Workbook 3 – MANOVA

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Question 2

A

```
> Sales.model<-lm(Knowledge~Treatment, data=Sales.scores)
> Sales.scores.an<-anova(Sales.model)
> Sales.scores.an
Analysis of Variance Table

Response: Knowledge
          Df  Sum Sq Mean Sq F value   Pr(>F)
Treatment  2  34.444 17.2220   6.702 0.002833 **
Residuals 45 115.635  2.5697
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In this case, if using a 0.05 significance level, we would reject the NULL hypothesis in favour of the alternative hypothesis as the P-value is significantly less than 0.05.

B

```
> Sales.model.motivation<-lm(Motivation~Treatment, data=Sales.scores)
> Sales.motivation.an<-anova(Sales.model.motivation)
> Sales.motivation.an
Analysis of Variance Table

Response: Motivation
          Df Sum Sq Mean Sq F value    Pr(>F)
Treatment  2 59.102 29.5512  15.674 6.828e-06 ***
Residuals 45 84.841  1.8854
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

If using the same significance level of 0.05, we would also reject the NULL hypothesis as the P-value is even less than 0.001.

C

```
> Sales.scores.man<-manova(cbind(Knowledge,Motivation)~Treatment,data=Sales.scores)
> Sales.scores.man
Call:
   manova(cbind(Knowledge, Motivation) ~ Treatment, data = Sales.scores)

Terms:
                Treatment Residuals
resp 1           34.44391 115.63467
resp 2           59.10232  84.84091
Deg. of Freedom         2        45

Residual standard errors: 1.603016 1.373082
Estimated effects may be unbalanced
>
>
> Sales.scores.man$coef
            Knowledge Motivation
(Intercept)  9.774437 10.6851250
TreatmentT2 -1.930188 -2.6883750
TreatmentT3 -0.305625 -0.9973125
```

3

```
> summary(Sales.scores.man)
          Df  Pillai approx F num Df den Df    Pr(>F)
Treatment  2 0.43739    6.298      4     90 0.0001629 ***
Residuals 45
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

Using 0.05 significance value. The P-value is much lower and therefore the NULL hypothesis would be rejected.

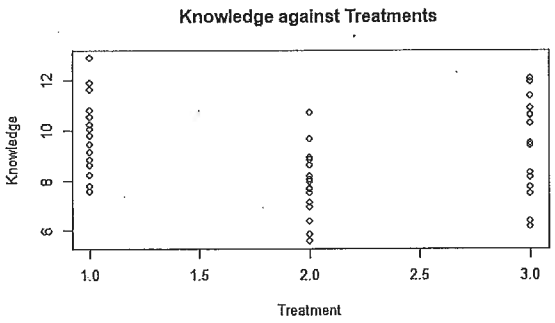
Looking at the individual tests:

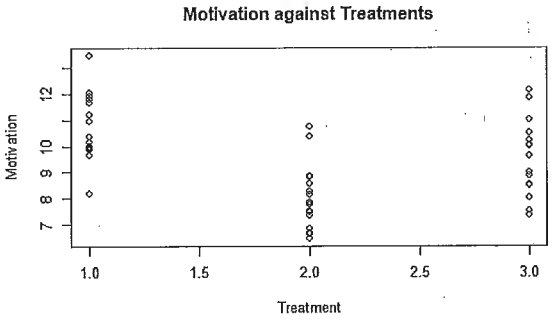
```
> summary.aov(Sales.scores.man)
 Response Knowledge :
            Df  Sum Sq Mean Sq F value   Pr(>F)
Treatment    2  34.444 17.2220   6.702 0.002833 **
Residuals   45 115.635  2.5697
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Response Motivation :
            Df Sum Sq Mean Sq F value    Pr(>F)
Treatment    2 59.102 29.5512  15.674 6.828e-06 ***
Residuals   45 84.841  1.8854
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Both P-values are below the significance level so the NULL hypotheses here are both rejected.

What are the null hypotheses?
What are your conclusions?





Looking at these graphs, we can clearly see the mean of treatment two is going to be considerably less than the means of treatment one and three as the plots of treatment 2 are displayed significantly lower.

Question 3

A

Sepal length

```
> Iris.sepal.length<-lm(Sepal.Length~Species, data=iris)
> Iris.sepal.length.an<-aov(Iris.sepal.length)
> tukey.sep.len<-TukeyHSD(Iris.sepal.length.an)
> Iris.sepal.length.an
Call:
   aov(formula = Iris.sepal.length)

Terms:
                  Species Residuals
Sum of Squares   63.21213  38.95620
Deg. of Freedom         2       147

Residual standard error: 0.5147894
Estimated effects may be unbalanced
>
>
> tukey.sep.len
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Iris.sepal.length)

$`Species`
                     diff       lwr       upr p adj
versicolor-setosa    0.930 0.6862273 1.1737727     0
virginica-setosa     1.582 1.3382273 1.8257727     0
virginica-versicolor 0.652 0.4082273 0.8957727     0
```

