GitHob:https://github.com/cindy930605/hw1/blob/main/README.md

健康大數據 hw1

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#Q1. Among adults aged ≥20 years in the 2021–2023 NHANES, observe the association between BMI and mean systolic blood pressure (SBP) and does the association vary between sex ?

```
# ================= Q1: BMI & SBP Cleaning and Visualization ==========
=======
# Load libraries -----------------------------------------------------
-------
pkgs <- c("tidyverse","haven","janitor","stringr","scales","skimr","nan
iar")
to_install <- setdiff(pkgs, rownames(installed.packages()))
if (length(to_install)) install.packages(to_install)
invisible(lapply(pkgs, library, character.only = TRUE))

## Warning: package 'ggplot2' was built under R version 4.3.3

## Warning: package 'purrr' was built under R version 4.3.3

## Warning: package 'lubridate' was built under R version 4.3.3

## ── Attaching core tidyverse packages ──────────────────────── tidyve
rse 2.0.0 ──
## ✓ dplyr     1.1.4     ✓ readr     2.1.5
## ✓ forcats   1.0.0     ✓ stringr   1.5.1
## ✓ ggplot2   3.5.2     ✓ tibble    3.2.1
## ✓ lubridate 1.9.4     ✓ tidyr     1.3.1
## ✓ purrr     1.1.0
## ── Conflicts ──────────────────────────────────────── tidyverse_co
nflicts() ──
## ✕ dplyr::filter() masks stats::filter()
## ✕ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to for
ce all conflicts to become errors

## Warning: package 'haven' was built under R version 4.3.3

## Warning: package 'janitor' was built under R version 4.3.3
```

```
##
## Attaching package: 'janitor'
##
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test

## Warning: package 'scales' was built under R version 4.3.3

##
## Attaching package: 'scales'
##
## The following object is masked from 'package:purrr':
##
##     discard
##
## The following object is masked from 'package:readr':
##
##     col_factor
##
##
## Attaching package: 'naniar'
##
## The following object is masked from 'package:skimr':
##
##     n_complete

dir.create("outputs", showWarnings = FALSE)
data_dir <- "/Users/cindytsai/Desktop/健康大數據"


# Load data -----------------------------------------------------------
------
demo <- read_xpt(file.path(data_dir,"DEMO_L.xpt")) %>% clean_names()
bpx  <- read_xpt(file.path(data_dir,"BPXO_L.xpt")) %>% clean_names()
bmx  <- read_xpt(file.path(data_dir,"BMX_L.xpt"))  %>% clean_names()

skimr::skim(demo)
```

Data summary

Name	demo
Number of rows	11933
Number of columns	27

Column type frequency:	
numeric	27

Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
seqn	0	1.00	136344.00	3444.90	130378.00	133361.00	136344.00	139327.00	142310.0	▇▇▇▇▇
sddsrvyr	0	1.00	12.00	0.00	12.00	12.00	12.00	12.00	12.0	▁▁▇▁▁
ridstatr	0	1.00	1.74	0.44	1.00	1.00	2.00	2.00	2.0	▂▁▁▁▇
riagendr	0	1.00	1.53	0.50	1.00	1.00	2.00	2.00	2.0	▇▁▁▁▇
ridageyr	0	1.00	38.32	25.60	0.00	13.00	37.00	62.00	80.0	▇▃▂▅▇
ridagemn	11556	0.03	11.63	6.81	0.00	6.00	11.00	17.00	24.0	▆▇▇▆▅
ridreth1	0	1.00	3.10	1.08	1.00	3.00	3.00	4.00	5.0	▂▂▅▂▂
ridreth3	0	1.00	3.32	1.52	1.00	3.00	3.00	4.00	7.0	▂▅▂▁▂
ridexmon	3073	0.74	1.52	0.50	1.00	1.00	2.00	2.00	2.0	▇▁▁▁▇
ridexagm	9146	0.23	121.91	67.16	0.00	66.00	122.00	179.50	239.0	▅▆▇▇▆
dmqmiliz	3632	0.70	1.92	0.28	1.00	2.00	2.00	2.00	7.0	▇▁▁▁

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
dmdborn4	19	1.00	1.16	0.36	1.00	1.00	1.00	1.00	2.0	▁ ▇▁ ▁▁
dmdyrusr	10058	0.16	7.33	15.83	1.00	3.00	6.00	6.00	99.0	▂ ▇▁ ▁▁
dmdeduc2	4139	0.65	3.80	1.15	1.00	3.00	4.00	5.00	9.0	▁ ▂▇ ▅▁
dmdmartz	4141	0.65	1.78	3.10	1.00	1.00	1.00	2.00	99.0	▁ ▇▁ ▁▁
ridexprg	10430	0.13	2.24	0.49	1.00	2.00	2.00	3.00	3.0	▁ ▁▁ ▇▁
dmdhhsiz	0	1.00	3.24	1.70	1.00	2.00	3.00	4.00	7.0	▂ ▇▂ ▂▂
dmdhrgnd	7818	0.34	1.56	0.50	1.00	1.00	2.00	2.00	2.0	▂ ▇▁ ▁▁
dmdhragz	7809	0.35	2.54	0.64	1.00	2.00	2.00	3.00	4.0	▇ ▁▇ ▁▇
dmdhredz	8187	0.31	2.17	0.66	1.00	2.00	2.00	3.00	3.0	▁ ▂▁ ▇▁
dmdhrmaz	7913	0.34	1.38	0.68	1.00	1.00	1.00	2.00	3.0	▃ ▇▁ ▂▁
dmdhsedz	9806	0.18	2.28	0.69	1.00	2.00	2.00	3.00	3.0	▁ ▂▁ ▇▁
wtint2yr	0	1.00	27404.14	19449.1	4584.46	14331.75	21670.19	33831.33	170968.	▇ ▇▂ ▁▁

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
				6					3	▁
wtmec2yr	0	1.00	27404.14	27962.96	0.00	0.00	21717.85	38341.15	227108.3	▇▃▁▁▁
sdmvstra	0	1.00	179.92	4.31	173.00	176.00	180.00	184.00	187.0	▇▇▇▇▇
sdmvpsu	0	1.00	1.49	0.50	1.00	1.00	1.00	2.00	2.0	▇▁▁▁▇
indfmpir	2041	0.83	2.71	1.67	0.00	1.18	2.50	4.50	5.0	▆▇▅▃▇

```
skimr::skim(bpx)
```

Data summary

Name	bpx
Number of rows	7801
Number of columns	12
_______________________	
Column type frequency:	
character	1
numeric	11
________________________	
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
bpaoarm	0	1	0	1	147	3	0

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
seqn	0	1.00	136349.49	3449.49	130378	133335	136382	139325	142310	▇▇

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
bpaocsz	190	0.98	3.52	0.67	2	3	4	4	5	▇▁▇▁▇▁
bpxosy1	284	0.96	119.29	18.56	61	106	117	130	232	▁▇▃▁▁
bpxodi1	284	0.96	72.75	11.90	33	64	72	80	142	▁▇▆▁▁
bpxosy2	296	0.96	119.08	18.57	59	106	116	129	233	▁▇▃▁▁
bpxodi2	296	0.96	72.09	11.85	32	64	71	79	139	▁▇▆▁▁
bpxosy3	321	0.96	118.92	18.50	50	106	116	129	232	▁▇▆▁▁
bpxodi3	321	0.96	71.81	11.77	24	64	71	79	136	▁▆▇▁▁
bpxopls1	284	0.96	72.34	12.72	35	63	71	80	158	▂▇▂▁▁
bpxopls2	296	0.96	73.09	12.78	32	64	72	81	141	▁▇▆▁▁
bpxopls3	321	0.96	73.69	12.89	31	65	73	82	154	▁▇▃▁▁

```
skimr::skim(bmx)
```

