homolog.db

October 16, 2009

R topics documented:

`homolog_dbconn` *Collect information about the package annotation DB*

Description

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

Usage

```
homolog_dbconn()
homolog_dbfile()
homolog_dbschema(file="", show.indices=FALSE)
homolog_dbInfo()
```

Arguments

`file`	A connection, or a character string naming the file to print to (see the file argument of the cat function for the details).
`show.indices`	The CREATE INDEX statements are not shown by default. Use show.indices=TRUE to get them.

Details

`homolog_dbconn` returns a connection object to the package annotation DB. IMPORTANT: Don't call `dbDisconnect` on the connection object returned by `homolog_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

`homolog_dbfile` returns the path (character string) to the package annotation DB (this is an SQLite file).

`homolog_dbschema` prints the schema definition of the package annotation DB.

`homolog_dbInfo` prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(homolog_dbconn(), "select * from homolog limit 3")

## The connection object returned by homolog_dbconn() was created with:
dbConnect(SQLite(), dbname=homolog_dbfile(), cache_size=64000, synchronous=0)

homolog_dbschema()

homolog_dbInfo()
```

`homolog.db` *annotation data package*

Description

Welcome to the homolog.db annotation Package. The annotation package was built using a downloadable R package - PAnnBuilder (download and build your own). The purpose is to provide detailed information about the homologs among eukaryotic gene sets from HomoloGene database: `ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data` 2 0 0

Each of these objects has their own manual page detailing where relevant data was obtained along with examples of how to use it. Many of these objects also have a reverse map available. When this is true, expect to usually find relevant information on the same manual page as the forward map.

Examples

```
# You can learn what objects this package supports with the following command:
ls("package:homolog.db")
```

`homologHOMOLOG2AC` *Tax identifier*

Description

homologHOMOLOG2AC map homolog group identifier to NCBI protein accession number.

Details

Mappings were based on data provided by:HomoloGene (`ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data`) on 2 0 0

Examples

```
# Convert to a list
xx <- as.list(homologHOMOLOG2AC)
if(length(xx) > 0){
    xx[1:5]
}
```

`homologHOMOLOG2GI` *Tax identifier*

Description

homologHOMOLOG2GI map homolog group identifier to NCBI protein GI.

Details

Mappings were based on data provided by:HomoloGene (`ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data`) on 2 0 0

Examples

```
# Convert to a list
xx <- as.list(homologHOMOLOG2GI)
if(length(xx) > 0){
    xx[1:5]
}
```

`homologHOMOLOG` *Tax identifier*

Description

homologHOMOLOG map Entrez gene identifier to homolog group identifier.

Details

Mappings were based on data provided by:HomoloGene (`ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data`) on 2 0 0

Examples

```
## Convert to a list
xx <- as.list(homologHOMOLOG)
if(length(xx) > 0){
    xx[1:5]
}

## For the reverse map homologHOMOLOG2GENEID
## Convert to a list
xx <- as.list(homologHOMOLOG2GENEID)
if(length(xx) > 0){
    xx[1:5]
}
```

`homologMAPCOUNTS` *Number of mapped keys for the maps in package homolog.db*

Description

homologMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package homolog.db.

Details

This "map count" information is precalculated and stored in the package annotation DB. This allows some quality control and is used by the `checkMAPCOUNTS` function defined in AnnotationDbi to compare and validate different methods (like `count.mappedkeys(x)` or `sum(!is.na(as.list(x)))`) for getting the "map count" of a given map.

See Also

`mappedkeys`, `count.mappedkeys`, `checkMAPCOUNTS`

Examples

```
homologMAPCOUNTS
mapnames <- names(homologMAPCOUNTS)
homologMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x)   # much faster!

## Check the "map count" of all the maps in package homolog.db
checkMAPCOUNTS("homolog.db")
```

`homologORGANISM` *Map tax identifiers to organism*

Description

homologORGANISM map tax identifier to the name the organism.

Details

Mappings were based on data provided by:HomoloGene (ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologe
on 2 0 0

Examples

```
# Convert to a list
xxx <- as.list(homologORGANISM)
# randomly display 2 proteins
sample(xxx, 2)
```

`homologSYMBOL` *Gene symbol*

Description

homologSYMBOL map Entrez gene identifier to its symbol.

Details

Mappings were based on data provided by:HomoloGene (`ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data`) on 2 0 0

Examples

```
# Convert to a list
xx <- as.list(homologSYMBOL)
if(length(xx) > 0){
    xx[1:5]
}
```

`homologTAXID` *Taxonomy identifier*

Description

homologTAXID map Entrez gene identifier to its taxonomy identifer.

Details

Mappings were based on data provided by:HomoloGene (`ftp://ftp.ncbi.nlm.nih.gov/pub/HomoloGene/current/homologene.data`) on 2 0 0

Examples

```
# Convert to a list
xx <- as.list(homologTAXID)
if(length(xx) > 0){
    xx[1:5]
}
```

Index