Package ‘transPlotR’

October 14, 2022

Title Visualize Transcript Structures in Elegant Way

Version 0.0.2

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

RoxygenNote 7.2.1

Imports cowplot, dplyr, ggplot2, purrr, magrittr, ggarchery, geomtextpath, stats

Depends R (>= 3.5.0), tidyverse

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

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

LazyData true

NeedsCompilation no

Author Junjun Lao [aut, cre] (<`https://orcid.org/0000-0001-7692-9105`>)

Maintainer Junjun Lao <`3219030654@stu.cpu.edu.cn`>

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R topics documented:

`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

`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').

Value

A ggplot object.

Author(s)

Junjun Lao

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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