R Training Book for IKU

Table of contents

Preface

Objectives

The Institute for Public Health (IPH) (Malay: Institut Kesihatan Umum, IKU) is a research institution under the Ministry of Health Malaysia, primarily focusing on public health research. In its daily activities, software like SPSS and STATA plays a crucial role in data analysis. However, using these softwares results in significant operational costs for the institute due to the purchase of software licenses. Recognising this issue, IKU is committed to transitioning towards using open-source and free software such as R and Python. This shift reduces cost burdens and empowers IKU staff with more flexible and advanced tools for data analysis.

R is a practical programming language for statistical analysis and graphics production. Its open-source and free nature makes it the preferred choice for research in public health. Through this book, it is hoped that the data analysis skills among IKU staff will be enhanced, leading to improvements in the quality of IKU's research.

Way Forward

R offers capabilities that extend well beyond statistical analysis. As more IKU staff become proficient in R, we anticipate leveraging R's diverse project capabilities to benefit IKU significantly:

1. Shiny: Develop interactive dashboards for dynamic and near-real-time result presentation.
2. Quarto: Utilize this publishing system for expedited reports and paper production.
3. IKU-specific R packages: Create tailored R packages incorporating functions for tasks such as sample size calculation, importing data from REDCap via API, standardising analysis of NHMS data, and uniform reporting of NHMS findings.

This forward-looking approach aims to harness R's full potential to streamline and enhance IKU's research and reporting processes, making them more efficient and impactful.

Collaborators Are Welcome

In the spirit of open science and continuous improvement, individuals both within and outside IPH are invites for collaboration. Whether one is an author with insights to share, an editor with an eye for detail, or possesses constructive suggestions, these contribution can significantly enhance the utility and reach of this manual. It is particularly interested in contributions in the following areas:

- Content Enhancement: The addition of new chapters or sections covering unexplored areas of R, the introduction of advanced statistical techniques, or the expansion on the applications of R in public health research are welcomed.
- Technical Review: Contributors can help ensure the accuracy of code examples, update or optimize R scripts, and contribute towards a repository of R functions tailored for public health data analysis.
- Case Studies: The IPH appreciates the sharing of real-world applications of R in public health, especially those within the context of IKU's research projects. This could include case studies on data visualization, statistical analysis, or the development of interactive applications with Shiny.
- Educational Materials: There is a need for developing tutorials, exercises, or additional learning resources that complement the manual's content, thereby facilitating a deeper understanding of R programming among IPH staff.

How to Contribute:

Individuals interested in contributing or who have suggestions to improve this manual are encouraged not to hesitate in reaching out. Your input is invaluable in making this resource more comprehensive, accurate, and beneficial for all users.

Contact Information:

Ideas, proposals for collaboration, or any feedback should be emailed to Mohd Azmi Bin Suliman at the Centre for Non-communicable Diseases Research (CNCDR). The institute looks forward to hearing from contributors and exploring how collaboration can further advance public health research through the power of R programming.

Mohd Azmi Bin Suliman
Centre for Non-communicable Diseases Research (CNCDR)
February 2024

1 How To Use This Book

2 Why Tidyverse?

3 Why dataset in SPSS file?

4 Introduction

4.1 R

4.2 RStudio

4.3 Quarto

5 Data Wrangling

In summary, this book has no content whatsoever.

```
1 + 1
```

```
[1] 2
```

6 Data Wrangling

In summary, this book has no content whatsoever.

```
1 + 1
```

```
[1] 2
```

7 Statistical Tests

Several statistical tests will be covered, which will be grouped into

- Bivariate analyses of categorical data
- Bivariate analyses of numerical data
- Linear regression
- Logistic regression

This book however was not intended to be a statistical book, nor should not be the main reference for statistical analyses. Please refer your statistical texts book for further information.

In addition of conducting the test in standard way, I'll also how to create a nice result table using related packages.

> ℹ Note
>
> dataset used in this example can be downloaded from github site: https://github.com/MohdAzmiSuliman/IKU_RBook/tree/master/dataset

7.1 Practical: Setup Project

1. Setup your project
   - Open your RStudio
   - Create New Project
2. Create Quarto document
   - update the YAML metadata to make the document self-contained

```
---
title: "Sesi 3 - Basic Statistical Analysis"
format:
  html:
    embed-resources: true
---
```

7.2 Bivariate Analyses of Categorical Data

Bivariate analysis involves examining the relationship or association between to variables. When both variables are categorical, bivariate analysis looks at how these categories are related. The bivariate analyses often involve the use of contingency tables, also know as cross-tabulation or crosstab.

7.2.1 Contingency Table

Contigency table, or crosstab, is a simple matrix that display the frequency of occurence of combination of two categories for two categorical variable.

For example, this contigency table show a cross tabulation between smoking status and lung cancer outcome.

Table 7.1: Contigency Table Structure

Status	Lung Cancer	No Lung Cancer	Total
Smoker	a	b	a+b
Non-Smoker	c	d	c+d
Total	a+c	b+d	N

In this example:

- the independent variable (or the predictor, i.e. the smoking status), is the row
- the dependent variable (or the outcome, i.e. the cancer status), is the column
- The letters a, b, c, and d represent the cell frequencies:
  - a: The number of smokers who have the disease.
  - b: The number of smokers who do not have the disease.
  - c: The number of non-smokers who have the disease.
  - d: The number of non-smokers who do not have the disease.
- "Total" is the sum of the frequencies in the respective row or column, with N being the grand total of all observations.

Example: Gender vs Employment Status

0. Download dataset

    - we will be using the `asthmads_clean.sav` dataset
    - this code below download directly from github package into your working directory
    - otherwise, you may download from the link: https://github.com/MohdAzmiSuliman/IKU_RBook/raw/master/dataset/asthmads_clean.sav and copy to the working directory

~~~
```{r}
#| eval: false

download.file(
  url = "https://github.com/MohdAzmiSuliman/IKU_RBook/raw/master/dataset/asthmads_clean.sav",
  destfile = "asthmads_clean.sav", mode = "wb")
```
~~~

1. Import dataset

~~~
```{r}
library(tidyverse)
library(haven)

asthmads <- read_sav("asthmads_clean.sav") %>%
  as_factor()
asthmads
```
~~~

```
# A tibble: 150 x 22
      id idR   Gender   Age WorkStatus Height  Ht_m Weight_Pre BMI_Pre
   <dbl> <chr> <fct>  <dbl> <fct>       <dbl> <dbl>      <dbl>   <dbl>
 1     1 nXSw  Female    34 Unemployed    179  1.79       84.2    26.3
 2     2 yg2t  Male      31 Unemployed    169  1.69       81.8    28.6
 3     3 QBW4  Male      25 Employed      164  1.64       88.5    32.9
 4     4 2×2S  Female    33 Unemployed    136  1.36       53.2    28.8
 5     5 mOnn  Male      28 Unemployed    172  1.72       71.3    24.1
 6     6 D3sl  Male      33 Unemployed    178  1.78       87.3    27.6
 7     7 le6j  Female    31 Unemployed    140  1.4        48.8    24.9
 8     8 r3gC  Female    34 Employed      140  1.4        49.1    25.0
 9     9 3Tyt  Male      31 Employed      171  1.71       60.1    20.6
10    10 cmKF  Male      28 Employed      163  1.63       93.1    35.0
# i 140 more rows
# i 13 more variables: BMI_PreCat <fct>, PA_HW <dbl>, Weight_Post <dbl>,
#   BMI_Post <dbl>, BMI_PostCat <fct>, Tx1 <fct>, Tx2 <fct>, PEFR_Pre <dbl>,
#   PEFR_Post <dbl>, SxWheeze_Pre <fct>, SxWheeze_Post <fct>, PS_Pre <dbl>,
#   PS_Post <dbl>
```

2. Create Contingency Table

~~~
```{r}
with(asthmads, table(Gender, WorkStatus))
```
~~~

```
        WorkStatus
Gender   Unemployed Employed
  Female         47       17
  Male           33       53
```

3. ***BONUS 1***: We can also use `tidyverse::`, `janitor::` and `gt::` package to create nice looking table with total row and total column

~~~
```{r}
#| tbl-cap: "2×2 Contigency Table for Gender by Employment Status, using tidyverse, janitor and gt"

asthmads %>%
  count(Gender, WorkStatus) %>%
  pivot_wider(names_from = WorkStatus, values_from = n,
              values_fill = list(n = 0)) %>%
  janitor::adorn_totals(c("row", "col")) %>%
  gt()
```
~~~

Table 7.2: 2x2 Contigency Table for Gender by Employment Status, using tidyverse, janitor and gt

Gender	Unemployed	Employed	Total
Female	47	17	64
Male	33	53	86
Total	80	70	150

3. ***BONUS 2***: We can also use `gtsummary::` package to create nice looking table with total row and total column

~~~
```{r}
#| tbl-cap: "2×2 Contigency Table for Gender by Employment Status, using gtsummary"

library(gtsummary)

asthmads %>%
  tbl_summary(include = Gender,
              by = WorkStatus,
              digits = all_categorical() ~ c(0,1))
```
~~~

Table 7.3: 2x2 Contigency Table for Gender by Employment Status, using gtsummary

Characteristic	**Unemployed**, N = 80	**Employed**, N = 70
Gender		
Female	47 (58.8%)	17 (24.3%)
Male	33 (41.3%)	53 (75.7%)

7.2.2 Pearson's Chi-Square Test

Pearson Chi-square Test is a statistical test used to determine whether there is a significant association between two categorical variable.

Pearson Chi-square Test is conducted with these assumptions:

- both variables must be **categorical** (either nominal or ordinal)
- the observation must be **independence**. This mean that the outcome of one observation is not influency by the outcome of another observation
- the groupings are **mutually exclusive**
- <20% of celss have **expected frequency of <5**
- minimum **expected frequency if >1**

Example: Gender vs Employment Status

1. Refer previous part to create contingency table
2. Calculate the chi-square test

~~~
```{r}
with(asthmads, table(Gender, WorkStatus)) %>%
  chisq.test(., correct = F)
```
~~~

```
	Pearson's Chi-squared test

data:  .
X-squared = 18.128, df = 1, p-value = 2.066e-05
```

3. Check the test's assumptions

~~~
```{r}
with(asthmads, table(Gender, WorkStatus)) %>%
  chisq.test(., correct = F) %>%
  .$expected
```
~~~

```
        WorkStatus
Gender   Unemployed Employed
  Female   34.13333 29.86667
  Male     45.86667 40.13333
```

> Tip
>
> If the assumptions for chi-square is violated, R will show warning message `In chisq.test(.) : Chi-squared approximation may be incorrect` which is most likely due to violation of small sample assumptions.

4. ***Bonus***: we can create a nice looking table with gtsummary

~~~
```{r}
#| tbl-cap: "Association between Gender and Employment Status"

library(gtsummary)

asthmads %>%
  tbl_summary(include = Gender,
              by = WorkStatus,
              digits = all_categorical() ~ c(0,1)) %>%
  add_p(test = all_categorical() ~ "chisq.test",
        test.args = all_tests("chisq.test") ~ list(correct = F))
```
~~~

Table 7.4: Association between Gender and Employment Status

Characteristic	**Unemployed**, N = 80	**Employed**, N = 70	**p-value**
Gender			<0.001
Female	47 (58.8%)	17 (24.3%)	
Male	33 (41.3%)	53 (75.7%)	

7.2.3 Small Sample

Pearson's Chi-square is only reliable with medium to large datasets. There are two (2) assumptions in the test that might be violated for a small sample, which were (1) <20% of cells have an expected frequency of >5 and (2) minimum expected frequency > 1.

There are two alternatives for a small sample, namely:

- Yates' Correction for Continuity
- Fisher Exact Test

7.2.3.1 Yates' Correction for Continuity

Yates' correction adjust the Chi-square statistics to account for the overestimation of significance due to the continuity assumption of the chi-square distribution.

In R, Yates' correction is the default option for Pearson Chi-square

> **Note**
>
> While Yates' correction is used for small sample (especially when it violate the chi-square assumptions), Yates' correction is not preferable for moderate or large sample, as it can be overly conservative, increasing the risk of Type II error

~~~
```{r}
with(asthmads, table(Gender, WorkStatus)) %>%
  chisq.test(.)
```
~~~

```

	Pearson's Chi-squared test with Yates' continuity correction

data:  .
X-squared = 16.746, df = 1, p-value = 4.273e-05
```

~~~
```{r}
asthmads %>%
  tbl_summary(include = Gender,
              by = WorkStatus,
              digits = all_categorical() ~ c(0,1)) %>%
  add_p()
```
~~~

Characteristic	**Unemployed**, N = 80	**Employed**, N = 70	**p-value**
Gender			<0.001
Female	47 (58.8%)	17 (24.3%)	
Male	33 (41.3%)	53 (75.7%)	

7.2.3.2 Fisher's Exact Test

Pearson's Chi-square test (and the Yates' Correction) is an approximation test, while Fisher Exact Test was based on calculating the exact probability of observing the data under the null hypothesis. Thus it is preferable compared to Pearson's Chi-square Test especially in small sample.

~~~
```{r}
with(asthmads, table(Gender, WorkStatus)) %>%
  fisher.test(.)
```
~~~

```

    Fisher's Exact Test for Count Data

data:  .
p-value = 2.96e-05
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 2.08176 9.60658
sample estimates:
odds ratio
  4.392789
```

~~~
```{r}
asthmads %>%
  tbl_summary(include = Gender,
              by = WorkStatus,
              digits = all_categorical() ~ c(0,1)) %>%
  add_p(test = all_categorical() ~ "fisher.test")
```
~~~

Characteristic	**Unemployed**, N = 80	**Employed**, N = 70	**p-value**
Gender			<0.001
Female	47 (58.8%)	17 (24.3%)	
Male	33 (41.3%)	53 (75.7%)	

7.2.4 McNemar Test

McNemar test is Pearson's Chi-square Test equivalence for paired data (e.g., pre-post data).

Example: Wheezing Symptom Pre and Post Intervention

1. Create Contingency Table

~~~
```{r}
with(asthmads, table(SxWheeze_Pre, SxWheeze_Post))
```
~~~

```
            SxWheeze_Post
SxWheeze_Pre No Yes
         No  43  19
         Yes 56  32
```

2. Calcualte the McNemar Test statistic

~~~
```{r}
with(asthmads, table(SxWheeze_Pre, SxWheeze_Post)) %>%
  mcnemar.test(correct = F)
```
~~~

```

	McNemar's Chi-squared test

data:  .
McNemar's chi-squared = 18.253, df = 1, p-value = 1.934e-05
```

> **Caution**
>
> Supposedly `gtsummary::` package can create table for paired data, unfortunately I unable to replicate the code, despite converted to long format.

