MS Lab 2

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Contents

1 Question 1: Test of outliers

Consider again the data set from the T1-9.dat file, National track records for women. In the first assignment we studied different distance measures between an observation and the sample average vector. The most common multivariate residual is the Mahalanobis distance and we computed this distance for all observations.

1.1 Conclude which countries can be regarded as outliers

The Mahalanobis distance is approximately chi–square distributed, if the data comes from a multivariate normal distribution and the number of observations is large. Use this chi– square approximation for testing each observation at the 0.1% significance level and conclude which countries can be regarded as outliers. Should you use a multiple–testing correction procedure? Compare the results with and without one. Why is (or maybe is not) 0.1% a sensible significance level for this task?

```
trackData = read.table("T1-9.dat")

colnames(trackData) = c("Countries", "100m", "200m", "400m", "800m", "1500m", "3000m", "Marathon")
samplesnames = c("100m", "200m", "400m", "800m", "1500m", "3000m", "Marathon")

Mahalanobis = function(obs){
  IdentityMat = diag(54)
  one_n = matrix(1,54,54) #matrix(1,7,1) %*% matrix(1,1,7)

  V = (IdentityMat - (1/54)*(one_n))

  X = as.matrix(obs)
  sample_variance = (t(X) %*% V %*% X)/54

  # sample mean formula from notes
  one = matrix(1, 54,54)
  sample_mean = (one %*% (obs))/54
  Xbar = obs - sample_mean

  ss = (Xbar) %*% solve(sample_variance) %*% t(Xbar)
  vec3 = diag(ss)
  return(vec3)
}
obs = as.matrix(trackData[,2:8])
Mahalanobis_vec = Mahalanobis(obs)
ndf = dim(trackData)[2] - 1 #degrees of freedom

alpha = 0.001 # 0.1% significance level
indices = 1-pchisq(Mahalanobis_vec, df=ndf) < alpha
trackData$Countries[indices]
```

```
## [1] KORN PNG  SAM
## 54 Levels: ARG AUS AUT BEL BER BRA CAN CHI CHN COK COL CRC CZE DEN ... USA
```

1.2 Mahalanobis vs Euclidean

One outlier is North Korea. This country is not an outlier with the Euclidean distance. Try to explain these seemingly contradictory results.

Answer: Euclidean distance only makes sense when all the dimensions have the same units (like meters or minutes in this case), since it involves adding the squared value of them. Unlike the Euclidean distance though, the Mahalanobis distance accounts for how correlated the variables are to one another. Because of high correlation between values, there is a lot of redundant information in that Euclidean distance calculation. By considering the covariance between the points in the distance calculation, we remove that redundancy. When using the Mahalanobis distance, we don't have to standardize the data like we need to do it for the Euclidean distance(which we did not do). The covariance matrix calculation takes care of this in Mahalanobis. Also, it removes redundant information from correlated variables. Even if your variables aren't very correlated it can't hurt to use Mahalanobis distance, it will just be quite similar to the results you'll get from Euclidean.Thus, Mahalanobis distance is almost always better to use than the Euclidean distance for the multivariate case.

source: https://waterprogramming.wordpress.com/2018/07/23/multivariate-distances-mahalanobis-vs-euclidean/

