Homework Chapter 4: MANOVA

Ho Huu Binh

2024-02-24

Table of contents

Loading Library **2**

Notes on MANOVA Model **2**

Exercise 4.10 **3**
Data Preprocessing . . . 3
Code . . . 4
Are there time effect differences on human skulls? . . . 4
Pairwise Comparison . . . 5
Checking Assumptions of MANOVA Model . . . 7

Exercise 4.9 **11**
Data Preprocessing . . . 11
Code . . . 12
Are there any differences among the 6 Treatments . . . 12

Exercise 4.8 **17**
Code . . . 17

Exercise 4.7 **19**
Code . . . 19

Exercise 4.6 **22**
Notes on Repeated Measures Design . . . 22
Code . . . 23

Exercise 4.2 **25**
Decompose the observations into mean, treatment, and residual components . . . 25
Construct the One-way MANOVA Table . . . 25

Hypothesis Testing on Method 25
Code 25

Exercise 4.3 **27**
Code 27

Appendix **29**
Paperwork on Problem 4.2 29

Loading Library

```
library(tidyverse)# data manipulation and visualization
library(dplyr)
library(forcats)
library(purrr)
library(ggpubr)# easy pipe-friendly statistical analyses
library(rstatix)# easy pipe-friendly statistical analyses
library(car) # MANOVA analyses
library(lsmeans) # Post-hoc tests
library(broom)# printing a nice summary of statistical tests as data frames
library(gridExtra) #plotting subplots
# suppressPackageStartupMessages(library(tidyverse)) # Suppress warnings from Tidyverse
```

Notes on MANOVA Model

The one-way MANOVA model is specified by

$$X_{lj} = \mu + \tau_l + e_{lj}, \quad j = 1, \ldots, n_l \text{ and } l = 1, \ldots, g.$$

where e_{lj} are independent multivariate Gaussian $\mathcal{N}_p(0, \Sigma)$ variables. The parameter vector μ is an overall mean level (mean effect) and τ_l represents the $l-$the time period effect with additional constraint $\sum_{l=1}^{g} n_l \tau_l = 0$.

The hypothesis of no time period effects is tested considering the relative size of the time effect and residual sums of squares and cross products.

$$H_0 : \tau_1 = \cdots = \tau_g = 0 \text{ vs } H_1 : \text{ at least one } \tau \neq 0$$

The summarization of the computations resulting in the test statistics is presented in a MANOVA table:

Source	Matrix of sum of squares	D.o.Fs
Treatment	$B = \sum_{l=1}^{g} n_l(\bar{x}_l - \bar{x})(\bar{x}_l - \bar{x})^T$	$g-1$
Residual	$W = \sum_{l=1}^{g}\sum_{j=1}^{n_l}(x_{lj} - \bar{x}_l)(x_{lj} - \bar{x}_l)^T$	$n_l - g$
Total	$B+W = \sum_{l=1}^{g}\sum_{j=1}^{n_l}(x_{lj} - \bar{x})(x_{lj} - \bar{x})^T$	$n_l - 1$

We reject the null hypothesis H_0 if the ratio of generalized variances

$$\Lambda^* = \frac{|W|}{|B+W|}$$

is critically small. The exact distribution of Λ^* can be derived for some special cases. Moreover, there is an asymptotic case that when $\sum_{l=1}^{g} n_l = n$ is large, Barlett proves that if H_0 is true then

$$-\left(n - 1 - \frac{p+g}{2}\right)\ln\Lambda^* = \left(n - 1 - \frac{p+g}{2}\right)\ln\left(\frac{|W|}{|B+W|}\right)$$

can be approximated by a Chi-square distribution with $p(g-1)$ degree of freedoms. Hence, with critical value $\alpha \in (0,1)$, we reject the null when

$$-\left(n - 1 - \frac{p+g}{2}\right)\ln\left(\frac{|W|}{|B+W|}\right) > \chi^2_{p(g-1)}(1-\alpha)$$

With $p = 4$, $g = 3$, we can derive the exact distribution of Λ^*, which is

$$\left(\frac{\sum_{l=1}^{g} n_l - p - 2}{p}\right)\left(\frac{1-\sqrt{\Lambda^*}}{\sqrt{\Lambda^*}}\right) \sim F_{2p,2(\sum_{l=1}^{g} n_l - p - 2)}$$

Exercise 4.10

Data Preprocessing

```
dat <- read.table('BT_4_10.dat', header = TRUE)

dat %>% rename(MB = X131, BH = X138, BL = X89, NH = X49, Period = X1) %>% mutate(Period =

n <- nrow(dat)
p <- ncol(dat) - 1 # Remove the Species group
```

The data includes four variable, denoted as X_1, X_2, X_3, X_4 respectively. The information of each variable is as follows:

- X_1: The width of the skull (mm)

- X_2: The height of the skull (mm)
- X_3: The basic length of the skull (mm)
- X_4: The basic height of the skull (mm)

Here we will represent some theoretical notes on the MANOVA one-way model and other questions will process in a similar manner

Code

Are there time effect differences on human skulls?

The value of Λ^* is 0.8180203.

```
mod1 <- manova(lm(cbind(MB,BH,BL,NH) ~ Period, data=dat))
mod2 <- Manova(lm(cbind(MB,BH,BL,NH) ~ Period, data=dat))

mod1_summary <- summary(mod1)
mod2_summary <- summary(mod2) # 0.8180203

B <- mod1_summary$SS$Period
W <- mod1_summary$SS$Residuals

# Wilk's Lambda
Lambda_mod1 <- det(W)/(det(B+W))
Lambda_mod2 <- 0.8180203

abs_diff <- abs(Lambda_mod1 - Lambda_mod2)
abs_diff
```

```
[1] 3.010851e-08
```

The test statistics is 2.192252

```
F_val <- ((n-p-2)/p) * ((1 -sqrt(Lambda_mod1))/sqrt(Lambda_mod1))
F_val
```

```
[1] 2.192252
```

and the critical value is 1.99456

```r
alpha <- 0.05
crit_val <- qf(1-alpha,df1=2*p,df2=2*(n-p-2))
crit_val
```

```
[1] 1.99456
```

Since the test statistics $2.19 > 1.99$, we reject the null hypothesis H_0 and conclude that the time effect differences are prevalent. This implies that there can be a difference of male Egyptian skulls for the three different time periods.

