

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

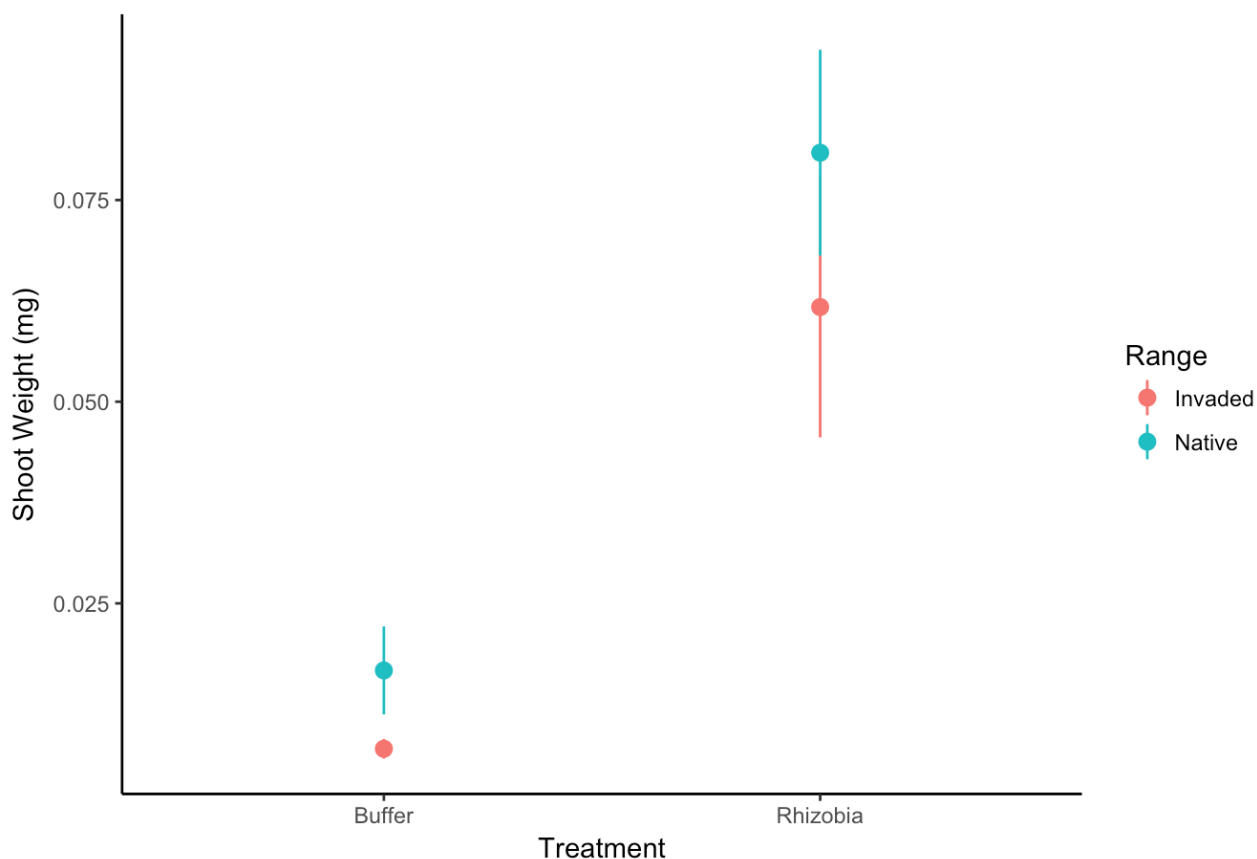
```
ShootMod <- lmer(ShootWeight ~ Treatment * Range + (1| Genotype), data = TrapBio)
```

```
## 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
```

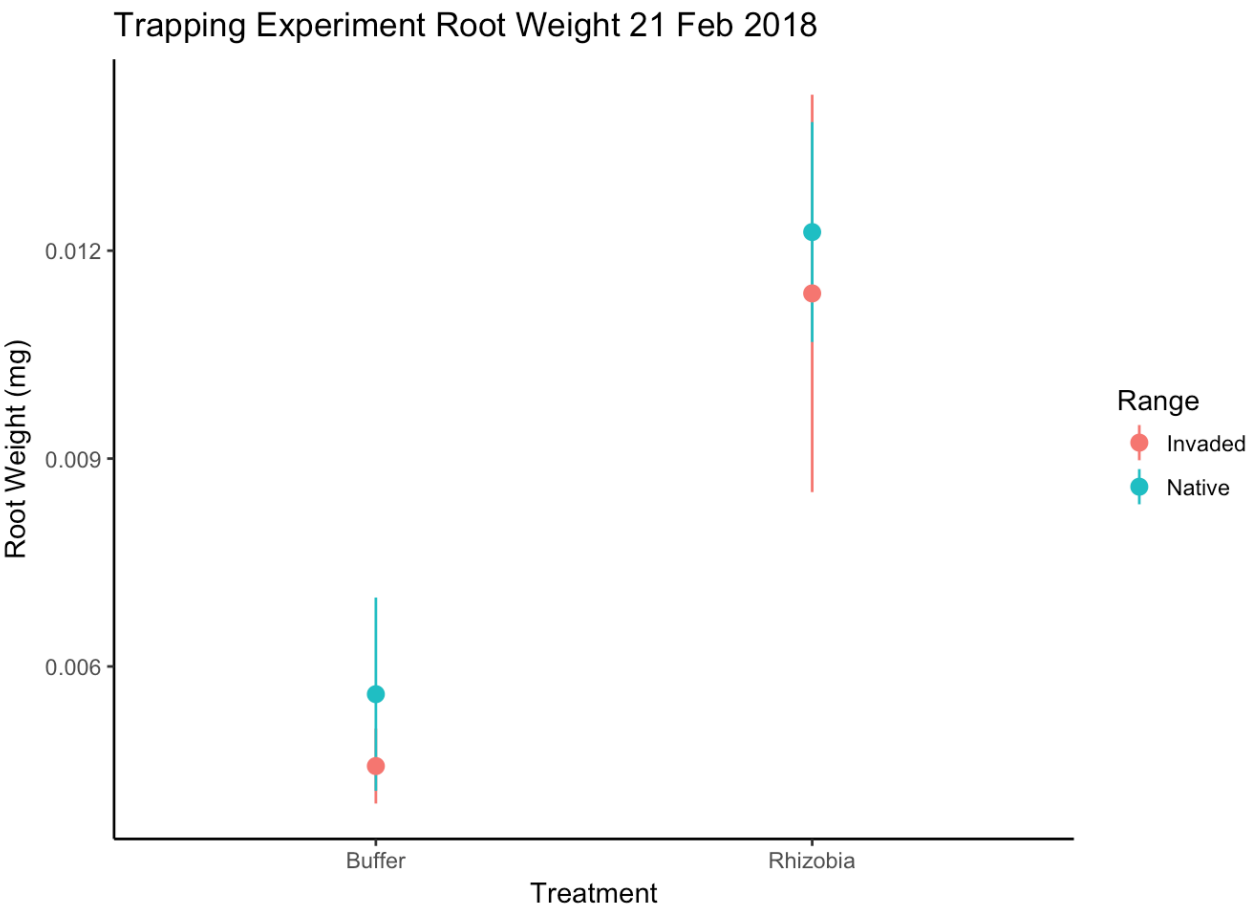
Trapping Experiment Shoot Weight 21 Feb 2018



Root data

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

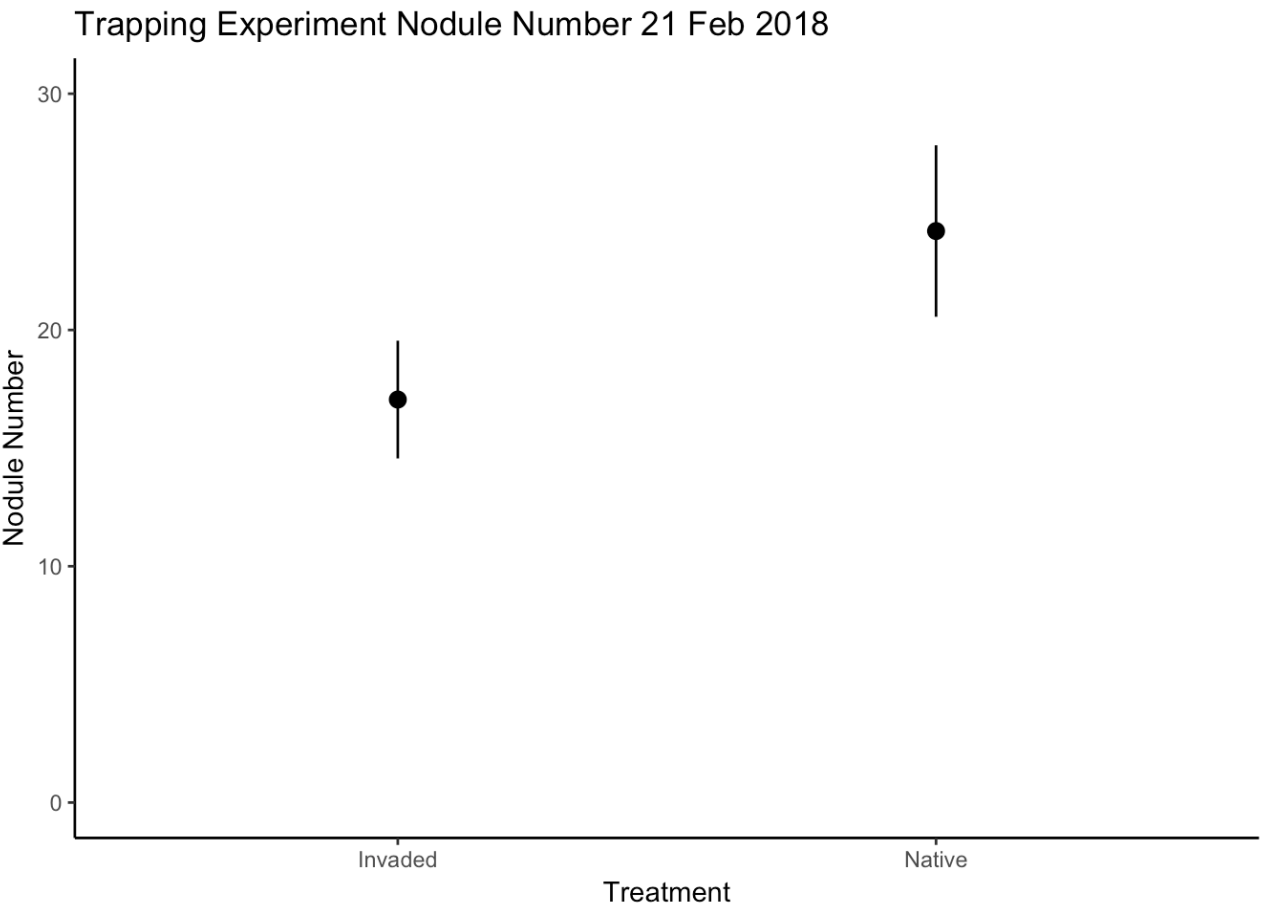
```
## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##           Sum Sq   Mean Sq NumDF   DenDF F.value    Pr(>F)
## Treatment      0.00081642 0.00081642     1 45.295 17.6854 0.0001214 ***
## Range          0.00002627 0.00002627     1 10.243  0.5690 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)
```

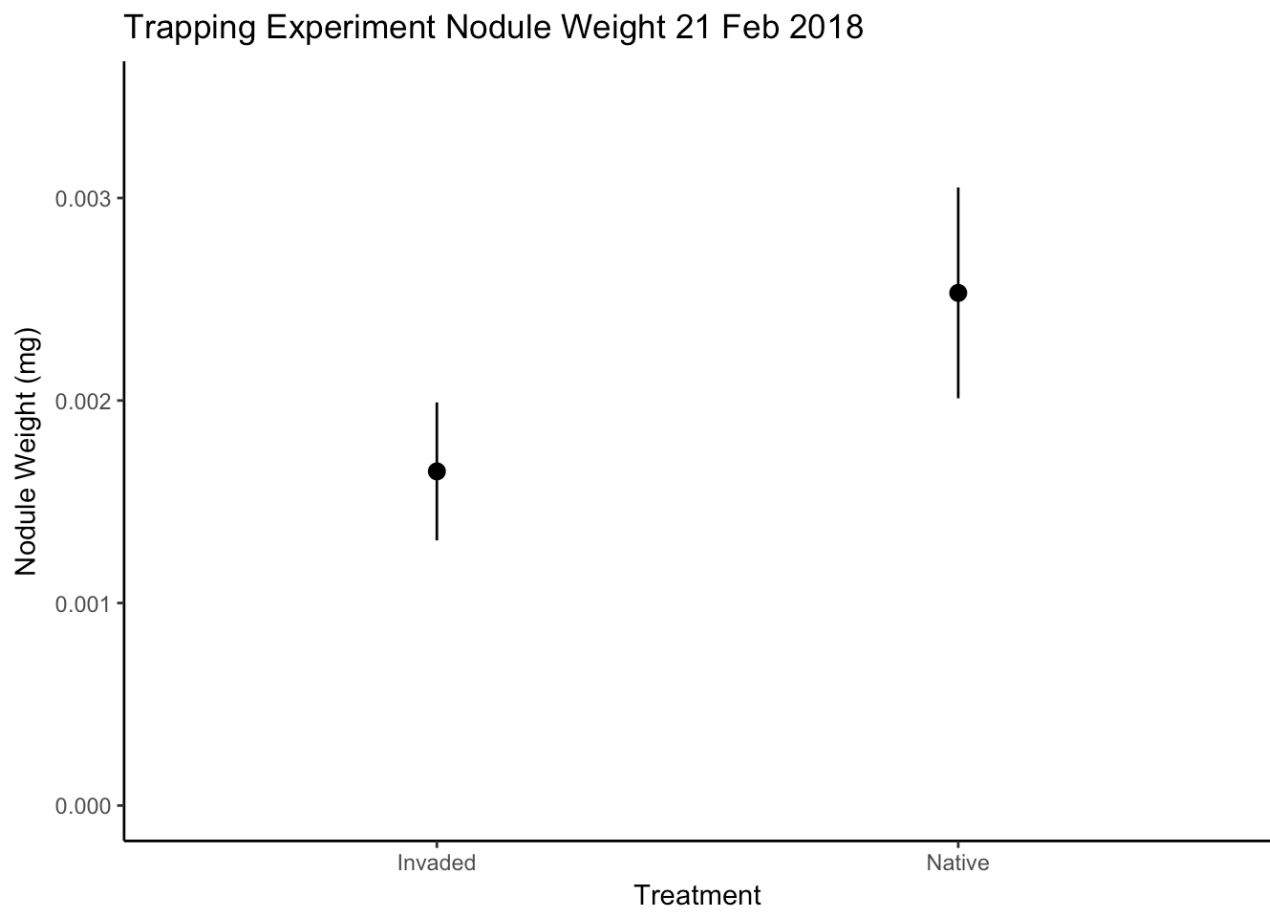
```
## Analysis of Variance Table of type III with Satterthwaite
## approximation for degrees of freedom
##           Sum Sq Mean Sq NumDF   DenDF F.value Pr(>F)
## Range 330.42   330.42     1 10.378  2.2672 0.162
```



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

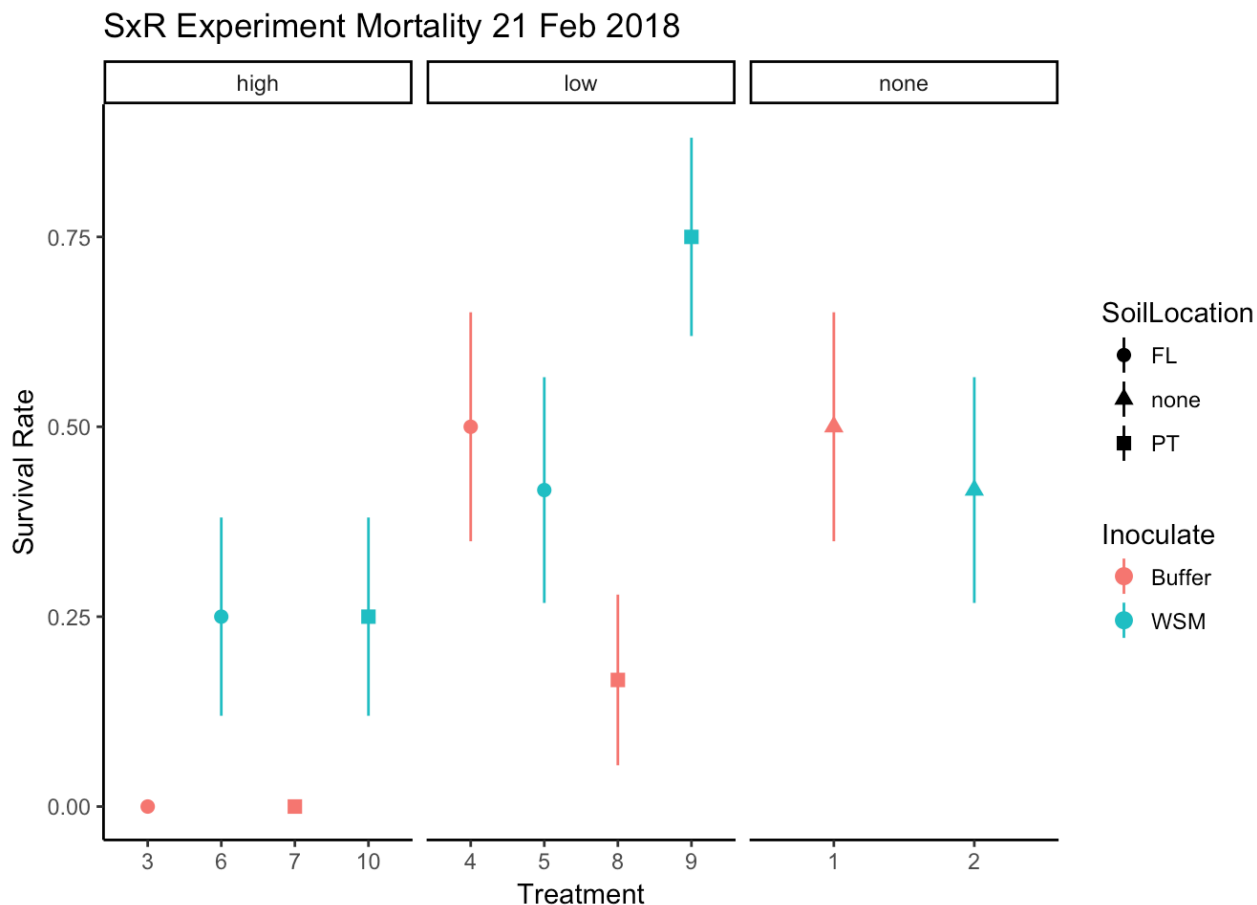
```
SRMortMod <- glm(DeadOrAlive ~ Treatment , family = binomial(link = "logit"), d
ata = SRMort)
```

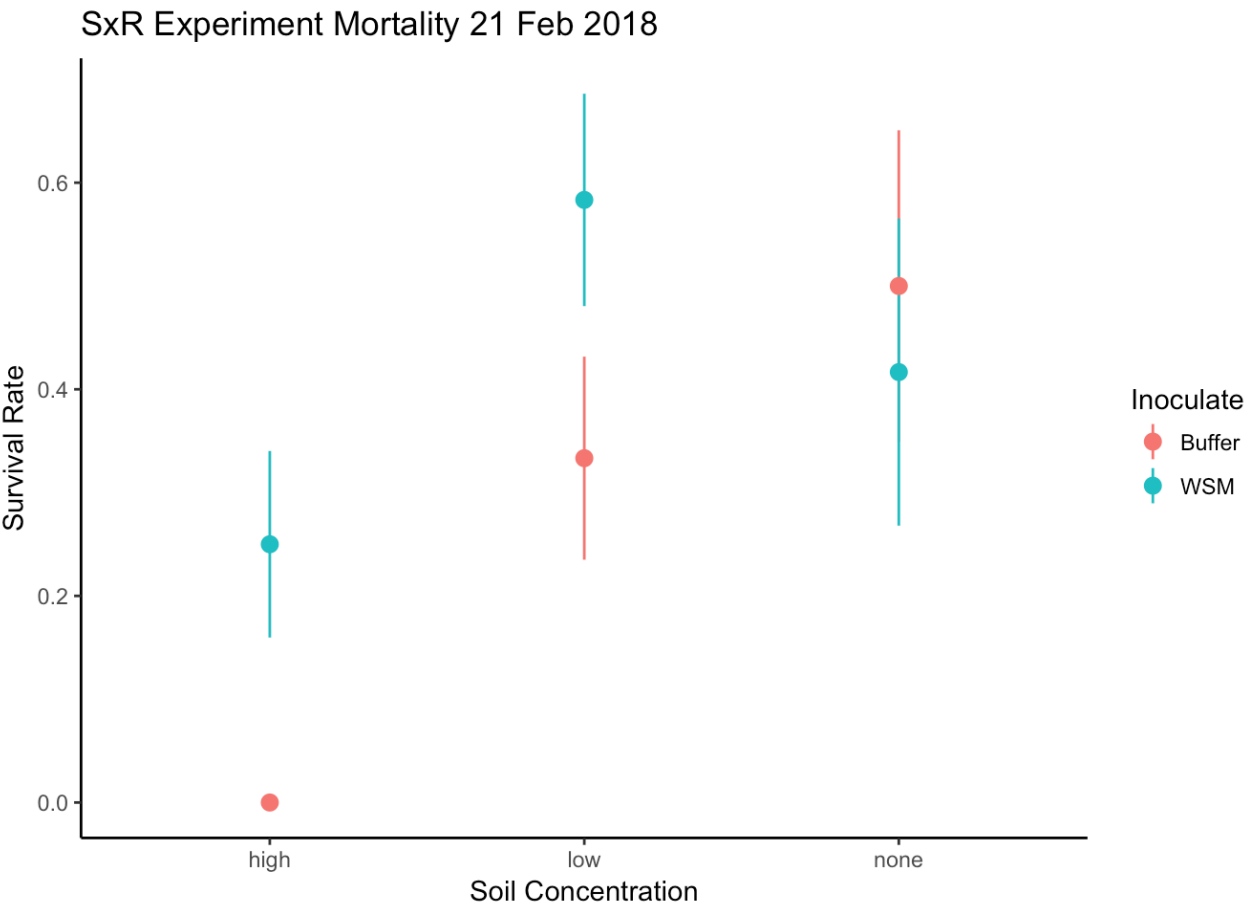
```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: DeadOrAlive
##
## Terms added sequentially (first to last)
##
##
```

