

Data for Soil Rhizobia Paper

FLM018: Rhizobia confer protection against pathogenic effect of soil microbiome in *M. polymorpha*

===== Project Description =====

This is a project initiated by Katie Wozniak where she grew 12 genotypes of *Medicago polymorpha* in the presence of soil inoculates and/or rhizobia. The initial project (Trapping experiment) used soil from 8 different locations in either Florida or Portugal. The second part of the experiment, Katie used only two MP genotypes and location matching soil at low and high concentrations. In both experiments, WSM was the rhizobia used for inoculations.

```
library(ggplot2)
library(reshape2)
library(plyr)
library(dplyr)
library(car)
library(multcomp)
library(data.table)
library(lme4)
library(lmerTest)
library(emmeans)
```

```
SRMort <- read.csv("Soil_Rhiz_All_Data20Feb2018.csv")
TrapMort <- read.csv("Trapping_Alll_Data20Feb2018.csv")

SRMort <- within(SRMort, Soil <- as.factor(paste(SoilConc, Inoculate)))
```

Trapping Experiment

Mortality

I compared survival rate using two models, in the first, I used the *Medicago* genotypes as a random variable along with a variable "Treat" that refers to the addition of soil, buffer, or WSM. The second

model uses the variable “Treatment”, which divides the soil variable into their identities. However, due to a deficiency of DFs, Genotype can not be included.

```
MortMod <- glmer(as.factor(Dead_0) ~ Treat * Range + (1 | Genotype), family = binomial(link = "logit"), data = TrapMort)
```

```
MortMod2 <- glm(as.factor(Dead_0) ~ Treatment * Range, family = binomial(link = "logit"), data = TrapMort)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: as.factor(Dead_0)
##              Chisq Df Pr(>Chisq)
## Treat          51.8972  2  5.379e-12 ***
## Range           0.0475  1    0.8275
## Treat:Range     0.0080  2    0.9960
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: as.factor(Dead_0)
##
## Terms added sequentially (first to last)
##
##
##              Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                                347      453.29
## Treatment          9  198.124      338      255.16 <2e-16 ***
## Range              1    0.019      337      255.14  0.8902
## Treatment:Range    9    8.957      328      246.19  0.4413
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results show that Treat(ment) **is significant** but that Range **is not significant**.

Biomass

I don't think the Biomass data should be included for this portion of the paper since data was only taken on the WSM and buffer plants. The results show that Treat(ment) **is significant** but that Range **is not significant** for all data.

Shoot data

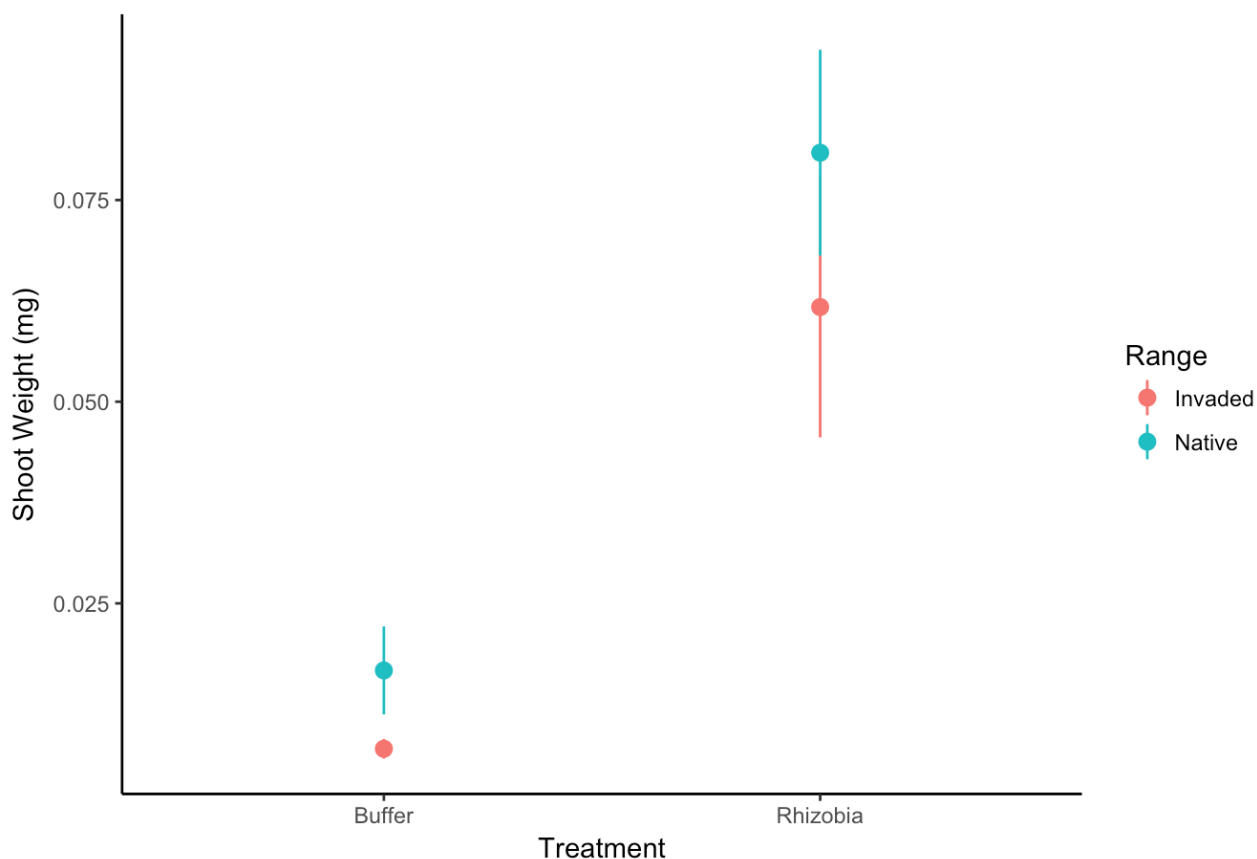
```
ShootMod <- lmer(ShootWeight ~ Treatment * Range + (1| Genotype), data = TrapBio)
```

```
## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##
```

| | Sum Sq | Mean Sq | NumDF | DenDF | F.value | Pr(>F) |
|-----------------|----------|----------|-------|--------|---------|---------------|
| Treatment | 0.052655 | 0.052655 | 1 | 45.914 | 29.7477 | 1.898e-06 *** |
| Range | 0.002725 | 0.002725 | 1 | 10.344 | 1.5395 | 0.2421 |
| Treatment:Range | 0.000224 | 0.000224 | 1 | 45.914 | 0.1264 | 0.7238 |

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

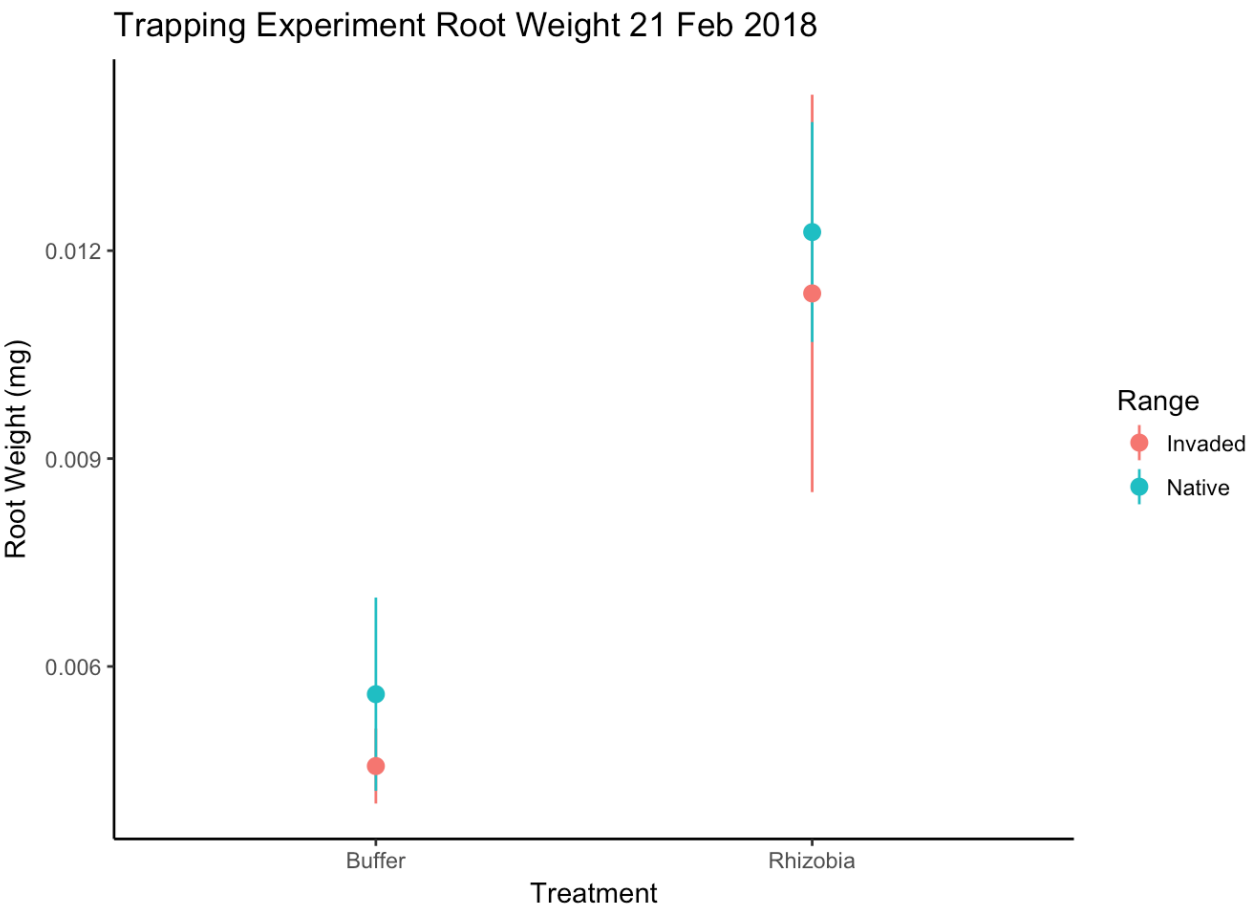
Trapping Experiment Shoot Weight 21 Feb 2018



Root data

