

Package ‘LRBaseDbi’

July 10, 2025

Title DBI to construct LRBase-related package

Description Interface to construct LRBase package (LRBase.XXX.eg.db).

Version 2.18.1

Author Koki Tsuyuzaki

Maintainer Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>

Depends R (>= 3.5.0)

Imports methods, stats, utils, AnnotationDbi, RSQLite, DBI, Biobase

Suggests testthat, BiocStyle, AnnotationHub

VignetteBuilder utils

biocViews Infrastructure

License Artistic-2.0

git_url <https://git.bioconductor.org/packages/LRBaseDbi>

git_branch RELEASE_3_21

git_last_commit 1976965

git_last_commit_date 2025-05-23

Repository Bioconductor 3.21

Date/Publication 2025-07-09

Contents

LRBaseDb-class	2
----------------	---

Index	5
--------------	---

LRBaseDb-class

LRBaseDb objects

Description

`LRBaseDb` is the simple class for providing the relationship between Entrez gene IDs and LRBase IDs. It provides the database connection and easily accessible with `columns`, `keytypes`, `keys` and `select`. Some users may use additional functions such as `dbconn`, `dbfile`, `dbschema`, `dbInfo`, `species`, `lrNomenclature`, `lrListDatabases`, and `lrVersion` for much complex data acquisition.

`columns` shows which kinds of data can be returned for the `LRBaseDb` object.

`keytypes` allows the user to discover which keytypes can be passed in to `select` or `keys` and the `keytype` argument.

`keys` returns keys for the database contained in the `LRBaseDb` object . This method is already documented in the `keys` manual page but is mentioned again here because it's usage with `select` is so intimate. By default it will return the primary keys for the database, but if used with the `keytype` argument, it will return the keys from that keytype.

`select` will retrieve the data as a `data.frame` based on parameters for selected `keys`, `columns`, and `keytype` arguments.

`dbconn` returns the connection with database in the package.

`dbfile` returns the absolute path sqlite file is saved.

`dbschema` returns the database schema.

`dbInfo` returns the many meta information about the package.

`species` returns the species name.

`lrNomenclature` returns the scientific name.

`lrListDatabases` returns the list of databases to correspond Gene ID of ligand gene and Gene ID of receptor gene.

`lrVersion` returns the version of `LRBaseDb`.

Usage

```
columns(x)
keytypes(x)
keys(x, keytype, ...)
select(x, keys, columns, keytype, ...)
dbconn(x)
dbfile(x)
dbschema(x, file = "", show.indices = FALSE)
dbInfo(x)
species(object)
lrNomenclature(x)
lrListDatabases(x)
lrVersion(x)
```

Arguments

x	the LRBaseDb object converted by LRBaseDbi::LRBaseDb.
object	same as x
keys	the keys to select records for from the database. All possible keys are returned by using the keys method.
columns	the columns or kinds of things that can be retrieved from the database. As with keys, all possible columns are returned by using the columns method.
keytype	the keytype that matches the keys used. For the select methods, this is used to indicate the kind of ID being used with the keys argument. For the keys method this is used to indicate which kind of keys are desired from keys
...	other arguments.
file	The file argument must be 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.

Value

keys, columns, keytypes, dbfile, dbInfo, species, and lrNomenclature each return a character vector or possible values. select, dbschema, lrListDatabases, and lrVersion each return a data.frame. dbconn returns database connection.

Author(s)

Koki Tsuyuzaki

See Also

[dbConnect](#)

Examples

```
# library("LRBaseDb")
# library("AnnotationHub")

# # Data retrieval from AnnotationHub
# ah <- AnnotationHub()
# dbfile <- query(ah, c("LRBaseDb", "Sus scrofa", "v001"))[[1]]

# # Constructor
# LRBase.Ssc.eg.db <- LRBaseDbi::LRBaseDb(dbfile)

# # show
# LRBase.Ssc.eg.db

# # dbconn
# dbconn(LRBase.Ssc.eg.db)
```

```
# # dbfile
# dbfile(LRBase.Ssc.eg.db)

# # dbschema
# dbschema(LRBase.Ssc.eg.db)

# # dbInfo
# dbInfo(LRBase.Ssc.eg.db)

# # species
# species(LRBase.Ssc.eg.db)

# # lrNomenclature
# lrNomenclature(LRBase.Ssc.eg.db)

# # lrListDatabases
# lrListDatabases(LRBase.Ssc.eg.db)

# # lrVersion
# lrVersion(LRBase.Ssc.eg.db)

# # columns
# cols <- columns(LRBase.Ssc.eg.db)

# # keytypes
# kts <- keytypes(LRBase.Ssc.eg.db)

# # keys
# ks <- keys(LRBase.Ssc.eg.db, keytype="GENEID_L")[seq(10)]

# # select
# out <- select(LRBase.Ssc.eg.db,
#   columns=cols,
#   keys=ks,
#   keytype="GENEID_L")
```

Index

cat, 3
class:LRBaseDb (LRBaseDb-class), 2
columns (LRBaseDb-class), 2
columns,LRBaseDb-method
(LRBaseDb-class), 2

dbconn (LRBaseDb-class), 2
dbconn,LRBaseDb-method
(LRBaseDb-class), 2
dbConnect, 3
dbfile (LRBaseDb-class), 2
dbfile,LRBaseDb-method
(LRBaseDb-class), 2
dbInfo (LRBaseDb-class), 2
dbInfo,LRBaseDb-method
(LRBaseDb-class), 2
dbschema (LRBaseDb-class), 2
dbschema,LRBaseDb-method
(LRBaseDb-class), 2

keys (LRBaseDb-class), 2
keys,LRBaseDb-method (LRBaseDb-class), 2
keytypes (LRBaseDb-class), 2
keytypes,LRBaseDb-method
(LRBaseDb-class), 2

LRBaseDb (LRBaseDb-class), 2
LRBaseDb-class, 2
lrListDatabases (LRBaseDb-class), 2
lrListDatabases,LRBaseDb-method
(LRBaseDb-class), 2
lrNomenclature (LRBaseDb-class), 2
lrNomenclature,LRBaseDb-method
(LRBaseDb-class), 2
lrVersion (LRBaseDb-class), 2
lrVersion,LRBaseDb-method
(LRBaseDb-class), 2

select (LRBaseDb-class), 2
select,LRBaseDb-method
(LRBaseDb-class), 2