Data summary

Name	bmx
Number of rows	8860
Number of columns	22
_______________________	
Column type frequency:	
numeric	22
________________________	
Group variables	None

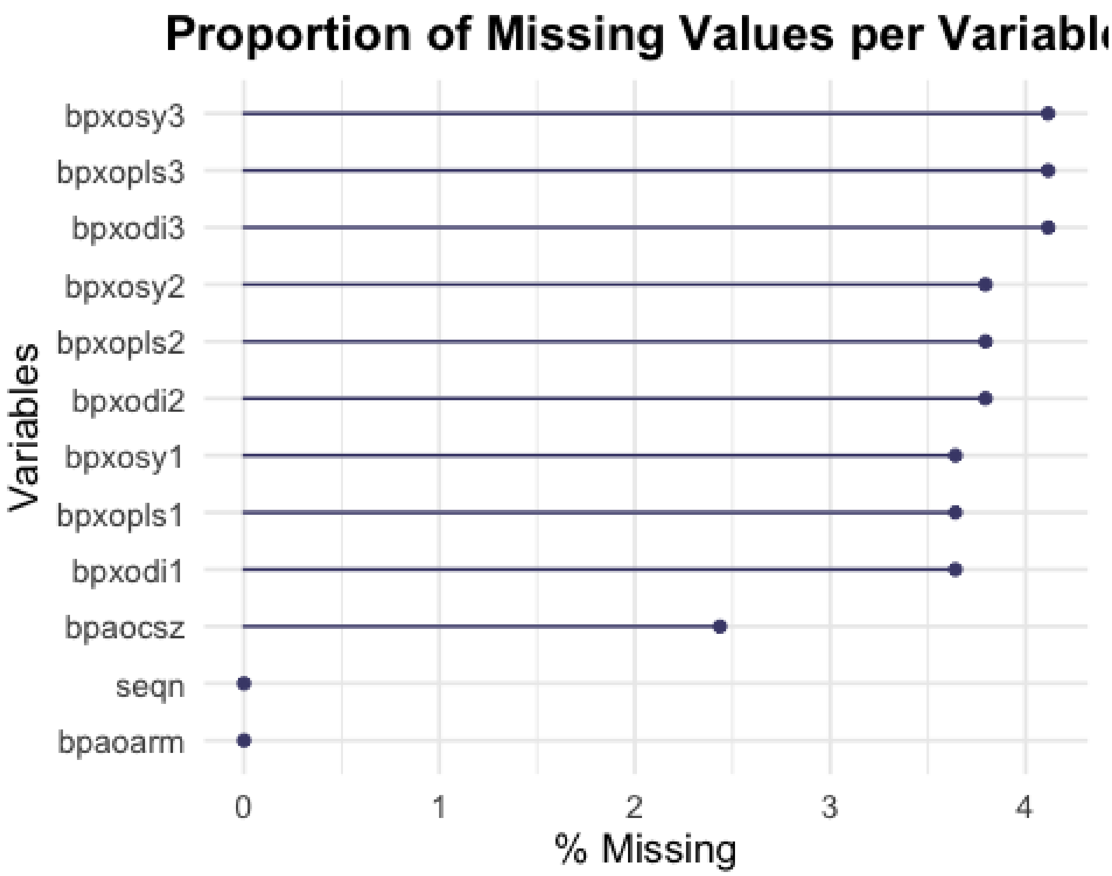
Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
seqn	0	1.00	136345.83	3453.78	130378.0	133319.75	136377.5	139336.2	142310.0	▇▇▇▇▇
bmdstats	0	1.00	1.13	0.50	1.0	1.00	1.0	1.0	4.0	▇▁▁▁▁
bmxwt	106	0.99	70.55	30.39	2.7	54.20	71.7	89.1	248.2	▂▇▂▁▁
bmiwt	8515	0.04	2.88	0.62	1.0	3.00	3.0	3.0	4.0	▁▁▁▇▁
bmxrecum	8406	0.05	84.33	14.06	48.5	73.48	84.7	96.1	118.8	▂▇▇▇▂
bmirecum	8842	0.00	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁
bmxhead	8790	0.01	41.93	2.80	34.4	40.20	42.4	44.0	46.5	▁▃▃▇▅
bmihead	8860	0.00	NaN	NA	NA	NA	NA	NA	NA	
bmxht	361	0.96	159.66	19.86	79.1	154.40	163.6	172.1	200.7	▁▁▂▇▂
bmiht	8726	0.02	2.31	0.95	1.0	1.00	3.0	3.0	3.0	▅▁▁▁▇
bmxbmi	389	0.96	27.25	8.14	11.1	21.60	26.4	31.7	74.8	▇▇▂▁▁
bmdbmic	6368	0.28	2.56	0.88	1.0	2.00	2.0	3.0	4.0	▁▇▁▂▂
bmxleg	1525	0.83	38.13	3.86	24.9	35.50	38.1	40.8	51.6	▁▂▇▂

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
bmileg	8464	0.04	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁
bmxarml	292	0.97	35.11	6.18	10.0	33.60	36.5	39.0	49.2	▁▁▂▇▁
bmiarml	8660	0.02	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁
bmxarmc	298	0.97	30.56	7.37	12.0	26.40	31.2	35.4	63.3	▂▇▇▁▁
bmiarmc	8655	0.02	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁
bmxwaist	670	0.92	92.12	22.05	39.8	77.50	92.7	107.0	187.0	▂▇▆▁▁
bmiwaist	8513	0.04	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁
bmxhip	2084	0.76	106.26	14.66	69.9	96.40	103.7	113.5	187.1	▂▇▂▁▁
bmihip	8499	0.04	1.00	0.00	1.0	1.00	1.0	1.0	1.0	▁▁▇▁▁

