

Package ‘igvR’

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Type Package

Title igvR: integrative genomics viewer

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Imports methods, BiocGenerics, httpuv, utils, MotifDb, seqLogo, rtracklayer, VariantAnnotation, 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/>

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biocViews Visualization, ThirdPartyClient, GenomeBrowsers

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'DataFrameAnnotationTrack.R' 'VariantTrack.R'
'QuantitativeTrack.R' 'DataFrameQuantitativeTrack.R'
'UCSCBedGraphQuantitativeTrack.R' 'GRangesAnnotationTrack.R'
'GRangesQuantitativeTrack.R' 'GenomicAlignmentTrack.R' 'igvR.R'

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R topics documented:

| | |
|--|-----------|
| DataFrameAnnotationTrack-class | 2 |
| DataFrameQuantitativeTrack-class | 3 |
| displayTrack,igvR-method | 5 |
| enableMotifLogoPopups,igvR-method | 6 |
| GenomicAlignmentTrack-class | 7 |
| getGenomicRegion,igvR-method | 8 |
| getSupportedGenomes,igvR-method | 8 |
| getTrackNames,igvR-method | 9 |
| GRangesAnnotationTrack-class | 10 |
| GRangesQuantitativeTrack-class | 11 |
| igvAnnotationTrack-class | 12 |
| igvR-class | 13 |
| ping,igvR-method | 14 |
| QuantitativeTrack-class | 15 |
| removeTracksByName,igvR-method | 16 |
| saveToSVG,igvR-method | 17 |
| setGenome,igvR-method | 17 |
| setTrackClickFunction,igvR-method | 18 |
| showGenomicRegion,igvR-method | 18 |
| Track-class | 19 |
| trackInfo,Track-method | 20 |
| trackSize,DataFrameAnnotationTrack-method | 21 |
| trackSize,DataFrameQuantitativeTrack-method | 21 |
| trackSize,GenomicAlignmentTrack-method | 22 |
| trackSize,GRangesAnnotationTrack-method | 22 |
| trackSize,GRangesQuantitativeTrack-method | 23 |
| trackSize,QuantitativeTrack-method | 23 |
| trackSize,UCSCBedAnnotationTrack-method | 24 |
| trackSize,UCSCBedGraphQuantitativeTrack-method | 24 |
| trackSize,VariantTrack-method | 25 |
| UCSCBedAnnotationTrack-class | 25 |
| UCSCBedGraphQuantitativeTrack-class | 26 |
| VariantTrack-class | 27 |
| Index | 29 |

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 motif log popups on or off
```

Description

Some tracks represent transcription factor binding sites, traditionally represented as a motif logo. use this method to enable that capability - which depends upon a properly constructed `tbl.regions` data.frame in a `DataFrameAnnotationTrack`: in addition to the usual (and mandatory) `chrom`, `start`, and `end` columns. To enable track-click popups over binding site, `tbl.regions` data.frame must also have a "name" column, which this format, by example: "MotifDb::Hsapiens-HOCOMOCov10-MEF2C_HUMAN.H10MO.C" The first part of the name, "MotifDb::", tells igv you want to view the specified MotifDb pwm (motif logo, a matrix) when the binding site track element is clicked.

Limitations: This method only works after a call to `setGenome(igv, "your genome of interest")`. It only works with `DataFrameAnnotationTrack` objects (for now)

Usage

```
## S4 method for signature 'igvR'
enableMotifLogoPopups(obj, status)
```

Arguments

| | |
|---------------------|--------------------------------------|
| <code>obj</code> | An object of class <code>igvR</code> |
| <code>status</code> | 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 an IGV track for bed-like objects expressed as GRanges

Usage

