Linear Models

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Contents

1. 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)
```

```
plant.emergence <- read.csv("data/PlantEmergence.csv")

plant.emergence$Treatment = as.factor(plant.emergence$Treatment)
plant.emergence$DaysAfterPlanting = as.factor(plant.emergence$DaysAfterPlanting)
plant.emergence$Rep = as.factor(plant.emergence$Rep)
```

2. 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.

Treatment had a strong effect on Emergence ($F = 307.95$, $p < .001$). On average, emergence occurred after 182.3 days (I'm unsure if these are the appropriate units?!), however, after Treatment2, this was 136.5 days earlier.

```
lm_model <- lm(Emergence ~ Treatment + DaysAfterPlanting + Treatment:DaysAfterPlanting,
               data = plant.emergence)
summary(lm_model)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment + DaysAfterPlanting + Treatment:DaysAfterPlanting,
##     data = plant.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
```

```
anova(lm_model)
```

```
## 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
```

3. Based on the results of the linear model in question 2, do you need to fit the interaction term? 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.

An interaction term was not necessary, since none exhibited statistical or practical significance within the linear model.

According to the simplified linear model, Treatment still has a strong effect on Emergence (all but Treatments 4, 7, and 9 were $p < .05$). However, this model also revealed that DaysAfterPlanting also had a strong effect (all ps $< .001$).

```
lm_model1 <- lm(Emergence ~ Treatment + DaysAfterPlanting,
                data = plant.emergence)
summary(lm_model1)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment + DaysAfterPlanting, data = plant.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
```

```
anova(lm_model1)
```

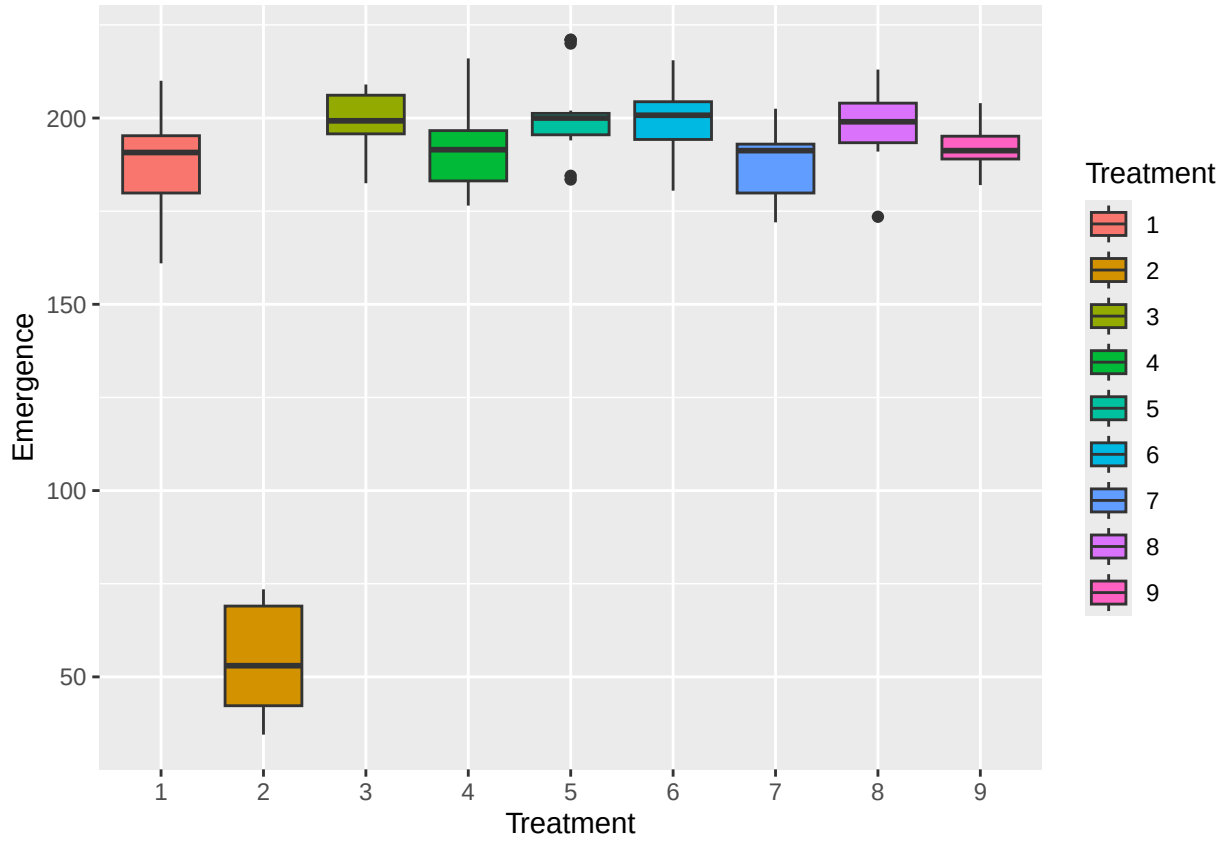
```
## Analysis of Variance Table
##
## Response: Emergence
##                    Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## 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
```

4. 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

According to visualisations and pairwise comparisons, the effect for Treatment2 was statistically different from all other treatment types. With a mean Emergence of 55.6 (units), Treatment2 was roughly 135 units sooner than all others (all ps $< .001$).

