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Basic Biostatistics with R
– The Practical -

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What is R

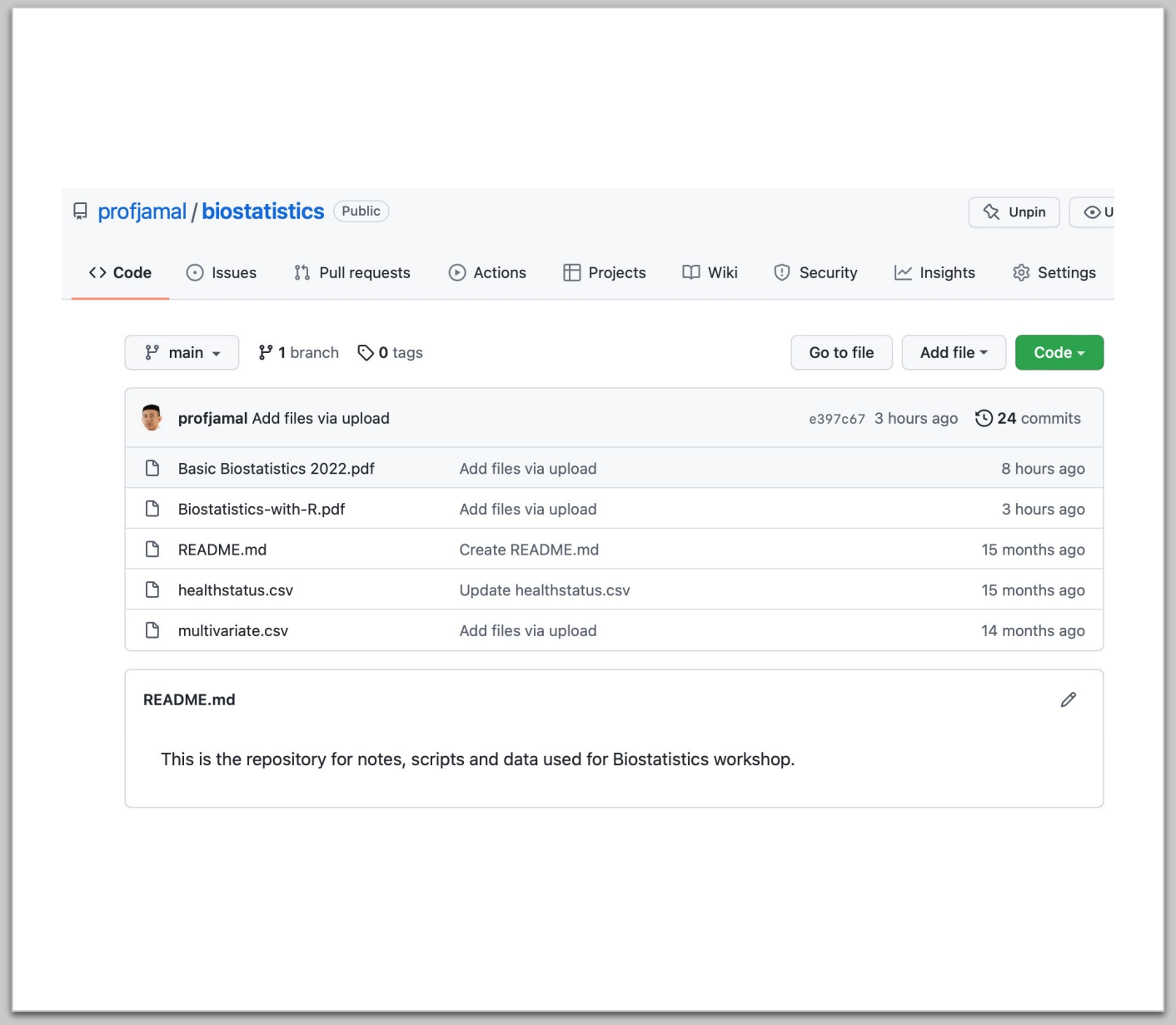
- Open-source programming language environment
- Used especially for **statistical** computing and **graphics**
- Free
- *Steep* learning curve
- Progressive

