Package ‘ctrdata’

November 24, 2023

Type Package

Title Retrieve and Analyze Clinical Trials in Public Registers

Version 1.16.0

Imports jsonlite, httr, curl (>= 5.1.0), clipr, xml2, nodbi (>= 0.9.3), stringi, tibble, lubridate, jqr, dplyr, zip, V8, readr

URL https://cran.r-project.org/package=ctrdata

BugReports https://github.com/rfhb/ctrdata/issues


Trial information is downloaded, converted and stored in a database ('PostgreSQL', 'SQLite', 'DuckDB' or 'MongoDB'; via package 'nodbi'). Documents in registers associated with trials can also be downloaded. Other functions identify deduplicated records, easily find and extract variables (fields) of interest even from complex nested data as used by the registers, merge variables and update queries.

The package can be used for meta-analysis and trend-analysis of the design and conduct as well as of the results of clinical trials.

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RoxygenNote 7.2.3

Suggests devtools, knitr, rmarkdown, RSQLite (>= 2.2.4), mongolite, tinytest (>= 1.2.1), R.rsp, RPostgres, duckdb

VignetteBuilder R.rsp

NeedsCompilation no
Description

A package for aggregating and analysing information on clinical studies, and for obtaining documents, from public registers

1 - Database connection

Package ctrdata retrieves trial information and stores it in a database collection, which has to be given as a connection object to parameter con for several ctrdata functions; this connection object is created in almost identical ways for these supported backends:

<table>
<thead>
<tr>
<th>Database</th>
<th>Connection object</th>
</tr>
</thead>
<tbody>
<tr>
<td>MongoDB</td>
<td>dbc &lt;- nodbi::src_mongo(db = &quot;my_db&quot;, collection = &quot;my_coll&quot;)</td>
</tr>
<tr>
<td>SQLite</td>
<td>dbc &lt;- nodbi::src_sqlite(dbname = &quot;my_db&quot;, collection = &quot;my_coll&quot;)</td>
</tr>
<tr>
<td>PostgreSQL</td>
<td>dbc &lt;- nodbi::src_postgres(dbname = &quot;my_db&quot;); dbc[[&quot;collection&quot;]]&lt;-&quot;my_coll&quot;</td>
</tr>
<tr>
<td>DuckDB</td>
<td>dbc &lt;- nodbi::src_duckdb(dbname = &quot;my_db&quot;, collection = &quot;my_coll&quot;)</td>
</tr>
</tbody>
</table>

Use a connection object with a ctrdata function, for example dbQueryHistory, or other packages,
for example `mongolite::mongo` or `nodbi::docdb_query`. Use a demo database: `dbc <- nodbi::src_sqlite(dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"), collection = "my_trials")`

2 - Operate on a clinical trial register

`ctrOpenSearchPagesInBrowser`, `ctrLoadQueryIntoDb` (load trial records into database collection); see `ctrdata-registers` for details on registers and how to search.

3 - Get a data frame from the database collection

`dbFindFields` (find names of fields of interest in trial records in a collection), `dbGetFieldsIntoDf` (create a data frame with fields of interest from collection), `dbFindIdsUniqueTrials` (get de-duplicated identifiers of clinical trials’ records that can be used to subset a data frame).

4 - Operate on a data frame with trial information

`dfTrials2Long` (convert fields with nested elements into long format), `dfName2Value` (get values for variable(s) of interest).

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See Also

Useful links:

- https://cran.r-project.org/package=ctrdata
- Report bugs at https://github.com/rfhb/ctrdata/issues

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ctrdata-registers  ctrdata: information on clinical trial registers

Description

Registers of clinical trials that can be accessed with package `ctrdata` as of September 2023.

