

STAT 511A Homework 7

Kathleen Wendt

10/25/2019

Load packages

```
library(readxl)
library(tidyverse)
library(broom)
library(car)
library(dunn.test)
library(emmeans)
```

Question 1

Power plant data

Read Problem 8.23 which concerns power plant reliability. This data is available from the Ott & Longnecker companion site. Note that the data is in “wide” format.

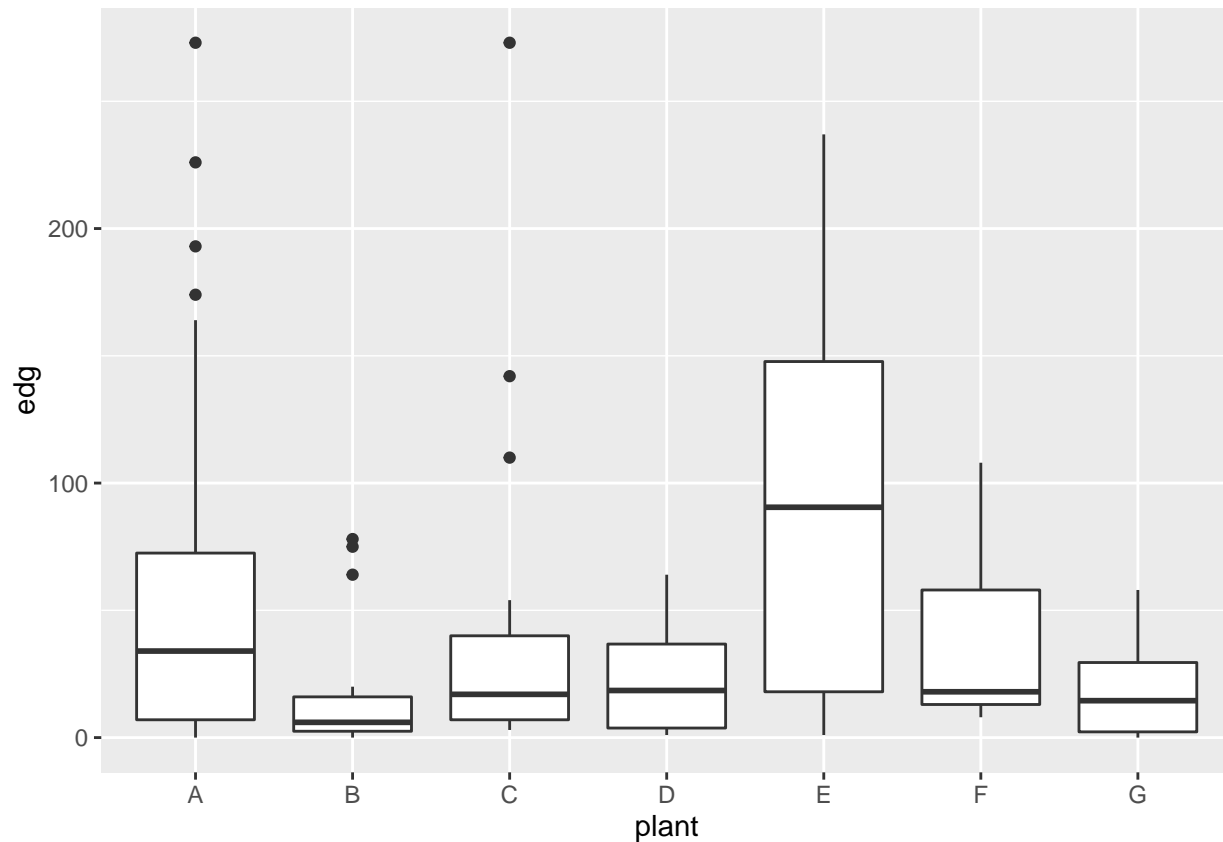
```
power_data <- read_xlsx("ex8-23.xlsx") %>%
  gather(key = "plant", value = "edg") %>%
  mutate(plant = as_factor(plant)) %>%
  drop_na() # remove 135 observations with NA for EDG
glimpse(power_data)
```

```
## Observations: 103
## Variables: 2
## $ plant <fct> A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, ...
## $ edg <dbl> 28, 50, 193, 55, 4, 7, 174, 76, 10, 0, 10, 84, 0, 9, 1, ...
```