Sepal Width

```
> Iris.sepal.width<-lm(Sepal.Width~Species, data=iris)
> Iris.sepal.width.an<-aov(Iris.sepal.width)
> tukey.sep.wid<-TukeyHSD(Iris.sepal.width.an)
> Iris.sepal.width.an
Call:
   aov(formula = Iris.sepal.width)

Terms:
                  Species Residuals
Sum of Squares  11.34493  16.96200
Deg. of Freedom        2       147

Residual standard error: 0.3396877
Estimated effects may be unbalanced
>
>
> tukey.sep.wid
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Iris.sepal.width)

$`Species`
                     diff         lwr        upr     p adj
versicolor-setosa    -0.658 -0.81885528 -0.4971447 0.0000000
virginica-setosa     -0.454 -0.61485528 -0.2931447 0.0000000
virginica-versicolor  0.204  0.04314472  0.3648553 0.0087802
```

Petal Length

```
> Iris.petal.length<-lm(Petal.Length~Species, data=iris)
> Iris.petal.length.an<-aov(Iris.petal.length)
> tukey.pet.len<-TukeyHSD(Iris.petal.length.an)
> Iris.petal.length.an
Call:
   aov(formula = Iris.petal.length)

Terms:
                  Species Residuals
Sum of Squares  437.1028   27.2226
Deg. of Freedom        2       147

Residual standard error: 0.4303345
Estimated effects may be unbalanced
>
>
> tukey.pet.len
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Iris.petal.length)

$`Species`
                     diff     lwr     upr p adj
versicolor-setosa    2.798 2.59422 3.00178     0
virginica-setosa     4.090 3.88622 4.29378     0
virginica-versicolor 1.292 1.08822 1.49578     0
```

Petal Width

```
> Iris.petal.width<-lm(Petal.Width~Species, data=iris)
> Iris.petal.width.an<-aov(Iris.petal.width)
> tukey.pet.wid<-TukeyHSD(Iris.petal.width.an)
> Iris.petal.width.an
Call:
   aov(formula = Iris.petal.width)

Terms:
                  Species Residuals
Sum of Squares  80.41333   6.15660
Deg. of Freedom         2       147

Residual standard error: 0.20465
Estimated effects may be unbalanced
>
>
> tukey.pet.wid
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Iris.petal.width)

$`Species`
                      diff       lwr       upr p adj
versicolor-setosa    1.08 0.9830903 1.1769097     0
virginica-setosa     1.78 1.6830903 1.8769097     0
virginica-versicolor 0.70 0.6030903 0.7969097     0
```

Petal features (petal length and width) differ more in each species when looking at the mean values of each. When compared to the differences of the sepal feature (sepal length and width) mean values. With no difference of mean being larger than 1 for Sepal width but even the lowest value in the petal width test is larger than this. The petal length mean value differences are overall significantly larger than the differences shown in the sepal length test.

B

With each test conducted, the chance of errors made increases thus increasing the error rate. This is when the NULL hypothesis may be rejected when in fact it showed be accepted. Bonferroni correction can be used to lower the effect of this and reduce the chance of receiving false-positive results. It adjusts the p values made and divides the critical p-value by the number of hypotheses tested.

C

```
> Iris.man<-manova(cbind(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width)~Species,data=iris)
> Iris.man
Call:
   manova(cbind(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) ~
    Species, data = iris)

Terms:
                Species Residuals
resp 1          63.2121   38.9562
resp 2          11.3449   16.9620
resp 3         437.1028   27.2226
resp 4          80.4133    6.1566
Deg. of Freedom       2       147

Residual standard errors: 0.5147894 0.3396877 0.4303345 0.20465
Estimated effects may be unbalanced
```

```
> summary(Iris.man)
           Df Pillai approx F num Df den Df    Pr(>F)
Species     2 1.1919   53.466      8    290 < 2.2e-16 ***
Residuals 147
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

✓ ($< 10^{-15}$).

Using the summary function, we can see the P-value of MANOVA is very small and so the NULL hypothesis should be rejected. What is H_0?

4.

This backs up the one-way ANOVA results which also show that the NULL hypothesis should be rejected and that the means for each species aren't the same.

One-way ANOVA's are used to find the differences between a group in one dependant variable and so when looking at multiple variables, will need to execute multiple tests and compare. This is why the Bonferroni correction process may be used. ✓

Whereas a MANOVA evaluates the differences of groups based on two or more dependant variables. This way the groups are tested against all the variables the must be tested against but in one execution. The dependant variables in a MANOVA should be related.

MANOVA checks more variables.

Question 4

Q4 7 – 10

A

```
> amino.matrix<-matrix(0,10,3)
> amino.matrix[1,1]<-7.0
> amino.matrix[2,1]<-7.3
> amino.matrix[3,1]<-8.0
... ... ...

