

Curry Co. SOD Analysis

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R setup and libraries

Reading and manipulating data

```
SODSites <- read_xlsx("BasicData.xlsx", 1)
SODSite.ord <- SODSites[-c(31),,drop=F] #removing HD-4331 as it skews results strongly

# Subsetting data
AllSites <- SODSites[-c(76, 78, 79, 82, 83, 84, 88, 97, 98, 99),,drop=F]
#removing HD-4376, 4378, 4379, 4382, 4383, 4384, 4388, 4397, 4398, 4399 as these sites were measured before and after treatment (removing treated data). Removing these duplicate sites to a data subset for separate analysis.
AllSites <- subset(AllSites, AllSites$Lineage != "U") #removing uninfested sites
AllSites$TrtBin <- as.factor(AllSites$TrtBin)

NA1 <- subset(AllSites, AllSites$Lineage == "NA1")

AllSeeds <- read_xlsx("BasicData.xlsx", 2)
AllSeeds <- column_to_rownames(AllSeeds, var = "New Site")
AllSeeds <- AllSeeds[-11] #removing CE as it skews results strongly
AllSeeds <- AllSeeds[-c(31),,drop=F] #removing HD-4331 as it skews results strongly

AllFire <- read_xlsx("BasicData.xlsx", 3)
AllFire$RX <- as.factor(AllFire$RX)

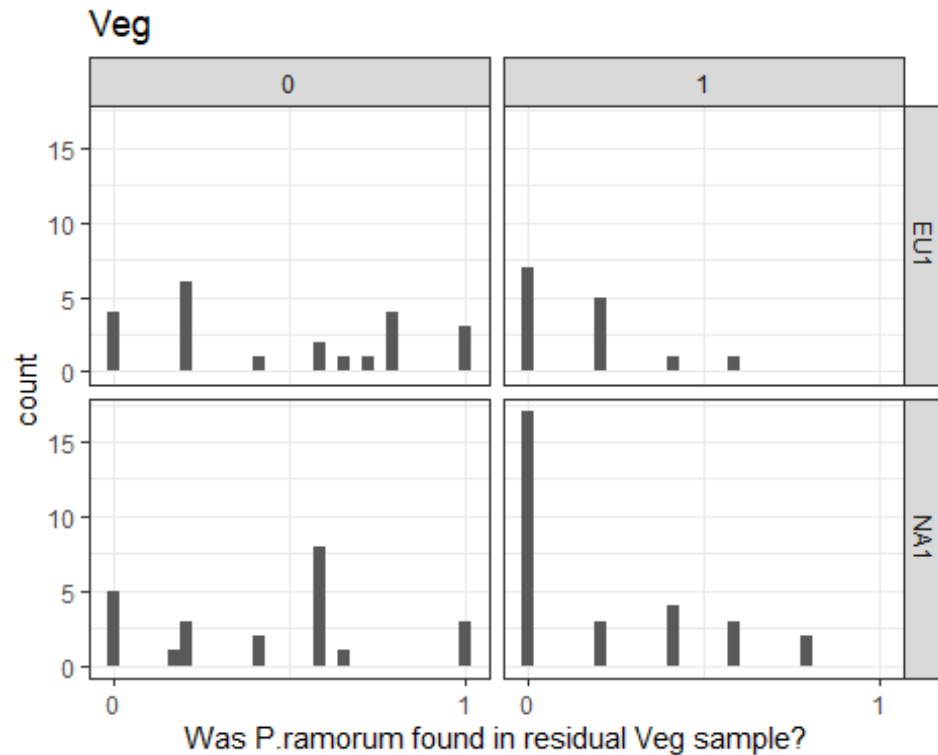
EU1wide <- read_xlsx("BasicData.xlsx", 4)
EU1long <- read_xlsx("BasicData.xlsx", 5)
```

Visualizing raw data

```
ggplot(AllSites, aes(x=x)) +
  geom_histogram(aes(x = VegProp, y = stat(count))) +
  scale_x_continuous(name = "Was P.ramorum found in residual Veg sample?",
    breaks = seq(0, 1)) +
  facet_grid(Lineage ~ TrtBin) +
```

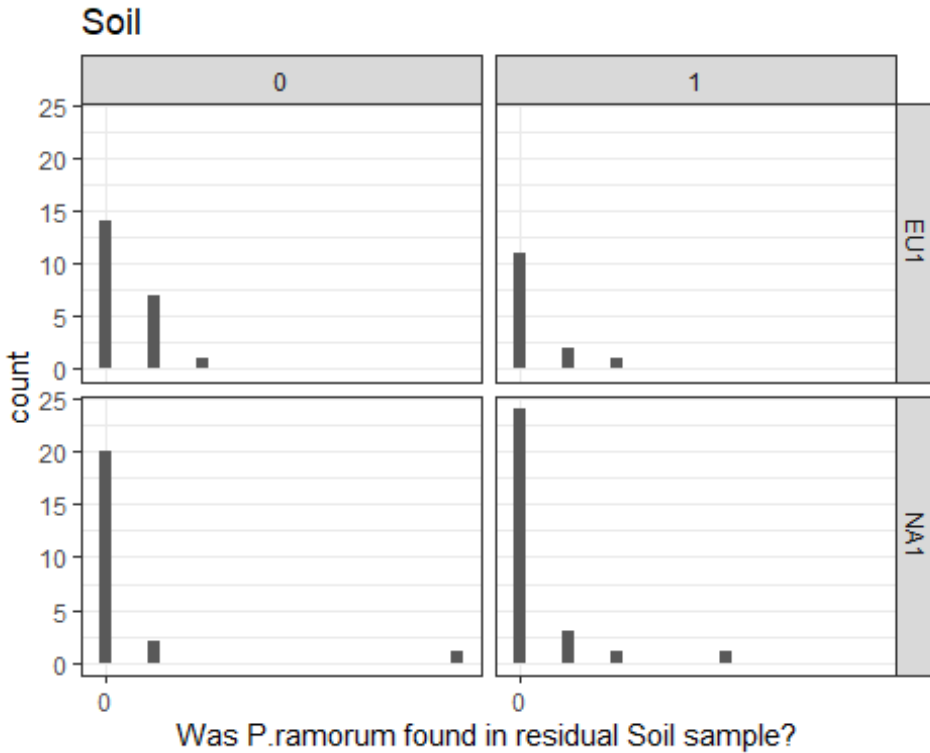
```
labs(title = "Veg") +
theme_bw()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
ggplot(AllSites, aes(x=x)) +
  geom_histogram( aes(x = SoilProp, y = stat(count))) +
  scale_x_continuous(name = "Was P.ramorum found in residual Soil sample?",
breaks = seq(0, 1)) +
  facet_grid(Lineage ~ TrtBin) +
  labs(title = "Soil") +
  theme_bw()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

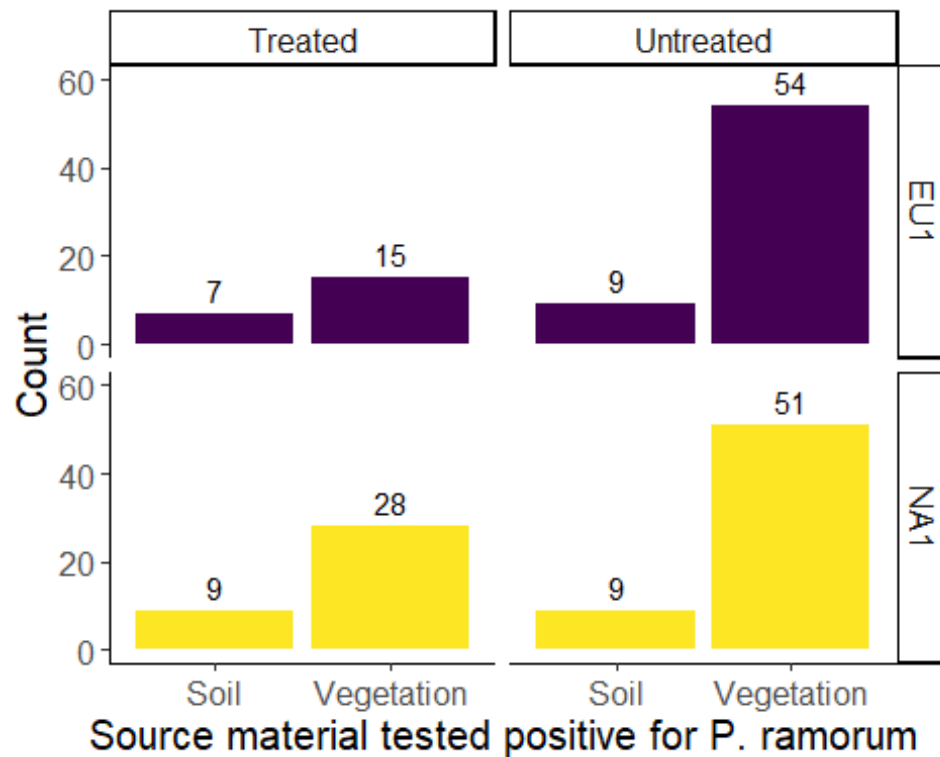


```

Trt <- c(rep("Untreated", 4), rep("Treated", 4))
Lin <- c("EU1", "EU1", "NA1", "NA1", "EU1", "EU1", "NA1", "NA1")
Tis <-
c("Vegetation", "Soil", "Vegetation", "Soil", "Vegetation", "Soil", "Vegetation", "S
oil")
Count <- c(54, 9, 51, 9, 15, 7, 28, 9)
df <- data.frame(Trt, Lin, Tis, Count)

ggplot(df, aes(x=Tis, y=Count, fill=Lin))+
  geom_bar(stat="identity", position="dodge")+
  scale_fill_discrete(name="Lineage", labels=c("EU1", "NA1"))+
  scale_fill_viridis_d() +
  theme_classic()+
  theme(legend.position="none", text = element_text(size=15))+
  xlab("Source material tested positive for P. ramorum")+
  ylab("Count")+
  ylim(0, 60)+
  geom_text(aes(label = Count), vjust = -0.5)+
  facet_grid(Lin~Trt)

```



#This visualization includes all 100 sites sampled, including uninfested sites, and EU1 sites that were sampled before and after treatment.

Vegetation

EU1 Repeated Measurement

```
V3 <- lme(VegProp ~ TrtBin, random = ~1|Plot, data = EU1long)
```

```
anova(V3)
```

```
##               numDF denDF   F-value p-value
## (Intercept)      1     9 16.286969  0.0029
## TrtBin           1     9  8.684625  0.0163
```

```
summary(V3)
```

```
## Linear mixed-effects model fit by REML
## Data: EU1long
##      AIC      BIC    logLik
## 24.68194 28.24342 -8.340968
##
## Random effects:
## Formula: ~1 | Plot
##      (Intercept) Residual
## StdDev:  0.08728716 0.3273545
##
```

```

## Fixed effects: VegProp ~ TrtBin
##               Value Std.Error DF   t-value p-value
## (Intercept)  0.5314286 0.1071354   9  4.960343  0.0008
## TrtBin       -0.4314286 0.1463974   9 -2.946969  0.0163
## Correlation:
##      (Intr)
## TrtBin -0.683
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.5033354 -0.3755643 -0.2234416  0.2972945  2.5651355
##
## Number of Observations: 20
## Number of Groups: 10

DTV <-array(c(1,8,0,1),
            dim=c(2, 2),
            dimnames=list(
              Time2=c("ThenPos", "ThenNeg"),
              Time1=c("FirstPos", "FirstNeg"))
            )

mcnemar.test(DTV, y=NULL, correct = FALSE)

##
## McNemar's Chi-squared test
##
## data:  DTV
## McNemar's chi-squared = 8, df = 1, p-value = 0.004678

chisq.test(EU1long$VegProp, EU1long$TrtBin)

## Warning in chisq.test(EU1long$VegProp, EU1long$TrtBin): Chi-squared
## approximation may be incorrect

##
## Pearson's Chi-squared test
##
## data:  EU1long$VegProp and EU1long$TrtBin
## X-squared = 13.733, df = 5, p-value = 0.0174

#correlations
VC3 <- cor.test(EU1wide$VegPre, EU1wide$VegPost, method=c("pearson",
"kendall", "spearman"))
VC3

##
## Pearson's product-moment correlation
##
## data:  EU1wide$VegPre and EU1wide$VegPost
## t = 0.18975, df = 8, p-value = 0.8542

```

```
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.5874476 0.6683936
## sample estimates:
##      cor
## 0.06693682
```

NA1 Veg Wildfire

```
V2 <- lm(VegProp ~ RX, data = AllFire)
```

```
anova(V2)
```

```
## Analysis of Variance Table
##
## Response: VegProp
##           Df Sum Sq Mean Sq F value    Pr(>F)
## RX           3 1.0706  0.35687    4.1361 0.01095 *
## Residuals  48 4.1416  0.08628
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(V2)
```

```
##
## Call:
## lm(formula = VegProp ~ RX, data = AllFire)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.43623 -0.24000 -0.04444  0.16377  0.56377
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.43623     0.06125   7.122 4.78e-09 ***
## RX1         -0.19623     0.09749  -2.013  0.0498 *
## RX2         -0.11623     0.14494  -0.802  0.4266
## RX3         -0.39179     0.11549  -3.392  0.0014 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2937 on 48 degrees of freedom
## Multiple R-squared:  0.2054, Adjusted R-squared:  0.1557
## F-statistic: 4.136 on 3 and 48 DF, p-value: 0.01095
```

```
summ(V2)
```

```
## MODEL INFO:
## Observations: 52
## Dependent Variable: VegProp
## Type: OLS linear regression
##
```

```
## MODEL FIT:
## F(3,48) = 4.14, p = 0.01
## R2 = 0.21
## Adj. R2 = 0.16
##
## Standard errors: OLS
## -----
##               Est.   S.E.   t val.   p
## -----
## (Intercept)    0.44   0.06    7.12   0.00
## RX1            -0.20   0.10   -2.01   0.05
## RX2            -0.12   0.14   -0.80   0.43
## RX3            -0.39   0.12   -3.39   0.00
## -----

# Contrast statement
levels(AllFire$RX)

## [1] "0" "1" "2" "3"

# 0 - No Wildfire or Treatment
# 1 - Only Treatment
# 2 - Only Wildfire
# 3 - Both Wildfire and Treatment

#Least Squares Means
V2.lsm <- lsmeans(V2, ~RX, adjst="tukey")
V2.lsm

##   RX lsmean      SE df lower.CL upper.CL
## 0  0.4362 0.0612 48   0.3131   0.559
## 1  0.2400 0.0758 48   0.0875   0.392
## 2  0.3200 0.1314 48   0.0559   0.584
## 3  0.0444 0.0979 48  -0.1524   0.241
##
## Confidence level used: 0.95

V2LSM <- as.data.frame(V2.lsm)