7.3 Bivariate Analyses of Numerical Data

Bivariate analysis involves examining the relationship or association between two variables, and bivariate analyses of numerical data is said when involving continuous dependent variables. Example of bivariate analyses of numerical data include

- Parametric Tests
  - Independent t-test
  - Paired t-test
  - Analysis of Variance (ANOVA)
  - Pearson' Correlation
- Non-Parametric Tests
  - Mann-Whitney U Test
  - Wilcoxon Signed Rank Test
  - Spearman's Correlation

Many of parametric tests were based on normal distribution and analyses of the variances, while non-parametric tests were based on rank.

7.3.1 Independent T-test

Independent t-test is a parametric test, commonly used to compare the mean of two independent sample, more specifically, compare the difference of the two means, in relation to the variation (i.e., the variance) of the data.

Independent t-test is conducted with these assumptions:

- samples was taken **randomly** (i.e., the sample representative of the population)
- the groups and measurements were **independents**.
- the outcome (or dependent variable) is **numerical** data.
- the outcome is **normally distributed** in each group.
- *the variance outcome between groups is approximately equal (**homogeneity of variance**)*

> ℹ Note
>
> 1. In large sample size, T-test can be robust to violation of normal distribution assumption, based on Central Limit Theorem.
> 2. The homogeneity of variance can be ignore if we use Welch T-test as default.

Example: Compare Height between Gender

1. We will use the same dataset as previous `asthmads`.
   - below is the code as recap

~~~
```{r}
#| eval: false

download.file(
  url = "https://github.com/MohdAzmiSuliman/IKU_RBook/raw/master/dataset/asthmads_clean.sav",
  destfile = "asthmads_clean.sav", mode = "wb")

asthmads <- read_sav("asthmads_clean.sav") %>%
  as_factor()
```
~~~

~~~
```{r}
asthmads
```
~~~

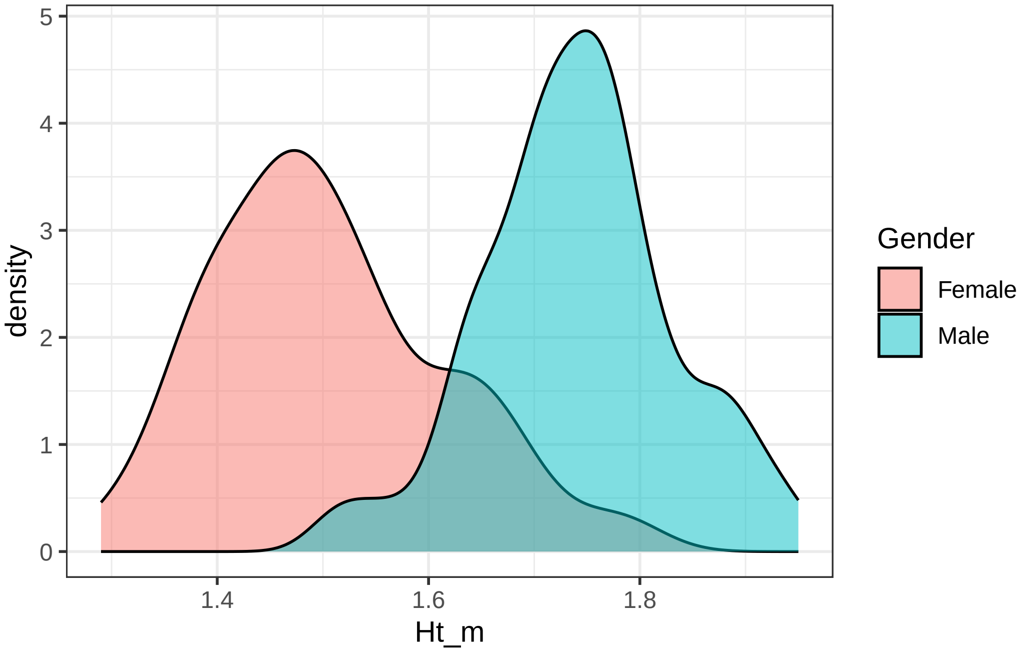
```
# A tibble: 150 x 22
      id idR   Gender   Age WorkStatus Height  Ht_m Weight_Pre BMI_Pre
   <dbl> <chr> <fct>  <dbl> <fct>       <dbl> <dbl>      <dbl>   <dbl>
 1     1 nXSw  Female    34 Unemployed    179  1.79       84.2    26.3
 2     2 yg2t  Male      31 Unemployed    169  1.69       81.8    28.6
 3     3 QBW4  Male      25 Employed      164  1.64       88.5    32.9
 4     4 2×2S  Female    33 Unemployed    136  1.36       53.2    28.8
 5     5 mOnn  Male      28 Unemployed    172  1.72       71.3    24.1
 6     6 D3sl  Male      33 Unemployed    178  1.78       87.3    27.6
 7     7 le6j  Female    31 Unemployed    140  1.4        48.8    24.9
 8     8 r3gC  Female    34 Employed      140  1.4        49.1    25.0
 9     9 3Tyt  Male      31 Employed      171  1.71       60.1    20.6
10    10 cmKF  Male      28 Employed      163  1.63       93.1    35.0
# i 140 more rows
```

```
# i 13 more variables: BMI_PreCat <fct>, PA_HW <dbl>, Weight_Post <dbl>,
#   BMI_Post <dbl>, BMI_PostCat <fct>, Tx1 <fct>, Tx2 <fct>, PEFR_Pre <dbl>,
#   PEFR_Post <dbl>, SxWheeze_Pre <fct>, SxWheeze_Post <fct>, PS_Pre <dbl>,
#   PS_Post <dbl>
```

2. Confirm data distribution

    - assumption for normal distributed in each group

~~~
```{r}
asthmads %>%
  ggplot(aes(x = Ht_m, fill = Gender)) +
  geom_density(alpha = .5) +
  theme_bw()
```
~~~



3. Calculate mean and SD of height for each gender

~~~
```{r}
asthmads %>%
  group_by(Gender) %>%
  summarise(mean = mean(Ht_m, na.rm = T),
            sd = sd(Ht_m, na.rm = T))
```
~~~

```
# A tibble: 2 x 3
  Gender  mean     sd
  <fct>  <dbl>  <dbl>
1 Female  1.50 0.110
2 Male    1.74 0.0898
```

4. Conduct the Welch's T-test

~~~
```{r}
t.test(Ht_m ~ Gender, asthmads)
```
~~~

```

	Welch Two Sample t-test

data:  Ht_m by Gender
t = -14.12, df = 119.43, p-value < 2.2e-16
alternative hypothesis: true difference in means between group Female and group Male is not equal to 0
95 percent confidence interval:
 -0.2703944 -0.2038862
sample estimates:
mean in group Female   mean in group Male 
            1.503906             1.741047 
```

! Important

In R, many functions require a formula parameter, especially in statistical modelling.

- The general form of a formula is `outcome ~ predictors, data`,
  - outcome = dependent variable
  - predictors = independent variable**s**.
- This formula structure is used in various functions, such as linear modelling.
- For a t-test, which compares means across groups,
  - the formula formed by `outcome ~ group, data`
  - `group` = categorical variable = groups

5. ***Bonus 1***: We can create a nice looking table with gtsummary

~~~
```{r}
#| tbl-cap: "Height Differences between Gender table, using gtsummary"

asthmads %>%
  tbl_summary(include = Ht_m,
              by = Gender,
              statistic = all_continuous() ~ "{mean} ({sd})") %>%
  add_difference()
```
~~~

Table 7.7: Height Differences between Gender table, using gtsummary

Characteristic	**Female**, N = 64	**Male**, N = 86	**Difference**	**95% CI**	**p-value**
Height (m)	1.50 (0.11)	1.74 (0.09)	-0.24	-0.27, -0.20	<0.001

6. ***Bonus 2***: the *classical* Student T-test

As mention previously, by default, R will use Welch's T-test, regardless of the assumption of homogeneity of variance. But if you still want to use the Student T-test, change the `var.equal = TRUE` parameter

~~~~
```{r}
t.test(Ht_m ~ Gender, asthmads, var.equal = T)
```
~~~~

```
    Two Sample t-test

data:  Ht_m by Gender
t = -14.539, df = 148, p-value < 2.2e-16
alternative hypothesis: true difference in means between group Female and group Male is not equal to 0
95 percent confidence interval:
 -0.2693719 -0.2049086
sample estimates:
mean in group Female   mean in group Male
            1.503906             1.741047
```

❗ Important

Interested to know why Welch's T-test is preferable? In short:

- Student T-test result biased when assumption for normality and homogeneity of variance were not met
- Welch's T-test provides better control of Type 1 error rates when assumption of homoegeneity of variance was not met.
- Using Welch's T-test as default skip the need to test for homogeneity of variance (i.e., the Levene's test)
- Real data commonly not normally distributed and it is reasonable to assume that variance is unequal in many studies

Source: https://doi.org/10.5334/irsp.82

7.3.2 Paired T-test

Paired T-test is a parametric test, used to compare the mean of two dependent sample, e.g., comparing the mean for pre and post measurement.

Independent t-test is conducted with these assumptions:

- The samples were **random**
- The measurement were **dependent** (i.e., paired, e.g., pre-post)
- The outcome variable is **numerical data**
- The **outcome differences** is **normally distributed**

Example: Weight differences from pre to post measurement

1. We will use the same dataset as previous: `asthmads`

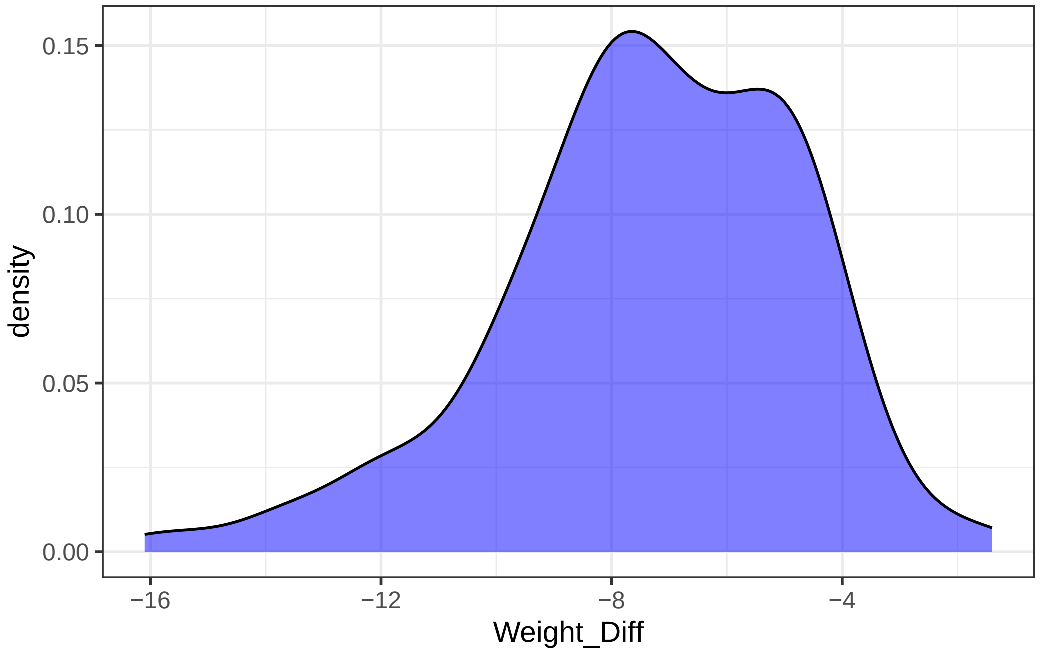
2. Check the differences data distribution

    - assumption for outcome difference is normally distributed
    - we need to calculate the differences

~~~
```{r}
#| eval: false

asthmads %>%
  mutate(Weight_Diff = Weight_Post - Weight_Pre)
```
~~~

    - then plot the differences to check the distribution

~~~
```{r}
asthmads %>%
  mutate(Weight_Diff = Weight_Post - Weight_Pre) %>%
  ggplot(aes(x = Weight_Diff)) +
  geom_density(alpha = .5, fill = "blue") +
  theme_bw()
```
~~~



- we can see that the data is approximately normally distributed

3. Calculate mean and SD of weight - pre & post

~~~
```{r}
asthmads %>%
  summarise(Weight_Pre_Mean = mean(Weight_Pre, na.rm = T),
            Weight_Pre_SD = sd(Weight_Pre, na.rm = T),
            Weight_Post_Mean = mean(Weight_Post, na.rm = T),
            Weight_Post_SD = sd(Weight_Post, na.rm = T))
```
~~~

```
# A tibble: 1 x 4
  Weight_Pre_Mean Weight_Pre_SD Weight_Post_Mean Weight_Post_SD
            <dbl>         <dbl>            <dbl>          <dbl>
1            75.9          21.3             68.6           20.5
```

4. Conduct the Paired T-test

~~~
```{r}
t.test(Pair(Weight_Post, Weight_Pre) ~ 1, asthmads)
```
~~~

```

    Paired t-test

data:  Pair(Weight_Post, Weight_Pre)
t = -34.658, df = 149, p-value < 2.2e-16
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -7.755671 -6.918996
sample estimates:
mean difference
      -7.337333
```

> Caution
>
> Since this is pre-post test, we need to write the post column first. In this example, the samples had reduction in body weight, thus the differences is in negative

