

Biochar and Soil Microbial Inocula Effects on Plant Growth and C mineralization - with graphs

Ariane L. Peralta, 2017 Microbial Ecology Class

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Project Description:

Initial Setup

```
rm(list=ls())
setwd("~/GitHub/BGE_ME_EXPT")
se <- function(x, ...){sd(x, na.rm = TRUE)/sqrt(length(na.omit(x)))}
ci <- function(x, ...){1.96 * sd(x, na.rm = TRUE)}

# Code Dependencies
require("reshape")
```

```
## Loading required package: reshape
```

```
## Warning: package 'reshape' was built under R version 3.2.5
```

```
require("ggplot2")
```

```
## Loading required package: ggplot2
```

```
## Warning: package 'ggplot2' was built under R version 3.2.5
```

Input Data

```
data1 <- read.csv("../data/2017_BGE_ME_expt_DATA.csv", header=TRUE)
str(data1)
```

```
## 'data.frame':    60 obs. of  9 variables:
##  $ ID             : Factor w/ 60 levels "B0_C_P_R1","B0_C_P_R2",...: 10 11 12 34 35 36 58 59 60 22 ..
##  $ Biochar         : int  0 0 0 2 2 2 5 5 5 10 ...
##  $ Microbe         : Factor w/ 2 levels "Microbes","NoMicrobes": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Plant           : Factor w/ 2 levels "NoPlant","Plant": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Replicate       : Factor w/ 3 levels "rep1","rep2",...: 1 2 3 1 2 3 1 2 3 1 ...
##  $ Cmin            : num  15.4 17.9 16 18.2 14.7 ...
##  $ ShootMass_g     : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ RootMass_g      : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ PercentMoisture : num  9.5 23.7 25.9 180 32.3 ...
```

*#NOTE: all parametric tests were run without testing for assumptions to simplify
#code for the class - so the 'proper' way to run these stats is to test for
#normality and homogeneity of variances or modeling fitting approaches*

Data Analysis - Carbon Mineralization

```
# hyp testing and plot - 3-way ANOVA - all interactions
data.lm <- lm(Cmin~Biochar*Microbe*Plant, data=data1)
anova(data.lm)

## Analysis of Variance Table
##
## Response: Cmin
##
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Biochar      1  52.49   52.492    6.7381 0.012239 *
## Microbe      1  78.09   78.090   10.0239 0.002584 **
## Plant        1  19.26   19.255    2.4717 0.121980
## Biochar:Microbe  1   3.71    3.705    0.4756 0.493489
## Biochar:Plant   1   3.86    3.861    0.4957 0.484552
## Microbe:Plant   1   0.82    0.819    0.1051 0.747060
## Biochar:Microbe:Plant 1   5.55    5.549    0.7123 0.402531
## Residuals     52 405.10    7.790
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(data.lm)

##
## Call:
## lm(formula = Cmin ~ Biochar * Microbe * Plant, data = data1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3992  -1.2088  -0.1563   1.2563   5.7432
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    16.03311     1.03758   15.452  <2e-16
## Biochar        -0.08763     0.10087   -0.869   0.389
## MicrobeNoMicrobes -1.93277     1.46736   -1.317   0.194
## PlantPlant       0.25623     1.46736    0.175   0.862
## Biochar:MicrobeNoMicrobes -0.01557     0.14266   -0.109   0.913
## Biochar:PlantPlant -0.15616     0.14266   -1.095   0.279
## MicrobeNoMicrobes:PlantPlant -1.72738     2.07516   -0.832   0.409
## Biochar:MicrobeNoMicrobes:PlantPlant 0.17028     0.20175    0.844   0.403
##
## (Intercept)                ***
## Biochar
## MicrobeNoMicrobes
## PlantPlant
## Biochar:MicrobeNoMicrobes
## Biochar:PlantPlant
## MicrobeNoMicrobes:PlantPlant
## Biochar:MicrobeNoMicrobes:PlantPlant
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.791 on 52 degrees of freedom
```

```
## Multiple R-squared:  0.2879, Adjusted R-squared:  0.192
## F-statistic: 3.003 on 7 and 52 DF,  p-value: 0.01003
```

```
#only Biochar and Microbe main effects significant
```

```
data.lm2 <- lm(Cmin~Biochar+Microbe, data=data1)
anova(data.lm2)
```

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

```
##
```

```
## Response: Cmin
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Biochar    1  52.49   52.492    6.8267 0.011463 *
## Microbe    1  78.09   78.090   10.1556 0.002335 **
## Residuals 57 438.29    7.689
```

```
## ---
```

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

```
summary(data.lm2)
```

```
##
```

```
## Call:
```

```
## lm(formula = Cmin ~ Biochar + Microbe, data = data1)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -12.392  -1.038    0.127    1.454    6.305
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    15.90383     0.62754   25.343 < 2e-16 ***
## Biochar         -0.13092     0.05011   -2.613  0.01146 *
## MicrobeNoMicrobes -2.28167     0.71598   -3.187  0.00234 **
```

```
## ---
```