```
GenomicAlignmentTrack(trackName, alignment, trackHeight = 50,  
  visibilityWindow = 30000, color = "gray")
```

Arguments

| | |
|------------------|---|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| alignment | A GAlignments object |
| trackHeight | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files) |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |
| color | A character string, either a recognized color ("red") or a hex string ("FF8532") |

Details

Detailed description goes here

Value

A GenomicAlignmentTrack object

Examples

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

getGenomicRegion, igvR-method

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

Description

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

Usage

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

Arguments

obj An object of class igvR

Value

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

Examples

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

getSupportedGenomes, igvR-method

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

Description

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

Usage

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

Arguments

obj An object of class igvR

Value

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

Examples

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

getTrackNames, igvR-method

Get the names of all the tracks currently displayed in igv

Description

Get the names of all the tracks currently displayed in igv

Usage

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

Arguments

obj An object of class igvR

Value

A character vector

Examples

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

GRangesAnnotationTrack-class

Constructor for GRangesAnnotationTrack

Description

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

Arguments

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

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

Value

An igvAnnotationTrack object

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

Description

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

Usage

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

Arguments

| | |
|-------------|---|
| portRange | The constructor looks for a free websocket port in this range. 15000:15100 by default |
| host | In practice, this is always "localhost" |
| title | Used for the web browser window, "igvR" by default |
| browserFile | The full path to the bundled html, js and libraries, and css which constitute the browser app |
| quiet | A logical variable controlling verbosity during execution |

Value

An object of the igvR class

Examples

```
if(interactive()){
  igv <- igvR(title="igv demo")
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  #-----
  # an easy transparent way to create a bed track
  #-----
  base.loc <- 88883100
  tbl <- data.frame(chrom=rep("chr5", 3),
```

```

start=c(base.loc, base.loc+100, base.loc + 250),
end=c(base.loc + 50, base.loc+120, base.loc+290),
name=c("a", "b", "c"),
score=runif(3),
strand=rep("*", 3),
stringsAsFactors=FALSE)

track <- DataFrameAnnotationTrack("dataframeTest", tbl, color="red", displayMode="EXPANDED")
displayTrack(igv, track)
showGenomicRegion(igv, sprintf("chr5:%d-%d", base.loc-100, base.loc+350))
} # if interactive

```

ping,igvR-method

Test the connection between your R session and the webapp

Description

Test the connection between your R session and the webapp

Usage

```
## S4 method for signature 'igvR'
ping(obj, msecDelay = 0)
```

Arguments

| | |
|-----------|---|
| obj | An object of class igvR |
| msecDelay | don't return until these many milliseconds have passed, default 0 |

Value

"pong"

Examples

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

 QuantitativeTrack-class

Constructor for QuantitativeTrack

Description

QuantitativeTrack creates an IGV track for genomic tracks in which a numerical value is associated with each reported location.

Usage

```
QuantitativeTrack(trackName, quantitativeData, fileFormat = c("wig",
  "bigWig", "bedGraph"), color = "gray", sourceType = "file",
  autoscale = TRUE, min = NA_real_, max = NA_real_,
  visibilityWindow = 1e+05)
```

Arguments

| | |
|------------------|---|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| quantitativeData | A polyvalent object, either a data.frame, GRanges, or UCSCBedGraphQuantitative object |
| fileFormat | only "bedGraph" supported at present; wig and bigWig support soon. |
| color | A CSS color name (e.g., "red" or "#FF0000") |
| sourceType | only "file" supported at present ("gcs" for Google Cloud Storage, and "ga4gh" for the Global Alliance API may come) |
| autoscale | Autoscale track to maximum value in view |
| min | Sets the minimum value for the data (y-axis) scale. Usually zero. |
| max | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

Details

Detailed description will go here

Value

A QuantitativeTrack object

```
removeTracksByName, igvR-method
      Remove named tracks
```

Description

Remove named tracks

Usage

```
## S4 method for signature 'igvR'
removeTracksByName(obj, trackNames)
```

Arguments

| | |
|------------|-------------------------|
| obj | An object of class igvR |
| trackNames | a character vector |

Value

A character vector

See Also

getTrackNames

Examples

