", as.is=TRUE, header=TRUE)
dim(tbl.bedpe) # 32 6
track <- BedpeInteractionsTrack("bedpe-6", tbl.bedpe)

#-----
# show the relevant portion of the genome
#-----

shoulder <- 10000
if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "Paired End Demo")
  roi <- with(tbl.bedpe, sprintf("%s:%d-%d", chrom1[1], min(start1)-shoulder, max(end2) + shoulder))
  showGenomicRegion(igv, roi)
  displayTrack(igv, track)
}
```

---

currently.supported.stock.genomes

*currently.supported.stock.genomes*

---

**Description**

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

**Usage**

```
currently.supported.stock.genomes(test = FALSE)
```

**Arguments**

test            logical

**Value**

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

---

 DataFrameAnnotationTrack-class

*Constructor for DataFrameAnnotationTrack*


---

## Description

DataFrameAnnotationTrack creates an IGV track for bed objects imported using rtracklayer

## Usage

```
DataFrameAnnotationTrack(
  trackName,
  annotation,
  color = "",
  displayMode = "SQUISHED",
  trackHeight = 50,
  expandedRowHeight = 30,
  squishedRowHeight = 15,
  maxRows = 500,
  searchable = FALSE,
  visibilityWindow = 1e+05
)
```

## Arguments

|                   |   |
|-------------------|---|
| trackName         | A character string, used as track label by igv, we recommend unique names per track.  |
| annotation        | A base R data.frame   |
| color             | A CSS color name (e.g., "red" or "#FF0000"), leave as default empty string if supplying bed9 format with itemRgb.   |
| displayMode       | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise.   |
| trackHeight       | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| expandedRowHeight | Height of each row of features in "EXPANDED" mode.  |
| squishedRowHeight | Height of each row of features in "SQUISHED" mode, for compact viewing.   |
| maxRows           | of features to display  |
| searchable        | If TRUE, labels on annotation elements may be used in search  |
| visibilityWindow  | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description goes here

**Value**

A DataFrameAnnotationTrack object

**Examples**

```
base.loc <- 88883100
tbl <- data.frame(chrom=rep("chr5", 3),
                  start=c(base.loc, base.loc+100, base.loc + 250),
                  end=c(base.loc + 50, base.loc+120, base.loc+290),
                  name=c("a", "b", "c"),
                  score=runif(3),
                  strand=rep("*", 3),
                  stringsAsFactors=FALSE)

track <- DataFrameAnnotationTrack("data.frame demo", tbl)

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "DataFrameAnnotationTrack demo")
  displayTrack(igv, track)
  roi <- sprintf("%s:%d-%d", tbl$chrom[1], min(tbl$start)-100, max(tbl$start) + 100)
  showGenomicRegion(igv, roi)
  Sys.sleep(1)
  zoomOut(igv)
}
```

---

DataFrameQuantitativeTrack-class

*Constructor for DataFrameQuantitativeTrack*

---

**Description**

DataFrameQuantitativeTrack creates and IGV track for bed objects imported using rtracklayer

**Usage**

```
DataFrameQuantitativeTrack(
  trackName,
  quantitativeData,
  color = "blue",
  trackHeight = 50,
  autoscale,
  min = NA_real_,
```

```

    max = NA_real_,
    visibilityWindow = 1e+05
  )

```

### Arguments

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| quantitativeData | A base R data.frame   |
| color            | A CSS color name (e.g., "red" or "#FF0000")   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| autoscale        | Autoscale track to maximum value in view  |
| min              | Sets the minimum value for the data (y-axis) scale. Usually zero.   |
| max              | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

### Details

Detailed description goes here

### Value

A DataFrameQuantitativeTrack object

### See Also

DataFrameAnnotationTrack  
 GRangesQuantitativeTrack  
 GRangesAnnotationTrack  
 DataFrameAnnotationTrack  
 DataFrameQuantitativeTrack  
 GRangesAnnotationTrack  
 GRangesQuantitativeTrack  
 GenomicAlignmentTrack  
 UCSCBedAnnotationTrack  
 UCSCBedGraphQuantitativeTrack  
 VariantTrack  
 igvAnnotationTrack

**Examples**

```

base.loc <- 88883100
tbl.blocks <- data.frame(chrom=rep("chr5", 3),
                        start=c(base.loc, base.loc+100, base.loc + 250),
                        end=c(base.loc + 50, base.loc+120, base.loc+290),
                        score=runif(3),
                        stringsAsFactors=FALSE)

track.blocks <- DataFrameQuantitativeTrack("blocks", tbl.blocks, autoscale=TRUE)

locs <- seq(from=base.loc, length.out=1000)
tbl.wig <- data.frame(chrom=rep("chr5", 1000), start=locs-1, end=locs,
                    score=runif(n=1000, min=-1, max=1))
track.wig <- DataFrameQuantitativeTrack("wig", tbl.wig, autoscale=FALSE,
                                       min=min(tbl.wig$score), max=max(tbl.wig$score),
                                       color="random")

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "DataFrameQuantitativeTrack demo")
  displayTrack(igv, track.blocks)
  roi <- sprintf("%s:%d-%d", tbl.blocks$chrom[1],
                min(tbl.blocks$start)-1000, max(tbl.blocks$end) + 1000)
  showGenomicRegion(igv, roi)
  displayTrack(igv, track.wig)
}

```

---

displayTrack, igvR-method

*display the specified track in igv*

---

**Description**

display the specified track in igv

**Usage**

```

## S4 method for signature 'igvR'
displayTrack(obj, track, deleteTracksOfSameName = TRUE)

```

**Arguments**

|                        |   |
|------------------------|---|
| obj                    | An object of class igvR                             |
| track                  | An object of some terminal (leaf) subclass of Track |
| deleteTracksOfSameName | logical, default TRUE                               |



**Value**

""

**Examples**