Part 1A

Create side-by-side boxplots and include them in your assignment.

```
power_data %>%  
  ggplot(aes(y = edg, x = plant)) +  
  geom_boxplot()
```



Part 1B

Run the one-way ANOVA on the original scale. Include the ANOVA table in your assignment.

```
power_lm <- lm(edg ~ plant, data = power_data)  
power_anova <- tidy(anova(power_lm))  
power_anova
```

A tibble: 2 x 6

##	term	df	sumsq	meansq	statistic	p.value
##	<chr>	<int>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	plant	6	58745.	9791.	2.68	0.0191
## 2	Residuals	96	351233.	3659.	NA	NA

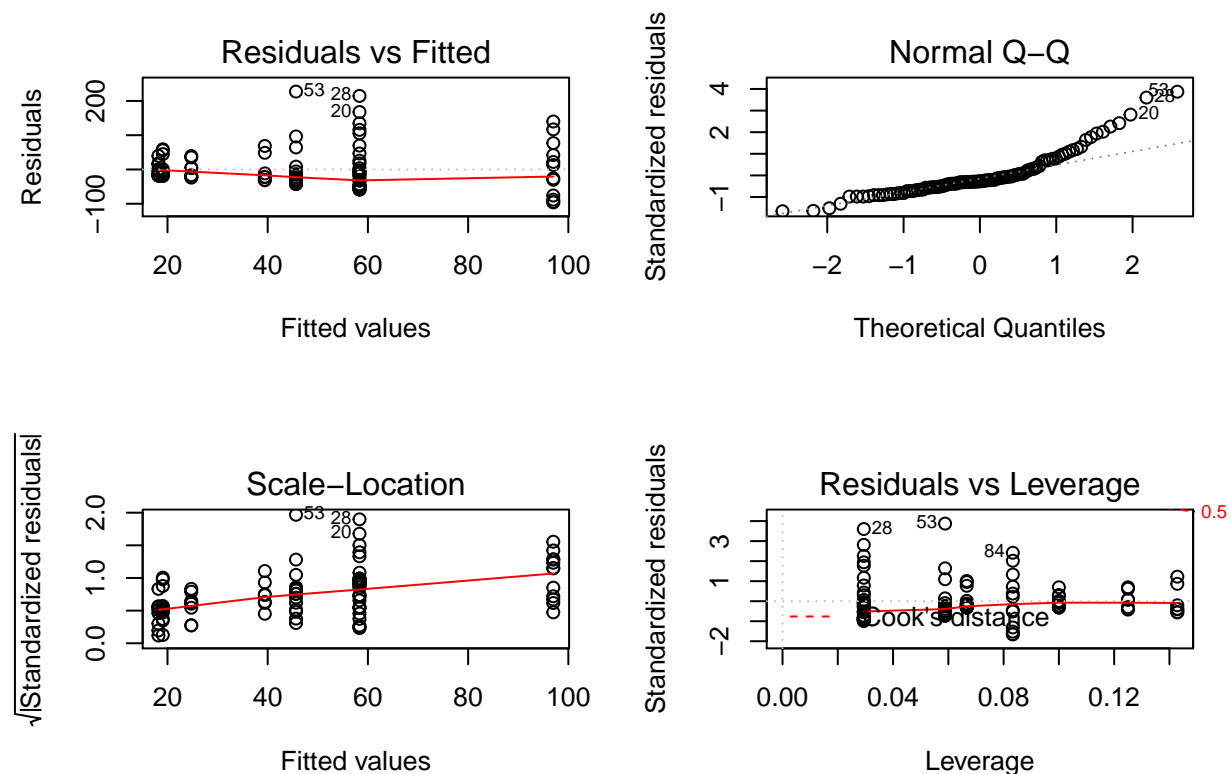
Note for parts C and D: plots do NOT need to be included in your assignment, just discuss. However, p-values from Levene's test and Shapiro-Wilk test should be included in your assignment.

Part 1C

Do the assumptions for one-way ANOVA appear to be satisfied for these data? In order to justify your response, consider residual diagnostic plots, Levene's test (using default center = "median") and Shapiro-Wilk test results. (4 pts)

Residual diagnostic plots

```
par(mfrow = c(2,2))
plot(power_lm)
```



- (1) Residuals vs Fitted values: This plot checks for violations of constant variance. Because there is a mega-phone pattern of the residuals, there is evidence for the violation of the assumption of constant variance.
- (2) Q-Q plot of residuals: This plot checks for normality of residuals. There are strong deviations from the Q-Q line on the upper-end of the plot. This indicates evidence of a heavy tail, and, therefore, a potential violation of the assumption of normally distributed residuals.

