HOME ASSIGNMENT 4

Multivariate Data Analysis

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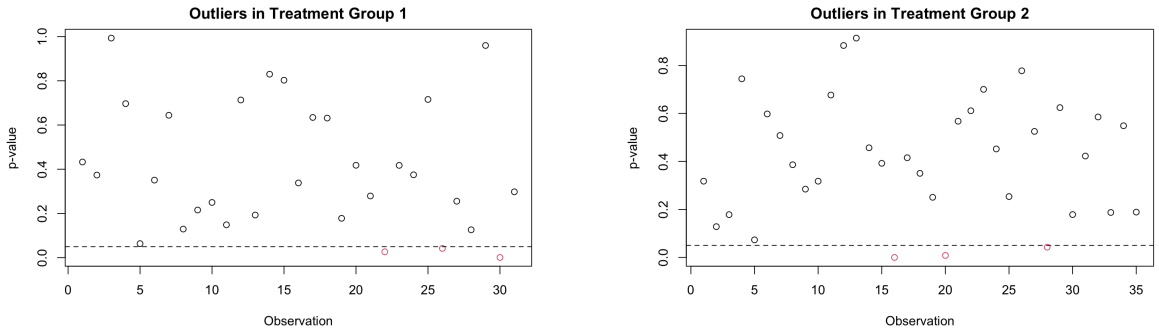
1 Exploratory Data Analysis

1.1 Task 1

Initially, the data is examined for potential outliers. By calculating the Mahalanobis Distance, *MD*, defined as

$$MD_i = \sqrt{(\mathbf{x}_i - \bar{\mathbf{x}})' \mathbf{S} (\mathbf{x}_i - \bar{\mathbf{x}})},$$

where $\bar{\mathbf{x}}$ and $\mathbf{S}$ is the sample mean vector and covariance matrix, respectively. The *MD* is χ^2- distributed with $p - 1$ degrees of freedom (d.f.) where p is the number of variables. Hence, we can compute the *MD* and the corresponding χ^2-statistics in order to detect anomalies at the significance level $\alpha = 0.05$. In Figure 1, the p-value for each observation in each treatment group is presented. The outliers in the *MD*-sense are marked as red points. Since, we have relatively few observations in each group (approximately 30 to 35), the detected outliers are removed (i.e., three observations per group) to prevent violation of the normality assumption. Thereby, the assumptions for paired comparisons are satisfied, and hypothesis testing can begin.

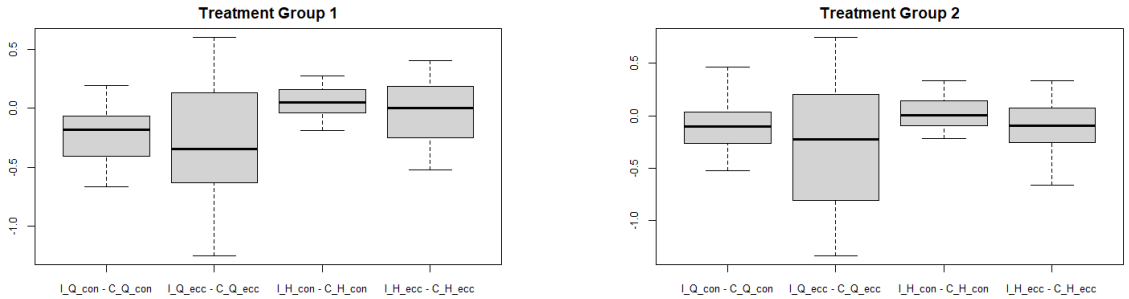


(a) Treatment group 1.

(b) Treatment group 2.

Figure 1: *The p-value, based on the χ^2-statistics, for each observation in each treatment group, respectively. The significance level, $\alpha = 0.05$, is visualized as a horizontal (dashed) line. The red points corresponds to outliers in the MD-sense.*

Further, the variables in each treatment group are visualized in Figure 2. For both treatment groups, the second variable, i.e., the difference in Quadriceps eccentric strength, shows a high variability which could be an indication of an actual difference between the injured and non-injured knees.



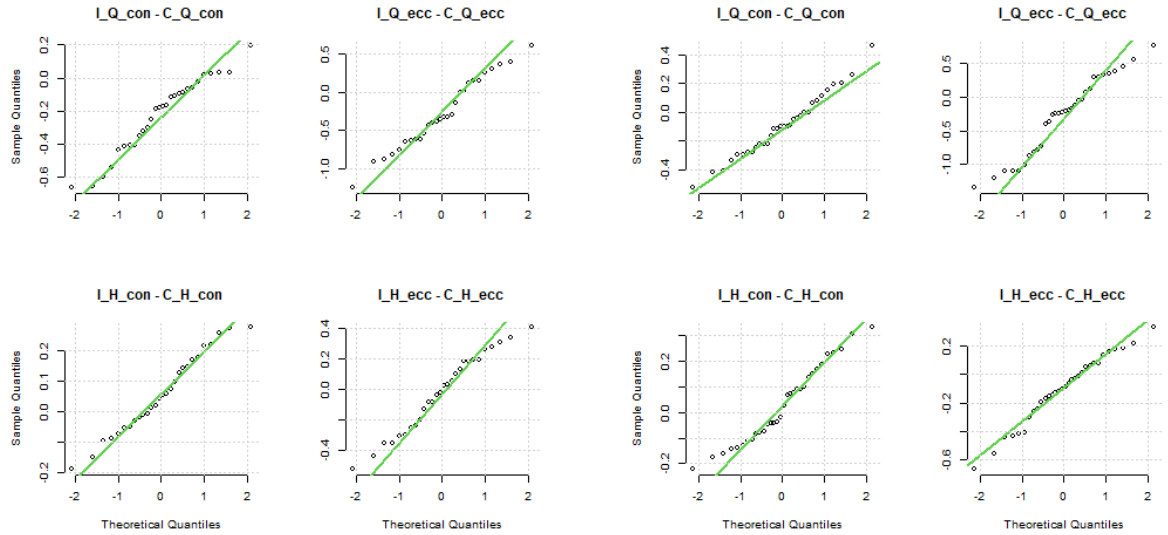
(a) Treatment group 1.

