Package 'trackViewer'

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Type Package

Title A bioconductor package with minimalist design for drawing elegant tracks or lollipop plot

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Author Jianhong Ou, Yong-Xu Wang, Lihua Julie Zhu

Maintainer Jianhong Ou <jianhong.ou@umassmed.edu>

Description Visualize mapped reads along with annotation as track layers for NGS dataset such as ChIP-seq, RNA-seq, miRNA-seq, DNA-seq, SNPs and methylation data.

License GPL (>= 2)

Depends R (>= 3.1.0), grDevices, methods, GenomicRanges, grid

Imports GenomicAlignments, GenomicFeatures, Gviz, pbapply, Rsamtools, rtracklayer, S4Vectors, scales, tools, IRanges, AnnotationDbi, grImport

Suggests biomaRt, TxDb.Hsapiens.UCSC.hg19.knownGene, RUnit, org.Hs.eg.db, BiocGenerics, BiocStyle, knitr, VariantAnnotation

biocViews Visualization

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

`trackViewer-package` *Minimal designed plotting tool for genomic data*

Description

A package that plot data and annotation information along genomic coordinates in an elegance style. This tool is based on Gviz but want to draw figures in minimal style for publication.

Details

Package:	trackViewer
Type:	Package
Version:	1.0
Date:	2013-10-18
License:	Artistic-2.0

This package is minimal designed to plot figure for publication.

Author(s)

Jianhong Ou, Julie Lihua Zhu

Maintainer: Jianhong Ou <jianhong.ou@umassmed.edu>

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(org.Hs.eg.db)
trs <- geneModelFromTxdb(TxDb.Hsapiens.UCSC.hg19.knownGene,
                         org.Hs.eg.db,
                         chrom="chr11",
                         start=122929275,
                         end=122930122)
extdata <- system.file("extdata", package="trackViewer",
                       mustWork=TRUE)
repA <- importScore(paste(extdata, "cpsf160.repA_+.wig", sep="/"),
                    paste(extdata, "cpsf160.repA_-.wig", sep="/"),
                    format="WIG")
```

```
strand(repA@dat) <- "+"
strand(repA@dat2) <- "-"
fox2 <- importScore(paste(extdata, "fox2.bed", sep="/"), format="BED")
dat <- coverageGR(fox2@dat)
fox2@dat <- dat[strand(dat)=="+"]
fox2@dat2 <- dat[strand(dat)=="-"]
gr <- GRanges("chr11", IRanges(122929275, 122930122), strand="-")
vp <- viewTracks(trackList(repA, fox2, trs), gr=gr, autoOptimizeStyle=TRUE)
addGuideLine(c(122929767, 122929969), vp=vp)
addArrowMark(list(x=unit(.5, "npc"),
                  y=unit(.39, "npc")),
             col="blue")
```

---

addArrowMark *Add arrow mark to the figure at a given position*

Description

A function to add arrow mark for emphasizing peaks

Usage

```
addArrowMark(pos=grid.locator(), label=NULL, angle=15,
             length=unit(.25, "inches"), col="red", cex=1, quadrant=4,
             type="closed", vp=NULL)
```

Arguments

pos	A unit object representing the location of arrow mark to be placed at current viewport. Default is the value of grid.locator, which will get the location of the mouse click.
label	A character or expression vector.
angle	A parameter passed into grid::arrow function. The angle of arrow head in degrees (smaller numbers produce narrower, pointier arrows). Essentially describes the width of the arrow head.
length	A parameter passed into grid::arrow function. Aunit specifying the length of the arrow head.
col	color of the arrow
cex	Multiplier applied to fontsize
quadrant	the direction of arrow, 1: to bottomleft, 2: to bottomright, 3: to topright, 4: to topleft
type	A parameter passed into grid::arrow function. One of "open" or "closed" indicating whether the arrow head should be a closed triangle.
vp	A Grid viewport object. It must be output of viewTracks

Value

invisible x, y position value.

Author(s)

Jianhong Ou

See Also

See Also as addGuideLine, arrow

Examples