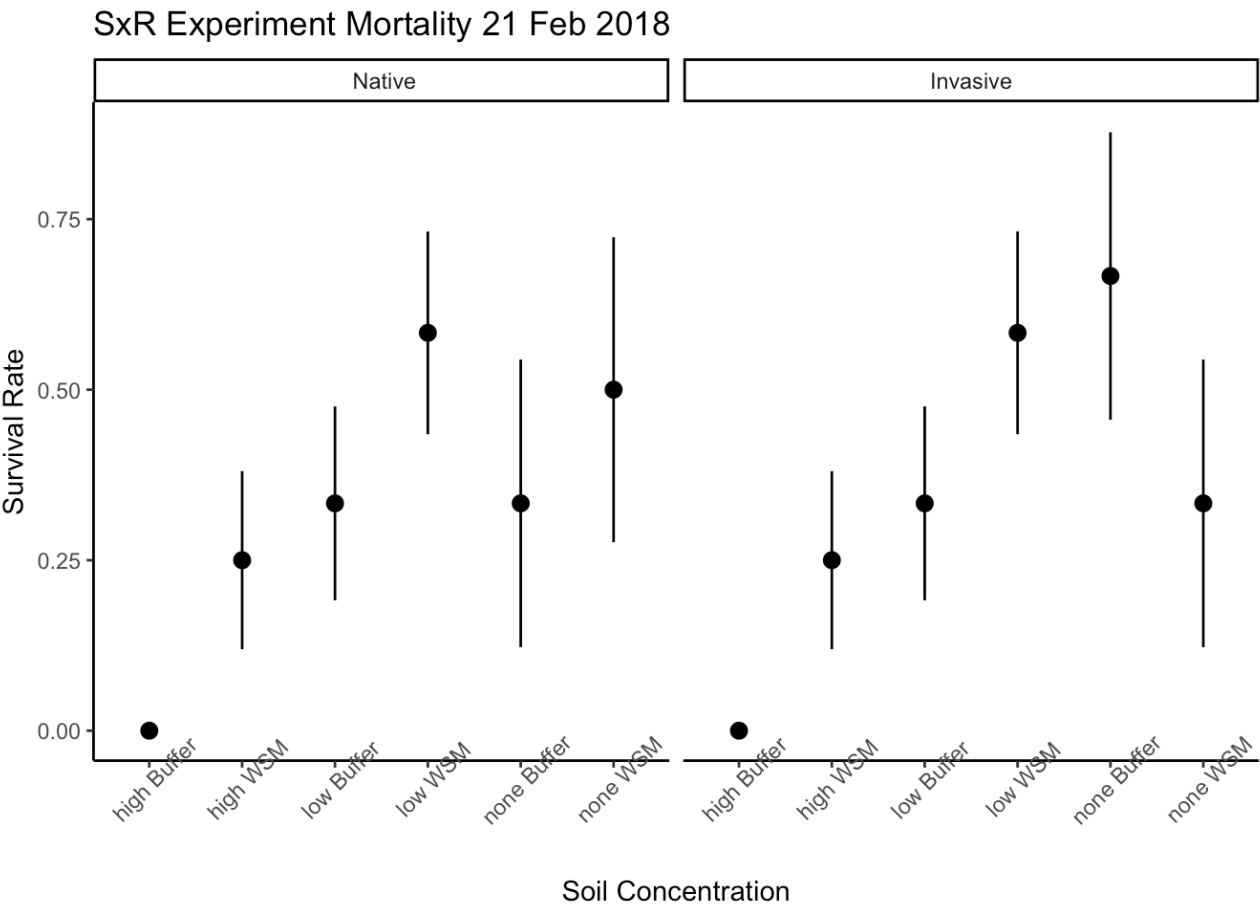
	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			119	151.34	
## Treatment	9	34.166	110	117.17	8.355e-05 ***

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

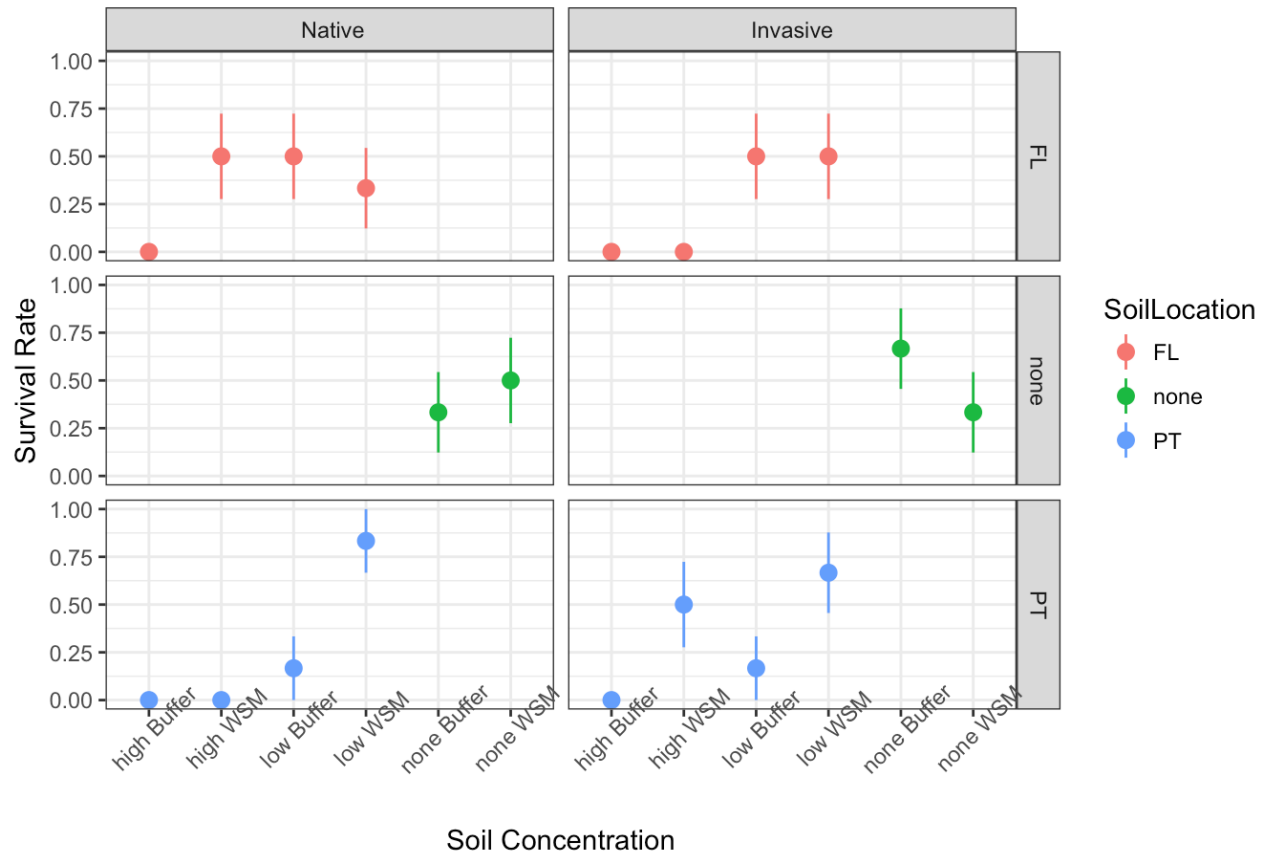
Treatment was *significant*. I also ran a Tukey mult comp test (results not shown). The only significance was between soil and buffer/wsm. All other comparisons were not significant.







SxR Experiment Mortality 21 Feb 2018



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
```

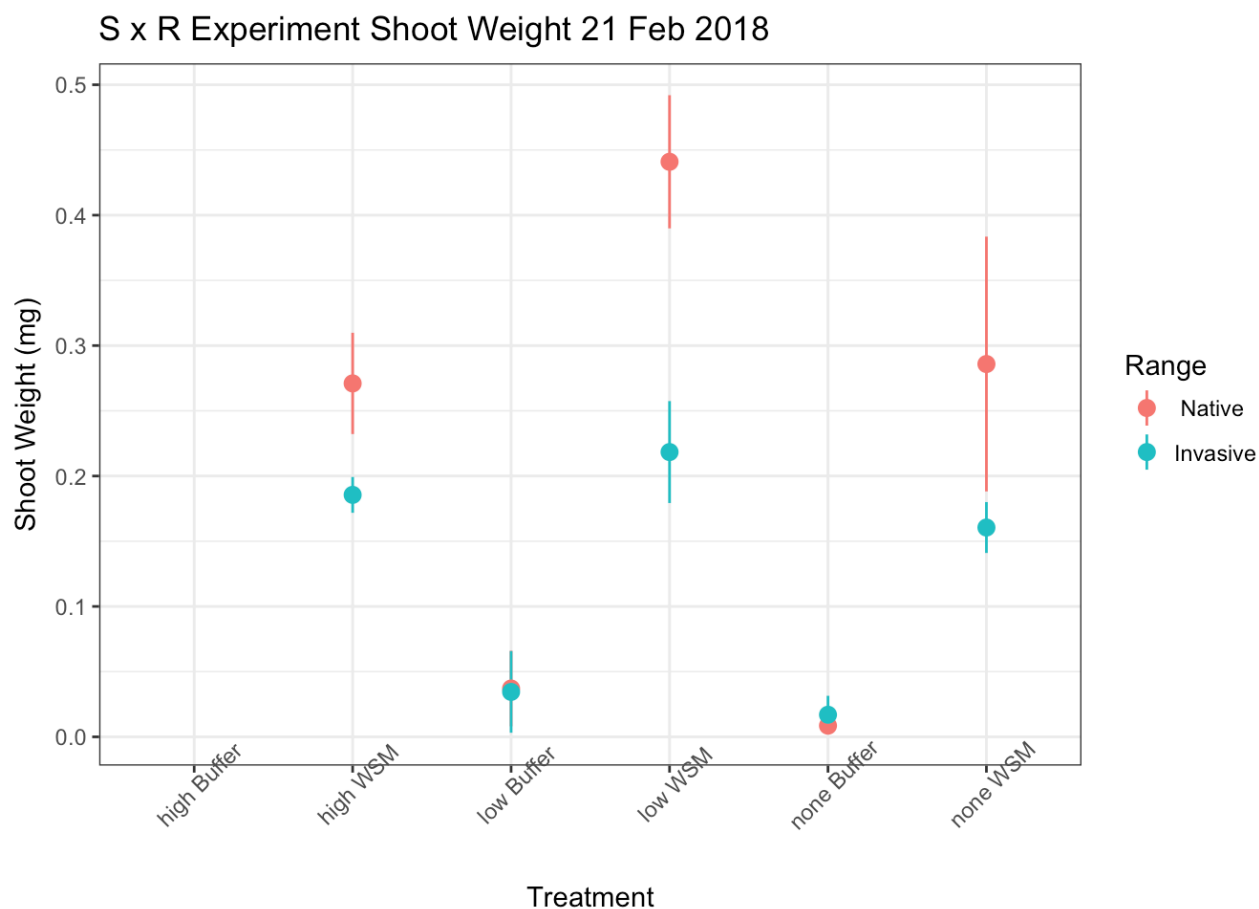
The main effects **are significantly different**

```
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	0.0254	*
## none WSM - high WSM == 0	0.007453	0.071151	0.105	1.0000	
## low WSM - low Buffer == 0	0.293887	0.052077	5.643	<0.001	***
## 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	<0.001	***
## none WSM - low WSM == 0	-0.093930	0.061217	-1.534	0.5436	
## none WSM - none Buffer == 0	0.221553	0.071151	3.114	0.0281	*

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

```
mod <- lm(ShootWeight ~ Soil * Range, data = SRMort)
tt = lsmeans(mod, specs = ~ Range | Soil)
dd = pairs(tt)
summary(dd, by = NULL)
```

##	contrast	Soil	estimate	SE	df	t.ratio	p.value
##	Native - Invasive	high WSM	0.08546667	0.07821987	29	1.093	0.2835
##	Native - Invasive	low Buffer	0.00257500	0.06774040	29	0.038	0.9699
##	Native - Invasive	low WSM	0.22255714	0.05120693	29	4.346	0.0002
##	Native - Invasive	none Buffer	-0.00835000	0.08296471	29	-0.101	0.9205
##	Native - Invasive	none WSM	0.12536667	0.08745248	29	1.434	0.1624

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  0.10967
## low WSM - high WSM == 0      0.16993    0.07950   2.138  0.25425
## none Buffer - high WSM == 0  -0.26240    0.10517  -2.495  0.14478
## 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  0.08183 .
## none Buffer - low WSM == 0   -0.43233    0.09237  -4.680  0.00269 **
## none WSM - low WSM == 0     -0.15506    0.07950  -1.951  0.33255
## none WSM - none Buffer == 0   0.27727    0.10517   2.636  0.11402
## ---
## 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  0.09862 .
## low WSM - high WSM == 0      0.03284    0.05050    0.650  0.96306
## none Buffer - high WSM == 0  -0.16858    0.05590   -3.016  0.05577 .
## none WSM - high WSM == 0    -0.02503    0.06681   -0.375  0.99521
## low WSM - low Buffer == 0     0.18390    0.04587    4.009  0.00832 **
## none Buffer - low Buffer == 0 -0.01752    0.05175   -0.339  0.99675
## none WSM - low Buffer == 0    0.12603    0.06338    1.988  0.31267
## none Buffer - low WSM == 0   -0.20142    0.04587   -4.391  0.00397 **
## none WSM - low WSM == 0     -0.05787    0.05868   -0.986  0.85451
## none WSM - none Buffer == 0   0.14355    0.06338    2.265  0.20606
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

SR Biomass Data =====

Root Data

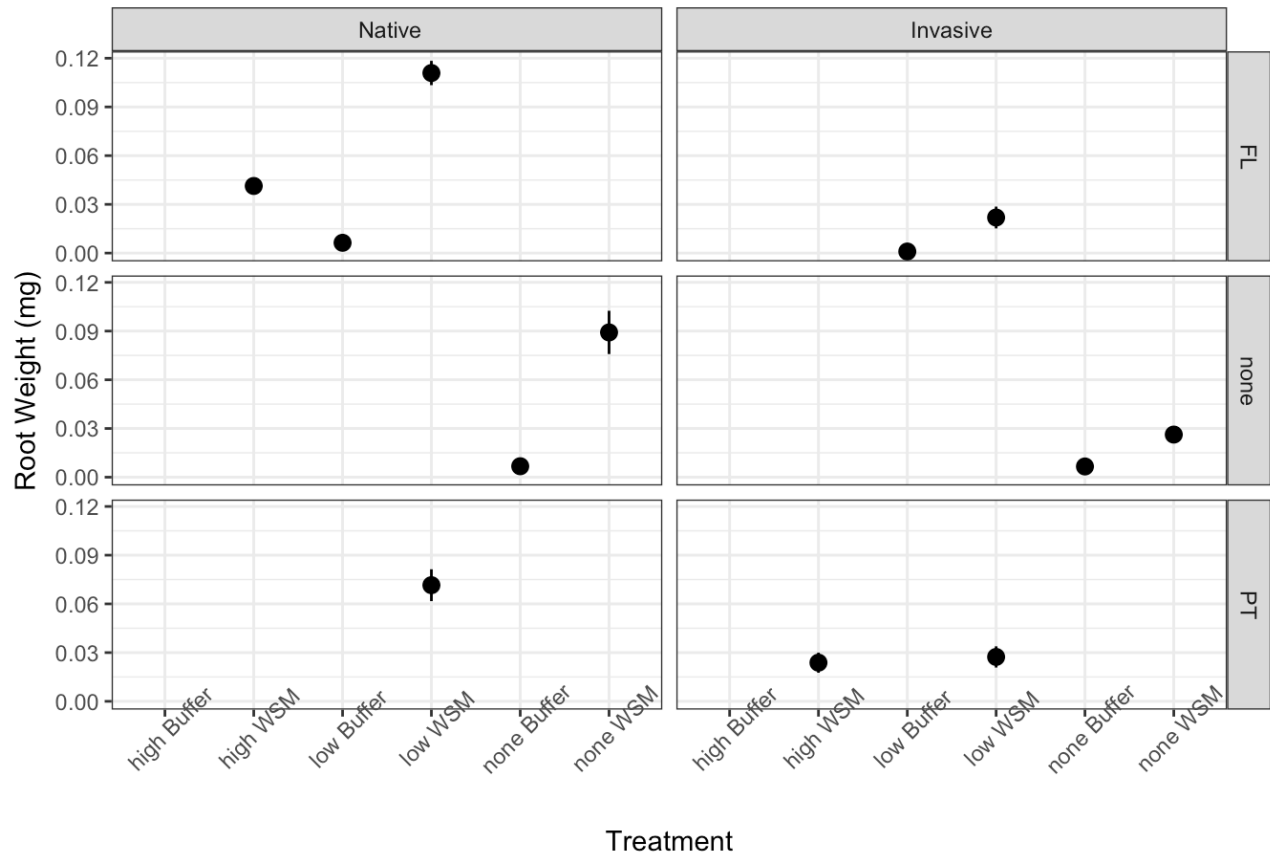
```
RootModSR <- lm(RootWeight ~ Treatment * Range, data = SRMort)
anova(RootModSR)
```

```
## 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
```

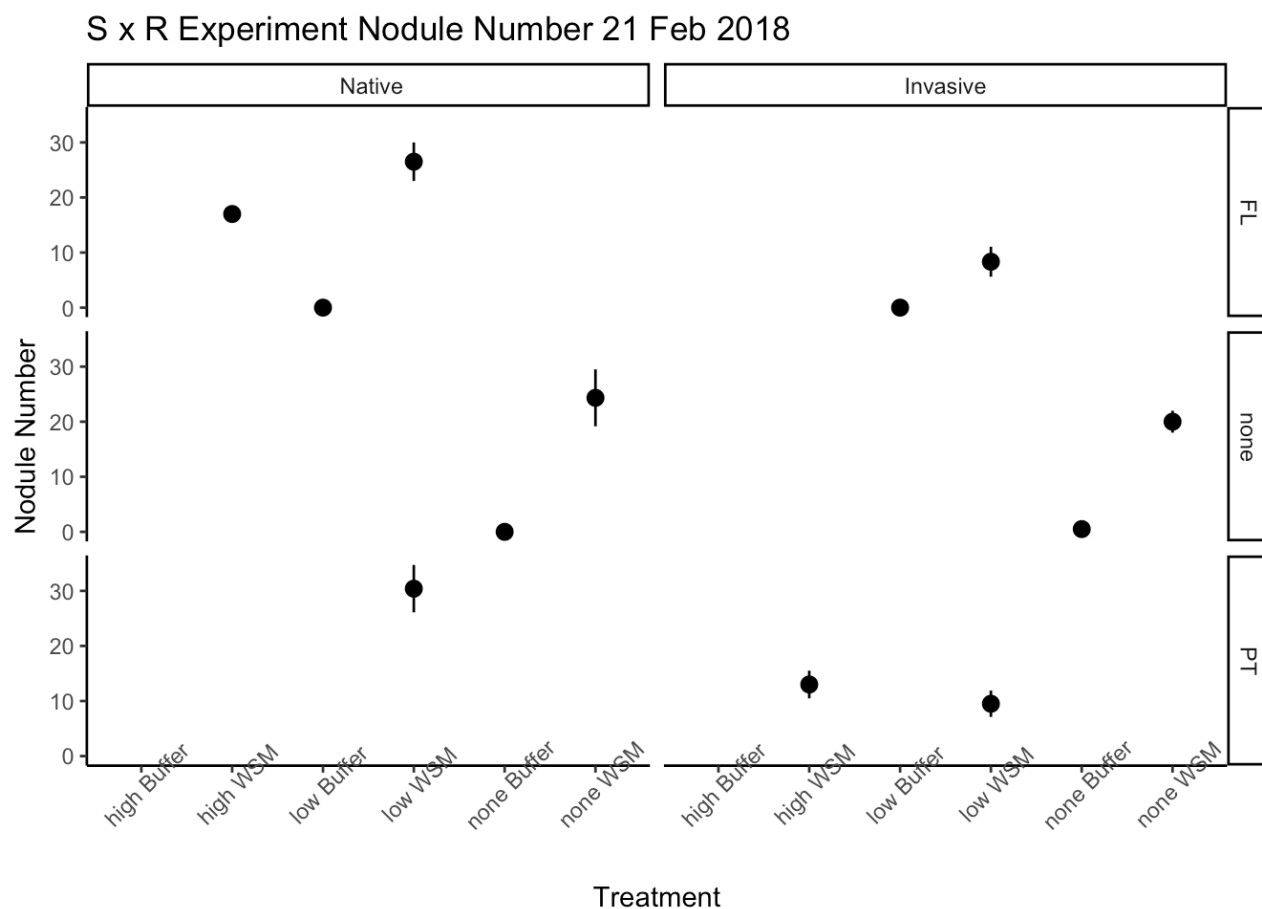
Nodule Number Data

```
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
```

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	0.08178 .
## low WSM - high WSM == 0	12.286	4.712	2.607	0.11991
## none Buffer - high WSM == 0	-17.000	6.234	-2.727	0.09759 .
## none WSM - high WSM == 0	7.333	5.576	1.315	0.68198
## low WSM - low Buffer == 0	27.036	4.280	6.317	< 0.001 ***
## none Buffer - low Buffer == 0	-2.250	5.914	-0.380	0.99488
## none WSM - low Buffer == 0	22.083	5.216	4.234	0.00612 **
## none Buffer - low WSM == 0	-29.286	5.475	-5.349	< 0.001 ***
## none WSM - low WSM == 0	-4.952	4.712	-1.051	0.82433
## none WSM - none Buffer == 0	24.333	6.234	3.903	0.01142 *

```
## ---
## 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	0.00814	**
## low WSM - high WSM == 0	-4.000	2.531	-1.581	0.52522	
## none Buffer - high WSM == 0	-12.500	2.801	-4.463	0.00343	**
## none WSM - high WSM == 0	7.000	3.348	2.091	0.26922	
## low WSM - low Buffer == 0	7.250	2.299	3.154	0.04325	*
## 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	0.01526	*
## none WSM - low WSM == 0	11.000	2.940	3.741	0.01405	*
## 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)
```

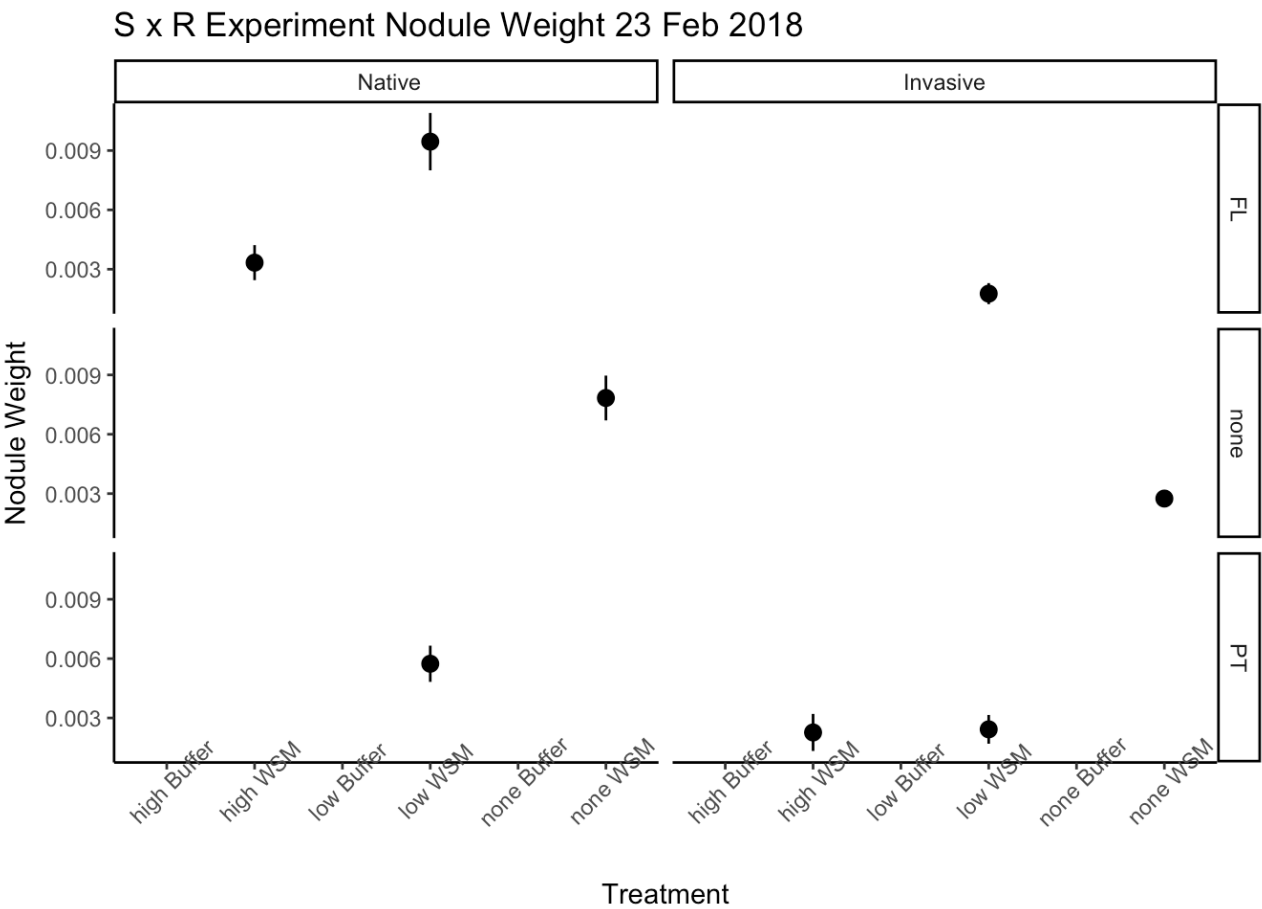
```
## Analysis of Variance Table
##
## Response: NodWeight
```

	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
```



Here is all of the data that was used in the results section, I didn't have time to organize it with thoughts to try and get it to you before your flight but I think that it is understandable.

