Multivariate Statistical Methods

Assignment 2. Inference about mean vectors

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Question 1.

A)

Outlier detection using mahalanobis distances.

Table 1: Outliers

	Country	d2values	pvalues
1	ARG	6.650003	0.0099156
5	BER	7.630567	0.0057387
11	COK	19.834001	0.0000084
13	CZE	10.901456	0.0009609
20	GRE	9.540322	0.0020101
29	KEN	7.625466	0.0057550
30	KORS	8.034918	0.0045884
31	KORN	26.167141	0.0000003
32	LUX	11.108846	0.0008592
33	MAS	8.237149	0.0041042
34	MRI	6.664985	0.0098325
35	MEX	14.230932	0.0001617
39	NOR	6.888063	0.0086773
40	PNG	30.507248	0.0000000
41	PHI	9.065884	0.0026042
46	SAM	35.014063	0.0000000
47	SIN	8.016395	0.0046356
51	TPE	10.183996	0.0014166
52	THA	7.815219	0.0051808
53	TUR	8.045368	0.0045620
54	USA	9.155697	0.0024794

The table shows 9 countries that could be assumed as outliers. Most countries that were classified as outliers with different distance functions from previous lab can be found on this list such as “COK”.

Table 2: Outliers Adjusted p-values

	Country	d2values	pvalues	adj_pvalues
11	COK	19.83400	0.0000084	0.0004561
31	KORN	26.16714	0.0000003	0.0000169
35	MEX	14.23093	0.0001617	0.0087313
40	PNG	30.50725	0.0000000	0.0000018
46	SAM	35.01406	0.0000000	0.0000002

The table above shows the result of adjusted p-values and the countries that still remain as outliers. The p-values are adjusted for a multiple-testing correction using Bonferroni correction. Multiple testing correction adjusts the individual p-value for each observation to keep the overall error rate to less than or equal to the user-specified p-cutoff value. Bonferroni correction takes each value and multiply by the number of observations. If corrected p-value is still below cutoff than the observation is significant.

B)

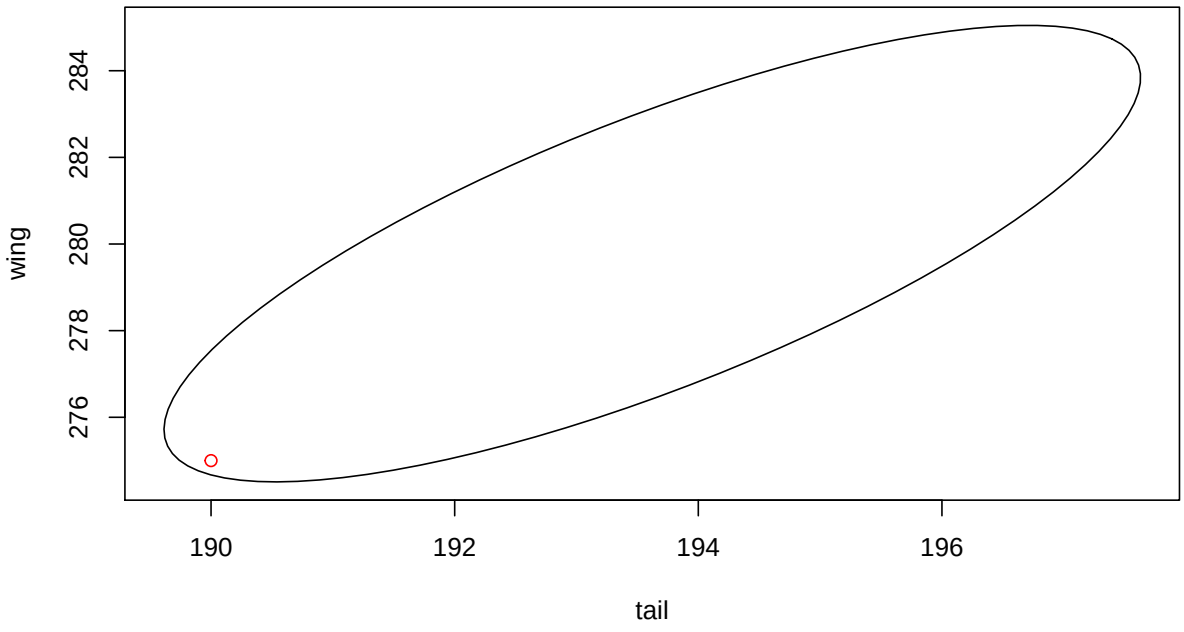
Euclidean distance assumes data to be Gaussian and treat each feature equally. Mahalanobis distance measures the correlation between variable and this can lead to different conclusions about the features.

