HW 6

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# 1

1. The overall trend for factor A is that as we increase the dosage of the first ingredient, the number of hours of relief increases.
2. The overall trend for factor B is that as we increase the dosage of the second ingredient, the number of hours of relief increases.
3. I would use the smallest multiplier out of the three for precision since all multipliers can be used.
4. If we assume no interaction effect, I would say increasing factor A is generally more important for increasing the number of hours of relief since there is a bigger increase from low to medium and medium to high for factor A compared to factor B.

# 2

1. The 95% confidence interval is .
2. We are 95% certain that the difference of hours of relief on average between low dosage of factor A and low dosage of factor B is around 0.5441676 to 0.9558324 lower. This means for low dosage of either drug, people are better off with drug B.
3. The 99% confidence interval for is . The 99% confidence interval for is .
4. The confidence interval for tells us that we are 99% certain that difference of hours of relief on average between a low dosage of drug A and a high dosage of drug A is around 5.6433579 to 6.2566421 lower.
5. The 90% confidence interval is . We are 90% certain that the difference of hours of relief on average between low dosage of factor A and high dosage of factor A is around 1.8041228 to 2.3958772 lower for those who took low dosage of factor B.

# 3

1. Yes, because 0 is not in our interval.
2. Yes, because 0 is not in our interval.
3. Yes, because 0 is not in our interval.
4. I would have them take a high dosage of drug A and drug B because we have clearly shown higher dosages of both drugs yields better results.

# 4

1. Yes, a weighted confidence interval changes the bounds compared to the unweighted confidence interval. Lets look at the equation for confidence interval:
   * We can tell that the weights can change not only the center of the confidence interval but also the spread of the confidence interval. Both of these will affect the bounds.
2. I would suggest equal weights because unequal weights will make the result difficult to interpret.
3. One reason to give unequal weights for smokers is due to the unequal sample sizes. Since the sample size of smokers is larger, we can assign a larger weight to this as it is more reliable information and indicates greater precision.
4. One reason to give equal weights is because unequal weights makes interpretation of the result difficult.

# 5

1. We are 95% certain that females on average have around 0.84 to 2.18 less lung capacity compared to males.
2. It would be unusual because -3 is not in our confidence interval.
3. We are 95% certain that nonsmokers on average have around 1.82 to 2.45 more lung capacity compared to smokers.
4. Yes, because 0 is not in our confidence interval.

# 6

1. Lets interpret the confidence interval for . The difference of lung capacity on average between non smokers and smokers is 0.4 to 2.6 more for females.
2. No, because our interval from (a) includes the interaction effect of A on B compared to (5c) which only accounted for factor B.
3. No, because our interval from (a) includes the interaction effect of A on B compared to (5c) which only accounted for factor B.
4. is our default modifier regardless of which group the subject belongs to. is our modifier if the subject is within Male group of factor A. is our modifier if the subject is within the smokers group of factor B.

# 7

1. True. If there is no interaction effect, we don’t expect a change in confidence interval if we choose to look at different groups in factor B when contrasting two means in factor A. We might as well compute the confidence interval for a contrast of or .
2. False. The multiplier used should be the smallest multiplier out of all the multipliers. Even though Bonferroni multiplier can be used for any contrast, it is not necessarily the smallest.
3. False. These multipliers are used for creating confidence intervals that contrast means, not for finding the true population mean.
4. True. The amount of parameters to estimate for the regression model is the same as the model we chose. In our case, we chose the no interaction model, which has parameters.

# I

1. The confidence interval for is .
2. The confidence interval for is . The confidence interval for is .
3. The confidence interval for is . The confidence interval for is .
4. Our results from C shows that the average days it takes for a Small systems, Exp experience programmer is around to more than Both systems, Exp experience programmer. The average days it takes for a Small systems, New experience programmer is around to more than Both systems, New experience programmer.
5. The largest difference of days we would expect for the average programmer with different types of experience is around 97.1478.
6. Yes, expereinced programmers do have significantly lower averages than other categories, because none of the confidence intervals in b contain 0.

