Package ‘KEGGlincs’
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[option]
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add_edge_data

Annotate KEGG edge mappings with user data

Description

Add data column[s] to object created from function expand_KEGG_edges

Usage

add_edge_data(expanded_edges, KEGG_mappings, user_data, data_column_no = 3,
only_mapped = FALSE)

Arguments

expanded_edges The data frame object generated via the function expand_KEGG_edges
KEGG_mappings KEGG_mappings The data.frame object generated by the function expand_KEGG_mappings
user_data A data frame where in which the first two columns contain gene symbols representing an edge and any/all other column[s] contain corresponding edge data.
data_column_no The column index for desired user data to be added
only_mapped A logical indicator; if set to FALSE will return 'de-novo' edges that 'exist' in data but are not documented in KEGG

Value

A data frame object with detailed KEGG edge mappings annotated with user data

Examples

p53_KGML <- get_KGML('hsa04115')
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)
p53_edges <- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)
p53_HA1E_data <- overlap_info(p53_KGML, p53_KEGG_mappings, 'HA1E',
data_type = '100_bing', only_mapped = FALSE)

p53_edges_HA1E_ALL <- add_edge_data(p53_edges, p53_KEGG_mappings,
p53_HA1E_data, c(3, 10, 12))
p53_edges_HA1E_MAPPED <- add_edge_data(p53_edges, p53_KEGG_mappings,
p53_HA1E_data, c(3, 10, 12),
only_mapped = TRUE)
cyto_vis

Send graph to Cytoscape via CyREST

Description

View the KEGG pathway in Cytoscape. With either the ‘expanded edges’ or ‘stacked nodes’ layout, users can visualize and interact with the graphs [strictly] as they are documented in the most recent KGML available from KEGG. This function is a modified version of the function send2cy(), which is part of the cyREST utility functions.

Usage

cyto_vis(graph_object, title = "Cytoscape Graph Window", edge_width_attribute = "summary_score", port.number = 1234)

Arguments

- **graph_object**: An igraph object such as the one generated by the function `get_graph_object`
- **title**: An optional title for the graph when it is in Cytoscape
- **edge_width_attribute**: The attribute that will be used for edge width; if data is not added or the attribute is not part of the graphing information, the edge width will default to 1.
- **port.number**: The port address for Cytoscape

Value

A dynamic map in Cytoscape automatically formatted for convenient viewing.

Examples

```r
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML, FALSE)
nodes <- node_mapping_info(p53_KEGG_mappings)
p53_edges <- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)
edges <- edge_mapping_info(p53_edges)
p53_graph_object <- get_graph_object(nodes, edges)
```

cyto_vis

Prepare edges for mapping

Description

Modify the mapping information for desired look when graphed in Cytoscape

Usage

edge_mapping_info(expanded_edges, data_added = FALSE, significance_markup = FALSE)
expand_KEGG_edges

**Arguments**

expanded_edges  The data frame object generated via the function expand_KEGG_edges() OR has been modified by the function add_edge_data()
data_added  A logical indicator; must be set to TRUE if user data has been added (i.e. edges modified by function add_edge_data())
significance_markup  A logical indicator; if set to TRUE will color edges based on direction and significance of correlation (as determined by user-data-analysis)

**Value**

A data.frame object for edges that will be passed on to the function get_graph_object

**Examples**

```r
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)

#Default; no data added to edges:
p53_edges <- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)
p53_edge_mapping_info <- edge_mapping_info(p53_edges)

#If data is added to edges as additional attribute[s]:
p53_HA1E_data <- overlap_info(p53_KGML, p53_KEGG_mappings, "HA1E", data_type = "100_bing")
p53_edges_HA1E_data_MAPPED <- add_edge_data(p53_edges, p53_KEGG_mappings, p53_HA1E_data, c(3, 10,12), only_mapped = TRUE)
p53_edge_mapping_HA1E <- edge_mapping_info(p53_edges_HA1E_data_MAPPED, data_added = TRUE)
```

**Description**

Extract relationship information from KGML object and re-map based on normalized node information

**Usage**

```r
expand_KEGG_edges(KGML_file, KEGG_mappings)
```

**Arguments**

KGML_file  An object of formal class KEGGPathway
KEGG_mappings  The data.frame object generated by the function expand_KEGG_mappings
**expand_KEGG_mappings**

**Value**

A dataframe object with unique entry information for all edges documented in the KEGG pathway. Note that each row has a unique combination of values for (entry1, entry2, entry1symbol, entry2symbol).

