

Package ‘graphsim’

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Type Package

Title Simulate Expression Data from 'igraph' Networks

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Description Functions to develop simulated continuous data (e.g., gene expression) from a sigma covariance matrix derived from a graph structure in 'igraph' objects. Intended to extend 'mvt-norm' to take 'igraph' structures rather than sigma matrices as input. This allows the use of simulated data that correctly accounts for pathway relationships and correlations. This allows the use of simulated data that correctly accounts for pathway relationships and correlations. Here we present a versatile statistical framework to simulate correlated gene expression data from biological pathways, by sampling from a multivariate normal distribution derived from a graph structure. This package allows the simulation of biological pathways from a graph structure based on a statistical model of gene expression. For example methods to infer biological pathways and gene regulatory networks from gene expression data can be tested on simulated datasets using this framework. This also allows for pathway structures to be considered as a confounding variable when simulating gene expression data to test the performance of genomic analyses.

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URL <https://github.com/TomKellyGenetics/graphsim/>

BugReports <https://github.com/TomKellyGenetics/graphsim/issues/>

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graphsimsim-package	<i>The graphsimsim package</i>
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Description

graphsimsim is a package to simulate normalised expression data from networks for biological pathways using 'igraph' objects and multivariate normal distributions.

Details

This package provides functions to develop simulated continuous data (e.g., gene expression) from a Sigma (Σ) covariance matrix derived from a graph structure in 'igraph' objects. Intended to extend 'mvtnorm' to take 'igraph' structures rather than sigma matrices as input. This allows the use of simulated data that correctly accounts for pathway relationships and correlations. Here we present a versatile statistical framework to simulate correlated gene expression data from biological pathways, by sampling from a multivariate normal distribution derived from a graph structure. This package allows the simulation of biological pathways from a graph structure based on a statistical model of gene expression, such as simulation of expression profiles that of log-transformed and normalised data from microarray and RNA-Seq data.

Introduction

This package enables the generation of simulated gene expression datasets containing pathway relationships from a known underlying network. These simulated datasets can be used to evaluate various bioinformatics methodologies, including statistical and network inference procedures.

These are computed by 1) resolving inhibitory states to derive a consistent matrix of positive and negative edges, 2) inferring relationships between nodes from paths in the graph, 3) weighting these in a Sigma (Σ) covariance matrix and 4) using this to sample a multivariate normal distribution.

Getting Started

The `generate_expression` function is a wrapper around all necessary functions to give a final simulated dataset.

Here we set up an example graph object using the `igraph` package.

```
library("igraph")
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                              c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
```

Then we can call `generate_expression` to return the simulated data based on the relationships defined in the graph structure. Various options are available to fine-tune this.

```
expr <- generate_expression(100, graph_structure,
                           cor = 0.8,
                           mean = 0,
                           sd = 1,
                           comm = FALSE,
                           dist = TRUE,
                           absolute = FALSE,
                           laplacian = FALSE)
```

Here we can see the final result. The graph structure defines the covariance matrix used by `rmvnorm` to generate a multivariate distribution.

```
dim(expr)
```

```
library("gplots")
heatmap.2(expr,
          scale = "none",
          trace = "none",
          col = bluered(50),
          colsep = 1:4,
          rowsep = 1:4)
```

This dataset consists of 9 rows (one for each vertex or gene) in the graph and 100 columns (one for each sample or observation).

Input with an adjacency matrix is available using the `generate_expression_mat` function.

Creating Input Data

Graph structures can be passed directly from the [igraph](#) package. Using this package, you can create an ‘igraph’ class object.

```
> class(graph_structure)
[1] "igraph"

> graph_structure
IGRAPH ba7fa2f DN-- 9 8 --
+ attr: name (v/c)
+ edges from ba7fa2f (vertex names):
[1] A->C B->C C->D D->E D->F F->G F->I H->I
```

This ‘igraph’ object class can be passed directly to [generate_expression](#) shown above and internal functions described below: [make_sigma_mat_graph](#), [make_sigma_mat_dist_graph](#), [make_distance_graph](#), and [make_state_matrix](#).

The ‘graphsim’ package also supports various matrix formats and has functions to handle these. The following functions will compute matrices from an ‘igraph’ object class:

- [make_adjmatrix_graph](#) to derive the adjacency matrix for a graph structure.
- [make_commonlink_graph](#) to derive the ‘common link’ matrix for a graph structure of mutually shared neighbours.
- [make_laplacian_graph](#) to derive the Laplacian matrix for a graph structure.

The following functions will compute matrices from an [adjacency matrix](#):

- [make_commonlink_adjmat](#) to derive the ‘common link’ matrix for a graph structure of mutually shared neighbours.
- [make_laplacian_adjmat](#) to derive the Laplacian matrix for a graph structure.

We provide some pre-generate pathways from Reactoem database for testing and demonstrations:

- [RAF_MAP_graph](#) for the interactions in the “RAF/MAP kinase” cascade (17 vertices and 121 edges).
- [Pi3K_graph](#) for the phosphoinositide-3-kinase cascade (35 vertices and 251 edges).
- [Pi3K_AKT_graph](#) for the phosphoinositide-3-kinase activation of Protein kinase B pathway “PI3K/AKT activation” (275 vertices and 21106 edges).
- [TGFBeta_Smad_graph](#) for the TGF- β receptor signaling activates SMADs pathway (32 vertices and 173 edges).

Please note that demonstrations on larger graph objects. These can be called directly from the package:

```
> graphsim::Pi3K_graph
IGRAPH 21437e3 DN-- 35 251 --
+ attr: name (v/c)
+ edges from 21437e3 (vertex names):
```



```
> states <- E(TGFBeta_Smad_graph)$state
> table(states)
states
1    2
103  70
```

Internal Functions

The following functions are used by `generate_expression` to compute a simulated dataset. They can be called separately to summarise the steps used to compute the final data matrix or for troubleshooting.

