Coding Challenge 7

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You can find the corresponding documents to this assignment on my GitHub: Theresa's PLPA 6820 Github Access

#Question 1. 4 pts. Read in the data called "PlantEmergence.csv" using a relative file path and load the following libraries. tidyverse, lme4, emmeans, multcomp, and multcompView. Turn the Treatment , DaysAfterPlanting and Rep into factors using the function as.factor

```
library(tidyverse)
library(lme4)
library(emmeans)
library(multcomp)
library(multcompView)


emergence <- read.csv("PlantEmergence.csv", na.strings = "na")

emergence$Treatment <- as.factor(emergence$Treatment)
emergence$DaysAfterPlanting <- as.factor(emergence$DaysAfterPlanting)
emergence$Rep <- as.factor(emergence$Rep)
```

#Question 2. 5 pts. Fit a linear model to predict Emergence using Treatment and DaysAfterPlanting along with the interaction. Provide the summary of the linear model and ANOVA results.

```
#Effect of one variable depends on the other; use the * sign to include the interaction
lm.interaction <- lm(Emergence ~ Treatment*DaysAfterPlanting, data = emergence)
summary(lm.interaction)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment * DaysAfterPlanting, data = emergence)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -21.250  -6.062  -0.875   6.750  21.875
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     1.823e+02  5.324e+00  34.229   <2e-16 ***
## Treatment2                     -1.365e+02  7.530e+00 -18.128   <2e-16 ***
## Treatment3                      1.112e+01  7.530e+00   1.477    0.142
## Treatment4                      2.500e+00  7.530e+00   0.332    0.741
```

```
## Treatment5                       8.750e+00  7.530e+00   1.162    0.248
## Treatment6                       7.000e+00  7.530e+00   0.930    0.355
## Treatment7                      -1.250e-01  7.530e+00  -0.017    0.987
## Treatment8                       9.125e+00  7.530e+00   1.212    0.228
## Treatment9                       2.375e+00  7.530e+00   0.315    0.753
## DaysAfterPlanting14              1.000e+01  7.530e+00   1.328    0.187
## DaysAfterPlanting21              1.062e+01  7.530e+00   1.411    0.161
## DaysAfterPlanting28              1.100e+01  7.530e+00   1.461    0.147
## Treatment2:DaysAfterPlanting14  1.625e+00  1.065e+01   0.153    0.879
## Treatment3:DaysAfterPlanting14 -2.625e+00  1.065e+01  -0.247    0.806
## Treatment4:DaysAfterPlanting14 -6.250e-01  1.065e+01  -0.059    0.953
## Treatment5:DaysAfterPlanting14  2.500e+00  1.065e+01   0.235    0.815
## Treatment6:DaysAfterPlanting14  1.000e+00  1.065e+01   0.094    0.925
## Treatment7:DaysAfterPlanting14 -2.500e+00  1.065e+01  -0.235    0.815
## Treatment8:DaysAfterPlanting14 -2.500e+00  1.065e+01  -0.235    0.815
## Treatment9:DaysAfterPlanting14  6.250e-01  1.065e+01   0.059    0.953
## Treatment2:DaysAfterPlanting21  3.500e+00  1.065e+01   0.329    0.743
## Treatment3:DaysAfterPlanting21 -1.000e+00  1.065e+01  -0.094    0.925
## Treatment4:DaysAfterPlanting21  1.500e+00  1.065e+01   0.141    0.888
## Treatment5:DaysAfterPlanting21  2.875e+00  1.065e+01   0.270    0.788
## Treatment6:DaysAfterPlanting21  4.125e+00  1.065e+01   0.387    0.699
## Treatment7:DaysAfterPlanting21 -2.125e+00  1.065e+01  -0.200    0.842
## Treatment8:DaysAfterPlanting21 -1.500e+00  1.065e+01  -0.141    0.888
## Treatment9:DaysAfterPlanting21 -1.250e+00  1.065e+01  -0.117    0.907
## Treatment2:DaysAfterPlanting28  2.750e+00  1.065e+01   0.258    0.797
## Treatment3:DaysAfterPlanting28 -1.875e+00  1.065e+01  -0.176    0.861
## Treatment4:DaysAfterPlanting28  3.264e-13  1.065e+01   0.000    1.000
## Treatment5:DaysAfterPlanting28  2.500e+00  1.065e+01   0.235    0.815
## Treatment6:DaysAfterPlanting28  2.125e+00  1.065e+01   0.200    0.842
## Treatment7:DaysAfterPlanting28 -3.625e+00  1.065e+01  -0.340    0.734
## Treatment8:DaysAfterPlanting28 -1.500e+00  1.065e+01  -0.141    0.888
## Treatment9:DaysAfterPlanting28 -8.750e-01  1.065e+01  -0.082    0.935
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.65 on 108 degrees of freedom
## Multiple R-squared:  0.9585, Adjusted R-squared:  0.945
## F-statistic: 71.21 on 35 and 108 DF,  p-value: < 2.2e-16
```

```r
anova(lm.interaction)
```

```
## Analysis of Variance Table
##
## Response: Emergence
##                             Df Sum Sq Mean Sq  F value    Pr(>F)
## Treatment                    8 279366   34921 307.9516 < 2.2e-16 ***
## DaysAfterPlanting            3   3116    1039   9.1603 1.877e-05 ***
## Treatment:DaysAfterPlanting  24    142       6   0.0522         1
## Residuals                  108  12247     113
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Question 3. 5 pts. Based on the results of the linear model in question 2, do you need to fit the interaction term? No, because the p-value for the interaction (Treatment:DaysAfterPlanting) is 1, which is > 0.05 and so is not significant.

#Provide a simplified linear model without the interaction term but still testing both main effects. Provide the summary and ANOVA results. Then, interpret the intercept and the coefficient for Treatment 2.

#Interpretation from below code (simplified linear model) = Intercept is 182.163, so emergence is 182.163 with treatment one at 7 days after planting. The coefficient for Treatment 2 is -134.531, which means a decrease in emergence (y/dependent variable) of 134.531 when treatment 2 is applied compared to treatment 1, holding days after planting constant*

