

01_table1_demographic

randy

2023-10-24

- Table1 has three different versions :
 - the basic training & testing
 - the basic training & testing + overall
 - the basic training & testing + pvalues
- Do we need to include too many variables not used in the paper?
 - ethnicity
 - genotype

Setup

```
## set seed
set.seed(555)
# load("data/sysdata.rda")
# load("final/epic_clean_full_data.Rdata")

# the code to prepare for
# epic, demog, test and train
# data0, data1, and data2
# they are all saved in sysdata.rda files
data <- left_join(epic, demog, by = "id") %>%
  mutate(sex = as.factor(sex))
test_id <- unique(test$id) %>% unlist()
train_id <- unique(train$id) %>% unlist()

data0 <- data %>%
  mutate(group = case_when(id %in% test_id ~ "testing",
                           TRUE ~ "training"))
data1 <- data0 %>%
  group_by(id, group) %>%
  summarize(age_mean = mean(age),
            age_min = min(age),
            age_max = max(age),
            age_n = length(age),
            visitn = n(),
            h_mean = mean(ht),
            h_max = max(ht),
            h_min = min(ht),
            w_mean = mean(wt),
```

```

        w_max = max(wt),
        w_min = min(wt),
        sex = sex,
        genotype = genotype,
        ethnic = ethnic,
        race = race) %>%

ungroup() %>%
unique()

# working dataset
data2 <- full_join(data1, data,
                   by = join_by(id, sex, genotype, ethnic, race)) %>%
  as.data.frame() %>%
  mutate(time = age - age_min,
         age_diff = age_max - age_min)

write.csv(data1, file = paste0("data/S01_table1_dataset_randy_", Sys.Date(), ".csv"))
write.csv(data2, file = paste0("data/S01_epic_clean_randy_", Sys.Date(), ".csv"))

```

Making table1

```

library(readr)
data1 <- read_csv("data/S01_table1_dataset_randy_2023-08-23.csv")

## table0 contains all the information about demgo for total
table0 <- data1 %>%
  unique() %>%
  dplyr::select(-id) %>%
  mutate(ethnic = case_when(ethnic == 1 ~ "Hispanic",
                           ethnic == 2 ~ "Non-Hispanic"),
         race = case_when(race == 1 ~ "White",
                          race != 1 ~ "Other"),
         sex = case_when(sex == "F" ~ "Female",
                         sex == "M" ~ "Male"),
         age_diff = age_max - age_min) %>%
  dplyr::select(group,
               Genotype = genotype,
               Gender = sex,
               Race = race,
               Ethnicity = ethnic,
               "Visit number" = visitn,
               # "Age mean" = age_mean,
               "Age baseline" = age_min,
               "Age final" = age_max,
               "Follow up years" = age_diff,
               # "Height mean" = h_mean,
               "Height baseline" = h_min) %>%
  # "Weight mean" = w_mean,
  # "Weight baseline" = w_min
## select all the variables for table1

```

```

tbl_summary(by = group) %>%
## just display all the variables in one column
modify_header(label = "***Characteristics**") %>%
# update the column header
bold_labels() %>%
italicize_labels() %>%
# as.data.frame()
as_flex_table() %>%
flextable::bold(part = "header") %>%
## auto adjust the column widths
flextable::autofit()

## table1 contains information of dataset grouped as training and testing
table1 <- data1 %>%
  unique() %>%
  dplyr::select(-id) %>%
  mutate(ethnic = case_when(ethnic == 1 ~ "Hispanic",
                             ethnic == 2 ~ "Non-Hispanic"),
         race = case_when(race == 1 ~ "White",
                           race != 1 ~ "Other"),
         sex = case_when(sex == "F" ~ "Female",
                          sex == "M" ~ "Male"),
         age_diff = age_max - age_min) %>%
  dplyr::select(group,
                Genotype = genotype,
                Gender = sex,
                Race = race,
                Ethnicity = ethnic,
                "Visit number" = visitn,
                # "Age mean" = age_mean,
                "Age baseline" = age_min,
                "Age final" = age_max,
                "Follow up years" = age_diff,
                # "Height mean" = h_mean,
                "Height baseline" = h_min) %>%
  # "Weight mean" = w_mean,
  # "Weight baseline" = w_min)
## select all the variables for table1
tbl_summary(by = group) %>%
## just display all the variables in one column
modify_header(label = "***Characteristics**") %>%
# update the column header
bold_labels() %>%
add_p() %>%
italicize_labels() %>%
as.data.frame()

## table1 contains information of dataset grouped as training and testing
table2 <- data1 %>%
  unique() %>%
  dplyr::select(-id) %>%
  mutate(ethnic = case_when(ethnic == 1 ~ "Hispanic",