(b) Treatment group 2.

Figure 2: *The difference between each variable within each treatment group, respectively.*

As a last step before the hypothesis testing, the assumption of normality for is validated. Under the assumption that each observation is independent, and that the different variables within each observation are uncorrelated, the univariate Q-Q plots can be examined. (The latter assumption is questionable, and will be discussed.) In Figure 3, the

Q-Q plots for each treatment group are presented. For some differences, there are heavy tails that could be problematic. Overall, however, the assumption of normality is plausible.



(a) Treatment group 1.

(b) Treatment group 2.

Figure 3: *The Q-Q plots of the difference between each variable within each treatment group, respectively.*

1.2 Task 2

First, summary statistics are presented in Table 1.

Table 1: *Number of observations, n, mean and standard deviation, sd, for the different trials respectively.*

Trial	Variable	n	mean	sd
1	Jump length	102	1.006	0.261
2	Jump length	102	1.069	0.267
3	Jump length	102	1.103	0.261

Next, the observations are visualized in Figure 4 and the normality assumption is validated by Figure 5.

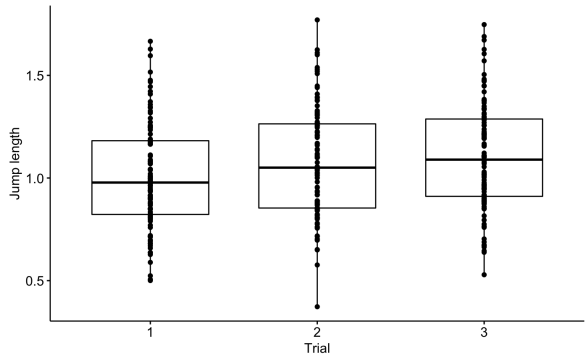


Figure 4: *Boxplot of the individual values corresponding to the different trials.*

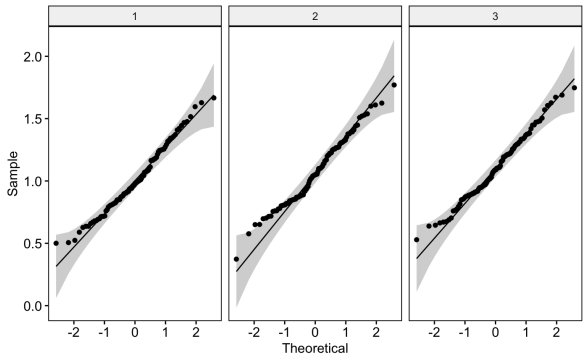


Figure 5: *QQ-plot of observations for the three trials respectively.*

Based on Figure 4 it can be concluded that there are no extreme outliers in the data. Moreover, Figure 5 validates that it is possible to assume normality of the observations since all the points corresponding to the different three trials fall

approximately along the reference line representing normal distribution.

1.3 Task 3

In addition to the data analysis conducted in Task 1 regarding the same exact variables used as response variables in this task, tests for the absence of multicollinearity, multivariate normality as well as homogeneity of covariance test between groups was also conducted.

To check the absence of multicollinearity a pairwise correlation test is conducted between all the variables which will add up to a total of six unique correlation tests between the variables. The results of these correlation test are presented in Table 2 where it is visible that all the unique dependent variables are correlated and hence there is a strong presence of multicollinearity in our response variables, as is confirmed by the respective p-values. This is somewhat troublesome when conducting MANOVA but is also rather expected given the nature of the response variables.

Table 2: *Correlation tests between each unique dependent variable. The correlation between each unique dependent variable is presented together with the p-value of the corresponding correlation test.*

Variable 1	Variable 2	Correlation	p-value
I_Q_con	I_Q_ecc	0.76	6.94e-14
I_Q_con	I_H_con	0.69	9.47e-11
I_Q_con	I_H_ecc	0.62	3.07e-08
I_Q_ecc	I_H_con	0.56	8.82e-07
I_Q_ecc	I_H_ecc	0.75	2.42e-13
I_H_con	I_H_ecc	0.69	1.50e-10

Furthermore, a test to check the multivariate normality was conducted. This was carried out using a multivariate Shapiro-Wilk normality test. This is resulted in a test-statistic with the value of approximately 0.98 which corresponds to a p-value of 0.21. This in return, makes it possible to conclude that the dependent variables seems to be normally distributed which is inline with the individual tests conducted in Task 1.

Lastly, the homogeneity of covariance between different groups should be analyzed. This was done by conducting a Box's M test for each of the two grouping variables on the dependent variables. Box's m test is based on the chi-square approximation. First off, a Box's M test for the grouping variable of gender was carried out. This resulted in an approximate chi-square statistic of 10.22 which corresponds to a p-value of 0.42. Secondly, a Box's M test for the grouping variable of treatment group was conducted.This resulted in an approximate chi-square statistic of 14.36 which corresponds to a p-value of 0.16. As a conclusion, one can say that there seems to be clear evidence of homogeneity of covariance between all the different groups that are to be analyzed in the task.

2 Method

2.1 Task 1

In this task, there are p responses, two treatments and n observations for each of the groups, respectively. Then, let

$$D_{jp} = X_{1jp} - X_{2jp}, \quad j = 1, \ldots, n,$$

where D_{jp} denotes the j^{th} difference for variable p, X_{1jp} and X_{2jp} denotes variable p under treatment 1 and 2, respectively. Further, let $\mathbf{D}_j' = [D_{j1}, D_{j2}, \ldots, D_{jp}]$ and assume that

$$\mathrm{E}(\mathbf{D}_j) = \boldsymbol{\delta} = \begin{bmatrix} \delta_1 \\ \delta_2 \\ \vdots \\ \delta_p \end{bmatrix} \quad \text{and} \quad \mathrm{Cov}(\mathbf{D}_j) = \boldsymbol{\Sigma}_d.$$

Since $\mathbf{D}_1, \mathbf{D}_2, \ldots, \mathbf{D}_n$ are independent, and assumed to be normally distributed, inferences about the vector of mean differences $\boldsymbol{\delta}$ is based on the T^2-statistics, i.e.,

$$T^2 = n(\bar{\mathbf{D}} - \boldsymbol{\delta})' \mathbf{S}_d^{-1} (\bar{\mathbf{D}} - \boldsymbol{\delta})$$

where

$$\bar{\mathbf{D}} = \frac{1}{n}\sum_{j=1}^{n}\mathbf{D}_j \quad \text{and} \quad \mathbf{S}_d = \frac{1}{n-1}\sum_{j=1}^{n}(\mathbf{D}_j - \bar{\mathbf{D}})(\mathbf{D}_j - \bar{\mathbf{D}})',$$

which has a $[(n-1)p/(n-p)]\, F_{p,n-p}(\alpha)$ distribution, independent of the true $\boldsymbol{\delta}$ and $\boldsymbol{\Sigma}_d$.

