STAT183 Individual Project

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Read and format data

```r
# read in data
bc_data <- read_excel("C:/Users/Emily Mai/Downloads/biochar study data.xls")

# rename columns for ease of access
bc_data <- bc_data %>%
  rename(shoot_weight = 'shoot weight (g)',
         shallow_root_weight = 'shallow root weight (g)',
         deep_root_weight = 'deep root weight (g)',
         total_root_weight = 'total root weight',
         root_shoot_ratio = 'root:shoot ratio') %>%
  na.omit()

attach(bc_data)
names(bc_data)
```

```
##  [1] "rep"                "type"               "Wheat"
##  [4] "Soil"               "Biochar"            "shoot_weight"
##  [7] "shallow_root_weight" "deep_root_weight"   "total_root_weight"
## [10] "root_shoot_ratio"
```

```r
bc_data <- subset(bc_data, select = -c(rep, type))
```

## Box Plots for Shoot Weight

```r
plot_shoot_weight <- bc_data[c("Wheat","Soil","Biochar","shoot_weight")]

g1 <- ggplot(data=plot_shoot_weight) +
  geom_boxplot(aes(x=Wheat, y=shoot_weight, fill=Wheat)) +
  scale_fill_manual(values=c("tan1", "steelblue2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g2 <- ggplot(data=plot_shoot_weight) +
  geom_boxplot(aes(x=Soil, y=shoot_weight, fill=Soil)) +
  scale_fill_manual(values=c("cornsilk", "plum2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g3 <- ggplot(data=plot_shoot_weight) +
```

```
   geom_boxplot(aes(x=Biochar, y=shoot_weight, fill=Biochar)) +
   scale_fill_manual(values=c("bisque", "cyan3")) +
   theme(axis.text.x = element_blank(),axis.ticks = element_blank())

grid.arrange(g1, g2, g3, nrow=1, top="Box Plot of Shoot Weight")
```



Box Plot of Shoot Weight
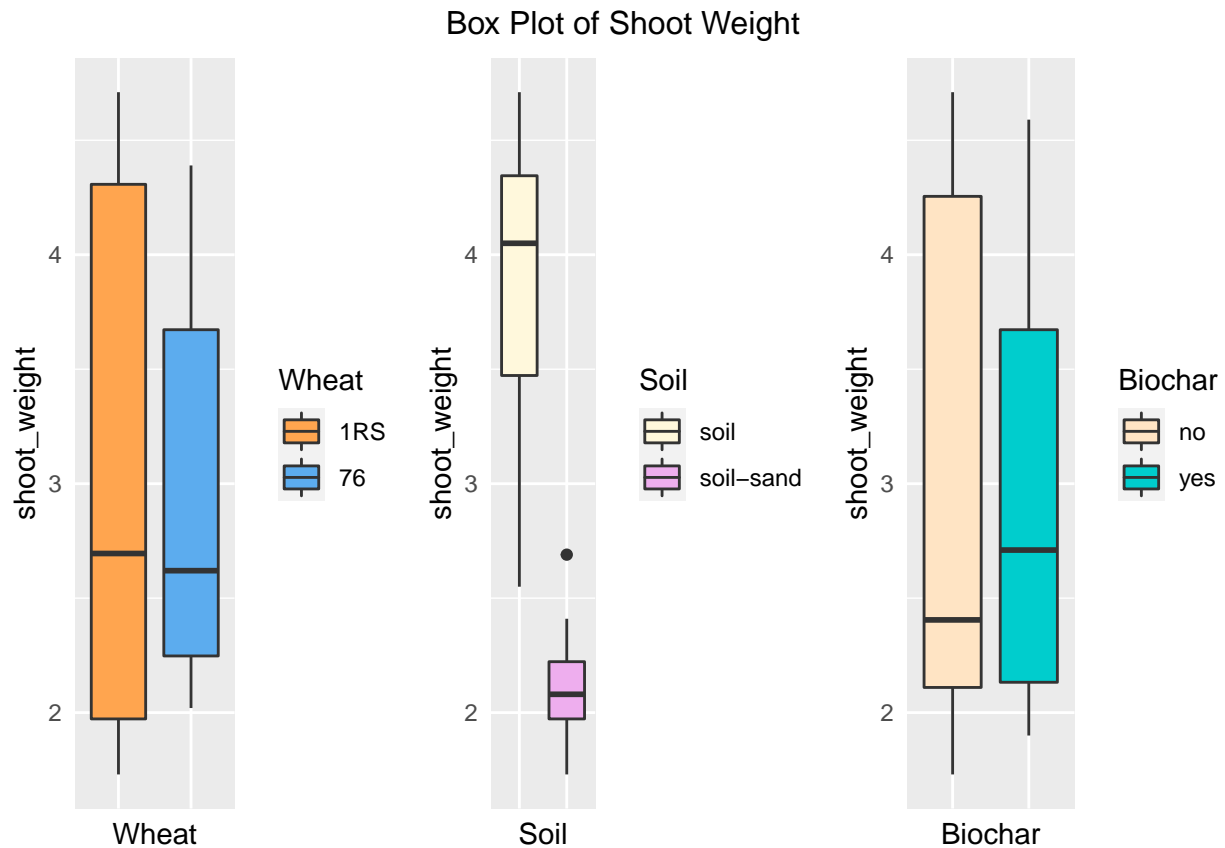
Shoot Weight

NOTE: All models and analysis performed below is for shoot weight only

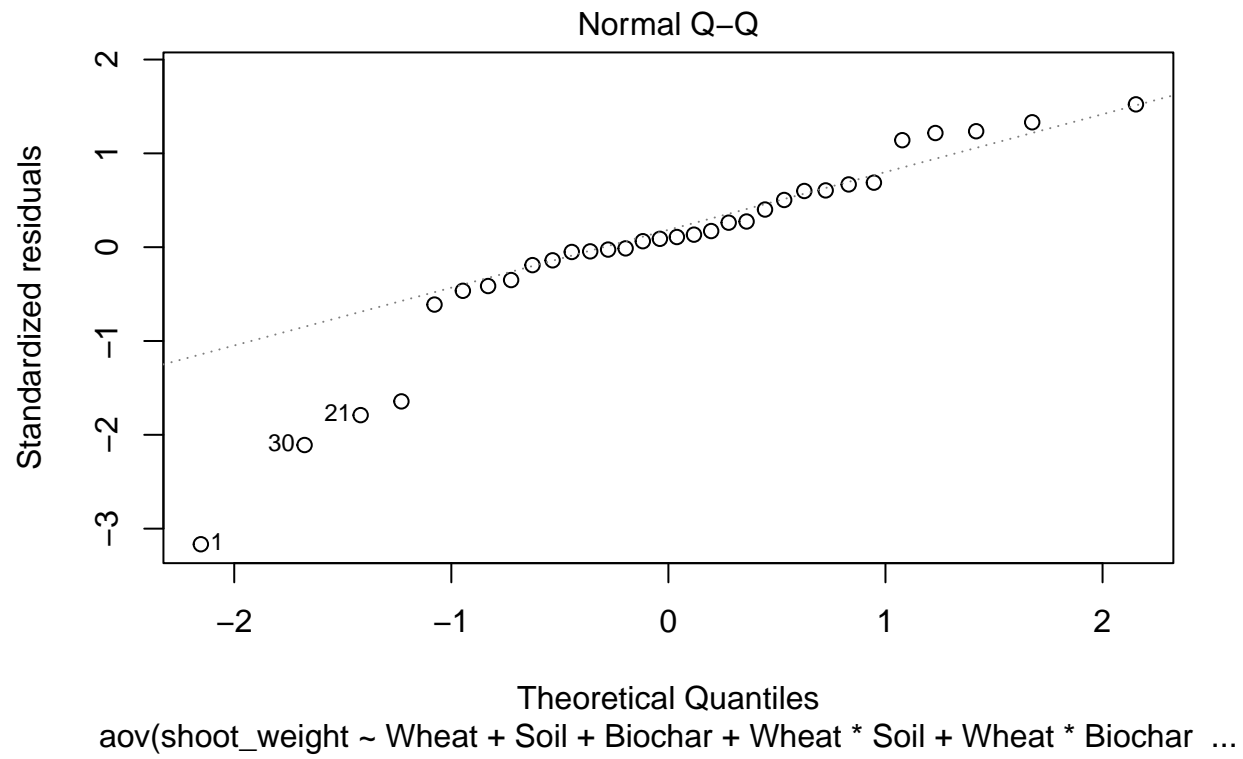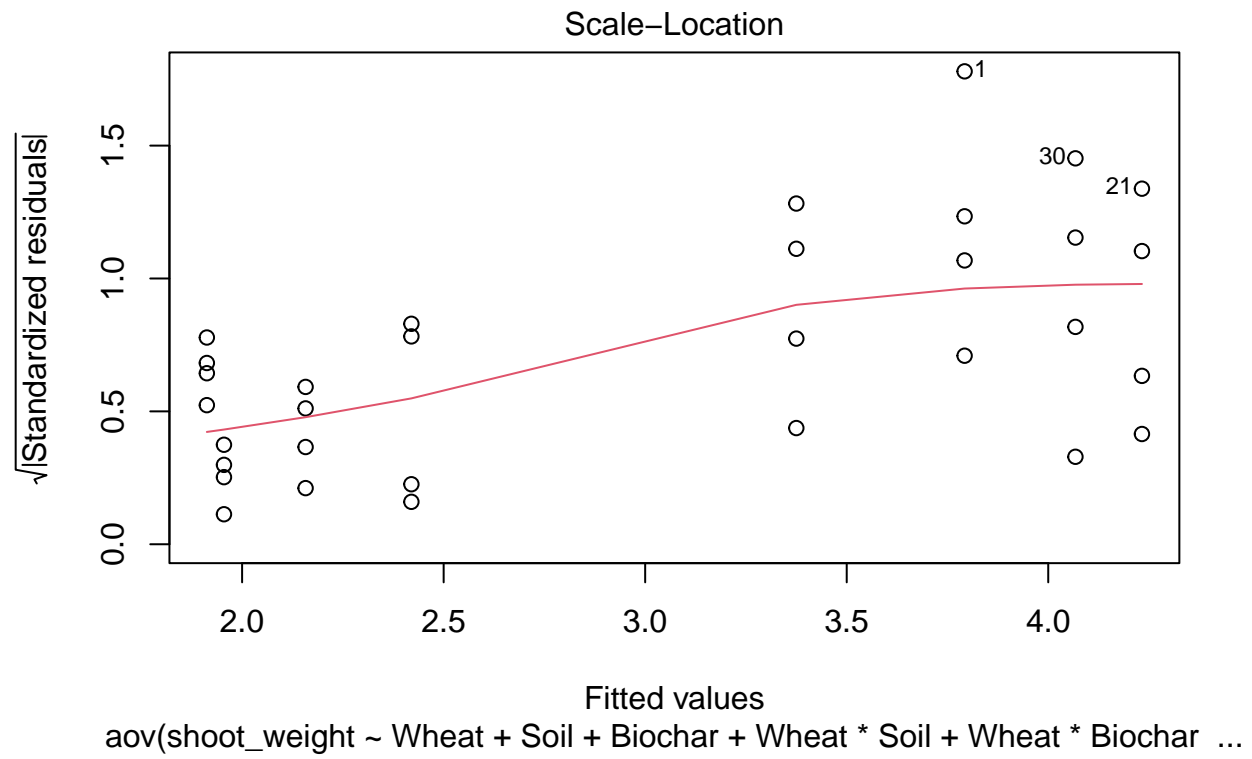## Fit Full Model

```
# fit full model
SW_model <- aov(shoot_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar + Whea
```

Check Model Assumptions

```
# check assumptions
plot(SW_model)
```

Residuals vs Fitted

Fitted values
aov(shoot_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biochar ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shoot_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biochar ...

Scale–Location

√|Standardized residuals|

Fitted values
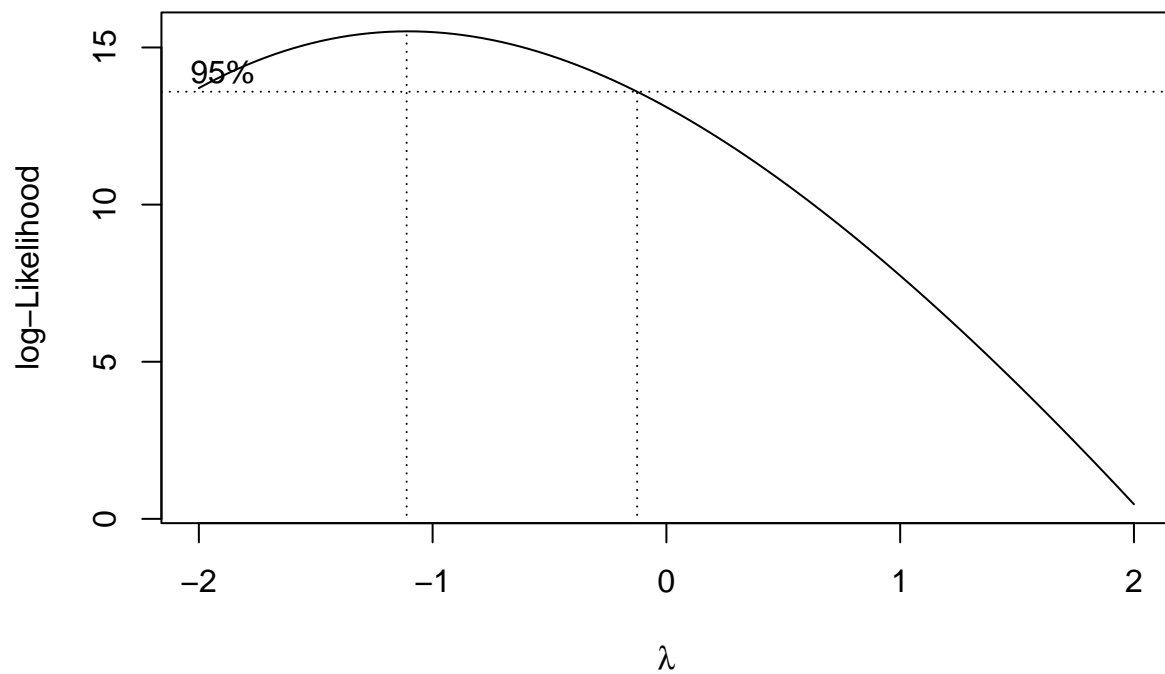aov(shoot_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biochar ...
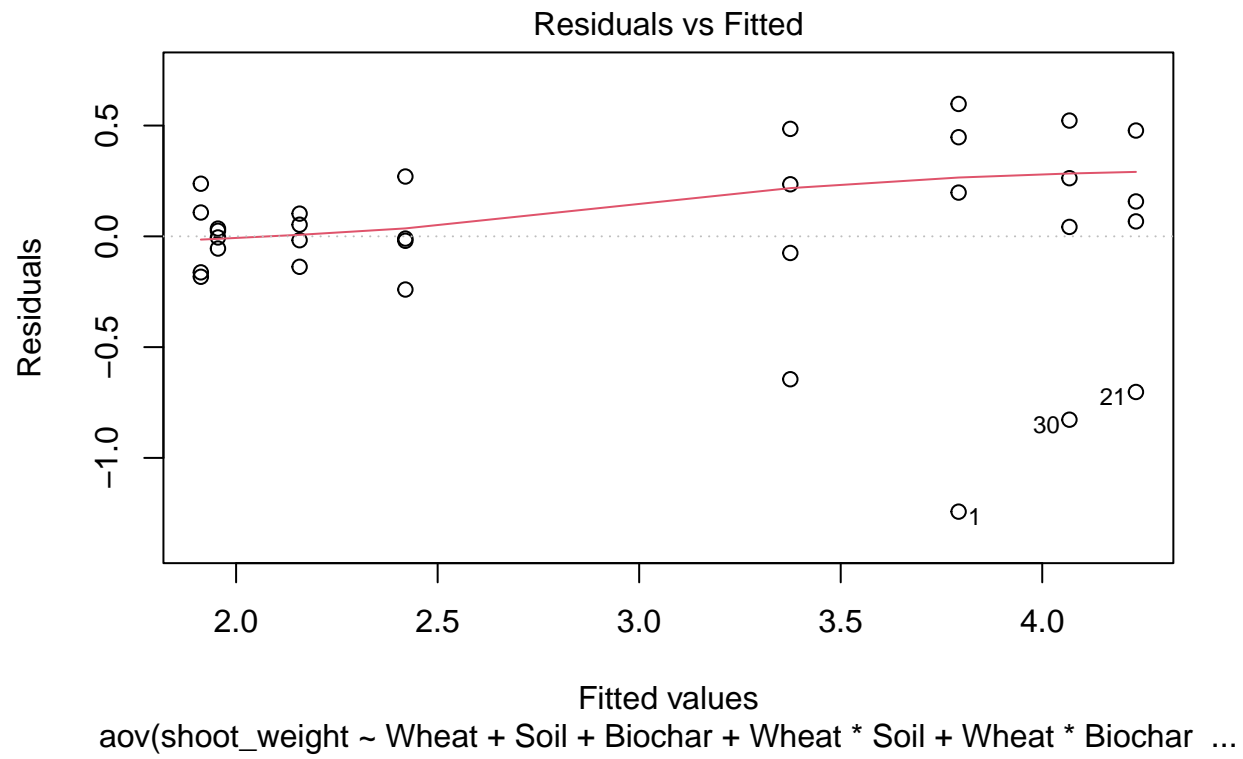
Perform Box-Cox Transformation

```
T <- boxcox(shoot_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar + Wheat*S
```
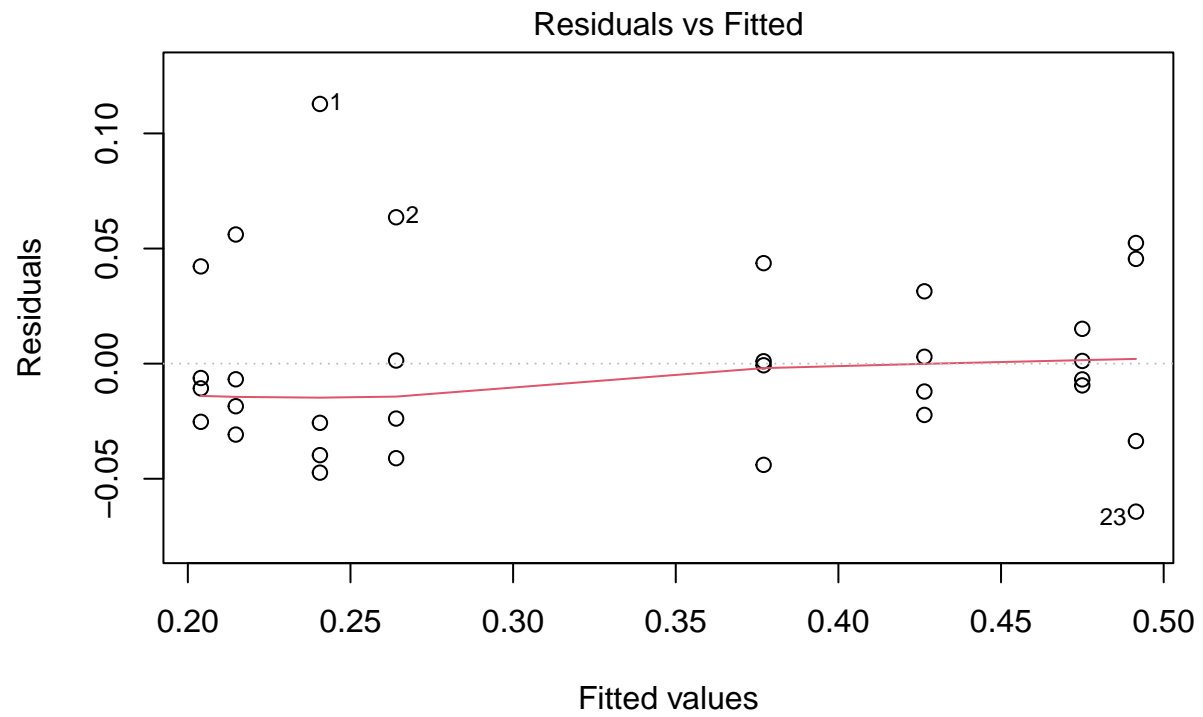
```r
lambda <- T$x[which(T$y == max(T$y))]
```

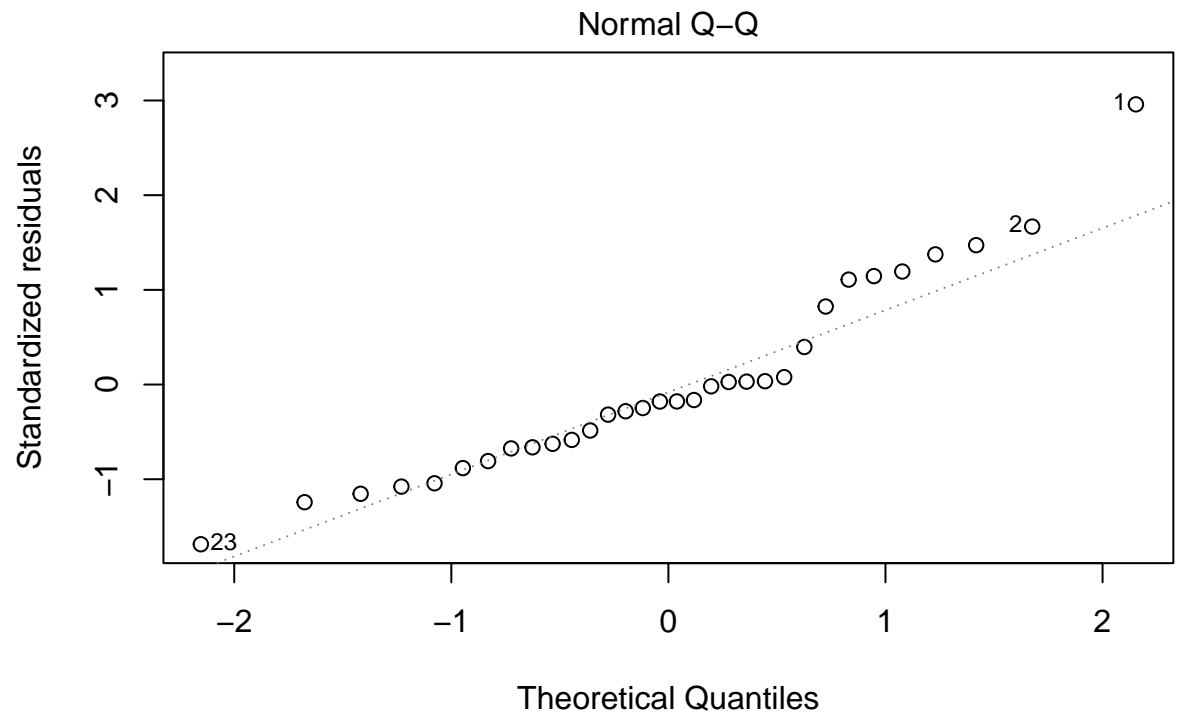**Refit and Check Assumptions after Transformation**

```r
shoot_weight_t <- shoot_weight**lambda

# refit model
SW_model_new <- aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar

# check assumptions
plot(SW_model_new)
```
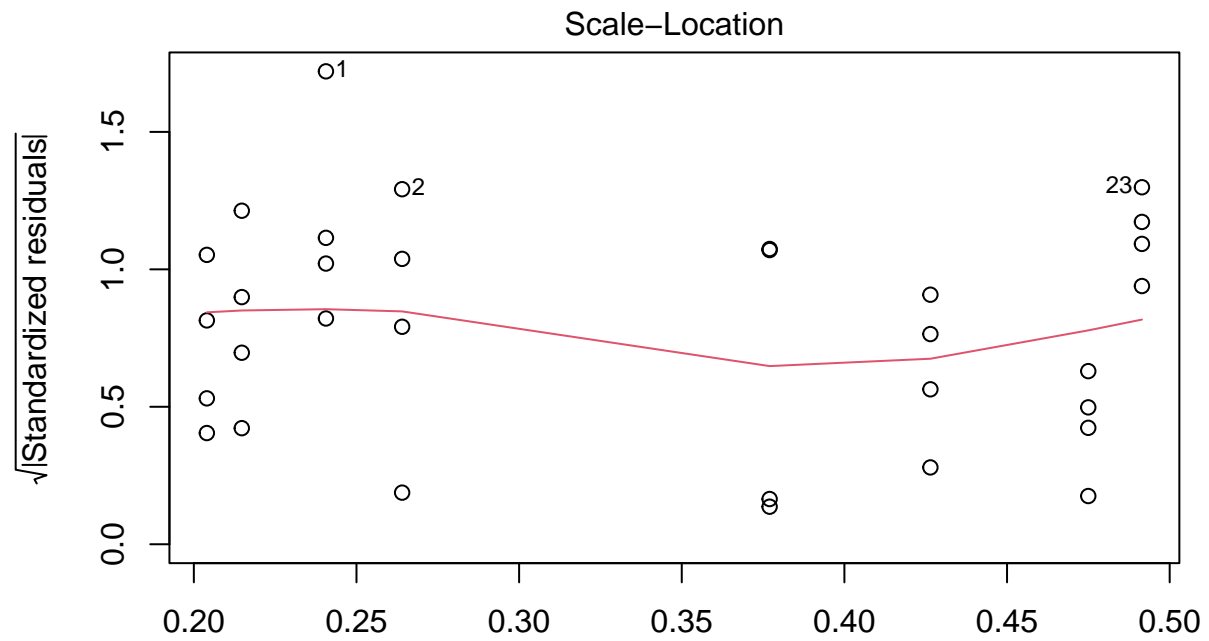
Residuals vs Fitted

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biocha ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biocha ...

Scale–Location

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biocha ...

Check for 3-way Interactions

```
anova(SW_model_new)
```

```
## Analysis of Variance Table
##
## Response: shoot_weight_t
##                   Df  Sum Sq Mean Sq  F value    Pr(>F)
## Wheat              1 0.00297 0.00297   1.5337 0.2275421
## Soil               1 0.35828 0.35828 184.9350 8.996e-13 ***
## Biochar            1 0.00050 0.00050   0.2603 0.6145718
## Wheat:Soil         1 0.03098 0.03098  15.9906 0.0005285 ***
## Wheat:Biochar      1 0.00020 0.00020   0.1057 0.7479045
## Soil:Biochar       1 0.00501 0.00501   2.5855 0.1209267
## Wheat:Soil:Biochar 1 0.00104 0.00104   0.5366 0.4709206
## Residuals         24 0.04650 0.00194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove 3 way interaction

Fit Model 2
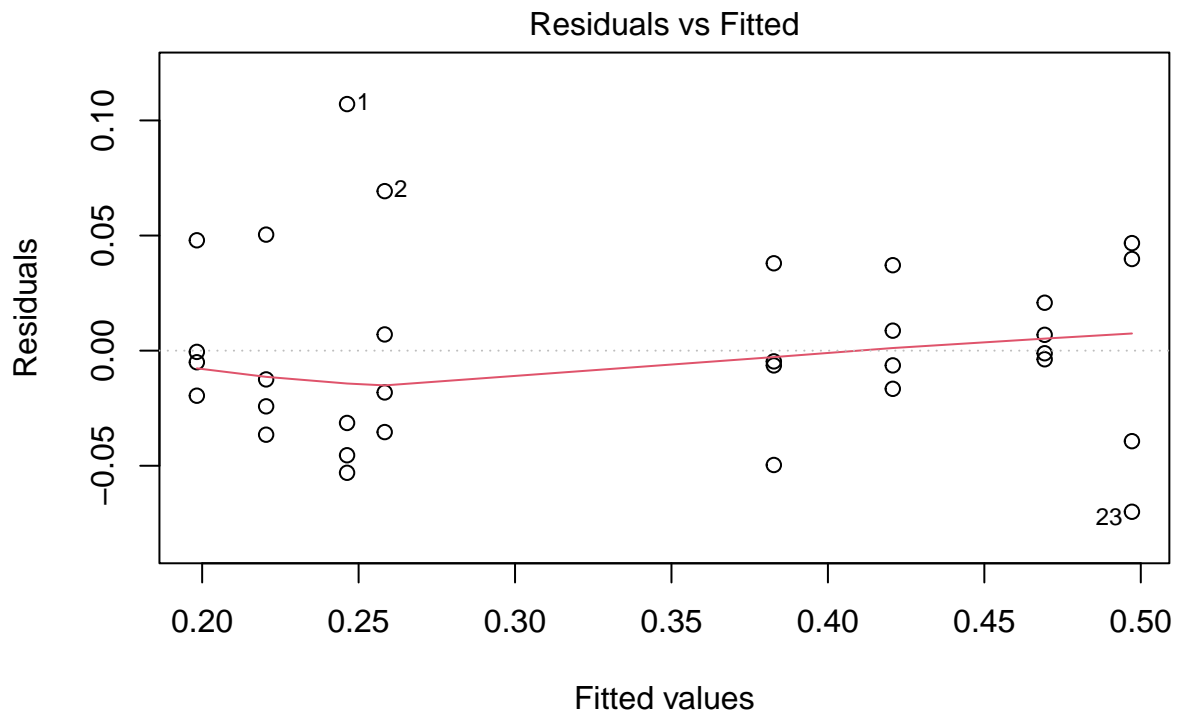
```
# fit full model
SW_model2 <- aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar, da
```

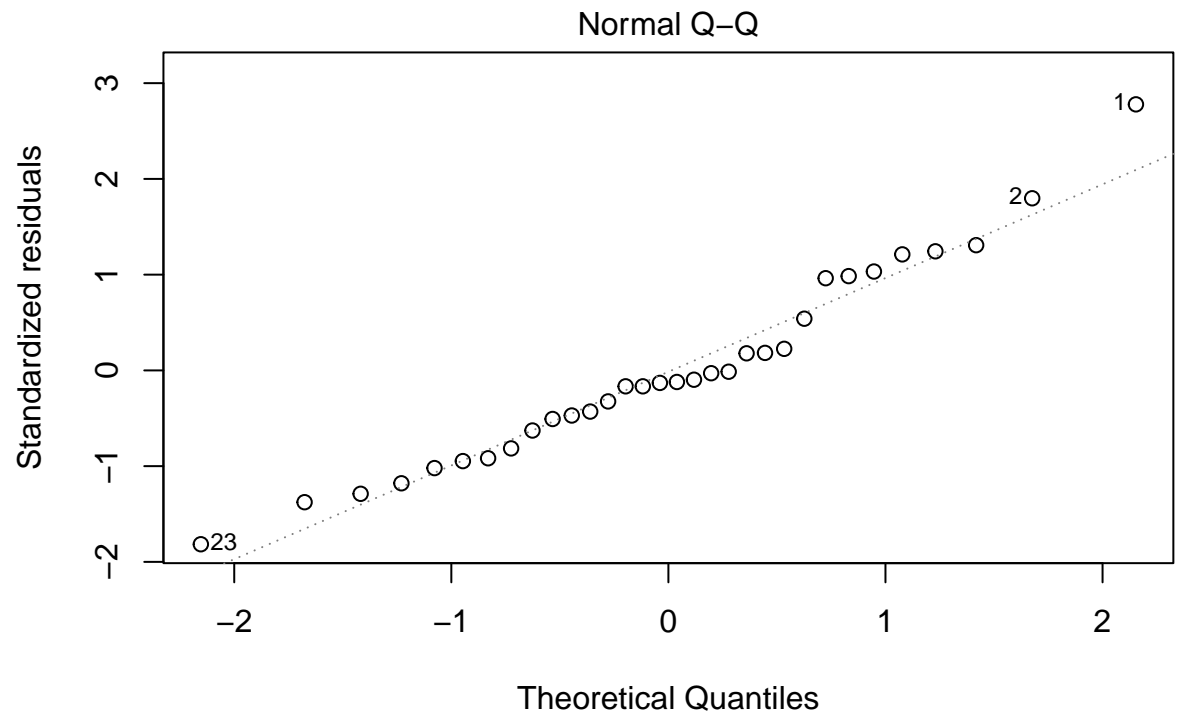**Check Model Assumptions**

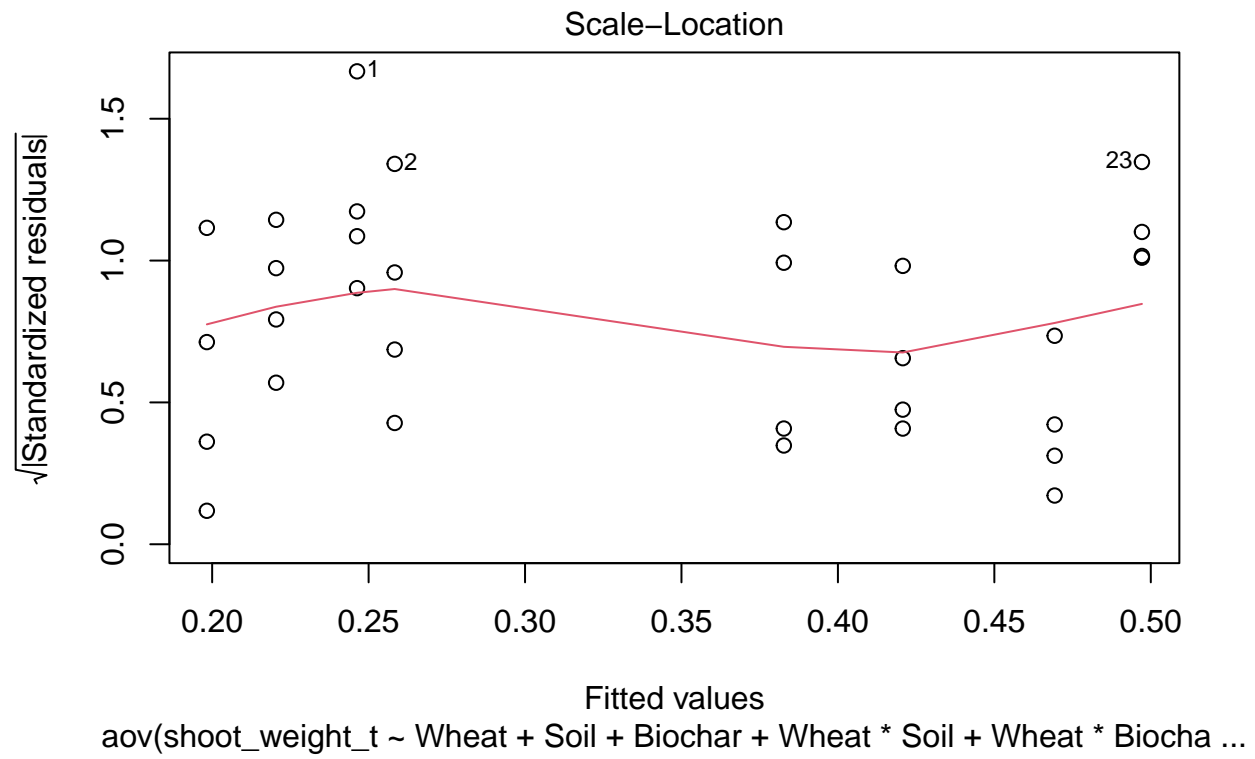```
# check assumptions
plot(SW_model2)
```

Normal Q–Q

aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biocha ...