2 Question 2: Test, confidence region and confidence inter- vals for a mean vector

2.1 Find and sketch 95% confidence for Eillpse

Find and sketch 95% confidence for Eillpse for the population mu1=190mm and mu2=275mm for male hook-billed kites. Are these plaussible values for the mean tail length and wing length for the female birds?

```
library(ellipse)
```

```
##
## Attaching package: 'ellipse'

## The following object is masked from 'package:car':
##
##     ellipse

## The following object is masked from 'package:graphics':
##
##     pairs
```

```
birddata = read.table("T5-12.DAT")
# Male hook-billed kites
n = nrow(birddata)
p = dim(birddata)[2]
mu = data.frame("mu1" = 190, "mu2" = 275)
meanVec =NULL
x_bar = NULL
meanMu = NULL
# x - x_bar
x_bar = data.frame("X1" = mean(birddata$V1), "X2" = mean(birddata$V2))

sample_var = function(obs){
  X = as.matrix(obs)
  IdentityMat = diag(nrow(obs))
  one_n = matrix(1,nrow(X),nrow(X))
  # sample var formula from notes
  mix = (IdentityMat - (1/nrow(X)) *(one_n))

  sample_variance = (1/nrow(X)) * (t(X) %*% mix %*% X)
  return(sample_variance)
}

S = sample_var(birddata)
S =  matrix(S, ncol=2, nrow=2)
eigenValVec = eigen(S)
meanMu = as.matrix(x_bar - mu)

# To check if mu is on the confidence region we need to check if t^2 is < F_{n,n-p}

Tsq = n * (meanMu) %*% solve(S) %*% t(meanMu)

F_val =  qf(0.95,df1=p, df=n-p) * (p*(n-1)/(n-p)) #5% significance level

cat("Is T^2 less than F_val? =",Tsq<F_val)
```

```
## Is T^2 less than F_val? = TRUE
```

```
cat("\nThus, we do not reject the NULL Hypothesis(H_0)")
```

```
##
## Thus, we do not reject the NULL Hypothesis(H_0)
```

```
# We conclude that it is in the region as  Tsq is less than F_val

axes_len = function(lam,n,p){
  sqrt(lam)* sqrt((p*(n-1))/ (n*(n-p)) * qf(0.95,df1=p, df2=(n-p)))
}

l1=axes_len(lam=eigenValVec$values[1],n=n,p=p)
l2=axes_len(lam=eigenValVec$values[2],n=n,p=p)

# plot(birddata)
# lines(ellipse(mu, S, npoints = 200))
# dataEllipse(birddata,levels=.95)
# length(c(mu$mu1,mu$mu2))
```

