

# STAT 6910: HW 4

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```
## Warning: package 'ggplot2' was built under R version 3.4.4
## Warning: package 'emmeans' was built under R version 3.4.4
## NOTE: As of emmeans versions > 1.2.3,
##       The 'cld' function will be deprecated in favor of 'CLD'.
##       You may use 'cld' only if you have package:multcomp attached.
```

## Problem 1 (3a)

The meat cooking experiment was described in Exercise 14 of Chap. 3, and the data were given in Table 3.14, p. 68.

- (a) Compare the effects of the six treatments, pairwise, using Scheffe's method of multiple comparisons and a 95% overall confidence level.

The data displayed below is represented by the codes 1, 2, 3, 4, 5, and 6 which denote the frying fat content at 10%, 15%, and 20% and the grilling fat content at 10%, 15% and 20% respectively for the post-cooking weight data (in grams) for the meat cooking experiment.

```
head(Post_grams)
```

```
##      [,1] [,2]
## [1,]   81    1
## [2,]   88    1
## [3,]   85    1
## [4,]   84    1
## [5,]   84    1
## [6,]   85    2
```

```
colnames(Post_grams) <- c( "Weight", "Code")
Post_grams <- data.frame(Post_grams)
Post_grams$Code <- factor(Post_grams$Code)
summary(Post_grams)
```

```
##      Weight      Code
## Min.   :71.00    1:5
## 1st Qu.:80.00    2:5
## Median :82.00    3:5
## Mean   :81.67    4:5
## 3rd Qu.:84.75    5:5
## Max.   :88.00    6:5
```

Assume the  $\tau_1, \tau_2, \dots, \tau_6$  represent the true mean of the coded 1, 2, ..., 6 respectively. We can see that the contrasts have the following 95% overall confidence intervals respectively using Scheffe's method of multiple comparisons and a 95% overall confidence level.

```
Post_weight_model <- aov(Weight ~ Code , data = Post_grams)
weight_means <- emmeans(object = Post_weight_model, specs = "Code")
estimates <- contrast(weight_means, method = "pairwise", adjust = "bonferroni")
alpha <- 0.05
v = 6
n = 30
wS <- sqrt((v-1) * qf(1-alpha, v-1, n-v))
cbind(summary(estimates)[, "estimate"] - wS* summary(estimates)[, "SE"],
       summary(estimates)[, "estimate"] + wS* summary(estimates)[, "SE"])
```

```
##           [,1]      [,2]
## [1,]  -3.5714537  8.771454
## [2,]   2.2285463 14.571454
## [3,]  -5.1714537  7.171454
## [4,]  -7.7714537  4.571454
## [5,]  -0.1714537 12.171454
## [6,]  -0.3714537 11.971454
## [7,]  -7.7714537  4.571454
## [8,] -10.3714537  1.971454
## [9,]  -2.7714537  9.571454
## [10,] -13.5714537 -1.228546
## [11,] -16.1714537 -3.828546
## [12,]  -8.5714537  3.771454
## [13,]  -8.7714537  3.571454
## [14,]  -1.1714537 11.171454
## [15,]   1.4285463 13.771454
```

We can observe that the contrasts  $\tau_1 - \tau_3, \tau_3 - \tau_4, \tau_3 - \tau_5$ , and  $\tau_5 - \tau_6$  don't include 0 and therefore can conclude that  $\tau_1 \neq \tau_3, \tau_3 \neq \tau_4, \tau_3 \neq \tau_5$ , and  $\tau_5 \neq \tau_6$  at the overall  $\alpha = .05$  level.  
## Problem 2 (5)

Exercise 15 of Chap. 3 (p. 67) concerns a study of the effects of four levels of sulfamerazine (0, 5, 10, 15 g per 100 lb of fish) on the hemoglobin content of trout blood. An analysis of variance test rejected the hypothesis that the four treatment effects are the same at significance level  $\alpha = 0.01$ .

- (a) Compare the four treatments using Tukey's method of pairwise comparisons and a 99% overall confidence level.

The Tukey's method of pairwise comparisons and 99% overall confidence level are displayed below.