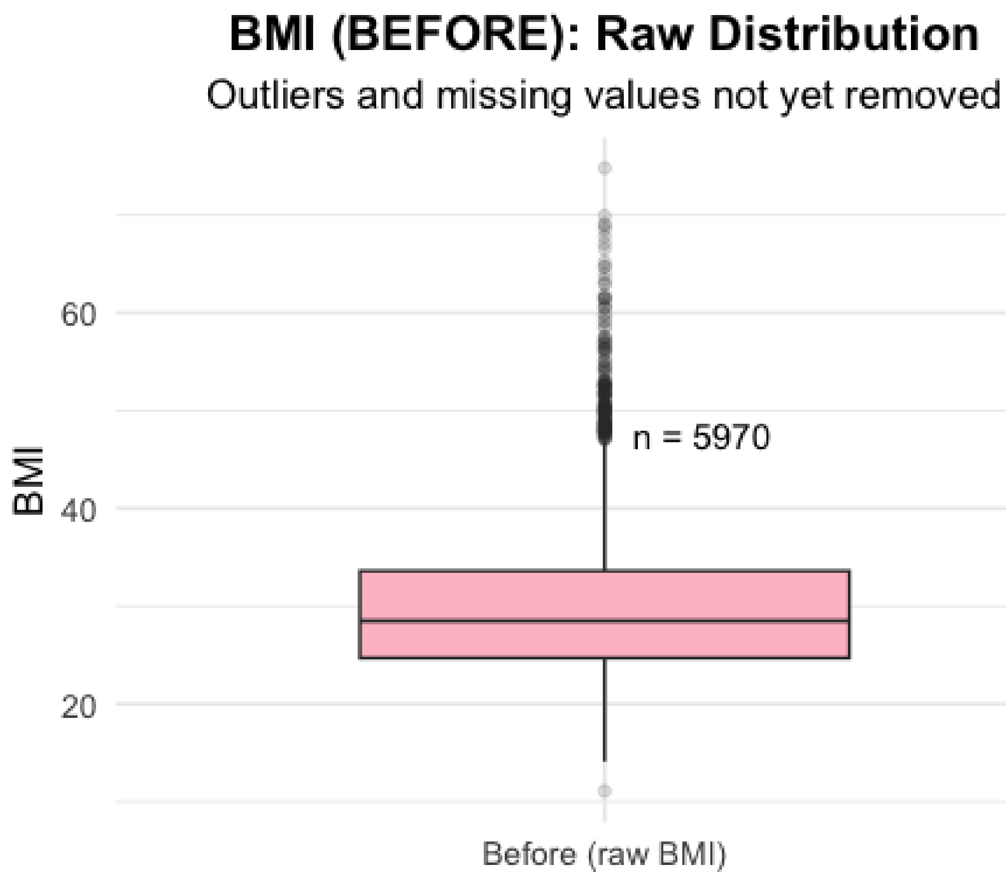
```r
# Plot missing proportion visually
gg_miss_var(bpx, show_pct = TRUE) +
  theme_minimal(base_size = 13) +
  labs(title = "Proportion of Missing Values per Variable") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5))
```



```
# Detect SBP/DBP columns ---------------------------------------------
------
sbp_cols <- names(bpx)[str_detect(names(bpx), "^bpxo?sy[1-3]$")]
dbp_cols <- names(bpx)[str_detect(names(bpx), "^bpxo?di[1-3]$")]

# Build raw BMI dataset ----------------------------------------------
------
bmi_raw <- bmx %>% transmute(seqn, bmi_raw = bmxbmi)
demo <- demo %>%
  mutate(riagendr = as.numeric(riagendr)) %>%
  filter(is.na(riagendr) | riagendr %in% c(1, 2))
demo_sex <- demo %>%
  transmute(seqn, age = ridageyr,
            sex = factor(riagendr, levels=c(1,2), labels=c("Male","Fema
le")))

dat_raw <- demo_sex %>%
  left_join(bmi_raw, by="seqn") %>%
  filter(age >= 20) %>%
  mutate(bmi_raw = ifelse(is.nan(bmi_raw), NA_real_, bmi_raw))

# BEFORE boxplot -----------------------------------------------------
------
```

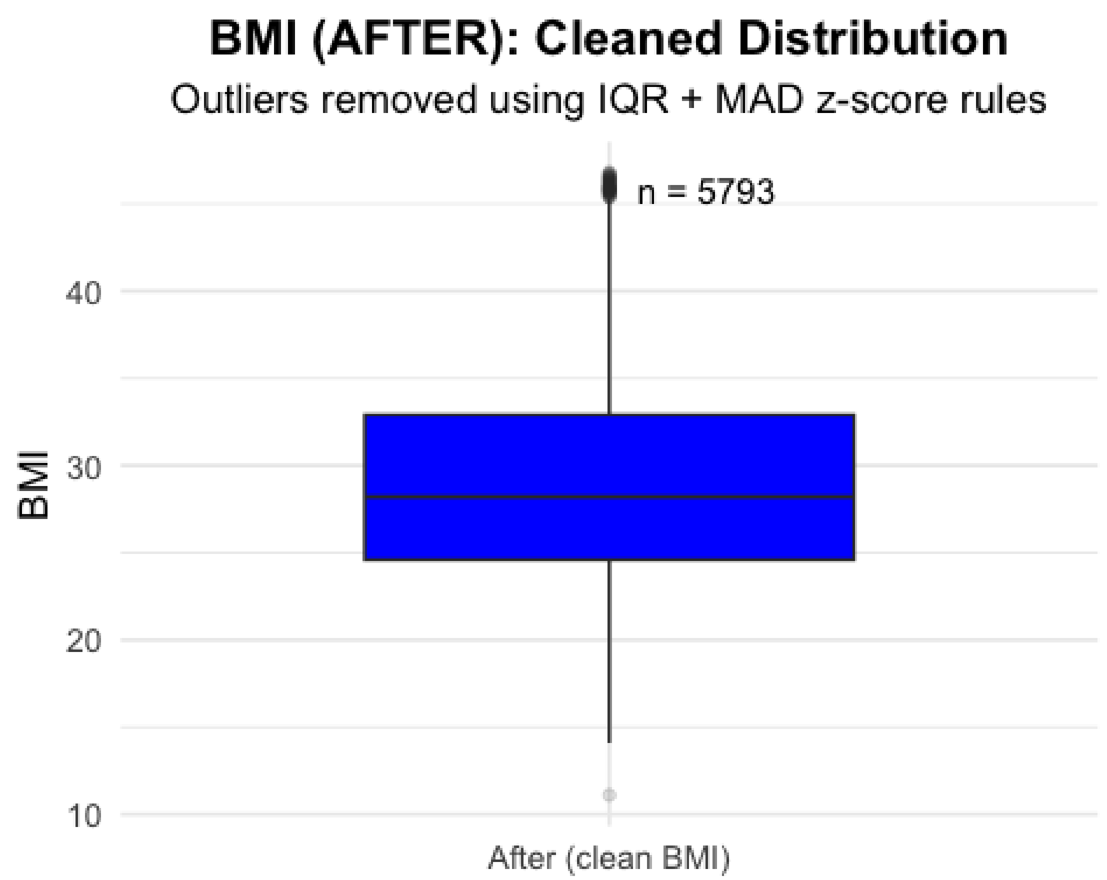
```r
bmi_before_df <- dat_raw %>% transmute(stage = "Before (raw BMI)", valu
e = bmi_raw)
x <- bmi_before_df$value
qs <- quantile(x, c(.25,.75), na.rm = TRUE)
iqr <- qs[2]-qs[1]
upper_whisker <- min(max(x, na.rm = TRUE), qs[2] + 1.5*iqr)
bmi_before_label_y <- upper_whisker + 0.05*iqr
bmi_before_N <- sum(!is.na(x))

ggplot(bmi_before_df, aes(stage, value, fill = stage)) +
  geom_boxplot(width = 0.6, outlier.alpha = 0.15, fatten = 1.2) +
  geom_text(data = tibble(stage="Before (raw BMI)", y=bmi_before_label_
y, N=bmi_before_N),
            aes(stage, y, label=paste0("n = ", N)), hjust = -0.2, size
= 4) +
  scale_fill_manual(values = c("Before (raw BMI)" = "pink")) +
  labs(title = "BMI (BEFORE): Raw Distribution",
       subtitle = "Outliers and missing values not yet removed",
       x = NULL, y = "BMI") +
  theme_minimal(base_size = 13) +
  theme(legend.position = "none",
        plot.title = element_text(face="bold", hjust=0.5),
        plot.subtitle = element_text(hjust=0.5))
```

```
## Warning: Removed 1839 rows containing non-finite outside the scale r
ange
## (`stat_boxplot()`).
```

