Package ‘trackViewer’

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Type Package

Title A R/Bioconductor package with web interface for drawing elegant interactive tracks or lollipop plot to facilitate integrated analysis of multi-omics data

Version 1.38.2

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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 (>= 3.5.0), grDevices, methods, GenomicRanges, grid

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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.

**Author(s)**

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**Examples**

```r
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@dat2 <- 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(0.25, "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 viewTracks

Value

invisible x, y position value.
addGuideLine

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

See Also

See Also as getCurTrackViewport, addArrowMark, viewTracks

Examples

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

Add annotation markers to the figure at a given position

Description

A function to add annotation markers for emphasizing interactions

Usage

addInteractionAnnotation(
  obj,
  idx,
  FUN = grid.polygon,
  panel = c("top", "bottom"),
  ...
)

Arguments

obj A GInteractions object, GRanges object or numeric vector. For numeric vector, the positive value will generate a line with slope 1 and negative value will generate a line at the position with slope -1.

idx The layer number of track.

FUN Function for plot. Available functions are grid.polygon, grid.lines, and grid.text for GInteractions object; grid.lines, and grid.text for GRanges object; FUN is not used for numeric vector.

panel Plot regions. Available values are "top", "bottom".

... Parameters will be passed to FUN.

Value

invisible viewport for plot region.

See Also

See Also as addGuideLine, addArrowMark

Examples

library(trackViewer)
library(InteractionSet)
gi <- readRDS(system.file("extdata", "nij.chr6.51120000.53200000.gi.rds", package="trackViewer"))
tads <- GInteractions(
  GRanges("chr6",
    IRanges(c(51130001, 51130001, 51450001, 52210001), width = 20000)),

  ...
GRanges("chr6",
   IRanges(c(51530001, 52170001, 52210001, 53210001), width = 20000))
range <- GRanges("chr6", IRanges(51120000, 53200000))
tr <- gi2track(gi)
viewTracks(trackList(tr),
   gr=range, autoOptimizeStyle = TRUE)
addInteractionAnnotation(tads, "tr", grid.lines,
   gp=gpar(col = "#E69F00", lwd=3, lty=3))

---

**ARA**

**Aggregate Region Analysis**

**Description**

Extract the interaction signal means from given coordinates.

**Usage**

ARA(gr, upstream = 2e+05, downstream = upstream, resolution = 10000, ...)  

**Arguments**

- **gr**
  A ‘GRanges‘ object. The center of the object will be used for alignment for all the given regions.
- **upstream, downstream**
  numeric(1L). Upstream and downstream from the center of given ‘gr‘ input will be used to extract the signals.
- **resolution**
  numeric(1L). The resolution will be passed to importGInteractions function.
- **...**
  The parameters used by importGInteractions function. Please note that the ranges resolution and out parameter should not be involved.

**Value**

A GInteractions object with scores which represent the mean values of the interactions.

**Examples**

hic <- system.file("extdata", "test_chr22.hic", package = "trackViewer", mustWork=TRUE)
gr <- GRanges("22", c(seq(20000001, 50000001, by=10000000), width=1))
sp <- ARA(gr, file=hic, format="hic")
rg <- GRanges("22", IRanges(1, 400000))
op <- optimizeStyle(trackList(gi2track(gi)))
heatmap <- op$tracks
sty <- op$style
setTrackViewerStyleParam(sty, "xat", c(1, 200000, 400000))
setTrackViewerStyleParam(sty, "xlabel",c("-20K", "center", "20K"))
viewTracks(heatmap, viewerStyle=sty, gr=rg)
browseTracks

Description

browse tracks by a web browser.

Usage

\[
\text{browseTracks(}
\text{trackList,}
\text{gr = GRanges(),}
\text{ignore.strand = TRUE,}
\text{width = NULL,}
\text{height = NULL,}
\text{...}
\text{)}
\]

Arguments

trackList an object of \text{trackList}

gr an object of \text{GRanges}

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 \text{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

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

*Shiny bindings for browseTracks*

**Description**

Output and render functions for using `browseTracks` within Shiny applications and interactive Rmd documents.

**Usage**

