ANOVA tests on Lantanna and Eucy mulch

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Loading the libraries

```
## 
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
## 
##     filter, lag

## The following objects are masked from 'package:base':
## 
##     intersect, setdiff, setequal, union

## ── Attaching packages ──────────────────────────────────── tidyverse 1.
3.2 ──
## ✔ ggplot2 3.3.6      ✔ purrr   0.3.4
## ✔ tibble  3.1.8      ✔ stringr 1.4.1
## ✔ tidyr   1.2.0      ✔ forcats 0.5.2
## ✔ readr   2.1.2
## ── Conflicts ───────────────────────────────────────── tidyverse_conflict
s() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
```

Purpose of the research: To show that lantana is better at suppressing biomass and emergence of weeds, compared to Eucy mulch.

Trial 1 One-way ANOVA test

```
trial_1 <- read_excel("biomass_t1 (1).xlsx")
trial_1$weed<-as.factor(trial_1$weed)
trial_1$mulch<-as.factor(trial_1$mulch)
trial_1$sample<-as.factor(trial_1$sample)
trial_1$treatment<-as.factor(trial_1$treatment)
df10<-trial_1 %>%
 filter(weed=="Rye")
df20<-trial_1 %>%
 filter(weed=="Radish")
## One way ANOVA for Rye
# Compute the analysis of variance for biomass
trial_1.anova10 <- aov(biomass ~ mulch, data = df10)
summary(trial_1.anova10)
```

```
##              Df  Sum Sq  Mean Sq F value Pr(>F)
## mulch        1 0.01993 0.019934   2.728  0.106
## Residuals   40 0.29228 0.007307

# Compute the analysis of variance for emergence
trial_1.anova11 <- aov(emergence ~ mulch, data = df10)
summary(trial_1.anova11)

##              Df Sum Sq Mean Sq F value  Pr(>F)
## mulch         1    384   384.0   9.293 0.00407 **
## Residuals    40   1653    41.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

One way ANOVA for radish
```
# Compute the analysis of variance for biomass
trial_1.anova20 <- aov(biomass ~ mulch, data = df20)
summary(trial_1.anova20)

##              Df Sum Sq Mean Sq F value Pr(>F)
## mulch         1 0.2131 0.21314   4.178 0.0476 *
## Residuals    40 2.0406 0.05102
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Compute the analysis of variance for emergence
trial_1.anova21 <- aov(emergence ~ mulch, data = df20)
summary(trial_1.anova21)

##              Df Sum Sq Mean Sq F value Pr(>F)
## mulch         1   6.88   6.881   2.051   0.16
## Residuals    40 134.19   3.355
```

Results of ANOVA for biomass:

As evident from the aforementioned analysis, there is no significant difference in means of biomass for the Lantanna and Eucy mulch as far as the Rye weed is concerned whereas, for the Radish weed, there is significant difference in means of biomass of the Lantanna and Eucy mulch because p value is less than the 0.05 significance level.

Results of ANOVA for emergence:

As evident from the aforementioned analysis, there is a significant difference in means of emergence for the Lantanna and Eucy mulch as far as the Rye weed is concerned because p value=0.00407 which is way less than the 0.05 significance level, whereas, for the Radish weed, there is no significant difference in means of emergence of the Lantanna and Eucy mulch because p value is gretaer than the 0.05 significance level.

Trial 1 Two-way ANOVA

```
##Two-way ANOVA test for Rye weed
aov2way1 <- aov(biomass ~ mulch + treatment, data = df10)
summary(aov2way1)

##             Df  Sum Sq Mean Sq F value   Pr(>F)
## mulch        1 0.01993 0.01993   30.66 3.44e-06 ***
## treatment    6 0.27018 0.04503   69.27  < 2e-16 ***
## Residuals   34 0.02210 0.00065
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

aov2way2 <- aov(emergence ~ mulch + treatment, data = df10)
summary(aov2way2)

