Assignment 2

Mohsen Pirmoradiyan, Ahmed Alhasan, Asad Enver, Ali Etminan, Mubarak Hussain

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Question 1: Test of outliers

```
## $Outliers
##   SAM   PNG  KORN
## 35.01 30.51 26.17
```

```
## $`Outliers after adjustment`
##   SAM   PNG
## 35.01 30.51
```

a)

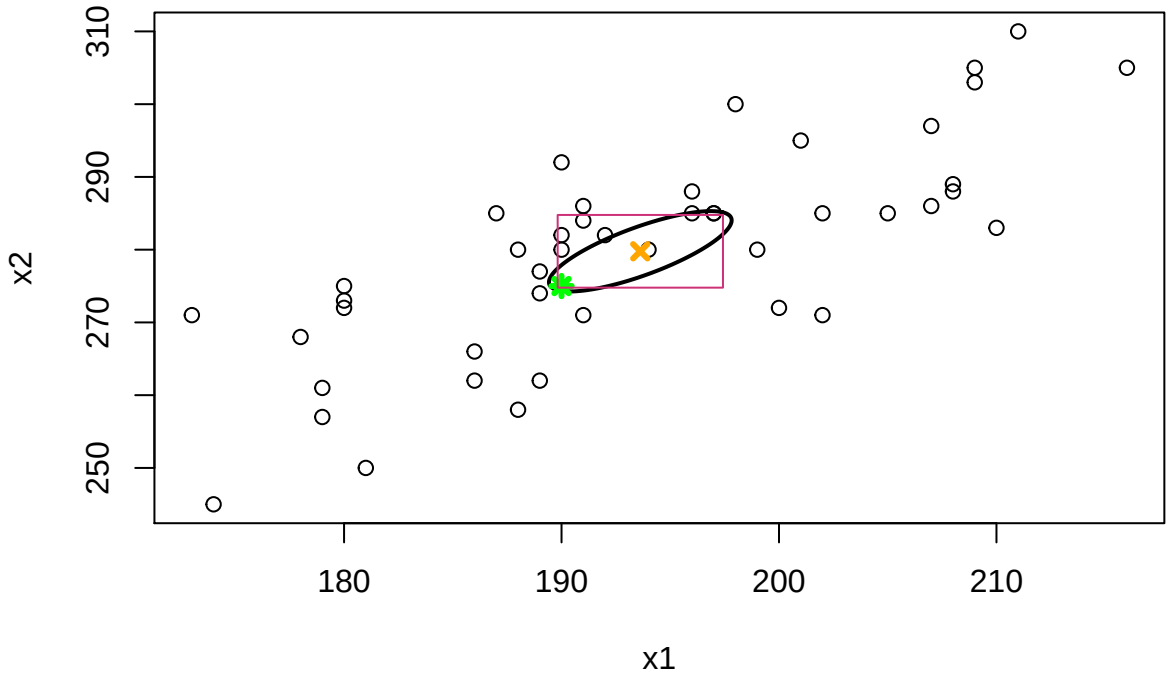
- Because confidence interval 0.001 means that there's a 0.1% chance of getting outliers, and because we are testing outliers in different races (7) there is a chance of getting different results with this threshold.
- Therefore, it is adviseable to do multiple testing correction. The simplest method to do this is Bonferroni adjustment which divide alpha by the number of tests (in this case 7)
- 0.1% is reasonable enough to reduce the change in getting different results, since there is trade off between not classifying any country as outlier (using low alpha) and capturing many outliers but with different results from different races (using high alpha)

b)

- Because the distribution of the records between each two races are in elipsoid shape its wise to use Mahalanobis to measure the distance for such distribution, however Mahalanobis penalize the distance on the short axis (or it give less weight to distances along the long axis) and because North Korea lies further way on the short axis it is treated as far as a country with longer distance from the center of the elipse but on the long axis.

Question 2: Test, confidence region and confidence intervals for a xbar vector

a)



The orange cross is the mean of sample and the green point is the location of μ_0. As it is clear the point is inside the ellipse, therefor this vector contains a plausible vlues for mesn.

- Because T^2 is smaller than the citical value at $\alpha = 5\%$ we can not reject the null hypotheses and we can conclude that the population means of the male birds are plausible means for the female birds.

b)

The related T^2 and $Benferroni$ intervals for μ_1:

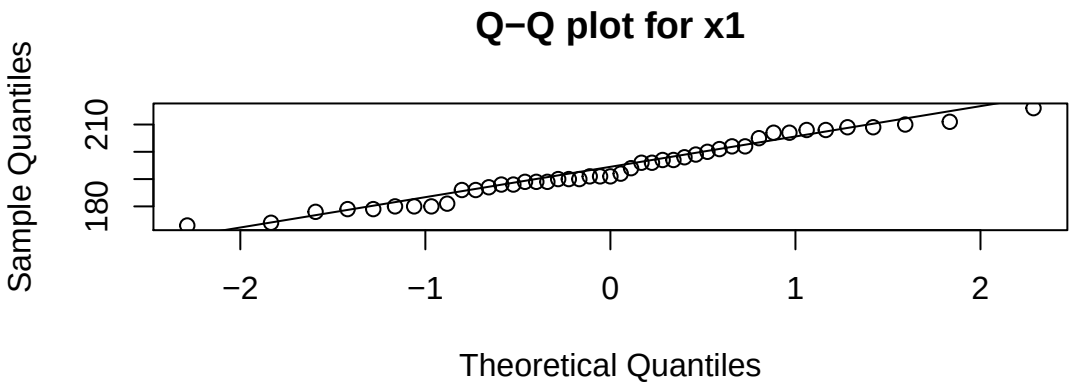
```
##      T2_mu1_Lo T2_mu1_Hi Bon_mu1_Lo Bon_mu1_Hi
## [1,]  189.4217  197.8227   189.8216   197.4229
```

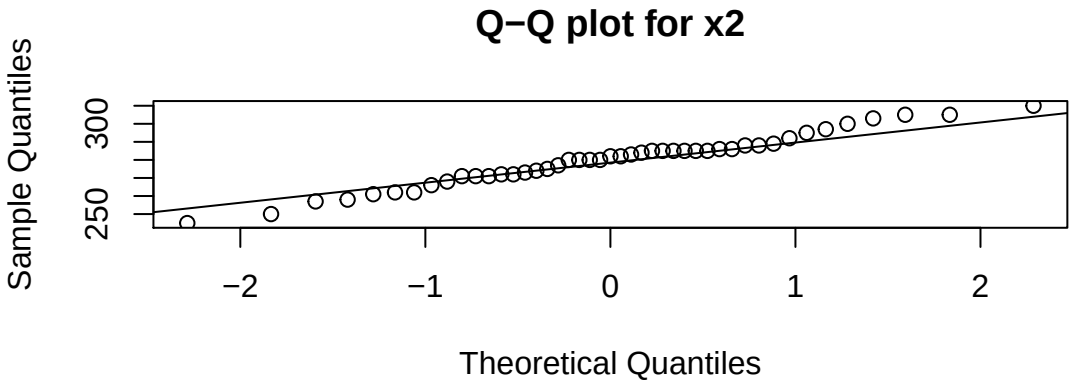
The related T^2 and $Benferroni$ intervals for μ_2:

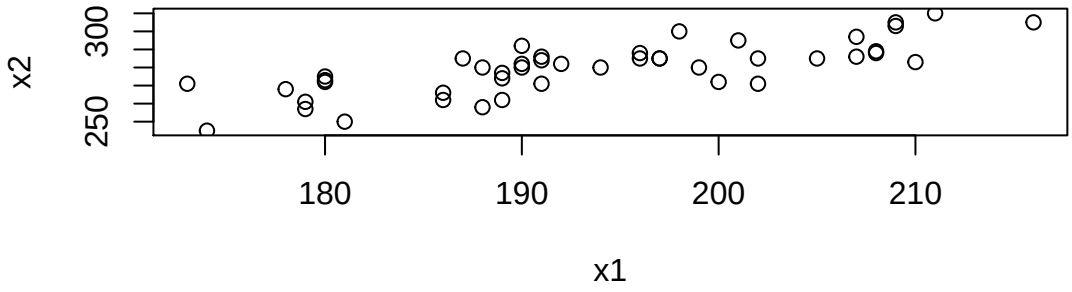
```
##      T2_mu2_Lo T2_mu2_Hi Bon_mu2_Lo Bon_mu2_Hi
## [1,]  274.2564  285.2992   274.7819   284.7736
```

As it can be identified from these values the Benferron intrvals are shorter than those calculted from T^2. Refer to the book: "The simultaneous confidence intervals(T^2) are ideal for "data snooping." The confidence coefficient $1 - \alpha$ remains unchanged for any choice of $\mathbf{a}$, so linear combinations of the components μ_i that merit inspection based upon an examination of the data can be estimated.

c)







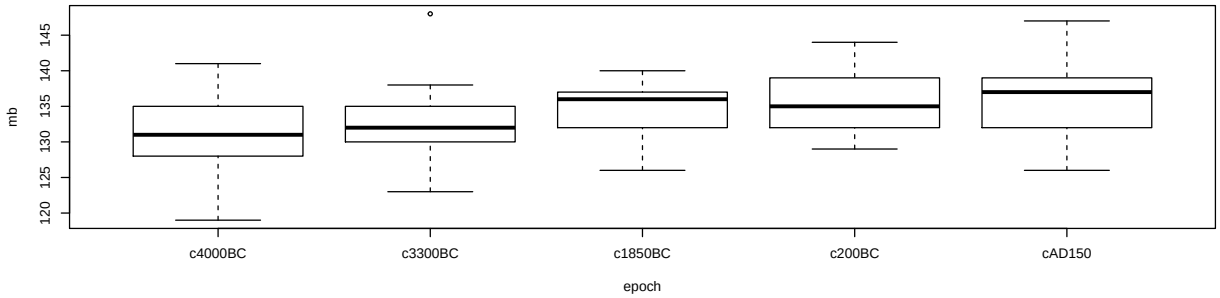
The Q-Q plot for both variables (x_1 & x_2) illustrate a linear trend. The scatterplot of two variables also indicates a linear relationship between these two features. These linear trends can lead us to this conclusion that the population can be considered as normal.