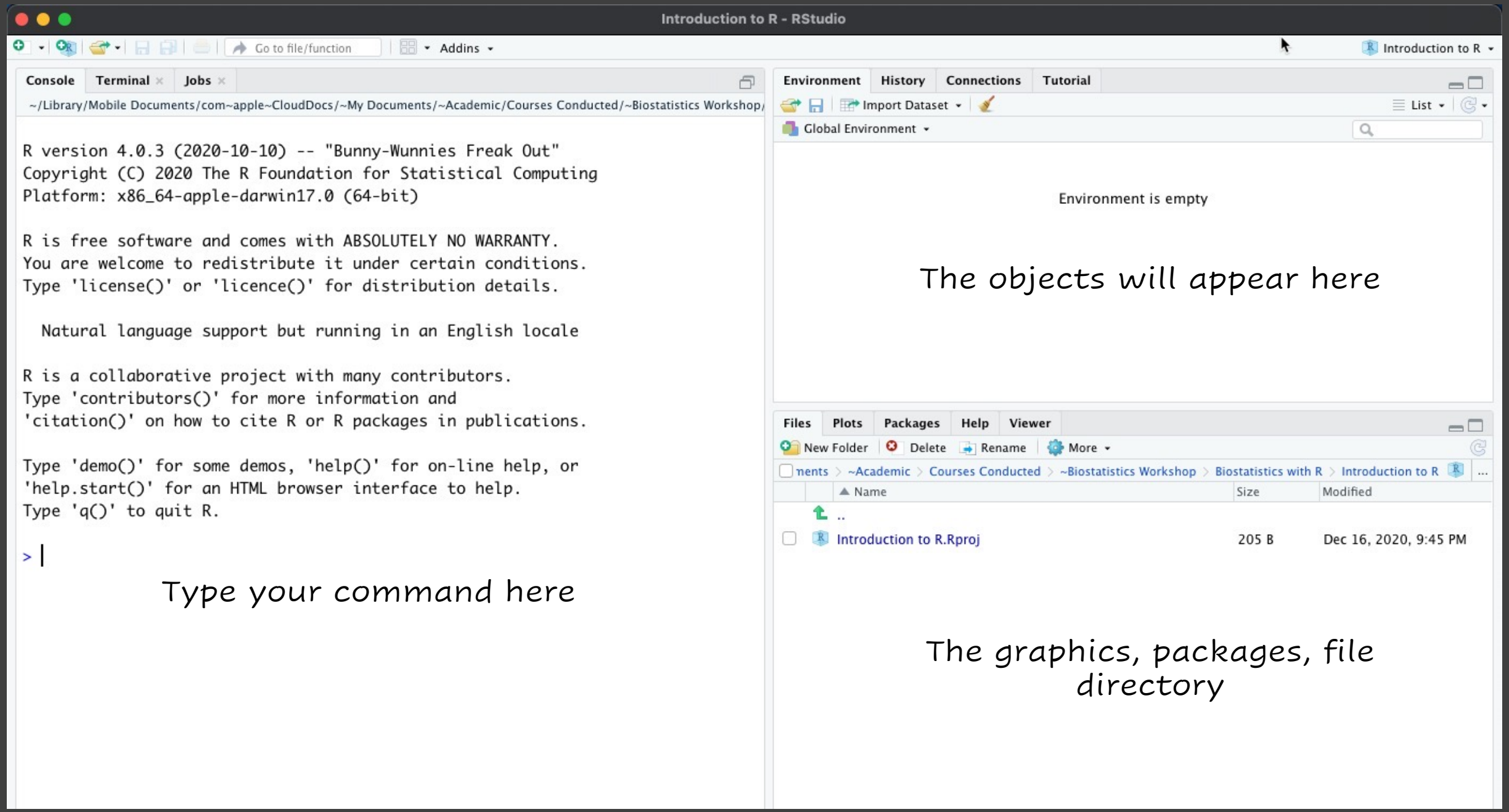
Install R & Rstudio

1. For R, download from https://cran.r-project.org
2. Then also download RStudio from https://rstudio.com

Repository for this workshop

- https://github.com/profjamal/biostatistics




Introduction to R - RStudio
Go to file/function
Addins
Introduction to R
Console
Terminal
Jobs
~/Library/Mobile Documents/com~apple~CloudDocs/~My Documents/~Academic/Courses Conducted/~Biostatistics Workshop/
R version 4.0.3 (2020-10-10) -- "Bunny-Wunnies Freak Out"
Copyright (C) 2020 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin17.0 (64-bit)
R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.
Natural language support but running in an English locale
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
>
Type your command here
Environment
History
Connections
Tutorial
Import Dataset
List
Global Environment
Environment is empty
The objects will appear here
Files
Plots
Packages
Help
Viewer
New Folder
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~Biostatistics Workshop
Biostatistics with R
Introduction to R
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Introduction to R.Rproj
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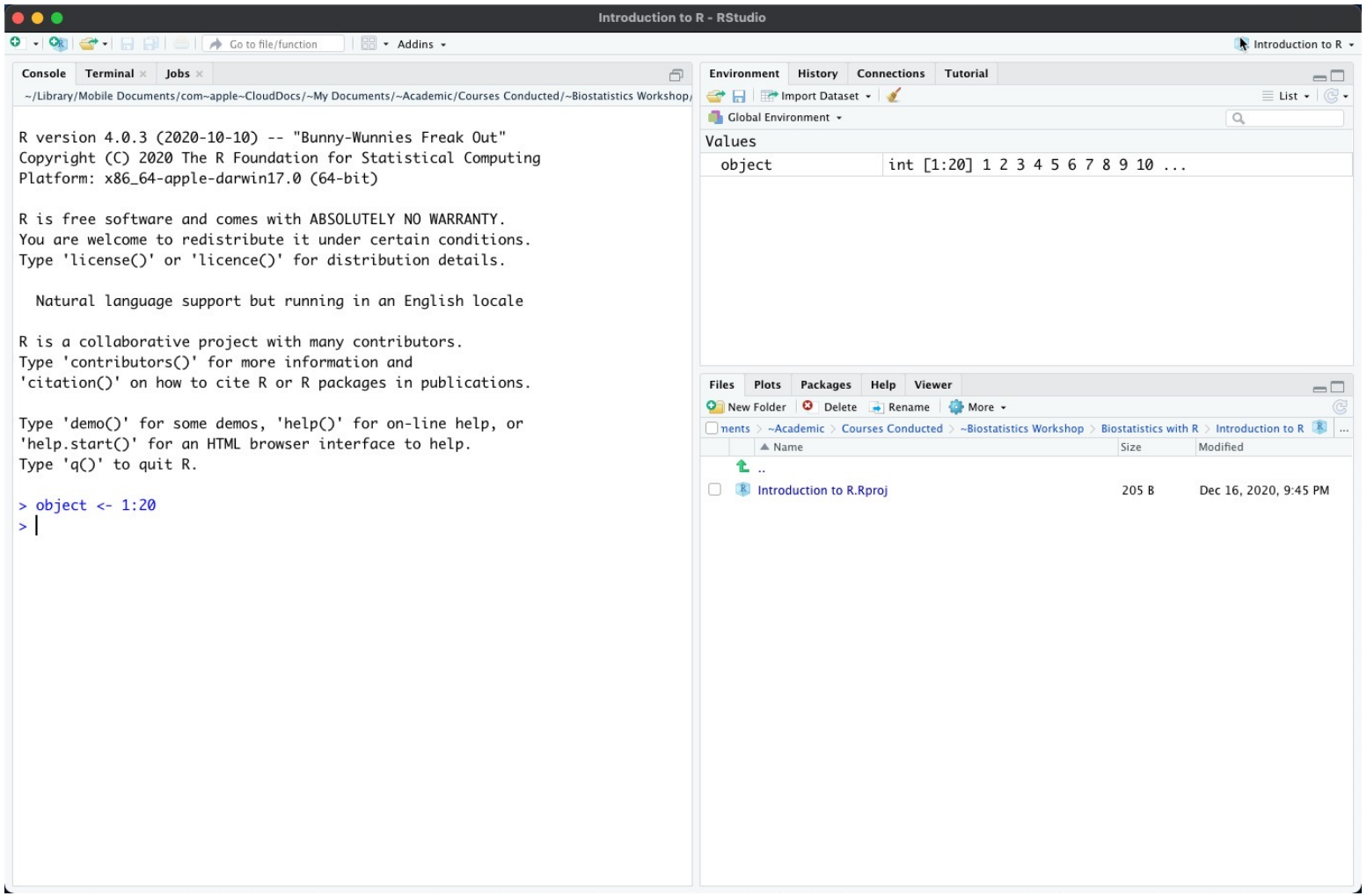
Dec 16, 2020, 9:45 PM
The graphics, packages, file directory



R command structure

Data types
(for each variable)

1. Character - similar like text in Excel
2. Numeric - any numbers including decimals
3. Integer - only accept whole number
4. Logical - TRUE, FALSE or NA
5. Complex - combination of data type
6. Date

Data structure (collection of variables)

1. Atomic vector
2. List
3. Matrix
4. Data frame
5. Factors

Starting R programming

- Google is your friend
- Set the working directory
- Packages can make or break you
- Practice, practice, practice

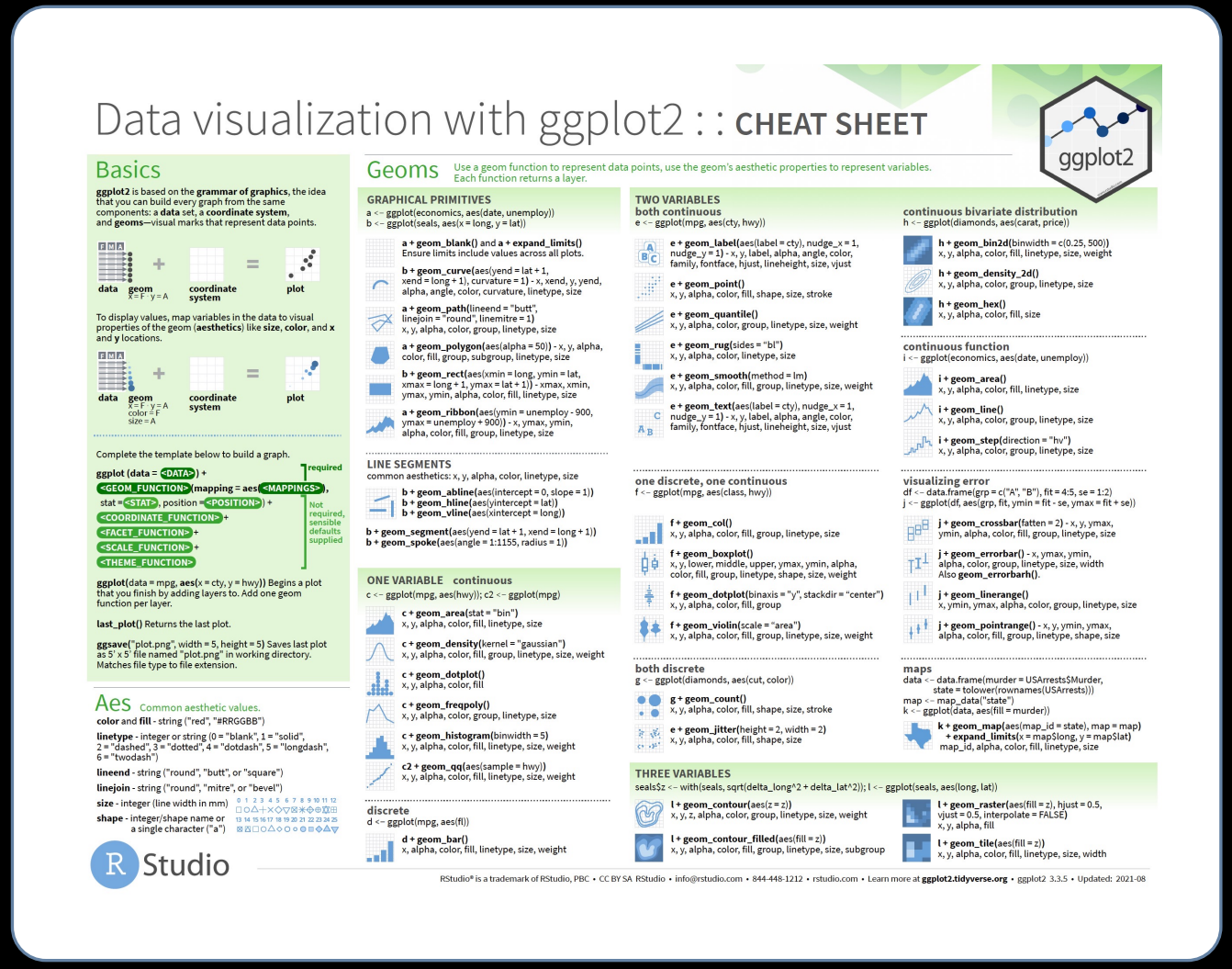
Recommended packages

- `tidyverse`, which contain
    1. `dplyr`
    2. `ggplot2`
    3. `readr`
    4. `forcats`
    5. `stringr`
    6. `purrr`
    7. `tidyr`
    8. `tibble`
- `ggpubr`
- `gtsummary`
- `psych`
- `car`

