Package ‘KEGGgraph’

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Type Package

Title KEGGgraph: A graph approach to KEGG PATHWAY in R and Bioconductor

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Description KEGGGraph is an interface between KEGG pathway and graph object as well as a collection of tools to analyze, dissect and visualize these graphs. It parses the regularly updated KGML (KEGG XML) files into graph models maintaining all essential pathway attributes. The package offers functionalities including parsing, graph operation, visualization and etc.

License GPL (>= 2)

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biocViews Pathways, GraphAndNetwork, Visualization, KEGG

NeedsCompilation no

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**expandKEGGNode**

**Expand KEGG node of paralogues**

**Description**

The function expands KEGG node of paralogues, and is mainly used internally. The end-users are not expected to call it unless they know exactly what they are doing.

**Usage**

```r
expandKEGGNode(node)
```

**Arguments**

- `node` An object of `KEGGNode-class`

**Author(s)**

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**expandKEGGPathway**

**Expand KEGG Pathway**

**Description**

The function expands paralogue nodes in KEGG pathway and returns expanded KEGG pathway, KEGG node and edge data is maintained.

**Usage**

```r
expandKEGGPathway(pathway)
```

**Arguments**

- `pathway` An object of `KEGGPathway-class`

**Details**

The function expands nodes with paralogues in KEGG pathway and copy neccessary edges.

**Value**

An object of `KEGGPathway-class`

**Author(s)**

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**See Also**

- `expandKEGGNode`
**Examples**

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
kegg.pathway <- parseKGML(sfile)
kegg.expandpathway <- expandKEGGPathway(kegg.pathway)
```

**Description**

In KGML files, 'graph' element has a 'name' attribute to store the displaying name of a node, which is straightforward for end users. For example, biologists have no idea about a node 'hsa:1432' but its display name 'MAPK14' helps them to link this node to their knowledge. This method extract DisplayName from graph objects for KEGGNode and graph, where the method for graph returns the display names of its nodes.

**Methods**

- `object = "KEGGNode"` An object of KEGGNode-class
- `object = "graph"` A KEGG graph object

**Author(s)**

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**References**


**Examples**

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
pathway <- parseKGML(sfile)
nodes <- nodes(pathway)
subnodes <- nodes[10:15]
sapply(subnodes, getDisplayName)
## compare them with getName, one 'displayName' may correspond to many paralogues
sapply(subnodes, getName)
```
**getEntryID-methods**

Get entry ID for single or list of KEGGNode or KEGGEdge object(s)

**Description**

The method extracts EntryIDs from KEGGNode-class or KEGGEdge-class object(s).

In case of KEGGEdge-class objects, the entryID of the nodes involved in the binary are returned as a vector in the order specified by the direction of the relation, that is, if the edge is defined as A->B, then the entryID returned from the edge equals to c(getEntryID(A), getEntryID(B)).

**Methods**

- `obj = "KEGGEdge"` Object of KEGGEdge-class
- `obj = "list"` A wrapper for list of KEGGNode-class or KEGGEdge-class objects

**Author(s)**

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**References**


**Examples**

```r
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
pathway <- parseKGML(sfile)

nodes <- nodes(pathway)
node <- nodes[[7]]
getEntryID(node)

edges <- edges(pathway)
edge <- edges[[7]]
getEntryID(edge)

getEntryID(nodes[1:4])
getEntryID(edges[1:4])
```

**getKEGGgeneLink-methods**

Get KEGG gene link

**Description**

Translate a object into a link point to the gene on KEGG website.

This method complies with the Gene link rule of the KEGG website.

**Methods**

- `object = "character"` A KEGGID, for example 'hsa:1423'
Examples

getKEGGgeneLink("hsa:1423")

getKEGGID-methods

Get KEGG ID

Description

Get KEGGID from a KEGGNode-class object.
The KEGGNode-class can be either another pathway (KEGGID in the form like 'hsa\d*'), KEGG Gene ('hsa:\d*') or compound ('cpd:C\d*'). In case of the KEGG Gene ID, the organism prefix is removed when the value is returned.

Methods

object = "KEGGNode" An object of KEGGNode-class

Examples

wntfile <- system.file("extdata/hsa04310.xml",package="KEGGgraph")
wnt <- parseKGML(wntfile)
nodes <- nodes(wnt)
getKEGGID(nodes[[1]])
getKEGGID(nodes[[26]])

getKEGGnodeData

Get or set list of KEGG node or edge data

Description

The 'get' methods extracts KEGG node (edge) attributes from a graph produced by calling parseKGML2Graph or KEGGpathway2Graph. The 'set' methods writes a list into the edge or node data.

Usage

getKEGGnodeData(graph, n)
getKEGGedgeData(graph, n)

Arguments

graph a graph object by parsing KGML file, where KEGG node and edge attributes are maintained

n optional character string, name of the desired node or edge. If is missing all node Data is returned

Details

Node and edge data is stored as list within environments in graphs to save memory and speed up graph manipulations. When using getKEGGnodeData or getKEGGedgeData is called, the list is extracted out of the environment and returned.
**getKGMLurl**

Value

Either a list or single item of **KEGGNode-class** or **KEGGEdge-class** object(s).

Note

These functions will be unified into `KEGGnodeData` and `KEGGnodeData<-` forms.

Author(s)

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Examples

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
gR <- parseKGML2Graph(sfile, expandGenes=TRUE)
getKEGGnodeData(gR, "hsa:4214")
getKEGGedgeData(gR, "hsa:4214~hsa:5605")
```

---

**getKGMLurl**

*Get KGML file (url) with KEGG PATHWAY ID and (optional) organism*

Description

The function simply returns the KGML file url given KEGG PATHWAY ID. If the KEGG PATHWAY ID contains no organism prefix, user can specify the `organism` parameter. Otherwise the `organism` option is ignored.

retrieveKGML is a simple wrapper to getKGMLurl, which downloads the KGML file with `download.file` in utils package.

Usage