```

# 26 Feb 2018
# testing the impact of soil on rhizobia
# SRMort_no_none has soil only removed
SRMort <- within(SRMort, Root_Shoot <- 1 / Shoot_Root)
SRMort_no_none <- subset(SRMort, SoilConc != "none")

# Mortality
mod <- glm(DeadOrAlive ~ Soil, family = binomial(link = "logit"), data = SRMort_no_none)
anova(mod, test = "Chisq")

```

```

## 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                                95    115.898
## Soil   3    25.752             92     90.146 1.075e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

mod <- glm(DeadOrAlive ~ SoilConc * Inoculate, family = binomial(link = "logit"), data = SRMort_no_none)
anova(mod, test = "Chisq")

```

```
## 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			95	115.898	
## SoilConc	1	13.5200	94	102.378	0.000236 ***
## Inoculate	1	8.6705	93	93.708	0.003234 **
## SoilConc:Inoculate	1	3.5618	92	90.146	0.059125 .

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

```
#Shoot - will continue with this b/c of line 320
mod <- lm(ShootWeight ~ SoilConc * Inoculate, data = SRMort_no_none)
anova(mod)
```

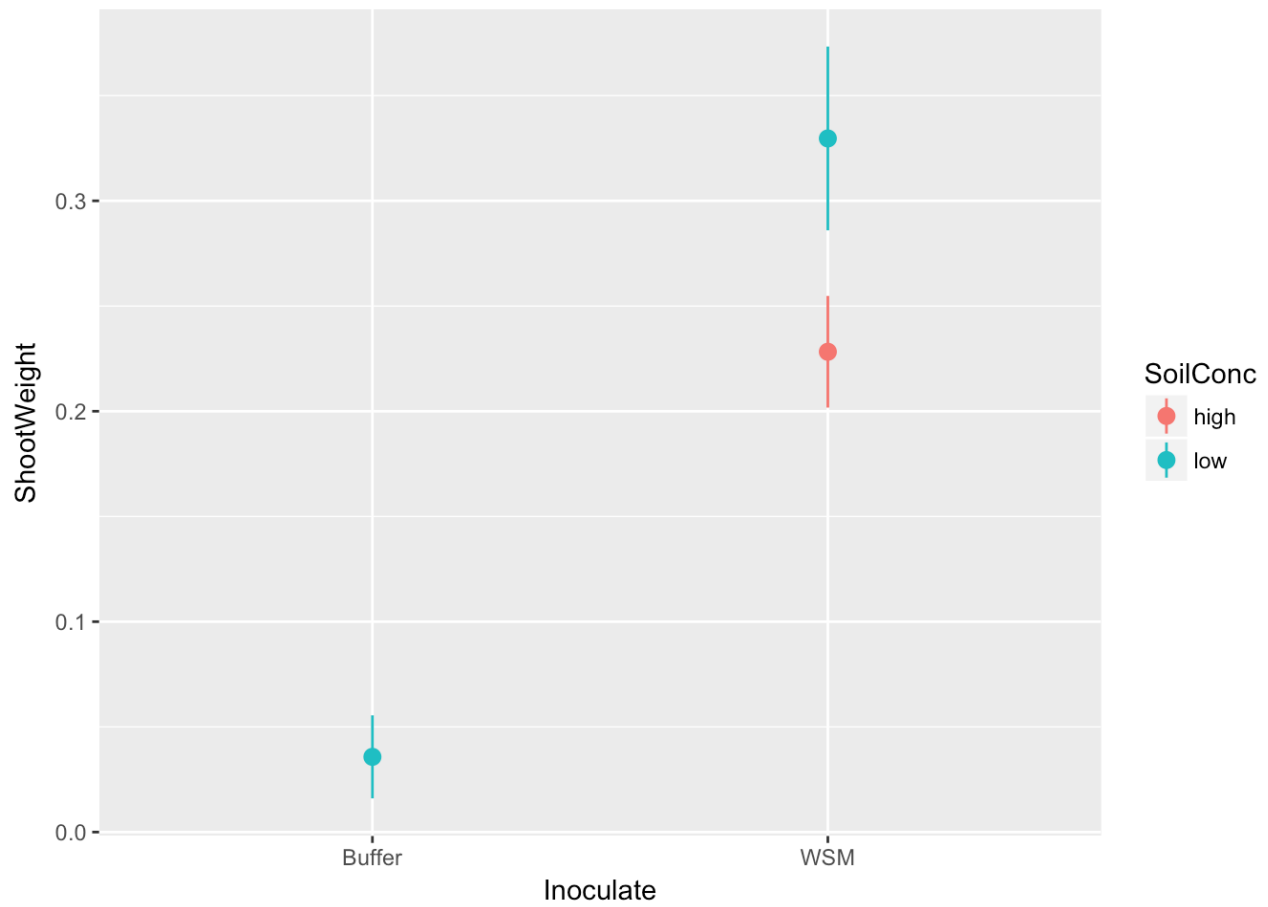
```
## Analysis of Variance Table
##
## Response: ShootWeight
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## SoilConc	1	0.00014	0.00014	0.0091	0.9248
## Inoculate	1	0.43970	0.43970	28.1909	1.677e-05 ***
## Residuals	25	0.38993	0.01560		

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

```
ggplot(SRMort_no_none, aes(x = Inoculate, y = ShootWeight, colour = SoilConc))
+ stat_summary(fun.data = "mean_se")
```

```
## Warning: Removed 68 rows containing non-finite values (stat_summary).
```

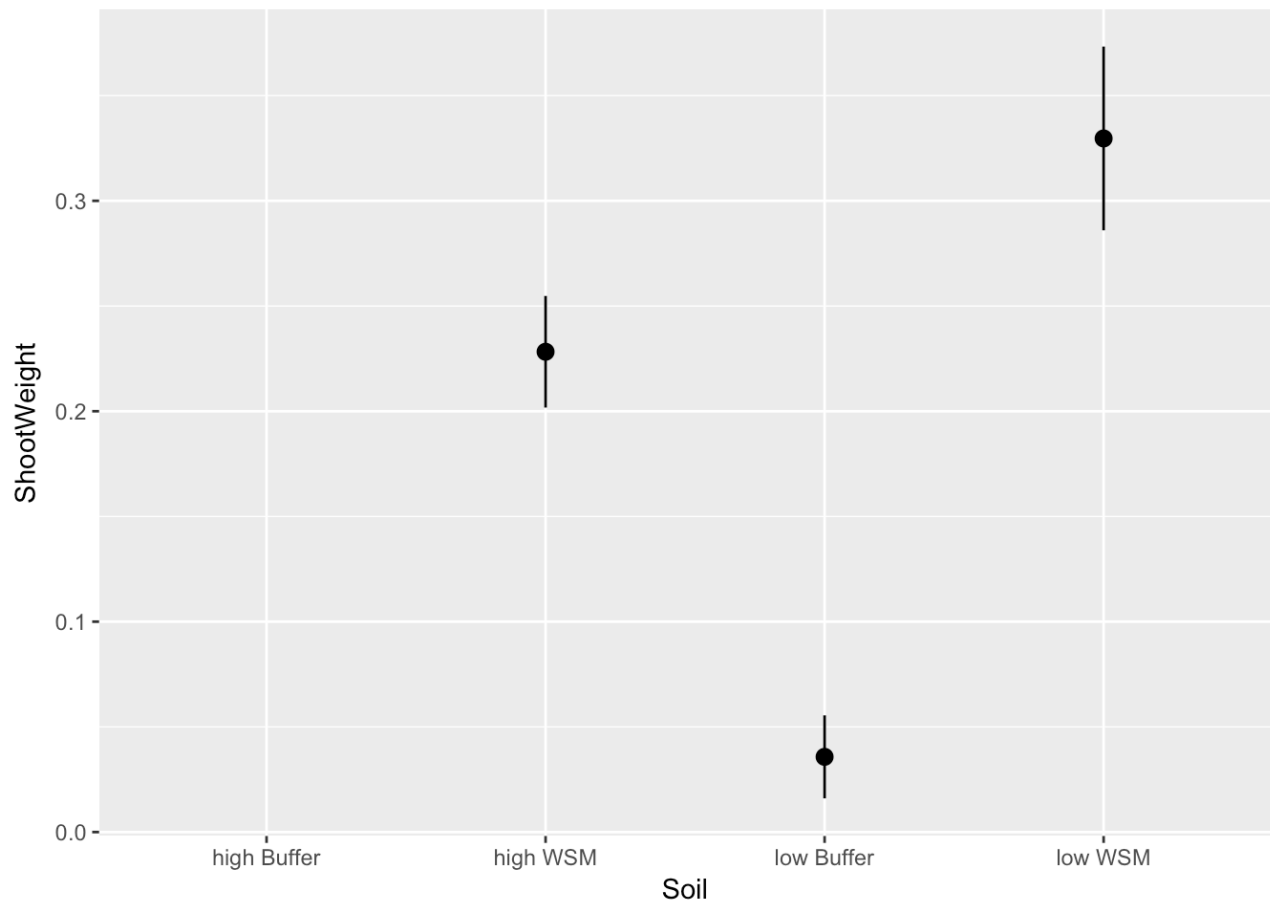


```
mod <- lm(ShootWeight ~ Soil, data = SRMort_no_none)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Soil         2  0.43984  0.219921    14.1 7.95e-05 ***
## Residuals   25  0.38993  0.015597
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMort_no_none, aes(x = Soil, y = ShootWeight)) + stat_summary(fun.data
= "mean_se")
```

```
## Warning: Removed 68 rows containing non-finite values (stat_summary).
```



```
# All high buffer plants died!
```

```
SRMortSub2 <- subset(SRMort_no_none, Inoculate == "WSM")
```

```
SRMortSub3 <- subset(SRMort, Inoculate == "WSM")
```

```
#Mortality
```

```
mod <- glm(DeadOrAlive ~ SoilConc * SoilLocation * Range, family = binomial(link = "logit"), data = SRMortSub2)
```

```
anova(mod, test = "Chisq")
```



```
## 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			47	65.203	
## SoilConc	1	5.6092	46	59.593	0.017867 *
## SoilLocation	1	1.5620	45	58.031	0.211373
## Range	1	0.0000	44	58.031	1.000000
## SoilConc:SoilLocation	1	1.2426	43	56.789	0.264971
## SoilConc:Range	1	0.0000	42	56.789	1.000000
## SoilLocation:Range	1	1.6913	41	55.098	0.193435
## SoilConc:SoilLocation:Range	1	9.4611	40	45.636	0.002099 **

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

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

```
## contrast SoilConc Range estimate SE df z.ratio p.value
## FL - PT high Native -18.5660685 2662.856186 Inf -0.007 0.9944
## FL - PT low Native 2.3025851 1.396424 Inf 1.649 0.0992
## FL - PT high Invasive 18.5660685 2662.856186 Inf 0.007 0.9944
## FL - PT low Invasive 0.6931472 1.190238 Inf 0.582 0.5603
##
## Results are given on the log odds ratio (not the response) scale.
```

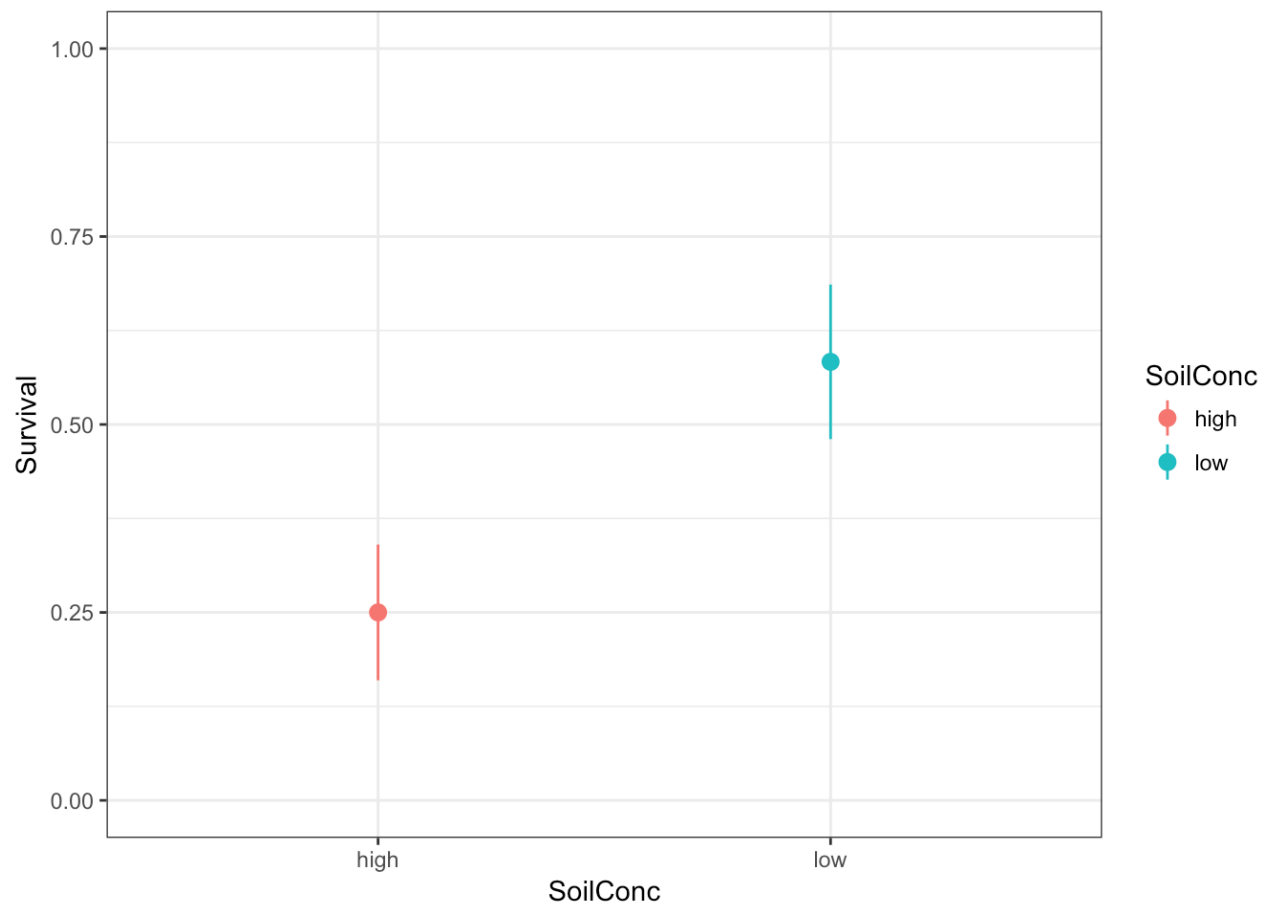
```
tt = lsmeans(mod, specs = ~ SoilConc | SoilLocation:Range)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilLocation Range      estimate      SE df z.ratio
## high - low FL          Native -0.6931472    1.190238 Inf  -0.582
## high - low PT          Native  20.1755064 2662.856286 Inf   0.008
## high - low FL          Invasive 18.5660685 2662.856186 Inf   0.007
## high - low PT          Invasive  0.6931472    1.190238 Inf   0.582
## p.value
## 0.5603
## 0.9940
## 0.9944
## 0.5603
##
## Results are given on the log odds ratio (not the response) scale.
```

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

```
## contrast      SoilLocation SoilConc      estimate      SE df
## Native - Invasive FL          high -18.5660685 2662.856186 Inf
## Native - Invasive PT          high  18.5660685 2662.856186 Inf
## Native - Invasive FL          low   0.6931472    1.190238 Inf
## Native - Invasive PT          low  -0.9162907    1.396424 Inf
## z.ratio p.value
## -0.007 0.9944
## 0.007 0.9944
## 0.582 0.5603
## -0.656 0.5117
##
## Results are given on the log odds ratio (not the response) scale.
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = Survival, colour = SoilConc)) + stat_s
ummary(fun.data = "mean_se") + coord_cartesian(ylim = c(0,1)) +theme_bw()
```



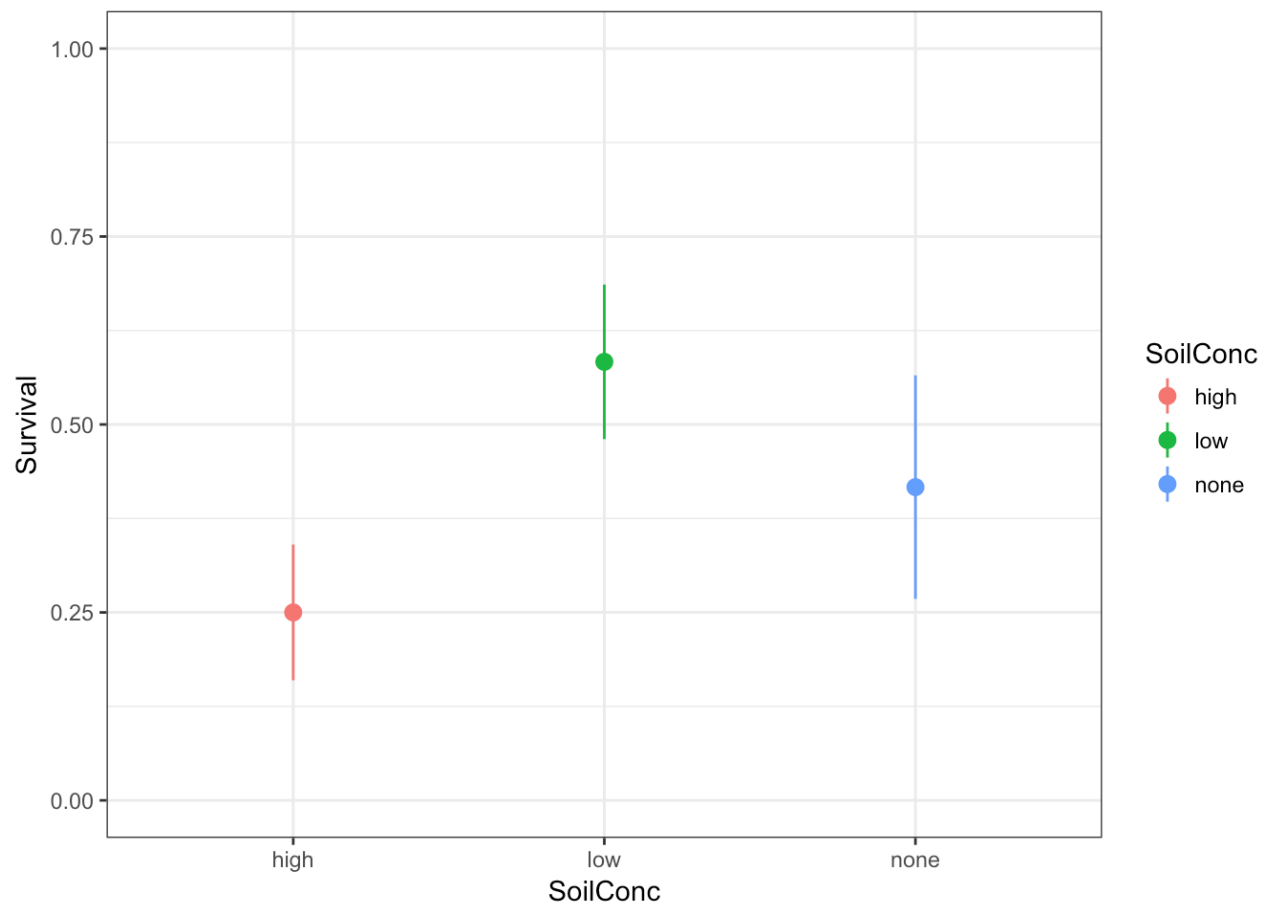
```
mod <- glm(DeadOrAlive ~ SoilConc * SoilLocation * Range, family = binomial(link = "logit"), data = SRMortSub3)
anova(mod, test = "Chisq")
```

```
## 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			59	81.503	
## SoilConc	2	5.6092	57	75.894	0.060531 .
## SoilLocation	1	1.5620	56	74.332	0.211373
## Range	1	0.0775	55	74.255	0.780741
## SoilConc:SoilLocation	1	1.2446	54	73.010	0.264583
## SoilConc:Range	2	0.2652	52	72.745	0.875815
## SoilLocation:Range	1	1.6913	51	71.053	0.193435
## SoilConc:SoilLocation:Range	1	9.4611	50	61.592	0.002099 **

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