Details

- **EUCTR**: The European Union Clinical Trials Register contains more than 43,500 clinical trials (using one or more medicines as investigational medicinal product, IMP; in the European Union and beyond)
- **CTGOV** and **CTGOV2**: ClinicalTrials.gov includes more than 465,000 interventional and observational studies (both the current and the classic website are supported)
- **ISRCTN**: The ISRCTN Registry includes almost 24,000 interventional or observational health studies
- **CTIS**: The EU Clinical Trials Information System was started in January 2023, including 410 publicly accessible trials on 2023-11-22. How to automatically get a query URL: here
ctrFindActiveSubstanceSynonyms

Find synonyms of an active substance

Description

An active substance can be identified by a recommended international nonproprietary name (INN), a trade or product name, or a company code(s). Retrieves the names of substance which are searched for by "CTGOV" when querying for a given active substance.

Usage

ctrFindActiveSubstanceSynonyms(activesubstance = "")

Arguments

activesubstance

An active substance, in an atomic character vector
Value

A character vector of the active substance (input parameter) and synonyms, or NULL if active substance was not found and may be invalid.

Examples

```r
# Not run:
ctrFindActiveSubstanceSynonyms(activesubstance = "imatinib")
# [1] "imatinib" "gleevec" "sti 571" "glivec" "CGP 57148" "st1571"
```

## ctrGetQueryUrl

### Get query details

Description

Extracts query parameters and register name from parameter ‘url‘ or from the clipboard, into which the URL of a register search was copied.

Usage

```r
ctrGetQueryUrl(url = "", register = "")
```

Arguments

- **url**: URL such as from the browser address bar. If not specified, clipboard contents will be checked for a suitable URL. For automatically copying the user’s query of a register in a web browser to the clipboard, see here. Can also contain a query term such as from `dbQueryHistory()"query-term"`.  
- **register**: Optional name of register (one of "EUCTR", "CTGOV", "ISRCTN" or "CTIS") in case ‘url‘ is a query term

Value

A data frame (or tibble, if tibble is loaded) with column names ‘query-term‘ and ‘query-register‘. The data frame (or tibble) can be passed as such as parameter ‘query-term‘ to `ctrLoadQueryIntoDb` and as parameter ‘url‘ to `ctrOpenSearchPagesInBrowser`.

Examples

```r
# user copied into the clipboard the URL from
# the address bar of the browser that shows results
# from a query in one of the trial registers
try(ctrGetQueryUrl(), silent = TRUE)
```
ctrLoadQueryIntoDb Load and store register trial information

Description
Retrieves information on clinical trials from registers and stores it in a collection in a database. Main function of ctrdata for accessing registers. A collection can store trial information from different queries or different registers. Query details are stored in the collection and can be accessed using dbQueryHistory. A previous query can be re-run, which replaces or adds trial records while keeping any user annotations of trial records.

Usage
ctrLoadQueryIntoDb(queryterm = NULL, 
register = "", 
querytoupdate = NULL, 
forcetoupdate = FALSE, 
euctrresults = FALSE, 
euctrresultshistory = FALSE, 
documents.path = NULL, 
documents.regexp = "prot|sample|statist|sap_|p1ar|p2ars|ctalett|lay|^\[0-9]+ ", 
annotation.text = "", 
annotation.mode = "append", 
only.count = FALSE, 
con = NULL, 
verbose = FALSE,
Arguments

**queryterm**
Either a string with the full URL of a search query in a register, or the data frame returned by the `ctrGetQueryUrl` or the `dbQueryHistory` functions, or, together with parameter `register`, a string with query elements of a search URL. The query details are recorded in the collection for later use to update records. For "CTIS", `queryterm` can be an empty string to obtain all trial records. For automatically copying the user's query of a register in a web browser to the clipboard, see here.

**register**
String with abbreviation of register to query, either "EUCTR", "CTGOV", "ISRCTN" or "CTIS". Not needed if `queryterm` provides a full URL to query results.