```
grid.newpage()
addArrowMark(list(x=unit(.5, "npc"),
                  y=unit(.5, "npc")),
             label="label1",
             col="blue")
## how to get the position by mouse click
if(interactive()){
    pos <- addArrowMark(label="byClick")
    addArrowMark(pos, label="samePosAsAbove")
}
```

---

addGuideLine *Add guide lines to the tracks*

Description

A function to add lines for emphasizing the positions

Usage

```
addGuideLine(guideLine, col="gray", lty="dashed", lwd=1, vp=NULL)
```

Arguments

guideLine	The genomic coordinates to draw the lines
col	A vector for the line color
lty	A vector for the line type
lwd	A vector for the line width
vp	A Grid viewport object. It must be output of viewTracks

Value

NULL

Author(s)

Jianhong Ou

See Also

See Also as getCurTrackViewport, addArrowMark, viewTracks

Examples

```
vp <- getCurTrackViewport(trackViewerStyle(), 10000, 10200)
addGuideLine(c(10010, 10025, 10150), vp=vp)
```

---

coverageGR *calculate coverage*

Description

calculate coverage for GRanges, GAlignments or GAlignmentPairs

Usage

```
coverageGR(gr)
```

Arguments

gr	an object of RGanges, GAlignments or GAlignmentPairs

Value

an object of GRanges

Author(s)

Jianhong Ou

See Also

See Also as coverage, coverage-methods

Examples

```
bed <- system.file("extdata", "fox2.bed", package="trackViewer",
                   mustWork=TRUE)
fox2 <- importScore(bed)
fox2@dat <- coverageGR(fox2@dat)
```

dandelion.plot *dandelion.plots*

Description

Plot variants and somatic mutations

Usage

```
dandelion.plot(SNP.gr, features=NULL, ranges=NULL,
                       type=c("fan", "circle", "pie", "pin"),
                       newpage=TRUE, ylab=TRUE,
                       xaxis=TRUE, legend=NULL,
                       cex=1, maxgaps=1/50, ...)
```

Arguments

SNP.gr	A object of GRanges or GRangesList. All the width of GRanges must be 1.
features	A object of GRanges or GRangesList.
ranges	A object of GRanges or GRangesList.
type	Character. Could be fan, circle, pie or pin.
newpage	plot in the new page or not.
ylab	plot ylab or not. If it is a character vector, the vector will be used as ylab.
xaxis	plot xaxis or not. If it is a numeric vector with length greater than 1, the vector will be used as the points at which tick-marks are to be drawn. And the names of the vector will be used to as labels to be placed at the tick points if it has names.
legend	If it is a list with named color vectors, a legend will be added.
cex	cex will control the size of circle.
maxgaps	maxgaps between the stem of dandelions. It is calculated by the width of plot region devided by maxgaps.
...	not used.

Details

In SNP.gr and features, metadata of the GRanges object will be used to control the color, fill, border, height, data source of pie if the type is pie.

Value

NULL

Author(s)

Jianhong Ou

Examples

```
SNP <- c(10, 100, 105, 108, 400, 410, 420, 600, 700, 805, 840, 1400, 1402)
SNP.gr <- GRanges("chr1", IRanges(SNP, width=1, names=paste0("snp", SNP)),
             score=sample.int(100, length(SNP))/100)
features <- GRanges("chr1", IRanges(c(1, 501, 1001),
                                    width=c(120, 500, 405),
                                    names=paste0("block", 1:3)),
                    color="black",
                    fill=c("#FF8833", "#51C6E6", "#DFA32D"),
                    height=c(0.1, 0.05, 0.08))
dandelion.plot(SNP.gr, features, type="fan")
```

`geneModelFromTxdb` *Prepare gene model from an object of TxDb*

Description

Generate an object of `track` for `viewTracks` by given parameters.

Usage