Constant need to search for guide

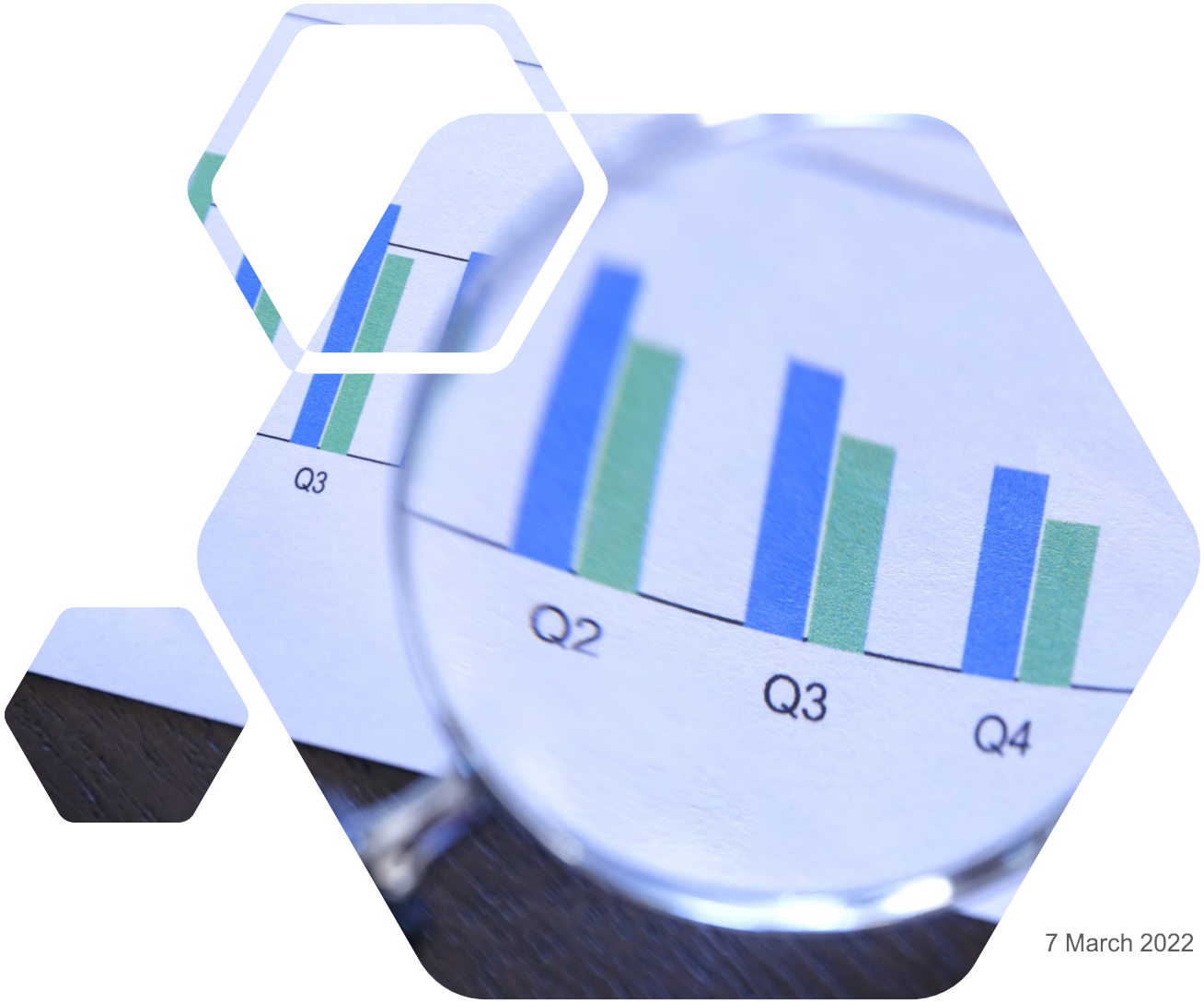
- Read the package documentation
- https://www.rdocumentation.org

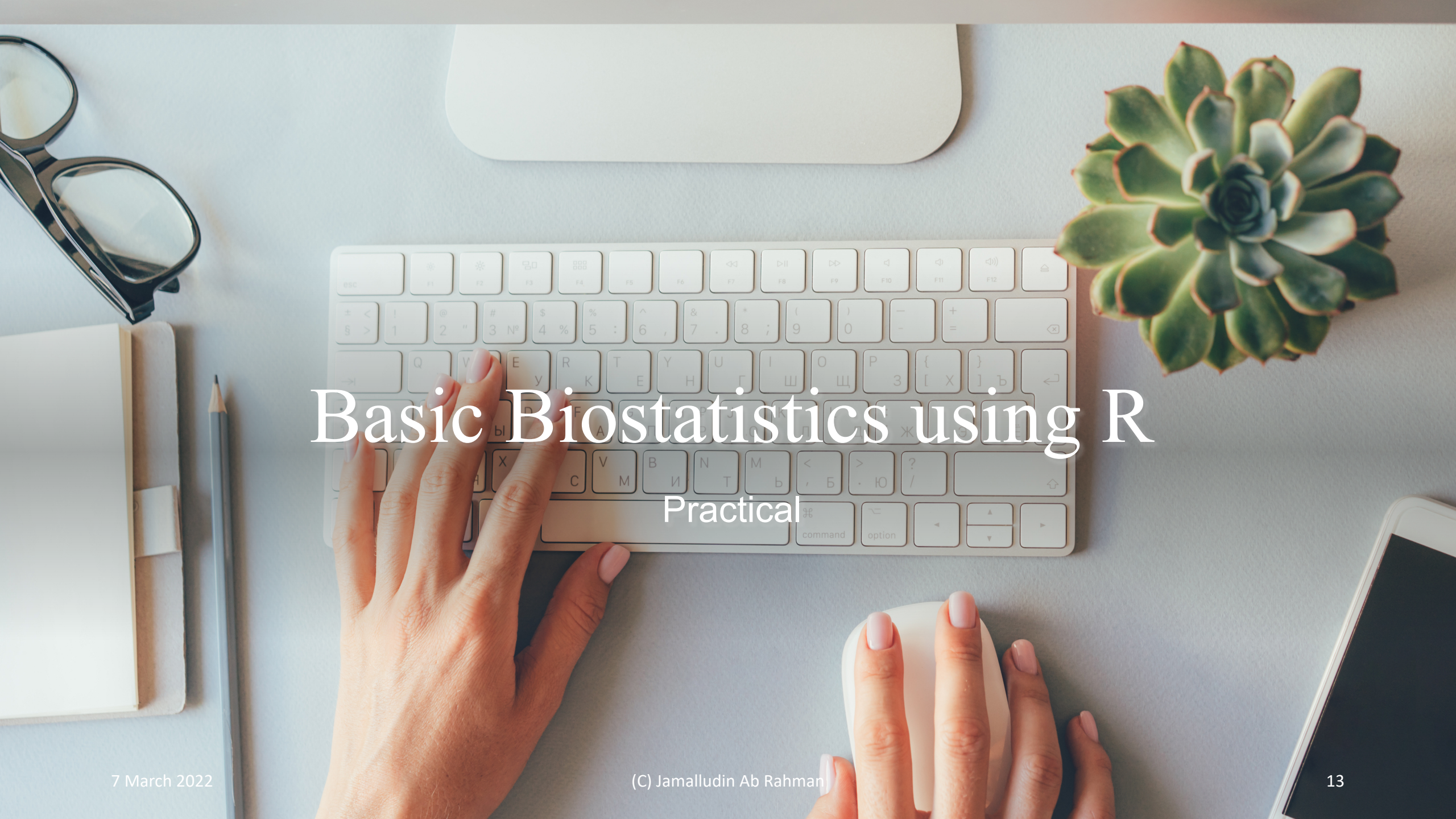
- Can download the cheat sheet
- https://www.rstudio.com/resources/cheatsheets/



Steps in statistics

1. Getting of data – import, or create
2. Examine the data – for errors, distribution
3. Analyse – descriptive & analytical
4. Interpret & conclude
5. Report





Basic Biostatistics using R

Practical

Content

1. Preparing the data – *create, read (import) and export data*
2. Checking the data
3. Descriptive statistics
4. Comparing proportions
5. Comparing two means
6. Comparing more than two means
7. Correlation analysis
8. Non-parametric tests
9. Comparing paired means

Before we begin

1. Download the practical script
2. Set your working directory
3. set.seed(1234) – for any random number generation

```
setwd(”Your Directory")
set.seed(1234)
```

Part 1

Create, export, import (read), format, check/screen data

Part 1.1 – Create data

- Practical to create a dummy set of data
- Create random values for ID, Age, Sex, SBP, DBP

```
set.seed(1234)
data <- cbind(1:120,
              rnorm(120,40,5),
              rbinom(120,1,.4),
              rnorm(120,130,10),
              rnorm(120,80,10)
              )
data <- as.data.frame(data)

colnames(data) <- c("ID", "Age", "Sex", "SBP", "DBP")
data$Sex <- factor(data$Sex, c(0,1), labels = c("Female", "Male") )

### Alternative method, and rounding numerics
set.seed(1234)
data2 <- data.frame(
  ID=1:120,
  Age=round(as.numeric(rnorm(120,40,5)),0),
  Sex=factor(rbinom(120,1,.4)),
  SBP=round(as.numeric(rnorm(120,130,10)), 0),
  DBP=round(as.numeric(rnorm(120,80,10)),0)
)

data2$Sex <- factor(data2$Sex, c(0,1), labels = c("Female", "Male") )
```

	ID	Age	Sex	SBP	DBP
1	1	33.96467	Female	102.67780	74.20043
2	2	41.38715	Female	129.00209	70.46721
3	3	45.42221	Female	139.76032	78.20571
4	4	28.27151	Male	134.13869	90.09808
5	5	42.14562	Male	139.12322	80.23627
6	6	42.53028	Female	149.83732	73.50972
7	7	37.12630	Male	141.69109	74.95626
8	8	37.26684	Female	124.91263	96.14391
9	9	37.17774	Male	137.04180	75.53040
10	10	35.54981	Male	128.01584	87.63177
11	11	37.61404	Female	124.61929	94.71719
12	12	35.00807	Female	101.44241	84.43665
13	13	36.11873	Female	122.10353	75.78278
14	14	40.32229	Female	134.87815	79.59998
15	15	44.79747	Female	151.68033	75.07720
16	16	39.44857	Female	135.00695	92.27717
17	17	37.44495	Female	136.20210	78.50446
18	18	35.44402	Female	120.34097	95.49983
19	19	35.81414	Female	131.62655	74.38387
20	20	52.07918	Female	109.21762	73.52883