```
RootMod <- lmer(RootWeight ~ Treatment * Range + (1| Genotype), data = TrapBio)
```

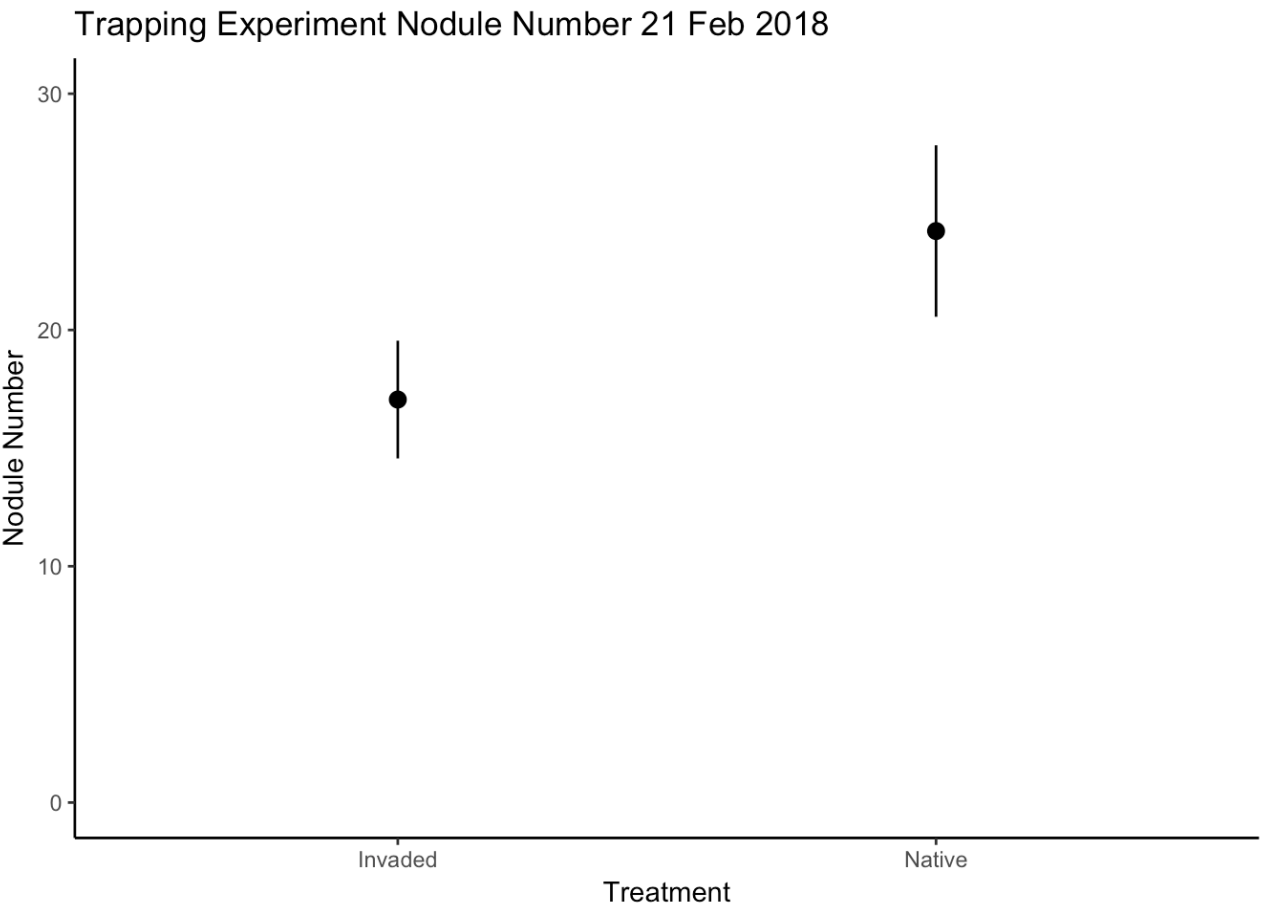
```
## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##           Sum Sq   Mean Sq NumDF   DenDF F.value    Pr(>F)
## Treatment      0.00081642 0.00081642     1 45.295 17.6854 0.0001214 ***
## Range          0.00002627 0.00002627     1 10.243  0.5690 0.4676507
## Treatment:Range 0.00004000 0.00004000     1 45.295  0.8665 0.3568678
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Nodule Number Data

```
NNMod <- lmer(NodNum ~ Range + (1| Genotype), data = TrapBio)
```

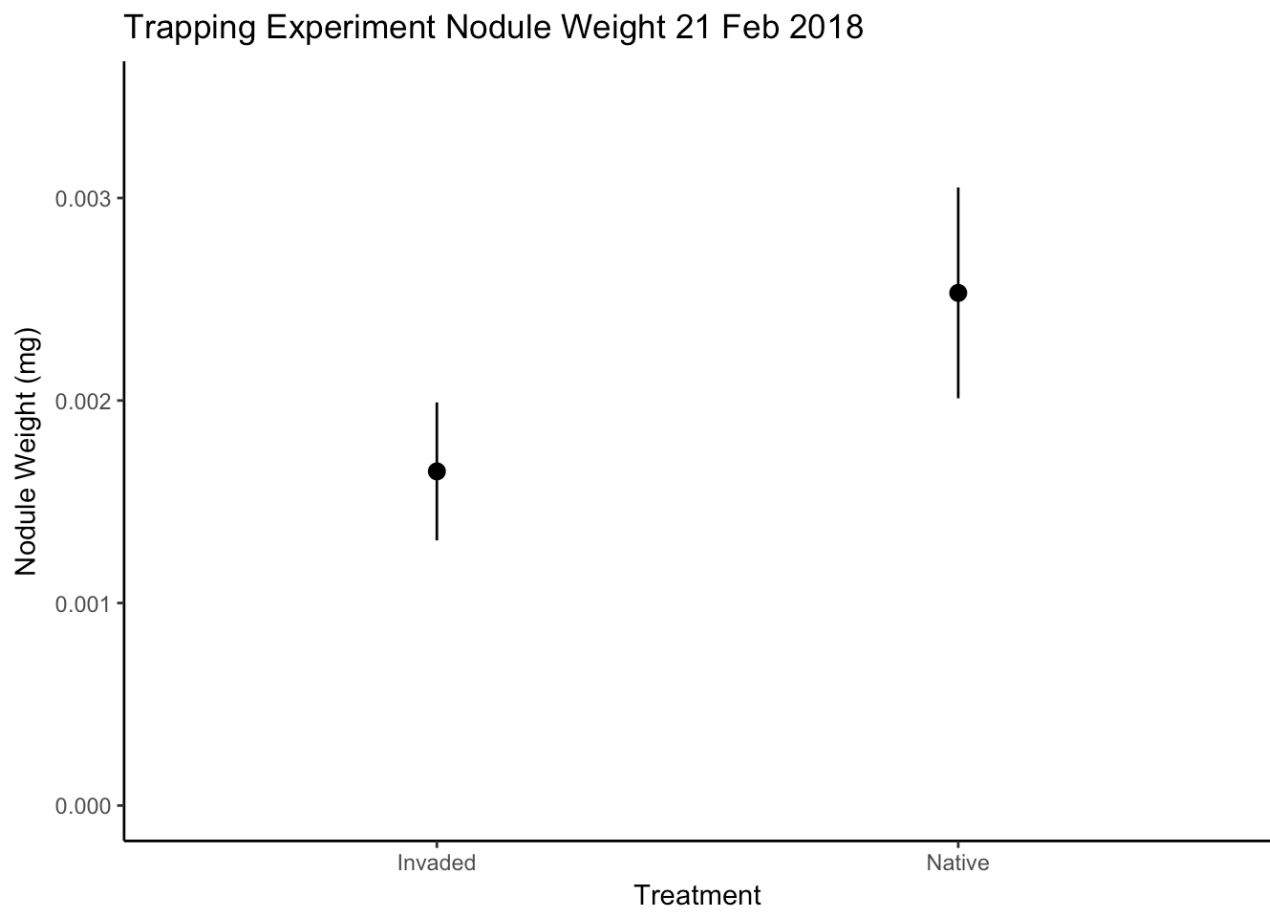
```
## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##           Sum Sq Mean Sq NumDF   DenDF F.value    Pr(>F)
## Range 330.42   330.42     1 10.378  2.2672  0.162
```