**Examples**

```r
p53_KGML &lt;- get_KGML("hsa04115")
p53_KEGG_mappings &lt;- expand_KEGG_mappings(p53_KGML, FALSE)
p53_edges &lt;- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)
```

**Description**

Extract mapping information from KGML object and normalize mappings based on multi-valued name attribute

**Usage**

```r
expand_KEGG_mappings(KGML_file, convert_KEGG_IDs = TRUE)
```

**Arguments**

- **KGML_file**: An object of formal class KEGGPathway
- **convert_KEGG_IDs**: A logical indicator; if set to FALSE will run faster however genes and compounds will remain labeled via KEGG codes (compounds) or accession numbers (genes). This option must be taken into account if data is being added. For example, the genes in 'KO_data' are identified by symbols, thus it is necessary to retain the default option to convert IDs to symbols when planning to add edge data of this type.

**Value**

A dataframe object with unique entry information for all [node] objects documented in the KEGG pathway. Note that if multiple objects (i.e. genes or compounds) have the same entryID, this indicates that they share the same node [location] in the pathway.

**Examples**

```r
p53_KGML &lt;- get_KGML("hsa04115")
p53_KEGG_mappings &lt;- expand_KEGG_mappings(p53_KGML, FALSE)
```
generate_mappings

The 'boilerplate' for this package’s desired graph style

Description

Generates an object that can be converted to a JSON file and subsequently applied to the graph for the markup specified by this package and the layout mirroring KEGG. Intended for use within cyto_vis

Usage

generate_mappings(style_name, map_edge_width, edge_width_attribute, min_score, max_score)

Arguments

- **style_name**: An argument to name style; when used inside of cyto_vis no name is needed
- **map_edge_width**: A logical indicator; if FALSE no continuous mapping of edge width will be applied
- **edge_width_attribute**: The attribute that will be used for edge width; if data is not added or the attribute is not part of the graphing information, the edge width will default to 1.
- **min_score**: The minimum attribute value for the column used to map edge width
- **max_score**: The maximum attribute value for the column used to map edge width

Value

A list that can be converted to a JSON file to apply desired style/layout in Cytoscape

Examples

```r
style.name = "myKEGGstyle"
mappings <- generate_mappings(style.name, FALSE)
```

get_fisher_info

Perform Fisher’s Exact test for edges in pathway

Description

Obtain a measure for strength and significance for the relationship (i.e. an edge) based on the concordance/discordance of UP-and-DOWN regulated genes shared by two different experimental gene-knockouts Intended for use within overlap_info

Usage

get_fisher_info(edges, method)
get_graph_object

Arguments

edges The set of edges to be analyzed; Although the intended use is for LINCS data overlaps, the function should work with any typical data object as long as it has columns labeled ("UP", "DOWN", "UK1_DK2", "DK1_UK2") that contain integer values.

method The method to correct/adjust p-values for multiple testing. For available methods, type ‘p.adjust.methods’ into command prompt and press enter.

Value

The input edge data.frame object with additional columns containing the results of the applied statistical test

Examples

ex.data <- data.frame("UP" = c(70,6), "DOWN" = c(8,20), "UK1_DK2" = c(4,47), "DK1_UK2" = c(3, 28))

overlaps <- get_fisher_info(ex.data, method = "BH")

Description

Obtain a graph object in the form of an igraph with KEGG-specific graphical information

Usage

generate_graph_object(node_mapping_info, expanded_edges, layered_nodes = FALSE)

Arguments

node_mapping_info The data.frame object generated by the function node_mapping_info()
expanded_edges The data.frame object generated by the function edge_mapping_info()
layered_nodes A logical indicator; if set to TRUE will create a graph with ‘stacked’ nodes that the user can manipulate when multiple nodes are mapped to one location

Value

A list object with the node and edge information from the graph required for mapping.

