

Multivariate Statistical Methods

Assignment 2

Allan Gholmi, Emma Wallentinsson, Rasmus Holm

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Question 1

a)

```
#> [1] "Outliers without correction"
#> [1] "KORN" "PNG"  "SAM"
#> [1] "Outliers with correction"
#> [1] "SAM"
```

Here are the countries that can be regarded as outliers since their Mahalanobis distance is greater than the critical set chi square distribution as 24.3218863. The countries are North Korea, Papa New Guinea and Samoa Island.

Using a significance level as low as 0.1 % makes it easy for a type 2 error – that is, when the null hypothesis is false and we do not reject it. We only believe there to be 0.1 % probability of random error and that is quite low.

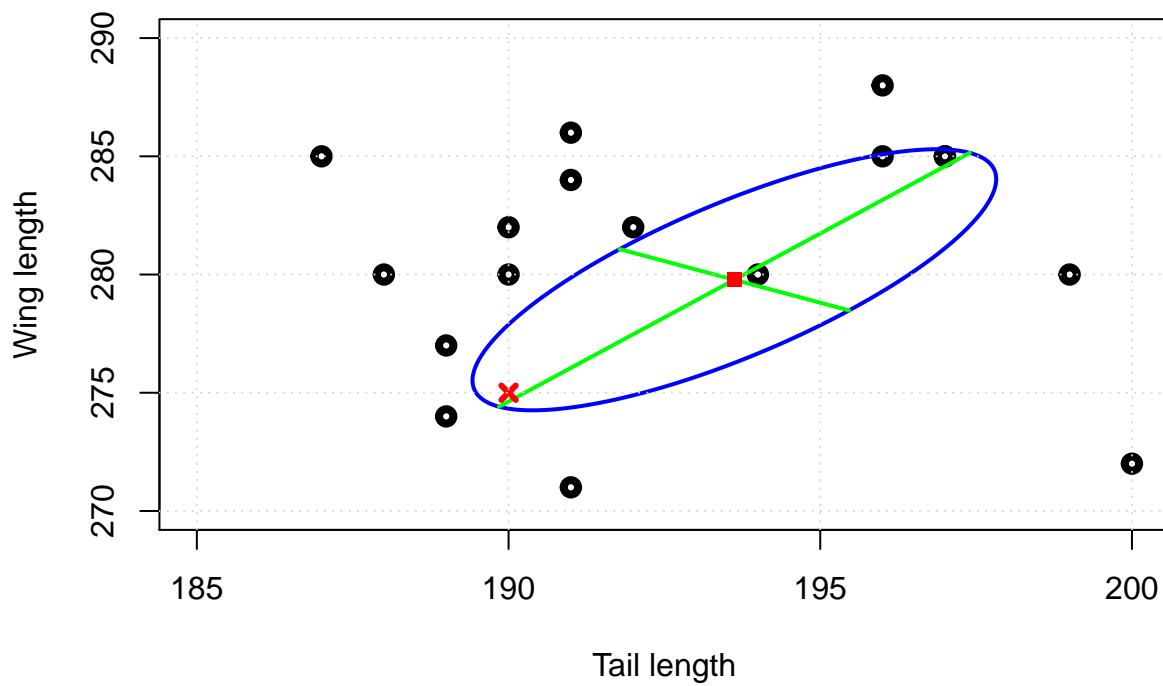
If we use the multiple-testing correction we get the critical value as 30.6729588 and the country that has a greater value than this is only Samoa Island. By using the multiple-testing correction we get a much smaller significance level since we divide the significance level by $2 * p$ ($2*7$). We already have a very low significance level set to 0.1 %, dividing that small number will increase the probability of a type 2 error.

b)

When using the Mahalanobis distance it takes the co-variances into account where the Euclidean distance assumes equal variance of the variables and zero covariates, skipping out on a lot of valuable information. Euclidean distance is not an ideal measurement to use in this dataset since the variables has very different units (e.g the time for 100 meter and marathon varies greatly).

Question 2

a)



Since the male mean (red cross) is inside the confidence region we do not reject the hypothesis that males and females have the same mean.

b)

T-square test always gives wider confidence intervals since it takes the correlation between the measured variables into account. Bonferroni intervals are more precise if you are interested in the individual component means, but if you are interested in the overall data mean you should consider the T-square intervals.