```r
getKGMLurl(pathwayid, organism = "hsa")
retrieveKGML(pathwayid, organism, destfile, method="wget", ...)
kglmNonmetabolicName2MetabolicName(destfile)
getricategoryIndepKGMUrl(pathwayid, organism="hsa", method="wget", ...)
```

Arguments

- **pathwayid**  
  KEGG PATHWAY ID, e.g. `hsa00020`
- **organism**  
  three-alphabet organism code, if pathwayid contains the code this option is ignored
- **destfile**  
  Destination file, to which the remote KGML file should be saved
- **method**  
  Method to be used for downloading files, passed to `download.file` function. Currently supports "internal", "wget" and "lynx"
- **...**  
  Parameters passed to `download.file`
getKGMLurl

Details

The function getKGMLurl takes the pathway identifier (can be in the form of 'hsa00020' or with 'pathway' prefix, for example 'path:hsa00020'), and returns the url to download KGML file.

The mapping between pathway identifier and pathway name can be found by KEGGPATHNAME2ID (or reversed mappings) in KEGG.db package. See vignette for example.

retrieveKGML calls download.file to download the KGML file from KEGG FTP remotely.

Since July 2011 the KGML is downloaded directly from the HTTP main page of each pathway, instead of from the FTP server. The FTP server is only open to subscribers. Commercial and other users should consider support the KEGG database by subscribing to the FTP service. See the references section below.

Value

KGML File URL of the given pathway.

Note

So far the function does not check the correctness of the 'organism' prefix, it is the responsibility of the user to guarantee the right spelling.

For Windows users, it is necessary to download and install wget program (http://gnuwin32.sourceforge.net/packages/wget.htm) to use the wget method to download files. Sometimes it may be necessary to modify searching path to add GnuWin32 folder (where wget execution file is located) and re-install R to make wget work.

Some user may experience difficulty of retrieving KGML files when the download method is set to 'auto'. In this case setting the method to 'wget' may solve the problem (thanks to the report by Gilbert Feng).

There were a period when the metabolic and non-metabolic pathways were saved separately in different directories, and KEGGgraph was able to handle them. kgmlNonmetabolicName2MetabolicName is used to translate non-metabolic pathway KGML URL to that of metabolic pathway. getCategoryIndepKGMLurl determines the correct URL to download by attempting both possibilities. They were mainly called internally. Now since the KGML file is to be downloaded in each pathway’s main page instead from the FTP server, these functions are no more needed and will be removed in the next release.

Author(s)

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References

Plea from KEGG (available as of Aug 2011) http://www.genome.jp/kegg/docs/plea.html

Examples

getKGMLurl("hsa00020")
getKGMLurl("path:hsa00020")
getKGMLurl("00020", organism="hsa")
getKGMLurl(c("00460", "hsa:00461", "path:hsa00453", "path:00453"))

## NOT RUN
tmp <- tempfile()
retrieveKGML(pathwayid='00010', organism='cel', destfile=tmp, method="wget")
getName-methods

Get 'name' attribute

Description

Get 'name' attribute for given object, this method can be used for almost all objects implemented in KEGGgraph package to extract their name slot. See manual pages of individual objects for examples.

Methods

object = "KEGGEdgeSubType"  An object of KEGGEEdgeSubType-class
object = "KEGGNode"  An object of KEGGNode-class
object = "KEGGPathway"  An object of KEGGPathway-class
object = "KEGGPathwayInfo"  An object of KEGGPathwayInfo-class
object = "KEGGReaction"  An object of KEGGReaction-class

Author(s)

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References


Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
pathway <- parseKGML(sfile)

## get pathway name
getName(pathway)

## get node name
nodes <- nodes(pathway)
getName(nodes[[2]])

## get edge name: it is not informative since the nodes are identified
## with file-dependent indices
edges <- edges(pathway)
getName(edges[[7]])

## get subtype name
subtype <- getSubtype(edges[[2]][[1]])
getName(subtype)
**getNamedElement**

*Extract the value in a vector by name*

**Description**

The function extracts the value(s) in a named vector by given name(s), in case no element is found with the given name, NA will be returned.

**Usage**

```r
getNamedElement(vector, name)
```

**Arguments**

- `vector` A named vector of any data type
- `name` Wanted name

**Value**

The elements with the given name, 'NA' in case no one was found

**Author(s)**

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**Examples**

```r
vec <- c(first="Hamburg", second="Hoffenheim",third="Bremen")
getNamedElement(vec, "third")
getNamedElement(vec, "last")
```

**getPathwayInfo-methods**

*Get KEGG pathway info*

**Description**

KEGG stores additional information of the pathways in their KGML files, which can be extracted by this function.

The method returns the attributes of the pathway including its full title, short name, organism, image file link (which can be downloaded from KEGG website) and web link.

**Methods**

```r
object = "KEGGPathway" An object of KEGGPathway-class
```

**Examples**

```r
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
pathway <- parseKGML(sfile)
getPathwayInfo(pathway)
```
getReactions-methods

Description

In KGML, the pathway element specifies one graph object with the *entry* elements as its nodes and the *relation* and *reaction* elements as its edges. The *relation* elements are saved as *edges* in objects of *KEGGPathway-class*, and the *reactions* elements are saved as a slot of the object, which can be retrieved with the function `getReactions`.

Regulatory pathways are always viewed as protein networks, so there is no 'reaction' information saved in their KGML files. Metabolic pathways are viewed both as both protein networks and chemical networks, hence the *KEGGPathway-class* object may have reactions information.

Methods

```r
object = "KEGGPathway"  # An object of *KEGGPathway-class*
```

Author(s)

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References

KGML Document manual  
http://www.genome.jp/kegg/docs/xml/

See Also

*KEGGPathway-class*

Examples

```r
mapfile <- system.file("extdata/map00260.xml", package="KEGGgraph")
maptest <- parseKGML(mapfile)
maptest

mapReactions <- getReactions(maptest)
mapReactions[1:3]
```

getRgraphvizEdgeNames  

Description

Get Rgraphviz compatible edge names, where the out- and in-nodes sharing a edge are concatenated by "~".

Usage

```r
getRgraphvizEdgeNames(graph)
```
getSubtype-methods

Arguments

graph A graph object

Value

A list of names, the order is determined by the edge order.

Author(s)

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References

Rgraphviz package

Examples

tnodes <- c("Hamburg", "Dortmund", "Bremen", "Paris")
tedges <- list("Hamburg"=c("Dortmund", "Bremen"),
"Dortmund"=c("Hamburg"), "Bremen"=c("Hamburg"), "Paris"=c())
tgraph <- new("graphNEL", nodes = tnodes, edgeL = tedges)
getRgraphvizEdgeNames(tgraph)

getSubtype-methods Get subtype

Description

KEGG stores sub-type of interactions between entities in the KGML files, which can be extracted
with this method. The descriptions for the subtypes can be explored at the KGML document manual
in the references.

See KEGGEdge-class for examples. The method for graphs is a wrapper to extract all subtype
information from one graph.

Methods

object = "graph" A graph object of KEGGgraph. The method returns a list of subtypes in the
same order of edges

object = "KEGGEdge" An object of KEGGEdge, which stores the subtype information

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

References

### Examples

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
pathway <- parseKGML(sfile)

edges <- edges(pathway)
subtype <- getSubtype(edges[[1]])
subtype
```

---

### Description

The methods get title attribute for given KGML element, for example for objects of `KEGGPathway-class` or `KEGGPathwayInfo-class`.