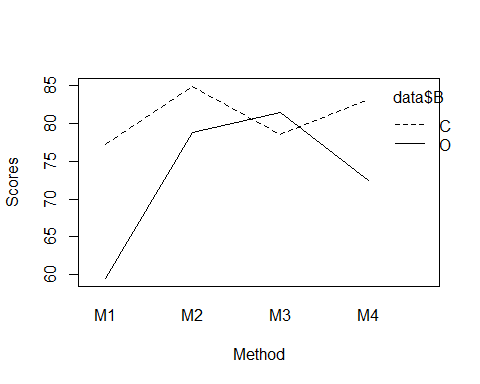
# II

* There are parameters total.

1. represents the estimated average for Medium Systems, High (Exp) Experience
2. represents the estimated average difference between Medium Systems, High Experience and Small Systems, High Experience ().
3. represents the interaction effect between Small Systems and Medium Experience.
4. represents the interaction effect between Small Systems and New Experience.

# III.a

Assuming that factor is Method and factor is Room.



# III.b.1

Here are the means for factor alone:

|  | x |
| --- | --- |
| M1 | 70.100 |
| M2 | 81.875 |
| M3 | 80.000 |
| M4 | 77.850 |

# III.b.2

Here are the means for factor alone:

|  | x |
| --- | --- |
| C | 80.84783 |
| O | 74.40476 |

# III.b.3

Here are the means for both factors and :

|  | x |
| --- | --- |
| C | 80.84783 |
| O | 74.40476 |

# III.c.1

Here are the counts for factor alone:

|  | x |
| --- | --- |
| M1 | 20 |
| M2 | 24 |
| M3 | 24 |
| M4 | 20 |

# III.c.2

Here are the counts for factor alone:

|  | x |
| --- | --- |
| C | 46 |
| O | 42 |

# III.c.3

Here are the means for both factors and :

|  | C | O |
| --- | --- | --- |
| M1 | 12 | 8 |
| M2 | 12 | 12 |
| M3 | 12 | 12 |
| M4 | 10 | 10 |

# III.d

The full model is:

The reduced model is:

There is no interaction effect. Don’t use the full model.

There is interaction effect. Use the full model.

Since , we accept . Therefore, we do not use the full model.

# III.e

# III.f

We would choose the Tukey multiplier because that multiplier assumes that we are making all possible pairwise confidence intervals. We can have the multiplier only account for factor B.

# Appendix

# Functions   
# Plus minus function  
plus.minus = function(value) {  
 return(c(-value, value))  
}  
  
# Find means  
find.means = function(the.data,fun.name = mean){  
 a = length(unique(the.data[,2]))  
 b = length(unique(the.data[,3]))  
 means.A = by(the.data[,1], the.data[,2], fun.name)  
 means.B = by(the.data[,1],the.data[,3],fun.name)  
 means.AB = by(the.data[,1],list(the.data[,2],the.data[,3]),fun.name)  
 MAB = matrix(means.AB,nrow = b, ncol = a, byrow = TRUE)  
 colnames(MAB) = names(means.A)  
 rownames(MAB) = names(means.B)  
 MA = as.numeric(means.A)  
 names(MA) = names(means.A)  
 MB = as.numeric(means.B)  
 names(MB) = names(means.B)  
 MAB = t(MAB)  
 results = list(A = MA, B = MB, AB = MAB)  
 return(results)  
}  
  
# Give me multipliers  
find.mult = function(alpha,a,b,dfSSE,g,group){  
 if(group == "A"){  
 Tuk = round(qtukey(1-alpha,a,dfSSE)/sqrt(2),3)  
 Bon = round(qt(1-alpha/(2\*g), dfSSE ) ,3)  
 Sch = round(sqrt((a-1)\*qf(1-alpha, a-1, dfSSE)),3)  
 }else if(group == "B"){  
 Tuk = round(qtukey(1-alpha,b,dfSSE)/sqrt(2),3)  
 Bon = round(qt(1-alpha/(2\*g), dfSSE ) ,3)  
 Sch = round(sqrt((b-1)\*qf(1-alpha, b-1, dfSSE)),3)  
 }else if(group == "AB"){  
 Tuk = round(qtukey(1-alpha,a\*b,dfSSE)/sqrt(2),3)  
 Bon = round(qt(1-alpha/(2\*g), dfSSE ) ,3)  
 Sch = round(sqrt((a\*b-1)\*qf(1-alpha, a\*b-1, dfSSE)),3)  
 }  
 results = c(Bon, Tuk,Sch)  
 names(results) = c("Bonferroni","Tukey","Scheffe")  
 return(results)  
}  
  
