Package ‘biodb’

April 3, 2024

Title  biodb, a library and a development framework for connecting to chemical and biological databases

Version  1.10.0

Description  The biodb package provides access to standard remote chemical and biological databases (ChEBI, KEGG, HMDB, ...), as well as to in-house local database files (CSV, SQLite), with easy retrieval of entries, access to web services, search of compounds by mass and/or name, and mass spectra matching for LCMS and MSMS. Its architecture as a development framework facilitates the development of new database connectors for local projects or inside separate published packages.

URL  https://github.com/pkrog/biodb

BugReports  https://github.com/pkrog/biodb/issues

biocViews  Software, Infrastructure, DataImport, KEGG

Depends  R (>= 4.1.0)

License  AGPL-3

Encoding  UTF-8

VignetteBuilder  knitr

Suggests  BiocStyle, roxyen2, devtools, testthat (>= 2.0.0), knitr, markdown, covr, xml2

Imports  BiocFileCache, R6, RCurl, RSQLite, Rcpp, XML, chk, git2r, jsonlite, lgr, lifecycle, methods, openssl, plyr, progress, rappdirs, stats, stringr, tools, withr, yaml

LinkingTo  Rcpp, testthat

NeedsCompilation  yes

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Collate  'BiodbPersistentCache.R' 'BiodbBiocPersistentCache.R'
          'BiodbConfig.R' 'BiodbConnBase.R' 'BiodbConn.R' 'BiodbEntry.R'
          'BiodbCsvEntry.R' 'BiodbCustomPersistentCache.R'
          'BiodbDbInfo.R' 'BiodbDbsInfo.R' 'BiodbEntryField.R'
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- 'BiodbMain.R'
- 'BiodbEntryFields.R'
- 'BiodbFactory.R'
- 'BiodbXmlEntry.R'
- 'BiodbHtmlEntry.R'
- 'BiodbJsonEntry.R'
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- 'spec-dist.R'
- 'test_framework.R'

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Description

The biodb package provides access to standard remote chemical and biological databases (ChEBI, KEGG, HMDB, ...), as well as to in-house local database files (CSV, SQLite), with easy retrieval of entries, access to web services, search of compounds by mass and/or name, and mass spectra matching for LCMS and MSMS. Its architecture as a development framework facilitates the development of new database connectors for local projects or inside separate published packages.

Details

To get a presentation of the biodb package and get started with it, please see the "biodb" vignette.

vignette('biodb', package='biodb')

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See Also

BiodbMain, BiodbConfig, BiodbFactory, BiodbPersistentCache, BiodbDbsInfo, BiodbEntryFields.
abstractClass  
Declares a class as abstract.

Description
Forbids instantiation of an abstract class. This method must be called from within a constructor of an abstract class. It will throw an error if a direct call is made to this constructor.

Usage
abstractClass(cls, obj)

Arguments
- cls  
The name of the abstract class to check.
- obj  
The object being instantiated.

Value
Nothing.

abstractMethod  
Declares a method as abstract

Description
This method must be called from within the abstract method.

Usage
abstractMethod(obj)

Arguments
- obj  
The object on which the abstract method is called.

Value
Nothing.
**BiodbBiocPersistentCache**

*A persistent cache implementation that uses BiocCache package.*

---

**Description**

A persistent cache implementation that uses BiocCache package.

A persistent cache implementation that uses BiocCache package.

**Super class**

`biodb::BiodbPersistentCache` -> `BiodbBiocPersistentCache`

**Methods**

**Public methods:**

- `BiodbBiocPersistentCache$new()`
- `BiodbBiocPersistentCache$clone()`

**Method `new()`**: New instance initializer. Cache objects must not be created directly. Instead, access the cache instance through the BiodbMain instance using the `getPersistentCache()` method.

*Usage:

BiodbBiocPersistentCache$new(...)*

*Arguments:*

... See the constructor of ExtGenerator for the parameters.

*Returns: Nothing.*

**Method `clone()`**: The objects of this class are cloneable with this method.

*Usage:

BiodbBiocPersistentCache$clone(deep = FALSE)*

*Arguments:*

deep Whether to make a deep clone.

**See Also**

`BiodbPersistentCache`, `BiodbBiocPersistentCache`. 
A class for storing configuration values.

Description

A class for storing configuration values.

Details

This class is responsible for storing configuration. You must go through the single instance of this class to create and set and get configuration values. To get the single instance of this class, call the getConfig() method of class BiodbMain.

Methods

Public methods:

- BiodbConfig$new()
- BiodbConfig$getKeys()
- BiodbConfig$getTitle()
- BiodbConfig$getDescription()
- BiodbConfig$getDefaultValue()
- BiodbConfig$hasKey()
- BiodbConfig$isDefined()
- BiodbConfig$isEnabled()
- BiodbConfig$get()
- BiodbConfig$set()
- BiodbConfig$reset()
- BiodbConfig$enable()
- BiodbConfig$disable()
- BiodbConfig$sprint()
- BiodbConfig$listKeys()
- BiodbConfig$getAssocEnvVar()
- BiodbConfig$define()
- BiodbConfig$notifyNewObservers()
- BiodbConfig$terminate()
- BiodbConfig$clone()

Method new(): New instance initializer. No BiodbConfig object must not be created directly. Instead, access the config instance through the BiodbMain instance using the getConfig() method.

Usage:

BiodbConfig$new(parent)

Arguments:
Methods:

- **getMethod()**: Get the list of available keys.

  Usage:
  ```r
  BiodbConfig$getKeys()
  ```

  Arguments:
  - `deprecated` If set to TRUE returns also the deprecated keys.

  Returns: A character vector containing the config key names.

- **getTitle()**: Get the title of a key.

  Usage:
  ```r
  BiodbConfig$getTitle(key)
  ```

  Arguments:
  - `key` The name of a configuration key.

  Returns: The title of the key as a character value.

- **getDescription()**: Get the description of a key.

  Usage:
  ```r
  BiodbConfig$getDescription(key)
  ```

  Arguments:
  - `key` The name of a configuration key.

  Returns: The description of the key as a character value.

- **getDefaultValue()**: Get the default value of a key.

  Usage:
  ```r
  BiodbConfig$getValue(key, as.chr = FALSE)
  ```

  Arguments:
  - `key` The name of a configuration key.
  - `as.chr` If set to TRUE, returns the value as character.

  Returns: The default value for that key.

- **hasKey()**: Test if a key exists.

  Usage:
  ```r
  BiodbConfig$hasKey(key)
  ```

  Arguments:
  - `key` The name of a configuration key.

  Returns: TRUE if a key with this name exists, FALSE otherwise.

- **isDefined()**: Test if a key is defined (i.e.: if a value exists for this key).

  Usage:
BiodbConfig$defined(key, fail = TRUE)

**Arguments:**
- **key** The name of a configuration key.
- **fail** If set to TRUE and the configuration key does not exist, then an error will be raised.

**Returns:** TRUE if the key has a value, FALSE otherwise.

**Method isEnabled():** Test if a boolean key is set to TRUE. This method will raise an error if the key is not a boolean key.

**Usage:**
BiodbConfig$isEnabled(key)

**Arguments:**
- **key** The name of a configuration key.

**Returns:** TRUE if the boolean key has a value set to TRUE, FALSE otherwise.

**Method get():** Get the value of a key.

**Usage:**
BiodbConfig$get(key)

**Arguments:**
- **key** The name of a configuration key.

**Returns:** The value associated with the key.

**Method set():** Set the value of a key.

**Usage:**
BiodbConfig$set(key, value)

**Arguments:**
- **key** The name of a configuration key.
- **value** A value to associate with the key.

**Returns:** Nothing.

**Method reset():** Reset the value of a key.

**Usage:**
BiodbConfig$reset(key = NULL)

**Arguments:**
- **key** The name of a configuration key. If NULL, all keys will be reset.

**Returns:** Nothing.

**Method enable():** Set a boolean key to TRUE.

**Usage:**
BiodbConfig$enable(key)

**Arguments:**
- **key** The name of a configuration key.
Returns: Nothing.

**Method** disable(): Set a boolean key to FALSE.

*Usage:*
BiodbConfig$disable(key)

*Arguments:*
key  The name of a configuration key.

*Returns:  Nothing.*

**Method** print(): Print list of configuration keys and their values.

*Usage:*
BiodbConfig$print()

*Returns: Nothing.*

**Method** listKeys(): Get the full list of keys as a data frame.

*Usage:*
BiodbConfig$listKeys()

*Returns: A data frame containing keys, titles, types, and default values.*

**Method** getAssocEnvVar(): Returns the environment variable associated with this configuration key.

*Usage:*
BiodbConfig$getAssocEnvVar(key)

*Arguments:*
key  The name of a configuration key.

*Returns:  The environment variable’s value.*

**Method** define(): Defines config properties from a structured object, normally loaded from a YAML file.

*Usage:*
BiodbConfig$define(def)

*Arguments:*
def  The list of key definitions.

*Returns: Nothing.*

**Method** notifyNewObservers(): Called by BiodbMain when a new observer is registered.

*Usage:*
BiodbConfig$notifyNewObservers(obs)

*Arguments:*
obs  The new observers registered by the BiodbMain instance.

*Returns: Nothing.*
Method **terminate()**: Terminates the instance. This method will be called automatically by the BiodbMain instance when you call

Usage:
BiodbConfig$terminate()

Arguments:
BiodbMain::terminate().

Returns: Nothing.

Method **clone()**: The objects of this class are cloneable with this method.

Usage:
BiodbConfig$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also

BiodbMain.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get the config instance:
config <- mybiodb$getConfig()

# Print all available keys
config$getKeys()

# Get a configuration value:
value <- config$get('cache.directory')

# Set a configuration value:
config$set('dwnld.timeout', 600)

# For boolean values, you can use boolean methods:
config$get('offline')
config$enable('offline') # set to TRUE
config$disable('offline') # set to FALSE
config$isEnabled('offline')

# Terminate instance.
mybiodb$terminate()
BiodbConn

The mother abstract class of all database connectors.

Description

The mother abstract class of all database connectors.

Details

This is the super class of all connector classes. All methods defined here are thus common to all connector classes. All connector classes inherit from this abstract class.

See section Fields for a list of the constructor’s parameters. Concrete classes may have direct web services methods or other specific methods implemented, in which case they will be described inside the documentation of the concrete class. Please refer to the documentation of each concrete class for more information. The database direct web services methods will be named "ws.*".

The constructor has the following arguments:

- id: The identifier of the connector.
- cache.id: The identifier used in the disk cache.

Super class

biodb::BiodbConnBase -> BiodbConn

Methods

Public methods:

- BiodbConn$new()
- BiodbConn$getBiodb()
- BiodbConn$getId()
- BiodbConn$print()
- BiodbConn$correctIds()
- BiodbConn$getEntry()
- BiodbConn$getCacheFile()
- BiodbConn$getEntryContent()
- BiodbConn$getEntryContentFromDb()
- BiodbConn$getEntryContentRequest()
- BiodbConn$getEntryIds()
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- BiodbConn$getEntryPageUrl()
- BiodbConn$getChromCol()
- BiodbConn$getMatchingMzField()
- BiodbConn$setMatchingMzField()
- BiodbConn$getMzValues()
- BiodbConn$getNbPeaks()
- BiodbConn$filterEntriesOnRt()
Method `new()`: New instance initializer. Connector objects must not be created directly. Instead, you create new connector instances through the `BiodbFactory` instance.

Usage:
```r
BiodbConn$new(id = NA_character_, cache.id = NA_character_, bdb, ...)```

Arguments:
- `id` The ID of the connector instance.
- `cache.id` The Cache ID of the connector instance.
- `bdb` The BiodbMain instance.
- `...` Remaining arguments will be passed to the constructor of the super class.

Returns: Nothing.

Method `getBiodb()`: Returns the biodb main class instance to which this object is attached.

Usage:
```r
BiodbConn$getBiodb()
```

Returns: The main biodb instance.

Method `getId()`: Get the identifier of this connector.

Usage:
```r
BiodbConn$getId()
```

Returns: The identifier of this connector.

Method `print()`: Prints a description of this connector.

Usage:
```r
BiodbConn$print()
```

Returns: Nothing.

Method `correctIds()`: Correct a vector of IDs by formatting them to the database official format, if required and possible.

Usage:
```r
BiodbConn$correctIds(ids)
```

Arguments:
- `ids` A character vector of IDs.

Returns: The vector of IDs corrected.
Method `getEntry()`: Return the entry corresponding to this ID. You can pass a vector of IDs, and you will get a list of entries.

Usage:
BiodbConn$`getEntry(id, drop = TRUE, nulls = TRUE)`

Arguments:
- `id` A character vector containing entry identifiers.
- `drop` If set to TRUE and only one entry is requested, then the returned value will be a single BiodbEntry object, otherwise it will be a list of BiodbEntry objects.
- `nulls` If set to TRUE, NULL entries are preserved. This ensures that the output list has the same length than the input vector `id`. Otherwise they are removed from the final list.

Returns: A list of BiodbEntry objects, the same size of the vector of IDs. The list will contain NULL values for invalid IDs. If `drop` is set to TRUE and only one entry was requested then a single BiodbEntry is returned instead of a list.

Method `getCacheFile()`: Get the path to the persistent cache file.

Usage:
BiodbConn$`getCacheFile(entry.id)`

Arguments:
- `entry.id` The identifiers (e.g.: accession numbers) as a character vector of the database entries.

Returns: A character vector, the same length as the vector of IDs, containing the paths to the cache files corresponding to the requested entry IDs.

Method `getEntryContent()`: Get the contents of database entries from IDs (accession numbers).

Usage:
BiodbConn$`getEntryContent(id)`

Arguments:
- `id` A character vector of entry IDs.

Returns: A character vector containing the contents of the requested IDs. If no content is available for an entry ID, then NA will be used.

Method `getEntryContentFromDb()`: Get the contents of entries directly from the database. A direct request or an access to the database will be made in order to retrieve the contents. No access to the biodb cache system will be made.

Usage:
BiodbConn$`getEntryContentFromDb(entry.id)`

Arguments:
- `entry.id` A character vector with the IDs of entries to retrieve.

Returns: A character vector, the same size of `entry.id`, with contents of the requested entries. An NA value will be set for the content of each entry for which the retrieval failed.

Method `getEntryContentRequest()`: Gets the URL to use in order to get the contents of the specified entries.
**Usage:**
BiodbConn$getEntryContentRequest(entry.id, concatenate = TRUE, max.length = 0)

**Arguments:**
- entry.id  A character vector with the IDs of entries to retrieve.
- concatenate  If set to TRUE, then try to build as few URLs as possible, sending requests with several identifiers at once.
- max.length  The maximum length of the URLs to return, in number of characters.

**Returns:**  A vector of URL strings.

**Method** getEntryIds(): Get entry identifiers from the database. More arguments can be given, depending on implementation in specific databases. For mass databases the ms.level argument can also be set.

**Usage:**
BiodbConn$getEntryIds(max.results = 0, ...)

**Arguments:**
- max.results  The maximum of elements to return from the method.
- ...  Arguments specific to connectors.

**Returns:**  A character vector containing entry IDs from the database. An empty vector for a remote database may mean that the database does not support requesting for entry accessions.

**Method** getNbEntries(): Get the number of entries contained in this database.

**Usage:**
BiodbConn$getNbEntries(count = FALSE)

**Arguments:**
- count  If set to TRUE and no straightforward way exists to get number of entries, count the output of getEntryIds().

**Returns:**  The number of entries in the database, as an integer.

**Method** isEditable(): Tests if this connector is able to edit the database (i.e.: the connector class implements the interface BiodbEditable). If this connector is editable, then you can call allowEditing() to enable editing.

**Usage:**
BiodbConn$isEditable()

**Returns:**  Returns TRUE if the database is editable.

**Method** editingIsAllowed(): Tests if editing is allowed.

**Usage:**
BiodbConn$editingIsAllowed()

**Returns:**  TRUE if editing is allowed for this database, FALSE otherwise.

**Method** allowEditing(): Allows editing for this database.

**Usage:**
BiodbConn$allowEditing()
Returns: Nothing.

**Method** disallowEditing(): Disallows editing for this database.

*Usage:*
BiodbConn$disallowEditing()

Returns: Nothing.

**Method** setEditingAllowed(): Allow or disallow editing for this database.

*Usage:*
BiodbConn$setEditingAllowed(allow)

*Arguments:*
allow  A logical value.

Returns: Nothing.

**Method** addNewEntry(): Adds a new entry to the database. The passed entry must have been previously created from scratch using BiodbFactory :createNewEntry() or cloned from an existing entry using BiodbEntry :clone().

*Usage:*
BiodbConn$addNewEntry(entry)

*Arguments:*
entry  The new entry to add. It must be a valid BiodbEntry object.

Returns: Nothing.

**Method** isWritable(): Tests if this connector is able to write into the database. If this connector is writable, then you can call allowWriting() to enable writing.

*Usage:*
BiodbConn$isWritable()

Returns: Returns TRUE if the database is writable.

**Method** allowWriting(): Allows the connector to write into this database.

*Usage:*
BiodbConn$allowWriting()

Returns: Nothing.

**Method** disallowWriting(): Disallows the connector to write into this database.

*Usage:*
BiodbConn$disallowWriting()

Returns: Nothing.

**Method** setWritingAllowed(): Allows or disallows writing for this database.

*Usage:*
BiodbConn$setWritingAllowed(allow)

*Arguments:*

allow If set to TRUE, allows writing.

Returns: Nothing.

Method writingIsAllowed(): Tests if the connector has access right to the database.

Usage:
BiodbConn$writingIsAllowed()

Returns: TRUE if writing is allowed for this database, FALSE otherwise.

Method write(): Writes into the database. All modifications made to the database since the last time write() was called will be saved.

Usage:
BiodbConn$write()

Returns: Nothing.

Method isSearchableByField(): Tests if a field can be used to search entries when using method searchForEntries().

Usage:
BiodbConn$isSearchableByField(field = NULL, field.type = NULL)

Arguments:
field The name of the field.
field.type The field type.

Returns: Returns TRUE if the database is searchable using the specified field or searchable by any field of the specified type, FALSE otherwise.

Method getSearchableFields(): Get the list of all searchable fields.

Usage:
BiodbConn$getSearchableFields()

Returns: A character vector containing all searchable fields for this connector.

Method searchForEntries(): Searches the database for entries whose name matches the specified name. Returns a character vector of entry IDs.

Usage:
BiodbConn$searchForEntries(fields = NULL, max.results = 0)

Arguments:
fields A list of fields on which to filter entries. To get a match, all fields must be matched (i.e. logical AND). The keys of the list are the entry field names on which to filter, and the values are the filtering parameters. For character fields, the filter parameter is a character vector in which all strings must be found inside the field’s value. For numeric fields, the filter parameter is either a list specifying a min-max range (list(min=1.0, max=2.5)) or a value with a tolerance in delta (list(value=2.0, delta=0.1)) or ppm (list(value=2.0, ppm=1.0)).

max.results If set, the number of returned IDs is limited to this number.

Returns: A character vector of entry IDs whose name matches the requested name.
**Method** searchByName(): DEPRECATED. Use searchForEntries() instead.

*Usage:*

BiodbConn$searchByName(name, max.results = 0)

*Arguments:*

name  A character value to search inside name fields.

max.results  If set, the number of returned IDs is limited to this number.

*Returns:* A character vector of entry IDs whose name matches the requested name.

**Method** isDownloadable(): Tests if the connector can download the database.

*Usage:*

BiodbConn$isDownloadable()

*Returns:* Returns TRUE if the database is downloadable.

**Method** isDownloaded(): Tests if the database has been downloaded.

*Usage:*

BiodbConn$isDownloaded()

*Returns:* TRUE if the database content has already been downloaded.

**Method** requiresDownload(): Tests if the connector requires the download of the database.

*Usage:*

BiodbConn$requiresDownload()

*Returns:* TRUE if the connector requires download of the database.

**Method** getDownloadPath(): Gets the path where the downloaded content is written.

*Usage:*

BiodbConn$getDownloadPath()

*Returns:* The path where the downloaded database is written.

**Method** setDownloadedFile(): Set the downloaded file into the cache.

*Usage:*

BiodbConn$setDownloadedFile(src, action = c("copy", "move"))

*Arguments:*

src  Path to the downloaded file.

action  Specifies if files have to be moved or copied into the cache.

*Returns:* Nothing.

**Method** isExtracted(): Tests if the downloaded database has been extracted (in case the database needs extraction).

*Usage:*

BiodbConn$isExtracted()

*Returns:* TRUE if the downloaded database content has been extracted, FALSE otherwise.

**Method** download(): Downloads the database content locally.
Usage:
BiodbConn$download()

Returns: Nothing.

Method `isRemotedb()`: Tests if the connector is connected to a remote database.

Usage:
BiodbConn$isRemotedb()

Returns: Returns TRUE if the database is a remote database.

Method `isCompounddb()`: Tests if the connector's database is a compound database.

Usage:
BiodbConn$isCompounddb()

Returns: Returns TRUE if the database is a compound database.

Method `searchCompound()`: This method is deprecated. Use `searchForEntries()` instead. Searches for compounds by name and/or by mass. At least one of name or mass must be set.

Usage:
BiodbConn$searchCompound(
  name = NULL,
  mass = NULL,
  mass.field = NULL,
  mass.tol = 0.01,
  mass.tol.unit = "plain",
  max.results = 0
)

Arguments:
name The name of a compound to search for.
mass The searched mass.

mass.field For searching by mass, you must indicate a mass field to use ("monoisotopic.mass", "molecular.mass", "average.mass" or "nominal.mass").
mass.tol The tolerance value on the molecular mass.
mass.tol.unit The type of mass tolerance. Either 'plain' or 'ppm'.
max.results The maximum number of matches to return.
description A character vector of words or expressions to search for inside description field.

The words will be searched in order. A match will be made only if all words are inside the description field.

Returns: A character vector of entry IDs.

Method `annotateMzValues()`: Annotates a mass spectrum with the database. For each matching entry the entry field values will be set inside columns appended to the data frame. Names of these columns will use a common prefix in order to distinguish them from other data from the input data frame.

Usage:
BiodbConn$annotateMzValues(
    x,
    mz.tol,
    ms.mode,
    mz.tol.unit = c("plain", "ppm"),
    mass.field = "monoisotopic.mass",
    max.results = 3,
    mz.col = "mz",
    fields = NULL,
    prefix = NULL,
    insert.input.values = TRUE,
    fieldsLimit = 0
)

Arguments:
- `x`: Either a data frame or a numeric vector containing the M/Z values.
- `mz.tol`: The tolerance on the M/Z values.
- `ms.mode`: The MS mode. Set it to either 'neg' or 'pos'.
- `mz.tol.unit`: The type of the M/Z tolerance. Set it to either to 'ppm' or 'plain'.
- `mass.field`: The mass field to use for matching M/Z values. One of: 'monoisotopic.mass', 'molecular.mass', 'average.mass', 'nominal.mass'.
- `max.results`: If set, it is used to limit the number of matches found for each M/Z value. To get all the matches, set this parameter to NA_integer_. Default value is 3.
- `mz.col`: The name of the column where to find M/Z values in case `x` is a data frame.
- `fields`: A character vector containing the additional entry fields you would like to get for each matched entry. Each field will be output in a different column.
- `prefix`: A prefix that will be inserted before the name of each added column in the output. By default it will be set to the name of the database followed by a dot.
- `insert.input.values`: Insert input values at the beginning of the result data frame.
- `fieldsLimit`: The maximum of values to output for fields with multiple values. Set it to 0 to get all values.

Returns: A data frame containing the input values, and annotation columns appended at the end. The first annotation column contains the IDs of the matched entries. The following columns contain the fields you have requested through the `fields` parameter.

Method `isMassdb()`: Tests if the connector’s database is a mass spectra database.

Usage:
BiodbConn$isMassdb()

Returns: Returns TRUE if the database is a mass database.

Method `checkDb()`: Checks that the database is correct by trying to retrieve all its entries.

Usage:
BiodbConn$checkDb()

Returns: Nothing.

Method `getAllVolatileCacheEntries()`: Get all entries stored in the memory cache (volatile cache).
Usage:
BiodbConn$getAllVolatileCacheEntries()

Returns: A list of BiodbEntry instances.

Method getAllCacheEntries(): This method is deprecated. Use getAllVolatileCacheEntries() instead.

Usage:
BiodbConn$getAllCacheEntries()

Returns: All entries cached in memory.

Method deleteAllEntriesFromVolatileCache(): Delete all entries from the volatile cache (memory cache).

Usage:
BiodbConn$deleteAllEntriesFromVolatileCache()

Returns: Nothing.

Method deleteAllEntriesFromPersistentCache(): Delete all entries from the persistent cache (disk cache).

Usage:
BiodbConn$deleteAllEntriesFromPersistentCache(deleteVolatile = TRUE)

Arguments:
deleteVolatile If TRUE deletes also all entries from the volatile cache (memory cache).

Returns: Nothing.

Method deleteWholePersistentCache(): Delete all files associated with this connector from the persistent cache (disk cache).

Usage:
BiodbConn$deleteWholePersistentCache(deleteVolatile = TRUE)

Arguments:
deleteVolatile If TRUE deletes also all entries from the volatile cache (memory cache).

Returns: Nothing.

Method deleteAllCacheEntries(): Delete all entries from the memory cache. This method is deprecated, please use deleteAllEntriesFromVolatileCache() instead.

Usage:
BiodbConn$deleteAllCacheEntries()

Returns: Nothing.

Method getCacheId(): Gets the ID used by this connector in the disk cache.

Usage:
BiodbConn$getCacheId()

Returns: The cache ID of this connector.
Method makesRefToEntry(): Tests if some entry of this database makes reference to another entry of another database.

Usage:
BiodbConn$makesRefToEntry(id, db, oid, any = FALSE, recurse = FALSE)

Arguments:
id A character vector of entry IDs from the connector’s database.
db Another database connector.
oid A entry ID from database db.
any If set to TRUE, returns a single logical value: TRUE if any entry contains a reference to oid, FALSE otherwise.
recurse If set to TRUE, the algorithm will follow all references to entries from other databases, to see if it can establish an indirect link to oid.

Returns: A logical vector, the same size as id, with TRUE for each entry making reference to oid, and FALSE otherwise.

Method makeRequest(): Makes a BiodbRequest instance using the passed parameters, and set itself as the associated connector.

Usage:
BiodbConn$makeRequest(...) 

Arguments:
... Those parameters are passed to the initializer of BiodbRequest.

Returns: The BiodbRequest instance.

Method getEntryImageUrl(): Gets the URL to a picture of the entry (e.g.: a picture of the molecule in case of a compound entry).

Usage:
BiodbConn$getEntryImageUrl(entry.id)

Arguments:
entry.id A character vector containing entry IDs.

Returns: A character vector, the same length as entry.id, containing for each entry ID either a URL or NA if no URL exists.

Method getEntryPageUrl(): Gets the URL to the page of the entry on the database web site.

Usage:
BiodbConn$getEntryPageUrl(entry.id)

Arguments:
entry.id A character vector with the IDs of entries to retrieve.

Returns: A list of BiodbUrl objects, the same length as entry.id.

Method getChromCol(): Gets a list of chromatographic columns contained in this database.

Usage:
BiodbConn$getChromCol(ids = NULL)
Arguments:
ids A character vector of entry identifiers (i.e.: accession numbers). Used to restrict the set of entries on which to run the algorithm.

Returns: A data.frame with two columns, one for the ID 'id' and another one for the title 'title'.

**Method** getMatchingMzField(): Gets the field to use for M/Z matching.

Usage:
BiodbConn$getMatchingMzField()

Returns: The name of the field (one of peak.mztheo or peak.mzexp).

**Method** setMatchingMzField(): Sets the field to use for M/Z matching.

Usage:
BiodbConn$setMatchingMzField(field = c("peak.mztheo", "peak.mzexp"))

Arguments:
field The field to use for matching.

Returns: Nothing.

**Method** getMzValues(): Gets a list of M/Z values contained inside the database.

Usage:
BiodbConn$getMzValues(
  ms.mode = NULL,
  max.results = 0,
  precursor = FALSE,
  ms.level = 0
)

Arguments:
ms.mode The MS mode. Set it to either 'neg' or 'pos' to limit the output to one mode.
max.results If set, it is used to limit the size of the output.
precursor If set to TRUE, then restrict the search to precursor peaks.
ms.level The MS level to which you want to restrict your search. 0 means that you want to search in all levels.

Returns: A numeric vector containing M/Z values.

**Method** getNbPeaks(): Gets the number of peaks contained in the database.

Usage:
BiodbConn$getNbPeaks(mode = NULL, ids = NULL)

Arguments:
mode The MS mode. Set it to either 'neg' or 'pos' to limit the counting to one mode.
ids A character vector of entry identifiers (i.e.: accession numbers). Used to restrict the set of entries on which to run the algorithm.

Returns: The number of peaks, as an integer.

**Method** filterEntriesOnRt(): Filters a list of entries on retention time values.
Usage:
BiodbConn$filterEntriesOnRt(
  entry.ids,
  rt,
  rt.unit,
  rt.tol,
  rt.tol.exp,
  chrom.col.ids,
  match.rt
)

Arguments:
entry.ids A character vector of entry IDs.
rt A vector of retention times to match. Used if input.df is not set. Unit is specified by rt.unit parameter.
rt.unit The unit for submitted retention times. Either ‘s’ or ‘min’.
rt.tol The plain tolerance (in seconds) for retention times: input.rt
  • rt.tol <= database.rt <= input.rt + rt.tol.
rt.tol.exp A special exponent tolerance for retention times: input.rt
  • input.rt ** rt.tol.exp <= database.rt <= input.rt + input.rt ** rt.tol.exp. This exponent is applied on the RT value in seconds. If both rt.tol and rt.tol.exp are set, the inequality expression becomes input.rt - rt.tol - input.rt ** rt.tol.exp <= database.rt <= input.rt + rt.tol + input.rt ** rt.tol.exp.
chrom.col.ids IDs of chromatographic columns on which to match the retention time.
match.rt If set to TRUE, filters on RT values, otherwise does not do any filtering.

Returns: A character vector containing entry IDs after filtering.

Method searchForMassSpectra(): Searches for entries (i.e.: spectra) that contain a peak around the given M/Z value. Entries can also be filtered on RT values. You can input either a list of M/Z values through mz argument and set a tolerance with mz.tol argument, or two lists of minimum and maximum M/Z values through mz.min and mz.max arguments.

Usage:
BiodbConn$searchForMassSpectra(
  mz.min = NULL,
  mz.max = NULL,
  mz = NULL,
  mz.tol = NULL,
  mz.tol.unit = c("plain", "ppm"),
  rt = NULL,
  rt.unit = c("s", "min"),
  rt.tol = NULL,
  rt.tol.exp = NULL,
  chrom.col.ids = NULL,
  precursor = FALSE,
  min.rel.int = 0,
  ms.mode = NULL,
  max.results = 0,
)
ms.level = 0,
include.ids = NULL
)

**Arguments:**

- **mz.min** A vector of minimum M/Z values.
- **mz.max** A vector of maximum M/Z values. Its length must be the same as **mz.min**.
- **mz** A vector of M/Z values.
- **mz.tol** The M/Z tolerance, whose unit is defined by **mz.tol.unit**.
- **mz.tol.unit** The type of the M/Z tolerance. Set it to either 'ppm' or 'plain'.
- **rt** A vector of retention times to match. Used if **input.df** is not set. Unit is specified by **rt.unit** parameter.
- **rt.unit** The unit for submitted retention times. Either 's' or 'min'.
- **rt.tol** The plain tolerance (in seconds) for retention times: **input.rt**
  - **rt.tol <= database.rt <= input.rt + rt.tol**.
- **rt.tol.exp** A special exponent tolerance for retention times: **input.rt**
  - **input.rt ** rt.tol.exp <= database.rt <= input.rt + input.rt ** rt.tol.exp**. This exponent is applied on the RT value in seconds. If both **rt.tol** and **rt.tol.exp** are set, the inequality expression becomes **input.rt - rt.tol - input.rt ** rt.tol.exp <= database.rt <= input.rt + rt.tol + input.rt ** rt.tol.exp**.
- **chrom.col.ids** IDs of chromatographic columns on which to match the retention time.
- **precursor** If set to TRUE, then restrict the search to precursor peaks.
- **min.rel.int** The minimum relative intensity, in percentage (i.e.: float number between 0 and 100).
- **ms.mode** The MS mode. Set it to either 'neg' or 'pos'.
- **max.results** If set, it is used to limit the number of matches found for each M/Z value.
- **ms.level** The MS level to which you want to restrict your search. 0 means that you want to search in all levels.
- **include.ids** A list of IDs to which to restrict the final results. All IDs that are not in this list will be excluded.

**Returns:** A character vector of spectra IDs.

**Method** `searchMsEntries()`: DEPRECATED. Use `searchForMassSpectra()` instead.

**Usage:**