Pairwise Comparison

For pairwise comparisons, the Bonferroni approach can be used to construct simultaneous confidence intervals for the components of the differences $\tau_k - \tau_l$. For the MANOVA model, with confidence level at $100(1-\alpha)\%$, the interval will be

$$\tau_{ki} - \tau_{li} \in \bar{x}_{ki} - \bar{x}_{li} \pm t_{n-g}\left(\frac{\alpha}{pg(g-1)}\right)\sqrt{\frac{w_{ii}}{n-g}\left(\frac{1}{n_k}+\frac{1}{n_l}\right)}$$

Here is the computation of the confidence intervals given $\alpha = 0.05$

```r
# Define the number of groups and the significance level
g <- 3
alpha <- 0.05
p <- ncol(dat) - 1

# Compute group sizes, means, and covariance matrices
n1 <- length(which((dat$Period==1)))
n2 <- length(which((dat$Period==2)))
n3 <- length(which((dat$Period==3)))
n <- n1+n2+n3
xbar1 <- colMeans(dat[dat$Period==1,-5])
xbar2 <- colMeans(dat[dat$Period==2,-5])
xbar3 <- colMeans(dat[dat$Period==3,-5])
xbar <- (n1*xbar1+n2*xbar2+n3*xbar3)/(n1+n2+n3)

S1 <- cov(dat[dat$Period==1,-5])
S2 <- cov(dat[dat$Period==2,-5])
S3 <- cov(dat[dat$Period==3,-5])
W <- (n1-1)*S1+(n2-1)*S2+(n3-1)*S3
```

```r
# Compute the qt level
qtlevel <- qt(1-alpha/(p*g*(g-1)),df=n-g)

# Initialize an empty dataframe to store the results
results <- tibble(comparison = character(), LCI = numeric(), UCI = numeric())

# Compute the pairwise comparisons
for (i in 1:p) {
  LCI12 <- (xbar1[i]-xbar2[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  UCI12 <- (xbar1[i]-xbar2[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  results <- results %>% bind_rows(tibble(comparison = paste0("tau1[",i,"]-tau2[",i,"]"),

  LCI13 <- (xbar1[i]-xbar3[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n3))
  UCI13 <- (xbar1[i]-xbar3[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n3))
  results <- results %>% bind_rows(tibble(comparison = paste0("tau1[",i,"]-tau3[",i,"]"),

  LCI23 <- (xbar2[i]-xbar3[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n2+1/n3))
  UCI23 <- (xbar2[i]-xbar3[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n2+1/n3))
  results <- results %>% bind_rows(tibble(comparison = paste0("tau2[",i,"]-tau3[",i,"]"),
}

# Print the results
print(results)
```

```
# A tibble: 12 x 3
   comparison         LCI   UCI
   <chr>            <dbl> <dbl>
 1 tau1[1]-tau2[1] -4.48  2.51
 2 tau1[1]-tau3[1] -6.58  0.406
 3 tau2[1]-tau3[1] -5.56  1.36
 4 tau1[2]-tau2[2] -2.86  4.36
 5 tau1[2]-tau3[2] -3.96  3.26
 6 tau2[2]-tau3[2] -4.68  2.48
 7 tau1[3]-tau2[3] -3.29  4.19
 8 tau1[3]-tau3[3] -0.255 7.22
 9 tau2[3]-tau3[3] -0.674 6.74
10 tau1[4]-tau2[4] -2.04  2.75
11 tau1[4]-tau3[4] -2.37  2.41
12 tau2[4]-tau3[4] -2.71  2.04
```

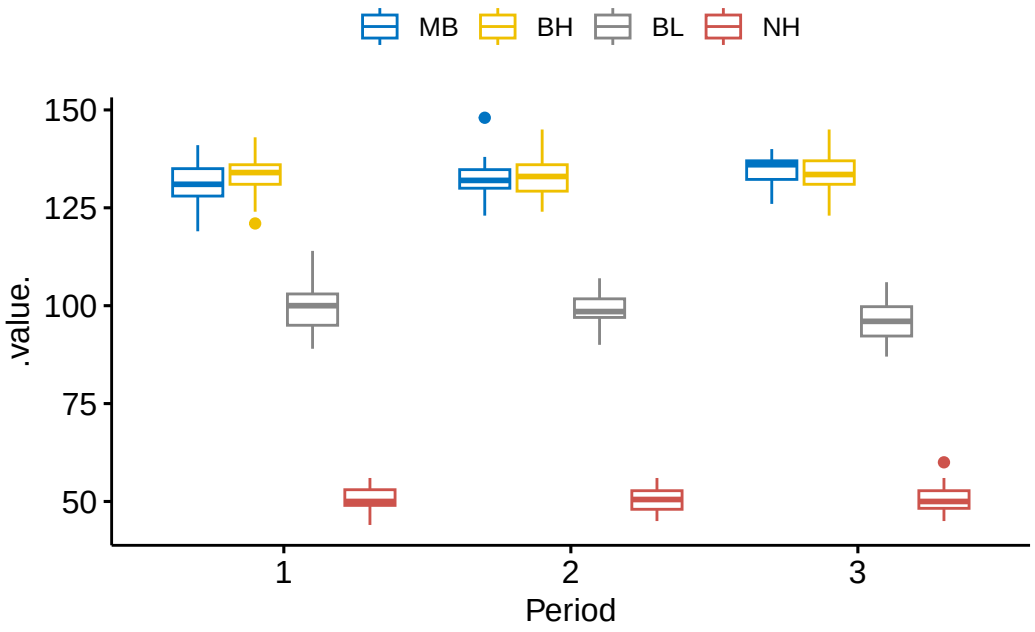
We see that all find all simultaneous confidence intervals cover zero, indicating that there is

no significant difference between three different time periods, which contradicts our conclusion earlier using MANOVA one-way model. Hence, we need to check the assumption of MANOVA model to see whether there are any violations.

Checking Assumptions of MANOVA Model

To get the taste of the data, we can visualize using boxplot.

```
features <- dat %>% select(where(is.numeric)) %>% colnames()
##Visualization
ggboxplot(
  dat, x = "Period", y = features,
  merge = TRUE, palette = "jco")
```



The figure shows an insignificant changes from period 1 to period 3; thereby we can expect the there are no differences at all.

The three assumptions of MANOVA models are:

1. The random samples from different populations are independent and samples from one population have same mean vectors.
2. Homogeneous variance populations (All populations have the same covariance matrix)

3. Multivariate normal population

The normality condition is the most important one since if it is not satisfied, the testing procedure would collapse immediately and leads to erroneous conclusion.

Equal Covariance

Since the Box test is prone to normality condition, we will use the Levene test. We reject the null (the samples to be compared come from a population with the same variance) if the p-value for the test is less than a threshold (usually 0.05). Since all four variables obtain large p-values, we fail to reject the null and conclude that the they may all have common variance.

```
box_m(dat[, features], dat$Period) # prone to errors if normality is not met
```

```
# A tibble: 1 x 4
  statistic p.value parameter method
      <dbl>   <dbl>     <dbl> <chr>
1      19.9   0.467        20 Box's M-test for Homogeneity of Covariance Matric~
```

```
dat %>%
  gather(key = "variable", value = "value", features) %>%
  group_by(variable) %>%
    levene_test(value ~ Period)
```

```
Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
i Please use `all_of()` or `any_of()` instead.
  # Was:
  data %>% select(features)

  # Now:
  data %>% select(all_of(features))

See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
```

```
# A tibble: 4 x 5
  variable   df1   df2 statistic     p
  <chr>    <int> <int>     <dbl> <dbl>
1 BH           2    86     0.283 0.754
2 BL           2    86     0.724 0.488
3 MB           2    86     1.47  0.236
4 NH           2    86     0.541 0.584
```

