Math 760

Chapter 6 HW

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2. Using the information in Example 6.1, construct the 95% Bonferroni simultaneous intervals for the components of the mean difference vector δ. Compare the lengths of these intervals with those of the simultaneous intervals constructed in the example.

The 95% Bonferroni simultaneous interval formula is: $\bar{x}_p \pm t_{n-1}\left(\frac{\alpha}{2p}\right)\sqrt{\frac{s_{pp}}{n}}$

```
## Commercial Lab: ( -22.29112 , 3.571124 )
## State Lab of Hygiene: ( -5.472651 , 32.01265 )
```

From Example 6.1, the simultaneous intervals are:

$$\delta_1: -9.35 \pm \sqrt{9.47}\sqrt{\frac{199.26}{11}} \Rightarrow (-22.46, 3.74)$$

$$\delta_2: 13.27 \pm \sqrt{9.47}\sqrt{\frac{418.61}{11}} \Rightarrow (-5.71, 32.25)$$

We see that the simultaneous intervals from Example 6.1 are larger than the Bonferroni ones, but not by much.

```
## Simultaneous - Bonferroni, d1 lower:  -0.1688761
## Simultaneous - Bonferroni, d1 upper:  0.1688761
## Simultaneous - Bonferroni, d2 lower:  -0.2373493
## Simultaneous - Bonferroni, d2 upper:  0.2373493
```

5. A researcher considered three indices measuring the severity of heart attacks. The values of these indices for n = 40 heart-attack patients arriving at a hospital emergency room produced the summary statistics

```
## xbar matrix:
##      [,1]
## [1,] 46.1
## [2,] 57.3
## [3,] 50.4
##
##  S matrix:
##       [,1] [,2] [,3]
## [1,] 101.3 63.0 71.0
```

```
## [2,]  63.0 80.2 55.6
## [3,]  71.0 55.6 97.4
```

(a) All three indices are evaluated ∀ patient. Test the equality of mean indices using (6-16) with $\alpha = 0.05$.

$$\boldsymbol{H_0}: \boldsymbol{C\mu} = \mathbf{0} \textbf{ vs } \boldsymbol{H_1}: \boldsymbol{C\mu} \neq \mathbf{0}$$

We will be using (6-16) to decide if we accept or reject H_0.
The formula is: $T^2 = n(C\bar{x})'(CSC')^{-1}(C\bar{x}) > \frac{(n-1)(q-1)}{n-q+1} F_{q-1,n-q+1}(\alpha)$
If our T^2 value is greater than the critical value, we will reject H_0. That said, our critical value is:

```
## [1] 6.660417
```

Our contrast matrix will be:

```
##      [,1] [,2] [,3]
## [1,]    1   -1    0
## [2,]    0    1   -1
```

Thus, our T^2 value is:

```
##          [,1]
## [1,] 90.49458
```

Because $T^2 = 90.49458 > 6.660417$, we reject H_0.

(b) Judge the differences in pairs of mean indices using 95% simultaneous confidence intervals. [See (6-18)]

The (6-18) formula is: $c'\mu: c'\bar{x} \pm \sqrt{\frac{(n-1)(q-1)}{n-q+1} F_{q-1,n-q+1}(\alpha)} \sqrt{\frac{c'Sc}{n}}$
We'll be finding these pairs: $\mu_1 - \mu_2$, $\mu_1 - \mu_3$, and $\mu_2 - \mu_3$.

```
## 95% simultaneous confidence intervals
##
##  mu1 - mu2: ( -14.23996 , -8.160045 )
## mu1 - mu3: ( -7.6251 , -0.9748998 )
## mu2 - mu3: ( 3.5749 , 10.2251 )
```

The differences in pairs of mean indices are all quite different from each other when looking at these intervals.

10. Consider the univariate one-way decomposition of the observation x_{lj} given by (6-34). Show that the mean vector $\bar{x}1$ is always perpendicular to the treatment effect vector $(\bar{x}_1 - \bar{x})\boldsymbol{\mu}_1 + (\bar{x}_2 - \bar{x})\boldsymbol{\mu}_2 + \ldots + (\bar{x}_g - \bar{x})\boldsymbol{\mu}_g$ where

$$\mathbf{u}_1 = \begin{bmatrix} 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix} \Big\} n_1 \quad , \mathbf{u}_2 = \begin{bmatrix} 0 \\ \vdots \\ 0 \\ 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix} \Big\} n_2 \quad , \ldots , \mathbf{u}_g = \begin{bmatrix} 0 \\ \vdots \\ 0 \\ 0 \\ \vdots \\ 0 \\ 1 \\ \vdots \\ 1 \end{bmatrix} \Big\} n_g$$

The formula of (6-34) is: $x_{lj} = \bar{x} + (\bar{x}_l - \bar{x}) + (x_{lj} - \bar{x}_l)$. In writing, this is: observation = overall sample mean + estimated treatment effect + residual.