	ID	Age	Sex	SBP	DBP
1	1	34	Female	103	74
2	2	41	Female	129	70
3	3	45	Female	140	78
4	4	28	Male	134	90
5	5	42	Male	139	80
6	6	43	Female	150	74
7	7	37	Male	142	75
8	8	37	Female	125	96
9	9	37	Male	137	76
10	10	36	Male	128	88
11	11	38	Female	125	95
12	12	35	Female	101	84
13	13	36	Female	122	76
14	14	40	Female	135	80
15	15	45	Female	152	75
16	16	39	Female	135	92
17	17	37	Female	136	79
18	18	35	Female	120	95
19	19	36	Female	132	74
20	20	52	Female	109	74

Part 1.2 – Export your data

- Use package `readr` or already available in `tidyverse`
- Export to your working directory unless specified otherwise

```
write_csv(data2, file = "data2.csv")
```

Part 1.3 – Import/Read external data

```
training <- read_csv("training.csv")
```

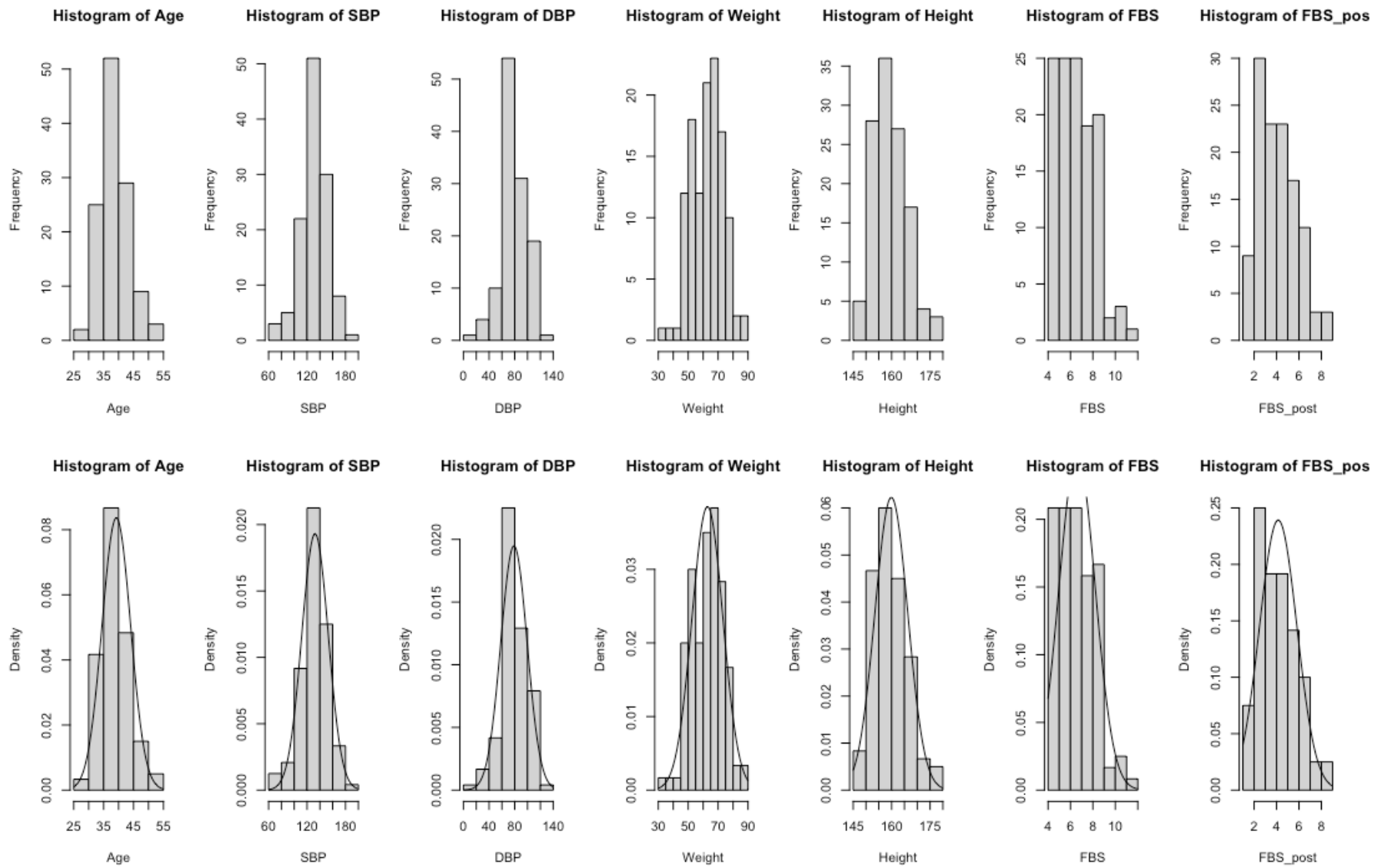
ID	Age	Sex	Smoking	SBP	DBP	Weight	Height	FBS	Intervention	FBS_post	Smoking2
1	34	Female	0	75	68	50.9	155	4.1	Diet & Exercise	2.3	No
2	41	Female	0	128	61	59.6	166	4.7	Diet & Exercise	2.3	No
3	45	Female	1	150	76	60.3	153	6.7	Diet	4.8	Yes
4	28	Male	0	138	100	67.2	168	4.7	Diet & Exercise	2.1	No
5	42	Male	1	148	80	52.4	166	6.2	Diet & Exercise	3.1	Yes
6	43	Female	0	170	67	59.9	149	8.1	Diet	6.3	No
7	37	Male	0	153	70	69.3	170	6.6	Diet & Exercise	3.8	No
8	37	Female	1	120	112	62.8	151	8.2	Diet & Exercise	5.4	Yes
9	37	Male	1	144	71	67.7	163	8.2	Diet & Exercise	5.2	Yes
10	36	Male	0	126	95	70.3	158	8.1	Diet & Exercise	5.1	No
11	38	Female	1	119	109	38.9	160	5.8	Diet & Exercise	2.9	Yes
12	35	Female	0	73	89	48.4	163	6.5	Diet & Exercise	3.8	No
13	36	Female	1	114	72	74.3	155	6.6	Diet	5.0	Yes
14	40	Female	1	140	79	61.4	151	8.1	Diet & Exercise	5.2	Yes
15	45	Female	0	173	70	67.4	158	9.0	Diet	7.1	No
16	39	Female	1	140	105	66.2	153	8.1	Diet	6.0	Yes
17	37	Female	0	142	77	73.7	148	8.3	Diet	6.3	No
18	35	Female	0	111	111	49.4	157	5.2	Diet & Exercise	2.0	No

Part 1.4 – Screen & prepare the data

```
# Assign proper data type for each variable
training$Sex <- factor(training$Sex)
training$Intervention <- factor(training$Intervention, levels = c(0,1), labels = c("Diet", "Diet & Exercise"))
training$Smoking2 <- factor(training$Smoking, levels = c(0,1), labels = c("No", "Yes"))

# Checking distribution for numerical variables
## Visually
par(mfrow= c(2,7))
hist(Age)
hist(SBP)
hist(DBP)
```

Only for 3 variables

```
# Showing Normal curve
hist(Age, probability = TRUE)
curve(dnorm(x, mean=mean(Age), sd=sd(Age)), add=TRUE)

hist(SBP, probability = TRUE)
curve(dnorm(x, mean=mean(SBP), sd=sd(SBP)), add=TRUE)

hist(DBP, probability = TRUE)
curve(dnorm(x, mean=mean(DBP), sd=sd(DBP)), add=TRUE)
```


Histogram of Age
Histogram of SBP
Histogram of DBP
Histogram of Weight
Histogram of Height
Histogram of FBS
Histogram of FBS_pos
Frequency
Age
SBP
DBP
Weight
Height
FBS
FBS_post
Histogram of Age
Histogram of SBP
Histogram of DBP
Histogram of Weight
Histogram of Height
Histogram of FBS
Histogram of FBS_pos
Density
Age
SBP
DBP
Weight
Height
FBS
FBS_post