Question 3: Comparison of xbar vectors (one{way MANOVA)

```
# fit manova model
sk.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
sk.mod
```

```
##
## Call:
## lm(formula = cbind(mb, bh, bl, nh) ~ epoch, data = Skulls)
##
## Coefficients:
##              mb         bh         bl         nh
## (Intercept)  133.97333  132.54667   96.46000   50.93333
## epoch.L        4.02663   -2.19251   -5.01748    1.07517
## epoch.Q       -0.46325   -1.26504   -0.08909    0.12472
## epoch.C       -0.46380   -0.78003    1.07517   -0.83273
## epoch^4        0.34263    0.80479   -0.66136   -0.41833
```

Boxplots:


mb
120
125
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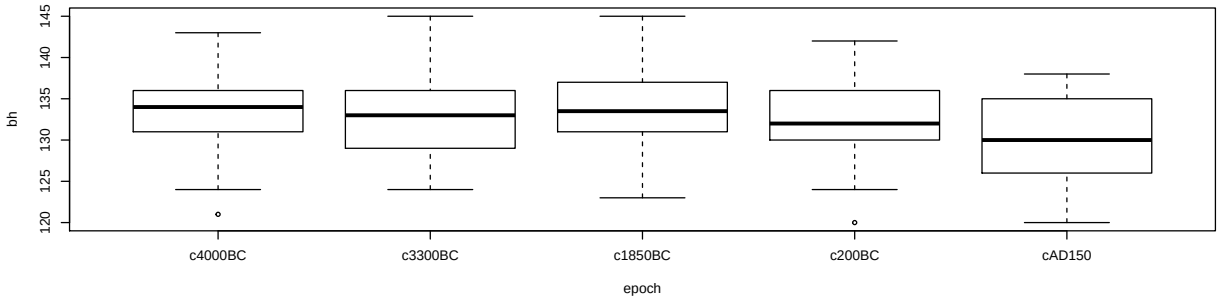
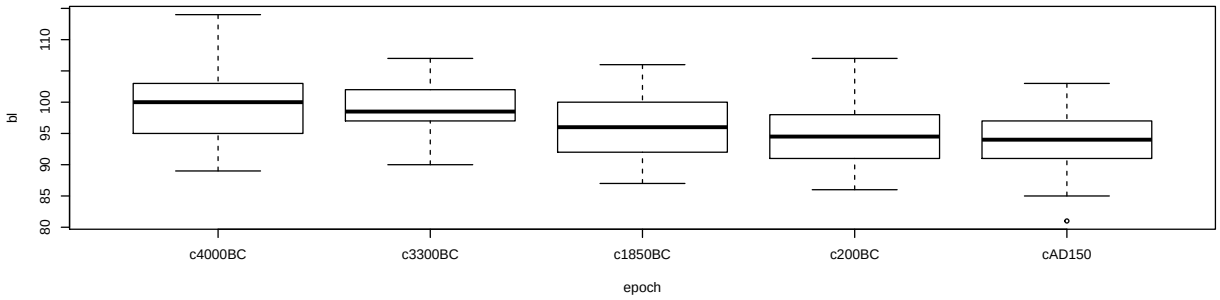
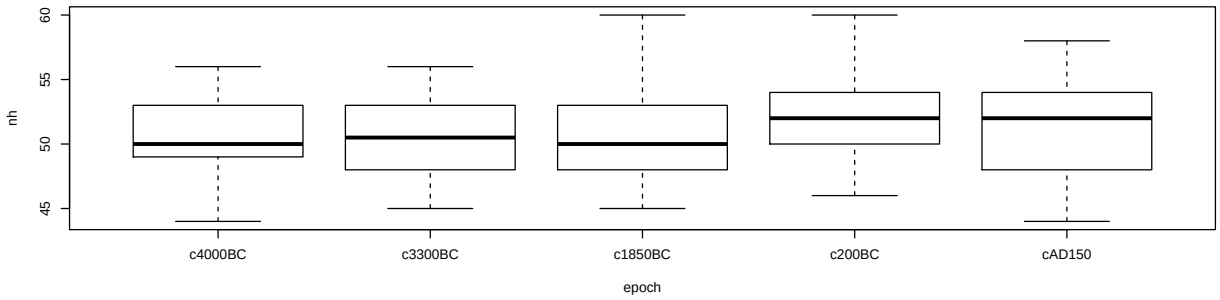
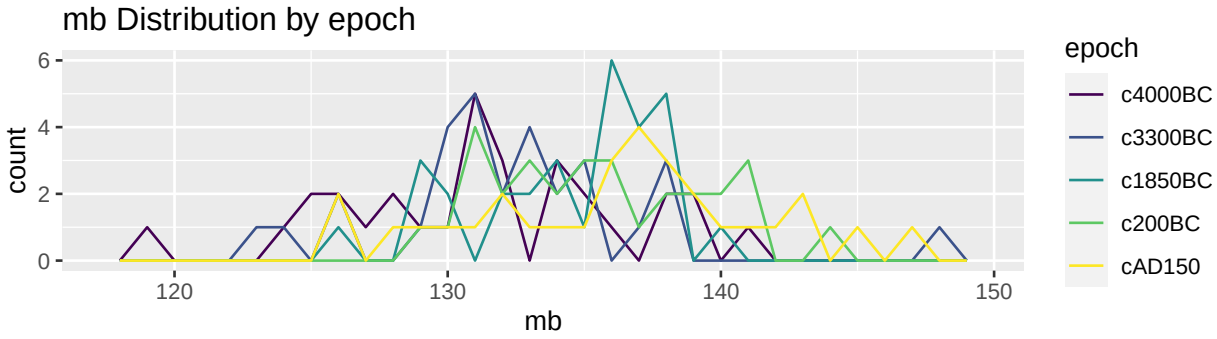
135
140
145
c4000BC
c3300BC
c1850BC
c200BC
cAD150
epoch