$$(\bar{x}1)'\left[(\bar{x}_1 - \bar{x})\mu_1 + \ldots + (\bar{x}_g - \bar{x})\mu_g\right] = \bar{x}\left[(\bar{x}_1 - \bar{x})n_1 + \ldots + (\bar{x}_g - \bar{x})n_g\right]$$
$$= \bar{x}\left[n_1\bar{x}_1 + \ldots + n_g\bar{x}_g - \bar{x}(n_1 + \ldots + n_g)\right] = \bar{x}\left[(n_1 + \ldots + n_g)\bar{x} - \bar{x}(n_1 + \ldots + n_g)\right] = 0$$

16. Four measures of the response stiffness on each of 30 boards are listed in Table 4.3 (see Example 4.14). The measures, on a given board, are repeated int he sense that they were made one after another. Assuming that the measures of stiffness arise from four treatments, test for the equality of treatments in a repeated measures design context. Set $\alpha = 0.05$. Construct a 95% (simultaneous) confidence interval for a contrast in the mean levels representing a comparison of the dynamic measurements with the static measurements.

$$\boldsymbol{H_0}: \boldsymbol{C\mu} = \mathbf{0} \text{ va } \boldsymbol{H_1}: \boldsymbol{C\mu} \neq \mathbf{0}$$

Our contrast, C, matrix is:

```
##      [,1] [,2] [,3] [,4]
## [1,]    1   -1    0    0
## [2,]    0    1   -1    0
## [3,]    0    0    1   -1
```

We'll be once again using (6-16) for this problem.

```
## The critical value is  9.53891
```

Now, we find our T^2 value and see if it's greater than our critical value

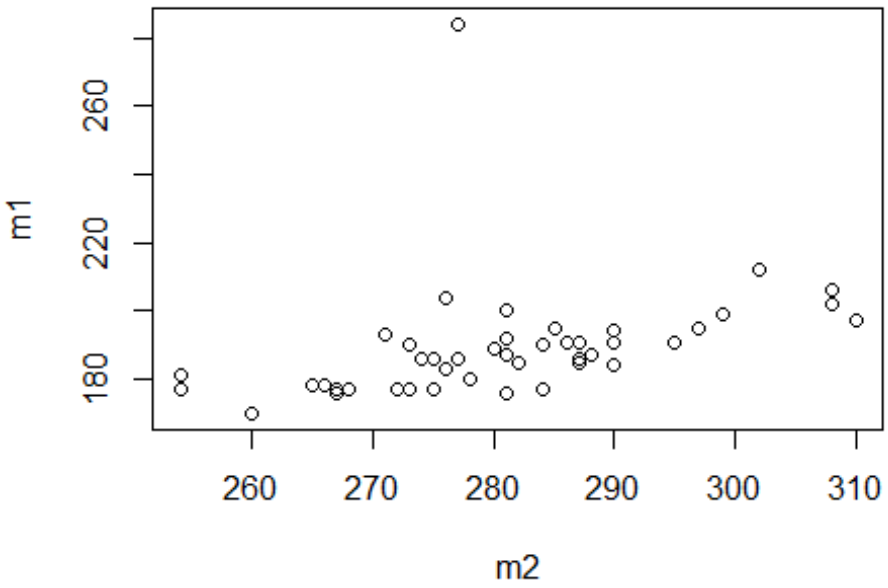
```
## Our T-squared value is  254.7158
## Is it greater than  9.53891 ?:  TRUE
```

Because $T^2 > 9.53891$, we reject H_0 at $\alpha = 0.05$ level.

Now, we will construct our 95% simultaneous confidence interval for dynamic and static measurements.

```
## The 95% simultaneous confidence interval is ( 247.0397 , 596.027 )
```

20. The tail lengths in measurements (x_1) and wing lengths in millimeters (x_2) for 45 male hook-billed kites are given in Table 6.11 on page 346. Similar measurements for female hook-billed kites were given in Table 5.12.
(a) Plot the male hook-billed kite data as a scatter diagram, and (visually) check for outliers. (Note, in particular, observation 31 with $x_1 = 284$)



Only one observation stands out:

```
##      V1  V2
## 31 284 277
```

(b) Test for equality of mean vectors for the populations of male and female hook-billed kites. Set $\alpha = 0.05$. If $H_0: \mu_1 - \mu_2 = 0$ is rejected, find the linear combination most responsible for the rejection of H_0. (You may want to eliminate any outliers found in (a) for the male hook-billed data before conducting this test. Alternatively, you may want to interperet $x_1 = 284$ for observation 31 as a misprint and conduct the test with $x_1 = 184$ for this observation. Does it make any difference in this case how observation 31 for the male hook-billed kite data is treated?)