Multicollinearity

The correlation between each variable must be moderate (below an extreme threshold like 0.9). Looking at the table, we observe that there are no multicollinearities between variables; thereby, we are safe to process the test.

```
dat %>% cor_test(features)
```

```
# A tibble: 16 x 8
   var1  var2     cor statistic      p conf.low conf.high method
   <chr> <chr>  <dbl>     <dbl>  <dbl>    <dbl>     <dbl> <chr>
 1 MB    MB     1       Inf     0        1          1     Pearson
 2 MB    BH     0.1       0.977 0.331   -0.106      0.306 Pearson
 3 MB    BL    -0.023    -0.218 0.828   -0.230      0.186 Pearson
 4 MB    NH     0.23      2.20  0.0307   0.0221     0.418 Pearson
 5 BH    MB     0.1       0.977 0.331   -0.106      0.306 Pearson
 6 BH    BH     1       Inf     0        1          1     Pearson
 7 BH    BL     0.088     0.820 0.414   -0.123      0.291 Pearson
 8 BH    NH     0.15      1.37  0.173   -0.0646     0.343 Pearson
 9 BL    MB    -0.023    -0.218 0.828   -0.230      0.186 Pearson
10 BL    BH     0.088     0.820 0.414   -0.123      0.291 Pearson
11 BL    BL     1       Inf     0        1          1     Pearson
12 BL    NH    -0.019    -0.175 0.862   -0.226      0.190 Pearson
13 NH    MB     0.23      2.20  0.0307   0.0221     0.418 Pearson
14 NH    BH     0.15      1.37  0.173   -0.0646     0.343 Pearson
15 NH    BL    -0.019    -0.175 0.862   -0.226      0.190 Pearson
16 NH    NH     1       Inf     0        1          1     Pearson
```

Normaility

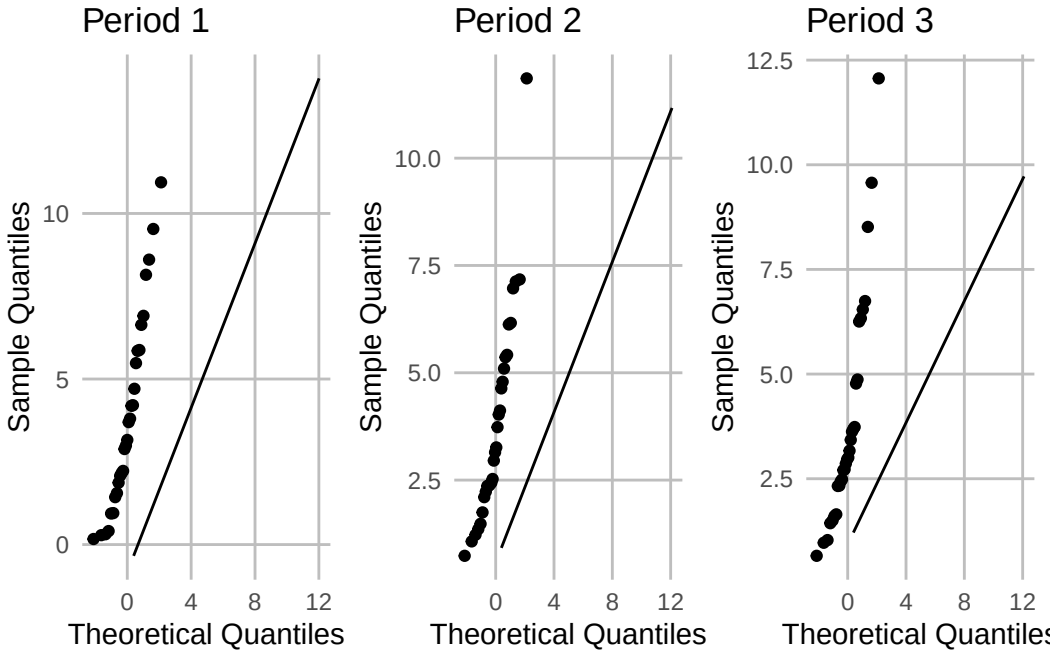
This condition is the most crucial to the test and it is realistically difficult to satisfy. We will check it by Q-Q plots and by multivariate Shapiro-Wilk test. For the former, if the sample quantile does not match the theoretical quantile (here we use the Mahalanobis distance which is Chi-square distributed), we conclude that the sample does not follow normality. For the latter, if the p-value is less than a threshold (i.e., 0.05), we reject the null hypothesis that we sample follows the multivariate normal distribution. We find that the normality assumption is violated for each period. Hence, we conclude that the usual MANOVA assumptions are not realistic for these data.

```
dat %>%
  select(all_of(features)) %>%
  mshapiro_test()
```

```
# A tibble: 1 x 2
  statistic p.value
      <dbl>   <dbl>
1     0.953 0.00270
```

```r
# Define a function to compute chi-square values
compute_chisq <- function(data, mean_vector, inv_cov_matrix) {
  diag(t(t(data) - mean_vector) %*% inv_cov_matrix %*% (t(data) - mean_vector))
}

# Compute inverse covariance matrices
S1inv <- solve(S1)
S2inv <- solve(S2)
S3inv <- solve(S3)

# Compute chi-square values
datachisq1 <- compute_chisq(dat[dat$Period==1,-5], xbar1, S1inv)
datachisq2 <- compute_chisq(dat[dat$Period==2,-5], xbar2, S2inv)
datachisq3 <- compute_chisq(dat[dat$Period==3,-5], xbar3, S3inv)

# Create QQ plots
qqplot1 <- ggplot() +
  geom_qq(aes(sample = datachisq1)) +
  geom_qq_line(aes(sample = datachisq1), distribution = qchisq, dparams = list(df = p)) +
  labs(title = "Period 1", x = "Theoretical Quantiles", y = "Sample Quantiles") +
  theme_minimal() +
  theme(panel.grid.major = element_line(colour = "grey"), panel.grid.minor = element_blank

qqplot2 <- ggplot() +
  geom_qq(aes(sample = datachisq2)) +
  geom_qq_line(aes(sample = datachisq2), distribution = qchisq, dparams = list(df = p)) +
  labs(title = "Period 2", x = "Theoretical Quantiles", y = "Sample Quantiles") +
  theme_minimal() +
  theme(panel.grid.major = element_line(colour = "grey"), panel.grid.minor = element_blank

qqplot3 <- ggplot() +
  geom_qq(aes(sample = datachisq3)) +
  geom_qq_line(aes(sample = datachisq3), distribution = qchisq, dparams = list(df = p)) +
  labs(title = "Period 3", x = "Theoretical Quantiles", y = "Sample Quantiles") +
  theme_minimal() +
  theme(panel.grid.major = element_line(colour = "grey"), panel.grid.minor = element_blank
```

```r
# Combine the plots
grid.arrange(qqplot1, qqplot2, qqplot3, ncol = 3)
```