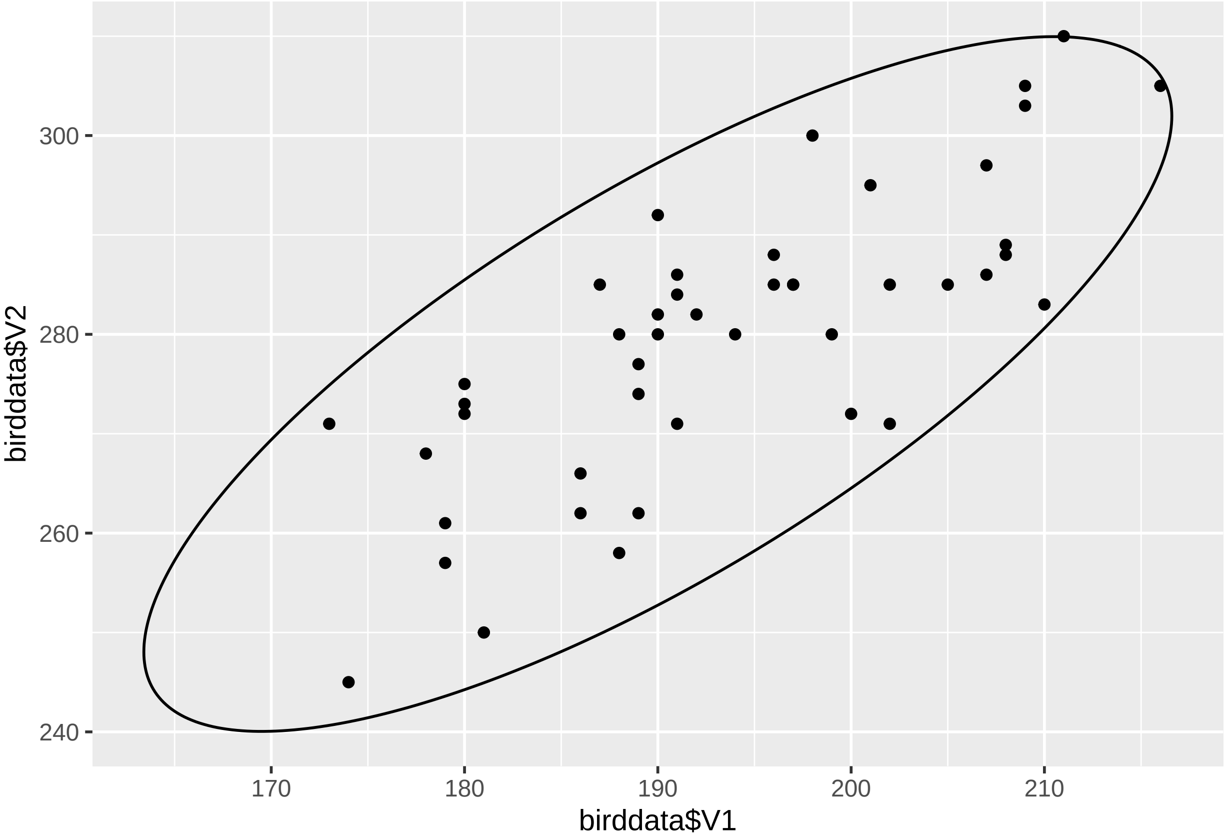
Are these plaussible values for the mean tail length and wing length for the female birds? **Answer** It is quite plaussible as female hook-billed vary a lot in size just like the male hook-billed. Sometimes the juveniles are bigger than the size than they are supposed to be. And thus the mean size of tail length and wing length could be same for the female hook-billed kites.

```
rotate = function(a,b,c){
  res = list()

  if (b==0 & a >= c){res$angle = 0}
  else if (b==0 & a<c) { res$angle = (pi/2)}
  else{ res$angle = atan2(eigenValVec$values[1]-a, b)}

  res$lam1 = (a+c)/2 + sqrt(((a-c)/2)^2 + b^2)
  res$lam2 = (a+c)/2 - sqrt(((a-c)/2)^2 + b^2)

  return(res)
}
# S = matrix(c(4,-2,-2,4),byrow = T, nrow = 2)
res = rotate(S[1,1],S[1,2],S[2,2])
```

```
chi95<-qchisq(.95,df=2)
axes95 <- sqrt(eigenValVec$values) * sqrt(chi95)


library(ggforce)
```

```
## Warning: package 'ggforce' was built under R version 3.5.2
```

```
ggplot()+
  geom_point(aes(birddata$V1, birddata$V2))+
  geom_ellipse(aes(x0=mu$mu1,y0=mu$mu2, a=axes95[1], b=axes95[2], angle = res$angle ))
```



```
# Simultaneous T2-intervals for the component means as shadows of the confidence ellipse on the axes

fsqrt = function(i){
  return(sqrt(p*(n-1)/ ((n-p)) * qf(0.95,df1=p, df=n-p)) * sqrt(S[i,i]/n))
}

CI = NULL
CI$Lower = (x_bar$X1) - fsqrt(1)
CI$Upper =(x_bar$X1) + fsqrt(1)
CI = as.data.frame(CI)
temp = c ((x_bar$X2) - fsqrt(2), (x_bar$X2) + fsqrt(2))
CI = rbind(CI, temp)
rownames(CI) = c("Mu_1_tail","Mu_2_wing")
# kableExtra::kable(CI)
CI
```

```
##              Lower    Upper
## Mu_1_tail 189.4687 197.7758
## Mu_2_wing 274.3180 285.2375
```

```
# Bonferroni's Confidence intervals
set.seed(12345)
ben_alpha = 0.95
Ber_CI = NULL
Ber_CI$Lower = x_bar$X1 - abs(qt(0.05/2*p, df=n-1))  * sqrt(S[1,1]/n)
Ber_CI$Upper= x_bar$X1 + abs(qt(0.05/2*p, df=n-1) ) * sqrt(S[1,1]/n)
Ber_CI = as.data.frame(Ber_CI)
temp = c(x_bar$X2 - abs(qt(0.05/2*p, df=n-1) ) * sqrt(S[2,2]/n),
         x_bar$X2 + abs(qt(0.05/2*p, df=n-1) ) * sqrt(S[2,2]/n))

Ber_CI = rbind(Ber_CI, temp)
rownames(Ber_CI) = c("Mu_1_tail", "Mu_2_wing")
Ber_CI
```

```
##              Lower    Upper
## Mu_1_tail 190.9012 196.3432
## Mu_2_wing 276.2011 283.3544
```

T^2 simultaneous CI is slightly wider than Bonferroni Intervals. Bonferroni method provides shorter intervals when m = p. Because they are easy to apply and provide the relatively short confi- dence intervals needed for inference.