```
if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg19")
  showGenomicRegion(igv, "MEF2C")
  # create three arbitrary tracks
  base.loc <- 88883100
  tbl <- data.frame(chrom=rep("chr5", 3),
                    start=c(base.loc, base.loc+100, base.loc + 250),
                    end=c(base.loc + 50, base.loc+120, base.loc+290),
                    name=c("a", "b", "c"),
                    score=runif(3),
                    strand=rep("*", 3),
                    stringsAsFactors=FALSE)
  track.1 <- DataFrameAnnotationTrack("track.1", tbl, color="red", displayMode="SQUISHED")
  track.2 <- DataFrameAnnotationTrack("track.2", tbl, color="blue", displayMode="SQUISHED")
  track.3 <- DataFrameAnnotationTrack("track.3", tbl, color="green", displayMode="SQUISHED")
  displayTrack(igv, track.1)
  displayTrack(igv, track.2)
  displayTrack(igv, track.3)
  removeTracksByName(igv, "track.2")
  #-----
  # bulk removal of the remaining tracks,
  # but leave the h19 reference track
  #-----
  removeTracksByName(igv, getTrackNames(igv)[-1])
}
```

saveToSVG,igvR-method *Get entire igv browser image in svg*

Description

Get entire igv browser image in svg

Usage

```
## S4 method for signature 'igvR'  
saveToSVG(obj, filename)
```

Arguments

| | |
|----------|--|
| obj | An object of class igvR |
| filename | character string, the name of the file to which the svg text will be written |

Value

A character vector

setGenome,igvR-method *Specify the reference genome, currently limited to hg38, hg19, mm10, tair10.*

Description

Specify the reference genome, currently limited to hg38, hg19, mm10, tair10.

Usage

```
## S4 method for signature 'igvR'  
setGenome(obj, genomeName)
```

Arguments

| | |
|------------|---|
| obj | An object of class igvR |
| genomeName | A character string, one of "hg38", "hg19", "mm10", "tair10" |

Value

An empty string, an error message if the requested genome is not yet supported

Examples

```
if(interactive()){  
  igv <- igvR()  
  setGenome(igv, "mm10")  
}
```

setTrackClickFunction,igvR-method

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

Description

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

Usage

```
## S4 method for signature 'igvR'
setTrackClickFunction(obj, javascriptFunction)
```

Arguments

obj An object of class igvR
 javascriptFunction expressed as a 2-element named list: body + args

Value

""

showGenomicRegion,igvR-method

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

Description

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

Usage

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

Arguments

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

Value

""

Examples

```

if(interactive()){
  igv <- igvR()
  setGenome(igv, "hg38")
  showGenomicRegion(igv, "MEF2C")
  x <- getGenomicRegion(igv)
  #-----
  # zoom out 2kb
  #-----
  showGenomicRegion(igv, with(x, sprintf("%s:%d-%d", chrom, start-1000, end+1000)))
}

```

Track-class

*Constructor for Track***Description**

Constructor for Track

Usage

```

Track(trackType = c("annotation", "quantitative", "alignment",
"variant"), sourceType = c("file", "gcs", "ga4gh"),
fileFormat = c("bed", "gff", "gff3", "gtf", "wig", "bigWig",
"bedGraph", "bam", "vcf", "seg"), trackName, onScreenOrder, color,
height, autoTrackHeight, minTrackHeight, maxTrackHeight,
visibilityWindow)

```

Arguments

| | |
|------------------|---|
| trackType | One of "annotation", "quantitative", "variant". |
| sourceType | Only "file" is currently supported. |
| fileFormat | One of "bed", "bedGraph", "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 min-Height and maxHeight, to accomodate features in view |
| minTrackHeight | In pixels, minimum allowed |
| maxTrackHeight | In pixels, maximum allowed |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

Value

An object of class Track

References

<https://github.com/igvteam/igv.js/wiki/Tracks>

https://www.w3schools.com/cssref/css_colors.asp

trackInfo, Track-method

Get basic info about a track: its type, file format, source and S4 class name

Description

Get basic info about a track: its type, file format, source and S4 class name

Usage

```
## S4 method for signature 'Track'  
trackInfo(obj)
```

Arguments

obj An object of base class Track

Value

A list with four fiels

Examples

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

trackSize,DataFrameAnnotationTrack-method

Retrieve the size of the DataFrameAnnotationTrack

Description

Retrieve the size of the DataFrameAnnotationTrack

Usage