Checking Normality

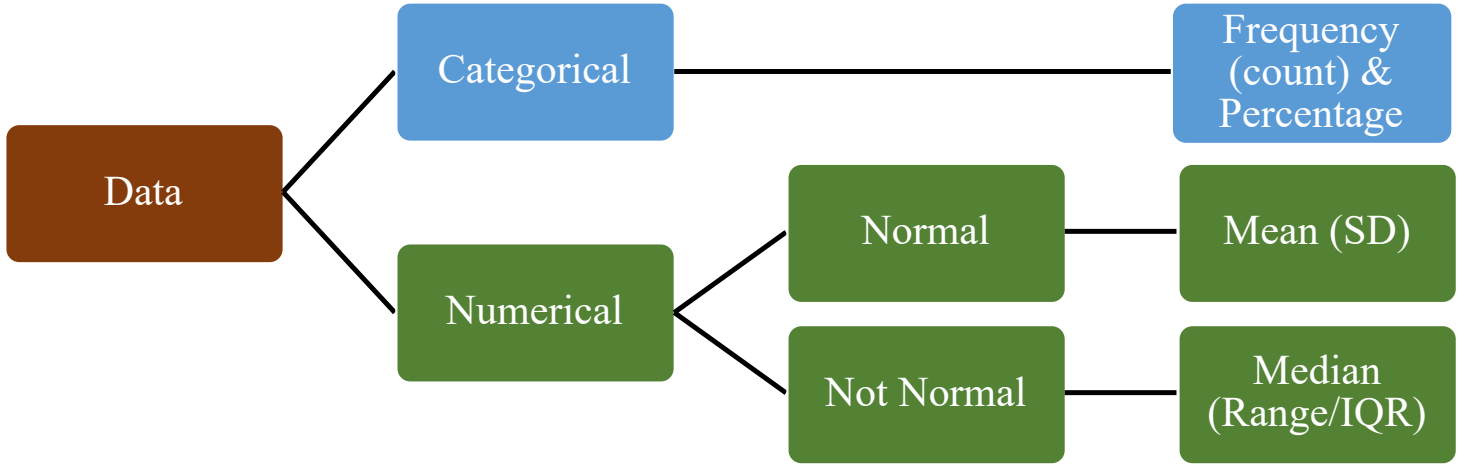
```
## Showing the moment values - determine
library(psych)
describe(Age)
describe(SBP)
describe(DBP)

# Normality test
shapiro.test(Age)
shapiro.test(SBP)
shapiro.test(DBP)
```

```
> ## Showing the moment values - determine
> library(psych)
> describe(Age)
   vars   n  mean   sd median trimmed  mad min max range skew kurtosis   se
X1    1 120 39.24 4.77     39    38.9 4.45  28  53    25 0.55      0.2 0.44
> describe(SBP)
   vars   n   mean    sd median trimmed   mad min max range  skew kurtosis   se
X1    1 120 132.45 20.67  135.5  132.96 17.05  65 188   123 -0.43     0.97 1.89
> describe(DBP)
   vars   n  mean    sd median trimmed   mad min max range  skew kurtosis   se
X1    1 120 78.81 20.48   78.5   79.23 18.53  12 125   113 -0.25     0.32 1.87
> # Normality test
> shapiro.test(Age)

        Shapiro-Wilk normality test

data:  Age
W = 0.97127, p-value = 0.01135

> shapiro.test(SBP)

        Shapiro-Wilk normality test

data:  SBP
W = 0.97457, p-value = 0.02247

> shapiro.test(DBP)

        Shapiro-Wilk normality test

data:  DBP
W = 0.98402, p-value = 0.1677
```

Part 2

Descriptive statistics

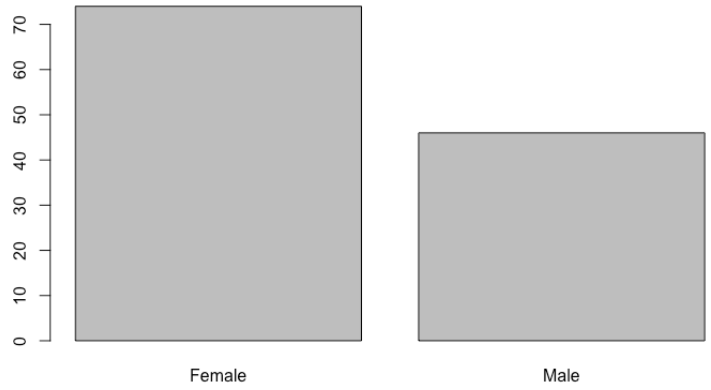
Descriptive statistics



Part 2.1 – Describe categorical variable

- `table(Sex)`
- `round(prop.table(table(Sex))*100, digit=1)`
- `plot(Sex) # Bar chart for the count`

```
> # Describe categorical variable (Sex)
> table(Sex)
Sex
Female   Male
    74     46
> round(prop.table(table(Sex))*100, digit=1)
Sex
Female   Male
  61.7   38.3
>
```



Using `gtsummary` for "Table 1"

```
# Using gtsummary to describe all variables
library(gtsummary)
library(tidyverse)

# The simplest format
training %>%
  tbl_summary()

# A better format
training %>%
  tbl_summary(
    statistic = list(all_continuous() ~ "{mean} ({sd})",
                     all_categorical() ~ "{n}/{N} ({p}%)"),
    digits = all_continuous() ~ 1
    )

# Even a better format
training %>%
  select(Age:Smoking2) %>%
  tbl_summary(
    statistic = list(c(Age, SBP, DBP, Weight, Height) ~ "{mean} ({sd})",
                     c(FBS, FBS_post) ~ "{median} ({p25}, {p75})",
                     all_categorical() ~ "{n}/{N} ({p}%)"),
    digit = all_continuous() ~ 1
    )
```

Characteristic	N = 120[1]
ID	60 (31, 90)
Age	39.0 (36.0, 42.0)
Sex	
Female	74 (62%)
Male	46 (38%)
Smoking	60 (50%)
SBP	136 (122, 144)
DBP	78 (67, 91)
Weight	64 (53, 70)
Height	160 (155, 164)
FBS	6.40 (5.27, 7.90)
Intervention	
Diet	58 (48%)
Diet & Exercise	62 (52%)
FBS_post	4.00 (2.80, 5.20)
Smoking2	60 (50%)

[1] Median (IQR); n (%)

Characteristic	N = 120[1]
ID	60.5 (34.8)
Age	39.2 (4.8)
Sex	
Female	74/120 (62%)
Male	46/120 (38%)
Smoking	60/120 (50%)
SBP	132.4 (20.7)
DBP	78.8 (20.5)
Weight	62.9 (10.4)
Height	159.9 (6.4)
FBS	6.6 (1.6)
Intervention	
Diet	58/120 (48%)
Diet & Exercise	62/120 (52%)
FBS_post	4.1 (1.7)
Smoking2	60/120 (50%)

[1] Mean (SD); n/N (%)

Characteristic	N = 120[1]
Age	39.2 (4.8)
Sex	
Female	74/120 (62%)
Male	46/120 (38%)
Smoking	60/120 (50%)
SBP	132.4 (20.7)
DBP	78.8 (20.5)
Weight	62.9 (10.4)
Height	159.9 (6.4)
FBS	6.4 (5.3, 7.9)
Intervention	
Diet	58/120 (48%)
Diet & Exercise	62/120 (52%)
FBS_post	4.0 (2.8, 5.2)
Smoking2	60/120 (50%)

[1] Mean (SD); n/N (%); Median (IQR)

Part 3

Analytical statistics – compare proportions

Cross-tabulate using Base

```
> # Cross-tabulate Sex with Smoking (Compare proportions
> table1 <- table(Smoking, Sex)
> table1
       Sex
Smoking Female Male
      0     41   19
      1     33   27
>
> margin.table(table1, 1) # Row (Smoking) total
Smoking
 0  1
60 60
> margin.table(table1, 2) # Column (Sex) total
Sex
Female   Male
    74     46
>
> # Results in %
> prop.table(table1, 1) # By Smoking status
       Sex
Smoking    Female      Male
      0 0.6833333 0.3166667
      1 0.5500000 0.4500000
> prop.table(table1, 2) # By Sex
       Sex
Smoking    Female      Male
      0 0.5540541 0.4130435
      1 0.4459459 0.5869565
>
```