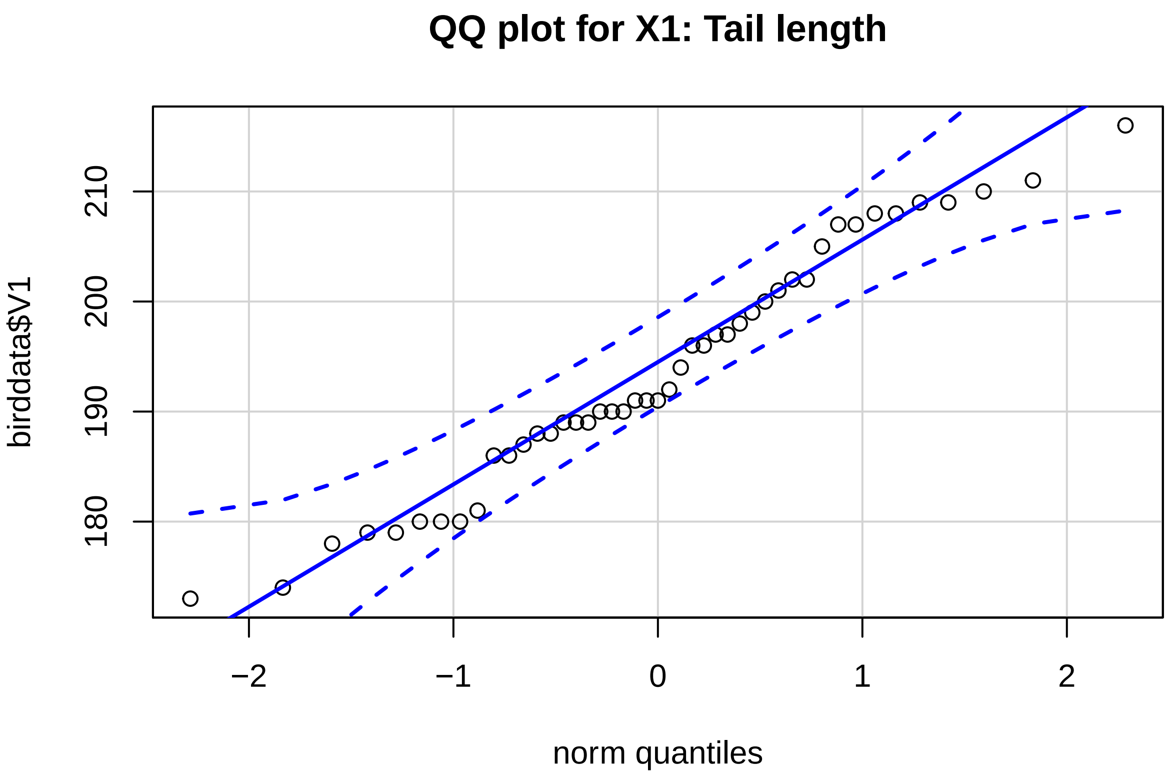
source: Applied multivariate Statistical Analysis - Pearson edition 2014

2.2 Q-Q plots and scatter plots

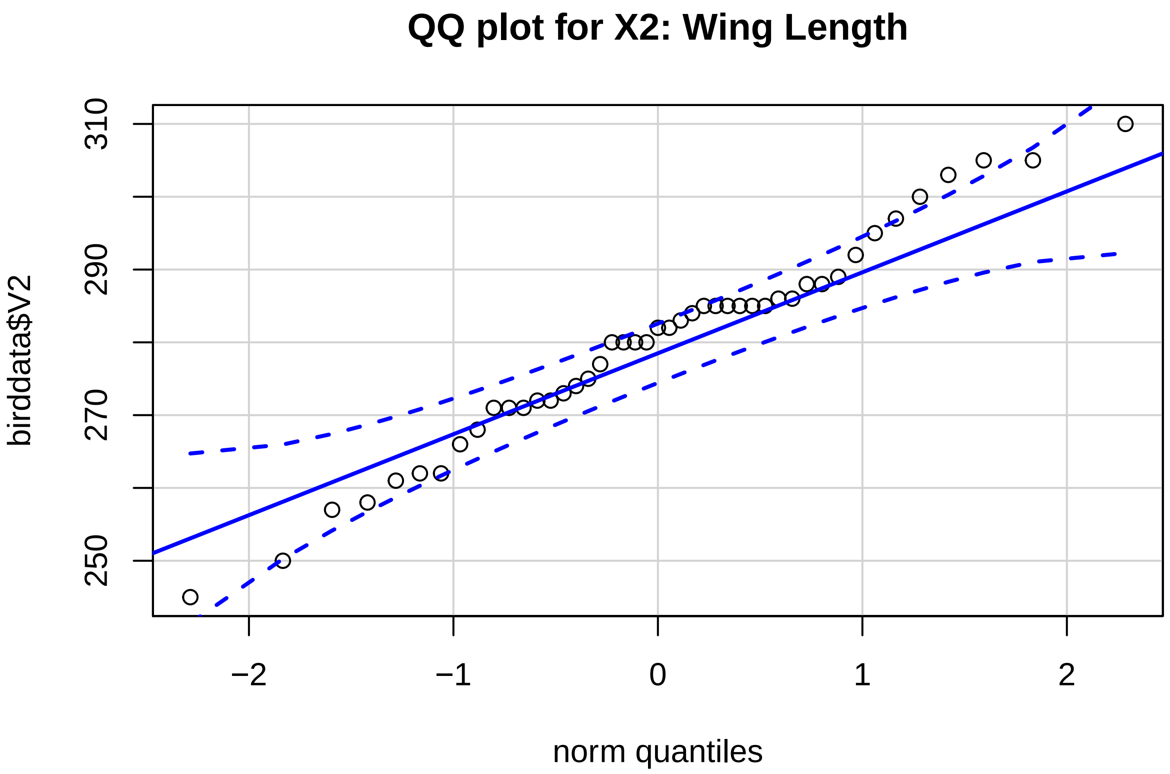
```
library(CARS)
```

```
## Warning: package 'CARS' was built under R version 3.5.2
```

```
qqPlot(birddata$V1, main ="QQ plot for X1: Tail length",id=F  )
```