```

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  base.loc <- 88883100
  tbl <- data.frame(chrom=rep("chr5", 3),
                    start=c(base.loc, base.loc+100, base.loc + 250),
                    end=c(base.loc + 50, base.loc+120, base.loc+290),
                    name=c("a", "b", "c"),
                    score=runif(3),
                    strand=rep("*", 3),
                    stringsAsFactors=FALSE)
  track <- DataFrameAnnotationTrack("dataframeTest", tbl, color="red",
                                    displayMode="EXPANDED")
  showGenomicRegion(igv, "chr5:88,881,962-88,885,045")
  displayTrack(igv, track)
}

```

---

enableMotifLogoPopups, igvR-method

*turn motif log popups on or off*


---

**Description**

Some tracks represent transcription factor binding sites, traditionally represented as a motif logo. use this method to enable that capability - which depends upon a properly constructed tbl.regions data.frame in a DataFrameAnnotationTrack: in addition to the usual (and mandatory) chrom, start, and end columns. To enable track-click popups over binding site, tbl.regions data.frame must also have a "name" column, which this format, by example: "MotifDb::Hsapiens-HOCOMOCov10-MEF2C\_HUMAN.H10MO.C" The first part of the name, "MotifDb:", tells igv you want to view the specified MotifDb pwm (motif logo, a matrix) when the binding site track element is clicked.

Limitations: This method only works after a call to setGenome(igv, "your genome of interest"). It only works with DataFrameAnnotationTrack objects (for now)

**Usage**

```

## S4 method for signature 'igvR'
enableMotifLogoPopups(obj, status)

```

**Arguments**

|        |                         |
|--------|-------------------------|
| obj    | An object of class igvR |
| status | TRUE or FALSE           |

**Examples**

```

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  new.region <- "chr5:88,882,214-88,884,364"
  showGenomicRegion(igv, new.region)
  base.loc <- 88883100
  element.names <- c("MotifDb::Hsapiens-HOCOMOCov10-MEF2C_HUMAN.H10M0.C",
                    "fubar",
                    "MotifDb::Hsapiens-jaspar2018-MEF2C-MA0497.1")

  tbl.regions <- data.frame(chrom=rep("chr5", 3),
                           start=c(base.loc, base.loc+100, base.loc + 250),
                           end=c(base.loc + 50, base.loc+120, base.loc+290),
                           name=element.names,
                           score=round(runif(3), 2),
                           strand=rep("*", 3),
                           stringsAsFactors=FALSE)

  track <- DataFrameAnnotationTrack("dataframeTest", tbl.regions, color="darkGreen", displayMode="EXPANDED")
  displayTrack(igv, track)
}

```

---

GenomicAlignmentTrack-class

*Constructor for GenomicAlignmentTrack*

---

**Description**

GenomicAlignmentTrack creates and IGV track for bed-like objects expressed as GRanges

**Usage**

```

GenomicAlignmentTrack(
  trackName,
  alignment,
  trackHeight = 50,
  visibilityWindow = 30000,
  color = "gray"
)

```

**Arguments**

|           |  |
|-----------|--|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| alignment | A GAlignments object   |

|                  |   |
|------------------|---|
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |
| color            | A character string, either a recognized color ("red") or a hex string ("#FF8532")   |

**Details**

Detailed description goes here

**Value**

A GenomicAlignmentTrack object

**Examples**

```
bamFile <- system.file(package="igvR", "extdata", "tumor.bam")
which <- GRanges(seqnames = "21", ranges = IRanges(10400126, 10400326))
param <- ScanBamParam(which=which, what = scanBamWhat())
x <- readGAlignments(bamFile, use.names=TRUE, param=param)
track <- GenomicAlignmentTrack("tumor", x)
```

---

getGenomicRegion,igvR-method

*Obtain the chromosome and coordinates of the currently displayed genomic region.*

---

**Description**

Some caution is needed with this function when called right after a lengthy browser operation - of which the main example is display a GenomicAlignmentTrack. igv.js does not at present allow us to delay the return from javascript pending completion of the track rendering. This does not pose much of a problem when you manipulate igv in the browser from R in normal interactive mode: simply wait for your last command to complete. But if you are running in programmatic mode, as we do when testing igvR, then caution is advised. See the test\_displayAlignment function in unitTests/test\_igvR.R.

**Usage**

```
## S4 method for signature 'igvR'
getGenomicRegion(obj)
```

**Arguments**

obj                    An object of class igvR

**Value**

A list with four fields: chrom (character), start(numeric), end(numeric), string(character)

**Examples**

```
if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  getGenomicRegion(igv)
  # list(chrom="chr5", start=88717241, end=88884466, string="chr5:88,717,241-88,884,466")
}
```

---

getSupportedGenomes, igvR-method

*Get the shorthand codes (eg, "hg38") for the genomes currently supported by our use of igv.js*

---

**Description**

Get the shorthand codes (eg, "hg38") for the genomes currently supported by our use of igv.js

**Usage**

```
## S4 method for signature 'igvR'
getSupportedGenomes(obj)
```

**Arguments**

obj                    An object of class igvR

**Value**

A character vector, the short form names of the currently supported genomes

**Examples**

```
if(interactive()){
  igv <- igvR()
  getSupportedGenomes(igv)
}
```

---

`getTrackNames, igvR-method`*Get the names of all the tracks currently displayed in igv*

---

**Description**

Get the names of all the tracks currently displayed in igv

**Usage**

```
## S4 method for signature 'igvR'  
getTrackNames(obj)
```

**Arguments**

`obj` An object of class `igvR`

**Value**

A character vector

**Examples**

```
if(interactive()){  
  igv <- igvR()  
  setGenome(igv, "hg19")  
  getTrackNames(igv) # "Gencode v18"  
}
```

---

`GFF3Track-class`*Constructor for GFF3Track*

---

**Description**

GFF3Track creates an IGV track for 9-column gene annotation tables

**Usage**

```
GFF3Track(  
  trackName,  
  tbl.track = data.frame(),  
  url = NA_character_,  
  indexURL = NA_character_,  
  trackColor = "black",  
  colorByAttribute = NA_character_,  
  colorTable = list(),
```