Levene's Test

```
power_levene <- tidy(leveneTest(edg ~ plant, data = power_data,
                                center = "median"))
power_levene
```

```
## # A tibble: 2 x 4
##   term      df statistic p.value
##   <chr> <int>    <dbl>   <dbl>
## 1 group      6      2.31  0.0396
## 2 ""        96      NA     NA
```

The Levene's Test yielded a p-value of 0.03962822, which is below $\alpha = 0.05$, therefore indicating a violation of the assumption of equal variances.

Shapiro-Wilk test

```
power_shapiro <- tidy(shapiro.test(power_data$edg))
power_shapiro
```

```
## # A tibble: 1 x 3
##   statistic p.value method
##   <dbl>    <dbl> <chr>
## 1    0.733 2.20e-12 Shapiro-Wilk normality test
```

The Shapiro-Wilk Test yielded a p-value close to 0, which is below $\alpha = 0.05$ and indicates non-normality.

Part 1D

Because the data are counts of the number of successes for the EDGs, a square root transformation may be an alternative to analysis on the original scale. Run the one-way ANOVA after square root transforming EDG. Include the ANOVA table in your assignment.

```
power_data <- power_data %>%
  group_by(plant) %>%
  mutate(edg_sq = sqrt(edg)) %>%
  ungroup()
glimpse(power_data)
```

```
## Observations: 103
## Variables: 3
## $ plant <fct> A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A, A...
## $ edg <dbl> 28, 50, 193, 55, 4, 7, 174, 76, 10, 0, 10, 84, 0, 9, 1,...
## $ edg_sq <dbl> 5.291503, 7.071068, 13.892444, 7.416198, 2.000000, 2.64...
```

```
power_sqrt_lm <- lm(edg_sq ~ plant, data = power_data)
power_sqrt_anova <- tidy(anova(power_sqrt_lm))
power_sqrt_anova
```

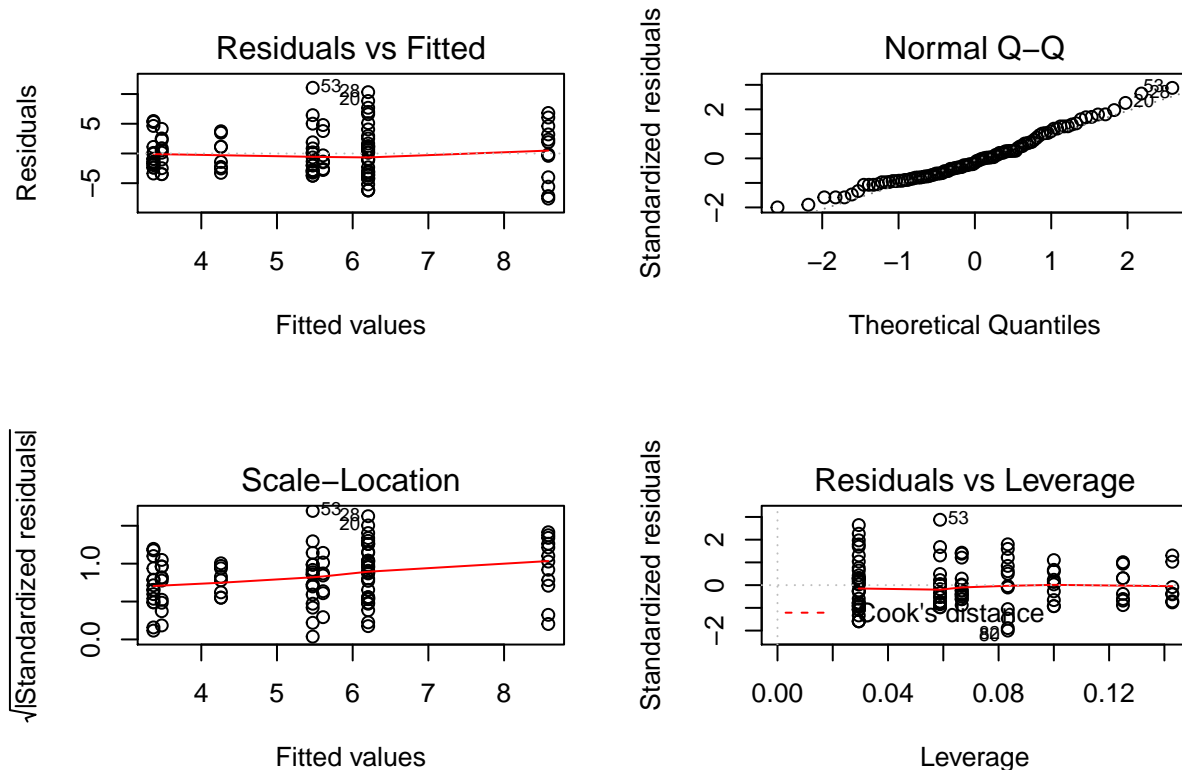
```
## # A tibble: 2 x 6
##   term      df sumsq meansq statistic p.value
##   <chr>    <int> <dbl> <dbl>    <dbl>   <dbl>
## 1 plant      6  252.   42.1     2.68  0.0189
## 2 Residuals  96 1506.   15.7     NA     NA
```