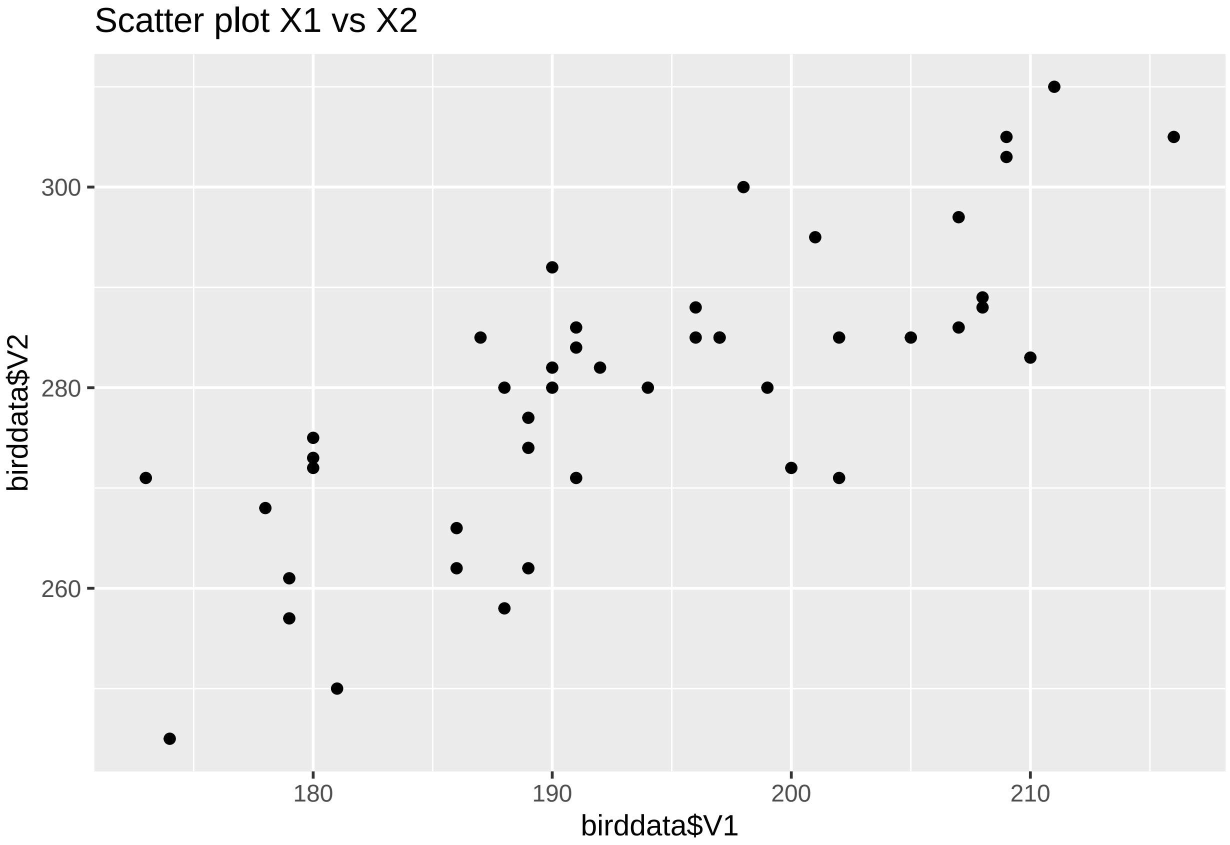


```
qqPlot(birddata$V2, main="QQ plot for X2: Wing Length",id=F )
```



```
Scat = ggplot()+
  geom_point(aes(x=birddata$V1,y=birddata$V2))+
  ggtitle(label = "Scatter plot X1 vs X2")
```

```
plot(Scat)
```