##             Df Sum Sq Mean Sq F value   Pr(>F)
## mulch        1  384.0   384.0  19.630 9.28e-05 ***
## treatment    6  987.8   164.6   8.416 1.25e-05 ***
## Residuals   34  665.1    19.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Two-way ANOVA test for Radish weed
aov2way3 <- aov(biomass ~ mulch + treatment, data = df20)
summary(aov2way3)

##             Df Sum Sq Mean Sq F value  Pr(>F)
## mulch        1 0.2131 0.21314   9.425 0.00419 **
## treatment    6 1.2717 0.21195   9.372 4.42e-06 ***
## Residuals   34 0.7689 0.02262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

aov2way4 <- aov(emergence ~ mulch + treatment, data = df20)
summary(aov2way4)

##             Df Sum Sq Mean Sq F value Pr(>F)
## mulch        1   6.88   6.881   1.893  0.178
## treatment    6  10.57   1.762   0.485  0.815
## Residuals   34 123.62   3.636
```

Results of Two-way ANOVA test

For rye weed:

From the Two-way ANOVA table, we can conclude that, both mulch and treatment are statistically significant. Treatment is the most significant factor variable . These results would lead us to believe that changing mulch or treatment, will impact significantly the biomass values.Both mulch and treatment are statistically significant for emergence as well.These results would lead us to believe that changing mulch or treatment, will impact significantly the emergence values as well.

From the Two-way ANOVA table, we can conclude that, both mulch and treatment are statistically significant. Treatment is the most significant factor variable in this case as well . These results would lead us to believe that changing mulch or treatment, will impact significantly the biomass values. Both mulch and treatment are not statistically significant for emergence.These results depict that changing mulch or treatment, will not impact the emergence values.

Trial 2 One-way ANOVA:

```
trial_2 <- read_excel("biomass_t2.xlsx")
trial_2$weed<-as.factor(trial_2$weed)
trial_2$mulch<-as.factor(trial_2$mulch)
trial_2$sample<-as.factor(trial_2$sample)
trial_2$treatment<-as.factor(trial_2$treatment)
df11<-trial_2 %>%
 filter(weed=="Rye")
df21<-trial_2 %>%
 filter(weed=="Radish")
## One way ANOVA for Rye
# Compute the analysis of variance for biomass
trial_2.anova10 <- aov(biomass ~ mulch, data = df11)
summary(trial_2.anova10)

##             Df Sum Sq Mean Sq F value Pr(>F)
## mulch        1 0.1000 0.09999   3.947 0.0568 .
## Residuals   28 0.7093 0.02533
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Compute the analysis of variance for emergence
trial_2.anova11 <- aov(emergence ~ mulch, data = df11)
summary(trial_2.anova11)

##             Df Sum Sq Mean Sq F value Pr(>F)
## mulch        1    472   472.0   5.459 0.0268 *
## Residuals   28   2421    86.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## One way ANOVA for radish
# Compute the analysis of variance for biomass
trial_2.anova20 <- aov(biomass ~ mulch, data = df21)
summary(trial_2.anova20)

##             Df Sum Sq Mean Sq F value   Pr(>F)
## mulch        1  3.005  3.0045   15.76 0.000456 ***
## Residuals   28  5.340  0.1907
```

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

```
# Compute the analysis of variance for emergence
trial_2.anova21 <- aov(emergence ~ mulch, data = df21)
summary(trial_2.anova21)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## mulch        1    7.5     7.5   0.528  0.473
## Residuals   28  397.5    14.2
```

Results of ANOVA for biomass:

As evident from the aforementioned analysis, there is no significant difference in means of biomass for the Lantanna and Eucy mulch as far as the Rye weed is concerned whereas, for the Radish weed, there is significant difference in means of biomass of the Lantanna and Eucy mulch because p value is less than the 0.05 significance level.

Results of ANOVA for emergence:

As evident from the aforementioned analysis, there is a significant difference in means of emergence for the Lantanna and Eucy mulch as far as the Rye weed is concerned because p value=0.000456 which is way less than the 0.05 significance level, whereas, for the Radish weed, there is no significant difference in means of emergence of the Lantanna and Eucy mulch because p value is gretaer than the 0.05 significance level.

Trial 2 Two-way ANOVA