Scale–Location

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Biocha ...

Check for Nonsignificant Interactions

```r
anova(SW_model2)
```

```
## Analysis of Variance Table
##
## Response: shoot_weight_t
##               Df  Sum Sq Mean Sq  F value    Pr(>F)
## Wheat          1 0.00297 0.00297   1.5626 0.2228583
## Soil           1 0.35828 0.35828 188.4274 3.821e-13 ***
## Biochar        1 0.00050 0.00050   0.2652 0.6110804
## Wheat:Soil     1 0.03098 0.03098  16.2926 0.0004512 ***
## Wheat:Biochar  1 0.00020 0.00020   0.1077 0.7455088
## Soil:Biochar   1 0.00501 0.00501   2.6343 0.1171235
## Residuals     25 0.04754 0.00190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
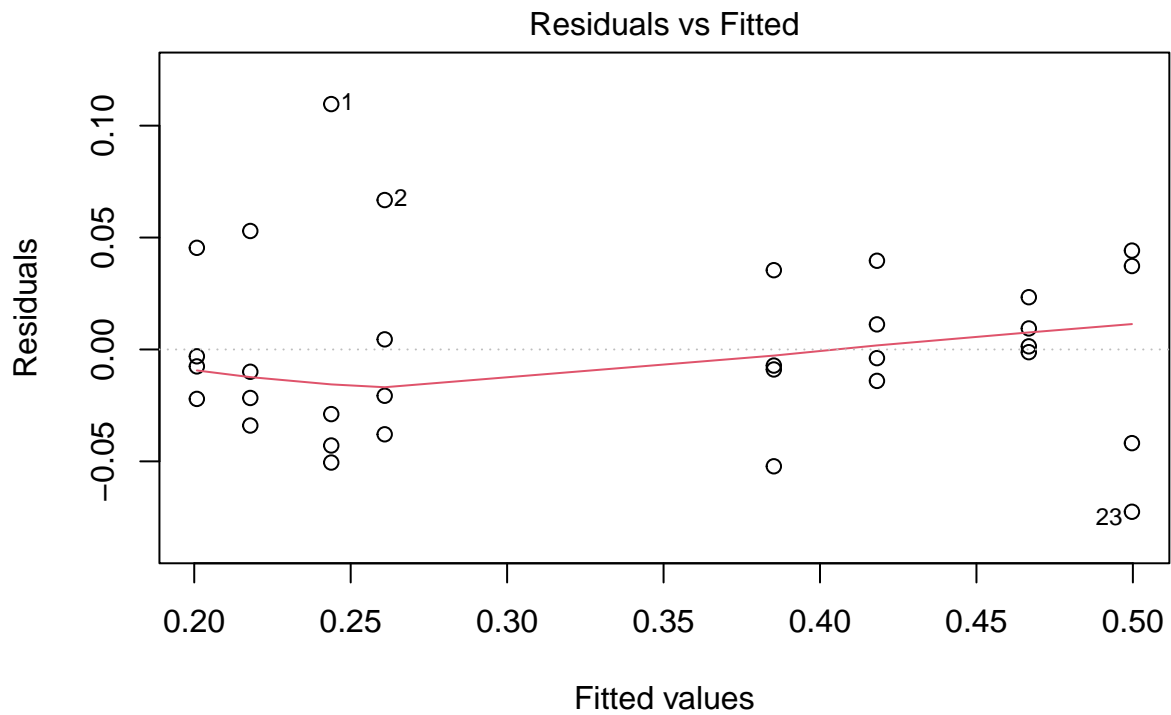
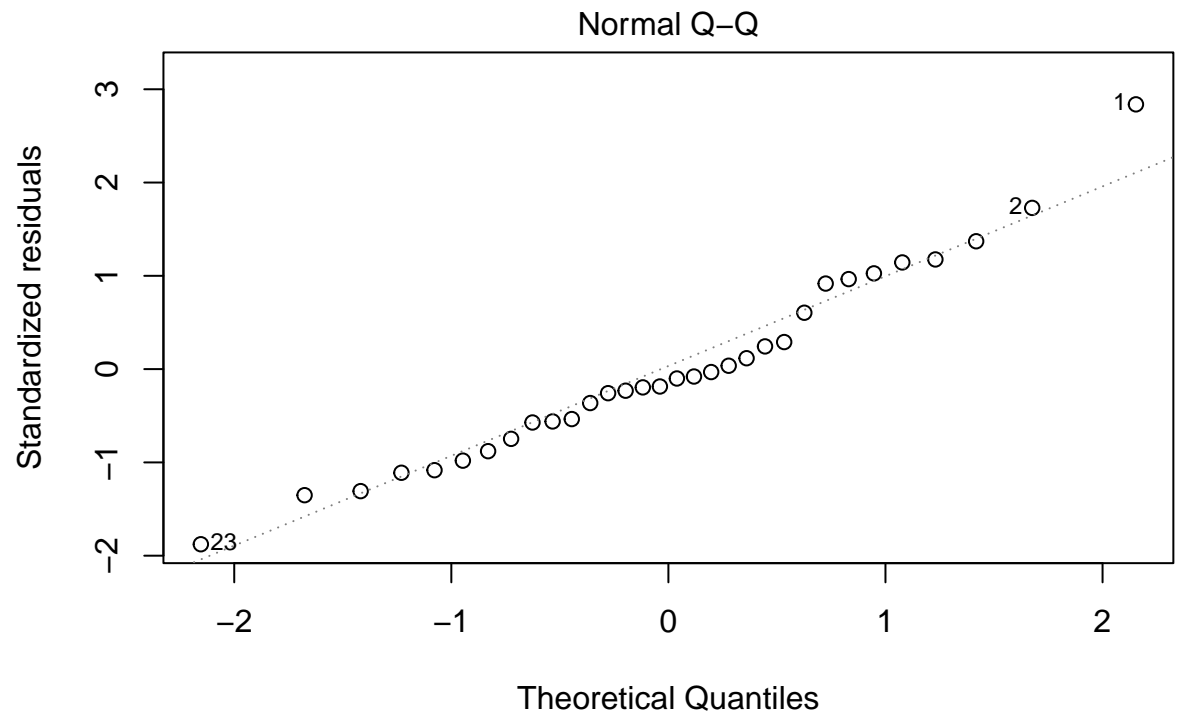**Remove Wheat:Biochar interaction**

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Fit Model 3

```
# fit full model
SW_model3 <- aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil + Soil*Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(SW_model3)
```

Residuals vs Fitted

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Biochar ...

Normal Q–Q

Theoretical Quantiles
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Biochar ...

Scale–Location
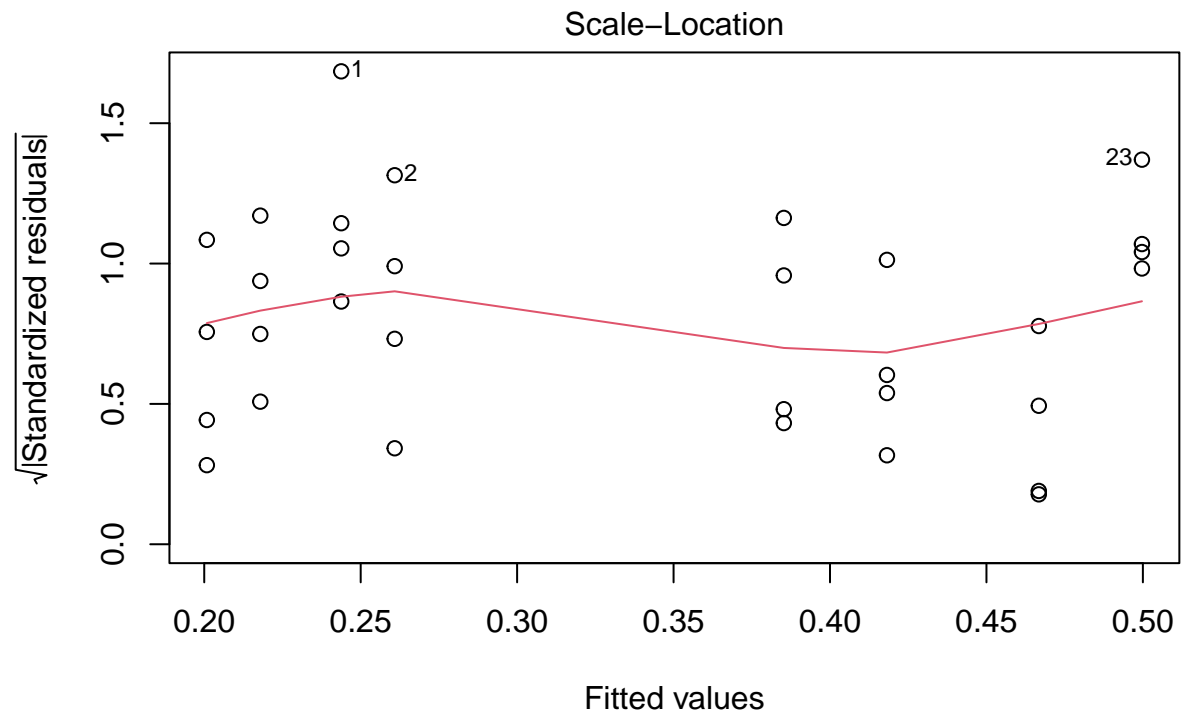
Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Biochar ...

Check for Nonsignificant Interactions

```
anova(SW_model3)
```

```
## Analysis of Variance Table
##
## Response: shoot_weight_t
##               Df  Sum Sq Mean Sq  F value    Pr(>F)
## Wheat          1 0.00297 0.00297   1.6181  0.214610
## Soil           1 0.35828 0.35828 195.1239 1.348e-13 ***
## Biochar        1 0.00050 0.00050   0.2746  0.604672
## Wheat:Soil     1 0.03098 0.03098  16.8716  0.000353 ***
## Soil:Biochar   1 0.00501 0.00501   2.7279  0.110637
## Residuals     26 0.04774 0.00184
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove Soil:Biochar interaction

Fit Model 4

```
# fit full model
SW_model4 <- aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil, data=bc_data)
```
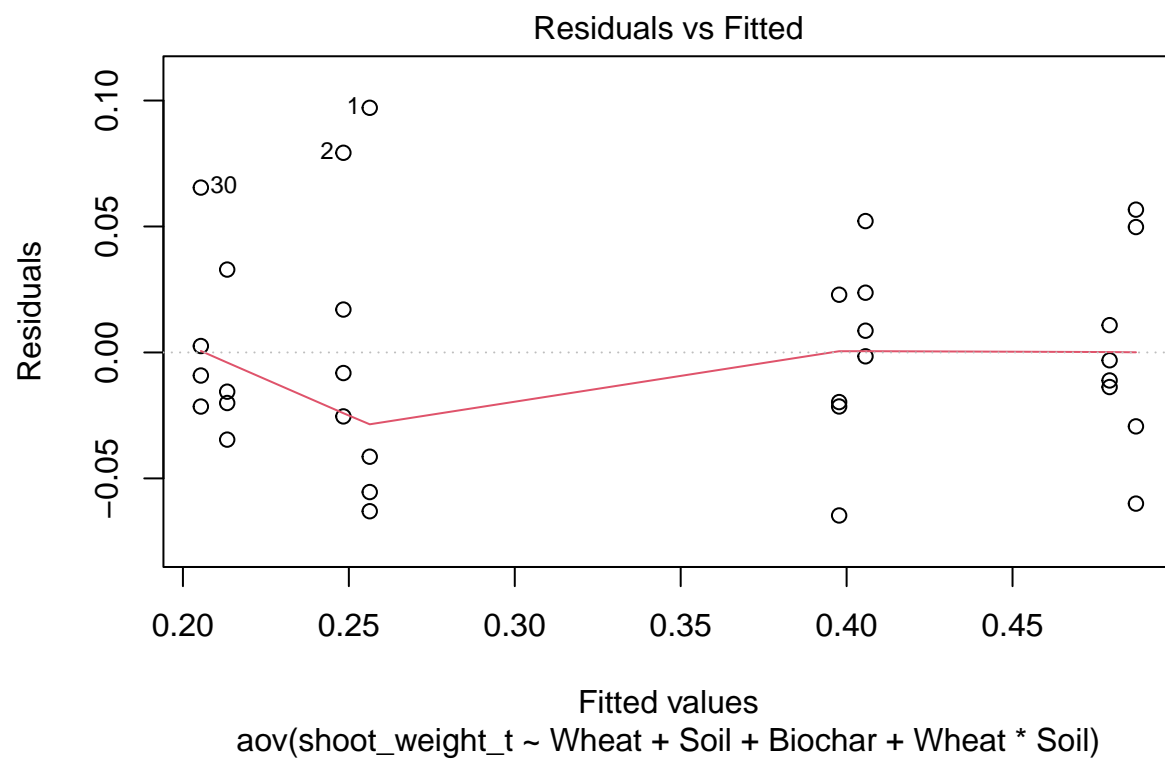
Check Model Assumptions

```
# check assumptions
plot(SW_model4)
```

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil)

Scale–Location

$\sqrt{|\text{Standardized residuals}|}$

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil)

Check for Nonsignificant Interactions

```
anova(SW_model4)
```

```
## Analysis of Variance Table
##
## Response: shoot_weight_t
##             Df  Sum Sq Mean Sq  F value     Pr(>F)
## Wheat        1 0.00297 0.00297   1.5208 0.2281245
## Soil         1 0.35828 0.35828 183.3877 1.488e-13 ***
## Biochar      1 0.00050 0.00050   0.2581 0.6155363
## Wheat:Soil   1 0.03098 0.03098  15.8568 0.0004641 ***
## Residuals   27 0.05275 0.00195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
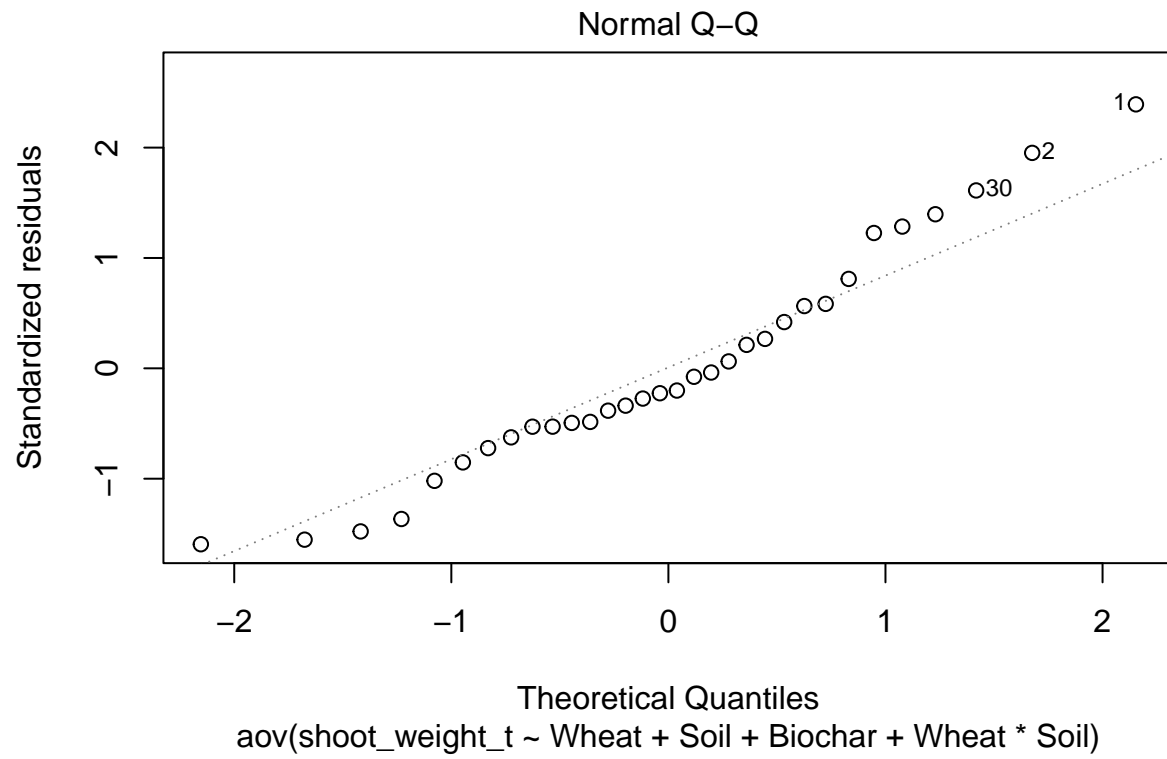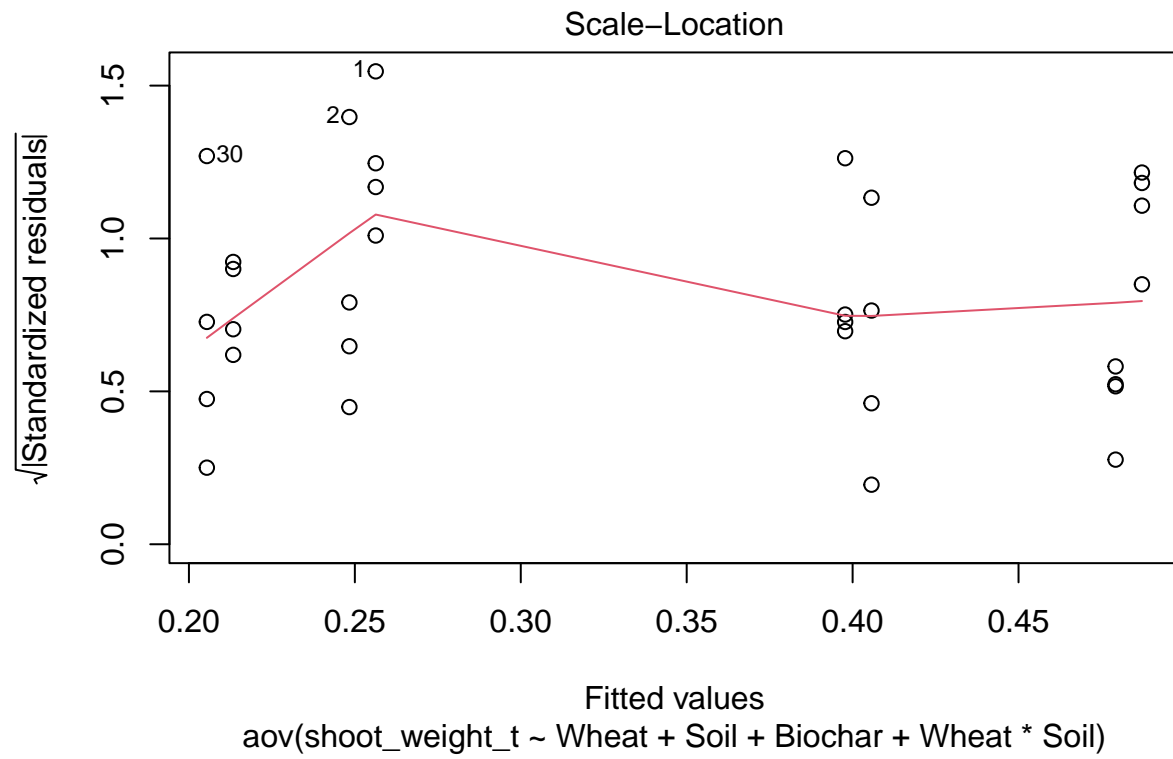
Remove Biochar

Fit Model 5

```
# fit full model
SW_model5 <- aov(shoot_weight_t ~ Wheat + Soil + Wheat*Soil, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(SW_model5)
```

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shoot_weight_t ~ Wheat + Soil + Wheat * Soil)

Scale−Location

√|Standardized residuals|

Fitted values
aov(shoot_weight_t ~ Wheat + Soil + Wheat * Soil)

Check for Nonsignificant Interactions

```
anova(SW_model5)
```

```
## Analysis of Variance Table
##
## Response: shoot_weight_t
##             Df  Sum Sq Mean Sq  F value     Pr(>F)
## Wheat        1 0.00297 0.00297   1.5622 0.2216880
## Soil         1 0.35828 0.35828 188.3789 5.884e-14 ***
## Wheat:Soil   1 0.03098 0.03098  16.2884 0.0003816 ***
## Residuals   28 0.05325 0.00190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
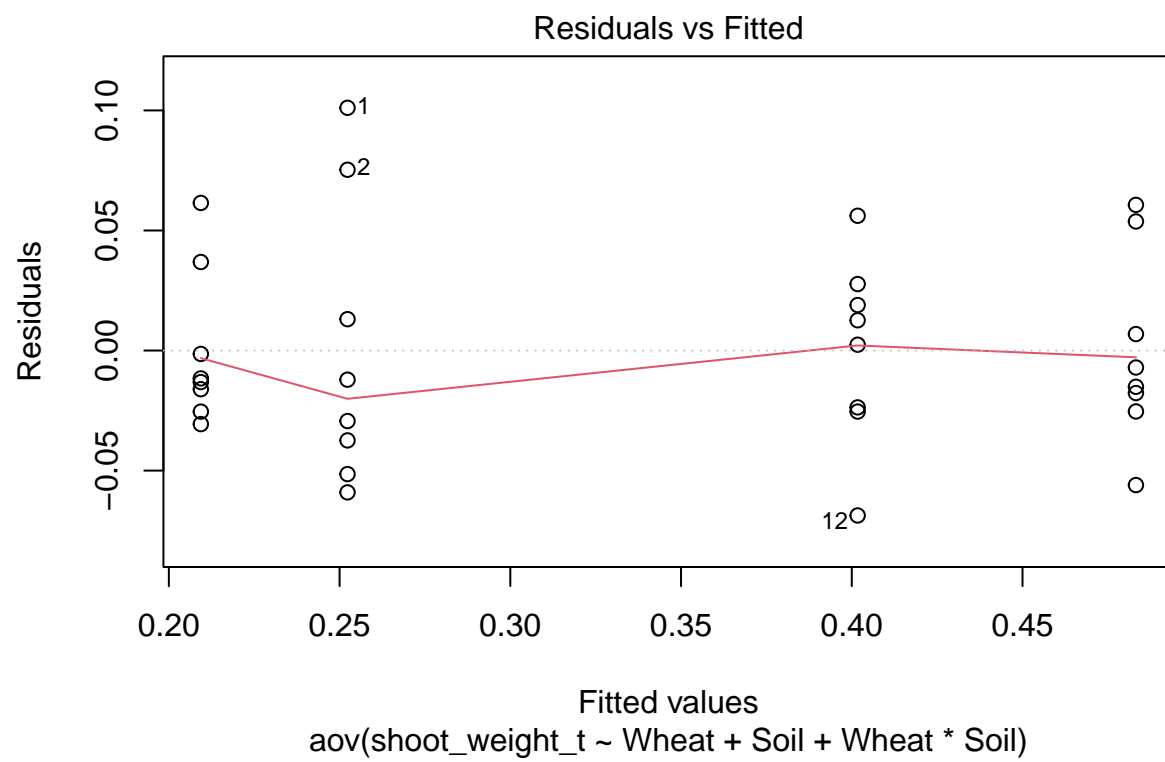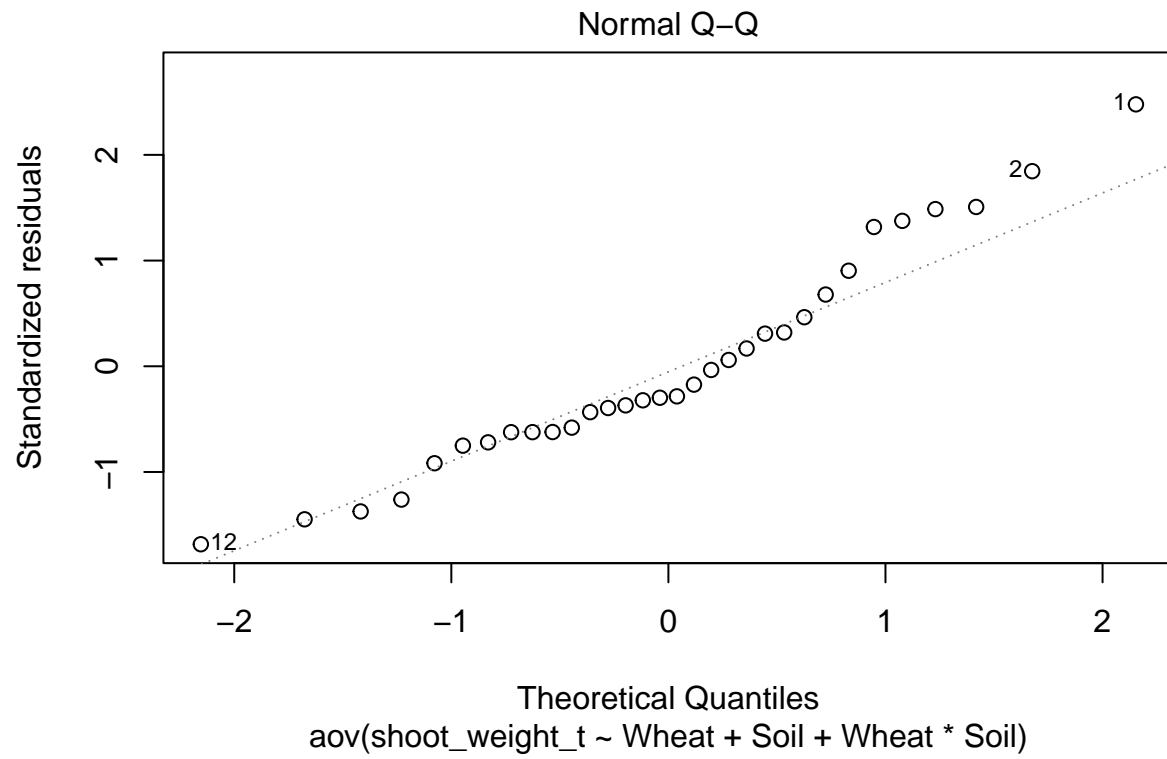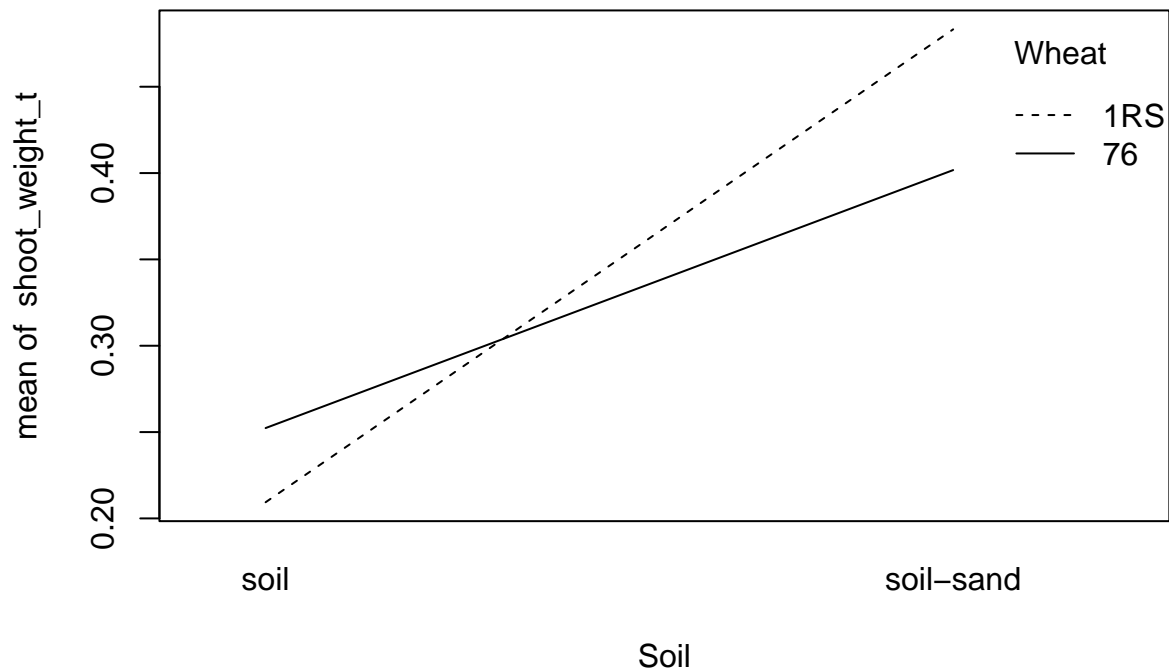
Final Model: Order 2 with interaction

Final Model: Shoot Weight = Wheat + Soil + Wheat*Soil

```
interaction.plot(Soil, Wheat, shoot_weight_t)
```

Multiple Comparison

```r
# compare the effect of Wheat at each level of Soil
emmeans(SW_model5, list(pairwise ~ Wheat|Soil))
```

```
## $`emmeans of Wheat | Soil`
## Soil = soil:
##  Wheat emmean     SE df lower.CL upper.CL
##  1RS    0.209 0.0154 28    0.178    0.241
##  76     0.252 0.0154 28    0.221    0.284
##
## Soil = soil-sand:
##  Wheat emmean     SE df lower.CL upper.CL
##  1RS    0.483 0.0154 28    0.452    0.515
##  76     0.402 0.0154 28    0.370    0.433
##
## Confidence level used: 0.95
##
## $`pairwise differences of Wheat | Soil`
## Soil = soil:
##  2        estimate     SE df t.ratio p.value
##  1RS - 76  -0.0430 0.0218 28  -1.970  0.0588
##
## Soil = soil-sand:
```

```
## 2           estimate     SE df t.ratio p.value
## 1RS - 76    0.0815 0.0218 28  3.738  0.0008
```

- The effect of wheat is significant when soil type is "soil-sand" (p-value = 0.0012 < 0.05) in terms of shoot weight.

```
# compare the effect of Soil at each level of Wheat
emmeans(SW_model5, list(pairwise ~ Soil|Wheat))
```

```
## $'emmeans of Soil | Wheat'
## Wheat = 1RS:
##  Soil       emmean     SE df lower.CL upper.CL
##  soil        0.209 0.0154 28    0.178    0.241
##  soil-sand   0.483 0.0154 28    0.452    0.515
##
## Wheat = 76:
##  Soil       emmean     SE df lower.CL upper.CL
##  soil        0.252 0.0154 28    0.221    0.284
##  soil-sand   0.402 0.0154 28    0.370    0.433
##
## Confidence level used: 0.95
##
## $'pairwise differences of Soil | Wheat'
## Wheat = 1RS:
##  2                 estimate     SE df  t.ratio p.value
##  soil - (soil-sand)  -0.274 0.0218 28 -12.559 <.0001
##
## Wheat = 76:
##  2                 estimate     SE df t.ratio p.value
##  soil - (soil-sand)  -0.149 0.0218 28  -6.851 <.0001
```

- The effect of Soil is significant at each level of wheat type (both p-value < 0.0001) in terms of shoot weight.