Exercise 4.9

Data Preprocessing

Since the factors present in the column names, we must extract these values and put them into new columns. Moreover, we can transform original data into wide format for transparency and complex modelling

```r
test <- "Wilk"
dat <- read.csv("data_exo_chap4\\mobile_3d_tasktime_multi.csv") |> as_tibble()

long_dat <- dat %>%
  pivot_longer(
    cols = starts_with("Trt"),  # Select all columns starting with "Trt"
    names_to = "Treatment",  # Keep the original column names as treatment
    values_to = "Value"  # The cell values become the new 'Value' column
  ) %>%
```

```
    mutate(
      # Extract display size and task from treatment name
      DisplaySize = as.numeric(substring(Treatment, 4, 4)),
      Task = as.numeric(substring(Treatment, 5, 5))
    ) %>%
    # Encode display size and task
    mutate(DisplaySize = factor(DisplaySize, levels = c(1, 2), labels = c(5, 7))) %>%
    mutate(Task = factor(Task, levels = c(1, 2, 3), labels = c(1, 2, 3)))

  wide_dat <- long_dat %>%
    pivot_wider(
      names_from = Treatment,
      values_from = Value) %>%
    mutate(across(where(is.numeric), ~replace(., is.na(.), 0)))
```

```
  print(dat)
```

```
# A tibble: 30 x 7
   SubjectID Trt11  Trt12  Trt13  Trt21  Trt22 Trt23
       <int> <dbl>  <dbl>  <dbl>  <dbl>  <dbl> <dbl>
 1         1 10.9   2.44   0.814  0.997  0.614  6.09
 2         2 14.1   0.381  1.01   0.680  1.09   7.83
 3         3  1.45  9.61   0.400  1.53   6.69   2.35
 4         4 14.4   9.28   3.49   4.92   6.31  12.6
 5         5 17.9   3.03   2.77   6.91   8.77   6.82
 6         6  9.48  8.50   4.23   5.58  11.2    3.24
 7         7 12.0  17.2    5.02   9.03   4.23  16.3
 8         8 16.6   8.55   3.65   7.58   3.45  26.3
 9         9 21.3   9.25   3.69   3.15   6.94  18.4
10        10 21.0  15.1   19.6   11.0    7.63  22.4
# i 20 more rows
```

Code

Are there any differences among the 6 Treatments

Two-way ANOVA (optional)

To be completed! #### MANOVA Formulation This MANOVA formulation is just my experiment to see if we can perform MANOVA to this two-factors ANOVA. Now we will perform MANOVA models.

```r
lm_mod_wide <- lm(cbind(Trt11, Trt12, Trt13, Trt21, Trt22, Trt23) ~ DisplaySize*Task, data
mod_wide <- manova(lm_mod_wide)
summary_mod_wide <- summary(mod_wide, test = test)
```

Here in all cases, the p-value is extremely small (2.2e-16), indicating very strong evidence against the null hypothesis (which states that there is no effect). Therefore, we can conclude that both display size and task, as well as their interaction, have a significant effect on the dependent variables. Now we will test whether the MANOVA's assumptions are met

Checking Assumptions of MANOVA Model

Here we see that the normality assumption is not satisfied; thereby we need to further resolve this issue to obtain a more reliable result.

```r
# Correlation test
wide_dat %>% cor_test(Trt11, Trt12, Trt13, Trt21, Trt22, Trt23)
```

```
# A tibble: 36 x 8
   var1  var2    cor statistic      p conf.low conf.high method
   <chr> <chr> <dbl>     <dbl>  <dbl>    <dbl>     <dbl> <chr>
 1 Trt11 Trt11  1       Inf    0         1      1        Pearson
 2 Trt11 Trt12 -0.15     -1.96 0.0511   -0.286  0.000640 Pearson
 3 Trt11 Trt13 -0.14     -1.82 0.0701   -0.276  0.0112   Pearson
 4 Trt11 Trt21 -0.15     -2.01 0.0458   -0.289 -0.00286  Pearson
 5 Trt11 Trt22 -0.11     -1.51 0.133    -0.255  0.0344   Pearson
 6 Trt11 Trt23 -0.16     -2.13 0.0346   -0.297 -0.0116   Pearson
 7 Trt12 Trt11 -0.15     -1.96 0.0511   -0.286  0.000640 Pearson
 8 Trt12 Trt12  1       Inf    0         1      1        Pearson
 9 Trt12 Trt13 -0.12     -1.60 0.111    -0.261  0.0277   Pearson
10 Trt12 Trt21 -0.13     -1.77 0.0793   -0.272  0.0154   Pearson
# i 26 more rows
```

```r
# Levene's Test
wide_dat %>%
  pivot_longer(cols = c(Trt11, Trt12, Trt13, Trt21, Trt22, Trt23), names_to = "variable",
  mutate(
    # Create a new factor that represents the combination of DisplaySize and Task
    Interaction = interaction(DisplaySize, Task)
  ) %>%
  group_by(variable) %>%
  levene_test(value ~ Interaction)
```

```
# A tibble: 6 x 5
  variable   df1   df2 statistic        p
  <chr>    <int> <int>     <dbl>    <dbl>
1 Trt11        5   174      52.1 7.56e-33
2 Trt12        5   174      71.7 1.95e-40
3 Trt13        5   174      77.3 2.21e-42
4 Trt21        5   174      46.9 1.53e-30
5 Trt22        5   174      16.0 5.53e-13
6 Trt23        5   174      43.2 8.24e-29
```

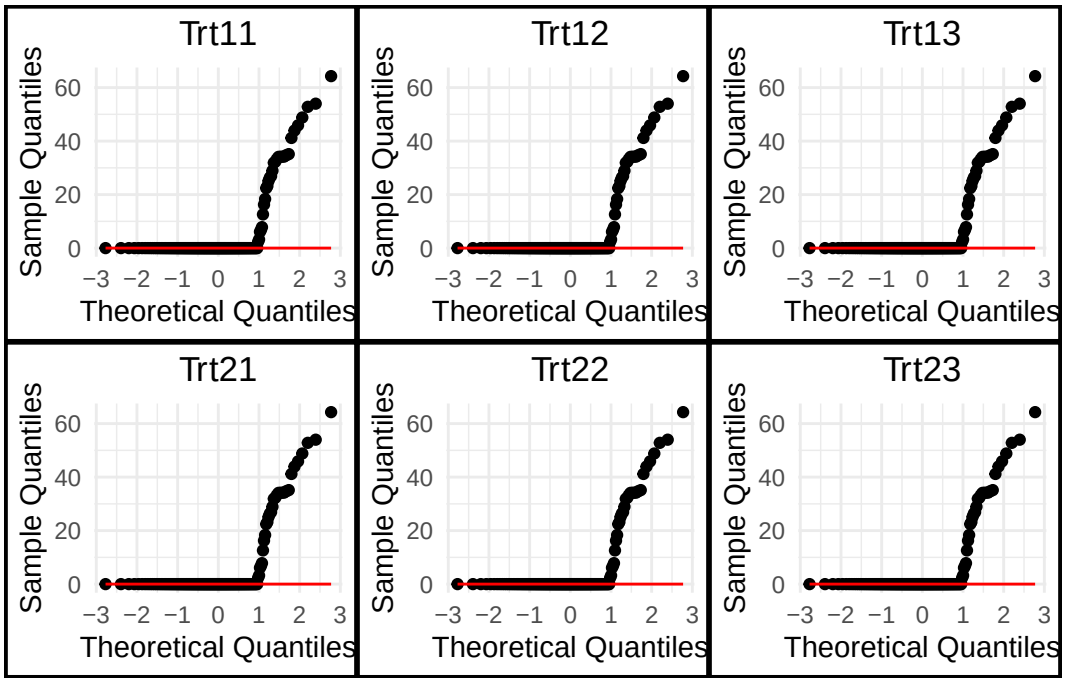
```r
# Shapiro-Wilk Test
wide_dat %>%
  select(c(Trt11, Trt12, Trt13, Trt21, Trt22, Trt23)) %>%
  mshapiro_test()
```

```
# A tibble: 1 x 2
  statistic  p.value
      <dbl>    <dbl>
1     0.413 5.79e-24
```

```r
# Create a list to store the plots
plots <- list()

# Loop over each treatment
for(treatment in c("Trt11", "Trt12", "Trt13", "Trt21", "Trt22", "Trt23")) {
  p <- ggplot(wide_dat, aes(sample = get(treatment))) +
    stat_qq() +
    stat_qq_line(color = 'red') +
    labs(title = treatment, x = "Theoretical Quantiles", y = "Sample Quantiles") +
    theme_minimal() +
    theme(plot.title = element_text(hjust = 0.5),
          plot.background = element_rect(color = "black", fill = NA, size = 1))
  plots[[treatment]] <- p
}
```

```
Warning: The `size` argument of `element_rect()` is deprecated as of ggplot2 3.4.0.
i Please use the `linewidth` argument instead.
```

```
# Arrange the plots in a 3x3 grid
grid.arrange(grobs = plots, ncol = 3)
```