### Methods

- `object = "KEGGPathway"` An object of `KEGGPathway-class`
- `object = "KEGGPathwayInfo"` An object of `KEGGPathwayInfo-class`

### Author(s)

Jitao David Zhang  
mailto:jitao_david.zhang@roche.com

### References


### Examples

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
pathway <- parseKGML(sfile)

getTitle(pathway)

pi <- getPathwayInfo(pathway)
getTitle(pi)
```
**getValue-methods**

Get type attribute

**Description**

This method can be used to extract generic type attribute from several objects implemented in KEGGgraph package.

The meanings and descriptions of the types can be found at KGML manual listed in the reference.

**Methods**

- object = "KEGGEdge" An object of KEGGEdge-class
- object = "KEGNNode" An object of KEGNNode-class
- object = "KEGGReaction" An object of KEGGReaction-class

**Author(s)**

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**References**


**Examples**

```r
mapfile <- system.file("extdata/map00260.xml", package="KEGGgraph")
maptest <- parseKGML(mapfile)

## node type
de <- nodes(maptest)[[3]]
getType(node)

## edge type
dge <- edges(maptest)[[5]]
getType(edge)

## reaction type
reaction <- getReactions(maptest)[[5]]
getType(reaction)
```

---

**getValue-methods**

Get 'value' attribute

**Description**

Get 'value' attribute, mainly used internally and is not expected to be called by users.

**Methods**

- object = "KEGGEdgeSubType" An object of KEGGEdgeSubType-class
graphDensity

Description

The graph density is defined as \( d = \frac{E}{V(V-1)/2} \) where \( E \) is the number of edges and \( V \) of nodes.

Usage

\texttt{graphDensity(graph)}

Arguments

- \texttt{graph} A graph object

Details

The density of a graph lies between \([0, 1]\)

Value

A value between \([0, 1]\)

Author(s)

Jitao David Zhang \texttt{jitao_david.zhang@roche.com}

References

Aittokallio and Schwikowski (2006), Graph-based methods for analysing networks in cell biology, Briefings in Bioinformatics, 7, 243-255.

Examples

```r
tnodes <- c("Hamburg", "Dortmund", "Bremen", "Paris")
tedges <- list("Hamburg" = c("Dortmund", "Bremen"),
"Dortmund" = c("Hamburg"), "Bremen" = c("Hamburg"), "Paris" = c())
tgraph <- new("graphNEL", nodes = tnodes, edgeL = tedges)
graphDensity(tgraph)
```
isHomoList  

_Determines whether a list is homogenous_

**Description**

If a list contains objects of the same class with the given class name, we call it a homogenous list and the function returns TRUE, otherwise it returns FALSE.

**Usage**

```r
isHomoList(list, class)
```

**Arguments**

- `list` A list
- `class` The class name to be validated

**Value**

logical

**Author(s)**

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**Examples**

```r
testlist <- list("home1"="Hamburg","home2"="Heidelberg", "home3"="Tianjin")
isHomoList(testlist,"character")
testlist$lucky <- 16
isHomoList(testlist,"character")
```

---

**KEGGEdge-class**  

_Class 'KEGGEdge'_

**Description**

A class to represent `relation` elements in KGML files and edge objects in a KEGG graph

**Objects from the Class**

Objects are normally created by `parseRelation` function, which is not intended to be called by user directly

**Slots**

- `entry1ID`: The entryID of the first KEGGNode
- `entry2ID`: The entryID of the second KEGGNode
- `type`: The type of the relation, see `getType-methods`
- `subtype`: The subtype(s) of the edge, a list of `KEGGEdgeSubType`
Methods

**getEntryID** signature(obj = "KEGGEdge"): Get entryIDs of the edge in the order specified by the direction of the edge

**getType** signature(object = "KEGGEdge"): Get the relation type

**getName** signature(object = "KEGGEdge"): Get the names of edges in the convention of Rgraphviz, 'node1~node2'

**show** signature(object = "KEGGEdge"): Show method

Author(s)

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References


See Also

KEGGNode-class

Examples

mapfile<- system.file("extdata/map00260.xml", package="KEGGgraph")
maptest <- parseKGML(mapfile)

x <- edges(maptest)[[1]]
class(x)

## examples to extract information from KEGGEdge
getName(x)
getEntryID(x)

getType(x)
getSubtype(x)

subtype <- getSubtype(x)[[1]]
getName(subtype)

<table>
<thead>
<tr>
<th>KEGGEdgeSubtype</th>
<th>Predefinitions of node or edge types</th>
</tr>
</thead>
</table>

Description

The KGML files define node and edge type and subtypes, which are summarized in these data frames.

Usage

data(KEGGEdgeSubtype)
data(KEGGNodeType)
data(KEGGEdgeType)
KEGGEdgeSubType-class

Format
They are stored as data frames

Details
They are used by graph render functions to identify different types of objects, user could use them to classify edges or nodes.

References

Examples
data(KEGGEdgeSubtype)
data(KEGGEdgeType)
data(KEGNNodeType)

KEGGEdgeSubType-class  Class "KEGGEdgeSubType"

Description
A class to represent subtype in KEGG

Objects from the Class
Objects can be created by calls of the form new("KEGGEdgeSubType", ...).

Slots
name: Object of class "character", name of the subtype
value: Object of class "character", value of the subtype

Methods
getName signature(object = "KEGGEdgeSubType"): getting subtype name
getValue signature(object = "KEGGEdgeSubType"): getting subtype value
show signature(object = "KEGGEdgeSubType"): show method

Note
Please note that 'KEGGEdgeSubtype' is a data frame storing subtype predefinitions, the 'type' with lowercases. 'KEGGEdgeSubType' is however a class representing these subtypes.

Author(s)
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See Also
KEGGEdge-class
Examples

showClass("KEGGEdgeSubType")
## use example(KEGGEdge-class) for more examples

Description

A class to represent `graphics` element in KGML files

Objects from the Class

This method is mainly used to extract visualization information from KGML files.
Objects can be created by calling `parseGraphics`

Slots

- name: Object of class "character" graphics name
- x: Object of class "integer" x coordinate in KEGG figure
- y: Object of class "integer" y coordinate in KEGG figure
- type: Object of class "character" graphics type (shape)
- width: Object of class "integer" width of the symbol
- height: Object of class "integer" height of the symbol
- fgcolor: Object of class "character" foreground color
- bgcolor: Object of class "character" background color

Author(s)

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References


See Also

`parseGraphics`

Examples

showClass("KEGGGraphics")
Description

Class to represent 'group' nodes in KEGG pathways.

Objects from the Class

The objects are usually created by parseEntry function and is not intended to be called directly by users.

Slots

- component: Component of the group
- entryID: see the slot of KEGGNode-class
- graphics: see the slot of KEGGNode-class
- link: see the slot of KEGGNode-class
- map: see the slot of KEGGNode-class
- name: see the slot of KEGGNode-class
- reaction: see the slot of KEGGNode-class
- type: see the slot of KEGGNode-class

Extends

Class "KEGGNode", directly.

Methods

- getComponent signature(object = "KEGGNode"): returns components of the group, in a vector of strings

Author(s)

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See Also

- KEGGNode-class

Examples

showClass("KEGGGroup")
Class "KEGGNode"

Description

The class to present 'entry' element in KGML files and nodes in KEGG graphs

Objects from the Class

Objects can be created by calls of the function `parseEntry` and is not intended to be directly created by users.

Slots

- `entryID`: entryID, the 'id' attribute of 'entry' elements in KGML files. In each KGML file the entryID is specified by auto-increment integers, therefore entryIDs from two individual KGML files are not unique. However, if 'expandGenes' option is specified in `KEGGpathway2Graph` function, the unique KEGGID will replace the default integer as the new entryID, which is unique in biological context.
- `name`: Name of the node
- `type`: Type of the node, use `data(KEGGNodeType)` to see available values
- `link`: URL link of the node
- `reaction`: Reaction of the node
- `map`: Map of the node
- `graphics`: Graphic details (including display name) of the node, an object of `KEGGGraphics`

Methods

- `getDisplayName` signature(object = "KEGGNode"): get display name
- `getEntryID` signature(obj = "KEGGNode"): get entryID, in case of gene-expanded graphs this is the same as getKEGGID
- `getKEGGID` signature(object = "KEGGNode"): get KEGGID
- `getType` signature(object = "KEGGNode"): get the type of the node
- `<-name` signature(object = "KEGGNode"): replace name
- `getComponent` signature(obj = "KEGGNode"): returns entryID (the same as getEntryID), for compatibility with `KEGGGroup-class`
- `show` signature(object = "KEGGNode"): show method

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

References


See Also

`KEGGEdge-class`, `parseEntry`
Examples