```r
BiodbConn$searchMsEntries(
  mz.min = NULL,
  mz.max = NULL,
  mz = NULL,
  mz.tol = NULL,
  mz.tol.unit = c("plain", "ppm"),
  rt = NULL,
  rt.unit = c("s", "min"),
  rt.tol = NULL,
  rt.tol.exp = NULL,
  chrom.col.ids = NULL,
  precursor = FALSE,
)```

```
Arguments:

- `mz.min` A vector of minimum M/Z values.
- `mz.max` A vector of maximum M/Z values. Its length must be the same as `mz.min`.
- `mz` A vector of M/Z values.
- `mz.tol` The M/Z tolerance, whose unit is defined by `mz.tol.unit`.
- `mz.tol.unit` The type of the M/Z tolerance. Set it to either "ppm" or "plain".
- `rt` A vector of retention times to match. Used if `input.df` is not set. Unit is specified by `rt.unit` parameter.
- `rt.unit` The unit for submitted retention times. Either 's' or 'min'.
- `rt.tol` The plain tolerance (in seconds) for retention times: `input.rt - rt.tol <= database.rt <= input.rt + rt.tol`.
- `rt.tol.exp` A special exponent tolerance for retention times: `input.rt - rt.tol.exp <= database.rt <= input.rt + rt.tol.exp`. This exponent is applied on the RT value in seconds. If both `rt.tol` and `rt.tol.exp` are set, the inequality expression becomes `input.rt - rt.tol - input.rt ** rt.tol.exp <= database.rt <= input.rt + rt.tol + input.rt ** rt.tol.exp`.
- `chrom.col.ids` IDs of chromatographic columns on which to match the retention time.
- `precursor` If set to TRUE, then restrict the search to precursor peaks.
- `min.rel.int` The minimum relative intensity, in percentage (i.e.: float number between 0 and 100).
- `ms.mode` The MS mode. Set it to either 'neg' or 'pos'.
- `max.results` If set, it is used to limit the number of matches found for each M/Z value.
- `ms.level` The MS level to which you want to restrict your search. 0 means that you want to search in all levels.

Returns: A character vector of spectra IDs.

Method `searchMsPeaks()`: For each M/Z value, searches for matching MS spectra and returns the matching peaks.

Usage:

```r
BiodbConn$searchMsPeaks(
    input.df = NULL,
    mz = NULL,
    mz.tol = NULL,
    mz.tol.unit = c("plain", "ppm"),
    min.rel.int = 0,
    ms.mode = NULL,
    ms.level = 0,
    max.results = 0,
    chrom.col.ids = NULL,
    rt = NULL,
```
rt.unit = c("s", "min"),
rt.tol = NULL,
rt.tol.exp = NULL,
precursor = FALSE,
precursor.rt.tol = NULL,
insert.input.values = TRUE,
prefix = NULL,
compute = TRUE,
fields = NULL,
fieldsLimit = 0,
input.df.colnames = c(mz = "mz", rt = "rt"),
match.rt = FALSE
)

Arguments:

input.df A data frame taken as input for searchMsPeaks(). It must contain a columns 'mz',
and optionally an 'rt' column.
mz A vector of M/Z values to match. Used if input.df is not set.
mz.tol The M/Z tolerance, whose unit is defined by mz.tol.unit.
mz.tol.unit The type of the M/Z tolerance. Set it to either 'ppm' or 'plain'.
min.rel.int The minimum relative intensity, in percentage (i.e.: float number between 0 and
100).
ms.mode The MS mode. Set it to either 'neg' or 'pos'.
ms.level The MS level to which you want to restrict your search. 0 means that you want to
search in all levels.
max.results If set, it is used to limit the number of matches found for each M/Z value.
chrom.col.ids IDs of chromatographic columns on which to match the retention time.
rt A vector of retention times to match. Used if input.df is not set. Unit is specified by rt.unit
parameter.
rt.unit The unit for submitted retention times. Either 's' or 'min'.
rt.tol The plain tolerance (in seconds) for retention times: input.rt
  • rt.tol <= database.rt <= input.rt + rt.tol.
rt.tol.exp A special exponent tolerance for retention times: input.rt
  • input.rt ** rt.tol.exp <= database.rt <= input.rt + input.rt ** rt.tol.exp. This exponent is
    applied on the RT value in seconds. If both rt.tol and rt.tol.exp are set, the inequality
    expression becomes input.rt - rt.tol - input.rt ** rt.tol.exp <= database.rt <= input.rt +
    rt.tol + input.rt ** rt.tol.exp.
precursor If set to TRUE, then restrict the search to precursor peaks.
precursor.rt.tol The RT tolerance used when matching the precursor.
insert.input.values Insert input values at the beginning of the result data frame.
prefix Add prefix on column names of result data frame.
compute If set to TRUE, use the computed values when converting found entries to data frame.
fields A character vector of field names to output. The data frame output will be restricted to
this list of fields.
fieldsLimit The maximum of values to output for fields with multiple values. Set it to 0 to
get all values.
input.df.colnames Names of the columns in the input data frame.
match.rt If set to TRUE, match also RT values.

Returns: A data frame with at least input MZ and RT columns, and annotation columns prefixed with prefix if set. For each matching found a row is output. Thus if n matchings are found for M/Z value x, then there will be n rows for x, each for a different match. The number of matching found for each M/Z value is limited to max.results.

Method msmsSearch(): Searches MSMS spectra matching a template spectrum. The mz.tol parameter is applied on the precursor search.

Usage:
BiodbConn$msmsSearch(
  spectrum,
  precursor.mz,
  mz.tol,
  mz.tol.unit = c("plain", "ppm"),
  ms.mode,
  npmin = 2,
  dist.fun = c("wcosine", "cosine", "pkernel", "pbachtttarya"),
  msms.mz.tol = 3,
  msms.mz.tol.min = 0.005,
  max.results = 0
)

Arguments:
spectrum A template spectrum to match inside the database.
precursor.mz The M/Z value of the precursor peak of the mass spectrum.
mz.tol The M/Z tolerance, whose unit is defined by mz.tol.unit.
mz.tol.unit The type of the M/Z tolerance. Set it to either to 'ppm' or 'plain'.
ms.mode The MS mode. Set it to either 'neg' or 'pos'.
npmin The minimum number of peak to detect a match (2 is recommended).
dist.fun The distance function used to compute the distance between two mass spectra.
msms.mz.tol M/Z tolerance to apply while matching MSMS spectra. In PPM.
msms.mz.tol.min Minimum of the M/Z tolerance (plain unit). If the M/Z tolerance computed with msms.mz.tol is lower than msms.mz.tol.min, then msms.mz.tol.min will be used.
max.results If set, it is used to limit the number of matches found for each M/Z value.

Returns: A data frame with columns id, score and peak.*. Each peak.* column corresponds to a peak in the input spectrum, in the same order and gives the number of the peak that was matched with it inside the matched spectrum whose ID is inside the id column.

Method collapseResultsDataFrame(): Collapse rows of a results data frame, by outputting a data frame with only one row for each MZ/RT value.

Usage:
BiodbConn$collapseResultsDataFrame(
  results.df,
  mz.col = "mz",
  rt.col = "rt",
  sep = "|"
)
Arguments:
results.df  Results data frame.
mz.col The name of the M/Z column in the results data frame.
rt.col The name of the RT column in the results data frame.
sep The separator used to concatenate values, when collapsing results data frame.

Returns: A data frame with rows collapsed.

Method searchMzRange(): Find spectra in the given M/Z range. Returns a list of spectra IDs.

Usage:
BiodbConn$searchMzRange(
mz.min,
mz.max,
min.rel.int = 0,
ms.mode = NULL,
max.results = 0,
precursor = FALSE,
ms.level = 0
)

Arguments:
mz.min A vector of minimum M/Z values.
mz.max A vector of maximum M/Z values. Its length must be the same as mz.min.
min.rel.int The minimum relative intensity, in percentage (i.e.: float number between 0 and 100).
ms.mode The MS mode. Set it to either 'neg' or 'pos'.
max.results If set, it is used to limit the number of matches found for each M/Z value.
precursor If set to TRUE, then restrict the search to precursor peaks.
ms.level The MS level to which you want to restrict your search. 0 means that you want to search in all levels.

Returns: A character vector of spectra IDs.

Method searchMzTol(): Find spectra containing a peak around the given M/Z value. Returns a character vector of spectra IDs.

Usage:
BiodbConn$searchMzTol(
mz,
mz.tol,
mz.tol.unit = "plain",
min.rel.int = 0,
ms.mode = NULL,
max.results = 0,
precursor = FALSE,
ms.level = 0
)

Arguments:
mz A vector of M/Z values.
mz.tol The M/Z tolerance, whose unit is defined by mz.tol.unit.
mz.tol.unit The type of the M/Z tolerance. Set it to either 'ppm' or 'plain'.
min.rel.int The minimum relative intensity, in percentage (i.e.: float number between 0 and 100).
ms.mode The MS mode. Set it to either 'neg' or 'pos'.
max.results If set, it is used to limit the number of matches found for each M/Z value.
precursor If set to TRUE, then restrict the search to precursor peaks.
ms.level The MS level to which you want to restrict your search. 0 means that you want to search in all levels.

Returns: A character vector of spectra IDs.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbConn$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also
Super class BiodbConnBase, and BiodbFactory class.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a compound CSV file database
chebi.tsv <- system.file("extdata", "chebi_extract.tsv", package='biodb')

# Create a connector
cconn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi.tsv)

# Get 10 identifiers from the database:
ids <- conn$getEntryIds(10)

# Get number of entries contained in the database:
n <- conn$getNbEntries()

# Terminate instance.
mybiodb$terminate()
**BiodbConnBase**

Base class of BiodbConn for encapsulating all needed information for database access.

**Description**

Base class of BiodbConn for encapsulating all needed information for database access.

**Details**

This is the base class for BiodbConn and BiodbDbInfo. When defining a new connector class, your class must not inherit from BiodbBaseConn but at least from BiodbConn (or BiodbRemoteConn or any subclass of BiodbConn). Its main purpose is to store property values. Those values are initialized from YAML files. The default definition file is located inside the package in "inst/definitions.yml" and is loaded at Biodb startup. However you can define your own files and load them using the BiodbMain::loadDefinitions() method.

Arguments to the constructor are:
- other: Another object inheriting from BiodbBaseConn, and from which property values will be copied.
- db.class: The class of the database ("mass.csv.file","comp.csv.file", ...).
- properties: Some properties to set at initialization.

**Methods**

**Public methods:**

- BiodbConnBase$new()
- BiodbConnBase$print()
- BiodbConnBase$hasProp()
- BiodbConnBase$getPropSlots()
- BiodbConnBase$hasPropSlot()
- BiodbConnBase$propExists()
- BiodbConnBase$isSlotProp()
- BiodbConnBase$getPropValSlot()
- BiodbConnBase$updatePropertiesDefinition()
- BiodbConnBase$getEntryFileExt()
- BiodbConnBase$getDbClass()
- BiodbConnBase$getConnClassName()
- BiodbConnBase$getConnClass()
- BiodbConnBase$getEntryClassName()
- BiodbConnBase$getEntryClass()
- BiodbConnBase$getEntryIdField()
- BiodbConnBase$getPropertyValue()
Method `new()`: New instance initializer. Connector objects must not be created directly. Instead, you create new connector instances through the BiodbFactory instance.

Usage:
BiodbConnBase$new(other = NULL, db.class = NULL, properties = NULL, cfg = NULL)

Arguments:
other Another BiodbConnBase instance as a model from which to copy property values.
db.class The class of the connector (i.e.: "mass.csv.file").
properties Some new values for the properties.
cfg The BiodbConfig instance from which will be taken some property values.

Returns: Nothing.

Method `print()`: Prints a description of this connector.

Usage:
BiodbConnBase$print()

Returns: Nothing.

Method `hasProp()`: Tests if this connector has a property.

Usage:
BiodbConnBase$hasProp(name)

Arguments:
name The name of the property to check.

Returns: Returns true if the property name exists.
**Method** `getPropSlots()`: Gets the slot fields of a property.

*Usage:*

\[ \text{BiodbConnBase}\$\text{getPropSlots(name)} \]

*Arguments:*

- `name` The name of a property.

*Returns:* Returns a character vector containing all slot names defined.

**Method** `hasPropSlot()`: Tests if a slot property has a specific slot.

*Usage:*

\[ \text{BiodbConnBase}\$\text{hasPropSlot(name, slot)} \]

*Arguments:*

- `name` The name of a property.
- `slot` The slot name to check.

*Returns:* Returns TRUE if the property `name` exists and has the slot `slot` defined, and FALSE otherwise.

**Method** `propExists()`: Checks if property exists.

*Usage:*

\[ \text{BiodbConnBase}\$\text{propExists(name)} \]

*Arguments:*

- `name` The name of a property.

*Returns:* Returns TRUE if the property `name` exists, and FALSE otherwise.

**Method** `isSlotProp()`: Tests if a property is a slot property.

*Usage:*

\[ \text{BiodbConnBase}\$\text{isSlotProp(name)} \]

*Arguments:*

- `name` The name of a property.

*Returns:* Returns TRUE if the property is a slot propert, FALSE otherwise.

**Method** `getPropValSlot()`: Retrieve the value of a slot of a property.

*Usage:*

\[ \text{BiodbConnBase}\$\text{getPropValSlot(name, slot, hook = TRUE)} \]

*Arguments:*

- `name` The name of a property.
- `slot` The slot name inside the property.
- `hook` If set to TRUE, enables the calls to hook methods associated with the property. Otherwise, all calls to hook methods are disabled.

*Returns:* The value of the slot `slot` of the property `name`.

**Method** `updatePropertiesDefinition()`: Update the definition of properties.

*Usage:*
BiodbConnBase$updatePropertiesDefinition(def)

Arguments:
def  A named list of property definitions. The names of the list must be the property names.

Returns:  Nothing.

Method getEntryFileExt():  Returns the entry file extension used by this connector.

Usage:
BiodbConnBase$getEntryFileExt()

Returns:  A character value containing the file extension.

Method getDbClass():  Gets the Biodb name of the database associated with this connector.

Usage:
BiodbConnBase$dbClass()

Returns:  A character value containing the Biodb database name.

Method getConnClassName():  Gets the name of the associated connector OOP class.

Usage:
BiodbConnBase$getConnClassName()

Returns:  Returns the connector OOP class name.

Method getConnClass():  Gets the associated connector OOP class.

Usage:
BiodbConnBase$getConnClass()

Returns:  Returns the connector OOP class.

Method getEntryClassName():  Gets the name of the associated entry class.

Usage:
BiodbConnBase$getEntryClassName()

Returns:  Returns the name of the associated entry class.

Method getEntryClass():  Gets the associated entry class.

Usage:
BiodbConnBase$getEntryClass()

Returns:  Returns the associated entry class.

Method getEntryIdField():  Gets the name of the corresponding database ID field in entries.

Usage:
BiodbConnBase$getEntryIdField()

Returns:  Returns the name of the database ID field.

Method getPropertyValue():  Gets a property value.

Usage:
BiodbConnBase$getPropertyValue(name, hook = TRUE)
Arguments:
name  The name of the property.
hook  If set to TRUE, enables the calls to hook methods associated with the property. Otherwise, all calls to hook methods are disabled.

Returns:  The value of the property.

Method setPropertyValue(): Sets the value of a property.
Usage:
BiodbConnBase$setPropertyValue(name, value)
Arguments:
name  The name of the property.
value  The new value to set the property to.

Returns:  Nothing.

Method setPropValSlot(): Set the value of the slot of a property.
Usage:
BiodbConnBase$setPropValSlot(name, slot, value, hook = TRUE)
Arguments:
name  The name of the property.
slot  The name of the property’s slot.
value  The new value to set the property’s slot to.
hook  If set to TRUE, enables the calls to hook methods associated with the property. Otherwise, all calls to hook methods are disabled.

Returns:  Nothing.

Method getBaseUrl(): Returns the base URL.
Usage:
BiodbConnBase$getBaseUrl()
Returns:  The base URL.

Method setBaseUrl(): Sets the base URL.
Usage:
BiodbConnBase$setBaseUrl(url)
Arguments:
url  A URL as a character value.

Returns:  Nothing.

Method getWsUrl(): Returns the web services URL.
Usage:
BiodbConnBase$getWsUrl()

Method setWsUrl(): Sets the web services URL.
**Usage:**
BiodbConnBase$setWsUrl(ws.url)

**Arguments:**
ws.url A URL as a character value.

**Returns:** Nothing.

**Method getToken():** Returns the access token.

**Usage:**
BiodbConnBase$getToken()

**Method setToken():** Sets the access token.

**Usage:**
BiodbConnBase$setToken(token)

**Arguments:**
token The token to use to access the database, as a character value.

**Returns:** Nothing.

**Method getName():** Returns the full database name.

**Usage:**
BiodbConnBase$getName()

**Method getEntryContentType():** Returns the entry content type.

**Usage:**
BiodbConnBase$getEntryContentType()

**Method getSchedulerNParam():** Returns the N parameter for the scheduler.

**Usage:**
BiodbConnBase$getSchedulerNParam()

**Method setSchedulerNParam():** Sets the N parameter for the scheduler.

**Usage:**
BiodbConnBase$setSchedulerNParam(n)

**Arguments:**
n The N parameter as a whole number.

**Returns:** Nothing.

**Method getSchedulerTParam():** Returns the T parameter for the scheduler.

**Usage:**
BiodbConnBase$getSchedulerTParam()

**Method setSchedulerTParam():** Sets the T parameter for the scheduler.

**Usage:**
BiodbConnBase$setSchedulerTParam(t)
Arguments:
  t  The T parameter as a whole number.

Returns:  Nothing.

Method getUrls(): Returns the URLs.
Usage:
  BiodbConnBase$getUrls()

Method getUrl(): Returns a URL.
Usage:
  BiodbConnBase$getUrl(name)

  Arguments:
  name  The name of the URL to retrieve.

  Returns:  The URL as a character value.

Method setUrl(): Sets a URL.
Usage:
  BiodbConnBase$setUrl(name, url)

  Arguments:
  name  The name of the URL to set.
  url   The URL value.

  Returns:  Nothing.

Method getXmlNs(): Returns the XML namespace.
Usage:
  BiodbConnBase$getXmlNs()

Method clone(): The objects of this class are cloneable with this method.
Usage:
  BiodbConnBase$clone(deep = FALSE)

  Arguments:
  deep  Whether to make a deep clone.

See Also

Sub-classes BiodbDbInfo and BiodbConn.
Examples