```r
#simplified = each variable impacts outcome, but they do not influence each others effect (independent&
simplified.lm <- lm(Emergence ~ Treatment + DaysAfterPlanting, data = emergence)

summary(simplified.lm)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment + DaysAfterPlanting, data = emergence)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.1632  -6.1536  -0.8542   6.1823  21.3958
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          182.163      2.797  65.136  < 2e-16 ***
## Treatment2          -134.531      3.425 -39.277  < 2e-16 ***
## Treatment3             9.750      3.425   2.847  0.00513 **
## Treatment4             2.719      3.425   0.794  0.42876
## Treatment5            10.719      3.425   3.129  0.00216 **
## Treatment6             8.812      3.425   2.573  0.01119 *
## Treatment7            -2.188      3.425  -0.639  0.52416
## Treatment8             7.750      3.425   2.263  0.02529 *
## Treatment9             2.000      3.425   0.584  0.56028
## DaysAfterPlanting14    9.722      2.283   4.258 3.89e-05 ***
## DaysAfterPlanting21   11.306      2.283   4.951 2.21e-06 ***
## DaysAfterPlanting28   10.944      2.283   4.793 4.36e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.688 on 132 degrees of freedom
## Multiple R-squared:  0.958,  Adjusted R-squared:  0.9545
## F-statistic: 273.6 on 11 and 132 DF,  p-value: < 2.2e-16
```

```r
anova(simplified.lm)
```

```
## Analysis of Variance Table
##
## Response: Emergence
##                    Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment           8 279366   34921 372.070 < 2.2e-16 ***
## DaysAfterPlanting   3   3116    1039  11.068 1.575e-06 ***
## Residuals         132  12389      94
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Question 4. 5 pts. Calculate the least square means for Treatment using the emmeans package and perform a Tukey separation with the compact letter display using the cld function.

#Interpret the results - First we are calculating the average emergence for each treatment (controlling days after planting). Treatment 2 has the lowest emergence, while the rest look rather uniform. Next, we use the cdl to group the treatments to compared least square means for statistical differences. Treatments in the same or overlapping groups are not significantly different from one another ($p > 0.05$). The group numbers start at the lowest emergence (1) and increase (here the highest is 3). Treatment 2 is in its own group (significantly different from the rest) and the lowest emergence(1).

```r
lsmeans <- emmeans(simplified.lm, ~Treatment)
lsmeans
```

```
##  Treatment emmean   SE  df lower.CL upper.CL
##  1          190.2 2.42 132    185.4    194.9
##  2           55.6 2.42 132     50.8     60.4
##  3          199.9 2.42 132    195.1    204.7
##  4          192.9 2.42 132    188.1    197.7
##  5          200.9 2.42 132    196.1    205.7
##  6          199.0 2.42 132    194.2    203.8
##  7          188.0 2.42 132    183.2    192.8
##  8          197.9 2.42 132    193.1    202.7
##  9          192.2 2.42 132    187.4    196.9
##
## Results are averaged over the levels of: DaysAfterPlanting
## Confidence level used: 0.95
```

```r
results_lsmeans <- cld(lsmeans, alpha = 0.05, details = TRUE)
results_lsmeans
```

```
## $emmeans
##  Treatment emmean   SE  df lower.CL upper.CL .group
##  2           55.6 2.42 132     50.8     60.4  1
##  7          188.0 2.42 132    183.2    192.8   2
##  1          190.2 2.42 132    185.4    194.9   23
##  9          192.2 2.42 132    187.4    196.9   23
##  4          192.9 2.42 132    188.1    197.7   23
##  8          197.9 2.42 132    193.1    202.7   23
##  6          199.0 2.42 132    194.2    203.8    3
##  3          199.9 2.42 132    195.1    204.7    3
##  5          200.9 2.42 132    196.1    205.7    3
##
## Results are averaged over the levels of: DaysAfterPlanting
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 9 estimates
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
##
```