> amino.matrix[8,3]<-26.1
> amino.matrix[9,3]<-27.5
> amino.matrix[10,3]<-28.1
```

```
> rownames(amino.matrix)<-c("Male","Male","Male","Male","Male","Fema
le","Female","Female","Female","Female")
> colnames(amino.matrix)<-c("Alanine","Aspartic acid", "Tyrosine")
> amino.matrix
       Alanine Aspartic acid Tyrosine
Male       7.0          17.0     19.7
Male       7.3          17.2     20.3
Male       8.0          19.3     22.6
Male       8.1          19.8     23.7
Male       7.9          18.4     22.0
Female     7.3          17.4     22.5
Female     7.7          19.8     24.9
Female     8.2          20.2     26.1
Female     8.3          22.6     27.5
Female     6.4          23.4     28.1
>

> gender<-rep(c("Male","Female"),rep(5,2))
> amino.man<-manova(amino.matrix~gender)
> amino.man
Call:
   manova(amino.matrix ~ gender)

Terms:
                gender Residuals
resp 1           0.016     3.320
resp 2          13.689    29.000
resp 3          43.264    30.820
Deg. of Freedom      1         8

Residual standard errors: 0.6442049 1.903943 1.962779
Estimated effects may be unbalanced
>
```

```
> summary(amino.man)
          Df  Pillai approx F num Df den Df   Pr(>F)
gender     1 0.91461   21.423      3      6 0.001317 **
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(amino.man, test="W")
          Df    Wilks approx F num Df den Df   Pr(>F)
gender     1 0.085386   21.423      3      6 0.001317 **
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(amino.man, test="H")
          Df Hotelling-Lawley approx F num Df den Df   Pr(>F)
gender     1           10.712   21.423      3      6 0.001317 **
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(amino.man, test="R")
          Df    Roy approx F num Df den Df   Pr(>F)
gender     1 10.712   21.423      3      6 0.001317 **
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

MANOVA shows mean vectors of amino acid levels differ M/F.

Not clear.

What does the MANOVA reveal in this case? Explore the MANOVA fit.

The differences between the values of each response variable against the Gender variable shows that there is some level of variation in the differences between genders over two of the three response variables. Looking at the P-value from the summary, we can see that the NULL hypothesis should again be rejected

Does it make any difference which of the four tests you use?

All four tests give the same P-value which is 0.001317 so to find the p-value of the MANOVA, any of the four tests can be used. They also give the same values for other attributes such as the approximation of F value, num df and den df. If the analyst us just trying to find the degrees of freedom information or the p-value for the MANOVA then any test can be used but if they are looking for the results of a specific test then they will have to add the type of test they wish to use.

3.

Test values

Pillai = 0.91461

Wilks = 0.085386

Hotelling-Lawley = 10.712

Roy = 10.712

B

```
> summary.aov(amino.man)
 Response Alanine :
            Df Sum Sq Mean Sq F value Pr(>F)
gender       1  0.016   0.016  0.0386 0.8492
Residuals    8  3.320   0.415

 Response Aspartic acid :
            Df Sum Sq Mean Sq F value Pr(>F)
gender       1 13.689  13.689  3.7763 0.0879 .
Residuals    8 29.000   3.625
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Response Tyrosine :
            Df Sum Sq Mean Sq F value  Pr(>F)
gender       1 43.264  43.264   11.23 0.01006 *
Residuals    8 30.820   3.853
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4

The P-values for the results of Alanine and Aspartic acid and are both above the 0.05 significance level, meaning they follow the NULL hypothesis that the means are the same among groups. Whereas the P-value for the Tyrosine variable test is below 0.05 and therefore follows the alternative hypothesis which is that the means among groups are not all the same. Therefore, the difference lies in the Tyrosine variable.

Q5 9/13

Question 5

A

Factor 1: Hormone treatment vs no treatment ✓ 2.

Factor 2: Males and Females

How males and females react to the hormone treatment.

B ✓

```
> hormone.man<-manova(cbind(Plasma.Ca,Water.loss)~Sex*Hormone)
> hormone.man
Call:
   manova(cbind(Plasma.Ca, Water.loss) ~ Sex * Hormone)

Terms:
                       Sex  Hormone Sex:Hormone Residuals
resp 1           14.7408 635.1075      7.2075  228.7533
resp 2           18.7500 102.0833     36.7500  151.3333
Deg. of Freedom        1        1           1         8

Residual standard errors: 5.347351 4.349329
Estimated effects may be unbalanced
>
> summary(hormone.man)
            Df  Pillai approx F num Df den Df  Pr(>F)
Sex          1 0.25408   1.1922      2      7 0.35844
Hormone      1 0.85574  20.7624      2      7 0.00114 **
Sex:Hormone  1 0.30894   1.5647      2      7 0.27435
Residuals    8
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> |
```

✓ ✓ main effect of hormone significant at 1% level.

P-values

Sex: 0.35844

Hormone: 0.00114

Sex:Hormone: 0.27435

cannot reject

Sex P-value is over 0.05 so we ~~keep~~ the NULL hypothesis.

Hormone P-value is significantly lower than 0.05 and therefore we reject the NULL hypothesis in favour of the alternative hypothesis. With the NULL hypothesis meaning there is no significant difference between the groups in terms of Hormone treatment, we can deduce the Hormone treatment has a greater effect on birds over the Sex variable and Sex:Hormone interaction.

Sex:Hormone interaction produces a P-value well above 0.05 and therefore we keep the NULL hypothesis over the alternative hypothesis.

It appears the Hormone variable best fits the model from the results so far. I then looked at the fitted values to see how the values differ per variable.