Shallow Root Weight

NOTE: All models and analysis performed below is for shoot weight only

Box Plot Shallow Root Weight

```
plot_shallow_root_weight <- bc_data[c("Wheat","Soil","Biochar","shallow_root_weight")]
gg_object <- ggplot(data=plot_shallow_root_weight)

g1 <- gg_object +
  geom_boxplot(aes(x=Wheat, y=shallow_root_weight, fill=Wheat)) +
  scale_fill_manual(values=c("tan1", "steelblue2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g2 <- gg_object +
  geom_boxplot(aes(x=Soil, y=shallow_root_weight, fill=Soil)) +
```
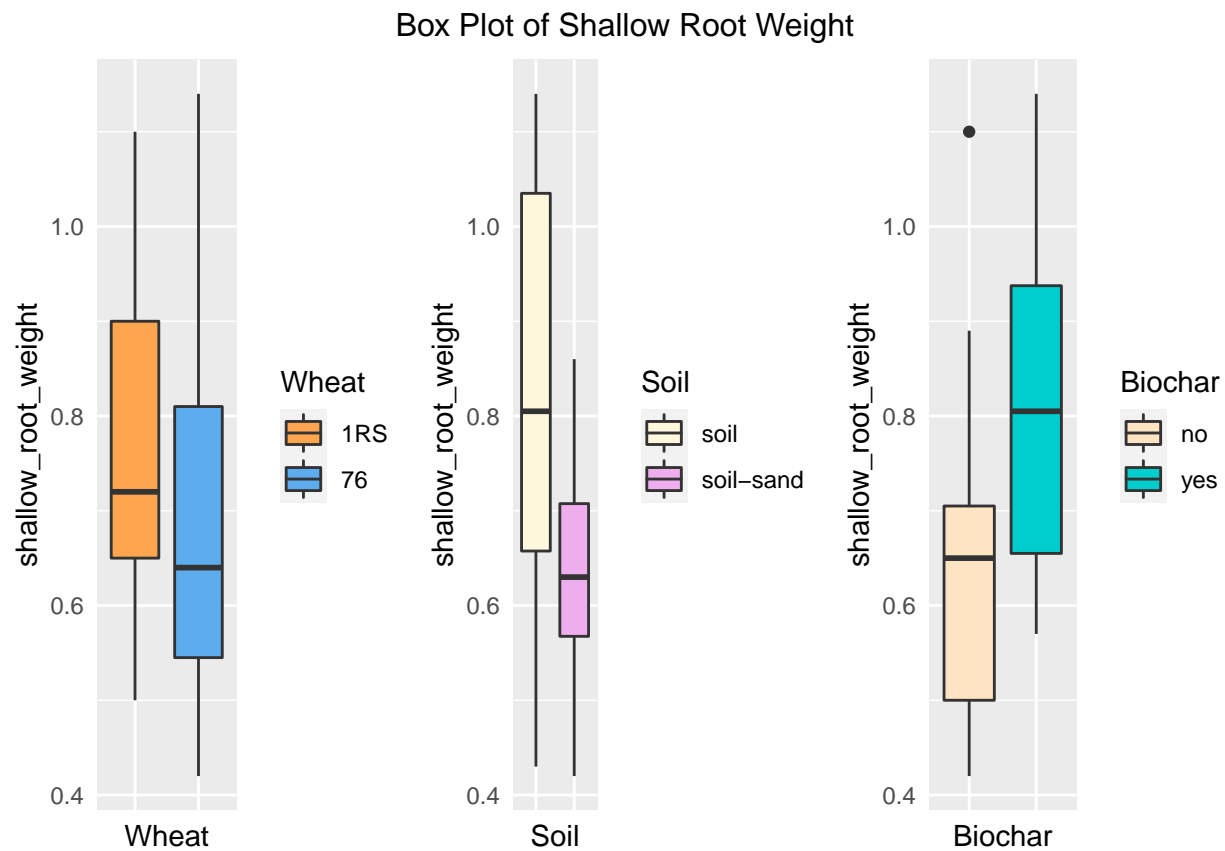
```
    scale_fill_manual(values=c("cornsilk", "plum2")) +
    theme(axis.text.x = element_blank(),axis.ticks = element_blank()))
g3 <- gg_object +
    geom_boxplot(aes(x=Biochar, y=shallow_root_weight, fill=Biochar)) +
    scale_fill_manual(values=c("bisque", "cyan3")) +
    theme(axis.text.x = element_blank(),axis.ticks = element_blank()))

grid.arrange(g1, g2, g3, nrow=1, top="Box Plot of Shallow Root Weight")
```

Box Plot of Shallow Root Weight

Fit Full Model

```
# fit full model
SRW_model <- aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Bioch
```
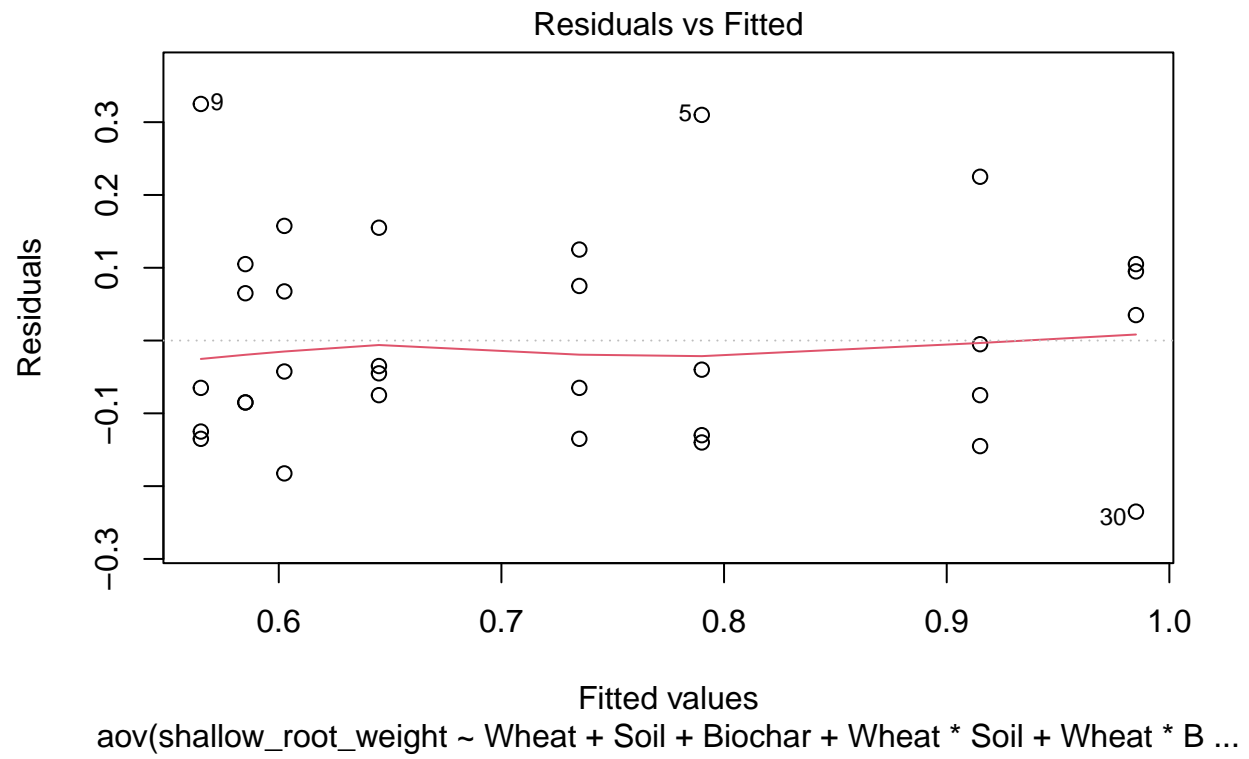
Check Model Assumptions

```
# check assumptions
plot(SRW_model)
```

Residuals vs Fitted

Residuals

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...

Normal Q–Q

Theoretical Quantiles
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...

Scale−Location

√|Standardized residuals|
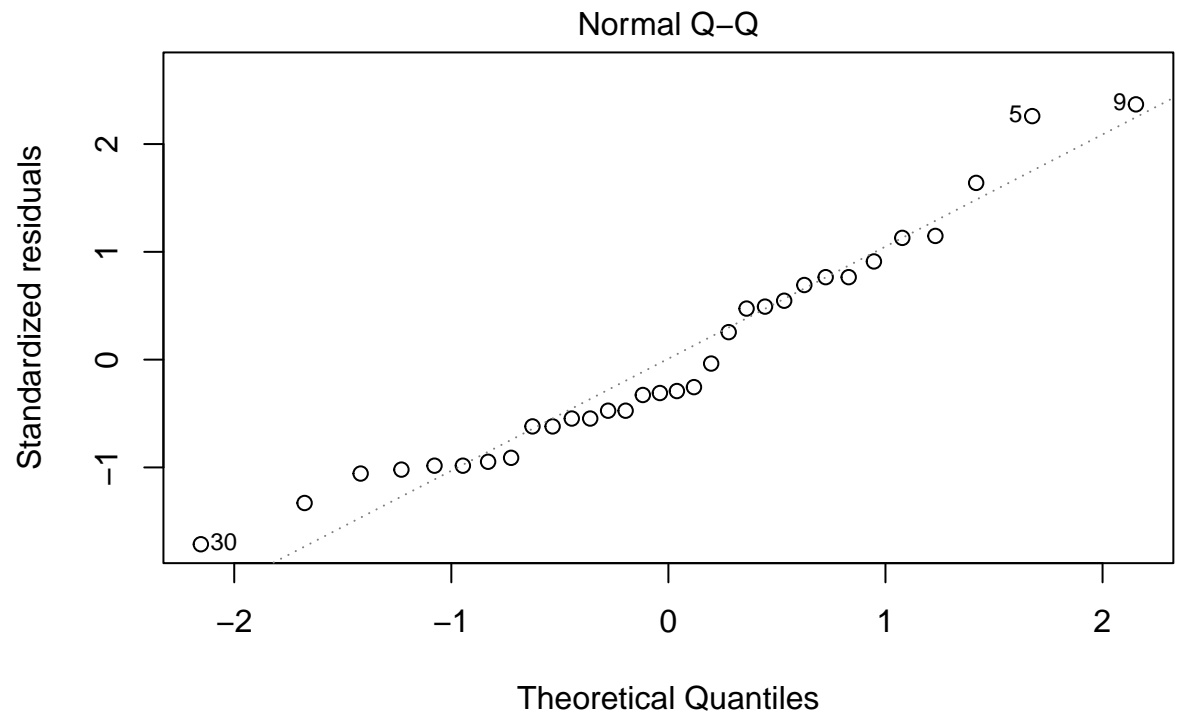
Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...
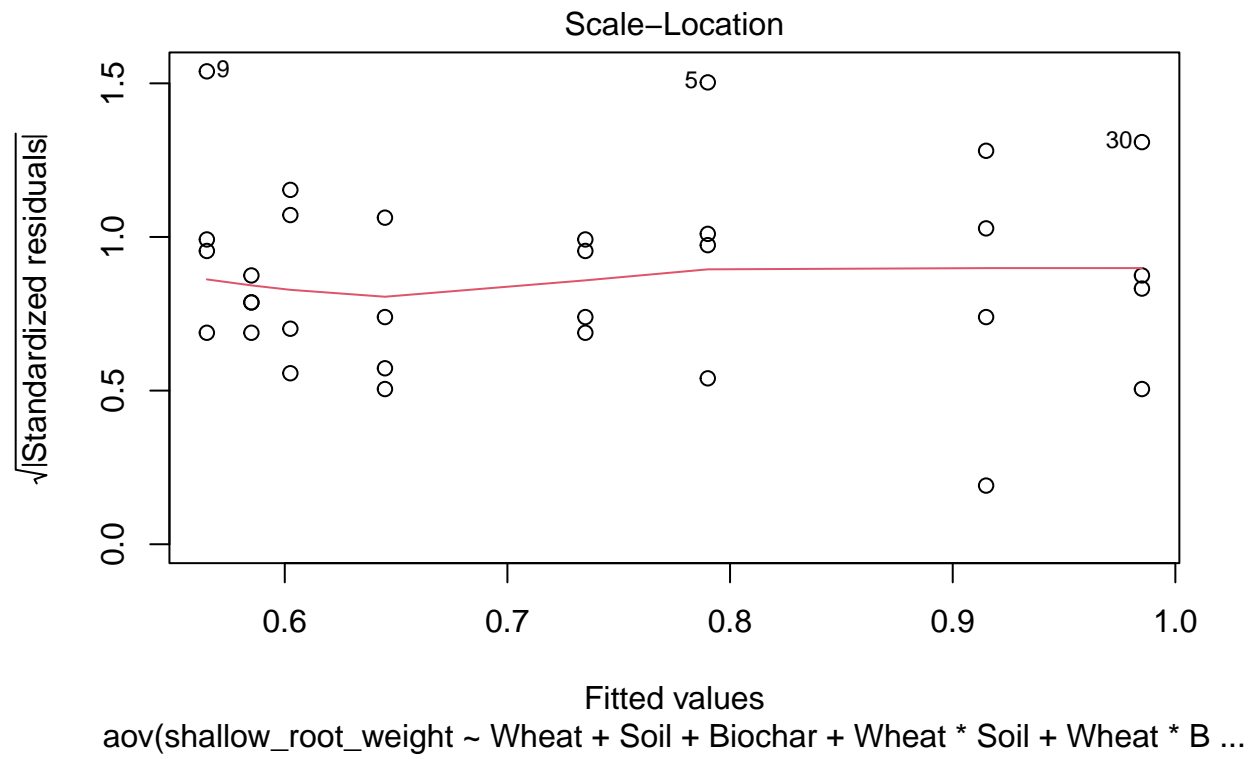
Transformation not necessary

Check for Nonsignificant Interactions

```
anova(SRW_model)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##                    Df  Sum Sq  Mean Sq F value   Pr(>F)
## Wheat               1 0.06753 0.067528  2.6900 0.114021
## Soil                1 0.23633 0.236328  9.4143 0.005274 **
## Biochar             1 0.27195 0.271953 10.8334 0.003076 **
## Wheat:Soil          1 0.02475 0.024753  0.9861 0.330615
## Wheat:Biochar       1 0.00113 0.001128  0.0449 0.833905
## Soil:Biochar        1 0.06213 0.062128  2.4749 0.128767
## Wheat:Soil:Biochar  1 0.03445 0.034453  1.3725 0.252889
## Residuals          24 0.60248 0.025103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove 3 way interaction

Fit Model 2

```
# fit full model
SRW_model2 <- aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Bioc
```
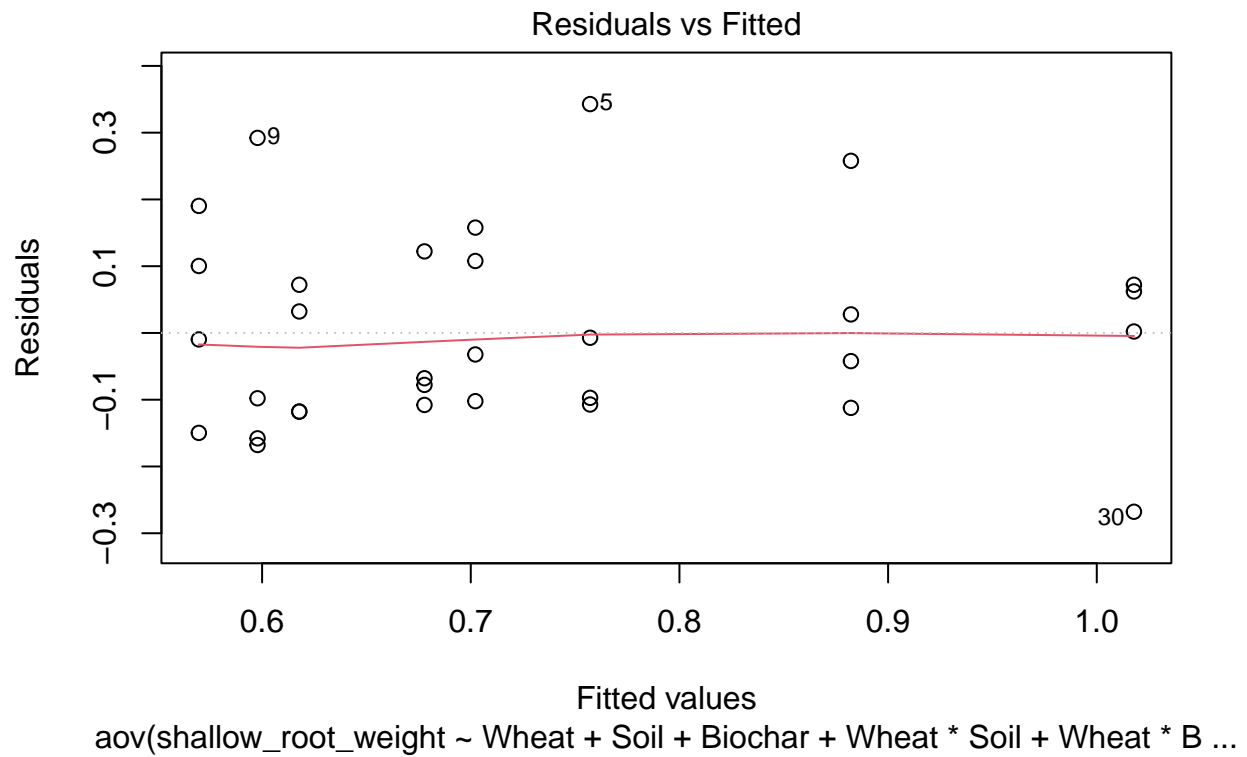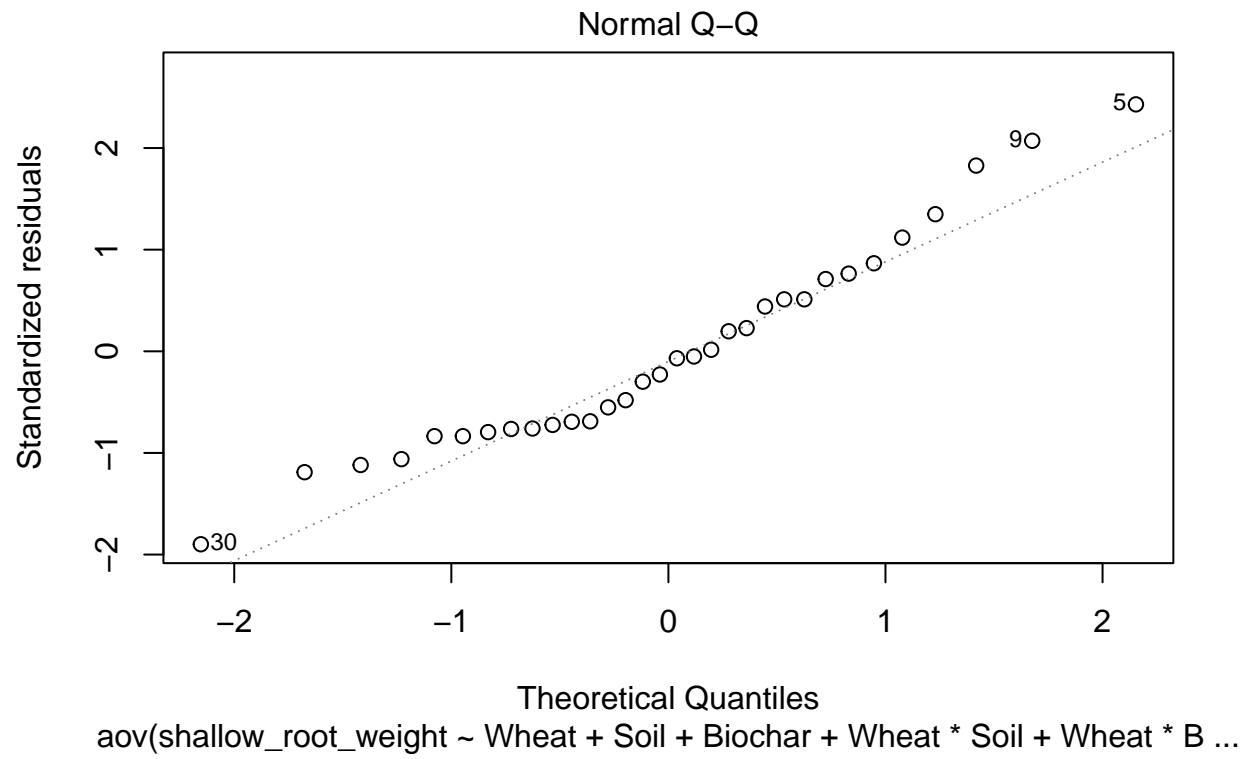
Check Model Assumptions

```
# check assumptions
plot(SRW_model2)
```

Residuals vs Fitted

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...

Normal Q–Q

Theoretical Quantiles
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...

Scale–Location

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * B ...
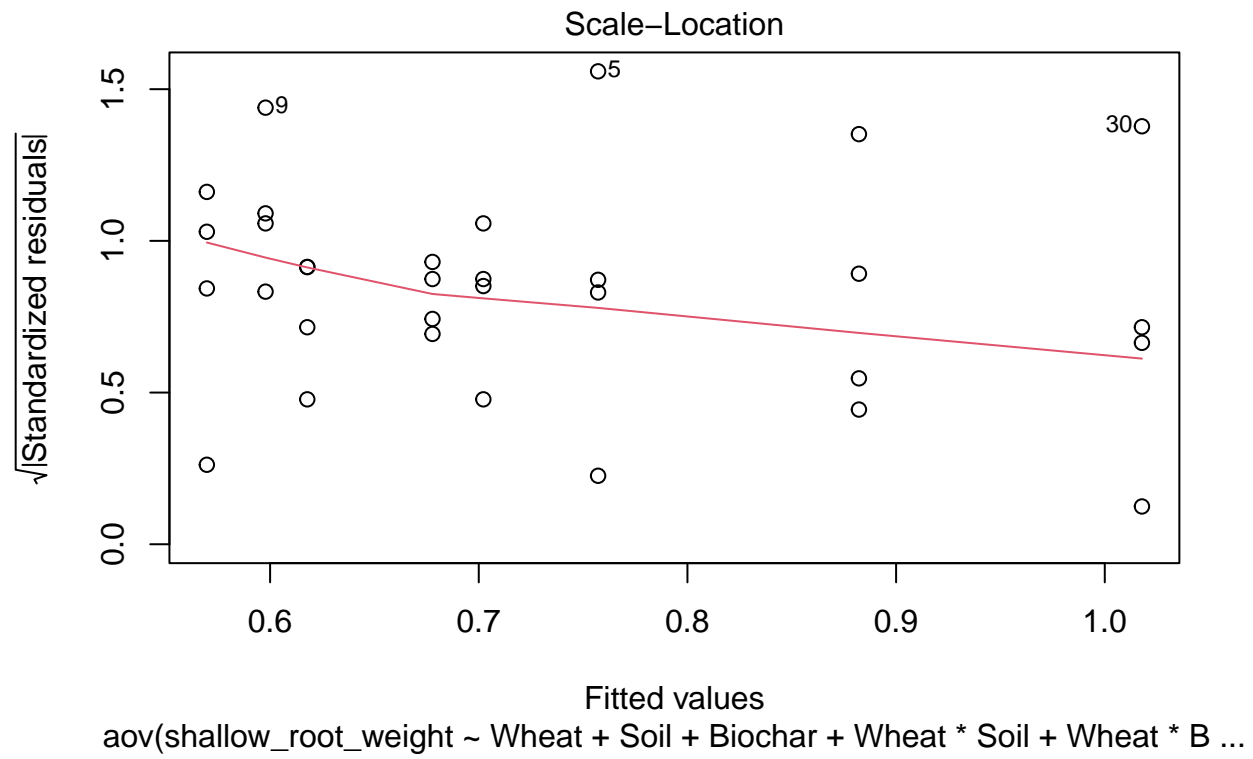
Check for Nonsignificant Interactions

```
anova(SRW_model2)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##               Df  Sum Sq  Mean Sq F value   Pr(>F)
## Wheat          1 0.06753 0.067528  2.6505 0.116054
## Soil           1 0.23633 0.236328  9.2761 0.005409 **
## Biochar        1 0.27195 0.271953 10.6744 0.003150 **
## Wheat:Soil     1 0.02475 0.024753  0.9716 0.333730
## Wheat:Biochar  1 0.00113 0.001128  0.0443 0.835039
## Soil:Biochar   1 0.06213 0.062128  2.4386 0.130954
## Residuals     25 0.63693 0.025477
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove Wheat:Biochar interaction

Fit Model 3

```
# fit full model
SRW_model3 <- aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Soil*Biochar, data=bc_data
```

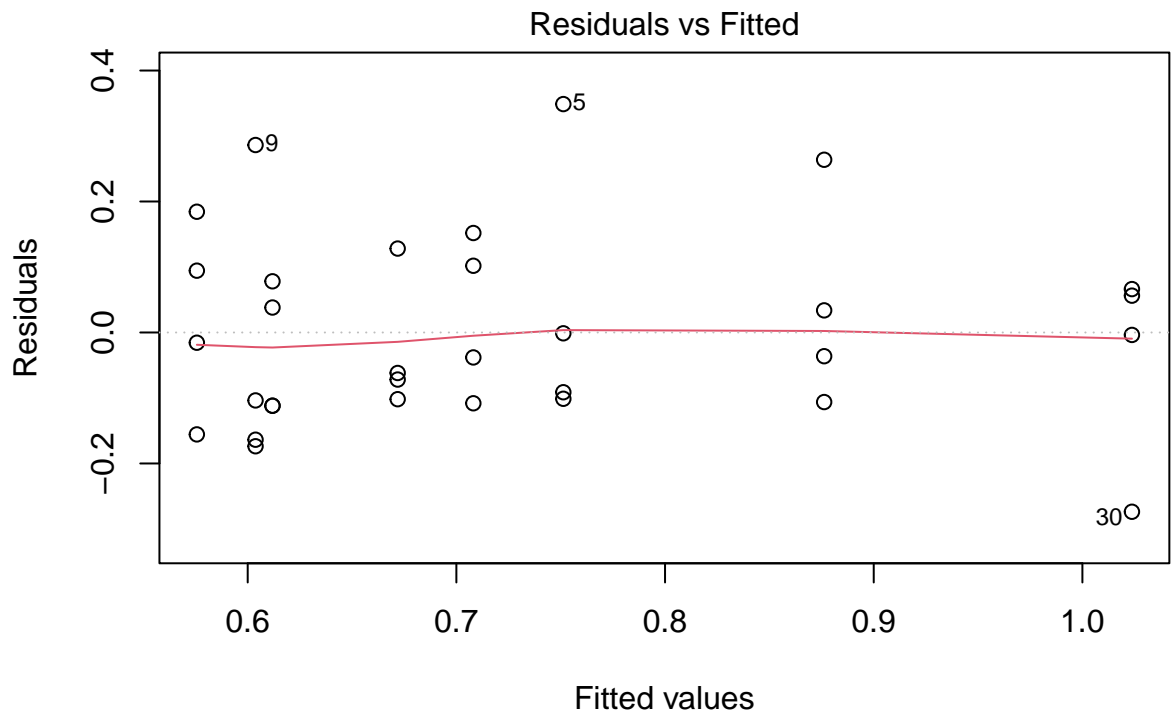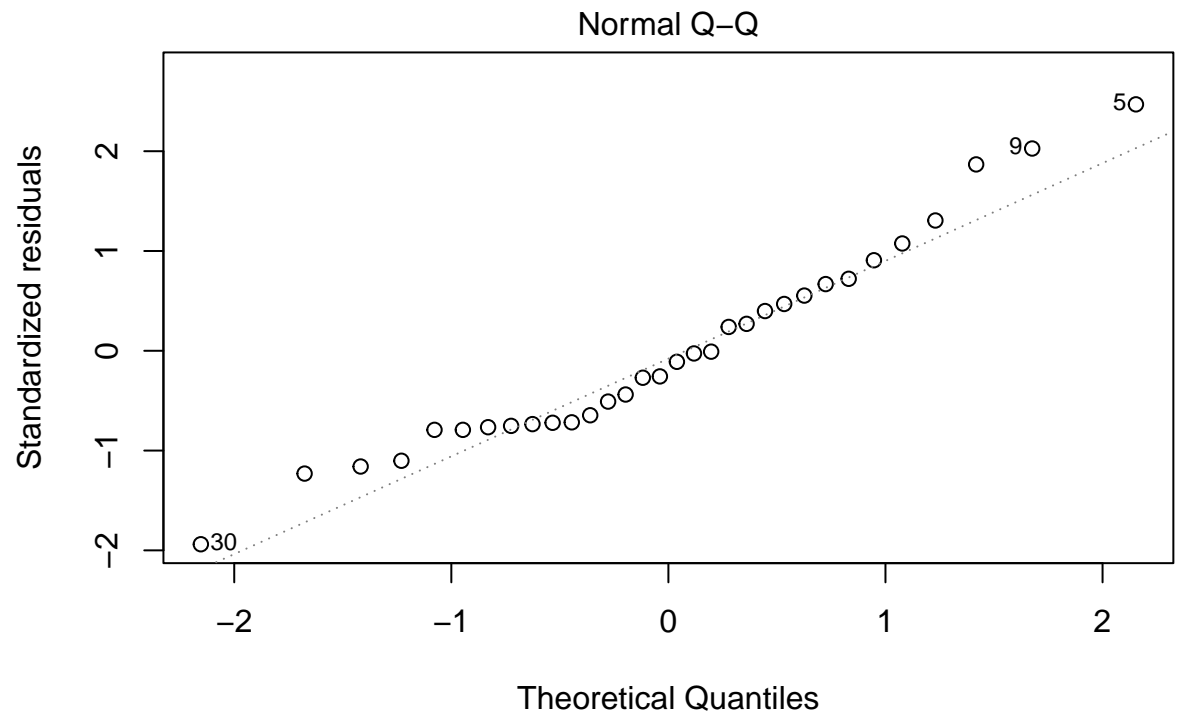**Check Model Assumptions**

```
# check assumptions
plot(SRW_model3)
```


Residuals vs Fitted

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bi ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bi ...

Scale−Location

√|Standardized residuals|

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bi ...