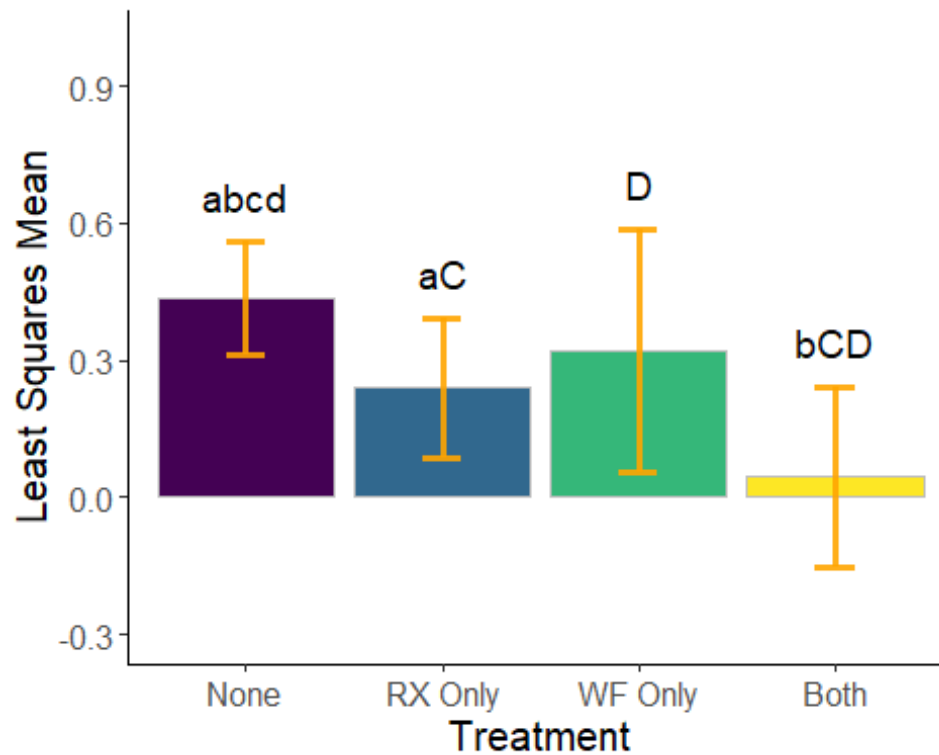
#Least Squares Means visualization
offset=5      # offsets for mean letters

ggplot(V2LSM,aes(x=RX,y=lsmean, fill=RX))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() + theme_classic()+
  scale_x_discrete(name="Treatment", labels=c("0" = "None", "1" = "RX
Only","2" = "WF Only", "3" = "Both"))+
  scale_y_continuous("Least Squares Mean", breaks = c(-0.3, 0, 0.3, 0.6,
0.9), limits = c(-0.3, 1))+
  geom_errorbar(aes(x=RX, ymin=lower.CL, ymax=upper.CL), width=0.2,
```

```

colour="orange", alpha=0.9, size=1.3)+
  theme(legend.position="none", text = element_text(size=15),
        strip.background = element_blank(),
        strip.text = element_blank())+
  geom_text(aes(x=RX, y=0.1+V2LSM$upper.CL,label=c("abcd", "aC", "D",
"bCD")),size = 5,position=position_dodge(.5))

```



#Contrasts

```

ConV2 <- contrast(V2.lsm, list (
  "0 v. 1" = c(-1, 1, 0, 0), #difference is RX
  "2 v. 3" = c(0, 0, -1, 1), #difference is RX
  "1 v. 2" = c(0, 1, -1, 0), #difference is both
  "3 v. 0" = c(-1, 0, 0, 1), #difference is both
  "0 v. 2" = c(-1, 0, 1, 0), #difference is WF; NS b/c small n & wide CI?
  "1 v. 3" = c(0, -1, 0, 1), #difference is WF
  "1&3 v. 2" = c(0, .5, -1, .5), #both RX to WF w/o RX
  "1&3 v. 0" = c(-1, .5, 0, .5), #both RX to noWF or RX
  "2&3 v. 0" = c(-1, 0, .5, .5), #both WF to noWF or RX
  "2&3 v. 1" = c(0, -1, .5, .5) #both WF to RX w/o WF
))

```

ConV2

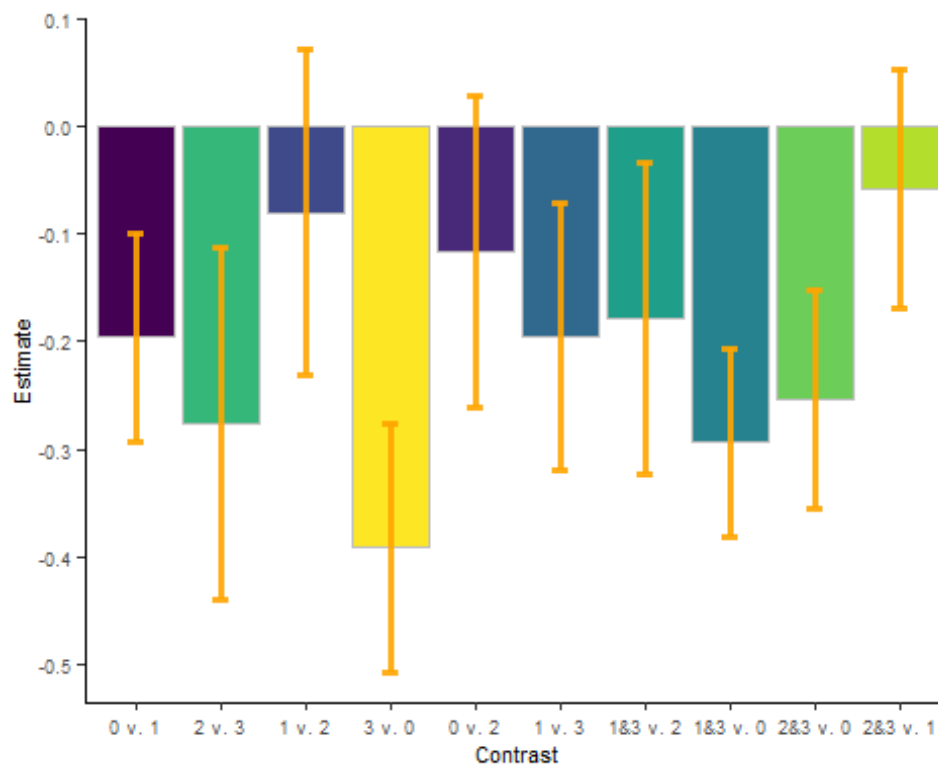
##	contrast	estimate	SE	df	t.ratio	p.value
##	0 v. 1	-0.1962	0.0975	48	-2.013	0.0498
##	2 v. 3	-0.2756	0.1638	48	-1.682	0.0991
##	1 v. 2	-0.0800	0.1517	48	-0.527	0.6003
##	3 v. 0	-0.3918	0.1155	48	-3.392	0.0014


```
## 0 v. 2    -0.1162 0.1449 48 -0.802  0.4266
## 1 v. 3    -0.1956 0.1239 48 -1.579  0.1209
## 1&3 v. 2  -0.1778 0.1452 48 -1.224  0.2269
## 1&3 v. 0  -0.2940 0.0871 48 -3.376  0.0015
## 2&3 v. 0  -0.2540 0.1023 48 -2.483  0.0166
## 2&3 v. 1  -0.0578 0.1116 48 -0.518  0.6072
```

```
CONV2 <- as.data.frame(Conv2)
```

```
#Contrasts visualization
```

```
ggplot(CONV2,aes(x=contrast,y=estimate, fill=contrast))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() + theme_classic()+
  theme(legend.position="none", text = element_text(size=8))+
  scale_x_discrete(name = "Contrast", limits=c("0 v. 1", "2 v. 3", "1 v. 2", "3
v. 0", "0 v. 2", "1 v. 3", "1&3 v. 2", "1&3 v. 0", "2&3 v. 0", "2&3 v. 1"))+
  ylab("Estimate")+
  geom_errorbar(aes(x=contrast, ymin=estimate-SE, ymax=estimate+SE),
width=0.2, colour="orange", alpha=0.9, size=1.3)
```



```
#Correlations of random effects not included in the model
```

```
VC2 <- cor.test(AllFire$VegProp, AllFire$TotalTO, method=c("pearson",
"kendall", "spearman"))
VC22 <- cor.test(AllFire$VegProp, AllFire$SoilProp, method=c("pearson",
"kendall", "spearman"))
```

```
VC2
```

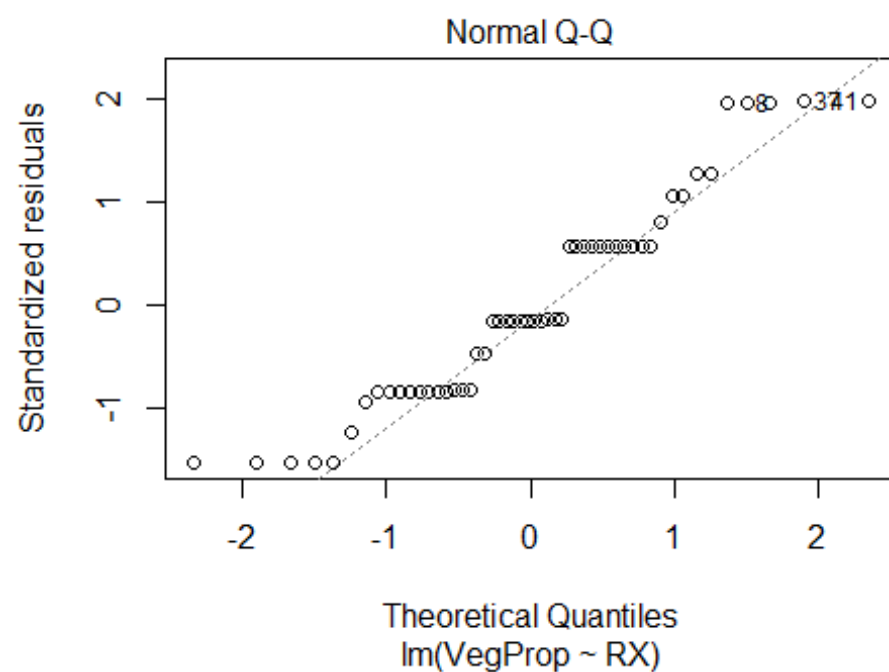
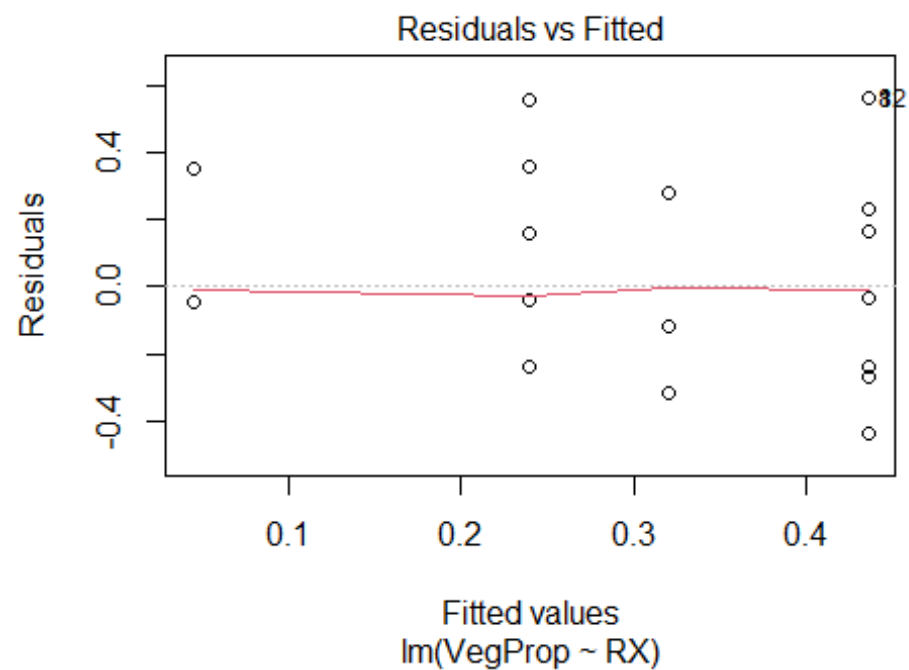
```
##  
## Pearson's product-moment correlation  
##  
## data: AllFire$VegProp and AllFire$TotalTO  
## t = 1.093, df = 50, p-value = 0.2796  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1253661 0.4086259  
## sample estimates:  
## cor  
## 0.1527605
```

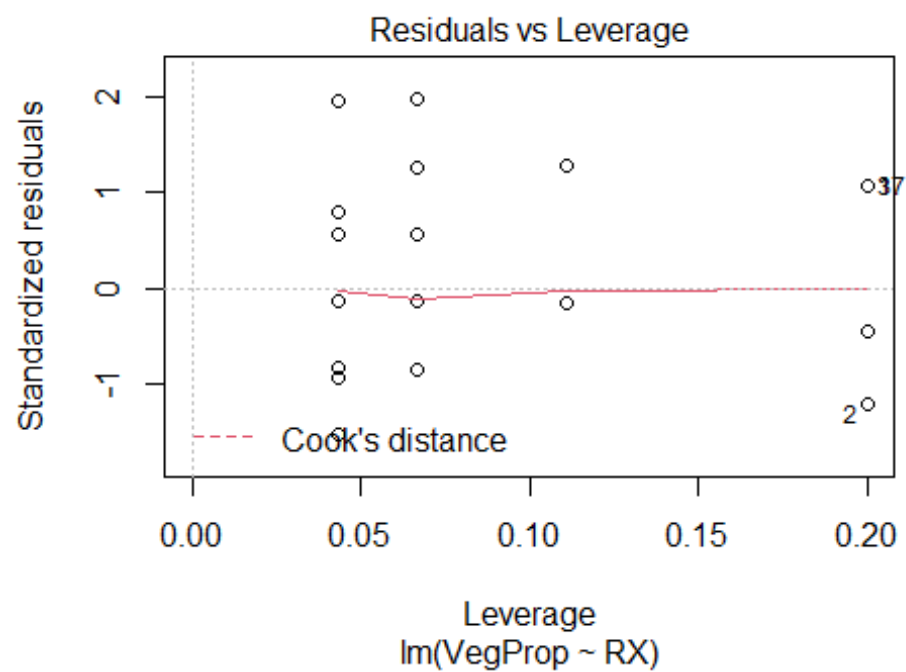
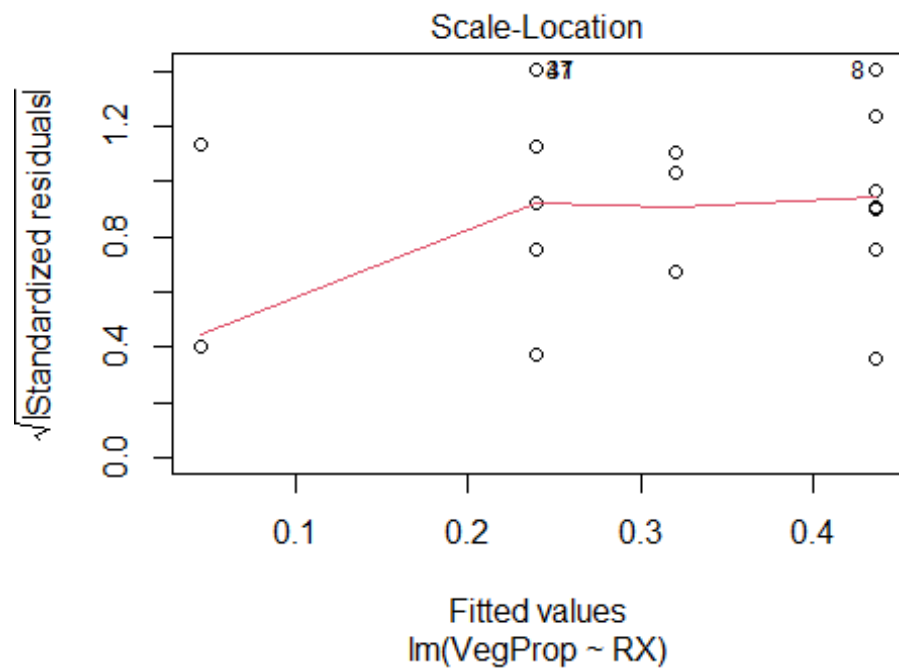
VC22 *#correlation between soil and veg!*

