

Package ‘ltertools’

February 23, 2024

Type Package

Title Tools Developed by the Long Term Ecological Research Community

Version 1.0.0

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Description Set of the data science tools created by various members of the Long Term Ecological Research (LTER) community. These functions were initially written largely as standalone operations and have later been aggregated into this package.

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Encoding UTF-8

Language en-US

LazyData true

URL <https://lter.github.io/ltertools/>

BugReports <https://github.com/lter/ltertools/issues>

RoxygenNote 7.2.3

Depends R (>= 3.5)

Imports dplyr, generics, ggplot2, magrittr, purrr, readxl, rlang,
stats, stringr, tidyr, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-02-23 19:00:02 UTC

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begin_key	<i>Generate the Skeleton of a Column Key</i>
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Description

Creates the start of a 'column key' for harmonizing data. A column key includes a column for the file names to be harmonized into a single data object as well as a column for the column names in those files. Finally, it includes a column indicating the tidied name that corresponds with each raw column name. Harmonization can accept this key object and use it to rename all raw column names—in a reproducible way—to standardize across datasets. Currently supports raw files of the following formats: CSV, TXT, XLS, and XLSX

Usage

```
begin_key(
  raw_folder = NULL,
  data_format = c("csv", "txt", "xls", "xlsx"),
  guess_tidy = FALSE
)
```

Arguments

raw_folder	(character) folder / folder path containing data files to include in key
data_format	(character) file extensions to identify within the raw_folder. Default behavior is to search for all supported file types.
guess_tidy	(logical) whether to attempt to "guess" what the tidy name equivalent should be for each raw column name. This is accomplished via coercion to lowercase and removal of special character/repeated characters. If FALSE (the default) the "tidy_name" column is returned empty

Value

(dataframe) skeleton of column key

Examples

```
# Generate two simple tables
## Dataframe 1
df1 <- data.frame("xx" = c(1:3),
                  "unwanted" = c("not", "needed", "column"),
                  "yy" = letters[1:3])
## Dataframe 2
df2 <- data.frame("LETTERS" = letters[4:7],
                  "NUMBERS" = c(4:7),
                  "BONUS" = c("plantae", "animalia", "fungi", "protista"))

# Generate a local folder for exporting
temp_folder <- tempdir()

# Export both files to that folder
utils::write.csv(x = df1, file = file.path(temp_folder, "df1.csv"), row.names = FALSE)
utils::write.csv(x = df2, file = file.path(temp_folder, "df2.csv"), row.names = FALSE)

# Generate a column key with "guesses" at tidy column names
ltertools::begin_key(raw_folder = temp_folder, data_format = "csv", guess_tidy = TRUE)
```

 convert_temp

Convert Temperature Values

Description

Converts a given set of temperature values from one unit to another

Usage

```
convert_temp(value = NULL, from = NULL, to = NULL)
```

Arguments

value	(numeric) temperature values to convert
from	(character) starting units of the value, not case sensitive.
to	(character) units to which to convert, not case sensitive.

Value

(numeric) converted temperature values

Examples

```
# Convert from Fahrenheit to Celsius
convert_temp(value = 32, from = "Fahrenheit", to = "c")
```

cv	<i>Calculate Coefficient of Variation</i>
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Description

Computes the coefficient of variation (CV), by dividing the standard deviation (SD) by the arithmetic mean of a set of numbers. If `na_rm` is TRUE then missing values are removed before calculation is completed

Usage

```
cv(x, na_rm = TRUE)
```

Arguments

x	(numeric) vector of numbers for which to calculate CV
na_rm	(logical) whether to remove missing values from both average and SD calculation

Value

(numeric) coefficient of variation

Examples

```
# Convert from Fahrenheit to Celsius  
cv(x = c(4, 5, 6, 4, 5, 5), na_rm = TRUE)
```

harmonize	<i>Harmonize Data via a Column Key</i>
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Description

A "column key" is meant to streamline harmonization of disparate datasets. This key must include three columns containing: (1) the name of each raw data file to be harmonized, (2) the name of all of the columns in each of those files, and (3) the "tidy name" that corresponds to each raw column name. This function accepts that key and the path to a folder containing all raw data files included in the key. Each dataset is then read in and the original column names are replaced with their respective "tidy_name" indicated in the key. Once this has been done to all files, a single dataframe is returned with only columns indicated in the column name. Currently the following file formats are supported for the raw data: CSV, TXT, XLS, and XLSX

Note that raw column names without an associated tidy name in the key are removed. We recommend using the `begin_key` function in this package to generate the skeleton of the key to make achieving the required structure simpler.

