

Package ‘igvR’

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Type Package

Title igvR: integrative genomics viewer

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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/>

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biocViews Visualization, ThirdPartyClient, GenomeBrowsers

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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 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 <- 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 reconized color ("red") or a hex string ("#FF8532")

Details

Detailed description goes here

Value

A GenomicAlignmentTrack object

Examples

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

getGenomicRegion, igvR-method

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

Description

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

Usage

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

Arguments

obj An object of class igvR

Value

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

Examples

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

```
getSupportedGenomes, igvR-method
```

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

Description

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

Usage

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

Arguments

obj An object of class igvR

Value

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

Examples

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

```
getTrackNames, igvR-method
```

Get the names of all the tracks currently displayed in igv

Description

Get the names of all the tracks currently displayed in igv

Usage

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

Arguments

obj An object of class igvR

Value

A character vector

Examples

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

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

Create an igvR object

Description

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

Usage

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

Arguments

portRange	The constructor looks for a free websocket port in this range. 15000:15100 by default
host	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

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

""

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)))
}
```

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 min-Height 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

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("*", 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 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)
```

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