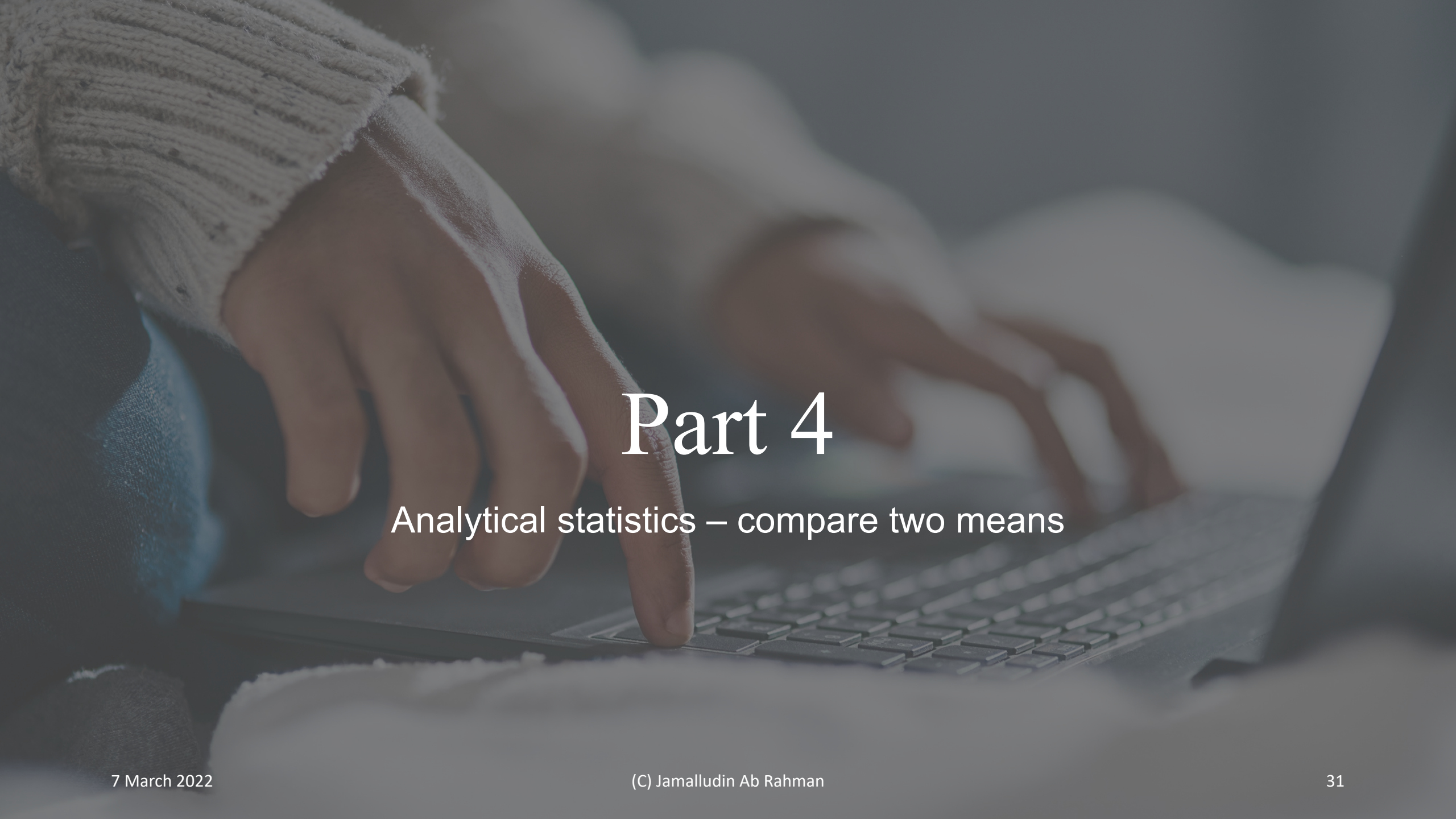
```
> # Results in % & rounded to 1 decimal point
> round(prop.table(table1, 1)*100, digit=1)
       Sex
Smoking Female Male
      0   68.3 31.7
      1   55.0 45.0
> round(prop.table(table1, 2)*100, digit=1)
       Sex
Smoking Female Male
      0   55.4 41.3
      1   44.6 58.7
>
> # Chi-square test
> chisq.test(table1, correct=FALSE) # Do continuity corr
 expected count < 5

        Pearson's Chi-squared test

data:  table1
X-squared = 2.2562, df = 1, p-value = 0.1331

>
> # To obtain the observed & expected count
> chisq.test(table1)$observed
       Sex
Smoking Female Male
      0     41   19
      1     33   27
> chisq.test(table1)$expected
       Sex
Smoking Female Male
      0     37   23
      1     37   23
>
```

Chi-square test using `gtsummary`

```
# Using gtsummary to compare proportions

training %>%

  select(Smoking2,Sex) %>%

  tbl_summary(by = Sex)%>%

  add_p(pvalue_fun = ~ style_pvalue(.x, digits = 3))
```

Characteristic	**Female**, N = 74[1]	**Male**, N = 46[1]	**p-value**[2]
Smoking2	33 (45%)	27 (59%)	0.133

[1] n (%)
[2] Pearson's Chi-squared test



Part 4

Analytical statistics – compare two means

Compare two means

```
# To check the variance assumption
var.test(FBS ~ Smoking2)

# By default, equal variance assumed
t.test(FBS ~ Smoking2)

# If equal variance can't be assumed
t.test(FBS ~ Smoking2, var.equal = FALSE)
```

```
> # Compare mean FBS by Smoking
>
> var.test(FBS ~ Smoking2) # To check the variance assumption, if P > 0.05 the equal variance can be
ssumed

        F test to compare two variances

data:  FBS by Smoking2
F = 1.4246, num df = 59, denom df = 59, p-value = 0.1771
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.8509299 2.3849163
sample estimates:
ratio of variances
          1.424569

> t.test(FBS ~ Smoking2) # By default, equal variance assumed

        Welch Two Sample t-test

data:  FBS by Smoking2
t = -0.48065, df = 114.49, p-value = 0.6317
alternative hypothesis: true difference in means between group No and group Yes is not equal to 0
95 percent confidence interval:
 -0.7255158  0.4421825
sample estimates:
 mean in group No mean in group Yes
         6.523333          6.665000

> t.test(FBS ~ Smoking2, var.equal = FALSE) # If equal variance can't be assumed

        Welch Two Sample t-test

data:  FBS by Smoking2
t = -0.48065, df = 114.49, p-value = 0.6317
alternative hypothesis: true difference in means between group No and group Yes is not equal to 0
95 percent confidence interval:
 -0.7255158  0.4421825
sample estimates:
 mean in group No mean in group Yes
         6.523333          6.665000
```

Compare means using gtsummary

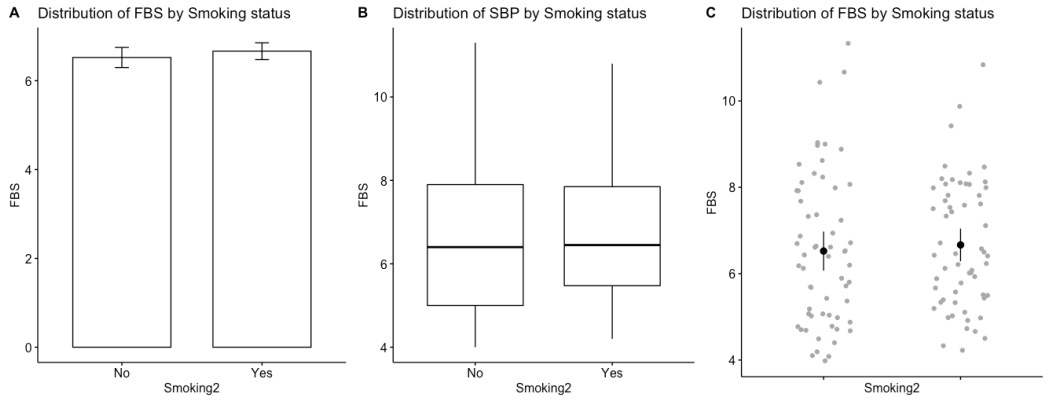
```
training %>%
  select(FBS, Smoking2) %>%
  tbl_summary(by = Smoking2,
              statistic = FBS ~ c("{mean} ({sd})")) %>%
  add_p(test.args = all_tests("t.test") ~ list(var.equal = TRUE),
        pvalue_fun = ~style_pvalue(.x, digits = 3)) %>%
  modify_spanning_header(all_stat_cols() ~ "**Smoking**")
```

	Smoking		
Characteristic	**No**, N = 60[1]	**Yes**, N = 60[1]	**p-value**[2]
FBS	6.52 (1.75)	6.66 (1.47)	0.467

[1] Mean (SD)
[2] Wilcoxon rank sum test

Visualising means by group

```
library(ggpubr)

A <- ggbarplot(data = training,
          x = "Smoking2",
          y = "FBS",
          main = "Distribution of FBS by Smoking status",
          add = "mean_se")
A

B <- ggboxplot(data = training,
          x = "Smoking2",
          y = "FBS",
          main = "Distribution of SBP by Smoking status")
B

C <- ggerrorplot(data = training, x="Smoking2", y="FBS",
            main = "Distribution of FBS by Smoking status",
            desc_stat = "mean_ci",
            add = "jitter",
            add.params = list(color = "darkgray"))
C

ggarrange(A, B, C + rremove("x.text"),
          labels = c("A", "B", "C"),
          ncol = 3, nrow = 1)
```



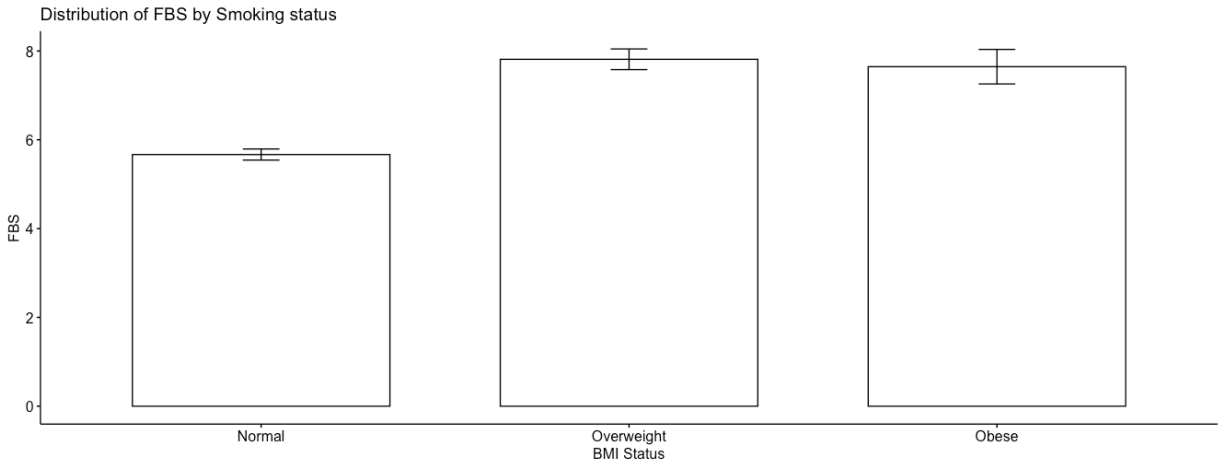
Part 5

Analytical statistics – compare more than two means

One-way ANOVA

```
> # Compare means FBS by BMI Status
> aov(training$FBS ~ training$BMI_Status)
Call:
   aov(formula = training$FBS ~ training$BMI_Status)

Terms:
                training$BMI_Status Residuals
Sum of Squares             130.6574  177.4685
Deg. of Freedom                   2       117

Residual standard error: 1.231594
Estimated effects may be unbalanced
> summary(aov(training$FBS ~ training$BMI_Status))
                     Df Sum Sq Mean Sq F value   Pr(>F)
training$BMI_Status   2  130.7   65.33   43.07 9.62e-15 ***
Residuals           117  177.5    1.52
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
# Visualising FBS by BMI Status
ggbarplot(data = training,
            x = "BMI_status",
            y = "FBS",
            main = "Distribution of FBS by Smoking status",
            add = "mean_se",
            xlab = "BMI Status")
```



