Multivariate Statistical Methods

Assignment 2

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Question 1

```r
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)
```

a)

Consider again the data set containing National track records for women. In lab 1 we studied different distance measures between an observation and the mean vector. The most common multivariate residual is the Mahalanobis distance and we computed this distance for all 54 observations. a) The Mahalanobis distance has an approximate chi square distribution, if the data come from a multivariate normal distribution and the number of observations is fairly large. Use the approximate chi square distribution for testing each observation at significance level 0.1 %, and conclude which countries can be regarded as outliers.

```r
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_mdist <- diag(mdist_sq)

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

outliers <- country_mdist > quantile
print("Outliers without correction")
#> [1] "Outliers without correction"
countries[outliers]
#> [1] "KORN" "PNG"  "SAM"

bonquantile <- qchisq(1 - significance_level / (2 * p), df=p)
paste("Critical chisquare value multiple testing corrected", round(bonquantile, 4))
#> [1] "Critical chisquare value multiple testing corrected 30.673"
outliers_bon <- country_mdist > bonquantile
print("Outliers with correction")
#> [1] "Outliers with correction"
countries[outliers_bon]
#> [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.

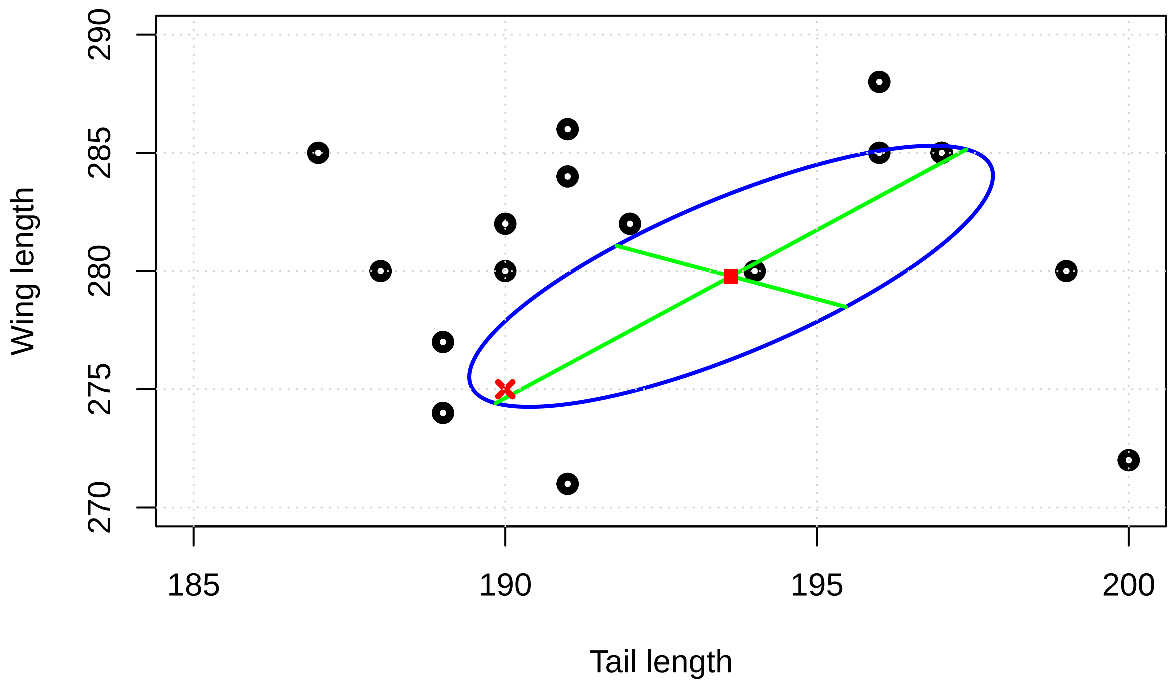
b)

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)