```r
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Accessing BiodbConnBase methods when using a BiodbDbInfo object
dbinf <- mybiodb$getDbInfo()$get('comp.csv.file')

# Test if a property exists
dbinf$hasProp('name')

# Get a property value
dbinf$getPropertyValue('name')

# Get a property value slot
dbinf$getPropertyValSlot('urls', 'base.url')

# Terminate instance.
mybiodb$terminate()
```

---

**BiodbCsvEntry**

*Entry class for content in CSV format.*

---

**Description**

Entry class for content in CSV format.

**Details**

This is an abstract class for handling database entries whose content is in CSV format.

**Super class**

`biodb::BiodbEntry` -> BiodbCsvEntry

**Methods**

**Public methods:**

- `BiodbCsvEntry$new()`
- `BiodbCsvEntry$clone()`

**Method** `new()`: New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

**Usage:**

`BiodbCsvEntry$new(sep = ",", na.strings = "NA", quotes = "", ...)`

**Arguments:**
The separator to use in CSV files.
na.strings The strings to recognize as NA values. This is a character vector.
quotes The characters to recognize as quotes. This is a single character value.
... The remaining arguments will be passed to the super class initializer.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbCsvEntry$clone(deep = FALSE)

Arguments:
dep Whether to make a deep clone.

See Also
Super class BiodbEntry.

Examples
# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbCsvEntry)
BiodbDbInfo

A class for describing the characteristics of a database.

Description

This class is used by BiodbDbsInfo for storing database characteristics, and returning them through the get() method. This class inherits from BiodbConnBase.

Super class

biodb::BiodbConnBase -> BiodbDbInfo

Methods

Public methods:

• BiodbDbInfo$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbDbInfo$clone(deep = FALSE)

Arguments:
  deep  Whether to make a deep clone.

See Also

Parent class BiodbDbsInfo and super class BiodbConnBase.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a BiodbDbInfo object for a database:
mybiodb$getDbsInfo()$get('comp.csv.file')

# Terminate instance.
mybiodb$terminate()
A class for describing the available databases.

Details

The unique instance of this class is handle by the `<BiodbMain>` class and accessed through the `getDbsInfo()` method.

Methods

Public methods:

- `BiodbDbsInfo$new()`
- `BiodbDbsInfo$define()`
- `BiodbDbsInfo$getId()`
- `BiodbDbsInfo$isDefined()`
- `BiodbDbsInfo$checkIsDefined()`
- `BiodbDbsInfo$get()`
- `BiodbDbsInfo$getAll()`
- `BiodbDbsInfo$print()`
- `BiodbDbsInfo$clone()`

Method `new()`: New instance initializer. The class must not be instantiated directly. Instead, access the BiodbDbsInfo instance through the BiodbMain instance using the `getDbsInfo()` method.

Usage:

`BiodbDbsInfo$new(cfg)`

Arguments:

- `cfg` The BiodbConfig instance.

Returns: Nothing.

Method `define()`: Define databases from a structured object, normally loaded from a YAML file.

Usage:

`BiodbDbsInfo$define(def, package = "biodb")`

Arguments:

- `def` A named list of database definitions. The names of the list will be the IDs of the databases.
- `package` The package to which belong the new definitions.

Returns: Nothing.
**Method** `getIds()`: Gets the database IDs.

*Usage:*

```r
BiodbDbsInfo$getIds()
```

*Returns:* A character vector containing all the IDs of the defined databases.

**Method** `isDefined()`: Tests if a database is defined.

*Usage:*

```r
BiodbDbsInfo$isDefined(db.id)
```

*Arguments:*

- `db.id` A database ID, as a character string.

*Returns:* TRUE if the specified id corresponds to a defined database, FALSE otherwise.

**Method** `checkIsDefined()`: Checks if a database is defined. Throws an error if the specified id does not correspond to a defined database.

*Usage:*

```r
BiodbDbsInfo$checkIsDefined(db.id)
```

*Arguments:*

- `db.id` A character vector of database IDs.

*Returns:* Nothing.

**Method** `get()`: Gets information on a database.

*Usage:*

```r
BiodbDbsInfo$get(db.id = NULL, drop = TRUE)
```

*Arguments:*

- `db.id` Database IDs, as a character vector. If set to NULL, informations on all databases will be returned.
- `drop` If TRUE and only one database ID has been submitted, returns a single BiodbDbInfo instance instead of a list.

*Returns:* A list of BiodbDbInfo instances corresponding to the specified database IDs.

**Method** `getAll()`: Gets informations on all databases.

*Usage:*

```r
BiodbDbsInfo$getAll()
```

*Returns:* A list of all BiodbDbInfo instances.

**Method** `print()`: Prints informations about this instance, listing also all databases defined.

*Usage:*

```r
BiodbDbsInfo$print()
```

*Returns:* Nothing.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```r
BiodbDbsInfo$clone(deep = FALSE)
```

*Arguments:*

- `deep` Whether to make a deep clone.
BiodbEntry

See Also

BiodbMain and child class BiodbDbInfo.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Getting the entry content type of a database:
db.inf <- mybiodb$getDbsInfo()$get('comp.csv.file')
cont.type <- db.inf$getPropertyValue('entry.content.type')

# Terminate instance.
mybiodb$terminate()

BiodbEntry

The mother abstract class of all database entry classes.

Description

The mother abstract class of all database entry classes.

Details

An entry is an element of a database, identifiable by its accession number. Each contains a list of fields defined by a name and a value. The details of all fields that can be set into an entry are defined inside the class BiodbEntryFields. From this class are derived other abstract classes for different types of entry contents: BiodbTxtEntry, BiodbXmlEntry, BiodbCsvEntry, BiodbJsonEntry and BiodbHtmlEntry. Then concrete classes are derived for each database: CompCsvEntry, MassCsvEntry, etc. For biodb users, there is no need to know this hierarchy; the knowledge of this class and its methods is sufficient.

Methods

Public methods:

- BiodbEntry$new()
- BiodbEntry$parentIsAConnector()
- BiodbEntry$getParent()
- BiodbEntry$getBiodb()
- BiodbEntry$cloneInstance()
- BiodbEntry$id()
- BiodbEntry$isNew()
- BiodbEntry$getDbClass()
- BiodbEntry$setFieldValue()
Method `new()`: New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:
```java
BiodbEntry$new(parent)
```

Arguments:
- `parent` A valid BiodbConn instance.

Returns: Nothing.

Method `parentIsAConnector()`: Tests if the parent of this entry is a connector instance.

Usage:
```java
BiodbEntry$parentIsAConnector()
```

Returns: TRUE if this entry belongs to a connector, FALSE otherwise.

Method `getParent()`: Returns the parent instance (A BiodbConn or BiodbFactory object) to which this object is attached.

Usage:
```java
BiodbEntry$getParent()
```

Returns: A BiodbConn instance or a BiodbFactory object.

Method `getBiodb()`: Returns the biodb main class instance to which this object is attached.

Usage:
```java
BiodbEntry$getBiodb()
```
Returns: The main biodb instance.

Method cloneInstance(): Clones this entry.
Usage:
BiodbEntry$cloneInstance(db.class = NULL)
Arguments:
db.class The database class (the Biodb database ID) of the clone. By setting this parameter, you can specify a different database for the clone, so you may clone an entry into another database if you wish. By default the class of the clone will be the same as the original entry.
Returns: The clone, as a new BiodbEntry instance.

Method getId(): Gets the entry ID.
Usage:
BiodbEntry$getId()
Returns: the entry ID, which is the value if the accession field.

Method isNew(): Tests if this entry is new.
Usage:
BiodbEntry$isNew()
Returns: TRUE if this entry was newly created, FALSE otherwise.

Method getDbClass(): Gets the ID of the database associated with this entry.
Usage:
BiodbEntry$getDbClass()
Returns: The name of the database class associated with this entry.

Method setFieldValue(): Sets the value of a field. If the field is not already set for this entry, then the field will be created. See BiodbEntryFields for a list of possible fields in biodb.
Usage:
BiodbEntry$setFieldValue(field, value)
Arguments:
field The name of a field.
value The value to set.
Returns: Nothing.

Method appendFieldValue(): Appends a value to an existing field. If the field is not defined for this entry, then the field will be created and set to this value. Only fields with a cardinality greater than one can accept multiple values.
Usage:
BiodbEntry$appendFieldValue(field, value)
Arguments:
field The name of a field.
value The value to append.
**Method getFieldNames():** Gets a list of all fields defined for this entry.

*Usage:*

```
BiodbEntry$getFieldNames()
```

*Returns:*
A character vector containing all field names defined in this entry.

**Method hasField():** Tests if a field is defined in this entry.

*Usage:*

```
BiodbEntry$hasField(field)
```

*Arguments:*

- `field` The name of a field.

*Returns:*
TRUE if the specified field is defined in this entry, FALSE otherwise.

**Method removeField():** Removes the specified field from this entry.

*Usage:*

```
BiodbEntry$removeField(field)
```

*Arguments:*

- `field` The name of a field.

*Returns:*
Nothing.

**Method getFieldValue():** Gets the value of the specified field.

*Usage:*

```
BiodbEntry$getFieldValue(
  field,  
  compute = TRUE,  
  flatten = FALSE,  
  last = FALSE,  
  limit = 0,  
  withNa = TRUE,  
  duplicatedValues = TRUE
)
```

*Arguments:*

- `field` The name of a field.

  *compute* If set to TRUE and a field is not defined, try to compute it using internal defined computing rules. If set to FALSE, let the field undefined.

  *flatten* If set to TRUE and a field’s value is a vector of more than one element, then export the field’s value as a single string composed of the field’s value concatenated and separated by the character defined in the 'multival.field.sep' config key. If set to FALSE or the field contains only one value, changes nothing.

  *last* If set to TRUE and a field’s value is a vector of more than one element, then export only the last value. If set to FALSE, changes nothing.

  *limit* The maximum number of values to get in case the field contains more than one value.

  *withNa* If set to TRUE, keep NA values. Otherwise filter out NAs values in vectors.
duplicatedValues  If set to TRUE, keeps duplicated values.

Returns: The value of the field.

Method getFieldsByType(): Gets the fields of this entry that have the specified type.

Usage:
BiodbEntry$getFieldsByType(type)

Arguments:
type  The type of fields to retrieve.

Returns: A character vector containing the field names.

Method getFieldsAsDataframe(): Converts this entry into a data frame.

Usage:
BiodbEntry$getFieldsAsDataframe(
  only.atomic = TRUE,
  compute = TRUE,
  fields = NULL,
  fields.type = NULL,
  flatten = TRUE,
  limit = 0,
  only.card.one = FALSE,
  own.id = TRUE,
  duplicate.rows = TRUE,
  sort = FALSE,
  virtualFields = FALSE
)

Arguments:
oonly.atomic  If set to TRUE, only export field’s values that are atomic
compute  If set to TRUE and a field is not defined, try to compute it using internal defined
computing rules. If set to FALSE, let the field undefined.
fields  Set to character vector of field names in order to restrict execution to this set of fields.
fields.type  If set, output all the fields of the specified type.
flatten  If set to TRUE and a field’s value is a vector of more than one element, then export
the field’s value as a single string composed of the field’s value concatenated and separated
by the character defined in the ‘multival.field.sep’ config key. If set to FALSE or the field
contains only one value, changes nothing.
limit  The maximum number of field values to write into new columns. Used for fields that
can contain more than one value.
only.card.one  If set to TRUE, only fields with a cardinality of one will be extracted.
own.id  If set to TRUE includes the database id field named <database_name>.id whose val-
ues are the same as the accession field.
duplicate.rows  If set to TRUE and merging field values with cardinality greater than one,
values will be duplicated.
sort  If set to TRUE sort the order of columns alphabetically, otherwise do not sort.
virtualFields  If set to TRUE includes also virtual fields, otherwise excludes them.
(i.e. of type vector).

Returns: A data frame containing the values of the fields.

Method `getFieldsAsJson()`: Converts this entry into a JSON string.

Usage:
BiodbEntry$getFieldsAsJson(compute = TRUE)

Arguments:
compute If set to TRUE and a field is not defined, try to compute it using internal defined computing rules. If set to FALSE, let the field undefined.

Returns: A JSON object from jsonlite package.

Method `parseContent()`: Parses content string and set values accordingly for this entry's fields. This method is called automatically and should be run directly by users.

Usage:
BiodbEntry$parseContent(content)

Arguments:
content A character string containing definition for an entry and obtained from a database. The format can be CSV, HTML, JSON, XML, or just text.

Returns: Nothing.

Method `computeFields()`: Computes fields. Look at all missing fields, and try to compute them using references to other databases, if a rule exists.

Usage:
BiodbEntry$computeFields(fields = NULL)

Arguments:
fields A list of fields to review for computing. By default all fields will be reviewed.

Returns: TRUE if at least one field was computed successfully, FALSE otherwise.

Method `print()`: Displays short information about this instance.

Usage:
BiodbEntry$print()

Returns: Nothing.

Method `getName()`: Gets a short text describing this entry instance.

Usage:
BiodbEntry$getName()

Returns: A character value concatenating the connector name with the entry accession.

Method `makesRefToEntry()`: Tests if this entry makes reference to another entry.

Usage:
BiodbEntry$makesRefToEntry(db, oid, recurse = FALSE)

Arguments:
db  Another database connector.
oid  A entry ID from database db.
recurse  If set to TRUE, the algorithm will follow all references to entries from other databases,
to see if it can establish an indirect link to oid.

Returns:  TRUE if this entry makes reference to the entry oid from database db, FALSE otherwise.

Method getField():  DEPRECATED. Gets the value of a field.

Usage:
BiodbEntry$getField(field)

Arguments:
field  The name of the field.

Returns:  The value of the field.

Method setField():  DEPRECATED. Sets the value of a field.

Usage:
BiodbEntry$setField(field, value)

Arguments:
field  The name of the field.
value  The new value of the field.

Returns:  Nothing.

Method getFieldClass():  Gets the class of a field.

Usage:
BiodbEntry$getFieldClass(field)

Arguments:
field  The name of the field.

Returns:  The class of the field.

Method getFieldDef():  Gets the definition of an entry field.

Usage:
BiodbEntry$getFieldDef(field)

Arguments:
field  The name of the field.

Returns:  An object BiodbEntryField which defines the field.

Method getFieldCardinality():  Gets the cardinality of the field.

Usage:
BiodbEntry$getFieldCardinality(field)

Arguments:
field  The name of the field.
Returns: The cardinality of the field.

Method fieldHasBasicClass(): DEPRECATED. Use BiodbEntryField::isVector() instead.

Usage:
BiodbEntry$fieldHasBasicClass(field)

Arguments:
field The name of the field.

Returns: TRUE if the field as a basic type (logical, numeric, character, ...).

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbEntry$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also
BiodbFactory, BiodbConn, BiodbEntryFields.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a compound CSV file database
chebi.tsv <- system.file("extdata", "chebi_extract.tsv", package='biodb')

# Get the connector of a compound database
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi.tsv)

# Get an entry:
entry <- conn$getEntry(conn$getEntryIds(1))

# Get all defined fields:
entry$getFieldNames()

# Get a field value:
accession <- entry$getFieldValue('accession')

# Test if a field is defined:
if (entry$hasField('name'))
  print(paste("The entry's name is ", entry$getFieldValue('name'), ".", sep=''))

# Export an entry as a data frame:
df <- entry$getFieldsAsDataframe()

# You can set or reset a field's value:
entry$setFieldValue('mass', 1893.1883)
# Terminate instance.
mybiodb$terminate()

---

**BiodbEntryField**  
A class for describing an entry field.

**Description**

A class for describing an entry field.

**Details**

This class is used by BiodbEntryFields for storing field characteristics, and returning them through the get() method. The constructor is not meant to be used, but for development purposes the constructor’s parameters are nevertheless described in the Fields section.

The constructor accepts the following arguments:

- **name**: The name of the field.
- **alias**: A character vector containing zero or more aliases for the field.
- **type**: A type describing the field. One of: "mass", "name" or "id". Optional.
- **class**: The class of the field. One of: "character", "integer", "double", "logical", "object", "data.frame".
- **card**: The cardinality of the field: either "1" or "*".
- **forbids.duplicates**: If set to TRUE, the field forbids duplicated values.
- **description**: A description of the field.
- **allowed.values**: The values authorized for the field.
- **lower.case**: Set to TRUE if you want all values set to the field to be forced to lower case.
- **case.insensitive**: Set to TRUE of you want the field to ignore case when checking a value.
- **computable.from**: The Biodb ID of a database, from which this field can be computed.
- **virtual**: If set to TRUE, the field is computed from other fields, and thus cannot be modified.
- **virtual.group.by.type**: For a virtual field of class data.frame, this indicates to gather all fields of the specified type to build a data frame.

**Methods**

**Public methods:**

- BiodbEntryField$new()
- BiodbEntryField$getName()
- BiodbEntryField$getType()
- BiodbEntryField$isOfType()
- BiodbEntryField$getDescription()
Method `new()`: New instance initializer. This class must not be instantiated directly. Instead, you access the instances of this class through the `BiodbEntryFields` instance that you get from the `BiodbMain` instance.

Usage:
```
BiodbEntryField$new(
  parent,
  name,
  alias = NA_character_,
  type = NA_character_,
```
BiodbEntryField

```r
class = c("character", "integer", "double", "logical", "object", "data.frame"),
card = c("one", "many"),
forbids.duplicates = FALSE,
description = NA_character_,
allowed.values = NULL,
lower.case = FALSE,
case.insensitive = FALSE,
computable.from = NULL,
virtual = FALSE,
virtual.group.by.type = NULL,
dataFrameGroup = NA_character_
)
```

**Arguments:**

- `parent` The BiodbEntryFields parent instance.
- `name` The field name.
- `alias` The field aliases as a character vector.
- `type` The field type.
- `class` The field class.
- `card` The field cardinality.
- `forbids.duplicates` Set to TRUE to forbid duplicated values.
- `description` The field description.
- `allowed.values` Restrict possible values to a set of allowed values.
- `lower.case` All values will be converted to lower case.
- `case.insensitive` Comparison will be made case insensitive for this field.
- `computable.from` A list of databases from which to compute automatically the value of this field.
- `virtual` Set to TRUE if this field is virtual.
- `virtual.group.by.type` In case of a virtual field, set the type of fields to group together into a data frame.
- `dataFrameGroup` The data frame group.

**Returns:** Nothing.

**Method** `getName()`: Gets the name.

**Usage:**

```r
BiodbEntryField$getName()
```

**Returns:** The name of this field.

**Method** `getType()`: Gets field's type.

**Usage:**

```r
BiodbEntryField$getType()
```

**Returns:** The type of this field.

**Method** `isOfType()`: Tests if this field is of the specified type.

**Usage:**

```r
BiodbEntryField$isOfType()
```
BiodbEntryField

`BiodbEntryField$нстype(type)`

**Arguments:**

`type` The type.

**Returns:** TRUE if this field is of the specified type, FALSE otherwise.

**Method** `getDescription()`: Get field's description.

**Usage:**

`BiodbEntryField$getDescription()`

**Returns:** The description of this field.

**Method** `hasAliases()`: Tests if this field has aliases.

**Usage:**

`BiodbEntryField$hasAliases()`

**Returns:** TRUE if this entry field defines aliases, FALSE otherwise.

**Method** `getAliases()`: Get aliases.

**Usage:**

`BiodbEntryField$getAliases()`

**Returns:** The list of aliases if some are defined, otherwise returns NULL.

**Method** `addAlias()`: Adds an alias to the list of aliases.

**Usage:**

`BiodbEntryField$addAlias(alias)`

**Arguments:**

`alias` The name of a valid alias.

**Returns:** Nothing.

**Method** `removeAlias()`: Removes an alias from the list of aliases.

**Usage:**

`BiodbEntryField$removeAlias(alias)`

**Arguments:**

`alias` The name of a valid alias.

**Returns:** Nothing.

**Method** `getAllNames()`: Gets all names.

**Usage:**

`BiodbEntryField$getAllNames()`

**Returns:** The list of all names (main name and aliases).

**Method** `isComputable()`: Tests if this field is computable from another field or another database.

**Usage:**

`BiodbEntryField$isComputable()`
**Returns:** TRUE if the field is computable, FALSE otherwise.

**Method** `getComputableFrom()`: Get the list of connectors that can be used to compute this field.

**Usage:**
BiodbEntryField$getComputableFrom()

**Returns:** A list of list objects. Each list object contains the name of the database from which the field is computable.

**Method** `getDataFrameGroup()`: Gets the defined data frame group, if any.

**Usage:**
BiodbEntryField$getDataFrameGroup()

**Returns:** The data frame group, as a character value.

**Method** `isComputableFrom()`: Gets the ID of the database from which this field can be computed.

**Usage:**
BiodbEntryField$isComputableFrom()

**Returns:** The list of databases where to find this field’s value.

**Method** `addComputableFrom()`: Adds a directive from the list of computableFrom.

**Usage:**
BiodbEntryField$addComputableFrom(directive)

**Arguments:**
directive A valid "computable from" directive.

**Returns:** Nothing.

**Method** `removeComputableFrom()`: Removes a directive from the list of computableFrom.

**Usage:**
BiodbEntryField$removeComputableFrom(directive)

**Arguments:**
directive A valid "computable from" directive.

**Returns:** Nothing.

**Method** `correctValue()`: Corrects a value so it is compatible with this field.

**Usage:**
BiodbEntryField$correctValue(value)

**Arguments:**
value A value.

**Returns:** The corrected value.

**Method** `isEnumerate()`: Tests if this field is an enumerate type (i.e.: it defines allowed values).

**Usage:**
BiodbEntryField$isEnumerate()

*Returns:* TRUE if this field defines some allowed values, FALSE otherwise.

**Method** isVirtual(): Tests if this field is a virtual field.

*Usage:*
BiodbEntryField$isVirtual()

*Returns:* TRUE if this field is virtual, FALSE otherwise.

**Method** getVirtualGroupByType(): Gets type for grouping field values when building a virtual data frame.

*Usage:*
BiodbEntryField$getVirtualGroupByType()

*Returns:* The type, as a character value.

**Method** getAllowedValues(): Gets allowed values.

*Usage:*
BiodbEntryField$getAllowedValues(value = NULL)

*Arguments:*
value If this parameter is set to particular allowed values, then the method returns a list of synonyms for this value (if any).

*Returns:* A character vector containing all allowed values.

**Method** addAllowedValue(): Adds an allowed value, as a synonym to already an existing value. Note that not all enumerate fields accept synonyms.