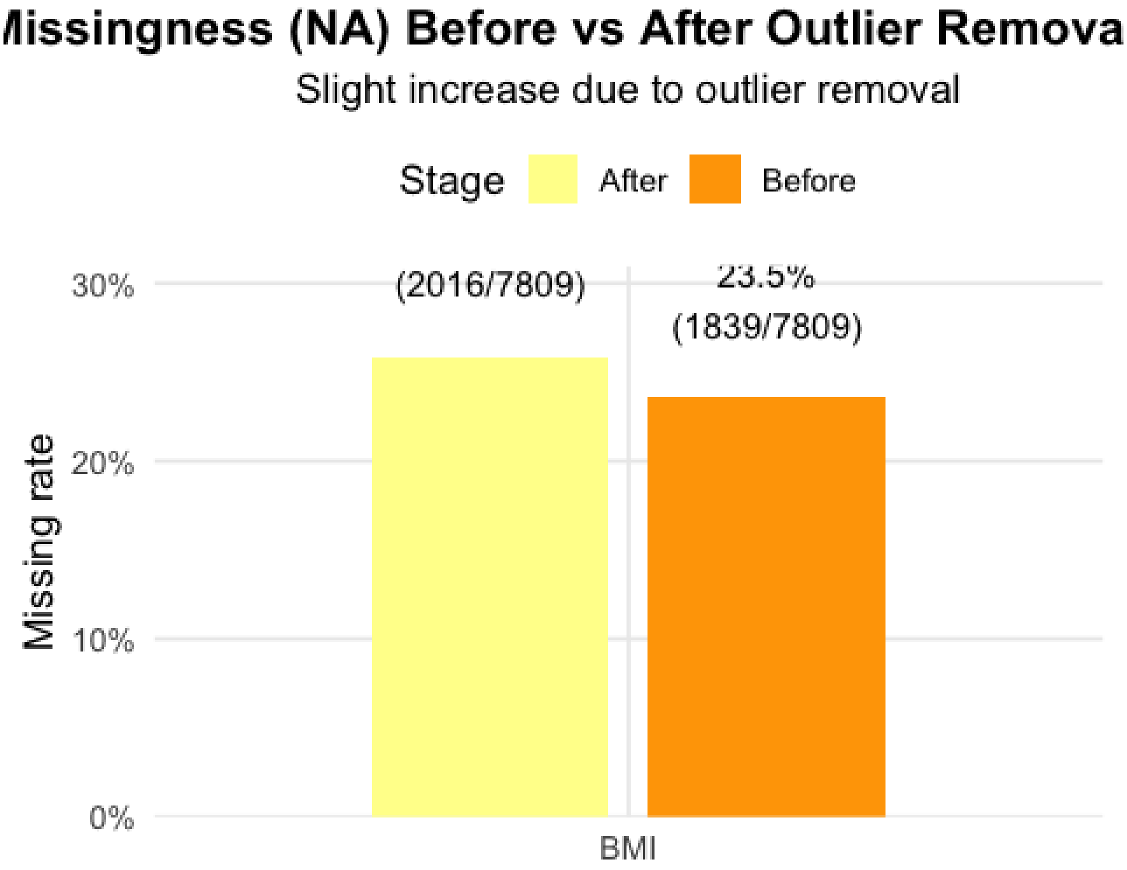


```r
# Outlier cleaning ----------------------------------------------------
------
BMI_LO <- 10; BMI_HI <- 80
bmi_clean <- bmx %>%
  transmute(seqn, bmxbmi) %>%
  mutate(
    q1 = quantile(bmxbmi, 0.25, na.rm=TRUE),
    q3 = quantile(bmxbmi, 0.75, na.rm=TRUE),
    iqr = q3 - q1,
    lo_iqr = q1 - 1.5*iqr,
    hi_iqr = q3 + 1.5*iqr,
    med = median(bmxbmi, na.rm=TRUE),
    madv = mad(bmxbmi, na.rm=TRUE),
    z = ifelse(madv > 0, (bmxbmi - med)/(madv*1.4826), 0),
    flag = (bmxbmi < BMI_LO | bmxbmi > BMI_HI) |
           (bmxbmi < lo_iqr | bmxbmi > hi_iqr) |
           (abs(z) > 3.5),
    bmxbmi_clean = ifelse(flag, NA_real_, bmxbmi)
  ) %>% select(seqn, bmxbmi_clean)

# Cleaned dataset -----------------------------------------------------
------
dat_clean <- demo_sex %>%
  left_join(bmi_clean, by="seqn") %>%
  filter(age >= 20) %>%
  mutate(bmxbmi_clean = ifelse(is.nan(bmxbmi_clean), NA_real_, bmxbmi_c
lean))

# AFTER boxplot -------------------------------------------------------
------
bmi_after_df <- dat_clean %>% transmute(stage = "After (clean BMI)", va
lue = bmxbmi_clean)
x <- bmi_after_df$value
qs <- quantile(x, c(.25,.75), na.rm = TRUE)
iqr <- qs[2]-qs[1]
upper_whisker <- min(max(x, na.rm = TRUE), qs[2] + 1.5*iqr)
bmi_after_label_y <- upper_whisker + 0.05*iqr
bmi_after_N <- sum(!is.na(x))

ggplot(bmi_after_df, aes(stage, value, fill = stage)) +
  geom_boxplot(width = 0.6, outlier.alpha = 0.15, fatten = 1.2) +
  geom_text(data = tibble(stage="After (clean BMI)", y=bmi_after_label_
y, N=bmi_after_N),
            aes(stage, y, label=paste0("n = ", N)), hjust = -0.2, size
= 4) +
  scale_fill_manual(values = c("After (clean BMI)" = "blue")) +
  labs(title = "BMI (AFTER): Cleaned Distribution",
       subtitle = "Outliers removed using IQR + MAD z-score rules",
       x = NULL, y = "BMI") +
  theme_minimal(base_size = 13) +
  theme(legend.position = "none",
        plot.title = element_text(face="bold", hjust=0.5),
        plot.subtitle = element_text(hjust=0.5))
```

```
## Warning: Removed 2016 rows containing non-finite outside the scale r
ange
## (`stat_boxplot()`).
```