We will have two male datasets: one with observation 31 as a misprint, and one without observation 31.

$$\boldsymbol{H_0: \mu_1 - \mu_2 = 0 \text{ vs } H_1: \mu_1 - \mu_2 \neq 0}$$

```
##
##  Hotelling's two sample T2-test
##
## data:  male1 and female
## T.2 = 6.713, df1 = 2, df2 = 87, p-value = 0.001944
## alternative hypothesis: true location difference is not equal to c(0,0)
##
##  Hotelling's two sample T2-test
##
## data:  male2 and female
## T.2 = 12.339, df1 = 2, df2 = 86, p-value = 1.944e-05
## alternative hypothesis: true location difference is not equal to c(0,0)
```

We see that with either male dataset, we will reject H_0 because $p < 0.05 = \alpha$.

We now will find the linear combination most responsible for this rejection. It is said that the coefficient vector for the linear combination most responsible for rejection is proportional to $S_{pooled}^{-1}(\bar{x_1} - \bar{x_2})$. Now, if we used the misprint dataset, there is a remark about datasets with the same sample size:

Remark: If $n_1 = n_2 = n$, then
$\frac{n-1}{n+n-2} = \frac{1}{2}$, so $\frac{1}{n_1}S_1 + \frac{1}{n_2}S_2 = \frac{1}{n}(S_1 + S_2) = \frac{(n-1)S_1 + (n-1)S_2}{n+n-2}\left(\frac{1}{n} + \frac{1}{n}\right) = S_{pooled}\left(\frac{1}{n} + \frac{1}{n}\right)$

With this in mind, our linear combination is:

```
##             [,1]
## [1,] -2.1886841
## [2,]  0.7353992
```

(c) Determine the 95% confidence region for $\mu_1 - \mu_2$ and 95% simultaneous confidence intervals for the components of $\mu_1 - \mu_2$.

The 95% confidence region formula for $\mu_1 - \mu_2$ is from **(6-30)**:

$$[(\bar{x_1} - \bar{x_2}) - (\mu_1 - \mu_2)]' \left(\frac{1}{n_1}S_1 + \frac{1}{n_2}S_2\right)^{-1} [(\bar{x_1} - \bar{x_2}) - (\mu_1 - \mu_2)] \leq \frac{vp}{v - p + 1} F_{p,v-p+1}(\alpha)$$

```
## The left side of the inequality is  4.142067
## The right side of the inequality is  2.888072
```

The 95% confidence region is $6.502715 \leq 2.888072$

For the 95% simultaneous intervals for the components of $\mu_1 - \mu_2$, we get:

Tail length (V_1): (-10.800065, -2.266602)
Wing length (V_2): (-6.204043, 8.159598)

```
##
##  Welch Two Sample t-test
##
## data:  male1$V1 and female$V1
## t = -3.0441, df = 85.679, p-value = 0.003099
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -10.800065  -2.266602
## sample estimates:
## mean of x mean of y
##  187.0889  193.6222
##
##  Welch Two Sample t-test
##
## data:  female$V2 and male1$V2
## t = 0.27088, df = 81.231, p-value = 0.7872
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -6.204043  8.159598
## sample estimates:
## mean of x mean of y
##  279.7778  278.8000
```

(d) Are male or female birds generally larger.

Female birds are generally larger, though more particularly with the tails as shown with the confidence intervals:

Tail length (V_1): (-10.800065, -2.266602)
Wing length (V_2): (-6.204043, 8.159598)

Wing length does include 0, which means no significance difference; but tail length is all negative.

25. Construct a one-way MANOVA of the crude-oil data listed in Table 11.7 on page 662. Construct 95% simultaneous confidence intervals to determine which mean components differ among the populations. (You may want to consider transformations of the data to make them more closely conform to the usual MANOVA assumptions.)

Without transforming the data, here are our results:

H_0: The mean components do not differ among populations
H_1: The mean components do differ among populations

```
##           Df   Wilks approx F num Df den Df    Pr(>F)
## pie        2 0.11591   18.985     10     98 < 2.2e-16 ***
## Residuals 53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Because the p-value is extremely small, we reject H_0, which means the mean components do differ among populations.

The 95% simultaneous confidence intervals will be based on groups in V6: Wilhelm, SubMuli, and Upper. The intervals are:

```
## tau1 - tau2
## tau1[1]-tau2[1] belongs to (-2.845798,0.412032)
## tau1[2]-tau2[2] belongs to (2.040458,18.92058)
## tau1[3]-tau2[3] belongs to (-0.2759328,0.1684003)
## tau1[4]-tau2[4] belongs to (-0.7699259,1.239536)
## tau1[5]-tau2[5] belongs to (3.570383,8.542344)
##
##  tau1 - tau3
## tau1[1]-tau3[1] belongs to (-5.383456,-2.612032)
## tau1[2]-tau3[2] belongs to (14.13887,28.49873)
## tau1[3]-tau3[3] belongs to (-0.5039587,-0.1259662)
## tau1[4]-tau3[4] belongs to (1.282835,2.992277)
## tau1[5]-tau3[5] belongs to (3.657291,7.88692)
##
##  tau2 - tau3
## tau2[1]-tau3[1] belongs to (-3.934361,-1.627362)
## tau2[2]-tau3[2] belongs to (4.861534,16.81502)
## tau2[3]-tau3[3] belongs to (-0.4185211,-0.1038712)
## tau2[4]-tau3[4] belongs to (1.191261,2.614241)
## tau2[5]-tau3[5] belongs to (-2.04468,1.476164)
```

Of all the simultaneous confidence intervals, the ones that don't cover 0 are:

$\tau_1 - \tau_2: V2, V5$
$\tau_1 - \tau_3: V1, V2, V3, V3, V5$
$\tau_2 - \tau_3: V1, V2, V3, V3, V5$

This means there are significant differences between the three different groups, especially between Wilhelm-Upper and SubMuli-Upper.

29. Using the data on bone mineral content in Table 1.8, investigate equality between the dominant and nondominant bones.

(a) Test using $\alpha = 0.05$

$$\boldsymbol{H_0: \mu_1 - \mu_2 = 0 \text{ vs } H_1: \mu_1 - \mu_2 \neq 0}$$

```
##
##  Hotelling's two sample T2-test
##
## data:  dom and weak
## T.2 = 0.29523, df1 = 3, df2 = 46, p-value = 0.8286
## alternative hypothesis: true location difference is not equal to c(0,0,0)
```

Because $p = 0.8286 > 0.05 = \alpha$, we fail to reject H_0 at 95% significance.

(b) Construct 95% simultaneous confidence intervals for the mean differences.

```
## Radius: ( -0.01458661 , 0.06554661 )
## Humerus Height: ( -0.0237914 , 0.1394714 )
## Ulna: ( -0.04262241 , 0.06374241 )
```

(c) Contruct the Bonferroni 95% simultaneous intervals, and compare these with the intervals in (b).

```
## Radius: ( -0.008338575 , 0.05929857 )
## Humerus Height: ( -0.01106171 , 0.1267417 )
## Ulna: ( -0.03432909 , 0.05544909 )
```

33. Refer to Exercise 6.32. The data in Table 6.18 are measurements on the variables X_1 [percent spectral reflectance at wavelength 560 nm (green)], X_2 [percent spectral reflectance at wavelength 720 nm (near infrared)] for three species (sitka spruce [SS], Japanese larch [JL], and lodgepole pine [LP]) of 1-year-old seedlings taken at three different times (Julian day 150 [1], Julian day 235 [2], and Julian day 320 [3]) during the growing season. The seedlings were all grown with the optimal level of nutrient.

(a) Perform a two-factor MANOVA using the data in Table 6.18. Test for a species effect, a time effect, and species-time interaction. Use $\alpha = 0.05$.

H_0: There is a species effect vs H_1: There is no species effect.

```
##           Df   Wilks approx F num Df den Df Pr(>F)
## x3         2 0.67704   3.4452      4     64  0.013 *
## Residuals 33
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Because $p = 0.013 < 0.05 = \alpha$, we reject H_0; there is no species effect.

H_0: There is a time effect vs H_1: There is no time effect.

```
##           Df   Wilks approx F num Df den Df   Pr(>F)
## x4         1 0.48184   17.744      2     33 5.86e-06 ***
## Residuals 34
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Because $p = 5.86e-06 < 0.05 = \alpha$, we reject H_0; there is no time effect.

H_0: There is a species-time effect vs H_1: There is no species-time effect.

```
##           Df   Wilks approx F num Df den Df    Pr(>F)
## x3         2 0.32499   10.935      4     58 1.125e-06 ***
## x4         1 0.26621   39.968      2     29 4.632e-09 ***
## x3:x4      2 0.42843    7.653      4     58 5.063e-05 ***
## Residuals 30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

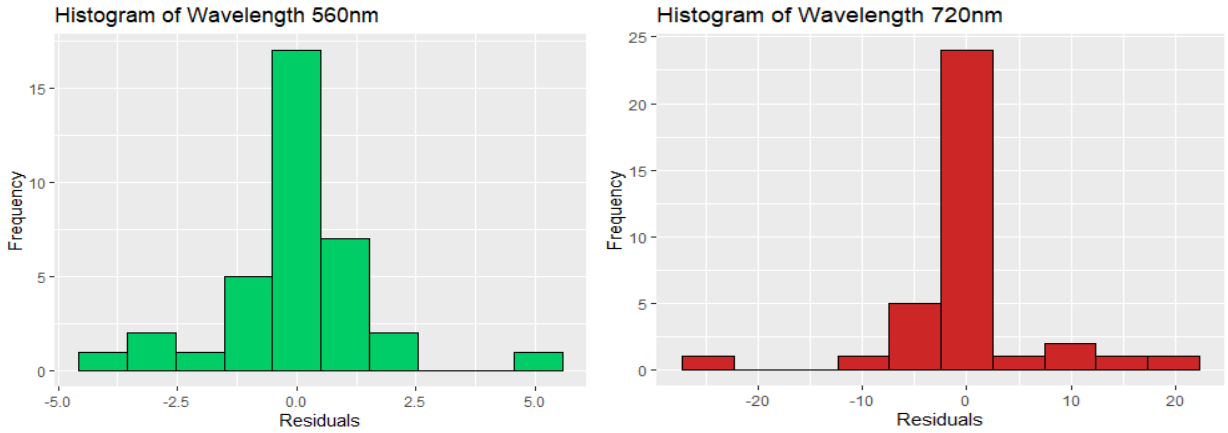
Because $p < 0.05 = \alpha$ for all variables, we reject H_0; there is no species-time effect.