```
##Two-way ANOVA test for Rye weed
aov2way1 <- aov(biomass ~ mulch + treatment, data = df11)
summary(aov2way1)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## mulch        1 0.1000 0.09999   51.59 2.01e-07 ***
## treatment    4 0.6628 0.16570   85.48 7.74e-14 ***
## Residuals   24 0.0465 0.00194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
aov2way2 <- aov(emergence ~ mulch + treatment, data = df11)
summary(aov2way2)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## mulch        1  472.0   472.0   26.48 2.87e-05 ***
## treatment    4 1993.1   498.3   27.95 1.01e-08 ***
## Residuals   24  427.8    17.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Two-way ANOVA test for Radish weed
aov2way3 <- aov(biomass ~ mulch + treatment, data = df21)
summary(aov2way3)

##              Df Sum Sq Mean Sq F value   Pr(>F)
## mulch         1  3.005  3.0045   58.67 6.75e-08 ***
## treatment     4  4.111  1.0277   20.07 2.26e-07 ***
## Residuals    24  1.229  0.0512
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

aov2way4 <- aov(emergence ~ mulch + treatment, data = df21)
summary(aov2way4)

##              Df Sum Sq Mean Sq F value Pr(>F)
## mulch         1    7.5    7.50   0.505  0.484
## treatment     4   41.1   10.28   0.693  0.604
## Residuals    24  356.3   14.85
```

Results of Two-way ANOVA test

For rye weed:

From the Two-way ANOVA table, we can conclude that, both mulch and treatment are statistically significant. Treatment is the most significant factor variable as its p value is way less than the significance level . These results would lead us to believe that changing mulch or treatment, will impact significantly the biomass values.Both mulch and treatment are statistically significant for emergence as well.These results would lead us to believe that changing mulch or treatment, will impact significantly the emergence values as well.

For radish weed:

From the Two-way ANOVA table, we can conclude that, both mulch and treatment are statistically significant. Treatment is the most significant factor variable in this case as well . These results would lead us to believe that changing mulch or treatment, will impact significantly the biomass values. Both mulch and treatment are not statistically significant for emergence.These results depict that changing mulch or treatment, will not impact the suppression of the emergence values.

Tukey multiple pairwise-comparisons

Since mulch has only two levels there is no need to conduct pairwise comparisons with respect to mulch. However, multiple pairwise-comparisons have been conducted for treatment variable against biomass and emergence.

```
TukeyHSD(aov2way1 , which = "treatment")

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
```

```
## 
## Fit: aov(formula = biomass ~ mulch + treatment, data = df11)
## 
## $treatment
##                   diff         lwr         upr      p adj
## T1-Control -0.27833333 -0.3532194 -0.20344730 0.0000000
## T2-Control -0.32750000 -0.4023860 -0.25261396 0.0000000
## T3-Control -0.37216667 -0.4470527 -0.29728063 0.0000000
## T4-Control -0.42600000 -0.5008860 -0.35111396 0.0000000
## T2-T1      -0.04916667 -0.1240527  0.02571937 0.3272593
## T3-T1      -0.09383333 -0.1687194 -0.01894730 0.0091627
## T4-T1      -0.14766667 -0.2225527 -0.07278063 0.0000498
## T3-T2      -0.04466667 -0.1195527  0.03021937 0.4201898
## T4-T2      -0.09850000 -0.1733860 -0.02361396 0.0059010
## T4-T3      -0.05383333 -0.1287194  0.02105270 0.2453059

TukeyHSD(aov2way2 , which = "treatment")

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
## 
## Fit: aov(formula = emergence ~ mulch + treatment, data = df11)
## 
## $treatment
##                   diff        lwr         upr      p adj
## T1-Control  -5.833333 -13.01444    1.3477691 0.1515949
## T2-Control  -8.666667 -15.84777   -1.4855642 0.0126358
## T3-Control -13.666667 -20.84777   -6.4855642 0.0000818
## T4-Control -24.166667 -31.34777  -16.9855642 0.0000000
## T2-T1       -2.833333 -10.01444    4.3477691 0.7720196
## T3-T1       -7.833333 -15.01444   -0.6522309 0.0277561
## T4-T1      -18.333333 -25.51444  -11.1522309 0.0000009
## T3-T2       -5.000000 -12.18110    2.1811025 0.2732180
## T4-T2      -15.500000 -22.68110   -8.3188975 0.0000131
## T4-T3      -10.500000 -17.68110   -3.3188975 0.0020515

