

sc.bacello.db

February 3, 2010

`sc.bacello_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

```
sc.bacello_dbconn()  
sc.bacello_dbfile()  
sc.bacello_dbschema(file="", show.indices=FALSE)  
sc.bacello_dbInfo()
```

Arguments

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

Details

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

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

`sc.bacello_dbschema` prints the schema definition of the package annotation DB.

`sc.bacello_dbInfo` prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(sc.bacello_dbconn(), "select * from bacello limit 3")

## The connection object returned by sc.bacello_dbconn() was created with:
dbConnect(SQLite(), dbname=sc.bacello_dbfile(), cache_size=64000, synchronous=0)

sc.bacello_dbschema()

sc.bacello_dbInfo()
```

```
sc.bacello.db      annotation data package
```

Description

Welcome to the sc.bacello.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 subcellular localization of proteins in eukaryotes from BaCelLo database: http://gpcr2.biocomp.unibo.it/bacello/datasets/animals_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/fungi_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/plants_dataset.zip Swiss-Prot 48

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:sc.bacello.db")
```

```
sc.bacelloMAPCOUNTS
      Number of mapped keys for the maps in package sc.bacello.db
```

Description

sc.bacelloMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package sc.bacello.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

```
sc.bacelloMAPCOUNTS
mapnames <- names(sc.bacelloMAPCOUNTS)
sc.bacelloMAPCOUNTS[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 sc.bacello.db
checkMAPCOUNTS("sc.bacello.db")
```

sc.bacelloSEQ *Map protein identifier to the protein sequence*

Description

sc.bacelloSEQ provides mappings between a Swss-Prot protein identifier and the protein Sequence.

Details

Mappings were based on data provided by: BaCelLo (http://gpcr2.biocomp.unibo.it/bacello/datasets/animals_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/fungi_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/plants_dataset.zip) on Swiss-Prot 48

Examples

```
# Convert to a list
xx <- as.list(sc.bacelloSEQ)
# Get the first one
xx[[1]]
```

sc.bacelloSUBCELL *Map protein identifier to the subcellular location*

Description

sc.bacelloSUBCELL provides mappings between a Swss-Prot protein identifier and the protein sub-cellular locations.

Details

Mappings were based on data provided by: BaCelLo (http://gpcr2.biocomp.unibo.it/bacello/datasets/animals_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/fungi_dataset.zip; http://gpcr2.biocomp.unibo.it/bacello/datasets/plants_dataset.zip) on Swiss-Prot 48

Examples

```
## Convert to a list
xx <- as.list(sc.bacelloSUBCELL)
## Get the first one
xx[[1]]

## For the reverse map sc.bacelloSUBCELL2SPID
## Convert to a list
xx <- as.list(sc.bacelloSUBCELL2SPID)
## Get the first one
xx[[1]]
```

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