```
> fitted.values(hormone.man)
```

```
> fitted.values(hormone.man)
   Plasma.Ca Water.loss
1   15.86667   70.33333
2   15.86667   70.33333
3   15.86667   70.33333
4   12.10000   76.33333
5   12.10000   76.33333
6   12.10000   76.33333
7   28.86667   68.00000
8   28.86667   68.00000
9   28.86667   68.00000
10  28.20000   67.00000
11  28.20000   67.00000
12  28.20000   67.00000
```

1-3: Untreated Female birds

4-6: Treated Female birds

7-9: Untreated Male birds

10-12: Treated Male birds

Bird Gender	Plasma.Ca fitted value	Water.loss fitted value
Untreated Female birds	15.86667	70.33333
Treated Female birds	12.10000	76.33333
Untreated Male birds	28.86667	68.00000
Treated Male birds	28.20000	67.00000

Looking at these results, first we can see that the treatment seems have a larger effect on females as the mean drops from 15.86667 to 12.10000, that's approximately a 3.8 difference. On the other hand, the effect on males doesn't even decrease by a full value, dropping only by approximately 0.7. A similar result is shown for the Water.loss values with a difference of 6 in females treated and females untreated. Water.loss in Males treated is only 1 less than Males untreated. In conclusion, the hormone treatment has a greater effect on female birds in comparison to male birds.

```
> summary.aov(hormone.man)
 Response Plasma.Ca :
             Df Sum Sq Mean Sq F value   Pr(>F)
Sex           1  14.74   14.74  0.5155 0.493191
Hormone       1 635.11  635.11 22.2111 0.001516 **
Sex:Hormone   1   7.21    7.21  0.2521 0.629151
Residuals     8 228.75   28.59
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Response Water.loss :
             Df Sum Sq Mean Sq F value  Pr(>F)
Sex           1  18.75  18.750  0.9912 0.34861
Hormone       1 102.08 102.083  5.3965 0.04869 *
Sex:Hormone   1  36.75  36.750  1.9427 0.20087
Residuals     8 151.33  18.917
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A look at the summary.aov results

When looking at the Plasma.Ca summary results, the P-value for the Sex variable in the ANOVA is 0.493191 which is just below the 0.05 significance level. The P-value for Hormone is 0.001516 which is significantly lower than that of the Sex P-value and considerably below the significance level. So, for both Sex and Hormone, the two P-values suggest rejecting the NULL hypothesis in favour of the alternative hypothesis. However, when looking at the interaction between Sex:Hormone, we see that the P-value is 0.629151 and therefore above the 0.05 significance level and the NULL hypothesis is then kept.

Hormone affects plasma Ca and H2O loss.

When looking at the Water.loss results, we see a similar pattern with the P-value of Sex being greater than Hormone but this time by a greater margin. With Water.loss, the P-value for the Sex variable is greater than the significance variable, and so the NULL hypothesis is accepted. The Sex:Hormone interaction shows a P-value below in between both but still greater than the significance level.

7.

Question 6

A

(M1, M2, M3) ~ Treatment

X

$\underline{y}_{ij} = \underline{\mu} + \underline{T}_i + \underline{\varepsilon}_{ij}$.

/6 11/18

B

```
> fields.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields)
> fields.man
Call:
   manova(cbind(M1, M2, M3) ~ Treatment, data = fields)

Terms:
                  Treatment Residuals
resp 1             1443.842    14.944
resp 2             1350.004    19.124
resp 3             5448.316     8.544
Deg. of Freedom           3        16

Residual standard errors: 0.9664368 1.093275 0.730753
Estimated effects may be unbalanced
>
```

```
> summary(fields.man)
          Df Pillai approx F num Df den Df    Pr(>F)
Treatment  3 1.1859   3.4864      9     48 0.002202 **
Residuals 16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(fields.man, test="W")
          Df     Wilks approx F num Df den Df     Pr(>F)
Treatment  3 0.0011538   57.464      9 34.223 < 2.2e-16 ***
Residuals 16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(fields.man, test="H")
          Df Hotelling-Lawley approx F num Df den Df     Pr(>F)
Treatment  3           705.31   992.66      9     38 < 2.2e-16 ***
Residuals 16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(fields.man, test="R")
          Df    Roy approx F num Df den Df     Pr(>F)
Treatment  3 705.09   3760.5      3     16 < 2.2e-16 ***
Residuals 16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

Pillai Summary: 0.002202 ~~= 0.00~~
Wilks Summary: 0.00000000000000022 ~~= 0.00~~
Hotelling-Lawley Summary: 0.00000000000000022 ~~= 0.00~~
Roy Summary: 0.00000000000000022 ~~= 0.00~~

For this set of data, the type of test executed for the summary does affect the p-value results with the Pillai summary having a significantly larger value than the other three, although still well below the 0.05 significance level. In all test cases the NULL hypothesis would be rejected in favour of the alternative hypothesis meaning the field treatment does have a notable effect on the fields.

4

C