Examples

p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)

p53_node_mapping_info <- node_mapping_info(p53_KEGG_mappings)
p53_edge_mapping_info <- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)
#Default graph object will have 'expanded edges':
expanded_edges_graph_object <- get_graph_object(p53_node_mapping_info,
p53_edge_mapping_info)

#Graph with layered nodes:
layered_nodes_graph_object <- get_graph_object(p53_node_mapping_info,
p53_edge_mapping_info,
layered_nodes = TRUE)

get_KGML

Description
Download and parse KGML file

Usage
get_KGML(pathwayid, get_if_no_edges = FALSE)

Arguments
pathwayid A KEGG pathway ID of the form "hsa12345" (only human pathways currently)
get_if_no_edges A logical indicator; if pathway has no edges returns null value if set to TRUE

Value
an object of Formal class KEGGPathway

Examples
mtor_KGML <- get_KGML("hsa04150")

# Some pathways contain only node information; since the purpose of this
# package is to explore pathways in an edge-focused manner, the default
# options return a warning message instead of a parsed KGML file if the
# input pathway has no edges.
ribosome_KGML <- get_KGML("hsa03020")
ribosome_KGML <- get_KGML("hsa03020", get_if_no_edges = TRUE)
**KEGG_lincs**

*Combines all other package functions for one-step pathway visualization*

**Description**

Combines all other package functions for one-step pathway visualization

**Usage**

```r
KEGG_lincs(pathwayid, cell_line = NA, refine_by_cell_line = NA, 
add_L1000_edge_data = TRUE, significance_markup = TRUE, 
data_type = "100_full", pert_time = 96, only_mapped = TRUE, 
layered_nodes = FALSE, graph_title = "default", get_data = FALSE, 
convert_KEGG_IDs = TRUE)
```

**Arguments**

- **pathwayid**
  A KEGG pathway ID of the form "hsa12345" (only human pathways currently)

- **cell_line**
  If left as NA will generate a pathway map without data-dependent attributes (such as edge width). To use in combination with LINCS data, choose from the set of cell lines: (A375,A549,ASC,HA1E,HCC515,HEK293T,HEKTE,HEPG2,HT29,MCF7,NCI-H716,NPC,PC3,SHSY5Y,SKL,SW480,VcAP)

- **refine_by_cell_line**
  A logical indicator

- **add_L1000_edge_data**
  A logical indicator

- **significance_markup**
  A logical indicator; if set to TRUE will color edges based on direction and significance of correlation (as determined by user-data-analysis)

- **data_type**
  Choose from data types: (100_full, 100_bing, 50_lm)

- **pert_time**
  Choose from (6,24,48,96,120,144,168)

- **only_mapped**
  A logical indicator; if set to FALSE will return 'de-novo' edges that 'exist' in data but are not documented in KEGG

- **layered_nodes**
  A logical indicator; if set to TRUE will create a graph with 'stacked' nodes that the user can manipulate when multiple nodes are mapped to one location

- **graph_title**
  An optional user-specified graph title

- **get_data**
  A logical indicator; if set to true, will return the 'expanded' edge information for the specified pathway

- **convert_KEGG_IDs**
  A logical indicator; if set to TRUE KEGG compounds will remain labeled via KEGG codes (do not need KEGGREST)

**Value**

A dynamic map in Cytoscape automatically formatted for convenient viewing and, if indicated by user, a data.frame object with detailed information for 'expanded' KEGG edges
### node_mapping_info

#### Prepare nodes for mapping

**Description**

Modify the mapping information for desired look when graphed in Cytoscape

**Usage**

```r
node_mapping_info(KEGG_mappings)
```

**Arguments**

- `KEGG_mappings` The data.frame object generated by the function `expand_KEGG_mappings()`

**Value**

A data.frame object for nodes that will be passed on to the function `get_graph_object`

**Examples**

```r
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML, FALSE)
p53_node_mapping_info <- node_mapping_info(p53_KEGG_mappings)
```
Get overlap information for pairs of gene knock-outs from LINCS data