QUESTION 2

A)

Table 3: Test value and the critical value

	Value
Test value	5.543130
Crit value	6.578471



In the table above presents the results of the calculated test statistics and the critical value. Since the test-statisctic is lower than the critical F-value means that the new mean values is in the confidence region and is therefore plausible values. That conclusion is also confirmed by the ellipse above which is representing the confidence region. The highlighted red circle is the tested mean vector and it is within the confidence region which should mean that that values are plausible.

B)

Table 4: T2 confidence intervals

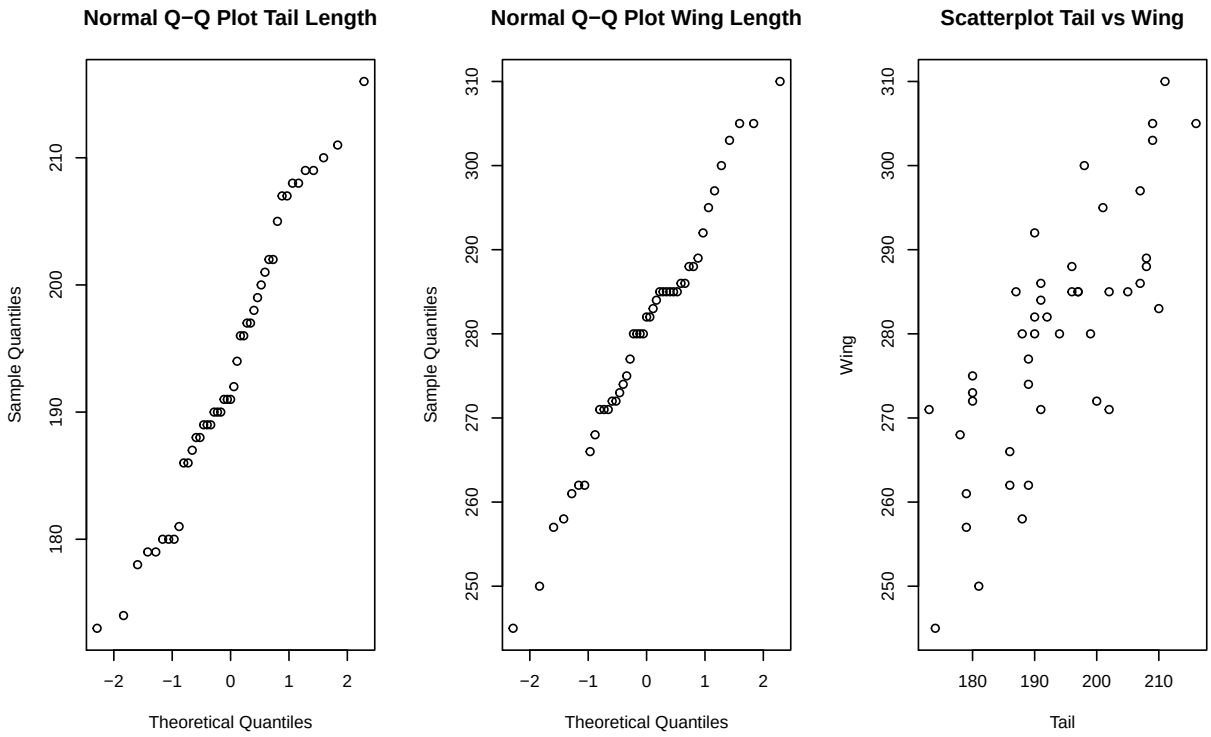
	Lower	Upper
Tail	189.4217	197.8227
Wing	274.2564	285.2992

Table 5: Bonferroni intervals

	Lower	Upper
Tail	189.8216	197.4229
Wing	274.7819	284.7736

T^2 intervals are largen than Bonferroni intervals. T^2-intervals takes the correlation between measured variables into account. #If only interested in the component means, the Bonferonni intervals provide more precise estimates. The difference does not depent on mean vector or covariance matrix. It depends on the critical value which obtains the length of the invervals.

