

# 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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**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** GenomeInfoDb, GenomicAlignments, GenomicFeatures, Gviz, pbapply, Rsamtools, rtracklayer, S4Vectors, scales, tools, IRanges, AnnotationDbi, grImport, htmlwidgets

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

**biocViews** Visualization

**VignetteBuilder** knitr

**NeedsCompilation** no

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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)

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## 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. A unit 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 <a href="#">viewTracks</a>

## 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**

<code>guideLine</code>	The genomic coordinates to draw the lines
<code>col</code>	A vector for the line color
<code>lty</code>	A vector for the line type
<code>lwd</code>	A vector for the line width
<code>vp</code>	A Grid viewport object. It must be output of <a href="#">viewTracks</a>

**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)
```

---

 browseTracks

*browse network*


---

**Description**

browse tracks by a web browser.

**Usage**

```
browseTracks(trackList,
             gr=GRanges(),
             ignore.strand=TRUE,
             width=NULL, height=NULL,
             ...)
```

**Arguments**

trackList	an object of <a href="#">trackList</a>
gr	an object of <a href="#">GRanges</a>
ignore.strand	ignore the strand or not when do filter. default TRUE
width	width of the figure
height	height of the figure
...	parameters not used

**Value**

An object of class `htmlwidget` that will intelligently print itself into HTML in a variety of contexts including the R console, within R Markdown documents, and within Shiny output bindings.

**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})
names(tracks) <- c("trackA", "trackB")
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))
browseTracks(trackList(tracks, fox2), gr=gr)
```

coverageGR                    *calculate coverage*

---

**Description**

calculate coverage for [GRanges](#), [GAlignments](#) or [GAlignmentPairs](#)

**Usage**

```
coverageGR(gr)
```

**Arguments**

gr                    an object of [RGRanges](#), [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 <a href="#">GRanges</a> or <a href="#">GRangesList</a> . All the width of GRanges must be 1.
features	A object of <a href="#">GRanges</a> or <a href="#">GRangesList</a> .
ranges	A object of <a href="#">GRanges</a> or <a href="#">GRangesList</a> .
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 divided 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 <a href="#">TxDb</a>
orgDb	An object of "OrgDb"
gr	An object of <a href="#">GRanges</a> .
chrom	chromosome name, must be a seqname of txdb
start	start position
end	end position
strand	strand
txdump	output of <a href="#">as.list(txdb)</a> , 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, subtract, multiply, divide)

**Usage**

```
GROperator(A, B, col="score", operator = c("+", "-", "*", "/", "^", "%"),  
          ignore.strand = TRUE)
```

**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. User-defined function also could be used.
ignore.strand	When set to TRUE, the strand information is ignored in the overlap calculations.

**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="/")
GRoperator(gr2, gr3, col="score", operator=mean)
```

---

ideogramPlot

*plot ideogram with data*

---

**Description**

plot ideogram with data for multiple chromosomes

**Usage**

```
ideogramPlot(ideo, dataList, layout=NULL,
             horiz=TRUE,
             parameterList=
               list(vp=plotViewport(margins=c(.1, 4.1, .3, .1)),
                  ideoHeight=unit(1/(1+length(dataList)), "npc"),
                  vgap=unit(.3, "lines"),
                  ylabs="auto",
                  ylabsRot=ifelse(horiz, 0, 90),
                  ylabsPos=unit(2.5, "lines"),
                  xaxis=FALSE, yaxis=FALSE,
                  xlab="",
                  types="barplot", heights=NULL,
                  dataColumn="score",
```

```

        gps=gpar(col="black", fill="gray")),
colorScheme=gieStain(),
gp=gpar(fill=NA, lwd=2), ...)

```

### Arguments

ideo	output of <a href="#">loadIdeogram</a> .
dataList	a <a href="#">GRangesList</a> of data to plot.
layout	The layout of chromosomes. Could be a list with chromosome names as its elements.
horiz	a logical value. If FALSE, the ideograms are drawn vertically to the left. If TRUE, the ideograms are drawn horizontally at the bottom.
parameterList	parameterList a list of parameters for each dataset in the dataList. The elements of the parameters could be xlabs, ylabs, etc. type could be barplot, line, point, heatmap.
colorScheme	A character vector of giemsa stain colors.
gp	parameters used for <a href="#">grid.roundrect</a> .
...	parameters not used.

### Author(s)

Jianhong Ou

### See Also

See Also as [loadIdeogram](#)

### Examples