(b) Do you think the usual MANOVA assumptions are satisfied for these data? Discuss with reference to a residual analysis, and the possibility of correlated observations over time.

The MANOVA assumptions are:

1. We assume that the observations are independent of one another, that the sample is completely random.
2. We assume that the independent variables are categorical and dependent variables are continuous or scale variables.
3. There is an absence of multicollinearity between the dependent variables.
4. The data follows a multivariate normal.
5. The variance between groups is equal.

We can check the 4th assumption with the histograms of Wavelength 560nm and Wavelength 720nm below. There are a few outliers in the data, but overall, they approximately follow a normal distribution.



Then, we can check with the rest of the assumptions. The χ^2 test is used for independence, and we see that the p-value is large, which means the 1st assumption does not hold. The correlation test is used to check for linearity, which can in turn tell us about the variance, because variance is part of the correlation equation. We see that p-value is small, which means there is multicollinearity between the dependent variables, which means variance is not equal between the groups. The 3rd and 5th assumptions do not hold.

```
## Warning in chisq.test(table(x1, x2)): Chi-squared approximation may be
## incorrect
##
##  Pearson's Chi-squared test
##
## data:  table(x1, x2)
## X-squared = 1188, df = 1156, p-value = 0.2504
##
##  Pearson's product-moment correlation
##
## data:  x1 and x2
## t = 8.144, df = 34, p-value = 1.691e-09
```

```
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6611588 0.9009499
## sample estimates:
##       cor
## 0.8130816
```

(b) Foresters are particularly interested in the interaction of species and time. Does interaction show up for one variable but not the other? Check by running a univariate two-factor ANOVA for each of the two responses.

```
## Analysis of Variance Table
##
## Response: x1
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## x3             2  965.18  482.59 169.973 5.027e-16 ***
## factor(x4)     2 1275.25  637.62 224.578 < 2.2e-16 ***
## x3:factor(x4)  4  795.81  198.95  70.073 7.341e-14 ***
## Residuals     27   76.66    2.84
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ------------------------------------------------------
## Analysis of Variance Table
##
## Response: x2
##               Df Sum Sq Mean Sq F value    Pr(>F)
## x3             2 2026.9 1013.43 15.4622 3.348e-05 ***
## factor(x4)     2 5573.8 2786.90 42.5207 4.537e-09 ***
## x3:factor(x4)  4  193.5   48.39  0.7383    0.5741
## Residuals     27 1769.6   65.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

After running a univariate two-factor ANOVA for each response, the interaction between predictor variables occurs for wavelength 560nm (green), but not for wavelength 720nm (near infrared).

(c) Can you think of another method of analyzing these data (or a different experimental design) that would allow for a potential time trend in the spectral reflectant numbers?

We could analyze the data by date. The time column goes from 1 to 3, so we can have 3 groups. Then, we can see if the spectral reflectance is either the same or not for all the species within that certain time.

Code Appendix

```
knitr::opts_chunk$set(echo = FALSE)
library(car)
library(DescTools)
library(dplyr)
library(GGally)
library(ggplot2)
library(graphics)
library(gridExtra)
library(gtools)
library(heplots)
library(investr)
library(matlib)
library(MVN)
library(mvnormtest)
library(robustbase)
library(SIBER)
effluent <- stiff <- read.table("D:/Coding/R Storage/T6-1.dat", header =
FALSE, sep = "")
# mats
dMat <- c(-9.36, 13.27)
Smat <- c(199.26, 88.38, 88.38, 418.61)
d <- matrix(dMat, nrow = 2, ncol = 1, byrow = TRUE)
S <- matrix(Smat, nrow = 2, ncol = 2, byrow = TRUE)
# vars
n <- dim(effluent)[1]
p <- dim(effluent)[2]
crit <- -qt(0.05/(2*p), df = n-1)
# comm
neg1 <- d[1] - crit*sqrt((S[1,1]/n))
pos1 <- d[1] + crit*sqrt((S[1,1]/n))
cat("Commercial Lab: (", neg1, ",", pos1, ") \n")
# state
neg2 <- d[2] - crit*sqrt((S[2,2]/n))
pos2 <- d[2] + crit*sqrt((S[2,2]/n))
cat("State Lab of Hygiene: (",neg2, ",", pos2, ")")
eneg1 <- -22.46
epos1 <- 3.74
eneg2 <- -5.71
epos2 <- 32.25
cat("Simultaneous - Bonferroni, d1 lower: ", eneg1 - neg1, "\n")
cat("Simultaneous - Bonferroni, d1 upper: ", epos1 - pos1, "\n")
cat("Simultaneous - Bonferroni, d2 lower: ", eneg2 - neg2, "\n")
cat("Simultaneous - Bonferroni, d2 upper: ", epos2 - pos2)
n <- 40
q <- 3
# mats
xbarMat <- c(46.1, 57.3, 50.4)
Smat <- c(101.3,63.0,71.0,63.0,80.2,55.6,71.0,55.6,97.4)
```