```r
browseTracksOutput(outputId, width = "100\%", height = "600px")
```

```r
renderbrowseTracks(expr, env = parent.frame(), quoted = FALSE)
```

**Arguments**

- **outputId**
  - output variable to read from

- **width, height**
  - Must be a valid CSS unit (like ‘100\%’, ‘400px’, ‘auto’) or a number, which will be coerced to a string and have ‘px’ appended.

- **expr**
  - An expression that generates a `browseTracks`

- **env**
  - The environment in which to evaluate `expr`.

- **quoted**
  - Is `expr` a quoted expression (with `quote()`)? This is useful if you want to save an expression in a variable.

---

### coverageGR

*calculate coverage*

**Description**

Calculate coverage for `GRanges`, `GAlignments` or `GAlignmentPairs`.

**Usage**

```r
coverageGR(gr)
```

**Arguments**

- **gr**
  - an object of `RGanges`, `GAlignments` or `GAlignmentPairs`

**Value**

- an object of `GRanges`
See Also

See Also as `coverage, coverage-methods`

Examples

```r
bbed <- 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**

```r
dandelion.plot(
    SNP.gr,
    features = NULL,
    ranges = NULL,
    type = c("fan", "circle", "pie", "pin"),
    newpage = TRUE,
    ylab = TRUE,
    ylab.gp = gpar(col = "black"),
    xaxis = TRUE,
    xaxis.gp = gpar(col = "black"),
    yaxis = FALSE,
    yaxis.gp = gpar(col = "black"),
    legend = NULL,
    cex = 1,
    maxgaps = 1/50,
    heightMethod = NULL,
    label_on_feature = FALSE,
    ...
)
```

**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.
**geneModelFromTxdb**  

Prepare gene model from an object of TxDb

---

**Description**

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

---

**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.

**ylab.gp, xaxis.gp, yaxis.gp**  
An object of class `gpar` for ylab, xaxis or yaxis.

**xaxis, yaxis**  
plot xaxis/yaxis 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. If a GRanges object is set, the dandelions stem will be clustered in each genomic range.

**heightMethod**  
A function used to determine the height of stem of dandelion. eg. Mean. Default is length.

**label_on_feature**  
Labels of the feature directly on them. Default FALSE.

**...**  
not used.

---

**Examples**

```r
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

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

Generate a list of track from a TxDb object.

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="-"
**geneTrack**

*track from TxDb*

---

**Description**

Generate a track object from TxDb by given gene ids

**Usage**

```
geneTrack(ids, txdb, symbols, type = c("gene", "transcript"), asList = TRUE)
```

**Arguments**

- `ids` Gene IDs. A vector of character. It should be keys in txdb.
- `txdb` An object of `TxDb`.
- `symbols` symbol of genes.
- `type` Output type of track, "gene" or "transcript".
- `asList` Output a list of tracks or not. Default TRUE.

**Value**

An object of `track`

**Examples**

```r
library(TxDB.Hsapiens.UCSC.hg19.knownGene)
library(org.Hs.eg.db)
ids <- c("3312", "390259", "341056", "79827")
symbols <- mget(ids, org.Hs.egSYMBOL)
geneTrack(ids, TxDb.Hsapiens.UCSC.hg19.knownGene, symbols)
```

---

**getCurTrackViewport**

*Get current track viewport*

---

**Description**

Get current track viewport for addGuideLine

**Usage**

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

Arguments

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

Value

an object of `viewport`

See Also

See Also as `addGuideLine`

Examples

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

getGeneIDsFromTxDb

get gene ids by genomic location

Description

retrieve gene ids from txdb object by genomic location.

Usage

geneIDsFromTxDb(gr, txdb)

Arguments

- `gr`: GRanges object.
- `txdb`: An object of `TxDb`.

Value

A character vector of gene ids

Examples

```r
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
gr <- parse2GRanges("chr11:122,830,799-123,116,707")
ids <- getGeneIDsFromTxDb(gr, TxDb.Hsapiens.UCSC.hg19.knownGene)
```
**getLocation**

get genomic location by gene symbol

**Description**

given a gene name, get the genomic coordinates.

**Usage**

ggetLocation(symbol, txdb, org)

**Arguments**

symbol  
Gene symbol

taxdb  
txdb will be used to extract the genes

org  
org package name

**Examples**