```

displayMode,
trackHeight,
visibilityWindow
)

```

### Arguments

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| tbl.track        | data.frame with 9 columns as defined at <a href="http://uswest.ensembl.org/info/website/upload/gff3.html">http://uswest.ensembl.org/info/website/upload/gff3.html</a> |
| url              | character the web location of a 9-column table, gzipped or not  |
| indexURL         | character the matching tabix index file   |
| trackColor       | character a recognized color name or RGB triple   |
| colorByAttribute | a name from a column 9 attribute  |
| colorTable       | list which maps the colorByAttribute values to different colors   |
| displayMode      | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise.   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types.       |

### Details

Detailed description goes here

### Value

A GFF3Track object

### Examples

```

tbl.gff3 <- read.table(system.file(package="igvR", "extdata", "GRCh38.94.NDUFS2.gff3"),
                      sep="\t", as.is=TRUE)
colnames(tbl.gff3) <- c("seqid", "source", "type", "start", "end", "score", "strand",
                      "phase", "attributes")
colors <- list("antisense" = "blueviolet",
              "protein_coding" = "blue",
              "retained_intron" = "rgb(0, 150, 150)",
              "processed_transcript" = "purple",
              "processed_pseudogene" = "#7fff00",
              "unprocessed_pseudogene" = "#d2691e",
              "default" = "black")
track <- GFF3Track("dataframe gff3", tbl.gff3, colorByAttribute="biotype", colorTable=colors,
                 url=NA_character_, indexURL=NA_character_, displayMode="EXPANDED", trackHeight=200,

```

```

visibilityWindow=100000)

# gff3 table structure is not bed-like. find chrom, start, end as seen below

roi <- with(tbl.gff3, sprintf("%s:%d-%d",
                             seqid[1],
                             as.integer(min(start)) - 1000,
                             as.integer(max(end)) + 1000))

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "GWAS demo")
  showGenomicRegion(igv, roi)
  displayTrack(igv, track)
}

```

---

GRangesAnnotationTrack-class

*Constructor for GRangesAnnotationTrack*


---

## Description

GRangesAnnotationTrack creates and IGV track for bed-like objects expressed as GRanges

## Usage

```

GRangesAnnotationTrack(
  trackName,
  annotationData,
  color = "darkGrey",
  displayMode = "SQUISHED",
  trackHeight = 50,
  expandedRowHeight = 30,
  squishedRowHeight = 15,
  maxRows = 500,
  searchable = FALSE,
  visibilityWindow = 1e+05
)

```

## Arguments

|                |  |
|----------------|--|
| trackName      | A character string, used as track label by igv, we recommend unique names per track. |
| annotationData | A GRanges object with optional name metadata column                                  |
| color          | A CSS color name (e.g., "red" or "#FF0000")  |
| displayMode    | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise.            |

|                   |   |
|-------------------|---|
| trackHeight       | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| expandedRowHeight | Height of each row of features in "EXPANDED" mode.  |
| squishedRowHeight | Height of each row of features in "SQUISHED" mode, for compact viewing.   |
| maxRows           | of features to display  |
| searchable        | If TRUE, labels on annotation elements may be used in search  |
| visibilityWindow  | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

### Details

Detailed description goes here

### Value

A GRangesAnnotationTrack object

### Examples

```
base.loc <- 88883100
tbl <- data.frame(chrom=rep("chr5", 3),
                 start=c(base.loc, base.loc+100, base.loc + 250),
                 end=c(base.loc + 50, base.loc+120, base.loc+290),
                 name=c("a", "b", "c"),
                 strand=rep("*", 3),
                 stringsAsFactors=FALSE)

gr <- GRanges(tbl)
track <- GRangesAnnotationTrack("GRangesQTest", gr)
```

---

GRangesQuantitativeTrack-class

*Constructor for GRangesQuantitativeTrack*

---

### Description

GRangesQuantitativeTrack creates and IGV track for bed objects imported using rtracklayer



**Usage**

```
GRangesQuantitativeTrack(
  trackName,
  quantitativeData,
  color = "blue",
  trackHeight = 50,
  autoscale = TRUE,
  min = NA_real_,
  max = NA_real_,
  visibilityWindow = 1e+05
)
```

**Arguments**

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| quantitativeData | A GRanges object with (at least) a "score" metadata column  |
| color            | A CSS color name (e.g., "red" or "#FF0000")   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| autoscale        | Autoscale track to maximum value in view  |
| min              | Sets the minimum value for the data (y-axis) scale. Usually zero.   |
| max              | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description goes here

**Value**

A GRangesQuantitativeTrack object

**Examples**

```
base.loc <- 88883100
tbl <- data.frame(chrom=rep("chr5", 3),
  start=c(base.loc, base.loc+100, base.loc + 250),
  end=c(base.loc + 50, base.loc+120, base.loc+290),
  name=c("a", "b", "c"),
  score=runif(3),
  strand=rep("*", 3),
  stringsAsFactors=FALSE)
```

```
gr <- GRanges(tbl)
track <- GRangesQuantitativeTrack("GRangesQTest", gr)
```

---

GWASTrack-class      *Constructor for GWASTrack*

---

### Description

GWASTrack creates an IGV manhattan track GWAS data

### Usage

```
GWASTrack(
  trackName,
  table,
  chrom.col,
  pos.col,
  pval.col,
  colorTable = list(),
  autoscale = TRUE,
  min = 0,
  max = 10,
  trackHeight = 50,
  visibilityWindow = 1e+05
)
```

### Arguments

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| table            | data.frame of 6 or more columns   |
| 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  |
| colorTable       | a named list of CSS colors, by chromosome name - exact matches to the names in the GWAS table.  |
| autoscale        | logical, controls how min and max of the y-axis are determined  |
| min              | numeric when autoscale is FALSE, use this minimum y   |
| max              | numeric when autoscale is FALSE, use this maximum y   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Value**

A GWASTrack object

**Examples**

```
file <- system.file(package="igvR", "extdata", "gwas-5k.tsv")
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)