T^2 intervals

$$189.4217 \leq \mu_1 \leq 197.8227$$

$$274.2564 \leq \mu_2 \leq 285.2992$$

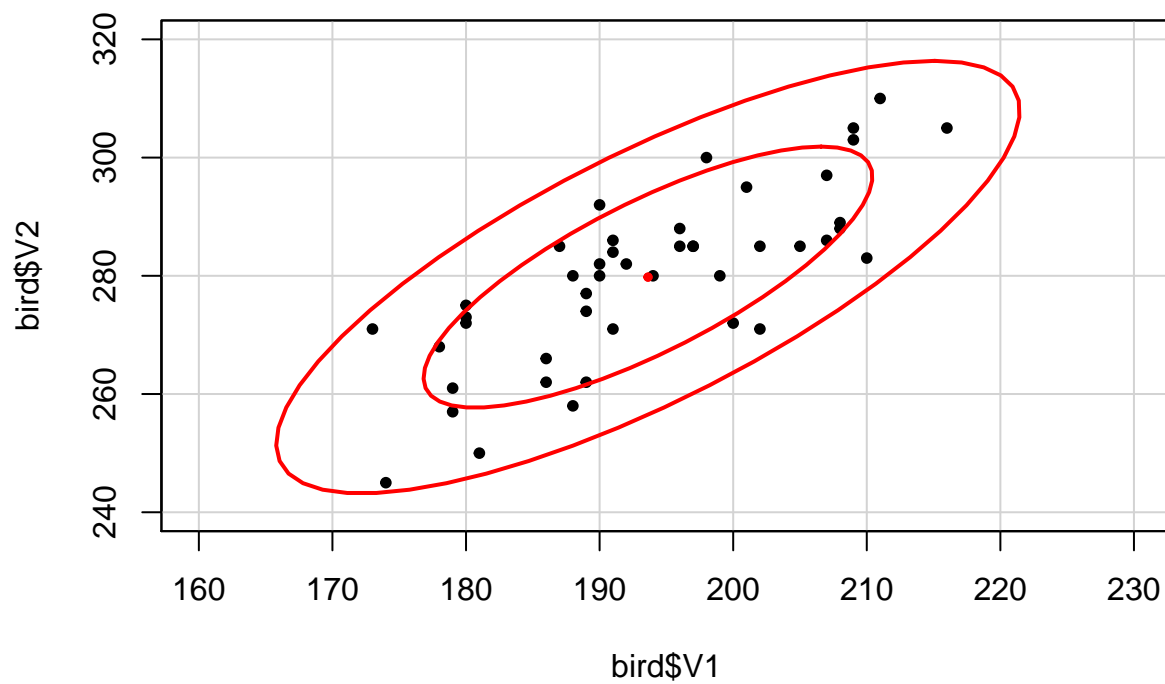
Bonferroni intervals

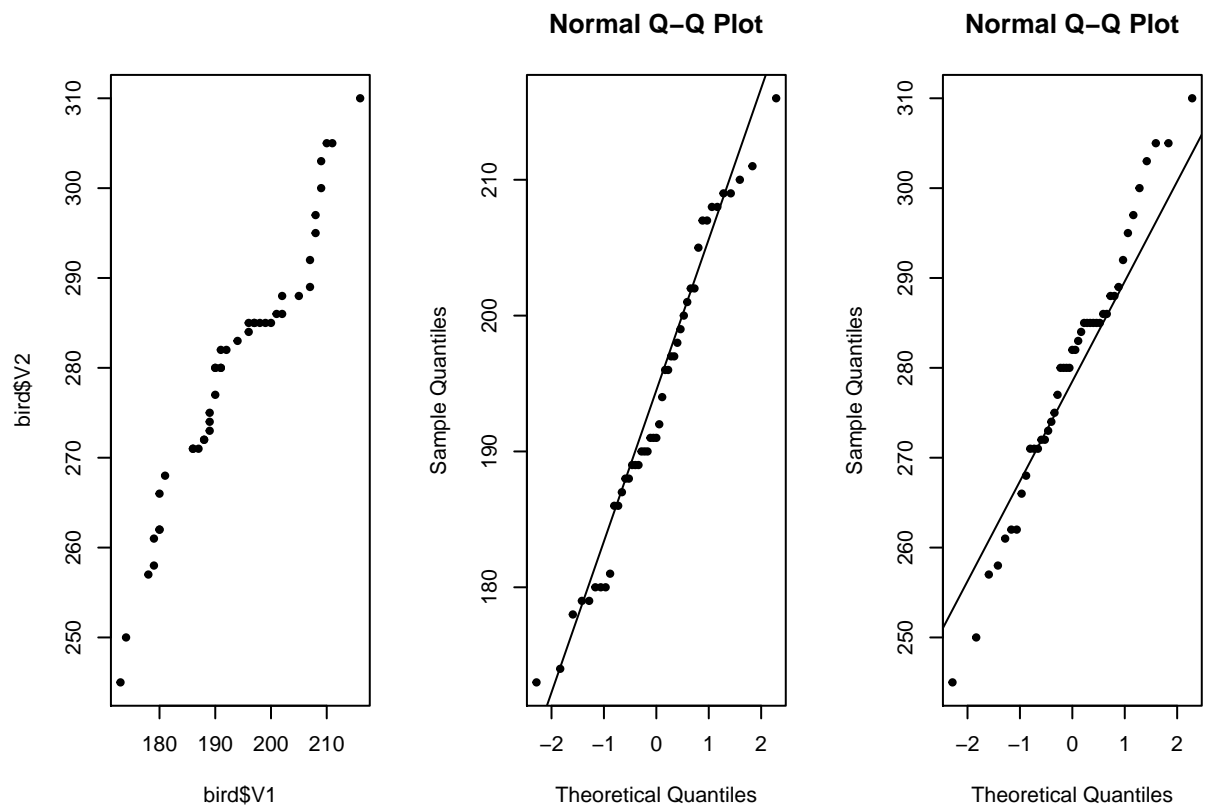
$$189.8216 \leq \mu_1 \leq 197.4229$$

$$274.7819 \leq \mu_2 \leq 284.7736$$

Figure 1: Confidence intervals.

c)