```
##  
## Pearson's product-moment correlation  
##  
## data: AllFire$VegProp and AllFire$SoilProp  
## t = 3.2198, df = 50, p-value = 0.002256  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.1595480 0.6174743  
## sample estimates:  
## cor  
## 0.4144049
```

NA1 Veg Wildfire Assumptions

plot(V2)





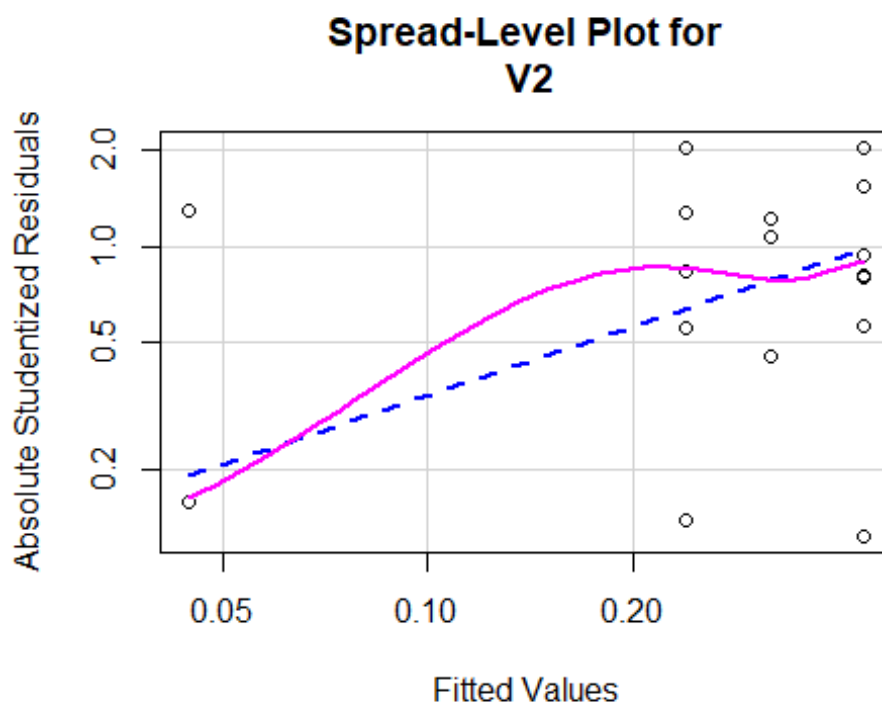
```
gvlma(V2)
```

```
##
```

```
## Call:
```

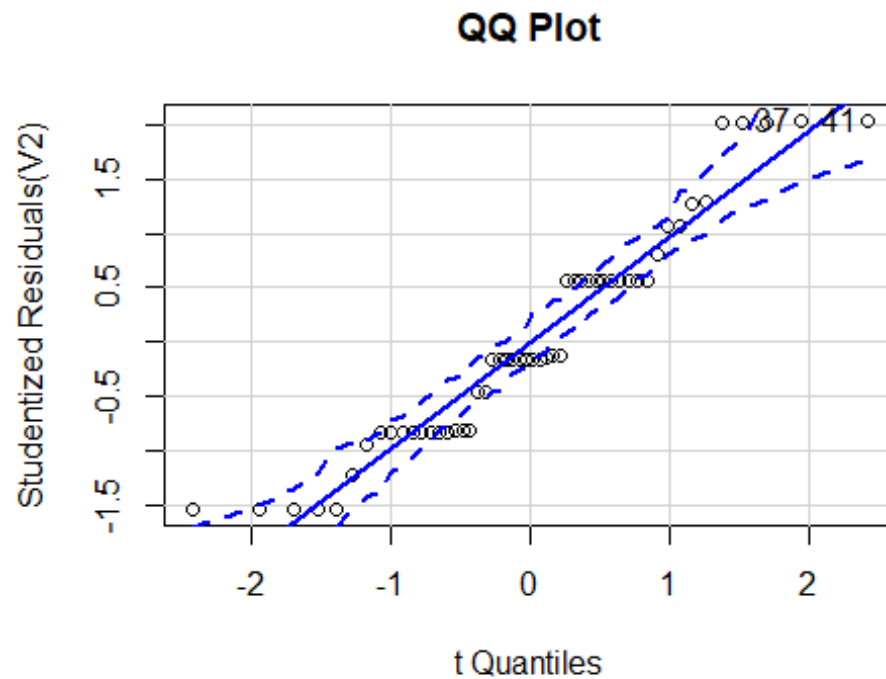
```
## lm(formula = VegProp ~ RX, data = AllFire)
##
## Coefficients:
## (Intercept)      RX1      RX2      RX3
##      0.4362     -0.1962     -0.1162     -0.3918
##
## ASSESSMENT OF THE LINEAR MODEL ASSUMPTIONS
## USING THE GLOBAL TEST ON 4 DEGREES-OF-FREEDOM:
## Level of Significance = 0.05
##
## Call:
## gvlma(x = V2)
##
##              Value p-value      Decision
## Global Stat      3.127e+00  0.5368 Assumptions acceptable.
## Skewness         1.354e+00  0.2445 Assumptions acceptable.
## Kurtosis         8.049e-01  0.3696 Assumptions acceptable.
## Link Function    -6.622e-16  1.0000 Assumptions acceptable.
## Heteroscedasticity 9.674e-01  0.3253 Assumptions acceptable.

#constant variance
spreadLevelPlot(V2)
```



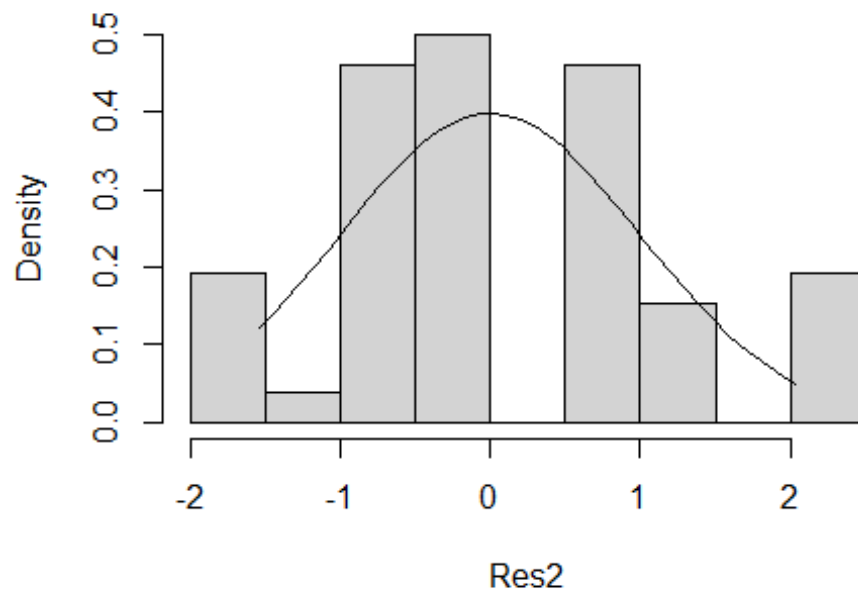
```
##
## Suggested power transformation: 0.2873349
```

```
#normality of residuals
Resq2 <- qqPlot(V2, main="QQ Plot")
```



```
Res2 <- studres(V2)
hist(Res2, freq = FALSE,
     main="Distribution of Studentized Residuals")
xfit2 <- seq(min(Res2), max(Res2), length = 40)
yfit2 <- dnorm(xfit2)
lines(xfit2, yfit2)
```

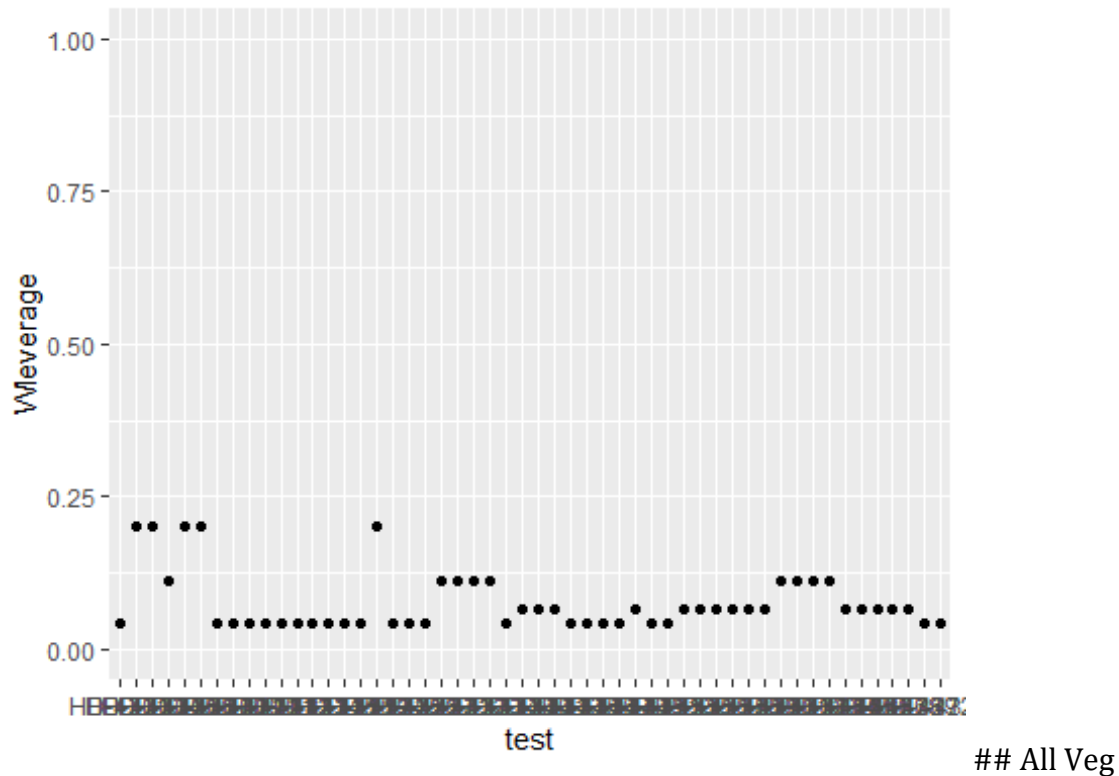
Distribution of Studentized Residuals



#outliers

```
AllFire$Wleverage <- hatvalues(V2)
```

```
ggplot(AllFire, aes(`New Site`, Wleverage)) + geom_point() + ylim(0,1) +  
xlab("test")
```



```
V1 <- lm(VegProp ~ Lineage * TrtBin, data = AllSites)
```

```
anova(V1)
```

Analysis of Variance Table

##

```
## Response: VegProp
```

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
## Lineage	1	0.0398	0.03984	0.4389	0.5095	
## TrtBin	1	1.6465	1.64646	18.1391	5.328e-05	***
## Lineage:TrtBin	1	0.0378	0.03785	0.4170	0.5202	
## Residuals	84	7.6245	0.09077			

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

```
summary(V1)
```

##

```
## Call:
```

```
## lm(formula = VegProp ~ Lineage * TrtBin, data = AllSites)
```

##

```
## Residuals:
```

##	Min	1Q	Median	3Q	Max
##	-0.47186	-0.19310	-0.05405	0.20690	0.60690

```
## Coefficients:
```

```
##           Estimate Std. Error t value Pr(>|t|)
```



```
## (Intercept)          0.47186    0.06423    7.346 1.21e-10 ***
## LineageNA1          -0.03563    0.08985   -0.397  0.69270
## TrtBin1             -0.32900    0.10300   -3.194  0.00198 **
## LineageNA1:TrtBin1   0.08588    0.13299    0.646  0.52021
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3013 on 84 degrees of freedom
## Multiple R-squared:  0.1844, Adjusted R-squared:  0.1553
## F-statistic: 6.332 on 3 and 84 DF,  p-value: 0.0006355
```

```
summ(V1)
```

```
## MODEL INFO:
## Observations: 88
## Dependent Variable: VegProp
## Type: OLS linear regression
##
```

```
## MODEL FIT:
## F(3,84) = 6.33, p = 0.00
## R2 = 0.18
## Adj. R2 = 0.16
##
```

```
## Standard errors: OLS
```

```
## -----
##               Est.    S.E.    t val.    p
## -----
## (Intercept)      0.47    0.06      7.35    0.00
## LineageNA1      -0.04    0.09     -0.40    0.69
## TrtBin1         -0.33    0.10     -3.19    0.00
## LineageNA1:TrtBin1  0.09    0.13      0.65    0.52
## -----
```

```
# Least Squares Means
```

```
V1.lsm <- lsmeans(V1, "TrtBin")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
V1.lsm
```

```
## TrtBin lsmean    SE df lower.CL upper.CL
## 0          0.454 0.0449 84    0.3647    0.543
## 1          0.168 0.0490 84    0.0705    0.265
##
```

```
## Results are averaged over the levels of: Lineage
## Confidence level used: 0.95
```

```
V1LSM <- as.data.frame(V1.lsm)
```

```
V1LSM
```

```

##   TrtBin    lsmean      SE df   lower.CL upper.CL
## 1      0 0.4540467 0.04492296 84 0.36471245 0.5433809
## 2      1 0.1679803 0.04902398 84 0.07049074 0.2654699

#Least Squares Means visualization
LSMVeg <- ggplot(V1LSM,aes(x=TrtBin,y=lsmean, fill=TrtBin))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() + theme_classic()+
  theme(legend.position="none", text = element_text(size=13),
axis.text.x=element_blank(), axis.title.x=element_blank())+
  scale_y_continuous("Least Squares Mean", limits = c(0, 1))+
  geom_errorbar(aes(x=TrtBin, ymin=lower.CL, ymax=upper.CL), width=0.1,
colour="orange", alpha=0.95, size=1)