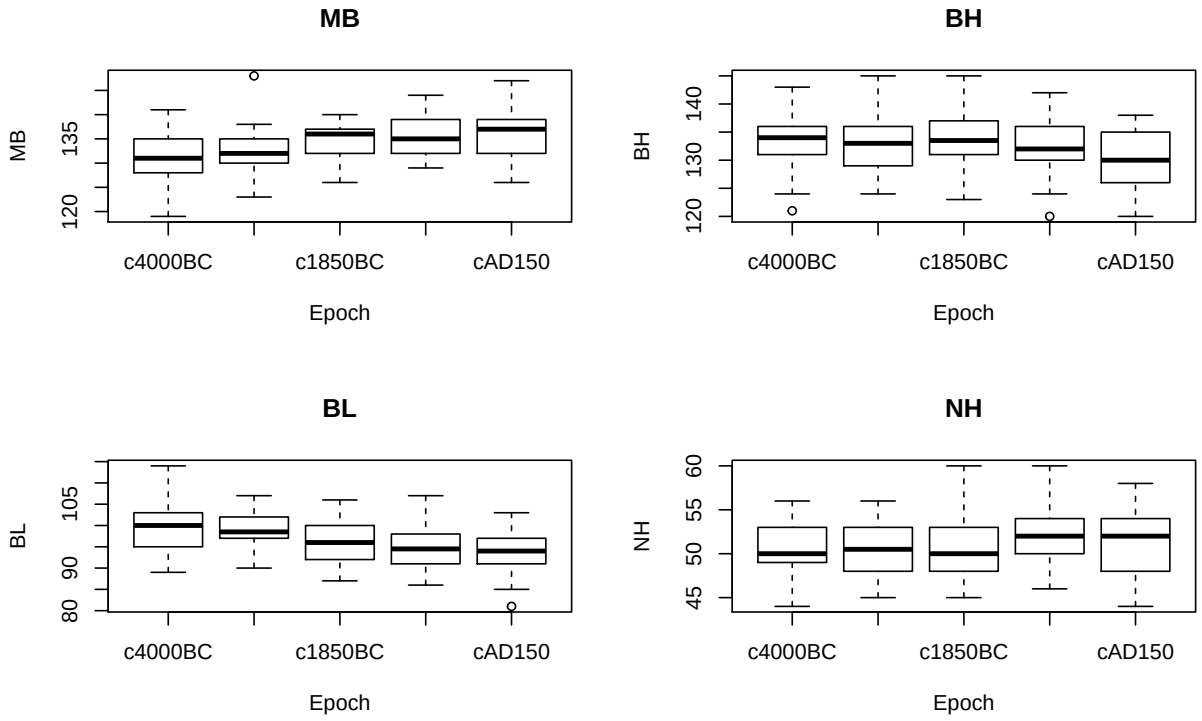
C)



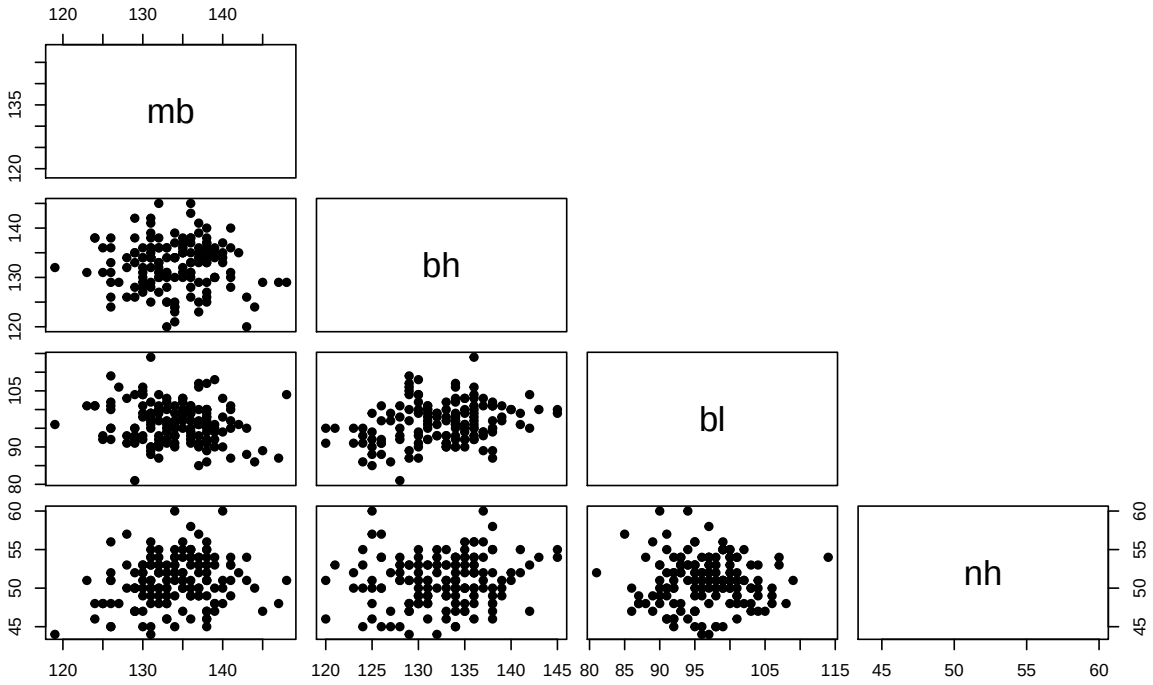
From the plots above, normality assumption seems not to be viable in this case. One possible solution could be transform the variables by a appropriate way.

