

Package ‘journalabbr’

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Type Package

Title Journal Abbreviations for BibTeX Documents

Version 0.3.1

Description Since the reference management software (such as 'Zotero', 'Mendeley') exports Bib file journal abbreviation is not detailed enough, the 'journalabbr' package only abbreviates the journal field of Bib file, and then outputs a new Bib file for generating reference format with journal abbreviation on other software (such as 'texstudio'). The abbreviation table is from 'JabRef'. At the same time, 'Shiny' application is provided to generate 'thebibliography', a reference format that can be directly used for latex paper writing based on 'Rmd' files.

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URL <https://github.com/zoushucai/journalabbr>

BugReports <https://github.com/zoushucai/journalabbr/issues>

Encoding UTF-8

Depends R (>= 4.0.0)

Imports data.table, stringr, stringi, dplyr, purrr, tibble, rlang,
httr, shiny

Suggests testthat, tidyr, rclipboard, tinytex, DT, rmarkdown (>= 2.7),
knitr (>= 1.33)

RoxygenNote 7.1.2

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abbr2bib	<i>Journal field abbreviation of BibTeX file</i>
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Description

Input Bib file with complete journal, output Bib file after abbreviation of journal, and return to the abbreviation table of journal

Usage

```
abbr2bib(
  file,
  outfile = tempfile(fileext = ".bib"),
  addcsvpath = "",
  csvsep = ";",
  csvheader = FALSE,
  ...
)
```

Arguments

file	character, input a .bib file.
outfile	character, file path to write the .bib file. An empty character string writes to stdout (default).
addcsvpath	path, Users can customize the path of journal abbreviation. The CSV file requires semicolon to segment data without header. The first column is the full name of the journal and the second column is the journal abbreviation.
csvsep	character, Customize the separator of CSV files. The default is semicolon, that is ;.
csvheader	logical, By default FALSE.
...	(generalized), Parameters from <code>data.table::fread</code> .

Value

output a new Bib file in the current directory, which only abbreviates the journal fields, and the rest remains unchanged. And return to a tibble, it has four columns:

JOURNAL Original journal field in bib

journal_abbr Field after abbreviation of original journal

originFile Abbreviate the source of the database file, see <https://github.com/JabRef/abbrv.jabref.org/tree/master/journals>

is_abbr There are only three cases, 1 represents that the item has a JOURNAL field and has been abbreviated successfully, - 1 means that the item does not have a JOURNAL field, and 0 represents that the item has a JOURNAL field, but the corresponding abbreviation is not found in the database, so the original JOURNAL field is used instead

Examples

```
require(journalabbr)
path = system.file("extdata", "testfile_1.bib", package = "journalabbr", mustWork = TRUE)
temptab = abbr2bib(file = path, outfile = tempfile(fileext = ".bib"))

# add user csv
csvpath = system.file("extdata", "myabbr.csv", package = "journalabbr", mustWork = TRUE)
temptab1 = abbr2bib(file = path, outfile = tempfile(fileext = ".bib"), addcsvpath = csvpath)
```

abbrTable

data abbrTable data

Description

There are four columns, each separated by a semicolon (;), as follows journal journal_abbr journal_lower. count_dot

Usage

```
abbrTable
```

Format

A data frame with columns:

journal Full name of Journal

journal_abbr Abbreviated format of Journal with dots

journal_lower The full name of the journal should be in lowercase and unique

count_dot The number of points in abbreviations of Journal with dots

originFile File source

abbr_len The char length of abbreviations of Journal

Source

<https://github.com/JabRef/abbrev.jabref.org>

Examples

```
require(journalabbr)
require(stringi)
abbrTable = journalabbr::abbrTable
# Unicode to UTF-8
abbrTable = as.data.frame(lapply(abbrTable, function(x)stringi::stri_unescape_unicode(x)))
```

rbind_bib

Merging multiple Bib file

Description

Use `read_bib2tib` to read multiple Bib files. For example, the returned objects are `tib1`, `rib2`, `tib3`, In general, the column names of `tib1`, `tib2`, ..., etc. are not the same. Therefore, this function is used to merge `tib1`, `TiB2`, if the column name does not exist, let it be NA

Usage

```
rbind_bib(..., fill = FALSE)
```

Arguments

```
...          (generalized) tibble or data.frame.
fill        logical, if TRUE the fills missing columns with NAs. By default FALSE.
```

Value

A tibble.

