

Package ‘transPlotR’

July 22, 2025

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

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Description

This is a test data for this package test data description

Usage

```
gtf
```

Format

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

Author(s)

Junjun Lao

trancryptVis	<i>trancryptVis</i>
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Description

This package is to visualize gene different isoforms.

Arguments

gtfFile	GTF file.
gene	Target gene to plot.
myTranscript	Specify which transcripts to plot use transcript 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 segment 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 bottom 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 negative 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  
transcriptVis(gtfFile = gtf,  
               gene = 'Xist')  
  
# coding gene  
transcriptVis(gtfFile = gtf,  
               gene = 'Nanog')  
  
# change fill color  
transcriptVis(gtfFile = gtf,  
               gene = 'Nanog',  
               exonFill = '#CCFF00')  
  
# change intron line size  
transcriptVis(gtfFile = gtf,  
               gene = 'Nanog',  
               intronSize = 1)  
  
# change label size,color and position  
transcriptVis(gtfFile = gtf,  
               gene = 'Nanog',  
               textLabelSize = 4,  
               textLabelColor = 'red',  
               relTextDist = 0)  
  
# aes by gene name  
transcriptVis(gtfFile = gtf,  
               gene = 'Nanog',  
               textLabel = 'gene_name')  
  
# color aes by transcript  
transcriptVis(gtfFile = gtf,  
               gene = 'Tpx2',  
               exonColorBy = 'transcript_id')  
  
# change arrow color and type
```

```
transcriptVis(gtffile = gtf,
              gene = 'Nanog',
              arrowCol = 'orange',
              arrowType = 'closed')

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

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

# draw specific transcript
p1 <- transcriptVis(gtffile = gtf,
                  gene = 'Commd7')

p2 <- transcriptVis(gtffile = gtf,
                  gene = 'Commd7',
                  myTranscript = c('ENSMUST00000071852', 'ENSMUST00000109782'))

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

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* **datasets**

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