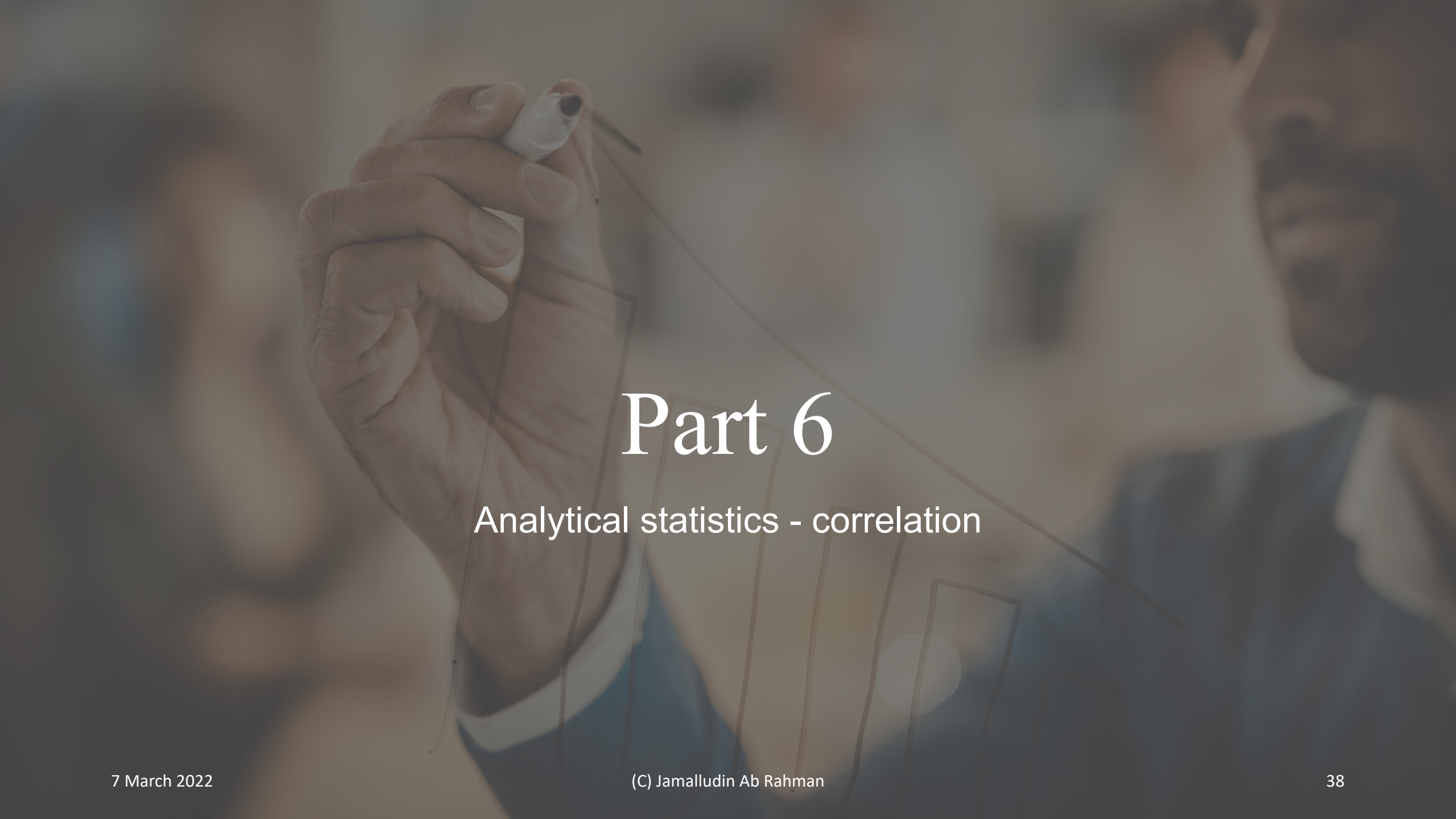
Post hoc test

```
> # Testing homogeneity assumption
> library(car)
>
> leveneTest(FBS ~ BMI_Status, training, center=mean)
Levene's Test for Homogeneity of Variance (center = mean)
       Df F value Pr(>F)
group   2  1.5498 0.2166
      117
>
> # Post-hoc test if equal variance
> pairwise.t.test(training$FBS, training$BMI_Status, p.adj = "bonf")

        Pairwise comparisons using t tests with pooled SD

data:  training$FBS and training$BMI_Status

           Normal  Overweight
Overweight 1.4e-13 -
Obese      3.8e-07 1

P value adjustment method: bonferroni
>
> # Post-hoc test if can't assume equal variance
> TukeyHSD(aov(training$FBS ~ training$BMI_Status))
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = training$FBS ~ training$BMI_Status)

$`training$BMI_Status`
                         diff       lwr       upr     p adj
Overweight-Normal  2.1459937  1.552252 2.7397356 0.0000000
Obese-Normal       1.9795025  1.144369 2.8146364 0.0000004
Obese-Overweight  -0.1664912 -1.058015 0.7250322 0.8974380
```

```
# Compare means using gtsummary
training %>%
  select(FBS, BMI_Status) %>%
  tbl_summary(by = BMI_Status,
              statistic = FBS ~ c("{mean} ({sd})"),
              digits = FBS ~ 1)%>%
  add_p(FBS ~ "aov",
        pvalue_fun = ~style_pvalue(.x, digits = 3)) %>%
  modify_spanning_header(all_stat_cols() ~ "**BMI Status**")
```

	BMI Status			
Characteristic	**Normal**, N = 67[1]	**Overweight**, N = 38[1]	**Obese**, N = 15[1]	**p-value**[2]
FBS	5.7 (1.0)	7.8 (1.4)	7.6 (1.5)	<0.001