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

```
##
```

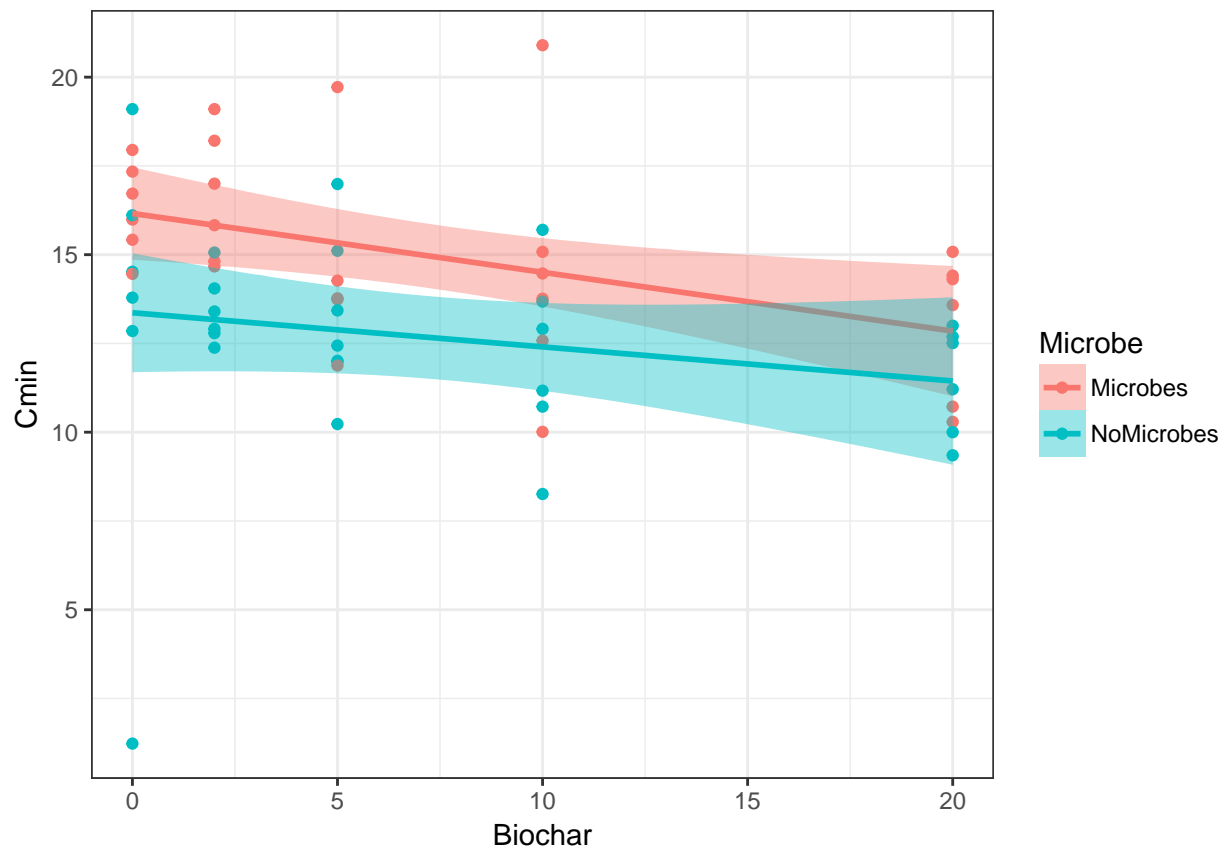
```
## Residual standard error: 2.773 on 57 degrees of freedom
```

```
## Multiple R-squared:  0.2295, Adjusted R-squared:  0.2025
```