```
Hemoglobin_2 <- matrix(c( rep(1, each = 10), rep(2, each = 10),
                        rep(3, each = 10), rep(4, each = 10),
```

```

        6.7, 7.8, 5.5, 8.4 ,7.0, 7.8, 8.6,7.4 ,5.8, 7.0,
        9.9, 8.4 ,10.4, 9.3 ,10.7 ,11.9, 7.1, 6.4 ,8.6, 10.6,
        10.4,8.1 ,10.6, 8.7, 10.7, 9.1, 8.8,8.1, 7.8, 8.0,
        9.3, 9.3 ,7.2, 7.8, 9.3, 10.2, 8.7, 8.6, 9.3, 7.2),
        byrow = FALSE, ncol = 2 )
Hemoglobin_2 <- data.frame(Hemoglobin_2)
Hemoglobin_2$X1 <- as.factor(Hemoglobin_2$X1)
colnames(Hemoglobin_2) <- c("Codes", "Hemo")

hem<- aov(Hemo ~ Codes, data = Hemoglobin_2)
hemoglobin_means<- emmeans(object = hem, specs = "Codes")

hemo.tukey <- contrast(hemoglobin_means,method = "pairwise", adjust = "tukey")
summary(hemo.tukey,infer = c(TRUE,TRUE), level = .99)

```

```

## contrast estimate      SE df lower.CL upper.CL t.ratio p.value
## 1 - 2          -2.13 0.5601141 36 -4.003146 -0.25685355 -3.803 0.0029
## 1 - 3          -1.83 0.5601141 36 -3.703146 0.04314645 -3.267 0.0122
## 1 - 4          -1.49 0.5601141 36 -3.363146 0.38314645 -2.660 0.0539
## 2 - 3           0.30 0.5601141 36 -1.573146 2.17314645 0.536 0.9498
## 2 - 4           0.64 0.5601141 36 -1.233146 2.51314645 1.143 0.6660
## 3 - 4           0.34 0.5601141 36 -1.533146 2.21314645 0.607 0.9292
##
## Confidence level used: 0.99
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates

```

We can see from the data that the only contrast that has a  $p$ -value less than 0.01 is  $\tau_1 - \tau_2$ .

- (b) Compare the effect of no sulfamerazine on the hemoglobin content of trout blood with the average effect of the other three levels. The overall confidence level of all intervals in parts (a) and (b) should be at least 98%.

We will use an  $\alpha = .01$  level in order to keep the overall confidence level of all intervals at least 98%. From the code below, we obtain a  $p$ -value of  $p = 0.003$  for the contrast  $(3, -1, -1, -1)$  which is greater than the  $\alpha$ . So our data do not provide evidence that no sulfamerazine on the hemoglobin content differs from the average effect of the other three levels.

