Coding_challenge_7

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Contents

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

STAND$Treatment <- as.factor(STAND$Treatment)$ # example shown here.

```
#load libraries
#Load packages
library(tidyverse)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.3
```

```
## Warning: package 'purrr' was built under R version 4.4.2
```

```
## Warning: package 'lubridate' was built under R version 4.4.2
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 4.4.2
```

```
## Loading required package: Matrix
```

```
## Warning: package 'Matrix' was built under R version 4.4.2
```

```
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
#install.packages("multcompView")
library(multcomp)
```

```
## Warning: package 'multcomp' was built under R version 4.4.2
```

```
## Loading required package: mvtnorm
```

```
## Warning: package 'mvtnorm' was built under R version 4.4.2
```

```
## Loading required package: survival
## Loading required package: TH.data
```

```
## Warning: package 'TH.data' was built under R version 4.4.2
```

```
## Loading required package: MASS
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
##
## Attaching package: 'TH.data'
##
## The following object is masked from 'package:MASS':
##
##     geyser
```

```
#install.packages("emmeans")
library(emmeans)
```

```
## Warning: package 'emmeans' was built under R version 4.4.3
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
#load data
datum <- read.csv("PlantEmergence.csv")
head(datum)
```

```
##   Plot Treatment Rep Emergence DatePlanted DateCounted DaysAfterPlanting
## 1  101         1   1     180.5    9-May-22   16-May-22                 7
## 2  102         2   1      54.5    9-May-22   16-May-22                 7
## 3  103         3   1     195.0    9-May-22   16-May-22                 7
## 4  104         4   1     198.5    9-May-22   16-May-22                 7
## 5  105         5   1     202.0    9-May-22   16-May-22                 7
## 6  106         6   1     184.0    9-May-22   16-May-22                 7
```

```
#Turn the Treatment , DaysAfterPlanting  and Rep into factors using the function as.factor

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

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.

```
model1 <- lm(Emergence ~ Treatment + DaysAfterPlanting + Treatment:DaysAfterPlanting, data = datum)
summary(model1)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment + DaysAfterPlanting + Treatment:DaysAfterPlanting,
##     data = datum)
##
## 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(model1)
```

```
## 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. 5 pts. 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.

Answer:

None of the interactions were significant so we can exclude the interactions. Lets consider with-interaction as 'complicated model'(model 1) and without-interaction as 'simple model'(model 2). So we will proceed with simple model for our analysis.

Interpretation:

- **Intercept is showing that Emergence value is 182.163 units when other independet variables(Treament, DaysAfterPlanting) are considered to be zero.**
- **Treatment 2: Plant that received treatment 2 had 134.531 units (SE +/- 3.42) lesser emergence. (p < < 2e-16)**

```
model2 <- lm(Emergence ~ Treatment + DaysAfterPlanting, data = datum)
summary(model2)
```

```
##
## Call:
## lm(formula = Emergence ~ Treatment + DaysAfterPlanting, data = datum)
```

```
##
## 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(model2)
```

```
## 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. 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.

Answer:

Interpretation Based on multiple comparison we found that statistically significant differences were only observed between Treatment 2 and other treatment groups.There was lower Emergence in group 2 compared to other groups.

```r
lsmeans <- emmeans(model2, ~ Treatment) # estimate lsmeans
Results_lsmeans <- cld(lsmeans, alpha = 0.05, reversed = TRUE, details = TRUE)
Results_lsmeans
```