*Usage:*
BiodbEntryField$addAllowedValue(key, value)

*Arguments:*
key The key associated with the value (i.e.: the key is the main name of an allowed value).
value The new value to add.

*Returns:* Nothing.

**Method** checkValue(): Checks if a value is correct. Fails if value is incorrect.

*Usage:*
BiodbEntryField$checkValue(value)

*Arguments:*
value The value to check.

*Returns:* Nothing.

**Method** hasCardOne(): Tests if this field has a cardinality of one.

*Usage:*
BiodbEntryField$hasCardOne()

*Returns:* TRUE if the cardinality of this field is one, FALSE otherwise.
Method hasCardMany(): Tests if this field has a cardinality greater than one.
Usage:
BiodbEntryField$hasCardMany()
Returns: TRUE if the cardinality of this field is many, FALSE otherwise.

Method forbidsDuplicates(): Tests if this field forbids duplicates.
Usage:
BiodbEntryField$forbidsDuplicates()
Returns: TRUE if this field forbids duplicated values, FALSE otherwise.

Method isCaseInsensitive(): Tests if this field is case sensitive.
Usage:
BiodbEntryField$isCaseInsensitive()
Returns: TRUE if this field is case insensitive, FALSE otherwise.

Method getClass(): Gets the class of this field's value.
Usage:
BiodbEntryField$getClass()
Returns: class) of this field.

Method isObject(): Tests if this field's type is a class.
Usage:
BiodbEntryField$isObject()
Returns: TRUE if field's type is a class, FALSE otherwise.

Method isDataFrame(): Tests if this field's type is data.frame.
Usage:
BiodbEntryField$isDataFrame()
Returns: TRUE if field's type is data frame, FALSE otherwise.

Method isAtomic(): Tests if this field's type is an atomic type.
Usage:
BiodbEntryField$isAtomic()
Returns: character, integer, double or logical), FALSE otherwise.

Method isVector(): Tests if this field's type is a basic vector type.
Usage:
BiodbEntryField$isVector()
Returns: character, integer, double or logical), FALSE otherwise.

Method equals(): Compares this instance with another, and tests if they are equal.
Usage:
BiodbEntryField$equals(other, fail = FALSE)
Arguments:
other  Another BiodbEntryField instance.
fail   If set to TRUE, then throws error instead of returning FALSE.

Returns: TRUE if they are equal, FALSE otherwise.

Method updateWithValuesFrom(): Updates fields using values from other instance. The updated fields

Usage:
BiodbEntryField$updateWithValuesFrom(other)

Arguments:
other  Another BiodbEntryField instance.
are    'alias' and 'computable.from'. No values will be removed from those vectors. The new
        values will only be appended. This allows to extend an existing field inside a new connector
definition.

Returns: Nothing.

Method print(): Print informations about this entry.

Usage:
BiodbEntryField$print()

Returns: Nothing.

Method getCardinality(): Gets the field's cardinality.

Usage:
BiodbEntryField$getCardinality()

Returns: The cardinality: "one" or "many".

Method check(): Checks if essential values are defined.

Usage:
BiodbEntryField$check()

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbEntryField$clone(deep = FALSE)

Arguments:
deep   Whether to make a deep clone.

See Also

Parent class BiodbEntryFields.
Examples

```r
# Get the class of the InChI field.
mybiodb <- biodb::newInst()
inchi.field.class <- mybiodb$getEntryFields()$get('inchi')$getClass()

# Test the cardinality of a field
card.one <- mybiodb$getEntryFields()$get('name')$hasCardOne()
card.many <- mybiodb$getEntryFields()$get('name')$hasCardMany()

# Get the description of a field
desc <- mybiodb$getEntryFields()$get('inchi')$getDescription()

# Terminate instance.
mybiodb$terminate()
```

BiodbEntryFields

A class for handling description of all entry fields.

Description

A class for handling description of all entry fields.

Details

The unique instance of this class is handle by the `BiodbMain` class and accessed through the `getEntryFields()` method.

Methods

Public methods:
- `BiodbEntryFields$new()`
- `BiodbEntryFields$notifyCfgUpdate()`
- `BiodbEntryFields$isAlias()`
- `BiodbEntryFields$formatName()`
- `BiodbEntryFields$isDefined()`
- `BiodbEntryFields$checkIsDefined()`
- `BiodbEntryFields$getRealName()`
- `BiodbEntryFields$get()`
- `BiodbEntryFields$getFieldNames()`
- `BiodbEntryFields$getDatabaseIdField()`
- `BiodbEntryFields$print()`
- `BiodbEntryFields$define()`
- `BiodbEntryFields$terminate()`
• **BiodbEntryFields$clone()**

**Method new():** New instance initializer. No BiodbEntryFields instance must be created directly. Instead, call the getEntryFields() method of BiodbMain.

**Usage:**
BiodbEntryFields$new(parent)

**Arguments:**
parent The BiodbMain instance.

**Returns:** Nothing.

**Method notifyCfgUpdate():** Call back method called when a value is modified inside the configuration.

**Usage:**
BiodbEntryFields$notifyCfgUpdate(k, v)

**Arguments:**
k The config key name.
v The value associated with the key.

**Returns:** Nothing.

**Method isAlias():** Tests if names are aliases.

**Usage:**
BiodbEntryFields$isAlias(name)

**Arguments:**
name A character vector of names or aliases to test.

**Returns:** A logical vector, the same length as name, with TRUE for name values that are an alias of a field, and FALSE otherwise.

**Method formatName():** Format field name(s) for biodb format: set to lower case and remove dot or underscore characters depending on configuration.

**Usage:**
BiodbEntryFields$formatName(name)

**Arguments:**
name A character vector of names or aliases to test.

**Returns:** A character vector of formatted names.

**Method isDefined():** Tests if names are defined fields.

**Usage:**
BiodbEntryFields$isDefined(name)

**Arguments:**
name A character vector of names or aliases to test.

**Returns:** A logical vector, the same length as name, with TRUE for name values that correspond to a defined field.
**Method** `checkIsDefined()`: Tests if names are valid defined fields. Throws an error if any name does not correspond to a defined field.

**Usage:**

\[\text{BiodbEntryFields.checkIsDefined(name)}\]

**Arguments:**

name A character vector of names or aliases to test.

**Returns:** Nothing.

**Method** `getRealName()`: Gets the real names (main names) of fields. If some name is not found neither in aliases nor in real names, an error is thrown.

**Usage:**

\[\text{BiodbEntryFields.getRealName(name, fail = TRUE)}\]

**Arguments:**

name A character vector of names or aliases.

fail Fails if name is unknown.

**Returns:** A character vector, the same length as name, with the real field name for each name given (i.e. each alias is replaced with the real name).

**Method** `get()`: Gets a `BiodbEntryField` instance.

**Usage:**

\[\text{BiodbEntryFields.get(name, drop = TRUE)}\]

**Arguments:**

name A character vector of names or aliases.

drop If TRUE and only one name has been submitted, returns a single `BiodbEntryField` instance instead of a list.

**Returns:** A named list of `BiodbEntryField` instances. The names of the list are the real names of the entry fields, thus they may be different from the one provided inside the name argument.

**Method** `getFieldNames()`: Gets the main names of all fields.

**Usage:**

\[\text{BiodbEntryFields.getFieldNames(type = NULL, computable = NULL)}\]

**Arguments:**

type Set this parameter to a character vector in order to return only the names of the fields corresponding to the types specified.

computable If set to TRUE, returns only the names of computable fields. If set to FALSE, returns only the names of fields that are not computable.

**Returns:** A character vector containing all selected field names.

**Method** `getDatabaseIdField()`: Gets a database ID field.

**Usage:**

\[\text{BiodbEntryFields.getDatabaseIdField(database)}\]

**Arguments:**
database  The name (i.e.: Biodb ID) of a database.

Returns:
accession numbers) for this database.

Method print(): Prints information about the instance.

Usage:
BiodbEntryFields$print()

Returns: Nothing.

Method define(): Defines fields.

Usage:
BiodbEntryFields$define(def)

Arguments:
def  A named list of field definitions. The names of the list are the main names of the fields.

Returns: Nothing.

Method terminate(): Terminates the instance. This method will be called automatically by the
BiodbMain instance when you call

Usage:
BiodbEntryFields$terminate()

Arguments:
BiodbMain :terminate().

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbEntryFields$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.

See Also

BiodbMain and child class BiodbEntryField.

Examples

# Getting information about the accession field:
mybiodb <- biodb::newInst()
entry.field <- mybiodb$getEntryFields()$get('accession')

# Test if a name is an alias of a field
mybiodb$getEntryFields()$isAlias('genesymbols')

# Test if a name is associated with a defined field
mybiodb$getEntryFields()$isDefined('name')

# Terminate instance.
mybiodb$terminate()
BiodbFactory

A class for constructing biodb objects.

Description

A class for constructing biodb objects.

Details

This class is responsible for the creation of database connectors and database entries. You must go through the single instance of this class to create and get connectors, as well as instantiate entries. To get the single instance of this class, call the getFactory() method of class BiodbMain.

Methods

Public methods:

- BiodbFactory$new()
- BiodbFactory$getBiodb()
- BiodbFactory$createConn()
- BiodbFactory$connExists()
- BiodbFactory$deleteConn()
- BiodbFactory$deleteConnByClass()
- BiodbFactory$getAllConnectors()
- BiodbFactory$deleteAllConnectors()
- BiodbFactory$getConn()
- BiodbFactory$getEntry()
- BiodbFactory$createNewEntry()
- BiodbFactory$createEntryFromContent()
- BiodbFactory$getAllCacheEntries()
- BiodbFactory$deleteAllEntriesFromVolatileCache()
- BiodbFactory$deleteAllCacheEntries()
- BiodbFactory$print()
- BiodbFactory$clone()

Method new(): New instance initializer. The BiodbFactory class must not be instantiated directly. Instead, call the getFactory() method from the BiodbMain instance.

Usage:
BiodbFactory$new(bdb)

Arguments:
bdb  The BiodbMain instance.

Returns:  Nothing.
Method getBiodb(): Returns the biodb main class instance to which this object is attached.

Usage:
BiodbFactory$getBiodb()

Returns: The main biodb instance.

Method createConn(): Creates a connector to a database.

Usage:
BiodbFactory$createConn(db.class, url = NULL, token = NA_character_, fail.if.exists = TRUE, get.existing.conn = TRUE, conn.id = NULL, cache.id = NULL)

Arguments:
- db.class: The type of a database. The list of types can be obtained from the class BiodbDescsInfo.
- url: An URL to the database for which to create a connection. Each database connector is configured with a default URL, but some allow you to change it.
- token: A security access token for the database. Some database require such a token for all or some of their webservices. Usually you obtain the token through your account on the database website.
- fail.if.exists: If set to TRUE, the method will fail if a connector for
- get.existing.conn: This argument will be used only if fail.if.exists is set to FALSE and an identical connector already exists. If it set to TRUE, the existing connector instance will be returned, otherwise NULL will be returned.
- conn.id: If set, this identifier will be used for the new connector. An error will be raised in case another connector already exists with this identifier.
- cache.id: If set, this ID will be used as the cache ID for the new connector. An error will be raised in case another connector already exists with this cache identifier.

Returns: An instance of the requested connector class.

Method connExists(): Tests if a connector exists.

Usage:
BiodbFactory$connExists(conn.id)

Arguments:
- conn.id: A connector ID.

Returns: TRUE if a connector with this ID exists, FALSE otherwise.

Method deleteConn(): Deletes an existing connector.

Usage:
BiodbFactory$deleteConn(conn)
Arguments:

conn  A connector instance or a connector ID.

Returns: Nothing.

Method deleteConnByClass(): Deletes all existing connectors from a same class.

Usage:
BiodbFactory$deleteConnByClass(db.class)

Arguments:

db.class  The type of a database. All connectors of this database type will be deleted.

Returns: Nothing.

Method getAllConnectors(): Gets all connectors.

Usage:
BiodbFactorygetAllConnectors()

Returns: A list of all created connectors.

Method deleteAllConnectors(): Deletes all connectors.

Usage:
BiodbFactory$deleteAllConnectors()

Returns: Nothing.

Method getConn(): Gets an instantiated connector instance, or create a new one.

Usage:
BiodbFactory$getConn(conn.id, class = TRUE, create = TRUE)

Arguments:

conn.id  An existing connector ID.

class  If set to TRUE, and "conn.id" does not correspond to any instantiated connector, then interpret "conn.id" as a database class and looks for the first instantiated connector of that class.

create  If set to TRUE, and "class" is also set to TRUE, and no suitable instantiated connector was found, then creates a new connector instance of the class specified by "conn.id".

Returns: The connector instance corresponding to the connector ID or to the database ID submitted (if class "parameter" is set to TRUE).

Method getEntry(): Retrieves database entry objects from IDs (accession numbers), for the specified connector.

Usage:
BiodbFactory$getEntry(conn.id, id, drop = TRUE, no.null = FALSE, limit = 0)

Arguments:

conn.id  An existing connector ID.

id  A character vector containing database entry IDs (accession numbers).

drop  If set to TRUE and the list of entries contains only one element, then returns this element instead of the list. If set to FALSE, then returns always a list.
no.null Set to TRUE to remove NULL entries.
limit Set to a positive value to limit the number of entries returned.

Returns: A list of BiodbEntry objects, the same length as id. A NULL value is put into the list for each invalid ID of id.

Method createNewEntry(): Creates a new empty entry object from scratch. This entry is not stored in cache, and is directly attached to the factory instance instead of a particular connector.

Usage:
BiodbFactory$createNewEntry(db.class)

Arguments:
db.class A database ID.

Returns: A new BiodbEntry object.

Method createEntryFromContent(): Creates an entry instance from a content.

Usage:
BiodbFactory$createEntryFromContent(conn.id, content, drop = TRUE)

Arguments:
conn.id A valid BiodbConn identifier.
content A list or character vector of contents to parse to create the entries.
drop If set to TRUE

Returns: A list of new BiodbEntry objects.

Method getAllCacheEntries(): For a connector, gets all entries stored in the cache.

Usage:
BiodbFactory$getAllCacheEntries(conn.id)

Arguments:
conn.id A connector ID.

Returns: A list of BiodbEntry objects.

Method deleteAllEntriesFromVolatileCache(): Deletes all entries stored in the cache of the given connector. This method is deprecated, please use deleteAllEntriesFromVolatileCache() instead.

Usage:
BiodbFactory$deleteAllEntriesFromVolatileCache(conn.id)

Arguments:
conn.id A connector ID.

Returns: Nothing.

Method deleteAllCacheEntries(): Deletes all entries stored in the cache of the given connector.

Usage:
BiodbFactory$deleteAllCacheEntries(conn.id)
Arguments:
conn.id A connector ID.

Returns: Nothing.

Method `print()`: Prints information about this instance.

Usage:
BiodbFactory$print()

Returns: Nothing.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
BiodbFactory$clone(deep = FALSE)

Arguments:
deepl Whether to make a deep clone.

See Also

`BiodbMain`, `BiodbConn` and `BiodbEntry`.

Examples

# Create a BiodbMain instance with default settings:
mybiodb <- biodb::newInst()

# Obtain the factory instance:
factory <- mybiodb$getFactory()

# Get a compound CSV file database
chebi.tsv <- system.file("extdata", "chebi_extract.tsv", package='biodb')

# Create a connector:
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi.tsv)

# Get a database entry:
entry <- conn$getEntry(conn$getEntryIds(1))

# Terminate instance.
mybiodb$terminate()
Description

Entry class for content in HTML format.

Details

This is an abstract class for handling database entries whose content is in HTML format.

Super classes

\texttt{biodb::BiodbEntry} -> \texttt{biodb::BiodbXmlEntry} -> \texttt{BiodbHtmlEntry}

Methods

Public methods:

\begin{itemize}
\item \texttt{BiodbHtmlEntry\$new()}
\item \texttt{BiodbHtmlEntry\$clone()}
\end{itemize}

Method \texttt{new()}: New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:
\texttt{BiodbHtmlEntry\$new(...)}

Arguments:
... All parameters are passed to the super class initializer.

Returns: Nothing.

Method \texttt{clone()}: The objects of this class are cloneable with this method.

Usage:
\texttt{BiodbHtmlEntry\$clone(\texttt{deep = FALSE})}

Arguments:

\begin{itemize}
\item deep Whether to make a deep clone.
\end{itemize}

See Also

Super class \texttt{BiodbXmlEntry}.

Examples

\begin{verbatim}
# Create a concrete entry class inheriting from this class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbHtmlEntry)
\end{verbatim}
BiodbJsonEntry

Entry class for content in JSON format.

Description

This is an abstract class for handling database entries whose content is in JSON format.

Super class

biodb::BiodbEntry -> BiodbJsonEntry

Methods

Public methods:

• BiodbJsonEntry$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:

BiodbJsonEntry$clone(deep = FALSE)

Arguments:

depth Whether to make a deep clone.

See Also

Super class BiodbEntry.

Examples

# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbJsonEntry)

BiodbListEntry

Entry class for content in list format.

Description

This is an abstract class for handling database entries whose content is in list format.

Super class

biodb::BiodbEntry -> BiodbListEntry
Methods

Public methods:

• BiodbListEntry$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbListEntry$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.

See Also

Super class BiodbEntry.

Examples

# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbListEntry)

BiodbMain

The central class of the biodb package.

Description

The central class of the biodb package.
The central class of the biodb package.

Details

The main class of the biodb package. In order to use the biodb package, you need first to create an instance of this class.
The constructor takes a single argument, autoloadExtraPkgs, to enable (TRUE or default) or disable (FALSE) autoloading of extra biodb packages.

Once the instance is created, some other important classes (BiodbFactory, BiodbPersistentCache, BiodbConfig, ...) are instantiated (just once) and their instances are later accessible through get*() methods.
Methods

Public methods:

- `BiodbMain$new()`
- `BiodbMain$terminate()`
- `BiodbMain$loadDefinitions()`
- `BiodbMain$getConfig()`
- `BiodbMain$getPersistentCache()`
- `BiodbMain$getDbsInfo()`
- `BiodbMain$getEntryFields()`
- `BiodbMain$getFactory()`
- `BiodbMain$getRequestScheduler()`
- `BiodbMain$addObservers()`
- `BiodbMain$getObservers()`
- `BiodbMain$convertEntryIdFieldToDbClass()`
- `BiodbMain$entriesFieldToVctOrLst()`
- `BiodbMain$entriesToDataframe()`
- `BiodbMain$addColsToDataframe()`
- `BiodbMain$entriesToJson()`
- `BiodbMain$collapseRows()`
- `BiodbMain$entriesToSingleFieldValues()`
- `BiodbMain$entryIdsToSingleFieldValues()`
- `BiodbMain$computeFields()`
- `BiodbMain$saveEntriesAsJson()`
- `BiodbMain$copyDb()`
- `BiodbMain$fieldIsAtomic()`
- `BiodbMain$getFieldClass()`
- `BiodbMain$clone()`

Method `new()`:

New instance initializer. The BiodbMain must not be instantiated directly. Instead use the `newInst()` global method.

Usage:

`BiodbMain$new(autoloadExtraPkgs = NULL)`

Arguments:

`autoloadExtraPkgs` Set to `TRUE` to allow automatic loading of extension packages. Set to `FALSE` to forbid it. If left to `NULL`, the default, `autoload.extra.pkgs` configuration value will be used.

Returns: Nothing.

Method `terminate()`:

Closes `BiodbMain` instance. Call this method when you are done with your `BiodbMain` instance.
Usage:
BiodbMain$terminate()
Returns: Nothing.

Method loadDefinitions(): Loads databases and entry fields definitions from YAML file.

Usage:
BiodbMain$loadDefinitions(file, package = "biodb")

Arguments:
file  The path to a YAML file containing definitions for \codeBiodbMain (databases, fields or configuration keys).
package  The package to which belong the new definitions.

Returns: Nothing.

Method getConfig(): Returns the single instance of the \codeBiodbConfig class.

Usage:
BiodbMain$getConfig()

Returns: The instance of the \codeBiodbConfig class attached to this BiodbMain instance.

Method getPersistentCache(): Returns the single instance of the BiodbPersistentCache class.

Usage:
BiodbMain$getPersistentCache()

Returns: The instance of the BiodbPersistentCache class attached to this BiodbMain instance.

Method getDbsInfo(): Returns the single instance of the \codeBiodbDbsInfo class.

Usage:
BiodbMain$getDbsInfo()

Returns: The instance of the \codeBiodbDbsInfo class attached to this BiodbMain instance.

Method getEntryFields(): Returns the single instance of the \codeBiodbEntryFields class.

Usage:
BiodbMain$getEntryFields()

Returns: The instance of the \codeBiodbEntryFields class attached to this BiodbMain instance.

Method getFactory(): Returns the single instance of the \codeBiodbFactory class.

Usage:
BiodbMain$getFactory()

Returns: The instance of the \codeBiodbFactory class attached to this BiodbMain instance.

Method getRequestScheduler(): Returns the single instance of the \codeBiodbRequestScheduler class.

Usage:
BiodbMain.getRequestScheduler()
**Returns:** The instance of the `BiodbRequestScheduler` class attached to this BiodbMain instance.

**Method addObservers():** Adds new observers. Observers will be called each time an event occurs. This is the way used in biodb to get feedback about what is going inside biodb code.

**Usage:**
BiodbMain$addObservers(observers)

**Arguments:**
observers Either an object or a list of objects.

**Returns:** Nothing.

**Method getObservers():** Gets the list of registered observers.

**Usage:**
BiodbMain$getObservers()

**Returns:** The list of registered observers.

**Method convertEntryIdFieldToDbClass():** Gets the database class name corresponding to an entry ID field.

**Usage:**
BiodbMain$convertEntryIdFieldToDbClass(entry.id.field)

**Arguments:**
entry.id.field The name of an ID field. It must end with "id".

**Method entriesFieldToVctOrLst():** Extracts the value of a field from a list of entries. Returns either a vector or a list depending on the type of the field.

**Usage:**
BiodbMain$entriesFieldToVctOrLst(
  entries,
  field,
  flatten = FALSE,
  compute = TRUE,
  limit = 0,
  withNa = TRUE
)

**Arguments:**
entries A list of `BiodbEntry` instances.
field The name of a field.
flatten If set to `TRUE` and the field has a cardinality greater than one, then values be converted into a vector of class character in which each entry values are collapsed.
compute If set to `TRUE`, computable fields will be output.
limit The maximum number of values to retrieve for each entry. Set to 0 to get all values.
withNa If set to `TRUE`, keep NA values. Otherwise filter out NAs values in vectors.

**Returns:** A vector if the field is atomic or flatten is set to `TRUE`, otherwise a list.
Method entriesToDataframe(): Converts a list of entries or a list of list of entries (BiodbEntry objects) into a data frame.

Usage:
BiodbMain$entriesToDataframe(
  entries,
  only.atomic = TRUE,
  null.to.na = TRUE,
  compute = TRUE,
  fields = NULL,
  limit = 0,
  drop = FALSE,
  sort.cols = FALSE,
  flatten = TRUE,
  only.card.one = FALSE,
  own.id = TRUE,
  prefix = ""
)

Arguments:
entries A list of BiodbEntry instances or a list of list of BiodbEntry instances.
only.atomic If set to TRUE, output only atomic fields, i.e.: the fields whose value type is one of integer, numeric, logical or character.
null.to.na If set to TRUE, each NULL entry in the list is converted into a row of NA values.
compute If set to TRUE, computable fields will be output.
fields A character vector of field names to output. The data frame output will be restricted to this list of fields.
limit The maximum number of field values to write into new columns. Used for fields that can contain more than one value. Set it to 0 to get all values.
drop If set to TRUE and the resulting data frame has only one column, a vector will be output instead of data frame.
sort.cols Sort columns in alphabetical order.
flatten If set to TRUE, then each field with a cardinality greater than one, will be converted into a vector of class character whose values are collapsed.
only.card.one Output only fields whose cardinality is one.
own.id If set to TRUE includes the database id field named <database_name>.id whose values are the same as the accession field.
prefix Insert a prefix at the start of all field names.

Returns: A data frame containing the entries. Columns are named according to field names.

Method entryIdsToDataframe(): Construct a data frame using entry IDs and field values of the corresponding entries.