Part 1E

Do the assumptions for one-way ANOVA appear to be satisfied for after square root transform? In order to justify your response, consider residual diagnostic plots, Levene's test (using default center = "median") and Shapiro-Wilk test results. (4 pts)

Residual diagnostic plots (square root transformation)

```
par(mfrow = c(2,2))
plot(power_sqrt_lm)
```



- (1) Residuals vs Fitted values: This plot checks for violations of constant variance and linearity. The square root transformation of the response variable minimized the previous mega-phone pattern of the residuals, therefore reducing the evidence for non-constant variance. The square root transformation helped.
- (2) Q-Q plot of residuals: This plot checks for normality of residuals. After the square root transformation of the response variable, there were no longer strong deviations from the Q-Q line on the upper-end of the plot. This indicates limited evidence of a heavy tail; therefore, I am no longer concerned about the potential violation of the assumption of normally distributed residuals. The square root transformation helped.

Levene's Test (square root transformation)

```
power_sqrt_levene <- tidy(leveneTest(edg_sq ~ plant, data = power_data,
                                     center = "median"))
power_sqrt_levene
```

```
## # A tibble: 2 x 4
##   term      df statistic p.value
##   <chr> <int>    <dbl>   <dbl>
## 1 group      6      1.65    0.143
## 2 ""       96      NA      NA
```

The Levene's Test yielded a p-value of 0.142764, which is above $\alpha = 0.05$, thus indicating that the square root transformation was successful in adjusting variances to support the reasonable assumption of equal variances.

Shapiro-Wilk test (square root transformation)

```
power_sqrt_shapiro <- tidy(shapiro.test(power_data$edg_sq))
power_sqrt_shapiro
```

```
## # A tibble: 1 x 3
##   statistic p.value method
##   <dbl>    <dbl> <chr>
## 1      0.920 0.0000102 Shapiro-Wilk normality test
```

After the square root transformation of the response variable, the Shapiro-Wilk Test yielded a p-value of lower than $\alpha = 0.05$, thus still indicative of non-normality. In this case, the square root transformation did not aid in normalizing the distribution. The data are still positively skewed.

Part 1F

Now run the Kruskal-Wallis test on the original scale (not square root transformed). Include the p-value and conclusion in your assignment.

```
power_kruskal <- tidy(kruskal.test(edg ~ plant, data = power_data))
power_kruskal
```

```
## # A tibble: 1 x 4
##   statistic p.value parameter method
##   <dbl>    <dbl>    <int> <chr>
## 1      12.5  0.0510         6 Kruskal-Wallis rank sum test
```

P-value

The p-value for the Kruskal-Wallis test on the original data is 0.0510032.

Conclusion

We fail to reject the null hypothesis; there is not sufficient evidence to suggest that there is a difference in mean EDG across power plants at $\alpha = 0.05$.

