

scop.db

October 16, 2009

R topics documented:

scopCHILDREN	1
scopCLASSIFICATION	2
scop_dbconn	2
scop.db	3
scopDE	4
scopMAPCOUNTS	4
scopNAME	5
scopPARENT	5
scopPDB2CF	6
scopPDB2CL	6
scopPDB2DM	7
scopPDB2FA	7
scopPDB2PX	8
scopPDB2SF	8
scopPDB2SP	9
scopTYPE	9
Index	11

scopCHILDREN	<i>Map SCOP identifiers to their children</i>
--------------	---

Description

scopCHILDREN maps SCOP entry identifier to their children.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopCHILDREN)
if(length(xx) > 0){
  xx[2:3]
}
```

scopCLASSIFICATION *Map SCOP identifiers to domain classification*

Description

scopCLASSIFICATION maps SCOP entry identifier to a compact representation of a SCOP domain classification.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopCLASSIFICATION)
if(length(xx) > 0){
  xx[2:3]
}
```

scop_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

```
scop_dbconn()
scop_dbfile()
scop_dbschema(file="", show.indices=FALSE)
scop_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

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

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

`scop_dbschema` prints the schema definition of the package annotation DB.

`scop_dbInfo` prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(scop_dbconn(), "select * from des limit 3")

## The connection object returned by scop_dbconn() was created with:
dbConnect(SQLite(), dbname=scop_dbfile(), cache_size=64000, synchronous=0)

scop_dbschema()

scop_dbInfo()
```

scop.db

annotation data package

Description

Welcome to the scop.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 structural classification of proteins from SCOP database: http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73 Release 1.73, November 2007

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:scop.db")
```

 scopDE

Map SCOP identifiers to their description

Description

scopDE maps SCOP entry identifier to their description.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopDE)
if (length(xx) > 0) {
  xx[2:3]
}
```

 scopMAPCOUNTS

Number of mapped keys for the maps in package scop.db

Description

scopMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package scop.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

```
scopMAPCOUNTS
mapnames <- names(scopMAPCOUNTS)
scopMAPCOUNTS[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 scop.db
checkMAPCOUNTS("scop.db")
```

`scopNAME`*Map SCOP identifiers to name*

Description

`scopNAME` maps SCOP entry identifier to a "short name"

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopNAME)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPARENT`*Map SCOP identifiers to their parents*

Description

`scopPARENT` maps SCOP entry identifier to their parents.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPARENT)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2CF`*Map PDB identifier to SCOP fold entry*

Description

scopPDB2CF maps a PDB identifier to a vector of SCOP fold entry. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2CF)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2CL`*Map PDB identifier to SCOP class identifier*

Description

scopPDB2CL maps a PDB identifier to a vector of SCOP class identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2CL)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2DM`*Map PDB identifier to SCOP protein domain identifier*

Description

scopPDB2DM maps a PDB identifier to a vector of SCOP protein domain identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2DM)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2FA`*Map PDB identifier to SCOP family identifier*

Description

scopPDB2FA maps a PDB identifier to a vector of SCOP family identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2FA)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2PX`*Map PDB identifier to SCOP domain entry identifier*

Description

scopPDB2PX maps a PDB identifier to a vector of SCP domain entry identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2PX)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2SF`*Map PDB identifier to SCOP superfamily identifier*

Description

scopPDB2SF maps a PDB identifier to a vector of SCOP superfamily identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2SF)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopPDB2SP`*Map PDB identifier to SCOP species identifier*

Description

scopPDB2SP maps a PDB identifier to a vector of SCOP species identifier. The vector name corresponds to the PDB chains.

Details

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopPDB2SP)
if(length(xx) > 0){
  xx[2:3]
}
```

`scopTYPE`*Map SCOP identifiers to their types*

Description

scopTYPE provides mappings between SCOP entry identifiers and their types.

Details

Possible entry types are: cl - class

cf - fold

sf - superfamily

fa - family

dm - protein domain

sp - species

px - domain entry

Mappings were based on data provided by: SCOP (http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73; http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) on Release 1.73, November 2007

Examples

```
# Convert to a list
xx <- as.list(scopTYPE)
if(length(xx) > 0){
  xx[2:3]
}
```

Index

*Topic **datasets**

- scopMAPCOUNTS, 4
- AnnDbObj, 2
- checkMAPCOUNTS, 4
- count.mappedkeys, 4
- dbDisconnect, 2
- mappedkeys, 4
- scop.db, 3
- scop_dbconn, 2
- scop_dbfile (scop_dbconn), 2
- scop_dbInfo (scop_dbconn), 2
- scop_dbschema (scop_dbconn), 2
- scopCHILDREN, 1
- scopCLASSIFICATION, 1
- scopDE, 3
- scopMAPCOUNTS, 4
- scopNAME, 4
- scopPARENT, 5
- scopPDB2CF, 5
- scopPDB2CL, 6
- scopPDB2DM, 6
- scopPDB2FA, 7
- scopPDB2PX, 7
- scopPDB2SF, 8
- scopPDB2SP, 8
- scopTYPE, 9