5. ***Bonus***: we can create a nice looking table with gtsummary

~~~
```{r}
asthmads %>%
  select(id, Weight_Post, Weight_Pre) %>%
  pivot_longer(cols = starts_with("Weight"),
               names_to = "Type",
~~~

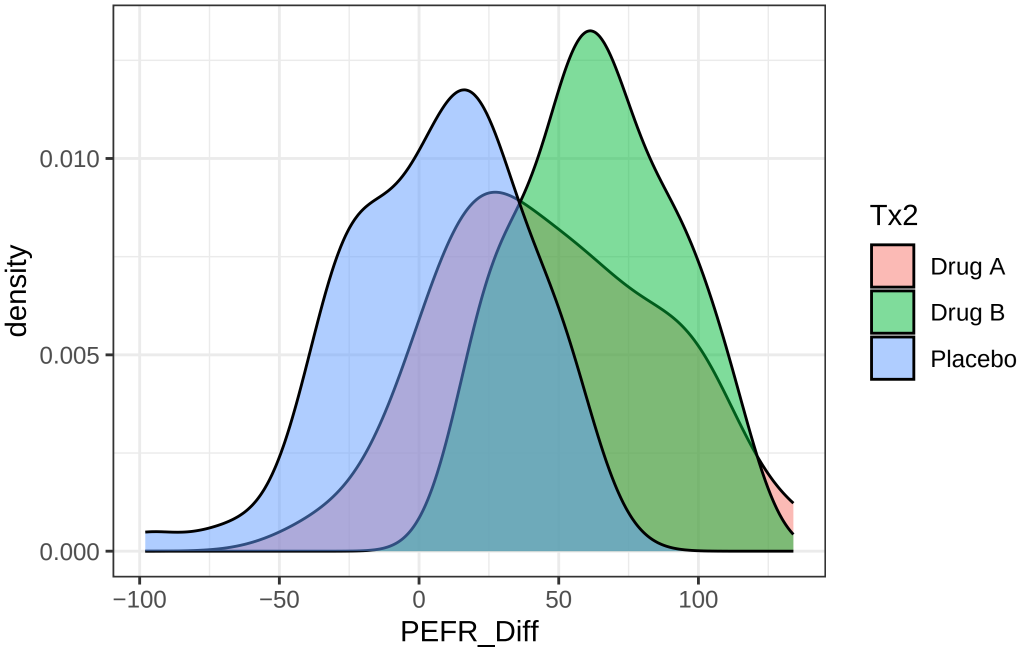
```
               values_to = "Weight",
               names_pattern = "Weight_(.*)") %>%
  mutate(Type = fct_relevel(Type, "Pre")) %>%
  tbl_summary(by = Type,
              include = Weight,
              statistic = all_continuous() ~ "{mean} ({sd})",
              digits = all_continuous() ~ 2) %>%
  add_difference(test = all_continuous() ~ "paired.t.test",
                 group = id)
```
```

Characteristic	**Pre**, N = 150	**Post**, N = 150	**Difference**	**95% CI**	**p-value**
Weight	75.89 (21.27)	68.55 (20.46)	-7.3	-7.8, -6.9	<0.001

7.3.3 ANOVA - Analysis of Variance

Analysis of Variance (ANOVA) is a parametric test, commonly used to compare the means of three or more independent (unrelated) groups, more specifically, in relation to the variation (i.e. the variance) of the data.

Note

There are severals test in ANOVA, which include one-way ANOVA, two-way ANOVA, N-way ANOVA, ANCOVA, Repeated Measure ANOVA, RM ANCOVA, MANOVA etc.
In this example, we will focus only to one-way ANOVA

One-way ANOVA is conducted with these assumptions:

- The samples were taken **randomly**
- The groups and measurements were **independents**
- The outcome is **numerical** data
- The outcome in approximately **normal distribution** in each group
- The variances of outcome in each group have approximately equal, i.e. **homogeneity of variance**.

Tip

note that almost all parametric tests have similar assumptions.

Example: PEFR improvement between Treatment Group

1. We will use the same dataset as previous, i.e., the `asthmads`

    - we will need to wrangle the dataset, to calculate the PEFR improvement

```
```{r}
asthmads <- asthmads %>%
  mutate(PEFR_Diff = PEFR_Post-PEFR_Pre)
```

~~~
```
~~~

2. Confirm data distribution

    - assumption for normal distributed in each group

~~~
```{r}
asthmads %>%
  ggplot(aes(x = PEFR_Diff, fill = Tx2)) +
  geom_density(alpha = .5) +
  theme_bw()
```
~~~



3. Calculate mean and SD of PEFR_Diff for each treatment group

~~~
```{r}
asthmads %>%
  group_by(Tx2) %>%
  summarise(mean = mean(PEFR_Diff, na.rm = T),
            sd = sd(PEFR_Diff, na.rm = T))
```
~~~

```
# A tibble: 3 x 3
  Tx2       mean    sd
  <fct>    <dbl> <dbl>
1 Drug A   47.9   38.7
2 Drug B   64     26.9
3 Placebo   5.92  31.9
```

4. Conduct the ANOVA

~~~
```{r}
oneway.test(PEFR_Diff ~ Tx2, asthmads)
```
~~~

```
	One-way analysis of means (not assuming equal variances)

data:  PEFR_Diff and Tx2
F = 56.384, num df = 2.000, denom df = 78.046, p-value = 7.064e-16
```

Note

In R, there are three related functions, but used differently, for ANOVA.

1. Function `oneway.test(_)` is for Welch's ANOVA
2. Function `aov(_)` is for ANOVA assuming equal variance
3. Function `anova(_)` is to compare between models.

5. Pair-wise post-hoc test

   - since the comparison by ANOVA is significant, we need to do post-hoc test to check which pair have significant difference.
   - since there are three pairwise comparison (Drug A vs B, Drug A vs Placebo and Drug B vs Placebo), in Bonferroni, the alpha level need to divide by 3 (i.e., 0.017)

Important

Type 1 error increase with the number of comparison being made. **Thus adjustment to the alpha level are necessary**.
Common post-hoc adjustment include Bonferroni Correction, in which the original alpha level (⊠) divided by the number of comparison.

~~~
```{r}
pairwise.t.test(asthmads$PEFR_Diff, asthmads$Tx2,
                p.adjust.method = "b")
```
~~~

```
	Pairwise comparisons using t tests with pooled SD

data:  asthmads$PEFR_Diff and asthmads$Tx2

        Drug A  Drug B
Drug B  0.09    -
Placebo 9.8e-09 4.8e-16
```

```
P value adjustment method: bonferroni
```

we can see that only Drug A vs B is not significant. other pairs were significant.

6. ***Bonus***: we can create nice looking table with gtsummary

~~~
```{r}
asthmads %>%
  tbl_summary(include = PEFR_Diff,
              by = Tx2,
              label = PEFR_Diff ~ "PEFR Difference (Post - Pre)",
              statistic = all_continuous() ~ "{mean} ({sd})",
              digits = all_continuous() ~ 2) %>%
  add_p(test = all_continuous() ~ "oneway.test")
```
~~~

Characteristic	**Drug A**, N = 35	**Drug B**, N = 43	**Placebo**, N = 72	**p-value**
PEFR Difference (Post - Pre)	47.89 (38.71)	64.00 (26.86)	5.92 (31.94)	<0.001

7.3.4 Pearson's Correlation

Pearson's correlation is a parametric test, commonly used to test correlation between two numerical data.

The Pearson's Correlation assumptions were:

- each observation/measurement were **independent**
- both variables were **numerical** data
- both variables should follow approximately **normal distribution**.
- the relationship between the two variables should be **linear**.
- the scatterplot of the two variables should show a roughly constant spread, the **homoscedasticity**

Tip

homogeneity and homoscedasticity is similar concept but mean differently. homogeneity means the variance between different groups were approximately equal, but homoscedasticity means the variances of residuals or best fit line were approximately constant.

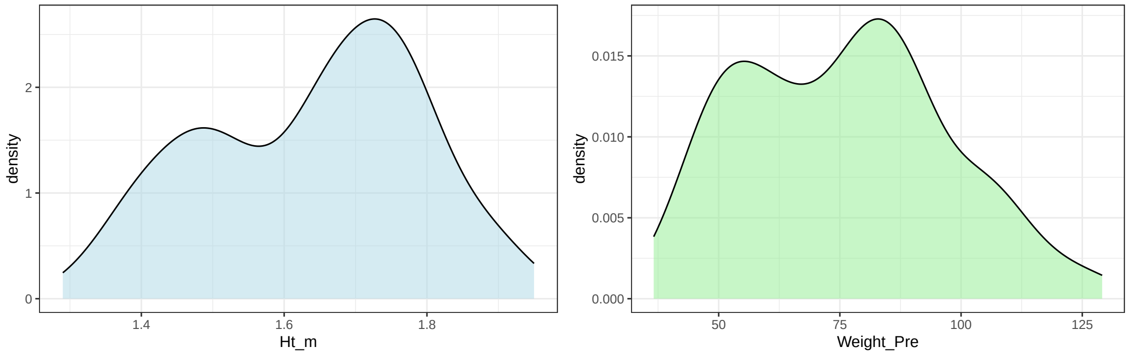
Example: Correlation between height and body weight

1. We will use the same dataset as previous, i.e. the `asthmads`.

2. Confirm data distribution

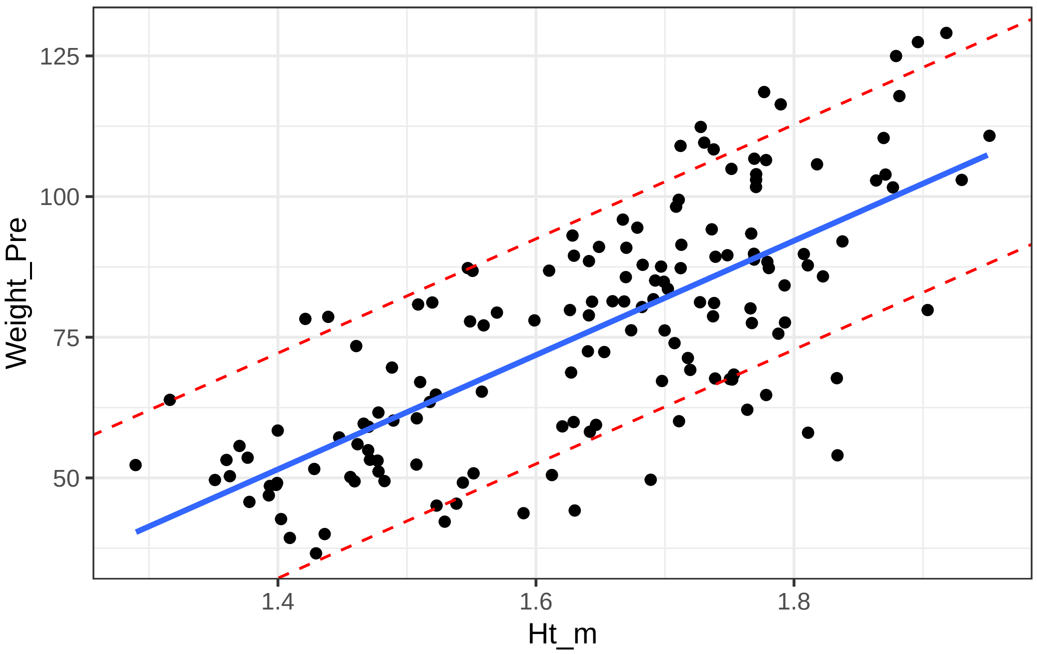
- assumptions for normal distribution

~~~
```{r}
#| layout-ncol: 2

asthmads %>%
  ggplot(aes(x = Ht_m)) +
  geom_density(fill = "lightblue", alpha = .5) +
  theme_bw()

asthmads %>%
  ggplot(aes(x = Weight_Pre)) +
  geom_density(fill = "lightgreen", alpha = .5) +
  theme_bw()
```
~~~



- assumption for linearity & homoscedasciticity

~~~
```{r}
modslope <- lm(Weight_Pre ~ Ht_m, data = asthmads) %>%
  broom::tidy() %>%
  filter(term == "Ht_m") %>%
  pull(estimate)

asthmads %>%
  ggplot(aes(x = Ht_m, y = Weight_Pre)) +
  geom_point(position = position_jitter()) +
  geom_smooth(method = "lm", se = F) +
  geom_abline(slope = modslope, intercept = -70,
              colour = "red", linetype = 2) +
  geom_abline(slope = modslope, intercept = -110,
              colour = "red", linetype = 2) +
  theme_bw()
```
~~~



4. Calculate the pearson correlation

```r
cor.test(~ Ht_m + Weight_Pre, asthmads, method = "pearson")
```

```

	Pearson's product-moment correlation

data:  Ht_m and Weight_Pre
t = 13.09, df = 148, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.6483493 0.7989693
sample estimates:
      cor 
0.7325001 
```

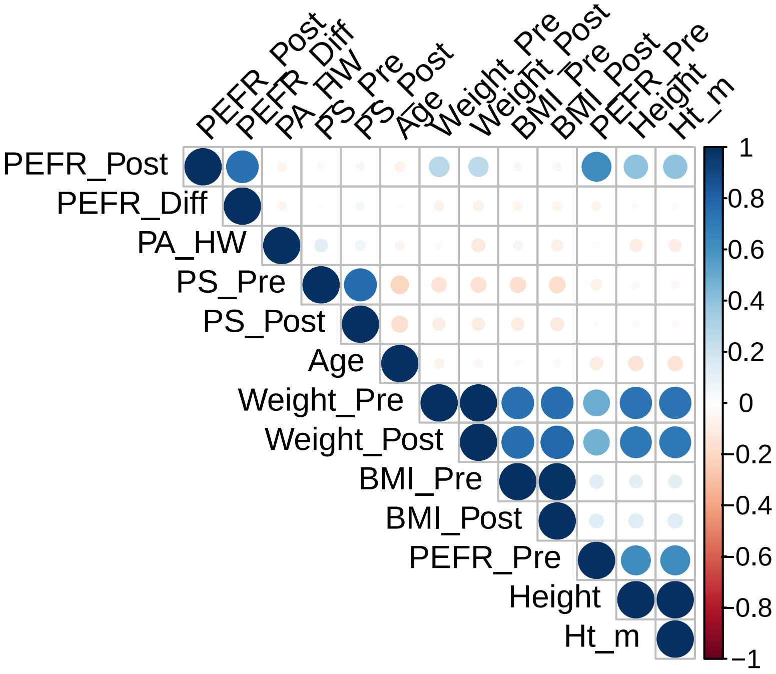
5. ***Bonus 1***: Create nice table with `apaTables::` package

~~~
```{r}
library(apaTables)

asthmads %>%
  select(Ht_m, Weight_Pre) %>%
  apa.cor.table(.)
```
~~~

```
Means, standard deviations, and correlations with confidence intervals


  Variable      M     SD    1
  1. Ht_m       1.64  0.15

  2. Weight_Pre 75.89 21.27 .73**
                            [.65, .80]


Note. M and SD are used to represent mean and standard deviation, respectively.
Values in square brackets indicate the 95% confidence interval.
The confidence interval is a plausible range of population correlations
that could have caused the sample correlation (Cumming, 2014).
 * indicates p < .05. ** indicates p < .01.
```

6. ***Bonus 2***: Correlation Plot

~~~
```{r}
library(corrplot)

asthmads %>%
  select(-id) %>%
  select(where(is.numeric)) %>%
  cor() %>%
  corrplot(type = "upper", order = "hclust",
           tl.col = "black", tl.srt = 45)
```
~~~



7.4 Linear Regression

Linear regression is a statistical method used to model the relationship between a dependent variable and one or more independent variables by fitting a linear equation to observed data.