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "GWAS demo")
  displayTrack(igv, track)
  Sys.sleep(1) # pause before zooming in
  showGenomicRegion(igv, "chr6:32,240,829-32,929,353")
}
```

---

GWASUrlTrack

*Constructor for GWASUrlTrack*


---

**Description**

GWASUrlTrack creates an IGV manhattan track GWAS data

**Usage**

```
GWASUrlTrack(
  trackName,
  url,
  chrom.col,
  pos.col,
  pval.col,
  colorTable = list(),
  autoscale = TRUE,
  min = 0,
  max = 10,
  trackHeight = 50,
  visibilityWindow = 1e+05
)
```

**Arguments**

|           |  |
|-----------|--|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| url       | character  |

|                  |   |
|------------------|---|
| 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  |
| colorTable       | a named list of CSS colors, by chromosome name - exact matches to the names in the GWAS table.  |
| autoscale        | logical, controls how min and max of the y-axis are determined  |
| min              | numeric when autoscale is FALSE, use this minimum y   |
| max              | numeric when autoscale is FALSE, use this maximum y   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Value**

A GWASUrlTrack object

**Examples**

```
track <- GWASUrlTrack("GWAS from url",
                     "https://s3.amazonaws.com/igv.org/demo/gwas_sample.tsv.gz",
                     chrom.col=12, pos.col=13, pval.col=28)

# note: this track is autoscaled. apparently some infinite values in the file,
# leading to a flat, low track. reproduce this in static html, report issue to igv.js
# temporary workaround: use the interactive track gear to set display range.

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "GWAS URL demo")
  displayTrack(igv, track)
}
```

---

igvAnnotationTrack-class

*Constructor for igvAnnotationTrack*

---

**Description**

Constructor for igvAnnotationTrack

**Usage**

```

igvAnnotationTrack(
  trackName,
  annotation,
  fileFormat = c("bed"),
  color = "gray",
  displayMode = c("SQUISHED", "COLLAPSED", "EXPANDED"),
  sourceType = "file",
  trackHeight = 30,
  expandedRowHeight = 30,
  squishedRowHeight = 15,
  maxRows = 500,
  searchable = FALSE,
  visibilityWindow = 1e+05
)

```

**Arguments**

|                   |   |
|-------------------|---|
| trackName         | A character string, used as track label by igv, we recommend unique names per track.  |
| annotation        | An opaque type, currently either a data.frame, GRanges, or UCSCBed object from rtracklayer.   |
| fileFormat        | Only "bed" is currently supported.  |
| color             | A CSS color name (e.g., "red" or "#FF0000")   |
| displayMode       | "COLLAPSED", "EXPANDED", or "SQUISHED"  |
| sourceType        | Only "file" sources are currently supported.  |
| trackHeight       | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| expandedRowHeight | Height of each row of features in "EXPANDED" mode.  |
| squishedRowHeight | Height of each row of features in "SQUISHED" mode, for compact viewing.   |
| maxRows           | of features to display  |
| searchable        | If TRUE, labels on annotation elements may be used in search  |
| visibilityWindow  | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Value**

An igvAnnotationTrack object

igvR-class

*Create an igvR object***Description**

The igvR class provides an R interface to igv.js, a rich, interactive, full-featured, javascript browser-based genome browser. One constructs an igvR instance on a specified port (default 9000), the browser code is loaded, and a websocket connection opened. After specifying the reference genome, any number of genome tracks may be created, displayed, and navigated.

**Usage**

```
igvR(
  portRange = 15000:15100,
  host = "localhost",
  title = "igvR",
  browserFile = igvBrowserFile,
  quiet = TRUE
)
```

**Arguments**

|             |   |
|-------------|---|
| portRange   | The constructor looks for a free websocket port in this range. 15000:15100 by default         |
| host        | character, often "localhost" but (as with RStudio Server deployment) can be a remote host     |
| title       | Used for the web browser window, "igvR" by default  |
| browserFile | The full path to the bundled html, js and libraries, and css which constitute the browser app |
| quiet       | A logical variable controlling verbosity during execution                                     |

**Value**

An object of the igvR class

**Examples**

```
if(interactive()){
  igv <- igvR(title="igv demo")
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  #-----
  # an easy transparent way to create a bed track
  #-----
  base.loc <- 88883100
  tbl <- data.frame(chrom=rep("chr5", 3),
                    start=c(base.loc, base.loc+100, base.loc + 250),
```

```

        end=c(base.loc + 50, base.loc+120, base.loc+290),
        name=c("a", "b", "c"),
        score=runif(3),
        strand=rep("*", 3),
        stringsAsFactors=FALSE)

track <- DataFrameAnnotationTrack("dataframeTest", tbl, color="red", displayMode="EXPANDED")
displayTrack(igv, track)
showGenomicRegion(igv, sprintf("chr5:%d-%d", base.loc-100, base.loc+350))
} # if interactive

```

---

```
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**

[currently.supported.stock.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)
```

---

ping,igvR-method

*Test the connection between your R session and the webapp*

---

**Description**

Test the connection between your R session and the webapp

**Usage**

```
## S4 method for signature 'igvR'
ping(obj, msecDelay = 0)
```

**Arguments**

obj                    An object of class igvR  
msecDelay              don't return until these many milliseconds have passed, default 0

**Value**

"pong"



**Examples**

```
if(interactive()){
  igv <- igvR()
  ping(igv)
}
```

---

 QuantitativeTrack-class

*Constructor for QuantitativeTrack*

---

**Description**

QuantitativeTrack creates an IGV track for genomic tracks in which a numerical value is associated with each reported location.

**Usage**