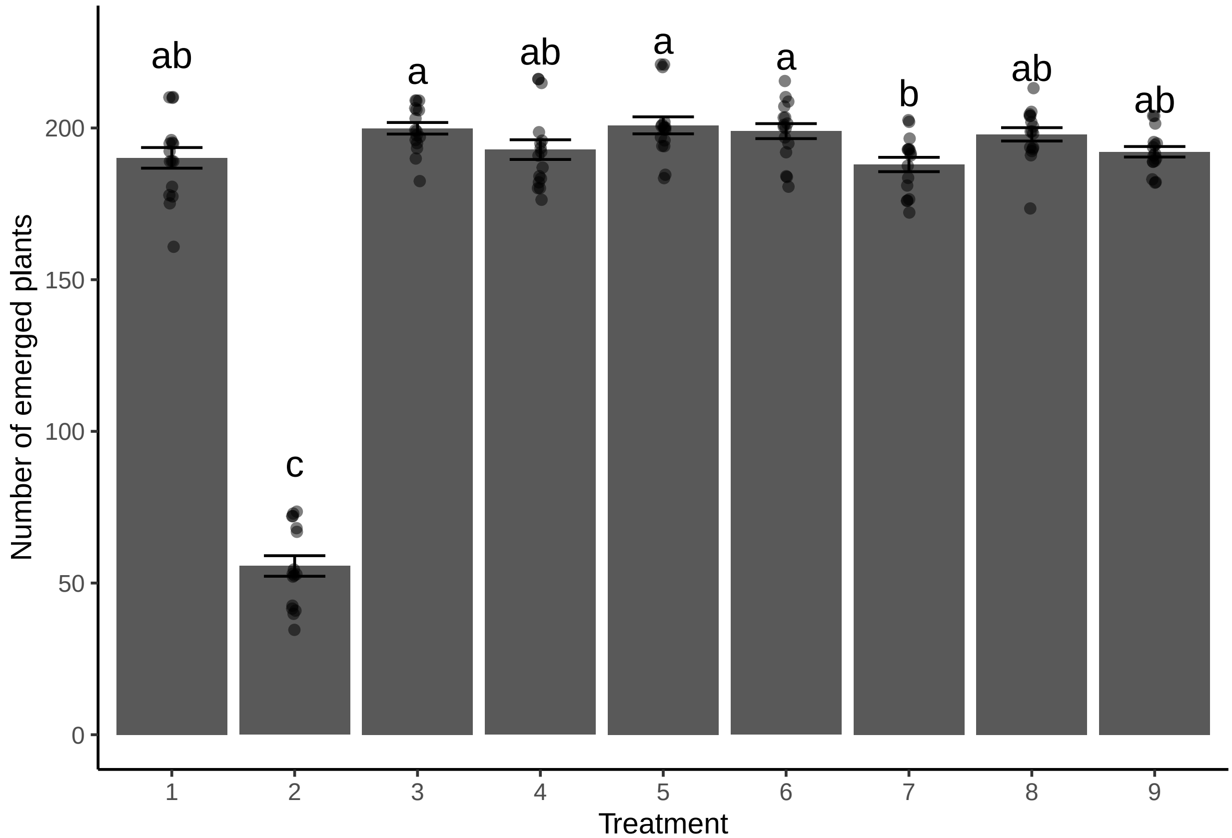
```
## $comparisons
##  contrast                estimate   SE  df t.ratio p.value
##  Treatment7 - Treatment2  132.344 3.43 132  38.638  <.0001
##  Treatment1 - Treatment2  134.531 3.43 132  39.277  <.0001
##  Treatment1 - Treatment7    2.188 3.43 132   0.639  0.9993
##  Treatment9 - Treatment2  136.531 3.43 132  39.861  <.0001
##  Treatment9 - Treatment7    4.188 3.43 132   1.223  0.9502
##  Treatment9 - Treatment1    2.000 3.43 132   0.584  0.9997
##  Treatment4 - Treatment2  137.250 3.43 132  40.071  <.0001
##  Treatment4 - Treatment7    4.906 3.43 132   1.432  0.8832
##  Treatment4 - Treatment1    2.719 3.43 132   0.794  0.9969
##  Treatment4 - Treatment9    0.719 3.43 132   0.210  1.0000
##  Treatment8 - Treatment2  142.281 3.43 132  41.540  <.0001
##  Treatment8 - Treatment7    9.938 3.43 132   2.901  0.0978
##  Treatment8 - Treatment1    7.750 3.43 132   2.263  0.3724
##  Treatment8 - Treatment9    5.750 3.43 132   1.679  0.7583
##  Treatment8 - Treatment4    5.031 3.43 132   1.469  0.8678
##  Treatment6 - Treatment2  143.344 3.43 132  41.850  <.0001
##  Treatment6 - Treatment7   11.000 3.43 132   3.212  0.0425
##  Treatment6 - Treatment1    8.812 3.43 132   2.573  0.2083
##  Treatment6 - Treatment9    6.812 3.43 132   1.989  0.5538
##  Treatment6 - Treatment4    6.094 3.43 132   1.779  0.6957
##  Treatment6 - Treatment8    1.062 3.43 132   0.310  1.0000
##  Treatment3 - Treatment2  144.281 3.43 132  42.124  <.0001
##  Treatment3 - Treatment7   11.938 3.43 132   3.485  0.0187
##  Treatment3 - Treatment1    9.750 3.43 132   2.847  0.1120
##  Treatment3 - Treatment9    7.750 3.43 132   2.263  0.3724
##  Treatment3 - Treatment4    7.031 3.43 132   2.053  0.5099
##  Treatment3 - Treatment8    2.000 3.43 132   0.584  0.9997
##  Treatment3 - Treatment6    0.938 3.43 132   0.274  1.0000
##  Treatment5 - Treatment2  145.250 3.43 132  42.406  <.0001
##  Treatment5 - Treatment7   12.906 3.43 132   3.768  0.0074
##  Treatment5 - Treatment1   10.719 3.43 132   3.129  0.0535
##  Treatment5 - Treatment9    8.719 3.43 132   2.545  0.2204
##  Treatment5 - Treatment4    8.000 3.43 132   2.336  0.3288
##  Treatment5 - Treatment8    2.969 3.43 132   0.867  0.9943
##  Treatment5 - Treatment6    1.906 3.43 132   0.557  0.9998
##  Treatment5 - Treatment3    0.969 3.43 132   0.283  1.0000
##
## Results are averaged over the levels of: DaysAfterPlanting
## P value adjustment: tukey method for comparing a family of 9 estimates
```