Nodule Weight Data

```
NWMod <- lmer(NodWeight ~ Range + (1| Genotype), data = TrapBio)

## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##           Sum Sq    Mean Sq NumDF  DenDF F.value Pr(>F)
## Range 4.6937e-06 4.6937e-06     1  9.6546  1.6373 0.2306
```



Soil plus/minus rhizobia Experiment

Mortality

First, I ran survival as a function of all 10 treatments as defined by Katie

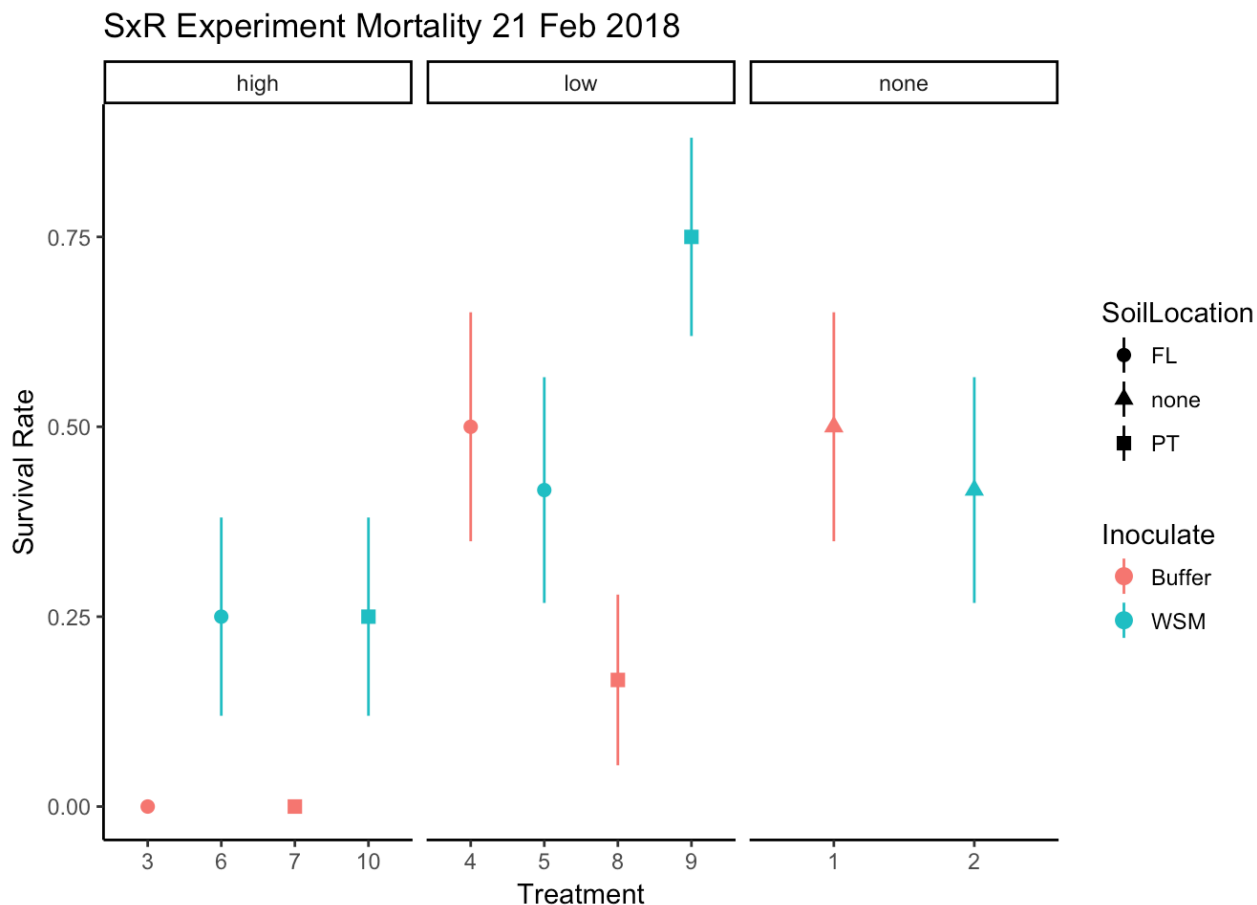
```
SRMortMod <- glm(DeadOrAlive ~ Treatment , family = binomial(link = "logit"), d  
ata = SRMort)
```

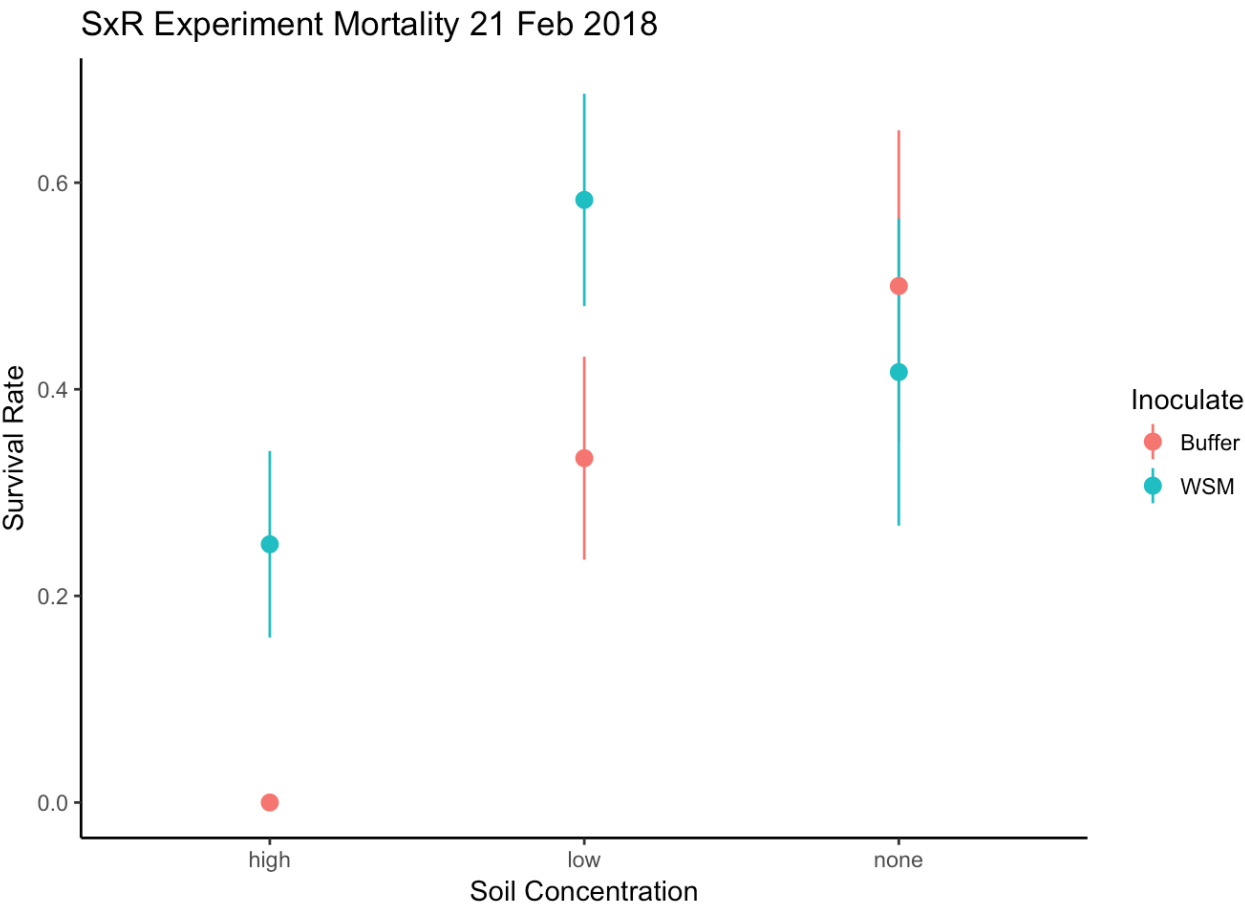
```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: DeadOrAlive
##
## Terms added sequentially (first to last)
##
##
```