**querytoupdate**
Either the word "last", or the row number of a query in the data frame returned by `dbQueryHistory` that should be run to retrieve any new or update trial records since this query was run the last time. This parameter takes precedence over `queryterm`. For "EUCTR", updates are available only for the last seven days; the query is run again if more time has passed since it was run last. Does not work with "CTIS" at this time.

**forcetoupdate**
If TRUE, run again the query given in `querytoupdate`, irrespective of when it was run last. Default is FALSE.

**euctrresults**
If TRUE, also download available results when retrieving and loading trials from EUCTR. This slows down this function. (For "CTGOV", "CTGOV2" and "CTIS", all available results are always retrieved and loaded into the collection.)

**euctrresultshistory**
If TRUE, also download available history of results publication in "EUCTR." This is quite time-consuming. Default is FALSE.

**documents.path**
If this is a relative or absolute path to a directory that exists or can be created, save any documents into it that are directly available from the register ("EUCTR", "CTGOV", "CTGOV2", "ISRCTN", "CTIS") such as PDFs on results, analysis plans, spreadsheets, patient information sheets, assessments or product information. Default is NULL, which disables saving documents.

**documents.regexp**
Regular expression, case insensitive, to select documents, if saving documents is requested (see `documents.path`). If set to NULL, empty placeholder files are saved for every document that could be saved. Default is "prot|sample|statist|sap_\_[p1ar][p2ars]\_ct"). Used with "CTGOV", "CTGOV2", "ISRCTN" and "CTIS" (but not "EUCTR", for which all available documents are saved in any case).

**annotation.text**
Text to be including into the field "annotation" in the records retrieved with the query that is to be loaded into the collection. The contents of the field "annotation" for a trial record are preserved e.g. when running this function again and loading a record of a with an annotation, see parameter `annotation.mode`.
ctrLoadQueryIntoDb

annotation.mode
One of "append" (default), "prepend" or "replace" for new annotation.text with respect to any existing annotation for the records retrieved with the query that is to be loaded into the collection.

only.count
Set to TRUE to return only the number of trial records found in the register for the query. Does not load trial information into the database. Default is FALSE.

con
A connection object, see section ‘Databases’ in ctrdata.

verbose
Printing additional information if set to TRUE; default is FALSE.

Value
A list with elements ‘n’ (number of trial records newly imported or updated), ‘success’ (a vector of _id’s of successfully loaded records), ‘failed’ (a vector of identifiers of records that failed to load) and ‘queryterm’ (the query term used). The returned list has several attributes (including database and collection name, as well as the query history of this database collection) to facilitate documentation.

Examples
## Not run:
dbc <- nodbi::src_sqlite(collection = "my_collection")

# Retrieve protocol- and results-related information
# on two specific trials identified by their EU number
ctrLoadQueryIntoDb(
  queryterm = "2005-001267-63+OR+2008-003606-33",
  register = "EUCTR",
  euctrresults = TRUE,
  con = dbc
)

# Retrieve all information on about 2,000 ongoing
# interventional cancer trials involving children
# into the same collection as used before
ctrLoadQueryIntoDb(
  queryterm = "cancer&recr=Open&type=Intr&age=0",
  register = "CTGOV",
  con = dbc
)

# Retrieve all information on more than 40 trials
# that are labelled as phase 3 and that mention
# either neuroblastoma or lymphoma from ISRCTN,
# into the same collection as used before
ctrLoadQueryIntoDb(
  queryterm = paste0("https://www.isrctn.com/search?",
    "q=neuroblastoma+OR+lymphoma&filters=phase%3APhase+III"),
  con = dbc
)
ctrOpenSearchPagesInBrowser

Open register to show query results or search page

Description

Open advanced search pages of register(s), or execute search in browser

Usage

ctrOpenSearchPagesInBrowser(url = "", register = "", copyright = FALSE)

Arguments

url of search results page to show in the browser. To open the browser with a previous search, the output of ctrGetQueryUrl or dbQueryHistory can be used. Can be left as empty string (default) to open the advanced search page of register.

register Register(s) to open, "EUCTR", "CTGOV", "CTGOV2", "ISRCTN" or "CTIS". Default is empty string, and this open the advanced search page of the register(s).

copyright (Optional) If set to TRUE, opens only the copyright pages of all registers.