```
geneModelFromTxdb(txdb, orgDb, gr,
                  chrom, start, end,
                  strand=c("*", "+", "-"),
                  txdump=NULL)
```

Arguments

`txdb`	An object of `TxDb`
`orgDb`	An object of "OrgDb"
`gr`	An object of GRanges.
`chrom`	chromosome name, must be a seqname of txdb
`start`	start position
`end`	end position
`strand`	strand
`txdump`	output of as.list(txdb), a list of data frames that can be used to make the db again with no loss of information.

Value

An object of `track`

Author(s)

Jianhong Ou

See Also

See Also as `importScore`, `importBam`, `viewTracks`

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(org.Hs.eg.db)
trs <- geneModelFromTxdb(TxDb.Hsapiens.UCSC.hg19.knownGene,
                         org.Hs.eg.db,
                         chrom="chr20",
                         start=22560000,
                         end=22565000,
                         strand="-")
```

`getCurTrackViewport` *Get current track viewport*

Description

Get current track viewport for addGuideLine

Usage

```
getCurTrackViewport(curViewerStyle, start, end)
```

Arguments

`curViewerStyle`	an object of `trackViewerStyle`
`start`	start position of current track
`end`	end position of current track

Value

an object of `viewport`

Author(s)

Jianhong Ou

See Also

See Also as `addGuideLine`

Examples

```
vp <- getCurTrackViewport(trackViewerStyle(), 10000, 10200)
addGuideLine(c(10010, 10025, 10150), vp=vp)
```

GRoperator *GRanges operator*

Description

GRanges operations (add, aubtract, multiply, divide)

Usage

```
GRoperator(A, B, col="score", operator = c("+", "-", "*", "/", "^", "%%"))
```

Arguments

A	an object of GRanges
B	an object of GRanges
col	colname of A and B to be calculated
operator	operator, "+" means A + B, and so on.

Value

an object of GRanges

Author(s)

Jianhong Ou

Examples

```
gr2 <- GRanges(seqnames=c("chr1", "chr1"),
           ranges=IRanges(c(7,13), width=3),
           strand=c("-", "-"), score=3:4)
gr3 <- GRanges(seqnames=c("chr1", "chr1"),
           ranges=IRanges(c(1, 4), c(3, 9)),
           strand=c("-", "-"), score=c(6L, 2L))
GRoperator(gr2, gr3, col="score", operator="+")
GRoperator(gr2, gr3, col="score", operator="-")
GRoperator(gr2, gr3, col="score", operator="*")
GRoperator(gr2, gr3, col="score", operator="/")
```

importBam *Reading data from a BAM file*

Description

Read a track object from a BAM file

Usage

```
importBam(file, file2, ranges=GRanges(), pairs=FALSE)
```

Arguments

file	The path to the BAM file to read.
file2	The path to the second BAM file to read.
ranges	An object of GRanges to indicate the range to be imported
pairs	logical object to indicate the BAM is paired or not. See readGAlignments

Value

a track object

Author(s)

Jianhong Ou

See Also

See Also as importScore, track, viewTracks

Examples

```
bamfile <- system.file("extdata", "ex1.bam", package="Rsamtools",
                       mustWork=TRUE)
dat <- importBam(file=bamfile, ranges=GRanges("seq1", IRanges(1, 50), strand="+"))
```

---

importData *Reading data from a BED or WIG file to RleList*

Description

Read a track object from a BED, bedGraph, WIG or BigWig file to RleList

Usage

```
importData(files, format=NA, ranges=GRanges())
```

Arguments

files	The path to the files to read.
format	The format of import file. Could be BAM, BED, bedGraph, WIG or BigWig
ranges	An object of GRanges to indicate the range to be imported

Value

a list of RleList.