Description

Get overlap information for pairs of gene knock-outs from LINCS data

Usage

```
overlap_info(KGML_file, KEGG_mappings, cell_type, data_type = "100_full",
pert_time = 96, only_mapped = TRUE, affy_based = FALSE,
keep_counts_only = TRUE, add_fisher_information = TRUE,
p.adjust.method = "BH")
```

Arguments

- **KGML_file**: An object of formal class KEGGPathway
- **KEGG_mappings**: The data.frame object generated by the function expand_KEGG_mappings
- **cell_type**: Choose from the set of cell lines: (A375, A549, ASC, HA1E, HCC515, HEK293T, HEKTE, HEPG2, HT29, SHSY5Y, SKL, SW480, VCAP)
- **data_type**: Choose from data types: (100_full, 100_bing, 50_lm)
- **pert_time**: Choose from (6, 24, 48, 96, 120, 144, 168)
- **only_mapped**: A logical indicator; if set to FALSE will return ‘de-novo’ edges that ‘exist’ in data but are not documented in KEGG
- **affy_based**: A logical indicator; if set to TRUE will return lists/counts based on probeID instead of gene symbol.
- **keep_counts_only**: A logical indicator; if set to FALSE will return data frame with lists [of gene symbols or probe ids] as well as counts
- **add_fisher_information**: A logical indicator; by default the relationships are analyzed for strength of correlation via Fisher’s Exact Test
- **p.adjust.method**: For available methods, type ‘p.adjust.methods’ into command prompt and press enter.

Value

A data frame where each row corresponds to information for pairs of experimental gene knock-outs from LINCS data (found in selected pathway).

Examples

```
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)
p53_edges <- expand_KEGG_edges(p53_KGML, p53_KEGG_mappings)

summary <- path_genes_by_cell_type(p53_KEGG_mappings)
p53_HA1E_data <- overlap_info(p53_KGML, p53_KEGG_mappings,
                               "HA1E", data_type = "100_bing",
                               only_mapped = FALSE)
```
**path_genes_by_cell_type**

*See how many pathway gene knock-outs are available from data*

**Description**

Check quantity of data across cell lines available from LINCS corresponding to the pathway of interest

**Usage**

```r
path_genes_by_cell_type(KEGG_mappings, pert_time = 96, get_KOs = FALSE, generate_plot = TRUE)
```

**Arguments**

- `KEGG_mappings`: The data.frame object generated by the function `expand_KEGG_mappings`
- `pert_time`: Choose from (6,24,48,96,120,144,168)
- `get_KOs`: Logical indicator to have data frame returned
- `generate_plot`: Logical indicator to generate histogram

**Value**

A plot depicting percentage of pathway genes knocked-out by cell line and a data frame object listing the genes [by cell line]

**Examples**

```r
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)
path_genes_by_cell_type(p53_KEGG_mappings)
```

---

**refine_mappings**

*Refine pathway by cell type*

**Description**

Reduce the KEGG pathway by only including genes that are expressed within a given cell type

**Usage**

```r
refine_mappings(KEGG_mappings, cell_line)
```

**Arguments**

- `KEGG_mappings`: The data.frame object generated by the function `expand_KEGG_mappings`
- `cell_line`: Choose from the set of cell lines with baseline data; cell-lines may or may not have corresponding KO data
toCytoscape

Value
A dataframe object with reduced set of pathway mappings to be passed on to other functions

Examples
p53_KGML <- get_KGML("hsa04115")

p53_KEGG_mappings <- expand_KEGG_mappings(p53_KGML)

MCF7_p53_mappings <- refine_mappings(p53_KEGG_mappings, "MCF7")

toCytoscape cyREST utility functions

Description
A subset of the R utility functions available from/defined by cyREST. The function mapAttributes is called from within toCytoscape which, in turn, is called from within cyto_vis.

Usage
toCytoscape(igraphobj)

mapAttributes(attr.names, all.attr, i)

Arguments
igraphobj A graph object compatible for use with the package igraph
attr.names Attribute names of an igraph object
all.attr The attribute value if an igraph object
i The index for a given igraph object

Value
A JSON object to be sent to Cytoscape
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