

# 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

**VignetteBuilder** knitr

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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("x", 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 an 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

|                     |                                      |
|---------------------|--------------------------------------|
| <code>obj</code>    | An object of class <code>igvR</code> |
| <code>status</code> | 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.H10MO.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 reconized 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 | <i>Constructor for GFF3Track</i> |
|-----------------|----------------------------------|

---

**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 | <i>Create an igvR object</i> |
|------------|------------------------------|

---

### 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



---

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.fa"                                                            |
| 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

*Constructor for Track*


---

**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 heterzygous 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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