```r
xbar <- matrix(xbarMat, nrow = 3, ncol = 1, byrow = TRUE)
S <- matrix(Smat, nrow = 3, ncol = 3, byrow = TRUE)
# print
cat("xbar matrix: \n")
xbar
cat("\n S matrix: \n")
S
crit <- qf(0.05, df1 = q-1, df2 = n-q+1, lower.tail = FALSE)
frac <- ((n-1)*(q-1))/(n-q+1)
right <- frac*crit
right
Cmat <- c(1,-1,0,0,1,-1)
C <- matrix(Cmat, nrow = 2, ncol = 3, byrow = TRUE)
C
Cx <- C %*% xbar
CSC <- C %*% S %*% t(C)
T2 <- n %*% t(Cx) %*% inv(CSC) %*% Cx
T2
m12 <- xbar[1] - xbar[2]
m13 <- xbar[1] - xbar[3]
m23 <- xbar[2] - xbar[3]
crit1 <- sqrt(right)
S1 <- (CSC/n)
# intervals
neg12 <- m12 - crit1*sqrt(S1[1,1])
neg13 <- m13 - crit1*sqrt(S1[2,2])
neg23 <- m23 - crit1*sqrt(S1[2,2])
pos12 <- m12 + crit1*sqrt(S1[1,1])
pos13 <- m13 + crit1*sqrt(S1[2,2])
pos23 <- m23 + crit1*sqrt(S1[2,2])
# print
cat("95% simultaneous confidence intervals \n")
cat("\n mu1 - mu2: (", neg12, ",", pos12, ") \n")
cat("mu1 - mu3: (", neg13, ",", pos13, ") \n")
cat("mu2 - mu3: (", neg23, ",", pos23, ") \n")
stiff <- read.table("D:/Coding/R Storage/T4-3.dat", header = FALSE, sep = "")
newStiff <- stiff[,1:4]
# cols
x1 <- newStiff$V1
x2 <- newStiff$V2
x3 <- newStiff$V3
x4 <- newStiff$V4
# vars
n <- dim(newStiff)[1]
q <- dim(newStiff)[2]
Cmat <- c(1,-1,0,0,0,1,-1,0,0,0,1,-1)
C <- matrix(Cmat, nrow = 3, ncol = 4, byrow = TRUE)
C
crit <- qf(0.05, df1 = q-1, df2 = n-q+1, lower.tail = FALSE)
frac <- ((n-1)*(q-1))/(n-q+1)
```

```r
right <- frac*crit
cat("The critical value is ", right)
Stiff <- as.matrix(newStiff)
# xbar
one <- as.matrix(rep(1, n))
xbar <- 1/n*t(Stiff)%*%one
# S
mean_matrix <- matrix(data = 1, nrow = n)%*%cbind(xbar[[1]], xbar[[2]],
xbar[[3]], xbar[[4]])
xstar <- Stiff - mean_matrix
S <- 1/(n-1) * t(xstar) %*% xstar
# T2
T2 <- n %*% t(C %*% xbar) %*% inv(C %*% S %*% t(C)) %*% (C %*% xbar)
ans <- T2 > right
# print
cat("Our T-squared value is ", T2, "\n")
cat("Is it greater than ", right, "?: ", ans)
cMat <- c(1,1,-1,-1)
c <- matrix(cMat, nrow = 4, ncol = 1, byrow = TRUE)
# ops
before <- t(c) %*% xbar
after <- sqrt(right) * sqrt((t(c) %*% S %*% c)/n)
cat("The 95% simultaneous confidence interval is (", before - after, ",",
before + after, ")")
male <- read.table("D:/Coding/R Storage/T6-11.dat", header = FALSE, sep = "")
female <- read.table("D:/Coding/R Storage/T5-12.dat", header = FALSE, sep =
"")
# cols
m1 <- male$V1 # tail length
m2 <- male$V2 # wing length
f1 <- female$V1 # tail length
f2 <- female$V2 # wing length
plot(m2,m1)
male[31,]
male1 <- male
male2 <- male
male1[31,] <- 184
male2 <- male2[-31,]
HotellingsT2Test(x = male1, y = female)
HotellingsT2Test(x = male2, y = female)
n <- 45
# xbar
onem1 <- as.matrix(rep(1, n))
onef <- as.matrix(rep(1, n))
xbarm1 <- 1/n*t(male1)%*%onem1
xbarf <- 1/n*t(female)%*%onef
# S
mean_matrixm1 <- matrix(data = 1, nrow = n)%*%cbind(xbarm1[[1]], xbarm1[[2]])
mean_matrixf <- matrix(data = 1, nrow = n)%*%cbind(xbarf[[1]], xbarf[[2]])
xstarm1 <- male1 - mean_matrixm1
```