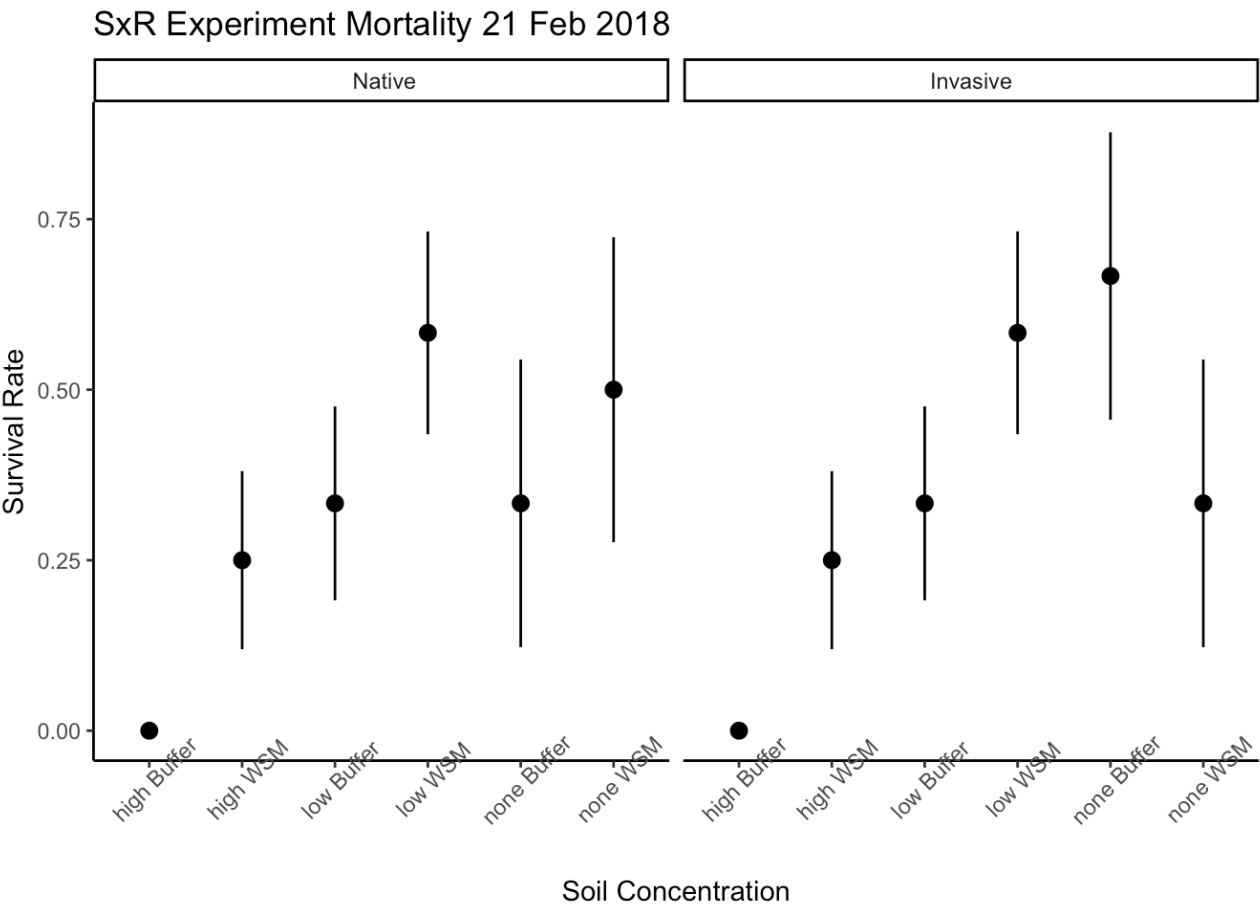
| | Df | Deviance | Resid. Df | Resid. Dev | Pr(>Chi) |
|--------------|----|----------|-----------|------------|---------------|
| ## NULL | | | 119 | 151.34 | |
| ## Treatment | 9 | 34.166 | 110 | 117.17 | 8.355e-05 *** |

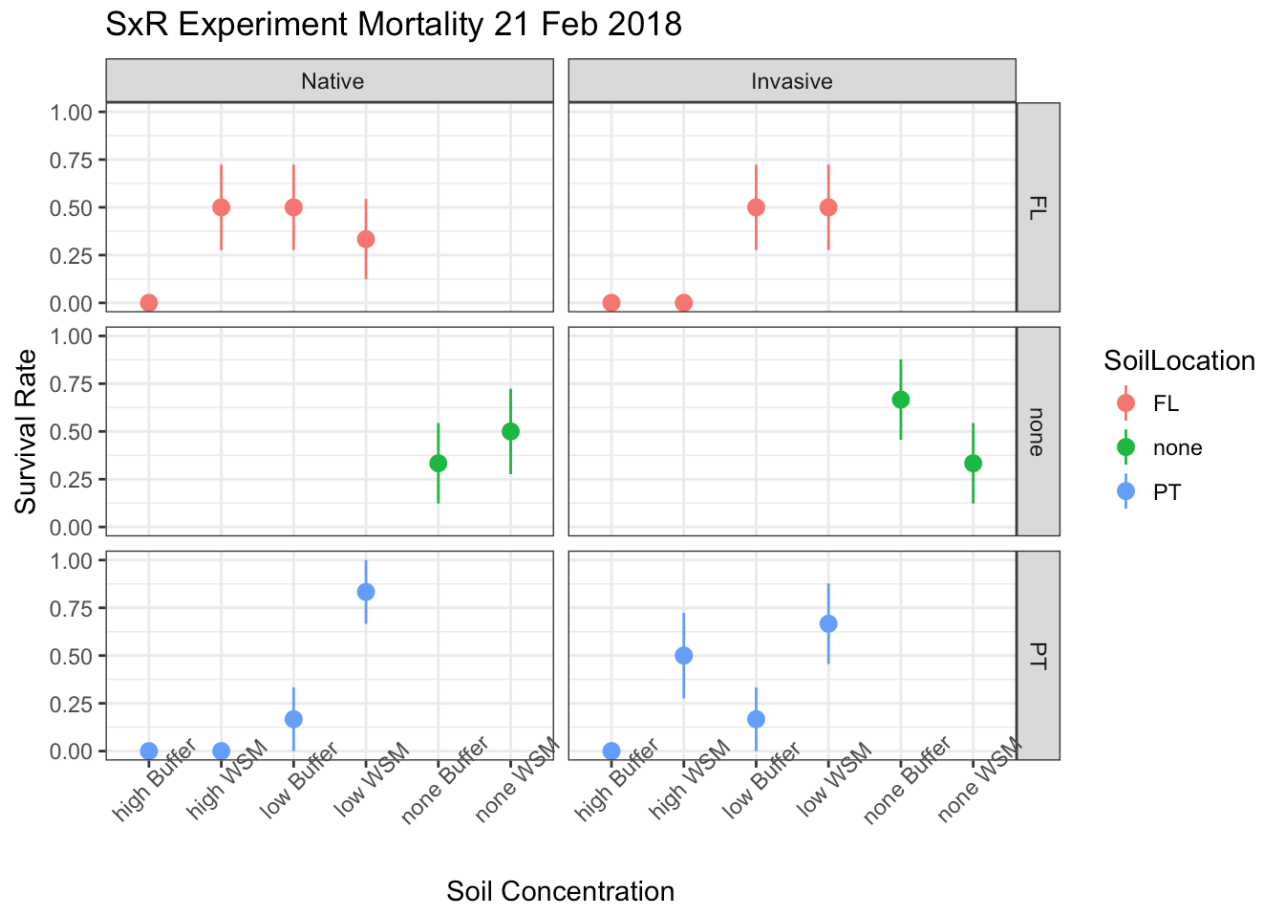
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Treatment was *significant*. I also ran a Tukey mult comp test (results not shown). The only significance was between soil and buffer/wsm. All other comparisons were not significant.