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Check for Nonsignificant Interactions

```
anova(SRW_model3)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##              Df  Sum Sq  Mean Sq F value   Pr(>F)
## Wheat         1 0.06753 0.067528  2.7517 0.109169
## Soil          1 0.23633 0.236328  9.6301 0.004574 **
## Biochar       1 0.27195 0.271953 11.0818 0.002612 **
## Wheat:Soil    1 0.02475 0.024753  1.0087 0.324480
## Soil:Biochar  1 0.06213 0.062128  2.5316 0.123671
## Residuals    26 0.63806 0.024541
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove Wheat:Soil interaction

Fit Model 4

```
# fit full model
SRW_model4 <- aov(shallow_root_weight ~ Wheat + Soil + Biochar + Soil*Biochar, data=bc_data)
```
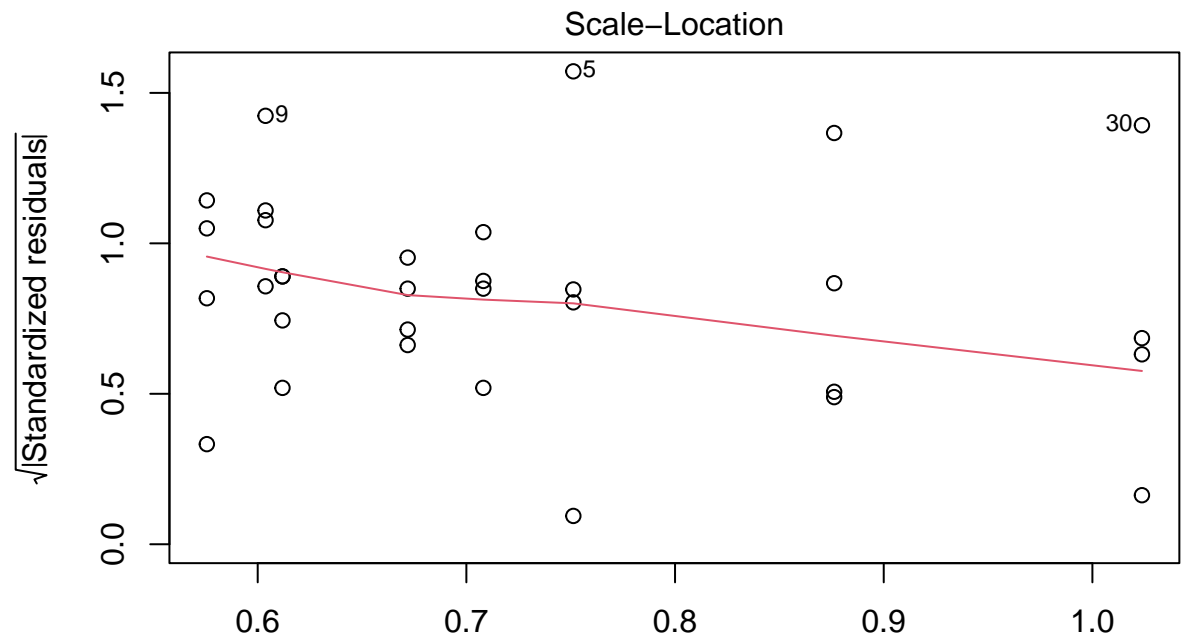
Check Model Assumptions

```
# check assumptions
plot(SRW_model4)
```


Residuals vs Fitted

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shallow_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

Scale−Location

aov(shallow_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

Fitted values

√|Standardized residuals|
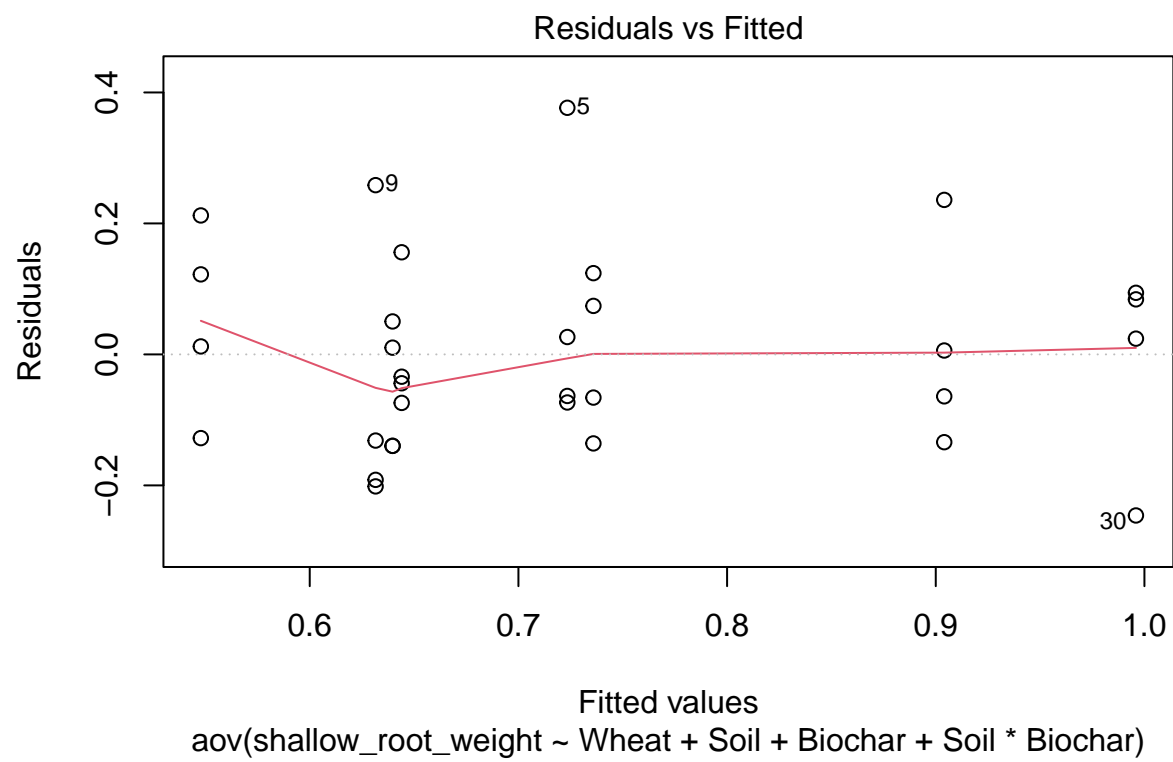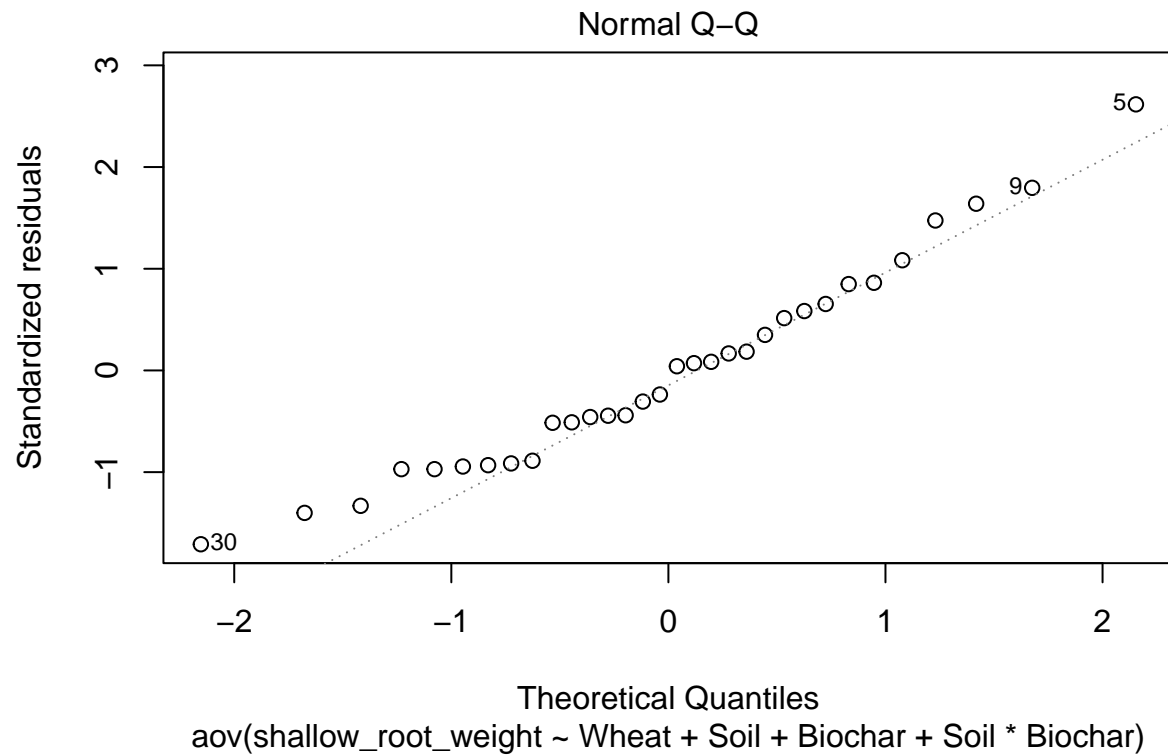
Check for Nonsignificant Interactions

```
anova(SRW_model4)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##              Df  Sum Sq  Mean Sq F value   Pr(>F)
## Wheat         1 0.06753 0.067528  2.7508 0.108780
## Soil          1 0.23633 0.236328  9.6270 0.004460 **
## Biochar       1 0.27195 0.271953 11.0782 0.002532 **
## Soil:Biochar  1 0.06213 0.062128  2.5308 0.123283
## Residuals    27 0.66281 0.024548
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
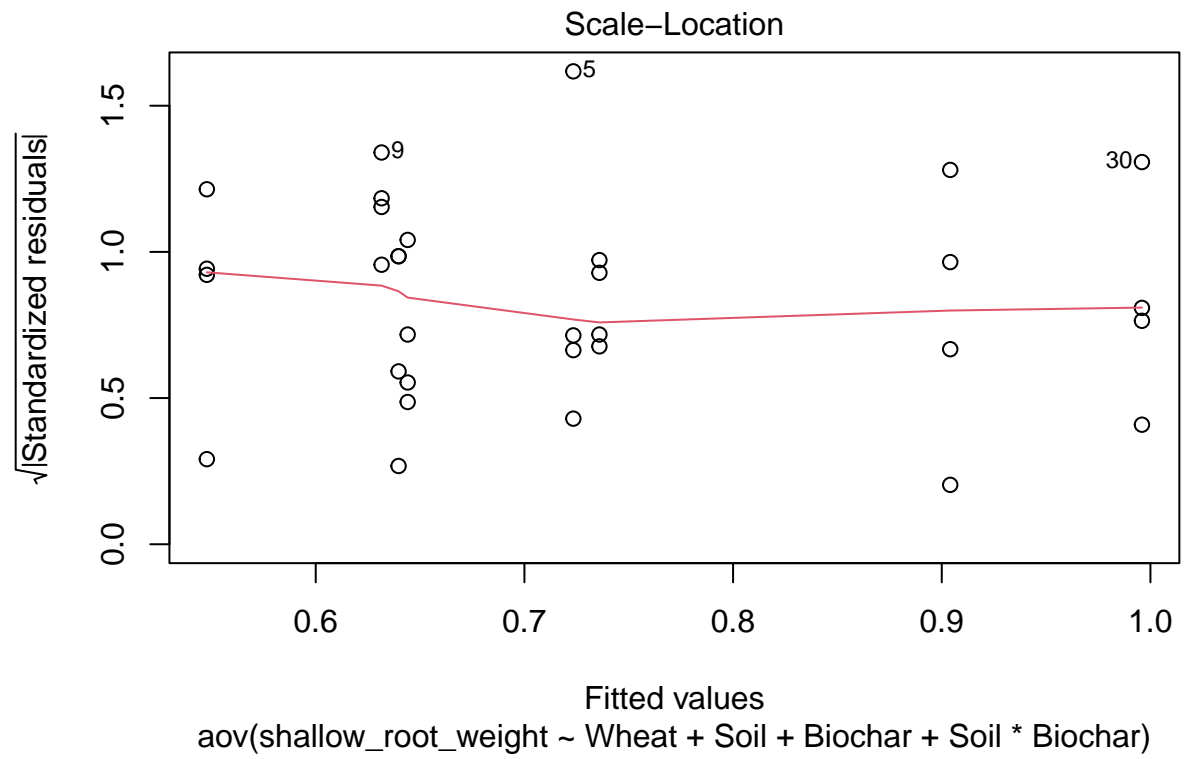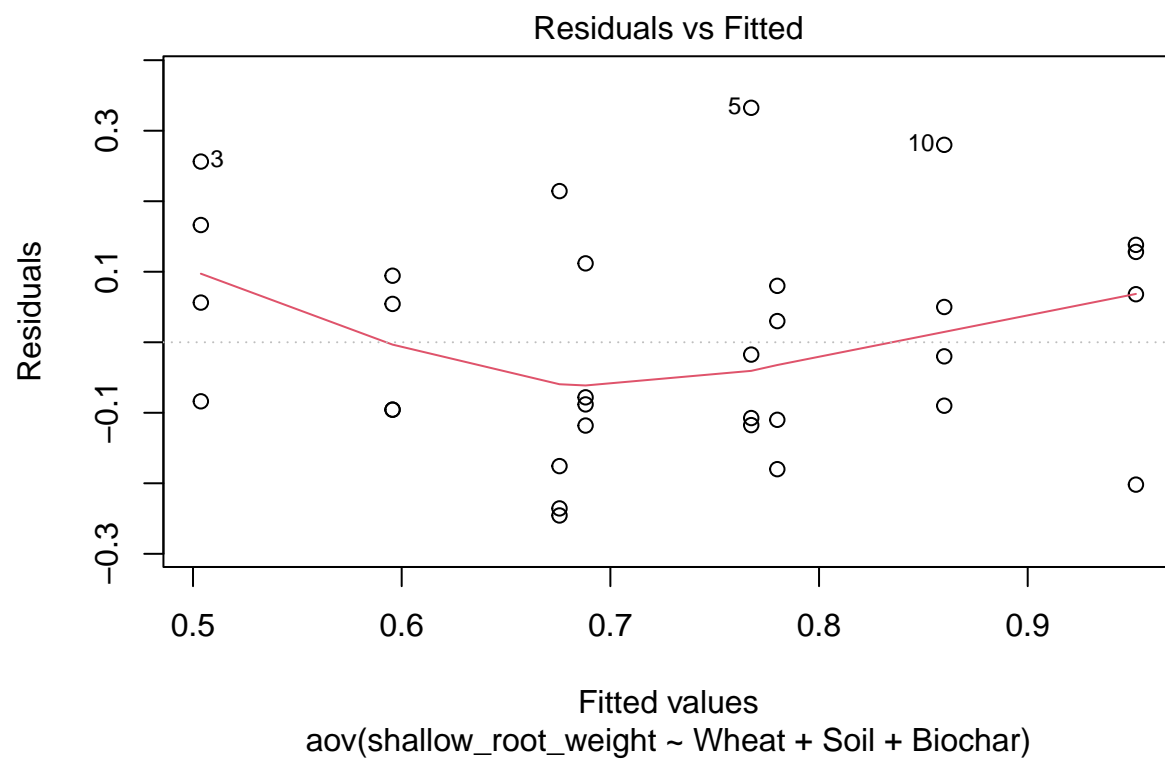
Remove Soil:Biochar

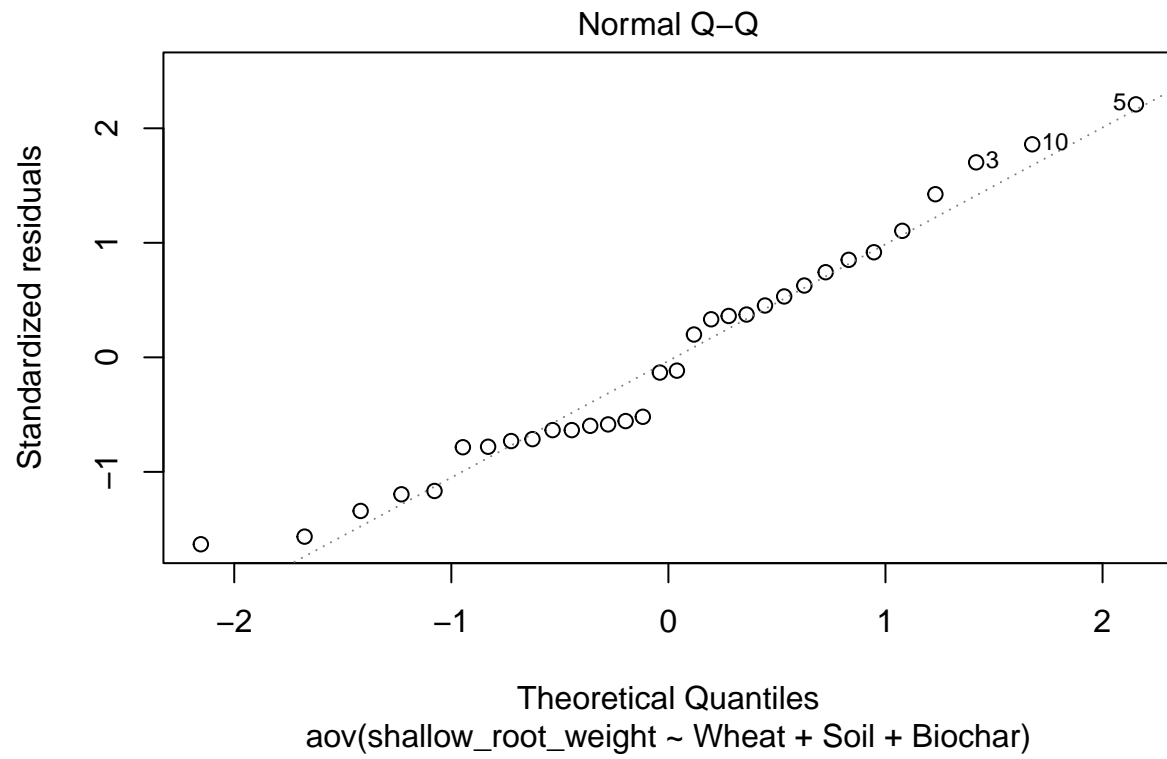# Fit Model 5

```
# fit full model
SRW_model5 <- aov(shallow_root_weight ~ Wheat + Soil + Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(SRW_model5)
```

Residuals vs Fitted

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shallow_root_weight ~ Wheat + Soil + Biochar)

Scale–Location

Fitted values
aov(shallow_root_weight ~ Wheat + Soil + Biochar)

Check for Nonsignificant Interactions

```
anova(SRW_model5)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##            Df  Sum Sq  Mean Sq F value   Pr(>F)
## Wheat       1 0.06753 0.067528  2.6082 0.117526
## Soil        1 0.23633 0.236328  9.1279 0.005329 **
## Biochar     1 0.27195 0.271953 10.5039 0.003069 **
## Residuals  28 0.72494 0.025891
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
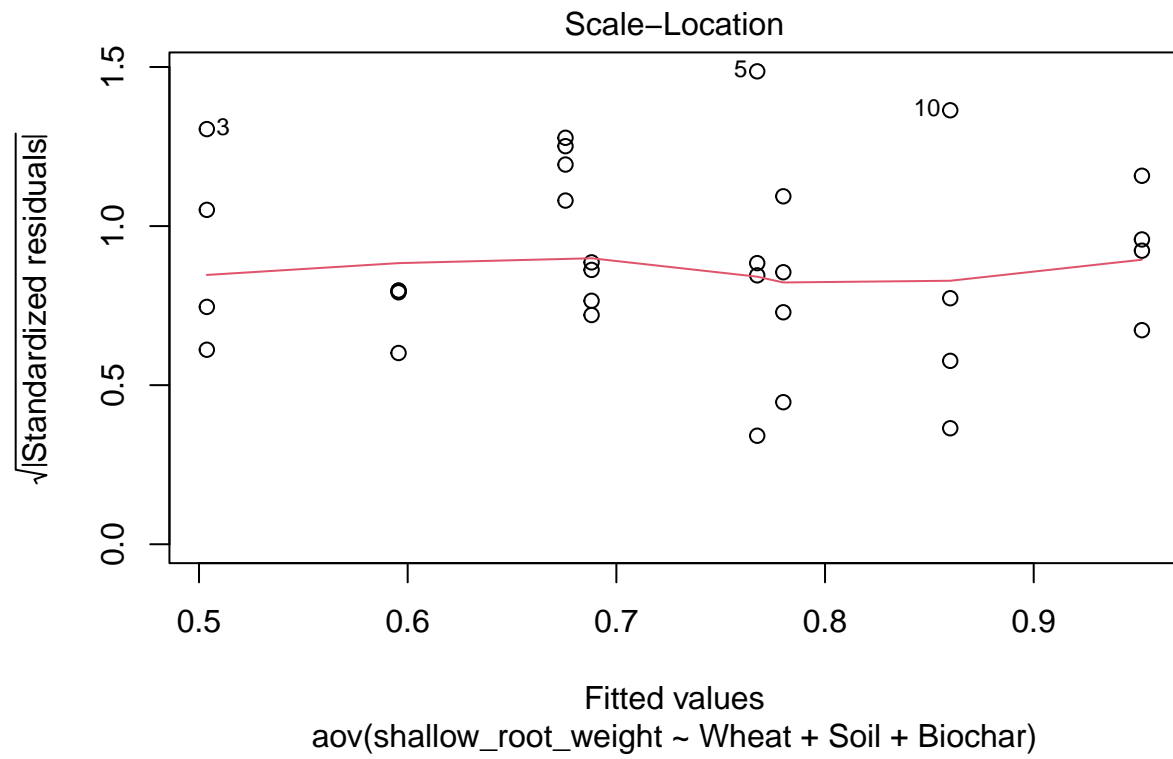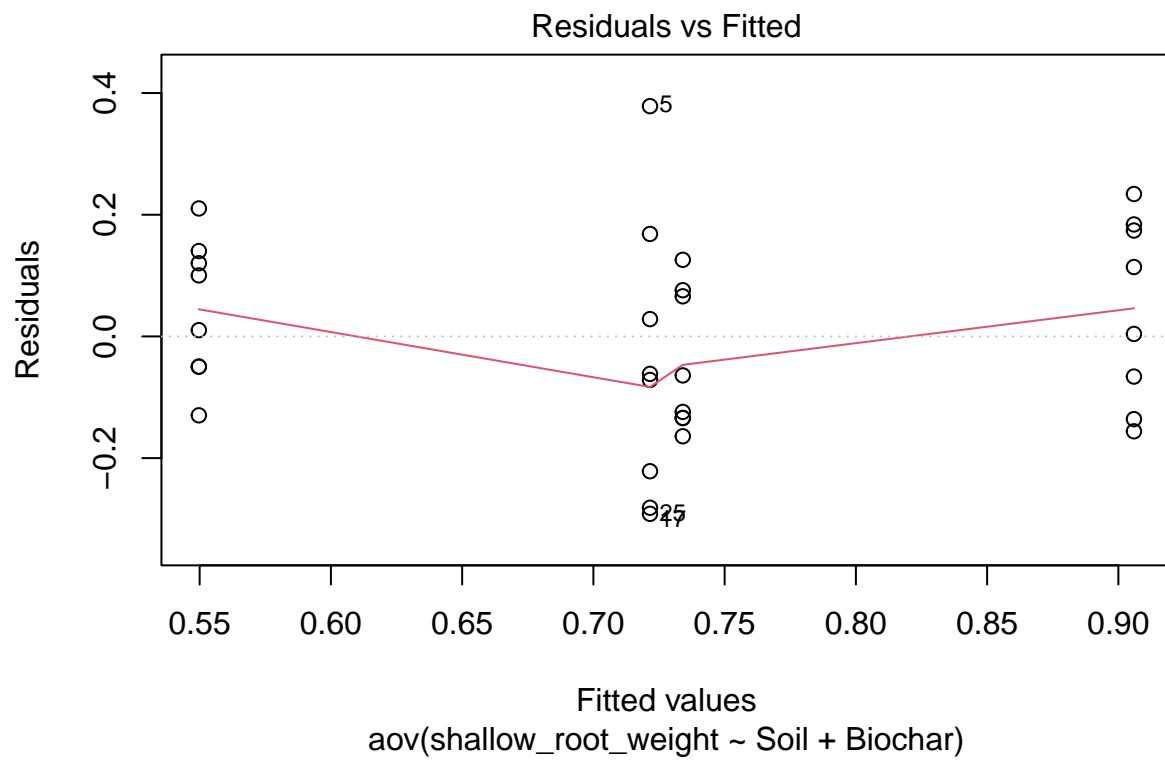
remove Wheat

Fit Model 6

```
# fit full model
SRW_model6 <- aov(shallow_root_weight ~ Soil + Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(SRW_model6)
```


Residuals vs Fitted

Fitted values
aov(shallow_root_weight ~ Soil + Biochar)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(shallow_root_weight ~ Soil + Biochar)

Scale−Location

Fitted values
aov(shallow_root_weight ~ Soil + Biochar)

Check for Nonsignificant Interactions

```
anova(SRW_model6)
```

```
## Analysis of Variance Table
##
## Response: shallow_root_weight
##            Df  Sum Sq  Mean Sq F value   Pr(>F)
## Soil        1 0.23633 0.236328  8.6483 0.006371 **
## Biochar     1 0.27195 0.271953  9.9520 0.003725 **
## Residuals  29 0.79247 0.027326
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
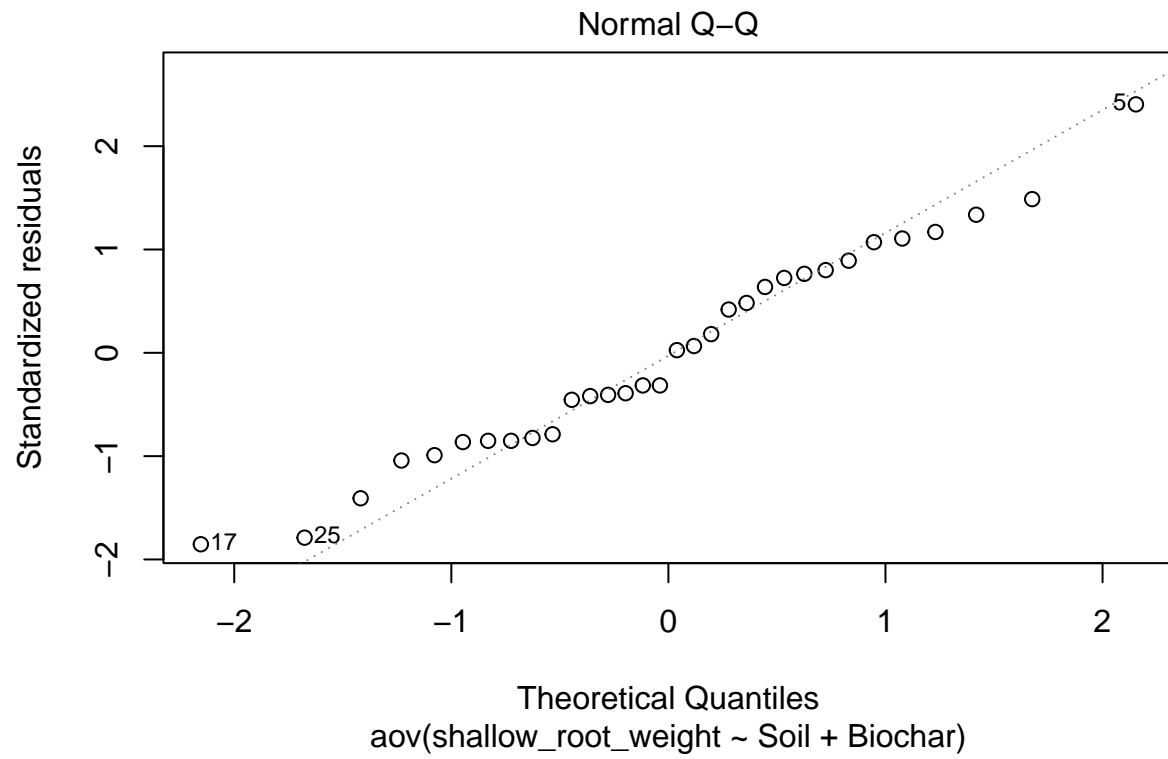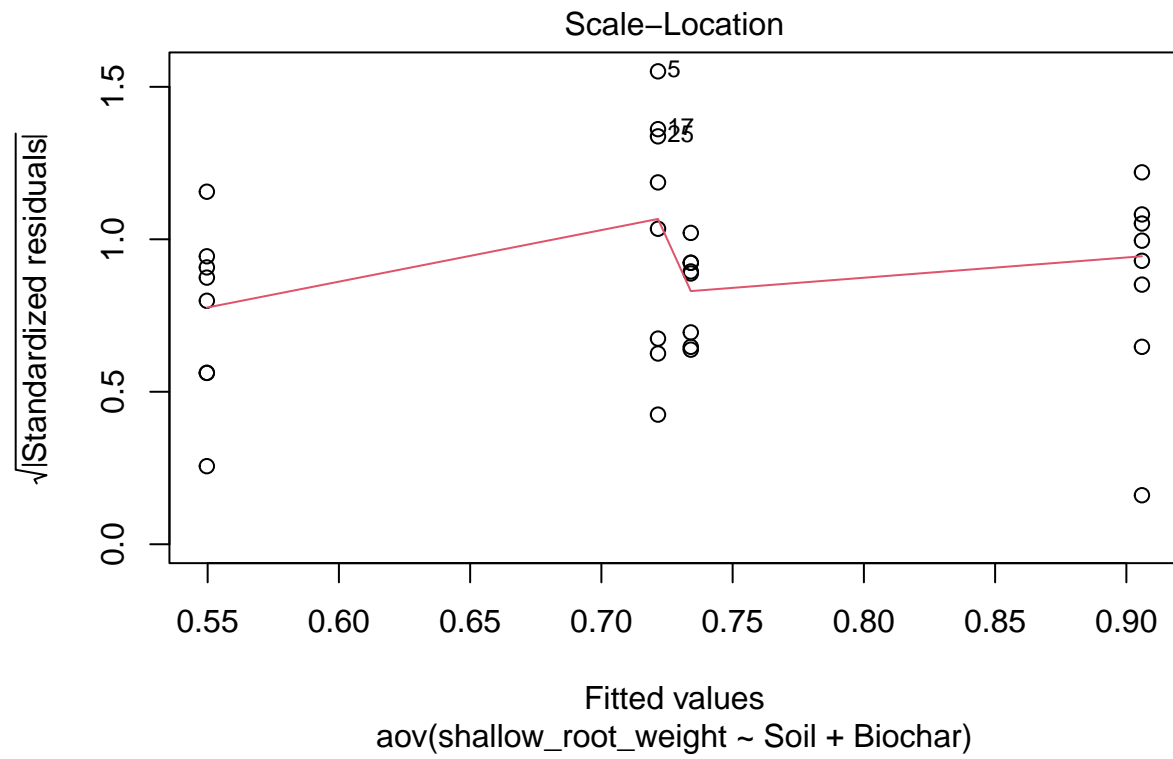
Final Model: Order 2 Model

Final Model: Shallow Root Weight = Soil + Biochar

Compare main Effects

```
TukeyHSD(SRW_model6)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = shallow_root_weight ~ Soil + Biochar, data = bc_data)
##
## $Soil
##                      diff        lwr         upr      p adj
## soil-sand-soil -0.171875 -0.2914081 -0.05234187 0.0063709
##
## $Biochar
##              diff        lwr        upr      p adj
## yes-no 0.184375 0.06484187 0.3039081 0.0037246
```

```
emmeans(SRW_model6,list(pairwise ~ Soil))
```

```
## $`emmeans of Soil`
##  Soil      emmean     SE df lower.CL upper.CL
##  soil       0.814 0.0413 29    0.729    0.898
##  soil-sand  0.642 0.0413 29    0.557    0.726
##
## Results are averaged over the levels of: Biochar
## Confidence level used: 0.95
##
## $`pairwise differences of Soil`
##  1                estimate     SE df t.ratio p.value
##  soil - (soil-sand)  0.172 0.0584 29   2.941  0.0064
##
## Results are averaged over the levels of: Biochar
```

```
emmeans(SRW_model6,list(pairwise ~ Biochar))
```

```
## $`emmeans of Biochar`
##  Biochar emmean     SE df lower.CL upper.CL
##  no       0.636 0.0413 29    0.551    0.720
##  yes      0.820 0.0413 29    0.735    0.905
##
## Results are averaged over the levels of: Soil
## Confidence level used: 0.95
##
## $`pairwise differences of Biochar`
##  1        estimate     SE df t.ratio p.value
##  no - yes   -0.184 0.0584 29  -3.155  0.0037
##
## Results are averaged over the levels of: Soil
```
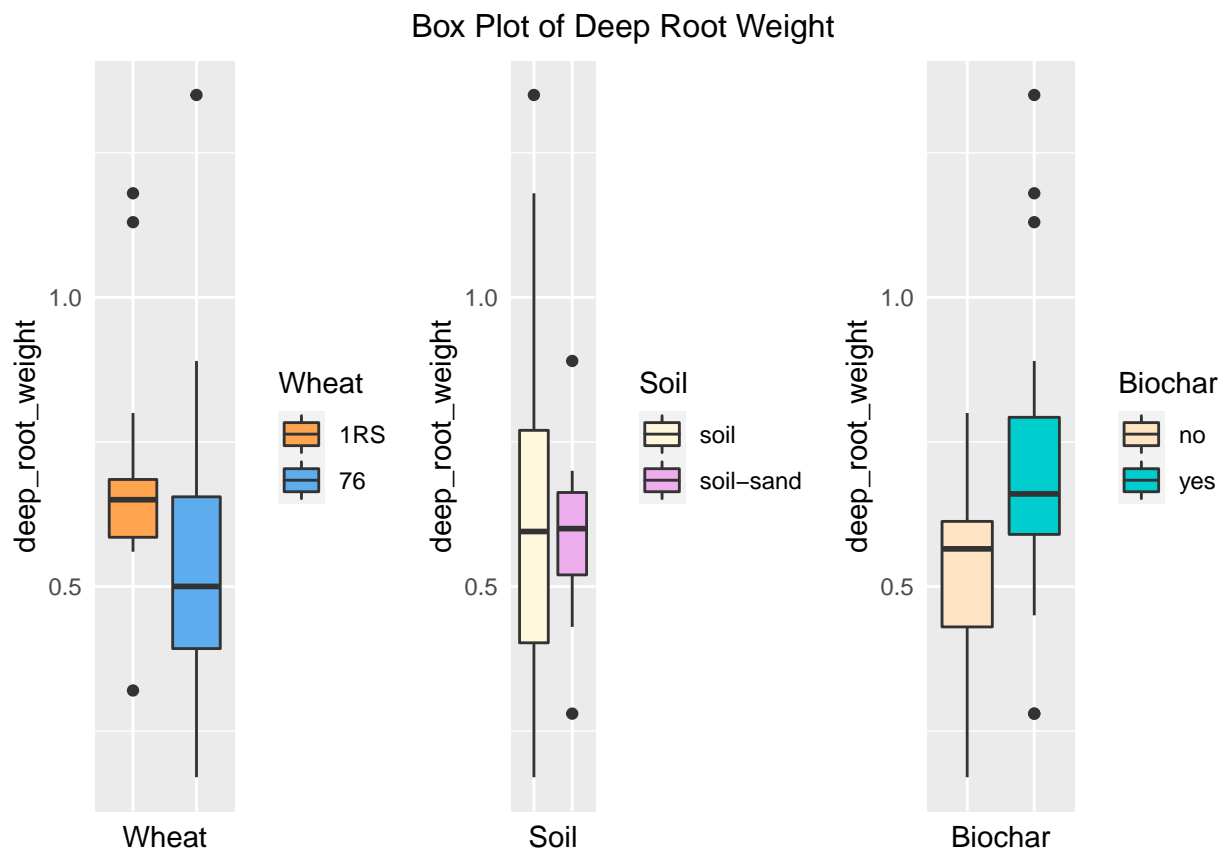
Deep Root Weight