For our observed differences $\mathbf{d}_j' = [d_{j1}, d_{j2}, \ldots d_{jp}]$, $j = 1, 2, \ldots, n$, an α-level test of H_0: $\boldsymbol{\delta} = \mathbf{0}$ versus H_1: $\boldsymbol{\delta} \neq \mathbf{0}$ rejects H_0 if the observed

$$T^2 = n(\bar{\mathbf{d}} - \boldsymbol{\delta})'\mathbf{S}_d^{-1}(\bar{\mathbf{d}} - \boldsymbol{\delta}) > \frac{(n-1)p}{(n-p)}F_{n,n-p}(\alpha)$$

where $F_{n,n-p}(\alpha)$ is the upper $100(1-\alpha)^{th}$ percentile of an F-distribution with p and $n-p$ d.f.

Lastly, to find which variables that significantly differs, the Bonferroni $100(1-\alpha)\%$ simultaneous confidence intervals (SCI) for the individual mean differences were computed as

$$\delta_i\text{: } \bar{d}_i \pm t_{n-1}\left(\frac{\alpha}{2p}\right)\sqrt{\frac{s_{d_i}^2}{n}}$$

where $t_{n-1}(\alpha/2p)$ is the upper $100(1-\alpha/2p)^{th}$ percentile of a t-distribution with $n-1$ d.f., $\bar{d}_i$ and $s_{d_i}^2$ corresponds to the i^{th} element of $\bar{\mathbf{d}}$ and the i^{th} diagonal element of $\mathbf{S}_d$, respectively.

2.2 Task 2

Three different conditions are compared to one response variable represented by the length of a long jump. The conditions are given by a first, second and third jump. The j:th observation can thus be represented by

$$\mathbf{X}_j = \begin{bmatrix} X_{j1} \\ X_{j2} \\ X_{j3} \end{bmatrix}, \quad j = 1, 2, \ldots, n$$

where X_{ji} is the response to the first, second or third condition on the j:th unit. Further, the contrast matrix, $\mathbf{C}$, is defined such that

$$\begin{bmatrix} \mu_2 - \mu_1 \\ \mu_3 - \mu_2 \end{bmatrix} = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \end{bmatrix}\begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{bmatrix} = \mathbf{C}\boldsymbol{\mu}$$

The null hypothesis that $\mathbf{C}\boldsymbol{\mu} = 0$, i.e.

$$\mathrm{H}_0 : \mu_1 = \mu_2 = \mu_3$$

is tested using T^2-statistics such that

$$T^2 = n(\mathbf{C}\bar{\mathbf{x}})'\left(\mathbf{C}\mathbf{S}\mathbf{C}'\right)^{-1}\mathbf{C}\bar{\mathbf{x}}$$

Thus, H_0 is rejected if

$$T^2 = n(\mathbf{C}\bar{\mathbf{x}})'\left(\mathbf{C}\mathbf{S}\mathbf{C}'\right)^{-1}\mathbf{C}\bar{\mathbf{x}} > \frac{(n-1)(q-1)}{(n-q+1)}F_{q-1,n-q^{+1}}(\alpha)$$

where $F_{q-1,n-q^{+1}}(\alpha)$ is the upper $100\cdot\alpha$ percentile of an F-distribution with $q-1$ and $n-q+1$ degrees of freedom and where the sample mean vector, $\bar{\mathbf{x}}$, and covariance matrix, $\mathbf{S}$, are defined as

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

Next, if a significant difference is found, pairwise comparisons between the different trials are performed in order to investigate which of the contrasts are responsible for the rejection of H_0. This is done using the fact that a confidence region for contrasts $\mathbf{C}\boldsymbol{\mu}$ is determined by the set of all $\mathbf{C}\boldsymbol{\mu}$ such that

$$n(\mathbf{C}\bar{\mathbf{x}} - \mathbf{C}\boldsymbol{\mu})' \left(\mathbf{CSC}'\right)^{-1} (\mathbf{C}\bar{\mathbf{x}} - \mathbf{C}\boldsymbol{\mu}) \leq \frac{(n-1)(q-1)}{(n-q+1)} F_{q-1,n-q+1}(\alpha)$$

Thus, $100(1-\alpha)\%$ confidence intervals for the contrast vectors of interest are defined by

$$\mathbf{c}'\boldsymbol{\mu}: \quad \mathbf{c}'\bar{\mathbf{x}} \pm \sqrt{\frac{(n-1)(q-1)}{(n-q+1)} F_{q-1,n-q+1}(\alpha)} \sqrt{\frac{\mathbf{c}'\mathbf{S}\mathbf{c}}{n}}$$

2.3 Task 3

In this task, different response variables are considered in the form of strengths in the Quadriceps and Hamstrings in the injured knees of the subjects tested. In addition to the different muscles, both the concentric and eccentric measurements are to be considered resulting in a total of four different measurements. The two variables of which their explanatory power is to be examined is the treatment group as well as the gender of the different subjects.