```r
## We show how to extract information from KEGGNode object
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
pathway <- parseKGML(sfile)

ns <- nodes(pathway)
node <- ns[[1]]

show(node)
getName(node)
getDisplayName(node)
getEntryID(node)
getKEGGID(node)
```

KEGGPathway-class

Class "KEGGPathway"

Description

A class to represent KEGG pathway

Objects from the Class

Objects can be created by calls of the form `new("KEGGPathway", ...)`. Normally they are created by `parseKGML`.

Slots

- `pathwayInfo`: An object of `KEGGPathwayInfo-class`
- `nodes`: List of objects of `KEGGNode-class`
- `edges`: List of objects of `KEGGEdge-class`
- `reactions`: List of objects of `KEGGReaction-class`

Methods

- `edges` signature: `signature(object = "KEGGPathway", which = "ANY")`: KEGGEdges of the pathway
- `edges<-` signature: `signature(object = "KEGGPathway")`: setting edges
- `getName` signature: `signature(object = "KEGGPathway")`: getting pathway name
- `getTitle` signature: `signature(object = "KEGGPathway")`: getting pathway title
- `nodes<-` signature: `signature(object = "KEGGPathway", value = "ANY")`: setting nodes
- `nodes` signature: `signature(object = "KEGGPathway")`: KEGGNodes of the pathway
- `getPathwayInfo` signature: `signature(object = "KEGGPathway")`: getting KEGGPathwayInfo
- `getTitle` signature: `signature(object = "KEGGPathway")`: getting title of the pathway
- `show` signature: `signature(object = "KEGGPathway")`: display method

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com
References


See Also

parseKGML, KEGGEclass, KEGGNode-class, KEGGReaction-class

Examples

```r
## We show how to extract information from KEGGPathway objects
## Parse KGML file into a 'KEGGPathway' object
mapfile <- system.file("extdata/map00260.xml", package="KEGGgraph")
maptest <- parseKGML(mapfile)

## short summary of the pathway
maptest

## get information of the pathway
getPathwayInfo(maptest)

## nodes of the pathway
nodes <- nodes(maptest)
node <- nodes[[3]]
getName(node)
getType(node)
getDisplayName(node)

## edges of the pathway
edges <- edges(maptest)
edge <- edges[[3]]
getEntryID(edge)
getSubtype(edge)
```

---

**KEGGpathway2Graph** *Parses KEGGpathway to graph*

**Description**

The function parses an object of `KEGGPathway-class` into graph.

**Usage**

`KEGGpathway2Graph(pathway, genesOnly = TRUE, expandGenes = TRUE)`

**Arguments**

- `pathway` An instance of `KEGGPathway-class`
- `genesOnly` logical, should only the genes are maintained and other types of nodes (compounds, etc) neglected? `TRUE` by default
- `expandGenes` logical, should homologue proteins expanded? `TRUE` by default
Details

When `expandGenes=TRUE`, the nodes have unique names of KEGGID (in the form of `org:xxxx`, for example `hsa:1432`), otherwise an auto-increment index given by KEGG is used as node names. In the latter case, the node names are duplicated and graphs cannot be simply merged before the nodes are unique.

KEGG node and edge data is stored in `nodeData` and `edgeData` slots respectively, which can be extracted by `getKEGGnodeData` and `getKEGGedgeData`.

Value

A directed graph.

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

See Also

`parseKGML2Graph`

Examples