[1] Mean (SD)
[2] One-way ANOVA



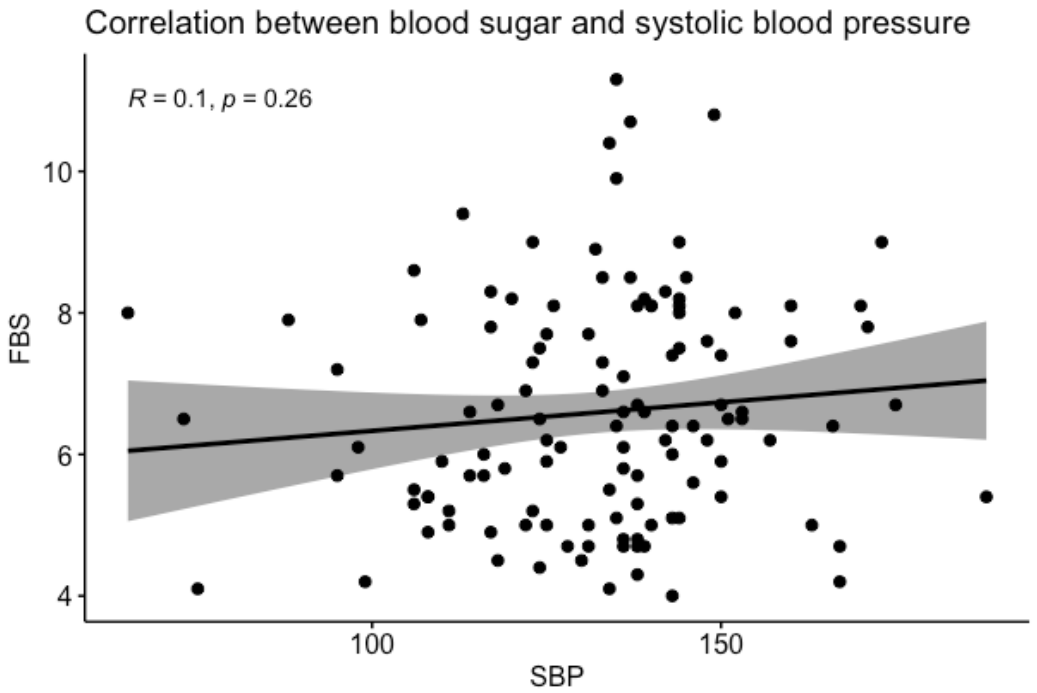
Part 6

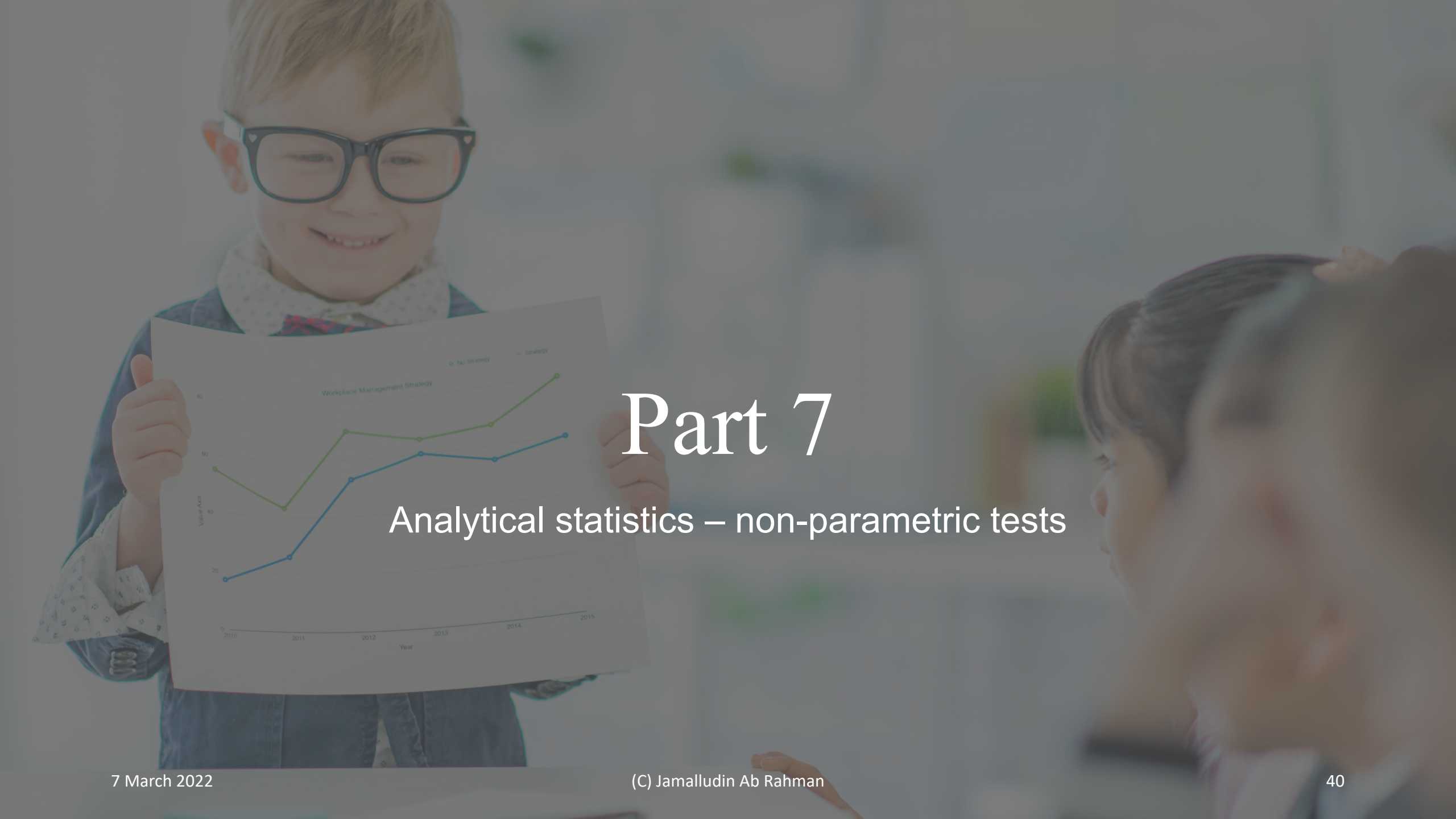
Analytical statistics - correlation

Correlation coefficient tests

```
> # Correlation test
> cor.test(training$FBS, training$SBP, method = "pearson") # If Normal

        Pearson's product-moment correlation

data:  training$FBS and training$SBP
t = 1.1321, df = 118, p-value = 0.2599
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.07701355  0.27773965
sample estimates:
      cor
0.1036587

> cor.test(training$FBS, training$SBP, method = "spearman", exact=FALSE) # If not Normal

        Spearman's rank correlation rho

data:  training$FBS and training$SBP
S = 248981, p-value = 0.1403
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.1354242
```

```
ggscatter(data = training,
          y = "FBS",
          x = "SBP",
          add = "reg.line", conf.int = TRUE, cor.coef = TRUE,
          main = "Correlation between blood sugar and systolic blood pressure")
```





Part 7

Analytical statistics – non-parametric tests

Wilcoxon Rank Sum Test

```
> # Compare two numericals
> # independent 2-group Mann-Whitney U Test
> wilcox.test(training$FBS ~ training$BP)

        Wilcoxon rank sum test with continuity correction

data:  training$FBS by training$BP
W = 2091.5, p-value = 0.07831
alternative hypothesis: true location shift is not equal to 0
```

```
training %>%
  select(FBS, BP) %>%
  tbl_summary(
    by = BP,
    statistic = FBS ~ "{median} ({p25}, {p75})"
  ) %>%
  add_p(all_continuous() ~ "wilcox.test") %>%
  modify_spanning_header(all_stat_cols() ~ "**Blood Pressure**")
```

	Blood Pressure		
Characteristic	**High**, N = 69[1]	**Normal**, N = 51[1]	**p-value**[2]
FBS	6.50 (5.40, 8.10)	6.10 (5.00, 7.15)	0.078

[1] Median (IQR)
[2] Wilcoxon rank sum test

Kruskall Wallis Test

```
> # Kruskal Wallis Test One Way Anova by Ranks
> kruskal.test(training$FBS ~ training$BMI_Status)

        Kruskal-Wallis rank sum test

data:  training$FBS by training$BMI_Status
Kruskal-Wallis chi-squared = 51.204, df = 2, p-value = 7.605e-12

>
> # Dunn Test, a post-hoc test for Kruskall Wallis
> library(FSA)
> dunnTest(FBS ~ BMI_status,
+          data = training,
+          method = "bonferroni")
Dunn (1964) Kruskal-Wallis multiple comparison
  p-values adjusted with the Bonferroni method.

           Comparison          Z      P.unadj        P.adj
1      Normal - Obese -4.4597645 8.204978e-06 2.461493e-05
2 Normal - Overweight -6.5550513 5.562277e-11 1.668683e-10
3  Obese - Overweight -0.1878895 8.509633e-01 1.000000e+00
>
```

```
training %>%
  select(FBS, BMI_status) %>%
  tbl_summary(
    by = BMI_status,
    statistic = FBS ~ "{median} ({p25}, {p75})"
  ) %>%
  add_p(all_continuous() ~ "kruskal.test") %>%
  modify_spanning_header(all_stat_cols() ~ "**BMI Status**")
```

	BMI Status			
Characteristic	**Normal**, N = 67[1]	**Overweight**, N = 38[1]	**Obese**, N = 15[1]	**p-value**[2]
FBS	5.50 (4.95, 6.30)	7.85 (6.98, 8.20)	8.00 (6.60, 8.50)	<0.001

[1] Median (IQR)
[2] Kruskal-Wallis rank sum test

Part 8

Paired samples

Paired t-test

```
> # Paired means - compare means FBS & FBS after as overall (within changes)
> t.test(training$FBS, training$FBS_post, paired = TRUE, alternative = "two.sided")

        Paired t-test

data:  training$FBS and training$FBS_post
t = 47.362, df = 119, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 2.342779 2.547221
sample estimates:
mean of the differences
                  2.445
```

```
# Table to show within and between changes
training %>%
  select(Intervention, FBS, FBS_post) %>%
    tbl_summary(
    by = Intervention,
    statistic = all_continuous() ~ "{mean} ({sd})",
    label = list(FBS ~ "Before",FBS_post ~ "After")) %>%
  add_n() %>%
  add_difference() %>%
  modify_header(label ~ "**FBS**") %>%
  modify_spanning_header(all_stat_cols() ~ "**Type of Intervention**")
```

		Type of Intervention				
FBS	**N**	**Diet**, N = 58[1]	**Diet & Exercise**, N = 62[1]	**Difference**[2]	**95% CI**[2,3]	**p-value**[2]
Before	120	6.76 (1.58)	6.44 (1.64)	0.32	-0.26, 0.90	0.3
After	120	4.81 (1.55)	3.53 (1.54)	1.3	0.73, 1.8	<0.001

[1] Mean (SD)
[2] Welch Two Sample t-test
[3] CI = Confidence Interval

Self Practice

Instruction

1. Please download the practice dataset from https://raw.githubusercontent.com/profjamal/biostatistics/main/healthstatus.csv - Use only variable age:hba1c
2. Fullfil the following objectives:
    1. Describe baseline characteristics (based on age, sex, exercise, smoking, BMI status and blood pressure status) of the study population. Summarise that in Table 1
    2. What are significant factors related to HbA1c? Summarise that in Table 2