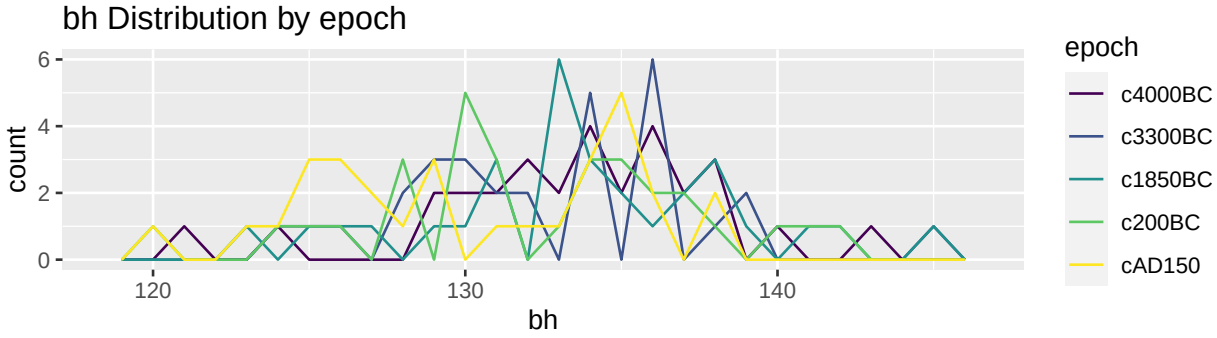

bh
120
125
130
135
140
145
c4000BC
c3300BC
c1850BC
c200BC
cAD150
epoch

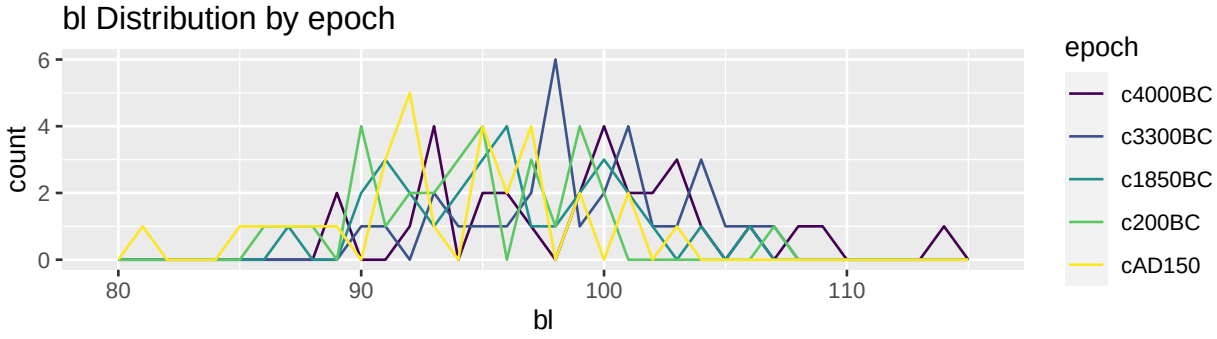

bl
80
85
90
95
100
110
c4000BC
c3300BC
c1850BC
c200BC
cAD150
epoch

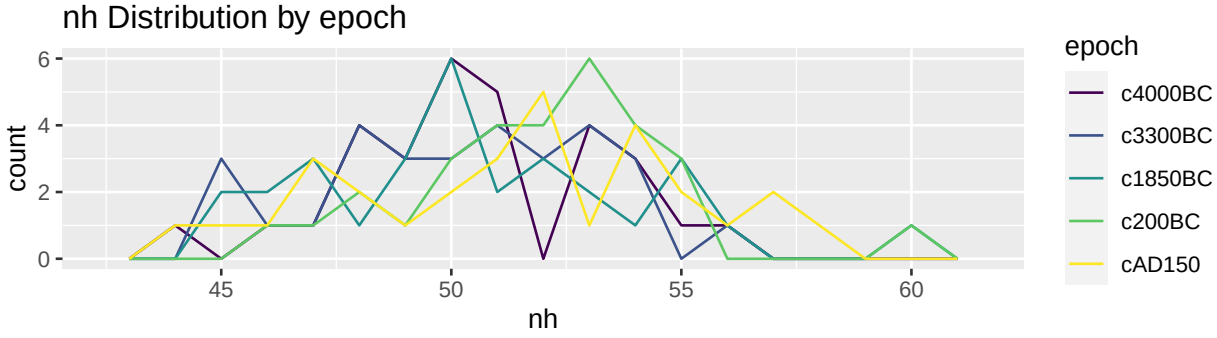

nh
45
50
55
60
c4000BC
c3300BC
c1850BC
c200BC
cAD150
epoch

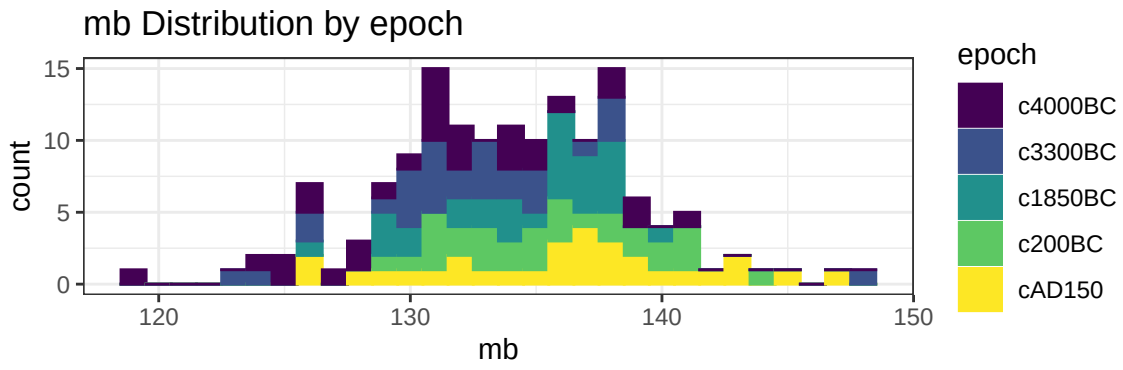
Features distributions with respect to the epochs:

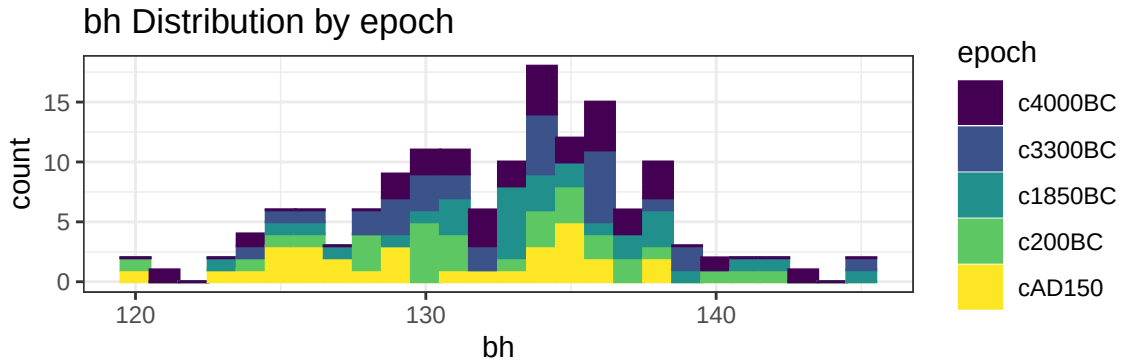


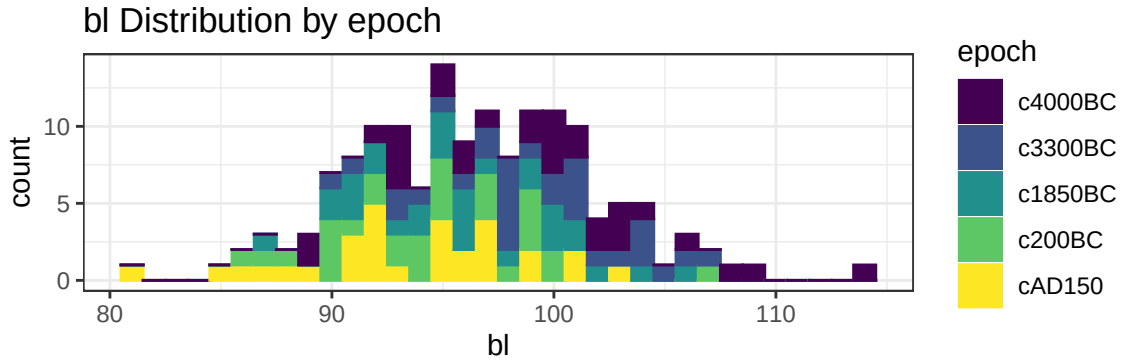


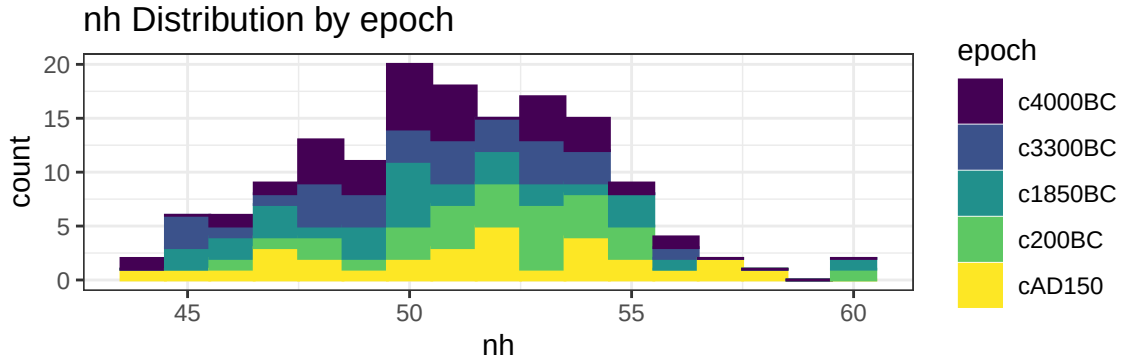




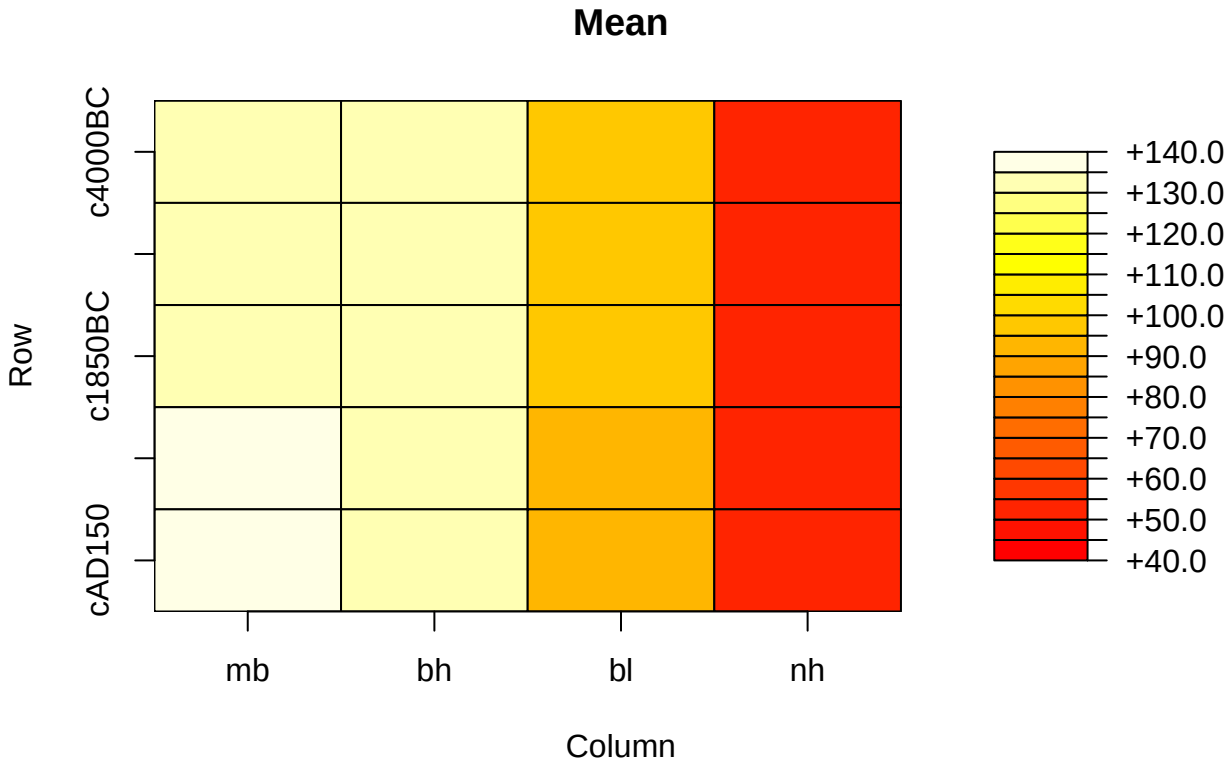

mb Distribution by epoch
count
mb
epoch
c4000BC
c3300BC
c1850BC
c200BC
cAD150


bh Distribution by epoch
count
bh
epoch
c4000BC
c3300BC
c1850BC
c200BC
cAD150

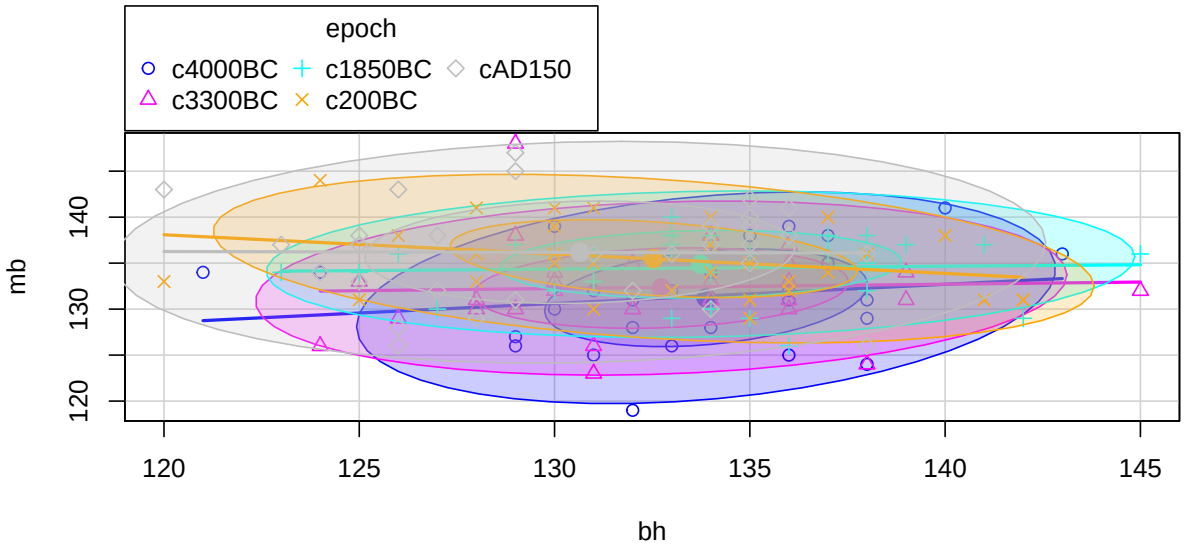

bl Distribution by epoch
count
bl
epoch
c4000BC
c3300BC
c1850BC
c200BC
cAD150

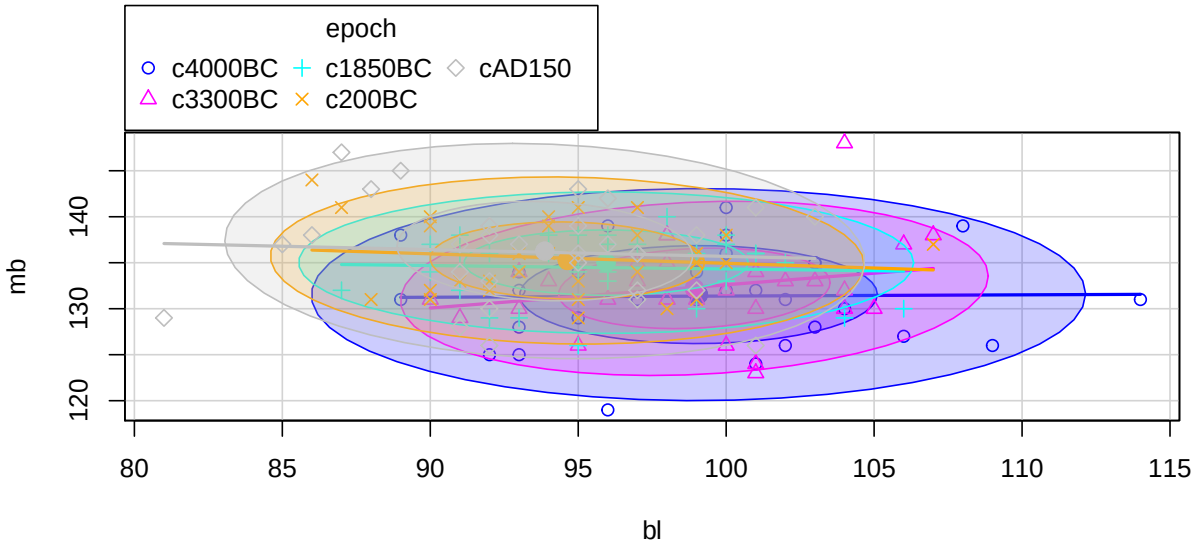

nh Distribution by epoch
count
nh
epoch
c4000BC
c3300BC
c1850BC
c200BC
cAD150

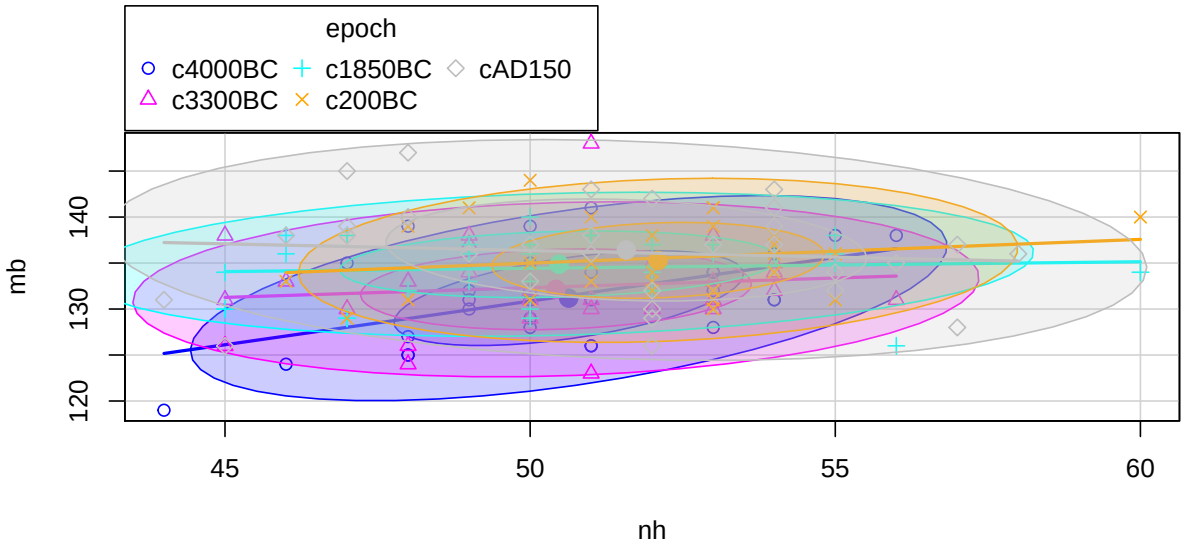
xbar matrix indicating the mean value for each feature with respect to epochs:



Scatter plots of features conditioning on epochs. The following plots illustrate the relationship between the different features mutually and the ellipses indicates the distribution of those relationships considering each epoch:






epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
mb
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50
55
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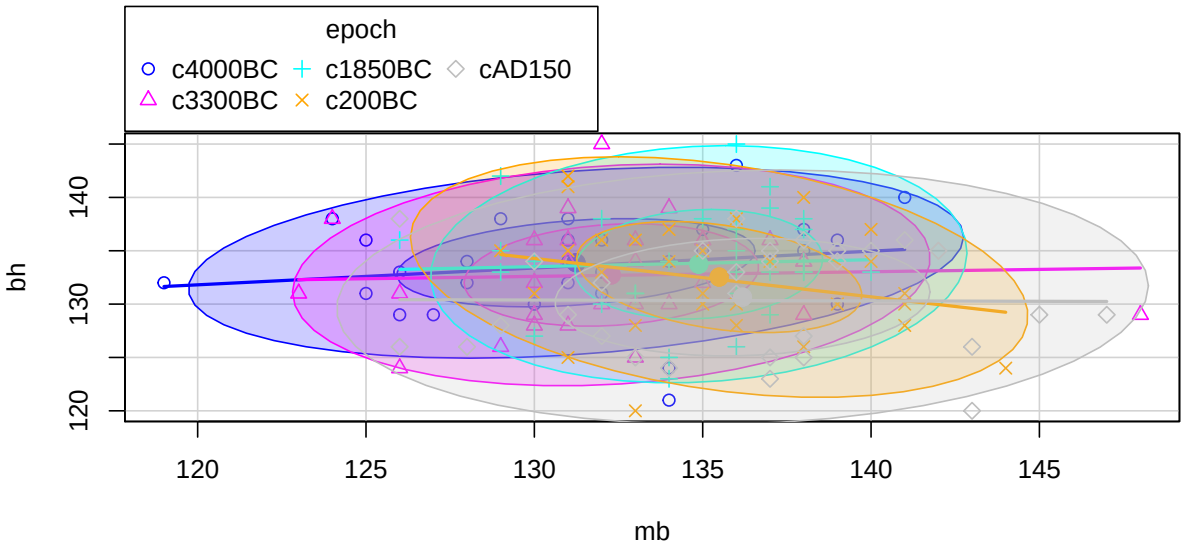
nh


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bh
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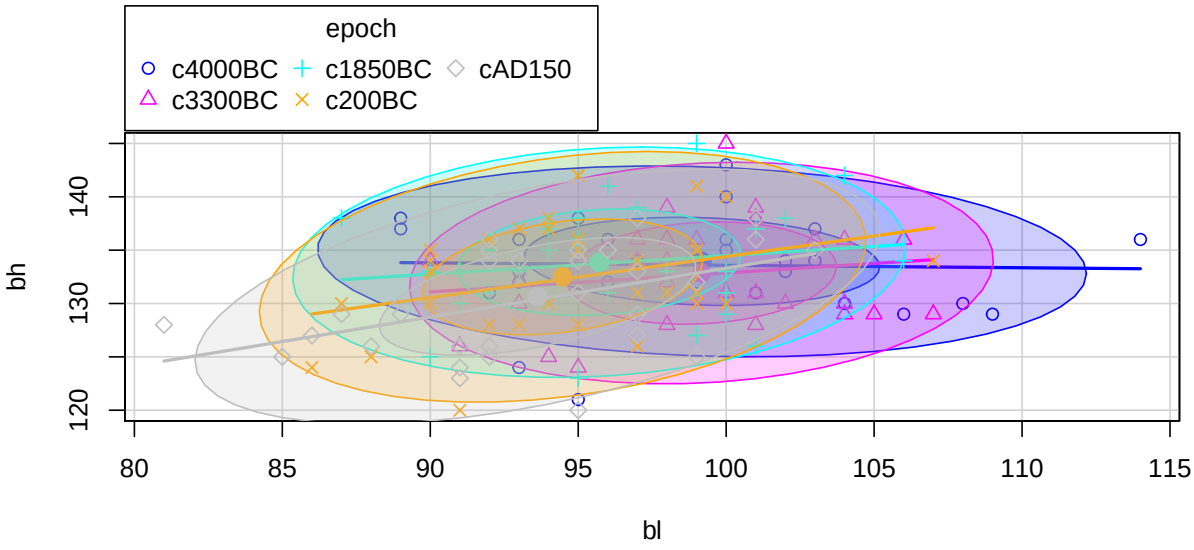
140
120
125
130
135
140
145
mb


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bh
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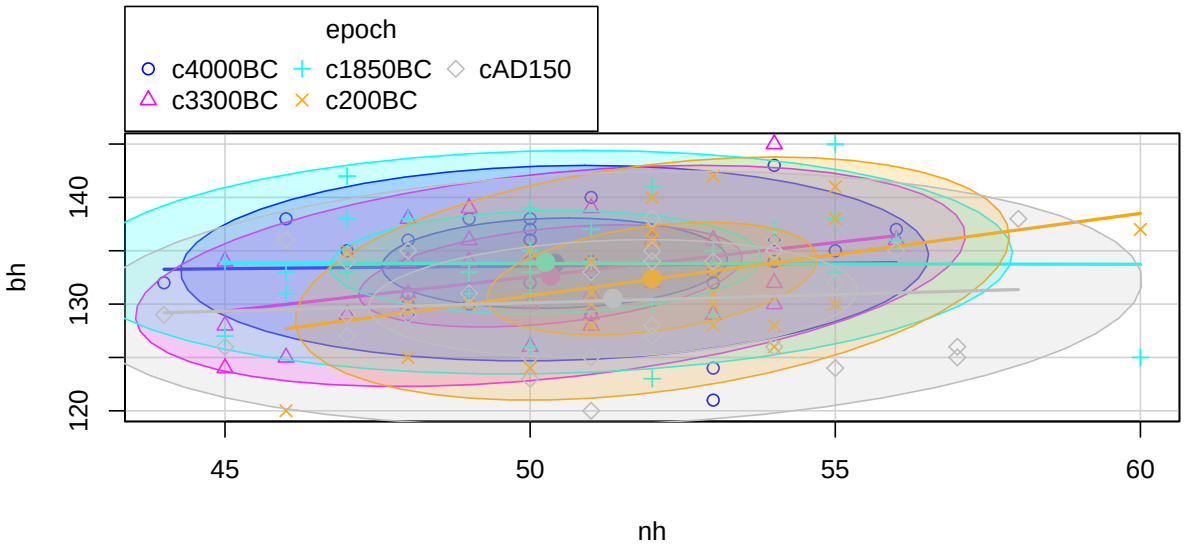
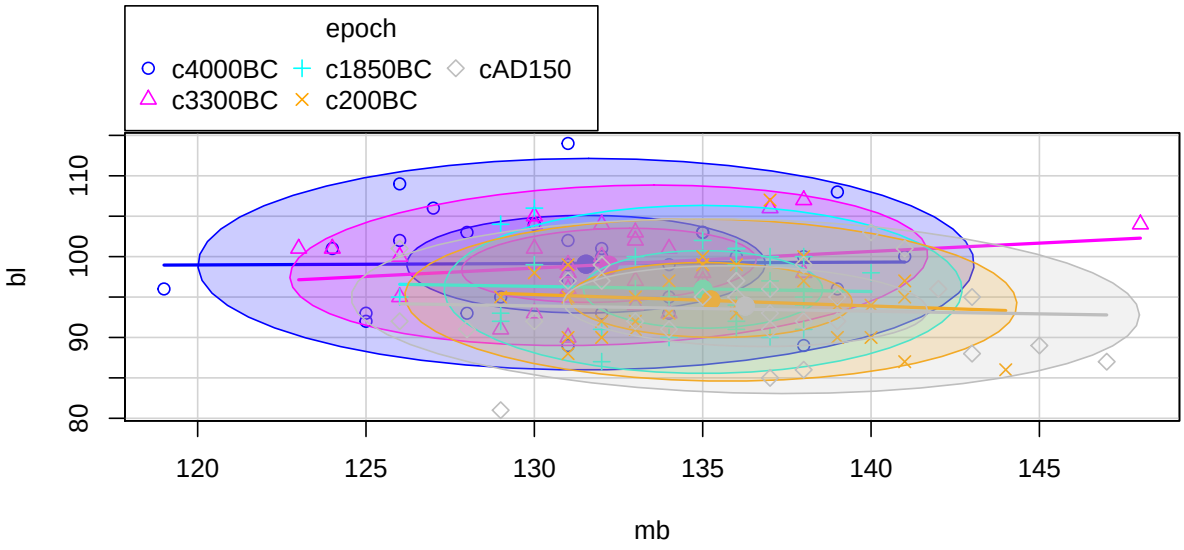
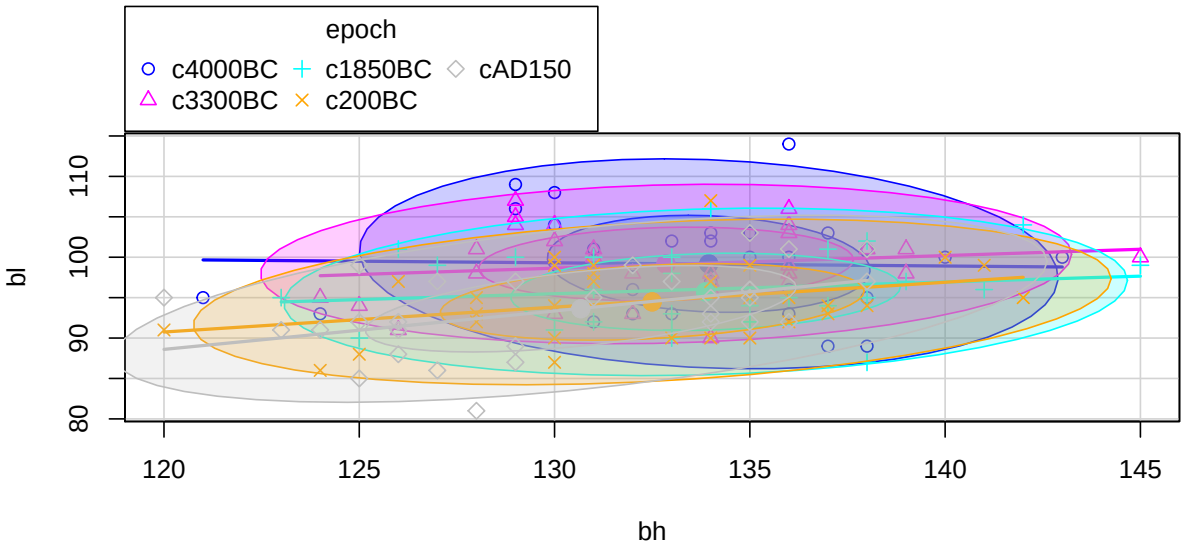
80
85
90
95
100
105
110
115
bl