Simultaneous Confidence Intervals

5 Inches vs 7 Inches (Display Size)

```
# library(multcomp)
# # Compute the simultaneous confidence intervals
# summary(glht(mod_wide, linfct = mcp(DisplaySize = "Tukey", Task = "Tukey")), test = adju

p <- 3
g <- 3
alpha <- 0.05
n1 <- length(which((wide_dat$DisplaySize==5)))
n2 <- length(which((wide_dat$DisplaySize==7)))
n <- n1+n2
xbar1 <- colMeans(wide_dat[wide_dat$DisplaySize==5,-c(1,2,3,7,8,9)])
xbar2 <- colMeans(wide_dat[wide_dat$DisplaySize==7,-c(1,2,3,4,5,6)])
```

```r
xbar <- (n1*xbar1+n2*xbar2)/(n1+n2)
S1 <- cov(wide_dat[wide_dat$DisplaySize==5,-c(1,2,3,7,8,9)])
S2 <- cov(wide_dat[wide_dat$DisplaySize==7,-c(1,2,3,4,5,6)])
W <- (n1-1)*S1+(n2-1)*S2

# Compute the qt level
qtlevel <- qt(1-alpha/(p*g*(g-1)),df=n-g)

# Initialize an empty dataframe to store the results
results <- tibble(comparison = character(), LCI = numeric(), UCI = numeric())

# Compute the pairwise comparisons
for (i in 1:p) {
  LCI57 <- (xbar1[i]-xbar2[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  UCI57 <- (xbar1[i]-xbar2[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  results <- results %>% bind_rows(tibble(comparison = paste0("tau5[",i,"]-tau7[",i,"]"),
}

# Print the results
print(results)
```

```
# A tibble: 3 x 3
  comparison          LCI   UCI
  <chr>             <dbl> <dbl>
1 tau5[1]-tau7[1]  -0.629  9.07
2 tau5[2]-tau7[2] -12.8    8.00
3 tau5[3]-tau7[3]  -9.18   3.82
```

Difficult vs Easy (Task)

```r
p <- 2
g <- 2
alpha <- 0.05
n1 <- length(which((wide_dat$Task==1)))
n2 <- length(which((wide_dat$Task==2)))
n <- n1+n2
xbar1 <- colMeans(wide_dat[wide_dat$Task==1,-c(1,2,3,4,6,7,9)])
xbar2 <- colMeans(wide_dat[wide_dat$Task==2,-c(1,2,3,4,6,7,9)])

xbar <- (n1*xbar1+n2*xbar2)/(n1+n2)
```

```r
S1 <- cov(wide_dat[wide_dat$Task==1,-c(1,2,3,4,6,7,9)])
S2 <- cov(wide_dat[wide_dat$Task==2,-c(1,2,3,4,6,7,9)])
W <- (n1-1)*S1+(n2-1)*S2

# Compute the qt level
qtlevel <- qt(1-alpha/(p*g*(g-1)),df=n-g)

# Initialize an empty dataframe to store the results
results <- tibble(comparison = character(), LCI = numeric(), UCI = numeric())

# Compute the pairwise comparisons
for (i in 1:p) {
  LCI12 <- (xbar1[i]-xbar2[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  UCI12 <- (xbar1[i]-xbar2[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
  results <- results %>% bind_rows(tibble(comparison = paste0("tau1[",i,"]-tau2[",i,"]"),
}

# Print the results
print(results)
```

```
# A tibble: 2 x 3
  comparison        LCI   UCI
  <chr>           <dbl> <dbl>
1 tau1[1]-tau2[1] -20.6 -8.61
2 tau1[2]-tau2[2] -28.6 -7.88
```

Exercise 4.8

Code

```r
dat <- read.table('data_exo_chap4\\exo4-8.dat')

dat$trt.meniscus <- factor(dat$trt.meniscus)

mod <- manova(cbind(loadFail,displace,stiff) ~ trt.meniscus, data = dat)
mod_summary <- summary(mod, test="Wilks")
mod_summary
```

```
            Df  Wilks approx F num Df den Df   Pr(>F)
```

```
trt.meniscus  2 0.2868   3.7582      6     26 0.007949 **
Residuals    15
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Print Wilk's Lambda
cat("Wilk's Lambda: ", mod_summary$stats[1, "Wilks"], "\n")
```

```
Wilk's Lambda:  0.2868046
```

```r
p_value <- mod_summary$stats[1, "Pr(>F)"]
cat("p-value: ", p_value, "\n")
```

```
p-value:  0.00794896
```

```r
# Conclude whether the effect is significant
if (p_value < 0.05) {
  cat("The effect of treatment on dependent variables is significant at a 0.05 level.\n")
} else {
  cat("The effect of treatment on dependent variables is not significant at a 0.05 level.\
}
```

```
The effect of treatment on dependent variables is significant at a 0.05 level.
```

```r
# Get the summary of each individual ANOVA
aov_summaries <- summary.aov(mod)

# Loop over each response variable
for (response in names(aov_summaries)) {
  # Get the p-value for the effect of trt.meniscus
  p_value <- aov_summaries[[response]][1,5]

  # Print the p-value
  cat(paste("The p-value for the effect of treatment on", response, "is", p_value, "\n"))

  # Conclude whether the effect is significant
  if (p_value < 0.05) {
```

```
    cat(paste("The effect of treatment on", response, "is significant at a 0.05 level.\n")
  } else {
    cat(paste("The effect of treatment on", response, "is not significant at a 0.05 level.
  }
}
```

```
The p-value for the effect of treatment on  Response loadFail is 0.000232387197857517
The effect of treatment on  Response loadFail is significant at a 0.05 level.
The p-value for the effect of treatment on  Response displace is 0.0137426112328135
The effect of treatment on  Response displace is significant at a 0.05 level.
The p-value for the effect of treatment on  Response stiff is 0.0219305736871826
The effect of treatment on  Response stiff is significant at a 0.05 level.
```