```
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 eigvactors 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)
```



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)

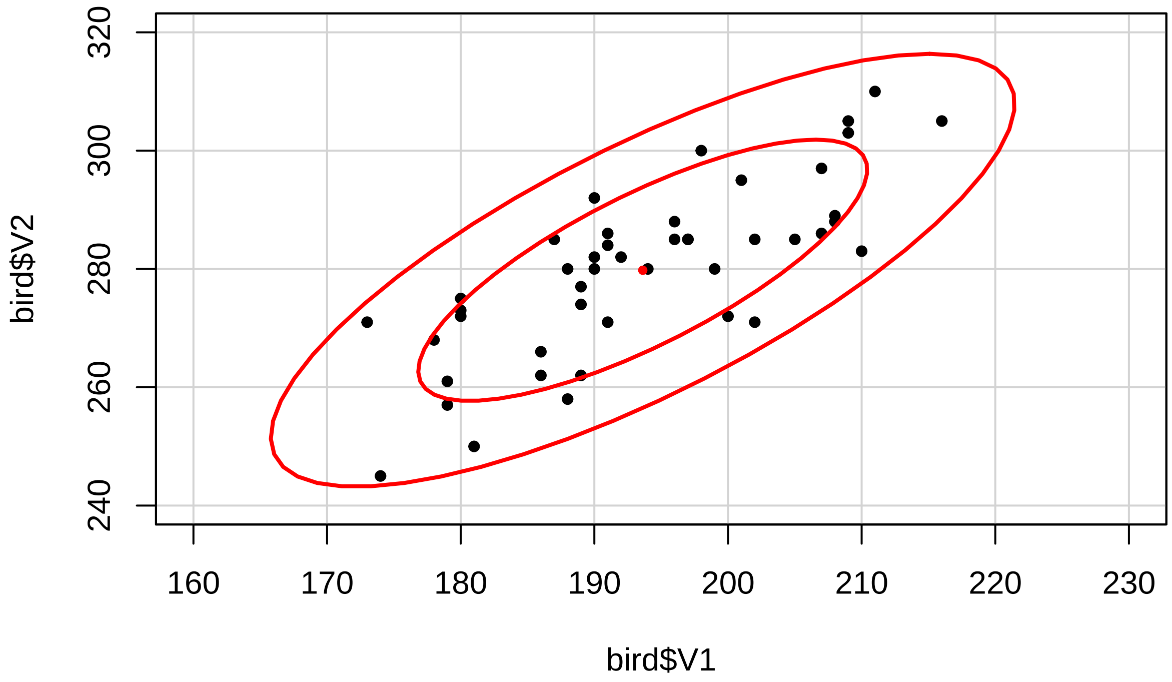
```
compute_tsq_intervals <- function(data, confidence=0.05) {
    n <- nrow(data)
    p <- ncol(data)
    x_bar <- colMeans(data)
    S <- cov(data)

    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)
}
```

```
print("T-square Confidence Intervals")
#> [1] "T-square Confidence Intervals"
compute_tsq_intervals(bird, confidence_level)
#>            V1       V2
#> [1,] 189.4217 274.2564
#> [2,] 197.8227 285.2992