```R
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(org.Hs.eg.db)
ggetLocation("HSPA8", TxDb.Hsapiens.UCSC.hg19.knownGene, "org.Hs.eg.db")
```

**gi2track**

convert GInteractions to track object

**Description**

Convert GInteractions object to track object

**Usage**

gi2track(gi, gi2)

**Arguments**

gi  
an object of GInteractions

`gi2`

an object of GInteractions

**Value**

an track object

**Examples**

```R
gi <- readRDS(system.file("extdata", "nij.chr6.51120000.53200000.gi.rds", package="trackViewer"))
gi2track(gi)
```
### giestain

**color scheme for the schema for Chromosome Band (Ideogram)**

**Description**

Describe the colors of giemsa stain results

**Usage**

```r
giestain()
```

**Value**

A character vector of colors

**Examples**

```r
giestain()
```

---

### GIoperator

**GInteractions operator**

**Description**

GInteractions operations (add, subtract, multiply, divide)

**Usage**

```r
GIoperator(gi_list, col = "score", operator = c("+", "-", "*", "/"))
```

**Arguments**

- `gi_list`: a list of GInteractions objects
- `col`: colname of metadata to be calculated
- `operator`: operator, "+" means A + B, and so on. User-defined function also could be used.

**Value**

an object of GInteractions
Examples

```r
library(InteractionSet)
gr2 <- GRanges(seqnames=c("chr1", "chr1"),
ranges=IRanges(c(7,13), width=3))
gr3 <- GRanges(seqnames=c("chr1", "chr1"),
ranges=IRanges(c(1, 4), c(3, 9)))
Gi <- GInteractions(gr2, gr3, score=c(1, 2))
Gi2 <- GInteractions(gr2, gr3, score=c(3, 4))
Gioperator(list(Gi, Gi2), col="score", operator="+")
Gioperator(list(Gi, Gi2), col="score", operator="-")
```

Description

plot GRanges metadata for different types

Usage

```r
gridPlot(gr, gp, type, xscale)
```

Arguments

- `gr`: an object of GRanges with metadata. All metadata must be numeric.
- `gp`: an object of gpar
- `type`: type of the figure, could be barplot, line, point and heatmap
- `xscale`: x scale of the viewport

GRoperator

GRanges operator

Description

GRanges operations (add, subtract, multiply, divide)

Usage

```r
GRoperator(
  A,
  B,
  col = "score",
  operator = c("+", "-", "\times", "/", \"^\", \"^\%\"),
  ignore.strand = TRUE
)
```
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(0.1, 4.1, 0.3, 0.1)), ideoHeight = unit(1/(1 + length(dataList)), "npc"), vgap = unit(0.3, "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"),
  colorSheme = gieStain(),
  gp = gpar(fill = NA, lwd = 2),
  ...
)

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

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
importBam

Reading data from a BAM file

Description

Read a track object from a BAM file

Usage

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

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**: A logical object to indicate the BAM is paired or not. See `readGAlignments`.

Value

A `track` object.

See Also

See Also as `importScore`, `track`, `viewTracks`.

Examples

