Package: transPlotR (via r-universe)

August 30, 2024

Title Visualize Transcript Structures in Elegant Way

Version 0.0.5

Description To visualize the gene structure with multiple isoforms better, I developed this package to draw different transcript structures easily.

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Encoding UTF-8

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Imports cowplot, dplyr, ggplot2, purrr, magrittr, ggarchery, geomtextpath, stats, rtracklayer, ggnewscale, future, furrr, ggh4x

Depends R (>= 2.10), tidyverse

URL https://github.com/junjunlab/transPlotR

BugReports https://github.com/junjunlab/transPlotR/issues

LazyData true

Repository https://junjunlab.r-universe.dev

RemoteUrl https://github.com/junjunlab/transplotr

RemoteRef HEAD

RemoteSha f77b0611046e97f7bc1b757b8d2cfbdffe862bf1

Contents

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bedVis   *bedVis*

Description

visualize peaks(bed files).

Arguments

bdFile	the bed file path, default(NULL).
chr	the chromesome of peak, default(NULL).
region.min	the peak start coordinate, default(NULL).
region.max	the peak end coordinate, default(NULL).
track.width	track width, default(0.1).
collapse	whether collapse the track, default(FALSE).
fill	track fill colors, default(NULL).
show.legend	whether show fill color legend, default(TRUE).
add.label	whether add peak name, default(FALSE).
label.column	the peak name column name, default(NULL).
label.vjsut	the peak label vjust, default(0.1).

Value

a ggplot object.

Author(s)

JunZhang

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calcuRotatedCoord   *calcuRotatedCoord*

Description

calculate the rotated rectangle coordinate with specified degree.

Arguments

data	data.frame
theta	rotate degree, default(45).
workers	how many workers for parallel calculation, default(1).
rx	x variable name, default(NULL).
ry	y variable name, default(NULL).

Value

a data.frame

Author(s)

JunZhang

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gtf *This is a test data for this package test data describtion*

Description

This is a test data for this package test data describtion

Usage

```
gtf
```

Format

An object of class `data.frame` with 1987 rows and 31 columns.

Author(s)

Junjun Lao

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linkVis *linkVis*

Description

visualize the coordinate relation like chromtin accessbility or peak sites correlation.

Usage

```
linkVis(
  linkData = NULL,
  start = NULL,
  end = NULL,
  group = NULL,
  base_size = 14,
  link.aescolor = NULL,
  link.color = NULL,
  line.size = 0.5,
  curvature = 0.5,
  yshift = 0.1,
```

```
    legend.title = "",
    facet = TRUE,
    facet.placement = "outside",
    facet.fill = "grey90",
    facet.color = "black",
    facet.text.angle = 90,
    facet.text.size = 14,
    xAixs.info = TRUE
)
```

Arguments

`linkData`	the link data with data.frame format, default(NULL).
`start`	link start position, default(NULL).
`end`	link end position, default(NULL).
`group`	facet group variable name, default(NULL).
`base_size`	theme base_size, default(14).
`link.aescolor`	link line color or mapping variable name, default(NULL).
`link.color`	colors to change the link line colors when "link.aescolor" is a mapping variable, default(NULL).
`line.size`	link line size, default(0.5).
`curvature`	the link line curvature, default(0.5).
`yshift`	the space upper the link line, default(0.1).
`legend.title`	the legend title, default("").
`facet`	whether show the plot with facet plot, default(TRUE).
`facet.placement`	
	the facet label placement, default("outside").
`facet.fill`	facet rectangle fill color, default("grey90").
`facet.color`	facet rectangle border color, default("black").
`facet.text.angle`	
	facet text angle, default(90).
`facet.text.size`	
	facet text size, default(14).
`xAixs.info`	whether remove X axis info, default(FASLE).

Value

a ggplot object.

Author(s)

JunZhang

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loadBigWig   *loadBigWig*

Description

read bigwig files.