```
> Cont.T1.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatme
nt %in% c("Control","T1"))

> Cont.T2.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatme
nt %in% c("Control","T2"))

> Cont.T3.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatme
nt %in% c("Control","T3"))

> T1.T2.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatment
%in% c("T1","T2"))

> T1.T3.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatment
%in% c("T1","T3"))

> T2.T3.man<-manova(cbind(M1,M2,M3)~Treatment,data=fields,subset=Treatment
%in% c("T2","T3"))
> summary(Cont.T1.man)
          Df  Pillai approx F num Df den Df   Pr(>F)
Treatment  1 0.99456   365.81      3      6 3.51e-07 ***
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(Cont.T2.man)
          Df Pillai approx F num Df den Df    Pr(>F)
Treatment  1 0.9998    10058      3      6 1.719e-11 ***
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(Cont.T3.man)
          Df  Pillai approx F num Df den Df    Pr(>F)
Treatment  1 0.99958   4780.8      3      6 1.599e-10 ***
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(T1.T2.man)
          Df  Pillai approx F num Df den Df   Pr(>F)
Treatment  1 0.99398    330.5      3      6 4.75e-07 ***
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(T1.T3.man)
          Df  Pillai approx F num Df den Df    Pr(>F)
Treatment  1 0.99587    482.3      3      6 1.538e-07 ***
Residuals  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(T2.T3.man)
          Df  Pillai approx F num Df den Df Pr(>F)
Treatment  1 0.28343  0.79107      3      6 0.5416
Residuals  8
> |
```

P-values

Control:T1 = 3.51e-07 ~~= 0.00~~
Control:T2 = 1.719e-11 ~~= 0.00~~
Control:T3 = 1.599e-10 ~~= 0.00~~
T1:T2 = 4.75e-7 = ~~0.00~~
T1:T3 = 1.538e-07 ~~= 0.00~~
T2:T3 = 0.5416 ≈ 0.54

The only pairwise comparison that follows the NULL hypothesis is the T2:T3 pairwise comparison which has a p-value of approximately 0.54, all other pairwise comparison results have p-values significantly below the 0.05 significance level.

Bonferroni Correction

As multiple tests have been executed with various variables on the same dataset, we need to address the type I error issue as each test has its own 0.05 error margin.

Calculating current error rate:

Significance level/alpha = 0.05

$1 - (1-0.05)^6 = 0.26490810937$

This error rate is obviously alarmingly high, and this is why we need Bonferroni correction here.

Bonferroni correction considering the 6 tests:

$0.05/6 = 0.00833333333$

If we use this value as the significance value for the test then once the 6 tests have been completed, the overall error rate should be around the 0.05 we are looking for.

$1 - (1-(0.05/6))^6 = 0.048969835310$

When testing this correction, we see that the new error rate almost matches our 0.05 significance value which is what we want. The significance value is slightly altered lowering by a small amount to 0.049 from 0.05.

difference in mean vectors (M_1, M_2, M_3) across treatment.

D

```
> summary.aov(Cont.T1.man)
 Response M1 :
            Df Sum Sq Mean Sq F value    Pr(>F)
Treatment    1 281.96 281.961  275.08 1.764e-07 ***
Residuals    8   8.20   1.025
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Response M2 :
            Df  Sum Sq Mean Sq F value    Pr(>F)
Treatment    1 251.001  251.00  241.23 2.941e-07 ***
Residuals    8   8.324    1.04
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Response M3 :
            Df Sum Sq Mean Sq F value    Pr(>F)
Treatment    1 1014.0  1014.0  1448.6 2.493e-10 ***
Residuals    8    5.6     0.7
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