In knowing that there are multiple dependent variables, two-way MANOVA is a natural choice in order to examine the affect of the treatment group as well as the gender. Given that we have $l = 1, 2$ different treatment groups, $k = 1, 2$ different genders and $n = 67$ different observations, the model can be presented as

$$\mathbf{X}_{lki} = \boldsymbol{\mu} + \boldsymbol{\tau}_l + \boldsymbol{\beta}_k + \boldsymbol{\gamma}_{lk} + \epsilon_{lki}$$

where the response variable $\mathbf{X}_{lkn}$ is a vector of $p = 4$ values, $i = 1, \ldots 67$ and $\boldsymbol{\mu}$ is the overall mean level vector. In addition $\boldsymbol{\tau}_l$ is the fixed effect of treatment group at level l and $\boldsymbol{\beta}_k$ is the fixed effect of gender at level k.Furthermore, γ_{lk} can be interpreted as the interaction between treatment group and gender at level l and k respectively. This model assumes that the random noise terms are independent between cases as well as $\epsilon_{lki} \sim N_4(0, \Sigma)$. Given this model, the null hypothesis for the dependency of the treatment groups can be presented as

$$\mathrm{H}_0 : \boldsymbol{\tau}_1 = \boldsymbol{\tau}_2 = \mathbf{0},$$

and for the dependency of the gender, the null hypothesis can be presented as

$$\mathrm{H}_0 : \boldsymbol{\beta}_1 = \boldsymbol{\beta}_2 = \mathbf{0},$$

and finally for the dependency of the interaction between the gender and the treatment group, the null hypothesis can be presented as

$$\mathrm{H}_0 : \boldsymbol{\gamma}_{11} = \boldsymbol{\gamma}_{12} = \boldsymbol{\gamma}_{21} = \boldsymbol{\gamma}_{22} = \mathbf{0},$$

Based on the above mentioned null hypothesis for tests regarding the individual grouping variables as well as the interaction one is able to construct the test statistic, Wilk's Lambda by the Likelihood Ratio Test (LRT)

$$\boldsymbol{\Lambda} = \frac{\max \ell_{\text{Restricted model}}}{\max \ell_{\text{Full model}}} = \frac{\left|\hat{\boldsymbol{\Sigma}}_{RM}\right|}{\left|\widehat{\boldsymbol{\Sigma}}_{FM}\right|},$$

which can then be be compared to a theoretical value of a distribution. The distribution with regards to this task will be the following given that we have $p = 4 \geq 1$ different variables and $k = l = 2$ different groups within each grouping variable

$$\frac{\sum n_k - p - 1}{p} \frac{1 - \Lambda}{\Lambda} \sim F_{p, \sum n_k - p - 1}.$$

Thus we can reject either of the null hypothesis, H_0 if the following holds

$$\boldsymbol{\Lambda} = \frac{\left|\hat{\boldsymbol{\Sigma}}_{RM}\right|}{\left|\widehat{\boldsymbol{\Sigma}}_{FM}\right|} > F_{p, \sum n_k - p - 1}.$$

On the basis of the above mentioned hypothesis testing we start of by testing the interaction term of the model, $\boldsymbol{\gamma}_{lk}$. If this turns out to have a significant effect on the response variables, i.e. we reject the null hypothesis then there is no point in examining the grouping variables by themselves since their effect will be disordered. If we do not reject the null hypothesis we do then examine the two grouping variables,$\boldsymbol{\tau}_l$ and $\boldsymbol{\beta}_k$ by themselves in order to examine whether

they affect the response variables. We do this by hypothesis testing on the null hypothesis regarding the treatment group as well as the null hypothesis regarding the gender.

Additionally, based on the results from the two-way MANOVA, one could and possibly should continue and examine the effects of the grouping variables on the individual response variables by themselves. By doing this it is possible to extract which of the response variables does depend on the grouping variables which where found to be significant in the two-way MANOVA.

These individual test can be easily done by simple t-tests where we examine the mean dependent on the grouping variable. The appropriate test-statistic given these conditions is

$$t = \frac{\left|\bar{X} - \mu_0\right|}{S/\sqrt{n}},$$

where $\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$ and $S^2 = \frac{1}{n-1}\sum_{i=1}^{n} (x_i \quad \bar{x})^2$ where $x_1, \ldots, x_n$ is sample from a univariate normal distribution. Given this, the null hypothesis of the individual t-test becomes

$$\mathrm{H}_0 : \mu = \mu_0.$$

Furthermore, under the null hypothesis we have that the test statistic t is Student's t distribution with $n-1$ degrees of freedom. This gives us the following rule in order to reject the null hypothesis, H_0

$$\frac{|\bar{x} - \mu|}{S/\sqrt{n}} > t_{n-1}(\alpha/2).$$

3 Results

3.1 Task 1

For treatment group 1 (subscript 1), i.e., subjects with knee surgery, we have $n_1 = 28$ and $p_1 = 4$ which, at significance $\alpha = 0.05$ level, results in

$$T_1^2 = 35.65 > 12.49 = \left[(n_1 - 1)p_1/(n_1 - p_1)\right] F_{p_1, n_1 - p_1}(\alpha).$$

Hence, we reject the null hypothesis and conclude that at least one variable differs within the first treatment group. The corresponding means and Bonferroni SCI's are presented in Table 3, from which it can be seen that the SCI's for the first two variables does not include zero. This means that the difference in Quadriceps concentric as well as eccentric strength, between injured and non-injured knees, within treatment group 1 significantly differs.

Table 3: *The sample means, $\bar{d}_{1i}$, for treatment group 1 along with Bonferroni 95% SCI for each variable. The lower and upper bounds corresponds to SCI_L and SCI_U, respectively.*

p_1	$\bar{d}_{1i}$	SCI_L	SCI_U
1	-0.2260	-0.3407	-0.1113
2	-0.2883	-0.5223	-0.0542
3	0.0560	-0.0095	0.1216
4	-0.0261	-0.1559	0.1038

Consequently, for treatment group 2 (subscript 2), i.e., subjects without knee surgery, we have $n_2 = 32$ and $p_2 = 4$ which, at significance $\alpha = 0.05$ level, results in

$$T_2^2 = 15.72 > 12.02 = \left[(n_2 - 1)p_2/(n_2 - p_2)\right] F_{p_2, n_2 - p_2}(\alpha).$$

Hence, we reject the null hypothesis and conclude that at least one variable differs within the first treatment group. The corresponding means and Bonferroni SCI's are presented in Table 4, from which it can be seen that the SCI's for the first variable does not include zero. This means that the difference in Quadriceps eccentric strength, between injured and non-injured knees, within treatment group 2 significantly differs.