Author(s)

Jianhong Ou

Examples

```
#import a BED file
bedfile <- system.file("tests", "test.bed", package="rtracklayer",
                       mustWork=TRUE)
dat <- importData(files=bedfile, format="BED",
                    ranges=GRanges("chr7", IRanges(127471197, 127474697)))

##import a WIG file
wigfile <- system.file("tests", "step.wig", package = "rtracklayer",
                       mustWork=TRUE)
dat <- importData(files=wigfile, format="WIG",
                  ranges=GRanges("chr19",
                                 IRanges(59104701, 59110920)))

##import a BigWig file
if(.Platform$OS.type!="windows"){
    ##this is because we are using rtracklayer::import
    bwfile <- system.file("tests", "test.bw", package = "rtracklayer",
                       mustWork=TRUE)
    dat <- importData(files=bwfile, format="BigWig",
                      ranges=GRanges("chr19", IRanges(1500, 2700)))
}
```

`importScore` *Reading data from a BED or WIG file*

Description

Read a `track` object from a BED, bedGraph, WIG or BigWig file

Usage

```
importScore(file, file2,
            format=c("BED", "bedGraph", "WIG", "BigWig"),
            ranges=GRanges(), ignore.strand=TRUE)
```

Arguments

`file`	The path to the file to read.
`file2`	The path to the second file to read.
`format`	The format of import file. Could be BED, bedGraph, WIG or BigWig
`ranges`	An object of `GRanges` to indicate the range to be imported
`ignore.strand`	ignore the strand or not when do filter. default TRUE

Value

a `track` object

Author(s)

Jianhong Ou

See Also

See Also as importBam, track, viewTracks

Examples

```
#import a BED file
bedfile <- system.file("tests", "test.bed", package="rtracklayer",
                       mustWork=TRUE)
dat <- importScore(file=bedfile, format="BED",
                   ranges=GRanges("chr7", IRanges(127471197, 127474697)))

##import a WIG file
wigfile <- system.file("tests", "step.wig", package = "rtracklayer",
                       mustWork=TRUE)
dat <- importScore(file=wigfile, format="WIG")

##import a BigWig file
if(.Platform$OS.type!="windows"){##this is because we are using rtracklayer::import
    bwfile <- system.file("tests", "test.bw", package = "rtracklayer",
                       mustWork=TRUE)
    dat <- importScore(file=bwfile, format="BigWig")
}

##import 2 file
wigfile1 <- system.file("extdata", "cpsf160.repA_+.wig", package="trackViewer",
                        mustWork=TRUE)
wigfile2 <- system.file("extdata", "cpsf160.repA_-.wig", package="trackViewer",
                        mustWork=TRUE)
dat <- importScore(wigfile1, wigfile2, format="WIG",
                   ranges=GRanges("chr11", IRanges(122817703, 122889073)))
```

---

lolliplot *Lolliplots*

Description

Plot variants and somatic mutations

Usage

```
lolliplot(SNP.gr, features = NULL, ranges = NULL,
          type = c("circle", "pie", "pin",
                   "pie.stack"),
          newpage = TRUE,
          ylab=TRUE, yaxis=TRUE, xaxis=TRUE,
          legend=NULL, cex=1,
          dashline.col="gray80", ...)
```

Arguments

SNP.gr	A object of GRanges, GRangesList or a list of GRanges. All the width of GRanges must be 1.

features	A object of GRanges, GRangesList or a list of GRanges. The metadata 'featureLayerID' are used for drawing features in different layers. See details in vignette.
ranges	A object of GRanges or GRangesList.
type	Character. Could be circle, pie, pin or pie.stack.
newpage	plot in the new page or not.
ylab	plot ylab or not. If it is a character vector, the vector will be used as ylab.
yaxis	plot yaxis or not.
xaxis	plot xaxis or not. If it is a numeric vector with length greater than 1, the vector will be used as the points at which tick-marks are to be drawn. And the names of the vector will be used to as labels to be placed at the tick points if it has names.
legend	If it is a list with named color vectors, a legend will be added.
cex	cex will control the size of circle.
dashline.col	color for the dashed line.
...	not used.

Details

In SNP.gr and features, metadata of the GRanges object will be used to control the color, fill, border, height, data source of pie if the type is pie. And also the controls for labels by name the metadata start as label.parameter.<properties> such as label.parameter.rot, label.parameter.gp. The parameter is used for grid.text. The metadata 'featureLayerID' for features are used for drawing features in different layers. The metadata 'SNPsideID' for SNP.gr are used for determining the side of lollipops. And the 'SNPsideID' could only be 'top' or 'bottom'.

