

# 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://paul-shannon.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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## R topics documented:

BedpeInteractionsTrack-class . . . . .	3
currently.supported.stock.genomes . . . . .	4
DataFrameAnnotationTrack-class . . . . .	5
DataFrameQuantitativeTrack-class . . . . .	6
displayTrack,igvR-method . . . . .	8
enableMotifLogoPopups,igvR-method . . . . .	9
GenomicAlignmentTrack-class . . . . .	10
getGenomicRegion,igvR-method . . . . .	11
getSupportedGenomes,igvR-method . . . . .	12
getTrackNames,igvR-method . . . . .	13
GFF3Track-class . . . . .	13
GRangesAnnotationTrack-class . . . . .	15
GRangesQuantitativeTrack-class . . . . .	16
GWASTrack-class . . . . .	18
GWASUrlTrack . . . . .	19
igvAnnotationTrack-class . . . . .	20
igvR-class . . . . .	21
parseAndValidateGenomeSpec . . . . .	23
ping,igvR-method . . . . .	24
QuantitativeTrack-class . . . . .	25
RemoteAlignmentTrack-class . . . . .	26
removeTracksByName,igvR-method . . . . .	27
saveToSVG,igvR-method . . . . .	28
setCustomGenome,igvR-method . . . . .	28
setGenome,igvR-method . . . . .	30
setTrackClickFunction,igvR-method . . . . .	31
setTrackHeight,igvR-method . . . . .	31
showGenomicRegion,igvR-method . . . . .	32
showTrackLabels,igvR-method . . . . .	33
Track-class . . . . .	33
trackInfo,Track-method . . . . .	34
trackSize,BedpeInteractionsTrack-method . . . . .	35
trackSize,DataFrameAnnotationTrack-method . . . . .	35
trackSize,DataFrameQuantitativeTrack-method . . . . .	36
trackSize,GenomicAlignmentTrack-method . . . . .	37
trackSize,GFF3Track-method . . . . .	37
trackSize,GRangesAnnotationTrack-method . . . . .	38
trackSize,GRangesQuantitativeTrack-method . . . . .	38
trackSize,GWASTrack-method . . . . .	39
trackSize,GWASUrlTrack-method . . . . .	39
trackSize,QuantitativeTrack-method . . . . .	40

*BedpeInteractionsTrack*-class 3

trackSize,UCSCBedAnnotationTrack-method . . . . .	40
trackSize,UCSCBedGraphQuantitativeTrack-method . . . . .	41
trackSize,VariantTrack-method . . . . .	41
UCSCBedAnnotationTrack-class . . . . .	42
UCSCBedGraphQuantitativeTrack-class . . . . .	43
url.exists . . . . .	44
VariantTrack-class . . . . .	45
zoomIn,igvR-method . . . . .	47
zoomOut,igvR-method . . . . .	47

**Index** 48

---

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 = "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 base R data.frame
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 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,
  color = "darkBlue",
  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
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)
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 <- GWASUrlTrack("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,
  color = "darkBlue",
  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
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)

`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

### 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://igv-data.systemsbiology.net/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"),
  color = "gray",
  sourceType = "file",
  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)
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"),
  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**

""

# Index

- .BedpeInteractionsTrack
  - (BedpeInteractionsTrack-class),  
[3](#)
- .DataFrameAnnotationTrack
  - (DataFrameAnnotationTrack-class),  
[5](#)
- .DataFrameQuantitativeTrack
  - (DataFrameQuantitativeTrack-class),  
[6](#)
- .GFF3Track (GFF3Track-class), [13](#)
- .GRangesAnnotationTrack
  - (GRangesAnnotationTrack-class),  
[15](#)
- .GRangesQuantitativeTrack
  - (GRangesQuantitativeTrack-class),  
[16](#)
- .GWASTrack (GWASTrack-class), [18](#)
- .GWASURLTrack (GWASTrack-class), [18](#)
- .GenomicAlignmentTrack
  - (GenomicAlignmentTrack-class),  
[10](#)
- .QuantitativeTrack
  - (QuantitativeTrack-class), [25](#)
- .RemoteAlignmentTrack
  - (RemoteAlignmentTrack-class),  
[26](#)
- .Track (Track-class), [33](#)
- .UCSCBedAnnotationTrack
  - (UCSCBedAnnotationTrack-class),  
[42](#)
- .UCSCBedGraphQuantitativeTrack
  - (UCSCBedGraphQuantitativeTrack-class),  
[43](#)
- .igvAnnotationTrack
  - (igvAnnotationTrack-class), [20](#)
- .igvR (igvR-class), [21](#)
- BedpeInteractionsTrack
  - (BedpeInteractionsTrack-class),  
[3](#)
- BedpeInteractionsTrack-class, [3](#)
- currently.supported.stock.genomes, [4](#)
- DataFrameAnnotationTrack
  - (DataFrameAnnotationTrack-class),  
[5](#)
- DataFrameAnnotationTrack-class, [5](#)
- DataFrameQuantitativeTrack
  - (DataFrameQuantitativeTrack-class),  
[6](#)
- DataFrameQuantitativeTrack-class, [6](#)
- displayTrack
  - (displayTrack, igvR-method), [8](#)
- displayTrack, igvR-method, [8](#)
- enableMotifLogoPopups
  - (enableMotifLogoPopups, igvR-method),  
[9](#)
- enableMotifLogoPopups, igvR-method, [9](#)
- GenomicAlignmentTrack
  - (GenomicAlignmentTrack-class),  
[10](#)
- GenomicAlignmentTrack-class, [10](#)
- getGenomicRegion
  - (getGenomicRegion, igvR-method),  
[11](#)
- getGenomicRegion, igvR-method, [11](#)
- getSupportedGenomes
  - (getSupportedGenomes, igvR-method),  
[12](#)
- getSupportedGenomes, igvR-method, [12](#)
- getTrackNames
  - (getTrackNames, igvR-method), [13](#)
- getTrackNames, igvR-method, [13](#)
- GFF3Track (GFF3Track-class), [13](#)
- GFF3Track-class, [13](#)
- GRangesAnnotationTrack
  - (GRangesAnnotationTrack-class),  
[15](#)