print("Bonferroni Confidence Intervals")
#> [1] "Bonferroni Confidence Intervals"
compute_bonferroni_intervals(bird, confidence_level)
#>            V1       V2
#> [1,] 189.8216 274.7819
#> [2,] 197.4229 284.7736
```

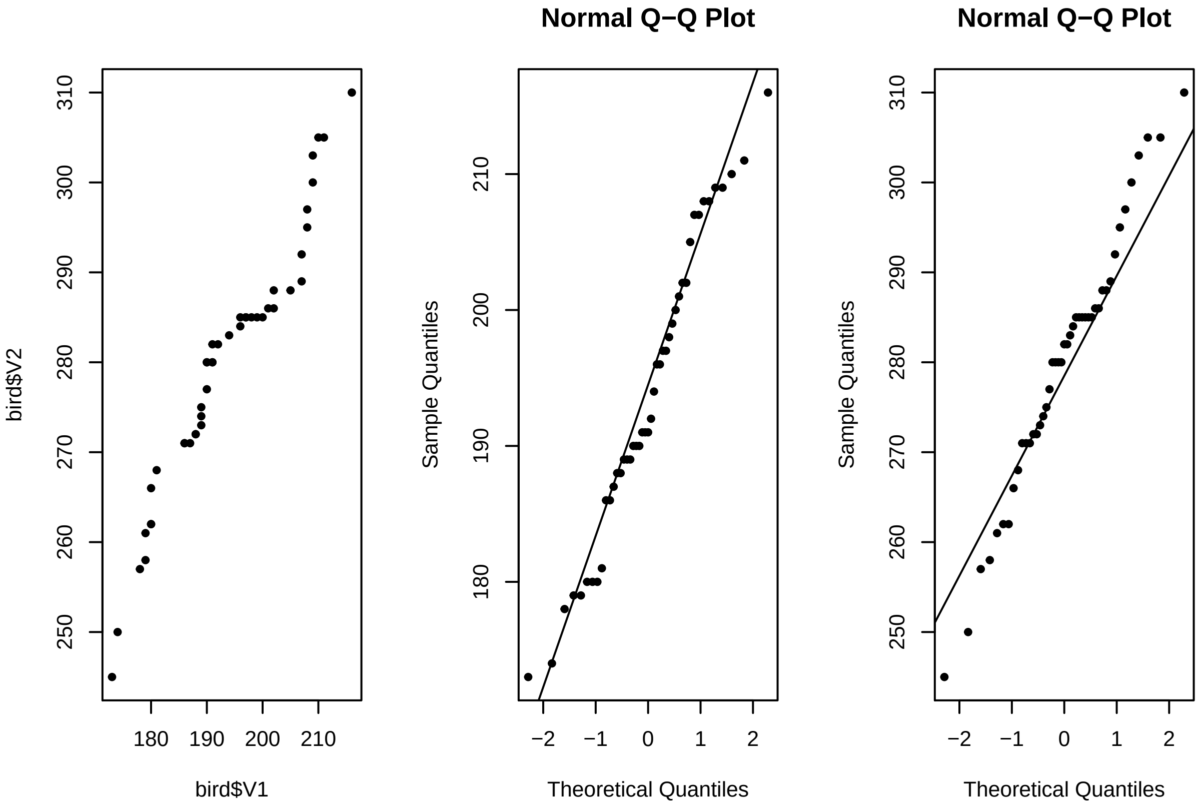
T-square test always gives wider confidence intervals since it takes the correlation between the measured variables into account. Bonferroni intervals are more precise if you are interested in the individual component means, but if you are interested in the overall data mean you should consider the T-square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

c)

```
library(car)

dataEllipse(x=bird$V1, y=bird$V2, pch=20, levels=c(0.68, 0.95),
            xlim=c(160, 230), ylim=c(240, 320), center.cex=0.5)
```



```
old <- par(mfrow=c(1, 3))
qqplot(bird$V1, bird$V2, pch=20)
qqnorm(bird$V1, pch=20)
qqline(bird$V1)
qqnorm(bird$V2, pch=20)
qqline(bird$V2)
```



