

# Package ‘codified’

September 11, 2018

**Title** Produce Standard/Formalized Demographics Tables

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

**Version** 0.2.0

**Date** 2018-09-06

**URL** <https://ouhscbbmc.github.io/codified/>, <https://github.com/0uhscBbmc/codified>, [https://github.com/higgi13425/nih\\_enrollment\\_table](https://github.com/higgi13425/nih_enrollment_table)

**BugReports** <https://github.com/0uhscBbmc/codified/issues>

**Depends** R(>= 3.0.0),  
stats

**Imports** checkmate (>= 1.8.4),  
dplyr (>= 0.7.0),  
kableExtra,  
knitr (>= 1.18.0),  
magrittr,  
methods,  
readr (>= 1.1.0),  
rlang,  
tibble (>= 1.4.0),  
tidyr (>= 0.7.0)

**Suggests** devtools,  
REDCapR,  
rmarkdown,  
testthat (>= 2.0)

**License** MIT + file LICENSE

**LazyData** TRUE

**VignetteBuilder** knitr

**Encoding** UTF-8

**RoxygenNote** 6.1.0

**Roxygen** list(markdown = TRUE)

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table_nih_enrollment	<i>Produce an NIH-compliant enrollment table.</i>
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**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)**

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**Examples**

```

library(magrittr)
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::spread(key=gender, value=n)

table_nih_enrollment(ds_1) %>%
  dplyr::mutate(
    gender_ethnicity = paste0(gender, " by ", ethnicity)
  ) %>%
  dplyr::select(-gender, -ethnicity) %>%
  tidyr::spread(key=gender_ethnicity, value=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
)

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