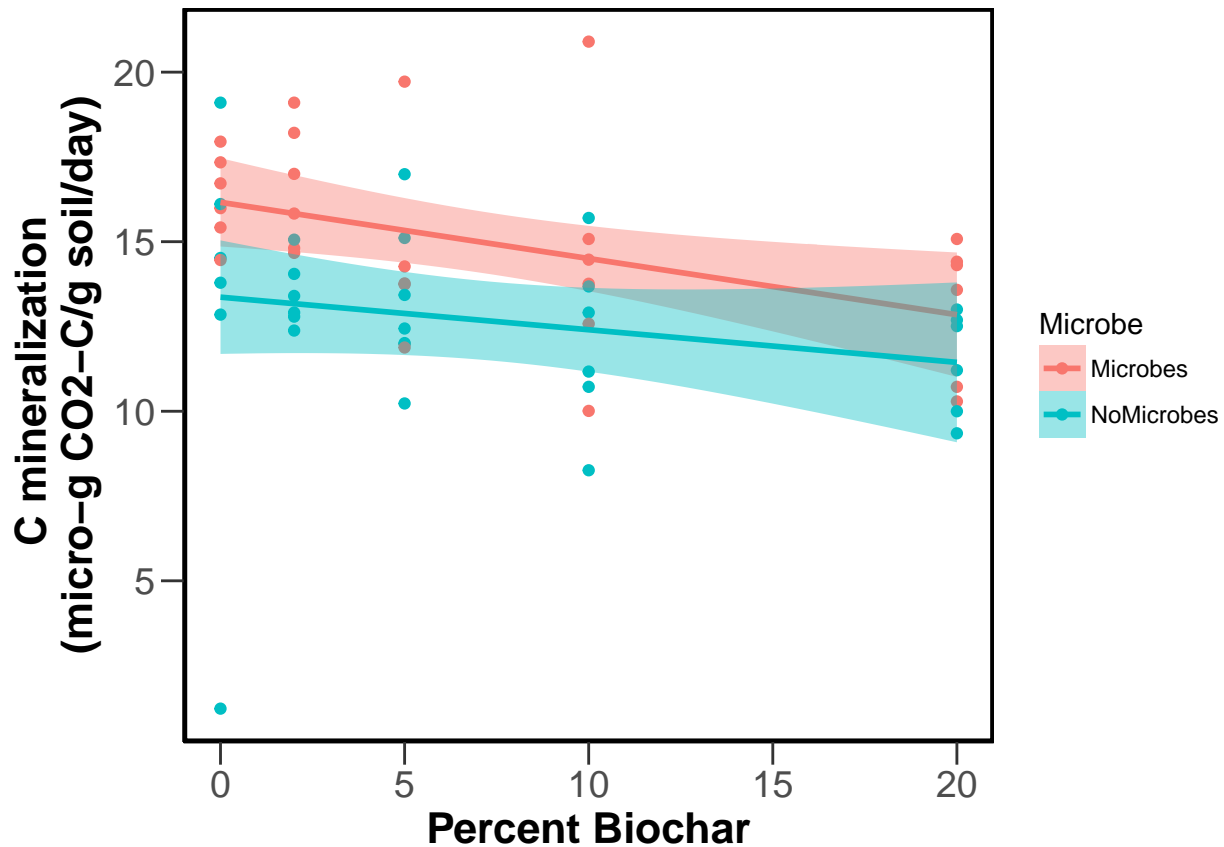
```
## F-statistic: 8.491 on 2 and 57 DF,  p-value: 0.000592
```

```
#graphing C mineralization by microbes only
```

```
p <- ggplot(data1, aes(x=Biochar, y=Cmin, color=Microbe))+geom_point()
p1=p+geom_smooth(method="lm",aes(fill=Microbe))
p1 + theme_bw()
```



```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.l
```



```
ggsave("../figures/Cmin.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA, dpi=300)
```

```
## Saving 6.5 x 4.5 in image
```

Data Analysis - Shoot Biomass

```
data.lm <- lm(ShootMass_g~Biochar*Microbe, data=data1)
anova(data.lm)
```

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

```
##
```

```
## Response: ShootMass_g
```

```
##           Df    Sum Sq Mean Sq F value    Pr(>F)
## Biochar      1 0.011717  0.011717   1.4560 0.238440
## Microbe      1 0.064218  0.064218   7.9801 0.008964 **
## Biochar:Microbe 1 0.018520  0.018520   2.3014 0.141325
## Residuals    26 0.209230  0.008047
```

```
## ---
```

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

```
summary(data.lm)
```

```
##
```

```
## Call:
```

```
## lm(formula = ShootMass_g ~ Biochar * Microbe, data = data1)
```

```
##
```