```
par(old)
```

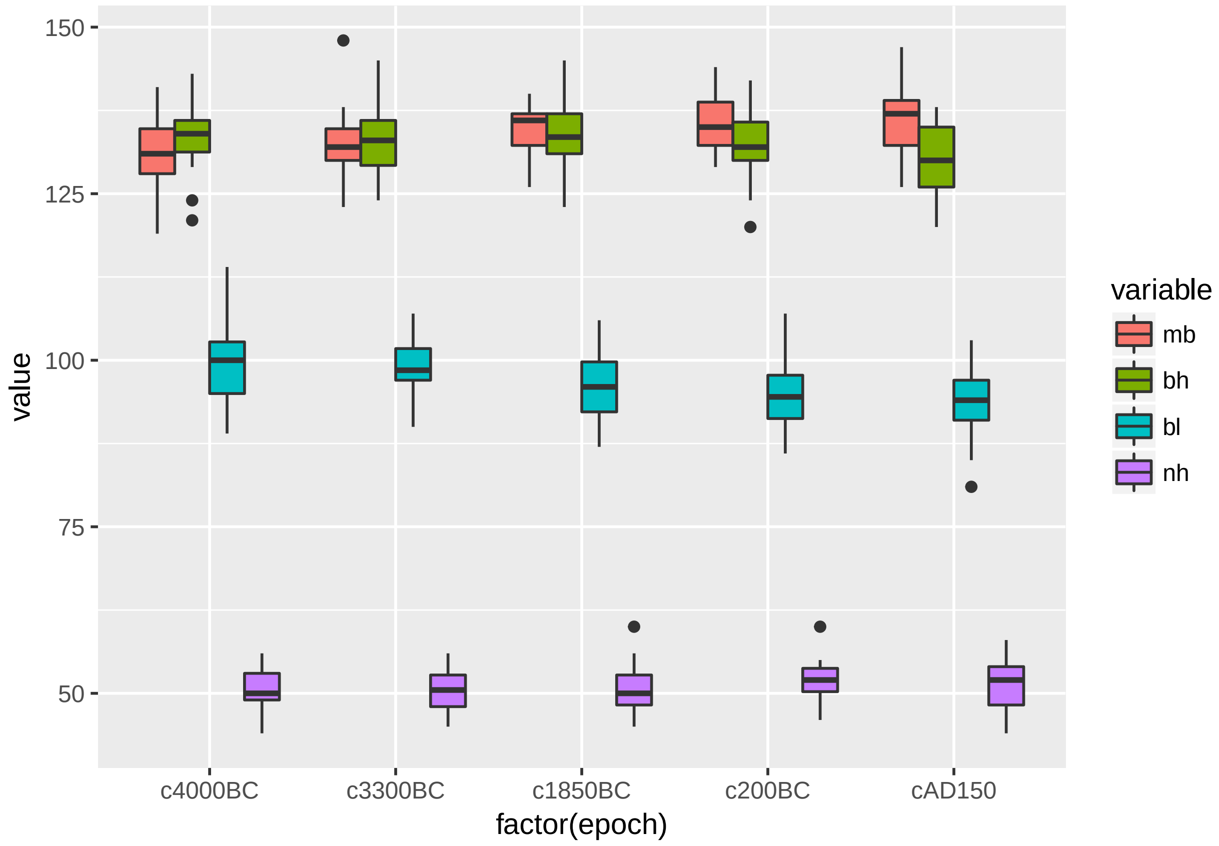
A bivariate normal distribution would be a viable population model. The qqplots do not deviate to much from the straight lines and the scatter plot shows that the points could very well have been generated from a bivariate normal distribution.

Question 3

```
library(heplots)
library(dplyr)
library(ggplot2)
library(reshape2)

data <- Skulls
numeric_data <- data[, -1]
colors <- as.numeric(data$epoch)
```

a)

```
# pairs(numeric_data, col=colors)
mm <- melt(data, id="epoch")
ggplot(mm) +
    geom_boxplot(aes(x=factor(epoch), y=value, fill=variable))
```



b)

```
group_means <- data %>%
    group_by(epoch) %>%
    summarise_all(funs(mean(., na.rm=TRUE)))

print("Group means")
#> [1] "Group means"
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

