

Package ‘igvR’

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Type Package

Title igvR: integrative genomics viewer

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Suggests RUnit, BiocStyle, knitr, rmarkdown

Description Access to igv.js, the Integrative Genomics Viewer running in a web browser.

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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' 'igvR.R'

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DataFrameAnnotationTrack-class

Constructor for DataFrameAnnotationTrack

Description

DataFrameAnnotationTrack creates and 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.

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()
  Sys.sleep(2)
  setGenome(igv, "hg38")
  Sys.sleep(5)
  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",
                                    autoscale=TRUE, displayMode="EXPANDED")
  displayTrack(igv, track)
}
```

getGenomicRegion, igvR-method

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

Description

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

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()
  Sys.sleep(2)
  setGenome(igv, "hg38")
  Sys.sleep(5)
  showGenomicRegion(igv, "MEF2C")
  getGenomicRegion(igv)
  # list(chrom="chr5", start=88717241, end=88884466, string="chr5:88,717,241-88,884,466")
}
```

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()
  Sys.sleep(2)
  setGenome(igv, "hg19")
  Sys.sleep(5)
  getTrackNames(igv)    # "Gencode v18"
}
```

GRangesAnnotationTrack-class

Constructor for GRangesAnnotationTrack

Description

GRangesAnnotationTrack creates an 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,
                   displayMode = c("SQUISHED", "COLLAPSED", "EXPANDED"),
                   sourceType = "file", trackHeight = 30, expandedRowHeight = 30,
                   squishedRowHeight = 15, maxRows = 500, searchable = FALSE,
                   visibilityWindow = 1e+05)
```

Arguments

trackName	A character string, used as track label by igv, we recommend unique names per track.
annotation	An opaque type, currently either a data.frame, GRanges, or UCSCBed object from rtracklayer.
fileFormat	Only "bed" is currently supported.
color	A CSS color name (e.g., "red" or "#FF0000")
displayMode	"COLLAPSED", "EXPANDED", or "SQUISHED"
sourceType	Only "file" sources are currently supported.
trackHeight	track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files)
expandedRowHeight	Height of each row of features in "EXPANDED" mode.
squishedRowHeight	Height of each row of features in "SQUISHED" mode, for compact viewing.

maxRows	of features to display
searchable	If TRUE, labels on annotation elements may be used in search
visibilityWindow	Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types.

Value

An igvAnnotationTrack object

igvR-class	<i>Create an igvR object</i>
------------	------------------------------

Description

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

Usage

```
igvR(portRange = 15000:15100, host = "localhost", title = "igvR",
      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
quiet	A logical variable controlling verbosity during execution

Value

An object of the igvR class

Examples

```
if(interactive()){
  igv <- igvR(title="igv demo")
  Sys.sleep(2)
  setGenome(igv, "hg38")
  Sys.sleep(5)
  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", autoscale=TRUE,
                                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)
```

Arguments

obj An object of class igvR

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, 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()
  Sys.sleep(2)
  setGenome(igv, "hg19")
  Sys.sleep(5) # give igv.js time to load
  # 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])
}
```

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()
  Sys.sleep(2)
  setGenome(igv, "mm10")
}
```

showGenomicRegion, igvR-method

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

Description

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

Usage

```
## S4 method for signature 'igvR'
showGenomicRegion(obj, region)
```

Arguments

obj	An object of class igvR
region	A genomic location (rendered "chr5:9,234,343-9,236,000" or as a list: list(chrom="chr9", start=9234343, end=9236000)) or a labeled annotation in a searchable track, often a gene symbol, eg "MEF2C"

Value

""

Examples

```
if(interactive()){
  igv <- igvR()
  Sys.sleep(2)
  setGenome(igv, "hg38")
  Sys.sleep(5)
  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 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,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,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 <- 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 <- 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 <- 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 <- 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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