```

```

        ethnic == 2 ~ "Non-Hispanic"),
  race = case_when(race == 1 ~ "White",
                  race != 1 ~ "Other"),
  sex = case_when(sex == "F" ~ "Female",
                 sex == "M" ~ "Male"),
  age_diff = age_max - age_min) %>%
dplyr::select(group,
              Genotype = genotype,
              Gender = sex,
              Race = race,
              Ethnicity = ethnic,
              "Visit number" = visitn,
              # "Age mean" = age_mean,
              "Age baseline" = age_min,
              # "Age final" = age_max,
              "Follow up years" = age_diff,
              # "Height mean" = h_mean,
              "Height baseline" = h_min) %>%
# "Weight mean" = w_mean,
# "Weight baseline" = w_min)
## select all the variables for table1
tbl_summary(by = group,
            statistic = list(all_continuous() ~ "{mean} ({sd})") ) %>%
## just display all the variables in one column
modify_header(label = "**Characteristics**") %>%
# update the column header
bold_labels() %>%
add_overall(last = TRUE) %>%
italicize_labels()

```

Saving for the table1

```
sessionInfo()
```

```

#> R version 4.2.2 (2022-10-31)
#> Platform: aarch64-apple-darwin20 (64-bit)
#> Running under: macOS 14.0
#>
#> Matrix products: default
#> BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
#> LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
#>
#> locale:
#> [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
#>
#> attached base packages:
#> [1] stats      graphics  grDevices  utils      datasets  methods   base
#>
#> other attached packages:
#> [1] flextable_0.9.2 gtsummary_1.7.1 lubridate_1.9.2 forcats_1.0.0
#> [5] stringr_1.5.0  dplyr_1.1.2    purrr_1.0.1   readr_2.1.4

```

```

#> [9] tidyr_1.3.0      tibble_3.2.1      ggplot2_3.4.3     tidyverse_2.0.0
#> [13] here_1.0.1
#>
#> loaded via a namespace (and not attached):
#> [1] Rcpp_1.0.11      freshr_1.0.2      rprojroot_2.0.3
#> [4] digest_0.6.33    utf8_1.2.3        mime_0.12
#> [7] R6_2.5.1         backports_1.4.1   evaluate_0.21
#> [10] pillar_1.9.0     gdtools_0.3.3     rlang_1.1.1
#> [13] uuid_1.1-0       curl_5.0.1        rstudioapi_0.15.0
#> [16] data.table_1.14.8 rmarkdown_2.23    textshaping_0.3.6
#> [19] bit_4.0.5        munsell_0.5.0     broom_1.0.5
#> [22] shiny_1.7.4.1    compiler_4.2.2    httpuv_1.6.11
#> [25] xfun_0.39        askpass_1.1       pkgconfig_2.0.3
#> [28] systemfonts_1.0.4 gfonts_0.2.0     htmltools_0.5.5
#> [31] openssl_2.1.0    tidyselect_1.2.0  fontBitstreamVera_0.1.1
#> [34] httpcode_0.3.0   fansi_1.0.4       crayon_1.5.2
#> [37] tzdb_0.4.0       withr_2.5.0       later_1.3.1
#> [40] crul_1.4.0       grid_4.2.2        jsonlite_1.8.7
#> [43] xtable_1.8-4     gtable_0.3.3      lifecycle_1.0.3
#> [46] magrittr_2.0.3   scales_1.2.1      zip_2.3.0
#> [49] vroom_1.6.3      cli_3.6.1         stringi_1.7.12
#> [52] broom.helpers_1.13.0 promises_1.2.0.1  xml2_1.3.5
#> [55] ragg_1.2.5       ellipsis_0.3.2    generics_0.1.3
#> [58] vctrs_0.6.3      tools_4.2.2       bit64_4.0.5
#> [61] glue_1.6.2       officer_0.6.2     fontquiver_0.2.1
#> [64] hms_1.1.3        parallel_4.2.2    fastmap_1.1.1
#> [67] yaml_2.3.7       timechange_0.2.0  colorspace_2.1-0
#> [70] fontLiberation_0.1.0 gt_0.9.0          knitr_1.43

```