```
ggplot(SRMortSub3, aes(x = SoilConc, y = Survival, colour = SoilConc)) + stat_s
ummary(fun.data = "mean_se") + coord_cartesian(ylim = c(0,1)) +theme_bw()
```



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

```
## contrast SoilConc Range estimate SE df z.ratio p.value
## FL - none high Native nonEst NA NA NA NA
## FL - PT high Native -18.5660685 2662.856189 Inf -0.007 1.0000
## none - PT high Native nonEst NA NA NA NA
## FL - none low Native nonEst NA NA NA NA
## FL - PT low Native 2.3025851 1.396424 Inf 1.649 0.2252
## none - PT low Native nonEst NA NA NA NA
## FL - none none Native nonEst NA NA NA NA
## FL - PT none Native nonEst NA NA NA NA
## none - PT none Native nonEst NA NA NA NA
## FL - none high Invasive nonEst NA NA NA NA
## FL - PT high Invasive 18.5660685 2662.856183 Inf 0.007 1.0000
## none - PT high Invasive nonEst NA NA NA NA
## FL - none low Invasive nonEst NA NA NA NA
## FL - PT low Invasive 0.6931472 1.190238 Inf 0.582 0.8296
## none - PT low Invasive nonEst NA NA NA NA
## FL - none none Invasive nonEst NA NA NA NA
## FL - PT none Invasive nonEst NA NA NA NA
## none - PT none Invasive nonEst NA NA NA NA
##
## Results are given on the log odds ratio (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

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

```
## contrast      SoilLocation Range      estimate      SE df z.ratio
## high - low    FL              Native -0.6931472    1.190238 Inf  -0.582
## high - none   FL              Native      nonEst      NA  NA      NA
## low - none    FL              Native      nonEst      NA  NA      NA
## high - low    none           Native      nonEst      NA  NA      NA
## high - none   none           Native      nonEst      NA  NA      NA
## low - none    none           Native      nonEst      NA  NA      NA
## high - low    PT              Native  20.1755064  2662.856289 Inf   0.008
## high - none   PT              Native      nonEst      NA  NA      NA
## low - none    PT              Native      nonEst      NA  NA      NA
## high - low    FL              Invasive 18.5660685  2662.856183 Inf   0.007
## high - none   FL              Invasive      nonEst      NA  NA      NA
## low - none    FL              Invasive      nonEst      NA  NA      NA
## high - low    none           Invasive      nonEst      NA  NA      NA
## high - none   none           Invasive      nonEst      NA  NA      NA
## low - none    none           Invasive      nonEst      NA  NA      NA
## high - low    PT              Invasive  0.6931472    1.190238 Inf   0.582
## high - none   PT              Invasive      nonEst      NA  NA      NA
## low - none    PT              Invasive      nonEst      NA  NA      NA
## p.value
## 0.8296
## NA
## NA
## NA
## NA
## NA
## 1.0000
## NA
## NA
## 1.0000
## NA
## NA
## NA
## NA
## NA
## NA
## 0.8296
## NA
## NA
##
## Results are given on the log odds ratio (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

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

```
## contrast      SoilLocation SoilConc      estimate      SE      df
## Native - Invasive FL          high    -18.5660685 2662.856183 Inf
## Native - Invasive none        high         nonEst      NA    NA
## Native - Invasive PT          high     18.5660685 2662.856189 Inf
## Native - Invasive FL          low      0.6931472   1.190238 Inf
## Native - Invasive none        low         nonEst      NA    NA
## Native - Invasive PT          low     -0.9162907   1.396424 Inf
## Native - Invasive FL          none         nonEst      NA    NA
## Native - Invasive none        none     -0.6931472   1.190238 Inf
## Native - Invasive PT          none         nonEst      NA    NA
## z.ratio p.value
## -0.007 0.9944
##      NA      NA
##  0.007 0.9944
##  0.582 0.5603
##      NA      NA
## -0.656 0.5117
##      NA      NA
## -0.582 0.5603
##      NA      NA
##
## Results are given on the log odds ratio (not the response) scale.
```

I you just compare high vs low WSM, there is a significant difference for survival. If no soil is included, then it becomes marginal due to ns difference from none treatment

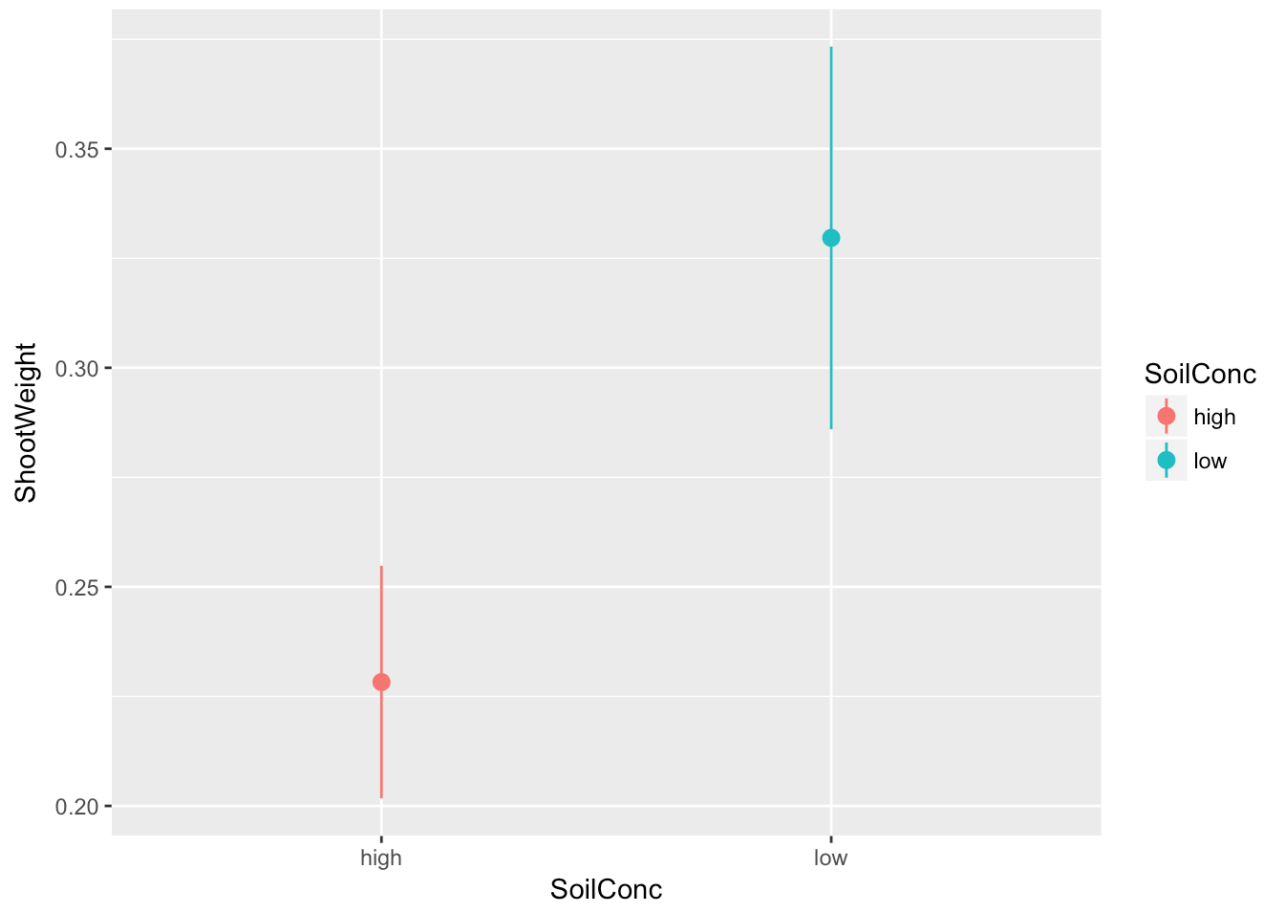
Shoot weight

```
mod <- lm(ShootWeight ~ SoilConc, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##           Df  Sum Sq Mean Sq F value Pr(>F)
## SoilConc   1 0.04317 0.04317   2.111 0.1635
## Residuals 18 0.36811 0.02045
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = ShootWeight, colour = SoilConc)) + stat_summary(fun.data = "mean_se")
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

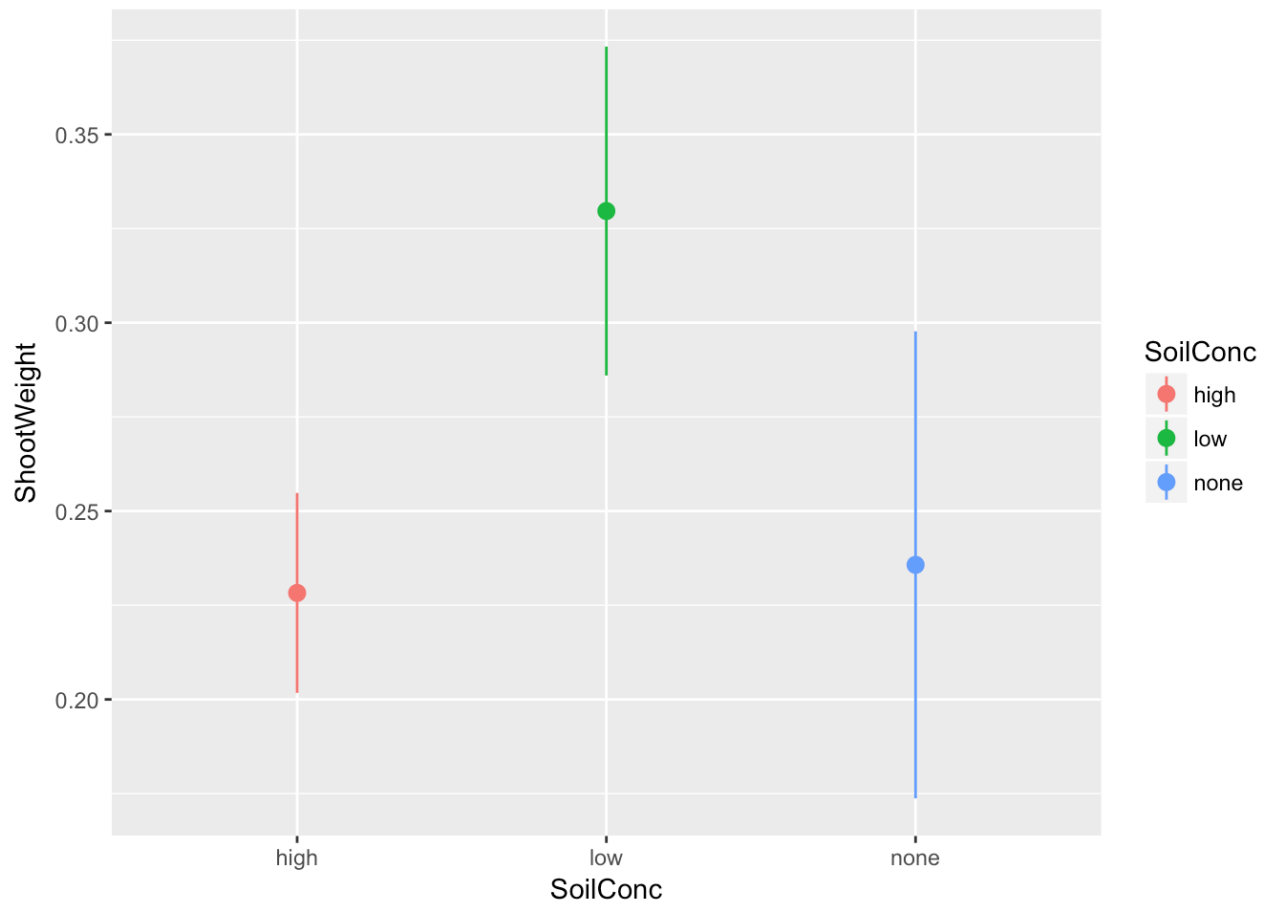



```
mod <- lm(ShootWeight ~ SoilConc, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##           Df Sum Sq Mean Sq F value Pr(>F)
## SoilConc   2  0.05931  0.029653   1.4661 0.2525
## Residuals 22  0.44497  0.020226
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = ShootWeight, colour = SoilConc)) + sta
t_summary(fun.data = "mean_se")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
summary(glht(mod, mcp(SoilConc = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = ShootWeight ~ SoilConc, data = SRMortSub3)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## low - high == 0  0.101383  0.069395   1.461   0.326
## none - high == 0  0.007453  0.086117   0.087   0.996
## none - low == 0  -0.093930  0.074094  -1.268   0.425
## (Adjusted p values reported -- single-step method)
```

```
# No sig difference for either subset for shoot weight
```

```
# Root weight
```

```
mod <- lm(RootWeight ~ SoilConc, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: RootWeight
```

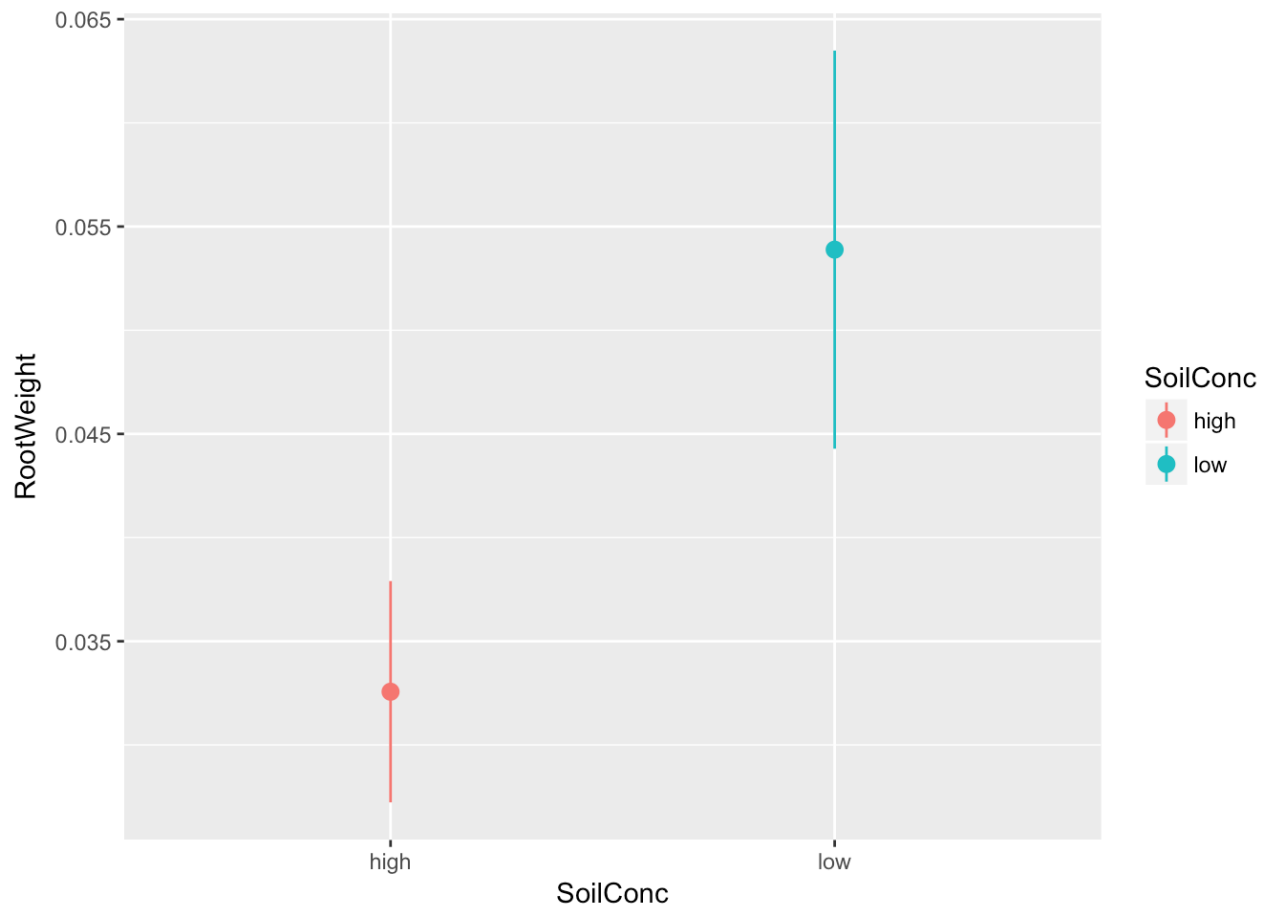
```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
```

```
## SoilConc   1 0.0019089 0.00190891   1.9488 0.1797
```

```
## Residuals 18 0.0176312 0.00097951
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = RootWeight, colour = SoilConc)) + stat_
_summary(fun.data = "mean_se")
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

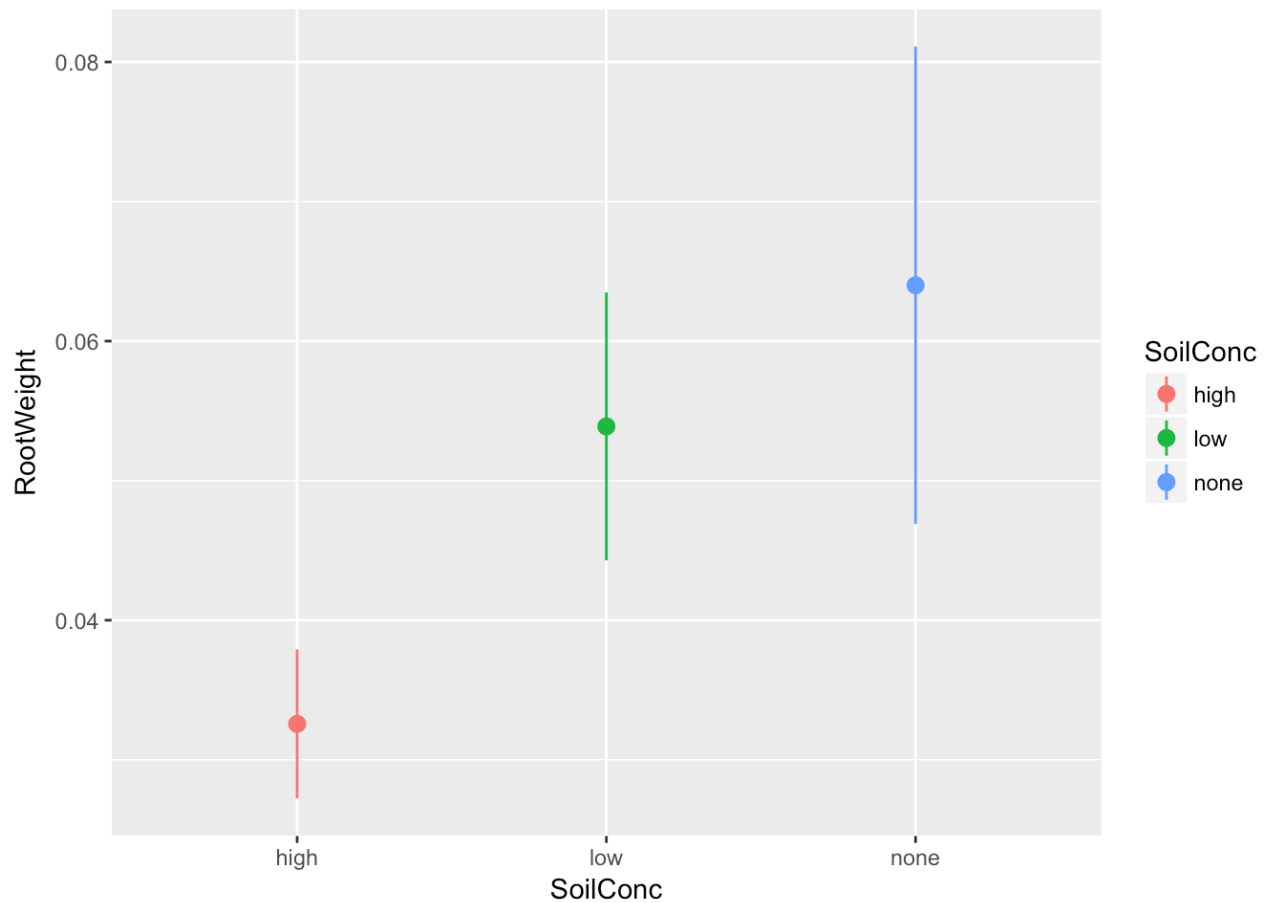


```
mod <- lm(RootWeight ~ SoilConc, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: RootWeight
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## SoilConc   2  0.0029992  0.0014996   1.4049  0.2666
## Residuals 22  0.0234836  0.0010674
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = RootWeight, colour = SoilConc)) + stat_
_summary(fun.data = "mean_se")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
# No sig diff for either subset, but there is a trend for increased root mass w  
ith decreasing soil
```