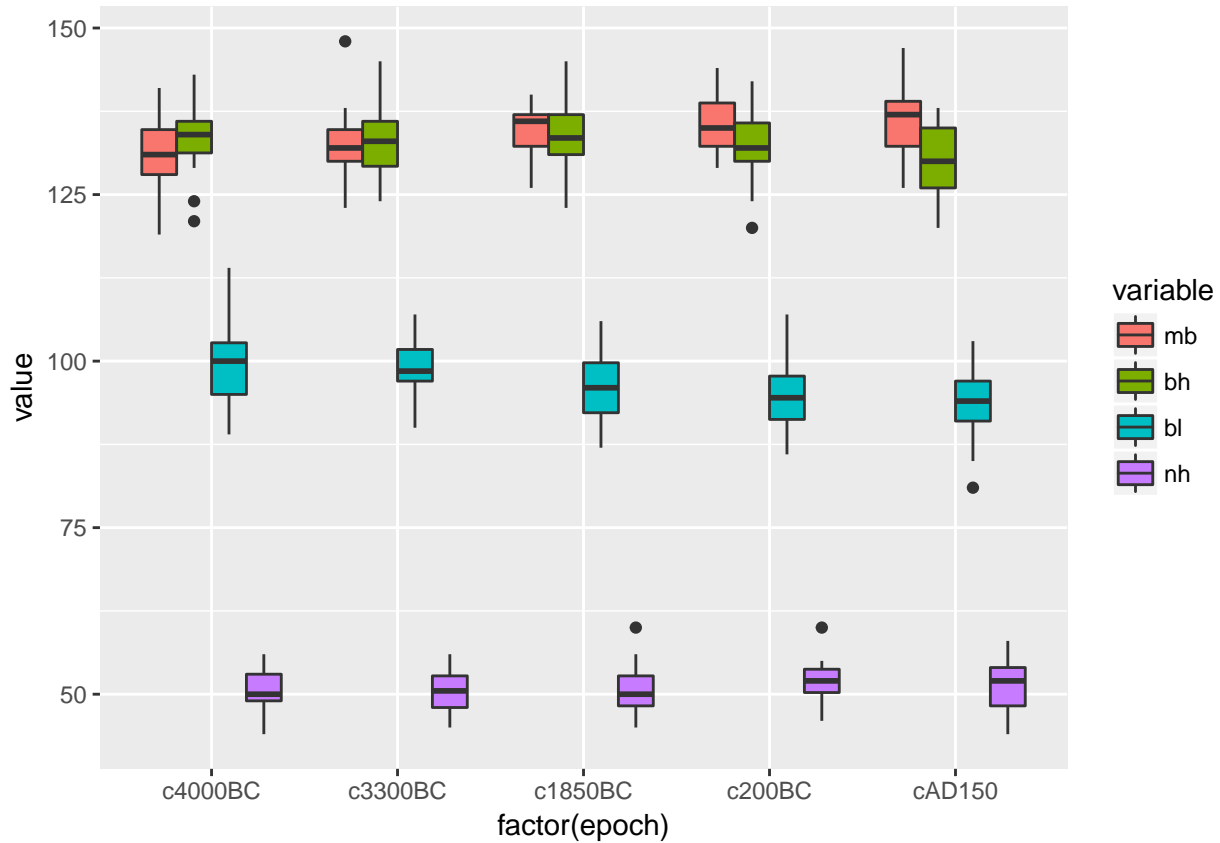




A bivariate normal distribution would be a viable population model. The qqplots do not deviate to much from the straight lines and the scatter plot shows that the points could very well have been generated from a bivariate normal distribution.

Question 3

a)



The nh variables seems to be relatively similar for all epochs. The bl appears to have a difference between the first epoch (c4000BC) and the last one (cAD150). The mb and bh has relatively similar values.

b)