#Contrasts
ConV1 <- contrast(V1.lsm, list (TvU = c(-1, 1)))
ConV1

## contrast estimate      SE df t.ratio p.value
## TvU          -0.286 0.0665 84 -4.302  <.0001
##
## Results are averaged over the levels of: Lineage

#correlations of random effects not included in the model
VC1 <- cor.test(AllSites$VegProp, AllSites$YrSinceTrt, method=c("pearson",
"kendall", "spearman"))
VC11 <- cor.test(AllSites$VegProp, AllSites$TotalT0, method=c("pearson",
"kendall", "spearman"))
VC111 <- cor.test(AllSites$VegProp, AllSites$Num_Seedlings,
method=c("pearson", "kendall", "spearman"))
VC1111 <- cor.test(AllSites$VegProp, AllSites$SoilProp, method=c("pearson",
"kendall", "spearman"))
VC1

##
## Pearson's product-moment correlation
##
## data: AllSites$VegProp and AllSites$YrSinceTrt
## t = -1.6704, df = 86, p-value = 0.09848
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.37286767 0.03341372
## sample estimates:
## cor
## -0.1772691

VC11

##
## Pearson's product-moment correlation
##

```

```
## data: AllSites$VegProp and AllSites$TotalT0
## t = 0.83633, df = 86, p-value = 0.4053
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1219169 0.2937354
## sample estimates:
##      cor
## 0.08981887
```

VC111

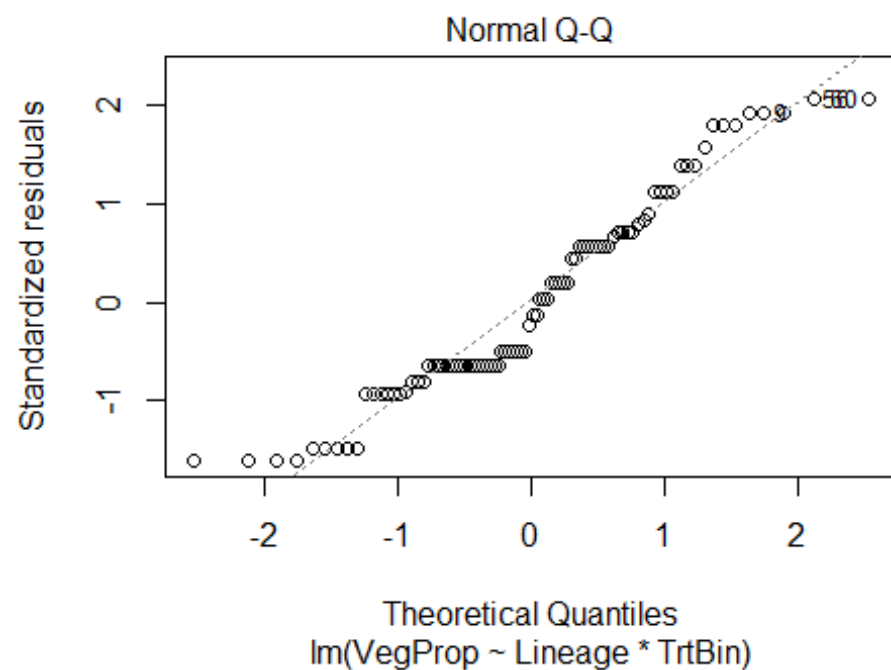
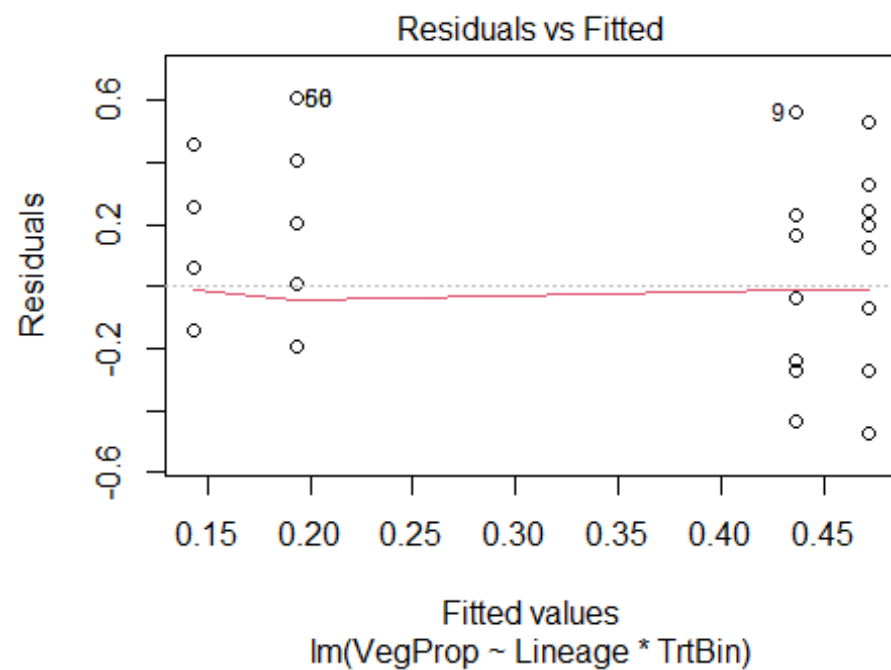
```
##
## Pearson's product-moment correlation
##
## data: AllSites$VegProp and AllSites$Num_Seedlings
## t = -1.1365, df = 86, p-value = 0.2589
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.32286202 0.09009204
## sample estimates:
##      cor
## -0.1216456
```

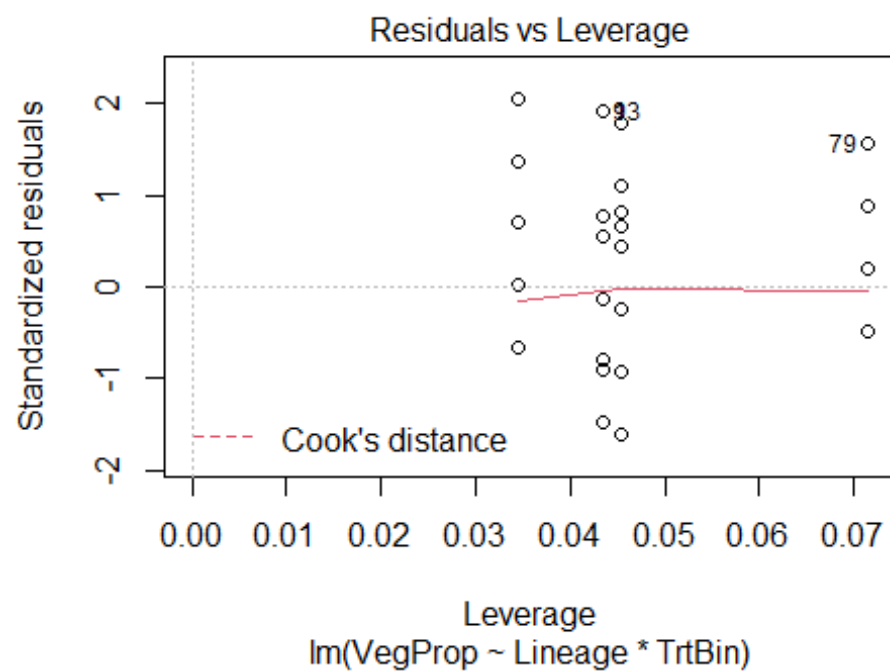
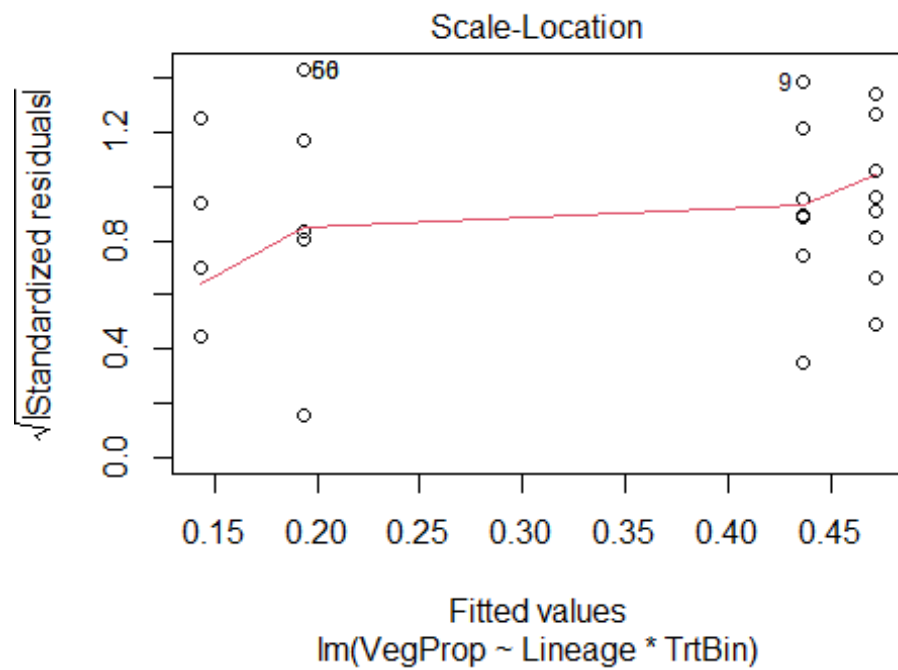
VC1111 *#correlation between soil and veg!*

```
##
## Pearson's product-moment correlation
##
## data: AllSites$VegProp and AllSites$SoilProp
## t = 2.931, df = 86, p-value = 0.004328
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.09811131 0.48047666
## sample estimates:
##      cor
## 0.301361
```

All Veg Assumptions

plot(V1)





```
gvlma(V1)
```

```
##
```

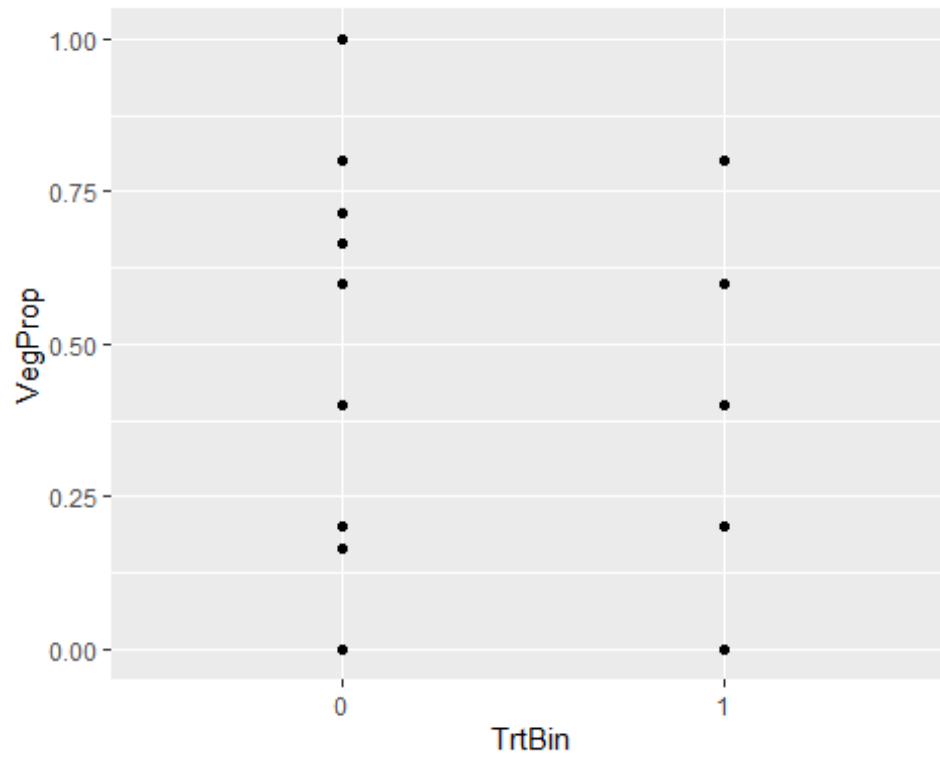
```
## Call:
```

```
## lm(formula = VegProp ~ Lineage * TrtBin, data = AllSites)
##
## Coefficients:
##          (Intercept)          LineageNA1          TrtBin1
LineageNA1:TrtBin1
##          0.47186          -0.03563          -0.32900
0.08588
##
##
## ASSESSMENT OF THE LINEAR MODEL ASSUMPTIONS
## USING THE GLOBAL TEST ON 4 DEGREES-OF-FREEDOM:
## Level of Significance = 0.05
##
## Call:
## gvlma(x = V1)
##
##              Value p-value              Decision
## Global Stat    5.533e+00  0.2368 Assumptions acceptable.
## Skewness       2.024e+00  0.1548 Assumptions acceptable.
## Kurtosis       2.295e+00  0.1298 Assumptions acceptable.
## Link Function  1.629e-14  1.0000 Assumptions acceptable.
## Heteroscedasticity 1.214e+00  0.2706 Assumptions acceptable.
```

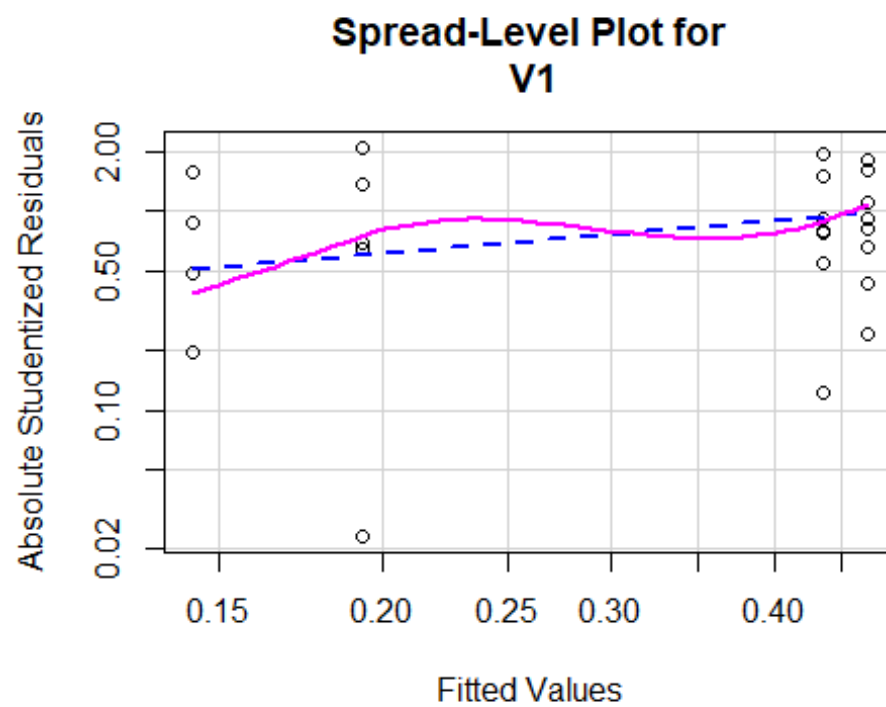
#linearity