```
# Root:Shoot
```

```
mod <- lm(Root_Shoot ~ SoilConc, data = SRMortSub2)  
anova(mod)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Root_Shoot
```

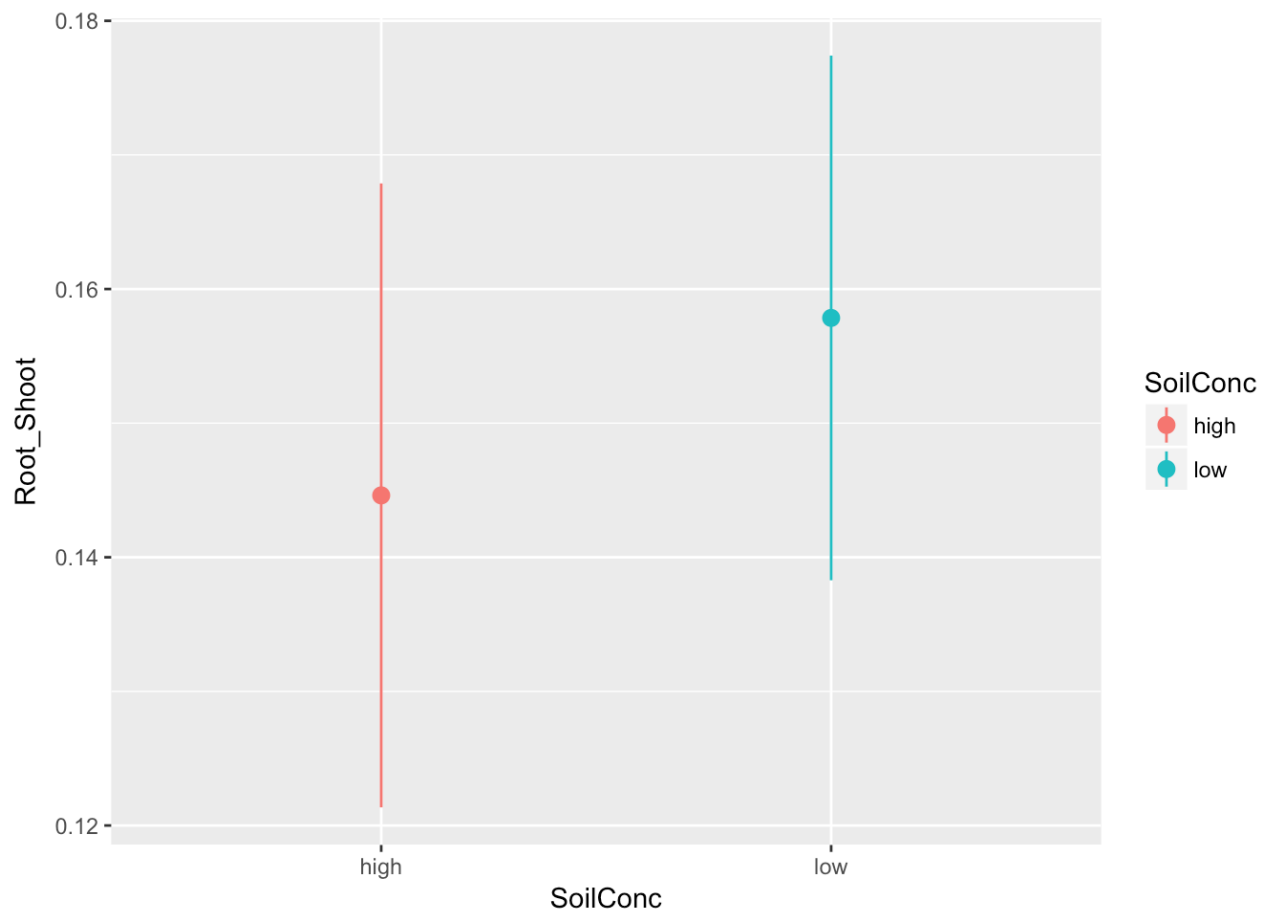
```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
```

```
## SoilConc   1 0.000735 0.0007354   0.1541 0.6992
```

```
## Residuals 18 0.085881 0.0047712
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = Root_Shoot, colour = SoilConc)) + stat  
_summary(fun.data = "mean_se")
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

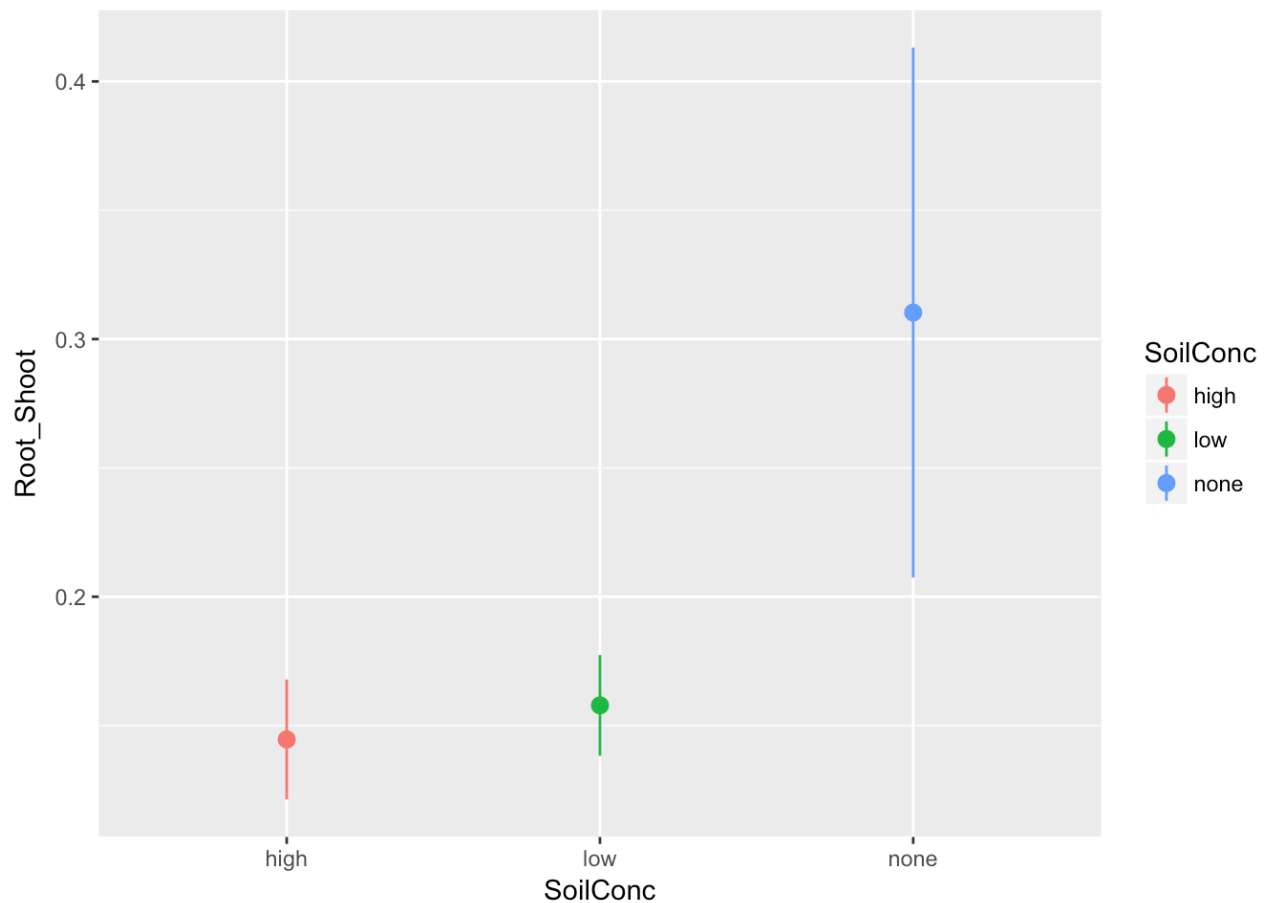


```
mod <- lm(Root_Shoot ~ SoilConc, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Root_Shoot
##           Df Sum Sq Mean Sq F value Pr(>F)
## SoilConc   2 0.09861  0.049305   3.6472 0.04286 *
## Residuals 22 0.29741  0.013519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = Root_Shoot, colour = SoilConc)) + stat_
_summary(fun.data = "mean_se")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
summary(glht(mod, mcp(SoilConc = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = Root_Shoot ~ SoilConc, data = SRMortSub3)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## low - high == 0    0.01323    0.05673   0.233   0.9702
## none - high == 0   0.16569    0.07040   2.353   0.0680 .
## none - low == 0    0.15245    0.06058   2.517   0.0489 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
# no sig diff for first subset, but second is significant ( p = 0.043). There is no diff between H-L, sig between N-L, marg between N-H.
```

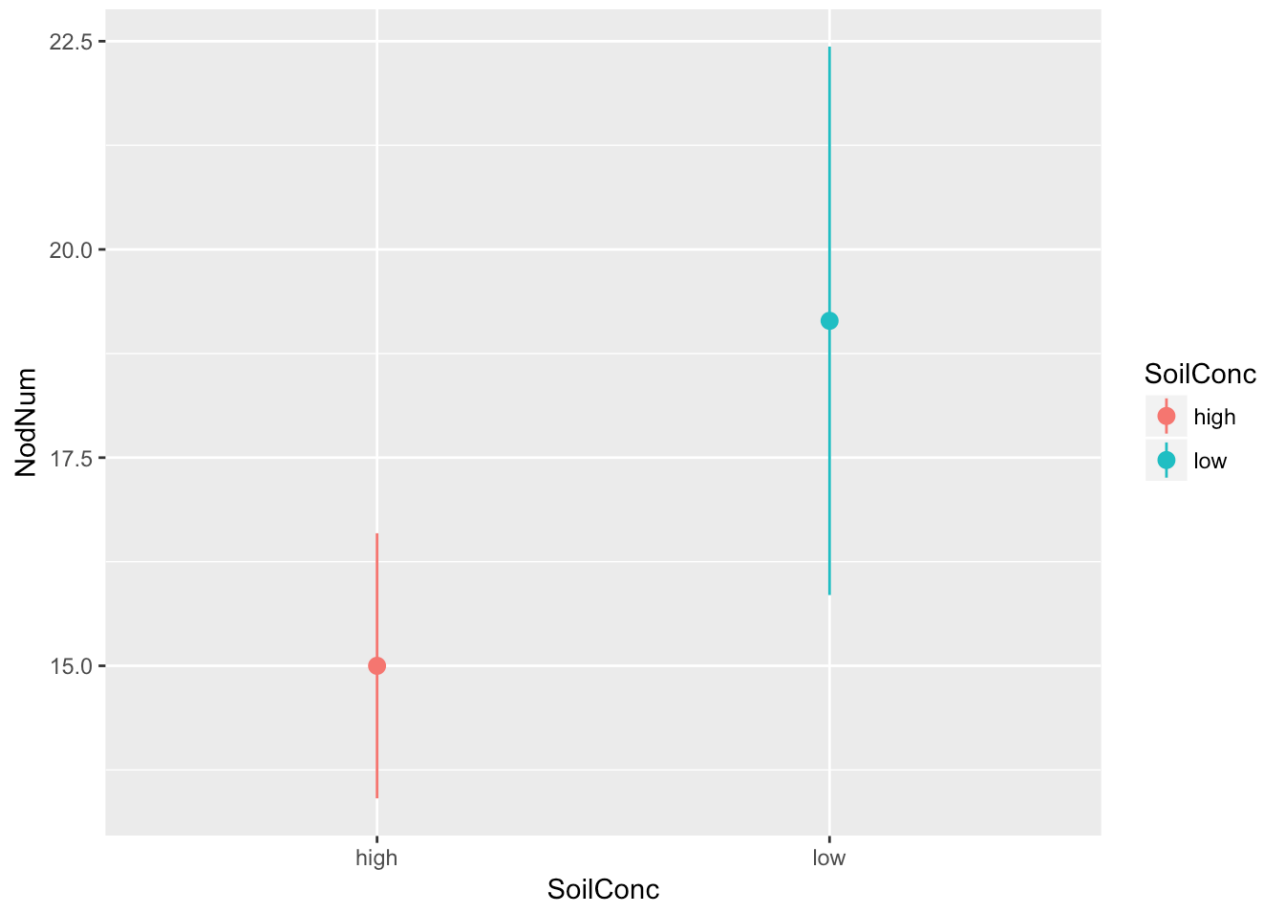
```
# Nod number
```

```
mod <- lm(NodNum ~ SoilConc, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##              Df   Sum Sq Mean Sq F value Pr(>F)
## SoilConc      1    72.09  72.086    0.633 0.4366
## Residuals    18 2049.71 113.873
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = NodNum, colour = SoilConc)) + stat_summary(fun.data = "mean_se")
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

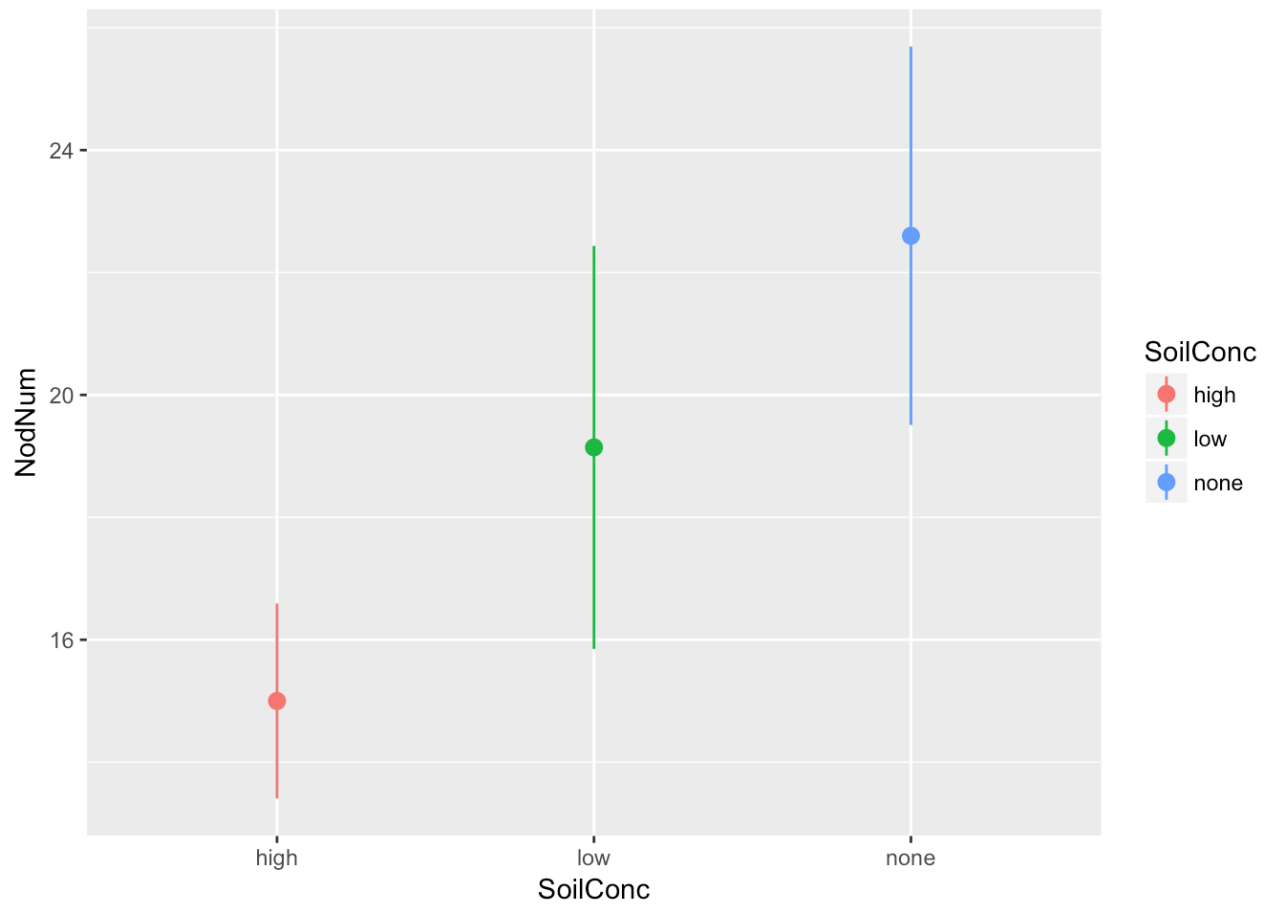


```
mod <- lm(NodNum ~ SoilConc, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##           Df Sum Sq Mean Sq F value Pr(>F)
## SoilConc   2  160.45   80.223   0.7876 0.4674
## Residuals 22 2240.91  101.860
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = NodNum, colour = SoilConc)) + stat_summary(fun.data = "mean_se")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```

```
summary(glht(mod, mcp(SoilConc = "Tukey")))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = NodNum ~ SoilConc, data = SRMortSub3)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## low - high == 0    4.143     4.925   0.841   0.679
## none - high == 0    7.600     6.111   1.244   0.438
## none - low == 0     3.457     5.258   0.657   0.788
## (Adjusted p values reported -- single-step method)
```

```
# No sig diff for either subset, but there is a trend for increased nod number  
with decreasing soil
```

```
# Nod Weight
```

```
mod <- lm(NodWeight ~ SoilConc, data = SRMortSub2)  
anova(mod)
```

```
## Analysis of Variance Table
```

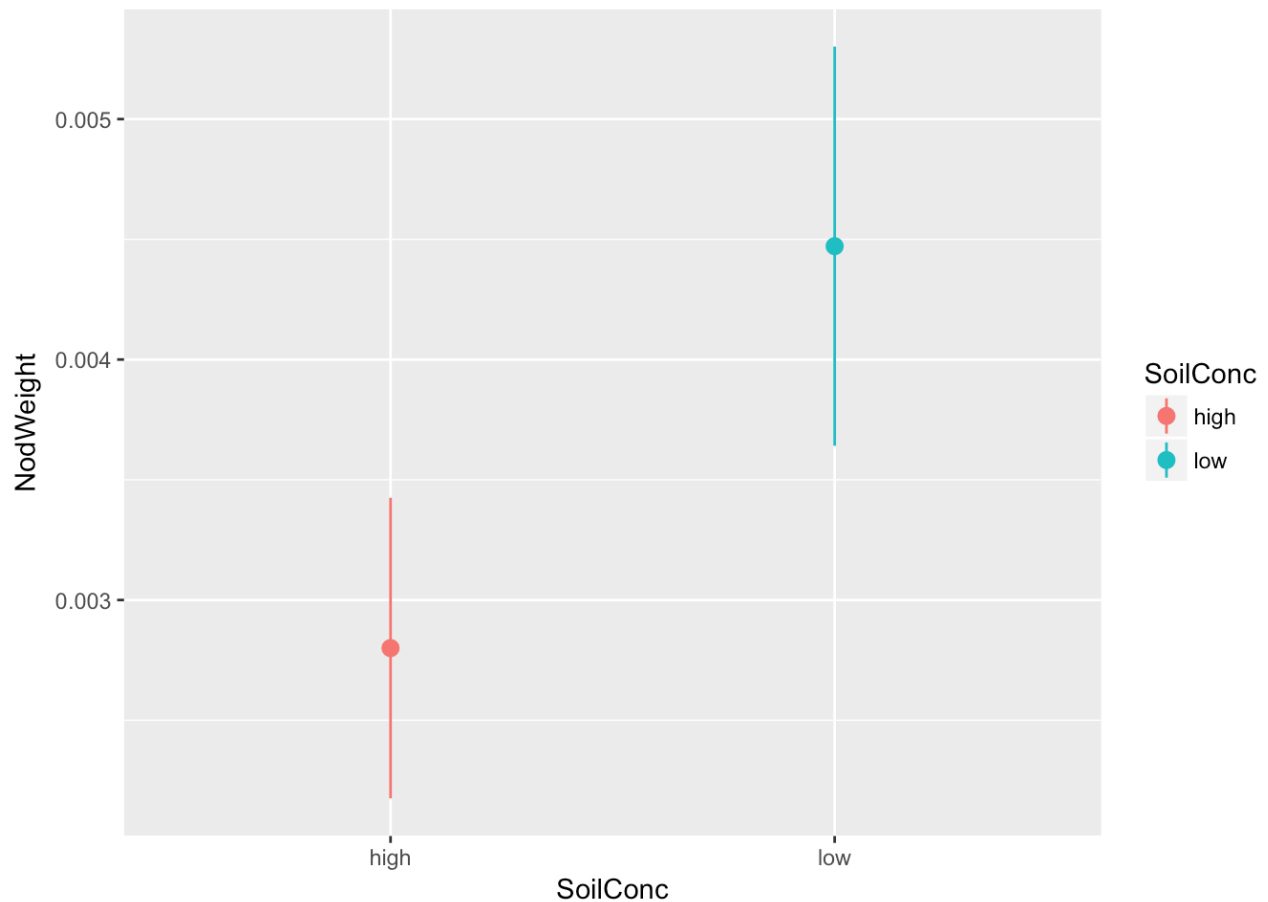
```
##
```

```
## Response: NodWeight
```

```
##           Df      Sum Sq   Mean Sq F value Pr(>F)  
## SoilConc    1 1.1733e-05 1.1733e-05   1.5397 0.2306  
## Residuals  18 1.3717e-04 7.6205e-06
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = NodWeight, colour = SoilConc)) + stat_  
summary(fun.data = "mean_se")
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

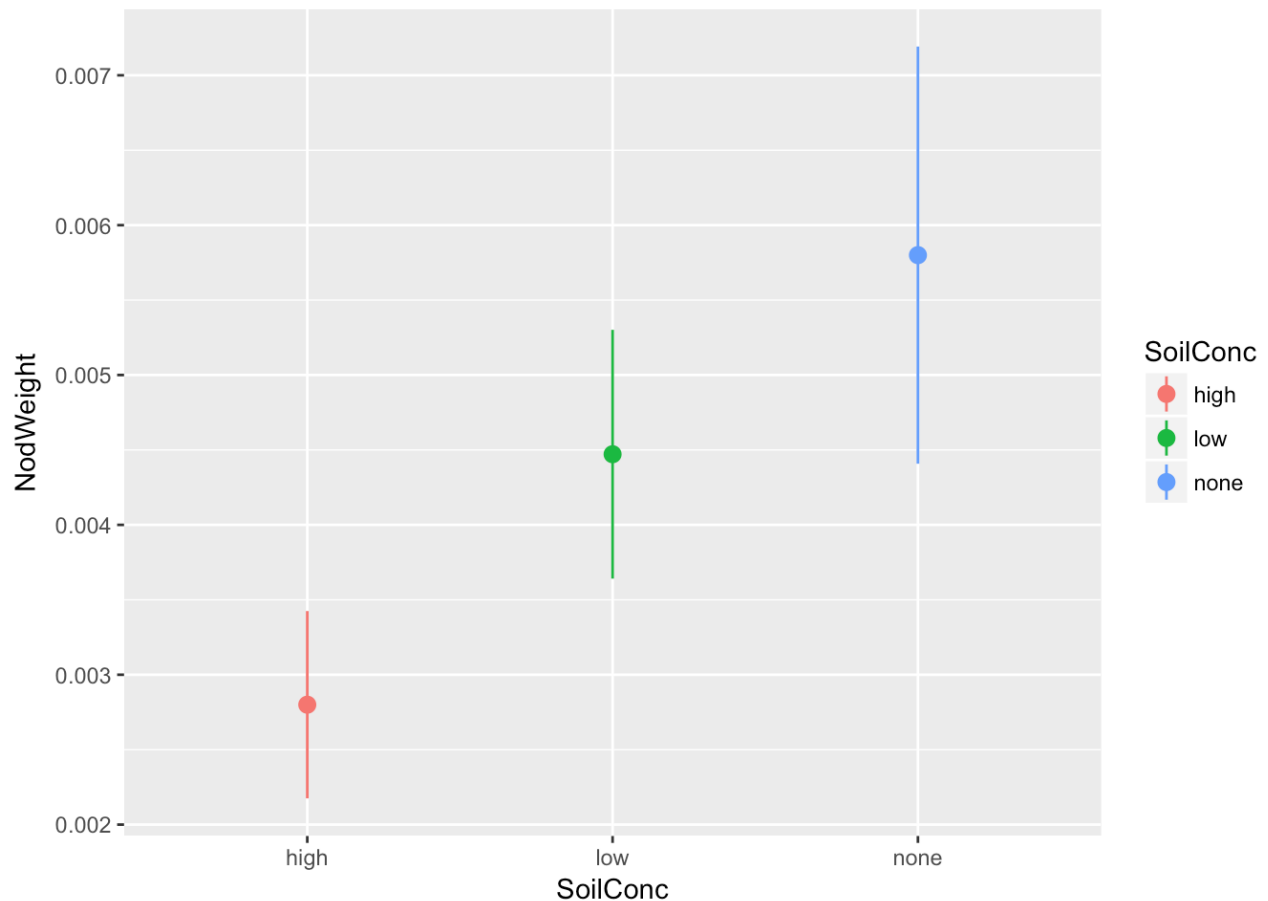