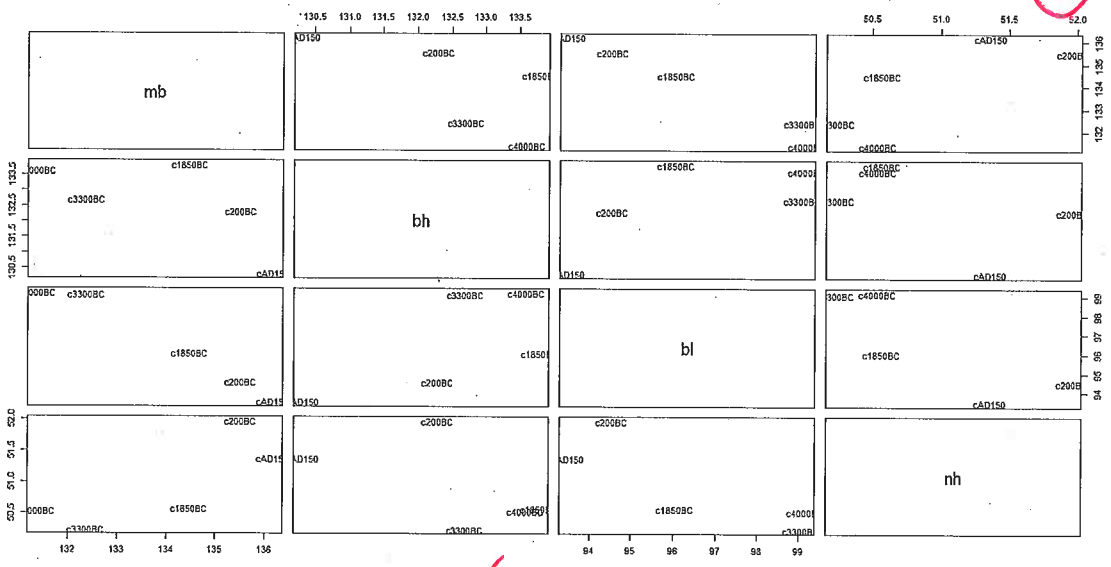
Shows the results for the results and p-value for each of the variables (M1, M2, M3) within the test, (Control, T1) and this can be used to see the results for the other tests. In this case all the P-values are below the 0.05 significance level. However, if looking at the summary.aov() results for T2 and T3, we should be able to see which variables affected these factors the most for the test to produce a p-value greater than 0.05.

Confused.

Q7

13/18

Question 7



The plots show that values do change over time. If they did not, the dates would be shown near the same spot. Looking at the positions of the plots and knowing the label of the row is the Y axis and label of the Column is the X axis, we can see how the values for the different measurements may change over time.

MB appears to increase over time.

BH decrease from 4000 to 3300, the increases to 1850 before decreasing until 150AD.

BL clearly decrease at a fairly consistent rate over time.

NB drops from 4000 to 3300 before climbing in values to 200BC and then dropping slightly during 150AD

```
> means
              mb       bh       bl       nh
c4000BC 131.3667 133.6000 99.16667 50.53333
c3300BC 132.3667 132.7000 99.06667 50.23333
c1850BC 134.4667 133.8000 96.03333 50.56667
c200BC  135.5000 132.3000 94.53333 51.96667
cAD150  136.1667 130.3333 93.50000 51.36667
> |
```

The means table displayed above shows how the average value changes over the time periods. In this case it shows similar results to what was discovered from the pairwise plot. Which is that mb values increase at a seemingly steady rate and appears to have to be overall largest values of the variables. Bh looks to sort of fluctuate around the low 130's and has the second highest values of the set of variables. Bl decreases but at what looks like a gradually faster rate with value differences increasing by a larger margin in the later time periods in comparison to the earlier tie periods. Nh values increase but only slightly and this variable has the lowest values by a large margin.

Manova's

```
> skulls.4000.3300.man
Call:
   manova(cbind(mb, bh, bl, nh) ~ epoch, data = skulls, subset = epoch %in%
    c("c4000BC", "c3300BC"))

Terms:
                   epoch Residuals
resp 1            15.000  1433.933
resp 2             12.15   1205.50
resp 3             0.150  1552.033
resp 4            1.3500  474.8333
Deg. of Freedom        1        58

Residual standard errors: 4.972222 4.559 5.172929 2.861255
Estimated effects are balanced
> skulls.4000.1850.man
Call:
   manova(cbind(mb, bh, bl, nh) ~ epoch, data = skulls, subset = epoch %in%
    c("c4000BC", "c1850BC"))

Terms:
                     epoch Residuals
resp 1             144.150  1114.433
resp 2                 0.6    1298.0
resp 3           147.2667 1605.1333
resp 4             0.0167  586.8333
Deg. of Freedom         1        58

Residual standard errors: 4.38342 4.730678 5.260676 3.180851
Estimated effects are balanced
```

```
> Skulls.4000.200.man
Call:
   manova(cbind(mb, bh, bl, nh) ~ epoch, data = skulls, subset = epoch %in%
    c("c4000BC", "c200BC"))

Terms:
                    epoch Residuals
resp 1           256.2667 1208.4667
resp 2             25.35   1343.50
resp 3           322.0167 1615.6333
resp 4            30.8167  452.4333
Deg. of Freedom         1        58

Residual standard errors: 4.564606 4.812878 5.277854 2.792951
Estimated effects are balanced
```

```
> Skulls.4000.AD150.man
Call:
   manova(cbind(mb, bh, bl, nh) ~ epoch, data = skulls, subset = epoch %in%
    c("c4000BC", "cAD150"))

Terms:
                    epoch Residuals
resp 1            345.600  1593.133
resp 2           160.0667 1295.8667
resp 3           481.6667 1745.6667
resp 4            10.4167  622.4333
Deg. of Freedom         1        58

Residual standard errors: 5.240975 4.726788 5.486137 3.275913
Estimated effects are balanced
```