3 Question 3: Comparison of mean vectors (one–way MANOVA)

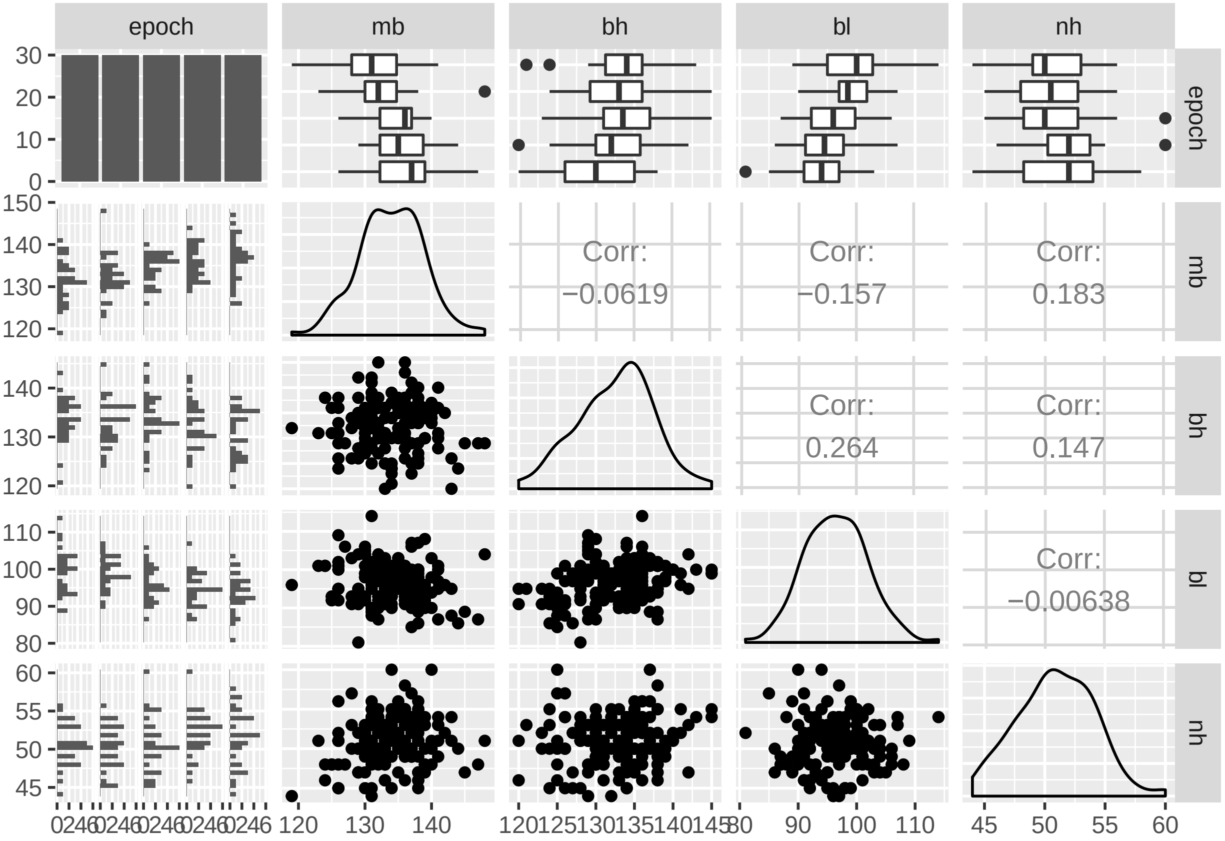
We will look at a data set on Egyptian skull measurements (published in 1905 and now in heplots R package as the object Skulls). Here observations are made from five epochs and on each object the maximum breadth (mb), basibregmatic height (bh), basialiveolar length (bl) and nasal height (nh) were measured.