Table 4: *The sample means, $\bar{d}_{2i}$, for treatment group 2 along with Bonferroni 95% SCI for each variable. The lower and upper bounds corresponds to SCI_L and SCI_U, respectively.*

p_2	$\bar{d}_{2i}$	SCI_L	SCI_U
1	-0.0974	-0.1995	0.0046
2	-0.2834	-0.5509	-0.0158
3	0.0278	-0.0428	0.0983
4	-0.1092	-0.2218	0.0033

3.2 Task 2

In Table 5 the T^2-statistics and F-value is presented.

Table 5: *Resulting T^2-statistics and F-value based on $\alpha = 0.05$.*

T^2	F-value
62.68767	6.23634

Based on the above table we have that $T^2 = 62.68767 > 6.23634 =$ F-value and thus we reject the null hypothesis meaning that not all level means are equal.

Further, Table 6 displays the result of pairwise t-tests using the Bonferroni method for adjusting p-values.

Table 6: *Resulting p-values based on pairwise comparisons between group levels.*

Group 1	Group 2	p-value
Trial 2	Trial 1	0.2663
Trial 3	Trial 1	0.0274
Trial 3	Trial 2	1.0000

Hence, it can be concluded that the rejection of H_0 depends on the contrast between the first and the third trial. This build upon the p-value of the pairwise t-test corresponding to the first and third trial being below the chosen significance level of 0.05 and thus proving statistically significant.

In Figure 6 the pairwise confidence intervals between the different trials are presented.

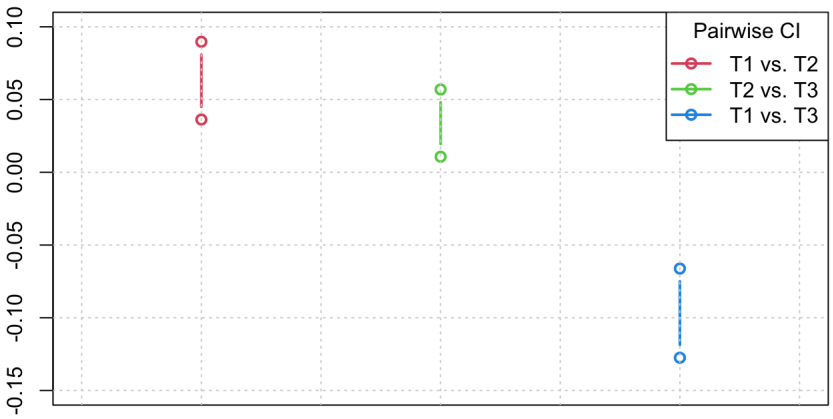


Figure 6: *Visualization of the pairwise confidence intervals between the different trials.*

The above figure further validates the results presented in Table 6 by showing that the confidence interval of the pair corresponding to trial 1 and 3 does not overlap with any of the other confidence intervals thus implying that the

difference between trial 1 and 3 is statistically significant.

3.3 Task 3

First off, a hypothesis test was carried out regarding the interaction term presented in the model in section 2.3. The result of this test is presented in Table 7 which shows us that the null hypothesis, $\mathrm{H}_0 : \boldsymbol{\gamma}_{11} = \boldsymbol{\gamma}_{12} = \boldsymbol{\gamma}_{21} = \boldsymbol{\gamma}_{22} = \mathbf{0}$, can not be rejected and hence the interaction term between the treatment groups and the different genders seems to have no effect on the different response variables.

Table 7: *Resulting Wilk's Lambda($\boldsymbol{\Lambda}$), approximate F-value as well as the corresponding p-value of the hypothesis testing of the interaction term in the two-way MANOVA.*

$\boldsymbol{\Lambda}$	**F-value**	**p-value**
0.97892	0.3230	0.8615

Given the results above, our next task was to examine the two grouping variables by themselves. This was done by the same type of hypothesis testing as for the interaction term but know to accept or reject the null hypothesis for the individual grouping variables presented in section 2.3. The result of the hypothesis testing is presented in Table 8 and it is clear by these results that the grouping variable gender has a significant effect on the different response variables while the treatment group does not seem to affect the response variables greatly.

Table 8: *Resulting Wilk's Lambda ($\boldsymbol{\Lambda}$), approximate F-value as well as the corresponding p-value of the hypothesis testing of the individual grouping variables in the two-way MANOVA.*

Variable	$\boldsymbol{\Lambda}$	**F-value**	**p-value**
Treatment group	0.92188	1.2923	0.283
Gender	0.65064	8.1885	$2.363 \cdot 10^{-5}$

Lastly, based on the result in Table 8, one should continue to examine the affect of the grouping variable gender on each of the four different response variables. This was done through simple t-test where the null hypothesis for each of the response variables was $\mathrm{H}_0 : \mu = \mu_0$. The result of these t-tests are presented in Table 9 which shows us that the concentric measurements seems to be the response variables that are affected by the grouping variable gender while the eccentric does not seem to be greatly impacted by this form of grouping.

Table 9: *Resulting t-value and the corresponding p-value of the hypothesis testing of the individual response variables dependent on the grouping variable gender through t-test.*

Response variable	**t-value**	**p-value**
I_Q_con	3.70	< 0.001
I_Q_ecc	1.21	0.229
I_H_con	4.67	$1.57 \cdot 10^{-5}$
I_H_ecc	1.59	0.119

4 Discussion & Conclusions

4.1 Task 1

Firstly, the assumption of uncorrelated differences between variables must be discussed. Since we have a multivariate response variable, we are naive to believe that independence between the subjects would imply uncorrelated differences, which is not necessarily true. Therefore, the reliability of the tests would increase if we could validate the multivariate normality, or by testing and (hopefully) rejecting the pairwise correlations. However, for this study, such a correlation is expected since a fit individual is likely to be strong over more than one variable. Hence, a more suitable assumption is that all variables are more or less correlated and in turn, taking that into consideration from the beginning.

