

Package: dmtools (via r-universe)

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Title Tools for Clinical Data Management

Version 0.2.6.9000

Description For checking the dataset from EDC(Electronic Data Capture) in clinical trials. 'dmtools' reshape your dataset in a tidy view and check events. You can reshape the dataset and choose your target to check, for example, the laboratory reference range.

Depends R (>= 3.6)

Imports magrittr (>= 1.5), dplyr (>= 1.0.0), readxl (>= 1.3.1), purrr (>= 0.3.3), lubridate (>= 1.7.4), httr (>= 1.4.1), tidyr (>= 1.1.0), tibble (>= 3.0.1), progress (>= 1.2.2)

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URL <https://github.com/KonstantinRyabov/dmtools>

BugReports <https://github.com/KonstantinRyabov/dmtools/issues>

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

Repository <https://konstantinryabov.r-universe.dev>

RemoteUrl <https://github.com/konstantinryabov/dmtools>

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add_cols	<i>Add columns if columns don't exist</i>
----------	---

Description

Add columns if columns don't exist

Usage

```
add_cols(dset, ds_part, target_cols)
```

Arguments

dset	A data frame. The dataset.
ds_part	A character scalar. Prefix or postfix.
target_cols	A character vector with necessary columns.

Value

A data frame. The dataset.

calc_diff	<i>Function for calculating the difference between two dates</i>
-----------	--

Description

Function for calculating the difference between two dates

Usage

```
calc_diff(st_inter, dt_item)
```

Arguments

st_inter	An interval. An object of interval.
dt_item	A date item. An object of date.

Value

An integer scalar. Differences between the two dates.

check	<i>Check the dataset</i>
-------	--------------------------

Description

Check the dataset

Usage

```
check(obj, dataset)
```

Arguments

obj	An object for check.
dataset	A dataset, a type is a data frame.

Value

An object with a check result.

Examples

```

id <- c("01", "02", "03")
screen_date_E1 <- c("1991-03-13", "1991-03-07", "1991-03-08")
rand_date_E2 <- c("1991-03-15", "1991-03-11", "1991-03-10")
ph_date_E3 <- c("1991-03-21", "1991-03-16", "1991-03-16")
bio_date_E3 <- c("1991-03-23", "1991-03-16", "1991-03-16")

df <- data.frame(id, screen_date_E1, rand_date_E2, ph_date_E3, bio_date_E3,
  stringsAsFactors = FALSE
)

timeline <- system.file("dates.xlsx", package = "dmtools")
obj_date <- date(timeline, id, dplyr::contains)

obj_date <- check(obj_date, df)

```

check.default

Check the dataset

Description

Check the dataset

Usage

```

## Default S3 method:
check(obj, dataset)

```

Arguments

obj An object for check.
dataset A dataset, a type is a data frame.

Value

An object with a check result.

Examples

```

id <- c("01", "02", "03")
screen_date_E1 <- c("1991-03-13", "1991-03-07", "1991-03-08")
rand_date_E2 <- c("1991-03-15", "1991-03-11", "1991-03-10")
ph_date_E3 <- c("1991-03-21", "1991-03-16", "1991-03-16")
bio_date_E3 <- c("1991-03-23", "1991-03-16", "1991-03-16")

df <- data.frame(id, screen_date_E1, rand_date_E2, ph_date_E3, bio_date_E3,
  stringsAsFactors = FALSE
)

```

```
timeline <- system.file("dates.xlsx", package = "dmtools")
obj_date <- date(timeline, id, dplyr::contains)

obj_date <- check(obj_date, df)
```

choose_test

Filter the final result

Description

Filter the final result

Usage

```
choose_test(obj, test, group_id)
```

Arguments

obj	An object for check.
test	Parameters, which use to filter the final dataset.
group_id	A logical scalar, default is TRUE. True is grouped by id, otherwise, it isn't grouped.

Value

The filtered dataset.

