Package 'BridgeDbR'

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Type Package

Title Code for using BridgeDb identifier mapping framework from within
R

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Imports RCurl

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, testthat

Description Use BridgeDb functions and load identifier mapping
databases in R.

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LazyLoad yes

URL https://github.com/bridgedb/BridgeDbR

BugReports https://github.com/egonw/BridgeDbR/issues

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R topics documented:

BridgeDbR-package   *BridgeDBR Package.*

Description

R package for using BridgeDB directly from R.

Author(s)

Christ Leemans

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---

fullNameExists   *Determines if the full name corresponds to any known data source.*

Description

Data sources are defined by a title and a short system code. This method determines if a data source is known with the given full name.

Usage

```
fullNameExists(name)
```

Arguments

name   full name of the data source

Value

exists   boolean that indicates if a data is known with the given name

Author(s)

Egon Willighagen

Examples

```
exists <- fullNameExists("HMDB")
```

---

getBridgeNames	*Method to list the BridgeDb identifier mapping file names as available from the download site.*

Description

This method returns a list of file names of BridgeDb identifier mapping files as they are available from the mapping file download site. The optional code parameter can be used to restrict the list to a specific organism.

Occassionally, the ID mapping file download website changes the pattern of the file names. In that case, you can provide an alternative filename pattern to recognize files on the download site.

Usage

```
getBridgeNames(code, website, pattern)
```

Arguments

code	the organism code
website	optional parameter that allows you to provide a different location to download BridgeDb Derby files from.
pattern	optional parameter to change the filename pattern of the BridgeDb Derby files.

Value

list	the list of available BridgeDb mapping files

Author(s)

Egon Willighagen Christ Leemans

Examples

```
files <- getBridgeNames("Hs")
## Not run:
prereleases <- getBridgeNames(
    website="http://bridgedb.org/data/gene_database/pre-release/",
    pattern="metabolites_\d*.bridge"
)

## End(Not run)
```

---

getDatabase   *Downloads a identifier mapping database for the given organism.*

Description

Downloads a identifier mapping database for the given organism. The optional location parameter can be used to indicate where the file should be stored. If not give, it will save it in a temporary folder.

Usage

```
getDatabase(organism,location,website)
```

Arguments

organism   the organism name

location   optional parameter to indicate where the database should be saved

website   optional URL of the server where to look for BridgeDb identifier mapping databases

Value

location   the location where the database was saved

Author(s)

Egon Willighagen Christ Leemans

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")
## Not run: location <- getDatabase("Homo sapiens")
```

---

getDataSource   *Return a DataSource object based on either a name or system code.*

Description

Return a DataSource object based on either a name or system code.

Usage

```
getDataSource(name,code)
```

Arguments

name   the name of the data source

code   the system code of the data source

Value

dataSource   a DataSource Java object

Author(s)

Egon Willighagen

Examples

```
dataSource <- getDataSource(code="Ce")
```

---

getFullName   *Return the name of a particular data source.*

Description

Data sources are defined by a title and a short system code. This method converts a system code into a full name.

Usage

```
getFullName(syscode)
```

Arguments

syscode   the system code of the data source

Value

systemCode   the full name of the data source

Author(s)

Egon Willighagen Christ Leemans

Examples

```
name <- getFullName("Ce")
```

---

getMatchingSources   *Return a list of data sources of which the identifier pattern matches the identifier given.*

Description

This method runs through all data sources it knows about, and looks for sources of which the identifier pattern matches the given identifier.

Usage

```
getMatchingSources(identifier)
```

Arguments

identifier   identifier to test

Value

list   list of matching data sources

Author(s)

Egon Willighagen Christ Leemans

Examples

```
list <- getMatchingSources("555")
```

---

getOrganismCode   *Return the code of a particular organism.*

Description

This method converts a organism latin name into a code.

Usage

```
getOrganismCode(name)
```

Arguments

name   latin name of an organism

Value

systemCode   the code of the organism

Author(s)

Egon Willighagen Christ Leemans

Examples

```
systemCode <- getOrganismCode("Mus musculus")
```

---

getSystemCode   *Return the system code of a particular data source.*

Description

Data sources are defined by a title and a short system code. This method converts a name into a system code.

Usage

```
getSystemCode(name)
```

Arguments

name   name of the data source

Value

systemCode   the system code of the data source

Author(s)

Egon Willighagen Christ Leemans

Examples

```
systemCode <- getSystemCode("ChEBI")
```

---

loadDatabase   *Loads a BridgeDb identifier mapping database (.bridge file) as an IDMapper Java-Object.*

Description

Loads a BridgeDb identifier mapping database (.bridge file) as an IDMapper Java-Object.

Usage

```
loadDatabase(location)
```

Arguments

location   location on the hard disk of the BridgeDb file

Details

The return Java-Object is a Java class implementing the BridgeDb IDMapper interface. It is the required mapper class that is used as input for other methods that need an IDMapper.

Value

mapper   an IDMapper object

Author(s)

Egon Willighagen

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")
mapper <- loadDatabase(location)
```

---

map   *Converts one identifier into other identifiers for the given target data*
                                 source.

Description

Converts one identifier into other identifiers for the given target data source.

Usage

```
map(mapper, source, identifier, target)
```

Arguments

mapper   loaded BridgeDb identifier mapper

source   system code of the data source

identifier   identifier to be converted

target   system code of the target data source (optional)

Value

mappings   a vector of mapped identifiers for the target data source

Author(s)

Egon Willighagen

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")
mapper <- loadDatabase(location)
map(mapper, "L", "885041", "X")
map(mapper, "L", "885041")
```

| registerDataSource | *Registers a new DataSource based on the given name or system code.* |

Description

Return a DataSource of the newly registered data source, based on either a name or system code.

Usage

```
registerDataSource(code,name)
```

Arguments

| code | the system code of the data source |
| name | the name of the data source |

Value

| dataSource | a DataSource Java object |

Author(s)

Egon Willighagen

Examples

```
newDataSource <- registerDataSource(code="Cks", name="KNApSAcK")
```

| systemCodeExists | *Determines if the system code corresponds to any known data source.* |

Description

Data sources are defined by a title and a short system code. This method determines if a data source is known with the given system code.

Usage

```
systemCodeExists(code)
```

Arguments

| code | system code of the data source |

Value

| exists | boolean that indicates if a data is known with the given system code |

Author(s)

Egon Willighagen

Examples

```
exists <- systemCodeExists("Ce")
```

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