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 (>= 2.7.20)

Imports methods, BiocGenerics, httpuv, utils, MotifDb, seqLogo, rtracklayer, VariantAnnotation, randomcoloR

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' 'igvR.R'

NeedsCompilation no

VignetteBuilder knitr

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R topics documented:

`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

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

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", "vdf"
`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,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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