```
mod <- lm(NodWeight ~ SoilConc, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: NodWeight
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## SoilConc   2 2.5129e-05 1.2564e-05  1.5714 0.2302
## Residuals 22 1.7591e-04 7.9958e-06
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = NodWeight, colour = SoilConc)) + stat_
summary(fun.data = "mean_se")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
summary(glht(mod, mcp(SoilConc = "Tukey")))
```

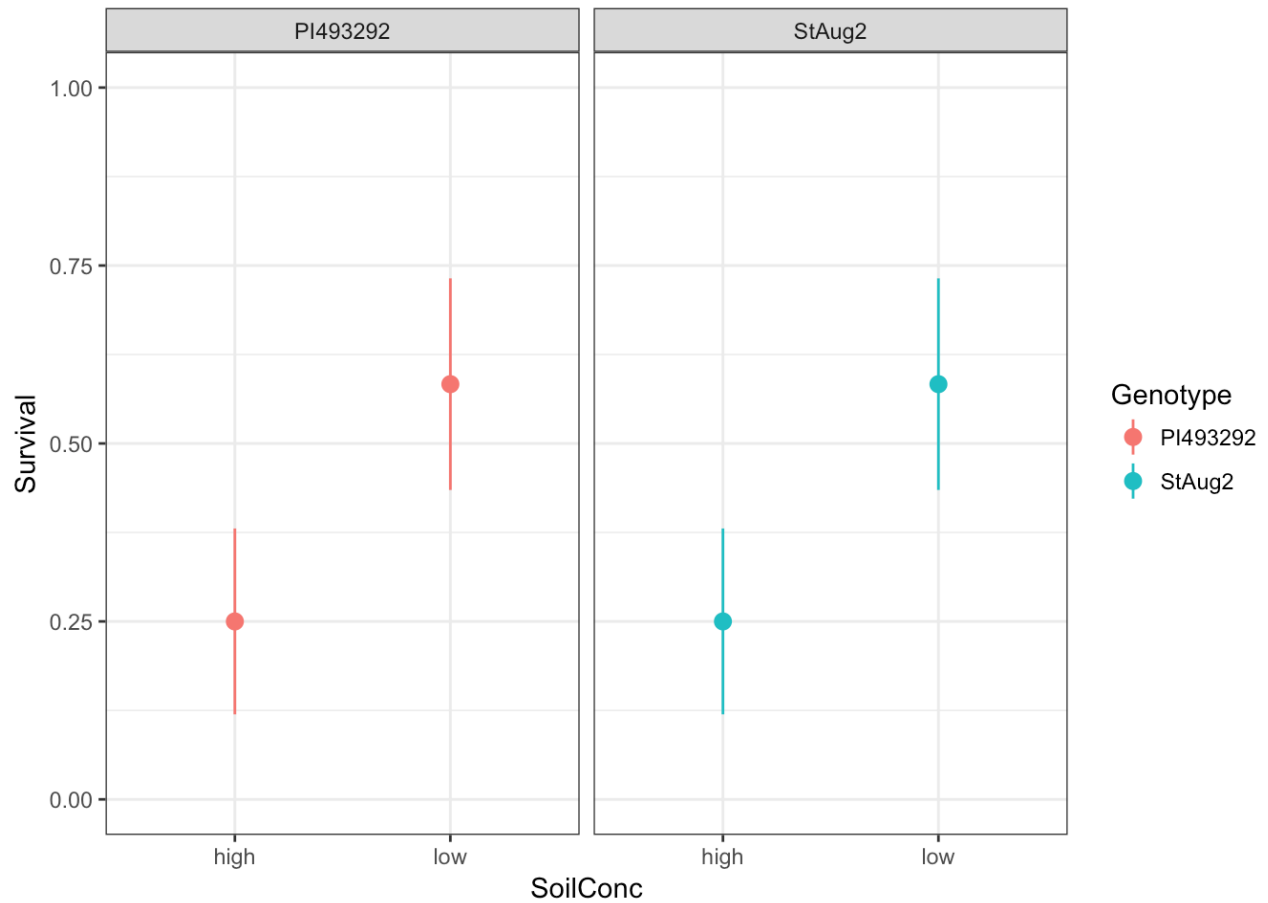
```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = NodWeight ~ SoilConc, data = SRMortSub3)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
## low - high == 0  0.001671   0.001380   1.211   0.456
## none - high == 0 0.003000   0.001712   1.752   0.207
## none - low == 0  0.001329   0.001473   0.902   0.642
## (Adjusted p values reported -- single-step method)
```

```
# No sig diff for either subset, but there is a trend for increased nod weight
with decreasing soil
```

```
# Now running models to see if there is a difference between genotypes
#Mortality
mod <- glm(DeadOrAlive ~ SoilConc * Genotype, family = binomial(link = "logit")
, data = SRMortSub2)
anova(mod, test = "Chisq")
```

```
## 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                      47      65.203
## SoilConc           1    5.6092      46      59.593 0.01787 *
## Genotype           1    0.0000      45      59.593 1.00000
## SoilConc:Genotype  1    0.0000      44      59.593 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

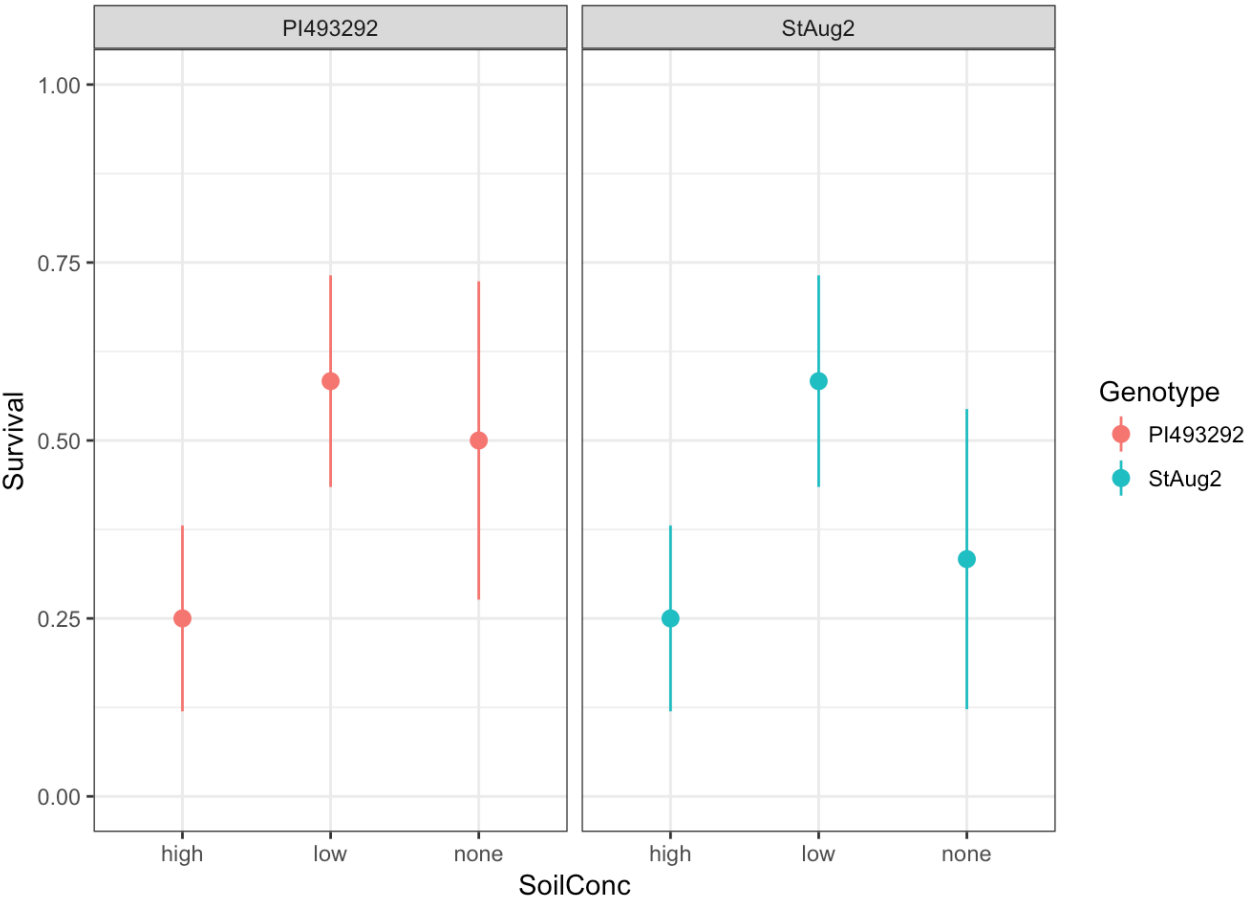
```
ggplot(SRMortSub2, aes(x = SoilConc, y = Survival, colour = Genotype)) + stat_summary(fun.data = "mean_se") + coord_cartesian(ylim = c(0,1)) + theme_bw() + facet_wrap(~Genotype)
```



```
mod <- glm(DeadOrAlive ~ SoilConc * Genotype, family = binomial(link = "logit"), data = SRMortSub3)
anova(mod, test = "Chisq")
```

```
## 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                      59      81.503
## SoilConc           2    5.6092      57    75.894 0.06053 .
## Genotype            1    0.0755      56    75.819 0.78350
## SoilConc:Genotype   2    0.2692      54    75.549 0.87406
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = Survival, colour = Genotype)) + stat_s
ummary(fun.data = "mean_se") + coord_cartesian(ylim = c(0,1)) +theme_bw() + fac
et_wrap(~ Genotype)
```



```
# Genotype NS for mortality for either
```

```
# Shoot weight
```

```
mod <- lm(ShootWeight ~ SoilConc* Genotype, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
```

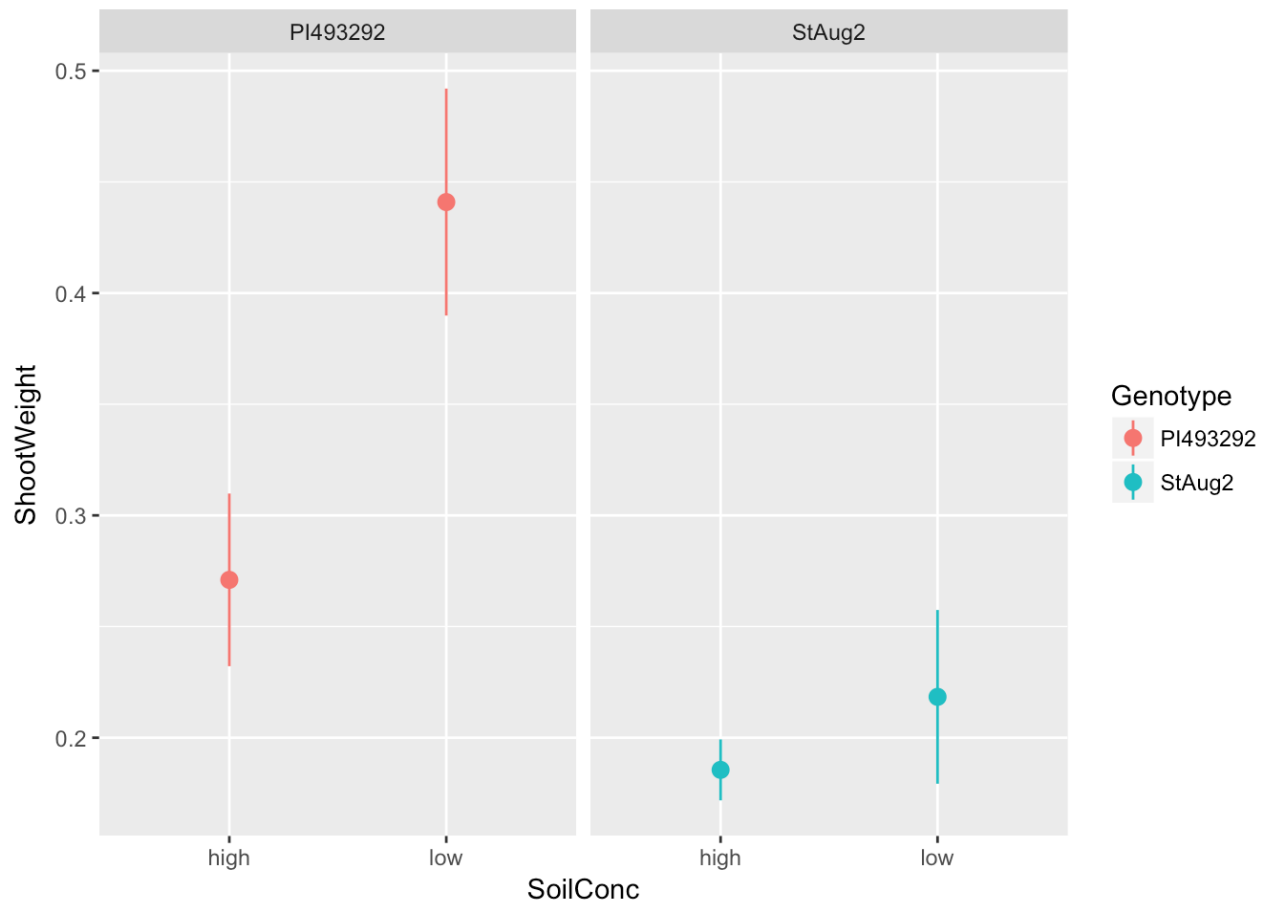
```
##
```

```
## Response: ShootWeight
```

```
##           Df    Sum Sq  Mean Sq F value    Pr(>F)
## SoilConc      1 0.043170  0.043170   3.7582 0.070396 .
## Genotype      1 0.164584  0.164584  14.3281 0.001622 **
## SoilConc:Genotype 1 0.019733  0.019733   1.7179 0.208462
## Residuals    16 0.183788  0.011487
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = ShootWeight, colour = Genotype)) + sta
t_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

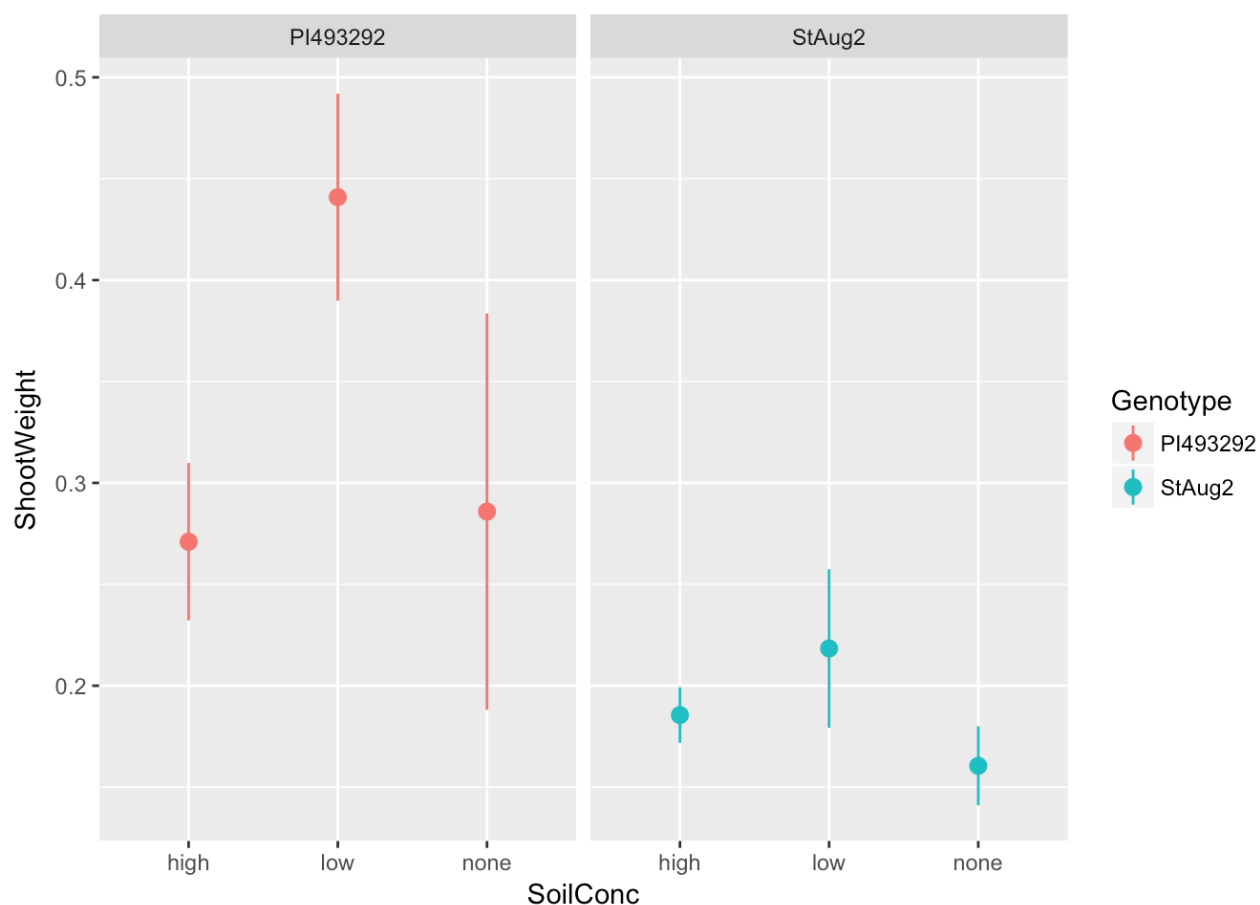


```
mod <- lm(ShootWeight ~ SoilConc * Genotype, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: ShootWeight
##              Df    Sum Sq  Mean Sq F value    Pr(>F)
## SoilConc      2  0.059307  0.029653   2.3301  0.12444
## Genotype      1  0.180403  0.180403  14.1759  0.00131 **
## SoilConc:Genotype 2  0.022775  0.011388   0.8948  0.42522
## Residuals    19  0.241795  0.012726
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = ShootWeight, colour = Genotype)) + sta
t_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```

```
tt = emmeans(mod, ~ SoilConc|Genotype)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast    Genotype    estimate      SE df t.ratio p.value
## high - low  PI493292 -0.16992857 0.07784616 19  -2.183  0.1000
## high - none PI493292 -0.01486667 0.09210882 19  -0.161  0.9858
## low - none  PI493292  0.15506190 0.07784616 19   1.992  0.1414
## high - low  StAug2    -0.03283810 0.07784616 19  -0.422  0.9070
## high - none StAug2     0.02503333 0.10298079 19   0.243  0.9680
## low - none  StAug2     0.05787143 0.09044907 19   0.640  0.8002
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
pairs(tt, simple = "Genotype")
```

```
## Genotype = PI493292:
## contrast      estimate      SE df t.ratio p.value
## high - low   -0.16992857 0.07784616 19  -2.183  0.1000
## high - none  -0.01486667 0.09210882 19  -0.161  0.9858
## low - none    0.15506190 0.07784616 19   1.992  0.1414
##
## Genotype = StAug2:
## contrast      estimate      SE df t.ratio p.value
## high - low   -0.03283810 0.07784616 19  -0.422  0.9070
## high - none    0.02503333 0.10298079 19   0.243  0.9680
## low - none     0.05787143 0.09044907 19   0.640  0.8002
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
tt = emmeans(mod, ~ Genotype| SoilConc)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilConc      estimate      SE df t.ratio p.value
## PI493292 - StAug2 high    0.08546667 0.09210882 19   0.928  0.3651
## PI493292 - StAug2 low     0.22255714 0.06029938 19   3.691  0.0016
## PI493292 - StAug2 none    0.12536667 0.10298079 19   1.217  0.2384
```

```
pairs(tt, simple = "Genotype")
```

```
## SoilConc = high:
## contrast      estimate      SE df t.ratio p.value
## PI493292 - StAug2 0.08546667 0.09210882 19   0.928  0.3651
##
## SoilConc = low:
## contrast      estimate      SE df t.ratio p.value
## PI493292 - StAug2 0.22255714 0.06029938 19   3.691  0.0016
##
## SoilConc = none:
## contrast      estimate      SE df t.ratio p.value
## PI493292 - StAug2 0.12536667 0.10298079 19   1.217  0.2384
```

```
# Using emmeans, there is a difference between ST. Aug and PI493292 at low WSM levels.
```

```
# Root weight
```

```
mod <- lm(RootWeight ~ SoilConc * Genotype, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
```