```r
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

```r
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`. 

importGInteractions

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)))
}

importGInteractions Reading data from a ginteractions, hic, cool, or validPairs file

Description

Read a track object from a ginteractions, hic, mcool, or validPairs file

Usage

importGInteractions(
  file,
  format = c("ginteractions", "hic", "cool", "validPairs"),
  ranges = GRanges(),
  ignore.strand = TRUE,
  out = c("track", "GInteractions"),
  resolution = 1e+05,
  unit = c("BP", "FRAG"),
                   "INTER_KR", "INTER_SCALE", "INTER_VC", "balanced"),
  matrixType = c("observed", "oe", "expected"),
  ...
)
Arguments

file  The path to the file to read.
format The format of import file. Could be ginteractions, hic, cool or validPairs
ranges An object of GRanges to indicate the range to be imported. For .hic file, if the length of ranges is 2, the first range will be used as anchor 1 and the second range will be used as anchor 2.
ignore.strand ignore the strand or not when do filter. default TRUE
out output format. Default is track. Possible values: track, GInteractions.
resolution Resolutions for the interaction data.
unit BP (base pair) or FRAG (fragment) (.hic file only).
normalization Type of normalization, NONE, VC, VC_SORT or KR for .hic and NONE, balanced for .cool.
matrixType Type of matrix for .hic file. Available choices are "observed", "oe", and "expected". default is "observed".

Value

a track object

See Also

See Also as listResolutions, listChromosomes, readHicNormTypes

Examples

# import a ginteractions file
#gi <- system.file("extdata", "test.ginteractions.tsv", package="trackViewer", 
#                   mustWork=TRUE)
#dat <- importGInteractions(file=gi, format="ginteractions", 
#                          ranges=GRanges("chr7", IRanges(127471197, 127474697)))

# import a hic file
if(!.Platform$OS.type!="windows"){
  hic <- system.file("extdata", "test_chr22.hic", package = "trackViewer", 
                     mustWork=TRUE)
  dat <- importGInteractions(file=hic, format="hic", 
                             ranges=GRanges("22", IRanges(1500000, 100000000)))
}

# import a cool file
cool <- system.file("extdata", "test.mcool", package = "trackViewer", 
                   mustWork=TRUE)
dat <- importGInteractions(file=cool, format="cool", 
                          resolution = 2, 
                          ranges=GRanges("chr1", IRanges(10, 28)))

# import a validPairs file
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

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
importScSeqScore

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)))

importScSeqScore    plot tracks for single cell RNAseq

Description

Plot single cell RNAseq data as heatmap track for Seurat object.

Usage

importScSeqScore(
    object,
    files,
    samplenames,
    ...,
    txdb,
    gene,
    id,
    idents,
    gr,
    color,
    withCoverageTrack = TRUE,
    flag = scanBamFlag(isSecondaryAlignment = FALSE, isUnmappedQuery = FALSE,
        isNotPassingQualityControls = FALSE, isSupplementaryAlignment = FALSE)
)

Arguments

object          Seurat object.
files           bam file to be scanned.
listChromosomes

Sample names for files.

... parameters used by readGAlignmentsList or readGAlignments

txDB TxDB object for gene model.
gene Gene name to plot. (row value)
id The id of gene used in txdb.
idents identity class to define the groups to plot. (column value)
gr GRanges object to define the plotting region.
color vector of colors used in heatmap.
withCoverageTrack plot coverage track or not.
flag An integer(2) vector used to filter reads based on their 'flag' entry.

Examples

## Not run:
library(TxDB.Hsapiens.UCSC.hg19.knownGene)
test_file <- "https://github.com/10XGenomics/subset-bam/raw/master/test/test.bam"
trs <- importScSeqScore(files=test_file,
    txdb=TxDB.Hsapiens.UCSC.hg19.knownGene,
    id="653635", gene = "WASH7P")

## End(Not run)

Description
List the available chromosome

Usage
listChromosomes(file, format = c("hic", "cool"))

Arguments

file character(1). File name of .hic or .cool/.mcool/.scool
format character(1). File format, "hic" or "cool".

Examples

hicfile <- system.file("extdata", "test_chr22.hic", package="trackViewer")
listChromosomes(hicfile)
coolfile <- system.file("extdata", "test.mcool", package="trackViewer")
listChromosomes(coolfile, format="cool")
listResolutions  \hspace{1em} \textit{List the available resolutions}

\textbf{Description}

List the resolutions available in the file.

\textbf{Usage}

\begin{verbatim}
listResolutions(file, format = c("hic", "cool"))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{file} \hspace{1em} character(1). File name of .hic or .cool/.mcool/.scool
  \item \texttt{format} \hspace{1em} character(1). File format, "hic" or "cool".
\end{itemize}

\textbf{Examples}

\begin{verbatim}
hicfile <- system.file("extdata", "test_chr22.hic", package="trackViewer")
listResolutions(hicfile)
coolfile <- system.file("extdata", "test.mcool", package="trackViewer")
listResolutions(coolfile, format="cool")
\end{verbatim}

loadIdeogram  \hspace{1em} \textit{load ideogram from UCSC}

\textbf{Description}

Download ideogram table from UCSC

\textbf{Usage}

\begin{verbatim}
loadIdeogram(genome, chrom = NULL, ranges = NULL, ...)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{genome} \hspace{1em} Assembly name assigned by UCSC, such as hg38, mm10.
  \item \texttt{chrom} \hspace{1em} A character vector of chromosome names, or NULL.
  \item \texttt{ranges} \hspace{1em} A \texttt{Ranges} object with the intervals.
  \item \ldots \hspace{1em} Additional arguments to pass to the \texttt{GRanges} constructor.
\end{itemize}

\textbf{Value}

A \texttt{GRanges} object.
lolliplot

See Also

See Also as ideogramPlot

Examples

