

# int.geneint.db

October 16, 2009

## R topics documented:

int.geneint_dbconn . . . . .	1
int.geneint.db . . . . .	2
int.geneintGGI . . . . .	2
int.geneintMAPCOUNTS . . . . .	3
int.geneintTAXID . . . . .	3

<b>Index</b>	<b>4</b>
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int.geneint\_dbconn *Collect information about the package annotation DB*

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## 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

`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**

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()
```

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int.geneint.db      *annotation data package*

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**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")
```

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int.geneintGGI      *Gene-Gene interaction*

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**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
```

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**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