The final graph suggests that there might be an effect of soil location on mortality.

```
SRMortMod3 <- glm(DeadOrAlive ~ Soil * Range * SoilLocation, family = binomial(
link = "logit"), data = SRMort)
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: DeadOrAlive
##
## Terms added sequentially (first to last)
##
##
```

| | Df | Deviance | Resid. Df | Resid. Dev | Pr(>Chi) |
|-----------------------------|----|----------|-----------|------------|---------------|
| ## NULL | | | 119 | 151.34 | |
| ## Soil | 5 | 28.2572 | 114 | 123.08 | 3.242e-05 *** |
| ## Range | 1 | 0.0463 | 113 | 123.04 | 0.82956 |
| ## Soil:Location | 1 | 0.0000 | 112 | 123.04 | 1.00000 |
| ## Soil:Range | 5 | 1.6576 | 107 | 121.38 | 0.89420 |
| ## Soil:Soil:Location | 3 | 5.9083 | 104 | 115.47 | 0.11616 |
| ## Range:Soil:Location | 1 | 1.1620 | 103 | 114.31 | 0.28105 |
| ## Soil:Range:Soil:Location | 3 | 9.9904 | 100 | 104.32 | 0.01865 * |

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

To try and parse out differences between will run some multiple comparisons and maybe some different contrasts.

```
tt = lsmeans(SRMortMod3, specs = ~ Range | Soil:Soil:Location)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      Soil      SoilLocation      estimate      SE      df
## Native - Invasive high Buffer FL      1.431178e-07 6208.832295 Inf
## Native - Invasive high WSM FL      -1.956607e+01 4390.307472 Inf
## Native - Invasive low Buffer FL      -1.661515e-15      1.154701 Inf
## Native - Invasive low WSM FL      6.931472e-01      1.190238 Inf
## Native - Invasive none Buffer FL      nonEst      NA NA
## Native - Invasive none WSM FL      nonEst      NA NA
## Native - Invasive high Buffer none      nonEst      NA NA
## Native - Invasive high WSM none      nonEst      NA NA
## Native - Invasive low Buffer none      nonEst      NA NA
## Native - Invasive low WSM none      nonEst      NA NA
## Native - Invasive none Buffer none      1.386294e+00      1.224745 Inf
## Native - Invasive none WSM none      -6.931472e-01      1.190238 Inf
## Native - Invasive high Buffer PT      -4.819478e-08 6208.832288 Inf
## Native - Invasive high WSM PT      1.956607e+01 4390.307474 Inf
## Native - Invasive low Buffer PT      -3.702069e-15      1.549193 Inf
## Native - Invasive low WSM PT      -9.162907e-01      1.396424 Inf
## Native - Invasive none Buffer PT      nonEst      NA NA
## Native - Invasive none WSM PT      nonEst      NA NA
## z.ratio p.value
## 0.000 1.0000
## -0.004 0.9964
## 0.000 1.0000
## 0.582 0.5603
## NA NA
## NA NA
## NA NA
## NA NA
## NA NA
## NA NA
## 1.132 0.2577
## -0.582 0.5603
## 0.000 1.0000
## 0.004 0.9964
## 0.000 1.0000
## -0.656 0.5117
## NA NA
## NA NA
##
## Results are given on the log odds ratio (not the response) scale.
```

```
pairs(dd, by = "Soil")
```

```
## Soil = high Buffer:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT 1.913126e-07 8780.614833
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df z.ratio p.value
## NA NA NA
## Inf 0.000 1.0000
## NA NA NA
##
## Soil = high WSM:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT -3.913214e+01 6208.832371
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df z.ratio p.value
## NA NA NA
## Inf -0.006 1.0000
## NA NA NA
##
## Soil = low Buffer:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT 2.040555e-15 1.932184
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df z.ratio p.value
## NA NA NA
## Inf 0.000 1.0000
## NA NA NA
##
## Soil = low WSM:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT 1.609438e+00 1.834848
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df z.ratio p.value
## NA NA NA
## Inf 0.877 0.6547
## NA NA NA
##
## Soil = none Buffer:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT nonEst NA
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df z.ratio p.value
```

```
##      NA      NA      NA
##      NA      NA      NA
##      NA      NA      NA
##
## Soil = none WSM:
## contrast                                estimate      SE
## Native - Invasive,FL - Native - Invasive,none      nonEst      NA
## Native - Invasive,FL - Native - Invasive,PT          nonEst      NA
## Native - Invasive,none - Native - Invasive,PT        nonEst      NA
## df z.ratio p.value
##      NA      NA      NA
##      NA      NA      NA
##      NA      NA      NA
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

I found a this on line:link (<https://rdrr.io/cran/emmeans/f/inst/doc/FAQs.Rmd#NAs>)

My ANOVA F is significant, but no pairwise comparisons are {#anova} This is a common misunderstanding of ANOVA. If F is significant, this implies only that some contrast among the means (or effects) is statistically significant (compared to a Scheffé critical value). That contrast may be very much unlike a pairwise comparison, especially when there are several means being compared. Another factor is that by default, P values for pairwise comparisons are adjusted using the Tukey method, and the adjusted P values can be quite a bit larger than the unadjusted ones. (But I definitely do not advocate using no adjustment to “repair” this problem.)

SR Biomass Data =====

Shoot Data

```
ShootModSR <- lm(ShootWeight ~ Treatment * Range, data = SRMort)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment      7 0.73327  0.104752 11.6884 1.633e-06 ***
## Range           1 0.09575  0.095754 10.6843  0.003139 **
## Treatment:Range  5 0.08405  0.016809  1.8756  0.134645
## Residuals      25 0.22405  0.008962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ShootModSR <- lm(ShootWeight ~ Soil * Range * SoilLocation, data = SRMort)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Soil         4 0.66769  0.166922 18.6253 3.286e-07 ***
## Range        1 0.11600  0.116001 12.9435  0.001381 **
## SoilLocation  1 0.03895  0.038953  4.3465  0.047456 *
## Soil:Range    4 0.08184  0.020460  2.2830  0.088648 .
## Soil:SoilLocation 1 0.00276  0.002760  0.3080  0.583863
## Range:SoilLocation 1 0.00348  0.003484  0.3888  0.538601
## Soil:Range:SoilLocation 1 0.00234  0.002340  0.2611  0.613833
## Residuals    25 0.22405  0.008962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