give.me.CI = function(the.data,MSE,equal.weights = TRUE,multiplier,group,cs){  
 if(sum(cs) != 0 & sum(cs !=0 ) != 1){  
 return("Error - you did not input a valid contrast")  
 }else{  
 the.means = find.means(the.data)  
 the.ns =find.means(the.data,length)  
 nt = nrow(the.data)  
 a = length(unique(the.data[,2]))  
 b = length(unique(the.data[,3]))  
 if(group =="A"){  
 if(equal.weights == TRUE){  
 a.means = rowMeans(the.means$AB)  
 est = sum(a.means\*cs)  
 mul = rowSums(1/the.ns$AB)  
 SE = sqrt(MSE/b^2 \* (sum(cs^2\*mul)))  
 N = names(a.means)[cs!=0]  
 CS = paste("(",cs[cs!=0],")",sep = "")  
 fancy = paste(paste(CS,N,sep =""),collapse = "+")  
 names(est) = fancy  
 } else{  
 a.means = the.means$A  
 est = sum(a.means\*cs)  
 SE = sqrt(MSE\*sum(cs^2\*(1/the.ns$A)))  
 N = names(a.means)[cs!=0]  
 CS = paste("(",cs[cs!=0],")",sep = "")  
 fancy = paste(paste(CS,N,sep =""),collapse = "+")  
 names(est) = fancy  
 }  
 }else if(group == "B"){  
 if(equal.weights == TRUE){  
 b.means = colMeans(the.means$AB)  
 est = sum(b.means\*cs)  
 mul = colSums(1/the.ns$AB)  
 SE = sqrt(MSE/a^2 \* (sum(cs^2\*mul)))  
 N = names(b.means)[cs!=0]  
 CS = paste("(",cs[cs!=0],")",sep = "")  
 fancy = paste(paste(CS,N,sep =""),collapse = "+")  
 names(est) = fancy  
 } else{  
 b.means = the.means$B  
 est = sum(b.means\*cs)  
 SE = sqrt(MSE\*sum(cs^2\*(1/the.ns$B)))  
 N = names(b.means)[cs!=0]  
 CS = paste("(",cs[cs!=0],")",sep = "")  
 fancy = paste(paste(CS,N,sep =""),collapse = "+")  
 names(est) = fancy  
 }  
 } else if(group == "AB"){  
 est = sum(cs\*the.means$AB)  
 SE = sqrt(MSE\*sum(cs^2/the.ns$AB))  
 names(est) = "someAB"  
 }  
 the.CI = est + c(-1,1)\*multiplier\*SE  
 results = c(est,the.CI)  
 names(results) = c(names(est),"lower bound","upper bound")  
 return(results)  
 }  
}

# 2.a   
a <- 3  
b <- 3  
nidot <- 12  
ndotj <- 12  
nT <- 36  
  
alpha <- 0.05  
g <- 1  
  
SSE <- 1.63  
dfSSE <- nT - a \* b  
MSE <- SSE / dfSSE  
  
mu1dot <- 3.88  
mudot1 <- 4.63  
  
all.mult <- find.mult(alpha = alpha, a = a, b = b,  
 dfSSE = dfSSE, g = g, group = "AB")  
the.mult <- min(all.mult)  
the.CI <- mu1dot - mudot1 + plus.minus(  
 the.mult \* sqrt(MSE \* (1 / nidot + 1 / ndotj))  
)

# 2.c   
alpha <- 0.01  
g <- 2  
  
mu3dot <- 9.83  
mudot3 <- 8.98  
  
all.mult <- find.mult(alpha = alpha, a = a, b = b,  
 dfSSE = dfSSE, g = g, group = "AB")  
the.mult <- min(all.mult)  
the.CI.1 <- mu1dot - mu3dot + plus.minus(  
 the.mult \* sqrt(MSE \* (1 / nidot + 1 / nidot))  
)  
the.CI.2 <- mudot1 - mudot3 + plus.minus(  
 the.mult \* sqrt(MSE \* (1 / ndotj + 1 / ndotj))  
)