QUESTION 3

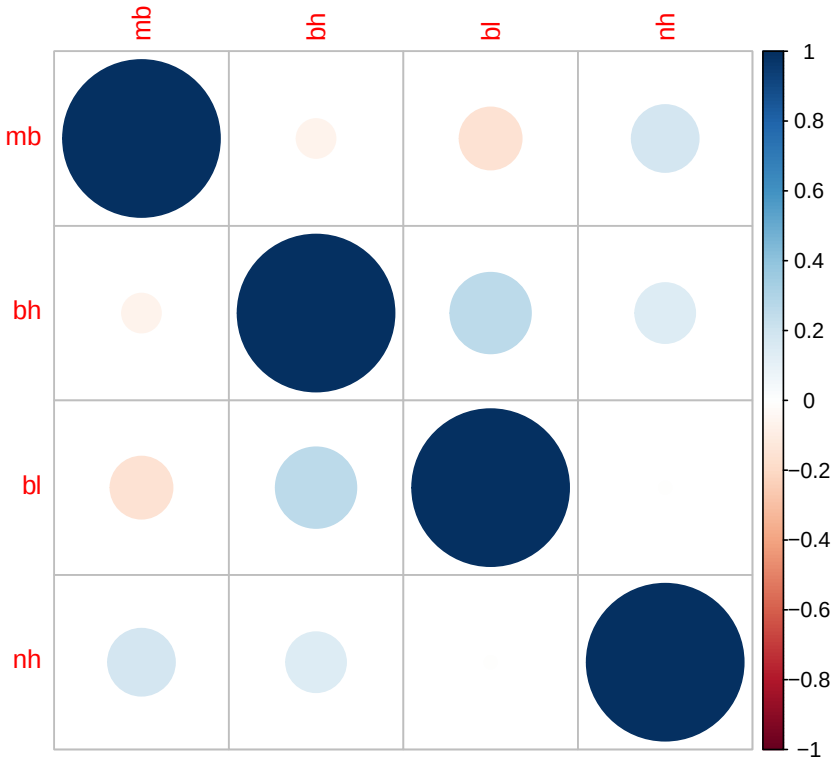
A)



In the figures above, changes for each variable over the different epochs are presented. One can see that there are differences within each variable across the different epochs.



The matrixplot scatterplot above presents the relation between the variables without considering the epochs. No patterns can be detected clearly which should be an indication of uncorrelated variables.



Also the correlation plot above shows that there are low correlations between each pair of variables.

B)

```
##        One Way Multivariate Analysis of Variance
##
## Method : Wilks
## The Value of Test Statistic = 0.6635858
##  F value = 3.901 , df1 = 16 , df2 = 434.4548 , p-value: 7.01e-07
##
##      Descriptive Statistics
## $c4000BC
##               mb         bh        bl        nh
## Means 131.366667 133.600000 99.166667 50.533333
## Sd      5.129249   4.469051  5.884423  2.763473
##
## $c3300BC
##               mb         bh        bl        nh
## Means 132.366667 132.700000 99.066667 50.233333
## Sd      4.810071   4.647209  4.346488  2.955805
##
## $c1850BC
##               mb         bh        bl        nh
## Means 134.466667 133.800000 96.033333 50.566667
## Sd      3.481313   4.978575  4.552251  3.549486
##
## $c200BC
##               mb         bh        bl        nh
## Means 135.500000 132.300000 94.533333 51.966667
## Sd      3.919448   5.133729  4.591847  2.822121
##
## $cAD150
##               mb         bh        bl        nh
## Means 136.166667 130.333333 93.500000 51.366667
## Sd      5.350368   4.971181  5.056576  3.718392
##
##
##
##    Detection important variable(s)
## [1] " Confidence Intervals are calculated only in the Roy Method."
```

MANOVA with Wilk´s method was applied. A p-value that is almost zero is obtained. Thus, there are differences between the mean vectors. There have been changes over time for the variables.