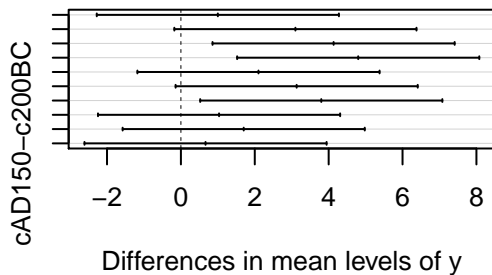
```
#> [1] "Group means"
#> # A tibble: 5 x 5
#>   epoch      mb      bh      bl      nh
#>   <ord>   <dbl>   <dbl>   <dbl>   <dbl>
#> 1 c4000BC 131.3667 133.6000 99.16667 50.53333
#> 2 c3300BC 132.3667 132.7000 99.06667 50.23333
#> 3 c1850BC 134.4667 133.8000 96.03333 50.56667
#> 4 c200BC 135.5000 132.3000 94.53333 51.96667
#> 5 cAD150 136.1667 130.3333 93.50000 51.36667
#>
#>      Df Pillai approx F num Df den Df      Pr(>F)
#> data$epoch    4 0.35331    3.512    16    580 4.675e-06 ***
#> Residuals 145
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

If there is more than one dependent variable, you can test them simultaneously using a multivariate analysis of variance MANOVA. Here is the summary for the manova model using the Pillai's trace as test statistic. There are 3 other test statistics in R but Pillai is considered to be the most reliable of them all and also offers the greatest protection against Type I errors with small sample sizes. Pillai's trace is the sum of the variance which can be explained by the calculation of discriminant variables. It calculates the amount of variance in the dependent variable which is accounted for by the greatest separation of the independent variables.