```
QuantitativeTrack(
  trackName,
  quantitativeData,
  fileFormat = c("wig", "bigWig", "bedGraph", "gwas"),
  color = "gray",
  sourceType = c("file", "url"),
  trackHeight = 50,
  autoscale = TRUE,
  min = NA_real_,
  max = NA_real_,
  visibilityWindow = 1e+05
)
```

**Arguments**

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.                                |
| quantitativeData | A polyvalent object, either a data.frame, GRanges, or UCSCBedGraphQuantitative object                               |
| fileFormat       | only "bedGraph" supported at present; wig and bigWig support soon.  |
| color            | A CSS color name (e.g., "red" or "#FF0000")   |
| sourceType       | only "file" supported at present ("gcs" for Google Cloud Storage, and "ga4gh" for the Global Alliance API may come) |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)                   |
| autoscale        | Autoscale track to maximum value in view  |
| min              | Sets the minimum value for the data (y-axis) scale. Usually zero.   |

|                  |   |
|------------------|---|
| max              | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description will go here

**Value**

A QuantitativeTrack object

---

RemoteAlignmentTrack-class

*Constructor for RemoteAlignmentTrack*

---

**Description**

RemoteAlignmentTrack creates an IGV track for remote bam files

**Usage**

```
RemoteAlignmentTrack(
    trackName,
    bamUrl,
    bamIndex = NULL,
    trackHeight = 50,
    visibilityWindow = 30000,
    color = "gray"
)
```

**Arguments**

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| bamUrl           | The URL of a bam file   |
| bamIndex         | The URL of a bam index file. Defaults to <bamUrl>.bai   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |
| color            | A character string, either a reconized color ("red") or a hex string ("#FF8532")  |

**Details**

Detailed description goes here

**Value**

A RemoteAlignmentTrack object

---

removeTracksByName, igvR-method  
*Remove named tracks*

---

**Description**

Remove named tracks

**Usage**

```
## S4 method for signature 'igvR'  
removeTracksByName(obj, trackNames)
```

**Arguments**

|            |                         |
|------------|-------------------------|
| obj        | An object of class igvR |
| trackNames | a character vector      |

**Value**

A character vector

**See Also**

getTrackNames

**Examples**

```
if(interactive()){  
  igv <- igvR()  
  setGenome(igv, "hg19")  
  showGenomicRegion(igv, "MEF2C")  
  # create three arbitrary tracks  
  base.loc <- 88883100  
  tbl <- data.frame(chrom=rep("chr5", 3),  
                   start=c(base.loc, base.loc+100, base.loc + 250),  
                   end=c(base.loc + 50, base.loc+120, base.loc+290),  
                   name=c("a", "b", "c"),  
                   score=runif(3),  
                   strand=rep("*", 3),  
                   stringsAsFactors=FALSE)
```

```

track.1 <- DataFrameAnnotationTrack("track.1", tbl, color="red", displayMode="SQUISHED")
track.2 <- DataFrameAnnotationTrack("track.2", tbl, color="blue", displayMode="SQUISHED")
track.3 <- DataFrameAnnotationTrack("track.3", tbl, color="green", displayMode="SQUISHED")
displayTrack(igv, track.1)
displayTrack(igv, track.2)
displayTrack(igv, track.3)
removeTracksByName(igv, "track.2")
#-----
# bulk removal of the remaining tracks,
# but leave the h19 reference track
#-----
removeTracksByName(igv, getTrackNames(igv)[-1])
}

```

---

saveToSVG, igvR-method *Get entire igv browser image in svg*

---

### Description

Get entire igv browser image in svg

### Usage

```

## S4 method for signature 'igvR'
saveToSVG(obj, filename)

```

### Arguments

|          |  |
|----------|--|
| obj      | An object of class igvR  |
| filename | character string, the name of the file to which the svg text will be written |

### Value

A character vector

---

setCustomGenome, igvR-method

*Specify the reference genome you wish to use, via full specification of all urls*

---

### Description

Specify the reference genome you wish to use, via full specification of all urls

**Usage**

```
## S4 method for signature 'igvR'
setCustomGenome(
  obj,
  id,
  genomeName,
  fastaURL,
  fastaIndexURL,
  chromosomeAliasURL = NA,
  cytobandURL = NA,
  geneAnnotationName = NA,
  geneAnnotationURL = NA,
  geneAnnotationTrackHeight = 200,
  geneAnnotationTrackColor = "darkblue",
  initialLocus = "all",
  visibilityWindow = 1e+06
)
```

**Arguments**

|                           |   |
|---------------------------|---|
| obj                       | An object of class igvR   |
| id                        | character string, a short name, displayed in the browser, e.g., "hg38", "tair10".   |
| genomeName                | character string, possibly longer, more descriptive than the id, e.g., "Human (GRCh38/hg38)"  |
| fastaURL                  | character string, e.g. "https://s3.amazonaws.com/igv.broadinstitute.org/genomes/seq/hg38/hg38.fa"   |
| fastaIndexURL             | character string, e.g. "https://s3.amazonaws.com/igv.broadinstitute.org/genomes/seq/hg38/hg38.fa.fai"   |
| chromosomeAliasURL        | character string, default NA, a tab-delimited file supporting multiple equivalent chromosome names. see details   |
| cytobandURL               | character string, default NA, a cytoband ideogram file in UCSC format, e.g. "https://s3.amazonaws.com/igv.broadinstitute.org/annotations/hg38/cytoBandIdeo.txt" |
| geneAnnotationName        | character string, e.g. "Refseq Genes", default NA   |
| geneAnnotationURL         | character string, e.g. "https://s3.amazonaws.com/igv.org/genomes/hg38/refGene.txt.gz", default NA   |
| geneAnnotationTrackHeight | numeric, pixels, e.g. 500. default 200  |
| geneAnnotationTrackColor  | character string, any legal CSS color, default "darkblue"   |
| initialLocus              | character string, e.g. "chr5:88,621,308-89,001,037" or "MEF2C"  |
| visibilityWindow          | numeric, number of bases over which to display features, default 1000000  |

**Value**

An empty string, an error message if any of the urls could not be reached

**Examples**

