Package 'pmparser'

January 13, 2024

Title Create and Maintain a Relational Database of Data from
PubMed/MEDLINE

Version 1.0.20

Description Provides a simple interface for extracting various elements from
the publicly available PubMed XML files, incorporating PubMed's regular
updates, and combining the data with the NIH Open Citation Collection. See
Schoenbachler and Hughey (2021) <doi:10.7717/peerj.11071>.

URL https://pmparser.hugheylab.org,

https://github.com/hugheylab/pmparser

License GPL-2

Encoding UTF-8

RoxygenNote 7.3.0

Depends R (>= 3.6)

Imports curl (>= 4.3.2), data.table (>= 1.12.2), DBI (>= 1.1.0),
foreach (>= 1.5.0), glue (>= 1.4.2), iterators (>= 1.0.12),
jsonlite (>= 1.7.0), R.utils (>= 2.10.1), RCurl (>= 1.98),
withr (>= 2.3.0), xml2 (>= 1.3.3)

Suggests bigrquery (>= 1.3.2), doParallel (>= 1.0.16), RMariaDB (>=
1.0.9), RPostgres (>= 1.2.0), RSQLite (>= 2.2.0), testthat (>=
2.3.2), knitr, rmarkdown

SystemRequirements head, unzip, sqlite

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

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getCitation   *Get public-domain citation data*

Description

Get the latest version of the NIH Open Citation Collection from figshare here, and optionally write it to the database. This function requires the shell command unzip, available by default on most Unix systems. This function should not normally be called directly, as it is called by modifyPubmedDb().

Usage

```
getCitation(
  localDir,
  filename = "open_citation_collection.zip",
  nrows = Inf,
  tableSuffix = NULL,
  overwrite = FALSE,
  con = NULL,
  checkMd5 = TRUE
)
```

Arguments

localDir	String indicating path to directory containing the citation file or to which the citation file should be downloaded.
filename	String indicating name of the citation file. This should not normally be changed from the default.
nrows	Number indicating how many rows of the citation file to read. This should not normally be changed from the default.
tableSuffix	String indicating suffix, if any, to append to the table name.
overwrite	Logical indicating whether to overwrite an existing table.
con	Connection to the database, created using DBI::dbConnect().
checkMd5	Logical indicating whether to download the citation file if the MD5 sums of the local and remote versions do not match. This should not normally be changed from the default.

Value

If con is NULL, the function returns a data.table with columns `citing_pmid` and `cited_pmid`. Beware this is a large table and could swamp the machine's memory. If con is not NULL, the function returns NULL invisibly.

See Also

[parsePmidStatus()](), [modifyPubmedDb()]()

Examples

```
## Not run:
dCitation = getCitation('.')

## End(Not run)
```

---

getPgParams *Get Postgres connection parameters*

Description

This is a helper function to get parameters from a .pgpass file. See here for details.

Usage

```
getPgParams(path = "~/.pgpass")
```

Arguments

path   Path to .pgpass file.

Value

A data.table with one row for each set of parameters.

See Also

[modifyPubmedDb()]()

Examples

```
pg = getPgParams(system.file('extdata', 'pgpass', package = 'pmparser'))
```

---

modifyPubmedDb   *Create or update a PubMed database*

Description

This function downloads PubMed/MEDLINE XML files, parses them, and adds the information to
the database, then downloads the NIH Open Citation Collection and adds it to the database. Only
the most recent version of each PMID is retained. Parsing of XML files will use a parallel backend
if one is registered, such as with `doParallel::registerDoParallel()`.

Usage

```
modifyPubmedDb(
  localDir,
  dbname,
  dbtype = c("postgres", "mariadb", "mysql", "sqlite"),
  nFiles = Inf,
  retry = TRUE,
  nCitations = Inf,
  mode = c("create", "update"),
  ...
)
```

Arguments

localDir	Directory in which to download the files from PubMed.
dbname	Name of database.
dbtype	Type of database, either 'postgres', 'mariadb', 'mysql', or 'sqlite'. Make sure to install the corresponding DBI driver package first: RPostgres, RMariaDB (for both 'mariadb' and 'mysql'), or RSQLite. Due to the large size of the database, SQLite is recommended only for small-scale testing.
nFiles	Maximum number of xml files to parse that are not already in the database. This should not normally be changed from the default.
retry	Logical indicating whether to retry parsing steps that fail.
nCitations	Maximum number of rows of the citation file to read. This should not normally be changed from the default.
mode	String indicating whether to create the database using the baseline files or to update the database using the update files.
...	Other arguments passed to `DBI::dbConnect()`.

Value

NULL, invisibly. Tab-delimited log files will be created in a logs folder in `localDir`.

See Also

parsePmidStatus(), getCitation(), getPgParams()

Examples

```
## Not run:
modifyPubmedDb('.', 'pmdb', mode = 'create')

## End(Not run)
```

---

parseElement   *Parse elements from a PubMed XML file*

Description

Elements are parsed according to the MEDLINE®PubMed® XML Element Descriptions and their Attributes here. These functions should not normally be called directly, as they are called by modifyPubmedDb().