Usage

```
loadBigWig(bwFile = NULL)
```

Arguments

bwFile   the path of bigwig files, default(NULL). bigwig files should end with ".bw" or
                ".bigwig" and directory should not be named "bw" or"bigwig".

Value

a data.frame

Author(s)

JunZhang

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trackVis   *trackVis*

Description

visualize bigwig files.

Arguments

bWData   the data.frame bigwig data, default(NULL).

gtf.file   whether supply gtf annotation file, default(NULL).

gene.name   the gene name to be choosed for visualization, default(NULL).

chr   chr the chromesome of peak, default(NULL).

region.min   the start coordinate, default(NULL).

region.max   the end coordinate, default(NULL).

show.legend   whether show color legend, default(FALSE).

legend.position

                 the legend position, default("right").

color   the track color, default(NULL).

extend.up	extend for upstream of start site, default(3000).
extend.dn	extend for downstream of start site, default(3000).
base_size	theme base size, default(14).
label.angle	the facet label angle, default(0).
label.face	the facet label face, default("bold").
space.y	the facet panel space, default(0.5).
sample.order	the sample order to be plotted in graph, default(NULL).
sampleName.dist	
	the facet label distance from Y axis, default(0.4).
sampleName.hjust	
	the facet label hjust, default(1).
sampleName.vjust	
	the facet label vjust, default(0.5).
xAxis.info	whether retain X axis info, default(TRUE).
yAxis.info	whether retain Y axis info, default(TRUE).
ticks.y.len	the y axis ticks length, default(0.3).
theme	plot theme, "bw" or "classic", default("classic").
scales	the facet scales settings, default("fixed").
ncol	the columns to be arranged, default(1).
mark.region	whether highlight regions in plot, default(FALSE).
mark.col	the colors of marked regions, default(NULL).
mark.alpha	the color alpha of marked regions, default(0.5).
new.yaxis	whether add new style Y axis, default(FALSE).
pos.ratio	the new style Y axis relative position, default(c(0.01,0.8)).
yinfo.text.size	
	the new style Y axis text size, default(5).
back.color	whether add panel background color, default(FALSE).
back.color.alpha	
	panel background color alpha, default(0.15).
y.max	the ylim, default(NULL).
new.label	whether add label in plot, default(FALSE).
label.color	the label color, default(NULL).
pos.label.ratio	
	the new label relative position, default(c(0.99,0.8)).
label.text.size	
	the new label text size, default(5).
label.hjust	the new label text hjust, default(1).
yinfo.hjust	the new style Y axis text hjust, default(0).
facetGroup	the annotation for samples, default(NULL).
annoLine.size	the annotation line size, default(1).
line.arrow	the annotation line arrow, default(NULL).

Value

a ggplot object.

Author(s)

JunZhang

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trancriptVis	*trancriptVis*

Description

This package is to visualize gene diffrent isoforms.

Arguments

gtfFile	GTF file.
gene	Target gene to plot.
myTranscript	Specify which transcripts to plot use transcipt id.
Chr	Chromosome number.
posStart	Region start position on genome.
posEnd	Region end position on genome.
collapse	Whether to collapse multiple transcripts into one, default(FALSE).
exonWidth	Exon width to plot, default(0.3).
relTextDist	Transcripts name or gene name relative to exon, default(0.3).
intronSize	Intron line size, default(0.5).
arrowBreak	How many gap distance to draw arrows, the smaller the more arrows, default(0.15).
exonColorBy	Whether color group by "transcript_id" or "gene_name", default(NULL).
exonFill	Exon fill color, default('#333399').
circle	Whether make plot into a circle plot, default(FALSE).
cicStart	Circle plot start position, default(pi).
circSegCol	Circle sgement color, default('#333399').
text_only	When circle plot labeled by gene name, whether remove the line connected with gene name, default(FALSE).
ylimLow	The Y axis lower limitation of Circle plot, default(-10).
openAngle	The gap of the circle plot, default(0.5).
arrowCol	Normal arrow color, default('#333399').
arrowAngle	Normal arrow angle, default(30).
arrowLength	Normal arrow length, default(0.1).
arrowType	Normal arrow type, default('open').