Further, it was shown that the healthy knees, w.r.t. the Quadriceps strength, was significantly stronger in the eccentric direction for both groups, and also in the concentric direction for the first group. Based on this result, one can

conclude that a surgery deteriorates the concentric Quadriceps strength. Regardless, one must also consider the long-term effects of having a surgery. Although the surgery decreases the strength to some extent, it could yield benefits in the long run, e.g., joint health and prevention of other negative side effects from not having a surgery.

4.2 Task 2

The exploratory analysis of Task 2 showed that there are no extreme outliers in the data and that the normality assumption looks plausible. Further, the results presented in Section 3.2 pointed at the difference between trial 1 and 3 being statistically significant. This result is not surprising since it is natural that there is a larger difference in tiredness in the leg between the first and third jump than between the first and second or second and third.

4.3 Task 3

The initial data analysis gave us both encouraging and less encouraging results. To begin with the encouraging results, the multivariate normality assumption was satisfied together with the assumption about homogeneity of covariances between groups for each of the two grouping variables. However, the test of collinearity between variables showed us that all response variables had a significant correlation between them. This should be taken into consideration when making conclusions about the results of the different hypothesis testing that was carried out. Although, this result is somewhat troublesome, the analysis does not pond on this assumption. Mostly because this is something we expect given the nature of the variables but also because the correlations are not very high (>0.9).

Regarding the results there is not much to discuss other than the fact that the treatment group does not seem to matter when analyzing the response variables given in the task. However, the gender of the subject does make a difference. More interestingly though, might be the fact that it is only the concentric measurements that seems to differ significantly between the gender and not the eccentric. What this is due to might have something to do with how our muscles are built but that analysis might be outside the scope of this course.

A Source Code

Listing 1: *The R source code used to solve Task 1.*

```
## ----
↪  warning=FALSE----------------------------------------------------------------------------------------
# import libraries
library(readxl)
library(stats)
library(matlib)
library(ggplot2)
library(qqplotr)
library(broom)
library(Hmisc)
library(dplyr)


##
↪  ------------------------------------------------------------------------------------------------------------
# read data
d = as.data.frame(read_excel('Knee.xlsx'))
d[d == "M"] = NA
# summary(d)


##
↪  ------------------------------------------------------------------------------------------------------------
# ------------------------------------------------------------------------
# Task 1

# Variable definitions:
# I_Q_conNm_weight (injured, concentric)
# C_Q_conNm_weight (healthy, concentric)
# I_Q_eccNm_weight (injured, eccentric)
# C_Q_eccNm_weight (healthy, eccentric)

# Test: Multivariate Hotelling's T-squared test statistic (Paired comparisons)

# extract relevant variables
d_t1 = cbind(
  group=d$Grupp,
  I_Q_con=d$I_Q_conNm_weight,
  I_Q_ecc=d$I_Q_eccNm_weight,
  I_H_con=d$I,
  I_H_ecc=d$I_H_eccNm_weight,
  C_Q_con=d$C_Q_conNm_weight,
  C_Q_ecc=d$C_Q_eccNm_weight,
  C_H_con=d$C_H_conNm_weight,
  C_H_ecc=d$C_H_eccNm_weight
)

# remove NA's and convert extracted data to data frame
D_t1_chr = as.data.frame(na.omit(d_t1))
D_t1 = as.data.frame(sapply(D_t1_chr, as.numeric))

# split into separate data frame for each group
D_t1_gr1 = D_t1[D_t1$group == 1, ]
D_t1_gr2 = D_t1[D_t1$group == 2, ]