NOTE: All models and analysis performed below is for deep root weight only

Box Plot for Deep Root Weight

```
plot_deep_root_weight <- bc_data[c("Wheat","Soil","Biochar","deep_root_weight")]
gg_object <- ggplot(data=plot_deep_root_weight)

g1 <- gg_object +
  geom_boxplot(aes(x=Wheat, y=deep_root_weight, fill=Wheat)) +
  scale_fill_manual(values=c("tan1", "steelblue2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g2 <- gg_object +
  geom_boxplot(aes(x=Soil, y=deep_root_weight, fill=Soil)) +
  scale_fill_manual(values=c("cornsilk", "plum2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g3 <- gg_object +
  geom_boxplot(aes(x=Biochar, y=deep_root_weight, fill=Biochar)) +
  scale_fill_manual(values=c("bisque", "cyan3")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())

grid.arrange(g1, g2, g3, nrow=1, top="Box Plot of Deep Root Weight")
```
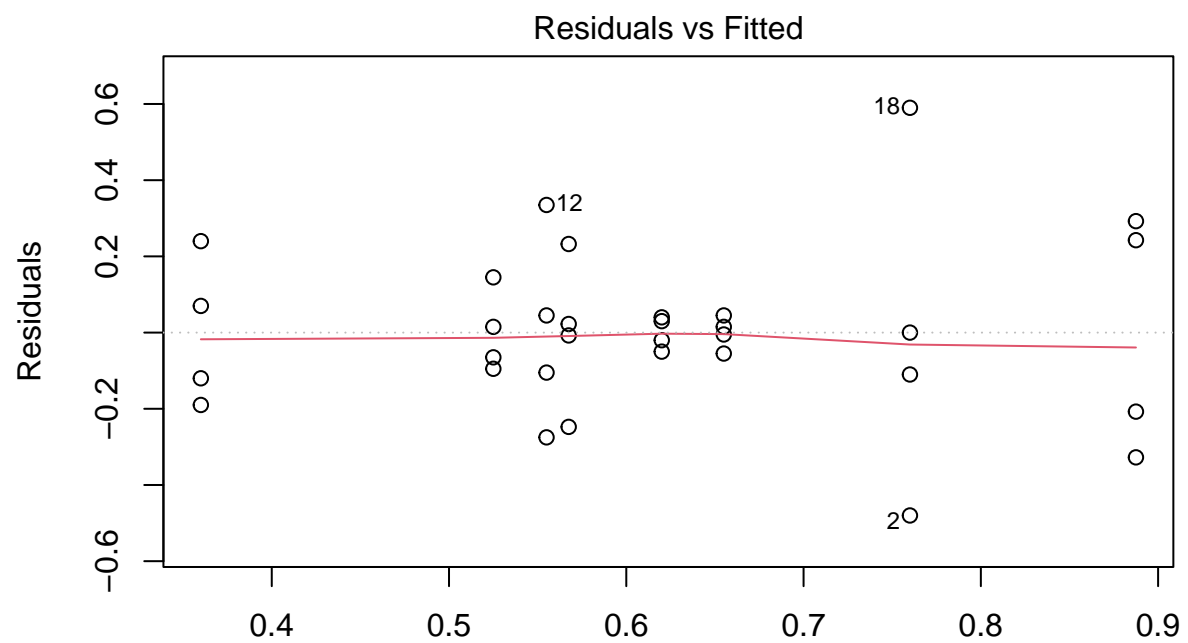

Box Plot of Deep Root Weight

Fit Full Model

```r
# fit full model
DRW_model <- aov(deep_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar +
```
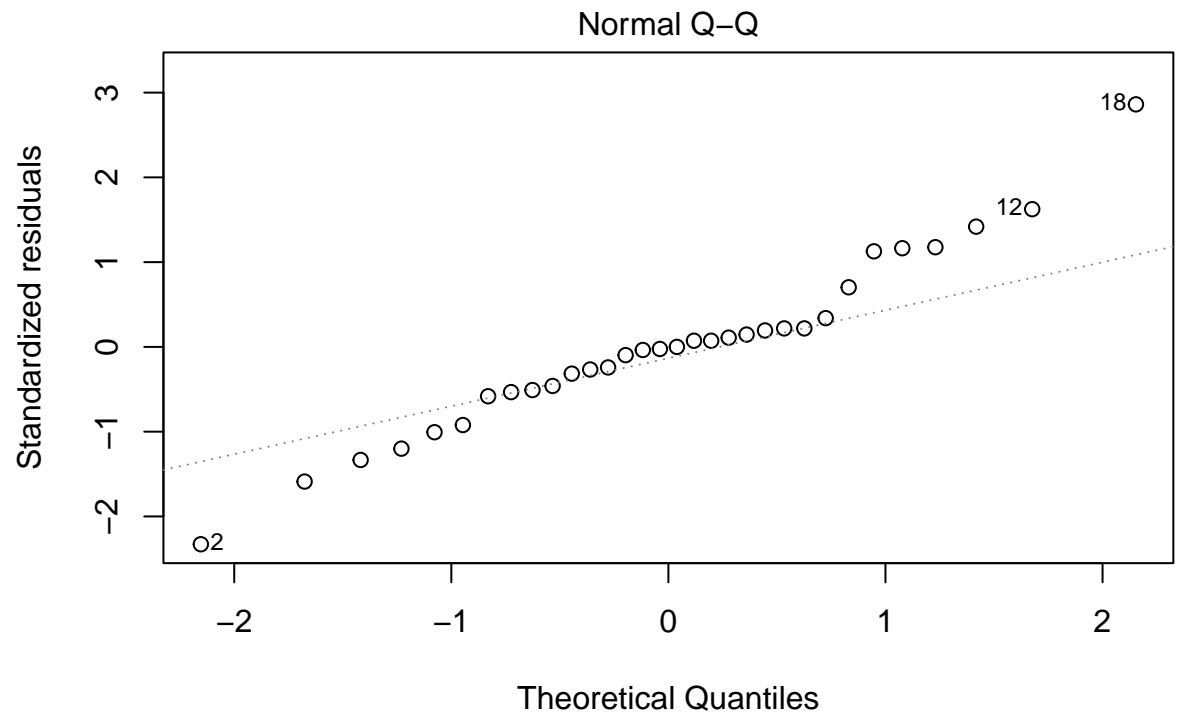
Check Model Assumptions

```r
# check assumptions
plot(DRW_model)
```

Residuals vs Fitted

aov(deep_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Normal Q–Q

Theoretical Quantiles
aov(deep_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...
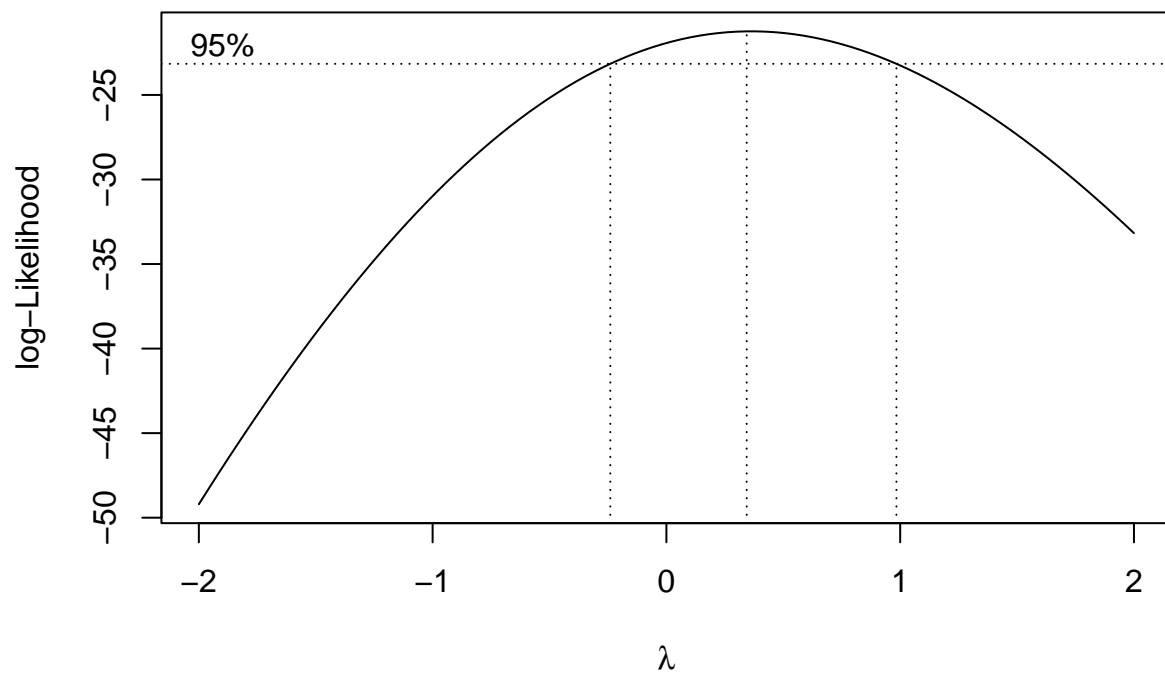
Scale–Location
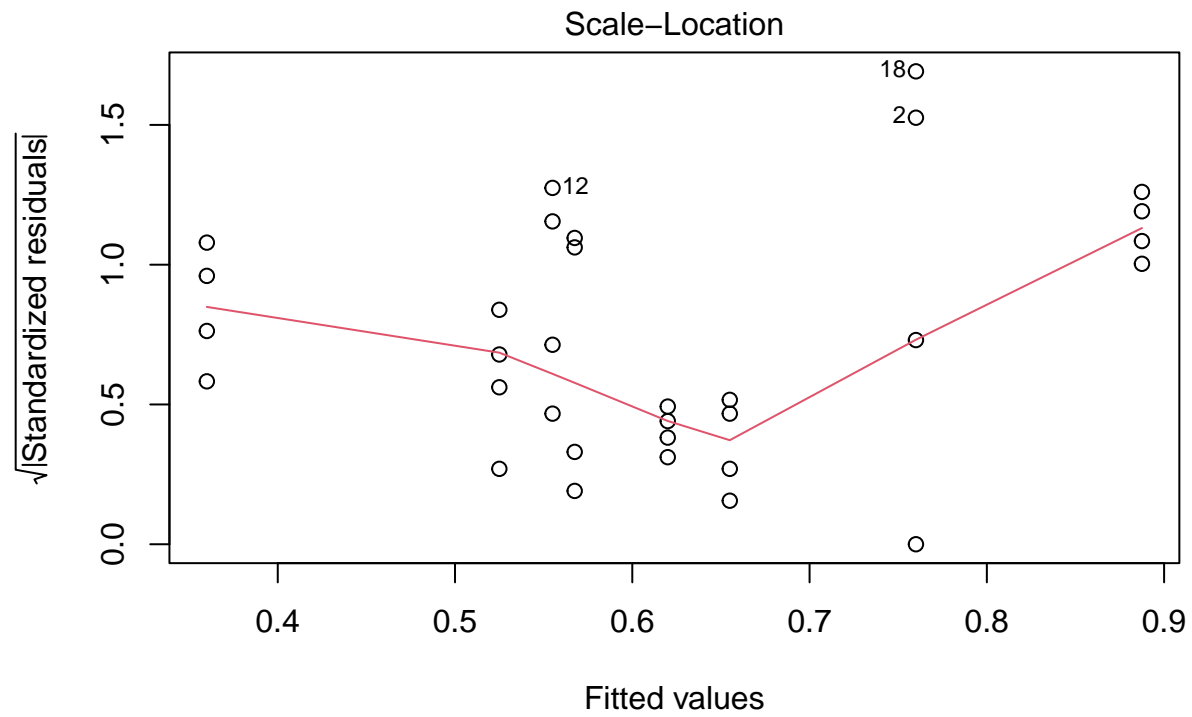
Fitted values
aov(deep_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Transformation is necessary

Perform Box-Cox Transformation

```
T1 <- boxcox(deep_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar + Wh
```

```r
lambda1 <- T1$x[which(T1$y == max(T1$y))]
```

Refit and Check Assumptions after Transformation

```r
deep_root_weight_t <- deep_root_weight**lambda1

# refit model
DRW_model_new <- aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Bi

# check assumptions
plot(DRW_model_new)
```
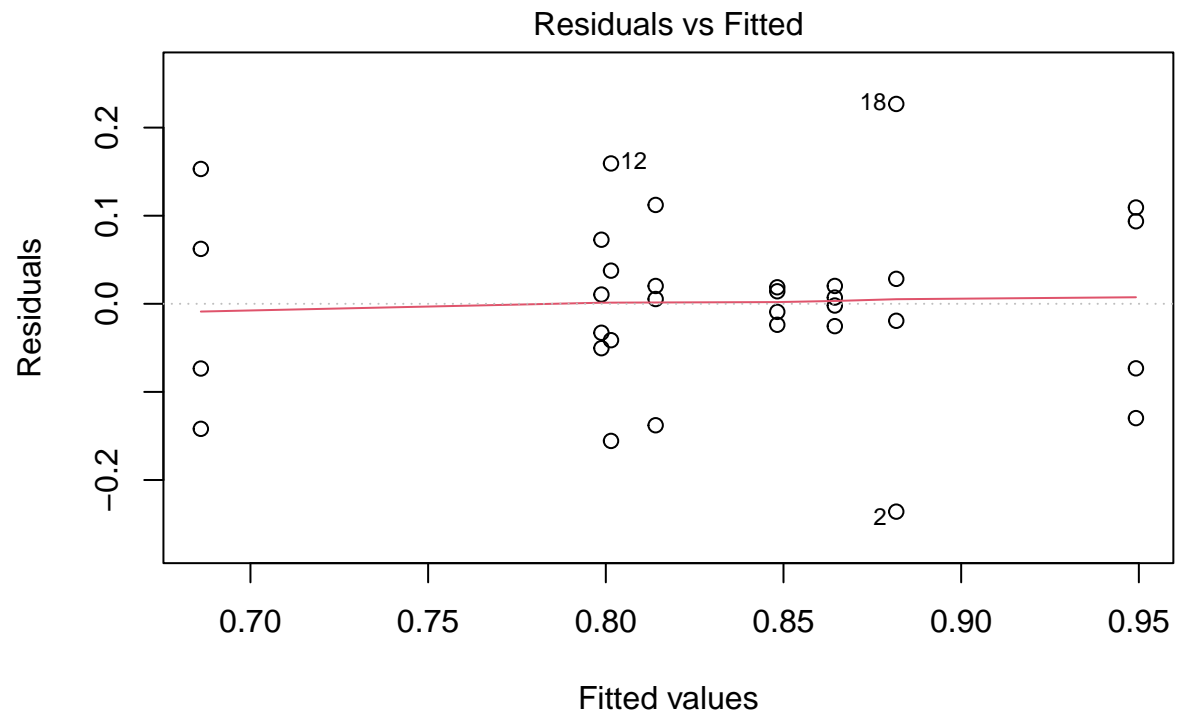
Residuals vs Fitted

Residuals

Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...

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Normal Q–Q

Theoretical Quantiles
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...

Scale–Location

Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...
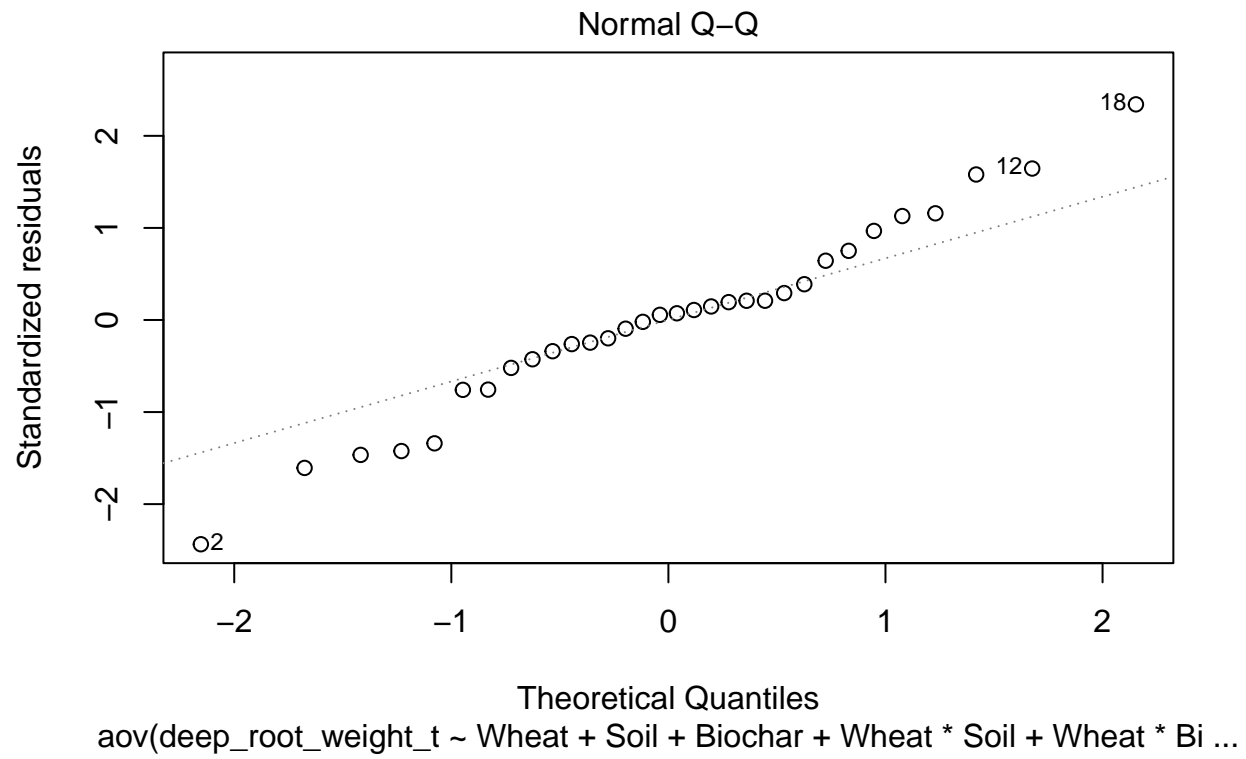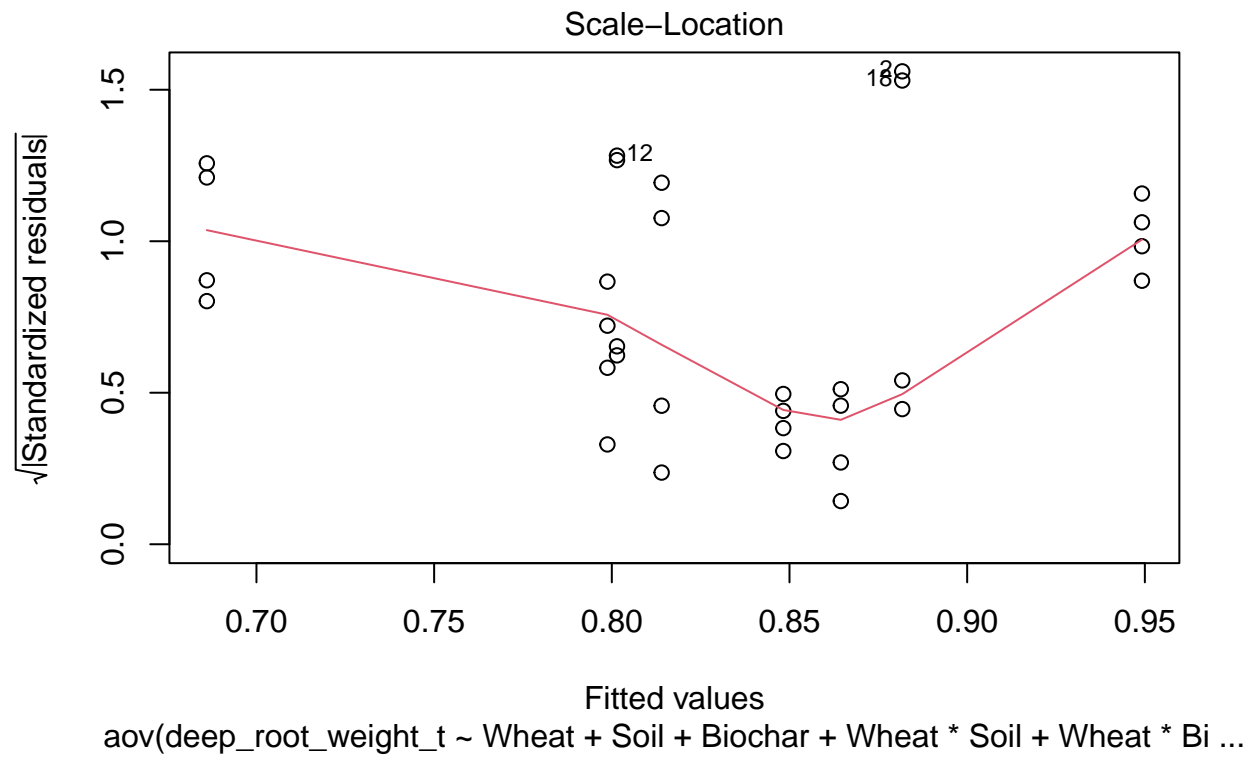
Check for Nonsignificant Interactions

```
anova(DRW_model_new)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##                    Df    Sum Sq   Mean Sq F value  Pr(>F)
## Wheat               1 0.047401  0.047401  3.7907 0.06333 .
## Soil                1 0.000163  0.000163  0.0130 0.91005
## Biochar             1 0.061163  0.061163  4.8912 0.03676 *
## Wheat:Soil          1 0.003442  0.003442  0.2752 0.60466
## Wheat:Biochar       1 0.001107  0.001107  0.0885 0.76865
## Soil:Biochar        1 0.048662  0.048662  3.8915 0.06016 .
## Wheat:Soil:Biochar  1 0.002740  0.002740  0.2191 0.64395
## Residuals          24 0.300112  0.012505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove 3 way interaction

Fit Model 2

```
# fit full model
DRW_model2 <- aov(deep_root_weight_t~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biocha
```

Check Model Assumptions

```
# check assumptions
plot(DRW_model2)
```

Residuals vs Fitted

Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...

Scale–Location

Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bi ...
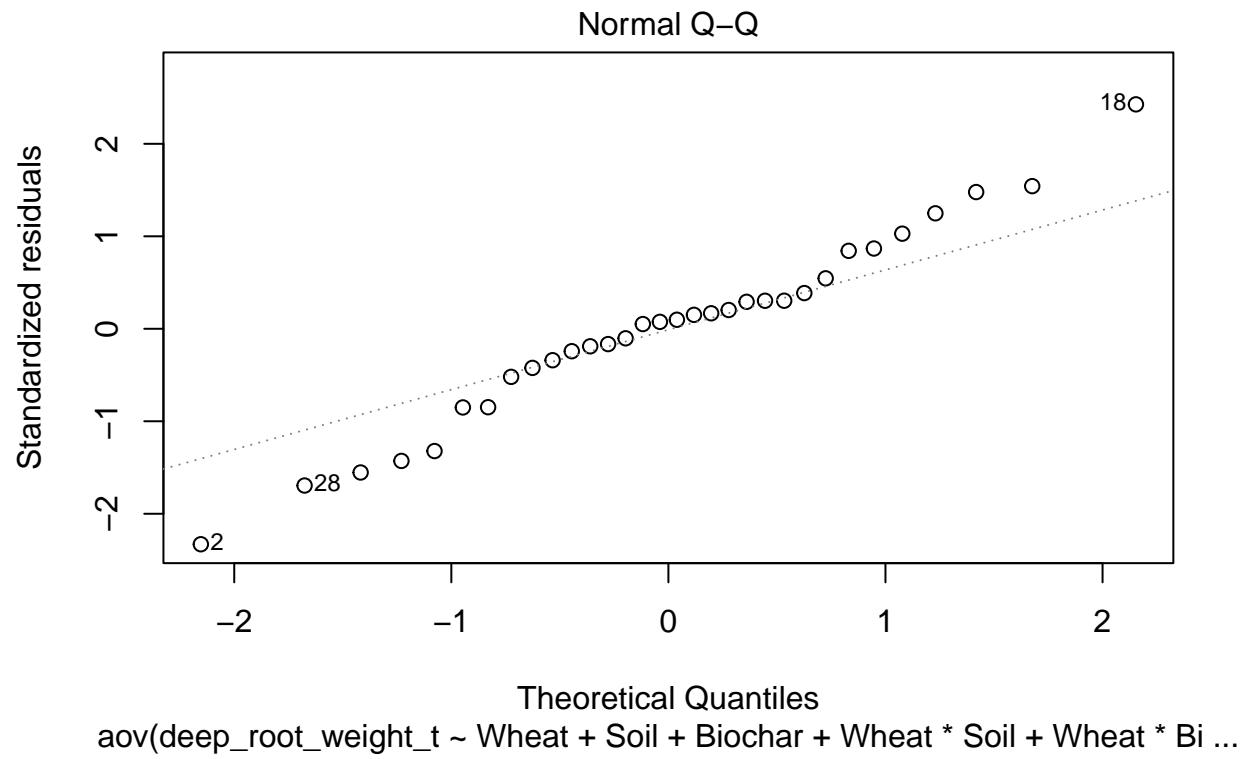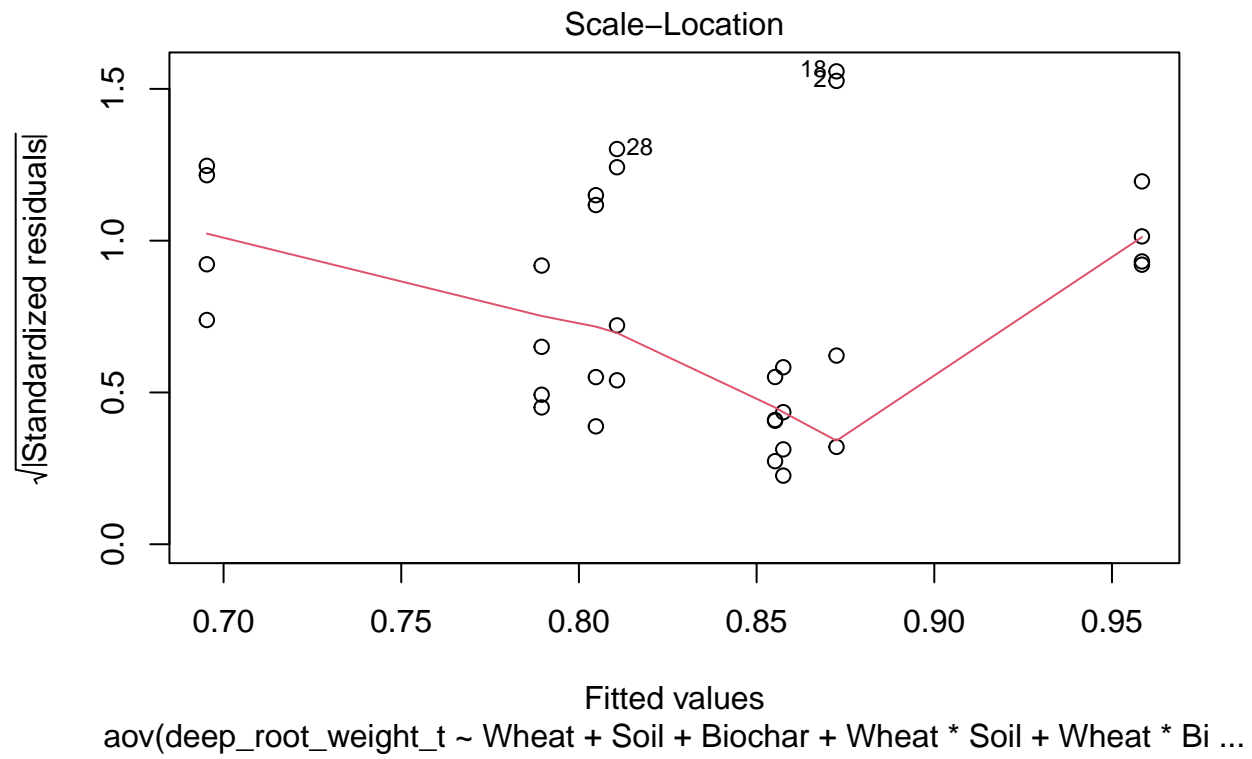
Check for Nonsignificant Interactions

```
anova(DRW_model2)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##               Df    Sum Sq  Mean Sq F value  Pr(>F)
## Wheat          1 0.047401 0.047401  3.9129 0.05904 .
## Soil           1 0.000163 0.000163  0.0135 0.90858
## Biochar        1 0.061163 0.061163  5.0489 0.03371 *
## Wheat:Soil     1 0.003442 0.003442  0.2841 0.59873
## Wheat:Biochar  1 0.001107 0.001107  0.0914 0.76496
## Soil:Biochar   1 0.048662 0.048662  4.0170 0.05599 .
## Residuals     25 0.302852 0.012114
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
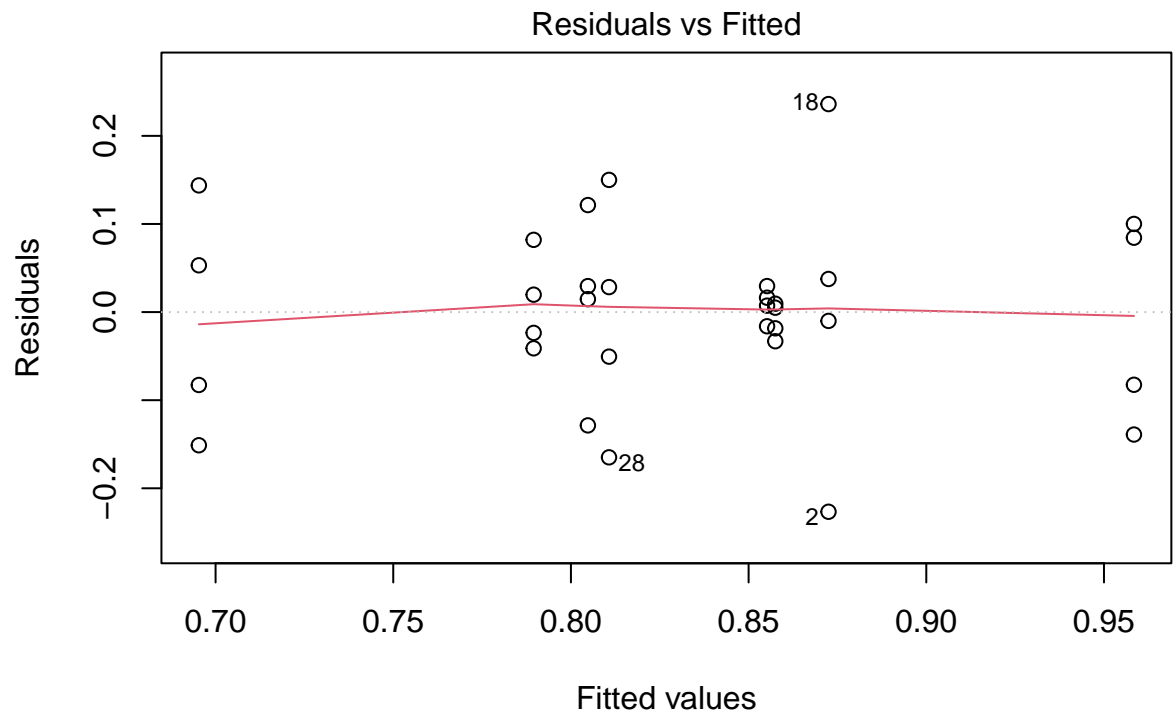
Remove Wheat:Biochar interaction

Fit Model 3

```
# fit full model
DRW_model3 <- aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat*Soil + Soil*Biochar, data=bc_data
```

**Check Model Assumptions**

```
# check assumptions
plot(DRW_model3)
```

Residuals vs Fitted

aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bio ...

Normal Q–Q

Theoretical Quantiles
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bio ...

