Package ‘keggorthology’

May 4, 2024

**Title**  graph support for KO, KEGG Orthology
**Version**  2.56.0
**Author**  VJ Carey <stvjc@channing.harvard.edu>
**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
**Maintainer**  VJ Carey <stvjc@channing.harvard.edu>
**License**  Artistic-2.0
**biocViews**  Pathways, GraphAndNetwork, Visualization, KEGG
**git_url**  https://git.bioconductor.org/packages/keggorthology
**git_branch**  RELEASE_3_19
**git_last_commit**  ca42fed
**git_last_commit_date**  2024-04-30
**Repository**  Bioconductor 3.19
**Date/Publication**  2024-05-03

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getKOfprobes

Description
obtain probe set IDs associated with a KO term

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

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 <stvc@channing.harvard.edu>

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

Indented textual rendering of nodes of a hierarchical graph

### Usage

```r
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

### 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](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
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
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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