TukeyHSD(aov2way3 , which = "treatment")

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
## 
## Fit: aov(formula = biomass ~ mulch + treatment, data = df21)
## 
## $treatment
##                   diff         lwr         upr      p adj
## T1-Control -0.80150000 -1.1864014 -0.4165986 0.0000225
## T2-Control -0.89966667 -1.2845680 -0.5147653 0.0000038
## T3-Control -0.93600000 -1.3209014 -0.5510986 0.0000020
## T4-Control -1.00550000 -1.3904014 -0.6205986 0.0000006
## T2-T1      -0.09816667 -0.4830680  0.2867347 0.9418404
## T3-T1      -0.13450000 -0.5194014  0.2504014 0.8392739
```
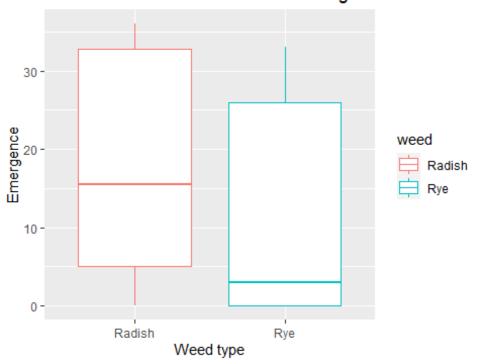
```
## T4-T1          -0.20400000 -0.5889014   0.1809014 0.5348885
## T3-T2          -0.03633333 -0.4212347   0.3485680 0.9985923
## T4-T2          -0.10583333 -0.4907347   0.2790680 0.9249717
## T4-T3          -0.06950000 -0.4544014   0.3154014 0.9831056

TukeyHSD(aov2way4 , which = "treatment")

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = emergence ~ mulch + treatment, data = df21)
##
## $treatment
##                     diff        lwr       upr      p adj
## T1-Control -1.0000000   -7.553887 5.553887 0.9910103
## T2-Control -2.1666667   -8.720554 4.387220 0.8641958
## T3-Control -1.8333333   -8.387220 4.720554 0.9205454
## T4-Control -3.5000000 -10.053887 3.053887 0.5277021
## T2-T1         -1.1666667   -7.720554 5.387220 0.9839747
## T3-T1         -0.8333333   -7.387220 5.720554 0.9955198
## T4-T1         -2.5000000   -9.053887 4.053887 0.7925468
## T3-T2          0.3333333   -6.220554 6.887220 0.9998778
## T4-T2         -1.3333333   -7.887220 5.220554 0.9738382
## T4-T3         -1.6666667   -8.220554 4.887220 0.9424185
```

Results: The treatment for which p adj value is less than 0.05, have significant effect on biomass and emergence respectively. On the other hand, if p adj value > 0.05, then those treatments don't have a significant effect on biomass and emergence values respectively.

Trial 3

```
#Visualizing using box plots
trial_3 <-read_excel("biomass_t3.xlsx")
trial_3$weed<-as.factor(trial_3$weed)
trial_3$mulch<-as.factor(trial_3$mulch)
trial_3$sample<-as.factor(trial_3$sample)
trial_3$treatment<-as.factor(trial_3$treatment)
df12<-trial_3 %>%
 filter(mulch=="Lantana")
ggplot(df12, aes(x=weed,y=emergence,color=weed))+
  geom_boxplot()+
  labs(title = "Lantanna effect on both weeds emergence ",x="Weed type",y="Em
ergence")
```

Lantanna effect on both weeds emergence


```
ggplot(df12,aes(x=weed,y=biomass,color=weed))+
  geom_boxplot()+
  labs(title = "Lantanna effect on both weeds biomass ",x="Weed type",y="Biom
ass")
```

Lantanna effect on both weeds biomass