- `make_sigma_mat_adjmat`, `make_sigma_mat_comm`, `make_sigma_mat_laplacian`, and `make_sigma_mat_graph` will compute a Sigma (Σ) covariance matrix from an adjacency matrix, common link matrix, Laplacian matrix, or an ‘igraph’ object. They are computed as above and passed to `rmvnorm`.
- `make_distance_adjmat`, `make_distance_comm`, `make_distance_laplacian`, and `make_distance_graph` will compute a distance matrix of relationships from an adjacency matrix, common link matrix, Laplacian matrix, or an ‘igraph’ object. They are computed as above and passed to `make_sigma`.
- `make_state_matrix` will compute a “state matrix” resolving positive and negative correlations from a vector of edge properties. This is called by `make_sigma` and `generate_expression` to ensure that the signs of correlations are consistent.

Examining Step-by-Step

These internal functions can be called to compute steps of the simulation procedure and examine the results.

1. first we create a graph structure and define the input parameters

```
library("igraph")
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
#sample size
data.n <- 100
#data distributions
data.cor <- 0.75
data.mean <- 3
data.sd <- 1.5
#inhibition states
edge_states <- c(1, 1, -1, -1, 1, 1, 1, 1)
```

2. examine the relationships between the genes.

Here we can see which nodes share an edge:

```

> adjacency_matrix <- make_adjmatrix_graph(graph_structure)
> adjacency_matrix
  A C B D E F G I H
A 0 1 0 0 0 0 0 0 0
C 1 0 1 1 0 0 0 0 0
B 0 1 0 0 0 0 0 0 0
D 0 1 0 0 1 1 0 0 0
E 0 0 0 1 0 0 0 0 0
F 0 0 0 1 0 0 1 1 0
G 0 0 0 0 0 1 0 0 0
I 0 0 0 0 0 1 0 0 1
H 0 0 0 0 0 0 0 1 0

```

Here we define a geometrically decreasing series of relationships between genes based on distance by paths in the graph:

```

> relationship_matrix <- make_distance_graph(graph_structure, absolute = FALSE)
> relationship_matrix
  A          C          B          D          E          F          G          I          H
A 1.00000000 0.20000000 0.10000000 0.10000000 0.06666667 0.06666667 0.05000000 0.05000000 0.04000000
C 0.20000000 1.00000000 0.20000000 0.20000000 0.10000000 0.10000000 0.06666667 0.06666667 0.05000000
B 0.10000000 0.20000000 1.00000000 0.10000000 0.06666667 0.06666667 0.05000000 0.05000000 0.04000000
D 0.10000000 0.20000000 0.10000000 1.00000000 0.20000000 0.20000000 0.10000000 0.10000000 0.06666667
E 0.06666667 0.10000000 0.06666667 0.20000000 1.00000000 0.10000000 0.06666667 0.06666667 0.05000000
F 0.06666667 0.10000000 0.06666667 0.20000000 0.10000000 1.00000000 0.20000000 0.20000000 0.10000000
G 0.05000000 0.06666667 0.05000000 0.10000000 0.06666667 0.20000000 1.00000000 0.10000000 0.06666667
I 0.05000000 0.06666667 0.05000000 0.10000000 0.06666667 0.20000000 0.10000000 1.00000000 0.20000000
H 0.04000000 0.05000000 0.04000000 0.06666667 0.05000000 0.10000000 0.06666667 0.20000000 1.00000000

```

Here we can see the resolved edge states through paths in the adjacency matrix:

```

> names(edge_states) <- apply(graph_structure_edges, 1, paste, collapse = "-")
> edge_states
A-C B-C C-D D-E D-F F-G F-I H-I
1  1 -1 -1  1  1  1  1
> state_matrix <- make_state_matrix(graph_structure, state = edge_states)
> state_matrix
  A C B D E F G I H
A 1 1 1 -1 1 -1 -1 -1 -1
C 1 1 1 -1 1 -1 -1 -1 -1
B 1 1 1 -1 1 -1 -1 -1 -1
D -1 -1 -1 1 -1 1 1 1 1
E 1 1 1 -1 1 -1 -1 -1 -1
F -1 -1 -1 1 -1 1 1 1 1
G -1 -1 -1 1 -1 1 1 1 1
I -1 -1 -1 1 -1 1 1 1 1
H -1 -1 -1 1 -1 1 1 1 1

```

3. define a Sigma (Σ) covariance matrix

Here we can see that the signs match the `state_matrix` and the covariance is based on the `relationship_matrix` weighted by the correlation (`cor`) and standard deviation (`sd`) parameters.

Note that where `sd = 1`, the diagonals will be 1 and the off-diagonal terms will be correlations.

```
> sigma_matrix <- make_sigma_mat_dist_graph(
+   graph_structure,
+   state = edge_states,
+   cor = data.cor,
+   sd = data.sd,
+   absolute = FALSE
+ )
> sigma_matrix
      A      C      B      D      E      F      G      I      H
A 2.250000 1.687500 0.843750 -0.84375 0.562500 -0.56250 -0.421875 -0.421875 -0.337500
C 1.687500 2.250000 1.687500 -1.68750 0.843750 -0.84375 -0.562500 -0.562500 -0.421875
B 0.843750 1.687500 2.250000 -0.84375 0.562500 -0.56250 -0.421875 -0.421875 -0.337500
D -0.843750 -1.687500 -0.843750 2.250000 -1.687500 1.68750 0.843750 0.843750 0.562500
E 0.562500 0.843750 0.562500 -1.68750 2.250000 -0.84375 -0.562500 -0.562500 -0.421875
F -0.562500 -0.843750 -0.562500 1.68750 -0.843750 2.25000 1.687500 1.687500 0.843750
G -0.421875 -0.562500 -0.421875 0.84375 -0.562500 1.68750 2.250000 0.843750 0.562500
I -0.421875 -0.562500 -0.421875 0.84375 -0.562500 1.68750 0.843750 2.250000 1.687500
H -0.337500 -0.421875 -0.337500 0.56250 -0.421875 0.84375 0.562500 1.687500 2.250000
```

4. generate an expression dataset using this sigma matrix

We use `generate_expression` to compute an expression dataset, simulated using these parameters:

```
> expression_data <- generate_expression(
+   n = data.n,
+   graph_structure,
+   state = edge_states,
+   cor = data.cor,
+   mean = data.mean,
+   sd = data.sd,
+   comm = FALSE,
+   dist = FALSE,
+   absolute = FALSE,
+   laplacian = FALSE
+ )
> dim(expression_data)
[1] 9 100
```

Here we also compute the final observed correlations in the simulated dataset:

```
> cor_data <- cor(t(expression_data))
> dim(cor_data)
[1] 9 9
```

These functions are demonstrated in more detail in the [main vignette](#).