Value

NULL

Author(s)

Jianhong Ou

Examples

```
SNP <- c(10, 100, 105, 108, 400, 410, 420, 600, 700, 805, 840, 1400, 1402)
x <- sample.int(100, length(SNP))
SNP.gr <- GRanges("chr1", IRanges(SNP, width=1, names=paste0("snp", SNP)),
            value1=x, value2=100-x)
SNP.gr$color <- rep(list(c("red", 'blue')), length(SNP))
SNP.gr$border <- sample.int(7, length(SNP), replace=TRUE)
features <- GRanges("chr1", IRanges(c(1, 501, 1001),
                                    width=c(120, 500, 405),
                                    names=paste0("block", 1:3)),
                    color="black",
                    fill=c("#FF8833", "#51C6E6", "#DFA32D"),
                    height=c(0.1, 0.05, 0.08),
                    label.parameter.rot=45)
lolliplot(SNP.gr, features, type="pie")
```

`optimizeStyle` *Optimize the style of plot*

Description

Automatic optimize the stlye of trackViewer

Usage

```
optimizeStyle(trackList, viewerStyle=trackViewerStyle(), theme=NULL)
```

Arguments

`trackList`	An object of `trackList`
`viewerStyle`	An object of `trackViewerStyle`
`theme`	A character string. Could be "bw" or "col".

Value

a list of a `trackList` and a `trackViewerStyle`

Author(s)

Jianhong Ou

See Also

See Also as `viewTracks`

Examples

```
extdata <- system.file("extdata", package="trackViewer",
                       mustWork=TRUE)
files <- dir(extdata, ".wig")
tracks <- lapply(paste(extdata, files, sep="/"),
                      importScore, format="WIG")
re <- optimizeStyle(trackList(tracks))
trackList <- re$tracks
viewerStyle <- re$style
```

parse2GRanges *parse text into GRanges*

Description

parse text like "chr13:99,443,451-99,848,821:-" into GRanges

Usage

```
parse2GRanges(text)
```

Arguments

text	character vector like "chr13:99,443,451-99,848,821:-" or "chr13:99,443,451-99,848,821"

Value

an object of GRanges

Author(s)

Jianhong Ou

Examples

```
parse2GRanges("chr13:99,443,451-99,848,821:-")
```

parseWIG *convert WIG format track to BED format track*

Description

convert WIG format track to BED format track for a given range

Usage

```
parseWIG(trackScore, chrom, from, to)
```

Arguments

trackScore	an object of track with WIG format
chrom	sequence name of the chromosome
from	start coordinate
to	end coordinate

Value

an object of track

Author(s)

Jianhong Ou

See Also

track

Examples

```
extdata <- system.file("extdata", package="trackViewer", mustWork=TRUE)
repA <- importScore(file.path(extdata, "cpsf160.repA_-.wig"),
                    file.path(extdata, "cpsf160.repA_+.wig"),
                    format="WIG")
strand(repA$dat) <- "-"
strand(repA$dat2) <- "+"
parseWIG(repA, chrom="chr11", from=122929275, to=122930122)
```

---

plotGRanges *plot GRanges data*

Description

A function to plot GRanges data for given range

Usage

```
plotGRanges(..., range=GRanges(),
            viewerStyle=trackViewerStyle(),
            autoOptimizeStyle=FALSE,
            newpage=TRUE)
```

Arguments

...	one or more objects of GRanges
range	an object of GRanges
viewerStyle	an object of trackViewerStyle
autoOptimizeStyle	should use optimizeStyle to optimize style
newpage	should be draw on a new page?

Value

An object of viewport for addGuideLine

Author(s)

Jianhong Ou

See Also

See Also as addGuideLine, addArrowMark

Examples

```
gr1 <- GRanges("chr1", IRanges(1:50, 51:100))
gr2 <- GRanges("chr1", IRanges(seq(from=10, to=80, by=5),
                               seq(from=20, to=90, by=5)))
vp <- plotGRanges(gr1, gr2, range=GRanges("chr1", IRanges(1, 100)))
addGuideLine(guideLine=c(5, 10, 50, 90), col=2:5, vp=vp)

gr <- GRanges("chr1", IRanges(c(1, 11, 21, 31), width=9),
              score=c(5, 10, 5, 1))
plotGRanges(gr, range=GRanges("chr1", IRanges(1, 50)))
```

---

pos-class *Class* "pos"

Description

An object of class "pos" represents a point location

Objects from the Class

Objects can be created by calls of the form new("pos", x, y, unit).