- GRangesAnnotationTrack-class, 15
- GRangesQuantitativeTrack
  - (GRangesQuantitativeTrack-class), 16
- GRangesQuantitativeTrack-class, 16
- GWASTrack (GWASTrack-class), 18
- GWASTrack-class, 18
- GWASUrlTrack, 19
  
- igvAnnotationTrack
  - (igvAnnotationTrack-class), 20
- igvAnnotationTrack-class, 20
- igvR (igvR-class), 21
- igvR-class, 21
  
- parseAndValidateGenomeSpec, 23
- ping (ping, igvR-method), 24
- ping, igvR-method, 24
  
- QuantitativeTrack
  - (QuantitativeTrack-class), 25
- QuantitativeTrack-class, 25
  
- RemoteAlignmentTrack
  - (RemoteAlignmentTrack-class), 26
- RemoteAlignmentTrack-class, 26
- removeTracksByName
  - (removeTracksByName, igvR-method), 27
- removeTracksByName, igvR-method, 27
  
- saveToSVG (saveToSVG, igvR-method), 28
- saveToSVG, igvR-method, 28
- setCustomGenome
  - (setCustomGenome, igvR-method), 28
- setCustomGenome, igvR-method, 28
- setGenome (setGenome, igvR-method), 30
- setGenome, igvR-method, 30
- setTrackClickFunction
  - (setTrackClickFunction, igvR-method), 31
- setTrackClickFunction, igvR-method, 31
- setTrackHeight
  - (setTrackHeight, igvR-method), 31
- setTrackHeight, igvR-method, 31
  
- showGenomicRegion
  - (showGenomicRegion, igvR-method), 32
- showGenomicRegion, igvR-method, 32
- showTrackLabels
  - (showTrackLabels, igvR-method), 33
- showTrackLabels, igvR-method, 33
  
- Track (Track-class), 33
- Track-class, 33
- trackInfo (trackInfo, Track-method), 34
- trackInfo, Track-method, 34
- trackSize
  - (trackSize, QuantitativeTrack-method), 40
- trackSize, BedpeInteractionsTrack-method, 35
- trackSize, DataFrameAnnotationTrack-method, 35
- trackSize, DataFrameQuantitativeTrack-method, 36
- trackSize, GenomicAlignmentTrack-method, 37
- trackSize, GFF3Track-method, 37
- trackSize, GRangesAnnotationTrack-method, 38
- trackSize, GRangesQuantitativeTrack-method, 38
- trackSize, GWASTrack-method, 39
- trackSize, GWASUrlTrack-method, 39
- trackSize, QuantitativeTrack-method, 40
- trackSize, UCSCBedAnnotationTrack-method, 40
- trackSize, UCSCBedGraphQuantitativeTrack-method, 41
- trackSize, VariantTrack-method, 41
  
- UCSCBedAnnotationTrack
  - (UCSCBedAnnotationTrack-class), 42
- UCSCBedAnnotationTrack-class, 42
- UCSCBedGraphQuantitativeTrack
  - (UCSCBedGraphQuantitativeTrack-class), 43
- UCSCBedGraphQuantitativeTrack-class, 43
- url.exists, 44

VariantTrack (VariantTrack-class), [45](#)

VariantTrack-class, [45](#)

zoomIn (zoomIn, igvR-method), [47](#)

zoomIn, igvR-method, [47](#)

zoomOut (zoomOut, igvR-method), [47](#)

zoomOut, igvR-method, [47](#)