Scale−Location
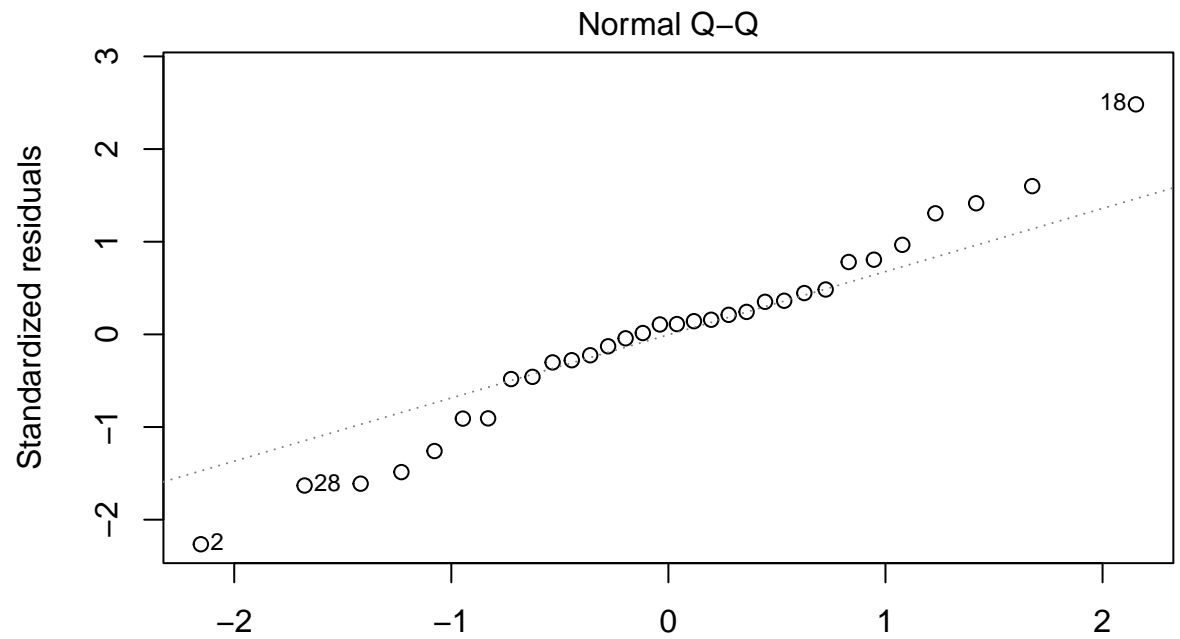
Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bio ...
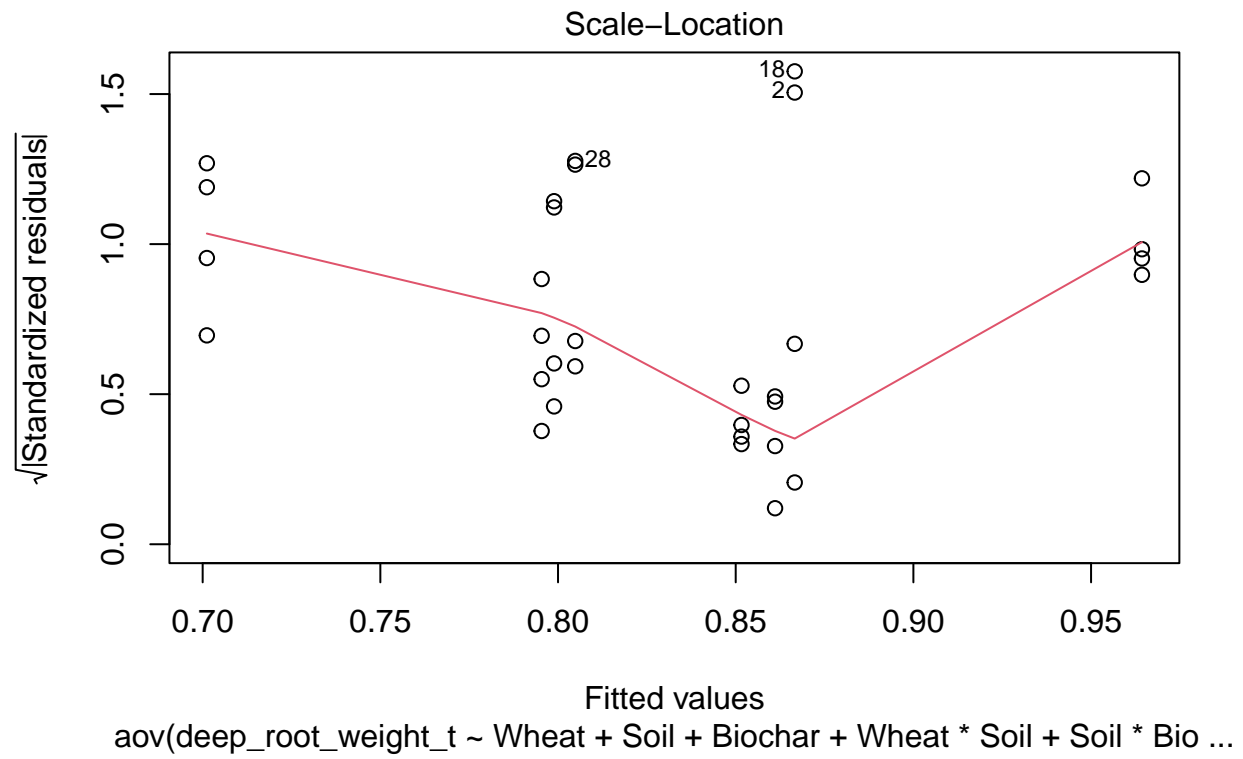
Check for Nonsignificant Interactions

```
anova(DRW_model3)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##               Df    Sum Sq   Mean Sq F value  Pr(>F)
## Wheat          1 0.047401 0.047401  4.0546 0.05451 .
## Soil           1 0.000163 0.000163  0.0139 0.90692
## Biochar        1 0.061163 0.061163  5.2318 0.03056 *
## Wheat:Soil     1 0.003442 0.003442  0.2944 0.59204
## Soil:Biochar   1 0.048662 0.048662  4.1625 0.05161 .
## Residuals     26 0.303958 0.011691
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
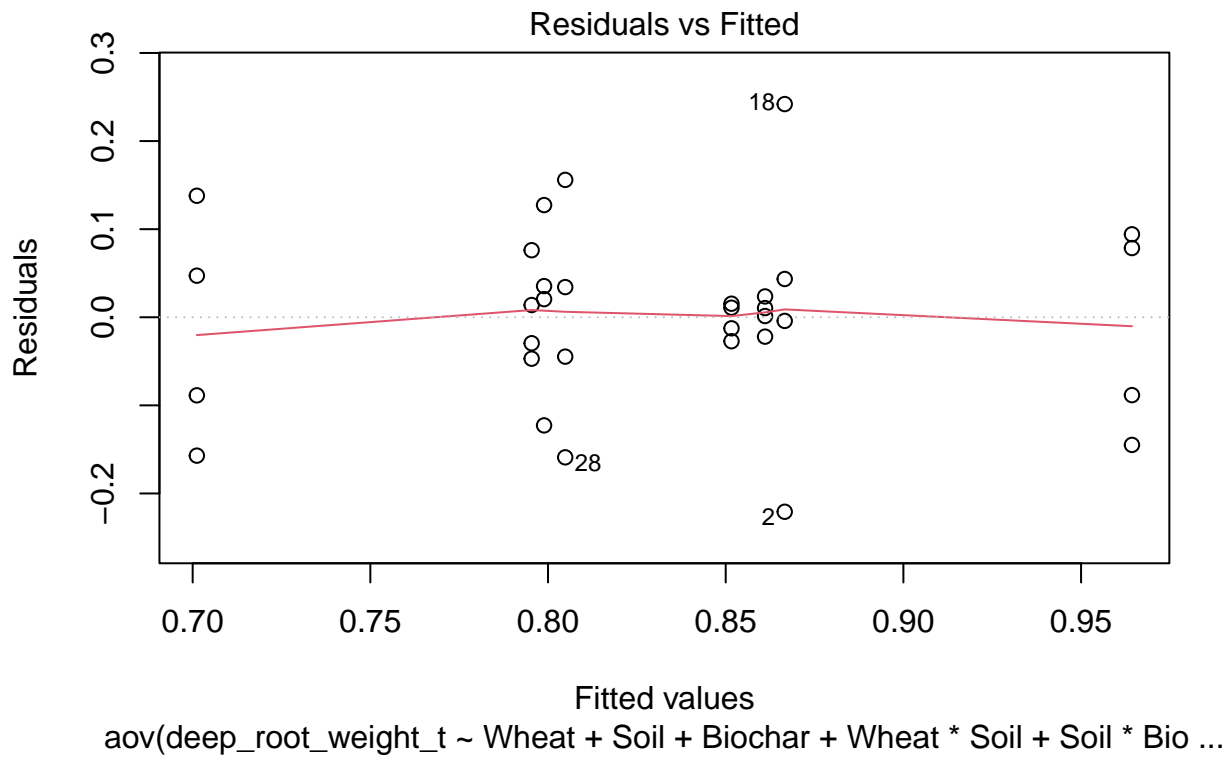
Remove Wheat:Soil interaction

# Fit Model 4

```
# fit full model
DRW_model4 <- aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Soil*Biochar, data=bc_data)
```

**Check Model Assumptions**

```
# check assumptions
plot(DRW_model4)
```

Residuals vs Fitted

Normal Q–Q

Standardized residuals (y-axis)

Theoretical Quantiles
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Soil * Biochar)

Scale–Location

Fitted values
aov(deep_root_weight_t ~ Wheat + Soil + Biochar + Soil * Biochar)
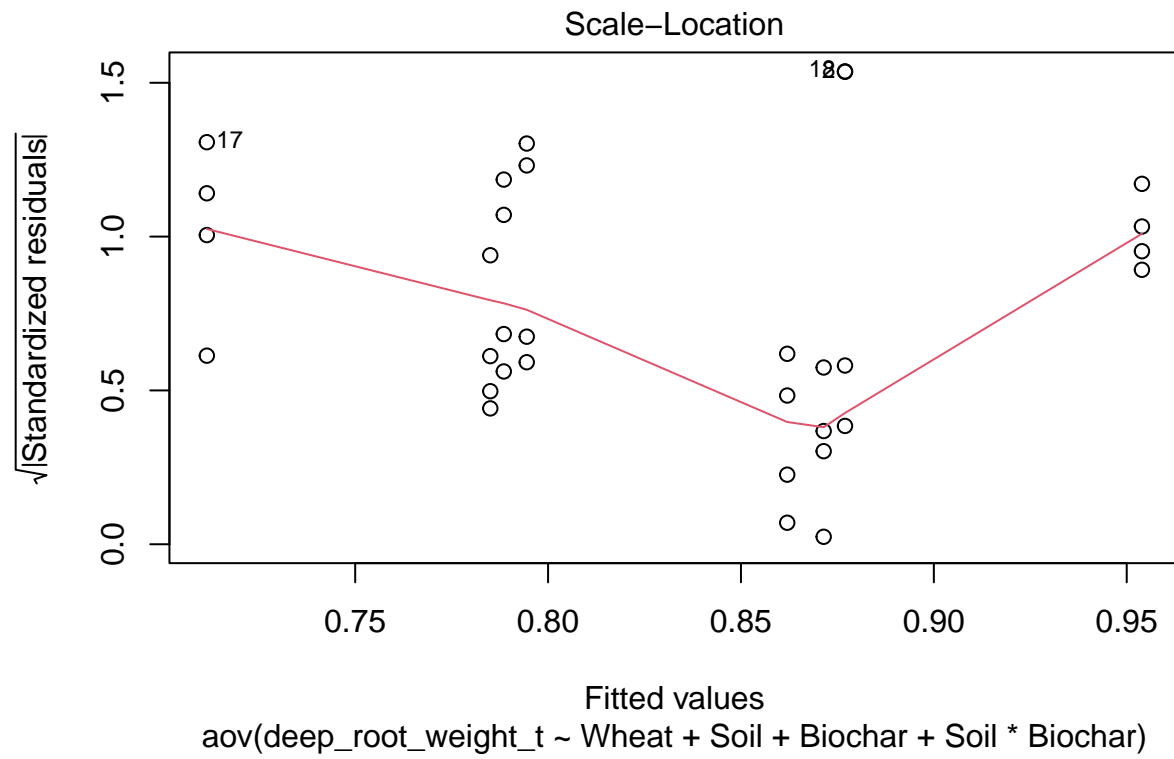
Check for Nonsignificant Interactions

```
anova(DRW_model4)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##              Df    Sum Sq  Mean Sq F value  Pr(>F)
## Wheat         1 0.047401 0.047401  4.1634 0.05120 .
## Soil          1 0.000163 0.000163  0.0143 0.90565
## Biochar       1 0.061163 0.061163  5.3722 0.02828 *
## Soil:Biochar  1 0.048662 0.048662  4.2742 0.04840 *
## Residuals    27 0.307400 0.011385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
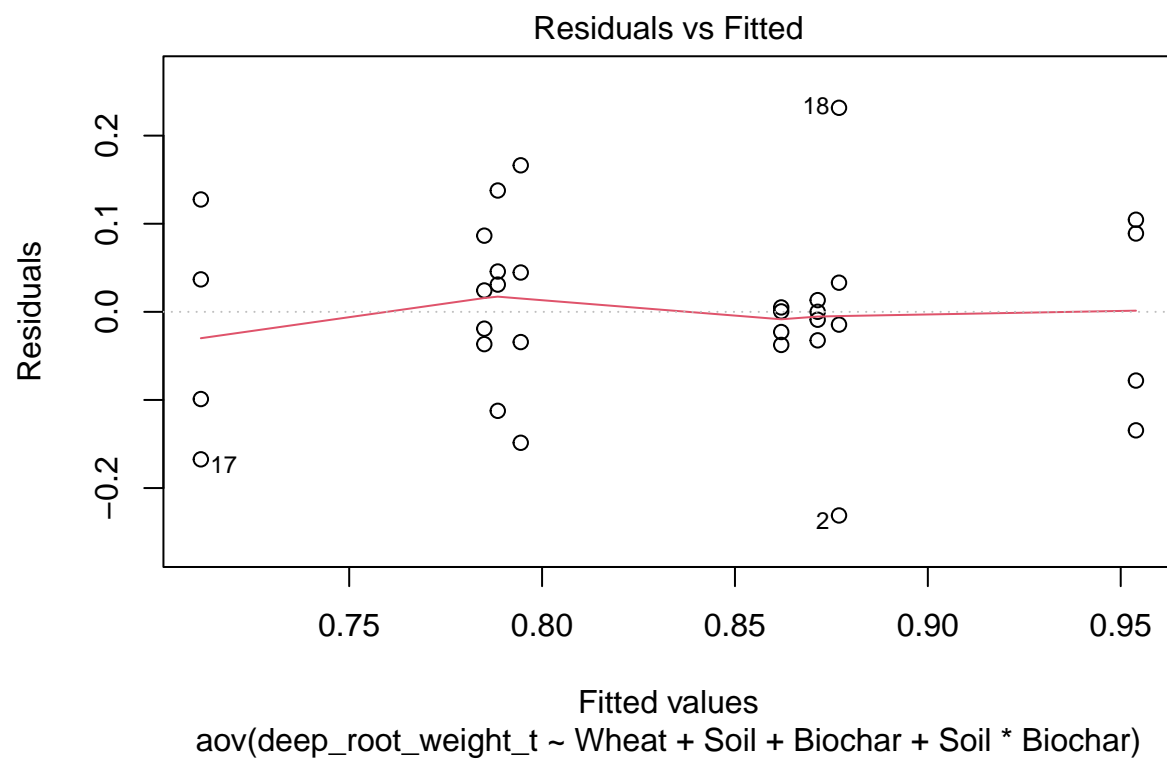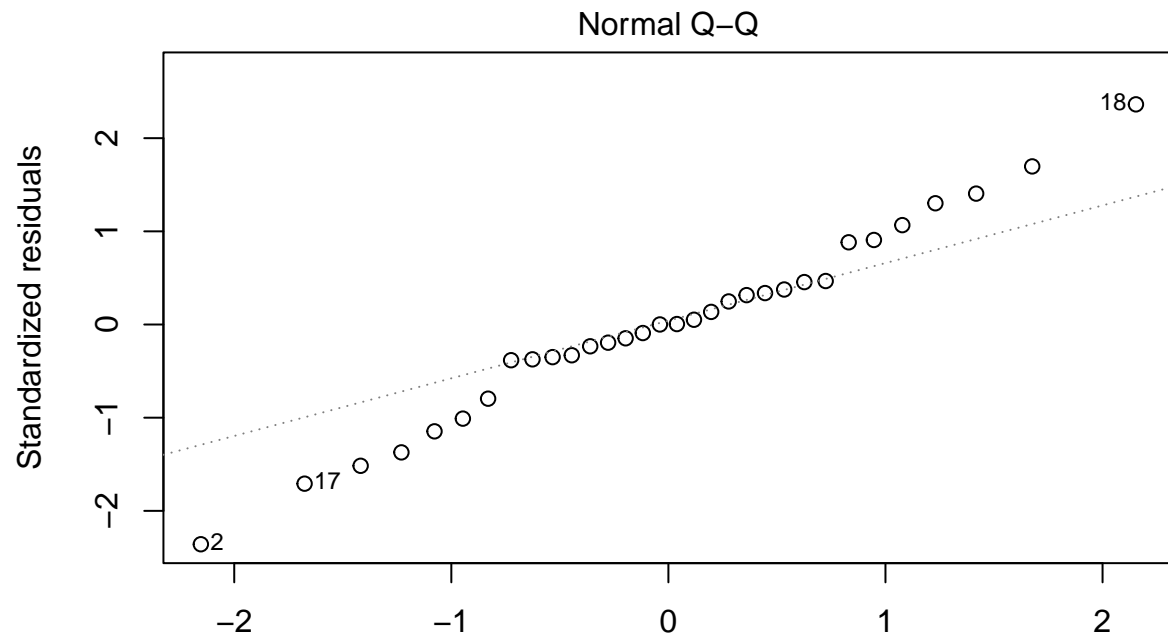
Remove Wheat

Fit Model 5

```
# fit full model
DRW_model5 <- aov(deep_root_weight_t ~ Soil + Biochar + Soil*Biochar, data=bc_data)
```
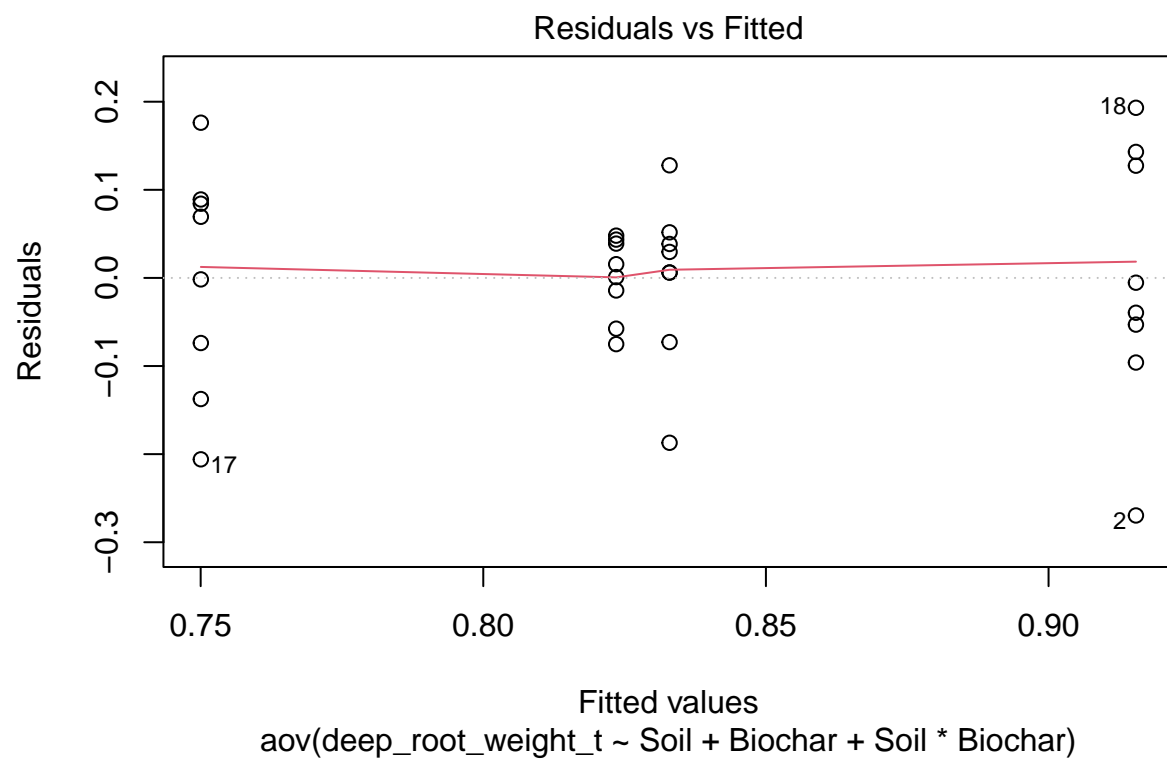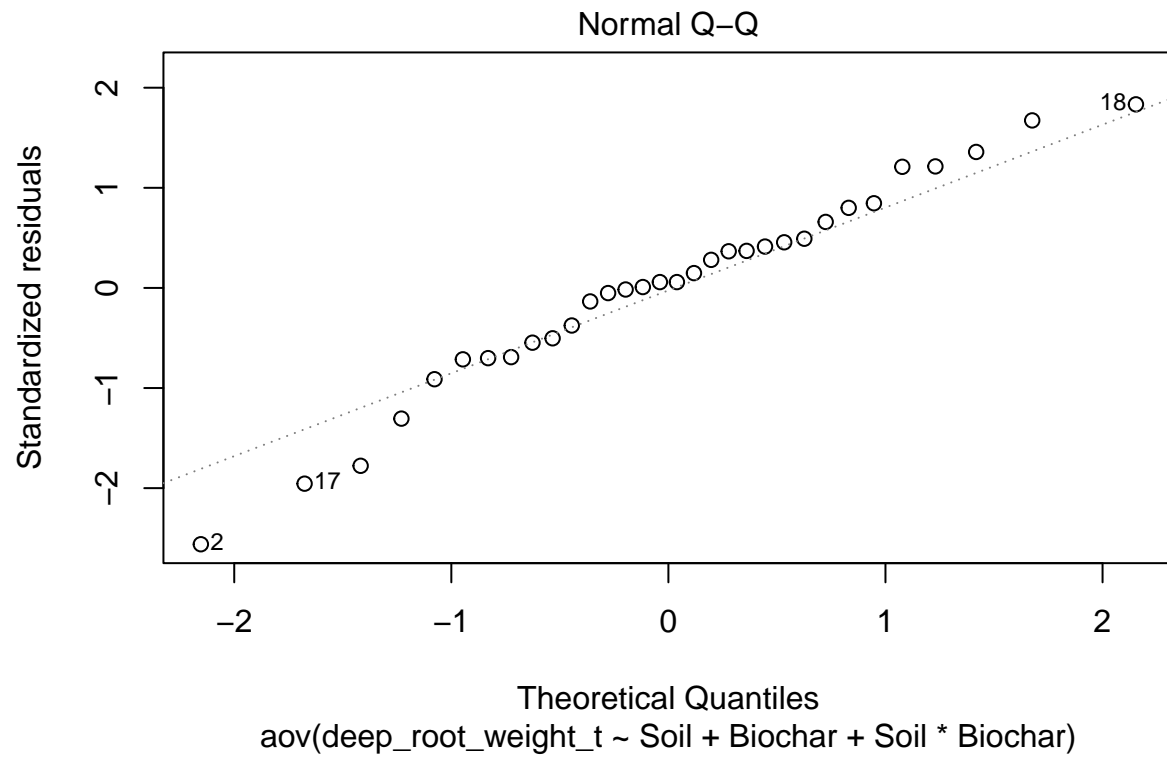
Check Model Assumptions

```
# check assumptions
plot(DRW_model5)
```

Normal Q–Q

Theoretical Quantiles
aov(deep_root_weight_t ~ Soil + Biochar + Soil * Biochar)

Scale−Location

√|Standardized residuals|

Fitted values
aov(deep_root_weight_t ~ Soil + Biochar + Soil * Biochar)

Check for Nonsignificant Interactions

```
anova(DRW_model5)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##               Df   Sum Sq   Mean Sq  F value  Pr(>F)
## Soil           1  0.00016  0.000163   0.0129  0.91051
## Biochar        1  0.06116  0.061163   4.8268  0.03646 *
## Soil:Biochar   1  0.04866  0.048662   3.8403  0.06006 .
## Residuals     28  0.35480  0.012671
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
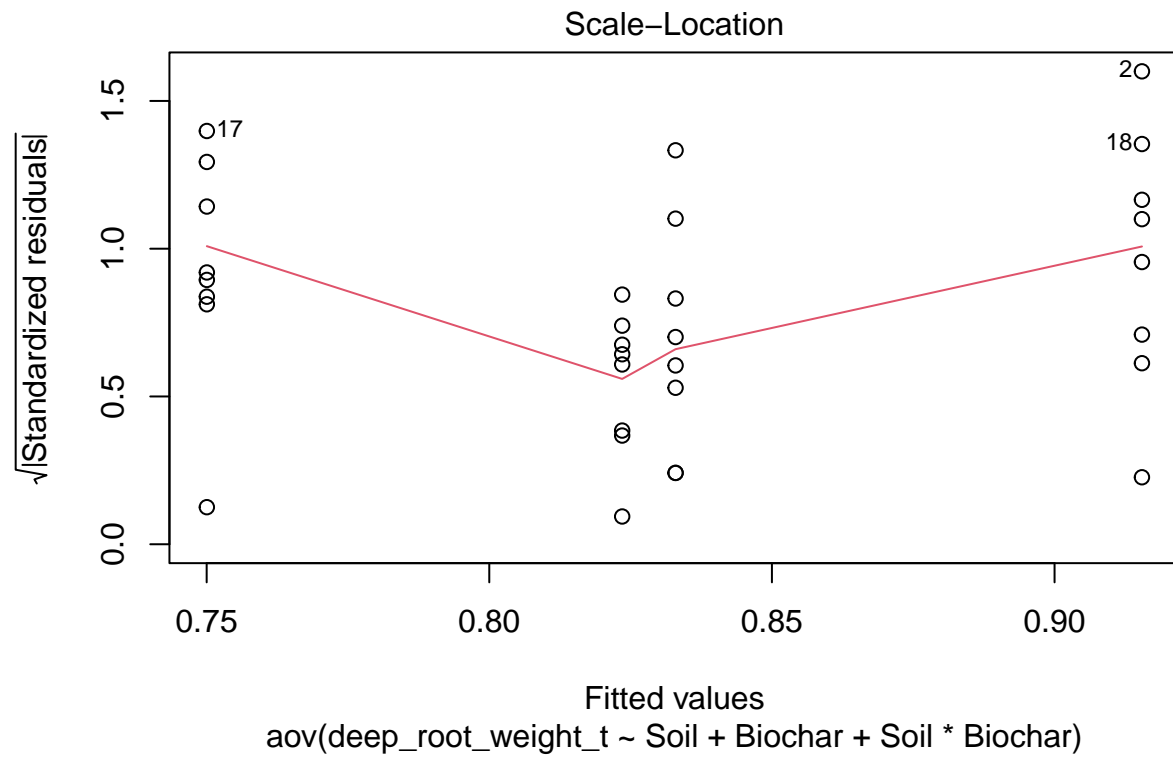
remove soil:biochar interaction

Fit Model 6

```
# fit full model
DRW_model6 <- aov(deep_root_weight_t ~ Soil + Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(DRW_model6)
```


Residuals vs Fitted

Fitted values
aov(deep_root_weight_t ~ Soil + Biochar)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(deep_root_weight_t ~ Soil + Biochar)

Scale–Location

√|Standardized residuals|

17

18 20

Fitted values
aov(deep_root_weight_t ~ Soil + Biochar)

Check for Nonsignificant Interactions

```
anova(DRW_model6)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##           Df  Sum Sq  Mean Sq F value  Pr(>F)
## Soil       1 0.00016 0.000163  0.0117 0.91455
## Biochar    1 0.06116 0.061163  4.3963 0.04485 *
## Residuals 29 0.40346 0.013913
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
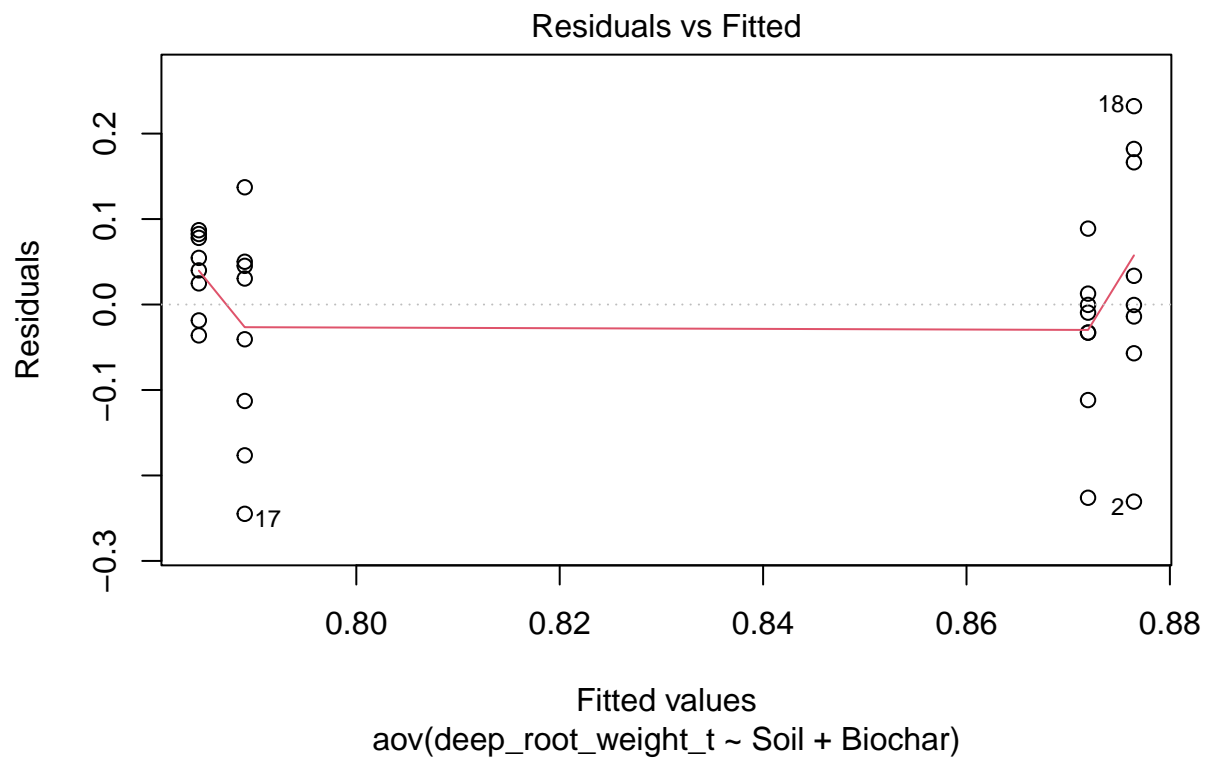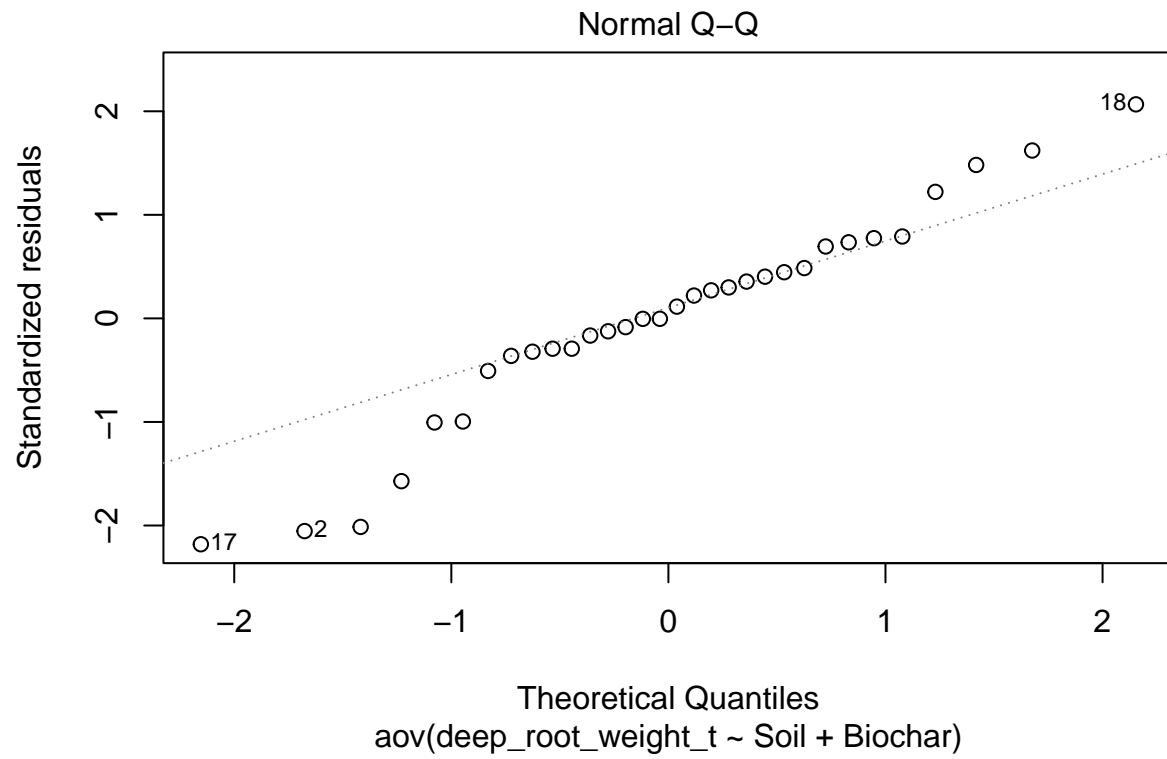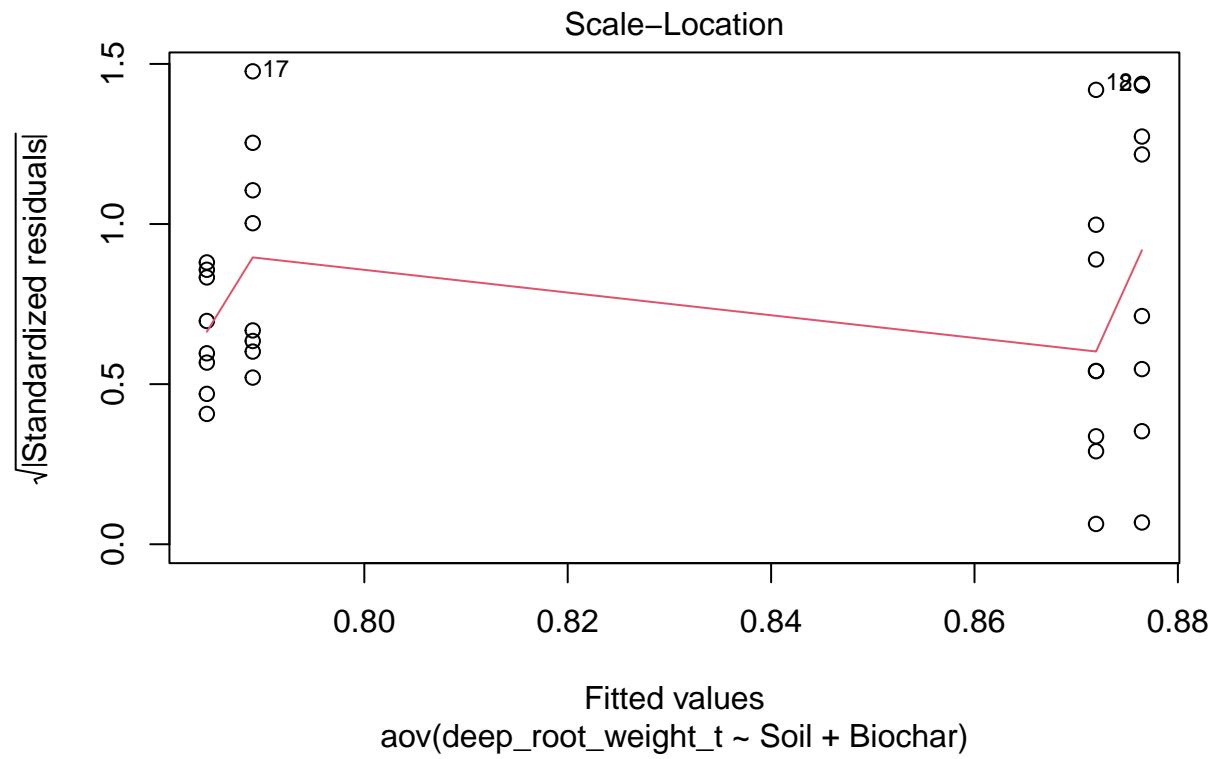
remove soil

