

int.geneint.db

February 3, 2010

`int.geneint_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

```
int.geneint_dbconn()  
int.geneint_dbfile()  
int.geneint_dbschema(file="", show.indices=FALSE)  
int.geneint_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

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

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

`int.geneint_dbschema` prints the schema definition of the package annotation DB.

`int.geneint_dbInfo` prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(int.geneint_dbconn(), "select * from geneint limit 3")

## The connection object returned by int.geneint_dbconn() was created with:
dbConnect(SQLite(), dbname=int.geneint_dbfile(), cache_size=64000, synchronous=0)

int.geneint_dbschema()

int.geneint_dbInfo()
```

```
int.geneint.db      annotation data package
```

Description

Welcome to the int.geneint.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 gene Interaction from NCBI database: <ftp://ftp.ncbi.nih.gov/gene/GeneRIF/interactions.gz>

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:int.geneint.db")
```

```
int.geneintGGI      Gene-Gene interaction
```

Description

int.geneintGGI gives gene-gene interactions from NCBI database.

Details

Mappings were based on data provided by: NCBI (<ftp://ftp.ncbi.nih.gov/gene/GeneRIF/interactions.gz>) on

Examples

```
# Convert to a list
xx <- as.list(int.geneintGGI)
if(length(xx) > 0){
  # Gets the first five interaction list
  xx[1:5]
}
```

```
int.geneintMAPCOUNTS
```

Number of mapped keys for the maps in package int.geneint.db

Description

int.geneintMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package int.geneint.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

```
int.geneintMAPCOUNTS
mapnames <- names(int.geneintMAPCOUNTS)
int.geneintMAPCOUNTS[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 int.geneint.db
checkMAPCOUNTS("int.geneint.db")
```

```
int.geneintTAXID Taxonomy identifier
```

Description

int.geneintTAXID map Entrez gene identifier to its taxonomy identifier.

Details

Mappings were based on data provided by: NCBI (<ftp://ftp.ncbi.nih.gov/gene/GeneRIF/interactions.gz>) on

Examples

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

Index

*Topic **datasets**

`int.geneintMAPCOUNTS`, 3

`AnnDbObj`, 1

`checkMAPCOUNTS`, 3

`count.mappedkeys`, 3

`dbDisconnect`, 1

`int.geneint.db`, 2

`int.geneint_dbconn`, 1

`int.geneint_dbfile`
(`int.geneint_dbconn`), 1

`int.geneint_dbInfo`
(`int.geneint_dbconn`), 1

`int.geneint_dbschema`
(`int.geneint_dbconn`), 1

`int.geneintGGI`, 2

`int.geneintMAPCOUNTS`, 3

`int.geneintTAXID`, 3

`mappedkeys`, 3