```
## $emmeans
##  Treatment emmean   SE  df lower.CL upper.CL .group
##  5          200.9 2.42 132    196.1    205.7  1
##  3          199.9 2.42 132    195.1    204.7  1
##  6          199.0 2.42 132    194.2    203.8  1
##  8          197.9 2.42 132    193.1    202.7  12
##  4          192.9 2.42 132    188.1    197.7  12
##  9          192.2 2.42 132    187.4    196.9  12
##  1          190.2 2.42 132    185.4    194.9  12
##  7          188.0 2.42 132    183.2    192.8   2
##  2           55.6 2.42 132     50.8     60.4    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
```

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.

Answer:

**Significance of letters: if the letters are same then there is no statically significant difference between groups. If letters are different between two groups then they are statistically signifcantly different from each other.

Example: Treament 2 (letter-c) versus Treamet 9 (letter- ab) – They are statically significantly different from each other.

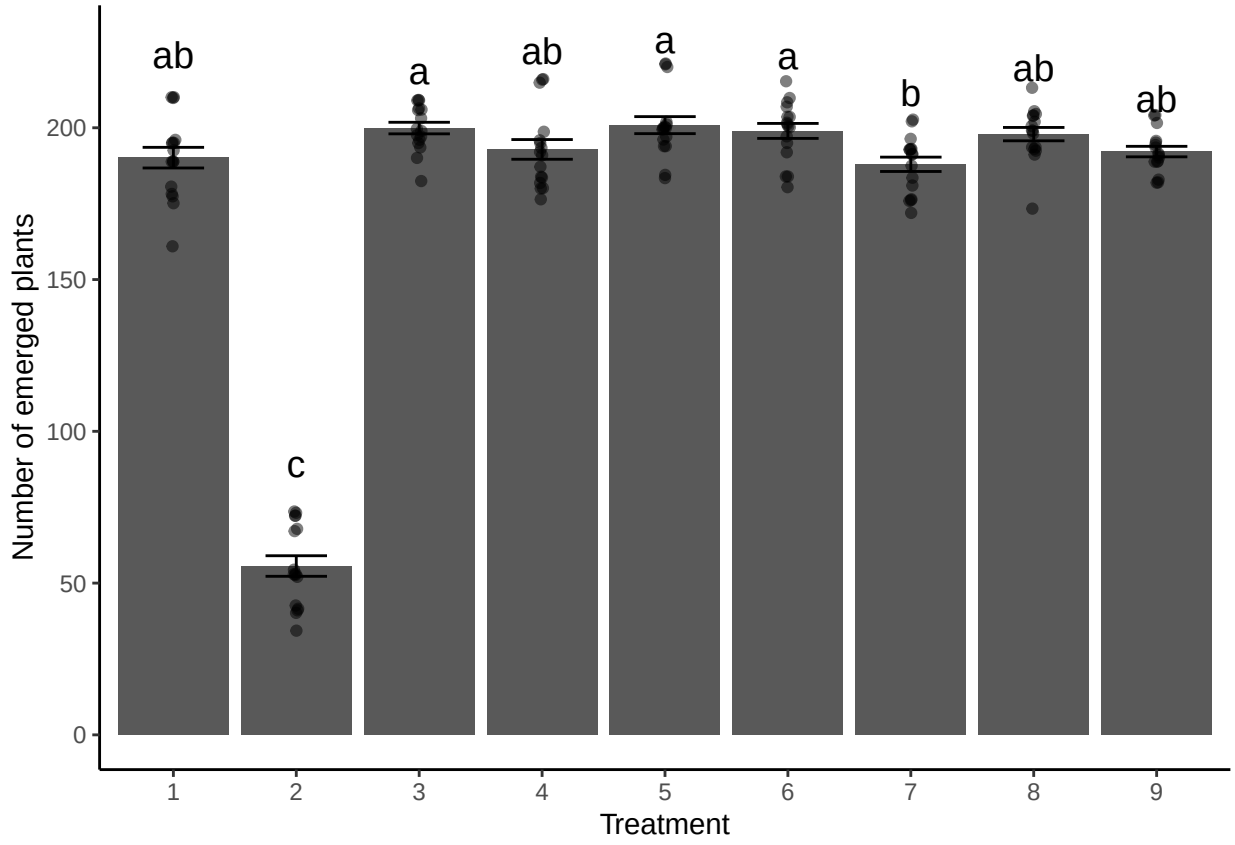
Treatment 8 (letter-ab) versus Treament 9 (letter- ab) - There is NO statiically signficant differnce between them

Function defined (from assignment)

```
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(model2, "Treatment") #I realized functions can make life easier
```



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.

Coding_challenge_7 Folder