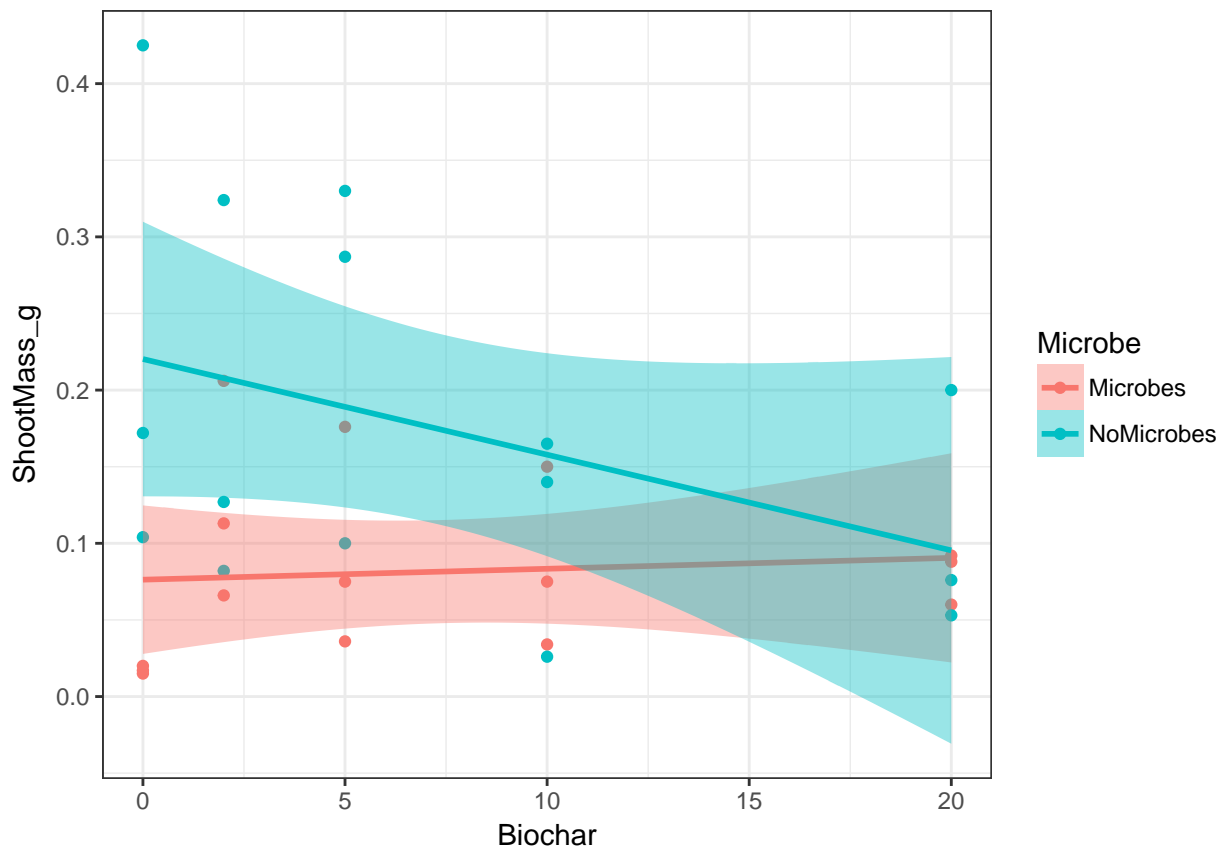
```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.13183 -0.05455 -0.01476  0.05879  0.20473
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0762675   0.0333478    2.287  0.03058 *
## Biochar           0.0007116   0.0032421    0.219  0.82798
## MicrobeNoMicrobes  0.1440047   0.0471609    3.053  0.00517 **
## Biochar:MicrobeNoMicrobes -0.0069556  0.0045850   -1.517  0.14132
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08971 on 26 degrees of freedom
## (30 observations deleted due to missingness)
## Multiple R-squared:  0.311, Adjusted R-squared:  0.2315
## F-statistic: 3.912 on 3 and 26 DF,  p-value: 0.01976
```

```
#graphing shoot biomass microbes x biochar
```

```
p <- ggplot(data1, aes(x=Biochar, y=ShootMass_g, color=Microbe))+geom_point()
p1=p+geom_smooth(method="lm",aes(fill=Microbe))
p1 + theme_bw()
```

```
## Warning: Removed 30 rows containing non-finite values (stat_smooth).
```

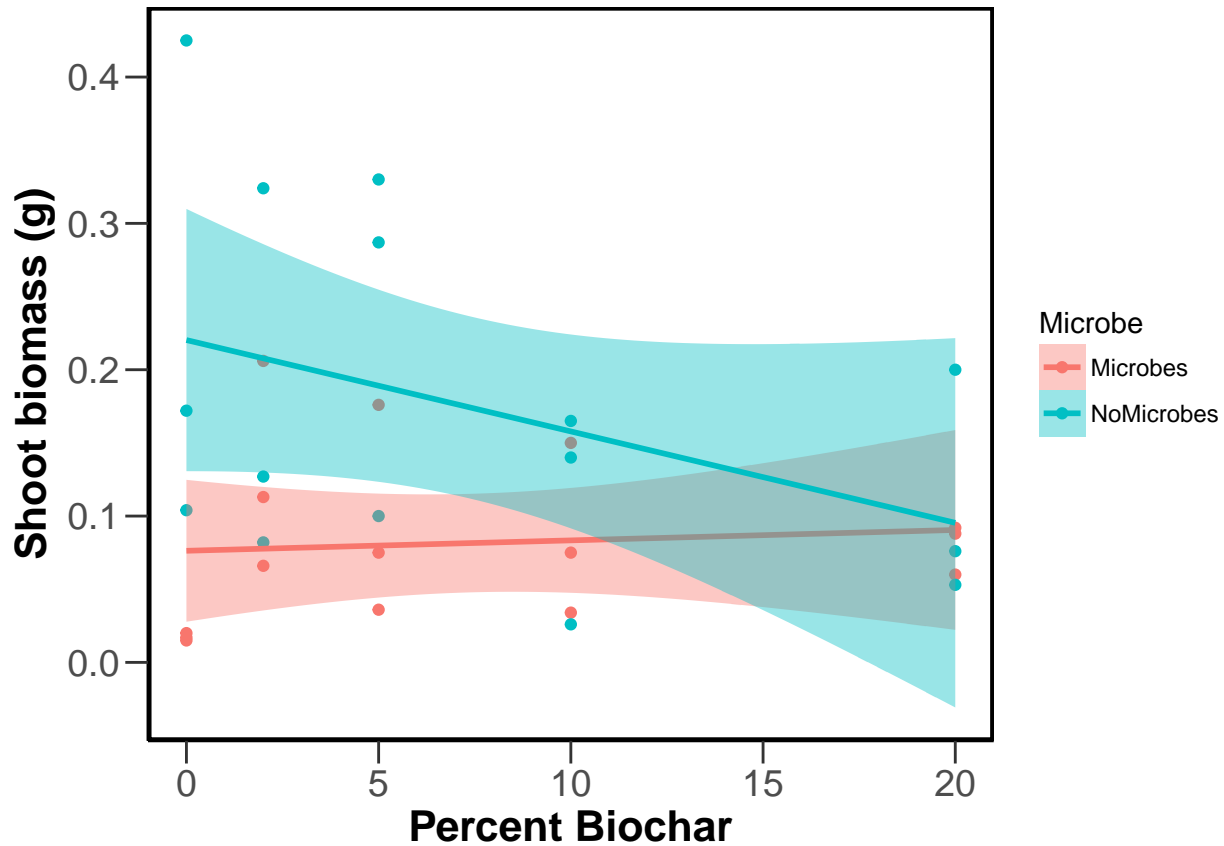
```
## Warning: Removed 30 rows containing missing values (geom_point).
```



```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.lin
```

```
## Warning: Removed 30 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 30 rows containing missing values (geom_point).
```



```
ggsave("../figures/Shoot.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA, c
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 30 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 30 rows containing missing values (geom_point).
```