```

if(interactive()){
  igv <- igvR()
  setCustomGenome(igv,
    id="hg38",
    genomeName="Human (GRCh38/hg38)",
    fastaURL="https://s3.amazonaws.com/igv.broadinstitute.org/genomes/seq/hg38/hg38.fa",
    fastaIndexURL="https://s3.amazonaws.com/igv.broadinstitute.org/genomes/seq/hg38/hg38.fa.fai",
    chromosomeAliasURL=NA,
    cytobandURL="https://s3.amazonaws.com/igv.broadinstitute.org/annotations/hg38/cytoBandIdeo.txt",
    geneAnnotationName="Refseq Genes",
    geneAnnotationURL="https://s3.amazonaws.com/igv.org/genomes/hg38/refGene.txt.gz",
    geneAnnotationTrackHeight=300,
    geneAnnotationTrackColor="darkgreen",
    initialLocus="chr5:88,621,308-89,001,037",
    visibilityWindow=5000000)
}

```

---

setGenome, igvR-method *Specify the reference genome, currently limited to hg38, hg19, mm10, tair10.*

---

**Description**

Specify the reference genome, currently limited to hg38, hg19, mm10, tair10.

**Usage**

```

## S4 method for signature 'igvR'
setGenome(obj, genomeName)

```

**Arguments**

|            |   |
|------------|---|
| obj        | An object of class igvR                                     |
| genomeName | A character string, one of "hg38", "hg19", "mm10", "tair10" |

**Value**

An empty string, an error message if the requested genome is not yet supported

**Examples**

```

if(interactive()){
  igv <- igvR()
  setGenome(igv, "mm10")
}

```

---

setTrackClickFunction, igvR-method  
*Specify (supply) the javascript function run on track click event*

---

### **Description**

Specify (supply) the javascript function run on track click event

### **Usage**

```
## S4 method for signature 'igvR'  
setTrackClickFunction(obj, javascriptFunction)
```

### **Arguments**

|                    |  |
|--------------------|--|
| obj                | An object of class igvR                          |
| javascriptFunction | expressed as a 2-element named list: body + args |

### **Value**

""

---

setTrackHeight, igvR-method  
*Remove named tracks*

---

### **Description**

Remove named tracks

### **Usage**

```
## S4 method for signature 'igvR'  
setTrackHeight(obj, trackName, newHeight)
```

### **Arguments**

|           |                         |
|-----------|-------------------------|
| obj       | An object of class igvR |
| trackName | a character string      |
| newHeight | integer, in ixels       |

### **Value**

nothing

**See Also**

getTrackNames

---

showGenomicRegion, igvR-method

*Set the visible region, by explicit chromLoc string, or by named features in any currently loaded annotation tracks*

---

**Description**

Set the visible region, by explicit chromLoc string, or by named features in any currently loaded annotation tracks

**Usage**

```
## S4 method for signature 'igvR'
showGenomicRegion(obj, region)
```

**Arguments**

|        |  |
|--------|--|
| obj    | An object of class igvR  |
| region | A genomic location (rendered "chr5:9,234,343-9,236,000" or as a list: list(chrom="chr9", start=9234343, end=9236000)) or a labeled annotation in a searchable track, often a gene symbol, eg "MEF2C" |

**Value**

""

**Examples**

```
if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  x <- getGenomicRegion(igv)
  #-----
  # zoom out 2kb
  #-----
  showGenomicRegion(igv, with(x, sprintf("%s:%d-%d", chrom, start-1000, end+1000)))
}
```



---

showTrackLabels,igvR-method  
*Hide or show igv track labels*

---

**Description**

Hide or show igv track labels

**Usage**

```
## S4 method for signature 'igvR'
showTrackLabels(obj, newState)
```

**Arguments**

|          |                               |
|----------|-------------------------------|
| obj      | An object of class igvR       |
| newState | logical, either TRUE or FALSE |

**Value**

""

---

|             |                              |
|-------------|------------------------------|
| Track-class | <i>Constructor for Track</i> |
|-------------|------------------------------|

---

**Description**

Constructor for Track

**Usage**

```
Track(
  trackType = c("annotation", "quantitative", "alignment", "variant", "gwas"),
  sourceType = c("file", "gcs", "ga4gh"),
  fileFormat = c("bed", "gff", "gff3", "gtf", "wig", "bigWig", "bedGraph", "bam", "vcf",
    "seg"),
  trackName,
  onScreenOrder,
  color,
  height,
  autoTrackHeight,
  minTrackHeight,
  maxTrackHeight,
  visibilityWindow
)
```

**Arguments**

|                  |   |
|------------------|---|
| trackType        | One of "annotation", "quantitative", "variant".   |
| sourceType       | Only "file" is currently supported.   |
| fileFormat       | One of "bed", "bedGraph", "vcf"   |
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| onScreenOrder    | Numeric, for explicit placement of track within the current set.  |
| color            | A CSS color name (e.g., "red" or "#FF0000")   |
| height           | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| autoTrackHeight  | If true, then track height is adjusted dynamically, within the bounds set by minHeight and maxHeight, to accomodate features in view                            |
| minTrackHeight   | In pixels, minimum allowed  |
| maxTrackHeight   | In pixels, maximum allowed  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Value**

An object of class Track

**References**

<https://github.com/igvteam/igv.js/wiki/Tracks>  
[https://www.w3schools.com/cssref/css\\_colors.asp](https://www.w3schools.com/cssref/css_colors.asp)

---

trackInfo,Track-method

*Get basic info about a track: its type, file format, source and S4 class name*

---

**Description**

Get basic info about a track: its type, file format, source and S4 class name

**Usage**

```
## S4 method for signature 'Track'
trackInfo(obj)
```

**Arguments**

obj                    An object of base class Track

**Value**

A list with four fields: trackType, fileFormat, source, class name

---

*trackSize,BedpeInteractionsTrack-method*  
*Retrieve the size of the BedpeInteractionsTrack*

---

**Description**

Retrieve the size of the BedpeInteractionsTrack

**Usage**

```
## S4 method for signature 'BedpeInteractionsTrack'  
trackSize(obj)
```

**Arguments**

obj                    An object of class BedpeInteractionsTrack

**Value**

The number of elements

---

*trackSize,DataFrameAnnotationTrack-method*  
*Retrieve the size of the DataFrameAnnotationTrack*

---

**Description**

Retrieve the size of the DataFrameAnnotationTrack

**Usage**