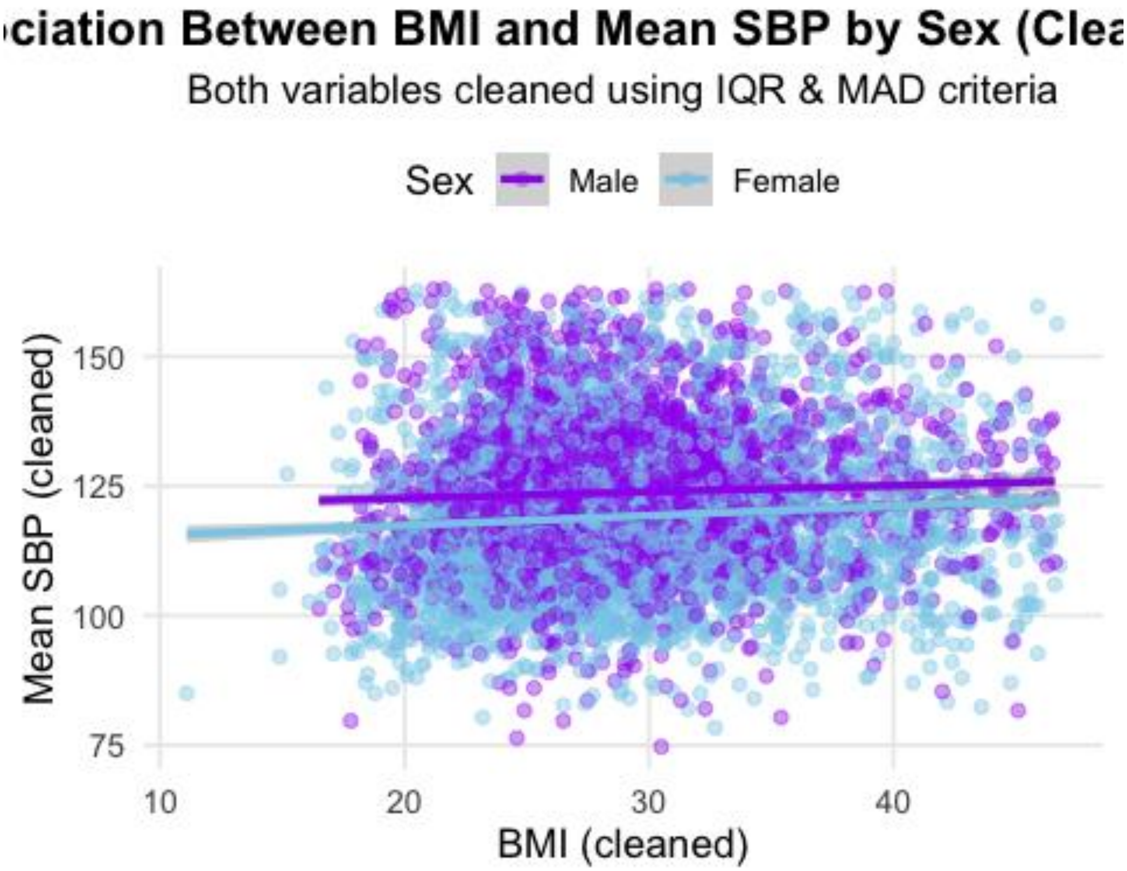
```r
# Missingness comparison ----------------------------------------------
------
miss_before <- tibble(
  stage     = "Before",
  variable  = "BMI",
  n_missing = sum(is.na(dat_raw$bmi_raw)),
  n_total   = nrow(dat_raw)
) %>% mutate(p_missing = n_missing / n_total)

miss_after <- tibble(
  stage     = "After",
  variable  = "BMI",
  n_missing = sum(is.na(dat_clean$bmxbmi_clean)),
  n_total   = nrow(dat_clean)
) %>% mutate(p_missing = n_missing / n_total)

miss_long <- bind_rows(miss_before, miss_after)

pos <- position_dodge(width = 0.7)
ggplot(miss_long, aes(variable, p_missing, fill = stage)) +
  geom_col(width = 0.6, position = pos) +
  geom_text(aes(label = paste0(scales::percent(p_missing, 0.1),
                               "\n(", n_missing, "/", n_total, ")")),
            position = pos, vjust = -0.8, size = 4) +
  scale_y_continuous(labels = scales::percent, expand = expansion(mult
= c(0, 0.2))) +
  scale_fill_manual(values = c("Before" = "orange", "After" = "#FF9"))
+
  labs(title = "Missingness (NA) Before vs After Outlier Removal (BMI)"
,
      subtitle = "Slight increase due to outlier removal",
      x = NULL, y = "Missing rate", fill = "Stage") +
  theme_minimal(base_size = 13) +
  theme(panel.grid.minor = element_blank(),
       plot.title = element_text(face = "bold", hjust = 0.5),
       plot.subtitle = element_text(hjust = 0.5),
       legend.position = "top")
```



```
# SBP mean (before cleaning) ------------------------------------------
------
sbp_raw <- bpx %>% transmute(seqn, sbp_mean_raw = rowMeans(select(., al
l_of(sbp_cols)), na.rm = TRUE))
dat_sbp_raw <- dat_raw %>%
  left_join(sbp_raw, by = "seqn") %>%
  filter(!is.na(bmi_raw) & !is.na(sbp_mean_raw))
```

```r
# SBP outlier cleaning ------------------------------------------------
------
SBP_LO <- 70; SBP_HI <- 260
sbp_clean <- bpx %>%
  transmute(seqn, across(all_of(sbp_cols))) %>%
  mutate(
    sbp_all = pmap_dbl(across(all_of(sbp_cols)), ~ mean(c(...), na.rm =
 TRUE)),
    q1 = quantile(sbp_all, 0.25, na.rm = TRUE),
    q3 = quantile(sbp_all, 0.75, na.rm = TRUE),
    iqr = q3 - q1,
    lo_iqr = q1 - 1.5 * iqr,
    hi_iqr = q3 + 1.5 * iqr,
    med = median(sbp_all, na.rm = TRUE),
    madv = mad(sbp_all, na.rm = TRUE),
    z = ifelse(madv > 0, (sbp_all - med) / (madv * 1.4826), 0),
    flag = (sbp_all < SBP_LO | sbp_all > SBP_HI) |
           (sbp_all < lo_iqr | sbp_all > hi_iqr) |
           (abs(z) > 3.5),
    sbp_mean_clean = ifelse(flag, NA_real_, sbp_all)
  ) %>% select(seqn, sbp_mean_clean)

# Combine BMI + SBP clean dataset -------------------------------------
-----
dat_final <- dat_clean %>%
  left_join(sbp_clean, by = "seqn") %>%
  filter(!is.na(bmxbmi_clean) & !is.na(sbp_mean_clean))

# Scatter plot: BMI vs SBP --------------------------------------------
-----
ggplot(dat_final, aes(x = bmxbmi_clean, y = sbp_mean_clean, color = sex
)) +
  geom_point(alpha = 0.4, size = 1.8) +
  geom_smooth(method = "lm", se = TRUE, lwd = 1.2) +
  labs(title = "Association Between BMI and Mean SBP by Sex (Cleaned Da
ta)",
       subtitle = "Both variables cleaned using IQR & MAD criteria",
       x = "BMI (cleaned)", y = "Mean SBP (cleaned)", color = "Sex") +
  scale_color_manual(values = c("Male" = "purple", "Female" = "skyblue"
)) +
  theme_minimal(base_size = 13) +
  theme(panel.grid.minor = element_blank(),
        plot.title = element_text(face = "bold", hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5),
        legend.position = "top")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



#Q2. Among all the subjects in 2021-2023 NHANES dataset, observe the distribution of BMI in different races and education levels

```
library(knitr)

## Warning: package 'knitr' was built under R version 4.3.3

# 檢查原始教育變項
demo %>% count(dmdeduc2)

## # A tibble: 7 × 2
##   dmdeduc2     n
##      <dbl> <int>
## 1        1   373
## 2        2   666
## 3        3  1749
## 4        4  2370
## 5        5  2625
## 6        9    11
## 7       NA  4139