Data Analysis - Root Biomass

```
data.lm <- lm(RootMass_g~Biochar*Microbe, data=data1)
anova(data.lm)
```

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

```
##
```

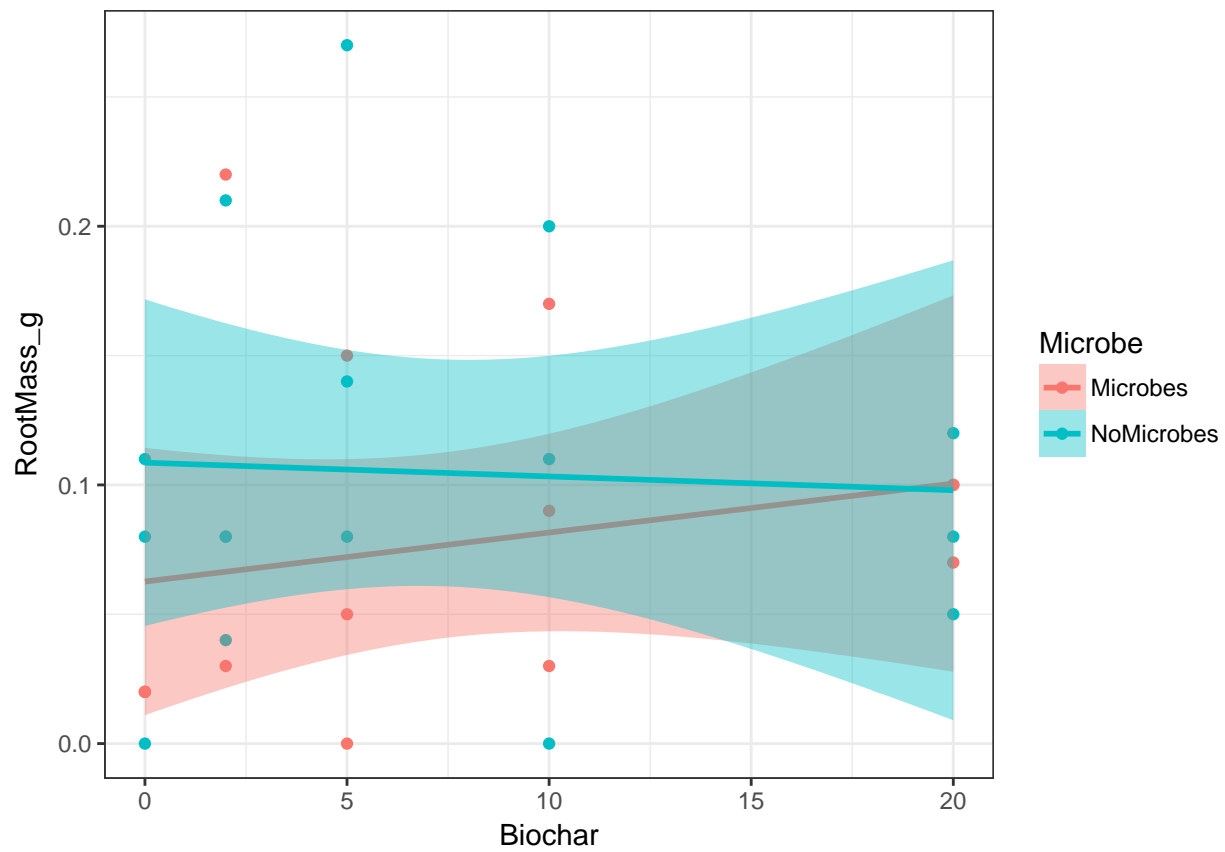
```
## Response: RootMass_g
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Biochar	1	0.000709	0.0007091	0.1374	0.7138
Microbe	1	0.005880	0.0058800	1.1397	0.2955
Biochar:Microbe	1	0.002255	0.0022545	0.4370	0.5144
Residuals	26	0.134143	0.0051593		

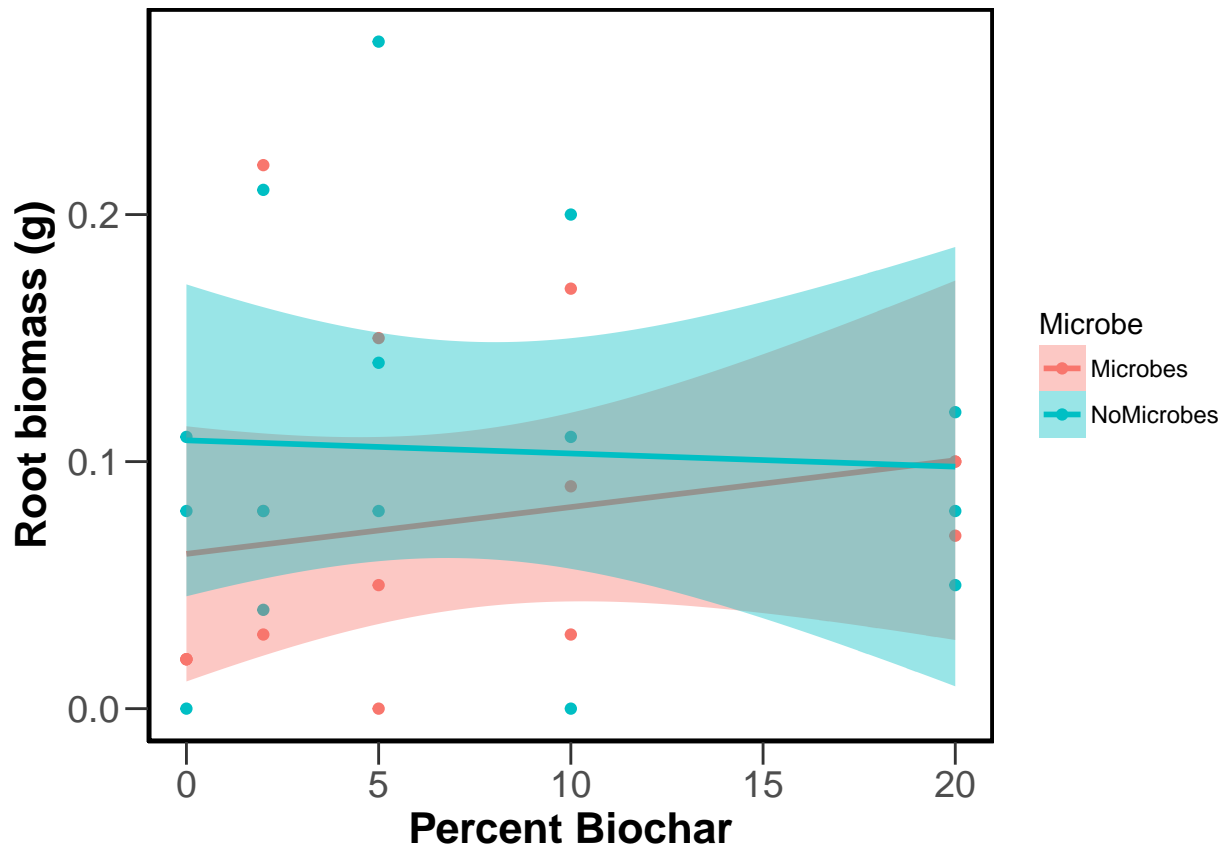
```
summary(data.lm)
```

```
##
## Call:
## lm(formula = RootMass_g ~ Biochar * Microbe, data = data1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.10861 -0.04265 -0.02004  0.01993  0.16405
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.062652   0.026702   2.346   0.0269 *
## Biochar          0.001894   0.002596   0.730   0.4722
## MicrobeNoMicrobes 0.045959   0.037762   1.217   0.2345
## Biochar:MicrobeNoMicrobes -0.002427  0.003671  -0.661   0.5144
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07183 on 26 degrees of freedom
## (30 observations deleted due to missingness)
## Multiple R-squared:  0.06185,    Adjusted R-squared:  -0.0464
## F-statistic: 0.5714 on 3 and 26 DF,  p-value: 0.6389
#graphing root biomass microbes x biochar
p <- ggplot(data1, aes(x=Biochar, y=RootMass_g, color=Microbe))+geom_point()
p1=p+geom_smooth(method="lm",aes(fill=Microbe))
p1 + theme_bw()