The formula for linear regression is

$$y = \beta_0 + \beta_1 x + \epsilon$$

where

- y is the dependent variable (outcome)
- x is the independent variable (predictor)
- β_0 is the y-intercept
- β_1 is the slope of the line, representing the change in y for one-unit change in x
- ϵ is the error term

For linear regression to provide reliable estimates, several key assumptions must be met

- each observation/measurement were **independent**
- the outcome variable is **numerical** data
- the residuals follow approximately **normal distribution**.
- the relationship between the predictor and the outcome should be **linear**.
- the residuals have constants variance at every level of the predictor, i.e., the **homoscedasticity**
- in multiple linear regression, there will be no or little **multicollinearity**, which independent variables are not too highly correlated with each other

> Tip
>
> note the similarity between pearson correlation and linear regression

Example: Finding factors associated with BMI changes

7.4.0.1 Simple Linear Regression

1. We will use the same dataset as previous, i.e. the `asthmads`

    - we need to do some data wrangling to calculate the BMI changes

~~~
```{r}
asthmads <- asthmads %>%
  mutate(BMI_Diff = BMI_Post-BMI_Pre)
```
~~~

2. Conduct the simple linear regression

    - in this example, the simple linear regression model is saved in R object, for used later

~~~
```{r}
slinm <- lm(BMI_Diff ~ PA_HW, asthmads)

summary(slinm)
```
~~~

```

Call:
lm(formula = BMI_Diff ~ PA_HW, data = asthmads)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.22966 -0.35884  0.02248  0.35711  1.39559 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1.84559    0.06743  -27.37   <2e-16 ***
PA_HW       -0.31476    0.01871  -16.82   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5182 on 148 degrees of freedom
Multiple R-squared:  0.6567,	Adjusted R-squared:  0.6544 
F-statistic: 283.1 on 1 and 148 DF,  p-value: < 2.2e-16
```

3. Test assumptions

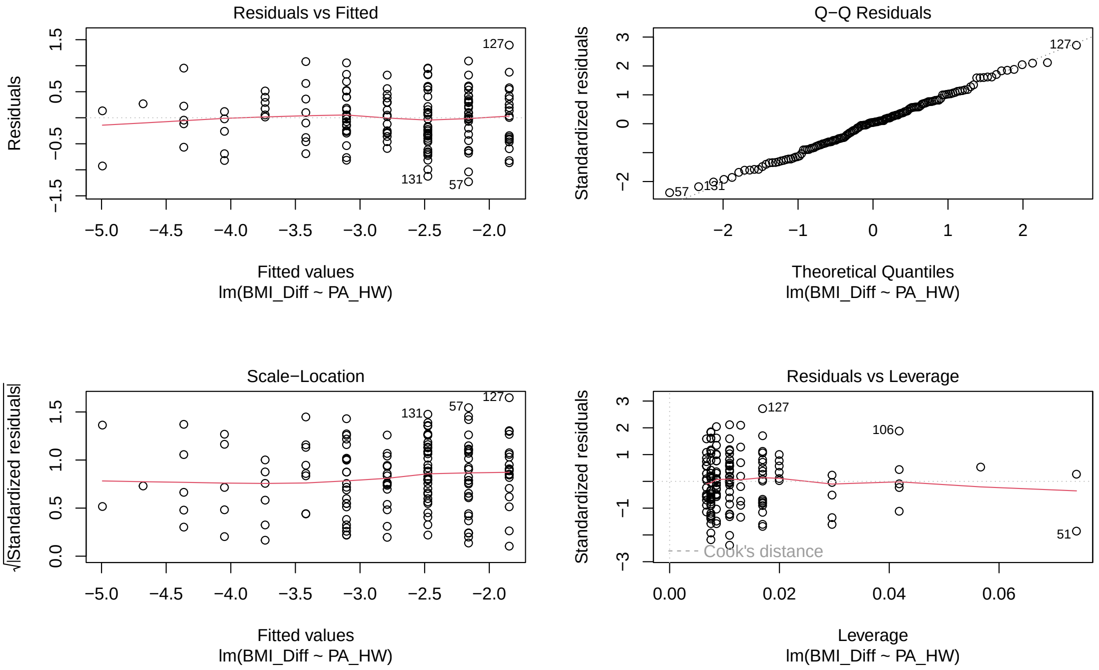
- the simplest way for assumptions testing, is to use `plot(_)` function

~~~
```{r}
#| layout-ncol: 2

plot(slinm)
```
~~~

- otherwise, we call also use `augment(_)` function from `broom::` package to extract the residuals and check the assumptions

~~~
```{r}
library(broom)

augment(slinm)
```
~~~

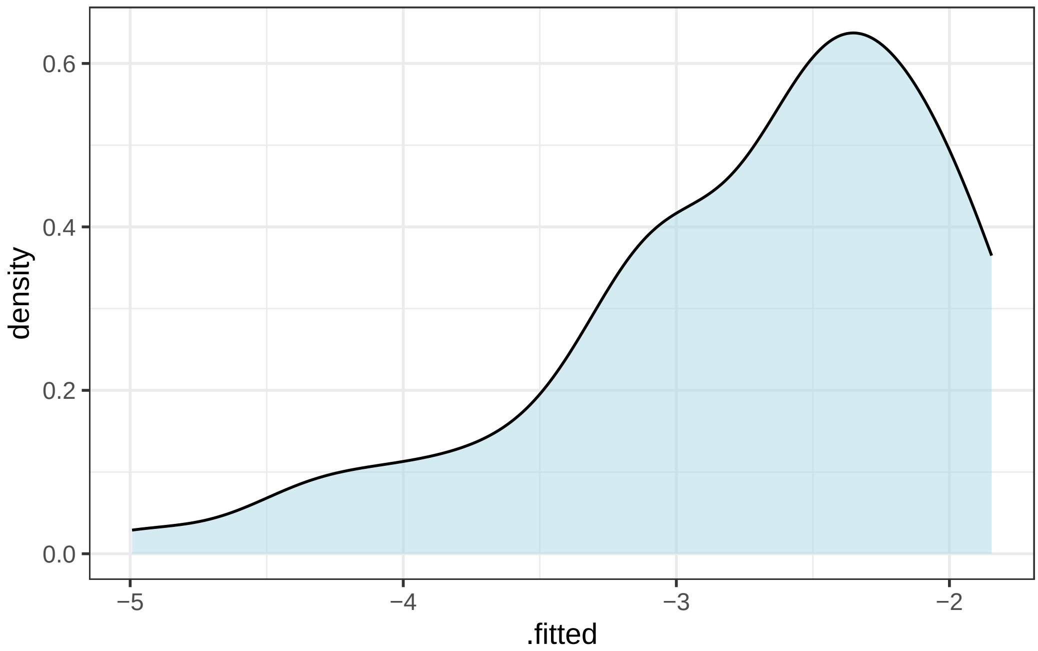
```
# A tibble: 150 x 8
   BMI_Diff PA_HW .fitted  .resid    .hat .sigma    .cooksd .std.resid
      <dbl> <dbl>   <dbl>   <dbl>   <dbl>  <dbl>      <dbl>      <dbl>
```



```
 1     -2.34      5    -3.42  1.08    0.0129    0.512 0.0288          2.10
 2     -2.14      1    -2.16  0.0203 0.0109    0.520 0.00000860      0.0395
 3     -1.63      1    -2.16  0.530   0.0109    0.518 0.00585         1.03
 4     -3.40      4    -3.10 -0.295   0.00852   0.519 0.00141        -0.572
 5     -2.70      2    -2.48 -0.225   0.00751   0.520 0.000718       -0.436
 6     -1.48      0    -1.85  0.366   0.0169    0.519 0.00436         0.711
 7     -3.52      5    -3.42 -0.101   0.0129    0.520 0.000250       -0.195
 8     -2.81      2    -2.48 -0.335   0.00751   0.519 0.00159        -0.649
 9     -1.84      1    -2.16  0.320   0.0109    0.519 0.00213         0.622
10     -2.6       1    -2.16 -0.440   0.0109    0.519 0.00402        -0.853
# i 140 more rows
```

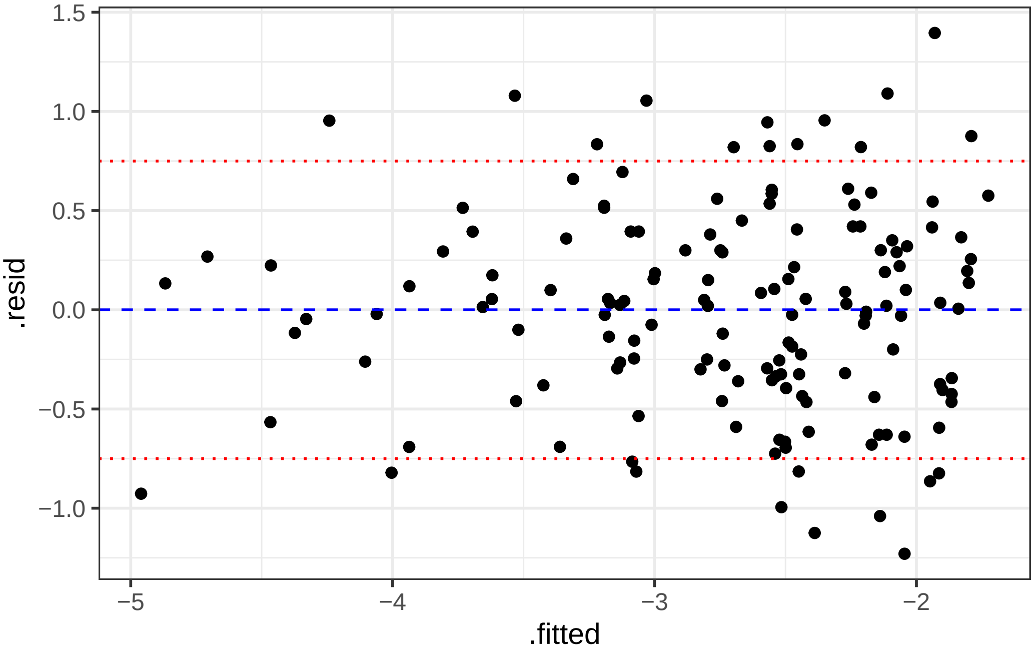
- using the dataset from augment, to plot the residual to check for normality

~~~
```{r}
augment(slinm) %>%
  ggplot(aes(.fitted)) +
  geom_density(fill = "lightblue", alpha = .5) +
  theme_bw()
```
~~~



- plot residual values vs predicted values (aka fitted values) for linearity and homoscedasticity
  - linearity: abscence of systematic patterns like curves
  - homoscedasticity: residuals randomly scttered around the horizontal line with no funnel-shapped patern

~~~
```{r}
augment(slinm) %>%
  ggplot(aes(x = .fitted, y = .resid)) +
  geom_point(position = position_jitter()) +
  geom_hline(yintercept = 0, linetype = 2, colour = "blue") +
  geom_hline(yintercept = .75, linetype = 3, colour = "red") +
  geom_hline(yintercept = -.75, linetype = 3, colour = "red") +
  theme_bw()
```
~~~



4. Check model fitness

- one of parameter to check our model fitness is by looking at the coefficient of determination r^2 from the model summary

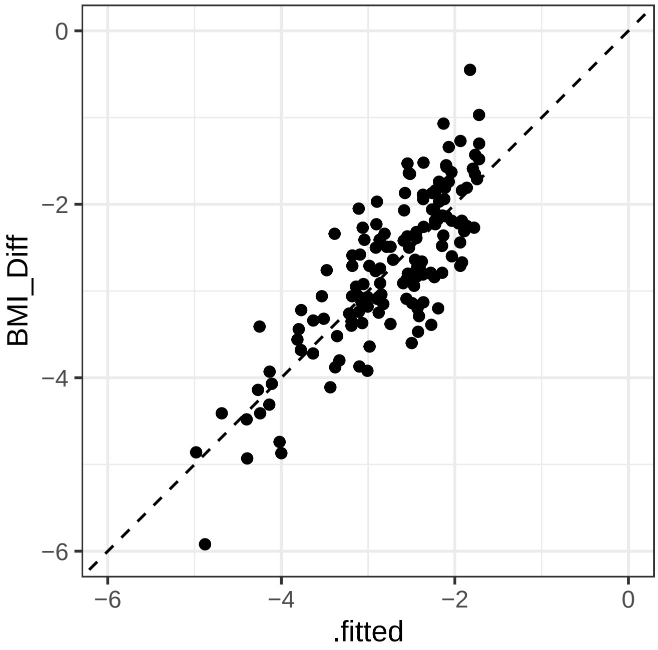
~~~
```{r}
summary(slinm)
```
~~~

```
Call:
lm(formula = BMI_Diff ~ PA_HW, data = asthmads)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.22966 -0.35884  0.02248  0.35711  1.39559 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1.84559    0.06743  -27.37   <2e-16 ***
PA_HW       -0.31476    0.01871  -16.82   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5182 on 148 degrees of freedom
Multiple R-squared:  0.6567,    Adjusted R-squared:  0.6544 
F-statistic: 283.1 on 1 and 148 DF,  p-value: < 2.2e-16
```

- we can also plot our observed vs predicted value to visualize the model fitness

- in this plot, the point should be close at the diagonal, i.e. observed = predicted

~~~
```{r}
slinm %>%
  augment() %>%
  ggplot(aes(x = .fitted, y = BMI_Diff)) +
  scale_x_continuous(limits = c(-6, 0)) +
  scale_y_continuous(limits = c(-6, 0)) +
  geom_point(position = position_jitter()) +
  geom_abline(intercept = 0, slope = 1, linetype = 2) +
  theme_bw() +
  theme(aspect.ratio = 1)
```
~~~



5. ***Bonus***: nice table with gtsummary

- `tbl_uvregression(_)` functions from gtsummary not only can create a nice table

~~~
```{r}
asthmads %>%
  tbl_uvregression(method = lm,
                   y = BMI_Diff,
                   include = PA_HW)
```
~~~

Characteristic	**N**	**Beta**	**95% CI**	**p-value**
Physical Activity (total hour per week)	150	-0.31	-0.35, -0.28	<0.001

- but also can simplified our simple linear regression involving several predictors

~~~~
```{r}
asthmads %>%
  select(BMI_Diff, Gender, Age, WorkStatus, Height, PA_HW) %>%
  tbl_uvregression(method = lm,
                   y = BMI_Diff,
                   pvalue_fun = partial(style_pvalue,
                                        digits = 3)) %>%
  bold_p()
```
~~~~

Characteristic	**N**	**Beta**	**95% CI**	**p-value**
Gender	150			
Female		—	—	
Male		0.23	-0.05, 0.52	0.108
Age (year)	150	0.01	-0.04, 0.06	0.609
Employment	150			
Unemployed		—	—	
Employed		0.02	-0.26, 0.31	0.884
Height (cm)	150	0.01	0.00, 0.02	0.070
Physical Activity (total hour per week)	150	-0.31	-0.35, -0.28	**<0.001**

7.4.1 Multiple Linear Regression

Real-world relationships between variables rarely occur in isolation; they are often influenced by third variables. These third variables can be categorized as:

- Confounders
- Mediators
- Moderators

Controlling for these third variables is crucial for accurately understanding the relationships among variables. While the optimal approach is to control for these variables at the study design level (e.g., through randomization, stratification, and setting proper inclusion and exclusion criteria), the presence of third variables can be inevitable and may significantly impact the observed relationships.