C)

```
## $`Epoch1-Epoch2`
##
##
##           Lower      Upper
## ---  ----------  ---------
## mb    -4.905276   2.905276
## bh    -3.218991   5.018991
## bl    -4.079451   4.279451
## nh    -2.408251   3.008251
```

```
##
## $`Epoch1-Epoch3`
##
##
##           Lower       Upper
## ---  ----------  ----------
## mb    -7.005276   0.8052757
## bh    -4.318991   3.9189912
## bl    -1.046117   7.3127839
## nh    -2.741584   2.6749174
##
## $`Epoch1-Epoch4`
##
##
##            Lower        Upper
## ---  -----------  -----------
## mb    -8.0386090   -0.2280576
## bh    -2.8189912    5.4189912
## bl     0.4538827    8.8127839
## nh    -4.1415841    1.2749174
##
## $`Epoch1-Epoch5`
##
##
##            Lower        Upper
## ---  -----------  -----------
## mb    -8.7052757   -0.8947243
## bh    -0.8523246    7.3856579
## bl     1.4872161    9.8461173
## nh    -3.5415841    1.8749174
##
## $`Epoch2-Epoch3`
##
##
##           Lower      Upper
## ---  ----------  ---------
## mb    -6.005276   1.805276
## bh    -5.218991   3.018991
## bl    -1.146117   7.212784
## nh    -3.041584   2.374917
##
## $`Epoch2-Epoch4`
##
##
##            Lower       Upper
## ---  -----------  ----------
## mb    -7.0386090   0.7719424
## bh    -3.7189912   4.5189912
## bl     0.3538827   8.7127839
## nh    -4.4415841   0.9749174
##
## $`Epoch2-Epoch5`
##
##
```

```
##           Lower       Upper
## ---  ----------  ----------
## mb    -7.705276   0.1052757
## bh    -1.752325   6.4856579
## bl     1.387216   9.7461173
## nh    -3.841584   1.5749174
##
## $`Epoch3-Epoch4`
##
##
##           Lower      Upper
## ---  ----------  ---------
## mb    -4.938609   2.871942
## bh    -2.618991   5.618991
## bl    -2.679451   5.679451
## nh    -4.108251   1.308251
##
## $`Epoch3-Epoch5`
##
##
##            Lower      Upper
## ---  -----------  ---------
## mb    -5.6052757   2.205276
## bh    -0.6523246   7.585658
## bl    -1.6461173   6.712784
## nh    -3.5082508   1.908251
##
## $`Epoch4-Epoch5`
##
##
##           Lower      Upper
## ---  ----------  ---------
## mb    -4.571942   3.238609
## bh    -2.152325   6.085658
## bl    -3.146117   5.212784
## nh    -2.108251   3.308251
```

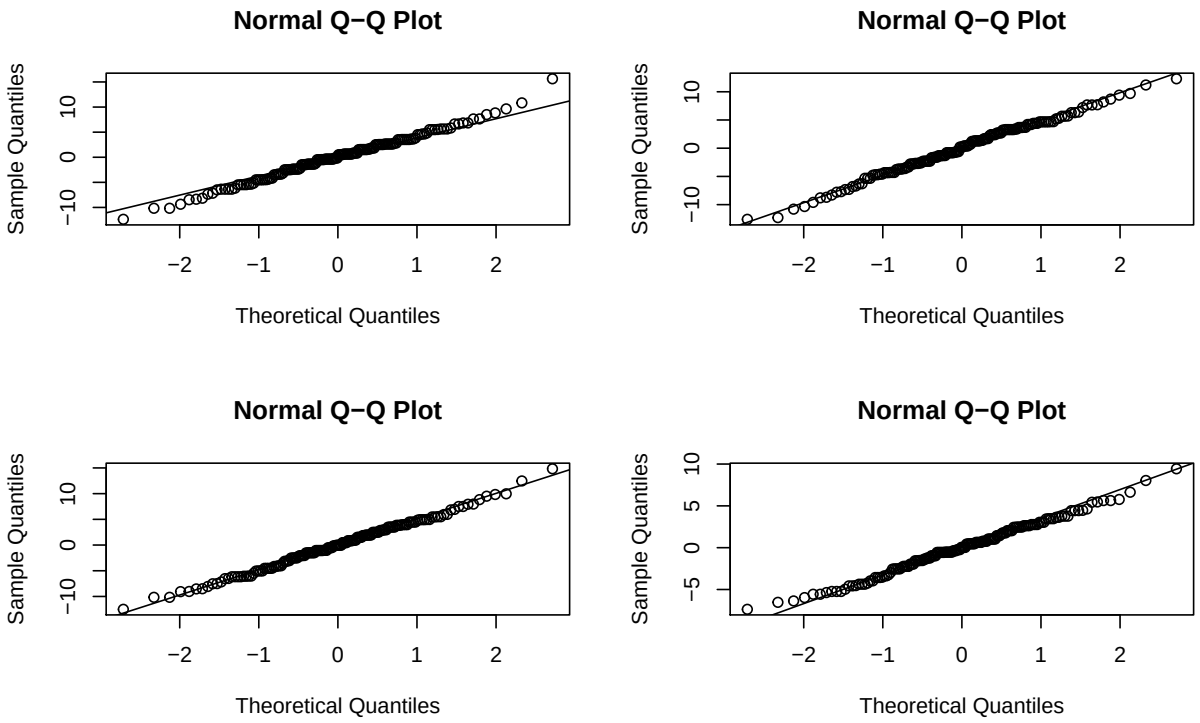
The tables above shows the simultaneous confidence intervals. If the intervals go through 0, this means that there are NO significant differences between the specified epochs for the specific variable.