```
## S4 method for signature 'DataFrameAnnotationTrack'  
trackSize(obj)
```

**Arguments**

obj                    An object of class UCSCBedAnnotationTrack

**Value**

The number of elements

**Examples**

```
base.loc <- 88883100
tbl <- data.frame(chrom=rep("chr5", 3),
                 start=c(base.loc, base.loc+100, base.loc + 250),
                 end=c(base.loc + 50, base.loc+120, base.loc+290),
                 name=c("a", "b", "c"),
                 score=runif(3),
                 strand=rep("*", 3),
                 stringsAsFactors=FALSE)

track <- DataFrameAnnotationTrack("dataframeTest", tbl)
trackSize(track)
```

---

trackSize,DataFrameQuantitativeTrack-method

*Retrieve the size of the DataFrameQuantitativeTrack*

---

**Description**

Retrieve the size of the DataFrameQuantitativeTrack

**Usage**

```
## S4 method for signature 'DataFrameQuantitativeTrack'
trackSize(obj)
```

**Arguments**

obj                    An object of class DataFrameQuantitativeTrack

**Value**

The number of elements

---

trackSize,GenomicAlignmentTrack-method  
*Retrieve the size of the GenomicAlignmentTrack*

---

**Description**

Retrieve the size of the GenomicAlignmentTrack

**Usage**

```
## S4 method for signature 'GenomicAlignmentTrack'  
trackSize(obj)
```

**Arguments**

obj                    An object of class GenomicAlignmentTrack

**Value**

The number of elements

---

trackSize,GFF3Track-method  
*Retrieve the size of the GFF3Track*

---

**Description**

Retrieve the size of the GFF3Track

**Usage**

```
## S4 method for signature 'GFF3Track'  
trackSize(obj)
```

**Arguments**

obj                    An object of class UCSCBedAnnotationTrack

**Value**

The number of elements

---

`trackSize,GRangesAnnotationTrack-method`

*Retrieve the size of the GRangesAnnotationTrack*

---

**Description**

Retrieve the size of the GRangesAnnotationTrack

**Usage**

```
## S4 method for signature 'GRangesAnnotationTrack'  
trackSize(obj)
```

**Arguments**

`obj`                    An object of class GRangesAnnotationTrack

**Value**

The number of elements

---

`trackSize,GRangesQuantitativeTrack-method`

*Retrieve the size of the GRangesQuantitativeTrack*

---

**Description**

Retrieve the size of the GRangesQuantitativeTrack

**Usage**

```
## S4 method for signature 'GRangesQuantitativeTrack'  
trackSize(obj)
```

**Arguments**

`obj`                    An object of class GRangesQuantitativeTrack

**Value**

The number of elements

---

trackSize,GWASTrack-method

*Retrieve the size of the GWASTrack*

---

### **Description**

Retrieve the size of the GWASTrack

### **Usage**

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

### **Arguments**

obj                    An object of class GWASTrack

### **Value**

The number of elements

---

trackSize,GWASUrlTrack-method

*Retrieve the size of the GWASUrlTrack*

---

### **Description**

Retrieve the size of the GWASUrlTrack

### **Usage**

```
## S4 method for signature 'GWASUrlTrack'  
trackSize(obj)
```

### **Arguments**

obj                    An object of class GWASUrlTrack

### **Value**

The number of elements

---

`trackSize,QuantitativeTrack-method`

*Retrieve the size of the QuantitativeTrack*

---

**Description**

Retrieve the size of the QuantitativeTrack

**Usage**

```
## S4 method for signature 'QuantitativeTrack'  
trackSize(obj)
```

**Arguments**

`obj`                    An object of class UCSCBedAnnotationTrack

**Value**

The number of elements

---

`trackSize,UCSCBedAnnotationTrack-method`

*Retrieve the size of theUCSCBedAnnotationTrack*

---

**Description**

Retrieve the size of theUCSCBedAnnotationTrack

**Usage**

```
## S4 method for signature 'UCSCBedAnnotationTrack'  
trackSize(obj)
```

**Arguments**

`obj`                    An object of class UCSCBedAnnotationTrack

**Value**

The number of elements



**Examples**

```
bed.filepath <- system.file(package = "rtracklayer", "tests", "test.bed")
gr.bed <- rtracklayer::import(bed.filepath)
track.1 <- UCSCBedAnnotationTrack("UCSC bed", gr.bed, color="blue", displayMode="SQUISHED")
trackSize(track.1)
```

---

trackSize,UCSCBedGraphQuantitativeTrack-method

*Retrieve the size of the UCSCBedGraphQuantitativeTrack*

---

**Description**

Retrieve the size of the UCSCBedGraphQuantitativeTrack

**Usage**

```
## S4 method for signature 'UCSCBedGraphQuantitativeTrack'
trackSize(obj)
```

**Arguments**

obj                    An object of class UCSCBedGraphQuantitativeTrack

**Value**

The number of elements

---

trackSize,VariantTrack-method

*Retrieve the size of the VariantTrack*

---

**Description**

Retrieve the size of the VariantTrack

**Usage**

```
## S4 method for signature 'VariantTrack'
trackSize(obj)
```

**Arguments**

obj                    An object of class VariantTrack

**Value**

The number of elements

---

 UCSCBedAnnotationTrack-class

*Constructor for UCSCBedAnnotationTrack*


---

### Description

UCSCBedAnnotationTrack creates and IGV track for bed objects imported using rtracklayer

### Usage