Slots

x A numeric value, indicates the x position

y A numeric value, indicates the y position

unit "character" apecifying the units for the corresponding numeric values. See unit

---

track-class *Class* "track"

Description

An object of class "track" represents scores of a given track.

Usage

```
    ## S4 method for signature 'track,character,ANY'
setTrackStyleParam(ts, attr, value)
    ## S4 method for signature 'track,character,ANY'
setTrackXscaleParam(ts, attr, value)
    ## S4 method for signature 'track,character,ANY'
setTrackYaxisParam(ts, attr, value)
```

Arguments

ts	An object of track.
attr	the name of slot of trackStyle object to be changed.
value	values to be assigned.

Objects from the Class

Objects can be created by calls of the form `new("track", dat, dat2, type, format, style, name)`.

Slots

`dat` Object of class `GRanges` the scores of a given track. It should contain score metadata.

`dat2` Object of class `GRanges` the scores of a given track. It should contain score metadata. When dat2 and dat is paired, dat will be drawn as positive value where dat2 will be drawn as negative value (-1 * score)

`type` The type of track. It could be 'data' or 'gene'.

`format` The format of the input. It could be "BED", "bedGraph", "WIG", "BigWig" or "BAM"

`style` Object of class `trackStyle`

`name` unused yet

Methods

setTrackStyleParam change the slot values of `trackStyle` object for an object of `track`

setTrackXscaleParam change the `xscale` slot values for an object of `track`

setTrackYaxisParam change the `yaxisStyle` values for an object of `track`

$, $<- Get or set the slot of `track`

show show the detials of `track`

See Also

Please try to use `importScore` and `importBam` to generate the object.

Examples

```
extdata <- system.file("extdata", package="trackViewer",
                       mustWork=TRUE)
fox2 <- importScore(file.path(extdata, "fox2.bed"), format="BED")
setTrackStyleParam(fox2, "color", c("red","green"))
setTrackXscaleParam(fox2, "gp", list(cex=.5))
setTrackYaxisParam(fox2, "gp", list(col="blue"))
fox2$dat <- GRanges(score=numeric(0))
```

---

trackList-class *List of tracks*

Description

An extension of List that holds only `track` objects.

constructor

trackList(..., heightDist=NA): Each tracks in ... becomes an element in the new trackList, in the same order. This is analogous to the list constructor, except every argument in ... must be derived from `track`. The heightDist is vector or NA to define the height of each track.

See Also

`track`.

trackStyle-class *Class* "trackStyle"

Description

An object of class "trackStyle" represents track style.

Objects from the Class

Objects can be created by calls of the form new("trackStyle", tracktype, color, height, marginTop, marginBo

Slots

tracktype "character" track type, could be peak or cluster. Default is "peak". "cluster" is not supported yet.

color "character" track color. If the track has dat and dat2 slot, it should have two values.

height "numeric" track height. It should be a value between 0 and 1

marginTop "numeric" track top margin

marginBottom "numeric" track bottom margin

xscale object of xscale, describe the details of x-scale

yaxis object of yaxisStyle, describe the details of y-axis

ylim "numeric" y-axis range

ylabpos "character", ylable postion, ylabpos should be 'left', 'right', 'topleft', 'bottomleft', 'topright' or 'bottomright'.

ylablas "numeric" y lable direction. It should be a integer 0-3. See par:las

ylabgp A "list" object, It will convert to an object of class gpar. This is basically a list of graphical parameter settings of y-label.

trackViewerStyle-class *Class* "trackViewerStyle"

Description

An object of class "trackViewerStyle" represents track viewer style.

