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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