Value

(String) Full URL corresponding to the shortened url in conjunction with register if any, or invisibly TRUE if no url is specified.

Examples

# Open all and check copyrights before using registers
ctrOpenSearchPagesInBrowser(copyright = TRUE)

# Open specific register advanced search page
ctrOpenSearchPagesInBrowser(register = "CTGOV")
ctrOpenSearchPagesInBrowser(register = "CTGOV2")
ctrOpenSearchPagesInBrowser(register = "CTIS")
ctrOpenSearchPagesInBrowser(register = "EUCTR")
ctrOpenSearchPagesInBrowser(register = "ISRCTN")
ctrOpenSearchPagesInBrowser(url = "status=Ended", register = "CTIS")

# Open all queries that were loaded into demo collection
dbc <- nodbi::src_sqlite(
    dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
    collection = "my_trials"
)

dbh <- dbQueryHistory(
    con = dbc
)

for (r in seq_len(nrow(dbh))) {
    ctrOpenSearchPagesInBrowser(dbh[r, ])
}

dbFindFields

Find names of fields in the database collection

Description
Given part of the name of a field of interest to the user, this function returns the full field names used in records that were previously loaded into a collection (using ctrLoadQueryIntoDb). The field names can be fed into function dbGetFieldsIntoDf to extract the data from the collection into a data frame.

Usage
dbFindFields(namepart = ",", con, verbose = FALSE)

Arguments
namepart A character string (can include a regular expression, including Perl-style) to be searched among all field names (keys) in the collection, case-insensitive. Use ".*" to find all fields.
con A connection object, see section 'Databases' in ctrdata.
verbose If TRUE, prints additional information (default FALSE).

Details
In addition to the full names of all child fields (e.g., clinical_results.outcome_list.outcome.measure.class_list.class.title) this function may return names of parent fields (e.g., clinical_results). Data in parent fields is typically complex (nested) and can be converted into individual data elements with dfTrials2Long, and subelements can then be accessed with dfName2Value. For field definitions of the registers, see row "Definition" in ctrdata-registry. Note: Only when dbFindFields is first called after ctrLoadQueryIntoDb, it will take a moment.
**dbFindIdsUniqueTrials**

**Value**

Vector of strings with full names of field(s) found, ordered by register and alphabet. Names of the vector elements are the register names for the respective fields.

Only names of fields that have a value in the collection are returned, and the names may be incomplete because they are from sampled records. See here for obtaining a complete set of field names (albeit without register names): https://github.com/rfhb/ctrdata/issues/26#issuecomment-1751452462

**Examples**

dbc <- nodbi::src_sqlite(
  dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
  collection = "my_trials"
)

dbFindFields(namepart = "date", con = dbc)

dbFindIdsUniqueTrials  *Get identifiers of deduplicated trial records*

**Description**

Records for a clinical trial can be loaded from more than one register into a collection. This function returns deduplicated identifiers for all trials in the collection, respecting the register(s) preferred by the user. All registers are recording identifiers also from other registers, which are used by this function to provide a vector of identifiers of deduplicated trials.