```
ggplot(AllSites, aes(TrtBin,VegProp)) +
  stat_smooth(method="loess") +
  stat_smooth(method="lm", color="red", fill="red", alpha=.25) +
  geom_point()

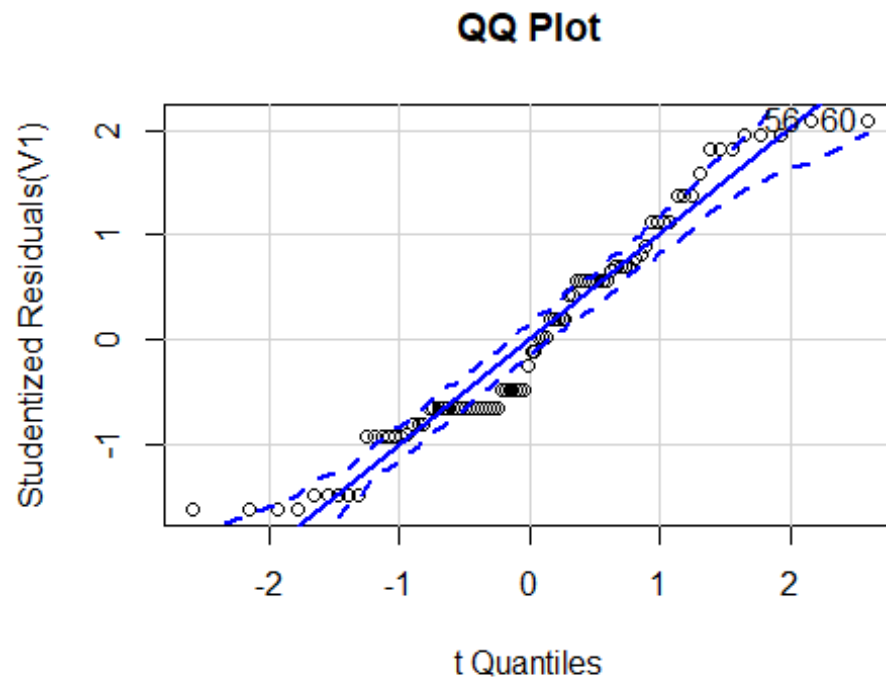
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```



```
#constant variance
spreadLevelPlot(V1)
```

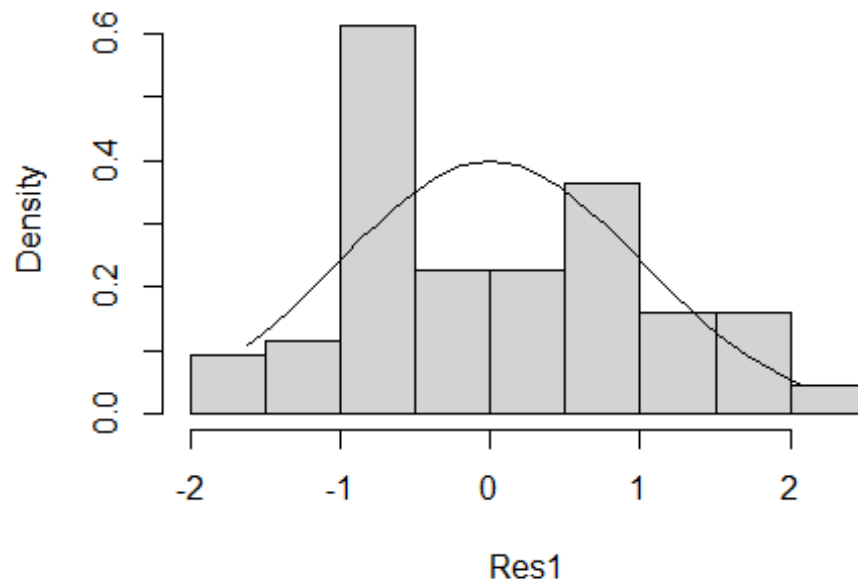


```
##
## Suggested power transformation: 0.4389184
#normality of residuals
Resq1 <- qqPlot(V1, main="QQ Plot")
```



```
Res1 <- studres(V1)
hist(Res1, freq = FALSE, main="Distribution of Studentized Residuals")
xfit1 <- seq(min(Res1), max(Res1), length = 40)
yfit1 <- dnorm(xfit1)
lines(xfit1, yfit1)
```


Distribution of Studentized Residuals



```
#multicollinearity
```

```
vif(V1)
```

```
##      Lineage      TrtBin Lineage:TrtBin
##      1.891843      2.570100      3.788390
```

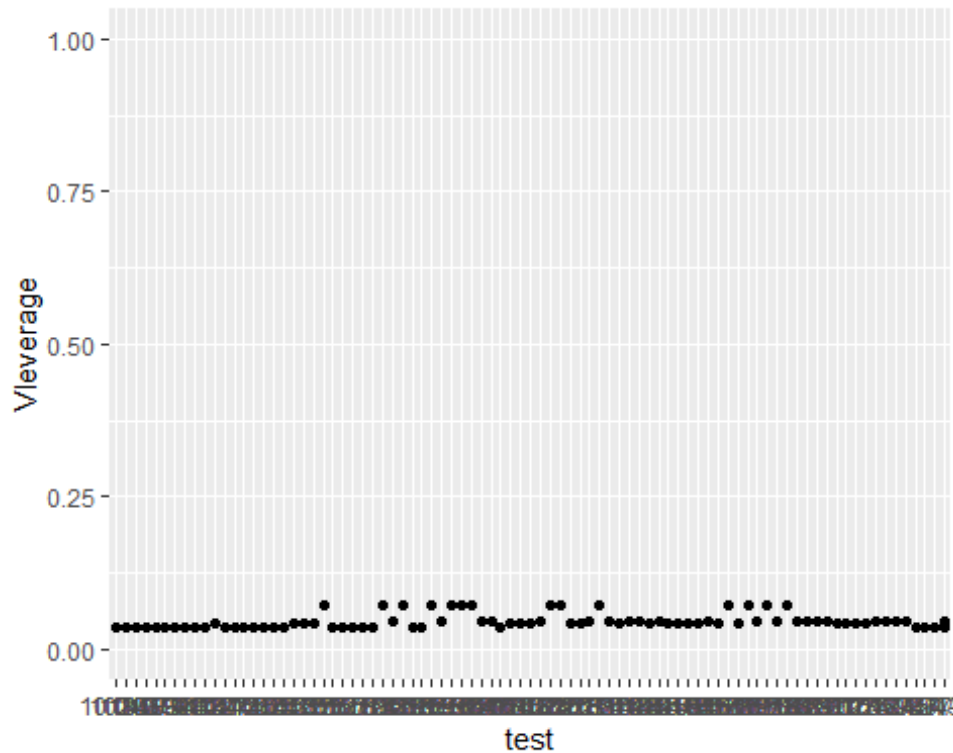
```
sqrt(vif(V1)) > 2
```

```
##      Lineage      TrtBin Lineage:TrtBin
##      FALSE      FALSE      FALSE
```

```
#outliers
```

```
AllSites$Vleverage <- hatvalues(V1)
```

```
ggplot(AllSites, aes(Plot, Vleverage)) + geom_point() + ylim(0,1) +
xlab("test")
```



Soil ## EU1

Repeated Measurement

```
S3 <- lme(SoilBin ~ TrtBin, random = ~1|Plot, data = EU1long)
```

```
anova(S3)
```

	numDF	denDF	F-value	p-value
## (Intercept)	1	9	10.755896	0.0095
## TrtBin	1	9	1.975647	0.1934

```
summary(S3)
```

```
## Linear mixed-effects model fit by REML
## Data: EU1long
##      AIC      BIC    logLik
##  37.05803 40.61952 -14.52902
##
## Random effects:
## Formula: ~1 | Plot
##      (Intercept)  Residual
## StdDev: 0.002064555 0.4772562
##
## Fixed effects: SoilBin ~ TrtBin
##              Value Std.Error DF   t-value p-value
## (Intercept)   0.5  0.1509231   9   3.312946  0.0090
## TrtBin        -0.3  0.2134355   9  -1.405577  0.1934
## Correlation:
##      (Intr)
```

```

## TrtBin -0.707
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.0476670 -0.5762123 -0.4190347  1.0476435  1.6762366
##
## Number of Observations: 20
## Number of Groups: 10

DTS <-array(c(1,4,1,4),
            dim=c(2, 2),
            dimnames=list(
              Time2=c("ThenPos", "ThenNeg"),
              Time1=c("FirstPos", "FirstNeg"))
            )
DTS

##           Time1
## Time2      FirstPos FirstNeg
##  ThenPos         1         1
##  ThenNeg         4         4

mcnemar.test(DTS, y=NULL, correct = FALSE)

##
## McNemar's Chi-squared test
##
## data:  DTS
## McNemar's chi-squared = 1.8, df = 1, p-value = 0.1797

chisq.test(EU1long$SoilBin, EU1long$TrtBin)

## Warning in chisq.test(EU1long$SoilBin, EU1long$TrtBin): Chi-squared
## approximation may be incorrect

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  EU1long$SoilBin and EU1long$TrtBin
## X-squared = 0.87912, df = 1, p-value = 0.3484

#correlations
SC3 <- cor.test(EU1wide$SoilPre, EU1wide$SoilPost, method=c("pearson",
"kendall", "spearman"))
SC3

##
## Pearson's product-moment correlation
##
## data:  EU1wide$SoilPre and EU1wide$SoilPost
## t = 0.13333, df = 8, p-value = 0.8972
## alternative hypothesis: true correlation is not equal to 0

```

```
## 95 percent confidence interval:
## -0.6003369 0.6572290
## sample estimates:
##      cor
## 0.04708816
```

NA1 Soil Wildfire

```
S2 <- glm(SoilBin ~ RX, data = AllFire)
```

```
anova(S2)
```

```
## Analysis of Deviance Table
##
## Model: gaussian, link: identity
##
## Response: SoilBin
##
## Terms added sequentially (first to last)
##
##
```

	Df	Deviance	Resid. Df	Resid. Dev
## NULL			51	6.7692
## RX	3	1.2272	48	5.5420

```
summary(S2)
```

```
##
## Call:
## glm(formula = SoilBin ~ RX, data = AllFire)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.6000  -0.1333  -0.1304   0.0000   0.8696
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.130435   0.070852   1.841  0.07181 .
## RX1          0.002899   0.112771   0.026  0.97960
## RX2          0.469565   0.167666   2.801  0.00733 **
## RX3         -0.130435   0.133599  -0.976  0.33380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1154589)
##
##      Null deviance: 6.7692  on 51  degrees of freedom
## Residual deviance: 5.5420  on 48  degrees of freedom
## AIC: 41.148
##
## Number of Fisher Scoring iterations: 2
```

```

summ(S2)

## MODEL INFO:
## Observations: 52
## Dependent Variable: SoilBin
## Type: Linear regression
##
## MODEL FIT:
## <math>\chi^2(3) = 1.23, p = 0.01</math>
## Pseudo-R2 (Cragg-Uhler) = 0.33
## Pseudo-R2 (McFadden) = 0.25
## AIC = 41.15, BIC = 50.90
##
## Standard errors: MLE
## -----
##               Est.   S.E.   t val.   p
## -----
## (Intercept)    0.13   0.07    1.84   0.07
## RX1             0.00   0.11    0.03   0.98
## RX2             0.47   0.17    2.80   0.01
## RX3            -0.13   0.13   -0.98   0.33
## -----
##
## Estimated dispersion parameter = 0.12

# Contrast statement
levels(AllFire$RX)

## [1] "0" "1" "2" "3"

# 0 - No Wildfire or Treatment
# 1 - Only Treatment
# 2 - Only Wildfire
# 3 - Both Wildfire and Treatment

S2.lsm <- lsmeans(S2, ~RX, adjst="tukey")
S2.lsm

##   RX lsmean      SE  df asymp.LCL asymp.UCL
## 0   0.130 0.0709 Inf  -0.00843    0.269
## 1   0.133 0.0877 Inf  -0.03862    0.305
## 2   0.600 0.1520 Inf   0.30216    0.898
## 3   0.000 0.1133 Inf  -0.22199    0.222
##
## Confidence level used: 0.95

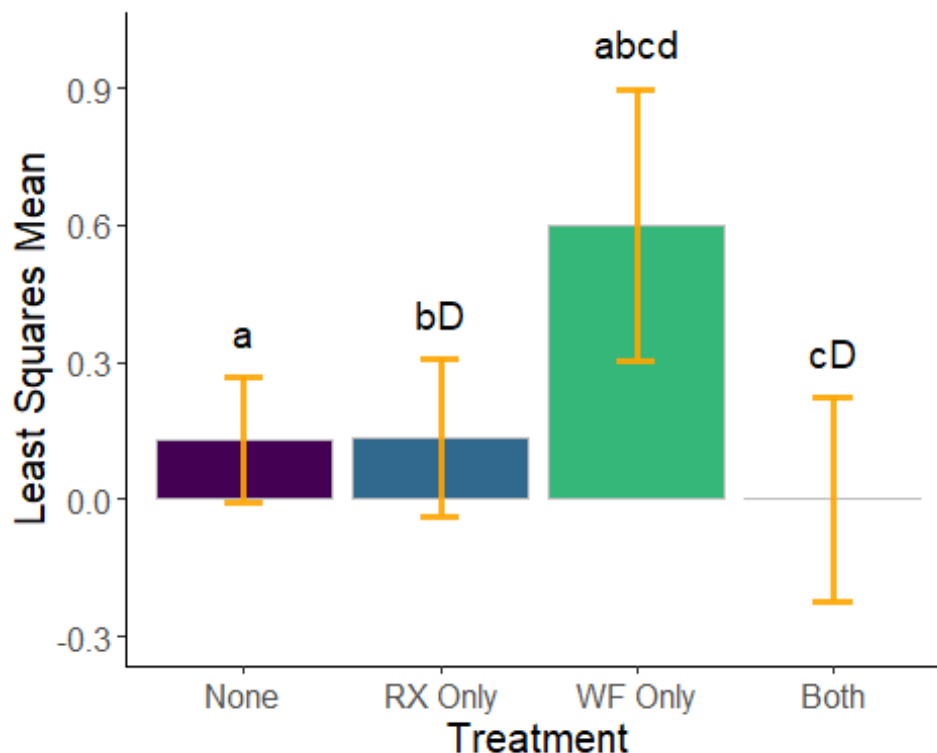
S2LSM <- as.data.frame(S2.lsm)
S2LSM

##   RX      lsmean      SE  df  asymp.LCL asymp.UCL
## 1  0  1.304348e-01 0.07085163 Inf -0.008431865 0.2693014