When third variables cannot be controlled through design alone, statistical methods can be employed to adjust for their influence, including (not limited to) Stratification, Multivariable Analysis or Multivariate Analysis

Example: Find factors associated with BMI changes

1. Conduct multiple linear regression
    - and check for model fitness (R^2)

~~~
```{r}
mlinm <- lm(BMI_Diff ~ Gender + Age + WorkStatus + PA_HW + BMI_PreCat,
            asthmads)

summary(mlinm)
```
~~~

```
Call:
lm(formula = BMI_Diff ~ Gender + Age + WorkStatus + PA_HW + BMI_PreCat,
    data = asthmads)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.18613 -0.32674  0.02218  0.28579  1.29659 

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)    
(Intercept)          -1.800884   0.479161  -3.758 0.000249 ***
GenderMale            0.157402   0.091767   1.715 0.088483 .  
Age                   0.005324   0.014421   0.369 0.712517    
WorkStatusEmployed   -0.159447   0.093687  -1.702 0.090962 .  
PA_HW                -0.312087   0.018950 -16.469  < 2e-16 ***
BMI_PreCatNormal     -0.140436   0.223807  -0.627 0.531347    
BMI_PreCatOverweight -0.336183   0.239738  -1.402 0.163011    
BMI_PreCatObese      -0.248582   0.205849  -1.208 0.229211    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5156 on 142 degrees of freedom
Multiple R-squared:  0.6739,	Adjusted R-squared:  0.6578 
F-statistic: 41.93 on 7 and 142 DF,  p-value: < 2.2e-16
```

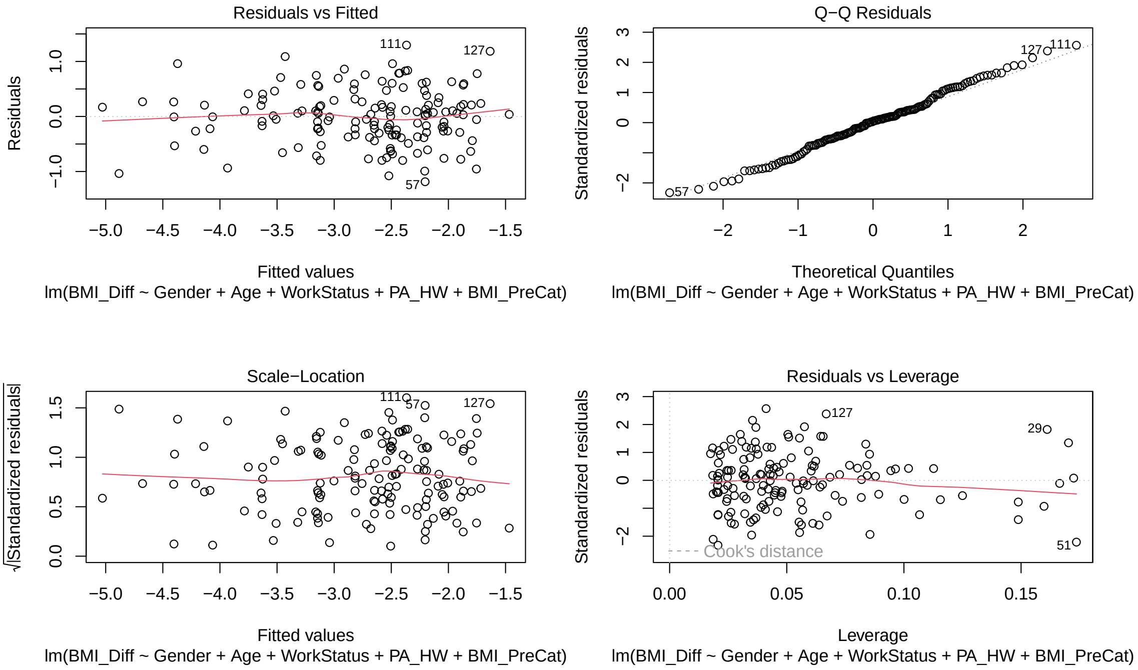
2. Test for assumptions

~~~
```{r}
#| layout-ncol: 2

plot(mlinm)
```
~~~

3. ***Bonus 1***: Model Comparison

   we can compare multiple model with `anova(_)` function

   - for example we have null model



~~~
```{r}
slinnulm <- lm(BMI_Diff ~ 1, asthmads)
```
~~~

- we want to compare our simple linear regression model with the null model

~~~
```{r}
anova(slinnulm, slinm)
```
~~~

```
Analysis of Variance Table

Model 1: BMI_Diff ~ 1
Model 2: BMI_Diff ~ PA_HW
  Res.Df     RSS Df Sum of Sq      F    Pr(>F)
1    149 115.774
2    148  39.748  1    76.026 283.08 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- we can also compare multiple models

~~~
```{r}
anova(slinnulm, slinm, mlinm)
```
~~~

```
Analysis of Variance Table

Model 1: BMI_Diff ~ 1
Model 2: BMI_Diff ~ PA_HW
Model 3: BMI_Diff ~ Gender + Age + WorkStatus + PA_HW + BMI_PreCat
  Res.Df     RSS Df Sum of Sq        F Pr(>F)
1    149 115.774
2    148  39.748  1    76.026 285.9702 <2e-16 ***
3    142  37.751  6     1.997   1.2518 0.2836
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- we can see that our multiple linear regression model is not significantly different with simple linear regression model. thus we can choose the simpler model i.e., the simple linear regression model.

4. ***Bonus 2***: Variable Selection

Important

variable selection should start with plausible relationship i.e., back up with prior knowledge. this should start even at study design, in which unlikely relationship should not be included as variable collected in the study. this is to avoid spurious significant association
further read: https://doi.org/10.1002%2Fbimj.201700067

While variable selection should be made purposely, i.e., the PI specifically select variable to be included in final model, variable selection by statistically software is still available to conduct.

- create null model

~~~
```{r}
mlinnulm <- lm(BMI_Diff ~ 1, asthmads)
```
~~~

- create full model

~~~
```{r}
mlinfulm <- lm(BMI_Diff ~ Gender + Age + WorkStatus + PA_HW + BMI_PreCat,
               asthmads)
```
~~~

- conduct forward selection

~~~
```{r}
step(mlinfulm,
     scope = list(lower = mlinnulm, upper = mlinfulm),
     direction = "forward",
     trace = 0)
```
~~~

```
Call:
lm(formula = BMI_Diff ~ Gender + Age + WorkStatus + PA_HW + BMI_PreCat,
    data = asthmads)

Coefficients:
         (Intercept)            GenderMale                   Age
           -1.800884              0.157402              0.005324
  WorkStatusEmployed                 PA_HW      BMI_PreCatNormal
           -0.159447             -0.312087             -0.140436
BMI_PreCatOverweight       BMI_PreCatObese
           -0.336183             -0.248582
```

- conduct backward selection

~~~
```{r}
step(mlinfulm,
     scope = list(lower = mlinnulm, upper = mlinfulm),
     direction = "backward",
     trace = 0)
```
~~~

```
Call:
lm(formula = BMI_Diff ~ Gender + WorkStatus + PA_HW, data = asthmads)

Coefficients:
       (Intercept)          GenderMale  WorkStatusEmployed               PA_HW
           -1.8527              0.1531             -0.1706             -0.3151
```

- conduct both selection

~~~
```{r}
step(mlinfulm,
     scope = list(lower = mlinnulm, upper = mlinfulm),
     direction = "both",
     trace = 0)
```
~~~

```
Call:
lm(formula = BMI_Diff ~ Gender + WorkStatus + PA_HW, data = asthmads)

Coefficients:
       (Intercept)          GenderMale  WorkStatusEmployed               PA_HW
           -1.8527              0.1531             -0.1706             -0.3151
```

5. ***Bonus 3***: Nice table with gtsummary
   - final model table based on variable selection, direction “both”

~~~
```{r}
lm(formula = BMI_Diff ~ Gender + WorkStatus + PA_HW,
   data = asthmads) %>%
  tbl_regression() %>%
  bold_p()
```
~~~

Characteristic	**Beta**	**95% CI**	**p-value**
Gender			
Female	—	—	
Male	0.15	-0.03, 0.33	0.093
Employment			
Unemployed	—	—	
Employed	-0.17	-0.35, 0.01	0.059
Physical Activity (total hour per week)	-0.32	-0.35, -0.28	**<0.001**

6. ***Bonus 4***: Another package that also create nice table, sjPlot

~~~
```{r}
library(sjPlot)

lm(formula = BMI_Diff ~ Gender + WorkStatus + PA_HW,
   data = asthmads) %>%
  tab_model()
```
~~~

		BMI Diff	
Predictors	Estimates	CI	p
(Intercept)	-1.85	-2.03 – -1.67	**<0.001**
Gender: Male	0.15	-0.03 – 0.33	0.093
Employment: Employed	-0.17	-0.35 – 0.01	0.059
Physical Activity(total hour per week)	-0.32	-0.35 – -0.28	**<0.001**
Observations	150		
R^2 / R^2 adjusted	0.668 / 0.661		

7.5 Logistic Regression

Similar to linear regression, logistic regression models the relationship between a dependent variable and one or more independent variables. However, while linear regression predicts continuous outcomes, binary logistic regression is used when the outcome is binary in nature, with two possible outcomes (0/1, yes/no, true/false). Logistic regression estimates the **probabilities** of the binary outcome

the formula is

$$\log\left(\frac{P}{1-P}\right) = \beta_0 + \beta_1 X$$

- P is the probability of outcome
- $\frac{P}{1-P}$ is the odd of event occuring
- $\log\left(\frac{P}{1-P}\right)$ - the log odds or logit
- X is the predictor
- β_0 is the y-intercept
- $\beta_1 X$ is the slope of the line, representing the change of probability in y for one-unit change in X

The assumptions for logistic regression are:

- each observation were **indepedent**.
- the outcome variable is **binary categorical** data
- The log odds of the outcome should have a **linear** relationship with the independent variables
- abscence (or minimal) **multicollinearity**
- **large sample size**. general rule of thumn, at least 10 cases with the least frequent outcome for each independent variable in the model
- no extreme **outlier**
- model should adequately fit the model, i.e., test for **goodness-of-fit**

Tip

note the similarities and differences between linear regression and logistic regression.

Example: Finding factors associated with BMI changes category

7.5.1 Simple Logistic Regression

1. We will use the same dataset as previous, i.e., the `asthmads`
   - we need to do some data wrangling to categorised the BMI changes.
   - assumed, if the BMI changes (reduced) by 2.5 kg/m^2, the changes is effective

~~~
```{r}
asthmads <- asthmads %>%
  mutate(BMI_DiffCat = cut(BMI_Diff,
                           breaks = c(0, -2, -6),
                           labels = c("Effective", "Not Effective")),
         BMI_DiffCat = fct_relevel(BMI_DiffCat, "Not Effective"))
```
~~~

2. Conduct the simple logistic regression

~~~
```{r}
slogm <- glm(BMI_DiffCat ~ PA_HW, family = binomial, asthmads)

summary(slogm)
```
~~~

~~~
```
~~~

```
Call:
glm(formula = BMI_DiffCat ~ PA_HW, family = binomial, data = asthmads)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)    
(Intercept)  -0.6381     0.3744  -1.705   0.0883 .  
PA_HW         1.0840     0.2299   4.715 2.41e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 155.5  on 149  degrees of freedom
Residual deviance: 111.3  on 148  degrees of freedom
AIC: 115.3

Number of Fisher Scoring iterations: 6
```

3. Exponentiate the estimate and confident interval

~~~
```{r}
exp(coef(slogm))

exp(confint(slogm))
```
~~~

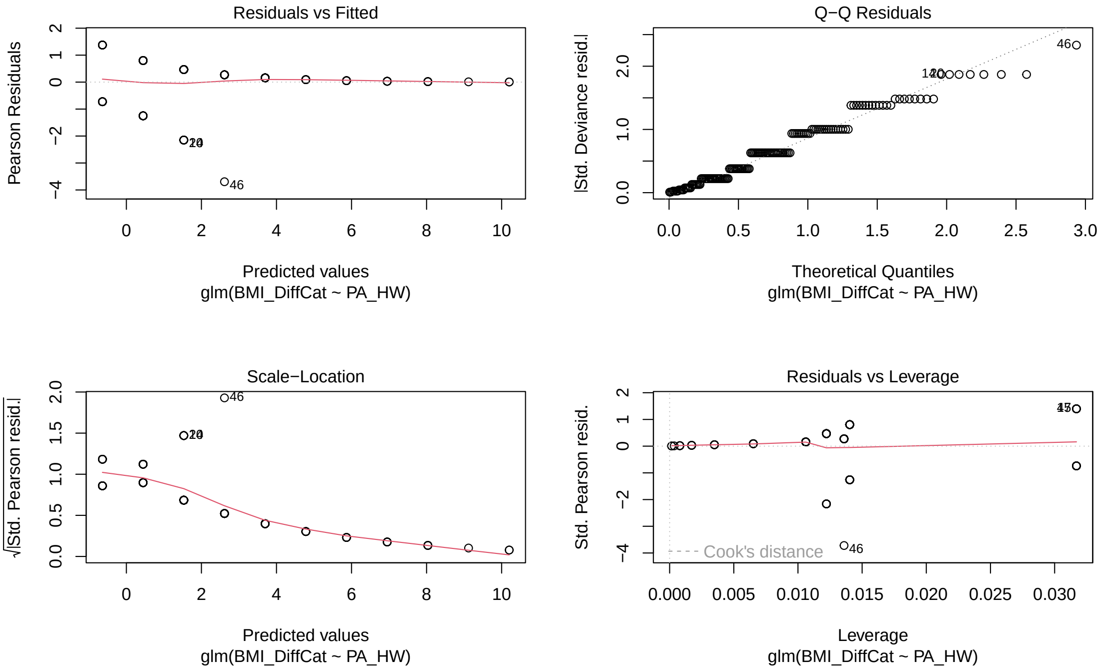
```
(Intercept)       PA_HW 
  0.5282878   2.9566236 
                2.5 %   97.5 %
(Intercept) 0.2459518 1.079780
PA_HW       1.9692051 4.872002
```

> ℹ Note
>
> exponentiating a coefficient gives you the odds ratio associated with a one-unit increase in the corresponding predictor variable, assuming other variables are held constant

4. Test assumption

    - similar to linear regression, simplest way for assumption testing is use `plot(_)` function

