Orthology.eg.db

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`Orthology.eg.db` *Bioconductor annotation data package*

Description

Welcome to the Orthology.eg.db annotation Package. The purpose of this package is to provide orthology mappings between species, based on NCBI Gene IDs and NCBI orthology mappings. This package is updated biannually.

Objects in this package are accessed using the `select()` interface. See ?select in the AnnotationDbi package for details.

Please note that this package is slightly different from other annotation packages; the keytypes and columns are species names, separated by a period (e.g. Homo.sapiens), and the keys are the NCBI Gene IDs that are to be mapped between species. See examples for more details.

See Also

- `AnnotationDb-class` for use of `keys()`, `columns()` and `select()`.

Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.
## Map NCBI Gene IDs from human to mouse
select(Orthology.eg.db, as.character(c(1,9,13:22)),"Mus.musculus","Homo.sapiens")

## get list of available species
head(keytypes(Orthology.eg.db))

## get list of Gene IDs for Electric eel
eeKeys <- keys(Orthology.eg.db, "Electrophorus.electricus")
head(eeKeys)

## map all availble Electric eel genes to human
ee2human <- select(Orthology.eg.db, eeKeys, "Homo.sapiens", "Electrophorus.electricus")
```

Orthology.eg_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

```
Orthology.eg_dbconn()
Orthology.eg_dbfile()
Orthology.eg_dbschema(file="", show.indices=FALSE)
Orthology.eg_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

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

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

Orthology.eg_dbschema prints the schema definition of the package annotation DB.

Orthology.eg_dbInfo prints other information about the package annotation DB.

Value

Orthology.eg_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

Orthology.eg_dbfile: a character string with the path to the package annotation DB.

Orthology.eg_dbschema: none (invisible NULL).

Orthology.eg_dbInfo: none (invisible NULL).

See Also

dbGetQuery, dbConnect, dbconn, dbfile, dbschema, dbInfo

Examples

```
library(DBI)
## Count the number of rows in the "genes" table:
dbGetQuery(Orthology.eg_dbconn(), "SELECT COUNT(*) FROM genes")

Orthology.eg_dbschema()

Orthology.eg_dbInfo()
```

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