**Usage**

dbFindIdsUniqueTrials(
  preferregister = c("EUCTR", "CTGOV", "CTGOV2", "ISRCTN", "CTIS"),
  prefermemberstate = "DE",
  include3rdcountrytrials = TRUE,
  con,
  verbose = FALSE
)

**Arguments**

preferregister  A vector of the order of preference for registers from which to generate unique _id’s, default c("EUCTR", "CTGOV", "CTGOV2", "ISRCTN", "CTIS")

prefermemberstate  Code of single EU Member State for which records should returned. If not available, a record for DE or lacking this, any random Member State’s record for the trial will be returned. For a list of codes of EU Member States, please
see vector countriesEUCTR. Specifying "3RD" will return the Third Country record of trials, where available.

include3rdcountrytrials
A logical value if trials should be retained that are conducted exclusively in third countries, that is, outside the European Union. Ignored if prefermemberstate is set to "3RD".

con
A connection object, see section 'Databases' in ctrdata.

verbose
If set to TRUE, prints out which fields of the registers are used to find corresponding trial records

Details
Note that the content of records may differ between registers (and, for "EUCTR", between records for different Member States). Such differences are not considered by this function.

Value
A named vector with strings of keys (field "._id") of records in the collection that represent unique trials, where names correspond to the register of the record.

Examples

dbc <- nodbi::src_sqlite(
    dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
    collection = "my_trials"
)
dbFindIdsUniqueTrials(con = dbc)

dbGetFieldsIntoDf(fields = "", con, verbose = FALSE, stopifnodata = TRUE)
Arguments

fields Vector of one or more strings, with names of sought fields. See function `dbFindFields` for how to find names of fields. "item.subitem" notation is supported.

con A connection object, see section 'Databases' in `ctrdata`.

verbose Printing additional information if set to `TRUE`; (default `FALSE`).

stopifnodata Stops with an error (default `TRUE`) or with a warning (`FALSE`) if the sought field is empty in all, or not available in any of the records in the database collection.

Value

A data frame (or tibble, if `tibble` is loaded) with columns corresponding to the sought fields. A column for the records’ `_id` will always be included. Each column can be either a simple data type (numeric, character, date) or a list (typically for nested data, see above). For complicated lists, use function `dfTrials2Long` followed by function `dfName2Value` to extract values for sought nested variables. The maximum number of rows of the returned data frame is equal to, or less than the number of records of trials in the database collection.

Examples

```r
dbc <- nodbi::src_sqlite(
  dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
  collection = "my_trials")

# get fields that are nested within another field
# and can have multiple values with the nested field
dbGetFieldsIntoDf(
  fields = "b1_sponsor.b31_and_b32_status_of_the_sponsor",
  con = dbc)

# fields that are lists of string values are
# returned by concatenating values with a slash
dbGetFieldsIntoDf(
  fields = "keyword",
  con = dbc)
```

---

**dbQueryHistory**: Show history of queries loaded into a database collection

**Description**

Show history of queries loaded into a database collection

**Usage**

```r
dbQueryHistory(con, verbose = FALSE)
```
### dfMergeVariablesRelevel

**Merge variables, keeping type, and optionally relevel factors**

#### Description

Merge variables in a data frame such as returned by `dbGetFieldsIntoDf` into a new variable, and optionally also map its values to new levels.

#### Usage

```r
dfMergeVariablesRelevel(df = NULL, colnames = "", levelslist = NULL)
```

#### Arguments

- `df`: A `data.frame` with the variables (columns) to be merged into one vector.
- `colnames`: A vector of names of columns in ‘df’ that hold the variables to be merged, or a selection of columns as per `select`.
- `levelslist`: A names list with one slice each for a new value to be used for a vector of old values (optional).

#### Value

A vector, with the type of the columns to be merged
Examples

dbc <- nodbi::src_sqlite(
  dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
  collection = "my_trials"
)

df <- dbGetFieldsIntoDf(
  fields = c("overall_status", "x5_trial_status"),
  con = dbc
)

statusvalues <- list(
  "ongoing" = c("Recruiting", "Active", "Ongoing"),
  "completed" = c("Completed", "Prematurely Ended", "Terminated"),
  "other" = c("Withdrawn", "Suspended", "No longer available")
)

dfMergeVariablesRelevel(
  df = df,
  colnames = c(Var contains("status"),
    levelslist = statusvalues
)

---

**dfName2Value**

*Get value for variable of interest*

**Description**

Get information for variable of interest (e.g., clinical endpoints) from long data frame of protocol- or result-related trial information as returned by `dfTrials2Long`. Parameters 'valuename', 'wherename' and 'wherevalue' are matched using Perl regular expressions and ignoring case.