```

```
## 2 1 1.333333e-01 0.08773404 Inf -0.038622233 0.3052889
## 3 2 6.000000e-01 0.15195982 Inf 0.302164222 0.8978358
## 4 3 -1.665335e-16 0.11326416 Inf -0.221993682 0.2219937
```

```
ggplot(S2LSM,aes(x=RX,y=lsmean, fill=RX))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() + theme_classic()+
  scale_x_discrete(name="Treatment", labels=c("0" = "None", "1" = "RX
Only","2" = "WF Only", "3" = "Both"))+
  scale_y_continuous("Least Squares Mean", breaks = c(-0.3, 0, 0.3, 0.6,
0.9), limits = c(-0.3, 1))+
  geom_errorbar(aes(x=RX, ymin=asympt.LCL, ymax=asympt.UCL), width=0.2,
colour="orange", alpha=0.9, size=1.3)+
  theme(legend.position="none", text = element_text(size=15),
  strip.background = element_blank(),
  strip.text = element_blank())+
  geom_text(aes(x=RX, y=0.1+S2LSM$asympt.UCL,label=c("a", "bD", "abcd",
"cD")),size = 5,position=position_dodge(.5))
```



```
ConS2 <- contrast(S2.lsm, list (
  "0 v. 1" = c(-1, 1, 0, 0), #difference is RX
  "2 v. 3" = c(0, 0, -1, 1), #difference is RX
  "1 v. 2" = c(0, -1, 1, 0), #difference is both
  "3 v. 0" = c(-1, 0, 0, 1), #difference is both
  "0 v. 2" = c(-1, 0, 1, 0), #difference is WF; NS b/c small n & wide CI?
  "1 v. 3" = c(0, -1, 0, 1), #difference is WF
  "1&3 v. 2" = c(0, .5, -1, .5), #both RX to WF w/o RX
```

```

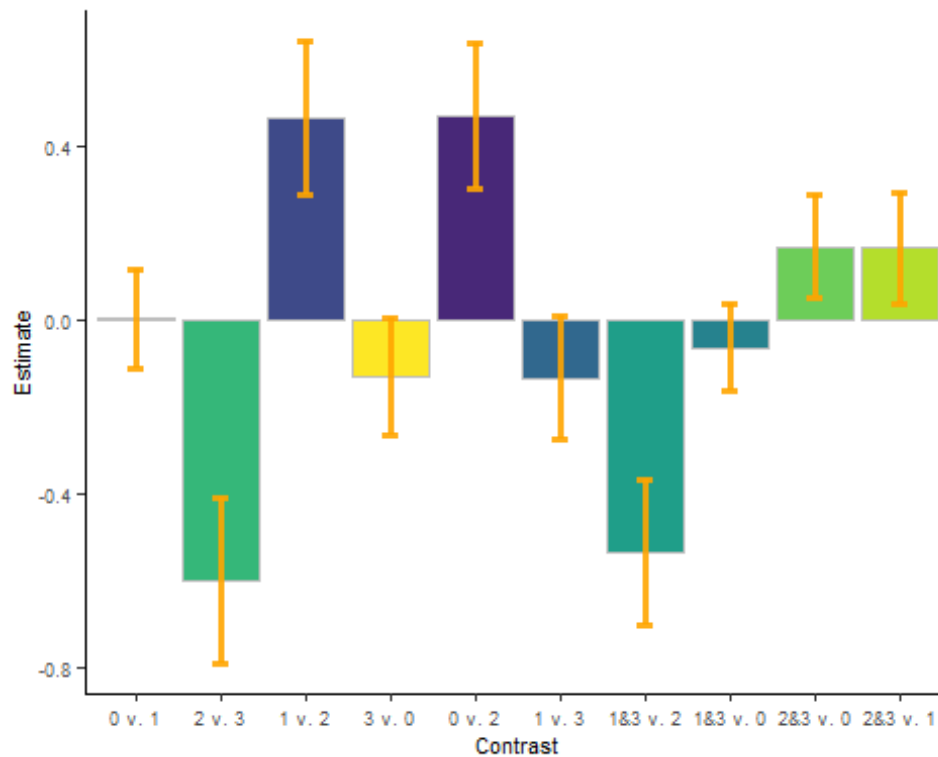
"1&3 v. 0" = c(-1, .5, 0, .5), #both RX to noWF or RX
"2&3 v. 0" = c(-1, 0, .5, .5), #both WF to noWF or RX
"2&3 v. 1" = c(0, -1, .5, .5) #both WF to RX w/o WF
))
ConS2

## contrast estimate SE df z.ratio p.value
## 0 v. 1 0.0029 0.113 Inf 0.026 0.9795
## 2 v. 3 -0.6000 0.190 Inf -3.166 0.0015
## 1 v. 2 0.4667 0.175 Inf 2.660 0.0078
## 3 v. 0 -0.1304 0.134 Inf -0.976 0.3289
## 0 v. 2 0.4696 0.168 Inf 2.801 0.0051
## 1 v. 3 -0.1333 0.143 Inf -0.931 0.3520
## 1&3 v. 2 -0.5333 0.168 Inf -3.175 0.0015
## 1&3 v. 0 -0.0638 0.101 Inf -0.633 0.5268
## 2&3 v. 0 0.1696 0.118 Inf 1.433 0.1518
## 2&3 v. 1 0.1667 0.129 Inf 1.291 0.1968

CONS2 <- as.data.frame(ConS2)

#Contrasts visualization
ggplot(CONS2,aes(x=contrast,y=estimate, fill=contrast))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() +
  theme_classic()+
  theme(legend.position="none", text = element_text(size=8))+
  xlab("Contrast")+
  scale_x_discrete(name = "Contrast", limits=c("0 v. 1","2 v. 3","1 v. 2", "3
v. 0", "0 v. 2", "1 v. 3", "1&3 v. 2", "1&3 v. 0", "2&3 v. 0", "2&3 v. 1"))+
  ylab("Estimate")+
  geom_errorbar(aes(x=contrast, ymin=estimate-SE, ymax=estimate+SE),
width=0.2, colour="orange", alpha=0.9, size=1.3)

```



#correlations of random effects not included in the model

```
SC2 <- cor.test(AllFire$VegProp, AllFire$TotalT0, method=c("pearson",
"kendall", "spearman"))
SC22 <- cor.test(AllFire$VegProp, AllFire$SoilProp, method=c("pearson",
"kendall", "spearman"))
```

SC2

```
##
## Pearson's product-moment correlation
##
## data: AllFire$VegProp and AllFire$TotalT0
## t = 1.093, df = 50, p-value = 0.2796
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1253661 0.4086259
## sample estimates:
## cor
## 0.1527605
```

SC22 *#correlation between soil and veg!*

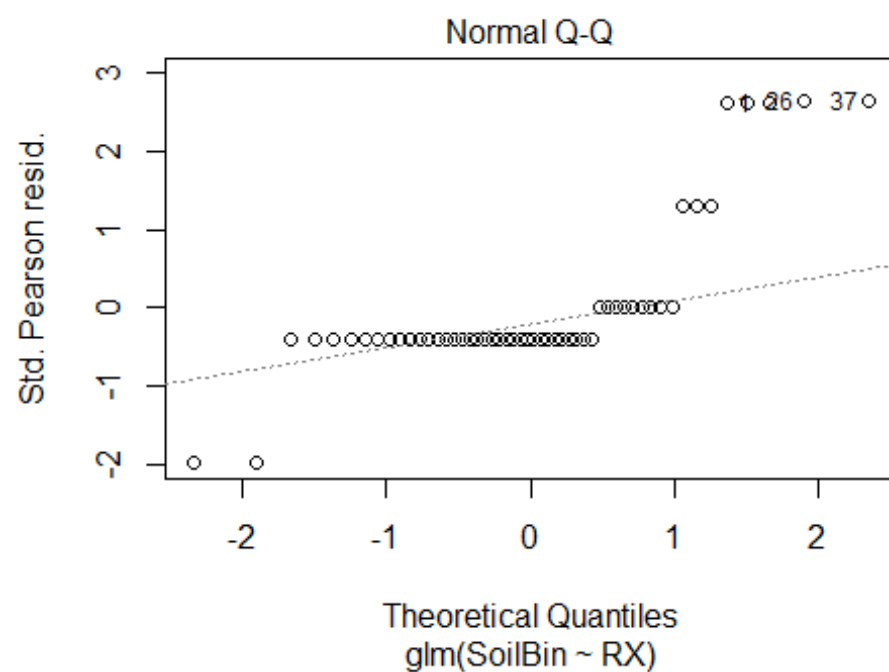
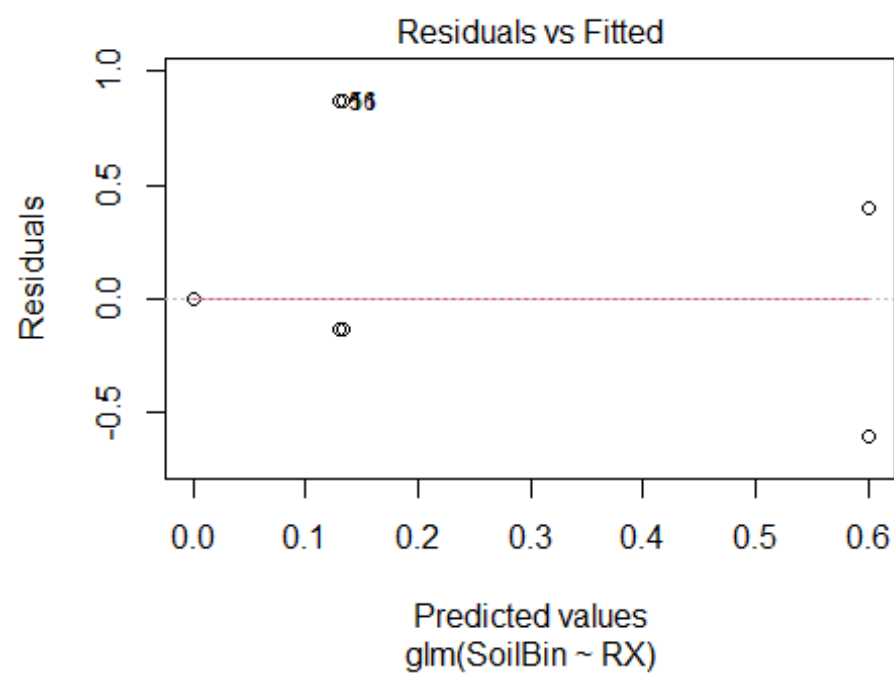
```
##
## Pearson's product-moment correlation
##
## data: AllFire$VegProp and AllFire$SoilProp
## t = 3.2198, df = 50, p-value = 0.002256
```

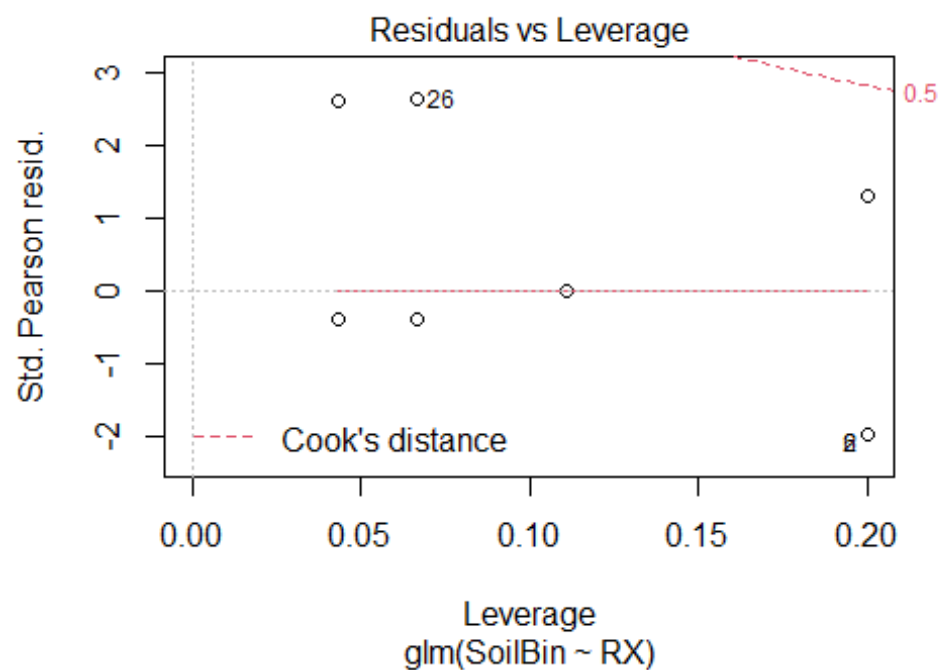
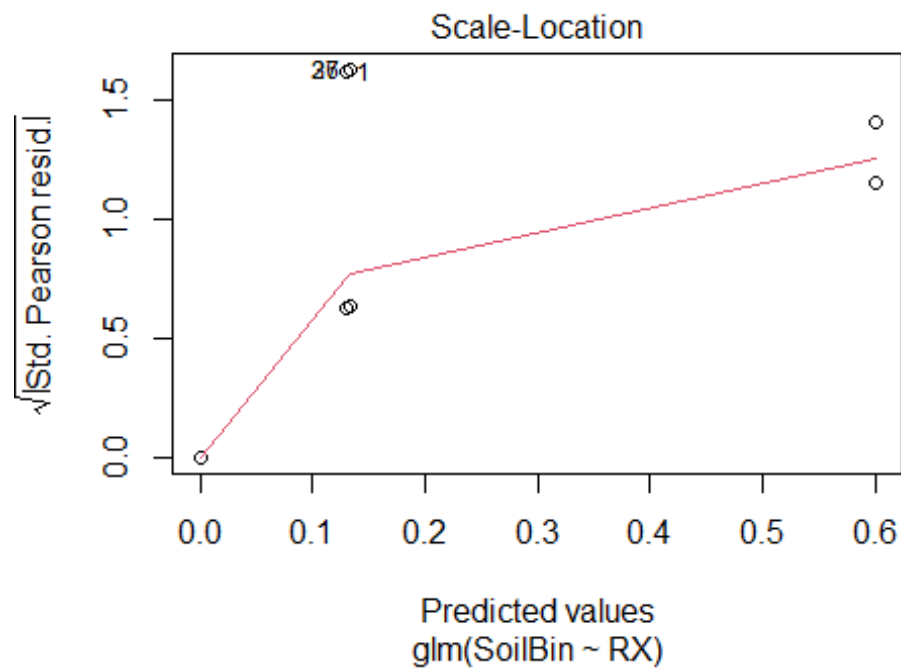


```
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1595480 0.6174743
## sample estimates:
##           cor
## 0.4144049
```

