

Package ‘LRBaseDbi’

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Title DBI to construct LRBase-related package

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

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Depends R (>= 3.5.0)

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

Suggests RUnit, BiocGenerics, BiocStyle

VignetteBuilder utils

biocViews Infrastructure

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| | |
|---------|--|
| columns | <i>A function to return the columns of LRBase that user can retrieve</i> |
|---------|--|

Description

This function returns the columns of LRBase that user can retrieve.

Usage

```
columns(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The columns of sqlite database

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("columns")
```

| | |
|--------|--|
| dbconn | <i>A function to return the connection to sqlite3 file</i> |
|--------|--|

Description

This function returns the connection to sqlite file.

Usage

```
dbconn(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The database connection to sqlite3 file

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("dbconn")
```

| | |
|--------|--|
| dbfile | <i>A function to return the directory that the sqlite3 file stored</i> |
|--------|--|

Description

This function returns the directory that the sqlite file stored.

Usage

```
dbfile(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The directory path to the sqlite3 file

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("dbfile")
```

| | |
|--------|--|
| dbInfo | <i>A function to return the database information</i> |
|--------|--|

Description

This function returns the database information, which is METADATA table in sqlite file.

Usage

```
dbInfo(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The information of LRBase.XXX.eg.db-type package

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("dbInfo")
```

 dbschema

A function to return the schema of sqlite-database

Description

This function returns the schema of sqlite-database.

Usage

```
dbschema(x, file = "", show.indices = FALSE)
```

Arguments

| | |
|--------------|--|
| x | LRBaseDb object such as LRBase.Mmu.eg.db |
| file | LRBaseDb file |
| show.indices | LRBaseDb show.indices |

Value

The schema for constructing sqlite database file

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("dbschema")
```

 FANTOM5

Data to construct user's original LRBaseDb package

Description

Correspondance between Ligand Entrez Gene ID and Receptor Entrez Gene ID of FANTOM5 project used for demo data. This is to demonstrate how to construct user's original LRBaseDb package.

Usage

```
data(FANTOM5)
```

Details

- 1st Column: Ligand Entrez gene ID
- 2nd Column: Receptor Entrez gene ID
- 3rd Column: Source ID. In this case, PMID is used.
- 4th Column: Source Database. In this case, FANTOM5

Value

The test data is loaded

Examples

```
data(FANTOM5)
head(FANTOM5)
```

keys

A function defined by AnnotationDbi to return the keys

Description

This function returns the keys.

Usage

```
keys(x, keytype, ...)
```

Arguments

| | |
|---------|--|
| x | LRBaseDb object such as LRBase.Mmu.eg.db |
| keytype | LRBaseDb What kind of key user want to specify |
| ... | LRBaseDb Other parameter |

Value

The keys for using select functions

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("keys")
```

| | |
|----------|--|
| keytypes | <i>A function to return the columns that user can specified in select function</i> |
|----------|--|

Description

This function returns the columns that user can specified in select function.

Usage

```
keytypes(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The columns that user can specify as key

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("keytypes")
```

| | |
|----------------|-------------------------|
| LRBaseDb-class | <i>LRBaseDb objects</i> |
|----------------|-------------------------|

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, and species 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.

Usage

```
LRBaseDb
```

Arguments

LRBaseDb the LRBaseDb object. But in practice this will mean an object derived from an LRBaseDb object such as a LRBase.Hsa.eg.db, LRBase.Mmu.eg.db or many other LRBase.XXX.eg.db (XXX means abbreviation of species name).

Value

the LRBaseDb object

Author(s)

Koki Tsuyuzaki

See Also

[dbConnect](#)

Examples

```
ls("package:LRBaseDbi")
```

lrListDatabases

A function to return the list of databases used in the package

Description

This function returns the list of databases used in the package.

Usage

```
lrListDatabases(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The list of source databases

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("lrListDatabases")
```

| | |
|----------------|---|
| lrNomenclature | <i>A function to return the scientific name</i> |
|----------------|---|

Description

This function returns the scientific name of species used in the package.

Usage

```
lrNomenclature(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The scientific name of organisms

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("lrNomenclature")
```

| | |
|---------------|--|
| lrPackageName | <i>A function to return the package name</i> |
|---------------|--|

Description

This function returns the package name

Usage

```
lrPackageName(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The name of LRBase.XXX.eg.db-type package

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("lrPackageName")
```

lrVersion

A function to return the LRBase version of package

Description

This function returns the version of LRBase used in the package.