Part 1G

Use Dunn's test to run pairwise comparisons after Kruskal-Wallis. Include the pairwise comparisons in your assignment. Which plants show evidence of a difference from plant G at the alpha = 0.05 level? (4pts)

```
dunn.test(x = power_data$edg, g = power_data$plant, method = "none")
```

```
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 12.5372, df = 6, p-value = 0.05
##
##
## Comparison of x by group
## (No adjustment)
## Col Mean-|
## Row Mean | A B C D E F
## -----|-----
## B | 2.286906
## | 0.0111*
## |
## C | 0.455880 -1.618775
## | 0.3242 0.0527
## |
## D | 0.994053 -0.726924 0.595221
## | 0.1601 0.2336 0.2758
## |
## E | -1.385870 -3.031778 -1.593366 -1.875307
## | 0.0829 0.0012* 0.0555 0.0304
## |
## F | -0.118471 -1.656043 -0.411029 -0.849750 0.875049
## | 0.4528 0.0489 0.3405 0.1977 0.1908
## |
## G | 1.596615 -0.329450 1.101424 0.387375 2.428228 1.265278
## | 0.0552 0.3709 0.1354 0.3492 0.0076* 0.1029
##
## alpha = 0.05
## Reject Ho if p <= alpha/2
```

There is a difference in EDG between Plant E and Plant G at $\alpha = 0.05$.

Question 2

Read Problem 9.13 which concerns a weight loss study. Use the following code to (1) transpose from wide to long and (2) reorder the levels of Trt so that S (standard) is first (for convenience for Dunnett's comparisons).

Weight data

```
weight_data <- read_xlsx("ex9-13.xlsx") %>%
  gather(key = "trt", value = "loss") %>%
  mutate(trt = as_factor(trt)) %>%
  mutate(trt = fct_relevel(trt, "S"))
glimpse(weight_data)

## Observations: 50
## Variables: 2
## $ trt <fct> A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A2, A2, A2, A2, A...
## $ loss <dbl> 12.4, 10.7, 11.9, 11.0, 12.4, 12.3, 13.0, 12.5, 11.2, 13....
```

```
levels(weight_data$trt)
```

```
## [1] "S" "A1" "A2" "A3" "A4"
```

Part 2A

Calculate a table of summary statistics including sample size, mean, sd and se by trt group. (4 pts)

```
weight_stats <- weight_data %>%  
  group_by(trt) %>%  
  summarize(n = n(),  
            mean = mean(loss),  
            sd = sd(loss),  
            se = sd / sqrt(n)) %>%  
  ungroup()  
  
weight_stats
```

```
## # A tibble: 5 x 5  
##   trt      n mean    sd    se  
##   <fct> <int> <dbl> <dbl> <dbl>  
## 1 S         10  9.27  1.16  0.366  
## 2 A1         10 12.0   0.829 0.262  
## 3 A2         10 11.0   1.12  0.355  
## 4 A3         10 10.3   1.03  0.325  
## 5 A4         10 12.2   0.756 0.239
```

Part 2B

Run the one-way ANOVA and include the ANOVA table in your assignment. Note: I will not formally ask you to evaluate assumptions for this group of questions but based on the residual diagnostic plots, I think the data looks OK. There does seem to be an outlier for one of the groups.

One-way ANOVA

```
weight_lm <- lm(loss ~ trt, data = weight_data)  
weight_anova <- tidy(anova(weight_lm))  
weight_anova  
  
## # A tibble: 2 x 6  
##   term      df sumsq meansq statistic    p.value  
##   <chr>    <int> <dbl> <dbl>    <dbl>    <dbl>  
## 1 trt         4  61.6  15.4    15.7 0.0000000416  
## 2 Residuals   45  44.2  0.982     NA      NA
```

Part 2C

Calculate unadjusted p-values for pairwise comparisons of means.

Pairwise comparisons

```
weight_em <- emmeans(weight_lm, pairwise ~ trt, adjust = "none")
weight_em
```

```
## $emmeans
##   trt emmean    SE df lower.CL upper.CL
##   S      9.27 0.313 45     8.64     9.9
##   A1     12.05 0.313 45    11.42    12.7
##   A2     11.02 0.313 45    10.39    11.7
##   A3     10.27 0.313 45     9.64    10.9
##   A4     12.24 0.313 45    11.61    12.9
##
## Confidence level used: 0.95
##
## $contrasts
##   contrast estimate    SE df t.ratio p.value
##   S - A1      -2.78 0.443 45  -6.272 <.0001
##   S - A2      -1.75 0.443 45  -3.948 0.0003
##   S - A3      -1.00 0.443 45  -2.256 0.0290
##   S - A4      -2.97 0.443 45  -6.700 <.0001
##   A1 - A2       1.03 0.443 45   2.324 0.0247
##   A1 - A3       1.78 0.443 45   4.016 0.0002
##   A1 - A4      -0.19 0.443 45  -0.429 0.6702
##   A2 - A3       0.75 0.443 45   1.692 0.0976
##   A2 - A4      -1.22 0.443 45  -2.752 0.0085
##   A3 - A4      -1.97 0.443 45  -4.444 0.0001
```