Exercise 4.7

Code

```
dat <- read.csv('data_exo_chap4\\nfl_db_wo2014.csv')
attach(dat)
```

```
The following object is masked from package:ggplot2:

    Position
```

```
Height_WO <- Height[Position=="WO"]
Weight_WO <- Weight[Position=="WO"]
HandLen_WO <- HandLen[Position=="WO"]
ArmLen_WO <- ArmLen[Position=="WO"]

Height_DB <- Height[Position=="DB"]
Weight_DB <- Weight[Position=="DB"]
HandLen_DB <- HandLen[Position=="DB"]
ArmLen_DB <- ArmLen[Position=="DB"]

X1 <- cbind(Height_WO, Weight_WO, HandLen_WO, ArmLen_WO)
X2 <- cbind(Height_DB, Weight_DB, HandLen_DB, ArmLen_DB)

n1 <- nrow(X1); n2 <- nrow(X2); p <- ncol(X1)
```

```r
I_n1 <- diag(n1)
J_n1 <- matrix(rep(1,n1^2),n1,n1)
I_n2 <- diag(n2)
J_n2 <- matrix(rep(1,n2^2),n2,n2)

(xbar1 <- (1/n1) * (t(X1) %*% rep(1,n1)))
```

```
                [,1]
Height_WO   72.416667
Weight_WO  200.520833
HandLen_WO   9.479167
ArmLen_WO   31.937500
```

```r
(xbar2 <- (1/n2) * (t(X2) %*% rep(1,n2)))
```

```
                [,1]
Height_DB   71.051282
Weight_DB  194.358974
HandLen_DB   9.211538
ArmLen_DB   31.346154
```

```r
(S1 <- (1/(n1-1)) * (t(X1) %*% (I_n1 - (1/n1) * J_n1) %*% X1))
```

```
            Height_WO Weight_WO HandLen_WO  ArmLen_WO
Height_WO   6.6737589  31.22518  0.1471631  2.7898936
Weight_WO  31.2251773 281.31871  2.5828901 14.2566489
HandLen_WO  0.1471631   2.58289  0.2076684  0.1389628
ArmLen_WO   2.7898936  14.25665  0.1389628  1.5664894
```

```r
(S2 <- (1/(n2-1)) * (t(X2) %*% (I_n2 - (1/n2) * J_n2) %*% X2))
```

```
              Height_DB  Weight_DB   HandLen_DB ArmLen_DB
Height_DB   2.260458839  7.4284750 -0.001265182 0.6692814
Weight_DB   7.428475034 72.6045884  0.813512146 3.4777328
HandLen_DB -0.001265182  0.8135121  0.269040992 0.1028909
ArmLen_DB   0.669281377  3.4777328  0.102890941 0.9189651
```

```
  (Sp <- ((n1-1) * S1 + (n2-1) * S2) / (n1+n2-2))
```

```
             Height_WO  Weight_WO HandLen_WO ArmLen_WO
Height_WO   4.70075415  20.586652 0.08080694 1.8418552
Weight_WO  20.58665158 188.011218 1.79187406 9.4378394
HandLen_WO  0.08080694   1.791874 0.23510558 0.1228365
ArmLen_WO   1.84185520   9.437839 0.12283654 1.2770079
```

```
  ### Test equality of mean based on Hotelling's T^2

  (Tsq <- t(xbar1-xbar2) %*% solve(((1/n1)+(1/n2)) * Sp) %*% (xbar1-xbar2))
```

```
         [,1]
[1,] 14.47333
```

```
  (CV.wt <- (n1+n2-2)*p/(n1+n2-p-1))
```

```
[1] 4.146341
```

```
  (Tsq.CV <- CV.wt * qf(.95,p,n1+n2-p-1))
```

```
[1] 10.29551
```

```
  (Tsq.PV <- 1-pf(Tsq/CV.wt, p, n1+n2-p-1))
```

```
          [,1]
[1,] 0.0110447
```

```
  ### Simultaneous CI's for differences of mean characteristics

  diff <- xbar1 - xbar2
  sediff <- sqrt(diag(Sp)*(1/n1+1/n2))
  simCILo <- diff - sqrt(Tsq.CV) * sediff
  simCIHi <- diff + sqrt(Tsq.CV) * sediff
  bonCILo <- diff - qt(1-.05/(2*4),n1+n2-2) * sediff
```

```
bonCIHi <- diff + qt(1-.05/(2*4),n1+n2-2) * sediff

oldlci <- cbind(diff,simCILo,simCIHi,bonCILo,bonCIHi)
colnames(oldlci) <- c("Diff","Sim Lo","Sim Hi", "Bon Lo", "Bon Hi")
round(oldlci, 3)
```

```
            Diff Sim Lo Sim Hi Bon Lo Bon Hi
Height_WO  1.365 -0.134  2.865  0.173  2.558
Weight_WO  6.162 -3.323 15.647 -1.382 13.705
HandLen_WO 0.268 -0.068  0.603  0.001  0.534
ArmLen_WO  0.591 -0.190  1.373 -0.030  1.213
```

```
### Linear combination with maximum population difference

(ahat <- solve(Sp) %*% (xbar1-xbar2))
```

```
                [,1]
Height_WO   0.35403510
Weight_WO  -0.01435271
HandLen_WO  1.15343480
ArmLen_WO  -0.05243558
```

```
detach(dat)
```

Exercise 4.6

Notes on Repeated Measures Design

Consider an $N_q(\mu, \Sigma)$ population, and let C be a contrast matrix. An α-level test of $H_0 : C\mu = 0$ (equal treatment means) versus $H_1 : C\mu \neq 0$ is as follows:

Reject H_0 if

$$T^2 = n(C^\top \bar{x})^\top (C^\top S C)^{-1} C\bar{x} > \frac{(n-1)(q-1)}{(n-q+1)} F_{q-1,n-q+1}(\alpha)$$

where $F_{q-1,n-q+1}(\alpha)$ is the upper (100α)th percentile of an F-distribution with $q-1$ and $n-q+1$ d.f. Here $\bar{x}$ and S are the sample mean vector and covariance matrix defined, respectively, by

$$\bar{x} = \frac{\sum_{j=1}^n x_j}{n} \quad , \quad S = \frac{\sum_{j=1}^n (x_j - \bar{x})(x_j - \bar{x}')}{(n-1)}$$