Now we check if mean of residuals are zero.

	Residual mean
mb	-4.11e-17
bh	2.18e-16
bl	-8.89e-17
nh	-2.57e-17

The table above shows values extremely close to zero which means that they can be considered as zeros.

Checking if the residuals are normally distributed by studying the following plots:



The plot shows theoretical quantiles versus residual values' quantiles of the variable. More observations deviated from the line means less likelihood of being normally distributed. The second and the third variables' residuals are mostly alligned on qqlines - residuals of variable 2 and 3 are normally distributed. Observations of residuals on the first and the fourth variables generally follow qqlines. However, compare to the second and the third variable, residual observations are deviated from qqlines, especially as they moves away from the mean 0.

APPENDIX

```
##Setup

knitr::opts_chunk$set(echo = TRUE)
library(knitr)
library(heplots)
library(corrplot)
library(MVTests)
knitr::opts_chunk$set(fig.width=8, fig.height=5)

###################-----Q1.A-----###################

my_data <- read.delim(file="C:\\Users\\Suat\\Desktop\\Master_courses\\732A97_Multivariate\\Materials\\T
colnames(my_data)<-c("Country","100m","200m","400m","800m","1500m","3000m","Marathon")

data<-my_data

charac <- data.frame(variable = as.numeric(), mean=as.numeric(), std_dev=as.numeric(), stringsAsFactors
for (i in 2:length(data)) {
  mean_v <- mean(data[[i]])
  std_dev_v <- sd(data[[i]])
  charac <- rbind(charac, data.frame(variable = colnames(data)[i], mean=mean_v, std_dev=std_dev_v))
}
mean_vect <- as.vector(charac[,2])
data_mat <- as.matrix(data[,-1])
mean_mat <- matrix(0, ncol=7, nrow=nrow(data_mat))
for (i in 1:nrow(data_mat)) {
  mean_mat[i,] <- mean_vect
}
mean_correct_mat <- data_mat - mean_mat
cov_mat<-cov(data[,-1])
cor_mat<-cor(data[,-1])
d2values<-vector()
for(i in 1:nrow(data)){
  d2values[i]<-t(mean_correct_mat[i,])%*%solve(cov_mat)%*%mean_correct_mat[i,]
}
frame_mah<-data.frame("Country"=my_data$Country,d2values)
frame_mah$pvalues<-1-pchisq(frame_mah$d2values,df=1)
kable(frame_mah[frame_mah$pvalues<0.01,],caption="Outliers") #Outliers

frame_mah$adj_pvalues<-p.adjust(frame_mah$pvalues,method = "bonferroni")
kable(frame_mlt

###################-----Q2.A-----###################

bird_data<-read.table("C:\\Users\\Suat\\Desktop\\Master_courses\\732A97_Multivariate\\Materials\\T5-12.
colnames(bird_data)<-c("tail","wing")

the_means<-apply(bird_data,2,mean)
one_matrix<-matrix(1,nrow=dim(bird_data)[1],ncol = 1)

#Cov matrix
```

```r
M_mean<-matrix(data=1,nrow=nrow(bird_data))%*%cbind(mean(bird_data$tail),mean(bird_data$wing))
diff_matrix<-as.matrix(bird_data-M_mean)
covs<-((nrow(bird_data)-1)^-1)*t(diff_matrix)%*%diff_matrix

#Confidence interval
mu1<-190
mu2<-275
n<-nrow(bird_data)
tmp_vector<-c(the_means[1]-mu1,the_means[2]-mu2)
theres<-matrix(c(n*t(tmp_vector)%*%solve(covs)%*%tmp_vector,2*(n-1)/(n-2)*qf(0.95,ncol(bird_data),n-2))
colnames(theres)<-"Value";rownames(theres)<-c("Test value", "Crit value")
kable(theres,caption="Test value and the critical value")



tmp<-ellipse::ellipse(covs/n,centre = the_means,level = 0.95)
plot(tmp,type = "l")
points(x=190,y=275,col="red")

###################-----Q2.B-----###################


mu1_vector<-c(1,0)
n_col<-ncol(bird_data)
n<-nrow(bird_data)
