TLG-cat-demogra-tbl.R

Admin

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```r
# Table _ Demography

library(tern)
```

```
## Loading required package: rtables
```

```
## Loading required package: formatters
```

```
##
## Attaching package: 'formatters'
```

```
## The following object is masked from 'package:base':
##
##      %||%
```

```
## Loading required package: magrittr
```

```
##
## Attaching package: 'rtables'
```

```
## The following object is masked from 'package:utils':
##
##      str
```

```
## Registered S3 method overwritten by 'tern':
##    method    from
##    tidy.glm broom
```

```r
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##      filter, lag
```

```
## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
```

```r
library(tidyr)
```

```
##
## Attaching package: 'tidyr'
```

```
## The following object is masked from 'package:magrittr':
##
##     extract
```

```r
adsl <- random.cdisc.data::cadsl
advs <- random.cdisc.data::cadvs
adsub <- random.cdisc.data::cadsub

# Ensure character variables are converted to factors and empty strings and NAs are explicit
missing levels.
adsl <- df_explicit_na(adsl)
advs <- df_explicit_na(advs)
adsub <- df_explicit_na(adsub)

# Change description in variable SEX.
adsl <- adsl %>%
  mutate(
    SEX = factor(case_when(
      SEX == "M" ~ "Male",
      SEX == "F" ~ "Female",
      SEX == "U" ~ "Unknown",
      SEX == "UNDIFFERENTIATED" ~ "Undifferentiated"
    )),
    AGEGR1 = factor(
      case_when(
        between(AGE, 18, 40) ~ "18-40",
        between(AGE, 41, 64) ~ "41-64",
        AGE > 64 ~ ">=65"
      ),
      levels = c("18-40", "41-64", ">=65")
    ),
    BMRKR1_CAT = factor(
      case_when(
        BMRKR1 < 3.5 ~ "LOW",
        BMRKR1 >= 3.5 & BMRKR1 < 10 ~ "MEDIUM",
        BMRKR1 >= 10 ~ "HIGH"
      ),
      levels = c("LOW", "MEDIUM", "HIGH")
    )
  ) %>%
  var_relabel(
    BMRKR1_CAT = "Biomarker 1 Categories"
  )
# The developer needs to do pre-processing to add necessary variables based on ADVS to analys
is dataset.
# Obtain SBP, DBP and weight.
get_param_advs <- function(pname, plabel) {
  ds <- advs %>%
    filter(PARAM == plabel & AVISIT == "BASELINE") %>%
    select(USUBJID, AVAL)

  colnames(ds) <- c("USUBJID", pname)

  ds
}
# The developer needs to do pre-processing to add necessary variables based on ADSUB to analy
sis dataset.
# Obtain baseline BMI (BBMISI).
get_param_adsub <- function(pname, plabel) {
```

```r
  ds <- adsub %>%
    filter(PARAM == plabel) %>%
    select(USUBJID, AVAL)

  colnames(ds) <- c("USUBJID", pname)

  ds
}
adsl <- adsl %>%
  left_join(get_param_advs("SBP", "Systolic Blood Pressure"), by = "USUBJID") %>%
  left_join(get_param_advs("DBP", "Diastolic Blood Pressure"), by = "USUBJID") %>%
  left_join(get_param_advs("WGT", "Weight"), by = "USUBJID") %>%
  left_join(get_param_adsub("BBMISI", "Baseline BMI"), by = "USUBJID")

vars <- c("AGE", "AGEGR1", "SEX", "ETHNIC", "RACE", "BMRKR1")
var_labels <- c(
  "Age (yr)",
  "Age Group",
  "Sex",
  "Ethnicity",
  "Race",
  "Continous Level Biomarker 1"
)

result <- basic_table(show_colcounts = TRUE) %>%
  split_cols_by(var = "ACTARM") %>%
  add_overall_col("All Patients") %>%
  analyze_vars(
    vars = vars,
    var_labels = var_labels
  ) %>%
  build_table(adsl)

result
```

```
##                                  A: Drug X   B: Placebo   C: Combination
All Patients
##                                    (N=134)     (N=134)       (N=132)
(N=400)
##
   ─────────────────────────────────────────────────────────────────────────

   ──────────

## Age (yr)
##     n                               134         134           132
400
##     Mean (SD)                    33.8 (6.6)   35.4 (7.9)    35.4 (7.7)
34.9 (7.4)
##     Median                          33.0        35.0          35.0
34.0
##     Min - Max                   21.0 - 50.0  21.0 - 62.0   20.0 - 69.0
20.0 - 69.0
## Age Group
##     n                               134         134           132
400
##     18-40                       113 (84.3%)  103 (76.9%)   106 (80.3%)
322 (80.5%)
##     41-64                        21 (15.7%)   31 (23.1%)    25 (18.9%)
77 (19.2%)
##     >=65                             0            0          1 (0.8%)
1 (0.2%)
## Sex
##     n                               134         134           132
400
##     Female                        79 (59%)    82 (61.2%)     70 (53%)
231 (57.8%)
##     Male                          55 (41%)    52 (38.8%)     62 (47%)
169 (42.2%)
## Ethnicity
##     n                               134         134           132
400
##     HISPANIC OR LATINO           15 (11.2%)   18 (13.4%)    15 (11.4%)
48 (12%)
##     NOT HISPANIC OR LATINO      104 (77.6%)  103 (76.9%)   101 (76.5%)
308 (77%)
##     NOT REPORTED                  6 (4.5%)    10 (7.5%)     11 (8.3%)
27 (6.8%)
##     UNKNOWN                       9 (6.7%)     3 (2.2%)      5 (3.8%)
17 (4.2%)
## Race
##     n                               134         134           132
400
##     ASIAN                        68 (50.7%)    67 (50%)     73 (55.3%)
208 (52%)
##     BLACK OR AFRICAN AMERICAN    31 (23.1%)   28 (20.9%)    32 (24.2%)
91 (22.8%)
##     WHITE                        27 (20.1%)   26 (19.4%)    21 (15.9%)
74 (18.5%)
##     AMERICAN INDIAN OR ALASKA NATIVE   8 (6%)  11 (8.2%)     6 (4.5%)
25 (6.2%)
##     MULTIPLE                         0         1 (0.7%)         0
```

```
1 (0.2%)
##    NATIVE HAWAIIAN OR OTHER PACIFIC ISLANDER            0         1 (0.7%)          0
1 (0.2%)
##    OTHER                                                0            0              0
0
##    UNKNOWN                                              0            0              0
0
## Continous Level Biomarker 1
##    n                                                  134          134            132
400
##    Mean (SD)                                      6.0 (3.6)    5.7 (3.3)      5.6 (3.5)
5.8 (3.4)
##    Median                                             5.4          4.8            4.6
4.8
##    Min - Max                                    0.4 - 17.7   0.6 - 14.2     0.2 - 21.4
0.2 - 21.4
```