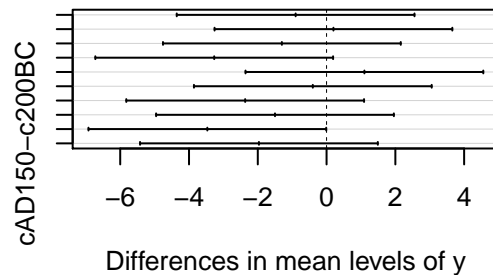
Since the P-value is smaller than 0.05, we reject the hypothesis that the mean between the epochs are equal.

c)

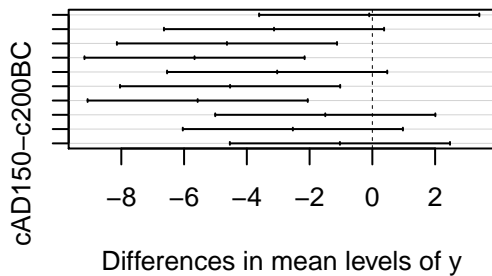
95% family-wise confidence level



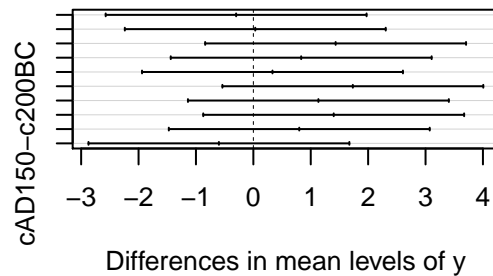
95% family-wise confidence level



95% family-wise confidence level



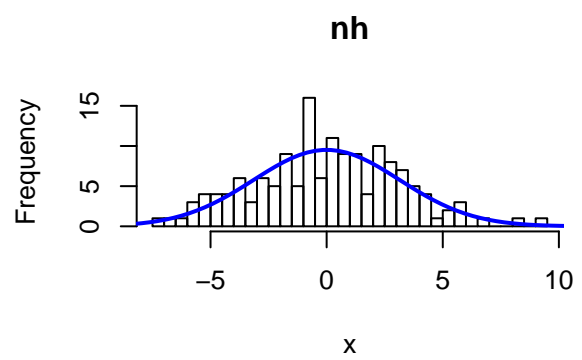
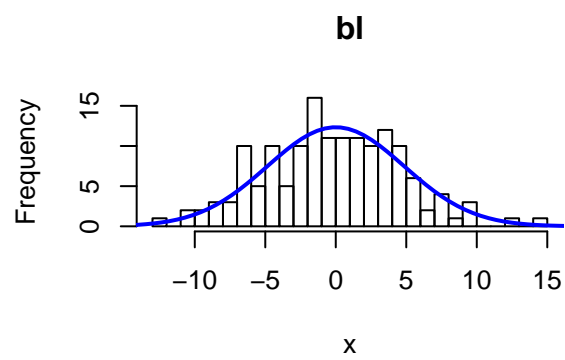
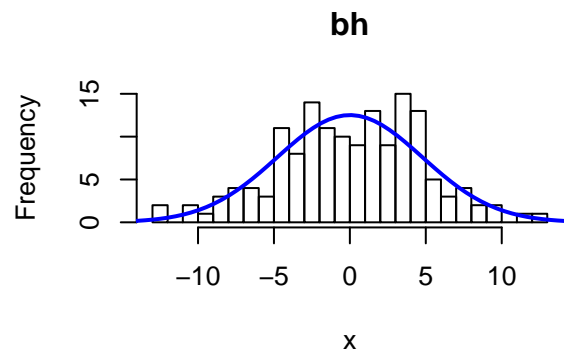
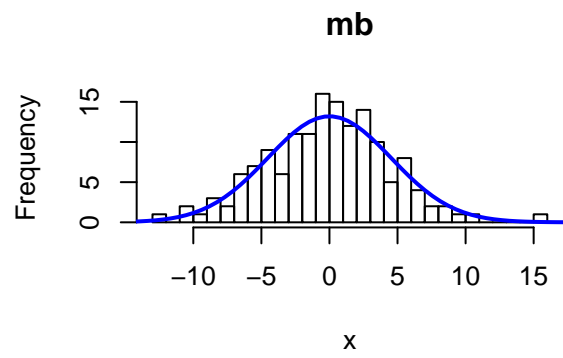
95% family-wise confidence level



```
#> [1] "epoch" "mb"    "bh"    "bl"    "nh"
```

The variables are mb, bh, bl, nh from left to right, top to bottom. In the variable nh (the plot bottom right) there seems to be no difference between the mean nasal heights. For all other variables can see that there exists differences. bh are very close to not having differences between their values. mb and bl seems to have intervals with more or less significant differences.