```r
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
kegg.pathway <- parseKGML(sfile)
gR.compact<- KEGGpathway2Graph(kegg.pathway,expandGenes=FALSE)
```

**Description**

Regulatory pathways are always viewed as protein networks, so there is no `reaction` information saved in their KGML files. Metabolic pathways are viewed both as both protein networks and chemical networks, hence the `KEGGPathway-class` object may have reactions information among chemical compounds.

This functions extracts reaction information from KEGG pathway, and convert the chemical compound reaction network into directed graph.

**Usage**

`KEGGpathway2reactionGraph(pathway)`

**Arguments**

- `pathway` A `KEGGPathway-class` object, usually as the result of the function `parseKGML`
Details

The direction of the graph is specified by the role of the compound in the reaction, the edges go always out of 'substrate' and points to 'product'.

For now there is no wrapper to parse the KGML file directly into a reaction graph. In future there maybe one, but we don’t want to confuse users with two similar functions to parse the file into a graph (since we assume that most users will need the protein graph, which can be conveniently parsed by parseKGML2Graph).

From version 1.18.0, reaction graphs returned by KEGGpathway2reactionGraph can be merged with other reaction graphs or pathway graphs. Thus users can combine pathway and reaction graph in one KGML file into a single graph.

Value

A directed graph with compounds as nodes and reactions as edges.

If the pathway does not contain any chemical reactions, a warning message will be printed and NULL is returned.

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

References


See Also

KEGGPathway-class

Examples

mapfile <- system.file("extdata/map00260.xml",package="KEGGgraph")
map <- parseKGML(mapfile)
cg <- KEGGpathway2reactionGraph(map)
cg
nodes(cg)[1:3]
edges(cg)[1:3]
Slots

name: Object of class "character" Pathway name
org: Object of class "character" Organism
number: Object of class "character" Number
title: Object of class "character" Title of the pathway
image: Object of class "character" Image URL
link: Object of class "character" URL Link

Methods

getTitle signature(object = "KEGGPathwayInfo"): get title of the pathway
show signature(object = "KEGGPathwayInfo"): show method

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

References


Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
pathway <- parseKGML(sfile)
pi <- getPathwayInfo(pathway)
class(pi)
getTitle(pi)

KEGGRreaction-class  Class "KEGGReaction"

Description

A class to present 'reaction' elements in KGML files

Objects from the Class

Objects can be created by calls of the function parseReaction.

Slots

name: Object of class "character" the KEGGID of this reaction, e.g. "rn:R02749"
type: Object of class "character" the type of this reaction, either 'reversible' or 'irreversible'
substrateName: Object of class "character", KEGG identifier of the COMPOUND database or the GLYCAN database e.g. "cpd:C05378"
substrateAltName: Object of class "character" alternative name of its parent substrate element
productName: Object of class "character" specifies the KEGGID of the product
productAltName: Object of class "character" alternative name of its parent product element
Methods

- `show` signature(object = "KEGGReaction"): show method
- `getName` signature(object = "KEGGReaction"): get the KEGGID of the reaction
- `getType` signature(object = "KEGGReaction"): get the type of the reaction
- `getSubstrate` signature(object = "KEGGReaction"): get the name of substrate
- `getProduct` signature(object = "KEGGReaction"): get the name of product

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

References


Examples

```r
## We show how to extract reactions from a 'KEGGPathway' object
mapfile <- system.file("extdata/map00260.xml", package="KEGGgraph")

maptest <- parseKGML(mapfile)
mapReactions <- getReactions(maptest)

## More details about reaction
reaction <- mapReactions[[1]]
getName(reaction)
getType(reaction)
getSubstrate(reaction)
getProduct(reaction)
```

kgmlFileName2PathwayName

Convert KGML file name to pathway name

Description

The function uses KEGG package and converts KGML file name into human readable pathway name.

Usage

kgmlFileName2PathwayName(filename)

Arguments

filename A KGML file name
mergeGraphs

Details

So far it only supports KGML files organized by species.

NOTE: there is issue of package loading sequence to use this function: the 'KEGG.db' must be loaded before 'KEGGgraph' to use it properly. Otherwise the mget returns error of 'KEGGPATHID2NAME' is not a environment. So far I don’t where does this bug come from, so I commented out the examples.

Value

A character string of pathway name

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

mergeGraphs A function to merge KEGG graphs

Description

The function merges a list of KEGG graphs into one graph object. The merged graph have unique nodes, and edges are merged into non-duplicate sets.

For the reason of speed, mergeGraphs discards KEGG node and edge informations. To maintain them while merging graphs, please use mergeKEGGgraphs.

Usage

mergeGraphs(list, edgemode = "directed")

Arguments

list A list of graph objects, which can be created by parseKGML2Graph
edgemode Edge mode of the graph product, by default 'directed'

Details

The function takes a list of graphs and merges them into a new graph. The nodes of individual graphs must be unique. The function takes care of the removal of duplicated edges.

Value

A directed graph

Note

It is known that graphs from C.elegance pathways have problem when merging, because the nodes name are not consistent between edge records and entry IDs.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>
mergeKEGGgraphs

See Also

parseKGML2Graph

mergeKEGGgraphs Merge KEGG graphs, also merging KEGGNode and KEGGEdge attributes

Description

mergeKEGGgraphs extends function `mergeGraphs` and merges a list of KEGG graphs. Both `mergeGraphs` and `mergeKEGGgraphs` can be used to merge graphs, while the latter form is able to merge the nodes and edges attributes from KEGG, so that the nodes and edges have a one-to-one mapping to the results from `getKEGGnodeData` and `getKEGGedgeData`.

See details below.

Usage

mergeKEGGgraphs(list, edgemode = "directed")

Arguments

list A list of named KEGG graphs
edgemode character, ‘directed’ by default

Details

`mergeGraphs` discards the node or edge attributes, hence `getKEGGnodeData` or `getKEGGedgeData` will return NULL on the resulting graph.

`mergeKEGGgraphs` calls `mergeGraphs` first to merge the graphs, then it also merges the KEGGnodeData and KEGGedgeData, so that they are one-to-one mapped to the nodes and edges in the merged graph.

Value

A graph with nodeData and edgeData

Note

From version 1.21.1, lists containing NULL should also work.

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

See Also

`mergeGraphs`
neighborhood

Examples

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
gR <- parseKGML2Graph(sfile, expandGenes=TRUE)

wntfile <- system.file("extdata/hsa04310.xml", package="KEGGgraph")
wntR <- parseKGML2Graph(wntfile, expandGenes=TRUE)

graphlist <- list(mapkG=gR, wntG=wntR)
mergedKEGG <- mergeKEGGgraphs(graphlist)

mergedKEGG
```

## list containing NULL works also

```r
nlist <- list(gR, wntR, NULL)
nmergedKEGG <- mergeKEGGgraphs(nlist)
```

### neighborhood

Return the neighborhood set of given vertices

Description

The function returns the neighborhood set of given vertices in the form of list. Optionally user can choose to include the given vertices in the list, too.

