

Package: codified (via r-universe)

June 21, 2024

Title Produce Standard/Formalized Demographics Tables

Description Augment clinical data with metadata to create output used in conventional publications and reports.

Version 0.3.0

URL <https://ouhscbbmc.github.io/codified/>,
<https://github.com/OuhscBbmc/codified>,
https://github.com/higgi13425/nih_enrollment_table

BugReports <https://github.com/OuhscBbmc/codified/issues>

Depends R(>= 4.1.0)

Imports checkmate (>= 1.8.4), dplyr (>= 1.0.0), kableExtra, knitr (>= 1.18.0), rlang, tibble (>= 1.4.0), tidyr (>= 1.0.0)

Suggests covr, readr (>= 1.1.0), REDCapR, rmarkdown, testthat (>= 3.0)

License MIT + file LICENSE

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.2.1

Roxygen list(markdown = TRUE)

Config/testthat/edition 3

Language en-US

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

RemoteUrl <https://github.com/ouhscbbmc/codified>

RemoteRef HEAD

RemoteSha a37760d3b1d6aa304bb949875993dfb02cb1770d

Contents

table_nih_enrollment 2

Index 5

table_nih_enrollment *Produce an NIH-compliant enrollment table.*

Description

Produce an NIH enrollment table, leveraging metadata to adapt to the observed [data.frame](#).

Usage

```
table_nih_enrollment(  
  d,  
  d_lu_gender = NULL,  
  d_lu_race = NULL,  
  d_lu_ethnicity = NULL,  
  variable_gender = "gender",  
  variable_race = "race",  
  variable_ethnicity = "ethnicity"  
)
```

Arguments

d [data.frame](#) of observed values in the investigation. Required.

d_lu_gender [data.frame](#) that maps the observed levels of gender to the NIH-recommended levels of gender. Required only if the levels are not the same.

d_lu_race [data.frame](#) that maps the observed levels of gender to the NIH-recommended levels of gender. Required only if the levels are not the same.

d_lu_ethnicity [data.frame](#) that maps the observed levels of gender to the NIH-recommended levels of gender. Required only if the levels are not the same.

variable_gender name of the gender variable in the d [data.frame](#). Defaults to gender.

variable_race name of the race variable in the d [data.frame](#). Defaults to race.

variable_ethnicity name of the ethnicity variable in the d [data.frame](#). Defaults to ethnicity.

Details

<https://grants.nih.gov/grants/how-to-apply-application-guide/forms-d/general/g.500-phs-inclusion-enrollment-report.htm>

Value

Table for publication

Author(s)

Will Beasley, Peter Higgins, Andrew Peters, Sreeharsha Mandem

Examples

```

ds_1 <- tibble::tribble(
  ~subject_id, ~gender, ~race, ~ethnicity,
  1L, "Male", "Black or African American", "Not Hispanic or Latino",
  2L, "Male", "Black or African American", "Not Hispanic or Latino",
  3L, "Female", "Black or African American", "Unknown/Not Reported Ethnicity",
  4L, "Male", "White", "Not Hispanic or Latino",
  5L, "Male", "White", "Not Hispanic or Latino",
  6L, "Female", "White", "Not Hispanic or Latino",
  7L, "Male", "White", "Hispanic or Latino",
  8L, "Male", "White", "Hispanic or Latino"
)

table_nih_enrollment(ds_1)
table_nih_enrollment_pretty(ds_1)

table_nih_enrollment(ds_1) |>
  tidyr::pivot_wider(names_from = gender, values_from = n)

table_nih_enrollment(ds_1) |>
  dplyr::mutate(
    gender_ethnicity = paste0(gender, " by ", ethnicity)
  ) |>
  dplyr::select(-gender, -ethnicity) |>
  tidyr::pivot_wider(names_from = gender_ethnicity, values_from = n)

ds_2 <- tibble::tribble(
  ~subject_id, ~gender, ~race, ~ethnicity,
  1L, "Male", "Black or African American", "Not Latino",
  2L, "Male", "Black or African American", "Not Latino",
  3L, "Female", "Black or African American", "Unknown",
  4L, "Male", "White", "Not Latino",
  5L, "Male", "White", "Not Latino",
  6L, "Female", "White", "Not Latino",
  7L, "Male", "White", "Latino",
  8L, "Male", "White", "Latino"
)

ds_lu_ethnicity <- tibble::tribble(
  ~input, ~displayed,
  "Not Latino", "Not Hispanic or Latino",
  "Latino", "Hispanic or Latino",
  "Unknown", "Unknown/Not Reported Ethnicity"
)

table_nih_enrollment(ds_2, d_lu_ethnicity = ds_lu_ethnicity)
table_nih_enrollment_pretty(ds_2, d_lu_ethnicity = ds_lu_ethnicity)

## Read a 500-patient fake dataset
path <- system.file("misc/example-data-1.csv", package = "codified")
ds_3 <- readr::read_csv(path) |>
  dplyr::mutate(
    gender = as.character(gender),

```

```

    race      = as.character(race),
    ethnicity = as.character(ethnicity)
  )

ds_lu_gender <- tibble::tribble(
  ~input, ~displayed,
  "0"    , "Female",
  "1"    , "Male",
  "U"    , "Unknown/Not Reported"
)

ds_lu_race <- tibble::tribble(
  ~input, ~displayed,
  "1"    , "American Indian/Alaska Native",
  "2"    , "Asian",
  "3"    , "Native Hawaiian or Other Pacific Islander",
  "4"    , "Black or African American",
  "5"    , "White",
  "M"    , "More than One Race",
  "6"    , "Unknown or Not Reported"
)

ds_lu_ethnicity <- tibble::tribble(
  ~input, ~displayed,
  "2"    , "Not Hispanic or Latino",
  "1"    , "Hispanic or Latino",
  "0"    , "Unknown/Not Reported Ethnicity"
)

table_nih_enrollment(
  d      = ds_3,
  d_lu_gender = ds_lu_gender,
  d_lu_race  = ds_lu_race,
  d_lu_ethnicity = ds_lu_ethnicity
)

table_nih_enrollment_pretty(
  d      = ds_3,
  d_lu_gender = ds_lu_gender,
  d_lu_race  = ds_lu_race,
  d_lu_ethnicity = ds_lu_ethnicity
)

```

Index

`data.frame`, 2

`table_nih_enrollment`, 2

`table_nih_enrollment_pretty`
 (`table_nih_enrollment`), 2