```
## S4 method for signature 'DataFrameAnnotationTrack'  
trackSize(obj)
```

Arguments

obj An object of class UCSCBedAnnotationTrack

Value

The number of elements

Examples

```
base.loc <- 88883100  
tbl <- data.frame(chrom=rep("chr5", 3),  
                  start=c(base.loc, base.loc+100, base.loc + 250),  
                  end=c(base.loc + 50, base.loc+120, base.loc+290),  
                  name=c("a", "b", "c"),  
                  score=runif(3),  
                  strand=rep("x", 3),  
                  stringsAsFactors=FALSE)  
  
track <- DataFrameAnnotationTrack("dataframeTest", tbl)  
trackSize(track)
```

trackSize,DataFrameQuantitativeTrack-method

Retrieve the size of the DataFrameQuantitativeTrack

Description

Retrieve the size of the DataFrameQuantitativeTrack

Usage

```
## S4 method for signature 'DataFrameQuantitativeTrack'  
trackSize(obj)
```

Arguments

obj An object of class DataFrameQuantitativeTrack

Value

The number of elements

trackSize,GenomicAlignmentTrack-method

Retrieve the size of the GenomicAlignmentTrack

Description

Retrieve the size of the GenomicAlignmentTrack

Usage

```
## S4 method for signature 'GenomicAlignmentTrack'  
trackSize(obj)
```

Arguments

obj An object of class GenomicAlignmentTrack

Value

The number of elements

trackSize,GRangesAnnotationTrack-method

Retrieve the size of the GRangesAnnotationTrack

Description

Retrieve the size of the GRangesAnnotationTrack

Usage

```
## S4 method for signature 'GRangesAnnotationTrack'  
trackSize(obj)
```

Arguments

obj An object of class GRangesAnnotationTrack

Value

The number of elements

trackSize,GRangesQuantitativeTrack-method

Retrieve the size of the GRangesQuantitativeTrack

Description

Retrieve the size of the GRangesQuantitativeTrack

Usage

```
## S4 method for signature 'GRangesQuantitativeTrack'  
trackSize(obj)
```

Arguments

obj An object of class GRangesQuantitativeTrack

Value

The number of elements

trackSize,QuantitativeTrack-method

Retrieve the size of the QuantitativeTrack

Description

Retrieve the size of the QuantitativeTrack

Usage

```
## S4 method for signature 'QuantitativeTrack'  
trackSize(obj)
```

Arguments

obj An object of class UCSCBedAnnotationTrack

Value

The number of elements

trackSize,UCSCBedAnnotationTrack-method

Retrieve the size of theUCSCBedAnnotationTrack

Description

Retrieve the size of theUCSCBedAnnotationTrack

Usage

```
## S4 method for signature 'UCSCBedAnnotationTrack'  
trackSize(obj)
```

Arguments

obj An object of class UCSCBedAnnotationTrack

Value

The number of elements

Examples

```
bed.filepath <- system.file(package = "rtracklayer", "tests", "test.bed")  
gr.bed <- rtracklayer::import(bed.filepath)  
track.1 <- UCSCBedAnnotationTrack("UCSC bed", gr.bed, color="blue", displayMode="SQUISHED")  
trackSize(track.1)
```

trackSize,UCSCBedGraphQuantitativeTrack-method

Retrieve the size of the UCSCBedGraphQuantitativeTrack

Description

Retrieve the size of the UCSCBedGraphQuantitativeTrack

Usage

```
## S4 method for signature 'UCSCBedGraphQuantitativeTrack'  
trackSize(obj)
```

Arguments

obj An object of class UCSCBedGraphQuantitativeTrack

Value

The number of elements

 trackSize, VariantTrack-method

Retrieve the size of the VariantTrack

Description

Retrieve the size of the VariantTrack

Usage

