org.HsMm.ortholog.db

October 16, 2009

R topics documented:

```
org.HsMm.ortholog_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

```
org.HsMm.ortholog_dbconn()
org.HsMm.ortholog_dbfile()
org.HsMm.ortholog_dbschema(file="", show.indices=FALSE)
org.HsMm.ortholog_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.

1

Details

org.HsMm.ortholog_dbconn returns a connection object to the package annotation DB. IM-
PORTANT: Don't call dbDisconnect on the connection object returned by org.HsMm.ortholog_dbconn
or you will break all the AnnDbObj objects defined in this package!

org.HsMm.ortholog_dbfile returns the path (character string) to the package annotation
DB (this is an SQLite file).

org.HsMm.ortholog_dbschema prints the schema definition of the package annotation DB.

org.HsMm.ortholog_dbInfo prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(org.HsMm.ortholog_dbconn(), "select * from ortholog limit 3")

## The connection object returned by org.HsMm.ortholog_dbconn() was created with:
dbConnect(SQLite(), dbname=org.HsMm.ortholog_dbfile(), cache_size=64000, synchronous=0)

org.HsMm.ortholog_dbschema()

org.HsMm.ortholog_dbInfo()
```

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org.HsMm.ortholog.db

annotation data package

Description

Welcome to the org.HsMm.ortholog.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 ortholog protein from Inparanoid eukaryotic ortholog
database: http://inparanoid.sbc.su.se/download/current/sequences/processed/
ensHOMSA.fa; http://inparanoid.sbc.su.se/download/current/sequences/
processed/modMUSMU.fa; http://inparanoid.sbc.su.se/download/current/
sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa Release 6.0, 09/07

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:org.HsMm.ortholog.db")
```

```
org.HsMm.orthologMAPCOUNTS
```
                            Number of mapped keys for the maps in package org.HsMm.ortholog.db

---

Description

org.HsMm.orthologMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package org.HsMm.ortholog.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

```
org.HsMm.orthologMAPCOUNTS
mapnames <- names(org.HsMm.orthologMAPCOUNTS)
org.HsMm.orthologMAPCOUNTS[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 org.HsMm.ortholog.db
checkMAPCOUNTS("org.HsMm.ortholog.db")
```

```
org.HsMm.orthologORGANISM
```
                            The Organism for org.HsMm.ortholog.db

---

Description

org.HsMm.orthologORGANISM is an R object that contains a single item: a character string that names the organism for which org.HsMm.ortholog.db was built.

Details

Although the package name is suggestive of the organism for which it was built, org.HsMm.orthologORGANISM provides a simple way to programmatically extract the organism name.

Examples

```
org.HsMm.orthologORGANISM
```

`org.HsMm.orthologORTHOLOG`
Map protein identifier to its ortholog

Description

org.HsMm.orthologORTHOLOG map protein identifier to its ortholog identifier.

Details

Mappings were based on data provided by: Inparanoid (`http://inparanoid.sbc.su.se/download/current/sequences/processed/ensHOMSA.fa;http://inparanoid.sbc.su.se/download/current/sequences/processed/modMUSMU.fa;http://inparanoid.sbc.su.se/download/current/sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa`) on Release 6.0, 09/07

Examples

```
## Convert to a list
xxx <- as.list(org.HsMm.orthologORTHOLOG)
## randomly display 10 proteins
sample(xxx, 10)

## For the reverse map org.HsMm.orthologORTHOLOG2PROTEIN
## Convert to a list
xxx <- as.list(org.HsMm.orthologORTHOLOG2PROTEIN)
## randomly display 10 proteins
sample(xxx, 10)
```

`org.HsMm.orthologSEQ`
Map protein identifier to the protein sequence

Description

org.HsMm.orthologSEQ provides mappings between a protein identifier and the protein Sequence.

Details

Mappings were based on data provided by: Inparanoid (`http://inparanoid.sbc.su.se/download/current/sequences/processed/ensHOMSA.fa;http://inparanoid.sbc.su.se/download/current/sequences/processed/modMUSMU.fa;http://inparanoid.sbc.su.se/download/current/sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa`) on Release 6.0, 09/07

Examples

```
# Convert to a list
xxx <- as.list(org.HsMm.orthologSEQ)
# randomly display 10 proteins
sample(xxx, 10)
```

Index