

# Package ‘KEGGlincs’

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**Type** Package

**Title** Visualize all edges within a KEGG pathway and overlay LINCS data

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**Description** See what is going on 'under the hood' of KEGG pathways by explicitly re-creating the pathway maps from information obtained from KGML files.

**License** GPL-3

**LazyData** true

**RoxygenNote** 6.1.1

**Depends** R (>= 3.3), KOdata, hgu133a.db, org.Hs.eg.db (>= 3.3.0)

**SystemRequirements** Cytoscape (>= 3.3.0), Java (>= 8)

**Suggests** BiocManager (>= 1.20.3), knitr, graph

**biocViews** NetworkInference, GeneExpression, DataRepresentation, ThirdPartyClient, CellBiology, GraphAndNetwork, Pathways, KEGG, Network

**Imports** AnnotationDbi, KEGGgraph, igraph, plyr, gtools, httr, RJSONIO, KEGGREST, methods, graphics, stats, utils, XML, grDevices

**VignetteBuilder** knitr

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add_edge_data	<i>Annotate KEGG edge mappings with user data</i>
---------------	---

---

### 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, map_type = "SYMBOL", only_mapped = TRUE)
```

### 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
map_type	If the genes in your data set are left untranslated set to "NUMBER" (assuming numbers are gene accession numbers)
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 <- add_edge_data(p53_edges, p53_KEGG_mappings,
                               p53_HA1E_data, c(3, 10,12))
```

---

 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**

<code>graph_object</code>	An igraph object such as the one generated by the function <a href="#">get_graph_object</a>
<code>title</code>	An optional title for the graph when it is in Cytoscape
<code>edge_width_attribute</code>	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.
<code>port.number</code>	The port address for Cytoscape

**Value**

A dynamic map in Cytoscape automatically formatted for convenient viewing.

**Examples**

```

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)

## Not run:
cyto_vis(p53_graph_object, "Default p53 Graph [no data added]")

#Workflow to visualize graph with data-dependent attributes:

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

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")
p53_edges_plus_data <- add_edge_data(p53_edges, p53_KEGG_mappings,
                                     p53_HA1E_data, c(3, 10,12),
                                     only_mapped = TRUE)

edges <- edge_mapping_info(p53_edges_plus_data, data_added = TRUE)

p53_plus_data_graph_object <- get_graph_object(nodes, edges)

cyto_vis(p53_plus_data_graph_object, "p53 Graph: Mapped Edges + HA1E Data",
         edge_width_attribute = "UP")

## End(Not run)

```

---

edge\_mapping\_info      *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, tidy_edge = TRUE)

```

**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)
- `tidy_edge` A logical indicator; must be set to `FALSE` for expanded edges

**Value**

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

**Examples**

```
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,
                                             data_column_no = c(3, 10,12),
                                             only_mapped = TRUE)

p53_edge_mapping_HA1E <- edge_mapping_info(p53_edges_HA1E_data_MAPPED,
                                           data_added = TRUE)
```

---

<code>expand_KEGG_edges</code>	<i>Get detailed KEGG mapping information for each relation [edge] documented in KEGG</i>
--------------------------------	--

---

**Description**

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

**Usage**

```
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

**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**

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

---

expand\_KEGG\_mappings    *Get detailed KEGG mapping information for each map entity*

---

**Description**

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

**Usage**

```
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

```
p53_KGML <- get_KGML("hsa04115")
p53_KEGG_mappings <- 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 <a href="#">cyto_vis</a> 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

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

---

get_fisher_info	<i>Perform Fisher's Exact test for edges in pathway</i>
-----------------	---

---

### 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)
```

### 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")
```

---

get_graph_object	<i>Generate graph object from nodes and edges</i>
------------------	---

---

### Description

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

### Usage

```
get_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

*Download and parse KGML file*


---

**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



---

KEGGlincs	<i>KEGGlincs: an R package designed to explore the edges in KEGG pathways</i>
-----------	---

---

**Description**

KEGGlincs: an R package designed to explore the edges in KEGG pathways

---

KEGG_lincs	<i>Combines all other package functions for one-step pathway visualization</i>
------------	--

---

**Description**

Combines all other package functions for one-step pathway visualization

**Usage**

```
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, tidy_edge = FALSE)
```

**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,NCIH716,NSH5Y5Y,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)
tidy_edge	A logical indicator; must be set to FALSE for expanded edges

**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

**Examples**