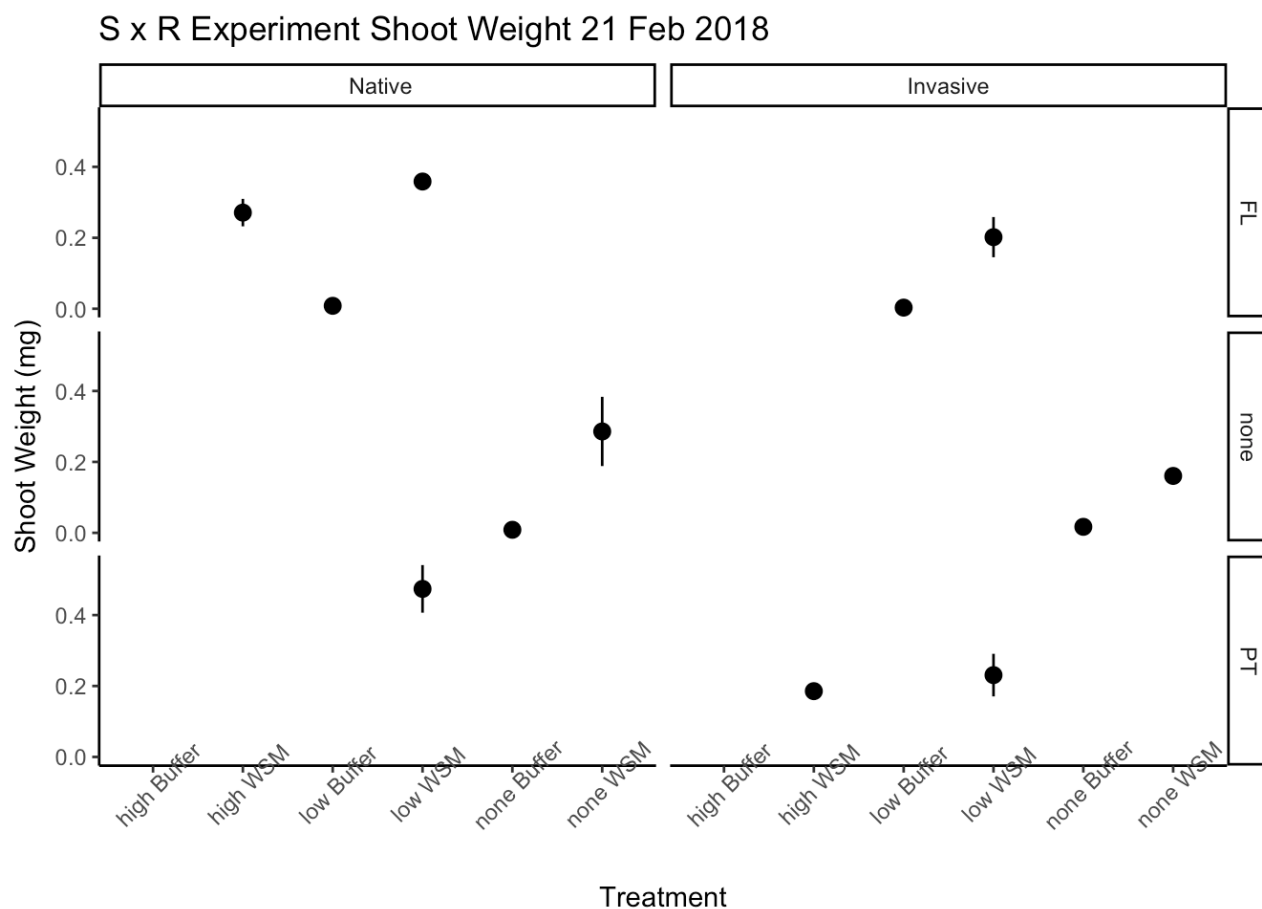
The main effects **are significantly different**

```
ShootModSR <- lm(ShootWeight ~ Soil, data = SRMort)
summary(glht(ShootModSR, mcp(Soil = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = ShootWeight ~ Soil, data = SRMort)
##
## Linear Hypotheses:
```

| | Estimate | Std. Error | t value | Pr(> t) | |
|----------------------------------|-----------|------------|---------|----------|-----|
| ## low Buffer - high WSM == 0 | -0.192504 | 0.063459 | -3.034 | 0.0341 | * |
| ## low WSM - high WSM == 0 | 0.101383 | 0.057335 | 1.768 | 0.4036 | |
| ## none Buffer - high WSM == 0 | -0.214100 | 0.067840 | -3.156 | 0.0253 | * |
| ## none WSM - high WSM == 0 | 0.007453 | 0.071151 | 0.105 | 1.0000 | |
| ## low WSM - low Buffer == 0 | 0.293887 | 0.052077 | 5.643 | <1e-04 | *** |
| ## none Buffer - low Buffer == 0 | -0.021596 | 0.063459 | -0.340 | 0.9969 | |
| ## none WSM - low Buffer == 0 | 0.199957 | 0.066987 | 2.985 | 0.0383 | * |
| ## none Buffer - low WSM == 0 | -0.315483 | 0.057335 | -5.502 | <1e-04 | *** |
| ## none WSM - low WSM == 0 | -0.093930 | 0.061217 | -1.534 | 0.5436 | |
| ## none WSM - none Buffer == 0 | 0.221553 | 0.071151 | 3.114 | 0.0282 | * |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Soil x Range is nearly significant, so will do comparisons of soil within each range

```
SRMort_N <- subset(SRMort, Range == " Native")
ShootModSRs <- lm(ShootWeight ~ Soil , data = SRMort_N)
anova(ShootModSRs)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Soil         4  0.55673  0.139183   10.487 0.0003839 ***
## Residuals   14  0.18581  0.013272
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(glht(ShootModSRs, mcp(Soil = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = ShootWeight ~ Soil, data = SRMort_N)
##
## Linear Hypotheses:
```

| | Estimate | Std. Error | t value | Pr(> t) |
|----------------------------------|----------|------------|---------|-------------|
| ## low Buffer - high WSM == 0 | -0.23395 | 0.08799 | -2.659 | 0.10981 |
| ## low WSM - high WSM == 0 | 0.16993 | 0.07950 | 2.138 | 0.25434 |
| ## none Buffer - high WSM == 0 | -0.26240 | 0.10517 | -2.495 | 0.14458 |
| ## none WSM - high WSM == 0 | 0.01487 | 0.09406 | 0.158 | 0.99984 |
| ## low WSM - low Buffer == 0 | 0.40388 | 0.07221 | 5.593 | < 0.001 *** |
| ## none Buffer - low Buffer == 0 | -0.02845 | 0.09977 | -0.285 | 0.99832 |
| ## none WSM - low Buffer == 0 | 0.24882 | 0.08799 | 2.828 | 0.08199 . |
| ## none Buffer - low WSM == 0 | -0.43233 | 0.09237 | -4.680 | 0.00268 ** |
| ## none WSM - low WSM == 0 | -0.15506 | 0.07950 | -1.951 | 0.33249 |
| ## none WSM - none Buffer == 0 | 0.27727 | 0.10517 | 2.636 | 0.11418 |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
SRMort_I <- subset(SRMort, Range == "Invasive")
ShootModSRs <- lm(ShootWeight ~ Soil , data = SRMort_I)
Anova(ShootModSRs, type = "3")
```

```
## Anova Table (Type III tests)
##
## Response: ShootWeight
##
```

| | Sum Sq | Df | F value | Pr(>F) |
|----------------|----------|----|---------|---------------|
| ## (Intercept) | 0.103268 | 1 | 19.2806 | 0.0005263 *** |
| ## Soil | 0.153393 | 4 | 7.1598 | 0.0019682 ** |
| ## Residuals | 0.080341 | 15 | | |

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

```
summary(glht(ShootModSRs, mcp(Soil = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = ShootWeight ~ Soil, data = SRMort_I)
##
## Linear Hypotheses:
```

| | Estimate | Std. Error | t value | Pr(> t) |
|----------------------------------|----------|------------|---------|------------|
| ## low Buffer - high WSM == 0 | -0.15106 | 0.05590 | -2.702 | 0.09858 . |
| ## low WSM - high WSM == 0 | 0.03284 | 0.05050 | 0.650 | 0.96306 |
| ## none Buffer - high WSM == 0 | -0.16858 | 0.05590 | -3.016 | 0.05587 . |
| ## none WSM - high WSM == 0 | -0.02503 | 0.06681 | -0.375 | 0.99521 |
| ## low WSM - low Buffer == 0 | 0.18390 | 0.04587 | 4.009 | 0.00835 ** |
| ## none Buffer - low Buffer == 0 | -0.01752 | 0.05175 | -0.339 | 0.99675 |
| ## none WSM - low Buffer == 0 | 0.12603 | 0.06338 | 1.988 | 0.31256 |
| ## none Buffer - low WSM == 0 | -0.20142 | 0.04587 | -4.391 | 0.00402 ** |
| ## none WSM - low WSM == 0 | -0.05787 | 0.05868 | -0.986 | 0.85452 |
| ## none WSM - none Buffer == 0 | 0.14355 | 0.06338 | 2.265 | 0.20604 |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

SR Biomass Data =====

Root Data

```
RootModSR <- lm(RootWeight ~ Treatment * Range, data = SRMort)
anova(RootModSR)
```