Fit Model 7

```
# fit full model
DRW_model7 <- aov(deep_root_weight_t ~ Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(DRW_model7)
```

Residuals vs Fitted

Fitted values
aov(deep_root_weight_t ~ Biochar)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(deep_root_weight_t ~ Biochar)

Scale−Location

√|Standardized residuals|

Fitted values
aov(deep_root_weight_t ~ Biochar)
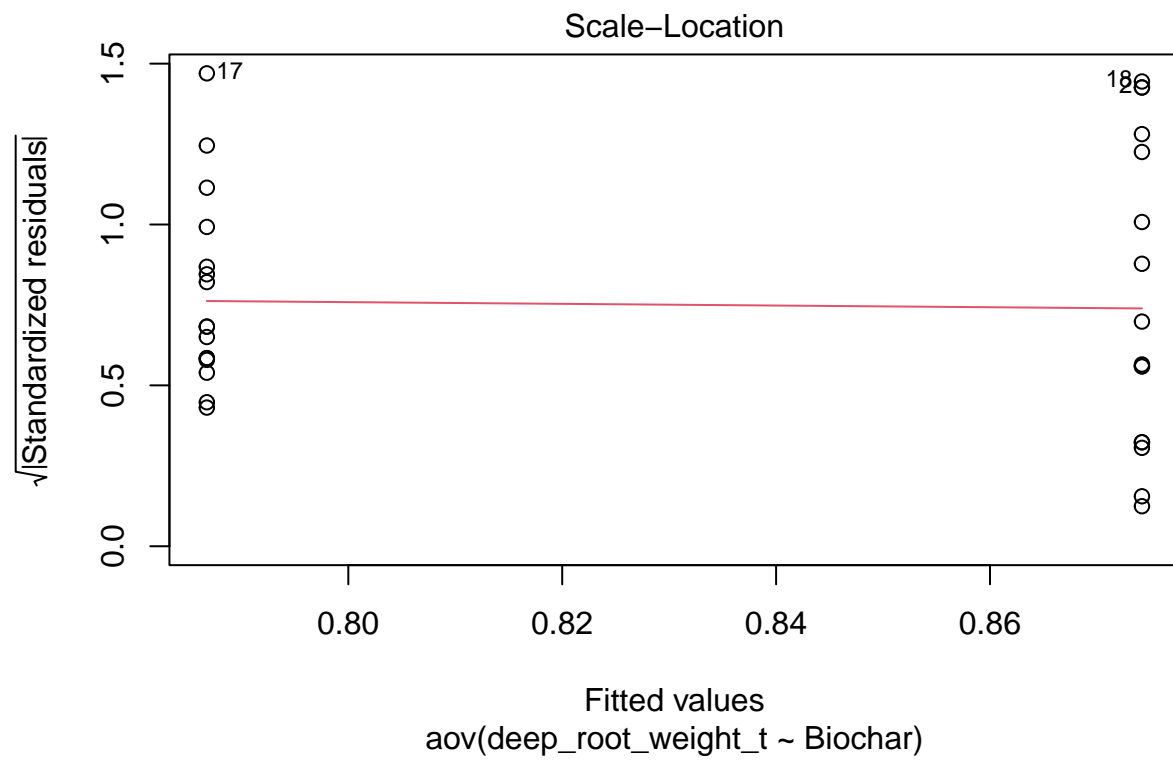
Check for Nonsignificant Interactions

```
anova(DRW_model7)
```

```
## Analysis of Variance Table
##
## Response: deep_root_weight_t
##           Df  Sum Sq  Mean Sq F value Pr(>F)
## Biochar    1 0.06116 0.061163   4.546 0.0413 *
## Residuals 30 0.40363 0.013454
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
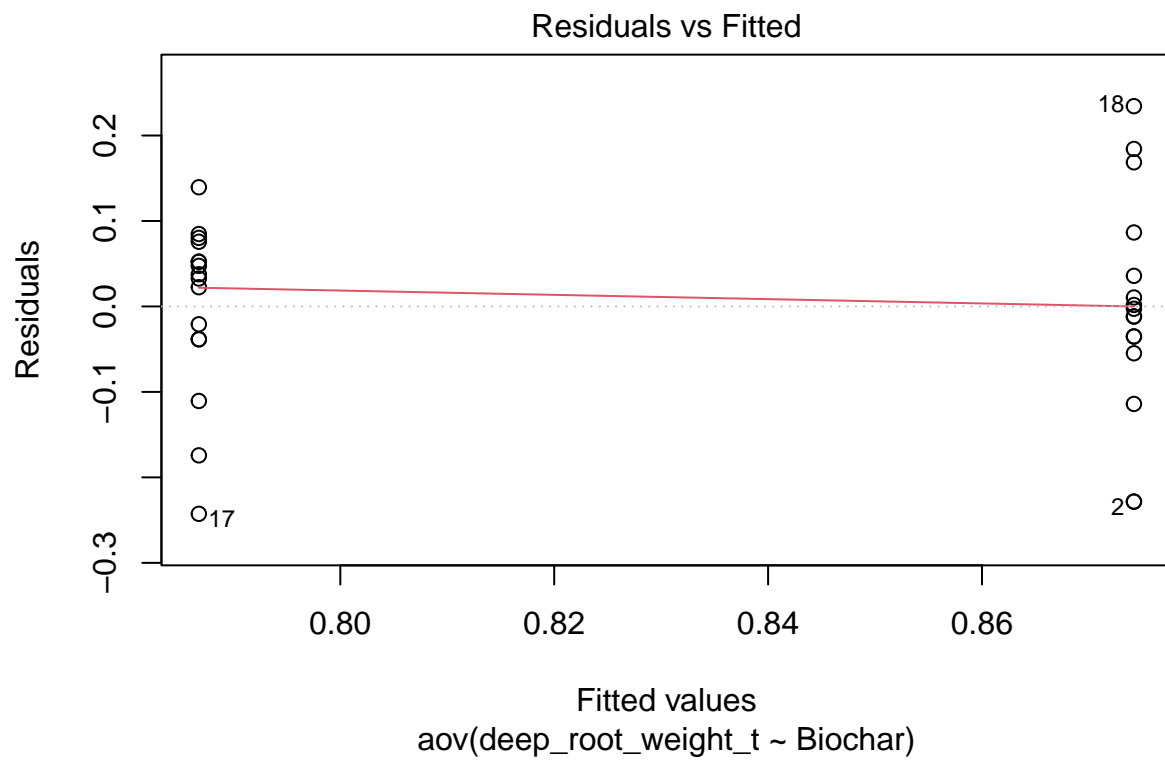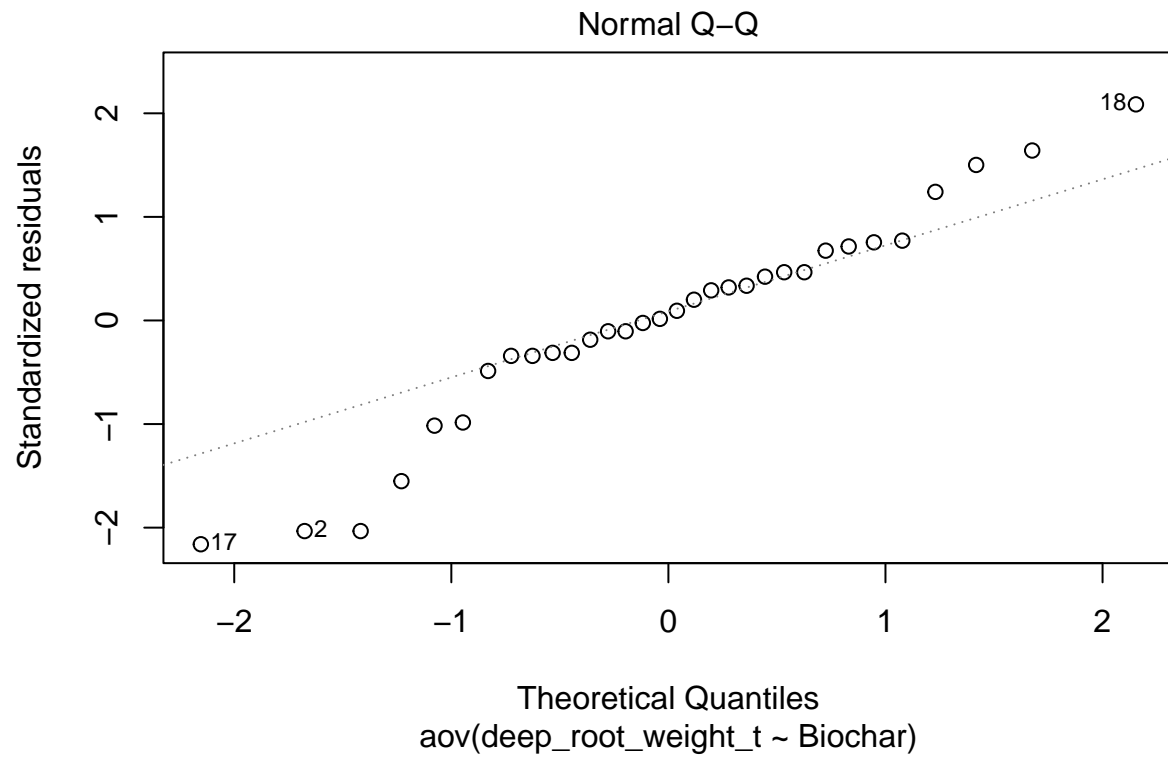
Final Model: One-Way

Final Model: Deep Root Weight = Biochar

Compare main effect

```
TukeyHSD(DRW_model7)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = deep_root_weight_t ~ Biochar, data = bc_data)
##
## $Biochar
##               diff          lwr       upr      p adj
## yes-no 0.08743797 0.003685406 0.1711905 0.0412984
```

```r
emmeans(DRW_model7,list(pairwise ~ Biochar))
```

```
## $'emmeans of Biochar'
##  Biochar emmean    SE df lower.CL upper.CL
##  no       0.787 0.029 30    0.728    0.846
##  yes      0.874 0.029 30    0.815    0.933
##
## Confidence level used: 0.95
##
## $'pairwise differences of Biochar'
##  1        estimate    SE df t.ratio p.value
##  no - yes  -0.0874 0.041 30  -2.132  0.0413
```

Total Root Weight

NOTE: All models and analysis performed below is for total root weight only

Box Plot for Total Root Weight

```r
plot_total_root_weight <- bc_data[c("Wheat","Soil","Biochar","total_root_weight")]
gg_object <- ggplot(data=plot_total_root_weight)

g1 <- gg_object +
  geom_boxplot(aes(x=Wheat, y=total_root_weight, fill=Wheat)) +
  scale_fill_manual(values=c("tan1", "steelblue2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g2 <- gg_object +
  geom_boxplot(aes(x=Soil, y=total_root_weight, fill=Soil)) +
  scale_fill_manual(values=c("cornsilk", "plum2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g3 <- gg_object +
  geom_boxplot(aes(x=Biochar, y=total_root_weight, fill=Biochar)) +
  scale_fill_manual(values=c("bisque", "cyan3")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())

grid.arrange(g1, g2, g3, nrow=1, top="Box Plot of Total Root Weight")
```

Box Plot of Total Root Weight
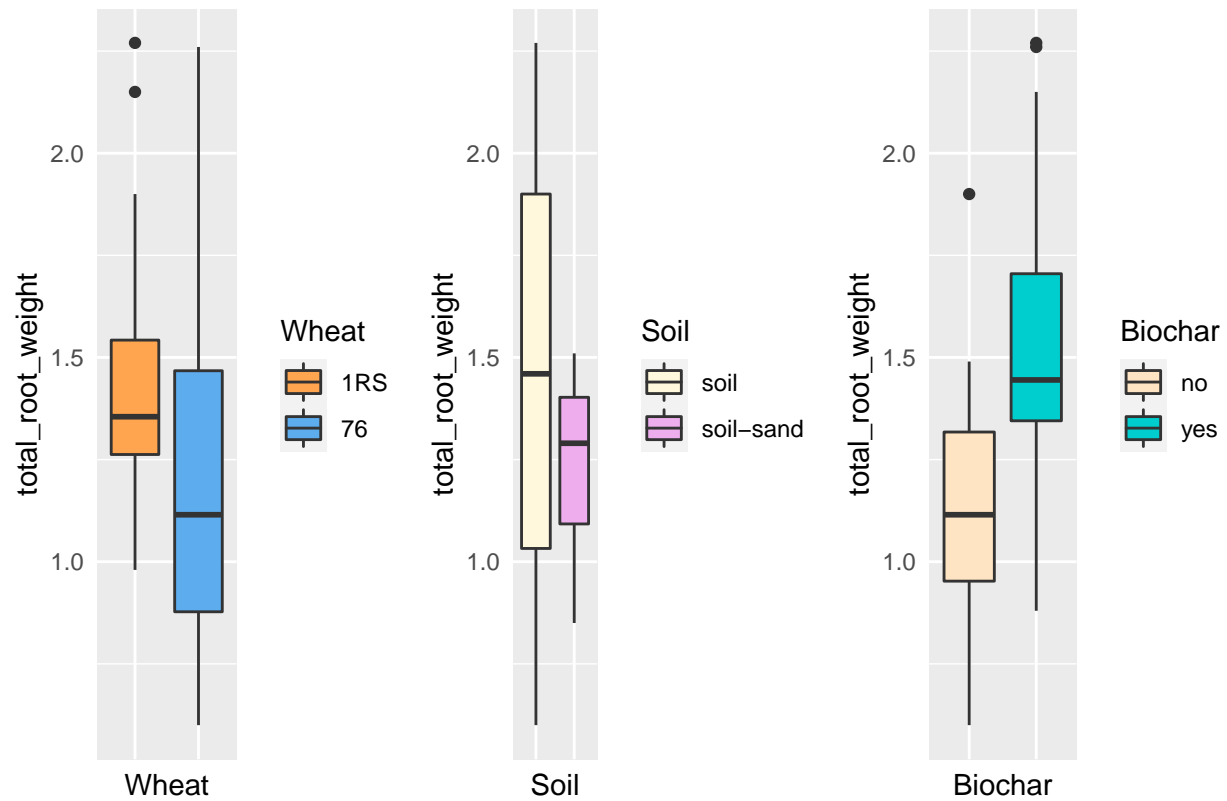
Fit Full Model

```r
# fit full model
TRW_model <- aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar
```

Check Model Assumptions

```r
# check assumptions
plot(TRW_model)
```

Residuals vs Fitted

aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...

Normal Q–Q

Theoretical Quantiles
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...

Scale–Location

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...
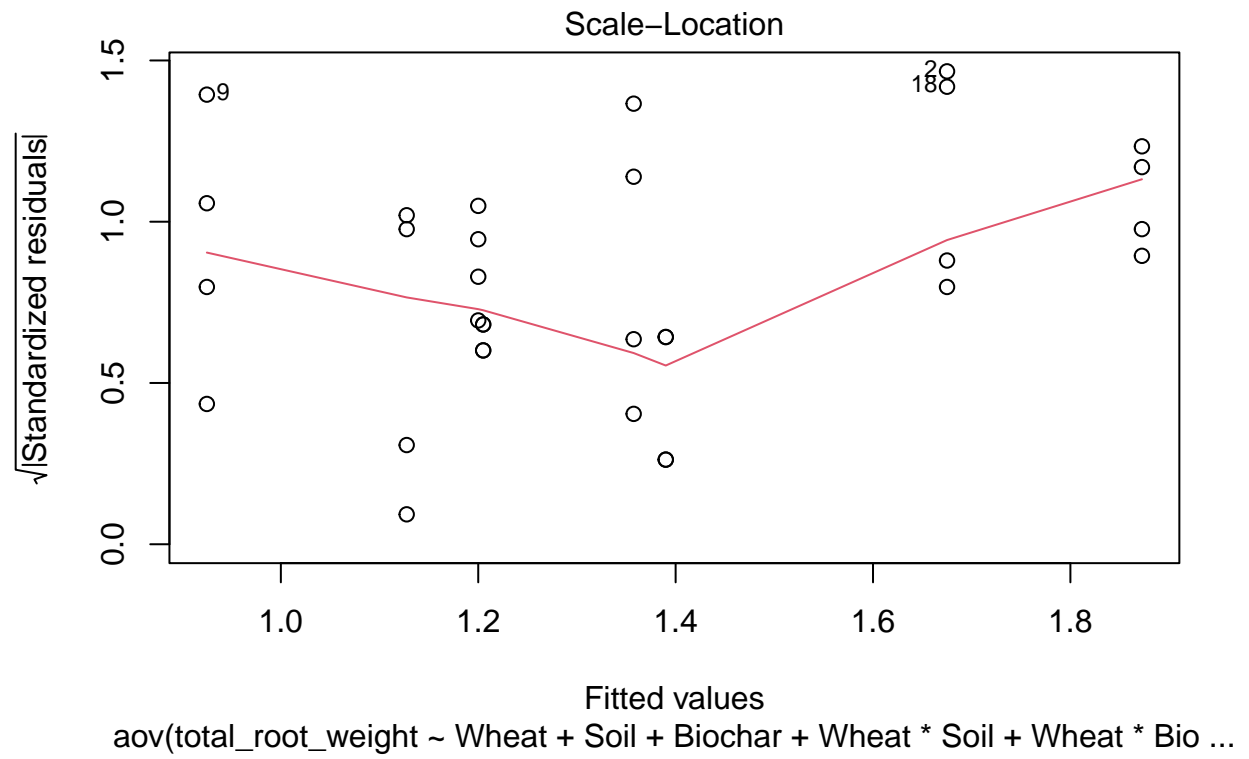
Check for 3-way Interactions

```
anova(TRW_model)
```

```
## Analysis of Variance Table
##
## Response: total_root_weight
##                   Df  Sum Sq Mean Sq F value    Pr(>F)
## Wheat              1 0.40275 0.40275  3.5740 0.070824 .
## Soil               1 0.41178 0.41178  3.6541 0.067943 .
## Biochar            1 1.15900 1.15900 10.2850 0.003776 **
## Wheat:Soil         1 0.06570 0.06570  0.5831 0.452561
## Wheat:Biochar      1 0.00750 0.00750  0.0666 0.798579
## Soil:Biochar       1 0.50753 0.50753  4.5038 0.044335 *
## Wheat:Soil:Biochar 1 0.06038 0.06038  0.5358 0.471268
## Residuals         24 2.70452 0.11269
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
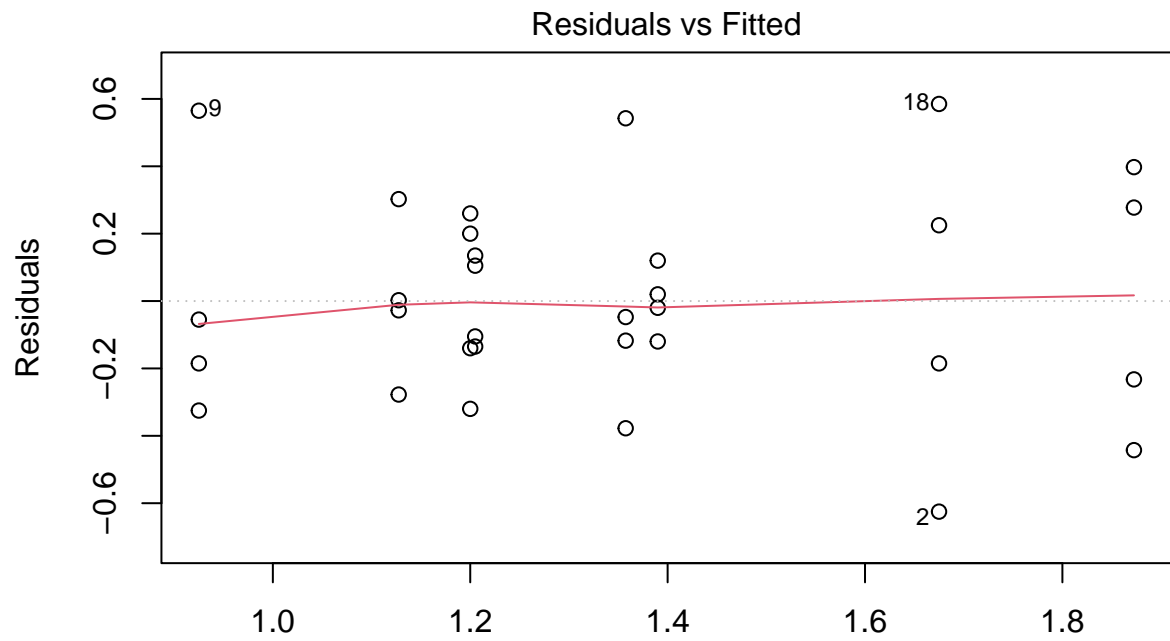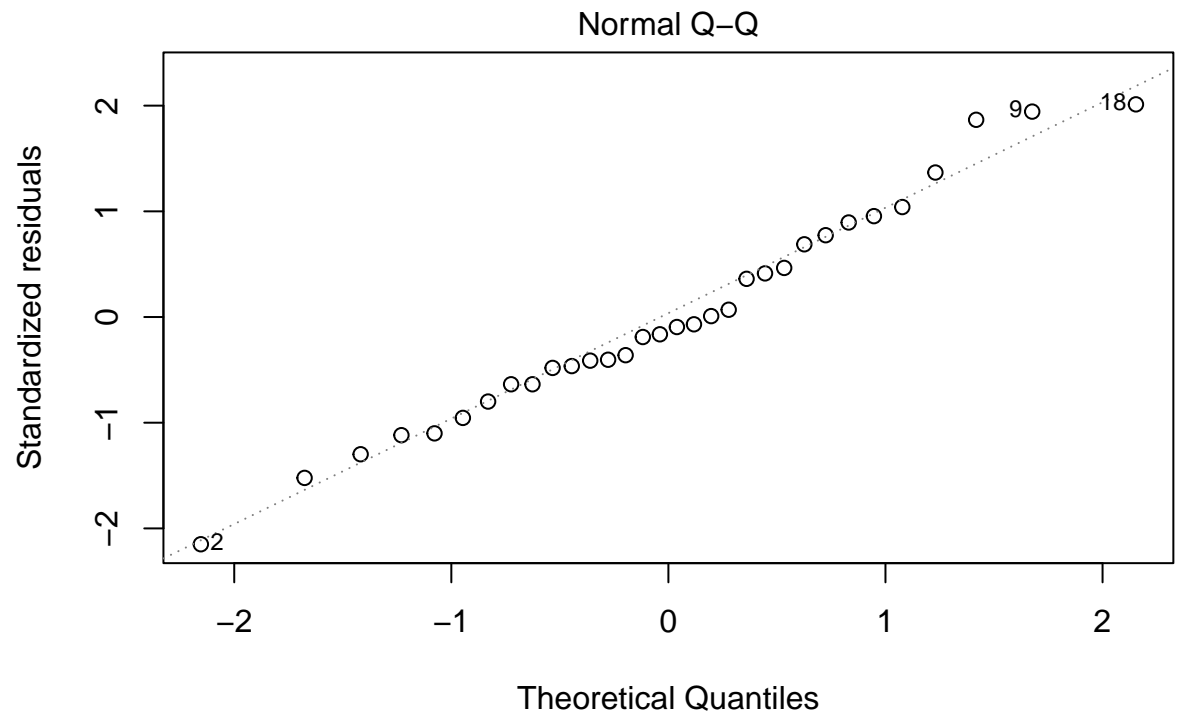
Remove 3 way interaction

Fit Model 2

```
# fit full model
TRW_model_2 <- aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Bioch
```

Check Model Assumptions

```
# check assumptions
plot(TRW_model_2)
```

Residuals vs Fitted

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...

Normal Q–Q

Theoretical Quantiles
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...

Scale−Location

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bio ...
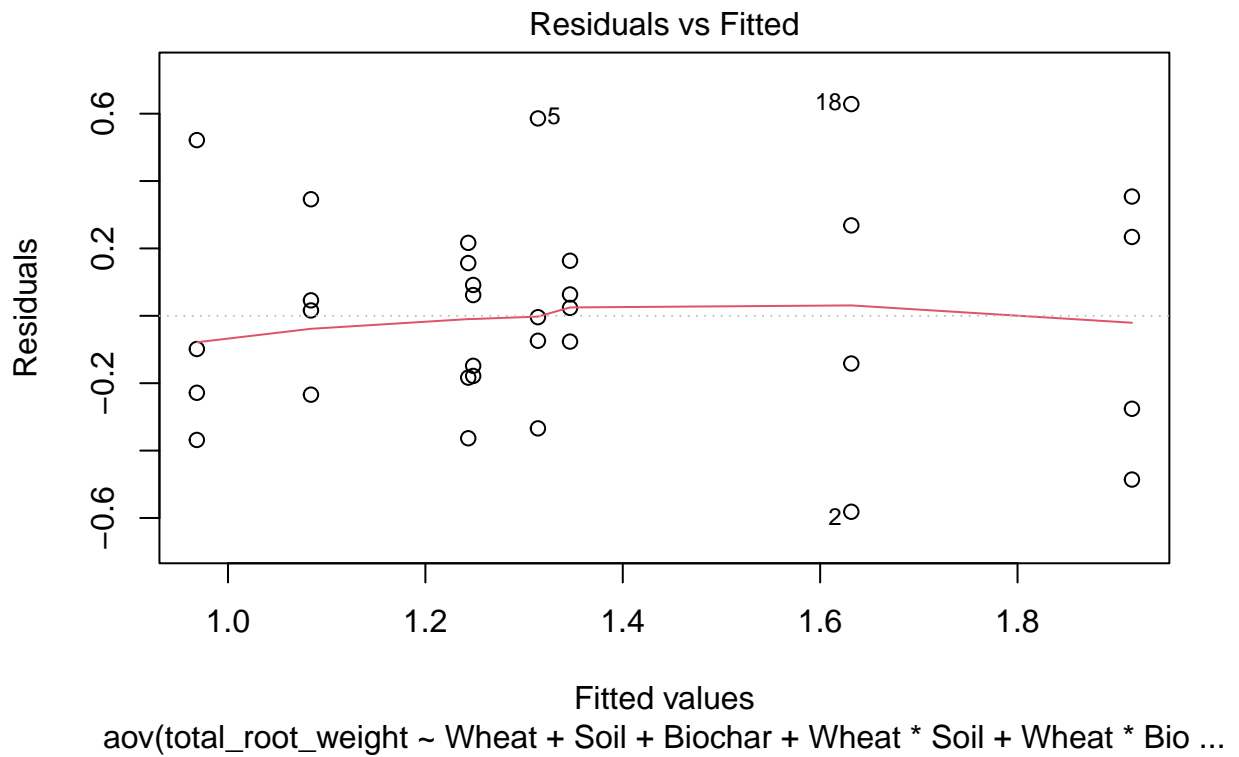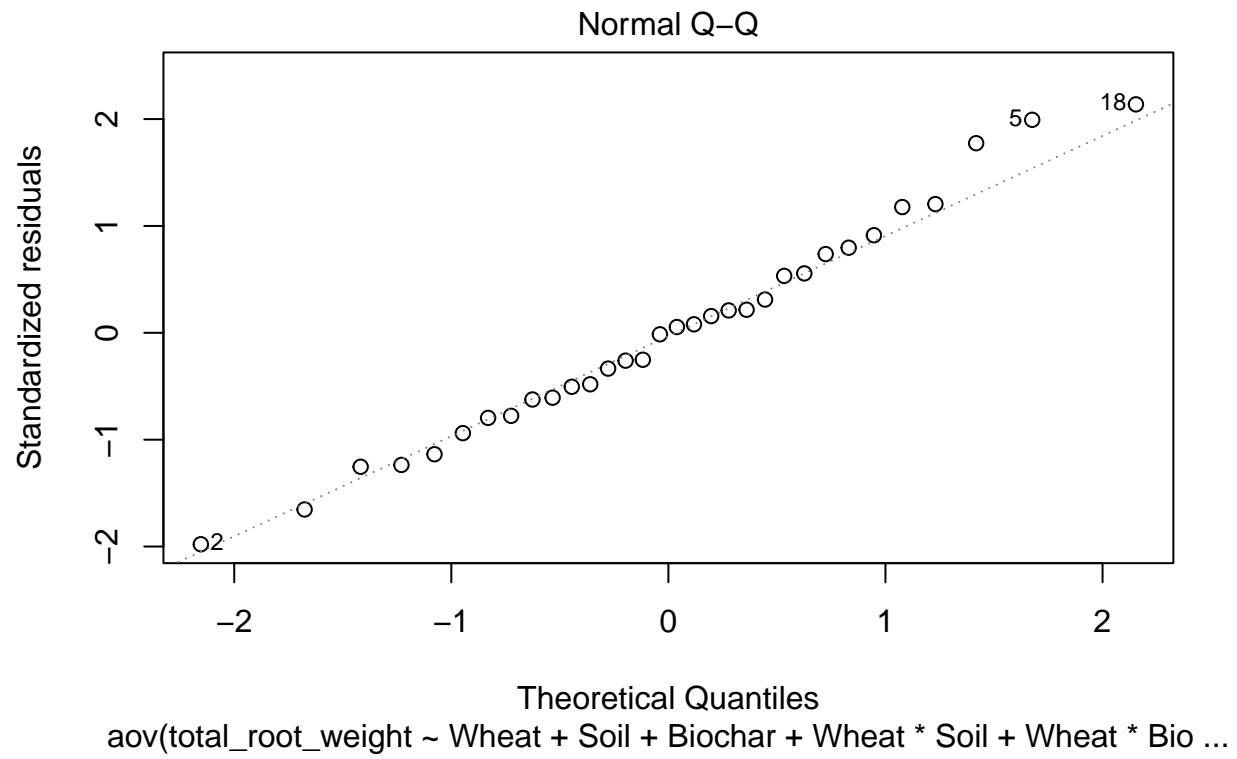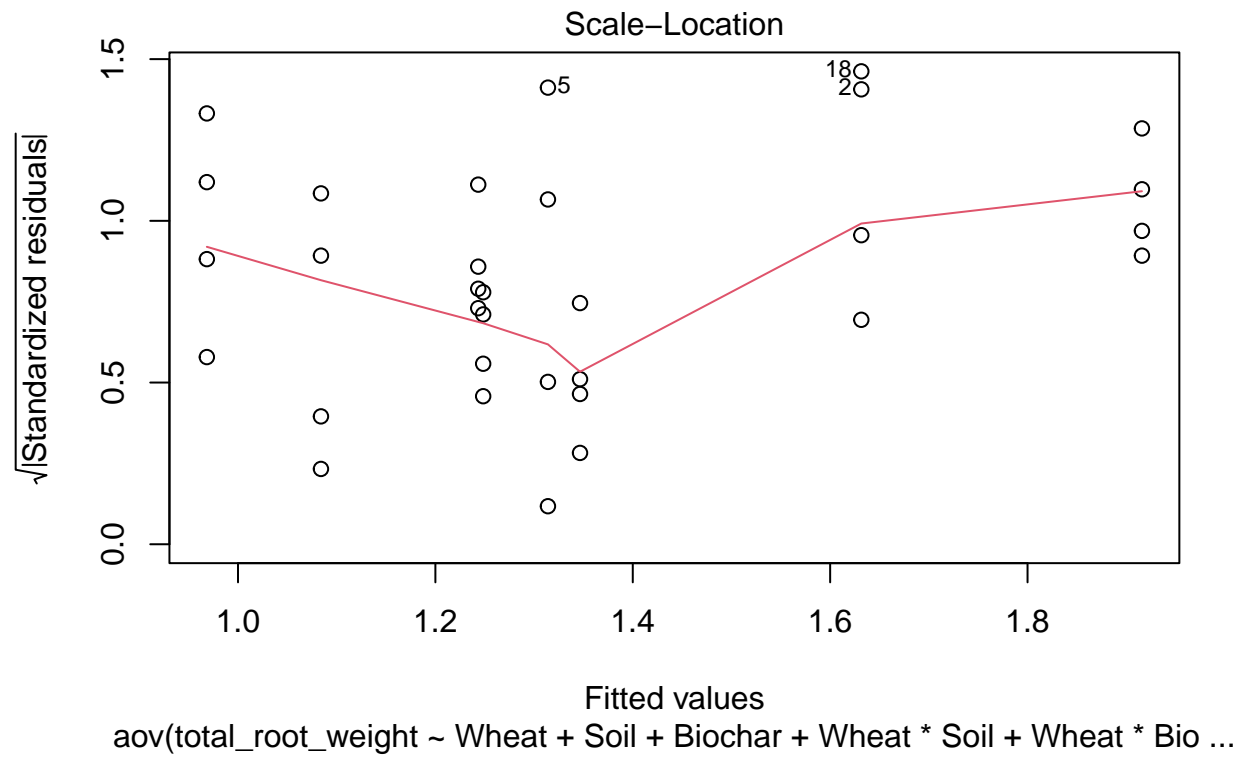
Check for Nonsignificant Interactions

```
anova(TRW_model_2)
```

```
## Analysis of Variance Table
##
## Response: total_root_weight
##                Df  Sum Sq Mean Sq F value    Pr(>F)
## Wheat           1 0.40275 0.40275  3.6417 0.067898 .
## Soil            1 0.41178 0.41178  3.7233 0.065083 .
## Biochar         1 1.15900 1.15900 10.4796 0.003392 **
## Wheat:Soil      1 0.06570 0.06570  0.5941 0.448069
## Wheat:Biochar   1 0.00750 0.00750  0.0678 0.796638
## Soil:Biochar    1 0.50753 0.50753  4.5890 0.042105 *
## Residuals      25 2.76490 0.11060
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove Wheat:Biochar interaction

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Fit Model 3

