

Package: ggtangle (via r-universe)

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Title Draw Network with Data

Version 0.0.3

Description Extends the 'ggplot2' plotting system to support network visualization. Inspired by 'ggtree', 'ggtangle' is designed to work with network associated data.

Imports ggfun (>= 0.1.7), ggplot2, ggrepel, igraph, rlang, yulab.utils (>= 0.1.7)

Suggests aplot, ggtree, knitr, prettydoc, rmarkdown, scatterpie (>= 0.2.4)

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

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Repository <https://guangchuangyu.r-universe.dev>

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`cnetplot`*category-item network plot*

Description

category-item network plot

Usage

```
cnetplot(  
  x,  
  layout = igraph::layout_nicely,  
  showCategory = 5,  
  color_category = "#E5C494",  
  size_category = 1,  
  color_item = "#B3B3B3",  
  size_item = 1,  
  color_edge = "grey",  
  size_edge = 0.5,  
  node_label = "all",  
  foldChange = NULL,  
  hilight = "none",  
  hilight_alpha = 0.3,  
  ...  
)
```

```
## S3 method for class 'list'  
cnetplot(  
  x,  
  layout = igraph::layout_nicely,  
  showCategory = 5,  
  color_category = "#E5C494",  
  size_category = 1,  
  color_item = "#B3B3B3",  
  size_item = 1,  
  color_edge = "grey",  
  size_edge = 0.5,  
  node_label = "all",  
  foldChange = NULL,  
  hilight = "none",  
  hilight_alpha = 0.3,  
  ...  
)
```

Arguments

x input object

layout	network layout
showCategory	selected category to be displayed
color_category	color of category node
size_category	relative size of the category
color_item	color of item node
size_item	relative size of the item (e.g., genes)
color_edge	color of edge
size_edge	relative size of edge
node_label	one of 'all', 'none', 'category' and 'item'
foldChange	numeric values to color the item (e.g, foldChange of gene expression values)
hilight	selected category to be highlighted
hilight_alpha	transparent value for not selected to be highlight
...	additional parameters

drag_network

Drag the nodes of a network to update the layout of the network

Description

Drag the nodes of a network to update the layout of the network

Usage

```
drag_network(p, g = NULL)
```

Arguments

p the network diagram as a ggplot/gg/ggraph object.
g an corresponding igraph object. Default is to extract from the 'ggraph' attribute.

Value

an updated ggplot/gg/ggraph object

Examples

```
## Not run:
library(igraph)
library(ggraph)

flow_info <- data.frame(from = c(1,2,3,3,4,5,6),
                        to = c(5,5,5,6,7,6,7))
g = graph_from_data_frame(flow_info)
p <- ggraph(g, layout='nicely') + geom_node_point() + geom_edge_link()
pp <- drag_network(p)

## End(Not run)
```

geom_edge	<i>layer to draw edges of a network</i>
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Description

layer to draw edges of a network

Usage

```
geom_edge(mapping = NULL, data = NULL, geom = geom_segment, ...)
```

Arguments

mapping	aesthetic mapping, default is NULL
data	data to plot, default is NULL
geom	geometric layer to draw lines
...	additional parameter passed to 'geom'

Value

line segments layer

Examples

```
flow_info <- data.frame(from = LETTERS[c(1,2,3,3,4,5,6)],
                       to = LETTERS[c(5,5,5,6,7,6,7)])

dd <- data.frame(
  label = LETTERS[1:7],
  v1 = abs(rnorm(7)),
  v2 = abs(rnorm(7)),
  v3 = abs(rnorm(7))
)

g = igraph::graph_from_data_frame(flow_info)

p <- ggplot(g) + geom_edge()
library(ggplot2)
library(scatterpie)

p %+% dd +
  geom_scatterpie(cols = c("v1", "v2", "v3")) +
  geom_text(aes(label=label), nudge_y = .2) +
  coord_fixed()
```

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