Usage

```r
neighborhood(graph, index, return.self = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>graph</td>
<td>An object of graphNEL</td>
</tr>
<tr>
<td>index</td>
<td>Names of nodes, whose neighborhood set should be returned</td>
</tr>
<tr>
<td>return.self</td>
<td>logical, should the vertex itself also be returned?</td>
</tr>
</tbody>
</table>

Details

Let \(v\) be a vertex in a (di)graph, the out-neighborhood or successor set \((N+(v), x \in V(G)\text{ and } v \rightarrow x)\) and the in-neighborhood or predecessor set \((N-(v), x \in V(G)\text{ and } x \rightarrow v)\) are jointly returned.

The returned list is indexed by the given node indices, NULL is returned in case of non-existing node. The nodes are unique, that is, duplicated nodes are removed in results.

Value

A list indexed by the given node indices, each entry containing the neighborhood set of that node (or furthermore including that node).

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>
parseEntry

References


Examples

```r
V <- c("Hamburg","Stuttgart","Berlin","Paris","Bremen")
E <- list("Hamburg"=c("Berlin","Bremen"),
          "Stuttgart"=c("Berlin","Paris"),
          "Berlin"=c("Stuttgart","Bremen"),
          "Paris"=c("Stuttgart"),
          "Bremen"=c("Hamburg","Berlin"))
g <- new("graphNEL", nodes=V, edgeL=E, edgemode="directed")
if(require(Rgraphviz) & interactive()) {
  plot(g, "neato")
}

## simple uses
neighborhood(g, "Hamburg")
neighborhood(g, c("Hamburg", "Berlin","Paris"))

## in case of non-existing nodes
neighborhood(g, c("Stuttgart","Ulm"))

## also applicable to non-directed graphs
neighborhood(ugraph(g), c("Stuttgart","Berlin"))
```

Description

ENTRY elements contain information of nodes (proteins, enzymes, compounds, maps, etc) in KEGG pathways. `parseEntry` function parses the elements into `link{KEGGNode-class}` or `KEGGGroup-class` objects. It is not expected to be called directly by the user.

Usage

```r
parseEntry(entry)
```

Arguments

entry XML node of KGML file

Details

See [http://www.genome.jp/kegg/docs/xml/](http://www.genome.jp/kegg/docs/xml/) for more details about ’entry’ as well as other elements in KGML files.

Value

An object of `link{KEGGNode}` or (in case of a group node) `link{KEGGGroup}`
parseGraphics

Author(s)
Jitao David Zhang <jitao_david.zhang@roche.com>

References
http://www.genome.jp/kegg/docs/xml/

See Also
parseGraphics, parseKGML, KEGGNode-class, KEGGGroup-class

parseGraphics  Parse ‘graphics’ elements in KGML files

Description
The function parses ‘graphics’ elements in KGML files, and it is mainly used internally.

Usage
parseGraphics(graphics)

Arguments
graphics  XML node

Details
The function is called by other parsing functions and not intended to be called directly by user.

Value
An object of KEGGGraphics-class.

Author(s)
Jitao David Zhang mailto:jitao_david.zhang@roche.com

References

See Also
KEGGraphics-class
parseKGML  

**KGML file parser**

**Description**

The function parses KGML files according to the KGML XML documentation.

**Usage**

```r
parseKGML(file)
```

**Arguments**

- `file`  
  Name of KGML file

**Details**

The function parses KGML file (depending on XML package).

**Value**

An object of `KEGGPathway-class`.

**Author(s)**

Jitao David Zhang  
mailto: jitao_david.zhang@roche.com

**References**

KGML Manual  
http://www.genome.jp/kegg/docs/xml/

**See Also**

`parseEntry`, `parseRelation`, `parseReaction`, `KEGGPathway-class`

**Examples**

```r
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
kegg.pathway <- parseKGML(sfile)
kegg.pathway
```
parseKGML2DataFrame  
Parse KGML file into a data frame

Description

This function extends the `parseKGML2Graph` function, by converting the resulting graph into a three-column data frame representing out-nodes (the `from` column in the data frame), in-nodes (to) and subtypes of edges that connect them (subtype). It can be used, for example, for exporting KEGG pathway networks in plain text files.

Usage

```r
parseKGML2DataFrame(file, reactions=FALSE,...)
```

Arguments

- `file`: A KGML file
- `reactions`: Logical, whether metabolic reactions should be parsed and returned as part of the data frame. Default: FALSE
- `...`: Other parameters passed to `KEGGpathway2Graph`

Details

The out- and in-nodes are represented in the form of KEGG identifiers. For human EntrezIDs the function `translateKEGGID2GeneID` can be used.

Multile edges are supported: in case more than one subtypes of edges exist between two nodes, they are all listed in the resulting data frame.

Value

A three-column data frame, representing the graph structure: out-nodes (the `from` column), in-nodes (to) and edge subtype (subtype).

Author(s)

Jitao David Zhang

See Also

`parseKGML2Graph`, `KEGGpathway2Graph` and `translateKEGGID2GeneID`.

Examples

```r
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
gdf <- parseKGML2DataFrame(sfile)
head(gdf)
dim(gdf)

rfile <- system.file("extdata/hsa00020.xml",package="KEGGgraph")
dim(dfW <- parseKGML2DataFrame(rfile, reactions=TRUE))
dim(dfWO <- parseKGML2DataFrame(rfile, reactions=FALSE))
stopifnot(nrow(dfW)>nrow(dfWO))
```
(parseKGML2Graph)

---

## not expanding genes: only the KGML-specific identifiers are used then
## only for expert use
## NOT RUN

gdf.ne <- parseKGML2DataFrame(sfile, expandGenes=FALSE)
dim(gdf.ne)
head(gdf.ne)
## NOT RUN

---

parseKGML2Graph  Parse KGML files into KEGG graph

Description

This function is a wrapper for parseKGML and KEGGpathway2Graph. It takes two actions: first it reads in the KGML file and parses it into an object of KEGGPathway-class, the second step it calls KEGGpathway2Graph function to return the graph model.

Usage

parseKGML2Graph(file, ...)

Arguments

- `file` Name of KGML file
- `...` other parameters passed to KEGGpathway2Graph, see KEGGpathway2Graph

Details

Note that groups of genes will be split into single genes by calling the KEGGpathway2Graph function. Edges that connected to groups will be duplicated to connect each member of the group.

Value

A graph object.

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
gR <- parseKGML2Graph(sfile,expandGenes=TRUE)
gR
Description

The function does several tasks implemented in the KEGGgraph package in sequence to make expanding maps easier.

Usage