NA1 Soil Wildfire Assumptions

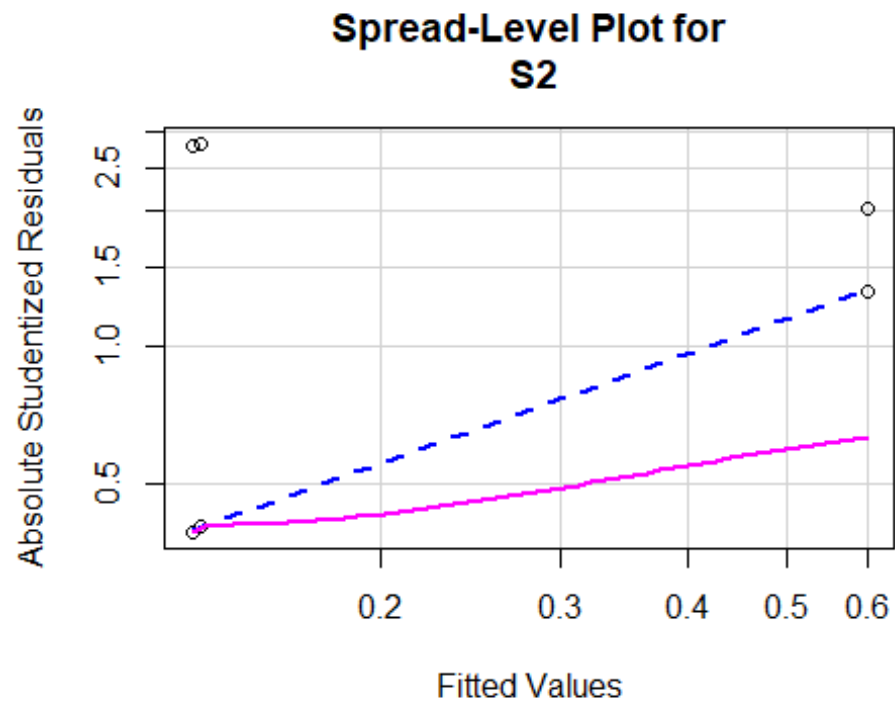
```
plot(S2)
```





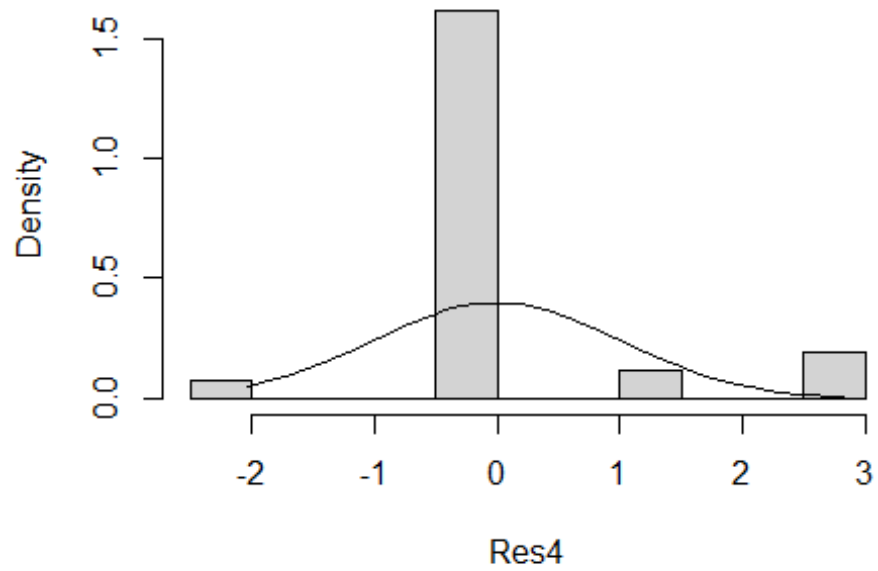
```
#constant variance
spreadLevelPlot(S2)
```

```
## Warning in spreadLevelPlot.lm(S2):  
## 9 negative fitted values removed
```



```
##  
## Suggested power transformation: 0.1937396  
  
#normality of residuals  
Res4 <- studres(S2)  
hist(Res4, freq = FALSE,  
      main="Distribution of Studentized Residuals")  
xfit4 <- seq(min(Res4), max(Res4), length = 40)  
yfit4 <- dnorm(xfit4)  
lines(xfit4, yfit4)
```

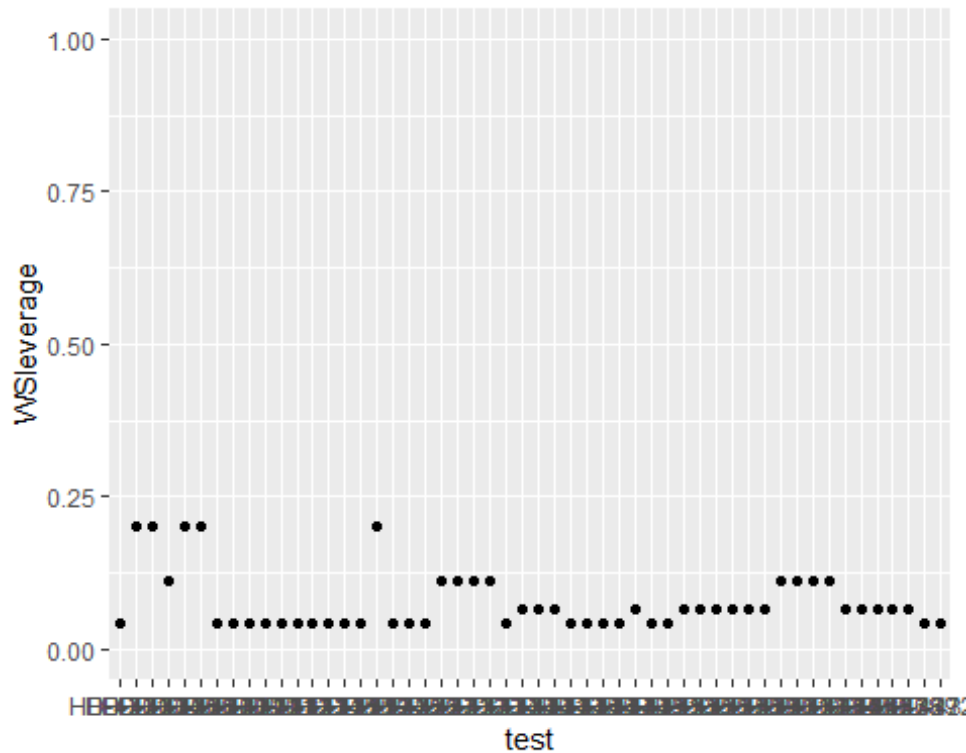
Distribution of Studentized Residuals



#outliers

```
AllFire$WSleverage <- hatvalues(S2)
```

```
ggplot(AllFire, aes(`New Site`, WSleverage)) + geom_point() + ylim(0,1) +  
xlab("test")
```



All Soil

```
S1 <- glm(SoilBin ~ Lineage + TrtBin, family = "binomial", data = AllSites)
```

```
anova(S1)
```

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

	Df	Deviance	Resid. Df	Resid. Dev
## NULL			87	91.816
## Lineage	1	2.85043	86	88.965
## TrtBin	1	0.15705	85	88.808

```
summary(S1)
```

```
##
## Call:
## glm(formula = SoilBin ~ Lineage + TrtBin, family = "binomial",
##      data = AllSites)
##
## Deviance Residuals:
```

```

##      Min      1Q   Median      3Q      Max
## -0.8831 -0.8076 -0.6092 -0.5524  1.9775
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.7404     0.4129  -1.793   0.073 .
## LineageNA1   -0.8496     0.5347  -1.589   0.112
## TrtBin1      -0.2127     0.5375  -0.396   0.692
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 91.816  on 87  degrees of freedom
## Residual deviance: 88.808  on 85  degrees of freedom
## AIC: 94.808
##
## Number of Fisher Scoring iterations: 4

summ(S1)

## MODEL INFO:
## Observations: 88
## Dependent Variable: SoilBin
## Type: Generalized linear model
## Family: binomial
## Link function: logit
##
## MODEL FIT:
## <math>\chi^2(2) = 3.01, p = 0.22</math>
## Pseudo- $R^2$  (Cragg-Uhler) = 0.05
## Pseudo- $R^2$  (McFadden) = 0.03
## AIC = 94.81, BIC = 102.24
##
## Standard errors: MLE
## -----
##              Est.   S.E.   z val.    p
## -----
## (Intercept)    -0.74   0.41   -1.79   0.07
## LineageNA1     -0.85   0.53   -1.59   0.11
## TrtBin1        -0.21   0.54   -0.40   0.69
## -----

# Contrast statement
S1.lsm <- lsmeans(S1, "TrtBin")
S1.lsm

## TrtBin lsmean   SE  df asymp.LCL asymp.UCL
## 0      -1.17 0.356 Inf    -1.86   -0.467
## 1      -1.38 0.398 Inf    -2.16   -0.597
##

```

```
## Results are averaged over the levels of: Lineage
## Results are given on the logit (not the response) scale.
## Confidence level used: 0.95
```

```
S1LSM <- as.data.frame(S1.lsm)
S1LSM
```

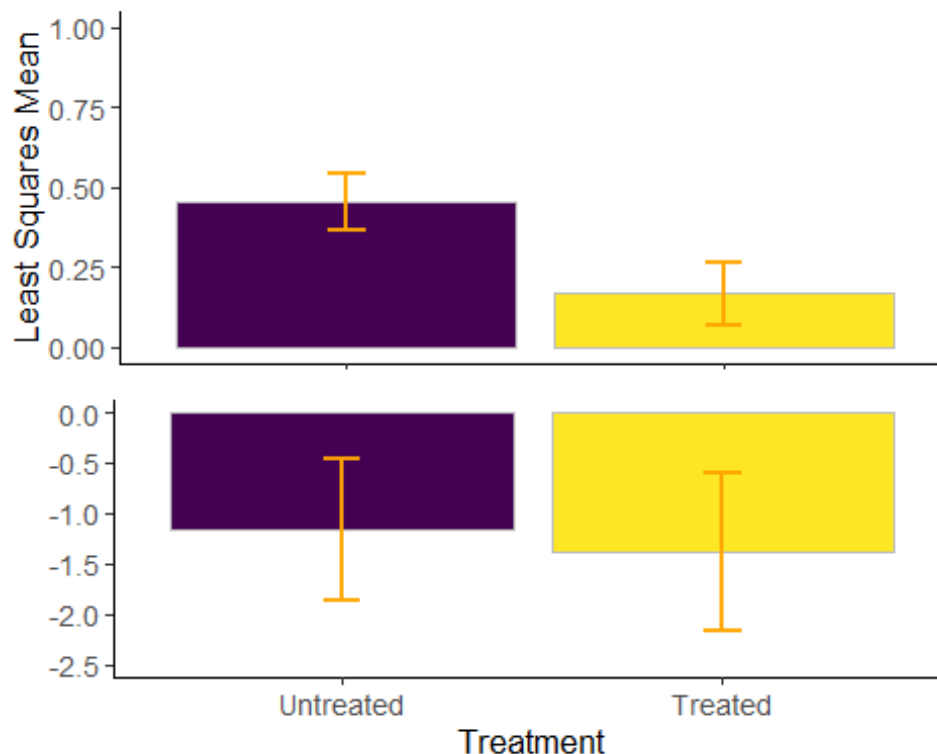
```
##   TrtBin    lsmean      SE  df asymp.LCL asymp.UCL
## 1      0 -1.165202 0.3563991 Inf -1.863731 -0.4666727
## 2      1 -1.377871 0.3984384 Inf -2.158796 -0.5969458
```

```
#Least Squares Means visualization
```

```
LSMSoil <- ggplot(S1LSM,aes(x=TrtBin,y=lsmean, fill=TrtBin))+
  geom_bar(stat="identity",position="dodge",color="gray")+
  scale_fill_viridis_d() + theme_classic()+
  theme(legend.position="none", text = element_text(size=13),
axis.title.y=element_text(color="white"))+
  scale_x_discrete(name="Treatment", breaks=c("0", "1"),labels=c("0" =
"Untreated", "1" = "Treated"))+
  scale_y_continuous(limits = c(-2.5, 0))+
  geom_errorbar(aes(x=TrtBin, ymin=asymp.LCL, ymax=asymp.UCL), width=0.1,
colour="orange", alpha=0.95, size=1)
```

```
#Combining veg and soil plots
```

```
grid.arrange(LSMVeg, LSMSoil, ncol=1)
```



#Contrasts

```
ConS1 <- contrast(S1.lsm, list (TvU = c(-1, 1)))
```

```
ConS1
```

```
## contrast estimate      SE  df z.ratio p.value
```

```
## TvU          -0.213 0.538 Inf -0.396  0.6924
```

```
##
```

```
## Results are averaged over the levels of: Lineage
```

```
## Results are given on the log odds ratio (not the response) scale.
```

```
CONS1 <- as.data.frame(ConS1)
```

#correlations of random effects not included in the model

```
SC1 <- cor.test(AllSites$SoilBin, AllSites$YrSinceTrt, method=c("pearson",  
"kendall", "spearman"))
```

```
SC11 <- cor.test(AllSites$SoilBin, AllSites$TotalTO, method=c("pearson",  
"kendall", "spearman"))
```

```
SC111 <- cor.test(AllSites$SoilBin, AllSites$Num_Seedlings,  
method=c("pearson", "kendall", "spearman"))
```

```
SC1111 <- cor.test(AllSites$SoilBin, AllSites$VegProp, method=c("pearson",  
"kendall", "spearman"))
```

```
SC1
```

```
##
```

```
## Pearson's product-moment correlation
```

```
##
```

```
## data: AllSites$SoilBin and AllSites$YrSinceTrt
```

```
## t = -0.66715, df = 86, p-value = 0.5065
```

```
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.2770337  0.1397882
```

```
## sample estimates:
```

```
##          cor
```

```
## -0.07175484
```

```
SC11
```

```
##
```

```
## Pearson's product-moment correlation
```

```
##
```

```
## data: AllSites$SoilBin and AllSites$TotalTO
```

```
## t = -0.020186, df = 86, p-value = 0.9839
```

```
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.2115225  0.2073601
```

```
## sample estimates:
```

```
##          cor
```

```
## -0.002176686
```

```
SC111
```