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bh
120
130
140
45
50
55
60
nh


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bl
80
90
100
110
120
125
130
135
140
145
mb


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bl
80
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120
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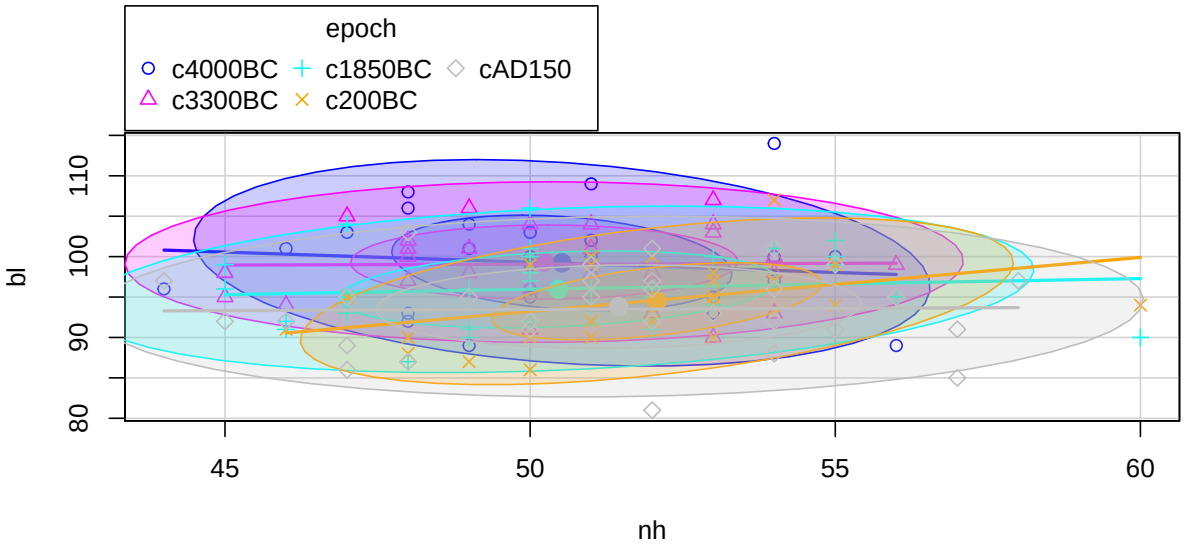
135
140
145
bh


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
bl
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110
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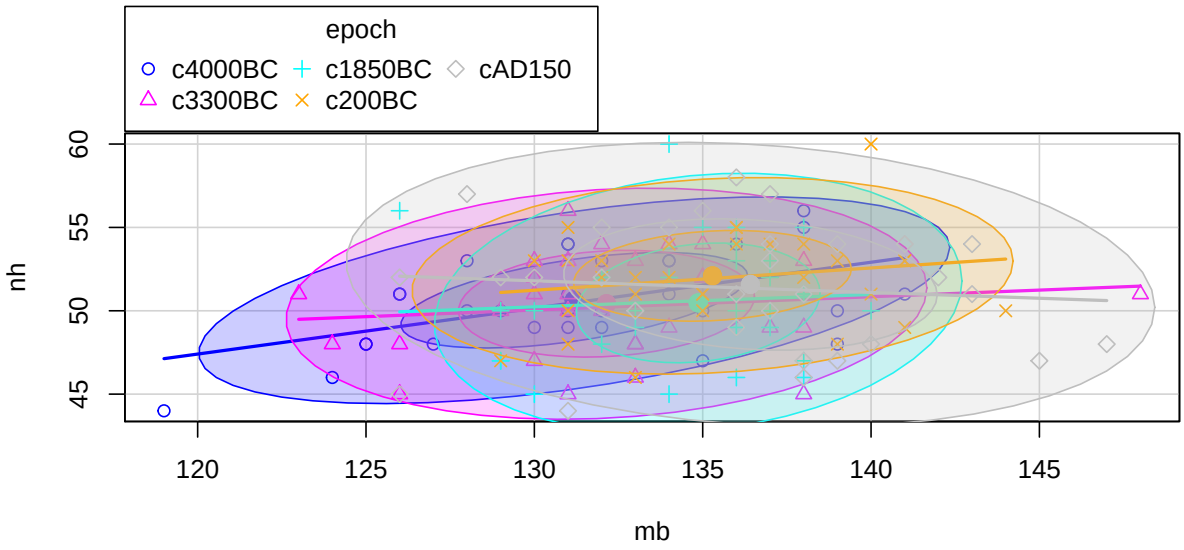
nh


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
nh
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50
55
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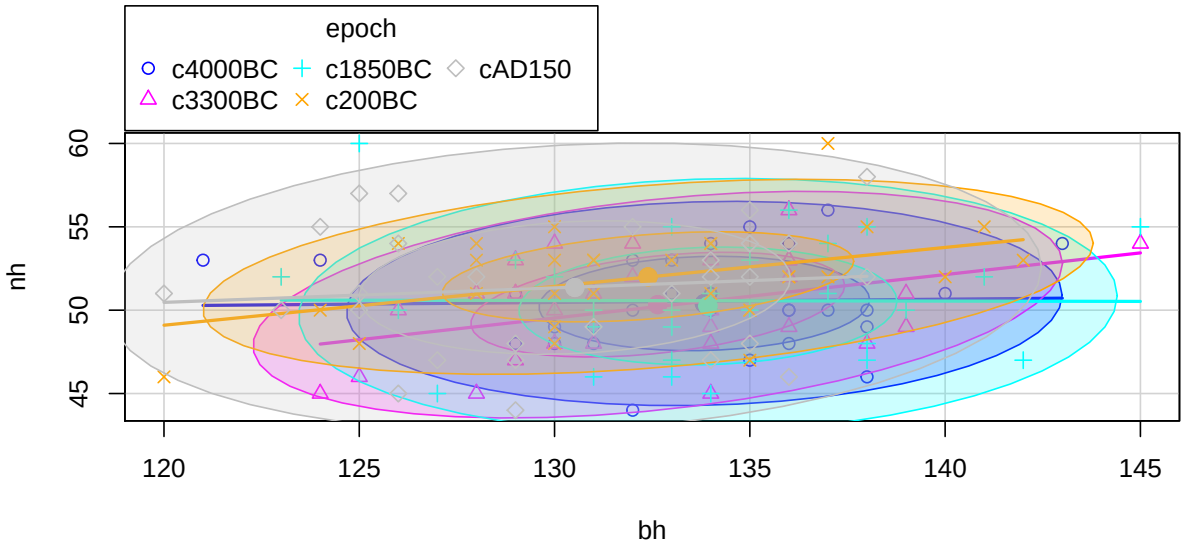
120
125
130
135
140
145
mb