```r
## Not run:
head(loadIdeogram("hg38", chrom = "chr1"))

## End(Not run)
```

## lolliplot

### lolliplot

#### Lolliplots

#### Description

Plot variants and somatic mutations

#### Usage

```
lolliplot(
    SNP.gr,
    features = NULL,
    ranges = NULL,
    type = "circle",
    newpage = TRUE,
    ylab = TRUE,
    ylab.gp = gpar(col = "black"),
    yaxis = TRUE,
    yaxis.gp = gpar(col = "black"),
    xaxis = TRUE,
    xaxis.gp = gpar(col = "black"),
    legend = NULL,
    cex = 1,
    dashline.col = "gray80",
    jitter = c("node", "label"),
    rescale = FALSE,
    label_on_feature = FALSE,
    lollipop_style_switch_limit = 10,
    ...
)
```

#### 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, pie.stack or flag.

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.

ylab.gp, xaxis.gp, yaxis.gp  An object of class gpar for ylab, xaxis or yaxis.

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.

rescale  logical(1), character(1), numeric vector, or a dataframe with rescale from and to. Rescalse the x-axis or not. if dataframe is used, colnames must be from.start, from.end, to.start, to.end. And the from scale must cover the whole plot region. The rescale parameter can be set as "exon" or "intron" to emphasise "exon" or "intron" region. The "exon" or "intron" can be followed with an integer e.g. "exon_80", or "intron_99". The integer indicates the total percentage of "exon" or "intron" region. Here "exon" indicates all regions in features. And "intron" indicates all flank regions of the features.

label_on_feature  Labels of the feature directly on them. Default FALSE.

lollipop_style_switch_limit  The cutoff value for lollipop style for the 'circle' type. If the max score is greater than this cutoff value, trackViewer will only plot one shape at the highest score. Otherwise trackViewer will draw the shapes like 'Tanghulu'.

...  not used.

Details

In SNP.gr and features, metadata of the GRanges object will be used to control the color, fill, border, alpha, shape, 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>, and for node labels by name the metadata start as node.label.<properties>, such as label.parameter.rot, label.parameter.gp. The parameter is used for grid.text or plotMotifLogoA. 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'.
optimizeStyle

Optimize the style of plot

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 style 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", "col" or "safe".

Value

a list of a trackList and a trackViewerStyle

See Also

See Also as viewTracks
Examples

```r
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

```r
parse2GRanges(text)
```

Arguments

text  

Value

an object of GRanges

Examples

```r
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

```r
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`

Examples

```r
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)
```

plotGInteractions

Description

plot graph for GInteractions

Usage

`plotGInteractions(gi, range, feature.gr, ...)`

Arguments

- `gi`: an object of `GInteractions`
- `range`: the region to plot. an object of `GRanges`
- `feature.gr`: the feature.gr to be added. an object of `GRanges`
- `...`: Not used.