Usage

```
parsePmidStatus(rawXml, filename, con = NULL, tableSuffix = NULL)

parseArticleId(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseArticle(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parsePubHistory(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseJournal(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parsePubType(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseMesh(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseKeyword(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseGrant(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseChemical(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseDataBank(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseComment(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseAbstract(pmXml, dPmid, con = NULL, tableSuffix = NULL)
```

```
parseOther(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseAuthor(pmXml, dPmid, con = NULL, tableSuffix = NULL)

parseInvestigator(pmXml, dPmid, con = NULL, tableSuffix = NULL)
```

Arguments

rawXml	An xml document obtained by loading a PubMed XML file using xml2::read_xml().
filename	A string that will be added to a column xml_filename.
con	Connection to the database, created using DBI::dbConnect().
tableSuffix	String to append to the table names.
pmXml	An xml nodeset derived from rawXml, such as that returned by parsePmidStatus(), where each node corresponds to a PMID.
dPmid	A data.table with one row for each node of pmXml, should have columns pmid, version, and possibly xml_filename.

Value

parsePmidStatus() returns a list of two objects. The first is an xml nodeset in which each node corresponds to a PubmedArticle in the rawXml object. The second is a data.table with columns pmid, version, xml_filename, and status, in which each row corresponds to a PubmedArticle in the rawXml object or a deleted pmid. The status column is parsed from the DeleteCitation and MedlineCitation sections.

The following functions return a data.table or list of data.tables with columns from dPmid plus the columns specified.

parseArticleId(): a data.table with columns id_type and id_value, parsed from the ArticleIdList section. Only id_types "doi" and "pmc" are retained.

parseArticle(): a data.table with columns title, language, vernacular_title, pub_model, and pub_date, parsed from the Article section.

parsePubHistory(): a data.table with columns pub_status and pub_date, parsed from the History section.

parseJournal(): a data.table with columns journal_name, journal_iso, pub_date, pub_year, pub_month, pub_day, medline_date, volume, issue, and cited_medium, parsed from the Journal section.

parsePubType(): a data.table with columns type_name and type_id, parsed from the PublicationTypeList section.

parseMesh(): a list of three data.tables parsed mostly from the MeshHeadingList section. The first has column indexing_method (parsed from the MedlineCitation section), the second has columns descriptor_pos, descriptor_name, descriptor_ui, and descriptor_major_topic, the third has columns descriptor_pos, qualifier_name, qualifier_ui, and qualifier_major_topic.

parseKeyword(): a list of two data.tables parsed from the KeywordList section. The first has column list_owner, the second has columns keyword_name and major_topic.

parseGrant(): a list of two data.tables parsed from the GrantList section. The first has column complete, the second has columns grant_id, acronym, agency, and country.

parseChemical(): a data.table with columns registry_number, substance_name, and substance_ui, parsed from the ChemicalList section.

parseDataBank(): a data.table with columns data_bank_name and accession_number, parsed from the DataBankList section.

parseComment(): a data.table with columns ref_type and ref_pmid, parsed from the CommentsCorrectionsList section.

parseAbstract(): a list of two data.tables parsed from the Abstract section. The first has column copyright. The second has columns text, label, and nlm_category.

parseAuthor(): a list of data.tables parsed from the AuthorList section. The first is for authors and has columns author_pos, last_name, fore_name, initials, suffix, valid, equal_contrib, and collective_name. The second is for affiliations and has columns author_pos, affiliation_pos, and affiliation. The third is for author identifiers and has columns author_pos, source, and identifier. The fourth is for author affiliation identifiers and has columns author_pos, affiliation_pos, source, and identifier. The fifth is for the author list itself and has a column complete.

parseInvestigator(): a list of data.tables similar to those returned by parseAuthor(), except parsed from the InvestigatorList section, with column names containing "investigator" instead of "author", and where the first data.table lacks columns for equal_contrib and collective_name and the fifth data.table does not exist.

parseOther(): a list of data.tables parsed from the OtherAbstract and OtherID sections. The first has columns text, type, and language. The second has columns source and id_value.

See Also

[getCitation()](), [modifyPubmedDb()]()

Examples

```
library('data.table')
library('xml2')

filename = 'pubmed20n1016.xml.gz'
rawXml = read_xml(system.file('extdata', filename, package = 'pmparser'))

pmidStatusList = parsePmidStatus(rawXml, filename)
pmXml = pmidStatusList[[1L]]
dPmidRaw = pmidStatusList[[2L]]
dPmid = dPmidRaw[status != 'Deleted', !'status']

dArticleId = parseArticleId(pmXml, dPmid)
dArticle = parseArticle(pmXml, dPmid)
dJournal = parseJournal(pmXml, dPmid)
dPubType = parsePubType(pmXml, dPmid)
dPubHistory = parsePubHistory(pmXml, dPmid)
meshRes = parseMesh(pmXml, dPmid)
keywordRes = parseKeyword(pmXml, dPmid)
grantRes = parseGrant(pmXml, dPmid)
```

```
dChemical = parseChemical(pmXml, dPmid)
dDataBank = parseDataBank(pmXml, dPmid)
dComment = parseComment(pmXml, dPmid)
abstractRes = parseAbstract(pmXml, dPmid)
authorRes = parseAuthor(pmXml, dPmid)
investigatorRes = parseInvestigator(pmXml, dPmid)
otherRes = parseOther(pmXml, dPmid)
```

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