Usage:
BiodbMain$entryIdsToDataframe(
  ids,
  db,
BiodbMain

```r
fields = NULL,
limit = 3,
prefix = "",
own.id = FALSE
)

Arguments:
ids A character vector of entry IDs or a list of character vectors of entry IDs.
db The biodb database name for the entry IDs, or a connector ID, as a single character value.
fields A character vector containing entry fields to add.
limit The maximum number of field values to write into new columns. Used for fields that
can contain more than one value. Set it to 0 to get all values.
prefix Insert a prefix at the start of all field names.
own.id If set to TRUE includes the database id field named <database_name>.id whose val-
ues are the same as the accession field.
A data frame containing in columns the requested field values, with one entry per line, in the
same order than in ids vector.

Method addColsToDataframe(): Add values from a database to an existing data frame using a
column containing entry identifiers.

Usage:
BiodbMain$addColsToDataframe(x, id.col, db, fields, limit = 3, prefix = "")

Arguments:
x A data frame containing at least one column with Biodb entry IDs identified by the parameter
id.col.
id.col The name of the column containing IDs inside the input data frame.
db The biodb database name for the entry IDs, or a connector ID, as a single character value.
fields A character vector containing entry fields to add.
limit The maximum number of field values to write into new columns. Used for fields that
can contain more than one value. Set it to 0 to get all values.
prefix Insert a prefix at the start of all field names.

Returns: A data frame containing x and new columns appended for the fields requested.

Method entriesToJson(): Converts a list of `BiodbEntry` objects into JSON. Returns a
vector of characters.

Usage:
BiodbMain$entriesToJson(entries, compute = TRUE)

Arguments:
entries A list of `BiodbEntry` instances. It may contain NULL elements.
compute If set to TRUE, computable fields will added to JSON too.

Returns: A list of JSON strings, the same length as entries list.

Method collapseRows(): Collapses rows of a data frame, by looking for duplicated values
in the reference columns (parameter cols). The values contained in the reference columns are
supposed to be ordered inside the data frame, in the sense that all duplicated values are supposed
to directly follow the original values. For all rows containing duplicated values, we look at values
in all other columns and concatenate values in each column containing different values.
Usage:
BiodbMain$collapseRows(x, sep = "|", cols = 1L)

Arguments:
x A data frame.
sep The separator to use when concatenating values in collapsed rows.
cols The indices or the names of the columns used as reference.

Returns: A data frame, with rows collapsed.

Method entriesToSingleFieldValues(): Extract all values of a field from a list of entries.

Usage:
BiodbMain$entriesToSingleFieldValues(
  entries,
  field,
  sortOutput = FALSE,
  uniq = TRUE
)

Arguments:
entries A list of BiodbEntry objects.
field The field for which to extract values.
sortOutput Set to TRUE to sort the values.
uniq Set to TRUE to remove duplicates.

Returns: The values of the field as a vector.

Method entryIdsToSingleFieldValues(): Extract all values of a field from a list of entries.

Usage:
BiodbMain$entryIdsToSingleFieldValues(
  ids,
  db,
  field,
  sortOutput = FALSE,
  uniq = TRUE
)

Arguments:
ids A list of entry identifiers.
db The database ID or connector ID where to find the entries.
field The field for which to extract values.
sortOutput Set to TRUE to sort the values.
uniq Set to TRUE to remove duplicates.

Returns: The values of the field as a vector.

Method computeFields(): Computes missing fields in entries, for those fields that are comptable.

Usage:
BiodbMain$computeFields(entries)
Arguments:
entries A list of BiodbEntry instances. It may contain NULL elements.
Returns: Nothing.

Method saveEntriesAsJson(): Saves a list of entries in JSON format. Each entry will be saved in a separate file.
Usage:
BiodbMain$saveEntriesAsJson(entries, files, compute = TRUE)
Arguments:
entries A list of BiodbEntry instances. It may contain NULL elements.
files A character vector of file paths, the same length as entries list.
compute If set to TRUE, computable fields will be saved too.
Returns: Nothing.

Method copyDb(): Copies all entries of a database into another database. The connector of the destination database must be editable.
Usage:
BiodbMain$copyDb(conn.from, conn.to, limit = 0)
Arguments:
conn.from The connector of the source database to copy.
conn.to The connector of the destination database.
limit The number of entries of the source database to copy. If set to NULL, copy the whole database.
Returns: Nothing.

Method print(): Prints object information.
Usage:
BiodbMain$print()
Returns: Nothing.

Method fieldIsAtomic(): DEPRECATED method to test if a field is an atomic field. The new method is BiodbEntryField :isVector().
Usage:
BiodbMain$fieldIsAtomic(field)
Arguments:
field The name of the field.
Returns: TRUE if the field's value is atomic.

Method getClass(): DEPRECATED method to get the class of a field. The new method is BiodbMain :getEntryFields()$get(field)$getClass().
Usage:
BiodbMain$getFieldClass(field)

*Arguments:*
field  The name of the field.

*Returns:*  The class of the field.

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*
BiodbMain$clone(deep = FALSE)

*Arguments:*
deep  Whether to make a deep clone.

**See Also**
BiodbFactory, BiodbPersistentCache, BiodbConfig, BiodbEntryFields, BiodbDbsInfo.

**Examples**

# Create an instance:
mybiodb <- biodb::newInst()

# Get the factory instance
fact <- mybiodb$getFactory()

# Terminate instance.
mybiodb$terminate()
mybiodb <- NULL

---

**BiodbPersistentCache**  *The abstract class for handling file caching.*

**Description**
The abstract class for handling file caching.

**Details**
This abstract class is the mother class of concrete classes that manage cache systems for saving downloaded files and request results.

It is designed for internal use, but you can still access some of the read-only methods if you wish.
Methods

Public methods:

- `BiodbPersistentCache$new()`
- `BiodbPersistentCache$isReadable()`
- `BiodbPersistentCache$isWritable()`
- `BiodbPersistentCache$getDir()`
- `BiodbPersistentCache$getFolderPath()`
- `BiodbPersistentCache$folderExists()`
- `BiodbPersistentCache$getPath()`
- `BiodbPersistentCache$filesExist()`
- `BiodbPersistentCache$fileExist()`
- `BiodbPersistentCache$fileExists()`
- `BiodbPersistentCache$markerExist()`
- `BiodbPersistentCache$markerExists()`
- `BiodbPersistentCache$setMarker()`
- `BiodbPersistentCache$getTmpFolderPath()`
- `BiodbPersistentCache$getUsedCacheIds()`
- `BiodbPersistentCache$loadFileContent()`
- `BiodbPersistentCache$saveContentToFile()`
- `BiodbPersistentCache$addFilesToCache()`
- `BiodbPersistentCache$copyFilesIntoCache()`
- `BiodbPersistentCache$moveFilesIntoCache()`
- `BiodbPersistentCache$erase()`
- `BiodbPersistentCache$deleteFile()`
- `BiodbPersistentCache$deleteAllFiles()`
- `BiodbPersistentCache$deleteFiles()`
- `BiodbPersistentCache$listFiles()`
- `BiodbPersistentCache$print()`
- `BiodbPersistentCache$enabled()`
- `BiodbPersistentCache$enable()`
- `BiodbPersistentCache$disable()`
- `BiodbPersistentCache$clone()`

Method `new()`: New instance initializer. Persistent cache objects must not be created directly. Instead, access the cache instance through the BiodbMain instance using the getPersistentCache() method.

Usage:
`BiodbPersistentCache$new(cfg, bdb = NULL)`

Arguments:
- `cfg` An instance of the BiodbConfig class.
- `bdb` An instance of the BiodbMain class.

Returns: Nothing.
Method `isReadable()`: Checks if the cache system is readable.

Usage:
BiodbPersistentCache$`isReadable`(conn = NULL)

Arguments:
c`conn` If not `NULL`, checks if the cache system is readable for this particular connector.

Returns: `TRUE` if the cache system is readable, `FALSE` otherwise.

Method `isWritable()`: Checks if the cache system is writable.

Usage:
BiodbPersistentCache$`isWritable`(conn = NULL)

Arguments:
c`conn` If not `NULL`, checks if the cache system is writable for this particular connector.

Returns: `TRUE` if the cache system is writable, `FALSE` otherwise.

Method `getDir()`: Gets the path to the persistent cache folder.

Usage:
BiodbPersistentCache$`getDir()`

Returns: The path to the cache folder as a character value.

Method `getFolderPath()`: Gets path to the cache system sub-folder dedicated to this cache ID.

Usage:
BiodbPersistentCache$`getFolderPath`(cache.id, create = TRUE, fail = FALSE)

Arguments:
cache.id The cache ID to use.
ccreate If set to `TRUE` and the folder does not exist, creates it.
cfail If set to `TRUE`, throws a warning if the folder does not exist.

Returns: A string containing the path to the folder.

Method `folderExists()`: Tests if a cache folder exists for this cache ID.

Usage:
BiodbPersistentCache$`folderExists`(cache.id)

Arguments:
cache.id The cache ID to use.

Returns: `TRUE` if a cache folder exists.

Method `getFilePath()`: Gets path of file in cache system.

Usage:
BiodbPersistentCache$`getFilePath`(cache.id, name, ext)

Arguments:
cache.id The cache ID to use.
cname A character vector containing file names.
ext  The extension of the files.

>Returns: A character vector, the same size as `codenames`, containing the paths to the files.

**Method** `filesExist()`: Tests if at least one cache file exist for the specified cache ID.

.Usage:
```
BiodbPersistentCache$filesExist(cache.id)
```

.Arguments:
- `cache.id` The cache ID to use.

>Returns: A single boolean value.

**Method** `fileExist()`: DEPRECATED. Use `fileExists()`.

.Usage:
```
BiodbPersistentCache$fileExist(cache.id, name, ext)
```

.Arguments:
- `cache.id` The cache ID to use.
- `name` A character vector containing file names.
- `ext` The extension of the files, without the dot ("html", "xml", etc).

>Returns: A logical vector, the same size as `codenames`, with `TRUE` value if the file exists in the cache, or `FALSE` otherwise.

**Method** `fileExists()`: Tests if a particular file exist in the cache.

.Usage:
```
BiodbPersistentCache$fileExists(cache.id, name, ext)
```

.Arguments:
- `cache.id` The cache ID to use.
- `name` A character vector containing file names.
- `ext` The extension of the files, without the dot ("html", "xml", etc).

>Returns: A logical vector, the same size as `codenames`, with `TRUE` value if the file exists in the cache, or `FALSE` otherwise.

**Method** `markerExist()`: DEPRECATED. Use `markerExists()`.

.Usage:
```
BiodbPersistentCache$markerExist(cache.id, name)
```

.Arguments:
- `cache.id` The cache ID to use.
- `name` A character vector containing marker names.

>Returns: A logical vector, the same size as `codenames`, with `TRUE` value if the marker file exists in the cache, or `FALSE` otherwise.

**Method** `markerExists()`: Tests if markers exist in the cache. Markers are used, for instance, by biodb to remember that a downloaded zip file from a database has been extracted correctly.

.Usage:
BiodbPersistentCache$markerExists(cache.id, name)

**Arguments:**
- cache.id: The cache ID to use.
- name: A character vector containing marker names.

**Returns:** A logical vector, the same size as `name`, with `TRUE` value if the marker file exists in the cache, or `FALSE` otherwise.

**Method** setMarker(): Sets a marker.

**Usage:**
BiodbPersistentCache$setMarker(cache.id, name)

**Arguments:**
- cache.id: The cache ID to use.
- name: A character vector containing marker names.

**Returns:** Nothing.

**Method** getTmpFolderPath(): Gets path to the cache system temporary folder.

**Usage:**
BiodbPersistentCache$getTmpFolderPath()

**Returns:** A string containing the path to the folder.

**Method** getUsedCacheIds(): Returns a list of cache IDs actually used to store cache files.

**Usage:**
BiodbPersistentCache$getUsedCacheIds()

**Returns:** A character vector containing all the cache IDs actually used inside the cache system.

**Method** loadFileContent(): Loads content of files from the cache.

**Usage:**
BiodbPersistentCache$loadFileContent(
  cache.id,
  name,
  ext,
  output.vector = FALSE
)

**Arguments:**
- cache.id: The cache ID to use.
- name: A character vector containing file names.
- ext: The extension of the files.
- output.vector: If set to `TRUE`, force output to be a `vector` instead of a `list`. Where the list contains a `NULL`, the `vector` will contain an `NA` value.

**Returns:** A list (or a vector if `output.vector` is set to `TRUE`), the same size as `name`, containing the contents of the files. If some file does not exist, a `NULL` value is inserted inside the list.
**Method** `saveContentToFile()`: Saves content to files into the cache.

*Usage:*

```r
BiodbPersistentCache$saveContentToFile(content, cache.id, name, ext)
```

*Arguments:*

- `content`: A list or a character vector containing the contents of the files. It must have the same length as `codename`.
- `cache.id`: The cache ID to use.
- `name`: A character vector containing file names.
- `ext`: The extension of the files.

*Returns:* Nothing.

**Method** `addFilesToCache()`: Adds existing files into the cache.

*Usage:*

```r
BiodbPersistentCache$addFilesToCache(src.file.paths, cache.id, name, ext, action = c("copy", "move")
```

*Arguments:*

- `src.file.paths`: The current paths of the source files, as a character vector.
- `cache.id`: The cache ID to use.
- `name`: A character vector containing file names.
- `ext`: The extension of the files.
- `action`: Specifies if files have to be moved or copied into the cache.

*Returns:* Nothing.

**Method** `copyFilesIntoCache()`: Copies existing files into the cache.

*Usage:*

```r
BiodbPersistentCache$copyFilesIntoCache(src.file.paths, cache.id, name, ext)
```

*Arguments:*

- `src.file.paths`: The current paths of the source files, as a character vector.
- `cache.id`: The cache ID to use.
- `name`: A character vector containing file names.
- `ext`: The extension of the files.

*Returns:* Nothing.

**Method** `moveFilesIntoCache()`: Moves existing files into the cache.

*Usage:*

```r
BiodbPersistentCache$moveFilesIntoCache(src.file.paths, cache.id, name, ext)
```

*Arguments:*
src.file.paths  The current paths of the source files, as a character vector.
cache.id  The cache ID to use.
nname  A character vector containing file names.
ext  The extension of the files.

Returns:  Nothing.

Method erase(): Erases the whole cache.

Usage:
BiodbPersistentCache$erase()

Returns:  Nothing.

Method deleteFile(): Deletes a list of files inside the cache system.

Usage:
BiodbPersistentCache$deleteFile(cache.id, name, ext)

Arguments:
cache.id  The cache ID to use.
nname  A character vector containing file names.
ext  The extension of the files, without the dot ("html", "xml", etc).

Returns:  Nothing.

Method deleteAllFiles(): Deletes, in the cache system, all files associated with this cache ID.

Usage:
BiodbPersistentCache$deleteAllFiles(cache.id, fail = FALSE, prefix = FALSE)

Arguments:
cache.id  The cache ID to use.
fail  If set to TRUE, a warning will be emitted if no cache files exist for this cache ID.
prefix  DEPRECATED If set to TRUE, use cache.id as a prefix, deleting all files whose cache.id starts with this prefix.

Returns:  Nothing.

Method deleteFiles(): Deletes all files with the specific extension of the cache ID in the cache system.

Usage:
BiodbPersistentCache$deleteFiles(cache.id, ext)

Arguments:
cache.id  The cache ID to use.
ext  The extension of the files, without the dot ("html", "xml", etc). Only files having this extension will be deleted.

Returns:  Nothing.

Method listFiles(): Lists files present in the cache system.
Usage:
BiodbPersistentCache$listFiles(
  cache.id,
  ext = NULL,
  extract.name = FALSE,
  full.path = FALSE
)

Arguments:
cache.id The cache ID to use.
ext The extension of the files, without the dot ("html", "xml", etc).
extract.name If set to `codeTRUE`, instead of returning the file paths, returns the list of names
  used to construct the file name: [cache_folder]/[cache.id]/[name].[ext].
full.path If set to `codeTRUE`, returns full path for files.

Returns: The files of found files, or the names of the files if `codeextract.name` is set to `codeTRUE`.

Method `print()`: Displays information about this object.

Usage:
BiodbPersistentCache$print()

Method `enabled()`: DEPRECATED method. Use now `codeBiodbConfig :isEnabled('cache.system')`.

Usage:
BiodbPersistentCache$enabled()

Method `enable()`: DEPRECATED method. Use now `codeBiodbConfig :enable('cache.system')`.

Usage:
BiodbPersistentCache$enable()

Method `disable()`: DEPRECATED method. Use now `codeBiodbConfig :disable('cache.system')`.

Usage:
BiodbPersistentCache$disable()

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
BiodbPersistentCache$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.

See Also
BiodbMain, BiodbBiocPersistentCache, BiodbBiocPersistentCache.
**Examples**

```r
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a compound CSV file database
chebi.tsv <- system.file("extdata", "chebi_extract.tsv", package='biodb')

# Get a connector instance:
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi.tsv)

# Get all entries
entries <- conn$getEntry(conn$getEntryIds())

# Get the cache instance:
cache <- mybiodb$getPersistentCache()

# Get list of files inside the cache:
files <- cache$listFiles(conn$getCacheId())

# Delete files inside the cache:
cache$deleteAllFiles(conn$getCacheId())

# Terminate instance.
mybiodb$terminate()
```

---

**BiodbRequest**  
*Class Request.*

**Description**

Class Request.

Class Request.

**Details**

This class represents a Request object that can be used with the Request Scheduler.

**Methods**

**Public methods:**
- `BiodbRequest$new()`
- `BiodbRequest$setConn()`
- `BiodbRequest$getConn()`
- `BiodbRequest$url()`
- `BiodbRequest$getMethod()`
- `BiodbRequest$encoding()`
Method `new()`: Initializer.

Usage:
```r
BiodbRequest$new(
  url,
  method = c("get", "post"),
  header = character(),
  body = character(),
  encoding = integer(),
  conn = NULL
)
```

Arguments:
- `url` A `BiodbUrl` object.
- `method` HTTP method. Either "get" or "post".
- `header` The header.
- `body` The body.
- `encoding` The encoding to use.
- `conn` A valid `BiodbConn` instance for which this request is built.

Returns: Nothing.

Method `setConn()`: Sets the associated connector (usually the connector that created this request).

Usage:
```r
BiodbRequest$setConn(conn)
```

Arguments:
- `conn` A valid `BiodbConn` object.

Returns: Nothing.

Method `getConn()`: gets the associated connector (usually the connector that created this request).

Usage:
```r
BiodbRequest$getConn()
```

Returns: The associated connector as a `BiodbConn` object.

Method `getUrl()`: Gets the URL.

Usage:
BiodbRequest$getUrl()

*Returns:* The URL as a BiodbUrl object.

**Method** getMethod(): Gets the method.

*Usage:*

BiodbRequest$getMethod()

*Returns:* The method as a character value.

**Method** getEncoding(): Gets the encoding.

*Usage:*

BiodbRequest$getEncoding()

*Returns:* The encoding.

**Method** getCurlOptions(): Gets the options object to pass to cURL library.

*Usage:*

BiodbRequest$getCurlOptions(useragent)

*Arguments:* useragent The user agent as a character value.

*Returns:* An RCurl options object.

**Method** getUniqueKey(): Gets a unique key to identify this request. The key is an MD5 sum computed from the string representation of this request.

*Usage:*

BiodbRequest$getUniqueKey()

*Returns:* A unique key as an MD5 sum.

**Method** getHeaderAsString(): Gets the HTTP header as a string, concatenating all its information into a single string.

*Usage:*

BiodbRequest$getHeaderAsString()

*Returns:* The header as a single character value.

**Method** getBody(): Gets the body.

*Usage:*

BiodbRequest$getBody()

*Returns:* The body as a character value.

**Method** print(): Displays information about this instance.

*Usage:*

BiodbRequest$print()

*Returns:* self as invisible.

**Method** toString(): Gets a string representation of this instance.
BiodbRequestScheduler

Usage:
BiodbRequest$toString()

Returns: A single string giving a representation of this instance.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbRequest$clone(deep = FALSE)

Arguments:
deepe Whether to make a deep clone.

See Also

BiodbRequestScheduler, BiodbUrl.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Create a request object
u <- 'https://www.ebi.ac.uk/webservices/chebi/2.0/test/getCompleteEntity'
url <- BiodbUrl$new(url=u)
url$setParam('chebiId', 15440)
request <- BiodbRequest$new(method='get', url=url)

# Send request
mybiodb$getRequestScheduler()$sendRequest(request)

# Terminate instance.
mybiodb$terminate()

BiodbRequestScheduler  Class for handling requests.

Description

Class for handling requests.

Class for handling requests.

Details

This class handles GET and POST requests, as well as file downloading. Each remote database connection instance creates an instance of BiodbRequestScheduler for handling database connection. A timer is used to schedule connections, and avoid sending too much requests to the database. This class is not meant to be used directly by the library user. See section Fields for a list of the constructor’s parameters.
Methods

Public methods:

• BioDbRequestScheduler$new()
• BioDbRequestScheduler$sendSoapRequest()
• BioDbRequestScheduler$sendRequest()
• BioDbRequestScheduler$downloadFile()
• BioDbRequestScheduler$notifyConnUrlsUpdated()
• BioDbRequestScheduler$notifyConnSchedulerFrequencyUpdated()
• BioDbRequestScheduler$getUrlString()
• BioDbRequestScheduler$getUrl()
• BioDbRequestScheduler$findRule()
• BioDbRequestScheduler$getConnectorRules()
• BioDbRequestScheduler$registerConnector()
• BioDbRequestScheduler$unregisterConnector()
• BioDbRequestScheduler$getAllRules()
• BioDbRequestScheduler$clone()

Method new(): New instance initializer. BioDbRequestScheduler class must not be instantiated directly. Instead, use the getRequestScheduler() method from BioDbMain.

Usage:
BiodbRequestScheduler$new(bdb)

Arguments:
bdb The BioDbMain instance.

Returns: Nothing.

Method sendSoapRequest(): Sends a SOAP request to a URL. Returns the string result.

Usage:
BiodbRequestScheduler$sendSoapRequest(
    url,
    soap.request,
    soap.action = NA_character_,
    encoding = integer()
)

Arguments:
url The URL to access, as a character string.
soap.request The XML SOAP request to send, as a character string.
soap.action The SOAP action to contact, as a character string.
encoding The encoding to use.

Returns: The results returned by the contacted server, as a single string value.

Method sendRequest(): Sends a request, and returns content result.

Usage:
BiodbRequestScheduler$sendRequest(request, cache.read = TRUE)

*Arguments:*

- **request**: A BiodbRequest instance.
- **cache.read**: If set to TRUE, the cache system will be used. In case the same request has already been run and its results saved into the cache, then the request is not run again, the targeted server not contacted, and the results are directly loaded from the cache system.

*Returns*: The results returned by the contacted server, as a single string value.

**Method** `downloadFile()`: Downloads the content of a URL and save it into the specified destination file.

*Usage:*

BiodbRequestScheduler$downloadFile(url, dest.file)

*Arguments:*

- **url**: The URL to access, as a BiodbUrl object.
- **dest.file**: A path to a destination file.

*Returns*: Nothing.

**Method** `notifyConnUrlsUpdated()`: Call back function called when connector URLs are changed.

*Usage:*

BiodbRequestScheduler$notifyConnUrlsUpdated(conn)

*Arguments:*

- **conn**: The connector instance for which the URLs were changed.

*Returns*: Nothing.

**Method** `notifyConnSchedulerFrequencyUpdated()`: Call back function called when connector T and N parameters (frequency) are changed.

*Usage:*

BiodbRequestScheduler$notifyConnSchedulerFrequencyUpdated(conn)

*Arguments:*

- **conn**: The connector instance for which the frequency were changed.

*Returns*: Nothing.

**Method** `getUrlString()`: Builds a URL object, using a base URL and parameters to be passed.

*Usage:*

BiodbRequestScheduler$getUrlString(url, params = list())

*Arguments:*

- **url**: A URL string.
- **params**: A list of URL parameters.

*Returns*: A BiodUrl object.

**Method** `getUrl()`: Sends a request and get the result.
Usage:

BiodbRequestScheduler$getUrl(
  url,
  params = list(),
  method = c("get", "post"),
  header = character(),
  body = character(),
  encoding = integer()
)

Arguments:

url    A URL string.
params A list of URL parameters.
method The method to use. Either 'get' or 'post'.
header The header to send.
body   The body to send.
encoding The encoding to use.

Returns: The results of the request.

Method findRule(): Searches for a rule by host name.

Usage:

BiodbRequestScheduler$findRule(url, create = TRUE)

Arguments:

url The host URL.
create Sets to TRUE to create a rule when none exists.

Returns: A BiodbRequestSchedulerRule object.

Method getConnectorRules(): Gets the rules associates with a connector.

Usage:

BiodbRequestScheduler$getConnectorRules(conn)

Arguments:

conn A valid connector object.

Returns: A list of rules.

Method registerConnector(): Registers a new connector with the scheduler.

Usage:

BiodbRequestScheduler$registerConnector(conn)

Arguments:

conn A valid connector object.

Returns: Nothing.

Method unregisterConnector(): Unregisters a connector from this scheduler.

Usage:
BiodbRequestScheduler$unregisterConnector(conn)

**Arguments:**
- conn  A valid connector object.

**Returns:** Nothing.

**Method getAllRules():** Gets all defined rules.

**Usage:**
BiodbRequestScheduler$getAllRules()

**Returns:** The list of all rules.

**Method clone():** The objects of this class are cloneable with this method.

**Usage:**
BiodbRequestScheduler$clone(deep = FALSE)

**Arguments:**
- deep  Whether to make a deep clone.

**See Also**
BiodbRequestSchedulerRule.

**Examples**

