Package: keggorthology (via r-universe)

September 15, 2024

Title graph support for KO, KEGG Orthology

Version 2.57.0

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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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biocViews Pathways, GraphAndNetwork, Visualization, KEGG

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/keggorthology

RemoteRef HEAD

RemoteSha 6669643c11fe5fe10731a806105e3922d29aa2ad

Contents

`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)

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

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)

Vince Carey <stvjc@channing.harvard.edu>

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.

Author(s)

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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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