```
parseKGMLexpandMaps(file, downloadmethod = "wget", genesOnly = TRUE, localdir,...)
```

Arguments

- `file` A KGML file
- `downloadmethod` passed to `download.file` function as 'method', see its documentation for more details
- `genesOnly` logical, should only the genes nodes remain in the returned graph object?
- `localdir` character string, if specified, the function tries to read files with the same base name from a local directory, useful when there are file copies on the client.
- `...` Other parameters passed to `download.file`

Details

In KEGG pathways there’re usually pathways contained (‘cross-linked’) in other pathways, for example see [http://www.genome.jp/kegg/pathway/hsa/hsa04115.html](http://www.genome.jp/kegg/pathway/hsa/hsa04115.html), where p53 signalling pathway contains other two pathways ’apoptosis’ and ’cell cycle’. This function parses these pathways (referred as ’maps’ in KGML manual), download their KGML files from KEGG FTP website, parse them individually, and merge all the children pathway graphs with the parental pathway into one graph object. The graph is returned as the function value.

Since different graphs does not have unique node identifiers unless the genes are expanded, so by using this function user has to expand the genes. Another disadvantage is that so far due to the implementation, the KEGGnodeData and KEGGedgeData is lost during the merging. This however will probably be changed in the future version.

Value

A directed graph object

Author(s)

Jitao David Zhang [jitao_david.zhang@roche.com](mailto:jitao_david.zhang@roche.com)

References


See Also

for most users it is enough to use `parseKGML2Graph`
parsePathwayInfo  Parse information of the pathway from KGML files

Description
The function parses the information of the given pathway from KGML files into an object of KEGGPathwayInfo-class. It is used internally and is not expected to be called by users directly.

Usage
parsePathwayInfo(root)

Arguments
root Root element of the KGML file

Value
An object of KEGGPathwayInfo-class

Author(s)
Jitao David Zhang mailto:jitao_david.zhang@roche.com

References

parseReaction Parse reaction from KGML files

Description
The function parses 'reaction' element in KGML files. It is used internally and not expected to be called by users.

Usage
parseReaction(reaction)

Arguments
reaction A node of the type 'reaction' in KGML files

Details
See the reference manual for more information about 'reaction' type

Value
An object of KEGGReaction-class
parseRelation

Author(s)
Jitao David Zhang mail:jitao_david.zhang@roche.com

References

parseRelation Parse RELATION elements from KGML files

Description
RELATION elements in KGML files record the binary relationships between ENTRY elements, corresponding to (directed) edges in a graph. `parseRelation` function parses RELATION elements into `KEGGEge-class` objects from KGML files. It is not expected to be called directly by the user.

Usage
parseRelation(relation)

Arguments
relation XML node of KGML file

Details
See http://www.genome.jp/kegg/docs/xml/ for more details about `relation` as well as other elements in KGML files.

Value
An object of link(KEGGEge).

Author(s)
Jitao David Zhang <jitao_david.zhang@roche.com>

References
http://www.genome.jp/kegg/docs/xml/

See Also
KEGGEge-class, parseEntry
**parseSubType**

*Parse KGML relation subtype*

**Description**

The function parses KGML relation subtype, called internally and not intended to be used by end users.

**Usage**

parseSubType(subtype)

**Arguments**

- **subtype**  
  KGML subtype node

**Value**

An object of `KEGGEdgeSubType-class`

**Author(s)**

Jitao David Zhang  
mailto:jitao_david.zhang@roche.com

---

**plotKEGGgraph**

*Plot KEGG graph with Rgraphviz*

**Description**

The function provides a simple interface to Rgraphviz to render KEGG graph with custom styles.  
`KEGGgraphLegend` gives the legend of KEGG graphs

**Usage**

plotKEGGgraph(graph, y = "neato", shortLabel = TRUE, useDisplayName=TRUE, nodeRenderInfos, ...)

**Arguments**

- **graph**  
  A KEGG graph, by calling `parseKGML2Graph`

- **y**  
  the layout method, neato by default

- **shortLabel**  
  logical, should be short label used instead of full node name?

- **useDisplayName**  
  logical, should the labels of nodes rendered as the 'display name' specified in the KGML file or render them simply with the node names?

- **nodeRenderInfos**  
  List of node rendering info

- **...**  
  Other functions passed to `renderGraph`, not implemented for now
Details

Users are not restricted to this function, alternatively you can choose other rendering functions.

Value

The graph after layout and rendering is returned.

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com

Examples