Usage

```
    ## S4 method for signature 'trackViewerStyle,character,ANY'
setTrackViewerStyleParam(tvs, attr, value)
```

Arguments

tvs	An object of trackViewerStyle.
attr	the name of slot to be changed.
value	values to be assigned.

Objects from the Class

Objects can be created by calls of the form `new("trackViewerStyle", margin, xlas,`

constructor

trackViewerStyle(...): Each argument in ... becomes an slot in the new trackViewerStyle.

Slots

`margin` `"numeric"`, specify the bottom, left, top and right margin.

`xlas` `"numeric"`, label direction of x-axis mark. It should be a integer 0-3. See `par:las`

`xgp` A `"list"` object, It will convert to an object of class `gpar`. This is basically a list of graphical parameter settings of x-axis. For y-axis, see `yaxisStyle`

`xaxis` `"logical"`, draw x-axis or not

`autolas` `"logical"` automatic determine y label direction

`flip` `"logical"` flip the x-axis or not, default FALSE

Methods

setTrackViewerStyleParam change the slot values of an object of `trackViewerStyle`

Examples

```
tvs <- trackViewerStyle()
setTrackViewerStyleParam(tvs, "xaxis", TRUE)
```

---

viewTracks *plot the tracks*

Description

A function to plot the data for given range

Usage

```
viewTracks(trackList, chromosome, start, end, strand, gr=GRanges(),
           ignore.strand=TRUE,
           viewerStyle=trackViewerStyle(), autoOptimizeStyle=FALSE,
           newpage=TRUE, operator=NULL)
```

Arguments

`trackList`	an object of `trackList`
`chromosome`	chromosome
`start`	start position
`end`	end position
`strand`	strand
`gr`	an object of `GRanges`

ignore.strand	ignore the strand or not when do filter. default TRUE
viewerStyle	an object of trackViewerStyle
autoOptimizeStyle	should use optimizeStyle to optimize style
newpage	should be draw on a new page?
operator	operator, could be +, -, *, /, ^, %%. "-" means dat - dat2, and so on.

Value

An object of viewport for addGuideLine

Author(s)

Jianhong Ou

See Also

See Also as addGuideLine, addArrowMark

Examples

```
extdata <- system.file("extdata", package="trackViewer",
                  mustWork=TRUE)
files <- dir(extdata, "-.wig")
tracks <- lapply(paste(extdata, files, sep="/"),
                  importScore, format="WIG")
tracks <- lapply(tracks, function(.ele) {strand(.ele@dat) <- "-"; .ele})
fox2 <- importScore(paste(extdata, "fox2.bed", sep="/"), format="BED")
dat <- coverageGR(fox2@dat)
fox2@dat <- dat[strand(dat)=="+"]
fox2@dat2 <- dat[strand(dat)=="-"]
gr <- GRanges("chr11", IRanges(122929275, 122930122), strand="-")
viewTracks(trackList(tracks, fox2), gr=gr, autoOptimizeStyle=TRUE)
```

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xscale-class *Class* "xscale"

Description

An object of class "xscale" represents x-scale style.

Objects from the Class

Objects can be created by calls of the form new("xscale", from, to, label, gp, draw).

Slots

from A pos class, indicates the start point postion of x-scale.

to A pos class, indicates the end point postion of x-scale.

label "character" the label of x-scale

gp A "list" object, It will convert to an object of class gpar. This is basically a list of graphical parameter settings of x-scale.

draw A "logical" value indicating whether the x-scale should be draw.

yaxisStyle-class *Class* "yaxisStyle"

Description

An object of class "yaxisStyle" represents y-axis style.

Objects from the Class

Objects can be created by calls of the form new("yaxisStyle", at, label, gp, draw, main).

Slots

at "numeric" vector of y-value locations for the tick marks

label "logical" value indicating whether to draw the labels on the tick marks.

gp A "list" object, It will convert to an object of class gpar. This is basically a list of graphical parameter settings of y-axis.

draw A "logical" value indicating whether the y-axis should be draw.

main A "logical" value indicating whether the y-axis should be draw in left (TRUE) or right (FALSE).

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