```
## S4 method for signature 'VariantTrack'
trackSize(obj)
```

Arguments

obj An object of class VariantTrack

Value

The number of elements

UCSCBedAnnotationTrack-class

Constructor for UCSCBedAnnotationTrack

Description

UCSCBedAnnotationTrack creates and IGV track for bed objects imported using rtracklayer

Usage

```
UCSCBedAnnotationTrack(trackName, annotation, color = "darkGrey",
  displayMode = "SQUISHED", trackHeight = 50, expandedRowHeight = 30,
  squishedRowHeight = 15, maxRows = 500, searchable = FALSE,
  visibilityWindow = 1e+05)
```

Arguments

| | |
|-------------------|---|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| annotation | A UCSCData object imported by rtracklayer |
| color | A CSS color name (e.g., "red" or "#FF0000") |
| displayMode | "COLLAPSED", "SQUISHED" or "EXPANDED". Spelling and case must be precise. |
| trackHeight | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files) |
| expandedRowHeight | Height of each row of features in "EXPANDED" mode. |

| | |
|-------------------|---|
| squishedRowHeight | Height of each row of features in "SQUISHED" mode, for compact viewing. |
| maxRows | of features to display |
| searchable | If TRUE, labels on annotation elements may be used in search |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

Details

Detailed description goes here

Value

A UCSCBedAnnotationTrack object

Examples

```
bed.filepath <- system.file(package = "rtracklayer", "tests", "test.bed")
gr.bed <- rtracklayer::import(bed.filepath)
track <- UCSCBedAnnotationTrack("UCSC bed", gr.bed, color="blue", displayMode="SQUISHED")
```

UCSCBedGraphQuantitativeTrack-class

Constructor for UCSCBedGraphQuantitativeTrack

Description

UCSCBedGraphQuantitativeTrack creates an IGV track for bedGraph objects imported with rtracklayer

Usage

```
UCSCBedGraphQuantitativeTrack(trackName, quantitativeData,
  color = "blue", trackHeight = 50, autoscale = TRUE,
  min = NA_real_, max = NA_real_, visibilityWindow = 1e+05)
```

Arguments

| | |
|------------------|---|
| trackName | A character string, used as track label by igv, we recommend unique names per track. |
| quantitativeData | A GRanges object with (at least) a "score" metadata column |
| color | A CSS color name (e.g., "red" or "#FF0000") |
| trackHeight | track height, typically in range 20 (for annotations) and up to 1000 (for large sample vcf files) |
| autoscale | Autoscale track to maximum value in view |
| min | Sets the minimum value for the data (y-axis) scale. Usually zero. |

| | |
|------------------|---|
| max | Sets the maximum value for the data (y-axis) scale. This value is ignored if autoscale is TRUE |
| visibilityWindow | Maximum window size in base pairs for which indexed annotations or variants are displayed. Defaults: 1 MB for variants, whole chromosome for other track types. |

Details

Detailed description goes here

Value

A UCSCBedGraphQuantitativeTrack object

Examples

```
bedGraph.filepath <- system.file(package = "rtracklayer", "tests", "test.bedGraph")
gr.bedGraph <- rtracklayer::import(bedGraph.filepath)
track <- UCSCBedGraphQuantitativeTrack("UCSCBedGraphTest", gr.bedGraph)
```

| | |
|--------------------|-------------------------------------|
| VariantTrack-class | <i>Constructor for VariantTrack</i> |
|--------------------|-------------------------------------|

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)
```

