

# Package ‘igvR’

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**Type** Package

**Title** igvR: integrative genomics viewer

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**Author** Paul Shannon

**Maintainer** Paul Shannon <paul.thurmond.shannon@gmail.com>

**Depends** R (>= 3.5.0), GenomicRanges, GenomicAlignments, BrowserViz (>= 2.9.1)

**Imports** methods, BiocGenerics, httpuv, utils, MotifDb, seqLogo, rtracklayer, VariantAnnotation, RColorBrewer

**Suggests** RUnit, BiocStyle, knitr, rmarkdown

**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' 'igvR.R'

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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
roi <- with(tbl.bedpe, sprintf("%s:%d-%d", chrom1[1], min(start1)-shoulder, max(end2) + shoulder))
# showGenomicRegion(igv, roi)

# displayTrack(igv, track)
```

---

 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("dataframeTest", tbl)
```

---

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.

<code>max</code>	Sets the maximum value for the data (y-axis) scale. This value is ignored if <code>autoscale</code> is <code>TRUE</code>
<code>visibilityWindow</code>	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 <- 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 <- DataFrameQuantitativeTrack("dataframeTest", tbl, autoscale=TRUE)
```

---

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")  
  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.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 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"  
}
```

---

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)
```

---

`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	In practice, this is always "localhost"
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
```

---

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

---

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

---

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

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

---

**Description**

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

**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**

""

---

showGenomicRegion, igvR-method

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

---

**Description**

Set the visible region, by explicit chromLoc string, or by named features in any curenly 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)))
}
```

Track-class

*Constructor for Track***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 fiels

**Examples**

```
track <- Track(trackType="annotation", sourceType="file", fileFormat="bed",
              trackName="demoTrack", onScreenOrder=NA_integer_, color="red",
              height=40, autoTrackHeight=FALSE, minTrackHeight=50, maxTrackHeight=200,
              visibilityWindow=100000)
trackInfo(track)
```

---

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("x", 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,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,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")
```

---

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)
```

---

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)
```

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