3.1 Explore the data first and present plots that you find informative.

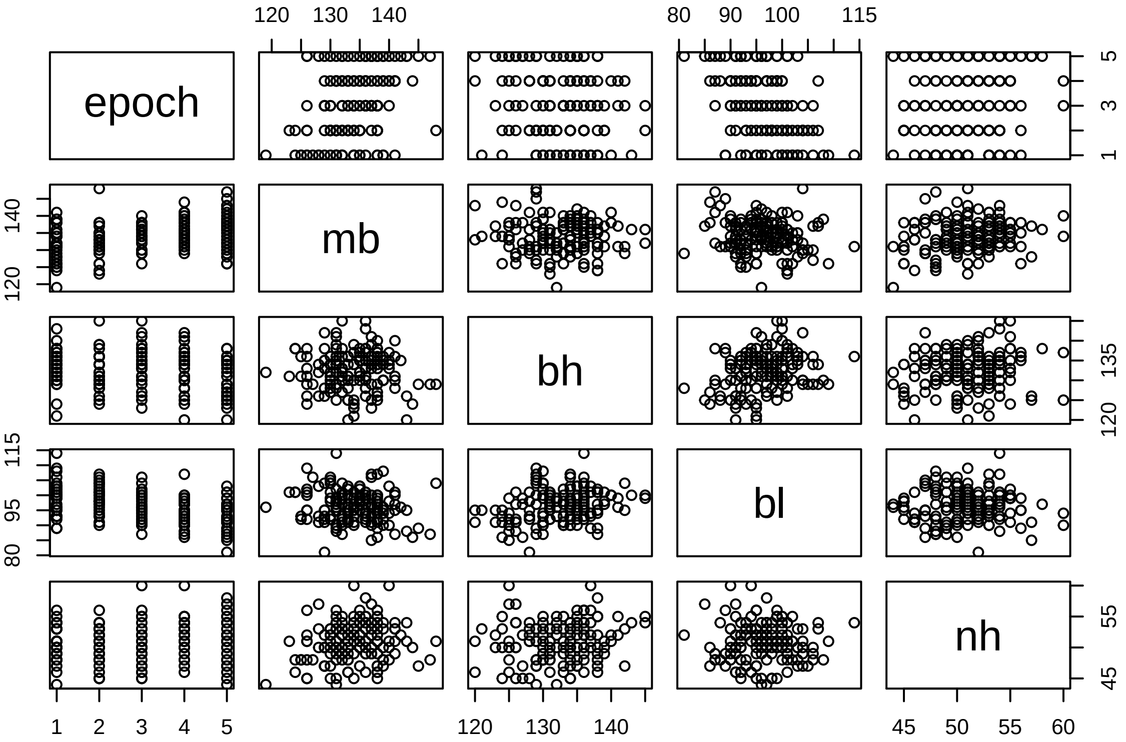
```
data("Skulls")


# summary(mann, test = "Wilks")
# mann
# Manova(data=(Skulls[,2:5]), group=Skulls$epoch,method = "Wilks", alpha=0.05,CI=TRUE)
#one-way manova
# summary(Anova(lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)))
# mann$residuals


mann = manova(cbind(mb,bh,bl, nh)~epoch, data = Skulls)
summary.aov(mann)
```

```
##  Response mb :
##              Df  Sum Sq Mean Sq F value    Pr(>F)
## epoch         4  502.83 125.707  5.9546 0.0001826 ***
## Residuals   145 3061.07  21.111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response bh :
##              Df Sum Sq Mean Sq F value  Pr(>F)
## epoch         4  229.9  57.477  2.4474 0.04897 *
## Residuals   145 3405.3  23.485
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response bl :
##              Df Sum Sq Mean Sq F value    Pr(>F)
## epoch         4  803.3 200.823  8.3057 4.636e-06 ***
## Residuals   145 3506.0  24.179
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response nh :
##              Df Sum Sq Mean Sq F value Pr(>F)
## epoch         4   61.2  15.300   1.507 0.2032
## Residuals   145 1472.1  10.153
```

```
ggpairs(Skulls)
```



```
pairs(Skulls)
```



```
# Simultaneous Confidence Intervals for Manova

#Groups or g = unique(Skulls$epoch)
```