```r
xstarf <- female - mean_matrixf
Sm1 <- 1/(n-1) * t(xstarm1) %*% as.matrix(xstarm1)
Sf <- 1/(n-1) * t(xstarf) %*% as.matrix(xstarf)
# combo
fracnum1 <- (n-1)*Sm1 + (n-1)*Sf
fracdenom1 <- n + n - 2
frac1 <- fracnum1/fracdenom1
frac2 <- (1/n)+(1/n)
Sp <- frac1*frac2
xbar <- xbarm1 - xbarf
combo <- inv(Sp)%*%xbar
combo
v <- 87
p <- 2
# crit
crit <- qf(0.05, df1 = v, df2 = v-p+1, lower.tail = FALSE)
frac <- (v*p)/(v-p+1)
right <- crit * frac
# mu
mumV1 <- mean(male1$V1)
mufV1 <- mean(female$V1)
mumV2 <- mean(male1$V2)
mufV2 <- mean(female$V2)
mu1 <- mumV1 - mufV1
mu2 <- mumV2 - mufV2
mu <- mu1 - mu2
# left
mux <- xbar - mu
left <- t(mux) %*% inv(Sp) %*% mux
# print
cat("The left side of the inequality is ", left, "\n")
cat("The right side of the inequality is ", right)
# t-test
t.test(x = male1$V1, y = female$V1)
t.test(x = female$V2, y = male1$V2)
oil <- read.table("D:/Coding/R Storage/T11-7.dat", header = FALSE, sep = "")
# cols
x1 <- oil$V1
x2 <- oil$V2
x3 <- oil$V3
x4 <- oil$V4
x5 <- oil$V5
pie <- oil$V6
# model
depend <- cbind(x1,x2,x3,x4,x5)
model1 <- manova(depend ~ pie, data = oil)
summary(model1, test = "Wilks")
g <- 3
n1 <- length(which(oil$V6 == "Wilhelm"))
n2 <- length(which(oil$V6 == "SubMuli"))
```

```r
n3 <- length(which(oil$V6 == "Upper"))
n <- n1+n2+n3
alpha <- 0.05
# subset
Wilhelm <- oil[1:7,]
Wilhelm <- Wilhelm[,-6]
SubMuli <- oil[8:18,]
SubMuli <- SubMuli[,-6]
Upper <- oil[19:56,]
Upper <- Upper[,-6]
# xbar
xbar1 <- colMeans(Wilhelm)
xbar2 <- colMeans(SubMuli)
xbar3 <- colMeans(Upper)
xbar <- (n1*xbar1 + n2*xbar2 + n3*xbar3)/n
# cov
S1 <- cov(Wilhelm)
S2 <- cov(SubMuli)
S3 <- cov(Upper)
W <- (n1-1)*S1 + (n2-1)*S2 + (n2-1)*S3
# crit
qtlevel <- qt(1-alpha/(p*g*(g-1)), df = n-g)
# loop
cat("tau1 - tau2 \n")
for ( i in 1:5 ){
# \tau_{11}-\tau_{21}
LCI12 <- (xbar1[i]-xbar2[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
UCI12 <- (xbar1[i]-xbar2[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n2))
cat("tau1[",i,"]-tau2[",i,"] belongs to (",LCI12,",",UCI12,")\n",sep="")
}
cat("\n tau1 - tau3 \n")
for ( i in 1:5 ){
# \tau_{11}-\tau_{31}
LCI13 <- (xbar1[i]-xbar3[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n3))
UCI13 <- (xbar1[i]-xbar3[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n1+1/n3))
cat("tau1[",i,"]-tau3[",i,"] belongs to (",LCI13,",",UCI13,")\n",sep="")
}
cat("\n tau2 - tau3 \n")
for ( i in 1:5 ){
# \tau_{21}-\tau_{31}
LCI23 <- (xbar2[i]-xbar3[i])-qtlevel*sqrt(W[i,i]/(n-g)*(1/n2+1/n3))
UCI23 <- (xbar2[i]-xbar3[i])+qtlevel*sqrt(W[i,i]/(n-g)*(1/n2+1/n3))
cat("tau2[",i,"]-tau3[",i,"] belongs to (",LCI23,",",UCI23,")\n",sep="")
}
bone <- read.table("D:/Coding/R Storage/T1-8.dat", header = FALSE, sep = "")
# vars
x1 <- bone$V1 # dom radius
x2 <- bone$V2 # radius
x3 <- bone$V3 # dom humerus
x4 <- bone$V4 # humerus
```