Usage

```
harmonize(
  key = NULL,
  raw_folder = NULL,
  data_format = c("csv", "txt", "xls", "xlsx"),
  quiet = TRUE
)
```

Arguments

key	(dataframe) key object including a "source", "raw_name" and "tidy_name" column. Additional columns are allowed but ignored
raw_folder	(character) folder / folder path containing data files to include in key
data_format	(character) file extensions to identify within the raw_folder. Default behavior is to search for all supported file types.
quiet	(logical) whether to suppress certain non-warning messages. Defaults to TRUE

Value

(dataframe) harmonized dataframe including all columns defined in the "tidy_name" column of the key object

Examples

```
# Generate two simple tables
## Dataframe 1
df1 <- data.frame("xx" = c(1:3),
                  "unwanted" = c("not", "needed", "column"),
                  "yy" = letters[1:3])

## Dataframe 2
df2 <- data.frame("LETTERS" = letters[4:7],
                  "NUMBERS" = c(4:7),
                  "BONUS" = c("plantae", "animalia", "fungi", "protista"))

# Generate a local folder for exporting
temp_folder <- tempdir()

# Export both files to that folder
utils::write.csv(x = df1, file = file.path(temp_folder, "df1.csv"), row.names = FALSE)
utils::write.csv(x = df2, file = file.path(temp_folder, "df2.csv"), row.names = FALSE)

# Generate a column key object manually
key_obj <- data.frame("source" = c(rep("df1.csv", 3),
                                  rep("df2.csv", 3)),
                     "raw_name" = c("xx", "unwanted", "yy",
                                     "LETTERS", "NUMBERS", "BONUS"),
                     "tidy_name" = c("numbers", NA, "letters",
                                     "letters", "numbers", "kingdom"))

# Use that to harmonize the 'raw' files we just created
```

```
ltertools::harmonize(key = key_obj, raw_folder = temp_folder, data_format = "csv")
```

lter_sites

Long Term Ecological Research Site Information

Description

There are currently 28 field sites involved with the Long Term Ecological Research (LTER) network. These sites occupy a range of habitats and were started / are renewed on site-specific timelines. To make this information more readily available to interested parties, this data object summarizes the key components of each site in an easy-to-use data format.

Usage

```
lter_sites
```

Format

Dataframe with 8 columns and 32 rows

name Full name of the LTER site

code Abbreviation (typically three letters) of the site name

habitat Simplified habitat designation of the site (or "mixed" for more complex habitat contexts)

start_year Year of initial funding by NSF as an official LTER site

end_year End of current funding cycle grant

latitude Degrees latitude of site

longitude Degrees longitude of site

site_url Website URL for the site

Source

Long Term Ecological Research Network Office. <https://lternet.edu/site/>

read

Read Data from Folder

Description

Reads in all data files of specified types found in the designated folder. Returns a list with one element for each data file. Currently supports CSV, TXT, XLS, and XLSX

Usage

```
read(raw_folder = NULL, data_format = c("csv", "txt", "xls", "xlsx"))
```

Arguments

`raw_folder` (character) folder / folder path containing data files to read

`data_format` (character) file extensions to identify within the `raw_folder`. Default behavior is to search for all supported file types.

Value

(list) data found in specified folder of specified file format(s)

Examples

```
# Generate two simple tables
## Dataframe 1
df1 <- data.frame("xx" = c(1:3),
                  "unwanted" = c("not", "needed", "column"),
                  "yy" = letters[1:3])
## Dataframe 2
df2 <- data.frame("LETTERS" = letters[4:7],
                  "NUMBERS" = c(4:7),
                  "BONUS" = c("plantae", "animalia", "fungi", "protista"))

# Generate a local folder for exporting
temp_folder <- tempdir()

# Export both files to that folder
utils::write.csv(x = df1, file = file.path(temp_folder, "df1.csv"), row.names = FALSE)
utils::write.csv(x = df2, file = file.path(temp_folder, "df2.csv"), row.names = FALSE)

# Read in all CSV files in that folder
read(raw_folder = temp_folder, data_format = "csv")
```

site_subset	<i>Subsets the LTER Site Information Table by Site Codes and Habitats</i>
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Description

Subsets the information on long term ecological research (LTER) sites based on user-specified site codes (i.e., three letter abbreviations), and/or desired habitats. See `lter_sites` for the full set of site information

Usage

```
site_subset(sites = NULL, habitats = NULL)
```

Arguments

sites	(character) three letter site code(s) identifying site(s) of interest
habitats	(character) habitat(s) of interest. See <code>unique(lter_sites\$habitat)</code>

Value

(dataframe) complete site information (8 columns) for all sites that meet the provided site code and/or habitat criteria

site_timeline	<i>Create a Timeline of Site(s) that Meet Criteria</i>
---------------	--

Description

Creates a `ggplot2` plot of all sites that meet the user-specified site code (i.e., three letter abbreviation) and/or habitat criteria. See `lter_sites` for the full set of site information including accepted site codes and habitat designations (unrecognized entries will trigger a warning and be ignored). Lines are grouped and colored by habitat to better emphasize possible similarities among sites

Usage

```
site_timeline(sites = NULL, habitats = NULL, colors = NULL)
```

Arguments

sites	(character) three letter site code(s) identifying site(s) of interest
habitats	(character) habitat(s) of interest. See <code>unique(lter_sites\$habitat)</code>
colors	(character) colors to assign to the timelines expressed as a hexadecimal (e.g, <code>#00FF00</code>). Note there must be as many colors as habitats included in the graph

Value

(ggplot2) plot object of timeline of site(s) that meet user-specified criteria

Examples

```
# Make the full timeline of all sites with default colors by supplying no arguments  
site_timeline()
```

```
# Or make a timeline of only sites that meet certain criteria  
site_timeline(habitats = c("grassland", "forest"))
```

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