Examples

```r
library(InteractionSet)
gi <- readRDS(system.file("extdata", "gi.rds", package="trackViewer"))
ranges <- GRanges("chr2", IRanges(234500000, 235000000))
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
feature.gr <- genes(TxDb.Hsapiens.UCSC.hg19.knownGene)
feature.gr <- subsetByOverlaps(feature.gr, regions(gi))
feature.gr$col <- sample(1:7, length(feature.gr), replace=TRUE)
```
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

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)
```r
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)))
```

---

### Description

plot ideogram for one chromosome

### Usage

```r
plotIdeo(
  ideo,
  chrom = seqlevels(ideo)[1],
  colorSheme = gieStain(),
  gp = gpar(fill = NA),
  ...
)
```

### Arguments

- **ideo**: output of `loadIdeogram`.
- **chrom**: A length 1 character vector of chromosome name.
- **colorSheme**: A character vector of giemsa stain colors.
- **gp**: parameters used for `grid.roundrect`.
- ... parameters not used.

### Examples

```r
## Not run:
ideo <- loadIdeogram("hg38")
library(grid)
grid.newpage()
plotIdeo(ideo)

## End(Not run)
```
plotOneIdeo plot ideogram with data for one chromosome

Description

plot ideogram with data for one chromosome

Usage

plotOneIdeo(
  ideogram, dataList,
  parameterList = list(wp = plotViewport(margins = c(0.1, 4.1, 1.1, 0.1)), ideoHeight = 
    unit(1/(1 + length(dataList)), "npc"), vgap = unit(1, "lines"), ylabs = 
    seqlevels(ideo)[1], ylabsRot = 90, ylabsPos = unit(2.5, "lines"), xaxis = FALSE, 
    yaxis = FALSE, xlab = "", types = "barplot", heights = NULL, dataColumn = "score", 
    gps = gpar(col = "black", fill = "gray"),
    chrom = seqlevels(ideo)[1],
    colorSheme = gieStain(),
    gp = gpar(fill = NA, lwd = 2),
    ...)

Arguments

ideo output of loadIdeogram.
dataList a GRangesList of data to plot.
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.
chrom A length 1 character vector of chromosome name.
colorSheme A character vector of giemsa stain colors.
gp parameters used for grid.roundrect.
...

Examples

## Not run:
ideo <- loadIdeogram("hg38")
library(rtracklayer)
library(grid)
dataList <- ideogram[seqnames(ideo) %in% "chr1"]
dataList$score <- as.numeric(dataList$gieStain)
dataList <- dataList[dataList$gieStain!="gneg"]
dataList <- GRangesList(dataList, dataList)
grid.newpage()
plotOneIdeo(ideo, dataList, chrom="chr1")
pos-class

## End(Not run)

pos-class

Class "pos"

Description

An object of class "pos" represents a point location

Slots

- x A numeric value, indicates the x position
- y A numeric value, indicates the y position
- unit "character" specifying the units for the corresponding numeric values. See unit

trackList-class

List of tracks

Description

An extension of List that holds only track objects.

Usage

## S4 replacement method for signature 'trackList'
seqlevelsStyle(x) <- value

trackList(..., heightDist = NA)

Arguments

- x trackList object.
- value values to be assigned.
- ... 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.
- heightDist A vector or NA to define the height of each track.

See Also

track.
trackStyle-class  

Description

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

Usage

## S4 method for signature 'track'
seqlevels(x)

## S4 method for signature 'track'
seqlevelsStyle(x)

## S4 replacement method for signature 'track'
seqlevelsStyle(x) <- value

## S4 method for signature 'track'
show(object)

## S4 method for signature 'track'
x$name

## S4 replacement method for signature 'track'
x$name <- value

setTrackStyleParam(ts, attr, value)

## S4 method for signature 'track,character'
setTrackStyleParam(ts, attr, value)

setTrackXscaleParam(ts, attr, value)

## S4 method for signature 'track,character'
setTrackXscaleParam(ts, attr, value)

setTrackYaxisParam(ts, attr, value)

## S4 method for signature 'track,character'
setTrackYaxisParam(ts, attr, value)

Arguments

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

Details

The attr of setTrackXscaleParam could not only be a slot of xscale, but also be position. If the attr is set to position, value must be a list of x, y and label. For example setTrackXscaleParam(track, attr="position", value=list(x=122929675, y=4, label=500))