```r
x5 <- bone$V5 # dom ulna
x6 <- bone$V6 # ulna
# subset
dom <- bone %>%
  select(V1, V3, V5)
weak <- bone %>%
  select(V2, V4, V6)
dom <- as.matrix(dom)
weak <- as.matrix(weak)
# new data
radius <- x1-x2
humerus <- x3-x4
ulna <- x5-x6
distance <- data.frame(radius, humerus, ulna)
# dim
n <- dim(distance)[1]
p <- dim(distance)[2]
# xbar
one <- as.matrix(rep(1, n))
xbar <- 1/n * t(distance) %*% one
# S
mean_matrix <- matrix(data = 1, nrow = n1) %*% cbind(xbar[[1]], xbar[[2]],
xbar[[3]])
xstar <- distance - mean_matrix
S <- 1/(n-1) * t(xstar) %*% as.matrix(xstar)
HotellingsT2Test(x = dom, y = weak)
# vars
crit1 <- qf(0.05, df1 = p, df2 = n-p, lower.tail = FALSE)
frac <- ((n-1)*p)/(n-p)
right <- sqrt(frac*crit1)
# Radius
bneg1 <- xbar[1] - crit1*sqrt((S[1,1]/n))
bpos1 <- xbar[1] + crit1*sqrt((S[1,1]/n))
cat("Radius: (", bneg1, ",", bpos1, ") \n")
# Humerus
bneg2 <- xbar[2] - crit1*sqrt((S[2,2]/n))
bpos2 <- xbar[2] + crit1*sqrt((S[2,2]/n))
cat("Humerus Height: (", bneg2, ",", bpos2, ") \n")
# Ulna
bneg3 <- xbar[3] - crit1*sqrt((S[3,3]/n))
bpos3 <- xbar[3] + crit1*sqrt((S[3,3]/n))
cat("Ulna: (", bneg3, ",", bpos3, ") \n")
# vars
crit2 <- -qt(0.05/(2*p), df = n-1)
# Radius
bneg1 <- xbar[1] - crit2*sqrt((S[1,1]/n))
bpos1 <- xbar[1] + crit2*sqrt((S[1,1]/n))
cat("Radius: (", bneg1, ",", bpos1, ") \n")
# Humerus
bneg2 <- xbar[2] - crit2*sqrt((S[2,2]/n))
```

```r
bpos2 <- xbar[2] + crit2*sqrt((S[2,2]/n))
cat("Humerus Height: (", bneg2, ",", bpos2, ") \n")
# Ulna
bneg3 <- xbar[3] - crit2*sqrt((S[3,3]/n))
bpos3 <- xbar[3] + crit2*sqrt((S[3,3]/n))
cat("Ulna: (", bneg3, ",", bpos3, ") \n")
specter <- read.table("D:/Coding/R Storage/T6-18.dat", header = FALSE, sep =
"")
# vars
x1 <- specter$V1 # percent spectral reflectance at wavelength 560nm (green)
x2 <- specter$V2 # percent spectral reflectance at wavelength 720nm (near
infrared)
x3 <- specter$V3 # species
x4 <- specter$V4 # time
x5 <- specter$V5 # replication
test1 <- manova(cbind(x1, x2)~ x3, data = specter)
summary(test1, test = 'Wilks')
test2 <- manova(cbind(x1, x2)~ x4, data = specter)
summary(test2, test = 'Wilks')
test3 <- manova(cbind(x1, x2)~ x3*x4, data = specter)
summary(test3, test = 'Wilks')
fit1 <- lm(x1 ~ x3*factor(x4), data = specter)
ggplot(data = specter, aes(x = fit1$residuals)) +
    geom_histogram(bins = 10, fill = 'springgreen3', color = 'black') +
    labs(title = 'Histogram of Wavelength 560nm',
         x = 'Residuals', y = 'Frequency')
# fit 2
fit2 <- lm(x2 ~ x3*factor(x4), data = specter)
ggplot(data = specter, aes(x = fit2$residuals)) +
    geom_histogram(bins = 10, fill = 'firebrick3', color = 'black') +
    labs(title = 'Histogram of Wavelength 720nm',
         x = 'Residuals', y = 'Frequency')
chisq.test(table(x1,x2))
cor.test(x1,x2)
anova(fit1)
cat("---------------------------------------------------- \n")
anova(fit2)
```