## Warning: Removed 30 rows containing non-finite values (stat_smooth).
## Warning: Removed 30 rows containing missing values (geom_point).
```

```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.lin  
## Warning: Removed 30 rows containing non-finite values (stat_smooth).  
## Warning: Removed 30 rows containing missing values (geom_point).
```



```
ggsave("../figures/Root.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA, dpi=300)
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 30 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 30 rows containing missing values (geom_point).
```

Data Analysis - testing moisture impact on shoot biomass

```
#testing moisture impact on shoot biomass - MICROBES addition only
attach(data1)
newdata <- data1[ which(Microbe=='Microbes'),]
detach(data1)
data.lm <- lm(ShootMass_g~PercentMoisture, data=newdata)
summary(data.lm)
```

```
##
```

```
## Call:
```

```
## lm(formula = ShootMass_g ~ PercentMoisture, data = newdata)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -0.057649 -0.019197  0.007484  0.023140  0.061372
```

```
##
```

```
## Coefficients:
```

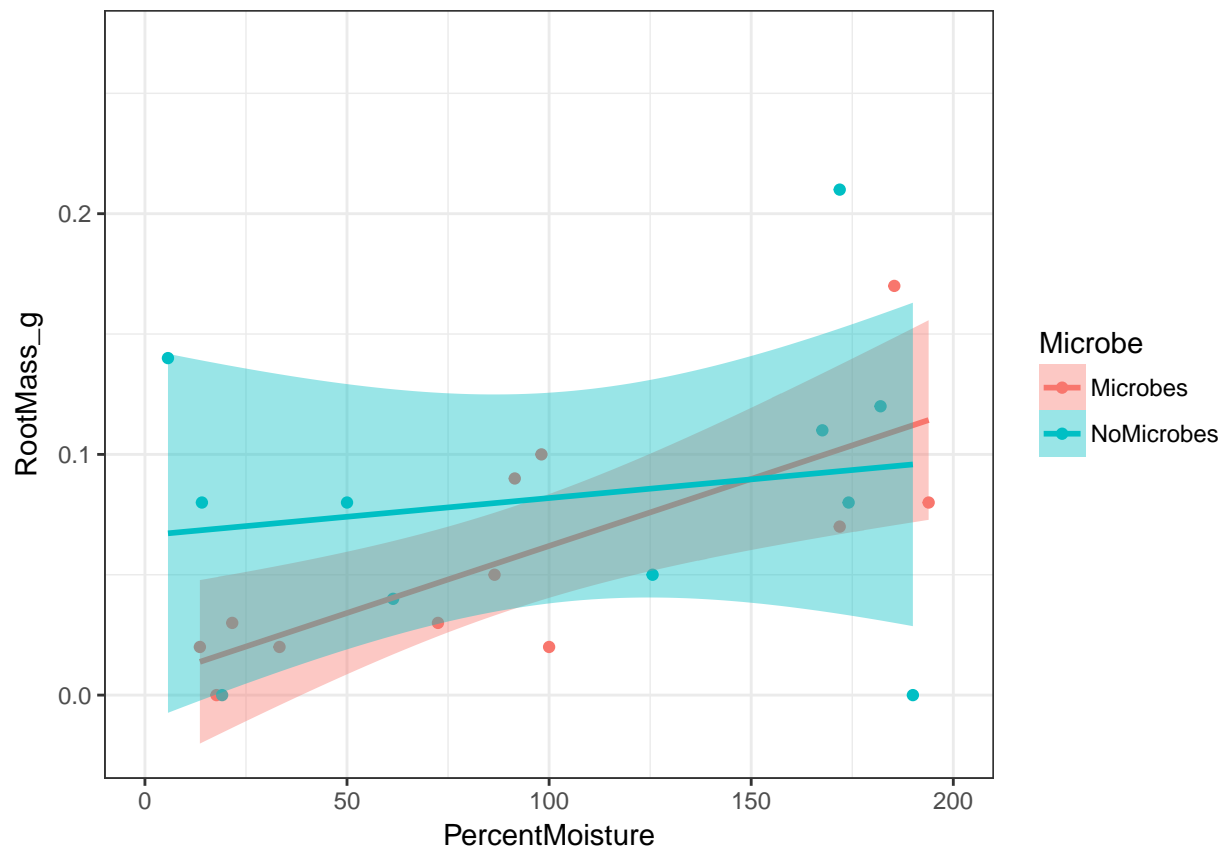
```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0122631  0.0178344   0.688 0.503781
## PercentMoisture 0.0006039  0.0001308   4.615 0.000484 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03731 on 13 degrees of freedom
## (15 observations deleted due to missingness)
## Multiple R-squared:  0.621, Adjusted R-squared:  0.5918
## F-statistic: 21.3 on 1 and 13 DF, p-value: 0.0004841

