

# 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, VariantAnnotation, rtracklayer,  
BrowserViz (>= 2.0)

**Imports** methods, BiocGenerics, httpuv, utils

**Suggests** RUnit, BiocStyle, knitr, rmarkdown

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

**License** MIT + file LICENSE

**LazyLoad** yes

**biocViews** Visualization, ThirdPartyClient

**Collate** 'Track.R' 'AnnotationTrack.R' 'UCSCBedAnnotationTrack.R'  
'DataFrameAnnotationTrack.R' 'VariantTrack.R'  
'QuantitativeTrack.R' 'DataFrameQuantitativeTrack.R'  
'UCSCBedGraphQuantitativeTrack.R' 'GRangesAnnotationTrack.R'  
'GRangesQuantitativeTrack.R' 'igvR.R'

**NeedsCompilation** no

**VignetteBuilder** knitr

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---

AnnotationTrack-class *Constructor for AnnotationTrack*

---

### Description

Constructor for AnnotationTrack

### Usage

```
AnnotationTrack(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 AnnotationTrack object

---

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.
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("x", 3),
                 stringsAsFactors=FALSE)

track <- DataFrameAnnotationTrack("dataframeTest", tbl)
```

---

DataFrameQuantitativeTrack-class

*Constructor for DataFrameQuantitativeTrack*

---

### Description

DataFrameQuantitativeTrack creates an IGV track for bed objects imported using rtracklayer

### Usage

```
DataFrameQuantitativeTrack(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 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),
                 name=c("a", "b", "c"),
                 score=runif(3),
                 strand=rep("*", 3),
                 stringsAsFactors=FALSE)

track <- DataFrameQuantitativeTrack("dataframeTest", tbl)
```

---

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)
```

**Arguments**

obj	An object of class igvR
track	An object of some terminal (leaf) subclass of Track

**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", 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)
```

igvR-class

*Create an igvR object***Description**

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

**Usage**

```
igvR(portRange = 15000:15100, host = "localhost", title = "igvR",
     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", 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

### 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](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*

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### 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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