Data Visualization

Heatmaps can be used from the [gplots](#) package to display these simulated datasets.

```
library("gplots")
heatmap.2(adjacency_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "white", "black"), key = FALSE)

heatmap.2(relationship_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

heatmap.2(state_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "royalblue", "palevioletred"),
          colsep = 1:length(V(graph_structure)),
          rowsep = 1:length(V(graph_structure)))

heatmap.2(sigma_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "royalblue", "white", "palevioletred"),
          colsep = 1:length(V(graph_structure)),
          rowsep = 1:length(V(graph_structure)))

heatmap.2(expression_data, scale = "none", trace = "none",
          col = colorpanel(50, "royalblue", "white", "palevioletred"),
          colsep = 1:length(V(graph_structure)),
          rowsep = 1:length(V(graph_structure)))

heatmap.2(cor_data, scale = "none", trace = "none",
          col = colorpanel(50, "royalblue", "white", "palevioletred"),
          colsep = 1:length(V(graph_structure)),
          rowsep = 1:length(V(graph_structure)))
```

In particular we can see here that the expected correlations show by the `sigma_matrix` are similar to the observed correlations in the `cor_data`.

Graph Visualization

The 'graphsimsim' package comes with a built-in plotting function to display graph objects.

```
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
plot_directed(graph_structure, layout = layout.kamada.kawai)
```

This supports the 'state' parameter to display activating relationships (with positive correlations) and inhibiting or repressive relationships (with negative correlations).

```
edge_states <- c(1, 1, -1, -1, 1, -1, 1, -1)
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
plot_directed(graph_structure, state = edge_states,
```

```
col.arrow = c("darkgreen", "red")[edge_states / 2 + 1.5]
layout = layout.kamada.kawai)
```

These states can also be passed from the ‘state’ edge attribute of the graph object.

```
graph_pathway <- identity(TGFBeta_Smad_graph)
edge_properties <- E(graph_pathway)$state
plot_directed(graph_pathway,
               col.arrow = c(alpha("navyblue", 0.25),
                             alpha("red", 0.25))[edge_properties],
               fill.node = c("lightblue"),
               layout = layout.kamada.kawai)
```

This plotting function is demonstrated in more detail in the plots_directed.Rmd plotting vignette.

Further information

The graphsime package is published in the *Journal of Open Source Software*. See the paper here for more details: [doi:10.21105/joss.02161](https://doi.org/10.21105/joss.02161)

The graphsime GitHub repository is here: [TomKellyGenetics/graphsime](https://github.com/TomKellyGenetics/graphsime) You can find the development version and submit an [issue](#) if you have questions or comments.

Citation

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See Also

Publication at *Journal of Open Source Software*:

- [doi:10.21105/joss.02161](https://doi.org/10.21105/joss.02161)

GitHub repository:

- <https://github.com/TomKellyGenetics/graphsim/>

Report bugs:

- <https://github.com/TomKellyGenetics/graphsim/issues>

Contributions:

- <https://github.com/TomKellyGenetics/graphsim/blob/master/CONTRIBUTING.md>

generate_expression *Generate Simulated Expression*

Description

Compute simulated continuous expression data from a graph network structure. Requires an [igraph](#) pathway structure and a matrix of states (1 for activating and -1 for inhibiting) for link signed correlations, from a vector of edge states to a signed adjacency matrix for use in [generate_expression](#). Uses graph structure to pass a sigma covariance matrix from [make_sigma_mat_graph](#) or [make_sigma_mat_dist_graph](#) on to [rmvnorm](#). By default data is generated with a mean of 0 and standard deviation of 1 for each gene (with correlations between derived from the graph structure).

Usage

```
generate_expression(
  n,
  graph,
  state = NULL,
  cor = 0.8,
  mean = 0,
  sd = 1,
  comm = FALSE,
  dist = FALSE,
  absolute = FALSE,
  laplacian = FALSE
)
```

```
generate_expression_mat(
  n,
  mat,
  state = NULL,
  cor = 0.8,
  mean = 0,
  sd = 1,
  comm = FALSE,
  dist = FALSE,
  absolute = FALSE,
  laplacian = FALSE
)
```

Arguments

n	number of observations (simulated samples).
graph	An igraph object. May must be directed if states are used.
state	numeric vector. Vector of length E(graph). Sign used to calculate state matrix, may be an integer state or inferred directly from expected correlations for each edge. May be applied a scalar across all edges or as a vector for each edge respectively. May also be entered as text for "activating" or "inhibiting" or as integers for activating (0,1) or inhibiting (-1,2). Compatible with inputs for plot_directed . Also takes a pre-computed state matrix from make_state if applied to the same graph multiple times.
cor	numeric. Simulated maximum correlation/covariance of two adjacent nodes. Default to 0.8.
mean	mean value of each simulated gene. Defaults to 0. May be entered as a scalar applying to all genes or a vector with a separate value for each.
sd	standard deviations of each gene. Defaults to 1. May be entered as a scalar applying to all genes or a vector with a separate value for each.
comm, absolute, laplacian	logical. Parameters for Sigma matrix generation. Passed on to make_sigma or make_sigma .

dist	logical. Whether a graph distance make_sigma_mat_graph or derived matrix make_sigma_mat_dist_graph is used to compute the sigma matrix (using make_distance).
mat	precomputed adjacency, laplacian, commonlink, or scaled distance matrix (generated by make_distance).