```
lsmeans <- emmeans(lm_model1, ~Treatment, data = plant.emergence)
ggplot(data = plant.emergence, aes(x = Treatment, y = Emergence, fill = Treatment)) +
  geom_boxplot()
```




```
summary(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
```

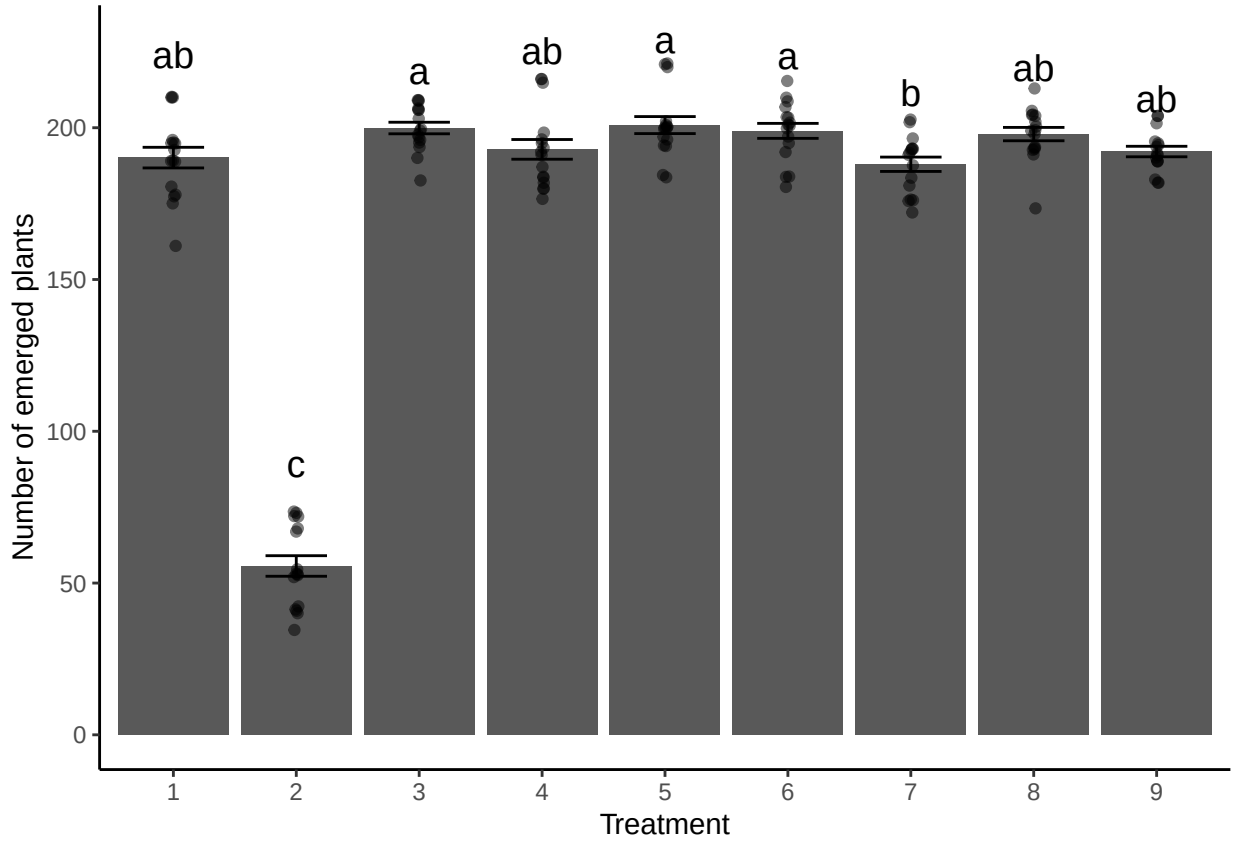
```
results_lsmeans <- cld(lsmeans, alpha = 0.05, details = TRUE)
summary(results_lsmeans)
```

```
##             Length Class       Mode
## emmeans     7      summary_emm list
## comparisons 6      summary_emm list
```

5. 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.

```
plot_cldbars_onefactor <- function(lm_model, factor) {
  data <- lm_model$model
  variables <- colnames(lm_model1$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) # contrast with Tukey adjustment by default.

# 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(lm_model1, "Treatment")
```



6. 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.

Coding Challenge 7