# 重編教育變項
dat_edu <- demo %>%
  transmute(
```

```r
    seqn,
    age = ridageyr,
    EDU = case_when(
      dmdeduc2 %in% 1:5 ~ dmdeduc2,
      TRUE ~ NA_real_
    )
  ) %>%
  mutate(
    EDU = factor(
      EDU,
      levels = 1:5,
      labels = c("<9th grade", "9-11th grade", "High school/GED",
                 "Some college/AA", "College or above")
    )
  ) %>%
  left_join(dat_clean %>% select(seqn, bmxbmi_clean), by = "seqn") %>%
  drop_na(EDU, bmxbmi_clean)

# 教育分布表
edu_dist <- dat_edu %>%
  count(EDU) %>%
  mutate(prop = n / sum(n)) %>%
  rename(category = EDU)

kable(edu_dist, digits = 3, caption = "Distribution of Educational Attainment (EDU)")
```

Distribution of Educational Attainment (EDU)

category	n	prop
<9th grade	278	0.048
9-11th grade	457	0.079
High school/GED	1227	0.212
Some college/AA	1749	0.302
College or above	2079	0.359

```r
# 檢查原始種族變項
demo %>% count(ridreth3)
```

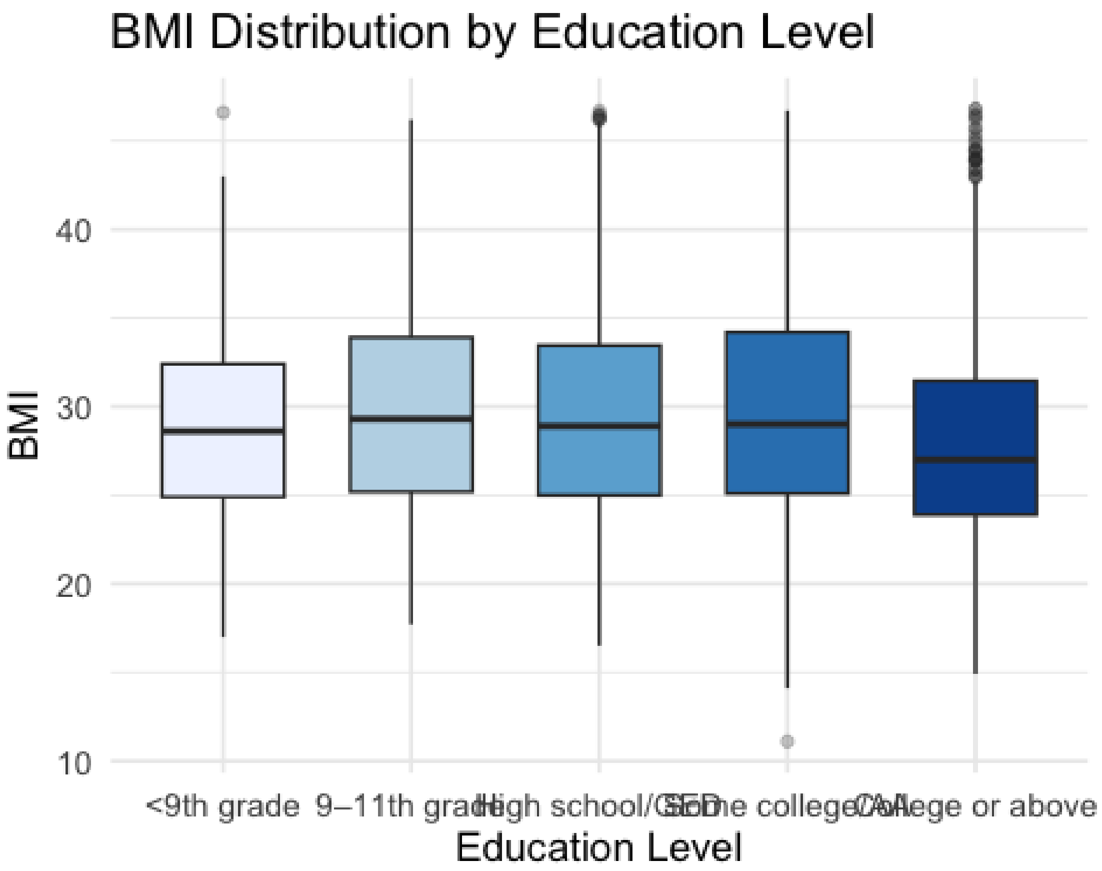
```
## # A tibble: 6 × 2
##   ridreth3     n
##      <dbl> <int>
## 1        1  1117
## 2        2  1373
## 3        3  6217
## 4        4  1597
## 5        6   681
## 6        7   948
```

```
# 重編種族變項
dat_race <- demo %>%
  transmute(
    seqn,
    age = ridageyr,
    Race = case_when(
      ridreth3 %in% 1:7 ~ ridreth3,
      TRUE ~ NA_real_
    )
  ) %>%
  mutate(
    Race = factor(
      Race,
      levels = 1:7,
      labels = c("Mexican American", "Other Hispanic", "Non-Hispanic Wh
ite",
                 "Non-Hispanic Black", "Non-Hispanic Asian",
                 "Other Race", "Multi-Racial")
    )
  ) %>%
  left_join(dat_clean %>% select(seqn, bmxbmi_clean), by = "seqn") %>%
  drop_na(Race, bmxbmi_clean)

# 種族分布表
race_dist <- dat_race %>%
  count(Race) %>%
  mutate(prop = n / sum(n)) %>%
  rename(category = Race)


kable(race_dist, digits = 3, caption = "Distribution of Race Categories
")
```

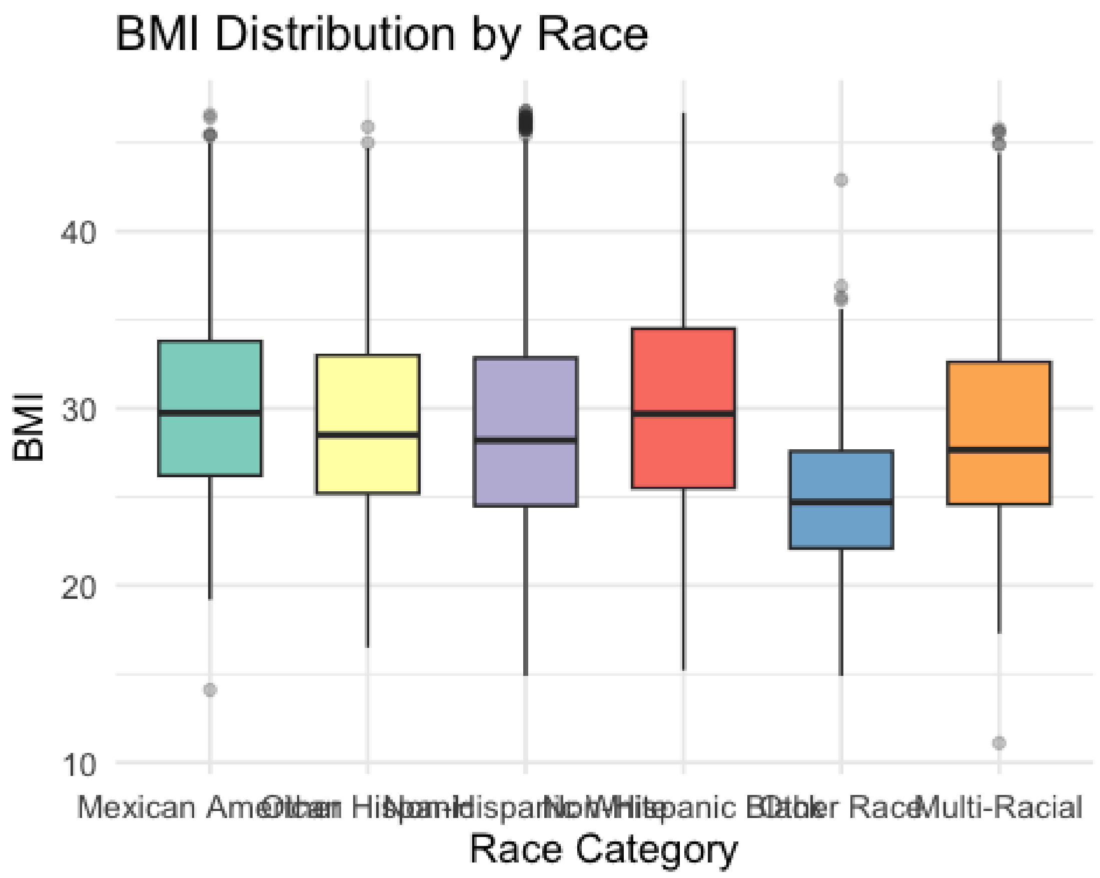
Distribution of Race Categories

category	n	prop
Mexican American	390	0.067
Other Hispanic	593	0.102
Non-Hispanic White	3427	0.592
Non-Hispanic Black	689	0.119
Other Race	330	0.057
Multi-Racial	364	0.063