Code

```r
dat <- read.table('data_exo_chap4\\exo4-6.dat')
```

```r
n <- nrow(dat)
X <- as.matrix.data.frame(dat)
q <- ncol(X)

xbar <- (1/n) * (t(X) %*% rep(1,n))

# # Construct covariance(tedious !!!)
# I_n <- diag(n)
# J_n <- matrix(rep(1,n^2),n,n)
# S <- (1/(n-1)) * (t(X) %*% (I_n - (1/n)*J_n) %*% X)

S <- cov(dat)

contrast_mat <- matrix(c(1,-1,0,0,1,0,-1,0,1,0,0,-1),byrow=T,ncol=4)

T2 <- n * (t(contrast_mat%*%xbar) %*% solve(contrast_mat%*%(S)%*%t(contrast_mat)) %*%(cont

crit_val <- ((n-1)*(q-1)/(n-q+1)) * qf(.95,q-1,n-q+1)
```

```r
print(paste("Test statistic:", T2))
```

```
[1] "Test statistic: 153.727505641501"
```

```r
print(paste("Critical value at alpha = 0.05:", crit_val))
```

```
[1] "Critical value at alpha = 0.05: 9.40913033581958"
```

```r
if (T2 > crit_val) {
  print("Reject the null hypothesis: there are significant differences among methods.")
} else {
  print("Fail to reject the null hypothesis: there is no significant evidence of differenc
}
```

```
[1] "Reject the null hypothesis: there are significant differences among methods."
```

```r
crit_ci = sqrt(crit_val)
contrast_vec1 <- c(-1,1,1,-1)
contrast_vec2 <- c(-1,1,-1,1)
contrast_vec3 <- c(1,-1,1,-1)

format_mean = t(contrast_vec1 %*% xbar)
format_sd = sqrt(n * (t(contrast_vec1) %*% S %*% contrast_vec1))
parity_mean = t(contrast_vec2 %*% xbar)
parity_sd = sqrt(n * (t(contrast_vec2) %*% S %*% contrast_vec2))
inter_mean = t(contrast_vec3 %*% xbar)
inter_sd = sqrt(n * (t(contrast_vec3) %*% S %*% contrast_vec3))

format_LB = format_mean - crit_ci * format_sd
format_UB = format_mean + crit_ci * format_sd

parity_LB = parity_mean - crit_ci * parity_sd
parity_UB = parity_mean + crit_ci * parity_sd

inter_LB = inter_mean - crit_ci * inter_sd
inter_UB = inter_mean + crit_ci * inter_sd

results <- tibble(
  Tests = c("Number Format", "Parity", "Interaction"),
  Lower_Bound = c(format_LB, parity_LB, inter_LB),
  Mean = c(format_mean, parity_mean, inter_mean),
  Upper_Bound = c(format_UB, parity_UB, inter_UB)
)
# Print the tibble
print(results)
```

```
# A tibble: 3 x 4
  Tests          Lower_Bound   Mean Upper_Bound
  <chr>                <dbl>  <dbl>       <dbl>
1 Number Format      -1713.    22.4       1758.
2 Parity             -2634. -206.        2222.
3 Interaction        -2222.   206.        2634.
```

Exercise 4.2

Decompose the observations into mean, treatment, and residual components

Paper work

Construct the One-way MANOVA Table

Paper work

Hypothesis Testing on Method

Paper work

Code

```
x1 <- c(6,5,8,4,7,3,1,2,2,5,3,2)
x2 <- c(7,9,6,9,9,3,6,3,3,1,1,3)
trt <- as.factor(c(1,1,1,1,1,2,2,2,3,3,3,3))

p <- 2
g <- length(levels(trt))
n <- length(x1)

lm_mod <- lm(cbind(x1,x2)~trt)
mod <- manova(lm_mod)
mod_summary <- summary(mod, test='Wilk')

B <- mod_summary$SS$trt
W <- mod_summary$SS$Residuals

# Wilk's Lambda
Lambda_mod <- det(W)/(det(B+W))
```

The test statistics is 17.02656

```
F_val <- ((n-p-2)/p) * ((1 -sqrt(Lambda_mod))/sqrt(Lambda_mod))
F_val
```

```
[1] 17.02656
```

and the critical value is 4.772578

```
alpha <- 0.01
crit_val <- qf(1-alpha,df1=2*p,df2=2*(n-p-2))
crit_val
```

```
[1] 4.772578
```

```
print(paste("Wilk's Lambda:", Lambda_mod))
```

```
[1] "Wilk's Lambda: 0.0361895867382676"
```

```
print(paste("Test statistic (F):", F_val))
```

```
[1] "Test statistic (F): 17.0265577076291"
```

```
print(paste("Critical value at alpha = 0.01:", crit_val))
```

```
[1] "Critical value at alpha = 0.01: 4.77257799972321"
```

```
if (F_val > crit_val) {
  print("Reject the null hypothesis: there are significant differences among the three met
} else {
  print("Fail to reject the null hypothesis: there is no significant evidence of differenc
}
```

```
[1] "Reject the null hypothesis: there are significant differences among the three methods."
```

```
Barlett_val <- -(n-1-(p+g)/2)*log(Lambda_mod)
crit_val <- qchisq(1-0.01,df=4) # df = p(g-1)
if (Barlett_val > crit_val) {
  print("Reject the null hypothesis: there are significant differences among the three met
} else {
```

```
  print("Fail to reject the null hypothesis: there is no significant evidence of differenc
}
```

```
[1] "Reject the null hypothesis: there are significant differences among the three methods."
```

Exercise 4.3

Code

```
n1 <- 10
n2 <- 8
n3 <- 16
n <- n1 + n2 + n3
p <- 2
g <- 3

xbar1 <- c(41, 9)
xbar2 <- c(50, 21)
xbar3 <- c(20, 5)

S1 <- matrix(c(20, 7, 7, 5), 2, 2, byrow = TRUE)
S2 <- matrix(c(30, 9, 9, 10), 2, 2, byrow = TRUE)
S3 <- matrix(c(25, 6, 6, 11), 2, 2, byrow = TRUE)

# Combined mean vector
xbar_pooled <- (n1 * xbar1 + n2 * xbar2 + n3 * xbar3) / n

# Within-group sum of squares and cross-products matrix
W <- matrix(0, nrow = 2, ncol = 2)
for (i in 1:g) {
  n_i <- c(n1, n2, n3)[i]
  x_i <- c(xbar1, xbar2, xbar3)[i]
  S_i <- c(S1, S2, S3)[i]
  W <- W + n_i * (outer(x_i - xbar_pooled, x_i - xbar_pooled) - S_i)
}

# Total sum of squares and cross-products matrix
T <- matrix(0, nrow = 2, ncol = 2)
for (i in 1:g) {
```

```
  n_i <- c(n1, n2, n3)[i]
  x_i <- c(xbar1, xbar2, xbar3)[i]
  T <- T + n_i * outer(x_i - xbar_pooled, x_i - xbar_pooled)
}

# Calculate Wilk's Lambda
Lambda <- det(solve(T) %*% W) # determinant for stable computation

F_val <- ((n-p-2)/p) * ((1 -sqrt(Lambda))/sqrt(Lambda))
F_val
```

```
[1] 0.3121426
```

```
alpha <- 0.01
crit_val <- qf(1-alpha,df1=2*p,df2=2*(n-p-2))
crit_val
```

```
[1] 3.649047
```

```
print(paste("Wilk's Lambda:", Lambda))
```

```
[1] "Wilk's Lambda: 0.959644958200021"
```

```
print(paste("Test statistic (F):", F_val))
```

```
[1] "Test statistic (F): 0.312142638970263"
```

```
print(paste("Critical value at alpha = 0.01:", crit_val))
```

```
[1] "Critical value at alpha = 0.01: 3.649047491095"
```

```
if (F_val > crit_val) {
  print("Reject the null hypothesis: there are significant differences among the three flo
} else {
  print("Fail to reject the null hypothesis: there is no significant evidence of differenc
```

```
}
```

```
[1] "Fail to reject the null hypothesis: there is no significant evidence of differences amo
```

Appendix

Paperwork on Problem 4.2

Hồ Hữu Bình - 23C23001.