addNormalArrow	Whether add normal arrow on plot, default(TRUE).
newStyleArrow	Whether add new style arrow on plot, default(FALSE).
absSpecArrowLen	
	Whether make new style arrow length to be relative to each transcript length or absolute length to the longest transcript, default(FALSE).
speArrowRelPos	The relative position to the transcript on horizontal direction of new style arrow, default(0).
speArrowRelLen	The relative length to the transcript length of new style arrow, default(0.05).
speArrowStart	The new style arrow start position on the vertical direction, default(-0.15).
speArrowRelHigh	
	The relative height of new style arrow to the vertical length, default(2).
speArrowLineSize	
	The new style arrow line size, default(0.5).
speArrowCol	The new style arrow line color, default('black').
speArrowAngle	The new style arrow angle, default(30).
speArrowLen	The new style arrow length, default(0.1).
speArrowType	The new style arrow type, default('closed').
textLabel	The text label aesthetic mappings, default('transcript_id').
textLabelSize	The text label size, default(5).
textLabelColor	The text label color, default('black').
base_size	Theme basesize, default(14).
marginX	Plot left and right margins, default(0.2).
marginY	Plot top and bottomn margins, default(0.2).
aspect.ratio	Plot ratio, default(NULL).
facetByGene	Whether facet by gene to plot, this useful for your genes which are far away from each other or not located on the same chromosome, default(FALSE).
ncolGene	The column numbers to plot, default(NULL).
scales	Facet plot scales, same as "facet_wrap" function, default('free').
strip.position	Facet plot strip.position, same as "facet_wrap" function, default('top').
forcePosRel	Whether force the genome coordinate to relative position to transcript start/end position, default('FALSE').
panel.spacing	Facet plot panel space, default(0.3).
revNegStrand	Whether reverse the negtive strand when set "forcePosRel=TRUE", default('FALSE').
xAxis.info	Whether retain X axis ticks and text, default(TRUE).
reverse.y	whether reverse the Y axis, default(FALSE).
text.pos	the label position(left/right), default(middle).
selecType	choose the representative transcript to show("lt(longest transcript)" or "lcds(longest CDS)"), default(NULL).
topN	the top number representative transcript to be shown, default(1).
show.legend	whether show color legend, default(FALSE).

Value

A ggplot object.

Author(s)

JunZhang

Examples

```
############################################################
# test function

#########################################################
# load data
data(gtf)

# non-coding gene
trancriptVis(gtfFile = gtf,
             gene = 'Xist')

# coding gene
trancriptVis(gtfFile = gtf,
             gene = 'Nanog')

# change fill color
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             exonFill = '#CCFF00')

# change inrton line size
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             intronSize = 1)

# change label size,color and position
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             textLabelSize = 4,
             textLabelColor = 'red',
             relTextDist = 0)

# aes by gene name
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             textLabel = 'gene_name')

# color aes by transcript
trancriptVis(gtfFile = gtf,
             gene = 'Tpx2',
             exonColorBy = 'transcript_id')

# change arrow color and type
```

```
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             arrowCol = 'orange',
             arrowType = 'closed')

# no intron gene and add arrow color
# change arrow color and type
trancriptVis(gtfFile = gtf,
             gene = 'Jun',
             textLabel = 'gene_name',
             arrowCol = 'white',
             arrowType = 'closed') +
  theme_void()

# add arrow breaks
trancriptVis(gtfFile = gtf,
             gene = 'Nanog',
             arrowCol = 'orange',
             arrowType = 'closed',
             arrowBreak = 0.1)

# draw specific transcript
p1 <- trancriptVis(gtfFile = gtf,
                   gene = 'Commd7')

p2 <- trancriptVis(gtfFile = gtf,
                   gene = 'Commd7',
                   myTranscript = c('ENSMUST00000071852','ENSMUST00000109782'))

# combine
cowplot::plot_grid(p1,p2,ncol = 2,align = 'hv')
```

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