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
nh
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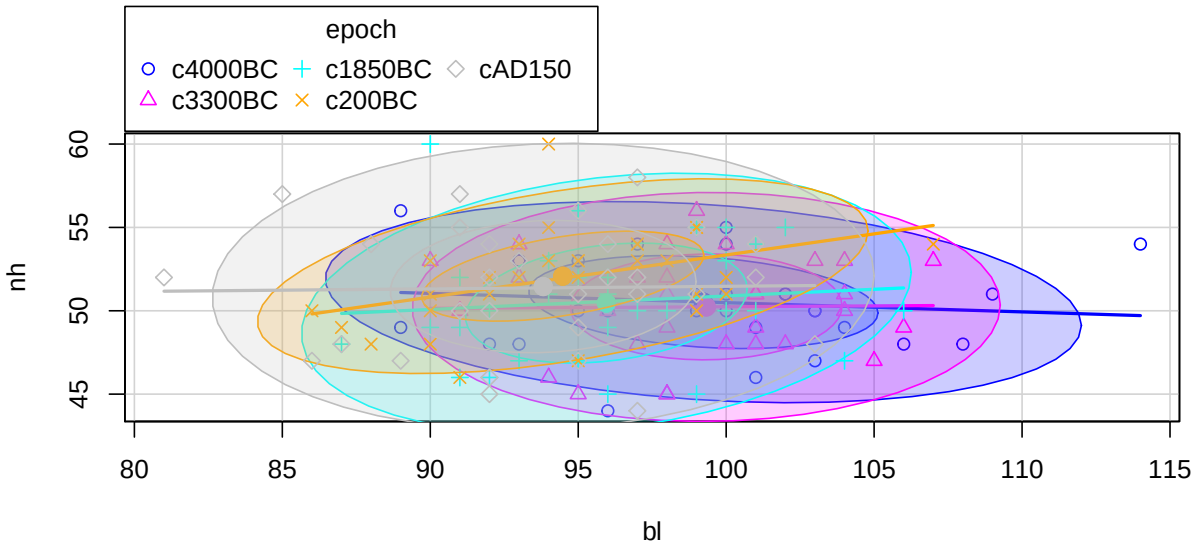
145
bh


epoch
c4000BC
c1850BC
cAD150
c3300BC
c200BC
nh
45
50
55
60
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85
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105
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115
bl

(b)

1)Summary of the manova model

```
##  Response mb :
##                    Df  Sum Sq Mean Sq F value    Pr(>F)
## as.factor(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)
## as.factor(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)
## as.factor(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)
## as.factor(epoch)   4   61.2  15.300   1.507 0.2032
## Residuals        145 1472.1  10.153
```

2)Different tests for MANOVA

2-1)Hotelling-Lawley

```
##                    Df Hotelling-Lawley approx F num Df den Df    Pr(>F)
## as.factor(epoch)   4          0.48182    4.231     16    562 8.278e-08 ***
## Residuals        145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2-2)Roy

```
##                    Df    Roy approx F num Df den Df    Pr(>F)
## as.factor(epoch)   4 0.4251    15.41      4    145 1.588e-10 ***
## Residuals        145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2-3)Pillai

```
##                    Df  Pillai approx F num Df den Df    Pr(>F)
## as.factor(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
```

2-4)Wilks

```
##                   Df   Wilks approx F num Df den Df   Pr(>F)
## as.factor(epoch)   4 0.66359   3.9009     16 434.45 7.01e-07 ***
## Residuals        145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3)Pairwise comparisons

3-1)4000BC, 3300BC and 185BC

```
##                   Df   Pillai approx F num Df den Df Pr(>F)
## as.factor(epoch)  1 0.027674  0.39135      4     55 0.8139
## Residuals        58
```

3-2)4000BC, AD150

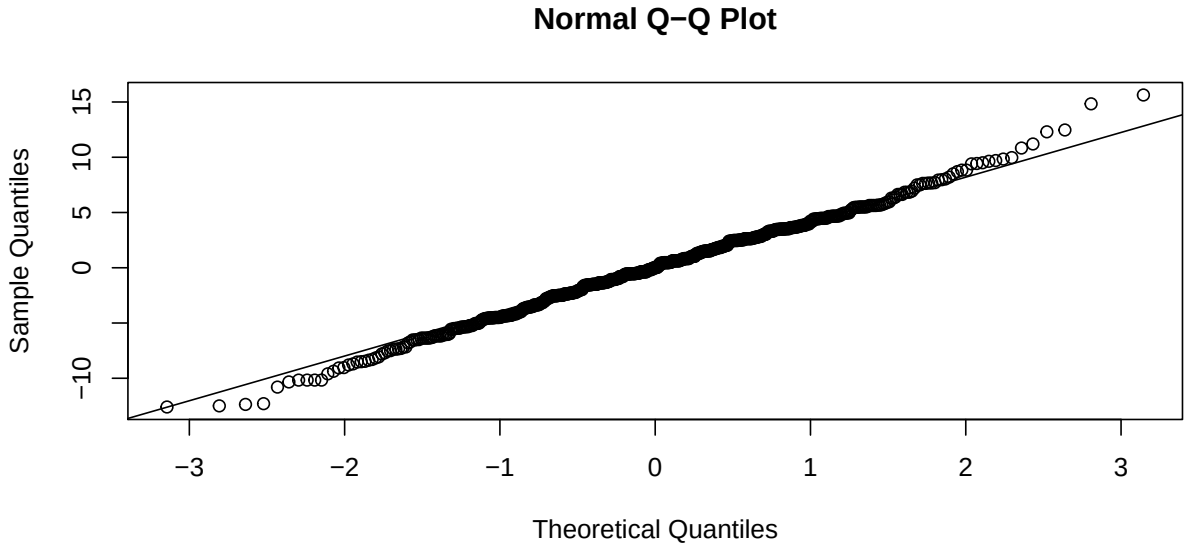
```
##                   Df  Pillai approx F num Df den Df    Pr(>F)
## as.factor(epoch)  1 0.36182   7.7956      4     55 4.736e-05 ***
## Residuals        58
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4)Simultaneous interval

	mb	bh	bl	nh
(epoch1 - epoch2)	(-4.905 2.905)	(-7.005 0.805)	(-8.039 -0.228)	(-8.705 -0.895)
(epoch1 - epoch3)	(-3.219 5.019)	(-4.319 3.919)	(-2.819 5.419)	(-0.852 7.386)
(epoch1 - epoch4)	(-4.079 4.279)	(-1.046 7.313)	(0.454 8.813)	(1.487 9.846)
(epoch1 - epoch5)	(-2.408 3.008)	(-2.742 2.675)	(-4.142 1.275)	(-3.542 1.875)

Analysis:

Applying MANOVA to the given variables gives strong evidence that the epoch means of these variables differ. The highlighted differences in the table above do not cover zero in their simulataneous intervals.



Analysis:

Yes, our histogram of residuals shows that the mean is zero. Since our residuals are normal, it means that our assumption is valid and model inference (confidence intervals, model predictions) should also be valid.

The data come from normal distribution.

Refrences

- http://www.biostathandbook.com/multiplecomparisons.html
- https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2907892/
- http://users.stat.umn.edu/~helwig/notes/mvmean-Notes.pdf