Index

- .DataFrameAnnotationTrack
(DataFrameAnnotationTrack-class),
[2](#)
- .DataFrameQuantitativeTrack
(DataFrameQuantitativeTrack-class),
[3](#)
- .GRangesAnnotationTrack
(GRangesAnnotationTrack-class),
[10](#)
- .GRangesQuantitativeTrack
(GRangesQuantitativeTrack-class),
[11](#)
- .GenomicAlignmentTrack
(GenomicAlignmentTrack-class),
[7](#)
- .QuantitativeTrack
(QuantitativeTrack-class), [15](#)
- .Track (Track-class), [19](#)
- .UCSCBedAnnotationTrack
(UCSCBedAnnotationTrack-class),
[25](#)
- .UCSCBedGraphQuantitativeTrack
(UCSCBedGraphQuantitativeTrack-class),GRangesQuantitativeTrack-class, [11](#)
[26](#)
- .igvAnnotationTrack
(igvAnnotationTrack-class), [12](#)
- .igvR (igvR-class), [13](#)
- DataFrameAnnotationTrack
(DataFrameAnnotationTrack-class),
[2](#)
- DataFrameAnnotationTrack-class, [2](#)
- DataFrameQuantitativeTrack
(DataFrameQuantitativeTrack-class),
[3](#)
- DataFrameQuantitativeTrack-class, [3](#)
- displayTrack
(displayTrack, igvR-method), [5](#)
- displayTrack, igvR-method, [5](#)
- enableMotifLogoPopups
(enableMotifLogoPopups, igvR-method),
[6](#)
- enableMotifLogoPopups, igvR-method, [6](#)
- GenomicAlignmentTrack
(GenomicAlignmentTrack-class),
[7](#)
- GenomicAlignmentTrack-class, [7](#)
- getGenomicRegion
(getGenomicRegion, igvR-method),
[8](#)
- getGenomicRegion, igvR-method, [8](#)
- getSupportedGenomes
(getSupportedGenomes, igvR-method),
[8](#)
- getSupportedGenomes, igvR-method, [8](#)
- getTrackNames
(getTrackNames, igvR-method), [9](#)
- getTrackNames, igvR-method, [9](#)
- GRangesAnnotationTrack
(GRangesAnnotationTrack-class),
[10](#)
- GRangesAnnotationTrack-class, [10](#)
- GRangesQuantitativeTrack
(GRangesQuantitativeTrack-class),
[11](#)
- igvAnnotationTrack
(igvAnnotationTrack-class), [12](#)
- igvAnnotationTrack-class, [12](#)
- igvR (igvR-class), [13](#)
- igvR-class, [13](#)
- ping (ping, igvR-method), [14](#)
- ping, igvR-method, [14](#)
- QuantitativeTrack
(QuantitativeTrack-class), [15](#)
- QuantitativeTrack-class, [15](#)
- removeTracksByName
(removeTracksByName, igvR-method),
[16](#)
- removeTracksByName, igvR-method, [16](#)
- saveToSVG (saveToSVG, igvR-method), [17](#)
- saveToSVG, igvR-method, [17](#)
- setGenome (setGenome, igvR-method), [17](#)

setGenome, igvR-method, [17](#)
setTrackClickFunction
 (setTrackClickFunction, igvR-method),
 [18](#)
setTrackClickFunction, igvR-method, [18](#)
showGenomicRegion
 (showGenomicRegion, igvR-method),
 [18](#)
showGenomicRegion, igvR-method, [18](#)

Track (Track-class), [19](#)
Track-class, [19](#)
trackInfo (trackInfo, Track-method), [20](#)
trackInfo, Track-method, [20](#)
trackSize
 (trackSize, QuantitativeTrack-method),
 [23](#)
trackSize, DataFrameAnnotationTrack-method,
 [21](#)
trackSize, DataFrameQuantitativeTrack-method,
 [21](#)
trackSize, GenomicAlignmentTrack-method,
 [22](#)
trackSize, GRangesAnnotationTrack-method,
 [22](#)
trackSize, GRangesQuantitativeTrack-method,
 [23](#)
trackSize, QuantitativeTrack-method, [23](#)
trackSize, UCSCBedAnnotationTrack-method,
 [24](#)
trackSize, UCSCBedGraphQuantitativeTrack-method,
 [24](#)
trackSize, VariantTrack-method, [25](#)

UCSCBedAnnotationTrack
 (UCSCBedAnnotationTrack-class),
 [25](#)
UCSCBedAnnotationTrack-class, [25](#)
UCSCBedGraphQuantitativeTrack
 (UCSCBedGraphQuantitativeTrack-class),
 [26](#)
UCSCBedGraphQuantitativeTrack-class,
 [26](#)

VariantTrack (VariantTrack-class), [27](#)
VariantTrack-class, [27](#)