3.6

a) Để xác định khoảng tin cậy đồng thời, ta có thể xác định dựa trên 2 công thức:
Scheffe (chính xác) và mẫu lớn (xấp xỉ) vì $\frac{(n-1)p}{n-p} F_{p,n-p}(\alpha) \approx \chi^2_p(\alpha)$ khi $n-p$ lớn,
Như vậy không tin cậy

4.2 Kết Quả trắc là $\begin{bmatrix} x_1 \\ x_2 \end{bmatrix}$.

a) Trung bình của từng phương pháp và trung bình tổng thì là

$\bar{x}_1 = \begin{bmatrix} 6 \\ 8 \end{bmatrix}$, $\bar{x}_2 = \begin{bmatrix} 2 \\ 1 \end{bmatrix}$, $\bar{x}_3 = \begin{bmatrix} 5 \\ 2 \end{bmatrix}$, $\bar{x} = \begin{bmatrix} 4 \\ 5 \end{bmatrix}$ với $\bar{x}_g = \sum_i x_{ig}/n_g$ và $\bar{x} = \sum_g \sum_i x_{ig}/n$.

Ta tách quan trắc thành trung bình, phương pháp và phần dư bằng $x_{ij} = \bar{x} + (\bar{x}_i - \bar{x}) + (x_{ij} - \bar{x}_i)$

với x_1, $\begin{bmatrix} 6 & 5 & 8 & 4 & 7 \\ 8 & 1 & 2 & & \\ 2 & 5 & 3 & 2 & \end{bmatrix} = \begin{bmatrix} 4 & 4 & 4 & 4 & 4 \\ 4 & 4 & 4 & & \\ 4 & 4 & 4 & 4 & \end{bmatrix} + \begin{bmatrix} 2 & 2 & 2 & 2 & 2 \\ -2 & -2 & -2 & & \\ -1 & -1 & -1 & -1 & \end{bmatrix} +$

$$\begin{bmatrix} 0 & -1 & 2 & -2 & 1 \\ 1 & -1 & 0 & & \\ -1 & 2 & 0 & -1 & \end{bmatrix}.$$

với x_2
$\begin{bmatrix} 7 & 9 & 6 & 9 & 9 \\ 3 & 6 & 3 & & \\ 3 & 1 & 1 & 3 & \end{bmatrix} = \begin{bmatrix} 5 & 5 & 5 & 5 & 5 \\ 5 & 5 & 5 & & \\ 5 & 5 & 5 & 5 & \end{bmatrix} + \begin{bmatrix} 3 & 3 & 3 & 3 & 3 \\ -1 & -1 & -1 & & \\ -3 & -3 & -3 & -3 & \end{bmatrix} +$

$$\begin{bmatrix} -1 & 1 & -2 & 1 & 1 \\ -1 & 2 & -1 & & \\ 1 & -1 & -1 & 1 & \end{bmatrix}.$$

b) Với x_1, ta có:

$SS_{quan\ trắc} = 6^2 + 5^2 + 8^2 + 4^2 + 7^2 + \ldots + 3^2 + 2^2 = 246$

$SS_{trung\ bình} = 4^2 \times 12 = 192.$

$SS_{phương\ pháp} = 5 \times 2^2 + 3 \times (-2)^2 + 1 \times (-1)^2 = 36$

$SS_{phần\ dư} = 0^2 + (-1)^2 + 2^2 + \ldots + (-1)^2 = 18.$

$\Rightarrow SS_{tổng} = SS_{quan\ trắc} - SS_{trung\ bình} = 246 - 192 = 54.$

Với x_2, tương tự như vậy, ta có:

$SS_{quan\ trắc} = 402$, $SS_{trung\ bình} = 300$, $SS_{phương\ pháp} = 84$, $SS_{phần\ dư} = 18 \Rightarrow SS_{tổng} = 102.$

Tích chéo : $SS_{quan\ sát} = 6\times 7 + 5\times 9 + 8\times 6 + \dots + 3\times 1 + 2\times 3 = 875$.

$SS_{trung\ bình} = 12\times 4\times 5 = 240$, $SS_{phương\ pháp} = 5\times 2\times 3 + 3\times(-2)\times(-1) + 4\times(-1)\times(-3) = 48$.

$SS_{phần\ dư} = 0\times(-1) + (-1)\times 1 + \dots + 0\times(-1) + (-1)\times 1 = 13$.

$\Rightarrow SS_{tổng} = SS_{quan\ sát} - SS_{trung\ bình} = 35$.

Như vậy, ta có bảng MANOVA 1 nhân tố như sau:

Nguồn biến thiên.	Ma trận tổng bình phương	Độ tự do.
phương pháp	$B = \begin{pmatrix} 36 & 48 \\ 48 & 64 \end{pmatrix}$	$3-1=2$.
phần dư	$W = \begin{pmatrix} 18 & -13 \\ -13 & 18 \end{pmatrix}$	$5+3+4-2=9$.
Tổng (hiệu chỉnh)	$B+W = \begin{pmatrix} 54 & 35 \\ 35 & 102 \end{pmatrix}$	$12-1=11$.

c) Ta có kiểm định như sau :

$H_0: \tau_1 = \tau_2 = \tau_3 = 0$ vs H_1 : ít nhất một $\tau_i \neq 0$.

$\Lambda^* = \dfrac{|W|}{|W+B|} = \dfrac{155}{4283} = 0.0362$. Như vậy với $p=2$, $g=3$, ta có thống kê kiểm định là

$$\left(\frac{\sum_{i=1}^{3} n_i - g - 1}{g-1}\right)\left(\frac{1-\sqrt{\Lambda^*}}{\sqrt{\Lambda^*}}\right) = 17.0266.$$

Với $\alpha = 0.01$, $F_{2(g-1),2\left(\sum_{i=1}^{3} n_i - g - 1\right)}(\alpha) = F_{4,16}(0.01) = 4.7726$.

Vì $17.0266 > 4.7725$, ta bác bỏ H_0 tại $\alpha = 0.01$ và kết luận ít nhất một τ_i khác 0.

Hơn nữa, xấp xỉ Chi square theo Barlett cho ta thống kê kiểm định :

$$-\left(n-1-\frac{p+g}{2}\right)\cdot\log(\Lambda^*) = 28.2114.$$

Với $\alpha = 0.01$, $\chi^2_{p(g-1)}(\alpha) = \chi^2_4(0.01) = 13.2767$.

Vì $28.2114 > 13.2767$, ta cũng bác bỏ H_0 tại $\alpha = 0.01$ và kết luận như trên.