Summaries

```
> summary(Skulls.4000.3300.man)
          Df   Pillai approx F num Df den Df Pr(>F)
epoch      1 0.027674  0.39135      4     55 0.8139
Residuals 58
>
>
> summary(Skulls.4000.1850.man)
          Df  Pillai approx F num Df den Df  Pr(>F)
epoch      1 0.18757   3.1744      4     55 0.02035 *
Residuals 58
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
>
> summary(Skulls.4000.200.man)
          Df  Pillai approx F num Df den Df    Pr(>F)
epoch      1 0.30297   5.9766      4     55 0.0004564 ***
Residuals 58
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
>
> summary(Skulls.4000.AD150.man)
          Df  Pillai approx F num Df den Df    Pr(>F)
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
>
```

Null hypothesis = Variables values remain the same across the time periods

Alternative hypothesis = Variable values change over the time periods

p-values

4000:3300 = 0.8139 ~~= 0.81~~

4000:1850 = 0.02035 ~~= 0.02~~

4000:200 = 0.0004564 ~~= 0.00~~

4000:AD150 = 0.00004736 ~~= 0.00~~

The p-values get gradually smaller over the time periods meaning the difference between the variables values at 4000BC have a greater difference with the values of the later time periods.

The p-value for the 4000:3300 MANOVA test is 0.81 which is above the 0.15 significance level provided in the assignment brief. Which means the NULL hypothesis is accepted for the 4000:3300 test and this tell us that the difference in values between these years is so small/insignificant that it is classed as the values remaining the same.

The p-value for the 4000:1850 MANOVA test is 0.02 which is larger than the following time periods' p-values but still well below the 0.15 significance level. For the two time periods that follow, the p-values are practically 0 and insignificant. Therefore, the three last time periods (1850BC, 200BC and AD150) all reject the NULL hypothesis in favour of the alternative hypothesis meaning there appears to be a significant difference/change in variable values within these time periods when compared to the initial values of the year 4000BC

I used summary.aov() to see the results for each of the variables for the 4000:3300 MANOVA test.

```
> summary.aov(skulls.4000.3300.man)
 Response mb :
            Df Sum Sq Mean Sq F value Pr(>F)
epoch        1   15.0  15.000  0.6067 0.4392
Residuals   58 1433.9  24.723

 Response bh :
            Df  Sum Sq Mean Sq F value Pr(>F)
epoch        1   12.15  12.150  0.5846 0.4476
Residuals   58 1205.50  20.785

 Response bl :
            Df  Sum Sq Mean Sq F value Pr(>F)
epoch        1    0.15   0.150  0.0056 0.9406
Residuals   58 1552.03  26.759

 Response nh :
            Df Sum Sq Mean Sq F value Pr(>F)
epoch        1   1.35  1.3500  0.1649 0.6862
Residuals   58 474.83  8.1868
```

could extend to other longitudinals.

13.

From this we can see that the bl variable is the one of which the values changed the least as the p-value is extremely high and fairly close to 1, although all the variables show very high p-values. Mb shows the greatest difference in its values but the change is still too small to be counted as significant.

Calculating current error rate:

Significance level/alpha = 0.15

$1 - (1\text{-}0.15)^4 = 0.47799375$

Bonferroni correction considering the 6 tests:

$$0.15/4 = 0.0375$$

Calculating new error rate:

$$1 - (1-(0.15/4))^4 = 0.14177145996$$

If we check each p-value of the tests against this new significance value (0.0375), we will achieve a final error rate closer to the desired significance level. Although this process will likely increase the number of false-positives.

With this new critical p-value/significance level, the hypotheses remain the same for the results with the 4000:3300 MANOVA accepting the NULL hypotheses and the other three MANOVAs rejecting the NULL hypothesis.

Question 8

A

```
> Q8.man<-manova(cbind(X1,X2,X3)~as.factor(group),data=Q8)
> Q8.man
Call:
   manova(cbind(X1, X2, X3) ~ as.factor(group), data = Q8)

Terms:
               as.factor(group) Residuals
resp 1                 15.48458  13.95500
resp 2                 15.89500  12.98333
resp 3                 0.351667  5.866667
Deg. of Freedom               3        20

Residual standard errors: 0.8353143 0.8057088 0.5416026
Estimated effects may be unbalanced
>
>
> summary(Q8.man)
                Df  Pillai approx F num Df den Df  Pr(>F)
as.factor(group)  3 0.84728   2.6239      9     60 0.01254 *
Residuals        20
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

P-value returned is 0.01. The p-value is below 0.05 and so the NULL hypothesis is rejected in favour of the alternative hypothesis, meaning that there is some level of difference involved.