```r
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get the scheduler
sched <- mybiodb$getRequestScheduler()

# Create a request object
u <- 'https://www.ebi.ac.uk/webservices/chebi/2.0/test/getCompleteEntity'
url <- BiodbUrl$new(url=u)
url$setParam('chebiId', 15440)
request <- BiodbRequest$new(method='get', url=url)

# Send request
sched$sendRequest(request)

# Terminate instance.
mybiodb$terminate()
mybiodb <- NULL
```
BiodbRequestSchedulerRule

Scheduler rule class.

Description

Scheduler rule class.
Scheduler rule class.

Details

This class represents a rule for the request scheduler.

Methods

Public methods:

- BiodbRequestSchedulerRule$new()
- BiodbRequestSchedulerRule$getHost()
- BiodbRequestSchedulerRule$getN()
- BiodbRequestSchedulerRule$getT()
- BiodbRequestSchedulerRule$setFrequency()
- BiodbRequestSchedulerRule$getConnectors()
- BiodbRequestSchedulerRule$addConnector()
- BiodbRequestSchedulerRule$removeConnector()
- BiodbRequestSchedulerRule$print()
- BiodbRequestSchedulerRule$waitAsNeeded()
- BiodbRequestSchedulerRule$recomputeFrequency()
- BiodbRequestSchedulerRule$computeSleepTime()
- BiodbRequestSchedulerRule$storeCurrentTime()
- BiodbRequestSchedulerRule$clone()

Method new(): Initializer.

Usage:
BiodbRequestSchedulerRule$new(host, conn = NULL)

Arguments:
host  The web host for which this rules is applicable.
conn  The connector instance that is concerned by this rule.

Returns: Nothing.

Method getHost(): Gets host.

Usage:
BiodbRequestSchedulerRule$getHost()
BiodbRequestSchedulerRule

Returns: Returns the host.

Method getN(): Gets N value. The number of connections allowed during a period of T seconds.
Usage:
BiodbRequestSchedulerRule\$getN()
Returns: Returns N as an integer.

Method getT(): Gets T value. The number of seconds during which N connections are allowed.
Usage:
BiodbRequestSchedulerRule\$getT()
Returns: Returns T as a numeric.

Method setFrequency(): Sets both N and T.
Usage:
BiodbRequestSchedulerRule\$setFrequency(n, t)
Arguments:
n The number of connections allowed during a period of t seconds, as an integer.
t The number of seconds during which n connections are allowed, as a numeric value.
Returns: Nothing.

Method getConnectors(): Gets connectors associated with this rule.
Usage:
BiodbRequestSchedulerRule\$getConnectors()
Returns: A list of BiodbConn objects.

Method addConnector(): Associate a connector with this rule.
Usage:
BiodbRequestSchedulerRule\$addConnector(conn)
Arguments:
conn A BiodbConn object.
Returns: Nothing.

Method removeConnector(): Disassociate a connector from this rule.
Usage:
BiodbRequestSchedulerRule\$removeConnector(conn)
Arguments:
conn A BiodbConn instance.
Returns: Nothing.

Method print(): Displays information about this instance.
Usage:
BiodbRequestSchedulerRule\$print()
BiodbRequestSchedulerRule

Returns: Nothing.

Method `waitAsNeeded()`: Wait (sleep) until a new request is allowed.

Usage:
BiodbRequestSchedulerRule$waitAsNeeded()

Returns: Nothing.

Method `recomputeFrequency()`: Recompute frequency from submitted N and T values.

Usage:
BiodbRequestSchedulerRule$recomputeFrequency()

Returns: Nothing.

Method `computeSleepTime()`: Compute the needed sleep time to wait until a new request is allowed, starting from the submitted time.

Usage:
BiodbRequestSchedulerRule$computeSleepTime(cur.time = Sys.time())

Arguments:
cur.time  Time from which to compute needed sleep time.

Returns: The needed sleep time in seconds.

Method `storeCurrentTime()`: Stores the current time.

Usage:
BiodbRequestSchedulerRule$storeCurrentTime(cur.time = Sys.time())

Arguments:
cur.time  The current time.

Returns: Nothing.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
BiodbRequestSchedulerRule$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.

See Also
BiodbRequestScheduler.
Description

Entry class for content in SDF format.
Entry class for content in SDF format.

Details

This is an abstract class for handling database entries whose content is in SDF format.

Super classes

biodb::BiodbEntry -> biodb::BiodbTxtEntry -> BiodbSdfEntry

Methods

Public methods:

• BiodbSdfEntry$new()
• BiodbSdfEntry$clone()

Method new(): New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:
BiodbSdfEntry$new(...)

Arguments:
... All parameters are passed to the super class initializer.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbSdfEntry$clone(deep = FALSE)

Arguments:
dead Whether to make a deep clone.

See Also

Super class BiodbTxtEntry.

Examples

# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbSdfEntry)
BiodbSqlBinaryOp

This class represents an SQL binary operator.

Description

This class represents an SQL binary operator.

Super class

`biodb::BiodbSqlExpr` -> BiodbSqlBinaryOp

Methods

Public methods:

- `BiodbSqlBinaryOp$new()`
- `BiodbSqlBinaryOp$toString()`
- `BiodbSqlBinaryOp$clone()`

Method `new()`: Initializer.

*Usage:*

```
BiodbSqlBinaryOp$new(lexpr, op, rexpr)
```

*Arguments:*

- `lexpr`: A BiodbSqlExpr instance for the left part.
- `op`: The binary operator, as a string.
- `rexpr`: A BiodbSqlExpr instance for the right part.

*Returns:*

Nothing.

Method `toString()`: Converts into a string.

*Usage:*

```
BiodbSqlBinaryOp$toString()
```

*Returns:*

A string containing the SQL expression.

Method `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
BiodbSqlBinaryOp$clone(deep = FALSE)
```

*Arguments:*

- `deep`: Whether to make a deep clone.
**BiodbSqlExpr**

The SQL Expression abstract class.

### Description

The SQL Expression abstract class.

### Details

This abstract class represents an SQL expression.

### Methods

**Public methods:**

- `BiodbSqlExpr$toString()`
- `BiodbSqlExpr$clone()`

**Method `toString()`**: Converts into a string.

**Usage:**

`BiodbSqlExpr$toString()`

**Returns**: A string containing the SQL expression.

**Method `clone()`**: The objects of this class are cloneable with this method.

**Usage:**

`BiodbSqlExpr$clone(deep = FALSE)`

**Arguments:**

depth Whether to make a deep clone.

---

**BiodbSqlField**

This class represents an SQL field.

### Description

This class represents an SQL field.

### Super class

```
biodb::BiodbSqlExpr -> BiodbSqlField
```
Methods

Public methods:

- `BiodbSqlField$new()`
- `BiodbSqlField$toString()`
- `BiodbSqlField$clone()`

Method `new()`: Initiator.

Usage:

```r
BiodbSqlField$new(table = NA_character_, field)
```

Arguments:

- `table` The table name.
- `field` The field name.

Returns: Nothing.

Method `toString()`: Converts into a string.

Usage:

```r
BiodbSqlField$toString()
```

Returns: A string containing the SQL expression.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```r
BiodbSqlField$clone(deep = FALSE)
```

Arguments:

- `deep` Whether to make a deep clone.

---

**BiodbSqlList**

*This class represents an SQL list.*

---

Description

This class represents an SQL list.

This class represents an SQL list.

Super class

```
biodb::BiodbSqlExpr -> BiodbSqlList
```
Methods

**Public methods:**

- `BiodbSqlList$new()`
- `BiodbSqlList$toString()`
- `BiodbSqlList$clone()`

**Method** `new()`: Initializer.

*Usage:*

```
BiodbSqlList$new(values)
```

*Arguments:*

- `values` The values of the list.

*Returns:*

Nothing.

**Method** `toString()`: Converts into a string.

*Usage:*

```
BiodbSqlList$toString()
```

*Returns:*

A string containing the SQL expression.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
BiodbSqlList$clone(deep = FALSE)
```

*Arguments:*

- `deep` Whether to make a deep clone.

---

**BiodbSqlLogicalOp**

This class represents an SQL logical operator.

---

**Description**

This class represents an SQL logical operator.

This class represents an SQL logical operator.

**Super class**

```
biodb::BiodbSqlExpr -> BiodbSqlLogicalOp
```
Methods

Public methods:

• `BiodbSqlLogicalOp$new()`
• `BiodbSqlLogicalOp$addExpr()`
• `BiodbSqlLogicalOp$toString()`
• `BiodbSqlLogicalOp$clone()`

Method `new()`: Initializer.

Usage:
BiodbSqlLogicalOp$new(op)

Arguments:
op  The logical operator, as a string.

Returns: Nothing.

Method `addExpr()`: Add an SQL expression to the logical operator.

Usage:
BiodbSqlLogicalOp$addExpr(expr)

Arguments:
expr  A BiodbSqlExpr instance.

Returns: Nothing.

Method `toString()`: Converts into a string.

Usage:
BiodbSqlLogicalOp$toString()

Returns:  A string containing the SQL expression.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
BiodbSqlLogicalOp$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.
BiodbSqlQuery

This class handles an SQL Query.

Description

This class handles an SQL Query.

Details

This class represents an SQL query. It is used internally to generate an SQL query string.

Methods

Public methods:

- BiodbSqlQuery$new()
- BiodbSqlQuery$setTable()
- BiodbSqlQuery$addField()
- BiodbSqlQuery$setDistinct()
- BiodbSqlQuery$setLimit()
- BiodbSqlQuery$addJoin()
- BiodbSqlQuery$setWhere()
- BiodbSqlQuery$getJoin()
- BiodbSqlQuery$getWhere()
- BiodbSqlQuery$getFields()
- BiodbSqlQuery$toString()
- BiodbSqlQuery$clone()

Method new(): Initializer.

Usage:
BiodbSqlQuery$new()

Returns: Nothing.

Method setTable(): Set the table.

Usage:
BiodbSqlQuery$setTable(table)

Arguments:

- table  The table name.

Returns: Nothing.

Method addField(): Set the fields.

Usage:
BiodbSqlQuery$addField(table = NULL, field)

Arguments:
table The table name.
field A field name.

Returns: Nothing.

Method setDistinct(): Set or unset distinct modifier.

Usage:
BiodbSqlQuery$setDistinct(distinct)

Arguments:
distinct Either TRUE or FALSE for setting or unsetting the distinct flag.

Returns: Nothing.

Method setLimit(): Set results limit.

Usage:
BiodbSqlQuery$setLimit(limit)

Arguments:
limit The limit to set, as an integer value.

Returns: Nothing.

Method addJoin(): Add a join.

Usage:
BiodbSqlQuery$addJoin(table1, field1, table2, field2)

Arguments:
table1 The first table.
field1 The field of the first table.
table2 The second table.
field2 The field of the second table.

Returns: Nothing.

Method setWhere(): Set the where clause.

Usage:
BiodbSqlQuery$setWhere(expr)

Arguments:
expr A BiodbSqlExpr representing the "where" clause.

Returns: Nothing.

Method getJoin(): Builds and returns the join expression.

Usage:
BiodbSqlQuery$getJoin()

Returns: A character vector representing the join expression.
**Method** `getWhere()`: Gets the where expression.

*Usage:*

`BiodbSqlQuery$getWhere()`

*Returns:* The `BiodbSqlExpr` instance representing the "where" clause.

**Method** `getFields()`: Gets the fields to retrieve.

*Usage:*

`BiodbSqlQuery$getFields()`

*Returns:* A string containing the list of fields to retrieve.

**Method** `toString()`: Generates the string representation of this query.

*Usage:*

`BiodbSqlQuery$toString()`

*Returns:* A string containing the full SQL query.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

`BiodbSqlQuery$clone(deep = FALSE)`

*Arguments:*

depth Whether to make a deep clone.

**See Also**

`BiodbRequestScheduler, BiodbRequest`

---

**BiodbSqlValue**

This class represents an SQL value.

**Description**

This class represents an SQL value.

**Super class**

`biodb::BiodbSqlExpr` -> `BiodbSqlValue`
Methods

Public methods:

- `BiodbSqlValue$new()`
- `BiodbSqlValue$toString()`
- `BiodbSqlValue$clone()`

Method `new()`: Initializer.

Usage:
`BiodbSqlValue$new(value)`

Arguments:
value The value.

Returns: Nothing.

Method `toString()`: Converts into a string.

Usage:
`BiodbSqlValue$toString()`

Returns: A string containing the SQL expression.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
`BiodbSqlValue$clone(deep = FALSE)`

Arguments:
deep Whether to make a deep clone.

-------

BiodbTestMsgAck A class for acknowledging messages during tests.

-------

Description

A class for acknowledging messages during tests.

Details

This observer is used to call a `testthat::expect_*()` method each time a message is received. This is used when running tests on Travis-CI, so Travis does not stop tests because no change is detected in output.
Methods

Public methods:

• BiodbTestMsgAck$\text{new}()  
• BiodbTestMsgAck$\text{notifyProgress}()  
• BiodbTestMsgAck$\text{clone}()


Usage:
BiodbTestMsgAck$\text{new}()

Returns: Nothing.

Method $\text{notifyProgress}()$: Call back method used to get progress advancement of a long process.

Usage:
BiodbTestMsgAck$\text{notifyProgress}(\text{what, index, total})

Arguments:
what  The reason as a character value.  
index  The index number representing the progress.  
total  The total number to reach for completing the process.

Returns: Nothing.

Method $\text{clone}()$: The objects of this class are cloneable with this method.

Usage:
BiodbTestMsgAck$\text{clone}(\text{deep} = \text{FALSE})

Arguments:
deep  Whether to make a deep clone.

Examples

# To use the acknowledger, set ack=TRUE when creating the Biodb test  
# instance:  
biodb <- biodb::createBiodbTestInstance(ack=TRUE)

# Terminate the BiodbMain instance  
biodb$\text{terminate}()
BiodbTxtEntry

Entry class for content in text format.

Description

Entry class for content in text format.
Entry class for content in text format.

Details

This is an abstract class for handling database entries whose content is in text format.

Super class

```
biodb::BiodbEntry -> BiodbTxtEntry
```

Methods

Public methods:

• `BiodbTxtEntry$new()`
• `BiodbTxtEntry$clone()`

Method `new()`: New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:

```
BiodbTxtEntry$new(...)
```

Arguments:

... All parameters are passed to the super class initializer.

Returns: Nothing.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
BiodbTxtEntry$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Super class `BiodbEntry`.

Examples

```
# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbTxtEntry)
```
BiodbUrl

Class URL

Description

This class represents a URL object that can be used in requests.

Details

This class represents a URL object that can be used in requests.

Methods

Public methods:

- BiodbUrl$new()
- BiodbUrl$getDomain()
- BiodbUrl$setUrl()
- BiodbUrl$setParam()
- BiodbUrl$print()
- BiodbUrl$toString()
- BiodbUrl$clone()

Method new(): Initializer.

Usage:
BiodbUrl$new(url = character(), params = character(), chompExtraSlashes = TRUE)

Arguments:
url  The URL to access, as a character vector.
params The list of parameters to append to this URL.
chompExtraSlashes If set to TRUE, then slashes at the end and the beginning of each element
of the url vector parameter will be removed before proper concatenation.

Returns: Nothing.

Method getDomain(): Gets the domain.

Usage:
BiodbUrl$getDomain()

Returns: The domain.

Method setUrl(): Sets the base URL string.

Usage:
BiodbUrl$setUrl(url)

Arguments:
url  The base URL string.

>Returns: Nothing.

**Method** `setParam()`: Sets a parameter.

>**Usage:**

`BiodbUrl$setParam(key, value)`

>**Arguments:**

key  The parameter name.
value  The value of the parameter.

>Returns: Nothing.

**Method** `print()`: Displays information about this instance.

>**Usage:**

`BiodbUrl$print()`

>Returns: self as invisible.

**Method** `toString()`: Gets the URL as a string representation.

>**Usage:**

`BiodbUrl$toString(encode = TRUE)`

>**Arguments:**

encode  If set to TRUE, then encodes the URL.

>Returns: The URL as a string, with all parameters and values set.

**Method** `clone()`: The objects of this class are cloneable with this method.

>**Usage:**

`BiodbUrl$clone(deep = FALSE)`

>**Arguments:**

deep  Whether to make a deep clone.

**See Also**

`BiodbRequestScheduler`, `BiodbRequest`.

**Examples**

```r
# Create a URL object
u <- c("https://www.uniprot.org", "uniprot")
p <- c(query="reviewed:yes+AND+organism:9606",
        columns='id,entry name,protein names',
        format="tab")
url <- BiodbUrl$new(url=u, params=p)
url$toString()
```
BiodbXmlEntry

Entry class for content in XML format.

Description

Entry class for content in XML format.
Entry class for content in XML format.

Details

This is an abstract class for handling database entries whose content is in XML format.

Super class

biodb::BiodbEntry -> BiodbXmlEntry

Methods

Public methods:

• BiodbXmlEntry$new()
• BiodbXmlEntry$clone()

Method new(): New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:
BiodbXmlEntry$new(...)  

Arguments:
... All parameters are passed to the super class initializer.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
BiodbXmlEntry$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also

Super class BiodbEntry.

Examples

# Create a concrete entry class inheriting from CSV class:
MyEntry <- R6::R6Class("MyEntry", inherit=biodb::BiodbXmlEntry)
checkDeprecatedCacheFolders

*Check deprecated default cache folders.*

**Description**

Searches for a deprecated location of the default cache folder, and moves files to the new location if possible. Otherwise raises a warning.

**Usage**

`checkDeprecatedCacheFolders()`

**Value**

Nothing.

**Examples**

`biodb::checkDeprecatedCacheFolders()`

---

closeMatchPpm

*Close match PPM*

**Description**

Matches peaks between two spectra.

**Usage**

`closeMatchPpm(x, y, xidx, yidx, xolength, dppm, dmz)`

**Arguments**

- `x` sorted M/Z values (ascending order) of input spectrum (no NA).
- `y` sorted M/Z values (ascending order) of reference spectrum (no NA).
- `xidx` indices of the M/Z peaks of x, taken from the original spectrum ordered in decreasing intensity values.
- `yidx` indices of the M/Z peaks of y, taken from the original spectrum ordered in decreasing intensity values.
- `xolength` The length of the output.
- `dppm` The M/Z tolerance in PPM.
- `dmz` Minimum M/Z tolerance.
Value

A list of results.

---

**CompCsvFileConn**

*Compound CSV File connector class.*

---

**Description**

Compound CSV File connector class.

*Compound CSV File connector class.*

---

**Details**

This is the connector class for a Compound CSV file database.

---

**Super classes**

`biodb::BiodbConnBase` -> `biodb::BiodbConn` -> `biodb::CsvFileConn` -> `CompCsvFileConn`

---

**Methods**

**Public methods:**

- `CompCsvFileConn$new()`
- `CompCsvFileConn$clone()`

**Method** `$new()`: New instance initializer. Connector classes must not be instantiated directly. Instead, you must use the `createConn()` method of the factory class.

*Usage:*

`CompCsvFileConn$new(...)`

*Arguments:*

... All parameters are passed to the super class initializer.

*Returns:* Nothing.

**Method** `$clone()`: The objects of this class are cloneable with this method.

*Usage:*

`CompCsvFileConn$clone(deep = FALSE)`

*Arguments:*

`deep` Whether to make a deep clone.

---

**See Also**

Super class `CsvFileConn`. 
Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector:
chebi_file <- system.file("extdata", "chebi_extract.tsv", package="biodb")
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi_file)

# Get an entry
e <- conn$getEntry('')

# Terminate instance.
mybiodb$terminate()

CompCsvFileEntry  Compound CSV File entry class.

Description

Compound CSV File entry class.

Compound CSV File entry class.

Details

This is the entry class for Compound CSV file databases.

Super classes

`biodb::BiodbEntry` - `biodb::BiodbCsvEntry` - `CompCsvFileEntry`

Methods

Public methods:

- `CompCsvFileEntry$new()`
- `CompCsvFileEntry$clone()`

Method $new()$: New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:

CompCsvFileEntry$new(...)

Arguments:

... All parameters are passed to the super class initializer.

Returns: Nothing.

Method $clone()$: The objects of this class are cloneable with this method.
CompSqliteConn

Usage:
CompCsvFileEntry$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also
Super class BiodbCsvEntry.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector that inherits from CsvFileConn:
chebi_file <- system.file("extdata", "chebi_extract.tsv", package="biodb")
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi_file)

# Get an entry
e <- conn$getEntry('')

# Terminate instance.
mybiodb$terminate()

CompSqliteConn  Class for handling a Compound database in SQLite format.

Description
This is the connector class for a Compound database.

Super classes
biodb::BiodbConnBase -> biodb::BiodbConn -> biodb::SqliteConn -> CompSqliteConn

Methods

Public methods:
• CompSqliteConn$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:
CompSqliteConn$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.
See Also

Super class SQLiteConn.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector:
chebi_file <- system.file("extdata", "chebi_extract.sqlite", package="biodb")
conn <- mybiodb$getFactory()$createConn("comp.sqlite", url=chebi_file)

# Get an entry
e <- conn$getEntry("1018")

# Terminate instance.
mybiodb$terminate()

CompSqliteEntry

Compound SQLite entry class.

Description

This is the entry class for a Compound SQLite database.

Super classes

biodb::BiodbEntry -> biodb::BiodbListEntry -> CompSqliteEntry

Methods

Public methods:

• CompSqliteEntry$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:

CompSqliteEntry$clone(deep = FALSE)

Arguments:

deeplWhether to make a deep clone.

See Also

Super class BiodbListEntry.
**Examples**

```r
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get path to LCMS database example file
lcmsdb <- system.file("extdata", "chebi_extract.sqlite", package="biodb")

# Create a connector
conn <- mybiodb$ConnectionFactory()$createConn('comp.sqlite', url=lcmsdb)

# Get an entry
e <- conn$getEntry('34.pos.col12.0.78')

# Terminate instance.
mybiodb$terminate()
```

---

**connNameToClassPrefix**  
Convert connector name into class prefix.

**Description**

Converts the connector name into the class prefix (e.g.: "mass.csv.file" -> "MassCsvFile").

**Usage**

```r
connNameToClassPrefix(connName)
```

**Arguments**

- `connName`: A connector name (e.g.: "mass.csv.file").

**Value**

The corresponding class prefix (e.g.: "MassCsvFile").

---

**createBiodbTestInstance**  
Creating a BiodbMain instance for tests.

**Description**

Creates a BiodbMain instance with options specially adapted for tests. You can request the logging of all messages into a log file. It is also possible to ask for the creation of a BiodbTestMsgAck observer, which will receive all messages and emit a testthat test for each message. This will allow the testthat output to not stall a long time while, for example, downloading or extracting a database. Do not forget to call `terminate()` on your instance at the end of your tests.
Usage

createBiodbTestInstance(ack = FALSE)

Arguments

ack  If set to TRUE, an instance of BiodbTestMsgAck will be attached to the Biodb-
Main instance.

Value

The created BiodbMain instance.

Examples

# Instantiate a BiodbMain instance for testing
biodb <- biodb::createBiodbTestInstance()

# Terminate the instance
biodb$terminate()

---

CsvFileConn  CSV File connector class.

Description

CSV File connector class.

Details

This is the abstract connector class for all CSV file databases.

Super classes

biodb::BiodbConnBase -> biodb::BiodbConn -> CsvFileConn

Methods

Public methods:

- CsvFileConn$new()
- CsvFileConn$getCsvQuote()
- CsvFileConn$setCsvQuote()
- CsvFileConn$getCsvSep()
- CsvFileConn$setCsvSep()
- CsvFileConn$getFieldNames()
- CsvFileConn$hasField()
- CsvFileConn$addField()
- CsvFileConn$getFieldColName()
- CsvFileConn$setField()
- CsvFileConn$getFieldsAndColumnsAssociation()
- CsvFileConn$getUnassociatedColumns()
- CsvFileConn$print()
- CsvFileConn$setDb()
- CsvFileConn$setIgnoreUnassignedColumns()
- CsvFileConn$clone()

**Method new()**: New instance initializer. Connector classes must not be instantiated directly. Instead, you must use the createConn() method of the factory class.