~~~
```{r}
#| layout-ncol: 2

~~~

```
plot(slogm)
```
```


Residuals vs Fitted
Pearson Residuals
Predicted values
glm(BMI_DiffCat ~ PA_HW)
20
46
Q−Q Residuals
|Std. Deviance resid.|
Theoretical Quantiles
glm(BMI_DiffCat ~ PA_HW)
46
120
Scale−Location
√|Std. Pearson resid.|
Predicted values
glm(BMI_DiffCat ~ PA_HW)
46
20
Residuals vs Leverage
Std. Pearson resid.
Leverage
glm(BMI_DiffCat ~ PA_HW)
Cook's distance
46
15
0
2
4
6
8
10
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.000
0.005
0.010
0.015
0.020
0.025
0.030

5. Check model fitness

- in R, the model fitness measured with AIC, which is from the `summary(_)` function

```
```{r}
summary(slogm)
```
```

```
Call:
glm(formula = BMI_DiffCat ~ PA_HW, family = binomial, data = asthmads)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.6381   0.3744 -1.705   0.0883 .
PA_HW   1.0840   0.2299   4.715 2.41e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 155.5 on 149 degrees of freedom
Residual deviance: 111.3 on 148 degrees of freedom
AIC: 115.3
```
```

```
Number of Fisher Scoring iterations: 6
```

- we can also conduct hosmer-lemeshow test.
- the outcome however need to change to binary numeric 0/1 first.

~~~
```{r}
asthmads <- asthmads %>%
  mutate(BMI_DiffCatN = case_when(BMI_DiffCat == "Not Effective" ~ 0,
                                  BMI_DiffCat == "Effective" ~ 1))

library(ResourceSelection)

hoslem.test(asthmads$BMI_DiffCatN,
            fitted(slogm), g = 5)
```
~~~

```

    Hosmer and Lemeshow goodness of fit (GOF) test

data:  asthmads$BMI_DiffCatN, fitted(slogm)
X-squared = 0.86611, df = 3, p-value = 0.8336
```

6. Check model performance

- model performance with accuracy, sensitivity and specificity
  - need to calculate the predicted outcome, using `broom::` package

~~~
```{r}
library(caret)
library(broom)

augment(slogm, type.predict = "response") %>%
  mutate(predcat = cut(.fitted,
                       breaks = c(0, .5, 1),
                       labels = c("Not Effective", "Effective")),
         predcat = fct_relevel(predcat, "Not Effective")) %>%
  with(., table(BMI_DiffCat, predcat)) %>%
  confusionMatrix(., positive = "Effective")
```
~~~

```
Confusion Matrix and Statistics

               predcat
BMI_DiffCat     Not Effective Effective
  Not Effective            11        21
  Effective                 8       110
```

```
               Accuracy : 0.8067
                 95% CI : (0.7343, 0.8665)
    No Information Rate : 0.8733
    P-Value [Acc > NIR] : 0.99266

                  Kappa : 0.3239

 Mcnemar's Test P-Value : 0.02586

            Sensitivity : 0.8397
            Specificity : 0.5789
         Pos Pred Value : 0.9322
         Neg Pred Value : 0.3438
             Prevalence : 0.8733
         Detection Rate : 0.7333
   Detection Prevalence : 0.7867
      Balanced Accuracy : 0.7093

       'Positive' Class : Effective
```

8 Complex Sampling Design in NHMS

8.1 Why Complex Sampling Design?

Surveys are essential for understanding population characteristics, offering a more efficient and resource-friendly alternative to censuses. Censuses, aiming to collect data from every individual within a population, are historically resource-intensive. In contrast, surveys, whether conducted by governments or researchers, enable effective population inferences with less expenditure.

Simple random sampling, while a traditional gold standard for its straightforward approach and unbiased estimates, often falls short in achieving comprehensive representativeness, particularly in diverse populations. This limitation becomes apparent in the context of the National Health and Morbidity Survey (NHMS), where both national and state-level representativeness are crucial. Simple random sampling might not adequately represent all geographic areas, especially when population densities and distributions vary significantly across different states. This could lead to over representation of more populous areas while leaving less populous regions under-represented.

Furthermore, this sampling method might not effectively capture the diversity within minority groups, as their smaller numbers in the overall population reduce the likelihood of their selection in a simple random sample. To overcome these challenges, NHMS employs more intricate sampling designs like stratified sampling. By dividing the population into distinct strata based on states or regions, and further considering sub-groups within these strata, it ensures that both geographic areas and minority groups are appropriately represented. Although these complex sampling designs introduce potential biases in selection probabilities and are more challenging to implement, they are indispensable for achieving the depth of representativeness required for national health assessments and policy planning.

One of the significant advantages of complex sampling designs is their feasibility without a comprehensive population list, focusing instead on broader stratifications like specific localities, simplifying the sampling process.

8.1.1 Benefits of Complex Sampling Design

The National Health and Morbidity Survey (NHMS), conducted by the Institut Kesihatan Umum (IKU), benefits extensively from complex sampling designs, showcasing several advantages:

1. **Cost Efficiency**: By clustering samples within selected strata or areas, operational costs are notably reduced, obviating the need to cover extensive and potentially scattered geographical locations.
2. **Enhanced Representativeness**: Stratification techniques ensure the sample accurately reflects specific subgroups or geographic areas, improving the survey's overall representativeness and reliability.
3. **Data Analysis Advantages**: Complex sampling designs facilitate the adjustment of sampling weights, enabling the generation of accurate national or state-level estimates. Furthermore, they support comprehensive subgroup analyses, ensuring sufficient statistical power.

8.1.2 Challenges in Implementing Complex Sampling Design

Despite their benefits, complex sampling designs require meticulous planning and sophisticated analytical techniques. These designs necessitate accounting for factors like clustering and weighting, demanding specialised expertise for both the sample's design and subsequent data analysis.

8.1.3 Example: Sampling Probability of a Sabahan

Problem: Consider a hypothetical scenario within a diverse group of 100 people, composed of 60% Malay, 20% Chinese, 15% Indian, and an additional 5% from other ethnic backgrounds, including 1% Sabahan. How sure are we, than when we randomly select 10 people from the group, at least one of the 10 people will be a Sabahan?

Answer: To calculate the probability of selecting at least one Sabahan in a 10-person sample, one might initially consider the likelihood of not choosing a Sabahan and subtract this figure from 1. With 99 of the 100 individuals not being Sabahan, the probability of not selecting a Sabahan in a single attempt is 99/100. Over 10 independent selections, this probability becomes (99/100)^10. Consequently, the probability of selecting at least one Sabahan is 1 - (99/100)^10, equating to approximately 9.56%. This calculation suggests a close to 10% chance that the sample will include at least one Sabahan.

Or in other word, since minorities were in fact had lower percentage, when we sample our population, we might even did not get the minorities in our sample!.

8.2 Practical

In complex survey analysis using the `survey::` package in R, it's crucial to account for the design aspects of the survey beyond just the outcome variables and covariates. This includes specifying:

Table 8.1: Required Information for Complex Sampling Design

Required Information/Specification	Common NHMS Variable Name
Cluster IDs (PSU)	EB ID
Strata	State.Strata, State.wt
Sampling Weight	ADW, weight_final, weight

8.2.1 Setup Project

1. Setup your project
2. Copy the NHMS dataset into the working directory
3. Create Quarto document
    - update the YAML metadata to make the document self-contained

```
---
title: "Sesi 4 - NHMS"
format:
  html:
    embed-resources: true
---
```

8.2.2 Analysis

8.2.2.1 Setup

0. Understand the dataset context
    - In this practical, the example was shown using NHMS NCD 2019's cholesterol dataset.
    - Two outcome will be selected
        - Categorical Type: known hypercholesterolaemia status (column `known_chol`)
        - Numerical Type: capillary total cholesterol level (column `u303`)

1. Import Dataset
    - On the `Files` pane, click on the spps .sav file
    - Select `Import Dataset` ...
    - Copy the code into the r code chunk
    - add function `as_factor(_)` to convert labelled code

~~~
```{r}
#| output: false

library(tidyverse)
library(haven)

nhms19ds <- read_sav("nhms19ds.sav") %>%
  as_factor()

nhms19ds
```
~~~

Note

there are 40 columns in the dataset, hence the dataset is not shown here.

2. Briefly (or in detail, up to you), explore the dataset.
    - Identify the outcome variable
        - data type: numerical, character or factor?
        - any missing data
    - Identify the complex sampling related variable:
        - the cluster ids
        - the strata
        - the sampling weight

Tip

some packages and functions that offer a quick data exploration:
- skimr :: package: skim(_) function.
- summarytools :: package: dfSummary(_) function.

~~~
```{r}
#| eval: false

library(skimr)

nhms19ds %>%
  select(known_chol, u303) %>%
  skim()
```
~~~

Variable Name	Variable Label
state	[Final] State
strata_gp	[Final] Locality
A2101	[Final] Gender
A2104	Age (Numerical)
A2104_grp	[Final] Age Group - 16 groups
A2106_5grp	Ethnicity (5 groups)
A2107	Citizenship
A2108_3grp	[Final] Marital Status (3 groups)
A2109_4grp	[Final] Highest Education Level (5 groups)
A2221	If working, type of occupation
A2222_7grp	Employement status (7 groups)
A2222_5grp	[Final] Occupation (5 groups)
indvid	_no label_
hh_id	_no label_
state_st	PSU
ebid	EB ID - Cluster
wtfinal_ncd	Sampling Weight
c01	ever had total blood cholesterol level measured
c02	ever told have high cholesterol level
c03	when told to have high cholesterol
c03a	years since was told to have high cholesterol
c04a	on medication for past 2 week
c04b	advice for special low fat diet
c04c	advice to loose weight
c04d	advice to exercise
c05	treatment - herbal/TCM
c06	common place to receive treatment
u303	Total Cholesterol (mmol/L)
known_chol	_no label_
undiagnosed_chol	_no label_
total_chol	_no label_
bodyweight1	Body Weight (kg)
bodyweight2	Body Weight (kg)
bodyheight1	Body Height (cm)
bodyheight2	Body Height (cm)
wc2	Waist Circumference (cm)
wc1	Waist Circumference (cm)
weight	Body Weight (kg)
height	Body Height (cm)
wc	Waist Circumference (cm)

NHMS NCD 2019 - Cholesterol Module Dataset: Variables List

Table 8.2: Data summary

Name	Piped data
Number of rows	10472
Number of columns	2
Column type frequency:	
factor	2
Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
known_chol	6	1.00	FALSE	2	No: 8451, Yes: 2015, N/A: 0
u303	594	0.94	FALSE	87	5: 448, 5.1: 383, 4.8: 378, 4.3: 373

Warning

- there are missing values in the outcome variable `known_chol`. while is it not a must to remove sample with no outcome, as the analysis will automatic remove sample with no outcome using `na.rm = T` parameter, it is advisable to remove any sample that do not have the outcome.
- the outcome variable of capillary total cholesterol was in categorical type. we need to convert it to numerical type

Tip

later in complex sampling design analysis, the analysis accept the variable outcome (i.e. the `known_chol`) variable in either numeric or factor type. but binary type is preferable

3. In this practical we will make some data wrangling

   - remove missing outcome
   - transform factor type to numerical binary type

~~~
```{r}
nhms19ds <- nhms19ds %>%
  as_factor() %>%
  filter(!is.na(known_chol)) %>%
  mutate(known_cholN = as.numeric(known_chol)-2,
         u303 = as.numeric(as.character(u303)))
```
~~~

Note

The variable `known_col` have there levels, which can be check using `levels(_)` function: `levels(nhms19ds$known_chol)`. When converted to numeric using `as.numeric(_)` function, the `known_chol` value was either 1 (correspond to NA), 2 (correspond to No) and 3 (correspond to Yes), thus the value need to minus 2, so that `No` is correspond to value `0` and `Yes` is correspond with value 1.

the conversion can be check by looking at both the variable

~~~
```{r}
#| eval: false

nhms19ds %>%
  select(known_chol, known_cholN)
```
~~~

4. Specifying the Complex Sampling Design

   - Add options at the top of Quarto file
   - These option is to handle in which if there is single PSU within strata or domains

   ~~~
   ```{r}
   library(survey)

   options(survey.lonely.psu = 'adjust',
           survey.adjust.domain.lonely = TRUE)
   ```
   ~~~

   - Unweighted Design
     - cluster ids set as 1 (i.e., no clustering)
     - weight as 1 (i.e., same probability)

   ~~~
   ```{r}
   nhms_unwdsg <- svydesign(id = ~1,
                            weights = ~1,
                            data = nhms19ds)
   ```
   ~~~

- we can use function `summary(_)` to view our complex sample design

```
summary(nhms_unwdsg)
```

```
Independent Sampling design (with replacement)
svydesign(id = ~1, weights = ~1, data = nhms19ds)
Probabilities:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
      1       1       1       1       1       1 
Data variables:
 [1] "state"              "strata_gp"          "A2101"              "A2104"             
 [5] "A2104_grp"          "A2106_5grp"         "A2107"              "A2108_3grp"        
 [9] "A2109_4grp"         "A2221"              "A2222_7grp"         "A2222_5grp"        
[13] "indvid"             "hh_id"              "state_st"           "ebid"              
[17] "wtfinal_ncd"        "c01"                "c02"                "c03"               
[21] "c03a"               "c04a"               "c04b"               "c04c"              
[25] "c04d"               "c05"                "c06"                "u303"              
[29] "known_chol"         "undiagnosed_chol"   "total_chol"         "bodyweight1"       
[33] "bodyweight2"        "bodyheight1"        "bodyheight2"        "wc2"               
[37] "wc1"                "weight"             "height"             "wc"                
[41] "known_cholN"       
```