Value

numeric matrix of simulated data (log-normalised counts)

Author(s)

Tom Kelly <tom.kelly@eriken.jp>

See Also

See also [make_sigma](#) for computing the Sigma (Σ) matrix, [make_distance](#) for computing distance from a graph object, and [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#), [make_commonlink](#), or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [make_adjmatrix](#), [make_commonlink](#), [make_distance](#), [make_laplacian](#), [make_sigma](#), [make_state](#), [plot_directed\(\)](#)

Other generate simulated expression functions: [make_distance](#), [make_sigma](#), [make_state](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)

# compute a simulated dataset for toy example
# n = 100 samples
# cor = 0.8 max correlation between samples
# absolute = FALSE (geometric distance by default)
test_data <- generate_expression(100, graph_test, cor = 0.8)
##' # visualise matrix
library("gplots")
# expression data
heatmap.2(test_data, scale = "none", trace = "none",
           col = colorpanel(50, "blue", "white", "red"))
# correlations
heatmap.2(cor(t(test_data)), scale = "none", trace = "none",
           col = colorpanel(50, "white", "red"))
# expected correlations ( $\Sigma$ )
sigma_matrix <- make_sigma_mat_graph(graph_test, cor = 0.8)
heatmap.2(make_sigma_mat_graph(graph_test, cor = 0.8),
           scale = "none", trace = "none",
```

```

        col = colorpanel(50, "white", "red"))

# compute adjacency matrix for toy example
adjacency_matrix <- make_adjmatrix_graph(graph_test)
# generate simulated data from adjacency matrix input
test_data <- generate_expression_mat(100, adjacency_matrix, cor = 0.8)

# compute a simulated dataset for toy example
# n = 100 samples
# cor = 0.8 max correlation between samples
# absolute = TRUE (arithmetic distance)
test_data <- generate_expression(100, graph_test, cor = 0.8, absolute = TRUE)
##' # visualise matrix
library("gplots")
# expression data
heatmap.2(test_data, scale = "none", trace = "none",
          col = colorpanel(50, "blue", "white", "red"))
# correlations
heatmap.2(cor(t(test_data)),
          scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))
# expected correlations ( $\Sigma$ )
sigma_matrix <- make_sigma_mat_graph(graph_test, cor = 0.8)
heatmap.2(make_sigma_mat_graph(graph_test, cor = 0.8),
          scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)

# compute a simulated dataset for toy network
# n = 250 samples
# state = edge_state (properties of each edge)
# cor = 0.95 max correlation between samples
# absolute = FALSE (geometric distance by default)
edge_state <- c(1, 1, -1, 1, 1, 1, 1, -1)
structure_data <- generate_expression(250, graph_structure,
                                     state = edge_state, cor = 0.95)

##' # visualise matrix
library("gplots")
# expression data
heatmap.2(structure_data, scale = "none", trace = "none",
          col = colorpanel(50, "blue", "white", "red"))
# correlations
heatmap.2(cor(t(structure_data)), scale = "none", trace = "none",
          col = colorpanel(50, "blue", "white", "red"))
# expected correlations ( $\Sigma$ )
sigma_matrix <- make_sigma_mat_graph(graph_structure,
                                     state = edge_state, cor = 0.8)
heatmap.2(make_sigma_mat_graph(graph_structure,
                               state = edge_state, cor = 0.8),
          state = edge_state, cor = 0.8),

```



```
heatmap.2(make_sigma_mat_graph(TGFBeta_Smad_graph, cor = 0.75, comm = TRUE),
          scale = "none", trace = "none",
          dendrogram = "none", Rowv = FALSE, Colv = FALSE,
          col = colorpanel(50, "blue", "white", "red"))
```

make_adjmatrix	<i>Generate Adjacency Matrix</i>
----------------	----------------------------------

Description

Compute the adjacency matrix of a (directed) [igraph](#) structure, preserving node/column/row names (and direction).

Usage

```
make_adjmatrix_graph(graph, directed = FALSE)
```

Arguments

graph	An igraph object. May be directed or weighted.
directed	logical. Whether directed information is passed to the adjacency matrix.

Value

An adjacency matrix compatible with generating an expression matrix

Author(s)

Tom Kelly <tom.kelly@riken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, [make_distance](#) for computing distance from a graph object, [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#) or [make_commonlink](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_commonlink](#), [make_distance](#), [make_laplacian](#), [make_sigma](#), [make_state](#), [plot_directed\(\)](#)

Other graph conversion functions: [make_commonlink](#), [make_laplacian](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)

# compute adjacency matrix for toy example
adjacency_matrix <- make_adjmatrix_graph(graph_test)
adjacency_matrix

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
# compute adjacency matrix for toy network
graph_structure_adjacency_matrix <- make_adjmatrix_graph(graph_structure)
graph_structure_adjacency_matrix

# import graph from package for reactome pathway
# TGF- $\beta$  receptor signaling activates SMADs (R-HSA-2173789)
TGFbeta_Smad_graph <- identity(TGFbeta_Smad_graph)

# compute adjacency matrix for TGF- $\beta$  receptor signaling activates SMADs
TGFbeta_Smad_adjacency_matrix <- make_adjmatrix_graph(TGFbeta_Smad_graph)
dim(TGFbeta_Smad_adjacency_matrix)
TGFbeta_Smad_adjacency_matrix[1:12, 1:12]
```

make_commonlink

Generate Common Link Matrix

Description

Compute the common link matrix of a (directed) [igraph](#) structure, preserving node / column / row names (and direction). We can compute the common links between each pair of nodes. This shows how many nodes are mutually connected to both of the nodes in the matrix (how many paths of length 2 exist between them).

Usage

```
make_commonlink_adjmat(adj_mat)
```

```
make_commonlink_graph(graph, directed = FALSE)
```

Arguments

adj_mat	precomputed adjacency matrix.
graph	An igraph object. May be directed or weighted.
directed	logical. Whether directed information is passed to the adjacency matrix.