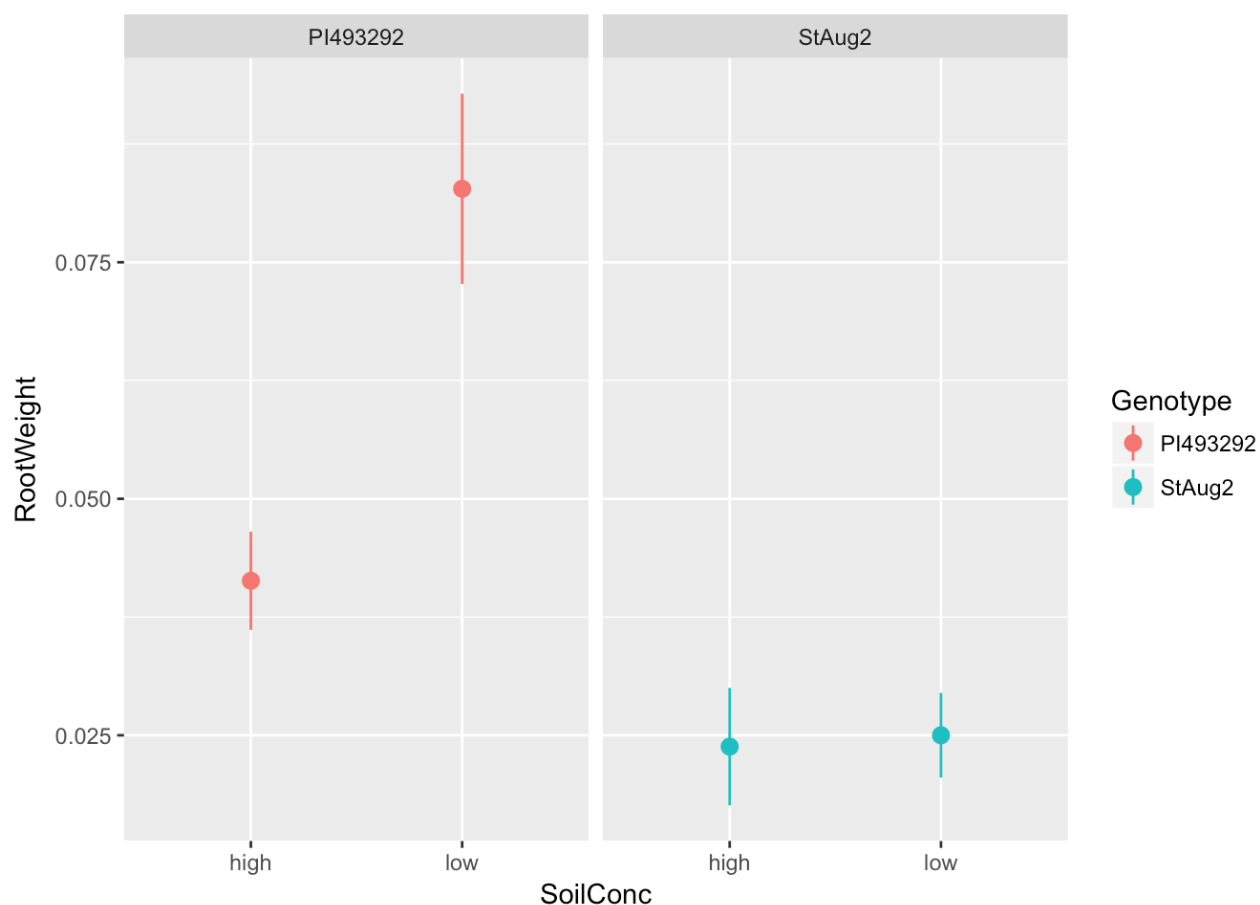
```
##
```

```
## Response: RootWeight
```

```
##           Df      Sum Sq   Mean Sq F value    Pr(>F)
## SoilConc      1 0.0019089 0.0019089   5.5647  0.03137 *
## Genotype      1 0.0104425 0.0104425  30.4409 4.684e-05 ***
## SoilConc:Genotype 1 0.0017001 0.0017001   4.9559  0.04072 *
## Residuals    16 0.0054886 0.0003430
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = RootWeight, colour = Genotype)) + stat_
_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

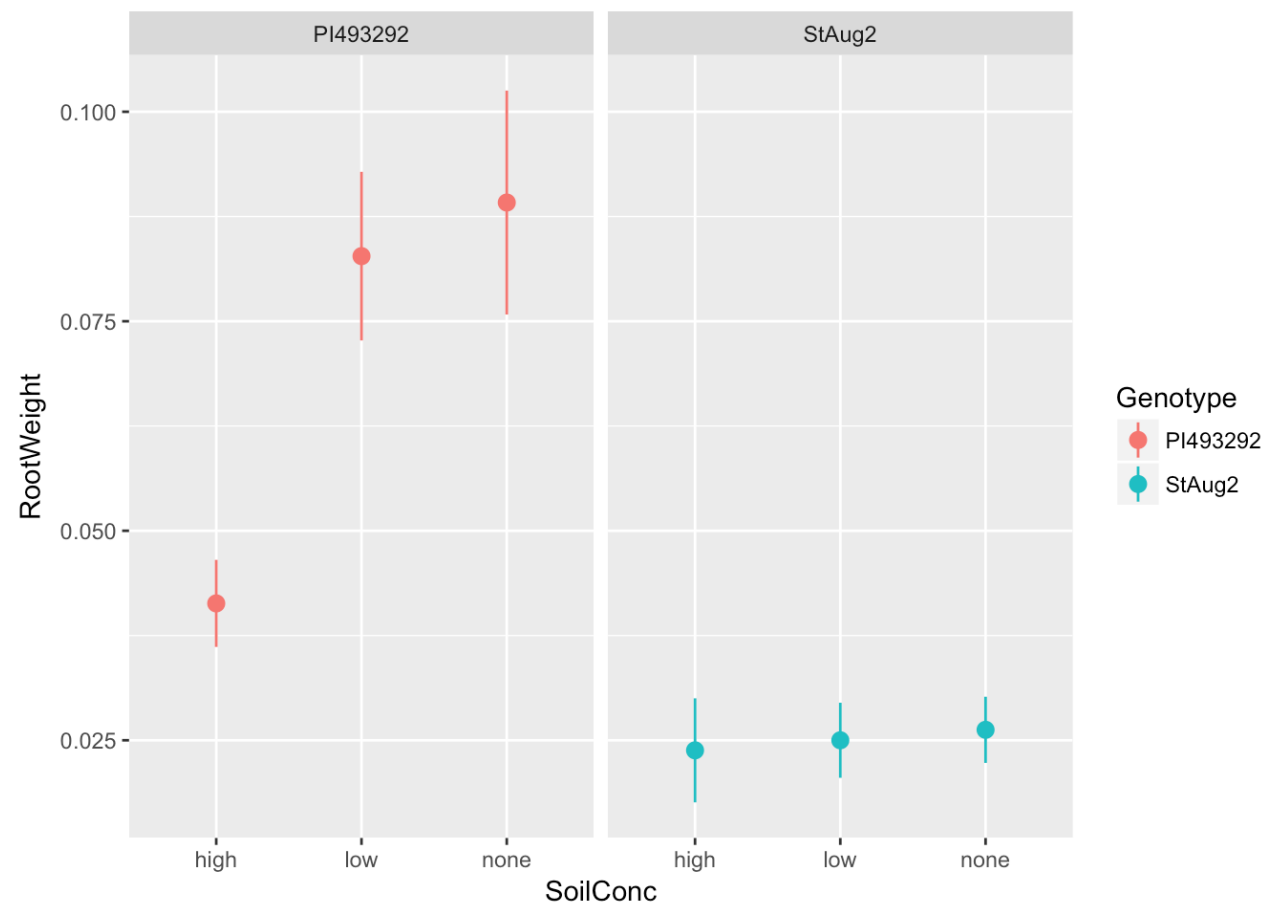


```
mod <- lm(RootWeight ~ SoilConc * Genotype, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: RootWeight
##              Df    Sum Sq  Mean Sq F value    Pr(>F)
## SoilConc      2  0.002992  0.001496   4.3231  0.02836 *
## Genotype      1  0.0149058  0.0149058  42.9702 2.819e-06 ***
## SoilConc:Genotype 2  0.0019869  0.0009935   2.8639  0.08183 .
## Residuals    19  0.0065909  0.0003469
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = RootWeight, colour = Genotype)) + stat_
_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
tt = emmeans(mod, ~ SoilConc|Genotype)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      Genotype      estimate      SE df t.ratio p.value
## high - low  PI493292 -0.041438095 0.01285240 19 -3.224 0.0119
## high - none PI493292 -0.047833333 0.01520717 19 -3.145 0.0141
## low - none  PI493292 -0.006395238 0.01285240 19 -0.498 0.8733
## high - low  StAug2 -0.001200000 0.01285240 19 -0.093 0.9952
## high - none StAug2 -0.002450000 0.01700213 19 -0.144 0.9886
## low - none  StAug2 -0.001250000 0.01493314 19 -0.084 0.9961
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
pairs(tt, simple = "Genotype")
```

```
## Genotype = PI493292:
## contrast      estimate      SE df t.ratio p.value
## high - low    -0.041438095 0.01285240 19  -3.224  0.0119
## high - none   -0.047833333 0.01520717 19  -3.145  0.0141
## low - none    -0.006395238 0.01285240 19  -0.498  0.8733
##
## Genotype = StAug2:
## contrast      estimate      SE df t.ratio p.value
## high - low    -0.001200000 0.01285240 19  -0.093  0.9952
## high - none   -0.002450000 0.01700213 19  -0.144  0.9886
## low - none    -0.001250000 0.01493314 19  -0.084  0.9961
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
tt = emmeans(mod, ~ Genotype | SoilConc)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilConc      estimate      SE df t.ratio p.value
## PI493292 - StAug2 high      0.01753333 0.015207169 19   1.153  0.2632
## PI493292 - StAug2 low      0.05777143 0.009955429 19   5.803  <.0001
## PI493292 - StAug2 none     0.06291667 0.017002132 19   3.701  0.0015
```

There is a sig diff in first subset between soil conc, genotype and interaction. In the second, the interaction becomes marginal. Then ran emmeans and found that in Native Geno: H-L and H-N are sig. None in Invasive. But the two genotypes vary sig within low and none for root weight.

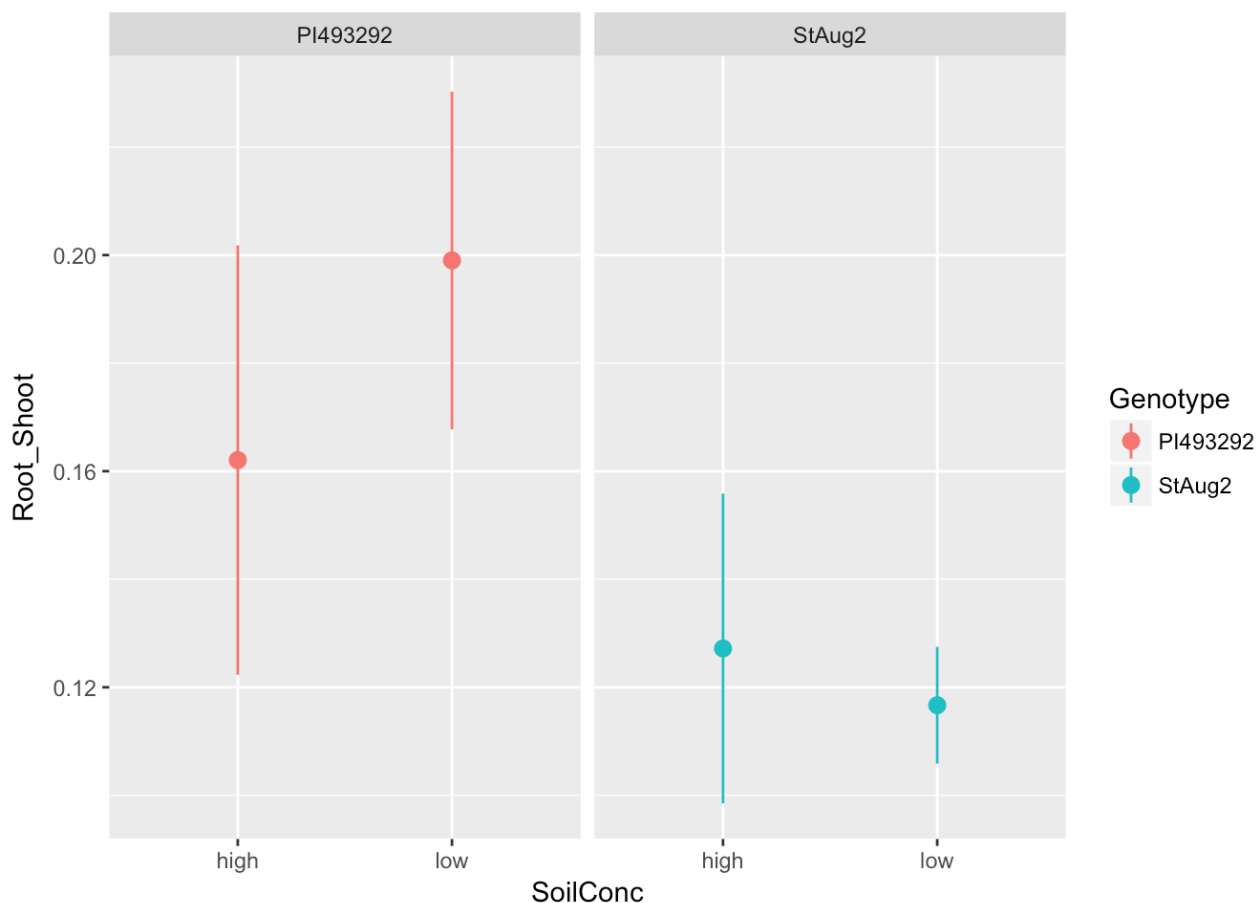
Root:Shoot

```
mod <- lm(Root_Shoot ~ SoilConc * Genotype, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Root_Shoot
##           Df    Sum Sq   Mean Sq F value   Pr(>F)
## SoilConc    1 0.000735 0.0007354   0.1951 0.66465
## Genotype     1 0.023189 0.0231887   6.1503 0.02465 *
## SoilConc:Genotype 1 0.002366 0.0023663   0.6276 0.43982
## Residuals   16 0.060326 0.0037704
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = Root_Shoot, colour = Genotype)) + stat_
_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```



```
mod <- lm(Root_Shoot ~ SoilConc * Genotype, data = SRMortSub3)
anova(mod)
```

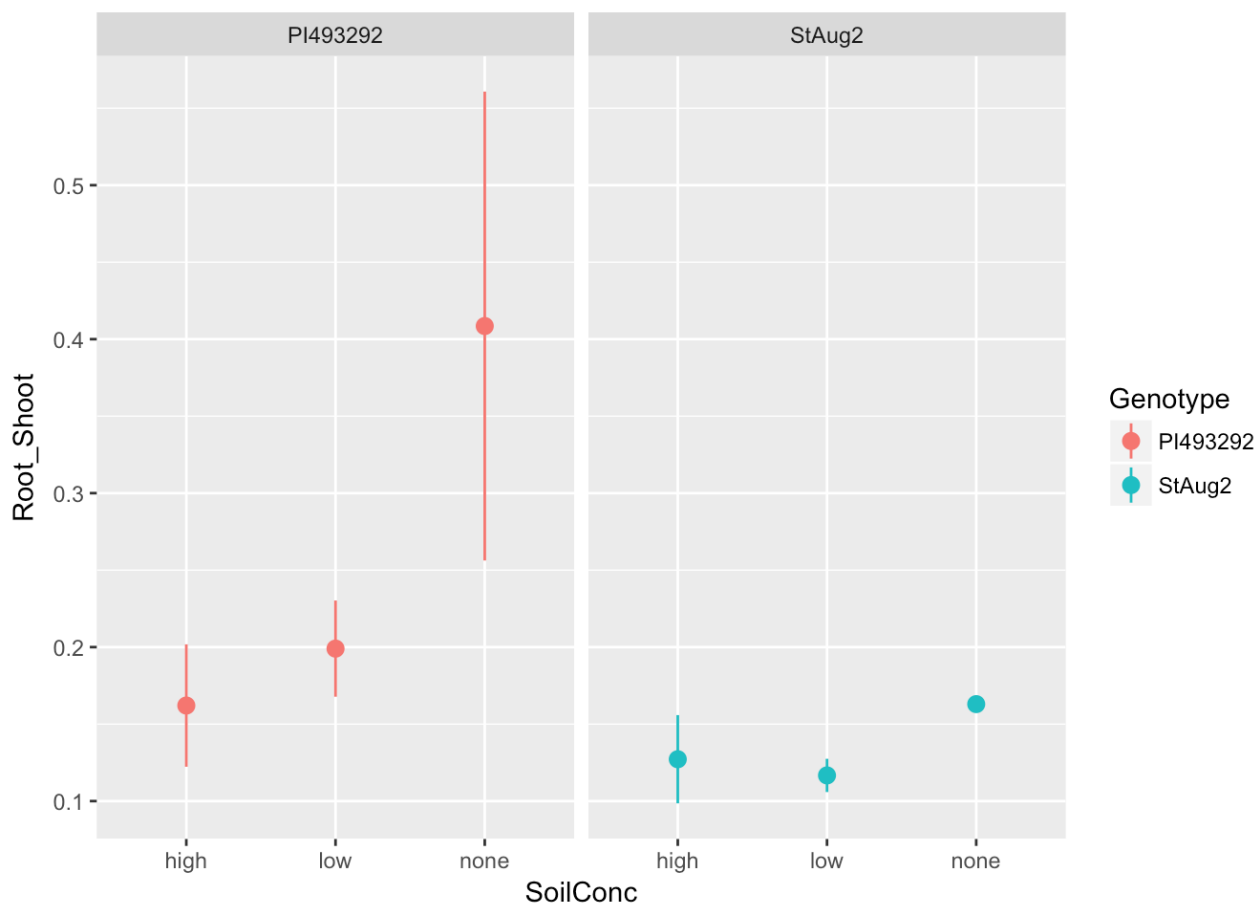
```
## Analysis of Variance Table
##
## Response: Root_Shoot
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
SoilConc	2	0.098610	0.049305	4.6958	0.02202 *
Genotype	1	0.065072	0.065072	6.1974	0.02223 *
SoilConc:Genotype	2	0.032841	0.016420	1.5639	0.23510
Residuals	19	0.199497	0.010500		

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

```
ggplot(SRMortSub3, aes(x = SoilConc, y = Root_Shoot, colour = Genotype)) + stat_
_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
tt = emmeans(mod, ~ SoilConc|Genotype)
dd = pairs(tt)
summary(dd, by = NULL)
```



```
## contrast      Genotype      estimate      SE df t.ratio p.value
## high - low    PI493292 -0.03696869 0.07071014 19  -0.523  0.8612
## high - none   PI493292 -0.24647493 0.08366537 19  -2.946  0.0216
## low - none    PI493292 -0.20950623 0.07071014 19  -2.963  0.0208
## high - low    StAug2      0.01050360 0.07071014 19   0.149  0.9879
## high - none   StAug2     -0.03578879 0.09354073 19  -0.383  0.9228
## low - none    StAug2     -0.04629238 0.08215776 19  -0.563  0.8409
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
pairs(tt, simple = "Genotype")
```

```
## Genotype = PI493292:
## contrast      estimate      SE df t.ratio p.value
## high - low    -0.03696869 0.07071014 19  -0.523  0.8612
## high - none   -0.24647493 0.08366537 19  -2.946  0.0216
## low - none    -0.20950623 0.07071014 19  -2.963  0.0208
##
## Genotype = StAug2:
## contrast      estimate      SE df t.ratio p.value
## high - low     0.01050360 0.07071014 19   0.149  0.9879
## high - none   -0.03578879 0.09354073 19  -0.383  0.9228
## low - none    -0.04629238 0.08215776 19  -0.563  0.8409
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
tt = emmeans(mod, ~ Genotype| SoilConc)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilConc      estimate      SE df t.ratio p.value
## PI493292 - StAug2 high      0.03487036 0.08366537 19   0.417  0.6815
## PI493292 - StAug2 low      0.08234265 0.05477184 19   1.503  0.1492
## PI493292 - StAug2 none     0.24555650 0.09354073 19   2.625  0.0167
```

```
# In the first subset, only genotype is s ( p = 0.025). In the second, soil and
genotype but not interaction are s (p = 0.022 for both). Using emmeans, in nati
ve sig dif between H-N and L-N (p = 0.0216, 0.0208) non for invasive. Between g
enotypes, only none is sig ( p= 0.0167)
```

```
# Nod number
```

```
mod <- lm(NodNum ~ SoilConc * Genotype, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: NodNum
```

```
##
```

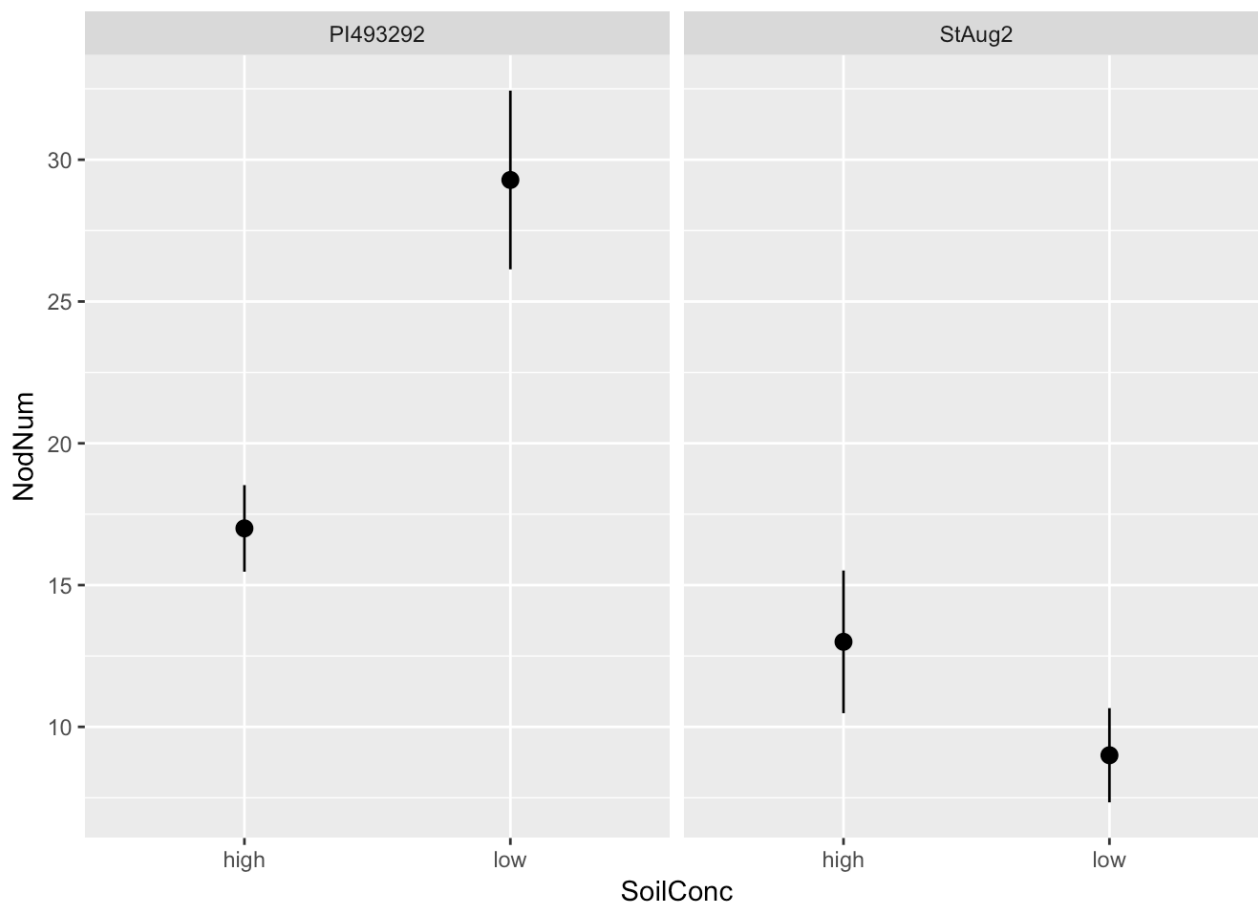
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## SoilConc	1	72.09	72.09	1.9701	0.17954
## Genotype	1	1185.80	1185.80	32.4084	3.331e-05 ***
## SoilConc:Genotype	1	278.49	278.49	7.6111	0.01398 *
## Residuals	16	585.43	36.59		