Appendix

```
knitr::opts_chunk$set(echo = TRUE)

# Question 1
setwd("E:/LiU/1st Semester/732A97-MStatistics/Assignments/2")
records <- read.table("T1-9.DAT")
colnames(records) <- c("Country","m100", "m200","m400", "m800", "m1500", "m3000", "Marathon")

# in the previous assignment we used abs(x-xbar(x))
# thats why we didnt get North Korea among the outliers
centered           <- apply(records[,-1], 2, function(x){x-mean(x)})
rownames(centered) <- records[[1]]

Cov   <- cov(records[,-1])
mah   <- ((centered) %*% solve(Cov)) %*% t(centered)
dist  <- (sort(diag(mah),decreasing = TRUE))

df    <- dim(records[,-1])[2]-1
alpha <- 0.001


chi      <- pchisq(dist, df, lower.tail = FALSE)
outliers <- list("Outliers" = round(dist[which(chi < alpha)],2))
outliers

Bonferroni  <- list("Outliers after adjustment" = round(dist[which(chi < (alpha/7))],2))
Bonferroni

# Question 2
setwd("E:/LiU/1st Semester/732A97-MStatistics/Assignments/2")
birds <- read.table("T5-12.DAT")
colnames(birds) <- c("Tail Length", "Wing Length")
birds
x1 <- birds$`Tail Length`
x2 <- birds$`Wing Length`
n = nrow(birds)
p = ncol(birds)
alpha <- 0.05
crit_value <- sqrt((p*(n-1)/(n* (n-p))) * qf(1-alpha, p, n-p))


mu0 = c(190, 275)

Mean = apply(birds, 2, mean)
Cov = cov(birds)


angles <- seq(0, 2*pi, length.out=200)
#eigen values and eigen vectors of covariance-variance matrix
eigVal <-eigen(Cov)$values
eigVec <- eigen(Cov)$vectors
```

```r
ellBase <- cbind(sqrt(eigVal[1])*crit_value*cos(angles), sqrt(eigVal[2])* crit_value*sin(angles))

ellRot <- eigVec%*%t(ellBase)

plot(x1,x2)
lines((ellRot+Mean)[1,], (ellRot + Mean)[2,], asp=1, type='l', lwd=2,
     main= "100(1-a)% Confidence Ellipsoid", xlab="x1", ylab="x2")
points(Mean[1], Mean[2], pch=4, col="orange", lwd=3)
points(mu0[1], mu0[2], pch=8, col="green", lwd=3)


bon11 <- Mean[1] - qt(1-alpha/(2*p), n-1)*sqrt(Cov[1,1]/n)
bon12 <- Mean[1] + qt(1-alpha/(2*p), n-1)*sqrt(Cov[1,1]/n)
bon21 <- Mean[2] - qt(1-alpha/(2*p), n-1)*sqrt(Cov[2,2]/n)
bon22 <- Mean[2] + qt(1-alpha/(2*p), n-1)*sqrt(Cov[2,2]/n)
rect(bon11, bon21, bon12, bon22, border= "violetred3")


T2_mu1_Lo <- mean(x1)- sqrt((p*(n-1)/(n* (n-p))) * qf(1-alpha, p, n-p)*var(x1))
T2_mu1_Hi <- mean(x1)+ sqrt((p*(n-1)/(n* (n-p))) * qf(1-alpha, p, n-p)*var(x1))
T2_mu2_Lo <- mean(x2)- sqrt((p*(n-1)/(n* (n-p))) * qf(1-alpha, p, n-p)*var(x2))
T2_mu2_Hi <- mean(x2)+ sqrt((p*(n-1)/(n* (n-p))) * qf(1-alpha, p, n-p)*var(x2))

Bon_mu1_Lo <- mean(x1) - qt(1-0.025/2, n-1)* sqrt(var(x1)/n)
Bon_mu1_Hi <- mean(x1) + qt(1-0.025/2, n-1)* sqrt(var(x1)/n)
Bon_mu2_Lo <- mean(x2) - qt(1-0.025/2, n-1)* sqrt(var(x2)/n)
Bon_mu2_Hi <- mean(x2) + qt(1-0.025/2, n-1)* sqrt(var(x2)/n)

cbind(T2_mu1_Lo, T2_mu1_Hi,Bon_mu1_Lo , Bon_mu1_Hi)
cbind(T2_mu2_Lo, T2_mu2_Hi,Bon_mu2_Lo , Bon_mu2_Hi)
qqnorm(x1, main = "Q-Q plot for x1")
qqline(x1)
qqnorm(x2, main = "Q-Q plot for x2")
qqline(x2)
plot(x1, x2)


# Question 3
library(heplots)
library(ggplot2)
data(Skulls)
data <- Skulls
# fit manova model
sk.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
sk.mod
#Boxplots
par(mfrow = c(4, 1))
boxplot(mb ~ epoch, data=data)
boxplot(bh ~ epoch, data=data)
boxplot(bl ~ epoch, data=data)
boxplot(nh ~ epoch, data=data)

par(mfrow = c(4, 1))
```

```r
ggplot(Skulls, aes(mb, colour = epoch)) +
  geom_freqpoly(binwidth = 1) + labs(title="mb Distribution by epoch")

ggplot(Skulls, aes(bh, colour = epoch)) +
  geom_freqpoly(binwidth = 1) + labs(title="bh Distribution by epoch")

ggplot(Skulls, aes(bl, colour = epoch)) +
  geom_freqpoly(binwidth = 1) + labs(title="bl Distribution by epoch")

ggplot(Skulls, aes(nh, colour = epoch)) +
  geom_freqpoly(binwidth = 1) + labs(title="nh Distribution by epoch")

c <- ggplot(Skulls, aes(x=mb, fill=epoch, color=epoch)) +
  geom_histogram(binwidth = 1) + labs(title="mb Distribution by epoch")
c + theme_bw()

c <- ggplot(Skulls, aes(x=bh, fill=epoch, color=epoch)) +
  geom_histogram(binwidth = 1) + labs(title="bh Distribution by epoch")
c + theme_bw()

c <- ggplot(Skulls, aes(x=bl, fill=epoch, color=epoch)) +
  geom_histogram(binwidth = 1) + labs(title="bl Distribution by epoch")
c + theme_bw()

c <- ggplot(Skulls, aes(x=nh, fill=epoch, color=epoch)) +
  geom_histogram(binwidth = 1) + labs(title="nh Distribution by epoch")
c + theme_bw()
#Mean matrix
epoch = levels(Skulls$epoch)

Mean = matrix(0, nrow = length(epoch), ncol = 4)
rownames(Mean) = levels(Skulls$epoch)
colnames(Mean) = colnames(Skulls)[-1]
for (i in epoch) {
  for (j in colnames(Mean)) {
    Mean[i,j] = mean(Skulls[,j][Skulls[1] == i])

  }
}
library(plot.matrix)
par(mar=c(5.1, 4.1, 4.1, 4.1))
plot(Mean, breaks = 20)


#Scatterplots
scatterplot(mb ~ bh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(mb ~ bl|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(mb ~ nh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright

scatterplot(bh ~ mb|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(bh ~ bl|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(bh ~ nh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
```

```r
scatterplot(bl ~ mb|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(bl ~ bh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(bl ~ nh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright

scatterplot(nh ~ mb|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(nh ~ bh|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright
scatterplot(nh ~ bl|epoch, data=Skulls, ellipse=TRUE, levels=0.68, smooth=FALSE, legend.coords="topright

manova_1 <- manova(cbind(mb, bh, bl, nh)~ as.factor(epoch), data= data)

summary.aov(manova_1)
summary(manova_1, test = "Hotelling-Lawley")
summary(manova_1, test = "Roy")
summary(manova_1, test = "Pillai")
summary(manova_1, test = "Wilks")
#Pairwise comparisons

#4000BC, 3300BC and 185BC
manova_2 <- manova(cbind(mb, bh, bl, nh)~ as.factor(epoch), data= data,
                   subset= as.factor(epoch) %in% c("c4000BC", "c3300BC", " c1850BC"))

#4000BC, AD150
manova_3 <- manova(cbind(mb, bh, bl, nh)~ as.factor(epoch), data= data,
                   subset= as.factor(epoch) %in% c("c4000BC", "cAD150"))

summary(manova_2)
summary(manova_3)
### 4)Simultaneous interval
w_mb <- sum(manova_1$residuals[,1]^2)
w_bh <- sum(manova_1$residuals[,2]^2)
w_bl <- sum(manova_1$residuals[,3]^2)
w_nh <- sum(manova_1$residuals[,4]^2)
w <- c(w_mb, w_bh, w_bl, w_nh)

epoch = as.character(unique(data$epoch))
g = length(unique(data$epoch))
p = ncol(data)
n = 150
a = 0.05
C <- -qt(a/((p-1)*g*(g-1)), (n-g)) * sqrt(2 * w/(30*(n-g)))
C_mat = matrix(c(1,1,1,1),4) %*% C

#Calculating the mean values of the samples and the differences between them.
xbar <- matrix(0, nrow = 5, ncol = 4, dimnames = list(epoch, names(data[,-1])))
dist <- matrix(0, 4,4)
for (i in 2:p) {
  for (j in 1:g) {
    xbar[j,(i-1)] = mean(data[which(data$epoch == epoch[j]),i])

  }
  for (k in 1:4) {

    dist[k, i-1] <- xbar[1, i-1] - xbar[k+1, i-1]
```

```
  }
}

#Calculating the intervals based on result 6.5
SI_lower = dist - C_mat
SI_upper = dist + C_mat

e1 = round(t(SI_lower),3)
e2 = round(t(SI_upper),3)

interval = matrix(0, 4,4)
for (i in 1:4) {
  for (j in 1:4) {
    #interval[i,j] = paste("(",e1[i,j],e2[i,j],")" ,sep = " ")
    interval[i,j] = paste("(",e1[i,j],e2[i,j],")" ,sep = " ")
  }

}

colnames(interval) = names(data[,-1])
rownames(interval) = c("(epoch1 - epoch2)", "(epoch1 - epoch3)",
                       "(epoch1 - epoch4)", "(epoch1 - epoch5)")
knitr::kable(interval)


# sk.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=data)
# #sk.mod
# summary(sk.mod)

#Histogram of Residuals
hist(sk.mod$resid, main="Histogram of Residuals",
     ylab="Residuals")

#Q-Q Plot
qqnorm(sk.mod$resid)
qqline(sk.mod$resid)
```