- in unweighted design, the probability for sample range from 1 to 1.
- Weighted Design
  - cluster `id` set as the PSU (commonly the variable `ebid`)
  - `strata` set as the stratification. since most NHMS applied two stage of stratification, the strata must include both 1st stage and 2nd stage (commonly the variable `state_st`)
  - `weights` set as the sampling weight
  - Note that parameter `nest = T` to ensure that the cluster is nested within the specified strata

~~~
```{r}
nhms_surdsg <- svydesign(id = ~ebid,
                         strata = ~state_st,
                         weights = ~wtfinal_ncd,
                         data = nhms19ds,
                         nest = T)
```
~~~

- we can use function `summary(_)` to view our complex sample design

~~~
```{r}
options(width = 70) # the output width limit

summary(nhms_surdsg)
```
~~~

```
Stratified 1 - level Cluster Sampling design (with replacement)
With (475) clusters.
svydesign(id = ~ebid, strata = ~state_st, weights = ~wtfinal_ncd,
    data = nhms19ds, nest = T)
Probabilities:
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
1.405e-05 3.608e-04 7.000e-04 2.850e-03 2.000e-03 1.200e-01
Stratum Sizes:
             1   2   3   4   5   6   7   8   9  10  11  12  13  14
obs        584 274 281 263 281 307 331 319 294 245 302 338 307 333
design.PSU  27  13  13  11  12  12  12  12  12  12  12  12  14  12
actual.PSU  27  13  13  11  12  12  12  12  12  12  12  12  14  12
            15  16  17  18  19  20  21  22  23  24  25  26  27  28 29
obs        317 265 258 294 898 224 301 341 405 429 388 358 504 420 99
design.PSU  16  11  12  12  53  11  11  13  20  19  16  14  25  19  4
actual.PSU  16  11  12  12  53  11  11  13  20  19  16  14  25  19  4
            30
obs        506
design.PSU  33
actual.PSU  33
Data variables:
 [1] "state"            "strata_gp"        "A2101"
 [4] "A2104"            "A2104_grp"        "A2106_5grp"
 [7] "A2107"            "A2108_3grp"       "A2109_4grp"
[10] "A2221"            "A2222_7grp"       "A2222_5grp"
[13] "indvid"           "hh_id"            "state_st"
[16] "ebid"             "wtfinal_ncd"      "c01"
[19] "c02"              "c03"              "c03a"
[22] "c04a"             "c04b"             "c04c"
[25] "c04d"             "c05"              "c06"
[28] "u303"             "known_chol"       "undiagnosed_chol"
[31] "total_chol"       "bodyweight1"      "bodyweight2"
[34] "bodyheight1"      "bodyheight2"      "wc2"
[37] "wc1"              "weight"           "height"
[40] "wc"               "known_cholN"
```

- in weighted design summary, several info were given
  - the sampling probabilities. in this dataset, each of the sample have probability from 0.00001 to 0.12
  - the number of strata, number of sample in each of the strata and number of PSU (EB) in each strata. in this dataset, there are total 30 strata (13 states + 3 federal territories, with each state have 2 locality urban and rural).

8.2.2.2 Count the unweighted sample

1. To count the number of sample, we will use function `svymean(_)` from `survey::`.
   - the outcome variable can be either factor type, or if it in numerical type, it must be binary 0-1 number.
   - to estimate the number of sample, we will use the unweighed design.
   - the `x =` parameter must be in formula form with ~ (tilde) symbol before the variable name, i.e. `~known_chol`.
2. this is if we want to use the original factor type.

~~~
```{r}
svytotal(x = ~known_chol,
         design = nhms_unwdsg,
         na.rm = T)
```
~~~

```
              total     SE
known_cholN/A     0  0.000
known_cholNo   8451 40.339
known_cholYes  2015 40.339
```

3. this is if we want to use the converted to binary 0-1 numerical type. noticed the output differences.

~~~
```{r}
svytotal(x = ~known_cholN,
         design = nhms_unwdsg,
         na.rm = T)
```
~~~

```
            total     SE
known_cholN  2015 40.339
```

Note

Note 1: noticed that parameter `na.rm =` were set as T (TRUE). this is so that any sample with missing at parameter `x =` (i.e. the `known_chol`) will be removed.

Note 2: From this point forward, I'll use `known_cholN` variable (the binary 0-1 numerical type) as the outcome. You are feel free to use the original factor type, and explore as you wish.

8.2.2.3 Estimating the estimated population

1. to estimate total number of population that have the outcome (i.e., `known_cholN`), same formula is used, with changes at the design used, i.e. the weighted design

~~~
```{r}
svytotal(x = ~known_cholN,
         design = nhms_surdsg,
         na.rm = T)
```
~~~

```
              total     SE
known_cholN 2868124 103013
```

8.2.2.4 Estimating Prevalence

0. Estimating the prevalence using the function of `svymean(_)` from `survey::` package.
    - if the outcome variable is factor type, both original factor type and converted numerical type can be used.
        - if original factor type is used, prevalence for both `No` and `Yes` will be estimated.
        - if the outcome have three or more levels, using original factor type is preferable.
        - when using the binary `0-1` numerical type (i.e., the `known_cholN`), `svymean(_)` will calculate prevalence by calculating how many `1` since `0` does not have value.
1. Using function `svymean(_)` to calculate

~~~
```{r}
svymean(x = ~known_cholN,
        design = nhms_surdsg,
        na.rm = T)
```
~~~

```
               mean     SE
known_cholN 0.13479 0.0051
```

8.2.2.5 Estimating Confidence Interval for Prevalence

1. To calculate the confidence interval for prevalence, function `svyciprop(_)` from package `survey::` will be used.

    - Generally, a generic function `confint(_)` can be used to calculate the confident interval for model parameter.
    - In R however, the function will treat proportion as mean of binary outcomes. While treating proportion as mean of binary outcomes is reasonable accepted to calculate the prevalence, however, when calculate the CI, it is preferable to treat apply logit transformation and transformed back to the original scale
    - the default method used in `svyciprop(_)` function is “logit”
    - however, to replicate result from SPSS and SUDAAN, the method parameter need to change to “xlogit”

~~~
```{r}
svyciprop(formula = ~known_cholN,
          design = nhms_surdsg,
          method = "xl") %>%
  attr(., "ci")
```
~~~

```
     2.5%     97.5%
0.1251425 0.1450549
```

> Note
>
> - function `attr(_)` is used to pull the attribute from the object (i.e., the output of the `svyciprop(_)` function), while the parameter `"ci"` in the `attr(_, "ci")` function is to pull the CI from the `svyciprop(_)`

8.2.2.6 Estimating the Unweighted Sample Proportion

Can you calculated the sample proportion using the same function?.

> Tip
>
> Hint:
>
> 1. Sample Proportion = Unweighted Proportion.
> 2. Unweighted design vs. Weighted design.

8.2.2.7 Estimating by Subpopulation

1. To estimates by subpopulation, we use `svyby(_)` function

2. Estimating the unweighted count by locality (urban vs rual)

  - Don't forget to use the unweighted design

~~~
```{r}
svyby(formula = ~known_cholN,
      by = ~strata_gp,
      design = nhms_unwdsg,
      FUN = svytotal,
      na.rm.all = T)
```
~~~

```
      strata_gp known_cholN       se
Urban     Urban        1198 32.57255
Rural     Rural         817 27.44622
```

3. Estimating the estimated population by locality (urban vs rual)

~~~
```{r}
svyby(formula = ~known_cholN,
      by = ~strata_gp,
      design = nhms_surdsg,
      FUN = svytotal,
      na.rm.all = T)
```
~~~

```
      strata_gp known_cholN       se
Urban     Urban   2282784.1 97025.32
Rural     Rural    585339.9 34607.55
```

4. Estimating the prevalence by locality (urban vs rual)

~~~
```{r}
svyby(formula = ~known_cholN,
      by = ~strata_gp,
      design = nhms_unwdsg,
      FUN = svymean,
      na.rm.all = T)
```
~~~

```
      strata_gp known_cholN          se
Urban     Urban   0.1878626 0.004891561
Rural     Rural   0.1998044 0.006253350
```

5. Estimating the prevalence CI by locality (urban vs rual).

   - unfortunately, `svyciprop(_)` can't be used with `svyby(_)` function.
   - to estimate the CI, we need to subset the sample, to only the sub-population.

Warning

This however, will affect the degree of freedom (df). thus, we need to specified the df in the subset analysis, using the df of the overall design. to achieve this, add parameter `df = degf(design)`, where the design is the overall design

~~~
```{r}
nhms_surdsg_urban <- subset(nhms_surdsg,
                            strata_gp == "Urban")

svyciprop(formula = ~known_cholN,
          design = nhms_surdsg_urban,
          method = "xl",
          df = degf(nhms_surdsg)) %>%
  attr(., "ci")
```
~~~

```
     2.5%     97.5%
0.1258899 0.1498218
```

alternatively, we can create custom function
(the custom function code is shown next page)

~~~
```{r}
svyciprop_by(x = ~known_cholN,
             by = ~strata_gp,
             design = nhms_surdsg,
             df = degf(nhms_surdsg),
             method = "xl")
```
~~~

```
  subset   ci.2.5.  ci.97.5.
1  Urban 0.1258899 0.1498218
2  Rural 0.1103945 0.1421803
```

the custom function code

~~~
```{r}
# create a svyby-like function specific for svyciprop
svyciprop_by <- function(x, by, design,
                         df = NULL, method = NULL) {
  # extract the levels in by
  by_var <- all.vars(by)[1]
  by_data <- model.frame(by, data = design$variables)
  by_levels <- sort(unique(by_data[[by_var]]))

  # run the svyciprop() functions on each levels in by
  calculate_ci <- function(stratum) {
    subset_design <-
      subset(design,
             design$variables[[by_var]] == stratum)
    # Use provided df or default to subset design df
    df_to_use <- if (is.null(df)) degf(subset_design) else df
    result <- svyciprop(x, design = subset_design,
                        method = method, df = df_to_use)
    return(attr(result, "ci"))
  }

  # tabulate the result
  ci_results <- lapply(by_levels, calculate_ci)
  results <- data.frame(subset = by_levels,
                        ci = do.call(rbind, ci_results))

  return(results)
}
```
~~~

ℹ Note

this custom function can be simplified, but i make it more general so it can be use to other too.

8.2.2.8 Total Sample and Estimated Population

Can you try calculate the total sample? Using the example from calculating the total number sample with the outcome.

The tutorial on estimated total population will be cover in Bonus II: Population Pyramid part

8.3 Bonus I: Regression (Linear Regression & Logistic Regression)

8.3.1 Logistic Regression

8.3.1.1 Simple Logistic Regression

~~~
```{r}
svyglm(known_chol ~ strata_gp,
       nhms_surdsg,
       family = quasibinomial) %>%
  summary()
```
~~~

```
Call:
svyglm(formula = known_chol ~ strata_gp, design = nhms_surdsg,
    family = quasibinomial)

Survey design:
svydesign(id = ~ebid, strata = ~state_st, weights = ~wtfinal_ncd,
    data = nhms19ds, nest = T)

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)    -1.83690    0.05134 -35.779   <2e-16 ***
strata_gpRural -0.10511    0.08976  -1.171    0.242
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 1.000096)

Number of Fisher Scoring iterations: 4
```

8.3.1.2 Multiple Logistic Regression

~~~
```{r}
svyglm(known_chol ~ strata_gp + A2101 + A2108_3grp,
       nhms_surdsg,
       family = quasibinomial) %>%
  summary()
```
~~~

```
Call:
svyglm(formula = known_chol ~ strata_gp + A2101 + A2108_3grp,
    design = nhms_surdsg, family = quasibinomial)

Survey design:
svydesign(id = ~ebid, strata = ~state_st, weights = ~wtfinal_ncd,
    data = nhms19ds, nest = T)

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                  -3.42541    0.17958 -19.075   <2e-16 ***
strata_gpRural               -0.13590    0.09510  -1.429    0.154
A2101Female                   0.01669    0.07898   0.211    0.833
A2108_3grpMarried             1.76977    0.18140   9.756   <2e-16 ***
A2108_3grpWidow(er)/Divercee  2.79062    0.19772  14.114   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 1.00007)

Number of Fisher Scoring iterations: 5
```

8.3.2 Linear Regression

8.3.2.1 Simple Linear Regression

~~~
```{r}
svyglm(u303 ~ strata_gp,
       nhms_surdsg,
       family = gaussian) %>%
  summary()
```
~~~

```
Call:
svyglm(formula = u303 ~ strata_gp, design = nhms_surdsg, family = gaussian)

Survey design:
svydesign(id = ~ebid, strata = ~state_st, weights = ~wtfinal_ncd,
    data = nhms19ds, nest = T)

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     4.77993    0.02913 164.080   <2e-16 ***
strata_gpRural -0.04295    0.04288  -1.002    0.317
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 1.329693)

Number of Fisher Scoring iterations: 2
```

8.3.2.2 Multiple Linear Regression

~~~
```{r}
options(width = 70) # the output width limit

svyglm(u303 ~ strata_gp+ A2101 + A2108_3grp,
       nhms_surdsg,
       family = gaussian) %>%
  summary()
```
~~~

```
Call:
svyglm(formula = u303 ~ strata_gp + A2101 + A2108_3grp, design = nhms_surdsg,
    family = gaussian)

Survey design:
svydesign(id = ~ebid, strata = ~state_st, weights = ~wtfinal_ncd,
    data = nhms19ds, nest = T)

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                   4.30828    0.04180 103.070  < 2e-16 ***
strata_gpRural               -0.03732    0.04205  -0.887    0.375
A2101Female                   0.40032    0.03174  12.612  < 2e-16 ***
A2108_3grpMarried             0.39027    0.03945   9.893  < 2e-16 ***
A2108_3grpWidow(er)/Divercee  0.38802    0.06279   6.180 1.46e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 1.251478)

Number of Fisher Scoring iterations: 2
```

8.4 Bonus II: Mapping the Prevalence

We can map our prevalence.