Value

An integer matrix of number of links shared between nodes

Author(s)

Tom Kelly <tom.kelly@eriken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, [make_distance](#) for computing distance from a graph object, [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#) or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_distance](#), [make_laplacian](#), [make_sigma](#), [make_state](#), [plot_directed\(\)](#)

Other graph conversion functions: [make_adjmatrix](#), [make_laplacian](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)

# compute adjacency matrix for toy example
adjacency_matrix <- make_adjmatrix_graph(graph_test)
# compute nodes with shared edges to a 3rd node
common_link_matrix <- make_commonlink_adjmat(adjacency_matrix)
common_link_matrix

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
# compute adjacency matrix for toy network
graph_structure_adjacency_matrix <- make_adjmatrix_graph(graph_structure)
# compute nodes with shared edges to a 3rd node
graph_structure_common_link_matrix <- make_commonlink_adjmat(graph_structure_adjacency_matrix)
graph_structure_common_link_matrix

# import graph from package for reactome pathway
# TGF- $\beta$  receptor signaling activates SMADs (R-HSA-2173789)
TGFBeta_Smad_graph <- identity(TGFBeta_Smad_graph)
# compute nodes with shared edges to a 3rd node
TGFBeta_Smad_adjacency_matrix <- make_adjmatrix_graph(TGFBeta_Smad_graph)
TGFBeta_Smad_common_link_matrix <- make_commonlink_adjmat(TGFBeta_Smad_adjacency_matrix)
```

```

# we show summary statistics as the graph is large
dim(TGFBeta_Smad_common_link_matrix)
TGFBeta_Smad_common_link_matrix[1:12, 1:12]
# visualise matrix
library("gplots")
heatmap.2(TGFBeta_Smad_common_link_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

```

make_distance

Generate Distance Matrix

Description

Compute the distance matrix of using shortest paths of a (directed) [igraph](#) structure, normalising by the diameter of the network, preserving node/column/row names (and direction). This is used to compute the simulated data for [generate_expression](#) (when `dist = TRUE`) by [make_sigma_mat_dist_graph](#).

Usage

```

make_distance_graph(graph, directed = FALSE, absolute = FALSE)

make_distance_adjmat(mat, directed = FALSE, absolute = FALSE)

make_distance_comm(mat, directed = FALSE, absolute = FALSE)

make_distance_laplacian(mat, directed = FALSE, absolute = FALSE)

```

Arguments

graph	An igraph object. May be directed or weighted.
directed	logical. Whether directed information is passed to the distance matrix.
absolute	logical. Whether distances are scaled as the absolute difference from the diameter (maximum possible). Defaults to TRUE. The alternative is to calculate a relative difference from the diameter for a geometric decay in distance.
mat	precomputed adjacency or commonlink matrix.

Value

A numeric matrix of values in the range [0, 1] where higher values are closer in the network

Author(s)

Tom Kelly <tom.kelly@riken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#), [make_commonlink](#), or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_commonlink](#), [make_laplacian](#), [make_sigma](#), [make_state](#), [plot_directed\(\)](#)

Other generate simulated expression functions: [generate_expression\(\)](#), [make_sigma](#), [make_state](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)

# compute adjacency matrix for toy example
adjacency_matrix <- make_adjmatrix_graph(graph_test)
# compute nodes with relationships between nodes (geometrically decreasing by default)
distance_matrix_geom <- make_distance_adjmat(adjacency_matrix)
distance_matrix_geom

# compute nodes with relationships between nodes (arithmetically decreasing)
distance_matrix_abs <- make_distance_adjmat(adjacency_matrix, absolute = TRUE)
distance_matrix_abs

# compute Laplacian matrix
laplacian_matrix <- make_laplacian_graph(graph_test)
# compute distances from Laplacian
distance_matrix <- make_distance_laplacian(laplacian_matrix)

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
# compute adjacency matrix for toy network
graph_structure_adjacency_matrix <- make_adjmatrix_graph(graph_structure)
# compute nodes with relationships between nodes (geometrically decreasing by default)
graph_structure_distance_matrix_geom <- make_distance_adjmat(graph_structure_adjacency_matrix)
graph_structure_distance_matrix_geom
# visualise matrix
library("gplots")
heatmap.2(graph_structure_distance_matrix_geom, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))
# compute nodes with relationships between nodes (arithmetically decreasing)
graph_structure_distance_matrix_abs <- make_distance_adjmat(graph_structure_adjacency_matrix,
                                                          absolute = TRUE)
graph_structure_distance_matrix_abs
```

```

# visualise matrix
library("gplots")
heatmap.2(graph_structure_distance_matrix_abs,
          scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

# import graph from package for reactome pathway
# TGF- $\beta$  receptor signaling activates SMADs (R-HSA-2173789)
TGFBeta_Smad_graph <- identity(TGFBeta_Smad_graph)
# compute nodes with relationships between nodes (geometrically decreasing by default)
TGFBeta_Smad_adjacency_matrix <- make_adjmatrix_graph(TGFBeta_Smad_graph)
TGFBeta_Smad_distance_matrix_geom <- make_distance_adjmat(TGFBeta_Smad_adjacency_matrix)
# visualise matrix
library("gplots")
heatmap.2(TGFBeta_Smad_distance_matrix_geom, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))
# compute nodes with relationships between nodes (arithmetically decreasing)
TGFBeta_Smad_distance_matrix_abs <- make_distance_adjmat(TGFBeta_Smad_adjacency_matrix,
                absolute = TRUE)

# visualise matrix
library("gplots")
heatmap.2(TGFBeta_Smad_distance_matrix_abs, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

```

make_laplacian	<i>Generate Laplacian Matrix</i>
----------------	----------------------------------

Description

Compute the Laplacian matrix of a (directed) [igraph](#) structure, preserving node/column/row names (and direction).

Usage

```
make_laplacian_adjmat(mat, directed = FALSE)
```

```
make_laplacian_graph(graph, directed = FALSE)
```

Arguments

mat	precomputed adjacency matrix.
directed	logical. Whether directed information is passed to the Laplacian matrix.
graph	An igraph object. May be directed or weighted.