```

contrast(hemoglobin_means,method = list(c(3,-1,-1,-1)))

```

```

## contrast      estimate      SE df t.ratio p.value
## c(3, -1, -1, -1)    -5.45 1.371994 36 -3.972 0.0003

```

### Problem 3 (7a and b)

The soap experiment was described in Sect. 2.5.1, p. 20, and an analysis was given in Sect. 3.7.2, p. 50.

- (a) Suppose that the experimenter had been interested only in the contrast  $\tau_1 - \frac{1}{2}(\tau_2 + \tau_3)$ , which compares the weight loss for the regular soap with the average weight loss for the other two soaps. Calculate a confidence interval for this single contrast.

Since it is being assumed that the experimenter might have been interested only in one contrast, there isn't a need to use a family-wise error rate. Therefore, using an  $\alpha$ -level of  $\alpha = .05$  and the results on pg. 51, we can calculate a confidence interval for this single contrast as follow:

$$\begin{aligned} & \sum_{i=1}^v b_i \hat{Y}_{i\bullet} \pm t_{n-v, \alpha/2} \sqrt{MSE \sum_{i=1}^v \frac{b_i^2}{r_i}} \\ &= -0.035 - \frac{1}{2}(2.7) - \frac{1}{2}(1.9925) \pm t_{9, .025} \sqrt{0.0772 \sum_{i=1}^v \frac{b_i^2}{r_i}} \\ &= -2.38125 \pm 2.262 \sqrt{0.0772 \left( \frac{1}{4} + \frac{1/4}{4} + \frac{1/4}{4} \right)} \\ &= -2.38125 \pm 2.262 \sqrt{0.0772 \left( \frac{3}{8} \right)} \\ &= -2.38125 \pm .38487 \end{aligned}$$

Therefore the 95% confidence interval for the specific contrast is (-2.76612, -1.99638).

- (b) Test the hypothesis that the regular soap has the same average weight loss as the average of the other two soaps. Do this via your confidence interval in part (a) and also via (4.3.13) and (4.3.15).

For this test, we will use the following:

The Null Hypothesis of No Difference Between Regular Soap and Others  $H_0 : \tau_1 = \frac{1}{2}(\tau_2 + \tau_4)$   
 vs. The Alternative Hypothesis of Some Difference Between Regular Soap and Others  
 $H_A : \tau_1 \neq \frac{1}{2}(\tau_2 + \tau_4)$

Using the confidence interval, we see that 0 is not in the interval and therefore we can reject the null hypothesis at the  $\alpha = .05$  level in favor of the alternative hypothesis that the regular soap does not have the same average weight loss as the average of the other two soaps. Next, using Equation 4.3.13 we get

$$\left| \frac{\sum c_i \bar{y}_i}{\sqrt{msE \sum c_i^2 / r_i}} \right| = \left| \frac{-2.38125}{\sqrt{0.0772 \left( \frac{3}{8} \right)}} \right| = 13.99525 > 2.262 = t_{9, .025}.$$

So we can reject the null hypothesis again. Lastly, Using Equation 4.3.15 we get

$$\left| \frac{\frac{(\sum c_i \bar{y}_i)^2}{\sum c_i^2 / r_i}}{msE} \right| = \left| \frac{\frac{5.67035}{3/8}}{.0772} \right|$$

$$= 195.8671 > 5.12 = F_{1,9,.05}.$$

and therefore we can reject the null hypothesis in favor of the alternative hypothesis again.

## Problem 4 (10)

Consider again the trout experiment in Exercise 15 of Chap. 3.

- (a) Suppose the experiment were to be repeated. Suggest the largest likely value for the error mean square  $msE$ .

From the code below we have that a 95% upper confidence limit for  $\sigma^2$  is 2.43. Therefore, the largest likely value for the error mean square  $msE$  is 2.43.

```
Hemoglobin_model <- aov(Hemo ~ Codes , data = Hemoglobin_2)
anova(Hemoglobin_model)

## Analysis of Variance Table
##
## Response: Hemo
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Codes       3 26.803   8.9343   5.6955 0.002685 **
## Residuals  36 56.471   1.5686
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ssE <- anova(Hemoglobin_model)[2,"Sum Sq"]
X_2_star <- qchisq(0.05,df = 36)
ssE/ X_2_star

## [1] 2.426918
```

- (b) How many observations should be taken on each treatment so that the length of each interval in a set of simultaneous 95% confidence intervals for pairwise comparisons should be at most 2 g per 100 ml?

Assuming that we want to look at all pairwise comparisons, we know that tukey's method will provide the narrowest confidence interval set of simultaneous 95% confidence intervals for pairwise comparisons. Therefore, using  $q_{4,12,.05} = 4.20$ , I'll assume  $\sigma^2 = 2.43$  from part (a), and also that  $r_i = r$ .

So we want

$$1 = \text{interval half-width} = \frac{1}{\sqrt{2}} q_{4,12,.05} \sqrt{\sigma^2 \left( \frac{2}{r} \right)}.$$

By trial and error we have that  $r = 27$  observations should be taken on each treatment so that the length of each interval in a set of simultaneous 95% confidence intervals for pairwise comparisons is at most 2 g per 100 ml.

$$\frac{1}{\sqrt{2}} 4.20 \sqrt{2.43 \left( \frac{2}{27} \right)} = .9984$$