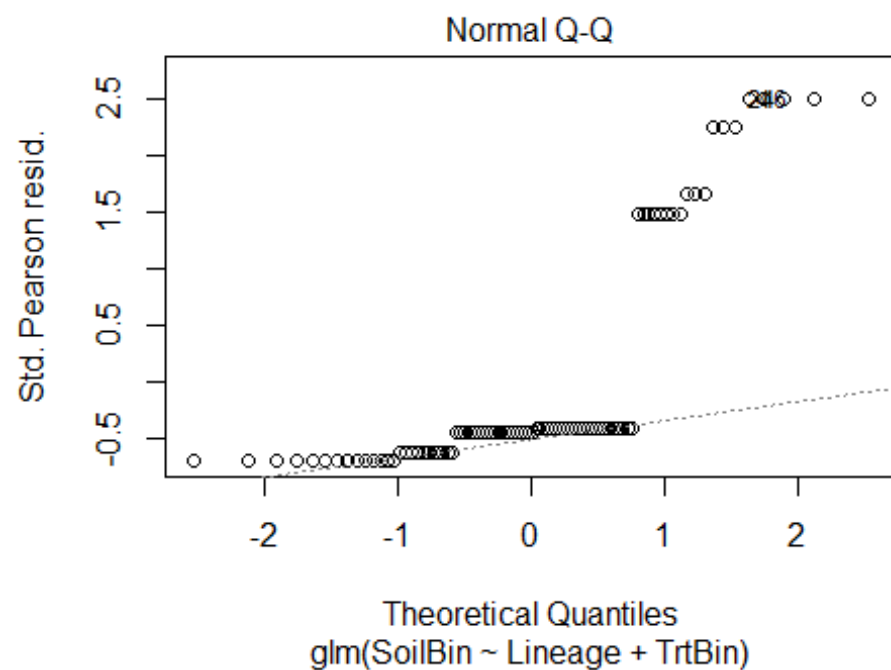
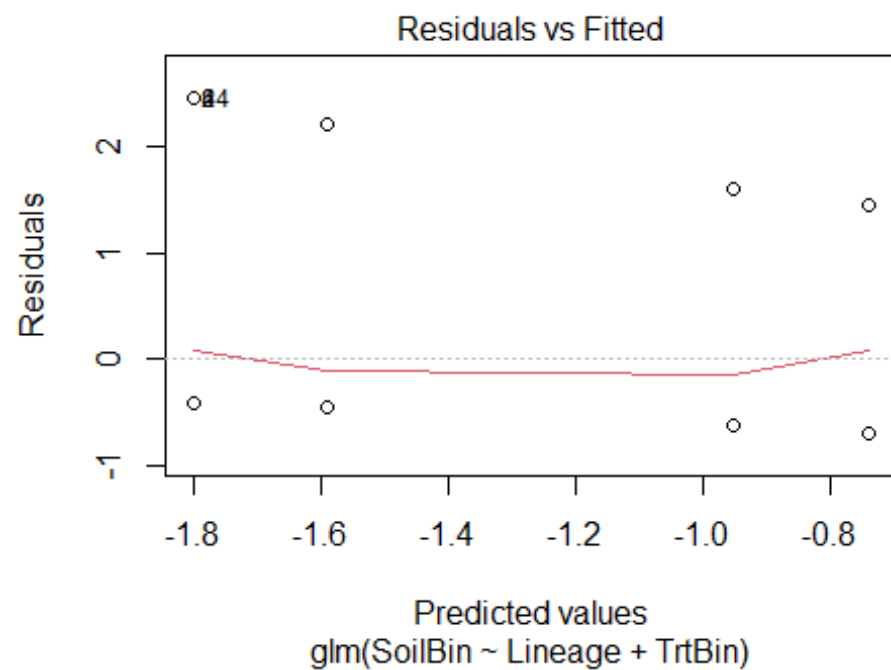
```
##  
## Pearson's product-moment correlation  
##  
## data: AllSites$SoilBin and AllSites$Num_Seedlings  
## t = -1.256, df = 86, p-value = 0.2125  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.33426265 0.07740132  
## sample estimates:  
## cor  
## -0.1342167
```

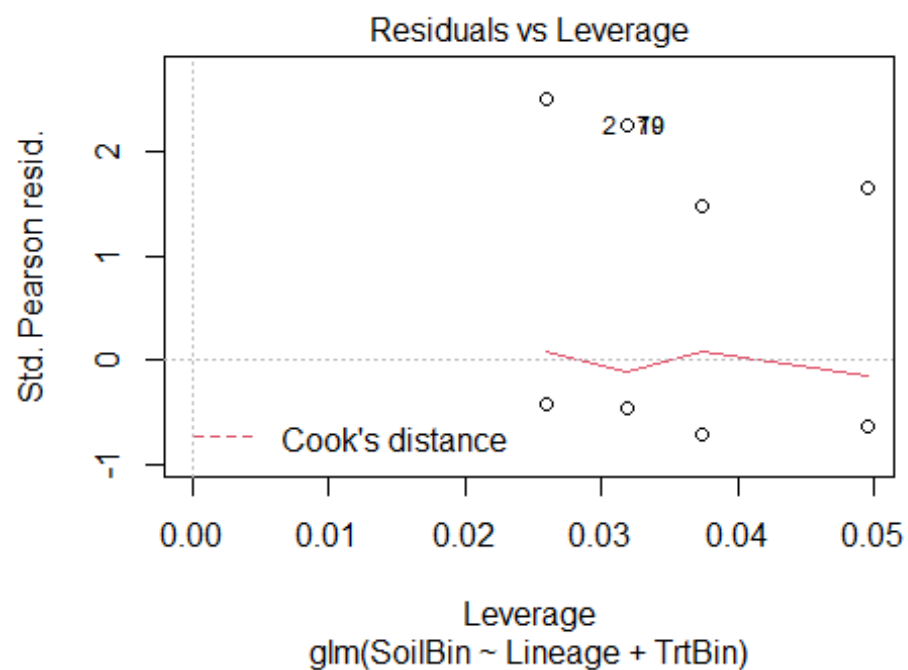
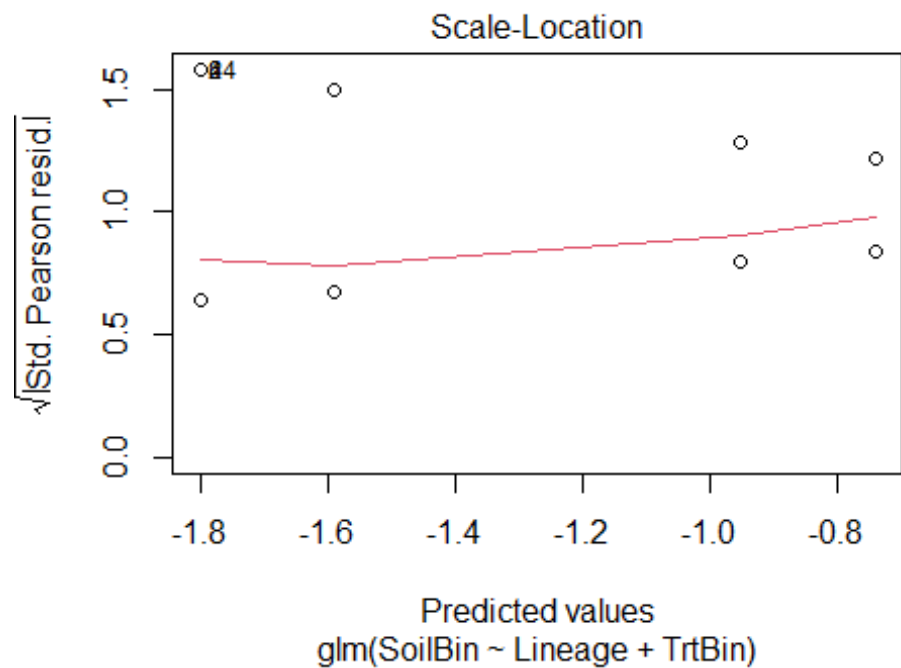
SC1111 *#correlation between soil and veg!*

```
##  
## Pearson's product-moment correlation  
##  
## data: AllSites$SoilBin and AllSites$VegProp  
## t = 2.6705, df = 86, p-value = 0.009055  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.0714214 0.4595330  
## sample estimates:  
## cor  
## 0.2767242
```

All Soil Assumptions

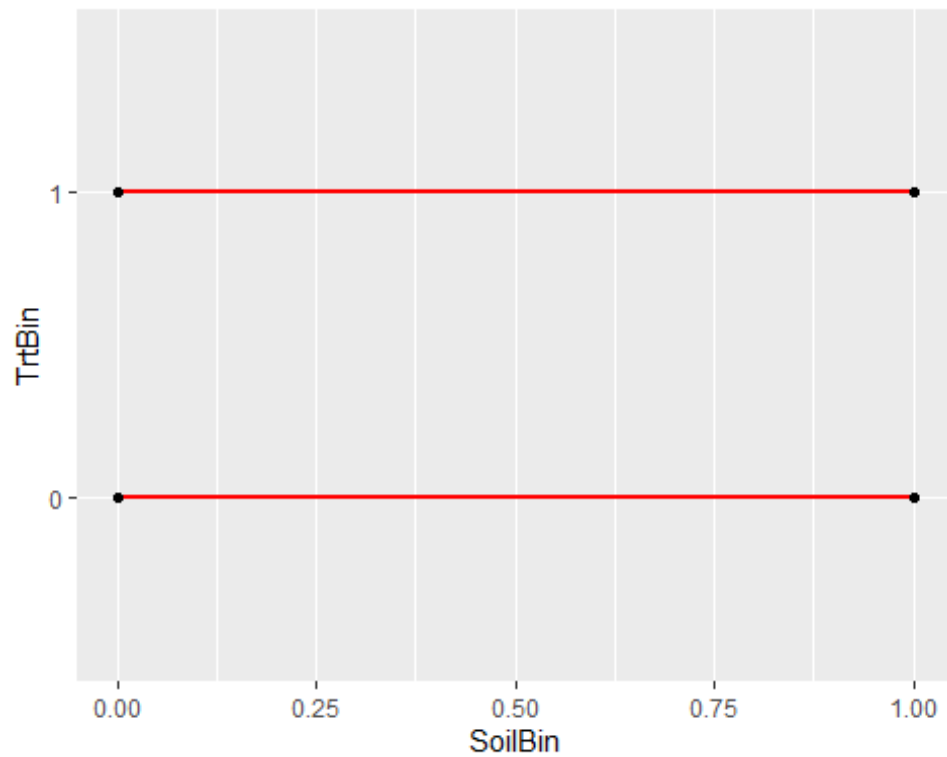
```
plot(S1)
```



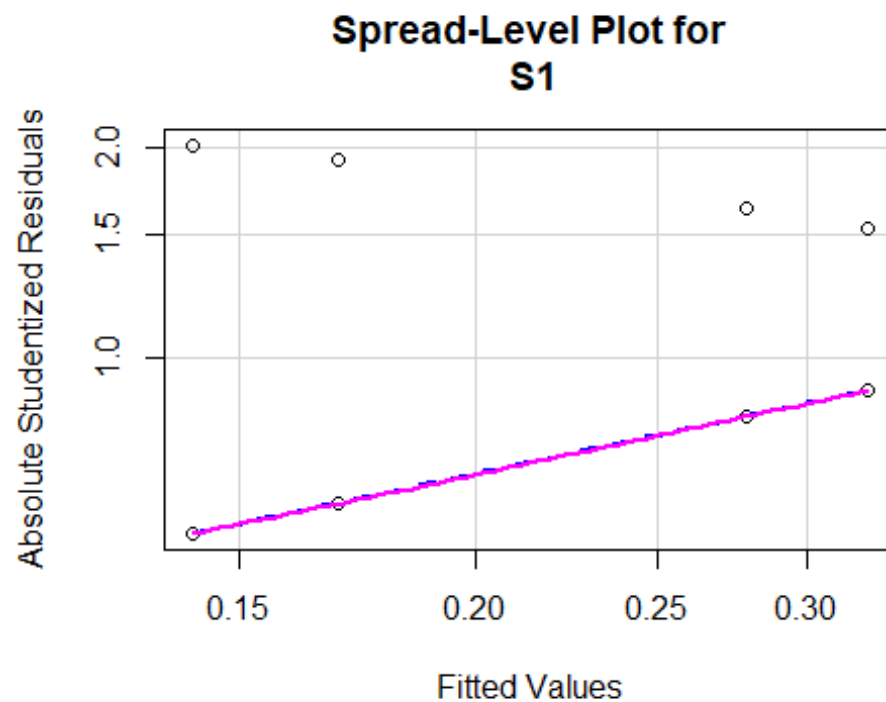


```
#linearity
ggplot(AllSites, aes(SoilBin,TrtBin)) +
  stat_smooth(method="loess") +
```

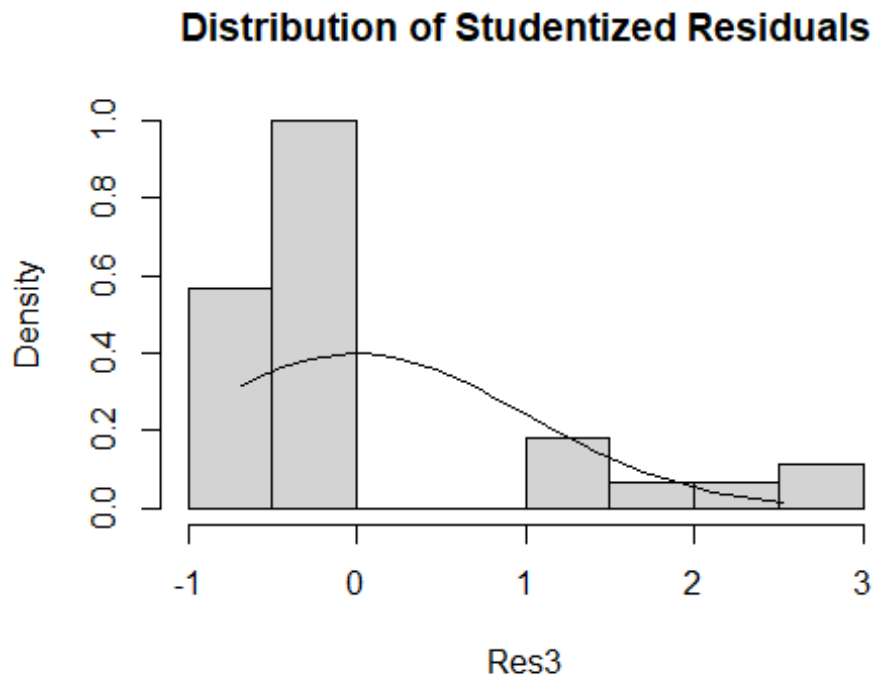
```
stat_smooth(method="lm", color="red", fill="red", alpha=.25) +  
geom_point()  
## `geom_smooth()` using formula 'y ~ x'
```



```
#constant variance  
spreadLevelPlot(S1)
```



```
##  
## Suggested power transformation: 0.4250135  
  
#normality of residuals  
Res3 <- studres(S1)  
hist(Res3, freq = FALSE,  
      main="Distribution of Studentized Residuals")  
xfit3 <- seq(min(Res3), max(Res3), length = 40)  
yfit3 <- dnorm(xfit3)  
lines(xfit3, yfit3)
```



#assumption violated?

#multicollinearity

```
vif(S1)
```

```
## Lineage TrtBin
```

```
## 1.024027 1.024027
```

```
sqrt(vif(S1)) > 2
```

```
## Lineage TrtBin
```

```
## FALSE FALSE
```

#outliers

```
AllSites$Sleverage <- hatvalues(S1)
```

```
ggplot(AllSites, aes(Plot, Sleverage)) + geom_point() + ylim(0,1) +  
xlab("test")
```