Value

An Laplacian matrix compatible with generating an expression matrix

Author(s)

Tom Kelly <tom.kelly@eriken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, [make_distance](#) for computing distance from a graph object, [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_commonlink](#) or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_commonlink](#), [make_distance](#), [make_sigma](#), [make_state](#), [plot_directed\(\)](#)

Other graph conversion functions: [make_adjmatrix](#), [make_commonlink](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)
# compute Laplacian matrix for toy example
laplacian_matrix <- make_laplacian_graph(graph_test)
laplacian_matrix

# compute Laplacian matrix from adjacency matrix
adjacency_matrix <- make_adjmatrix_graph(graph_test)
laplacian_matrix <- make_laplacian_adjmat(adjacency_matrix)
laplacian_matrix

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)
# compute Laplacian matrix for toy network
graph_structure_laplacian_matrix <- make_laplacian_graph(graph_structure)
graph_structure_laplacian_matrix

# import graph from package for reactome pathway
# TGF- $\beta$  receptor signaling activates SMADs (R-HSA-2173789)
TGFBeta_Smad_graph <- identity(TGFBeta_Smad_graph)

# compute Laplacian matrix for TGF- $\beta$  receptor signaling activates SMADs
TGFBeta_Smad_laplacian_matrix <- make_laplacian_graph(TGFBeta_Smad_graph)
dim(TGFBeta_Smad_laplacian_matrix)
TGFBeta_Smad_laplacian_matrix[1:12, 1:12]
# visualise matrix
library("gplots")
```

```
heatmap.2(TGFBeta_Smad_laplacian_matrix, scale = "none", trace = "none",
          col = colorpanel(50, "blue", "white", "red"))
```

make_sigma

Generate Sigma (Σ) Matrix

Description

Compute the Sigma (Σ) matrix from an [igraph](#) structure or pre-computed matrix. These are compatible with [rmvnorm](#) and [generate_expression](#). By default data is generated with a mean of 0 and standard deviation of 1 for each gene (with correlations between derived from the graph structure). Thus where the Sigma (Σ) matrix has diagonals of 1 (for the variance of each gene) then the symmetric non-diagonal terms (for covariance) determine the correlations between each gene in the output from [generate_expression](#).

Usage

```
make_sigma_mat_adjmat(mat, state = NULL, cor = 0.8, sd = 1)
```

```
make_sigma_mat_comm(mat, state = NULL, cor = 0.8, sd = 1)
```

```
make_sigma_mat_laplacian(mat, state = NULL, cor = 0.8, sd = 1)
```

```
make_sigma_mat_graph(
  graph,
  state = NULL,
  cor = 0.8,
  sd = 1,
  comm = FALSE,
  laplacian = FALSE,
  directed = FALSE
)
```

```
make_sigma_mat_dist_adjmat(
  mat,
  state = NULL,
  cor = 0.8,
  sd = 1,
  absolute = FALSE
)
```

```
make_sigma_mat_dist_graph(
  graph,
  state = NULL,
  cor = 0.8,
  sd = 1,

```

```

    absolute = FALSE
  )

```

Arguments

mat	precomputed adjacency, laplacian, commonlink, or scaled distance matrix (generated by make_distance).
state	numeric vector. Vector of length E(graph). Sign used to calculate state matrix, may be an integer state or inferred directly from expected correlations for each edge. May be applied a scalar across all edges or as a vector for each edge respectively. May also be entered as text for "activating" or "inhibiting" or as integers for activating (0,1) or inhibiting (-1,2). Compatible with inputs for plot_directed . Also takes a pre-computed state matrix from make_state if applied to the same graph multiple times.
cor	numeric. Simulated maximum correlation/covariance of two adjacent nodes. Default to 0.8.
sd	standard deviations of each gene. Defaults to 1. May be entered as a scalar applying to all genes or a vector with a separate value for each.
graph	An igraph object. May be directed or weighted.
comm	logical whether a common link matrix is used to compute sigma. Defaults to FALSE (adjacency matrix).
laplacian	logical whether a Laplacian matrix is used to compute sigma. Defaults to FALSE (adjacency matrix).
directed	logical. Whether directed information is passed to the distance matrix.
absolute	logical. Whether distances are scaled as the absolute difference from the diameter (maximum possible). Defaults to TRUE. The alternative is to calculate a relative difference from the diameter for a geometric decay in distance.

Value

a numeric covariance matrix of values in the range [-1, 1]

Author(s)

Tom Kelly <tom.kelly@eriken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_distance](#) for computing distance from a graph object, and [make_state](#) for resolving inhibiting states.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#), [make_commonlink](#), or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_commonlink](#), [make_distance](#), [make_laplacian](#), [make_state](#), [plot_directed\(\)](#)

Other generate simulated expression functions: [generate_expression\(\)](#), [make_distance](#), [make_state](#)

Examples

```

# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)
# compute sigma ( $\Sigma$ ) matrix for toy example
sigma_matrix <- make_sigma_mat_graph(graph_test, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from adjacency matrix for toy example
adjacency_matrix <- make_adjmatrix_graph(graph_test)
sigma_matrix <- make_sigma_mat_adjmat(adjacency_matrix, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from shared edges for toy example
common_link_matrix <- make_commonlink_graph(graph_test)
sigma_matrix <- make_sigma_mat_comm(common_link_matrix, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from Laplacian for toy example
laplacian_matrix <- make_laplacian_graph(graph_test)
sigma_matrix <- make_sigma_mat_laplacian(laplacian_matrix, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from distance matrix for toy example
distance_matrix <- make_distance_graph(graph_test, absolute = FALSE)
sigma_matrix <- make_sigma_mat_dist_adjmat(distance_matrix, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from geometric distance directly from toy example graph
sigma_matrix <- make_sigma_mat_dist_graph(graph_test, cor = 0.8)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from absolute distance directly from toy example graph
sigma_matrix <- make_sigma_mat_dist_graph(graph_test, cor = 0.8, absolute = TRUE)
sigma_matrix

# compute sigma ( $\Sigma$ ) matrix from geometric distance with sd = 2
sigma_matrix <- make_sigma_mat_dist_graph(graph_test, cor = 0.8, sd = 2)
sigma_matrix

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)

# compute sigma ( $\Sigma$ ) matrix from geometric distance directly from synthetic graph network
sigma_matrix_graph_structure <- make_sigma_mat_dist_graph(graph_structure,
                                                         cor = 0.8, absolute = FALSE)

sigma_matrix_graph_structure
# visualise matrix

```



```

                                                                    absolute = FALSE)
# visualise matrix
library("gplots")
heatmap.2(sigma_matrix_TFGBeta_Smad, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))
# compute with states removed (all positive)
sigma_matrix_TFGBeta_Smad <- make_sigma_mat_dist_graph(TFGBeta_Smad_graph,
                                                       state = 1,
                                                       cor = 0.8,
                                                       absolute = FALSE)