fit <- manova(cbind(mb, bh, bl, nh) ~ data$epoch, data)
summary(fit)
#>              Df  Pillai approx F num Df den Df    Pr(>F)
#> data$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
```

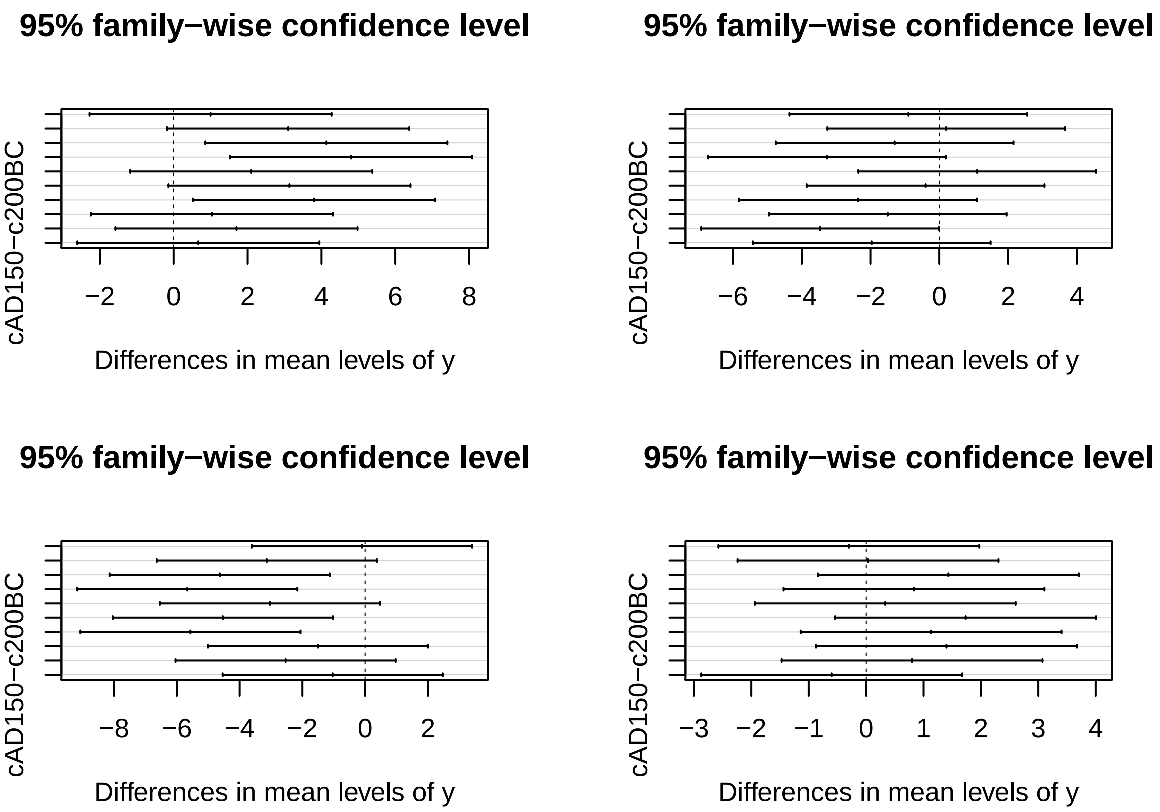
If there is more than one dependent variable, you can test them simultaneously using a multivariate analysis of variance MANOVA. Here is the summary for the manova model using the Pillai's trace as test statistic. There are 3 other test statistics in R but Pillai is considered to be the most reliable 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.

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

```
X <- as.matrix(data[,2:5])
y <- as.factor(data[,1])

old <- par(mfrow=c(2,2))

compareX1 = aov(X[,1] ~ y)
plot(TukeyHSD(compareX1))