# 2.e   
alpha <- 0.1  
g <- 1  
  
nij <- 4  
  
mu11 <- 2.48  
mu13 <- 4.58  
  
all.mult <- find.mult(alpha = alpha, a = a, b = b,  
 dfSSE = dfSSE, g = g, group = "AB")  
the.mult <- min(all.mult)  
the.CI <- mu11 - mu13 + plus.minus(  
 the.mult \* sqrt(MSE \* (1 / nij + 1 / nij))  
)

# I.a   
data <- read.csv("Prog.csv")  
  
data.I.a <- subset(data, type == "Small")  
result <- t.test(data.I.a$days)  
conf\_interval <- round(result$conf.int, 4)

# I.b   
alpha <- 0.1  
  
n <- nrow(data)  
a <- length(unique(data$type))  
b <- length(unique(data$years))  
  
names(data) = c("Y","A","B")  
AB = lm(Y ~ A \* B, data)  
SSE <- AB$residuals ^ 2  
dfSSE <- n - a \* b  
MSE <- SSE / dfSSE  
  
the.mult <- find.mult(alpha, a, b, dfSSE, 1, "B")[2]  
  
CI.1 <- give.me.CI(data, MSE, equal.weights = TRUE, the.mult, "B", c(1, -1, 0))  
CI.1 <- round(CI.1, 4)  
  
CI.2 <- give.me.CI(data, MSE, equal.weights = TRUE, the.mult, "B", c(1, 0, -1))  
CI.2 <- round(CI.2, 4)

# I.c   
alpha <- 0.01  
  
the.mult <- find.mult(alpha, a, b, dfSSE, 1, "AB")[3]  
  
# Note - i indices are flipped. In R, i = 1 is Both  
# However, in the HW, i = 1 is Small  
AB.cs <- matrix(0, nrow = a, ncol = b)  
AB.cs[2, 1] <- 1  
AB.cs[1, 1] <- -1  
CI.1 <- give.me.CI(data, MSE, equal.weights = TRUE, the.mult, "AB", AB.cs)  
CI.1 <- round(CI.1, 4)  
  
AB.cs <- matrix(0, nrow = a, ncol = b)  
AB.cs[2, 3] <- 1  
AB.cs[1, 3] <- -1  
CI.2 <- give.me.CI(data, MSE, equal.weights = TRUE, the.mult, "AB", AB.cs)  
CI.2 <- round(CI.2, 4)

# II   
co <- coef(AB)

# III.a   
data <- read.csv("Teaching.csv")  
names(data) = c("Y","A","B")  
interaction.plot(x.factor = data$A, trace.factor = data$B, response = data$Y, xlab = "Method", ylab = "Scores")

# III.b   
the.means <- find.means(data)

# III.b.1   
knitr::kable(the.means[1])

# III.b.2   
knitr::kable(the.means[2])

# III.b.3   
knitr::kable(the.means[2])

# III.c   
the.counts <- find.means(data, fun.name = length)

# III.c.1   
knitr::kable(the.counts[1])

# III.c.2   
knitr::kable(the.counts[2])

# III.c.3   
knitr::kable(the.counts[3])

# III.d   
the.data <- data  
AB = lm(Y ~ A\*B,the.data)  
A.B = lm(Y ~ A + B,the.data)  
all.models = list(AB,A.B)  
SSE = t(as.matrix(sapply(all.models,function(M) sum(M$residuals^2))))  
colnames(SSE) = c("AB","(A+B)")  
rownames(SSE) = "SSE"  
  
# Conduct ANOVA test  
anova\_result <- anova(A.B, AB)  
  
# Get the F-statistic and p-value  
f\_statistic <- anova\_result$F[2] # Extracting F-statistic from the first row  
p\_value <- anova\_result$Pr[2] # Extracting p-value from the first row

# III.e   
the.params <- round(coef(A.B), 4)  
# knitr::kable(the.params)