```
ggplot(dat_edu, aes(x = EDU, y = bmxbmi_clean, fill = EDU)) +
  geom_boxplot(outlier.alpha = 0.25, width = 0.65) +
  scale_fill_brewer(palette = "Blues") +
  labs(title = "BMI Distribution by Education Level",
       x = "Education Level", y = "BMI") +
  theme_minimal(base_size = 13) +
  theme(legend.position = "none")
```



```
ggplot(dat_race, aes(x = Race, y = bmxbmi_clean, fill = Race)) +
  geom_boxplot(outlier.alpha = 0.25, width = 0.65) +
  scale_fill_brewer(palette = "Set3") +
  labs(title = "BMI Distribution by Race",
       x = "Race Category", y = "BMI") +
   theme_minimal(base_size = 13) +
  theme(legend.position = "none")
```



```
cat("
### Observation & Interpretation (Q2)

- BMI tends to increase slightly as education level decreases.
- Participants with 'College or above' education generally show lower B
MI median values.
- Across race groups, Non-Hispanic Black and Hispanic groups have relat
ively higher BMI median compared to Non-Hispanic White and Asian partic
ipants.
- These differences might reflect socioeconomic and lifestyle factors a
ffecting BMI distribution.
")
```

```
##
## ### Observation & Interpretation (Q2)
##
## - BMI tends to increase slightly as education level decreases.
## - Participants with 'College or above' education generally show lowe
r BMI median values.
## - Across race groups, Non-Hispanic Black and Hispanic groups have re
latively higher BMI median compared to Non-Hispanic White and Asian par
ticipants.
```

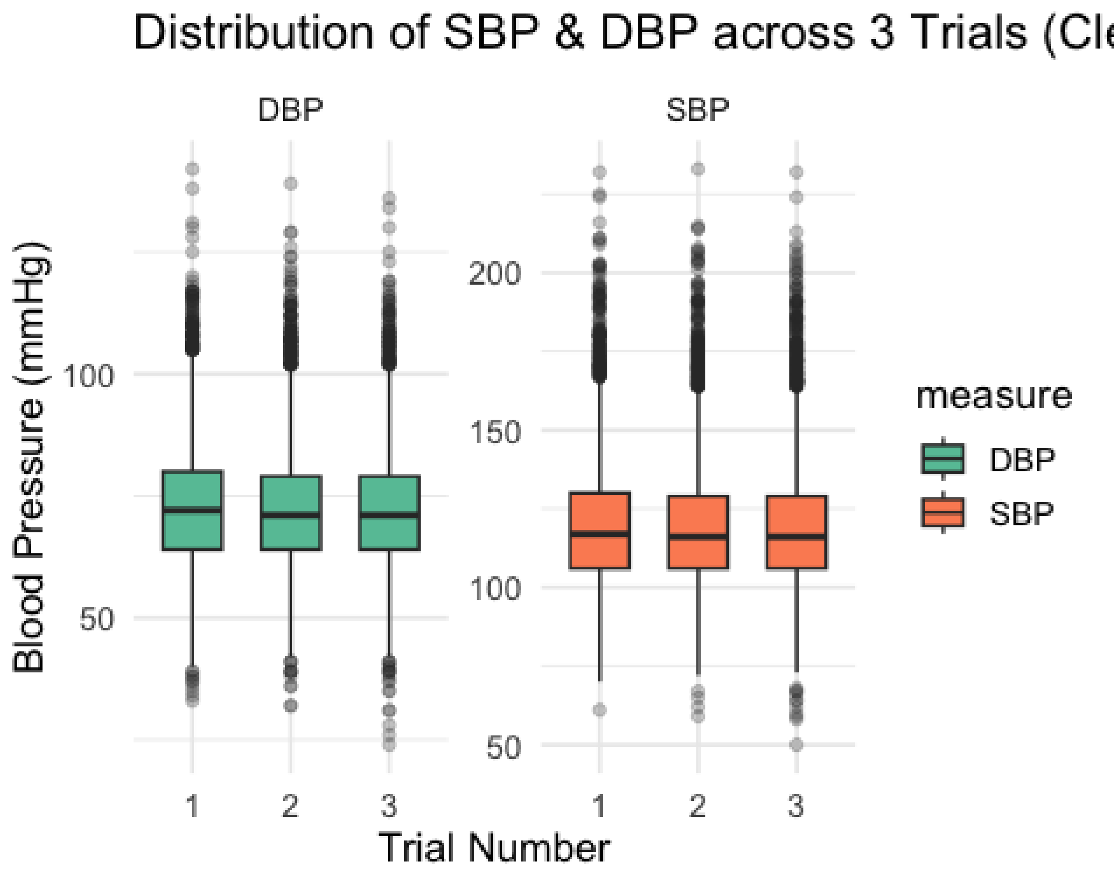
```
## - These differences might reflect socioeconomic and lifestyle factor
s affecting BMI distribution.
```

#Q3. Among all the subjects in 2021-2023 NHANES dataset, BPX is the data including three times of examination of blood pressure (SBP & DBP). The values were recorded in different columns (bpxosy1-3; bpxodi1-3) (Reminder: please use the “cleaned” BP data)

```
library(tidyverse)

# 偵測 SBP 與 DBP 欄位名稱
sbp_cols <- names(bpx)[stringr::str_detect(names(bpx), "^bpxo?sy[1-3]$"
)]
dbp_cols <- names(bpx)[stringr::str_detect(names(bpx), "^bpxo?di[1-3]$"
)]

# 轉換為長格式 (Long format)
bpx_long_clean <- bpx %>%
  select(seqn, all_of(c(sbp_cols, dbp_cols))) %>%
  pivot_longer(
    cols = -seqn,
    names_to = c("measure", "trial"),
    names_pattern = "^bpxo?([sd]i|sy)([1-3])$",
    values_to = "value"
  ) %>%
  mutate(
    measure = recode(measure, "sy" = "SBP", "di" = "DBP"),
    trial = as.integer(trial)
  )