# visualise matrix
library("gplots")
heatmap.2(sigma_matrix_TFGBeta_Smad, scale = "none", trace = "none",
          col = colorpanel(50, "white", "red"))

#restore edge attributes
TFGBeta_Smad_graph <- set_edge_attr(TFGBeta_Smad_graph, "state",
                                   value = TFGBeta_Smad_state)
TFGBeta_Smad_state <- E(TFGBeta_Smad_graph)$state
# states are edge attributes
sigma_matrix_TFGBeta_Smad_inhib <- make_sigma_mat_dist_graph(TFGBeta_Smad_graph,
                                                             cor = 0.8,
                                                             absolute = FALSE)

# visualise matrix
library("gplots")
heatmap.2(sigma_matrix_TFGBeta_Smad_inhib, scale = "none", trace = "none",
          col = colorpanel(50, "blue", "white", "red"))

```

make_state

Make State Matrix

Description

Functions to compute the matrix of states (1 for activating and -1 for inhibiting) for link signed correlations, from a vector of edge states to a signed adjacency matrix for use in [generate_expression](#). This resolves edge states to determine the sign of all correlations between nodes in a network. These are computed internally for sigma matrices as required.

Usage

```
make_state_matrix(graph, state = NULL)
```

Arguments

graph An [igraph](#) object. May be directed or weighted as long as a shortest path can be computed.

state numeric vector. Vector of length $E(\text{graph})$. Sign used to calculate state matrix, may be an integer state or inferred directly from expected correlations for each edge. May be applied a scalar across all edges or as a vector for each edge respectively. May also be entered as text for "activating" or "inhibiting" or as integers for activating (0,1) or inhibiting (-1,2). Compatible with inputs for [plot_directed](#). Vector input is supported either directly calling the function with a value for each edge in $E(\text{graph})$ or as an edge "attribute" in the igraph object (using $E(g)\$state \leftarrow \text{states}$).

Value

An integer matrix indicating the resolved state (activating or inhibiting for each edge or path between nodes)

Author(s)

Tom Kelly <tom.kelly@riken.jp>

See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, and [make_distance](#) for computing distance from a graph object.

See also [plot_directed](#) for plotting graphs or [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#), [make_commonlink](#), or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_commonlink](#), [make_distance](#), [make_laplacian](#), [make_sigma](#), [plot_directed\(\)](#)

Other generate simulated expression functions: [generate_expression\(\)](#), [make_distance](#), [make_sigma](#)

Examples

```
# construct a synthetic graph module
library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)

# compute state matrix for toy example
state_matrix <- make_state_matrix(graph_test)

# construct a synthetic graph network
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                             c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)

# compute state matrix for toy network
graph_structure_state_matrix <- make_state_matrix(graph_structure)
graph_structure_state_matrix
```

```

# compute state matrix for toy network with inhibitions
edge_state <- c(1, 1, -1, 1, 1, 1, 1, -1)
# edge states are a variable
graph_structure_state_matrix <- make_state_matrix(graph_structure, state = edge_state)
graph_structure_state_matrix

# compute state matrix for toy network with inhibitions
E(graph_structure)$state <- c(1, 1, -1, 1, 1, 1, 1, -1)
# edge states are a graph attribute
graph_structure_state_matrix <- make_state_matrix(graph_structure)
graph_structure_state_matrix

library("igraph")
graph_test_edges <- rbind(c("A", "B"), c("B", "C"), c("B", "D"))
graph_test <- graph.edgelist(graph_test_edges, directed = TRUE)
state_matrix <- make_state_matrix(graph_test)

# import graph from package for reactome pathway
# TGF- $\beta$  receptor signaling activates SMADs (R-HSA-2173789)
TGFBeta_Smad_graph <- identity(TGFBeta_Smad_graph)

# compute sigma ( $\Sigma$ ) matrix from geometric distance directly from TGF- $\beta$  pathway
TFGBeta_Smad_state <- E(TGFBeta_Smad_graph)$state
table(TFGBeta_Smad_state)
# states are edge attributes
state_matrix_TFGBeta_Smad <- make_state_matrix(TGFBeta_Smad_graph)
# visualise matrix
library("gplots")
heatmap.2(state_matrix_TFGBeta_Smad , scale = "none", trace = "none",
          dendrogram = "none", Rowv = FALSE, Colv = FALSE,
          col = colorpanel(50, "blue", "white", "red"))

# compare the states to the sign of expected correlations in the sigma matrix
sigma_matrix_TFGBeta_Smad_inhib <- make_sigma_mat_dist_graph(TGFBeta_Smad_graph,
                                                            cor = 0.8,
                                                            absolute = FALSE)

# visualise matrix
heatmap.2(sigma_matrix_TFGBeta_Smad_inhib,
          scale = "none", trace = "none",
          dendrogram = "none", Rowv = FALSE, Colv = FALSE,
          col = colorpanel(50, "blue", "white", "red"))

# compare the states to the sign of final correlations in the simulated matrix
TFGBeta_Smad_data <- generate_expression(100, TGFBeta_Smad_graph, cor = 0.8)
heatmap.2(cor(t(TFGBeta_Smad_data)), scale = "none", trace = "none",
          dendrogram = "none", Rowv = FALSE, Colv = FALSE,
          col = colorpanel(50, "blue", "white", "red"))

```

Description

Reactome pathway R-HSA-198203 for the interactions in the phosphoinositide-3-kinase activation of Protein kinase B (PKB), also known as Akt

Usage

Pi3K_AKT_graph

Format

A graph object of 275 vertices and 21106 edges:

V gene symbol (human)

E directed relationship for pathway

state type of relationship (activating or inhibiting) as edge attribute

Source

PathwayCommons <https://reactome.org/content/detail/R-HSA-198203>

Pi3K_graph

PI3K Cascade

Description

Reactome pathway R-HSA-109704 for the interactions in the phosphoinositide-3-kinase cascade

Usage

Pi3K_graph

Format

A graph object of 35 vertices and 251 edges:

V gene symbol (human)

E directed relationship for pathway

state type of relationship (activating or inhibiting) as edge attribute

Source

PathwayCommons <https://reactome.org/content/detail/R-HSA-109704>

Description

Functions to plot_directed or graph structures including customised colours, layout, states, arrows. Uses graphs functions as an extension of [igraph](#). Designed for plotting directed graphs.

Usage