crit_value<-sqrt((n_col*(n-1))*qf(0.95,n_col,n-n_col)/(n-n_col))
t2_res<-matrix(NA,ncol = 2,nrow = 2);colnames(t2_res)<-c("Lower","Upper");rownames(t2_res)<-c("Tail","W
#mu1
t2_res[1,1]<-t(mu1_vector)%*%the_means-crit_value*sqrt((t(mu1_vector)%*%covs%*%mu1_vector)/n)
t2_res[1,2]<-t(mu1_vector)%*%the_means+crit_value*sqrt((t(mu1_vector)%*%covs%*%mu1_vector)/n)
#mu2
mu2_vector<-c(0,1)
t2_res[2,1]<-t(mu2_vector)%*%the_means-crit_value*sqrt((t(mu2_vector)%*%covs%*%mu2_vector)/n)
t2_res[2,2]<-t(mu2_vector)%*%the_means+crit_value*sqrt((t(mu2_vector)%*%covs%*%mu2_vector)/n)
kable(t2_res,caption="T2 confidence intervals")

bon_res<--matrix(NA,ncol = 2,nrow = 2);colnames(bon_res)<-c("Lower","Upper");rownames(bon_res)<-c("Tail
crit_value_bon<-qt(1-(0.05/(2*n_col)),n-1)

bon_res[1,1]<-t(mu1_vector)%*%the_means-crit_value_bon*sqrt((t(mu1_vector)%*%covs%*%mu1_vector)/n)
bon_res[1,2]<-t(mu1_vector)%*%the_means+crit_value_bon*sqrt((t(mu1_vector)%*%covs%*%mu1_vector)/n)
#mu2
mu2_vector<-c(0,1)
bon_res[2,1]<-t(mu2_vector)%*%the_means-crit_value_bon*sqrt((t(mu2_vector)%*%covs%*%mu2_vector)/n)
bon_res[2,2]<-t(mu2_vector)%*%the_means+crit_value_bon*sqrt((t(mu2_vector)%*%covs%*%mu2_vector)/n)
kable(bon_res,caption="Bonferroni intervals")


###################-----Q2.C-----###################

par(mfrow=c(1,3),pch=1)
qqnorm(bird_data$tail,main = "Normal Q-Q Plot Tail Length")
```

```r
qqnorm(bird_data$wing,main = "Normal Q-Q Plot Wing Length")
plot(bird_data$tail,bird_data$wing,xlab = "Tail",ylab="Wing",main="Scatterplot Tail vs Wing")


###################-----Q3.A-----###################

skulls<-Skulls

par(mfrow=c(2,2))
boxplot(skulls$mb~skulls$epoch,xlab = "Epoch",ylab="MB",main="MB")
boxplot(skulls$bh~skulls$epoch,xlab = "Epoch",ylab="BH",main="BH")
boxplot(skulls$bl~skulls$epoch,xlab = "Epoch",ylab="BL",main="BL")
boxplot(skulls$nh~skulls$epoch,xlab = "Epoch",ylab="NH",main="NH")

pairs(skulls[,-1],pch=19,upper.panel = NULL)

corrplot(cor(skulls[,-1]))

###################-----Q3.B-----###################

my_manova<-Manova(data=skulls[,-1],group = skulls[,1])
summary(my_manova)

###################-----Q3.C-----###################

ep<-5
p<-ncol(skulls[,-1])
split1<-skulls[skulls$epoch=="c4000BC",]
split2<-skulls[skulls$epoch=="c3300BC",]
split3<-skulls[skulls$epoch=="c1850BC",]
split4<-skulls[skulls$epoch=="c200BC",]
split5<-skulls[skulls$epoch=="cAD150",]
n1<-30;n2<-30;n3<-30;n4<-30;n5<-30
n<-150

means1<-apply(split1[,-1],2,mean)
means2<-apply(split2[,-1],2,mean)
means3<-apply(split3[,-1],2,mean)
means4<-apply(split4[,-1],2,mean)
means5<-apply(split5[,-1],2,mean)

S1<-cov(split1[,-1])
S2<-cov(split2[,-1])
S3<-cov(split3[,-1])
S4<-cov(split4[,-1])
S5<-cov(split5[,-1])

critical<-qt(1-0.05/(p*ep*(ep-1)),df=n-ep)

W <- (n1-1)*S1+(n2-1)*S2+(n3-1)*S3+(n4-1)*S4+(n5-1)*S5

CI12<-matrix(NA,ncol=2,nrow=4);colnames(CI12)<-c("Lower","Upper");rownames(CI12)<-c("mb","bh","bl","nh")
for(i in 1:p){
```

```
  CI12[i,1]<-(means1[i]-means2[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n2))
  CI12[i,2]<-(means1[i]-means2[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n2))
}
CI13<-matrix(NA,ncol=2,nrow=4);colnames(CI13)<-c("Lower","Upper");rownames(CI13)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI13[i,1]<-(means1[i]-means3[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n3))