Examples

```
id <- c("01", "02", "03")
screen_date_E1 <- c("1991-03-13", "1991-03-07", "1991-03-08")
rand_date_E2 <- c("1991-03-15", "1991-03-11", "1991-03-10")
ph_date_E3 <- c("1991-03-21", "1991-03-16", "1991-03-16")
bio_date_E3 <- c("1991-03-23", "1991-03-16", "1991-03-16")

df <- data.frame(id, screen_date_E1, rand_date_E2, ph_date_E3, bio_date_E3,
  stringsAsFactors = FALSE
)

timeline <- system.file("dates.xlsx", package = "dmtools")
obj_date <- date(timeline, id, dplyr::contains)

obj_date <- check(obj_date, df)
choose_test(obj_date, "out")
```

choose_test.date *Filter the final result of the object date*

Description

Filter the final result of the object date

Usage

```
## S3 method for class 'date'  
choose_test(obj, test = "out", group_id = T)
```

Arguments

obj	An object for calculation. Class date.
test	A character scalar. Parameters, which use to filter the final dataset, default: "out": "out" - dates, which are out of the protocol's timeline, "uneq" - dates, which are unequal, "ok" - correct dates, "skip" - empty dates.
group_id	A logical scalar, default is TRUE. True is grouped by id, otherwise, it isn't grouped.

Value

The dataset by a value of test.

Examples

```
id <- c("01", "02", "03")  
screen_date_E1 <- c("1991-03-13", "1991-03-07", "1991-03-08")  
rand_date_E2 <- c("1991-03-15", "1991-03-11", "1991-03-10")  
ph_date_E3 <- c("1991-03-21", "1991-03-16", "1991-03-16")  
bio_date_E3 <- c("1991-03-23", "1991-03-16", "1991-03-16")  
  
df <- data.frame(id, screen_date_E1, rand_date_E2, ph_date_E3, bio_date_E3,  
  stringsAsFactors = FALSE  
)  
  
timeline <- system.file("dates.xlsx", package = "dmttools")  
obj_date <- date(timeline, id, dplyr::contains)  
  
obj_date <- check(obj_date, df)  
choose_test(obj_date, "out")
```

choose_test.lab	<i>Filter the final result of the object lab</i>
-----------------	--

Description

Filter the final result of the object lab

Usage

```
## S3 method for class 'lab'
choose_test(obj, test = "mis", group_id = T)
```

Arguments

obj	An object. Class lab.
test	A character scalar. Parameters, which use to filter the final dataset, default: "mis": "ok" - analysis, which has a correct estimate of the result, "mis" - analysis, which has an incorrect estimate of the result, "skip" - analysis, which has an empty value of the estimate, "null" - analysis, which has an empty result and value of the estimate.
group_id	A logical scalar, default is TRUE. True is grouped by id, otherwise, it isn't grouped.

Value

The filtered dataset by a value of test.

Examples

```
ID <- c("01", "02", "03")
SITE <- c("site 01", "site 02", "site 03")
AGE <- c("19", "20", "22")
SEX <- c("f", "m", "f")
GLUC_V1 <- c(5.5, 4.1, 9.7)
GLUC_IND_V1 <- c("norm", "no", "c1")
AST_V2 <- c("30", "48", "31")
AST_IND_V2 <- c(NA, "norm", "norm")

df <- data.frame(
  ID, SITE, AGE, SEX,
  GLUC_V1, GLUC_IND_V1,
  AST_V2, AST_IND_V2,
  stringsAsFactors = FALSE
)

refs <- system.file("labs_refer.xlsx", package = "dmtools")
obj_lab <- lab(refs, ID, AGE, SEX, "norm", "no")
```

```
obj_lab <- check(obj_lab, df)
choose_test(obj_lab, "mis")
```

create_spec	<i>For creating part of the specification</i>
-------------	---

Description

For creating part of the specification

Usage

```
create_spec(df_spec, all_colname, part_spec, is_pst)
```

Arguments

df_spec	A dataset, a type is a data frame.
all_colname	A character vector with all names in the dataset.
part_spec	A character scalar. Prefixes or postfixes.
is_pst	A logical scalar, default is TRUE. True is postfix, otherwise, prefix.

Value

A data frame. Part of the specification.

date	<i>Create object date</i>
------	---------------------------

Description

Create object date

Usage

```
date(file, id, get_visit, get_date = dplyr::contains, str_date = "DAT")
```

Arguments

file	A character scalar. Path to the date's parameters in the excel table.
id	A column name of the subject id in the dataset, without quotes.
get_visit	A function, which select necessary visit or event e.g. dplyr::start_with, dplyr::contains.
get_date	A function, which select dates from necessary visit e.g. dplyr::matches, dplyr::contains, default: dplyr::contains.
str_date	A date's pattern in column names, default: "DAT".

Value

The object date.