**Usage**

dfName2Value(df, valuename = "", wherename = "", wherevalue = "")

**Arguments**

df
A data frame (or tibble) with four columns ('_id', 'identifier', 'name', 'value') as returned by `dfTrials2Long`  
valuename
A character string for the name of the field that holds the value of the variable of interest (e.g., a summary measure such as "endPoints.*tendencyValue.value")  
wherename
(optional) A character string to identify the variable of interest among those that repeatedly occur in a trial record (e.g., "endPoints.endPoint.title")  
wherevalue
(optional) A character string with the value of the variable identified by 'wherename' (e.g., "response")
Value

A data frame (or tibble, if tibble is loaded) that includes the values of interest, with columns 
`'_id'`, 'identifier', 'name', 'value' (and 'where', with the contents of 'wherevalue' found at 'wher-
ename'). Contents of 'value' are strings unless all its elements are numbers. The 'identifier' is 
generated by function dfTrials2Long to identify matching elements, e.g. endpoint descriptions and 
measurements.

Examples

dbc <- nodbi::src_sqlite(
  dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
  collection = "my_trials"
)
dfwide <- dbGetFieldsIntoDf(
  fields = c(
    ## ctgov - typical results fields
    # "clinical_results.baseline.analyzed_list.analyzed.count_list.count",
    # "clinical_results.baseline.group_list.group",
    # "clinical_results.baseline.analyzed_list.analyzed.units",
    "clinical_results.outcome_list.outcome",
    "study_design_info.allocation",
    ## euctr - typical results fields
    # "trialInformation.fullTitle",
    # "baselineCharacteristics.baselineReportingGroups.baselineReportingGroup",
    # "trialChanges.hasGlobalInterruptions",
    # "subjectAnalysisSets",
    # "adverseEvents.seriousAdverseEvents.seriousAdverseEvent",
    "endPoints.endPoint",
    "subjectDisposition.recruitmentDetails"
  ), con = dbc
)
dflong <- dfTrials2Long(df = dfwide)

## get values for the endpoint 'response'
dfName2Value(
  df = dflong,
  valuename = paste0(
    "clinical_results.*measurement.value|",
    "clinical_results.*outcome.measure.units|",
    "endPoints.endPoint.*tendencyValue.value|",
    "endPoints.endPoint.unit"
  ),
  wherename = paste0(
    "clinical_results.*outcome.measure.title|",
    "endPoints.endPoint.title"
  ),
  wherevalue = "response"
)
dfTrials2Long  

Convert data frame with trial records into long format

Description

The function works with protocol- and results-related information. It converts lists and other values that are in a data frame returned by `dbGetFieldsIntoDf` into individual rows of a long data frame. From the resulting long data frame, values of interest can be selected using `dfName2Value`. The function is particularly useful for fields with complex content, such as node field "clinical_results" from EUCTR, for which `dbGetFieldsIntoDf` returns as a multiply nested list and for which this function then converts every observation of every (leaf) field into a row of its own.

Usage

```
dfTrials2Long(df)
```

Arguments

- `df` Data frame (or tibble) with columns including the trial identifier (`id`) and one or more variables as obtained from `dbGetFieldsIntoDf`

Value

A data frame (or tibble, if tibble is loaded) with the four columns: `id`, `identifier`, `name`, `value`

Examples

```r
dbc <- nodbi::src_sqlite(
    dbname = system.file("extdata", "demo.sqlite", package = "ctrdata"),
    collection = "my_trials")

dfwide <- dbGetFieldsIntoDf(
    fields = "clinical_results.participant_flow",
    con = dbc)

dfTrials2Long(df = dfwide)
```
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