```
plot_directed(  
  graph,  
  state = NULL,  
  labels = NULL,  
  layout = layout.fruchterman.reingold,  
  cex.node = 1,  
  cex.label = 0.75,  
  cex.arrow = 1.25,  
  cex.main = 0.8,  
  cex.sub = 0.8,  
  arrow_clip = 0.075,  
  pch = 21,  
  border.node = "grey33",  
  fill.node = "grey66",  
  col.label = NULL,  
  col.arrow = NULL,  
  main = NULL,  
  sub = NULL,  
  xlab = "",  
  ylab = "",  
  frame.plot = F  
)
```

Arguments

graph	An igraph object. Must be directed with known states.
state	character or integer. Defaults to "activating" if no "state" edge attribute found. May be applied a scalar across all edges or as a vector for each edge respectively. Accepts non-integer values for weighted edges provided that the sign indicates whether links are activating (positive) or inhibiting (negative). May also be entered as text for "activating" or "inhibiting" or as integers for activating (0,1) or inhibiting (-1,2). Compatible with inputs for <code>make_state_matrix</code> or <code>generate_expression_graph</code> in the <code>graphsim</code> package https://github.com/TomKellyGenetics/graphsim . Vector input is supported
labels	character vector. For labels to plot nodes. Defaults to vertex names in graph object. Entering "" would yield unlabelled nodes.

layout	function. Layout function as selected from layout_ . Defaults to layout.fruchterman.reingold. Alternatives include layout.kamada.kawai, layout.reingold.tilford, layout.sugiyama, and layout.davidson.harel. A 2-column layout matrix giving x and y co-ordinates of each node can be given.
cex.node	numeric. Defaults to 1.
cex.label	numeric. Defaults to 0.75.
cex.arrow	numeric Defaults to 1.25. May take a scalar applied to all edges or a vector with values for each edge respectively.
cex.main	numeric. Defaults to 0.8.
cex.sub	numeric. Defaults to 0.8.
arrow_clip	numeric Defaults to 0.075 (7.5%).
pch	parameter passed to plot. Defaults to 21. Recommends using selecting between 21-25 to preserve colour behaviour. Otherwise entire node will inherit border.node as it's colour, in which case a light colour is recommended to see labels.
border.node	character. Specifies the colours of node border passed to plot. Defaults to grey33. Applies to whole node shape if pch has only one colour.
fill.node	character. Specifies the colours of node fill passed to plot. Defaults to grey66.
col.label	character. Specifies the colours of node labels passed to plot. Defaults to par("fg").
col.arrow	character. Specifies the colours of arrows passed to plot. Defaults to par("fg"). May take a scalar applied to all edges or a vector with colours for each edge respectively.
main, sub, xlab, ylab	Plotting parameters to specify plot titles or axes labels
frame.plot	logical. Whether to frame plot with a box. Defaults to FALSE.

Value

base R graphics

Author(s)

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See Also

See also [generate_expression](#) for computing the simulated data, [make_sigma](#) for computing the Sigma (Σ) matrix, [make_distance](#) for computing distance from a graph object, [make_state](#) for resolving inhibiting states.

See also [heatmap.2](#) for plotting matrices.

See also [make_laplacian](#), [make_commonlink](#), or [make_adjmatrix](#) for computing input matrices.

See also [igraph](#) for handling graph objects and [plot.igraph](#) for base R [plot](#) methods.

Other graphsim functions: [generate_expression\(\)](#), [make_adjmatrix](#), [make_commonlink](#), [make_distance](#), [make_laplacian](#), [make_sigma](#), [make_state](#)

Examples

```

# generate example graphs
library("igraph")
graph_structure_edges <- rbind(c("A", "C"), c("B", "C"), c("C", "D"), c("D", "E"),
                              c("D", "F"), c("F", "G"), c("F", "I"), c("H", "I"))
graph_structure <- graph.edgelist(graph_structure_edges, directed = TRUE)

# plots with igraph defaults
plot(graph_structure, layout = layout.fruchterman.reingold)
plot(graph_structure, layout = layout.kamada.kawai)

# plots with scalar states
plot_directed(graph_structure, state="activating")
plot_directed(graph_structure, state="inhibiting")

# plots with vector states
plot_directed(graph_structure, state = c(1, 1, 1, 1, -1, 1, 1, 1))
plot_directed(graph_structure, state = c(1, 1, -1, 1, -1, 1, -1, 1))
plot_directed(graph_structure, state = c(1, 1, -1, 1, 1, 1, 1, -1))

# plots states with graph attributes
E(graph_structure)$state <- 1
plot_directed(graph_structure)
E(graph_structure)$state <- c(1, 1, -1, 1, -1, 1, -1, 1)
plot_directed(graph_structure)

# plot layout customised
plot_directed(graph_structure, state=c(1, 1, -1, 1, -1, 1, -1, 1), layout = layout.kamada.kawai)

```

RAF_MAP_graph

#' RAF/MAP kinase cascade

Description

Reactome pathway R-HSA-5673001 for the interactions in the RAF/MAP kinase cascade

Usage

```
RAF_MAP_graph
```

Format

A graph object of 17 vertices and 121 edges:

V gene symbol (human)

E directed relationship for pathway

Source

PathwayCommons <https://reactome.org/content/detail/R-HSA-5673001>

TGFBeta_Smad_graph *TGF- β receptor signaling activates SMADs*

Description

Reactome pathway R-HSA-2173789 for the interactions in the TGF- β receptor signaling activates SMADs

Usage

TGFBeta_Smad_graph

Format

A graph object of 32 vertices and 173 edges:

V gene symbol (human)

E directed relationship for pathway

state type of relationship (activating or inhibiting) as edge attribute

Source

PathwayCommons <https://reactome.org/content/detail/R-HSA-2173789>

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