```r
opar <- par(ask=TRUE)
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
gR <- parseKGM2Graph(sfile,expandGenes=TRUE)
gR.sub <- subGraph(subs, gR)
if(require(Rgraphviz))
  plotKEGGgraph(gR.sub)
KEGGgraphLegend()
par(opar)
```

**pvalue2asterisk**

*Return common significance sign (asterisk) associated with given p value*

Description

A p-value of 0.05, 0.01, 0.001 correspond to one, two or three asterisks. If ‘sig.1’ is set to TRUE, then the p-value of 0.1 returns ‘.’.

Usage

`pvalue2asterisk(pvalues, sig.1 = FALSE)`

Arguments

- `pvalues` A numeric value
- `sig.1` logical, whether the significance sign of 0.1 should be returned

Value

A character string containing the signs

Author(s)

Jitao David Zhang mailto:jitao_david.zhang@roche.com
queryKEGGsubgraph

Examples
pvalue2asterisk(0.03)
pvalue2asterisk(0.007)
pvalue2asterisk(3e-5)
pvalue2asterisk(0.55)

queryKEGGsubgraph  Query the subgraph of a given KEGG graph with Entrez GeneID (s)

Description
Given a list of genes (identified by Entrez GeneID), the function subsets the given KEGG graph of the genes as nodes (and maintaining all the edges between).

Usage
queryKEGGsubgraph(geneids, graph, organism = "hsa", addmissing = FALSE)

Arguments
geneids  A vector of Entrez GeneIDs
graph  A KEGG graph
organism  a three-alphabet code of organism
addmissing  logical, in case the given gene is not found in the graph, should it be added as a single node to the subgraph?

Details
This function solves the questions like 'How is the list of gene interact with each other in the context of pathways?'
Limited by the translateKEGGID2GeneID, this function supports only human for now. We are working to include other organisms.
If 'addmissing' is set to TRUE, the missing gene in the given list will be added to the returned subgraph as single nodes.

Value
A subgraph with nodes representing genes and edges representing interactions.

Author(s)
Jitao David Zhang <jitao_david.zhang@roche.com>

See Also
translateGeneID2KEGGID
Examples
sfile <- system.file("extdata/hsa04010.xml", package="KEGGgraph")
gR <- parseKML2Graph(sfile, expandGenes=TRUE)
geneids <- c(5594, 5595, 6197, 5603, 1843, 5530, 5603)
sub <- queryKEGGsubgraph(geneids, gR)
if(require(Rgraphviz) & & interactive()) {
  plot(sub, "neato")
}

## add missing nodes
list2 <- c(geneids, 81029)
sub2 <- queryKEGGsubgraph(list2, gR, addmissing=TRUE)
if(require(Rgraphviz) & & interactive()) {
  plot(sub2, "neato")
}

randomSubGraph

Randomly subset the given graph

Description
The function is intended to be a test tool. It subset the given graph repeatedly.

Usage
randomSubGraph(graph, per = 0.25, N = 10)

Arguments
graph  A graph object
per    numeric, the percentage of the nodes to be sampled, value between (0,1)
N      Repeat times

Value
The function is called for its side effect, NULL is returned

Author(s)
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Examples
tnodes <- c("Hamburg", "Dortmund", "Bremen", "Paris")
tedges <- list("Hamburg"=c("Dortmund", "Bremen"),
             "Dortmund"=c("Hamburg"), "Bremen"=c("Hamburg"), "Paris"=c())
tgraph <- new("graphNEL", nodes = tnodes, edgeL = tedges)
randomSubGraph(tgraph, 0.5, 10)
Description

The function split 'group' entries in KGML files. Most of the cases they are complexes. During the splitting the function copies the edges between groups and nodes (or between groups and groups) correspondingly, so that the existing edges also exist after the groups are split.

Usage

splitKEGGgroup(pathway)

Arguments

pathway An object of KEGGPathway-class

Details

By default the groups (complexes) in KEGG pathways are split.

Value

An object of KEGGPathway-class

Author(s)

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References


See Also

KEGGpathway2Graph

Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
kegg.pathway <- parseKGM(sfile)
kegg.pathway.split <- splitKEGGgroup(kegg.pathway)

## compare the different number of edges
length(edges(kegg.pathway))
length(edges(kegg.pathway.split))
subGraphByNodeType

Subset KEGG graph by node types

Description

The function subsets KEGG graph by node types, mostly used in extracting gene networks.

Usage

subGraphByNodeType(graph, type = "gene", kegg=TRUE)

Arguments

graph A KEGG graph object produced by calling parseKGML2Graph
type node type, see KEGGNodeType for details
kegg logical, should the KEGG Node and Edge attributes be maintained during the subsetting? By default set to ‘TRUE’

Value

A subgraph of the original graph

Author(s)

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Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
sGraph <- parseKGML2Graph(sfile,expandGenes=TRUE, genesOnly=FALSE)
sGraphGene <- subGraphByNodeType(sGraph, type="gene")

subKEGGgraph

Subset KEGG graph, including subsetting node and edge attributes

Description

subKEGGgraph extends generic method subGraph and subsets the KEGG graph. Both 'subKEGGgraph' and 'subGraph' can be used to subset the graph, the difference lies in whether the node and edge attributes from KEGG are also subset (subKEGGgraph) or not (subGraph).

See details below.

Usage

subKEGGgraph(nodes, graph)

Arguments

nodes Node names to subset
graph A graph parsed from KGML files, produced by parseKGML2Graph, KEGGpathway2Graph or parseKGMLExpandMaps
Details

subGraph does not subset the node or edge attributes, hence the results of `getKEG Gn odeData` and `getKEGG edgeData` do not map to the nodes and edges in the subgraph in a one-to-one manner, with attributes of removed nodes and edges still remaining in the subGraph.

subKEGGgraph calls subGraph first to subset the graph, and then it also subsets the KEGGNodeData and KEGGEdgeData so that they are one-to-one mapped to the nodes and edges in the subgraph.

Value

A graph with nodeData and edgeData.

Author(s)

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Examples

```r
sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
gR <- parseKGML2Graph(sfile,expandGenes=TRUE)
gR.keggsub <- subKEGGgraph(subs, gR)
gR

subKEGGgraph(subs, gR)
```

subtypeDisplay-methods

*Get display information for relation subtypes*

Description

To render KEGG pathway graphs, we have created a custom style of edges to represent their subtypes. `subtypeDisplay` extracts this information.

Methods

- `object = "graph"` An KEGG graph
- `object = "KEGGEdge"` An object of KEGGEdge-class
- `object = "KEGGEdgeSubType"` An object of KEGGEdgeSubType-class
Description

Colorectal cancer dataset provided by SPIA package. It is just a copy during the development of SPIA package in case the package is not available. It will be removed when the SPIA package is stable.

see the description of SPIA package.

Usage

data(colorectalcancerSPIA)

Format

see the format of SPIA package.

Source


translateKEGGgraph

Translate the KEGG graph from being indexed by KEKGID to another identifier

Description

The function translates the KEGG graph into a graph of equivalent topology while index with unique identifiers given by user. The new identifiers could be, for example, GeneSymbol or other identifiers mapped to KEKGID.

Usage

translateKEGGgraph(graph, newNodes)

Arguments

graph A KEGG graph
newNodes A character vector giving the new nodes, must be of the same length and same order of the nodes of the given graph

Details

The function is still experimental and users are welcomed to report any difficulties
translateKEGGID2GeneID

Translate between KEGGID and Entrez Gene ID

Value

Another graph indexed by the given identifier

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

Examples

sfile <- system.file("extdata/hsa04010.xml",package="KEGGgraph")
gR <- parseKGML2Graph(sfile,expandGenes=TRUE)

subG <- subKEGGgraph(c("hsa:1848","hsa:1432","hsa:2002","hsa:8986"),gR)
symbols <- c("DUSP6","MAPK14","ELK1","RPS6KA4")
sub2G <- translateKEGGgraph(subG, symbols)
sub2G

if(require(Rgraphviz) & interactive()) {
  plot(sub2G, "neato")
}

translateKEGGID2GeneID

Translate between KEGGID and Entrez Gene ID

Description

translateKEGGID2GeneID translates KEGGID to NCBI Entrez Gene ID, and translateGeneID2KEGGID translates Entrez Gene ID back to KEGGID.

Usage

translateKEGGID2GeneID(x, organism="hsa")
translateGeneID2KEGGID(x, organism="hsa")

Arguments

x

KEGGID, e.g. 'hsa:1432', or Entrez Gene ID, e.g. '1432'

organism

Three alphabet code for organisms. The mapping between the organisms and codes can be found at http://www.genome.jp/kegg/kegg3.html

Details

The KEGGID are unique identifiers used by KEGG PATHWAY to identify gene products. After parsing the KEGG pathway into graph, the graph use KEGGID as its nodes’ names.

translateKEGGID2GeneID converts KEGGIDs into entrez GeneID, which can be translated to other types of identifiers, for example with biomaRt package or organism-specific annotation packages. See vignette for examples.

translateKEGG2GeneID is maintained for back-compatibility and wraps translateKEGGID2GeneID.
Value

Entrez GeneID of the given KEGG ID(s)

Note

This function works so far only with human KEGGIDs, since for them the Entrez GeneID can be derived easily with removing the organism prefix.

The complete functional function will be implemented in the later release of the package.

Author(s)

Jitao David Zhang

Examples

egNodes <- c("hsa:1432", "hsa:11072")
translateKEGGID2GeneID(egNodes)
translateGeneID2KEGGID("1432")
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