*Usage:*
CsvFileConn$new(...)  

*Arguments:*  
... All parameters are passed to the super class initializer.  

*Returns:* Nothing.

**Method getCsvQuote()**: Gets the characters used to delimit quotes in the CSV database file.

*Usage:*
CsvFileConn$getCsvQuote()  

*Returns:* The characters used to delimit quotes as a single character value.

**Method setCsvQuote()**: Sets the characters used to delimit quotes in the CSV database file.

*Usage:*
CsvFileConn$setCsvQuote(quote)  

*Arguments:*  
quote The characters used to delimit quotes as a single character value. You may specify several characters. Example \"".  

*Returns:* Nothing.

**Method getCsvSep()**: Gets the current CSV separator used for the database file.

*Usage:*
CsvFileConn$getCsvSep()  

*Returns:* The CSV separator as a character value.

**Method setCsvSep()**: Sets the CSV separator to be used for the database file. If this method is called after the loading of the database, it will throw an error.

*Usage:*
CsvFileConn$setCsvSep(sep)  

*Arguments:*  
sep The CSV separator as a character value.
Returns: Nothing.

**Method getFieldNames():** Get the list of all biodb fields handled by this database.

*Usage:*

```r
CsvFileConn$getFieldNames()
```

*Returns:* A character vector of the biodb field names.

**Method hasField():** Tests if a field is defined for this database instance.

*Usage:*

```r
CsvFileConn$hasField(field)
```

*Arguments:*

- `field`: A valid Biodb entry field name.

*Returns:* TRUE of the field is defined, FALSE otherwise.

**MethodaddField():** Adds a new field to the database. The field must not already exist. The same single value will be set to all entries for this field. A new column will be written in the memory data frame, containing the value given.

*Usage:*

```r
CsvFileConn$addField(field, value)
```

*Arguments:*

- `field`: A valid Biodb entry field name.
- `value`: The value to set for this field.

*Returns:* Nothing.

**Method getFieldColName():** Get the column name corresponding to a Biodb field.

*Usage:*

```r
CsvFileConn$getFieldColName(field)
```

*Arguments:*

- `field`: A valid Biodb entry field name. This field must be defined for this database instance.

*Returns:* The column name from the CSV file.

**Method setField():** Sets a field by making a correspondence between a Biodb field and one or more columns of the loaded data frame.

*Usage:*

```r
CsvFileConn$setField(field, colname, ignore.if.missing = FALSE)
```

*Arguments:*

- `field`: A valid Biodb entry field name. This field must not be already defined for this database instance.
- `colname`: A character vector containing one or more column names from the CSV file.
- `ignore.if.missing`: Deprecated parameter.

*Returns:* Nothing.
Method `getFieldsAndColumnsAssociation()`: Gets the association between biodb field names and CSV file column names.

Usage:
```r
CsvFileConn$getFieldsAndColumnsAssociation()
```

Returns: A list with names being the biodb field names and values being a character vector of column names from the CSV file.

Method `getUnassociatedColumns()`: Gets the list of unassociated column names from the CSV file.

Usage:
```r
CsvFileConn$getUnassociatedColumns()
```

Returns: A character vector containing column names.

Method `print()`: Prints a description of this connector.

Usage:
```r
CsvFileConn$print()
```

Returns: Nothing.

Method `setDb()`: Sets the database directly from a data frame. You must not have set the database previously with the URL parameter.

Usage:
```r
CsvFileConn$setDb(db)
```

Arguments:

db A data frame containing your database.

Returns: Nothing.

Method `setIgnoreUnassignedColumns()`: Tells the connector to ignore or not the columns found in the CSV file for which no assignment were found.

Usage:
```r
CsvFileConn$setIgnoreUnassignedColumns(ignore)
```

Arguments:

ignore Set to TRUE to ignore the unassigned columns, and to FALSE otherwise.

Returns: Nothing.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
```r
CsvFileConn$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Super classes `BiodbConn`, and sub-classes `CompCsvFileConn, MassCsvFileConn`. 
Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector that inherits from CsvFileConn:
chebi_file <- system.file("extdata", "chebi_extract.tsv", package="biodb")
conn <- mybiodb$getFactory()$createConn('comp.csv.file', url=chebi_file)

# Get an entry
e <- conn$getEntry('1018')

# Terminate instance.
mybiodb$terminate()

---

**df2str**

*Convert a data.frame into a string.*

**Description**

Prints a data frame (partially if too big) into a string.

**Usage**

```r
df2str(x, rowCut = 5, colCut = 5)
```

**Arguments**

- `x` The data frame object.
- `rowCut` The maximum of rows to print.
- `colCut` The maximum of columns to print.

**Value**

A string containing the data frame representation (or part of it).

**Examples**

# Converts the first 5 rows and first 6 columns of a data frame into a string:
x <- data.frame(matrix(1:160, nrow=10, byrow=TRUE))
s <- df2str(x, rowCut=5, colCut=6)
doesRCurlRequestUrlExist

Test if a URL is valid according to RCurl

Description
Test if a URL is valid according to RCurl

Usage
doesRCurlRequestUrlExist(request, useragent = NULL)

Arguments
- request: A BiodbRequest object, from which the URL will be gotten.
- useragent: The user agent identification.

Value
Returns TRUE if the URL

error
Throw an error and log it too.

Description
Throws an error and logs it too with biodb logger.

Usage
error(...) 

Arguments
... Values to be passed to sprintf().

Value
Nothing.

Examples
# Throws an error:
tryCatch(biodb::error('Index is %d.', 10), error=function(e){e$message})
### error0

*Throw an error and log it too.*

#### Description

Throws an error and logs it too with biodb logger, using paste0().

#### Usage

`error0(…)`

#### Arguments

`…` Values to be passed to paste0().

#### Value

Nothing.

#### Examples

```
# Throws an error:
tryCatch(biodb::error0('Index is ', 10, '.'), error=function(e){e$message})
```

### ExtConnClass

*Extension connector clas*

#### Description

A class for generating a new connector class.

#### Details

This class generates a new connector class from given parameters. The new class inherits from BiodbConn. It can be defined as a compound or mass database connector, and made downloadable, editable and/or writable.

#### Super classes

`biodb::ExtGenerator` -> `biodb::ExtFileGenerator` -> `ExtConnClass`
Methods

Public methods:

- ExtConnClass$new()
- ExtConnClass$clone()

Method new(): Initializer.

Usage:
ExtConnClass$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtConnClass$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

# Generate a new connector class inside R folder:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtConnClass$new(path=pkgFolder, dbName='foo.db',
dbTitle='Foo database',
connType='mass', remote=TRUE)$generate()
Methods

Public methods:

- `ExtCpp$new()`
- `ExtCpp$clone()`

Method `new()`: Initializer.

Usage:
`ExtCpp$new(...)`

Arguments:

... See the constructor of ExtGenerator for the parameters.

Returns: Nothing.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:
`ExtCpp$clone(deep = FALSE)`

Arguments:

depth Whether to make a deep clone.

Examples

```r
# Generate C++ files
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtCpp$new(path=pkgFolder)$generate()
```

---

**ExtDefinitions**

**Extension definitions file class**

Description

A class for generating the definitions.yml file of a new extension package.

Details

This class generates the definitions.yml of a new extension package, needed for defining the new connector.

Super classes

`biodb::ExtGenerator` → `biodb::ExtFileGenerator` → `ExtDefinitions`
Methods

Public methods:

• ExtDefinitions$new()
• ExtDefinitions$clone()

Method new(): Initializer.

Usage:
ExtDefinitions$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters. offers this possibility.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtDefinitions$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

# Generate the biodb definitions.yml file inside "inst" folder:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtDefinitions$new(path=pkgFolder, dbName='foo.db', dbTitle='Foo database')$generate()
Methods

Public methods:

- ExtDescriptionFile$new()
- ExtDescriptionFile$clone()

Method new(): Initializer.

Usage:
ExtDescriptionFile$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtDescriptionFile$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

# Generate the DESCRIPTION file:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtDescriptionFile$new(path=pkgFolder, dbName='foo.db',
                                dbTitle='Foo database', email='j.smith@e.mail',
                                firstname='John', lastname='Smith', rcpp=TRUE,
                                entryType='xml')$generate()
Methods

Public methods:

• ExtEntryClass$new()
• ExtEntryClass$clone()

Method new():

Usage:
ExtEntryClass$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone():
The objects of this class are cloneable with this method.

Usage:
ExtEntryClass$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

Examples

# Generate a new entry class inside R folder:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtEntryClass$new(path=pkgFolder, dbName='foo.db',
                        dbTitle='Foo database',
                        connType='mass', entryType='xml')$generate()
Methods

Public methods:

• ExtFileGenerator$new()
• ExtFileGenerator$clone()

Method new(): Initializer.

Usage:
ExtFileGenerator$new(
  filename = NULL,
  overwrite = FALSE,
  folder = character(),
  template = NULL,
  upgrader = c("fullReplacer", "lineAdder"),
  ...
)

Arguments:
filename The name of the generated file.
overwrite If set to TRUE, then overwrite existing destination file, even whatever the version
of the template file. If set to FALSE, only overwrite if the version of the template file is
strictly greater than the existing destination file.
folder The destination subfolder inside the package directory, as a character vector of subfolders
hierarchy.
template The filename of the template to use.
upgrader The type of upgrader to use. "fullReplacer" replaces the whole destination file by
the template if it is newer (it compares version numbers). "lineAdder" only adds to the
destination file the missing lines from the template file.
... See the constructor of ExtGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtFileGenerator$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtConnClass$new(path=pkgFolder, dbName='foo.db',
  dbTitle='Foo database',
  connType='mass', remote=TRUE)$generate()
ExtGenerator

Extension generator abstract class

Description

The mother class of all generators for biodb extension packages.

Details

All generator classes for biodb extensions must inherit from this class.

Methods

Public methods:

- ExtGenerator$new()
- ExtGenerator$generate()
- ExtGenerator$upgrade()
- ExtGenerator$clone()

Method new(): Initializer.

Usage:
ExtGenerator$new(
  path,
  loadCfg = TRUE,
  saveCfg = TRUE,
  pkgName = getPkgName(path),
  email = "author@e.mail",
  dbName = "foo.db",
  dbTitle = "Foo database",
  pkgLicense = getLicenses(),
  firstname = "Firstname of author",
  lastname = "Lastname of author",
  newPkg = FALSE,
  connType = getConnTypes(),
  entryType = getEntryTypes(),
  editable = FALSE,
  writable = FALSE,
  remote = FALSE,
  downloadable = FALSE,
  makefile = FALSE,
  travis = FALSE,
  rcpp = FALSE,
  vignetteName = getPkgName(path),
  githubRepos = getReposName(path, default = "myaccount/myrepos")
)

Arguments:
**path** The path to the package folder.

**loadCfg** Set to FALSE to disable loading of tag values from config file "biodb_ext.yml".

**saveCfg** Set to FALSE to disable saving of tag values into config file "biodb_ext.yml".

**pkgName** The package name. If set to NULL, the folder name pointer by the "path" parameter will be used as the package name.

**email** The email of the author.

**dbName** The name of the database (in biodb format "my.db.name"), that will be used in "definitions.yml" file and for connector and entry classes.

**dbTitle** The official name of the database (e.g.: HMDB, UniProtKB, KEGG).

**pkgLicense** The license of the package.

**firstname** The firstname of the author.

**lastname** The lastname of the author.

**newPkg** Set to TRUE if the package is not yet published on Bioconductor.

**connType** The type of connector class to implement.

**entryType** The type of entry class to implement.

**editable** Set to TRUE to allow the generated connector to create new entries in memory.

**writable** Set to TRUE to enable the generated connector to write into the database.

**remote** Set to TRUE if the database to connect to is not local.

**downloadable** Set to TRUE if the database needs to be downloaded or offers this possibility.

**makefile** Set to TRUE if you want a Makefile to be generated.

**travis** Set to TRUE if you want a .travis.yml file to be generated.

**rcpp** Set to TRUE to enable Rcpp C/C++ code inside the package.

**vignetteName** Set to the name of the default/main vignette.

**githubRepos** Set to the name of the associated GitHub repository. Example: myaccount/myrepos.

**Returns:** Nothing.

**Method** generate(): Generates the destination file(s).

**Usage:**

```
ExtGenerator$generate(overwrite = FALSE, fail = TRUE)
```

**Arguments:**

**overwrite** If set to TRUE and destination files exist, overwrite the destination files.

**fail** If set to FALSE, do not fail if destination files exist, just do nothing and return.

**Examples:**

# Generate a new extension package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
biodb::ExtPackage$new(pkgFolder)$generate()

**Method** upgrade(): Upgrade the destination file(s).

**Usage:**

```
ExtGenerator$upgrade(generate = TRUE)
```

**Arguments:**

**generate** If set to FALSE, and destination file(s) do not exist, then do not generate them.
**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

`ExtGenerator$clone(deep = FALSE)`

*Arguments:*

deep Whether to make a deep clone.

**Examples**

```r
# Generate a new connector class inside the R folder:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtConnClass$new(path=pkgFolder, dbName='foo.db',
    dbTitle='Foo database',
    connType='mass', remote=TRUE)$generate()
```

```r
## ------------------------------------------------
## Method `ExtGenerator$generate`
## ------------------------------------------------
```

```r
# Generate a new extension package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
biodb::ExtPackage$new(pkgFolder)$generate()
```

**Description**

A class for generating the .gitignore file of an extension package.

**Details**

This class can be used to generate a new .gitignore file or to keep one up to date.

**Super classes**

`biodb::ExtGenerator` -> `biodb::ExtFileGenerator` -> `ExtGitignore`

**Methods**

**Public methods:**

- `ExtGitignore$new()`
- `ExtGitignore$clone()`

**Method** new(): Initializer.

*Usage:*
ExtLicense

ExtGitignore$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtGitignore$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.

Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtGitignore$new(path=pkgFolder)$generate()
... See the constructor of ExtFileGenerator for the parameters.

*Returns:* Nothing.

**Method clone()**: The objects of this class are cloneable with this method.

*Usage:*

```r
ExtLicense$clone(deep = FALSE)
```

*Arguments:*

- `deep` Whether to make a deep clone.

**Examples**

```r
# Generate a new connector class inside R folder:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtLicense$new(path=pkgFolder)$generate()
```

---

**Description**

A class for generating a Makefile for an extension package.

**Details**

This class generates a Makefile, usable on UNIX-like platforms, for managing a biodb extension package. Targets are automatically generated for running CRAN check, Bioconductor check, test-that tests, compiling, generating documentation, cleaning, etc.

**Super class**

*biodb::ExtGenerator -> ExtMakefile*

**Methods**

**Public methods:**

- `ExtMakefile$new()`
- `ExtMakefile$clone()`

**Method new()**: Initializer.

*Usage:*

```r
ExtMakefile$new(...)
```

*Arguments:*

... See the constructor of ExtGenerator for the parameters.
Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtMakefile$clone(deep = FALSE)

Arguments:
  deep  Whether to make a deep clone.

Examples
  # Generate a new connector class inside R folder:
  pkgFolder <- file.path(tempfile(), 'biodbFoo')
  dir.create(pkgFolder, recursive=TRUE)
  biodb::ExtMakefile$new(path=pkgFolder)$generate()
Arguments:
... See the constructor of ExtGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtPackage$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtPackage$new(path=pkgFolder, dbName='foo.db',
dbTitle='Foo database', rcpp=TRUE,
connType='mass', entryType='txt', downloadable=TRUE,
remote=TRUE)$generate()

ExtPackageFile

Description

A class for generating the package.R file for a biodb extension.

Details

This class generates the package.R file, writing a reference to the generated skeleton vignette, and possibly including directives for C++ code.

Super classes

biodb::ExtGenerator - biodb::ExtFileGenerator - ExtPackageFile

Methods

Public methods:
- ExtPackageFile$new()
- ExtPackageFile$clone()

Method new(): Initializer.

Usage:
ExtPackageFile$new(...)

Extension package file class.
Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtPackageFile$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.

Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtPackageFile$new(path=pkgFolder, dbName='foo.db')$generate()
Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtRbuildignore$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.

Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtRbuildignore$new(path=pkgFolder)$generate()

ExtReadme

Extension README file class

Description

A class for generating a README file for a new extension package.

Details

Write a README file inside package directory, using a template file.

Super classes

biodb::ExtGenerator -> biodb::ExtFileGenerator -> ExtReadme

Methods

Public methods:
• ExtReadme$new()
• ExtReadme$clone()

Method new(): Initializer.

Usage:
ExtReadme$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtReadme$clone(deep = FALSE)

Arguments:
depth Whether to make a deep clone.
Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtReadme$new(path=pkgFolder, dbName='foo.db',
        dbTitle='Foo database')$generate()

---

**ExtTests**  
*Extension tests class*

Description

A class for generating test files.

Details

This class generates a test file for running biodb generic tests, and a test file containing an example of a custom test for this extension.

Super class

*biodb::ExtGenerator* -> ExtTests

Methods

Public methods:

- `ExtTests$new()`
- `ExtTests$clone()`

**Method** `new()`: Initializer.

Usage:

`ExtTests$new(...)`

Arguments:

... See the constructor of ExtGenerator for the parameters.

Returns: Nothing.

**Method** `clone()`: The objects of this class are cloneable with this method.

Usage:

`ExtTests$clone(deep = FALSE)`

Arguments:

deep  Whether to make a deep clone.
Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtTests$new(path=pkgFolder, dbName='foo.db', rcpp=TRUE, remote=TRUE)$generate()

---

ExtTravisFile  
Extension Travis YAML file generator class

Description

A class for generating a .travis.yml file for a new extension package.

Details

Write a .travis.yml file inside the package directory, using a template file.

Super classes

biodb::ExtGenerator -> biodb::ExtFileGenerator -> ExtTravisFile

Methods

Public methods:

• ExtTravisFile$new()
• ExtTravisFile$clone()

Method new(): Initializer.

Usage:
ExtTravisFile$new(...)

Arguments:
...  See the constructor of ExtFileGenerator for the parameters.

Returns:  Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtTravisFile$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.
Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtTravisFile$new(path=pkgFolder, email='myname@e.mail')$generate()

---

ExtVignette

Extension vignette class

Description

A class for generating a vignette example for an extension package.

Details

This class generates a vignette file, serving as example to demonstrate the use of the extension package.

Super classes

biodb::ExtGenerator -> biodb::ExtFileGenerator -> ExtVignette

Methods

Public methods:

- ExtVignette$new()
- ExtVignette$clone()

Method new(): Initializer.

Usage:
ExtVignette$new(...)

Arguments:
... See the constructor of ExtFileGenerator for the parameters.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
ExtVignette$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.
Examples

# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::ExtVignette$new(path=pkgFolder, dbName='foo.db',
  dbTitle='Foo database', vignetteName='main',
  firstname='John', lastname='Smith',
  remote=TRUE)$generate()

FileTemplate

File template class.

Description

A class for reading a file template, replacing tags inside, and writing the results in an output file.

Methods

Public methods:
- FileTemplate$new()
- FileTemplate$replace()
- FileTemplate$choose()
- FileTemplate$select()
- FileTemplate$write()
- FileTemplate$getLines()
- FileTemplate$clone()

Method new():

Usage:
FileTemplate$new(path)

Arguments:
path The path to the template file.

Returns: Nothing.

Method replace():

Usage:
FileTemplate$replace(tag, value)

Arguments:
tag The tag to replace.
value The value to replace the tag with.

Returns: invisible(self) for chaining method calls.
Method choose(): Choose one case among a set of cases.

Usage:
FileTemplate$choose(set, case)

Arguments:
set  The name of the case set.
case  The name of case.

Returns: invisible(self) for chaining method calls.

Method select(): Select or remove sections that match a name.

Usage:
FileTemplate$select(section, enable)

Arguments:
section  The name of the section.
enable  Set to TRUE to select the section (and keep it), and FALSE to remove it.

Returns: invisible(self) for chaining method calls.

Method write(): Write template with replaced values to disk.

Usage:
FileTemplate$write(path, overwrite = FALSE, checkRemainingTags = TRUE)

Arguments:
path  Path to output file.
overwrite  If set to FALSE and the destination file already exists, a message is thrown. Otherwise writes into the destination.
checkRemainingTags  If set to TRUE, checks first, before writing, if there any remaining tags that have not been processed. A warning is thrown for each found tag.

Returns: Nothing.

Method getLines(): Get the lines of the templates.

Usage:
FileTemplate$getLines()

Returns: A vector containing the lines of the templates.

Method clone(): The objects of this class are cloneable with this method.

Usage:
FileTemplate$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.
genNewExtPkg

Generate a new extension package for biodb.

Description
Generates all the necessary files for a new extension package.

Usage
`genNewExtPkg(...)`

Arguments
... Parameters passed to `ExtPackage` constructor.

Value
Nothing.

See Also
`ExtPackage`.

Examples
```r
# Generate a new package:
pkgFolder <- file.path(tempfile(), 'biodbFoo')
dir.create(pkgFolder, recursive=TRUE)
biodb::genNewExtPkg(path=pkgFolder, dbName='foo.db',
dbTitle='Foo database', rcpp=TRUE,
connType='mass', entryType='txt', downloadable=TRUE,
remote=TRUE)
```

getBaseUrlContent
Get URL content using base::url().

Description
Get URL content using base::url().

Usage
`getBaseUrlContent(u, binary = FALSE)`
getConnClassName

**Description**

Gets the name of the connector class corresponding to a connector.

**Usage**

getConnClassName(connName)

**Arguments**

connName  
A connector name (e.g.: "mass.csv.file").

**Value**

The name of the corresponding connector class (e.g.: "MassCsvFileConn").

---

getBaseUrlRequestResult

*Get URL request result using base::url().*

**Description**

Get URL request result using base::url().

**Usage**

getBaseUrlRequestResult(request)

**Arguments**

request  
A BiodbRequest object.

**Value**

A RequestResult object.

---

getConnClassName

*Get connector class name.*

**Description**

Get connector class name.

**Usage**

getConnClassName(connName)

**Arguments**

connName  
A connector name (e.g.: "mass.csv.file").

**Value**

The URL content as a character single value.

---

**Arguments**

u  
The URL as a character value.

binary  
Set to TRUE if the content to be retrieved is binary.

---

**Value**

The URL content as a character single value.
**getConnTypes**

**Examples**

```
biodb::getConnClassName('foo.db')
```

---

**getDefaultCacheDir**

**Description**

Returns the path to the default cache folder.

**Usage**

```
getDefaultCacheDir()
```

**Value**

The path to the cache folder.

**Examples**

```
cacheFolderPath <- biodb::getDefaultCacheDir()
```
**getEntryClassNames**  
*Get entry class name.*

**Description**  
Gets the name of the entry class corresponding to a connector.

**Usage**  
getEntryClassName(connName)

**Arguments**  
connName  
A connector name (e.g.: "mass.csv.file").

**Value**  
The name of the corresponding entry class (e.g.: "MassCsvFileEntry").

**Examples**  
```r  
biodb::getEntryClassName('foo.db')  ```

**getEntryTypes**  
*Get entry types.*

**Description**  
Get the list of available entry types.

**Usage**  
getEntryTypes()

**Value**  
A character vector containing the entry types.

**Examples**  
```r  
biodb::getEntryTypes()  ```
getLicenses

Get the available licenses for extension packages.

Description
Get the available licenses for extension packages.

Usage
getLicenses()

Value
A character vector containing license names.

Examples
biodb::getLicenses()

getLogger

Get the main package logger.

Description
Gets the main package logger, parent of all loggers of this package.

Usage
getLogger()

Value
The main package logger (named "biodb") as a lgr::Logger object.

Examples
biodb::getLogger()
getPkgName  
*Get the package name from a package folder path.*

**Description**

The package name is extracted from the path by taking the basename.

**Usage**

```r
getPkgName(pkgRoot, check = TRUE)
```

**Arguments**

- `pkgRoot` The path to the root folder of the package.
- `check` If set to TRUE the extracted package name is checked against regular expression `^biodb[A-Z][A-Za-z0-9]+$`, to ensure the format is respected.

**Value**

The package name of the biodb extension.

**Examples**

```r
biodb::getPkgName('/my/path/to/my/extension/biodbFoo')
```

---

getRCurlContent  
*Get URL content using RCurl::getURL().*

**Description**

Get URL content using RCurl::getURL().

**Usage**

