Package ‘biodbUniprot’

May 10, 2024

Title  biodbUniprot, a library for connecting to the Uniprot Database
Version  1.10.0
Description  The biodbUniprot library is an extension of the biodb framework package. It provides access to the UniProt database. It allows to retrieve entries by their accession number, and run web service queries for searching for entries.

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

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

biocViews  Software, Infrastructure, DataImport

Depends  R (>= 4.1.0)
License  AGPL-3
Encoding  UTF-8

VignetteBuilder  knitr

Suggests  BiocStyle, roxygen2, devtools, testthat (>= 2.0.0), knitr, rmarkdown, lgr, covr

Imports  R6, biodb (>= 1.4.2)

RoxygenNote  7.2.1

Collate  'UniprotConn.R' 'UniprotEntry.R' 'package.R'

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Author  Pierrick Roger [aut, cre](<https://orcid.org/0000-0001-8177-4873>)

Maintainer  Pierrick Roger <pierrick.roger@cea.fr>
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UniprotConn The connector class to Uniprot database.

Description

The connector class to Uniprot database.
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Details

This is a concrete connector class. It must never be instantiated directly, but instead be instantiated
through the factory BiodbFactory. Only specific methods are described here. See super classes for
the description of inherited methods.

Super classes

biodb::BiodbConnBase -> biodb::BiodbConn -> UniprotConn

Methods

Public methods:

• UniprotConn$wsSearch()
• UniprotConn$wsQuery()
• UniprotConn$geneSymbolToUniprotIds()
• UniprotConn$clone()

Method wsSearch(): Calls search service on the database for searching for compounds. See
https://www.uniprot.org/help/programmatic_access for details.

Usage:

UniprotConn$wsSearch(
    query = "",
    fields = NULL,
    format = NULL,
    size = NULL,
    retfmt = c("plain", "parsed", "ids", "request")
)

Arguments:

query The query to send to the database.
fields The field columns to retrieve from the database (e.g.: ’id’, ’entry name’, ’pathway’, ’organism’, ’sequence’, etc).
format  The return format (e.g.: 'tsv').
size  The maximum number of entries to return.
refmt  Use to set the format of the returned value. 'plain' will return the raw results from
       the server, as a character value. 'parsed' will return the parsed results, as a JSON object.
       'request' will return a BiodbRequest object representing the request as it would have been
       sent. 'ids' will return a character vector containing the IDs of the matching entries.

Returns:  Depending on 'refmt' parameter.

Method  wsQuery():  Calls query service on the database for searching for compounds. See http
       //www.uniprot.org/help/api_queries for details.

Usage:
UniprotConn$wsQuery(
    query = "",
    columns = NULL,
    format = NULL,
    limit = NULL,
    refmt = c("plain", "parsed", "ids", "request")
)

Arguments:
query  The query to send to the database.
columns  The field columns to retrieve from the database (e.g.: 'id', 'entry name', 'pathway',
         'organism', 'sequence', etc).
format  The return format (e.g.: 'tsv').
limit  The maximum number of entries to return.
refmt  Use to set the format of the returned value. 'plain' will return the raw results from
       the server, as a character value. 'parsed' will return the parsed results, as a JSON object.
       'request' will return a BiodbRequest object representing the request as it would have been
       sent. 'ids' will return a character vector containing the IDs of the matching entries.

Returns:  Depending on 'refmt' parameter.

Method  geneSymbolToUniprotIds():  Gets UniProt IDs associated with gene symbols.

Usage:
UniprotConn$geneSymbolToUniprotIds(
    genes,
    ignore.nonalphanum = FALSE,
    partial.match = FALSE,
    filtering = TRUE,
    max.results = 0
)

Arguments:
genes  A vector of gene symbols to convert to UniProt IDs.
ignore.nonalphanum  If set to TRUE, do not take into account non-alphanumeric characters
        when comparing gene symbols.
partial.match  If set to TRUE, a match will be valid even if the provided gene symbol is only
        a substring of the found gene symbol.
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filtering If set to FALSE, do not run any filtering and return all the UniProt IDs given by UniProt search web service. DEPRECATED: new UniProt REST API returns only exact match.

max.results Maximum of UniProt IDs returned for each gene symbol.

Returns: A named list of vectors of UniProt IDs. The names are gene symbols provided with the genes parameter. For each gene symbol, a vector of found UniProt IDs is set.

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

Usage:

UniprotConn$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

Examples

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

# Get Uniprot connector
uniprot <- mybiodb$getFactory()$createConn('uniprot')

# Access web service "search":
result <- uniprot$wsSearch(query='protein_name:"prion protein"',
fields=c('id', 'entry name'),
format='tsv', size=10)

# Terminate instance.
mybiodb$terminate()

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UniprotEntry Uniprot entry class.

Description

This is the entry class for Uniprot database.

Super classes

biodb::BiodbEntry -> biodb::BiodbXmlEntry -> UniprotEntry

Methods

Public methods:

• UniprotEntry$clone()

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

Arguments:
deep  Whether to make a deep clone.

Examples

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

# Create a connector
conn <- mybiodb$getFactory()$createConn('uniprot')

# Get an entry
e <- conn$getEntry('P01011')

# Terminate instance.
mybiodb$terminate()
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