```
> summary(Q8.man,test="W")
                Df   Wilks approx F num Df den Df   Pr(>F)
as.factor(group)  3 0.25036   3.7439      9 43.958 0.001469 **
Residuals        20
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

B

Using the code provided for this part of the question. I retrieved the following:

```
> Lambda
[1] 0.2503629
```

X

Edit the same chunk of code to answer the three questions: 1 vs 4, 2 vs 3, 1 and 4 vs 2 and 3

```
> Y<-as.matrix(Q8[,1:3])
> N<-6
>
> sample.mean1<-apply(Y[1:N,],2,mean)
> sample.mean2<-apply(Y[(N+1):(2*N),],2,mean)
> sample.mean3<-apply(Y[(2*N+1):(3*N),],2,mean)
> sample.mean4<-apply(Y[(3*N+1):(4*N),],2,mean)
> overall.mean<-apply(Y,2,mean)

> Total.SSP<-matrix(0,3,3)
> for (i in 1:24){
+     Total.SSP<-Total.SSP+(Y[i,]- sample.mean1)%*%t(Y[i,]- sample.mean4)
+ }

> Between.SSP<-matrix(0,3,3)
> for (i in 1:4){
+     sample.mean<-apply(Y[((i-1)*N+1):(i*N),],2,mean)
+     Between.SSP<-Between.SSP+N*(sample.mean- sample.mean1)%*%t(sample.me
an- sample.mean4)
+ }

> Within.SSP<-Total.SSP-Between.SSP

> Lambda<-det(Within.SSP)/det(Within.SSP+Between.SSP)
>
```

1 and 4

```
> Total.SSP<-matrix(0,3,3)
> for (i in 1:24){
+     Total.SSP<-Total.SSP+(Y[i,]-sample.mean1)%*%t(Y[i,]-sample.mean4)
+ }
>
> Between.SSP<-matrix(0,3,3)
> for (i in 1:4){
+     sample.mean<-apply(Y[((i-1)*N+1):(i*N),],2,mean)
+     Between.SSP<-Between.SSP+N*(sample.mean-sample.mean1)%*%t(sample.mea
n-sample.mean4)
+ }
>
> Within.SSP<-Total.SSP-Between.SSP
> Lambda.1v4<-det(Within.SSP)/det(Within.SSP+Between.SSP)
```

2 and 3

```
> Total.SSP<-matrix(0,3,3)
> for (i in 1:24){
+     Total.SSP<-Total.SSP+(Y[i,]-sample.mean2)%*%t(Y[i,]-sample.mean3)
```

```
+ }
>
> Between.SSP<-matrix(0,3,3)
> for (i in 1:4){
+     sample.mean<-apply(Y[((i-1)*N+1):(i*N),],2,mean)
+     Between.SSP<-Between.SSP+N*(sample.mean-sample.mean2)%*%t(sample.mea
n-sample.mean3)
+ }
>
> Within.SSP<-Total.SSP-Between.SSP
> Lambda.2v3<-det(Within.SSP)/det(Within.SSP+Between.SSP)
```

1,4 and 2, 3

```
>  Total.SSP<-matrix(0,3,3)
>  for (i in 1:24){
+         Total.SSP<-Total.SSP+(Y[i,]-(sample.mean1+sample.mean4))%*%t(Y[i,]-(sample.mean2+sample.mean3))
+     }
>
>     Between.SSP<-matrix(0,3,3)
>     for (i in 1:4){
+         sample.mean<-apply(Y[((i-1)*N+1):(i*N),],2,mean)
+         Between.SSP<-Between.SSP+N*(sample.mean-(sample.mean1+sample.mean4))%*%t(sample.mean-(sample.mean2+sample.mean3))
+     }
>
>     Within.SSP<-Total.SSP-Between.SSP
>     Lambda.14v23<-det(Within.SSP)/det(Within.SSP+Between.SSP)
```

Sample means

Sample Mean Nº	X1	X2	X3	Mean
1	3.100000	5.033333	7.866667	5.333
2	4.283333	6.166667	7.566667	6.006
3	4.366667	6.516667	7.600000	6.161
4	2.466667	4.516667	7.600000	4.861
Overall	3.554167	5.558333	7.658333	5.590

✓

Contrast lambdas

Contrast	Lambda
Overall	0.2503629
1 vs 4	0.2037491
2 vs 3	0.1703486
1,4 vs 2,3	0.0005620253

X.

Total number of observations per group = 18 (as 6 observation and 3 variables) 6 obs. per group.

Total number of observations for all groups = 72

Total number of observations for two groups = 36

F approximation

Using equation:

$$F = \left(\frac{1 - lambda}{lambda}\right) * \left(\frac{N - g - p + 1}{p}\right)$$

Where N = number of observations, g = number of groups, p = number of variables.

1 vs 4:

N = (18 * 2) = 36

g = 2

p = 3

$$41.6853 = 3.907997 * 10.66667$$

2 vs 3:

N = (18 * 2) = 36

g = 2

p = 3

$$51.95003 = 4.870315 * 10.66667$$

1,4 vs 2,3:

N = (18 * 4) = 72

g = 4

p = 3

$$39122.14 = 1778.279 * 22$$

```
> summary(sample.mean1)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  3.100   4.067   5.033   5.333   6.450   7.867
>
> summary(sample.mean2)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  4.283   5.225   6.167   6.006   6.867   7.567
>
> summary(sample.mean3)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  4.367   5.442   6.517   6.161   7.058   7.600
>
> summary(sample.mean4)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  2.467   3.492   4.517   4.861   6.058   7.600
>
> summary(overall.mean)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  3.554   4.556   5.558   5.590   6.608   7.658
```