#testing moisture impact on shoot biomass - NO microbe addition only
attach(data1)
newdata2 <- data1[ which(Microbe=='NoMicrobes'),]
detach(data1)
data.lm2 <- lm(ShootMass_g~PercentMoisture, data=newdata2)
summary(data.lm2)

##
## Call:
## lm(formula = ShootMass_g ~ PercentMoisture, data = newdata2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.15279 -0.06360 -0.04134  0.07873  0.22849
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.1217974  0.0604919   2.013  0.0652 .
## PercentMoisture 0.0003932  0.0003942   0.997  0.3367
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.117 on 13 degrees of freedom
## (15 observations deleted due to missingness)
## Multiple R-squared:  0.07109, Adjusted R-squared: -0.0003619
## F-statistic: 0.9949 on 1 and 13 DF, p-value: 0.3367

#need to graph root biomass on y-axis and moisture on x-axis by microbe treatment
p <- ggplot(data1, aes(x=PercentMoisture, y=RootMass_g, color=Microbe))+geom_point()
p1=p+geom_smooth(method="lm",aes(fill=Microbe))
p1 + theme_bw() + xlim(0,200)

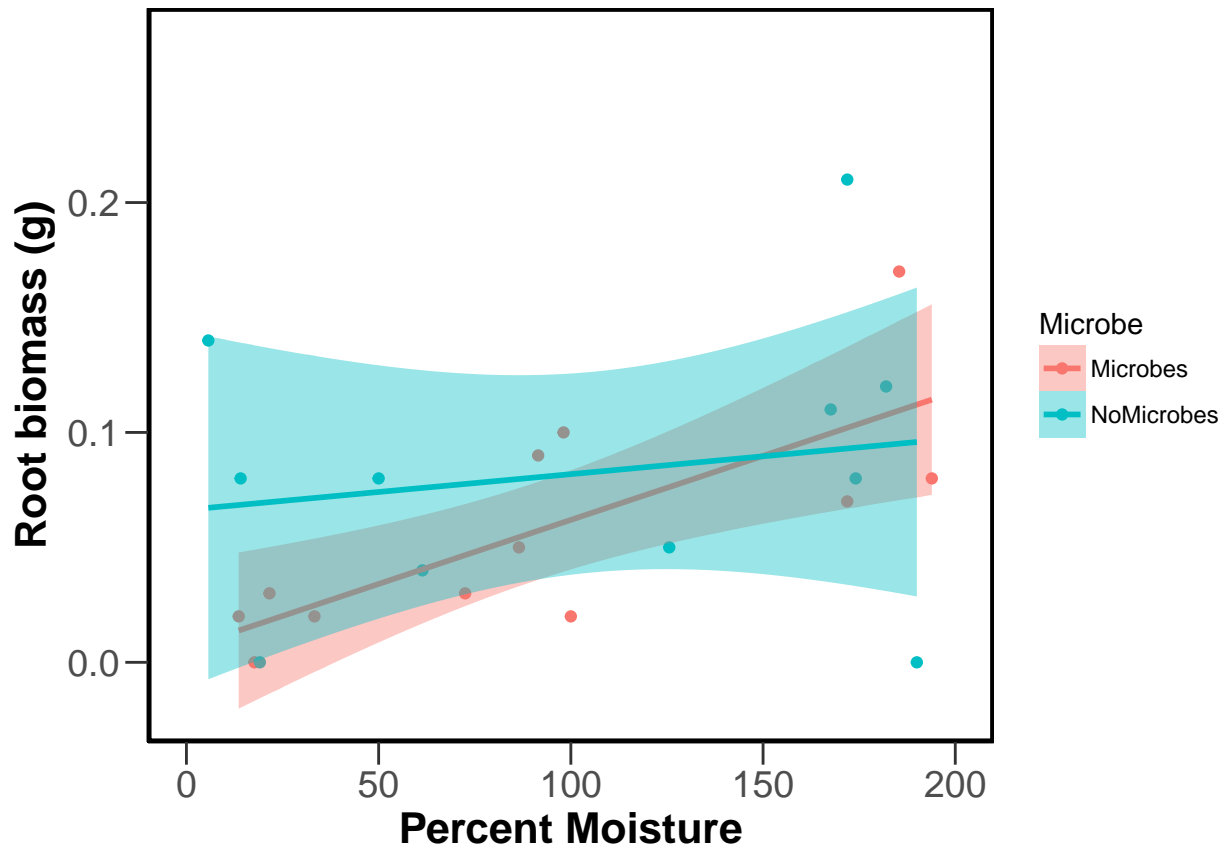
## Warning: Removed 37 rows containing non-finite values (stat_smooth).
## Warning: Removed 37 rows containing missing values (geom_point).
```



```
p1 + theme_bw() + xlim(0,200) + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
```

```
## Warning: Removed 37 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 37 rows containing missing values (geom_point).
```



```
ggsave("../figures/Moisture-Root.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 37 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 37 rows containing missing values (geom_point).
```