Examples

```
obj_date <- date("dates.xlsx", id, dplyr::contains)
obj_date <- date("dates.xlsx", id, dplyr::contains, "uneq")
```

dmtools	<i>dmtools: package to validate data</i>
---------	--

Description

for checking the dataset from EDC in clinical trials

find_colnames	<i>Find column names</i>
---------------	--------------------------

Description

Find column names

Usage

```
find_colnames(obj, dataset, row_file)
```

Arguments

obj	An object for check.
dataset	A dataset, a type is a data frame.
row_file	A row of the file.

Value

A data frame. Result of run_tests.

find_colnames.date *Find column names with dates*

Description

Find column names with dates

Usage

```
## S3 method for class 'date'  
find_colnames(obj, dataset, row_file)
```

Arguments

obj	An object for validation.
dataset	A data frame. Class date.
row_file	A data frame. A data frame with analysis parameters.

Value

A data frame. Visit's dates.

find_colnames.default *Find column names*

Description

Find column names

Usage

```
## Default S3 method:  
find_colnames(obj, dataset, row_file)
```

Arguments

obj	An object for validation.
dataset	A dataset, a type is a data frame.
row_file	A row of the file.

Value

A data frame. Result of run_tests.

get_result	<i>Get the final result of the check</i>
------------	--

Description

Get the final result of the check

Usage

```
get_result(obj, group_id = T)
```

Arguments

obj	An object. Can be all classes: short, lab, date.
group_id	A logical scalar, default is TRUE. True is grouped by id, otherwise, it isn't grouped.

Value

A data frame. The final result.

Examples

```
id <- c("01", "02", "03")
site <- c("site 01", "site 02", "site 03")
sex <- c("f", "m", "f")
preg_yn_e2 <- c("y", "y", "y")
preg_res_e2 <- c("neg", "neg", "neg")
preg_yn_e3 <- c("y", "y", "n")
preg_res_e3 <- c("neg", "pos", "unnes")

df <- data.frame(
  id, site, sex,
  preg_yn_e2, preg_res_e2,
  preg_yn_e3, preg_res_e3,
  stringsAsFactors = FALSE
)

preg <- system.file("preg.xlsx", package = "dmtools")
obj_short <- short(preg, id, "LBORRES", c("site", "sex"))

obj_short <- check(obj_short, df)
get_result(obj_short)
```

lab*Create object lab*

Description

Create object lab

Usage

```
lab(  
  file,  
  id,  
  age,  
  sex,  
  normal,  
  abnormal,  
  is_post = T,  
  name_to_find = "LBNRIND"  
)
```

Arguments

<code>file</code>	A character scalar. Path to the laboratory's reference in the excel table.
<code>id</code>	A column name of the subject id in the dataset, without quotes.
<code>age</code>	A column name of the subject age in the dataset, without quotes.
<code>sex</code>	A column name of the subject sex in the dataset, without quotes.
<code>normal</code>	A normal estimate, for example, "NORMAL".
<code>abnormal</code>	An abnormal estimate, for example, "ABNORMAL".
<code>is_post</code>	A logical scalar, default is TRUE. True is postfix, otherwise, prefix.
<code>name_to_find</code>	A character scalar. For search prefixes or postfixes, default is "LBNRIND".

Value

The object lab.

Examples

```
obj_lab <- lab("lab_refer.xlsx", ID, AGE, SEX, 1, 2)  
obj_lab <- lab("lab_refer.xlsx", ID, AGE, SEX, "NORMAL", "ABNORMAL")  
obj_lab <- lab("lab_refer.xlsx", ID, AGE, SEX, "norm", "no", FALSE)
```

list_parse	<i>A list to a tibble.</i>
------------	----------------------------

Description

A list to a tibble.

Usage

```
list_parse(to_tibble)
```

Arguments

to_tibble A list with nested lists.

Value

A tibble.

Examples

```
temp_list <- list(list(a = 1, b = 3), list(a = 4, b = 5))
list_parse(temp_list)
```

meddra_auth	<i>Get the token</i>
-------------	----------------------

Description

Get the token

Usage

```
meddra_auth(target_url, meddra_id, api_key)
```

Arguments

target_url The url for authenticate.
meddra_id The user's meddra id.
api_key The user's api key.

Value

A string scalar. The user's token.

Examples

```
## Not run:
meddra_auth(url, id, key)

## End(Not run)
```

meddra_post	<i>Create the post query</i>
-------------	------------------------------

Description

Create the post query

Usage

```
meddra_post(target_url, json, token)
```

Arguments

target_url	The url for a post query.
json	A string scalar or a list. The json query.
token	The user's token.

