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/`

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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'

NeedsCompilation no

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.1.1

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R topics documented:

`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 mottif 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 coordiates 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 opague 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 openend. 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

`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 descirptive then 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`

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

---

Description

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

---

Description

Set the visible region, by explicit chromLoc string, or by named features in any curently 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 accomdodate 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 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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