```
## Not run:

#Default KEGG pathway with colored edges representing type of relationship:
KEGG_lincs("hsa04115", convert_KEGG_IDs = FALSE)

#KEGG pathway with edge width and color based on observed experimental data:
KEGG_lincs("hsa04115", "HA1E")

#Have edge information data.frame to be output to the global environment:
p53_edge_info <- KEGG_lincs("hsa04115", graph_title = "p53"
                           convert_KEGG_IDs = FALSE, get_data = TRUE)

## End(Not run)
```

---

KL_compare	<i>Combines all other package functions for one-step cell line comparison</i>
------------	---

---

**Description**

Combines all other package functions for one-step cell line comparison

**Usage**

```
KL_compare(pathwayid, cell_line1 = NA, cell_line2 = NA,
           refine_by_cell_line = TRUE, data_type = "100_full", pert_time = 96,
           only_mapped = TRUE, get_data = FALSE, convert_KEGG_IDs = TRUE,
           graph_title = "default", tidy_edge = TRUE, layered_nodes = FALSE)
```

**Arguments**

pathwayid	A KEGG pathway ID of the form "hsa12345" (only human pathways currently)
cell_line1	Choose from the set of cell lines: (A375,A549,ASC,HA1E,HCC515,HEK293T,HEKTE,HEPG2,HT29,MSHSY5Y,SKL,SW480,VCAP)
cell_line2	A cell line such that cell_line1 != cell_line2
refine_by_cell_line	A logical indicator
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
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)
graph_title	An optional user-specified graph title
tidy_edge	A logical indicator; must be set to FALSE for expanded edges
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 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

**Examples**

```
## Not run:

# Compare p53 pathway between cell lines A375 and A549:
KL_compare("hsa04115", "A375", "A549")

## End(Not run)
```

---

node\_mapping\_info      *Prepare nodes for mapping*

---

**Description**

Modify the mapping information for desired look when graphed in Cytoscape

**Usage**

```
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**

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

p53_node_mapping_info <- node_mapping_info(p53_KEGG_mappings)
```

---

overlap_info	<i>Get overlap information for pairs of gene knock-outs from LINCS data</i>
--------------	---

---

**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 <code>KEGGPathway</code>
KEGG_mappings	The data.frame object generated by the function <code>expand_KEGG_mappings</code>
cell_type	Choose from the set of cell lines: (A375,A549,ASC,HA1E,HCC515,HEK293T,HEKTE,HEPG2,HT29,MSHSY5Y,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 <code>FALSE</code> will return 'de-novo' edges that 'exist' in data but are not documented in KEGG
affy_based	A logical indicator; if set to <code>TRUE</code> will return lists/counts based on probeID instead of gene symbol.
keep_counts_only	A logical indicator; if set to <code>FALSE</code> 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

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

### Arguments

KEGG_mappings	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**

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

path_genes_by_cell_type(p53_KEGG_mappings)
```

---

refine_mappings	<i>Refine pathway by cell type</i>
-----------------	------------------------------------

---

**Description**

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

**Usage**

```
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

**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")
```

---

tidy_edge	<i>Tidy up pathway by combining edges inside of edge_mapping_info</i>
-----------	---

---

**Description**

Combine edges that share nodes and have other commonalities

**Usage**

```
tidy_edge(edges, edge_id, data_added = FALSE, by_significance = FALSE,
  by_number = TRUE)
```

**Arguments**

edges	The edge dataframe
edge_id	The numeric value for the edge_id
data_added	A logical indicator; set to TRUE if data is added
by_significance	A logical indicator; option if data is added
by_number	A logical indicator; gives rough estimate of edge amount

**Value**

A data frame that has had the given edge condensed for viewing

**Examples**

```
## Not run:
if (tidy_edge == TRUE) {
  edge_IDs <- seq(min(expanded_edges$edgeID), max(expanded_edges$edgeID))
  for (i in edge_IDs){
    if(data_added == TRUE){
      expanded_edges <- tidy_edge(edges = expanded_edges,
                                  edge_id = edge_IDs[i],
                                  data_added = TRUE,
                                  by_significance = TRUE)
    }
    if(data_added == FALSE){
      expanded_edges <- tidy_edge(edges = expanded_edges,
                                  edge_id = edge_IDs[i],
                                  data_added = FALSE)
    }
  }
}

## End(Not run)
```

---

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**

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

**Value**

A JSON object to be sent to Cytoscape

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