```
UCSCBedAnnotationTrack(
  trackName,
  annotation,
  color = "darkGrey",
  displayMode = "SQUISHED",
  trackHeight = 50,
  expandedRowHeight = 30,
  squishedRowHeight = 15,
  maxRows = 500,
  searchable = FALSE,
  visibilityWindow = 1e+05
)
```

### Arguments

|                   |   |
|-------------------|---|
| trackName         | A character string, used as track label by igv, we recommend unique names per track.  |
| annotation        | A UCSCData object imported by rtracklayer   |
| color             | A CSS color name (e.g., "red" or "#FF0000")   |
| displayMode       | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise.   |
| trackHeight       | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| expandedRowHeight | Height of each row of features in "EXPANDED" mode.  |
| squishedRowHeight | Height of each row of features in "SQUISHED" mode, for compact viewing.   |
| maxRows           | of features to display  |
| searchable        | If TRUE, labels on annotation elements may be used in search  |
| visibilityWindow  | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description goes here

**Value**

A UCSCBedAnnotationTrack object

**Examples**

```
bed.filepath <- system.file(package = "rtracklayer", "tests", "test.bed")
gr.bed <- rtracklayer::import(bed.filepath)
track <- UCSCBedAnnotationTrack("UCSC bed", gr.bed, color="blue", displayMode="SQUISHED")

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "UCSC bed10 demo")
  showGenomicRegion(igv, "chr7:127,469,879-127,476,276")
  displayTrack(igv, track)
}
```

---

UCSCBedGraphQuantitativeTrack-class

*Constructor for UCSCBedGraphQuantitativeTrack*

---

**Description**

UCSCBedGraphQuantitativeTrack creates an IGV track for bedGraph objects imported with rtracklayer

**Usage**

```
UCSCBedGraphQuantitativeTrack(
  trackName,
  quantitativeData,
  color = "blue",
  trackHeight = 50,
  autoscale = TRUE,
  min = NA_real_,
  max = NA_real_,
  visibilityWindow = 1e+05
)
```

**Arguments**

|           |  |
|-----------|--|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
|-----------|--|

|                  |   |
|------------------|---|
| quantitativeData | A GRanges object with (at least) a "score" metadata column  |
| color            | A CSS color name (e.g., "red" or "#FF0000")   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| autoscale        | Autoscale track to maximum value in view  |
| min              | Sets the minimum value for the data (y-axis) scale. Usually zero.   |
| max              | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description goes here

**Value**

A UCSCBedGraphQuantitativeTrack object

**Examples**

```
bedGraph.filepath <- system.file(package = "rtracklayer", "tests", "test.bedGraph")
gr.bedGraph <- rtracklayer::import(bedGraph.filepath)
track <- UCSCBedGraphQuantitativeTrack("UCSCBedGraphTest", gr.bedGraph)

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  setBrowserWindowTitle(igv, "UCSC BedGraph demo")
  displayTrack(igv, track)
  Sys.sleep(1) # pause before zoomin
  showGenomicRegion(igv, "chr18:59,103,373-59,105,673")
}
```

---

url.exists

*url.exists*

---

**Description**

a helper function for mostly internal use, tests for availability of a url, modeled after file.exists  
a helper function for mostly internal use, tests for availability of a url, modeled after file.exists

**Usage**

```
url.exists(url)
```

```
url.exists(url)
```

**Arguments**

url                    character the http address to test

**Value**

logical TRUE or FALSE

logical TRUE or FALSE

**Examples**

```
if(interactive()){  
  igv <- igvR()  
  ping(igv)  
}
```

---

VariantTrack-class      *Constructor for VariantTrack*

---

**Description**

VariantTrack creates an IGV track for VCF (variant call format) objects, either local or at a remote url

**Usage**

```
VariantTrack(  
  trackName,  
  vcf,  
  trackHeight = 50,  
  anchorColor = "pink",  
  homvarColor = "rgb(17,248,254)",  
  hetvarColor = "rgb(34,12,253)",  
  homrefColor = "rgb(200,200,200)",  
  displayMode = "EXPANDED",  
  visibilityWindow = 1e+05  
)
```

**Arguments**

|                  |   |
|------------------|---|
| trackName        | A character string, used as track label by igv, we recommend unique names per track.  |
| vcf              | A VCF object from the VariantAnnotation package, or a list(url=x, index=y) pointing to a vcf file   |
| trackHeight      | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)   |
| anchorColor      | CSS color name (e.g., "red" or "#FF0000") for the "anchoring" graphical segment in the track  |
| homvarColor      | CSS color name for homozygous variant samples, rgb(17,248,254) by default (~turquoise)  |
| hetvarColor      | CSS color name for heterozygous variant samples, rgb(34,12,253) by default (~royalBlue)   |
| homrefColor      | CSS color names for homozygous reference samples, rgb(200,200,200) by default (~lightGray)  |
| displayMode      | "COLLAPSED", "EXPANDED", or "SQUISHED"  |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

**Details**

Detailed description goes here

**Value**

A VariantTrack object

**Examples**

```
#-----
# first, from a local file
#-----

f <- system.file("extdata", "chr22.vcf.gz", package="VariantAnnotation")
roi <- GRanges(seqnames="22", ranges=IRanges(start=c(50301422, 50989541),
                                             end=c(50312106, 51001328),
                                             names=c("gene_79087", "gene_644186")))
vcf.sub <- VariantAnnotation::readVcf(f, "hg19", param=roi)
track.local <- VariantTrack("chr22-tiny", vcf.sub)

#-----
# now try a url track
#-----

data.url <- sprintf("%s/%s", "https://s3.amazonaws.com/1000genomes/release/20130502",
                    "ALL.wgs.phase3_shapeit2_mvncall_integrated_v5b.20130502.sites.vcf.gz")
```

```
index.url <- sprintf("%s.tbi", data.url)
url <- list(data=data.url, index=index.url)

track.url <- VariantTrack("1kg", url)
```

---

zoomIn,igvR-method      *zoom the genome view in by a factor of 2*

---

**Description**

zoom the genome view in by a factor of 2

**Usage**

```
## S4 method for signature 'igvR'
zoomIn(obj)
```

**Arguments**

obj                      An object of class igvR

**Value**

""

---

zoomOut,igvR-method      *zoom the genome view out by a factor of 2*

---

**Description**

zoom the genome view out by a factor of 2

**Usage**

```
## S4 method for signature 'igvR'
zoomOut(obj)
```

**Arguments**

obj                      An object of class igvR

**Value**

""

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