#Question 5. 4 pts. The provided function lets you dynamically add a linear model plus one factor from that model and plots a bar chart with letters denoting treatment differences. Use this model to generate the plot shown below.

#Explain the significance of the letters - The letters have the same meaning as the numbers in the previous question. Treatments in the same or overlapping groups are not significantly different from one another ($p > 0.05$). The group numbers start at the highest emergence (a) and decrease (here the lowest is c). Treatment 2 is in its own group (significantly different from the rest) and the lowest emergence (c).

```
plot_cldbars_onefactor <- function(lm_model, factor) {
  data <- lm_model$model
  variables <- colnames(lm_model$model)
```

```
  dependent_var <- variables[1]
  independent_var <- variables[2:length(variables)]

  lsmeans <- emmeans(lm_model, as.formula(paste("~", factor))) # estimate lsmeans
  Results_lsmeans <- cld(lsmeans, alpha = 0.05, reversed = TRUE, details = TRUE, Letters = letters) # c

  # Extracting the letters for the bars
  sig.diff.letters <- data.frame(Results_lsmeans$emmeans[,1],
                                 str_trim(Results_lsmeans$emmeans[,7]))
  colnames(sig.diff.letters) <- c(factor, "Letters")

  # for plotting with letters from significance test
  ave_stand2 <- lm_model$model %>%
    group_by(!!sym(factor)) %>%
    dplyr::summarize(
      ave.emerge = mean(.data[[dependent_var]], na.rm = TRUE),
      se = sd(.data[[dependent_var]]) / sqrt(n())
    ) %>%
    left_join(sig.diff.letters, by = factor) %>%
    mutate(letter_position = ave.emerge + 10 * se)

  plot <- ggplot(data, aes(x = !! sym(factor), y = !! sym(dependent_var))) +
    stat_summary(fun = mean, geom = "bar") +
    stat_summary(fun.data = mean_se, geom = "errorbar", width = 0.5) +
    ylab("Number of emerged plants") +
    geom_jitter(width = 0.02, alpha = 0.5) +
    geom_text(data = ave_stand2, aes(label = Letters, y = letter_position), size = 5) +
    xlab(as.character(factor)) +
    theme_classic()

  return(plot)
}

plot_cldbars_onefactor(simplified.lm, "Treatment")
```



#Question 6. 2 pts. Generate the gfm .md file along with a .html, .docx, or .pdf. Commit, and push the .md file to github and turn in the .html, .docx, or .pdf to Canvas. Provide me a link here to your github.

```
#Link to github is a clickable link at the top of the document.
```