# keggorth

April 22, 2010

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getKOprobes          *obtain probe set IDs associated with a KO term*

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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)
```

**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 keggorth 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>

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## Examples

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

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| indRender | *indented textual rendering of nodes of a hierarchical graph* |
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## 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 keggorth 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")
```

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keggDF2graph       *create a graph from a specific data frame format for KEGG orthology*

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### 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 keggorth 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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