```

```r

##
↪ ----------------------------------------------------------------------------------------------------
# compute paired comparison statistics
paired_comp = function(gr1, gr2, a=.05) {
  # compute parameters
  D = gr1 - gr2
  D_bar = as.matrix(colMeans(D))
  S = cov(D)
  n = dim(gr1)[1]
  p = dim(gr1)[2]

  # compute statistics (H0: delta = 0)
  H_T2 = n * t(D_bar) %*% inv(S) %*% D_bar

  # compute F-statistics
  scale_p = (p * (n - 1)) / (n - p)
  F1 = qf(1 - (a), p, n-p)
  F_stat = scale_p * F1

  # hypothesis testing
  if (H_T2 > F_stat) {
    cat("Reject null hypothesis\n\n")
    cat("Test-stat:", H_T2, "\n")
    cat("F-quantile:", F_stat)
  } else {
    print("Do not reject null")
  }
  return(data.frame(Hotellings_T2=H_T2, F_qnt=F_stat))
}


##
↪ ----------------------------------------------------------------------------------------------------
# compute Bonferroni CI
bonf_CI = function(gr1, gr2, a=.05) {
  # compute parameters
  D = gr1 - gr2
  D_bar = as.matrix(colMeans(D))
  S = cov(D)
  n = dim(gr1)[1]
  p = dim(gr1)[2]
  bon_CI = matrix(rep(0, p * 3), nrow=p)
  for (i in 1:p) {
    bon_CI[i, 1] <- D_bar[i]
    bon_CI[i, 2] <- D_bar[i] - qt(1 - a / (2 * p), n - 1) * sqrt(S[i, i]/n)
    bon_CI[i, 3] <- D_bar[i] + qt(1 - a / (2 * p), n - 1) * sqrt(S[i, i]/n)
  }
  return(data.frame(estimate=bon_CI[, 1], L=bon_CI[, 2], U=bon_CI[, 3]))
}



##
↪ ----------------------------------------------------------------------------------------------------
# compare injured to non-injured by paired comparisons
# group 1 (operated)
gr1_I = D_t1_gr1[ , c(2:5)] # injured
gr1_NI = D_t1_gr1[ , c(6:9)] # non-injured
```

```
D = gr1_I - gr1_NI


##
↪ ----------------------------------------------------------------------------------------------------
m_vec = mahalanobis(D, colMeans(D), cov(D))
m_p = pchisq(m_vec, df=3, lower.tail=FALSE)
idx_rm = which(m_p < 0.05)
m_col = rep("1", 31)
m_col[idx_rm] = "2"
plot(
  1:length(m_p), m_p, ylab="p-value",
  xlab="Observation", col=m_col, main="Outliers in Treatment Group 1"
)
abline(h=0.05, lty=2)

##
↪ ----------------------------------------------------------------------------------------------------
c_n = c()
I_n = colnames(gr1_I)
NI_n = colnames(gr1_NI)
for (i in 1:4) {
  c_n[i] = paste(I_n[i], "-", NI_n[i])
}
boxplot(D[-idx_rm, ], main="Treatment Group 1", names=c_n, cex.axis=.8)


##
↪ ----------------------------------------------------------------------------------------------------
# check normality group 1
png(file="plot/qq_trt1.png")
par(mfrow=c(2, 2))
for (i in 1:4) {
  qqnorm(
    D[-idx_rm, i], pch=1, frame=FALSE, xlab=if (i > 2) "Theoretical Quantiles" else "",
    ylab=if (i %in% c(1, 3)) "Sample Quantiles" else "",
    main=paste(colnames(gr1_I)[i], "-", colnames(gr1_NI)[i])
  )
  qqline(D[-idx_rm, i], col="3", lwd=2)
  grid()
}


##
↪ ----------------------------------------------------------------------------------------------------
# compute test statistic within trt group 1
stat_g1 = paired_comp(gr1_I[-idx_rm,], gr1_NI[-idx_rm, ])


##
↪ ----------------------------------------------------------------------------------------------------
# compute CI within trt group 1
CI_g1 = bonf_CI(gr1_I[-idx_rm, ], gr1_NI[-idx_rm, ])
CI_g1

# sign. difference between the test 1 and 2:
# reason to believe that NI > I in these instances

##
↪ ----------------------------------------------------------------------------------------------------
```

```
print(latex(CI_g1 %>% mutate_if(is.numeric, round, digits=4), file=""))


##
↪  ------------------------------------------------------------------------------------------------------------
# compare injured to non-injured by paired comparisons
# group 2 (treated but not operated)
gr2_I = D_t1_gr2[ , c(2:5)] # injured
gr2_NI = D_t1_gr2[ , c(6:9)] # non-injured
D = gr2_I - gr2_NI


##
↪  ------------------------------------------------------------------------------------------------------------
m_vec = mahalanobis(D, colMeans(D), cov(D))
m_p = pchisq(m_vec, df=3, lower.tail=FALSE)
idx_rm = which(m_p < 0.05)
m_col = rep("1", 35)
m_col[idx_rm] = "2"
plot(
  1:length(m_p), m_p, ylab="p-value",
  xlab="Observation", col=m_col, main="Outliers in Treatment Group 2"
)
abline(h=0.05, lty=2)

##
↪  ------------------------------------------------------------------------------------------------------------
c_n = c()
I_n = colnames(gr1_I)
NI_n = colnames(gr1_NI)
for (i in 1:4) {
  c_n[i] = paste(I_n[i], "-", NI_n[i])
}
boxplot(D[-idx_rm, ], main="Treatment Group 2", names=c_n, cex.axis=.8)


##
↪  ------------------------------------------------------------------------------------------------------------
# check normality group 2
png(file="plot/qq_trt2.png")
par(mfrow=c(2, 2))
for (i in 1:4) {
  qqnorm(
    D[-idx_rm, i], pch=1, frame=FALSE, xlab=if (i > 2) "Theoretical Quantiles" else "",
    ylab=if (i %in% c(1, 3)) "Sample Quantiles" else "",
    main=paste(colnames(gr1_I)[i], "-", colnames(gr1_NI)[i])
  )
  qqline(D[-idx_rm, i], col="3", lwd=2)
  grid()
}


##
↪  ------------------------------------------------------------------------------------------------------------
# compute test statistic within trt group 2
stat_g2 = paired_comp(gr2_I[-idx_rm, ], gr2_NI[-idx_rm, ])


##
↪  ------------------------------------------------------------------------------------------------------------
```

```r
# compute CI within trt group 2
CI_g2 = bonf_CI(gr2_I[-idx_rm, ], gr2_NI[-idx_rm, ])
CI_g2

# sign. difference between the test 2:
# reason to believe that NI > I in these instances

##
print(latex(CI_g2 %>% mutate_if(is.numeric, round, digits=4), file=""))
```

Listing 2: *The R source code used to solve Task 2.*

```r
# Exploratory analysis

# load relevant data
data2 = subset(dat, select=c(1,18:20))

# remove rows with missing values
data2 = subset(data2, C_D_Length3!='M')

# get values for each jump
jump1 = as.double(data2$C_D_Length1)
jump2 = as.double(data2$C_D_Length2)
jump3 = as.double(data2$C_D_Length3)

# assign label to each jump
col = c('Jump','label')
jump1 = data.frame(jump1,rep(1,102))
colnames(jump1) = col
jump2 = data.frame(jump2,rep(2,102))
colnames(jump2) = col
jump3 = data.frame(jump3,rep(3,102))
colnames(jump3) = col

data2_temp = rbind(jump1,jump2,jump3)
jump_id = data2$subject
data2 = cbind(jump_id,data2_temp)

# get summary statistics
data2 %>%
  group_by(label) %>%
  get_summary_stats(Jump, type = "mean_sd")

# create boxplot
bxp <- ggboxplot(data2, x = "label", y = "Jump", add = "point", xlab ="Trial",
                 ylab = "Jump length",)
bxp

# identify outliers
data2 %>%
  group_by(label) %>%
  identify_outliers(Jump)

# check normality assumption
data2 %>%
```

```
  group_by(label) %>%
  shapiro_test(Jump)

ggqqplot(data2, "Jump", facet.by = "label")

# Test computation

# extract relevant variables
d_t2 = cbind(
  group=d$Grupp,
  C_D_1=d$C_D_Length1,
  C_D_2=d$C_D_Length2,
  C_D_3=d$C_D_Length3
)

# remove NA's and convert extracted data to data frame
D_t2_chr = as.data.frame(na.omit(d_t2))
D_t2 = as.data.frame(sapply(D_t2_chr, as.numeric))

# define contrast matrix
C1 = matrix(c(-1, 0, 1, -1, 0, 1), nrow=2)
C1

C2 = matrix(c(1, 1, 0, -1, -1, 0), nrow=2)
C2

# repeated measures design
rep_mes = function(X, C, a=.05) {
  q = ncol(X)
  n = nrow(X)
  X_bar = as.matrix(colMeans(X))
  S = cov(X)
  S_c = C %*% S %*% t(C)
  X_c = C %*% X_bar
  T2 = n * t(C %*% X_bar) %*% solve(S_c) %*% (C %*% X_bar)
  m = q - 1
  F_stat =  (n - 1) * (q - 1)/(n - q + 1) * qf(1 - a, q - 1, n - q + 1)
  CI = matrix(rep(0, m * 3), nrow=m)
  for (i in 1:m) {
    CI[i, 1] = X_c[i]
    CI[i, 2] = X_c[i] - sqrt(F_stat * S_c[i, i] / n)
    CI[i, 3] = X_c[i] + sqrt(F_stat * S_c[i, i] / n)
  }

  # hypothesis testing
  if (T2 > F_stat) {
    cat("Reject null hypothesis\n\n")
    cat("Test-stat:", T2, "\n")
    cat("F-quantile:", F_stat)
  } else {
    print("Do not reject null")
  }

  return(data.frame(estimate=CI[, 1], L=CI[, 2], U=CI[, 3]))
}

res_c1 = rep_mes(D_t2[, c(2:4)], C1)
res_c1