Author(s)

ShuCai Zou

Examples

```
# Read from .bib file:
require(journalabbr)
path1 = system.file("extdata", "testfile_2.bib", package = "journalabbr", mustWork = TRUE)
path2 = system.file("extdata", "testfile_3.bib", package = "journalabbr", mustWork = TRUE)
path3 = system.file("extdata", "testfile_4.bib", package = "journalabbr", mustWork = TRUE)
tib1 <- read_bib2tib(path1)
tib2 <- read_bib2tib(path2)
tib3 <- read_bib2tib(path3)
df = rbind_bib(tib1, tib2, fill=TRUE)
```

```
df1 = rbind_bib(tib1,tib2,tib3,fill=TRUE)
## dont run
# rbind_bib(tib1,tib2)
```

read_bib2tib	<i>Parse a BibTeX file to a tibble</i>
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Description

The BibTeX file is read, parsed, tidied and written to a tibble.

Usage

```
read_bib2tib(file)
```

Arguments

file character, path or URL to a bib file.

Details

Read, parse and collate bibtex file to form a Tibble. Different BIB may produce different tibble columns.

Value

A tibble.

Author(s)

ShuCai Zou

See Also

[abbrTable](#).

Examples

```
# Read from .bib file:
require(journalabbr)
path = system.file("extdata", "testfile_1.bib", package = "journalabbr", mustWork = TRUE)
bib <- read_bib2tib(path)
str(bib)
```

runExample

The Shiny Program for the 'journalabbr' Package

Description

The Shiny Program for the 'journalabbr' Package

Usage

```
runExample()
```

unique_bib

Delete duplicate.

Description

Delete duplicates based on a column (keybib).

Usage

```
unique_bib(tib, on = "keybib", retent_method = c("namin", "first", "last"))
```

Arguments

tib A tibble.

on character, A column in a tibble data frame, The default is keybib

retent_method character, Keep an entry from a duplicate in some way.

"namin" If it is repeated, the row containing the smallest number of NA values is retained. If there are multiple minimum values, the first one is retained

"first" If repeated, keep the first item

"last" If repeated, keep the last item

Value

A tibble.

Examples

```
# Read from .bib file:
require(journalabbr)
path1 = system.file("extdata", "testfile_2.bib", package = "journalabbr", mustWork = TRUE)
path2 = system.file("extdata", "testfile_3.bib", package = "journalabbr", mustWork = TRUE)
path3 = system.file("extdata", "testfile_4.bib", package = "journalabbr", mustWork = TRUE)
tib1 <- read_bib2tib(path1)
tib2 <- read_bib2tib(path2)
tib3 <- read_bib2tib(path3)
df = rbind_bib(tib1,tib2,fill=TRUE)
df1 = rbind_bib(tib1,tib2,tib3,fill=TRUE)
m1 = unique_bib(df1,retent_method='namin')
m2 = unique_bib(df1,retent_method='first')
m3 = unique_bib(df1,retent_method='last')
identical(m1,m2)
identical(m1,m3)
identical(m2,m3)
```

write_tib2bib

Export a BibTeX tibble to a .bib file.

Description

The BibTeX tibble is written to a .bib file.

Usage

```
write_tib2bib(
  tib,
  file = tempfile(fileext = ".bib"),
  append = FALSE,
  isformat = TRUE,
  isdelkeywords = FALSE,
  connect_author = c("nothing", "\\&", "&", "and")
)
```

Arguments

tib	tibble, in the format as returned by read_bib2tib .
file	character, file path to write the .bib file.
append	logical, if TRUE the tibble will be appended to an existing file.
isformat	logical, if TRUE the Fields in tibble will complete braces to make them appear in pairs.
isdelkeywords	logical, if TRUE and there is a picture of column 'isdelkeywords', column 'isdelkeywords' in the tibble will be deleted.
connect_author	character, what symbols are used to connect multiple authors, 'nothing', '\\&', '&', 'and', where 'nothing' stand for do nothing(default).

Value

file as a character string, invisibly.

Examples

```
# Read from .bib file:
require(journalabbr)
path = system.file("extdata", "testfile_1.bib", package = "journalabbr", mustWork = TRUE)
bib <- read_bib2tib(path)
```

```
# Write to .bib file:
write_tib2bib(bib, file = tempfile(fileext = ".bib"))
# Use `append = TRUE` to add lines to an existing .bib file:
```


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