# 檢查轉換後的資料結構
glimpse(bpx_long_clean)
```

```
## Rows: 46,806
## Columns: 4
## $ seqn    <dbl> 130378, 130378, 130378, 130378, 130378, 130378, 1303
79, 130379…
## $ measure <chr> "SBP", "SBP", "SBP", "DBP", "DBP", "DBP", "SBP", "SB
P", "SBP",…
## $ trial   <int> 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3
, 1, 2, 3,…
## $ value   <dbl> 135, 131, 132, 98, 96, 94, 121, 117, 113, 84, 76, 76
, 111, 112…
```

```
ggplot(bpx_long_clean, aes(x = factor(trial), y = value, fill = measure
)) +
  geom_boxplot(outlier.alpha = 0.25, width = 0.6) +
  facet_wrap(~ measure, scales = "free_y") +
  scale_fill_brewer(palette = "Set2") +
  labs(
    title = "Distribution of SBP & DBP across 3 Trials (Cleaned Data)",
    x = "Trial Number", y = "Blood Pressure (mmHg)"
  ) +
   theme_minimal(base_size = 13)

## Warning: Removed 1802 rows containing non-finite outside the scale r
ange
## (`stat_boxplot()`).
```



```
# 計算每位受試者在三次測量中的最大差值 (SBP 和 DBP 分開)
bpx_diff <- bpx_long_clean %>%
  group_by(seqn, measure) %>%
  summarise(
    diff_range = max(value, na.rm = TRUE) - min(value, na.rm = TRUE),
    .groups = "drop"
  )

## Warning: There were 1132 warnings in `summarise()`.
## The first warning was:
## ℹ In argument: `diff_range = max(value, na.rm = TRUE) - min(value, n
a.rm =
##   TRUE)`.
## ℹ In group 37: `seqn = 130401` and `measure = "DBP"`.
## Caused by warning in `max()`:
```

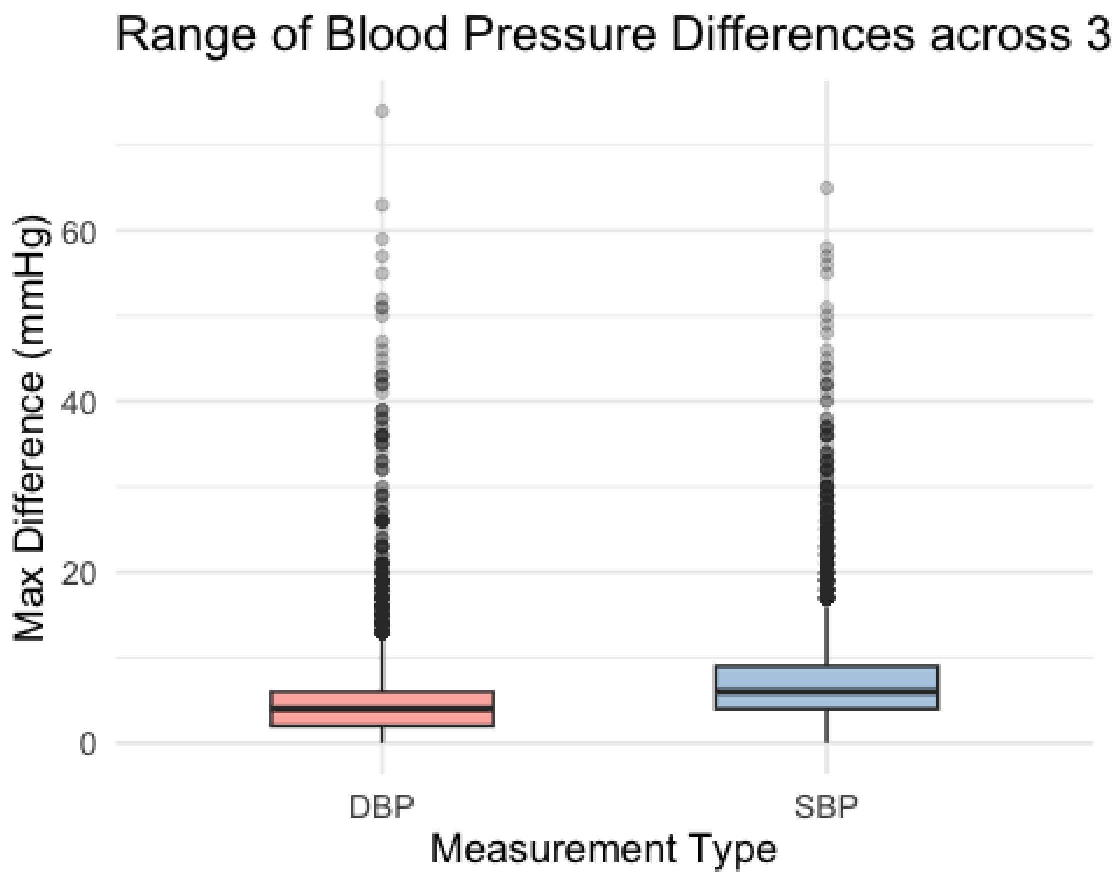
```
## ! no non-missing arguments to max; returning -Inf
## ℹ Run `dplyr::last_dplyr_warnings()` to see the 1131 remaining warni
ngs.
```

```r
# 取出最大差異前 5 位作為示例 (方便檢查)
head(bpx_diff[order(-bpx_diff$diff_range), ], 5)
```

```
## # A tibble: 5 × 3
##     seqn measure diff_range
##    <dbl> <chr>        <dbl>
## 1 141202 DBP             74
## 2 136053 SBP             65
## 3 135594 DBP             63
## 4 131306 DBP             59
## 5 141202 SBP             58
```

```r
# 視覺化：不同測量型別的最大差值分布
ggplot(bpx_diff, aes(x = measure, y = diff_range, fill = measure)) +
  geom_boxplot(outlier.alpha = 0.25, width = 0.5) +
  scale_fill_brewer(palette = "Pastel1") +
  labs(
    title = "Range of Blood Pressure Differences across 3 Trials",
    x = "Measurement Type", y = "Max Difference (mmHg)"
  ) +
   theme_minimal(base_size = 13)+
  theme(legend.position = "none")
```

```
## Warning: Removed 566 rows containing non-finite outside the scale ra
nge
## (`stat_boxplot()`).
```



```
cat("
### Observation & Interpretation

- Both SBP and DBP show relatively small variations across the three tr
ials, usually within ±10 mmHg.
- The distributions of the 1st, 2nd, and 3rd readings are quite close,
and there is no clear systematic shift.
- This pattern indicates that the three measurements were likely taken
**on the same day**, probably within a short interval, to ensure measur
ement reliability.
- Larger outliers (e.g., >20 mmHg difference) may reflect temporary phy
siological fluctuations or measurement error rather than time gaps.
")
```

```
##
## ### Observation & Interpretation
##
## - Both SBP and DBP show relatively small variations across the three
 trials, usually within ±10 mmHg.
## - The distributions of the 1st, 2nd, and 3rd readings are quite clos
e, and there is no clear systematic shift.
## - This pattern indicates that the three measurements were likely tak
en **on the same day**, probably within a short interval, to ensure mea
```

```
surement reliability.
## - Larger outliers (e.g., >20 mmHg difference) may reflect temporary
physiological fluctuations or measurement error rather than time gaps.
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.