Usage

```
lrVersion(x)
```

Arguments

x LRBaseDb object such as LRBase.Mmu.eg.db

Value

The version of LR database

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("lrVersion")
```

makeLRBasePackage

Making LRBaseDb packages from corresponding table as single data frame.

Description

makeLRBasePackage is a method that generates a package that will load an appropriate LRBaseDb object that will in turn point to existing annotation packages.

Usage

```
makeLRBasePackage(pkgname, data, metadata, organism, version,  
                  maintainer, author, destDir, license="Artistic-2.0")
```

Arguments

| | |
|------------|---|
| pkgname | The package name. We highly recommend that the name is ABC.XXX.eg.db-type, where ABC is some character and XXX is a abbreviation of organisms such as Hsa: Homo sapiens |
| data | Data frame contains Ligand GENEID (e.g., 100036770), Receptor GENEID (e.g., 100036770), SOURCEID (PMID), and SOURCEID (e.g., FANTOM5) |
| metadata | Data frame contains metadata of the package |
| organism | The name of the organism this package represents |
| version | The version number of this package |
| maintainer | The maintainer who creates the package (must include email to be valid) |
| author | The creator of the package |
| destDir | A path where the package source should be assembled. |
| license | The license and it's version |

Details

The purpose of this method is to create a special package that will depend on existing annotation packages and which will load a special LRBaseDb object that will allow proper dispatch of special select methods. These methods will allow the user to easily query across multiple annotation resources via information contained by the LRBaseDb object. Because the end result will be a package that treats all the data mapped together as a single source, the user is encouraged to take extra care to ensure that the different packages used are from the same build etc.

Value

A special package to load an [LRBaseDb](#) object.

Author(s)

Koki Tsuyuzaki

See Also

[LRBaseDb](#)

Examples

```
if(interactive()){
  ## makeLRBasePackage enable users to construct
  ## user's own custom LRBase package
  data(FANTOM5)
  head(FANTOM5)

  # We are also needed to prepare meta data as follows.
  data(metaFANTOM5)
  metaFANTOM5

  ## sets up a temporary directory for this example
  ## (users won't need to do this step)
  tmp <- tempfile()
  dir.create(tmp)
```

```
## makes an Organism package for human called Homo.sapiens
makeLRBasePackage(pkghname = "FANTOM5.Hsa.eg.db",
  data = FANTOM5,
  metadata = metaFANTOM5,
  organism = "Homo sapiens",
  version = "0.99.0",
  maintainer = "Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>",
  author = "Koki Tsuyuzaki",
  destDir = tmp,
  license="Artistic-2.0")
}
```

metaFANTOM5

Metadata to construct user's original LRBaseDb package

Description

Meta data to construct user's custom LRBaseDb

Usage

```
data(metaFANTOM5)
```

Details

- SOURCEDATE: The date the source data is retrived
- SOURCENAME: Type of source data
- SOURCEURL: The URL of source data
- DBSCHEMA: Database schema
- DBSCHEMAVERSION: The version of database schema
- ORGANISM: The scientific name
- SPECIES: The common name of the species
- package: The pacakge name
- Db type: The type of name (or class name)
- LRVERSION: The version for numbering of ligand-receptor data

Value

The test data is loaded

Examples

```
data(metaFANTOM5)
head(metaFANTOM5)
```

| | |
|--------|---|
| select | <i>select function defined by AnnotationDbi-class</i> |
|--------|---|

Description

This function returns the corresponding rows that user specified

Usage

```
select(x, keys, columns, keytype, ...)
```

Arguments

| | |
|---------|--|
| x | LRBaseDb object such as LRBase.Mmu.eg.db |
| keys | LRBaseDb keys vector |
| columns | LRBaseDb columns the user want to retrieve |
| keytype | LRBaseDb What kind of key the user want to specify |
| ... | LRBaseDb Other parameter |

Value

select function defined by AnnotationDbi package

Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("select")
```

| | |
|---------|--|
| species | <i>A function to return the name of organism</i> |
|---------|--|

Description

This function returns the name of organism.

Usage

```
species(object)
```

Arguments

| | |
|--------|--|
| object | LRBaseDb object such as LRBase.Mmu.eg.db |
|--------|--|

Value

The common name of organisms

species

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Author(s)

Koki Tsuyuzaki

Examples

```
showMethods("species")
```

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