Package ‘MSEADbi’

October 14, 2021

Title DBI to construct MSEA-related package

Description Interface to construct annotation package for MSEA (MSEA.XXX.pb.db). The program design is same as Bioconductor LRBaseDbi or MeSHDbi pacakge, and the usage is also the same as these packages.

Version 1.2.0

Depends R (>= 4.0)

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

Suggests RUnit, BiocGenerics, BiocStyle, knitr, testthat (>= 2.1.0)

VignetteBuilder knitr

biocViews Infrastructure

License Artistic-2.0

RoxygenNote 7.1.1

Encoding UTF-8

PackageStatus Deprecated

git_url https://git.bioconductor.org/packages/MSEADbi

git_branch RELEASE_3_13

git_last_commit 79634ad

git_last_commit_date 2021-05-19

Date/Publication 2021-10-14

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R topics documented:

`columns` *A function to return the columns of MSEA that user can retrieve*

Description

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

Usage

```
columns(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The columns of sqlite database

Author(s)

Kozo Nishida

Examples

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

`dbconn` *A function to return the connection to sqlite3 file*

Description

This function returns the connection to sqlite file.

Usage

```
dbconn(x)
```

Arguments

x	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The database connection to sqlite3 file

Author(s)

Kozo Nishida

Examples

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

`dbfile` *A function to return the directory that the sqlite3 file stored*

Description

This function returns the directory that the sqlite file stored.

Usage

```
dbfile(x)
```

Arguments

x	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The directory path to the sqlite3 file

Author(s)

Kozo Nishida

Examples

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

`dbInfo` *A function to return the database information*

Description

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

Usage

```
dbInfo(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The information of MSEA.XXX.pb.db package

Author(s)

Kozo Nishida

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`	`MSEADb` object such as `MSEA.Ath.pb.db`
`file`	`MSEADb` file
`show.indices`	`MSEADb` show.indices

Value

The schema for constructing sqlite database file

Author(s)

Kozo Nishida

Examples

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

`keys` *A function defined by AnnotationDbi to return the keys*

Description

This function returns the keys.

Usage

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

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`
`keytype`	`MSEADb` What kind of key user want to specify
`...`	`MSEADb` Other parameter

Value

The keys for using select functions

Author(s)

Kozo Nishida

Examples

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

`keytypes` *A function to return the columns that user can specified in select function*

Description

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

Usage

```
keytypes(x)
```

Arguments

x	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The columns that user can specify as key

Author(s)

Kozo Nishida

Examples

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

`makeMSEAPackage` *Making MSEADb packages from corresponding table as single data frame.*

Description

`makeMSEAPackage` is a method that generates a package that will load an appropriate `MSEADb` object that will in turn point to existing annotation packages.

Usage

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

Arguments

`pkgname`	What is the desired package name.
`data`	Data frame contains PathBankID, PathwayName, PathwaySubject, MetaboliteID, MetaboliteName, HMDBID, KEGGID, ChEBIID, DrugBankID, CAS, Formula, IUPAC, SMILES, InChI, and InChIKey
`metadata`	Data frame contains metadata of the package
`organism`	The name of the organism this package represents
`version`	What is the version number for this package?
`maintainer`	Who is the package maintainer? (must include email to be valid)
`author`	Who is the creator of this package?
`destDir`	A path where the package source should be assembled.
`license`	What is 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 `MSEADb` 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 `MSEADb` 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 MSEADb object.

Author(s)

Kozo Nishida

Examples

```
## makeMSEAPackage enable users to construct
## user's own custom MSEA annotation package

## this is test data which means the relationship between
## PathBank pathway IDs of Arabidopsis thaliana
## and its compound DB IDs (e.g., HMDB, CAS, etc...).
tmp <- tempdir()
ath <- system.file("extdata","MSEA.Ath.pb.db_DATA.csv",package="MSEADbi")
meta <- system.file("extdata","MSEA.Ath.pb.db_METADATA.csv",
    package="MSEADbi")
athDf <- read.csv(ath, fileEncoding="utf8")
metaDf <- read.csv(meta)
# We need to avoid DOT from the column names (to query with the names)
names(athDf) <- gsub("\\.", "", names(athDf))
names(metaDf) <- gsub("\\.", "", names(metaDf))

makeMSEAPackage(pkgname = "MSEA.Ath.pb.db", data=athDf, metadata=metaDf,
    organism = "Arabidopsis thaliana", version = "0.99.0",
    maintainer = "Kozo Nishida <kozo.nishida@gmail.com>",
    author = "Kozo Nishida",
    destDir = tmp, license = "Artistic-2.0")

mseaPackageDir = paste(tmp, "MSEA.Ath.pb.db", sep="/")
install.packages(mseaPackageDir, repos=NULL, type="source")
```

`MSEADb-class` *MSEADb objects*

Description

`MSEADb` is the simple class for providing the relationship between PathBank pathway IDs and metabolite IDs contained in the pathway. 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 `MSEADb` 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 `MSEADb` 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

```
MSEADb
```

Arguments

`MSEADb`	the `MSEADb` object. But in practice this will mean an object derived from an `MSEADb` object such as a `MSEA.Ath.pb.db` or many other MSEA.XXX.pb.db (XXX means abbreviation of species name).

Value

the `MSEADb` object

Author(s)

Kozo Nishida

See Also

`dbConnect`

Examples

```
ls("package:MSEADbi")
```

`mseaListPathwaySubjects` *A function to return the subject of pathways used in the package*

Description

This function returns the list of pathway subjects used in the package.

Usage

```
mseaListPathwaySubjects(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The list of pathway subjects

Author(s)

Kozo Nishida

Examples

```
showMethods("mseaListPathwaySubjects")
```

`mseaNomenclature` *A function to return the scientific name*

Description

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

Usage

```
mseaNomenclature(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The scientific name of organisms

Author(s)

Kozo Nishida

Examples

```
showMethods("mseaNomenclature")
```

`mseaPackageName` *A function to return the package name*

Description

This function returns the package name

Usage

```
mseaPackageName(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The name of MSEA.XXX.pb.db package

Author(s)

Kozo Nishida

Examples

```
showMethods("mseaPackageName")
```

`mseaVersion` *A function to return the MSEA data source version of package*

Description

This function returns the version of MSEA data source used in the package.

Usage

```
mseaVersion(x)
```

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The version of MSEA database

Author(s)

Kozo Nishida

Examples

```
showMethods("mseaVersion")
```

`select` *select function defined by AnnotationDbi-class*

Description

This function returns the corresponding rows that user specified

Usage

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

Arguments

`x`	`MSEADb` object such as `MSEA.Ath.pb.db`
`keys`	`MSEADb` keys vector
`columns`	`MSEADb` columns the user want to retrieve
`keytype`	`MSEADb` What kind of key the user want to specify
`...`	`MSEADb` Other parameter

Value

select function defined by AnnotationDbi package

Author(s)

Kozo Nishida

Examples

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

`species` *A function to return the name of organism*

Description

This function returns the name of organism.

Usage

```
species(object)
```

Arguments

`object`	`MSEADb` object such as `MSEA.Ath.pb.db`

Value

The common name of organisms

Author(s)

Kozo Nishida

Examples

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

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