```

```r
res_c2 = rep_mes(D_t2[, c(2:4)], C2)
res_c2

#Plot pairwise confidence intervals
plot(
  c(1.1, 1.1), res_c1[1, 2:3],
  type="b", ylim=c(-.15, .1), xlim=c(1.09, 1.15), col="2",
  ylab="", xlab="", lwd=2, xaxt="n"
)
points(c(1.12, 1.12), res_c1[2, 2:3], type="b", col="3", lwd=2)
points(c(1.14, 1.14), res_c2[1, 2:3], type="b", col="4", lwd=2)
grid()
legend(
  "topright",
  c("T1 vs. T2", "T2 vs. T3", "T1 vs. T3"),
  col=c("2", "3", "4"),
  pch=1, title="Pairwise CI",
  lwd=2
)

#Perform pairwise t-test
s_dat2 = stack(D_t2[, 2:4])
res = pairwise.t.test(s_dat2$values, s_dat2$ind, p.adjust.method="bonferroni")
tidy(res)
```

Listing 3: *The R source code used to solve Task 3.*

```r
## ----warning=FALSE----------------------------------------------------------------------------------------------------
# import libraries
library(readxl)
library(rstatix)
library(corpcor)
library(Hotelling)
library(tidyverse)
library(ggpubr)

## ---------------------------------------------------------------------------------------------------------------------
# read data
dat = read_excel('Knee.xlsx')

## ---------------------------------------------------------------------------------------------------------------------
# ---------------------------------------------------------------------------
# Task 3

# Variable definitions:
# I_Q_conNm_weight (injured, concentric)
# C_Q_conNm_weight (healthy, concentric)
# I_Q_eccNm_weight (injured, eccentric)
# C_Q_eccNm_weight (healthy, eccentric)
# Gender
# Grupp (1=opererad, 2=icke-opererad, 3=kontroll)

# Test: MANOVA
```

```r
# e.g.: stats::manova()


##
#Load relevant
data3 = subset(dat, select=c(2,5,51,53,55,57))

#Remove missing values and control group
data3 = subset(data3, I_Q_conNm_weight!='M' & I != 'M'& Grupp != 3)

##
#Check model assumptions

data3$I_Q_conNm_weight = as.double(data3$I_Q_conNm_weight)
data3$I_Q_eccNm_weight = as.double(data3$I_Q_eccNm_weight)
data3$I = as.double(data3$I)
data3$I_H_eccNm_weight = as.double(data3$I_H_eccNm_weight)

#Normality of responses (univariate)

par(mfrow=c(2,2))

X1 = as.double(data3$I_Q_conNm_weight)
ggqqplot(X1)


X2 = as.double(data3$I_Q_eccNm_weight)
ggqqplot(X2)

X3 = as.double(data3$I)
ggqqplot(X3)

X4 = as.double(data3$I_H_eccNm_weight)
ggqqplot(X4)

#Multivariate
mshapiro_test(data3[3:6])

#Normality of variance-covariance matrices
box_m(data3[3:6], data3$Gender)
box_m(data3[3:6], data3$Grupp)

#Check for multicollinarity between variables
cor_test(data3[3:6])

##
#Create model

mdl3 =
  manova(cbind(as.double(I_Q_conNm_weight),as.double(I_Q_eccNm_weight),as.double(I),as.double(I_H_eccNm_weigh
  ~ Gender*Grupp, data=data3)

summary(mdl3,test='Wilks')

mdl3_indi =
  manova(cbind(as.double(I_Q_conNm_weight),as.double(I_Q_eccNm_weight),as.double(I),as.double(I_H_eccNm_weigh
  ~ Gender+Grupp, data=data3)
```

```
80
81 summary(mdl3_indi,test='Wilks')
82
83 ##
   ↪ ----------------------------------------------------------------------------------------------------------------
84 #Separate models for each variable to check for dependencies
85 mdl_1 = lm(I_Q_conNm_weight~Gender,data = data3)
86 summary(mdl_1)
87
88 ##
   ↪ ----------------------------------------------------------------------------------------------------------------
89 mdl_2 = lm(I_Q_eccNm_weight~Gender,data = data3)
90 summary(mdl_2)
91
92 ##
   ↪ ----------------------------------------------------------------------------------------------------------------
93 mdl_3 = lm(I~Gender,data = data3)
94 summary(mdl_3)
95
96 ##
   ↪ ----------------------------------------------------------------------------------------------------------------
97 mdl_3 = lm(I_H_eccNm_weight~Gender,data = data3)
98 summary(mdl_3)
```