```r
getRCurlContent(
    u, 
    opts = NULL, 
    enc = integer(), 
    header.fct = NULL, 
    ssl.verifypeer = TRUE, 
    method = c("get", "post"), 
    binary = FALSE
)
```

---
getRCurlRequestResult

Arguments

- `u` The URL as a character value.
- `opts` A valid RCurl options object.
- `enc` The encoding.
- `header.fct` An RCurl header gatherer function.
- `ssl.verifypeer` Set to TRUE to enable SSL verify peer.
- `method` The HTTP method to use, either 'get' or 'post'.
- `binary` Set to TRUE if the content to be retrieved is binary.

Value

The URL content as a character single value.

getRCurlRequestResult Get URL request result using RCurl::getURL().

Description

Get URL request result using RCurl::getURL().

Usage

getRCurlRequestResult(request, useragent = NULL, ssl.verifypeer = TRUE)

Arguments

- `request` A BiodbRequest object.
- `useragent` The user agent identification.
- `ssl.verifypeer` Set to TRUE to enable SSL verify peer.

Value

A RequestResult object.
getReposName

Extract the repository name from a package folder.

**Description**

Given the root path of a package, returns the GitHub repository name.

**Usage**

```
getReposName(pkgRoot, default = NULL)
```

**Arguments**

- `pkgRoot` The path to the root folder of the package.
- `default` A default value to return in case git4r package is not available or the folder is not a Git repository.

**Value**

The repository name.

**Examples**

```
biodb::getReposName('/my/path/to/my/extension/biodbFoo')
```

getTestOutputDir

Get the test output directory.

**Description**

Returns the path to the test output directory. The function creates this directory if it does not exist.

**Usage**

```
getTestOutputDir()
```

**Value**

The path to the test output directory, as a character value.

**Examples**

```
# Get the test output directory:
biodb::getTestOutputDir()
```
**getUrlContent**

Get a URL content.

**Description**

Get a URL content.

**Usage**

```
getUrlContent(u, binary = FALSE)
```

**Arguments**

- `u` The URL as a single character value.
- `binary` Set to TRUE if the content to be retrieved is binary.

**Value**

The content, as a single character value.

---

**getUrlRequestResult**

Send a request and get results.

**Description**

Send a request and get results.

**Usage**

```
getUrlRequestResult(request, useragent = NULL, ssl.verifypeer = TRUE)
```

**Arguments**

- `request` A BiodbRequest object.
- `useragent` The user agent identification.
- `ssl.verifypeer` Set to TRUE to enable SSL verify peer.

**Value**

A RequestResult object.
listTestRefEntries  List test reference entries.

Description

DEPRECATED. Use TestRefEntries class instead.

Usage

listTestRefEntries(conn.id, pkgName, limit = 0)

Arguments

conn.id A valid Biodb connector ID.
pkgName The name of the
limit The maximum number of entries to retrieve.

Details

Lists the reference entries in the test folder for a specified connector. The test reference files must be in <pkg>/inst/testref/ folder and their names must match entry-<database_name>-<entry_accession>.json (e.g.: entry-comp.csv.file-1018.json).

Value

A list of entry IDs.

Examples

# List IDs of test reference entries:
biodb::listTestRefEntries('comp.csv.file', pkgName='biodb')

loadFileContents  Loads the contents of files in memory.

Description

This function loads the contents of a list of files and returns the contents as a list, each element being the content of a single file, in the same order. If a file could not be opened, a NULL value is used as the content. NA values are interpreted by default, but this behaviour can be turned off.

Usage

loadFileContents(x, naValues = "NA", outVect = FALSE)
logDebug

Arguments

- `x` A character vector containing the paths of the files.
- `naValues` A character vector listing the content values to convert into NA value. Set to NULL to disable the interpretation of NA values. Set to a different set of values to be interpreted.
- `outVect` If set to TRUE outputs a character vector (converting any NULL value into NA), otherwise outputs a list.

Value

A list with the contents of the files.

Description

Logs a debug level message with biodb logger.

Usage

```r
logDebug(...)
```

Arguments

- `...` Values to be passed to sprintf().

Value

Nothing.

Examples

```r
# Logs a debug message:
biodb::logDebug('Index is %d.', 10)
```
logDebug0  

*Log debug message.*

**Description**
Logs a debug level message with biodb logger, using paste0().

**Usage**
```
logDebug0(...)  
```

**Arguments**
```
...  
```
Values to be passed to paste0()

**Value**
Nothing.

**Examples**
```
# Logs a debug message:
biodb::logDebug0('Index is ', 10, '.
```

logInfo  

*Log information message.*

**Description**
Logs an information level message with biodb logger.

**Usage**
```
logInfo(...)  
```

**Arguments**
```
...  
```
Values to be passed to sprintf().

**Value**
Nothing.

**Examples**
```
# Logs an info message:
biodb::logInfo('Index is %d.', 10)
```
logInfo0

Description
Logs an information level message with biodb logger, using paste0().

Usage
logInfo0(...)  

Arguments
... Values to be passed to paste0().

Value
Nothing.

Examples
# Logs an info message:
biodb::logInfo0('Index is ', 10, ' .')

logTrace

Description
Logs a trace level message with biodb logger.

Usage
logTrace(...)  

Arguments
... Values to be passed to sprintf().

Value
Nothing.

Examples
# Logs a trace message:
biodb::logTrace('Index is %d.', 10)
logTrace0  

*Log trace message.*

**Description**

Logs a trace level message with biodb logger, using paste0().

**Usage**

```
logTrace0(...)  
```

**Arguments**

```
...  
```

Values to be passed to paste0()

**Value**

Nothing.

**Examples**

```
# Logs a trace message:
biodb::logTrace0('Index is ', 10, '.')  
```

---

lst2str  

*Convert a list into a string.*

**Description**

Prints a string (partially if too big) into a string.

**Usage**

```
lst2str(x, nCut = 10)  
```

**Arguments**

```
x  The list to convert into a string.  
nCut  The maximum of elements to print.  
```

**Value**

A string containing the list representation (or part of it).
Examples

# Converts the first 5 elements of a list into a string:
s <- lst2str(1:10, nCut=5)

Usage

makeRCurlOptions(
  useragent = NULL,
  httpheader = NULL,
  postfields = NULL,
  timeout.ms = 60000,
  verbose = FALSE
)

Arguments

useragent      The user agent identification.
httpheader     The HTTP header to send.
postfields     POST fields, in case of a POST method.
timeout.ms     The timeout in milliseconds.
verbose        Set to TRUE to get verbose output in RCurl.

Value

An RCurl::CURLOptions object.
MassCsvFileConn

Description

Mass CSV File connector class.

Details

This is the connector class for a MASS CSV file database.

Super classes

biodb::BiodbConnBase -> biodb::BiodbConn -> biodb::CsvFileConn -> MassCsvFileConn

Methods

Public methods:

• MassCsvFileConn$new()
• MassCsvFileConn$getPrecursorFormulae()
• MassCsvFileConn$isAPrecursorFormula()
• MassCsvFileConn$setPrecursorFormulae()
• MassCsvFileConn$addPrecursorFormulae()
• MassCsvFileConn$clone()

Method new(): New instance initializer. Connector classes must not be instantiated directly. Instead, you must use the createConn() method of the factory class.

Usage:
MassCsvFileConn$new(...)  
Arguments:
... All parameters are passed to the super class initializer.  
Returns: Nothing.

Method getPrecursorFormulae(): Gets the list of formulae used to recognize precursors.

Usage:
MassCsvFileConn$getPrecursorFormulae()  
Returns: A character vector containing chemical formulae.

Method isAPrecursorFormula(): Tests if a formula is a precursor formula.

Usage:
MassCsvFileConn$isAPrecursorFormula(formula)  
Arguments:
formula  A chemical formula, as a character value.

Returns:  TRUE if the submitted formula is considered a precursor.

Method setPrecursorFormulae(): Sets the list precursor formulae.

Usage:
MassCsvFileConn$setPrecursorFormulae(formulae)

Arguments:
formulae  A character vector containing formulae.

Returns:  Nothing.

Method addPrecursorFormulae(): Adds new formulae to the list of formulae used to recognize precursors.

Usage:
MassCsvFileConn$addPrecursorFormulae(formulae)

Arguments:
formulae  A character vector containing formulae.

Returns:  Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
MassCsvFileConn$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.

See Also

Super class CsvFileConn.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get path to LCMS database example file
lcmsdb <- system.file("extdata", "massbank_extract_lcms_2.tsv", package="biodb")

# Create a connector
conn <- mybiodb$getFactory()$createConn('mass.csv.file', url=lcmsdb)

# Get an entry
e <- conn$getEntry('PR010001')

# Terminate instance.
mybiodb$terminate()
MassCsvFileEntry  

Mass CSV File entry class.

Description

Mass CSV File entry class.
Mass CSV File entry class.

Details

This is the entry class for Mass CSV file databases.

Super classes

biodb::BiodbEntry -> biodb::BiodbCsvEntry -> MassCsvFileEntry

Methods

Public methods:

- MassCsvFileEntry$new()
- MassCsvFileEntry$clone()

Method new(): New instance initializer. Entry objects must not be created directly. Instead, they are retrieved through the connector instances.

Usage:
MassCsvFileEntry$new(...)

Arguments:
... All parameters are passed to the super class initializer.

Returns: Nothing.

Method clone(): The objects of this class are cloneable with this method.

Usage:
MassCsvFileEntry$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

See Also

Super class BiodbCsvEntry.
Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get path to LCMS database example file
lcmsdb <- system.file("extdata",
  "massbank_extract_lcms_2.tsv", package="biodb")

# Create a connector
conn <- mybiodb$getFactory()$createConn('mass.csv.file', url=lcmsdb)

# Get an entry
e <- conn$getEntry('PR010001')

# Terminate instance.
mybiodb$terminate()

MassSqliteConn

Class for handling a Mass spectrometry database in SQLite format.

Description

This is the connector class for a MASS SQLite database.

Super classes

biodb::BiodbConnBase -> biodb::BiodbConn -> biodb::SqliteConn -> MassSqliteConn

Methods

Public methods:

• MassSqliteConn$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:
MassSqliteConn$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

See Also

Super class SqliteConn.
MassSqliteEntry

Mass spectra SQLite entry class.

Description

This is the entry class for a Mass spectra SQLite database.

Super classes

biodb::BiodbEntry -> biodb::BiodbListEntry -> MassSqliteEntry

Methods

Public methods:

• MassSqliteEntry$clone()

Method clone(): The objects of this class are cloneable with this method.

Usage:
MassSqliteEntry$clone(deep = FALSE)

Arguments:

deepe Whether to make a deep clone.

See Also

Super class BiodbListEntry.
newInst

Create a new BiodbMain instance.

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get path to LCMS database example file
lcmsdb <- system.file("extdata", "massbank_extract.sqlite", package="biodb")

# Create a connector
cconn <- mybiodb$getFactory()$createConn('mass.sqlite', url=lcmsdb)

# Get an entry
e <- cconn$getEntry('34.pos.col12.0.78')

# Terminate instance.
mybiodb$terminate()

Description

Instatiates a new BiodbMain object by calling the constructor.

Usage

newInst(...)  

Arguments

...  
The parameters to pass to the BiodbMain constructor. See BiodbMain.

Value

A new BiodbMain instance.

See Also

BiodbMain.

Examples

# Create a new BiodbMain instance:
mybiodb <- biodb::newInst()

# Terminate the instance:
mybiodb$terminate()
prepareFileContents  Prepares file contents for saving.

Description
Prepares file contents for saving.

Usage
prepareFileContents(contents)

Arguments
contents  File contents, as a list or a character vector.

Value
File contents.

Progress  Progress class.

Description
A class for informing user about the progress of a process.

Details
This class displays progress of a process to user, and sends notifications of this progress to observers too.

Methods
Public methods:
• Progress$new()
• Progress$increment()
• Progress$clone()

Method new(): Initializer.
Usage:
Progress$new(biodb = NULL, msg, total = NA_integer_)
Arguments:
biodb  A BiodbMain instance that will be used to notify observers of progress.
msg  The message to display to the user.
Range

Range class.

Description

Range class.

Range class.

Details

A class for storing min/max range or value/tolerance.

Methods

Public methods:

- `Range$new()`
- `Range$getValue()`
- `Range$getMin()`
- `Range$getMax()`
• `Range$getMinMax()`
• `Range$getDelta()`
• `Range$getPpm()`
• `Range$getTolExpr()`
• `Range$clone()`

**Method new():** Initializer.

*Usage:*
`Range$new(
    min = NULL,
    max = NULL,
    value = NULL,
    delta = NULL,
    ppm = NULL,
    tol = NULL,
    tolType = c("delta", "plain", "ppm")
)`

*Arguments:*
- `min` The minimum value of the range.
- `max` The maximum value of the range.
- `value` The value.
- `delta` The delta tolerance.
- `ppm` The PPM tolerance.
- `tol` The tolerance value, whose type (ppm or delta) is specified by the "tolType" parameter.
- `tolType` The type of the tolerance value specified by the "tol" parameter.

*Returns:* Nothing.

*Examples:*

```
# Create an instance from min and max:
Range$new(min=1.2, max=1.5)
```

**Method getValue():** Gets the middle value of the range.

*Usage:*
`Range$getValue()`

*Returns:* The middle value.

**Method getMin():** Gets the minimum value of the range.

*Usage:*
`Range$getMin()`

*Returns:* The minimum value.

**Method getMax():** Gets the maximum value of the range.

*Usage:*
`Range$getMax()`
Returns: The maximum value.

Method getMinMax(): Get the min/max range.
Usage:
Range$getMinMax()

Returns: A list containing two fields: "min" and "max.

Method getDelta(): Gets the delta tolerance of the range.
Usage:
Range$getDelta()

Returns: The delta tolerance.

Method getPpm(): Gets the PPM tolerance of the range.
Usage:
Range$getPpm()

Returns: The tolerance in PPM.

Method getTolExpr(): Gets the tolerance expression as a list.
Usage:
Range$getTolExpr()

Returns: A list containing the tolerance range expression.

Method clone(): The objects of this class are cloneable with this method.
Usage:
Range$clone(deep = FALSE)
Arguments:
deed Whether to make a deep clone.

Examples

# Convert a min/max range into a value/ppm tolerance:
rng <- Range$new(min=0.4, max=0.401)
value <- rng$getValue()
ppm <- rng$getPpm()

# Create an instance from min and max:
Range$new(min=1.2, max=1.5)
Class RequestResult.

Description

Class RequestResult.

Details

Represents the result of a request.

Methods

Public methods:

- RequestResult$new()
- RequestResult$content()
- RequestResult$getRetry()
- RequestResult$ErrMsg()
- RequestResult$getStatus()
- RequestResult$getRetryAfter()
- RequestResult$getLocation()
- RequestResult$processRequestErrors()
- RequestResult$clone()

Method `new()`: New instance initializer.

Usage:

```php
RequestResult$new(
    content = NULL,
    retry = FALSE,
    errMsg = NULL,
    status = 0,
    statusMessage = "",
    retryAfter = NULL,
    location = NULL
)
```

Arguments:

- `content` The result content.
- `retry` If request should be resent.
- `errMsg` Error message.
- `status` HTTP status.
- `statusMessage` Status message.
- `retryAfter` Time after which to retry.
location  New location.
Returns:  Nothing.

**Method** getContent(): Get content.
Usage:
RequestResult$getContent()
Returns:  The content as a character value or NULL.

**Method** getRetry(): Get the retry flag.
Usage:
RequestResult$getRetry()
Returns:  TRUE if the URL request should be sent again, FALSE otherwise.

**Method** getErrMsg(): Get the error message.
Usage:
RequestResult$getErrMsg()
Returns:  The error message as a character value or NULL.

**Method** getStatus(): Get the HTTP status of the response.
Usage:
RequestResult$getStatus()
Returns:  The status as an integer.

**Method** getRetryAfter(): Get the time to wait before retrying.
Usage:
RequestResult$getRetryAfter()
Returns:  The time.

**Method** getLocation(): Get the redirect location.
Usage:
RequestResult$getLocation()
Returns:  The redirect location as a character value or NULL.

**Method** processRequestErrors(): Process possible HTTP error.
Usage:
RequestResult$processRequestErrors()
Returns:  Nothing.

**Method** clone(): The objects of this class are cloneable with this method.
Usage:
RequestResult$clone(deep = FALSE)
Arguments:
deep  Whether to make a deep clone.
runGenericTests

Run generic tests.

Description

This function must be used in tests on all connector classes, before any specific tests.

Usage

runGenericTests(
  conn,
  pkgName,
  testRefFolder = NULL,
  opt = NULL,
  short = TRUE,
  long = FALSE,
  maxShortTestRefEntries = 1
)

Arguments

  conn          A valid biodb connector.
  pkgName       The name of your package.
  testRefFolder The folder where to find test reference files.
  opt           A set of options to pass to the test functions.
  short         Run short tests.
  long          Run long tests.
  maxShortTestRefEntries
                 The maximum number of reference entries to use in short tests.

Value

Nothing.

Examples

# Instantiate a Biodb instance for testing
biodb <- biodb::createBiodbTestInstance()

# Create a connector instance
lcmsdb <- system.file("extdata", "massbank_extract.tsv", package="biodb")
conn <- biodb$getFactory()$createConn('mass.csv.file', lcmsdb)

# Run generic tests
biodb::runGenericTests(conn)
saveContentsToFiles

# Terminate the instance
biodb$terminate()

---

saveContentsToFiles  Saves contents to files.

Description

Saves contents to files.

Usage

saveContentsToFiles(files, contents, prepareContents = FALSE)

Arguments

files        The file paths to use for saving contents.
contents     The contents to save, as a list or a character vector.
prepareContents

If set to TRUE, then calls prepareFileContents() on the contents before saving them.

Value

Nothing.

---

SqliteConn  SQLite connector class.

Description

SQLite connector class.

Details

This is the abstract connector class for all SQLite databases.

Super classes

biodb::BiodbConnBase -> biodb::BiodbConn -> SqliteConn
Methods

**Public methods:**

- `SqliteConn$new()`
- `SqliteConn$hasField()`
- `SqliteConn$getQuery()`
- `SqliteConn$clone()`

**Method new():** New instance initializer. Connector classes must not be instantiated directly. Instead, you must use the `createConn()` method of the factory class.

  **Usage:**
  `SqliteConn$new(...)`

  **Arguments:**
  ...

  **Returns:** Nothing.

**Method hasField():** Tests if a field is defined for this database instance.

  **Usage:**
  `SqliteConn$hasField(field)`

  **Arguments:**
  field A valid Biodb entry field name.

  **Returns:** TRUE of the field is defined, FALSE otherwise.

**Method getQuery():** Run a query using a biodb SQL object.

  **Usage:**
  `SqliteConn$getQuery(query)`

  **Arguments:**
  query A valid BiodbSqlQuery object.

  **Returns:** The result returned by `DBI::dbGetQuery()` call.

**Method clone():** The objects of this class are cloneable with this method.

  **Usage:**
  `SqliteConn$clone(deep = FALSE)`

  **Arguments:**
  deep Whether to make a deep clone.

**See Also**

Super class `BiodbConn` and sub-classes `CompSqliteConn`, and `MassSqliteConn`. 
testContext

Examples

# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector that inherits from SqliteConn:
chebi_file <- system.file("extdata", "chebi_extract.sqlite", package="biodb")
conn <- mybiodb$getFactory()$createConn('comp.sqlite', url=chebi_file)

# Get an entry
e <- conn$getEntry('1018')

# Terminate instance.
mybiodb$terminate()

testContext

Set a test context.

Description

Define a context for tests using testthat framework. In addition to calling testthat::context().

Usage

testContext(text)

Arguments

text The text to print as test context.

Value

No value returned.

Examples

# Define a context before running tests:
biodb::testContext("Test my database connector.")

# Instantiate a BiodbMain instance for testing
biodb <- biodb::createBiodbTestInstance()

# Terminate the instance
biodb$terminate()
TestRefEntries

A class for accessing the test reference entries.

Description

A class for accessing the test reference entries.

Details

The test reference entries are stored as JSON files inside inst/testref folder of each extension package.

Methods

Public methods:

- `TestRefEntries$new()`
- `TestRefEntries$getAllIds()`
- `TestRefEntries$getContents()`
- `TestRefEntries$getRealEntries()`
- `TestRefEntries$saveEntriesAsJson()`
- `TestRefEntries$getRealEntry()`
- `TestRefEntries$getRefEntry()`
- `TestRefEntries$getAllRefEntriesDf()`
- `TestRefEntries$clone()`

Method `new()`: New instance initializer.

Usage:

```
TestRefEntries$new(db.class, pkgName, folder = NULL, bdb = NULL)
```

Arguments:

- `db.class`: Identifier of the database.
- `pkgName`: Name of the package in which are stored the reference entry files.
- `folder`: The folder where to find test reference files for the package. Usually it is "inst/testref".
- `bdb`: A valid BiodbMain instance or NULL.

Returns: Nothing.

Method `getAllIds()`: Retrieve all identifiers.

Usage:

```
TestRefEntries$getAllIds(limit = 0)
```

Arguments:

- `limit`: The maximum number of identifiers to return.

Returns: A character vector containing the IDs.
Method \texttt{getContents()}: Get the reference contents for the specified IDs.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$getContents(ids)
\end{verbatim}

\textit{Arguments:}
- \texttt{ids}  The reference IDs for which to get the contents.

\textit{Returns:} A character vector.

Method \texttt{getRealEntries()}: Retrieve all real entries from database corresponding to the reference entries.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$getRealEntries(ids = NULL)
\end{verbatim}

\textit{Arguments:}
- \texttt{ids}  A character vector of entry identifiers.

\textit{Returns:} A list containing \texttt{BiodbEntry} instances.

Method \texttt{saveEntriesAsJson()}: Saves a list of entries into separate JSON files, inside the test output folder.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$saveEntriesAsJson(ids, entries)
\end{verbatim}

\textit{Arguments:}
- \texttt{ids}  The IDs of the entries.
- \texttt{entries}  A list of entries. It can contain NULL values.

\textit{Returns:} Nothing.

Method \texttt{getRealEntry()}: Retrieves one real entry from database corresponding to one reference entry.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$getRealEntry(id)
\end{verbatim}

\textit{Arguments:}
- \texttt{id}  The identifier of the entry.

\textit{Returns:} A \texttt{BiodbEntry} instance.

Method \texttt{getRefEntry()}: Retrieves the content of a single reference entry.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$getRefEntry(id)
\end{verbatim}

\textit{Arguments:}
- \texttt{id}  The identifier of the reference entry to retrieve.

\textit{Returns:} The content of the reference entry as a list.

Method \texttt{getAllRefEntriesDf()}: Load all reference entries.

\textit{Usage:}
\begin{verbatim}
TestRefEntries$getAllRefEntriesDf()
\end{verbatim}
**Returns:** A data frame containing all the reference entries with their values.

**Method** `clone()`: The objects of this class are cloneable with this method.

**Usage:**
`TestRefEntries$clone(deep = FALSE)`

**Arguments:**
deep Whether to make a deep clone.

**Examples**

```r
# Creates an instance
refEntries <- TestRefEntries$new('comp.sqlite', pkgName='biodb')

# Gets identifiers of all reference entries
refEntries$getAllIds()

# Gets a data frame with the content of the reference entries
refEntries$getAllRefEntriesDf()
```

---

**testThat**

*Run a test.*

**Description**

Run a test function, using testthat framework. In addition to calling `testthat::test_that()`.

**Usage**

`testThat(msg, fct, biodb = NULL, conn = NULL, opt = NULL)`

**Arguments**

- `msg`: The test message.
- `fct`: The function to test.
- `biodb`: A valid BiodbMain instance to be passed to the test function.
- `conn`: A connector instance to be passed to the test function.
- `opt`: A set of options to pass to the test function.

**Value**

No value returned.
upgradeExtPkg

Upgrading an existing extension package for biodb.

Description

Upgrades some of the files previously generated (.gitignore, .travis.yml, .Rbuildignore, Makefile, etc) to the latest versions.

Usage

upgradeExtPkg(...)  

Arguments

... Parameters passed to ExtPackage constructor.

Value

Nothing.

Examples

# Generate a new package:  
pkgFolder <- file.path(tempfile(), 'biodbFoo')  
dir.create(pkgFolder, recursive=TRUE)  
biodb::genNewExtPkg(path=pkgFolder, dbName='foo.db',  
dbTitle='Foo database', rcpp=TRUE,  
connType='mass', entryType='txt', downloadable=TRUE,  
remote=TRUE)

# Upgrade it later
biodb::upgradeExtPkg(path=pkgFolder)

warn

Throw a warning and log it too.

Description
Thr...
Examples

# Throws a warning:
tryCatch(biodb::warn0('Index is ', 10, '.'), warning=function(w){w$message})
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