Package ‘keggorthology’

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Title graph support for KO, KEGG Orthology
Version 2.26.0
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Description graphical representation of the Feb 2010 KEGG Orthology. The KEGG orthology is a set of pathway IDs that are not to be confused with the KEGG ortholog IDs.
Depends R (>= 2.5.0), stats, graph, hgu95av2.db
Imports AnnotationDbi, graph, DBI, graph, grDevices, methods, stats, tools, utils
Suggests RBGL, ALL
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License Artistic-2.0
biocViews Pathways, GraphAndNetwork, Visualization, KEGG
NeedsCompilation no

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Description

obtain probe set IDs associated with a KO term

Usage

getKOprobes(str, useAcc=TRUE, plat="hgu95av2", na.action=na.omit)

1
Arguments

str string giving a KEGG orthology term
useAcc logical – use all accessible terms?
plat platform corresponding to a bioconductor annotation package, e.g., hgu95av2.db
na.action function for dealing with NA

Details

Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then keggDF2graph to construct the graph.

Looks up the requested term and gives back the unique probe set ids on the platform.

Value

character vector, typically processed by na.omit

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

getKOtags("insulin")
es = acc(KOgraph, "Endocrine System")
nm = names(es[[1]])
nm
esp = lapply(nm, getKOprobes)
names(esp) = nm
sapply(esp, length)

indRender

indented textual rendering of nodes of a hierarchical graph

Description

indented textual rendering of nodes of a hierarchical graph

Usage

indRender(klike, from=nodes(klike)[1], indent=" ")

Arguments

klike a graph, with tree structure similar to KOgraph
from a node name from which the rendering should proceed to all leaves
indent token to use for indentation – will be replicated to depth of node to be rendered to its left
Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on `ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg` and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then `keggDF2graph` to construct the graph.

### Value
NULL

### Author(s)
Vince Carey <stvjc@channing.harvard.edu>

### Examples
```r
data(KOgraph)
indRender(KOgraph, "Human Diseases")
```

### Description
create a graph from a specific data frame format for KEGG orthology

### Usage
```r
keggDF2graph(df, root="KO.June07root")
data(KOgraph)
```

### Arguments
- `df`: the data frame
- `root`: a name for root node

### Details
the obvious directed graph structure from root to leaf nodes (pathway names) is instantiated for the orthology, nodeData attribute tag is loaded with the numerical tag for the term in KEGG, and nodeData attribute depth is loaded with depth from root

Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on `ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg` and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then `keggDF2graph` to construct the graph.

### Value
- a `graphNEL-class` instance
Note

This is only a support function. The graph is serialized in the package data directory.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```r
data(keggOrthDF)
keggOrthDF[1:5,]
data(KOgraph)
nodes(KOgraph)[1:4]
nodeData(KOgraph,"tag")[1:5]
nodeData(KOgraph,"depth")[1:5]
```
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