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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getKOprobes obtain probe set IDs associated with a KO term

Description
obtain probe set IDs associated with a KO term

Usage
getKOprobes(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)

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Examples

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

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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
keggDF2graph

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.

Value

NULL

Author(s)

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Examples

data(KOgraph)
indRender(KOgraph, "Human Diseases")

keggDF2graph

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

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.

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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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