```
## ---
```

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

```
ggplot(SRMortSub2, aes(x = SoilConc, y = NodNum, Genotype = SoilConc)) + stat_s
ummary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```

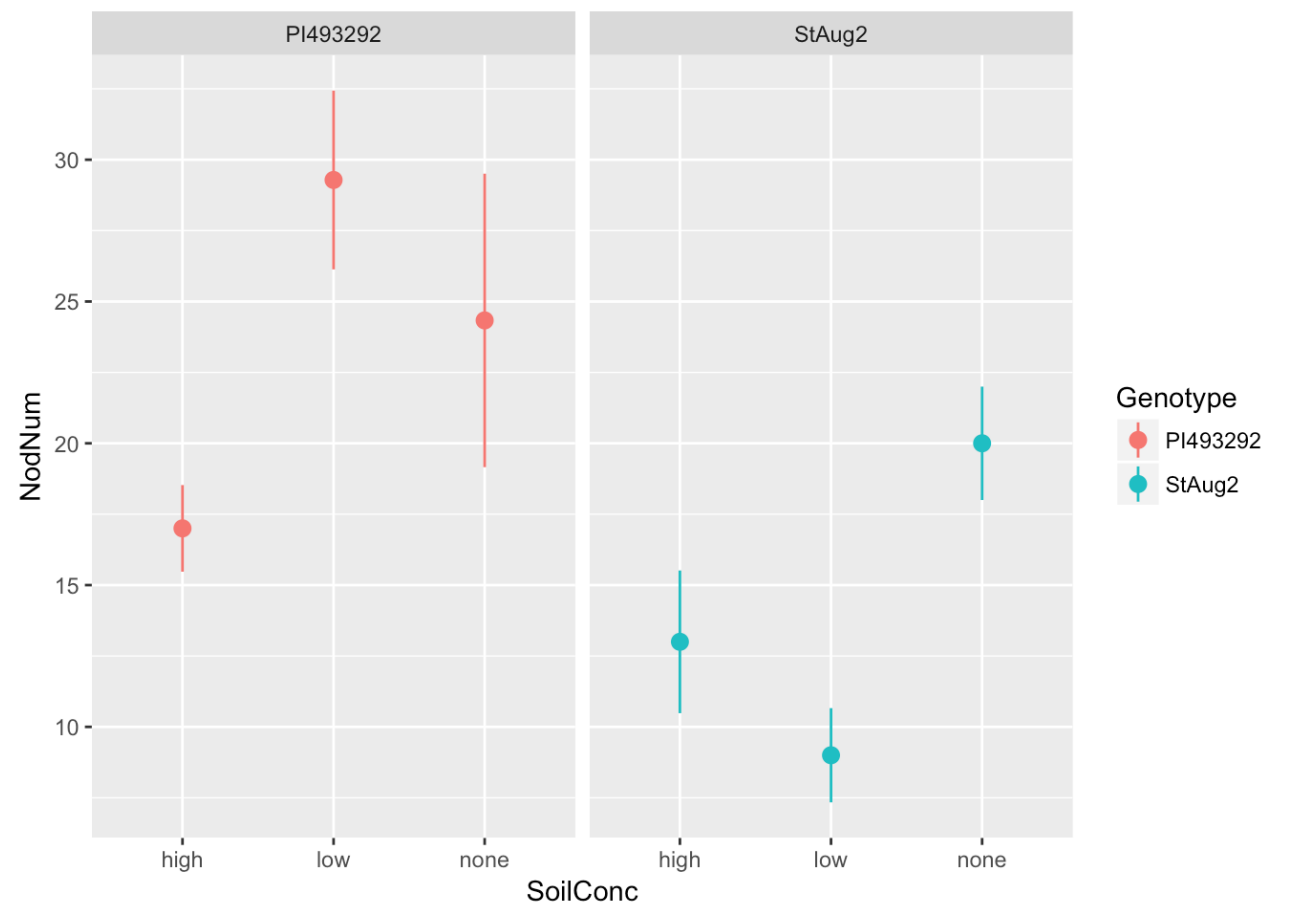


```
mod <- lm(NodNum ~ SoilConc * Genotype, data = SRMortSub3)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: NodNum
##
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## SoilConc    2   160.45    80.22   2.0213   0.16000
## Genotype     1  1089.81  1089.81  27.4587 4.663e-05 ***
## SoilConc:Genotype  2   397.01   198.50   5.0014   0.01799 *
## Residuals   19   754.10    39.69
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub3, aes(x = SoilConc, y = NodNum, colour = Genotype)) + stat_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
tt = emmeans(mod, ~ SoilConc|Genotype)
dd = pairs(tt)
summary(dd, by = NULL)
```

##	contrast	Genotype	estimate	SE	df	t.ratio	p.value
##	high - low	PI493292	-12.285714	4.347370	19	-2.826	0.0278
##	high - none	PI493292	-7.333333	5.143878	19	-1.426	0.3482
##	low - none	PI493292	4.952381	4.347370	19	1.139	0.5026
##	high - low	StAug2	4.000000	4.347370	19	0.920	0.6346
##	high - none	StAug2	-7.000000	5.751031	19	-1.217	0.4578
##	low - none	StAug2	-11.000000	5.051188	19	-2.178	0.1010
##	P value adjustment: tukey method for comparing a family of 3 estimates						

```
pairs(tt, simple = "Genotype")
```

```
## Genotype = PI493292:
## contrast      estimate      SE df t.ratio p.value
## high - low    -12.285714  4.347370 19  -2.826  0.0278
## high - none   -7.333333  5.143878 19  -1.426  0.3482
## low - none     4.952381  4.347370 19   1.139  0.5026
##
## Genotype = StAug2:
## contrast      estimate      SE df t.ratio p.value
## high - low     4.000000  4.347370 19   0.920  0.6346
## high - none   -7.000000  5.751031 19  -1.217  0.4578
## low - none   -11.000000  5.051188 19  -2.178  0.1010
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
tt = emmeans(mod, ~ Genotype| SoilConc)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilConc estimate      SE df t.ratio p.value
## PI493292 - StAug2 high      4.000000  5.143878 19   0.778  0.4464
## PI493292 - StAug2 low      20.285714  3.367459 19   6.024 <.0001
## PI493292 - StAug2 none      4.333333  5.751031 19   0.753  0.4604
```

```
# Genotype and interaction are sig in both subsets. Within Native, H-L is sig (
0.0278). Between genotypes, low is sig ( p < 0.001)
```

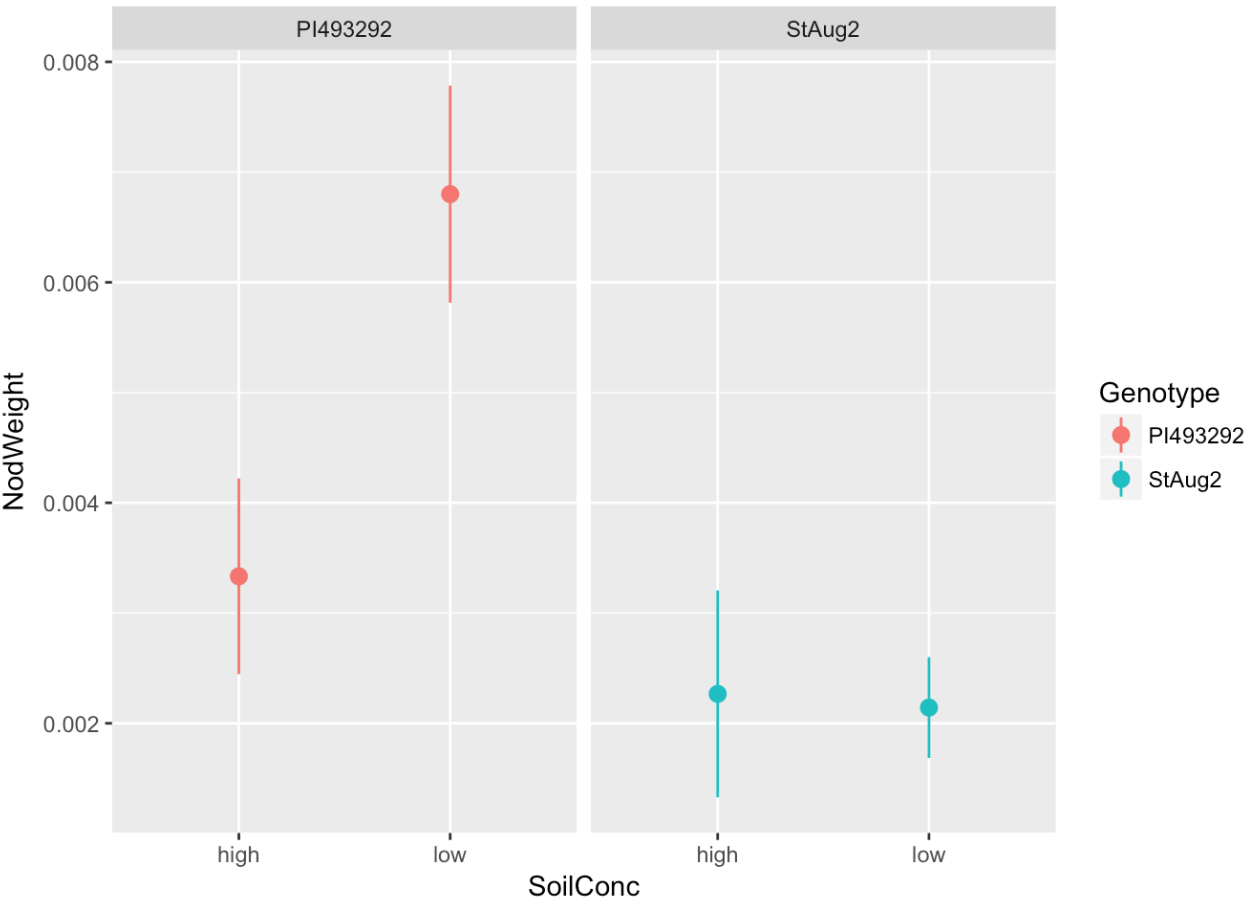
```
# Nod Weight
```

```
mod <- lm(NodWeight ~ SoilConc * Genotype, data = SRMortSub2)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: NodWeight
##              Df      Sum Sq    Mean Sq F value    Pr(>F)
## SoilConc       1  1.1733e-05  1.1733e-05   3.1525 0.0948301 .
## Genotype       1  6.4082e-05  6.4082e-05  17.2175 0.0007543 ***
## SoilConc:Genotype 1  1.3536e-05  1.3536e-05   3.6369 0.0746312 .
## Residuals     16  5.9550e-05  3.7220e-06
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(SRMortSub2, aes(x = SoilConc, y = NodWeight, colour = Genotype)) + stat_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 28 rows containing non-finite values (stat_summary).
```



```
mod <- lm(NodWeight ~ SoilConc * Genotype, data = SRMortSub3)
anova(mod)
```

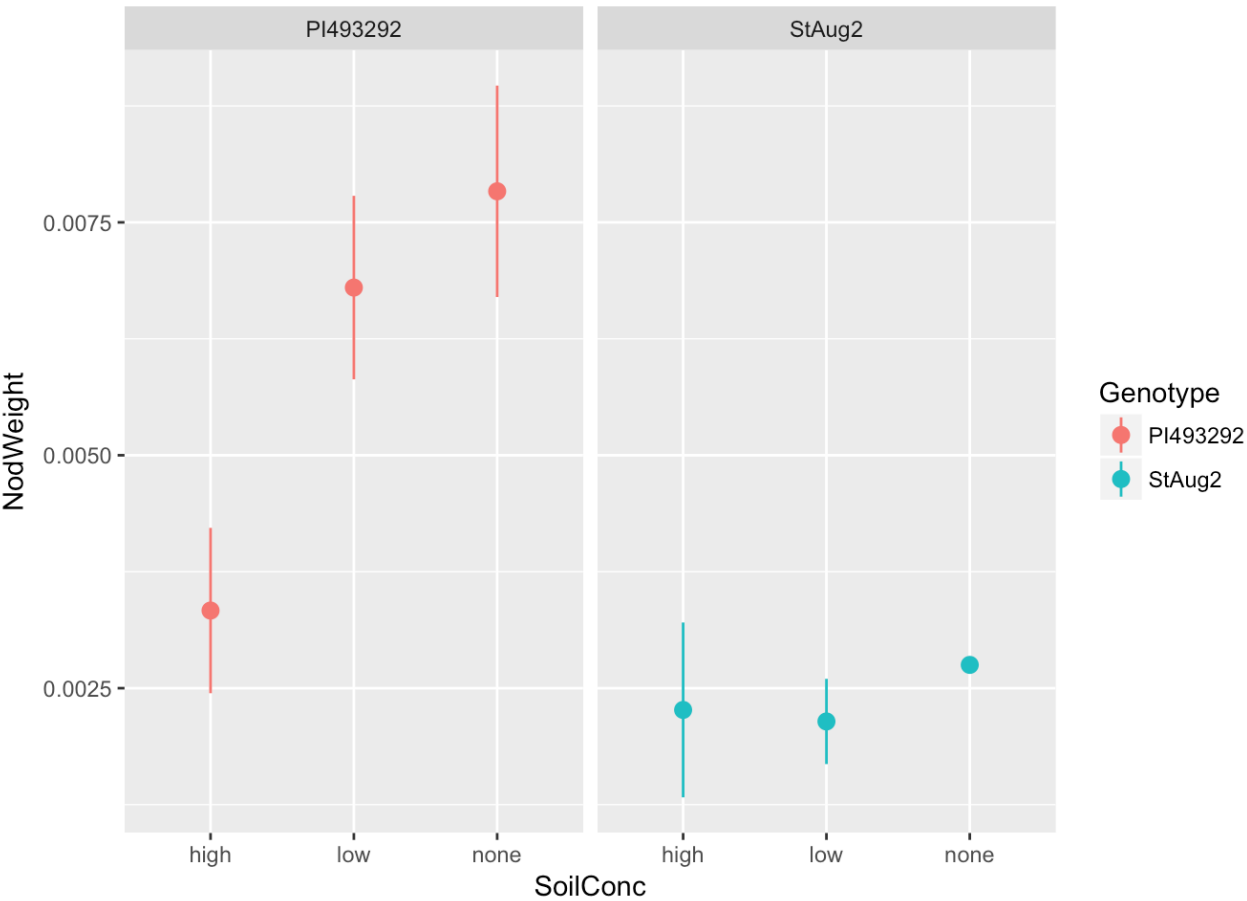
```
## Analysis of Variance Table
##
## Response: NodWeight
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
SoilConc	2	2.5129e-05	1.2565e-05	3.5481	0.04905 *
Genotype	1	9.2903e-05	9.2903e-05	26.2352	6.058e-05 ***
SoilConc:Genotype	2	1.5723e-05	7.8620e-06	2.2201	0.13600
Residuals	19	6.7282e-05	3.5410e-06		

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

```
ggplot(SRMortSub3, aes(x = SoilConc, y = NodWeight, colour = Genotype)) + stat_summary(fun.data = "mean_se") + facet_wrap(~ Genotype)
```

```
## Warning: Removed 35 rows containing non-finite values (stat_summary).
```



```
tt = emmeans(mod, ~ SoilConc|Genotype)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      Genotype      estimate      SE df t.ratio p.value
## high - low   PI493292 -0.003466667 0.001298564 19  -2.670  0.0385
## high - none  PI493292 -0.004500000 0.001536482 19  -2.929  0.0224
## low - none   PI493292 -0.001033333 0.001298564 19  -0.796  0.7101
## high - low   StAug2      0.0001238095 0.001298564 19   0.095  0.9950
## high - none  StAug2     -0.0004833333 0.001717839 19  -0.281  0.9574
## low - none   StAug2     -0.0006071429 0.001508795 19  -0.402  0.9150
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
pairs(tt, simple = "Genotype")
```

```
## Genotype = PI493292:
## contrast      estimate      SE df t.ratio p.value
## high - low   -0.0034666667 0.001298564 19  -2.670  0.0385
## high - none  -0.0045000000 0.001536482 19  -2.929  0.0224
## low - none   -0.0010333333 0.001298564 19  -0.796  0.7101
##
## Genotype = StAug2:
## contrast      estimate      SE df t.ratio p.value
## high - low    0.0001238095 0.001298564 19   0.095  0.9950
## high - none  -0.0004833333 0.001717839 19  -0.281  0.9574
## low - none   -0.0006071429 0.001508795 19  -0.402  0.9150
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
tt = emmeans(mod, ~ Genotype | SoilConc)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      SoilConc      estimate      SE df t.ratio p.value
## PI493292 - StAug2 high    0.001066667 0.001536482 19   0.694  0.4959
## PI493292 - StAug2 low    0.004657143 0.001005864 19   4.630  0.0002
## PI493292 - StAug2 none    0.005083333 0.001717839 19   2.959  0.0081
```

```
# First subset, genotype is sig ( p < 0.001). 2nd subset, soil and genotype are
sig ( p = 0.049, p < 0.001). Within genotype, native H-N is sig ( p = 0.0224). be
tween genotypes, sig for low and none ( p = 0.002, p = 0.0081)
```

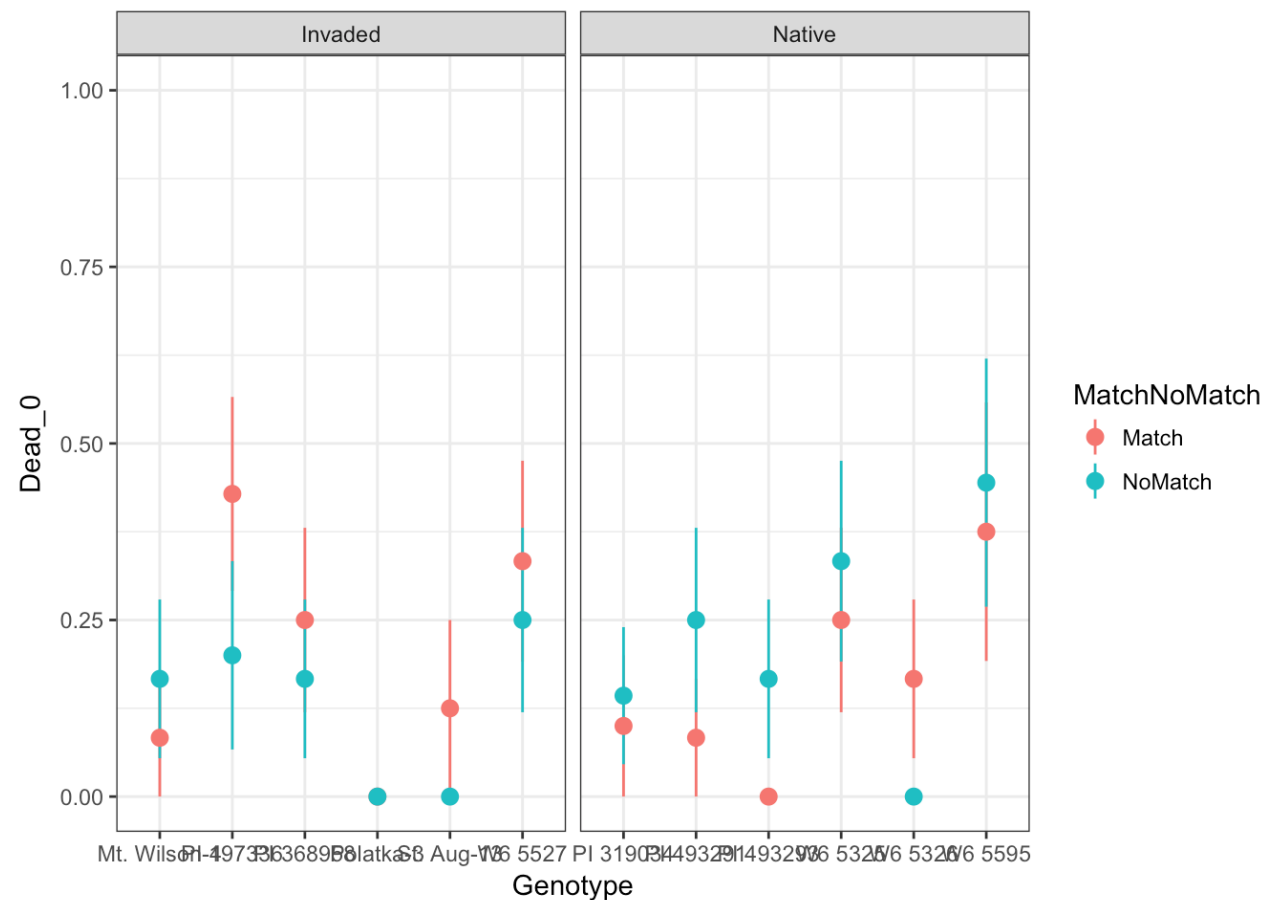
```
# Going back to trapping data to check for match x no match for mortality
```

```
# Create match variable
```

```
TrapMort <- within(TrapMort, MatchNoMatch <- ifelse(Range == "Native" & grepl("
PT", Treatment), "Match", ifelse(Range == "Invaded" & grepl("FL", Treatment), "
Match", "NoMatch")))
```

```
TrapMortSub <- subset(TrapMort, Treat == "Soil")
```

```
ggplot(TrapMortSub, aes(x = Genotype, y = Dead_0, colour = MatchNoMatch)) + sta
t_summary(fun.data = "mean_se") + coord_cartesian(ylim = c(0,1)) + theme_bw() +
facet_wrap(~ Range, scales = "free_x")
```

```
mod <- glm(as.factor(Dead_0) ~ MatchNoMatch * Range, family = binomial(link = "logit"), data = TrapMortSub)
anova(mod, test = "Chisq")
```

```
## 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			269	255.76	
## MatchNoMatch	1	0.02493	268	255.74	0.8745
## Range	1	0.00242	267	255.73	0.9608
## MatchNoMatch:Range	1	2.13596	266	253.60	0.1439

```
tt = emmeans(mod, ~ Range | MatchNoMatch)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      MatchNoMatch estimate      SE df z.ratio p.value
## Invaded - Native Match      0.4418328 0.4506021 Inf  0.981  0.3268
## Invaded - Native NoMatch    -0.4928071 0.4624031 Inf -1.066  0.2865
##
## Results are given on the log odds ratio (not the response) scale.
```

```
tt = emmeans(mod, ~ MatchNoMatch | Range)
dd = pairs(tt)
summary(dd, by = NULL)
```

```
## contrast      Range estimate      SE df z.ratio p.value
## Match - NoMatch Invaded  0.5291748 0.4631177 Inf  1.143  0.2532
## Match - NoMatch Native  -0.4054651 0.4498676 Inf -0.901  0.3674
##
## Results are given on the log odds ratio (not the response) scale.
```

```
# No Significance
```