1. save the prevalence by state into object to be used later

~~~
```{r}
kcprev_state <- svyby(formula = ~known_cholN,
                      by = ~state,
                      design = nhms_surdsg,
                      FUN = svymean,
                      na.rm.all = T) %>%
  as_tibble()

kcprev_state
```
~~~

```
# A tibble: 16 x 3
   state        known_cholN      se
   <fct>              <dbl>   <dbl>
 1 Johor             0.106  0.0112
 2 Kedah             0.168  0.0214
 3 Kelantan          0.106  0.00732
 4 Melaka            0.154  0.0189
 5 N. Sembilan       0.188  0.0293
 6 Pahang            0.112  0.0138
 7 P. Pinang         0.185  0.0270
 8 Perak             0.202  0.0248
 9 Perlis            0.177  0.0190
10 Selangor          0.120  0.0137
11 Terengganu        0.130  0.0138
12 Sabah             0.0836 0.0116
13 Sarawak           0.154  0.0156
14 WP Kl             0.154  0.0177
15 WP Labuan         0.149  0.0154
16 WP Putrajaya      0.146  0.0188
```

2. download the state map (geojson file) from DOSM github page

~~~
```{r}
#| eval: false

download.file(
  url = "https://raw.githubusercontent.com/dosm-malaysia/data-open/main/datasets/geodata/administrat
  destfile = "administrative_1_state.geojson",
  mode = "wb")
```
~~~

❗ Important

dosm github link to download the map dataset: https://raw.githubusercontent.com/dosm-malaysia/data-open/main/datasets/geodata/administrative_1_state.geojson

3. in R, map files like geojson and shp file is manipulated using `sf::` package
   - load sf package, if not available, please install first.

~~~
```{r}
library(sf)
```
~~~

4. convert the geojson file and save in r object.
   - in the same time, we can do some data wrangling, to ensure the name of state in dosm dataaset and our dataset is consistent.

~~~
```{r}
my_state_sf <- read_sf("administrative_1_state.geojson") %>%
  arrange(code_state) %>%
  mutate(state = fct_recode(state,
                          "P. Pinang" = "Pulau Pinang",
                          "N. Sembilan" = "Negeri Sembilan",
                          "WP Kl" = "W.P. Kuala Lumpur",
                          "WP Putrajaya" = "W.P. Putrajaya",
                          "WP Labuan" = "W.P. Labuan"))
```
~~~

5. Join both prevalence by state result and dosm state map.
   - the combined dataset need to convert to sf object

~~~
```{r}
#| eval: false

kcprev_state_mapds <- left_join(kcprev_state, my_state_sf) %>%
  st_as_sf()

kcprev_state_mapds
```
~~~

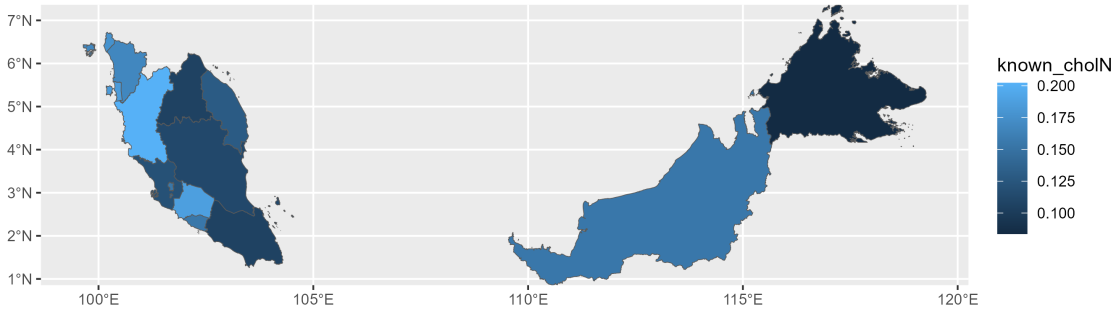
ℹ Note

any sf item must have geometry column, which contain the information of the location

```
Simple feature collection with 16 features and 4 fields
Geometry type: MULTIPOLYGON
Dimension:     XY
Bounding box:  xmin: 99.6409 ymin: 0.85539 xmax: 119.269 ymax: 7.36098
Geodetic CRS:  WGS 84
# A tibble: 16 x 5
   state      known_cholN      se code_state                  geometry
   <fct>            <dbl>   <dbl>      <int>        <MULTIPOLYGON [°]>
 1 Johor           0.106  0.0112           1 (((103.416 1.31868, 103.~
 2 Kedah           0.168  0.0214           2 (((100.7375 5.30512, 100~
 3 Kelantan        0.106  0.00732          3 (((101.8147 4.75934, 101~
 4 Melaka          0.154  0.0189           4 (((102.3322 2.04767, 102~
 5 N. Sembil~      0.188  0.0293           5 (((102.6248 2.62871, 102~
 6 Pahang          0.112  0.0138           6 (((103.9788 2.70211, 103~
 7 P. Pinang       0.185  0.0270           7 (((100.5371 5.2666, 100.~
 8 Perak           0.202  0.0248           8 (((100.7609 4.0423, 100.~
 9 Perlis          0.177  0.0190           9 (((100.2104 6.72068, 100~
10 Selangor        0.120  0.0137          10 (((101.7533 2.81998, 101~
11 Terengganu      0.130  0.0138          11 (((103.4645 4.57023, 103~
12 Sabah           0.0836 0.0116          12 (((118.6798 4.07375, 118~
13 Sarawak         0.154  0.0156          13 (((110.7571 1.55217, 110~
14 WP Kl           0.154  0.0177          14 (((101.6672 3.24432, 101~
15 WP Labuan       0.149  0.0154          15 (((115.1419 5.18637, 115~
16 WP Putraj~      0.146  0.0188          16 (((101.6985 2.97171, 101~
```

6. we can then plot the prevalence using ggplot

~~~
```{r}
#| eval: false

CholPrevMalMap <- kcprev_state_mapds %>%
  ggplot(aes(fill = known_cholN))
```
~~~



8.5 Bonus III: Population Pyramid:

Despite weight adjustment which include post-stratification, the total estimated population may differ from the original population. Here, plotting population pyramid can help to compare NHMS estimated population and DOSM 2019 Population

1. Download the DOSM Population 2019 from DOSM opendata

~~~
```{r}
#| eval: false

download.file(
  url = "https://storage.dosm.gov.my/population/population_malaysia.parquet",
  destfile = "population_malaysia.parquet",
  mode = "wb")
```
~~~

Important

dosm open website to download the dataset:
https://open.dosm.gov.my/data-catalogue/population_malaysia

2. Import downloaded dataset and wrangle it
   - to exclude data not required
   - to make data “compatible” with our NHMS dataset

the data wrangling code is in the next page

~~~
```{r}
dosmpop19
```
~~~

```
# A tibble: 32 x 4
   gender age_grp type  population
   <fct>  <fct>   <chr>      <dbl>
 1 Male   0-4     dosm     1331100
 2 Male   5-9     dosm     1317700
 3 Male   10-14   dosm     1299400
 4 Male   15-19   dosm     1480100
 5 Male   20-24   dosm     1675900
 6 Male   25-29   dosm     1746200
 7 Male   30-34   dosm     1502400
 8 Male   35-39   dosm     1304000
 9 Male   40-44   dosm     1022300
10 Male   45-49   dosm      895900
# i 22 more rows
```

~~~
```{r}
library(arrow)
dosmpop19 <- read_parquet("population_malaysia.parquet") %>%
  filter(date == "2019-01-01",             # to get 2019 population only
         sex != "overall_sex",             # exclude overall
         ethnicity == "overall_ethnicity", # exclude overall
         age != "overall_age") %>%         # exclude overall
  rename("gender" = "sex") %>%
  mutate(type = "dosm",
         gender = fct_recode(gender,
                             "Male" = "male",
                             "Female" = "female"),
         gender = fct_relevel(gender, "Male"),
         age_grp = case_when(age %in% c("75-79",
                                        "80-84",
                                        "85+") ~ "75+",
                             .default = age),
         age_grp = fct_relevel(age_grp,
                               "0-4", "5-9", "10-14",
                               "15-19", "20-24", "25-29",
                               "30-34", "35-39", "40-44",
                               "45-49", "50-54", "55-59",
                               "60-64", "65-69", "70-74",
                               "75+"),
         population = population * 1000) %>%
  select(-c(date, state, ethnicity, age)) %>% # not required
  group_by(gender, age_grp, type) %>%
  summarise(population = sum(population, na.rm = T)) %>%
  ungroup()
```
~~~

2. Calculate Total NHMS Estimated Population

   - this require a bit of a work, since we want to calculate all sample
   - one way of doing it, is by create a new column, with value of 1
   - this new column need to be done in the original dataset, thus a new survey design need to be constructed
   - then we can count the unweighted count and the estimated population, by age group and gender, using `svyby(_)` function
   - save the estimated population to an R object to used later

~~~
```{r}
nhms19ds_all <- nhms19ds %>%
  mutate(cholall = 1)
```
~~~

~~~
```{r}
nhms_surdsg_all <- svydesign(id = ~ebid,
                             strata = ~state_st,
                             weights = ~wtfinal_ncd,
                             data = nhms19ds_all,
                             nest = TRUE)

nhmspop19 <- svyby(formula = ~cholall,
                   by = ~A2104_grp+A2101,
                   design = nhms_surdsg_all,
                   FUN = svytotal) %>%
  as_tibble() %>%
  rename("gender" = "A2101",
         "age_grp" = "A2104_grp",
         "population" = "cholall") %>%
  mutate(type = "nhms",
         age_grp = fct_recode(age_grp,
                              "75+" = "75  & above")) %>%
  select(-se)

nhmspop19
```
~~~

```
# A tibble: 26 x 4
   age_grp gender population type 
   <fct>   <fct>       <dbl> <chr>
 1 15-19   Male      497478. nhms 
 2 20-24   Male     1496318. nhms 
 3 25-29   Male     1585427. nhms 
 4 30-34   Male     1412422. nhms 
 5 35-39   Male     1221228. nhms 
 6 40-44   Male      965349. nhms 
 7 45-49   Male      824204. nhms 
 8 50-54   Male      758598. nhms 
 9 55-59   Male      672648. nhms 
10 60-64   Male      549455. nhms 
# i 16 more rows
```

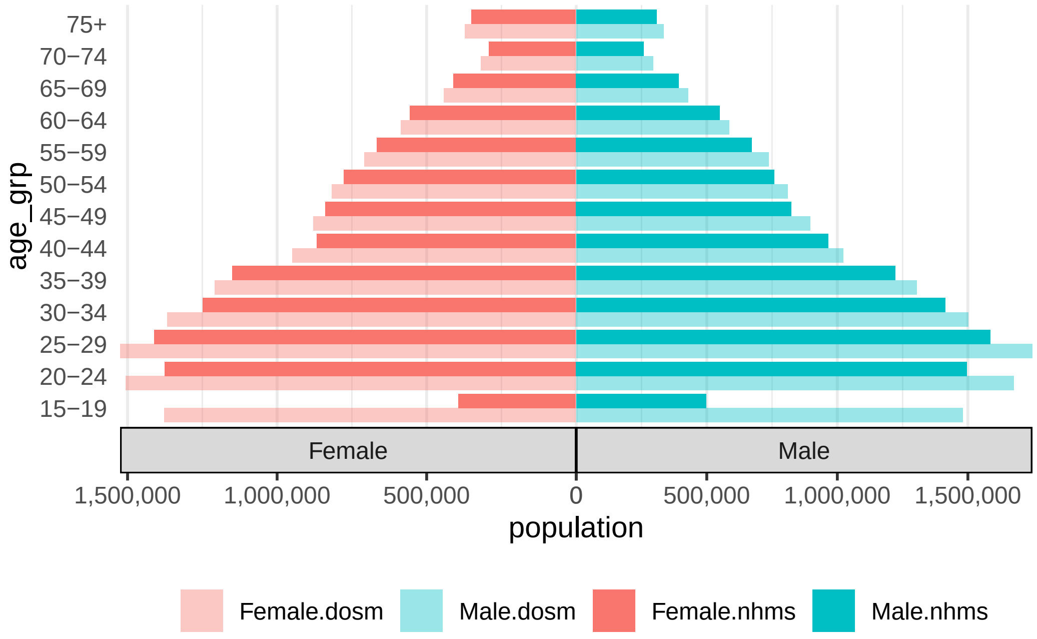
3. Join DOSM population and NHMS population
    - since we want female on left side, the female population need to be in negative form
    - the `female` also need to be in lower level
    - and save the join dataset to R object, to be used later

~~~
```{r}
join_pop19 <- full_join(dosmpop19, nhmspop19) %>%
  arrange(gender, age_grp) %>%
  filter(!age_grp %in% c("0-4", "5-9", "10-14")) %>%
  mutate(population = case_when(gender == "Male" ~ population,
                                gender == "Female" ~ 0 - population),
         gender = fct_relevel(gender, "Female"))

join_pop19
```
~~~

```
# A tibble: 52 x 4
   gender age_grp type  population
   <fct>  <fct>   <chr>      <dbl>
 1 Male   15-19   dosm    1480100
 2 Male   15-19   nhms     497478.
 3 Male   20-24   dosm    1675900
 4 Male   20-24   nhms    1496318.
 5 Male   25-29   dosm    1746200
 6 Male   25-29   nhms    1585427.
 7 Male   30-34   dosm    1502400
 8 Male   30-34   nhms    1412422.
 9 Male   35-39   dosm    1304000
10 Male   35-39   nhms    1221228.
# i 42 more rows
```

4. we can plot the pyramid plot

~~~
```{r}
join_pop19 %>%
  ggplot(aes(x = age_grp,
             y = population,
             fill = interaction(gender, type))) +
  geom_col(position = "dodge") +
  scale_y_continuous(expand = c(0, 0),
                     labels = function(x) scales::label_comma()(abs(x)),
                     breaks = scales::pretty_breaks()) +
  scale_fill_manual(values = hcl(h = c(15, 195, 15, 195),
                                 c = 100,
                                 l = 65,
                                 alpha = c(.4, .4, 1, 1)),
                    name = "") +
  coord_flip() +
  facet_wrap(. ~gender,
             scales = "free_x",
             strip.position = "bottom") +
  theme_bw() +
  theme(panel.border = element_blank(),
        axis.ticks.y = element_blank(),
        panel.grid.major.y = element_blank(),
        legend.position = "bottom",
        panel.spacing.x = unit(0, "pt"),
        strip.background = element_rect(colour = "black"))
```
~~~


age_grp
Female
Male
population
Female.dosm
Male.dosm
Female.nhms
Male.nhms