```

## Not run:
ideo <- loadIdeogram("hg38")
library(rtracklayer)
library(grid)
dataList <- ideo
dataList$score <- as.numeric(dataList$gieStain)
dataList <- dataList[dataList$gieStain!="gneg"]
dataList <- GRangesList(dataList)
grid.newpage()
ideogramPlot(ideo, dataList,
             layout=list("chr1", "chr2", c("chr3", "chr22"),
                        c("chr4", "chr21"), c("chr5", "chr20"),
                        c("chr6", "chr19"), c("chr7", "chr18"),
                        c("chr8", "chr17"), c("chr9", "chr16"),
                        c("chr10", "chr15"), c("chr11", "chr14"),
                        c("chr12", "chr13"), c("chrX", "chrY")),
             parameterList = list(types="heatmap"))

## End(Not run)

```

---

importBam	<i>Reading data from a BAM file</i>
-----------	-------------------------------------

---

**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 <a href="#">GRanges</a> to indicate the range to be imported
pairs	logical object to indicate the BAM is paired or not. See <a href="#">readGAlignments</a>

**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	<i>Reading data from a BED or WIG file to RleList</i>
------------	---

---

**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 <a href="#">GRanges</a> 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)))
```

---

loadIdeogram	<i>load ideogram from UCSC</i>
--------------	--------------------------------

---

**Description**

Download ideogram table from UCSC

**Usage**

```
loadIdeogram(genome, chrom = NULL, ranges = NULL, ...)
```

**Arguments**

genome	Assembly name assigned by UCSC, such as hg38, mm10.
chrom	A character vector of chromosome names, or NULL.
ranges	A <a href="#">Ranges</a> object with the intervals.
...	Additional arguments to pass to the <a href="#">GRanges</a> constructor.

**Value**

A [GRanges](#) object.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [ideogramPlot](#)

**Examples**

```
## Not run:  
head(loadIdeogram("hg38"))  
  
## End(Not run)
```

---

lollipoplot	<i>Lollipoplots</i>
-------------	---------------------

---

**Description**

Plot variants and somatic mutations

**Usage**

```
lollipoplot(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",
            jitter=c("node", "label"),
            ...)
```

**Arguments**

SNP.gr	A object of <a href="#">GRanges</a> , <a href="#">GRangesList</a> or a list of <a href="#">GRanges</a> . All the width of <a href="#">GRanges</a> must be 1.
features	A object of <a href="#">GRanges</a> , <a href="#">GRangesList</a> or a list of <a href="#">GRanges</a> . The metadata 'featureLayerID' are used for drawing features in different layers. See details in vignette.
ranges	A object of <a href="#">GRanges</a> or <a href="#">GRangesList</a> .
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.
jitter	jitter the position of nodes or labels.
...	not used.

**Details**

In SNP.gr and features, metadata of the [GRanges](#) object will be used to control the color, fill, border, height, cex, dashline.col, 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)
lollipop(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 <a href="#">trackList</a>
viewerStyle	An object of <a href="#">trackViewerStyle</a>
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 <a href="#">GRanges</a>
range	an object of <a href="#">GRanges</a>
viewerStyle	an object of <a href="#">trackViewerStyle</a>
autoOptimizeStyle	should use <a href="#">optimizeStyle</a> 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" apcifying 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 <a href="#">trackStyle</a> 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 <a href="#">GRanges</a> the scores of a given track. It should contain score metadata.
dat2	Object of class <a href="#">GRanges</a> 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 <a href="#">trackStyle</a>
name	unused yet

### Methods

<b>setTrackStyleParam</b>	change the slot values of <a href="#">trackStyle</a> object for an object of track
<b>setTrackXscaleParam</b>	change the <a href="#">xscale</a> slot values for an object of track
<b>setTrackYaxisParam</b>	change the <a href="#">yaxisStyle</a> values for an object of track
<b>\$, \$&lt;-</b>	Get or set the slot of <a href="#">track</a>
<b>show</b>	show the details of <a href="#">track</a>

### 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	<i>List of tracks</i>
-----------------	-----------------------

---

**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	<i>Class "trackStyle"</i>
------------------	---------------------------

---

**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 position, ylabpos should be 'left', 'right', 'topleft', 'bottomleft', 'topright' or 'bottomright'. For gene type track, it also could be 'upstream' or 'downstream'

ylablas "numeric" y label 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	<i>plot the tracks</i>
------------	------------------------

---

### 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 <a href="#">trackList</a>
chromosome	chromosome
start	start position
end	end position
strand	strand
gr	an object of <a href="#">GRanges</a>
ignore.strand	ignore the strand or not when do filter. default TRUE
viewerStyle	an object of <a href="#">trackViewerStyle</a>
autoOptimizeStyle	should use <a href="#">optimizeStyle</a> 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(track=tracks, fox2=fox2), gr=gr, autoOptimizeStyle=TRUE)
```

---

xscale-class	<i>Class "xscale"</i>
--------------	-----------------------

---

### 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 position of x-scale.

`to` A [pos](#) class, indicates the end point position 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	<i>Class "yaxisStyle"</i>
------------------	---------------------------

---

### 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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