TukeyHSD(compareX1)$y[2,]
#>        diff         lwr         upr       p adj
#>  3.10000000 -0.17713439  6.37713439  0.07323876
```

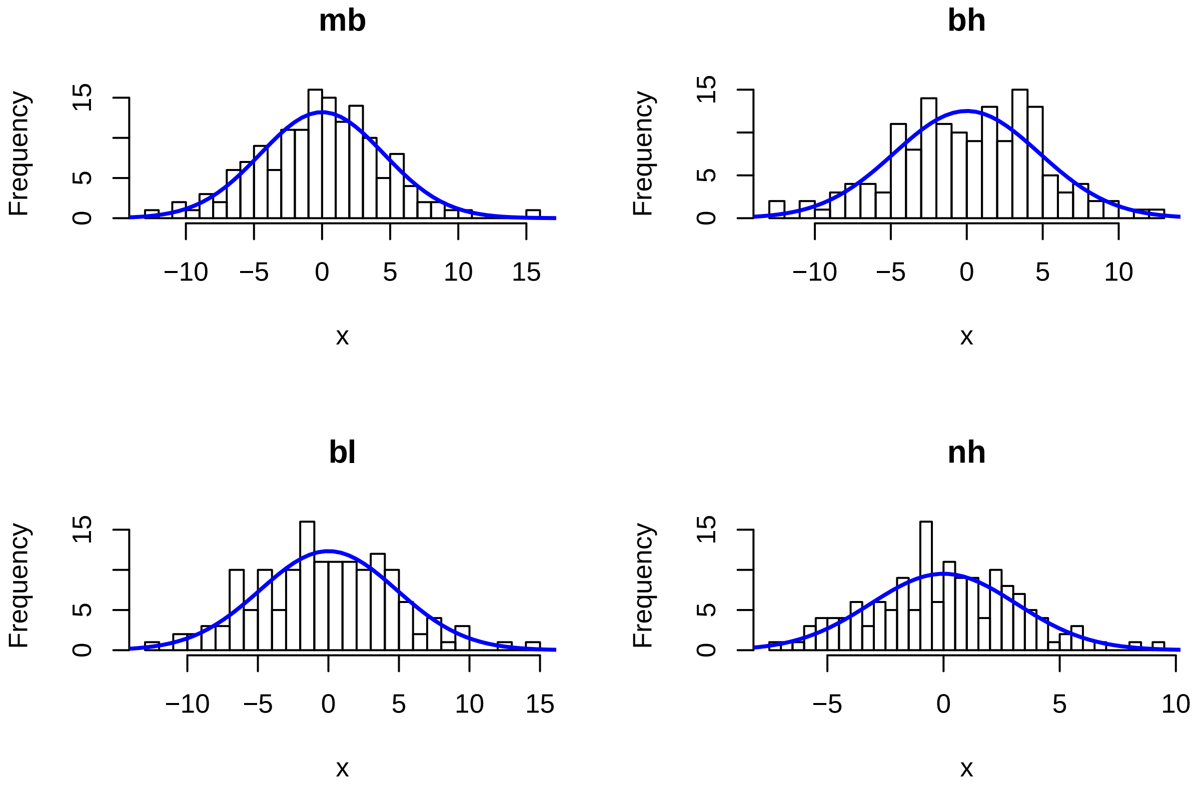
```
compareX2 = aov(X[,2] ~ y)
plot(TukeyHSD(compareX2))

compareX3 = aov(X[,3] ~ y)
plot(TukeyHSD(compareX3))

TukeyHSD(compareX3)$y[2,]
#>       diff        lwr        upr      p adj
#> -3.1333333 -6.6405432  0.3738765  0.1037609

compareX4 = aov(X[,4] ~ y)
plot(TukeyHSD(compareX4))
```



```
par(old)
```

c)

```
residuals <- fit$res
col_names <- c("mb", "bh", "bl", "nh")

old <- par(mfrow=c(2, 2))

for (col in 1:ncol(residuals)) {
    x <- residuals[, col]
    main <- col_names[col]
    h <- hist(x, breaks=25, main=main)
    offset <- (max(x) - min(x)) / 2
    xfit <- seq(min(x) - offset, max(x) + offset, length = 100)
    yfit <- dnorm(xfit, mean = mean(x), sd = sd(x))
    yfit <- yfit * diff(h$mids[1:2]) * length(x)
    lines(xfit, yfit, col="blue", lwd=2)
}
```



```
par(old)
```

Appendix

Code

```r
# 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_mdist <- diag(mdist_sq)

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

outliers <- country_mdist > 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_mdist > 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 eigvactors 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)
}

print("T-square Confidence Intervals")
compute_tsq_intervals(bird, confidence_level)

print("Bonferroni Confidence 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))
```

```r
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)
```