Part 2D

Calculate Tukey adjusted p-values for pairwise comparisons of means.

```
weight_em_tukey <- emmeans(weight_lm, pairwise ~ trt, adjust = "tukey")
weight_em_tukey
```

```
## $emmeans
##   trt emmean    SE df lower.CL upper.CL
##   S      9.27 0.313 45     8.64     9.9
##   A1     12.05 0.313 45    11.42    12.7
##   A2     11.02 0.313 45    10.39    11.7
##   A3     10.27 0.313 45     9.64    10.9
##   A4     12.24 0.313 45    11.61    12.9
##
## Confidence level used: 0.95
##
## $contrasts
##   contrast estimate    SE df t.ratio p.value
##   S - A1      -2.78 0.443 45  -6.272 <.0001
##   S - A2      -1.75 0.443 45  -3.948 0.0024
##   S - A3      -1.00 0.443 45  -2.256 0.1784
##   S - A4      -2.97 0.443 45  -6.700 <.0001
##   A1 - A2       1.03 0.443 45   2.324 0.1563
##   A1 - A3       1.78 0.443 45   4.016 0.0020
```

```
## A1 - A4      -0.19 0.443 45 -0.429 0.9927
## A2 - A3       0.75 0.443 45  1.692 0.4490
## A2 - A4     -1.22 0.443 45 -2.752 0.0618
## A3 - A4     -1.97 0.443 45 -4.444 0.0005
##
## P value adjustment: tukey method for comparing a family of 5 estimates
```

Part 2E

Comparing unadjusted and Tukey adjusted results, how many comparisons yield p-values less than 0.05? Just count the number of p-values less than 0.05.

The Tukey adjustment is more conservative and yielded fewer differences in means (5 pairs) at $\alpha = 0.05$. In contrast, there were 8 pairs with p-values lower than $\alpha = 0.05$ using unadjusted pairwise comparisons of means.

Part 2F

Calculate the Tukey HSD 0.05 value (95% Tukey ME). In R, use `qtukey(0.95, 5, 45)` to find the exact table value.

```
# Tukey critical value
# df = N - group# = 50 - 5 = 45
tukey_cv <- qtukey(0.95, 5, 45)

# calculate square root of mean square of residuals/error
mse <- weight_anova$meansq[2]

# create number per group (n) object
# N = 50; 5 groups; 10 per group
n <- 10

# plug values into HSD formula
hsd <- tukey_cv*sqrt((mse)/n)
hsd
```

```
## [1] 1.259489
```

The Tukey HSD 0.05 value is 1.2594887.

Part 2G

Create a “cld” display with Tukey adjustment.

```
CLD(weight_em$emmeans, adjust = "tukey")

## trt emmean SE df lower.CL upper.CL .group
## S      9.27 0.313 45      8.43      10.1 1
## A3     10.27 0.313 45      9.43      11.1 12
## A2     11.02 0.313 45     10.18      11.9 23
## A1     12.05 0.313 45     11.21      12.9 3
## A4     12.24 0.313 45     11.40      13.1 3
##
## Confidence level used: 0.95
```

```
## Conf-level adjustment: sidak method for 5 estimates
## P value adjustment: tukey method for comparing a family of 5 estimates
## significance level used: alpha = 0.05
```

Part 2H

Calculate Dunnett adjusted p-values to compare each of the “A” treatments versus “S” (standard). Summarize your conclusions from the Dunnett adjusted pairwise comparisons. Which Trts show evidence of differences as compared to the standard at the $\alpha = 0.05$ level? (4pts)

```
weight_dunnett <- emmeans(weight_lm, dunnett ~ trt)
weight_dunnett$contrasts
```

```
## contrast estimate    SE df t.ratio p.value
## A1 - S          2.78 0.443 45 6.272  <.0001
## A2 - S          1.75 0.443 45 3.948  0.0010
## A3 - S          1.00 0.443 45 2.256  0.0961
## A4 - S          2.97 0.443 45 6.700  <.0001
##
## P value adjustment: dunnettx method for 4 tests
```

Using Dunnett adjustments with $\alpha = 0.05$, Treatments A1, A2, and A4 yielded different (higher) average weight loss, as compared to the Standard treatment.