Slots

tracktype "character" track type, could be peak or cluster. Default is "peak". "cluster" is not supported yet. For interaction data, it could be "heatmap" or "link".
color "character" track color. If the track has dat and dat2 slot, it should have two values.
NAcolor "character" NA color for interactionData.
breaks "numeric" breaks for color keys of interactionData.
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", ylab position, ylabpos should be 'left', 'right', 'topleft', 'bottomleft', 'topright', 'bottomright', 'abovebaseline' or 'underbaseline'. For gene type track, it also could be 'upstream' or 'downstream'
ylalas "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.
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', 'gene', 'transcript', 'scSeq', 'lollipopData' or 'interactionData'.
format The format of the input. It could be "BED", "bedGraph", "WIG", "BigWig" or "BAM"
style Object of class trackStyle
name unused yet
See Also

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

Examples

```r
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))
```

trackViewerStyle-class

Class "trackViewerStyle"

Description

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

Usage

```r
trackViewerStyle(...)

setTrackViewerStyleParam(tvs, attr, value)
```

## S4 method for signature 'trackViewerStyle,character'

```r
setTrackViewerStyleParam(tvs, attr, value)
```

Arguments

... Each argument in ... becomes an slot in the new trackViewerStyle.
tvs An object of trackViewerStyle.
attr the name of slot to be changed.
value values to be assigned.

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
xat "numeric", the values will be passed to grid.xaxis as 'at' parameter.
viewGene

xlabel "character", the values will be passed to grid.xaxis as 'label' parameter.
autoslas "logical" automatic determine y label direction
flip "logical" flip the x-axis or not, default FALSE

Examples

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

---

viewGene  

*plot tracks based on gene name*

Description

given a gene name, plot the tracks.

Usage

```r
viewGene(
  symbol,
  filenames,
  format,
  txdb,
  org,
  upstream = 1000,
  downstream = 1000,
  anchor = c("gene", "TSS"),
  plot = FALSE
)
```

Arguments

- **symbol**: Gene symbol
- **filenames**: files used to generate tracks
- **format**: file format used to generate tracks
- **txdb**: txdb will be used to extract the genes
- **org**: org package name
- **upstream**: upstream from anchor
- **downstream**: downstream from anchor
- **anchor**: TSS, or gene
- **plot**: plot the tracks or not.

Value

an invisible list of a `trackList`, a `trackViewerStyle` and a `GRanges`
Examples

```r
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(org.Hs.eg.db)
extdata <- system.file("extdata", package="trackViewer", mustWork=TRUE)
filename = file.path(extdata, "fox2.bed")
optSty <- viewGene("HSPA8", filenames=filename, format="BED",
    txdb=TxDB.Hsapiens.UCSC.hg19.knownGene,
    org="org.Hs.eg.db")
```

```r
viewTracks plot the tracks
```

Description

A function to plot the data for given range

Usage

```r
viewTracks(
    trackList, chromosome, start, end, strand,
    gr = GRanges(),
    ignore.strand = TRUE,
    viewerStyle = trackViewerStyle(),
    autoOptimizeStyle = FALSE,
    newpage = TRUE,
    operator = NULL,
    smooth = FALSE,
    lollipop_style_switch_limit = 10
)
```

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 +, -, *, /, ^, %% and NA. '-' means dat - dat2, and so on. NA means do not apply any operator. Note: if multiple operator is supplied, please make sure the length of operator keep same as the length of trackList.

smooth
logical(1) or numeric(). Plot smooth curve or not. If it is numeric, eg n, mean of nearby n points will be used for plot. If it is numeric, the second number will be the color. Default color is 2 (red).

lollipop_style_switch_limit
The cutoff value for lollipop style for the 'circle' type. If the max score is greater than this cutoff value, trackViewer will only plot one shape at the highest score. Otherwise trackViewer will draw the shapes like 'Tanghulu'.

Value
An object of viewport for addGuideLine

See Also
See Also as addGuideLine, addArrowMark

Examples

```r
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)
```

Slots

from A pos class, indicates the start position of x-scale.
to A pos class, indicates the end 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 Class "yaxisStyle"

Description

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

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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