  CI13[i,2]<-(means1[i]-means3[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n3))
}

CI14<-matrix(NA,ncol=2,nrow=4);colnames(CI14)<-c("Lower","Upper");rownames(CI14)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI14[i,1]<-(means1[i]-means4[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n4))
  CI14[i,2]<-(means1[i]-means4[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n4))
}

CI15<-matrix(NA,ncol=2,nrow=4);colnames(CI15)<-c("Lower","Upper");rownames(CI15)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI15[i,1]<-(means1[i]-means5[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n5))
  CI15[i,2]<-(means1[i]-means5[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n1+1/n5))
}
CI23<-matrix(NA,ncol=2,nrow=4);colnames(CI23)<-c("Lower","Upper");rownames(CI23)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI23[i,1]<-(means2[i]-means3[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n3))
  CI23[i,2]<-(means2[i]-means3[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n3))
}
CI24<-matrix(NA,ncol=2,nrow=4);colnames(CI24)<-c("Lower","Upper");rownames(CI24)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI24[i,1]<-(means2[i]-means4[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n4))
  CI24[i,2]<-(means2[i]-means4[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n4))
}
CI25<-matrix(NA,ncol=2,nrow=4);colnames(CI25)<-c("Lower","Upper");rownames(CI25)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI25[i,1]<-(means2[i]-means5[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n5))
  CI25[i,2]<-(means2[i]-means5[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n2+1/n5))
}
CI34<-matrix(NA,ncol=2,nrow=4);colnames(CI34)<-c("Lower","Upper");rownames(CI34)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI34[i,1]<-(means3[i]-means4[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n3+1/n4))
  CI34[i,2]<-(means3[i]-means4[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n3+1/n4))
}
CI35<-matrix(NA,ncol=2,nrow=4);colnames(CI35)<-c("Lower","Upper");rownames(CI35)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI35[i,1]<-(means3[i]-means5[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n3+1/n5))
  CI35[i,2]<-(means3[i]-means5[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n3+1/n5))
}
CI45<-matrix(NA,ncol=2,nrow=4);colnames(CI45)<-c("Lower","Upper");rownames(CI45)<-c("mb","bh","bl","nh")
for(i in 1:p){
  CI45[i,1]<-(means4[i]-means5[i])-critical*sqrt(W[i,i]/(n-ep)*(1/n4+1/n5))
  CI45[i,2]<-(means4[i]-means5[i])+critical*sqrt(W[i,i]/(n-ep)*(1/n4+1/n5))
}

my_list<-list("Epoch1-Epoch2"=CI12,"Epoch1-Epoch3"=CI13,"Epoch1-Epoch4"=CI14,"Epoch1-Epoch5"=CI15,"Epoch
     "Epoch2-Epoch4"=CI24,"Epoch2-Epoch5"=CI25,"Epoch3-Epoch4"=CI34,"Epoch3-Epoch5"=CI35,"Epoch4-Epoch5
```

```
lapply(X = my_list, FUN = function(i) {
  kable(x = i, caption = names(i),booktabs="TRUE")

tmp1 <- manova(cbind(mb, bh, bl, nh)~epoch, data= Skulls)
res <- tmp1$residuals

res_mean <- c()
for (i in 1:4) {
  meanval <- mean(res[,i])
  res_mean <- append(res_mean, meanval)
}
res_mean<-as.matrix(res_mean)
rownames(res_mean)<-c("mb","bh","bl","nh");colnames(res_mean)<-"Residual mean"
res_mean[1:4]<-format(res_mean[1:4],digits=3)
kable(res_mean)


par(mfrow=c(2,2))
for (i in 1:4) {
  qqnorm(res[,i])
  qqline(res[,i])
}
```