```
## Analysis of Variance Table
##
## Response: RootWeight
```

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------|----|-----------|-----------|---------|---------------|
| ## Treatment | 7 | 0.0210114 | 0.0030016 | 16.305 | 7.011e-08 *** |
| ## Range | 1 | 0.0107698 | 0.0107698 | 58.501 | 5.277e-08 *** |
| ## Treatment:Range | 5 | 0.0079005 | 0.0015801 | 8.583 | 7.710e-05 *** |
| ## Residuals | 25 | 0.0046024 | 0.0001841 | | |

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

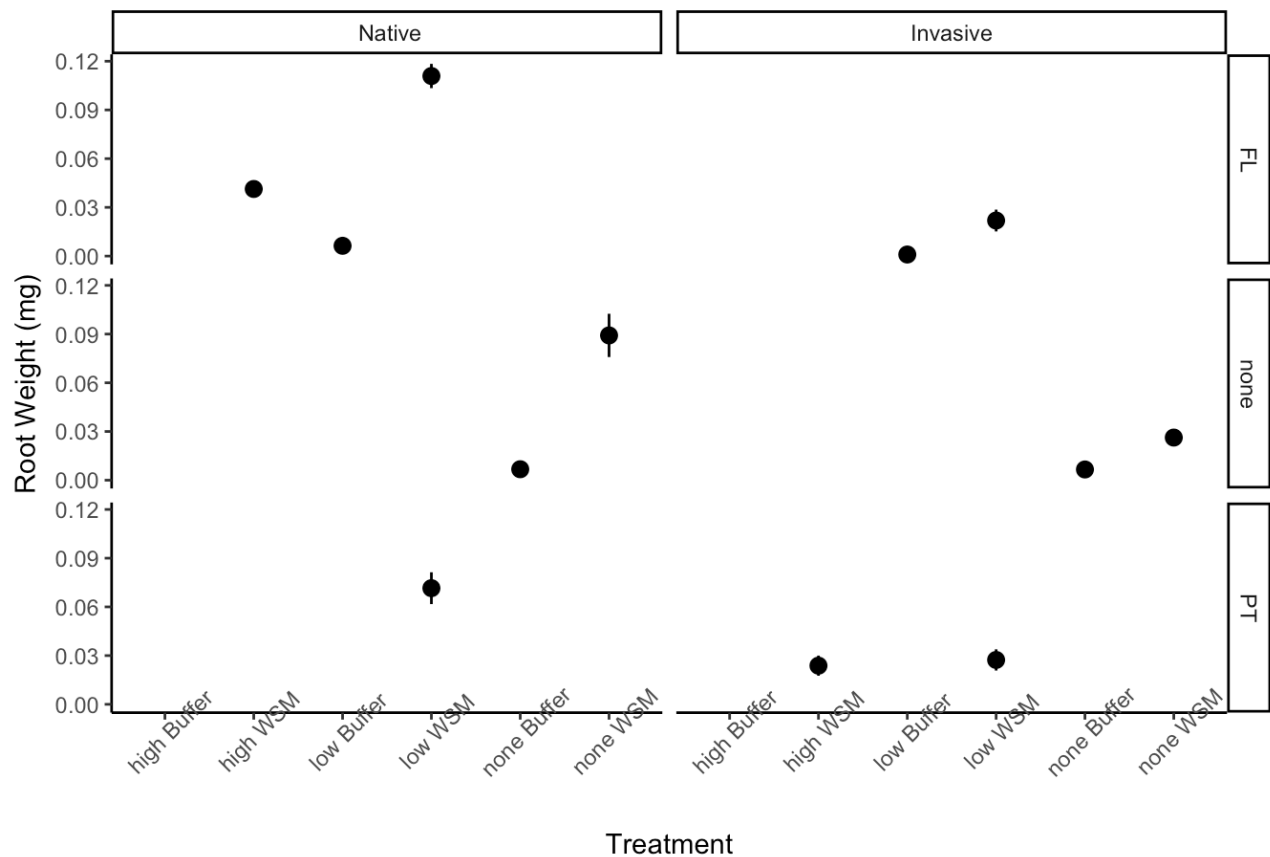
```
RootModSR <- lm(RootWeight ~ Soil * Range * SoilLocation, data = SRMort)
anova(RootModSR)
```

```
## Analysis of Variance Table
##
## Response: RootWeight
##
```

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | |
|-------------------------|----|-----------|-----------|---------|-----------|-----|
| Soil | 4 | 0.0200836 | 0.0050209 | 27.2732 | 8.506e-09 | *** |
| Range | 1 | 0.0104877 | 0.0104877 | 56.9683 | 6.676e-08 | *** |
| SoilLocation | 1 | 0.0000243 | 0.0000243 | 0.1323 | 0.7191603 | |
| Soil:Range | 4 | 0.0065723 | 0.0016431 | 8.9250 | 0.0001277 | *** |
| Soil:SoilLocation | 1 | 0.0009471 | 0.0009471 | 5.1446 | 0.0322140 | * |
| Range:SoilLocation | 1 | 0.0009994 | 0.0009994 | 5.4285 | 0.0281815 | * |
| Soil:Range:SoilLocation | 1 | 0.0005673 | 0.0005673 | 3.0817 | 0.0914281 | . |
| Residuals | 25 | 0.0046024 | 0.0001841 | | | |

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

S x R Experiment Root Weight 21 Feb 2018



Root biomass show **significant** differences in main effects and some interactions.

```
tt = lsmeans(RootModSR, specs = ~ Range | Soil:SoilLocation)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      Soil      SoilLocation      estimate      SE df
## Native - Invasive high WSM      FL      nonEst      NA NA
## Native - Invasive low Buffer      FL      0.005366667 0.011078402 25
## Native - Invasive low WSM      FL      0.089000000 0.012386030 25
## Native - Invasive none Buffer      FL      nonEst      NA NA
## Native - Invasive none WSM      FL      nonEst      NA NA
## Native - Invasive high WSM      none      nonEst      NA NA
## Native - Invasive low Buffer      none      nonEst      NA NA
## Native - Invasive low WSM      none      nonEst      NA NA
## Native - Invasive none Buffer      none      0.000150000 0.011750420 25
## Native - Invasive none WSM      none      0.062916667 0.012386030 25
## Native - Invasive high WSM      PT      nonEst      NA NA
## Native - Invasive low Buffer      PT      0.007900000 0.019188355 25
## Native - Invasive low WSM      PT      0.044195000 0.009101836 25
## Native - Invasive none Buffer      PT      nonEst      NA NA
## Native - Invasive none WSM      PT      nonEst      NA NA
## t.ratio p.value
##      NA      NA
## 0.484 0.6323
## 7.186 <.0001
##      NA      NA
##      NA      NA
##      NA      NA
##      NA      NA
##      NA      NA
## 0.013 0.9899
## 5.080 <.0001
##      NA      NA
## 0.412 0.6841
## 4.856 0.0001
##      NA      NA
##      NA      NA
```

```
pairs(dd, by = "Soil")
```

```

## Soil = high WSM:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT nonEst NA
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df t.ratio p.value
## NA NA NA
## NA NA NA
## NA NA NA
##
## Soil = low Buffer:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT -0.002533333 0.02215680
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df t.ratio p.value
## NA NA NA
## 25 -0.114 0.9928
## NA NA NA
##
## Soil = low WSM:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT 0.044805000 0.01537066
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df t.ratio p.value
## NA NA NA
## 25 2.915 0.0196
## NA NA NA
##
## Soil = none Buffer:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT nonEst NA
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df t.ratio p.value
## NA NA NA
## NA NA NA
## NA NA NA
##
## Soil = none WSM:
## contrast estimate SE
## Native - Invasive,FL - Native - Invasive,none nonEst NA
## Native - Invasive,FL - Native - Invasive,PT nonEst NA
## Native - Invasive,none - Native - Invasive,PT nonEst NA
## df t.ratio p.value

```

```
## NA NA NA
## NA NA NA
## NA NA NA
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Nodule Number Data