```
#> [1] "T-square Confidence Intervals"
#>      mb      bh      bl      nh
#> [1,] 132.7147 131.2755 95.076 50.10776
#> [2,] 135.2320 133.8178 97.844 51.75890
```



All of the residuals seems to be normally distributed with a mean zero.

Appendix

Code

```
# Question 1
data <- read.table("../data/T1-9.dat")
names(data) <- c("country", "100m", "200m", "400m", "800m", "1500m", "3000m", "marathon")
numeric_data <- data[, -1]

countries <- as.character(data$country)
X <- as.matrix(numeric_data)
means <- colMeans(X)
covariances <- cov(X)
X_central <- X - rep(1, nrow(X)) %*% t(means)

mdist_sq <- X_central %*% solve(covariances) %*% t(X_central)
country_mdists <- diag(mdist_sq)

significance_level <- 0.001
p <- ncol(X)
quantile <- qchisq(1 - significance_level, df=p)

outliers <- country_mdists > quantile
print("Outliers without correction")
countries[outliers]

bonquantile <- qchisq(1 - significance_level / (2 * p), df=p)
# paste("Critical chisquare value multiple testing corrected", round(bonquantile, 4))
outliers_bon <- country_mdists > bonquantile
print("Outliers with correction")
countries[outliers_bon]

# Question 2

bird <- read.table("../data/T5-12.DAT")

mu <- c(190, 275) #mus
x_bar <- colMeans(bird)
S <- cov(bird)
angles <- seq(0, 2 * pi, length.out=200) # make angles for circle

n <- nrow(bird)
p <- ncol(bird)

confidence_level <- 0.05

## eigenvalues and eigenvectors from covariance matrix S
eigVal <- eigen(S)$values
eigVec <- eigen(S)$vectors

quantile <- qf(1 - confidence_level, df1=p, df2=n - p)
scale <- sqrt(eigVal * p * (n - 1) * quantile / (n * (n - p)))
```



```

scaled <- eigVec %*% diag(scale) # scale eigenvectors to length = square-root

xMat <- rbind(x_bar[1] + scaled[1, ], x_bar[1] - scaled[1, ])
yMat <- rbind(x_bar[2] + scaled[2, ], x_bar[2] - scaled[2, ])
ellBase <- cbind(scale[1]*cos(angles), scale[2]*sin(angles)) # making a circle base...

ellax <- eigVec %*% t(ellBase) # where the ellips axis goes through eigenvectors.
plot(bird, lwd="4", xlab="Tail length", ylab="Wing length", xlim=c(185, 200), ylim=c(270, 290))
lines((ellax + x_bar)[1, ], (ellax + x_bar)[2, ], asp=1, type="l", lwd=2, col="blue")
matlines(xMat, yMat, lty=1, lwd=2, col="green") #
points(mu[1], mu[2], pch=4, col="red", lwd=3)
grid()
points(mean(bird[,1]), mean(bird[,2]), type="p", col="red", pch=15)
compute_tsq_intervals <- function(data, confidence=0.05) {
  n <- nrow(data)
  p <- ncol(data)
  x_bar <- colMeans(data)
  S <- cov(data)

  offset <- sqrt(p * (n - 1) * qf(1 - confidence, df1=p, df2=n - p) / (n - p) * diag(S) / n)
  rbind(x_bar - offset, x_bar + offset)
}

compute_bonferroni_intervals <- function(data, confidence=0.05) {
  n <- nrow(data)
  p <- ncol(data)
  x_bar <- colMeans(data)
  S <- cov(data)

  offset <- sqrt(diag(S) / n * qt(1 - confidence / (2 * p), df=n - 1)
  rbind(x_bar - offset, x_bar + offset)
}

tsq_intervals <- compute_tsq_intervals(bird, confidence_level)
bon_intervals <- compute_bonferroni_intervals(bird, confidence_level)

# Question 3
library(heplots)
library(dplyr)
library(ggplot2)
library(reshape2)

data <- Skulls
numeric_data <- data[, -1]
colors <- as.numeric(data$epoch)
# pairs(numeric_data, col=colors)
mm <- melt(data, id="epoch")
ggplot(mm) +
  geom_boxplot(aes(x=factor(epoch), y=value, fill=variable))
group_means <- data %>%
  group_by(epoch) %>%
  summarise_all(funs(mean(., na.rm=TRUE)))

```

```
print("Group means")
group_means

fit <- manova(cbind(mb, bh, bl, nh) ~ data$epoch, data)
summary(fit)
```