Value

A list. The result of query.

Examples

```
## Not run:
meddra_post(url, json_body, token)

## End(Not run)
```

rename_dataset	<i>For rename dataset</i>
----------------	---------------------------

Description

For rename dataset

Usage

```
rename_dataset(
  dataset,
  path_crfs,
  no_readable_name,
  readable_name,
  num_sheet = 1,
  extension = "*.xlsx",
  is_post = T
)
```

Arguments

dataset	A dataset, a type is a data frame.
path_crfs	A character scalar. Path to the specification files the in excel table.
no_readable_name	A character scalar. A column name of no_readable values.
readable_name	A character scalar. A column name of readable values.
num_sheet	An integer scalar, default is the first sheet. A position of a sheet in the excel document.
extension	A character scalar. A extension of files, default is *.xlsx.
is_post	A logical scalar, default is TRUE. True is postfix, otherwise, prefix.

Value

The list with two values: data - renamed dataset, spec - common specification. The common specification is data frame of two values: no_readable_var, readable_var.

Examples

```
id <- c("01", "02", "03")
age <- c("19", "20", "22")
sex <- c("f", "m", "f")
bio_date_post <- c("1991-03-23", "1991-03-16", "1991-03-16")
gluc_post <- c("5.5", "4.1", "9.7")
gluc_res_post <- c("norm", "no", "norm")

df <- data.frame(
  id, age, sex,
  bio_date_post,
  gluc_post, gluc_res_post,
  stringsAsFactors = FALSE
)

crfs <- system.file("forms", package = "dmttools")

result <- rename_dataset(df, crfs, "old_name", "new_name")
result[["data"]]
```

short

Create object short

Description

Create object short

Usage

```
short(  
  file,  
  id,  
  name_to_find,  
  common_cols = NULL,  
  extra = NULL,  
  is_post = T,  
  is_add_cols = F  
)
```

Arguments

file	A character scalar. Path to the excel table.
id	A column name of the subject id in the dataset, without quotes.
name_to_find	A character scalar. For search prefixes or postfixes.
common_cols	A character vector. A column names in the dataset, which common for all events.
extra	A character scalar. For additional information.
is_post	A logical scalar, default is TRUE. True is postfix, otherwise, prefix.
is_add_cols	A logical scalar, default is FALSE. If necessary add columns.

Value

The object short.

Examples

```
obj_short <- short("preg.xlsx", id, "res", c("site", "sex"))  
obj_short <- short("labs.xlsx", id, "name_labs", c("site"), "human_name")
```

to_dbl	<i>Cast to double type</i>
--------	----------------------------

Description

Cast to double type

Usage

```
to_dbl(vals)
```

Arguments

vals A character or double vector.

Value

A double vector.

to_long	<i>Reshape the dataset to a long view</i>
---------	---

Description

Reshape the dataset to a long view

Usage

```
to_long(obj, dataset, row_file, part)
```

Arguments

obj An object for check.
dataset A data frame.
row_file A data frame. A data frame with parameters.
part A character scalar. Prefixes or postfixes.

Value

A data frame. The part of final result.

to_long.date	<i>Reshape the dataset to a long view</i>
--------------	---

Description

Reshape the dataset to a long view

Usage

```
## S3 method for class 'date'
to_long(obj, dataset, row_file, date)
```

Arguments

obj	An object for validation.
dataset	A data frame. Class date.
row_file	A data frame. A data frame with analysis parameters.
date	A column name with dates.

Value

A data frame. Result of the date's validation.

to_long.lab	<i>Reshape the dataset to a long view</i>
-------------	---

Description

Reshape the dataset to a long view

Usage

```
## S3 method for class 'lab'
to_long(obj, dataset, row_file, part)
```

Arguments

obj	An object. Class lab.
dataset	A data frame.
row_file	A data frame. A data frame with parameters.
part	A character scalar. Prefixes or postfixes.

Value

A data frame. The part of the final result.

to_long.short	<i>Reshape the dataset to a long view</i>
---------------	---

Description

Reshape the dataset to a long view

Usage

```
## S3 method for class 'short'  
to_long(obj, dataset, row_file, part)
```

Arguments

obj	An object. Class short.
dataset	A data frame.
row_file	A data frame. A data frame with parameters.
part	A character scalar. Prefixes or postfixes.

Value

A data frame. The part of the final result.

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