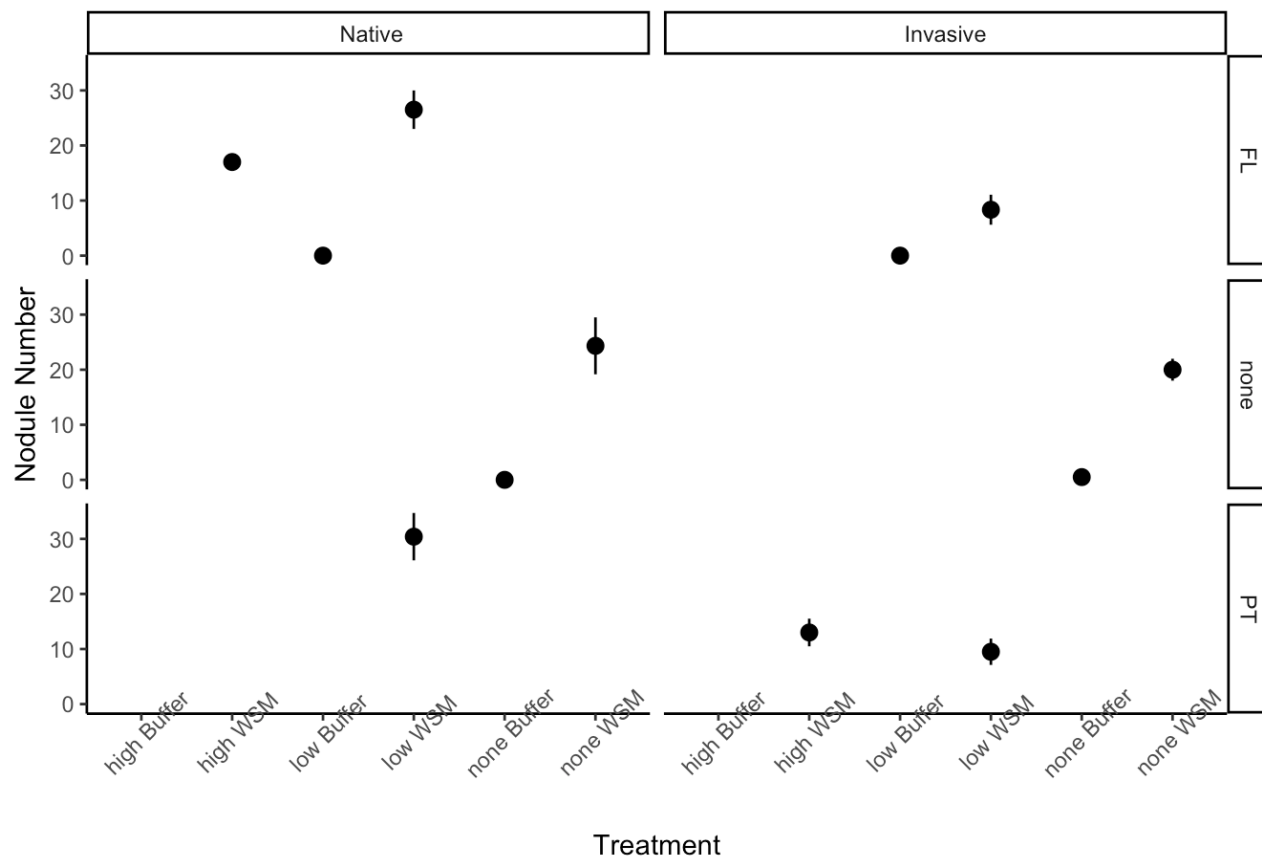
```
NNModSR <- lm(NodNum ~ Treatment * Range, data = SRMort)
anova(NNModSR)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment      7 3153.07   450.44  15.3621 1.255e-07 ***
## Range           1  684.20   684.20  23.3344 5.780e-05 ***
## Treatment:Range  5  707.39   141.48   4.8251 0.003178 **
## Residuals      25  733.03    29.32
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
NNModSR <- lm(NodNum ~ Soil * Range * SoilLocation, data = SRMort)
anova(NNModSR)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Soil           4 2935.44   733.86  25.0282 1.993e-08 ***
## Range           1  714.52   714.52  24.3686 4.393e-05 ***
## SoilLocation    1  171.53   171.53   5.8499 0.023190 *
## Soil:Range      4  684.11   171.03   5.8328 0.001856 **
## Soil:SoilLocation 1   31.74    31.74   1.0825 0.308106
## Range:SoilLocation 1    7.19     7.19   0.2451 0.624898
## Soil:Range:SoilLocation 1  0.14     0.14   0.0046 0.946215
## Residuals      25  733.03    29.32
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

S x R Experiment Nodule Number 21 Feb 2018



Soil x Range interaction was **significant** so looked at each within range for nodule number.

```
# Native
NNModSRs <- lm(NodNum ~ Soil , data = SRMort_N)
anova(NNModSRs)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Soil         4 2654.31   663.58   14.23 7.731e-05 ***
## Residuals   14   652.85    46.63
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(glht(NNModSRs, mcp(Soil = "Tukey")))
```



```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = NodNum ~ Soil, data = SRMort_N)
##
## Linear Hypotheses:
```

| | Estimate | Std. Error | t value | Pr(> t) |
|----------------------------------|----------|------------|---------|--------------|
| ## low Buffer - high WSM == 0 | -14.750 | 5.216 | -2.828 | 0.081783 . |
| ## low WSM - high WSM == 0 | 12.286 | 4.712 | 2.607 | 0.119782 |
| ## none Buffer - high WSM == 0 | -17.000 | 6.234 | -2.727 | 0.097674 . |
| ## none WSM - high WSM == 0 | 7.333 | 5.576 | 1.315 | 0.681947 |
| ## low WSM - low Buffer == 0 | 27.036 | 4.280 | 6.317 | 0.000129 *** |
| ## none Buffer - low Buffer == 0 | -2.250 | 5.914 | -0.380 | 0.994881 |
| ## none WSM - low Buffer == 0 | 22.083 | 5.216 | 4.234 | 0.006130 ** |
| ## none Buffer - low WSM == 0 | -29.286 | 5.475 | -5.349 | 0.000740 *** |
| ## none WSM - low WSM == 0 | -4.952 | 4.712 | -1.051 | 0.824294 |
| ## none WSM - none Buffer == 0 | 24.333 | 6.234 | 3.903 | 0.011294 * |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
# Invasive
NNModSRs <- lm(NodNum ~ Soil , data = SRMort_I)
Anova(NNModSRs, type = "3")
```

```
## Anova Table (Type III tests)
##
## Response: NodNum
```

| | Sum Sq | Df | F value | Pr(>F) |
|----------------|--------|----|---------|---------------|
| ## (Intercept) | 507.00 | 1 | 37.695 | 1.893e-05 *** |
| ## Soil | 747.20 | 4 | 13.889 | 6.251e-05 *** |
| ## Residuals | 201.75 | 15 | | |

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

```
summary(glht(NNModSRs, mcp(Soil = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = NodNum ~ Soil, data = SRMort_I)
##
## Linear Hypotheses:
```

| | Estimate | Std. Error | t value | Pr(> t) | |
|----------------------------------|----------|------------|---------|----------|-----|
| ## low Buffer - high WSM == 0 | -11.250 | 2.801 | -4.016 | 0.00821 | ** |
| ## low WSM - high WSM == 0 | -4.000 | 2.531 | -1.581 | 0.52525 | |
| ## none Buffer - high WSM == 0 | -12.500 | 2.801 | -4.463 | 0.00343 | ** |
| ## none WSM - high WSM == 0 | 7.000 | 3.348 | 2.091 | 0.26919 | |
| ## low WSM - low Buffer == 0 | 7.250 | 2.299 | 3.154 | 0.04320 | * |
| ## none Buffer - low Buffer == 0 | -1.250 | 2.593 | -0.482 | 0.98757 | |
| ## none WSM - low Buffer == 0 | 18.250 | 3.176 | 5.746 | < 0.001 | *** |
| ## none Buffer - low WSM == 0 | -8.500 | 2.299 | -3.698 | 0.01523 | * |
| ## none WSM - low WSM == 0 | 11.000 | 2.940 | 3.741 | 0.01399 | * |
| ## none WSM - none Buffer == 0 | 19.500 | 3.176 | 6.140 | < 0.001 | *** |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Nodule Weight Data

```
NWModSR <- lm(NodWeight ~ Treatment * Range, data = SRMort)
anova(NWModSR)
```

```
## Analysis of Variance Table
##
## Response: NodWeight
```

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------|----|------------|------------|---------|---------------|
| ## Treatment | 6 | 3.6340e-05 | 6.0570e-06 | 2.1965 | 0.09444 . |
| ## Range | 1 | 1.0723e-04 | 1.0723e-04 | 38.8893 | 9.038e-06 *** |
| ## Treatment:Range | 3 | 2.0160e-05 | 6.7200e-06 | 2.4371 | 0.10004 |
| ## Residuals | 17 | 4.6876e-05 | 2.7570e-06 | | |

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

```
NWModSR <- lm(NodWeight ~ Soil * Range * SoilLocation, data = SRMort)
anova(NWModSR)
```

```
## Analysis of Variance Table
##
## Response: NodWeight
##              Df      Sum Sq   Mean Sq F value    Pr(>F)
## Soil           4 3.3576e-05  8.3940e-06   3.0442  0.04611 *
## Range          1 9.1427e-05  9.1427e-05  33.1568 2.318e-05 ***
## SoilLocation    1 1.4000e-08  1.4000e-08   0.0050  0.94439
## Soil:Range      3 2.3847e-05  7.9490e-06   2.8828  0.06622 .
## Range:SoilLocation 1 1.4869e-05  1.4869e-05   5.3925  0.03290 *
## Residuals     17 4.6876e-05  2.7570e-06
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