```
# fit full model
TRW_model_3 <- aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat*Soil + Soil*Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(TRW_model_3)
```

Residuals vs Fitted

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioc ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioc ...

Scale–Location

aov(total_root_weight ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioc ...

Check for Nonsignificant Interactions

```r
anova(TRW_model_3)
```

```
## Analysis of Variance Table
##
## Response: total_root_weight
##              Df  Sum Sq Mean Sq F value   Pr(>F)
## Wheat         1 0.40275 0.40275  3.7771 0.062859 .
## Soil          1 0.41178 0.41178  3.8617 0.060169 .
## Biochar       1 1.15900 1.15900 10.8693 0.002831 **
## Wheat:Soil    1 0.06570 0.06570  0.6162 0.439568
## Soil:Biochar  1 0.50753 0.50753  4.7597 0.038365 *
## Residuals    26 2.77241 0.10663
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
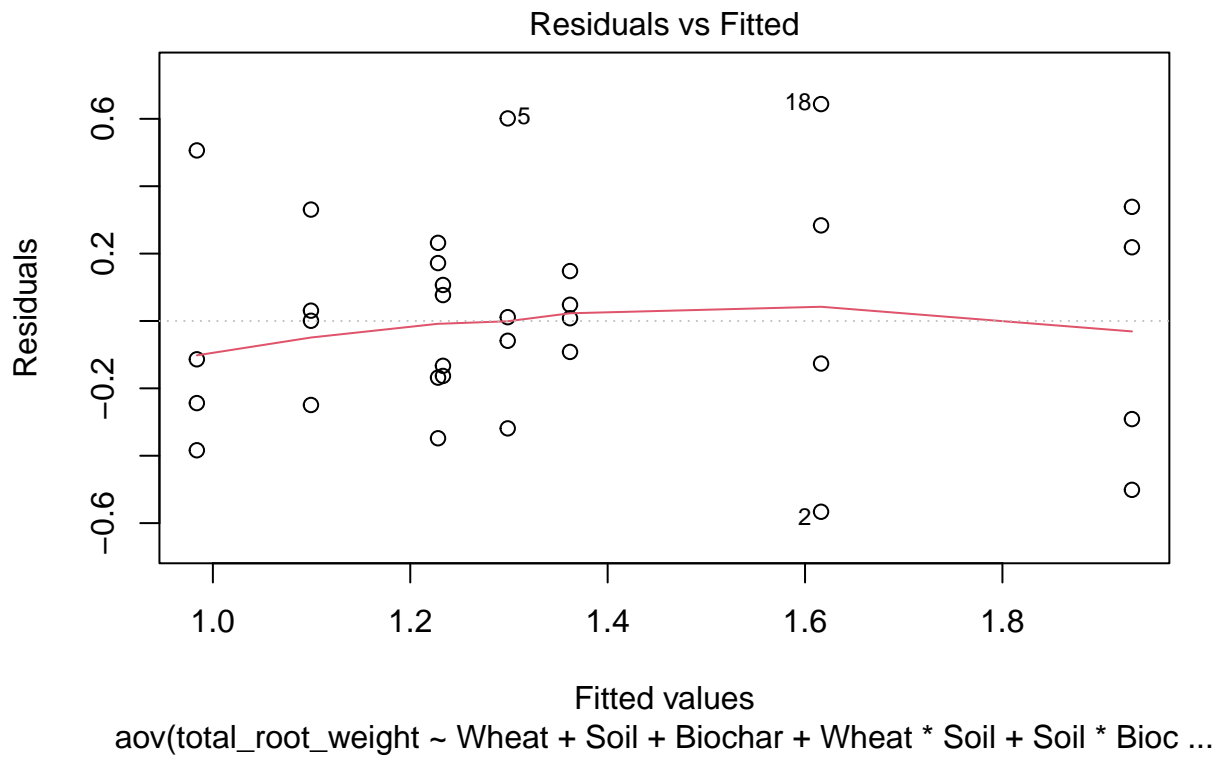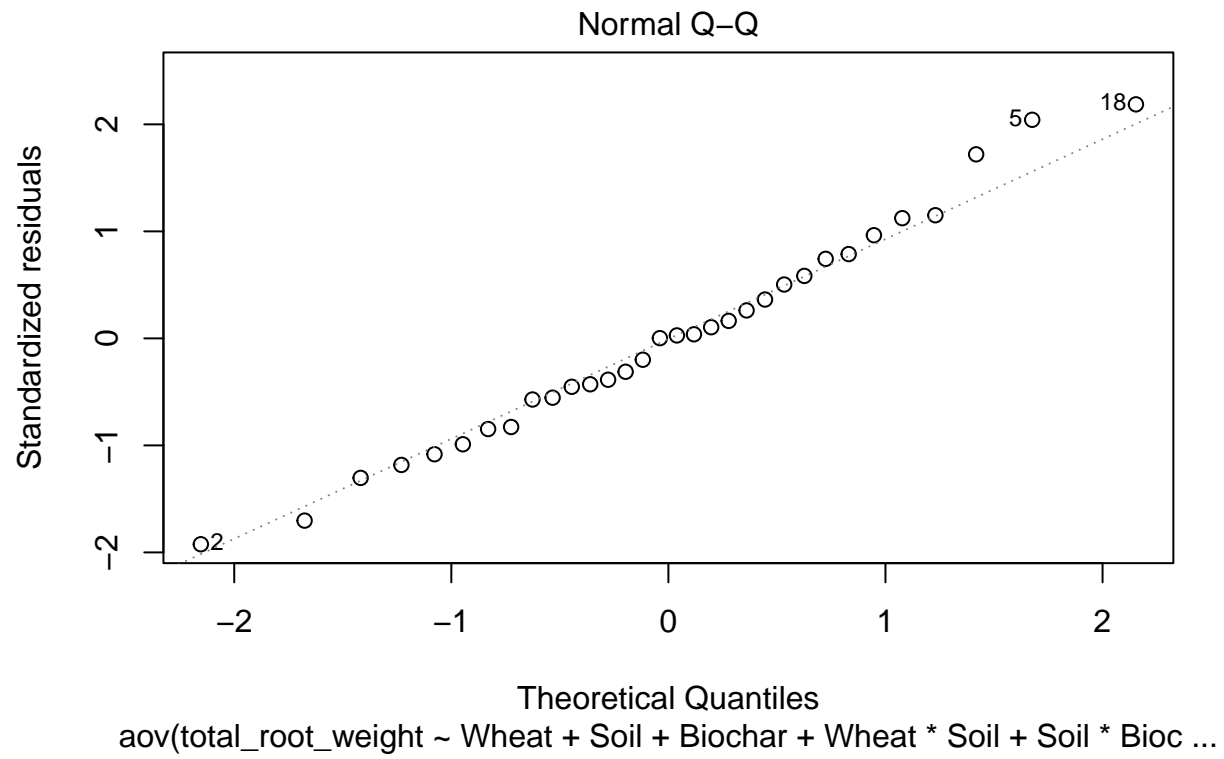
Remove Wheat:Soil interaction

Fit Model 4

```
# fit full model
TRW_model_4 <- aov(total_root_weight ~ Wheat + Soil + Biochar + Soil*Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(TRW_model_4)
```


Residuals vs Fitted

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(total_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

Scale–Location

Fitted values
aov(total_root_weight ~ Wheat + Soil + Biochar + Soil * Biochar)

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Check for Nonsignificant Interactions

```r
anova(TRW_model_4)
```

```
## Analysis of Variance Table
##
## Response: total_root_weight
##              Df  Sum Sq Mean Sq F value   Pr(>F)
## Wheat         1 0.40275 0.40275  3.8315 0.060708 .
## Soil          1 0.41178 0.41178  3.9174 0.058069 .
## Biochar       1 1.15900 1.15900 11.0260 0.002583 **
## Soil:Biochar  1 0.50753 0.50753  4.8283 0.036756 *
## Residuals    27 2.83811 0.10512
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
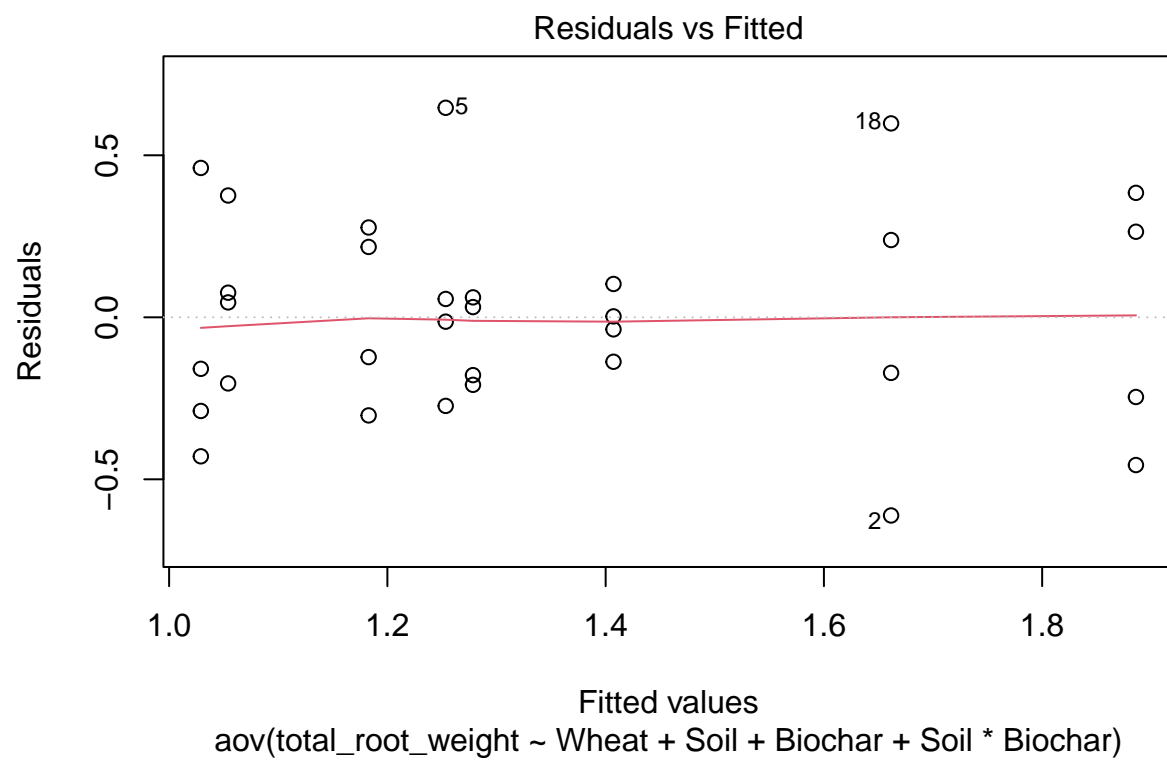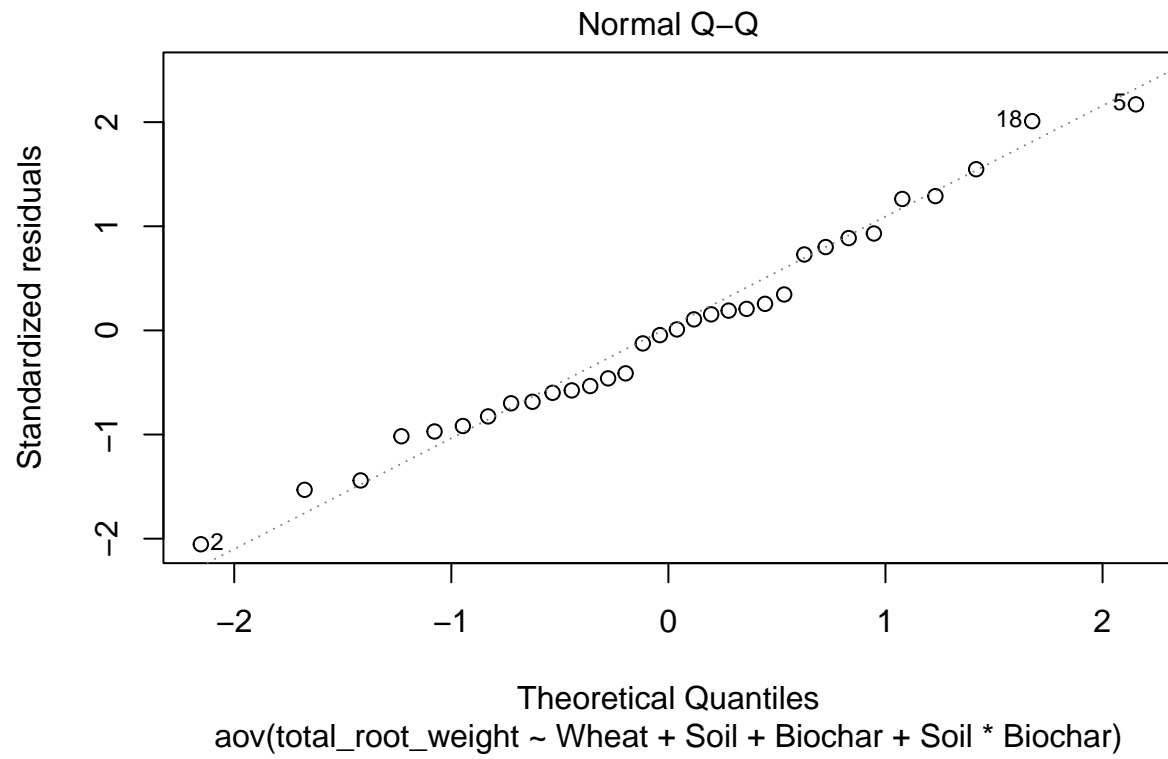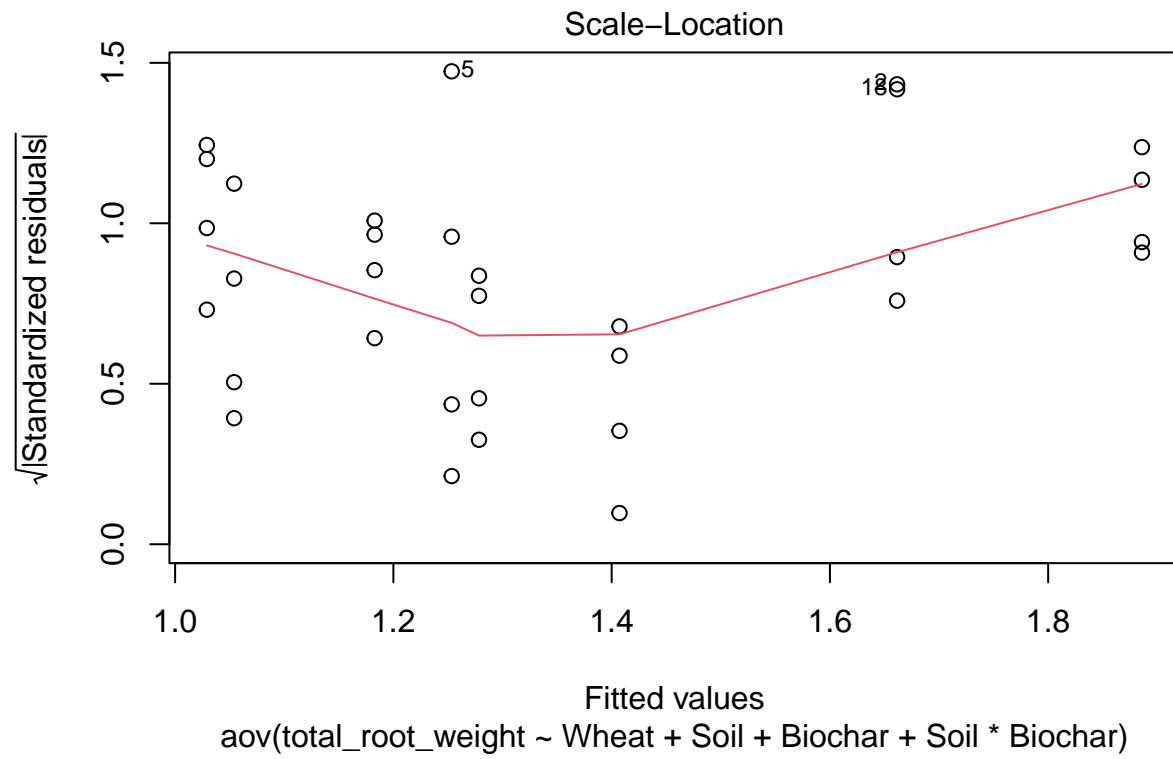
Remove Wheat

Fit Model 5

```
# fit full model
TRW_model_5 <- aov(total_root_weight ~ Soil + Biochar + Soil*Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(TRW_model_5)
```

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(total_root_weight ~ Soil + Biochar + Soil * Biochar)

Scale−Location

√|Standardized residuals|

Fitted values
aov(total_root_weight ~ Soil + Biochar + Soil * Biochar)

Check for Nonsignificant Interactions

```
anova(TRW_model_5)
```

```
## Analysis of Variance Table
##
## Response: total_root_weight
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Soil          1 0.4118 0.41178  3.5576 0.069684 .
## Biochar       1 1.1590 1.15900 10.0134 0.003726 **
## Soil:Biochar  1 0.5075 0.50753  4.3849 0.045435 *
## Residuals    28 3.2409 0.11575
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
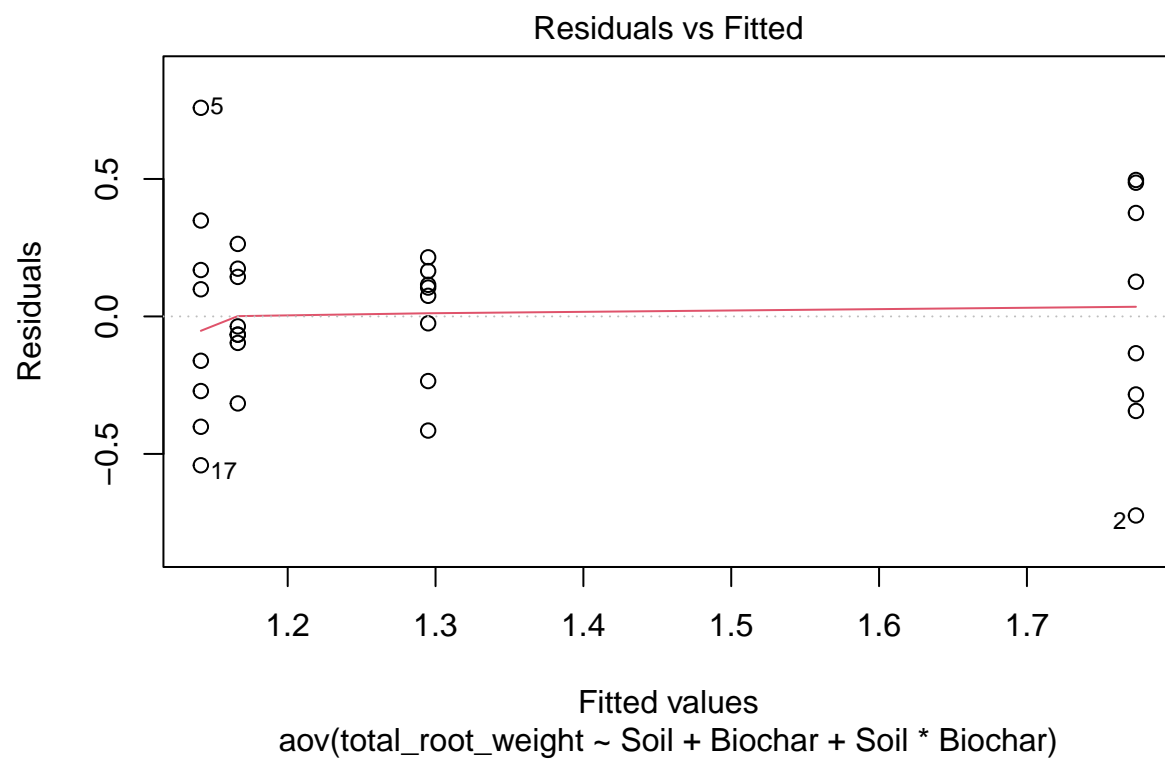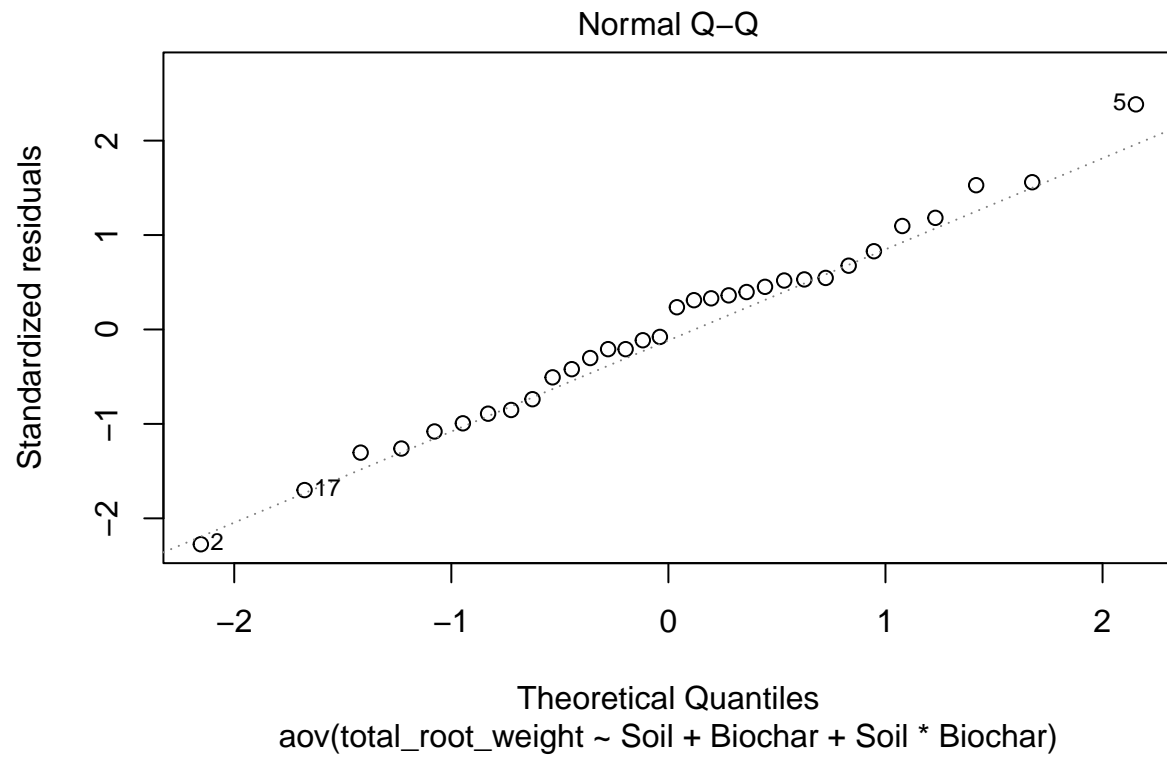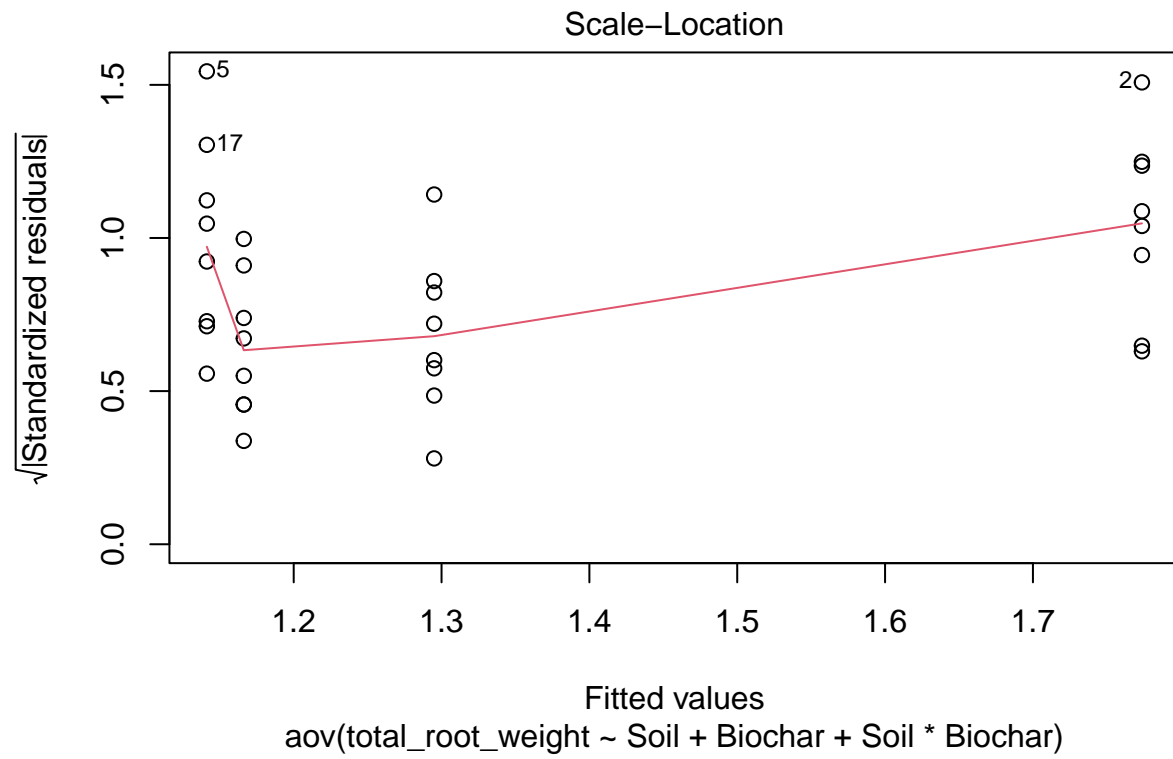
Final Model: Order 2 Model with interaction

Final Model: Total Root Weight = Soil + Biochar + Soil:Biochar

```
interaction.plot(Biochar, Soil, total_root_weight)
```
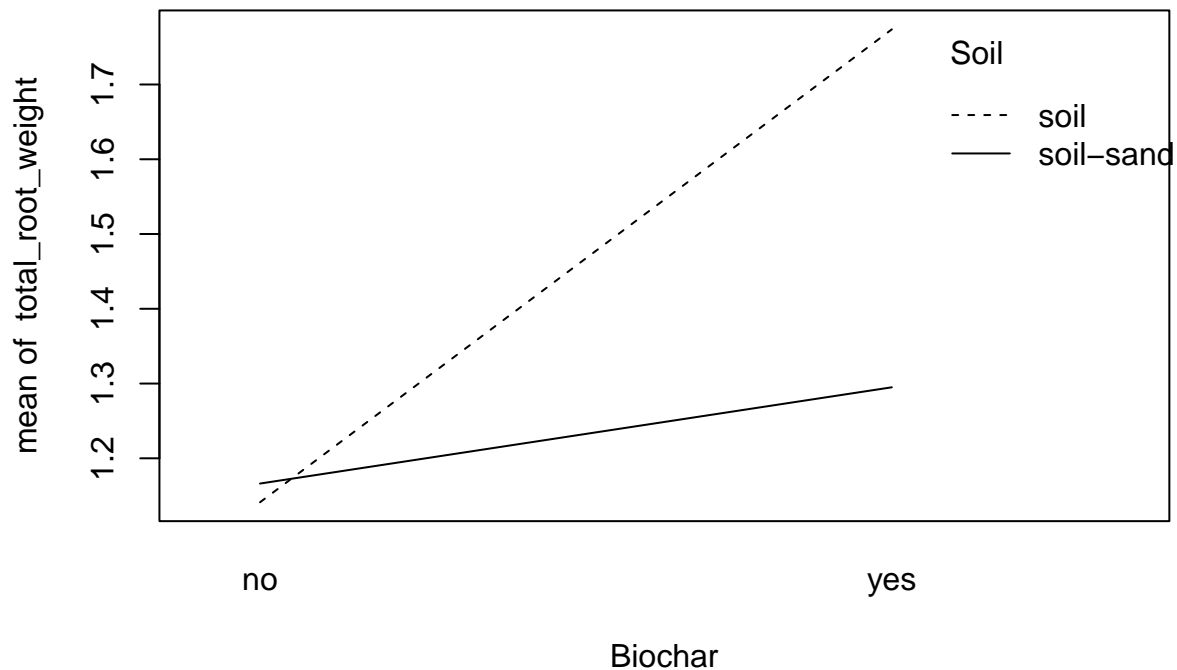
Multiple Comparison

```
# compare the effect of Wheat at each level of Soil
emmeans(TRW_model_5, list(pairwise ~ Soil|Biochar))
```

```
## $`emmeans of Soil | Biochar`
## Biochar = no:
##  Soil       emmean   SE df lower.CL upper.CL
##  soil         1.14 0.12 28    0.895     1.39
##  soil-sand    1.17 0.12 28    0.920     1.41
##
## Biochar = yes:
##  Soil       emmean   SE df lower.CL upper.CL
##  soil         1.77 0.12 28    1.527     2.02
##  soil-sand    1.29 0.12 28    1.049     1.54
##
## Confidence level used: 0.95
##
## $`pairwise differences of Soil | Biochar`
## Biochar = no:
##  2                 estimate   SE df t.ratio p.value
##  soil - (soil-sand)  -0.025 0.17 28  -0.147  0.8842
##
## Biochar = yes:
```

```
## 2                estimate   SE df t.ratio p.value
## soil - (soil-sand)    0.479 0.17 28  2.814  0.0088
```

- The effect of Soil is significant when Biochar treatment is "yes" (p-value = 0.0088 < 0.05) in terms of total root weight.

```
# compare the effect of Soil at each level of Wheat
emmeans(TRW_model_5, list(pairwise ~ Biochar|Soil))
```

```
## $`emmeans of Biochar | Soil`
## Soil = soil:
##  Biochar emmean   SE df lower.CL upper.CL
##  no        1.14 0.12 28    0.895     1.39
##  yes       1.77 0.12 28    1.527     2.02
##
## Soil = soil-sand:
##  Biochar emmean   SE df lower.CL upper.CL
##  no        1.17 0.12 28    0.920     1.41
##  yes       1.29 0.12 28    1.049     1.54
##
## Confidence level used: 0.95
##
## $`pairwise differences of Biochar | Soil`
## Soil = soil:
##  2        estimate   SE df t.ratio p.value
##  no - yes   -0.632 0.17 28 -3.718  0.0009
##
## Soil = soil-sand:
##  2        estimate   SE df t.ratio p.value
##  no - yes   -0.129 0.17 28 -0.757  0.4554
```

- The effect of Biochar is significant when Soil type is "soil" (p-value = 0.0009 < 0.05) in terms of total root weight.

Root Shoot Ratio

NOTE: All models and analysis performed below is for root shoot ratio only

Box Plot for Root Shoot Ratio

```
plot_root_shoot_ratio <- bc_data[c("Wheat","Soil","Biochar","deep_root_weight")]
gg_object <- ggplot(data=plot_root_shoot_ratio)

g1 <- gg_object +
  geom_boxplot(aes(x=Wheat, y=root_shoot_ratio, fill=Wheat)) +
  scale_fill_manual(values=c("tan1", "steelblue2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank())
g2 <- gg_object +
  geom_boxplot(aes(x=Soil, y=root_shoot_ratio, fill=Soil)) +
```
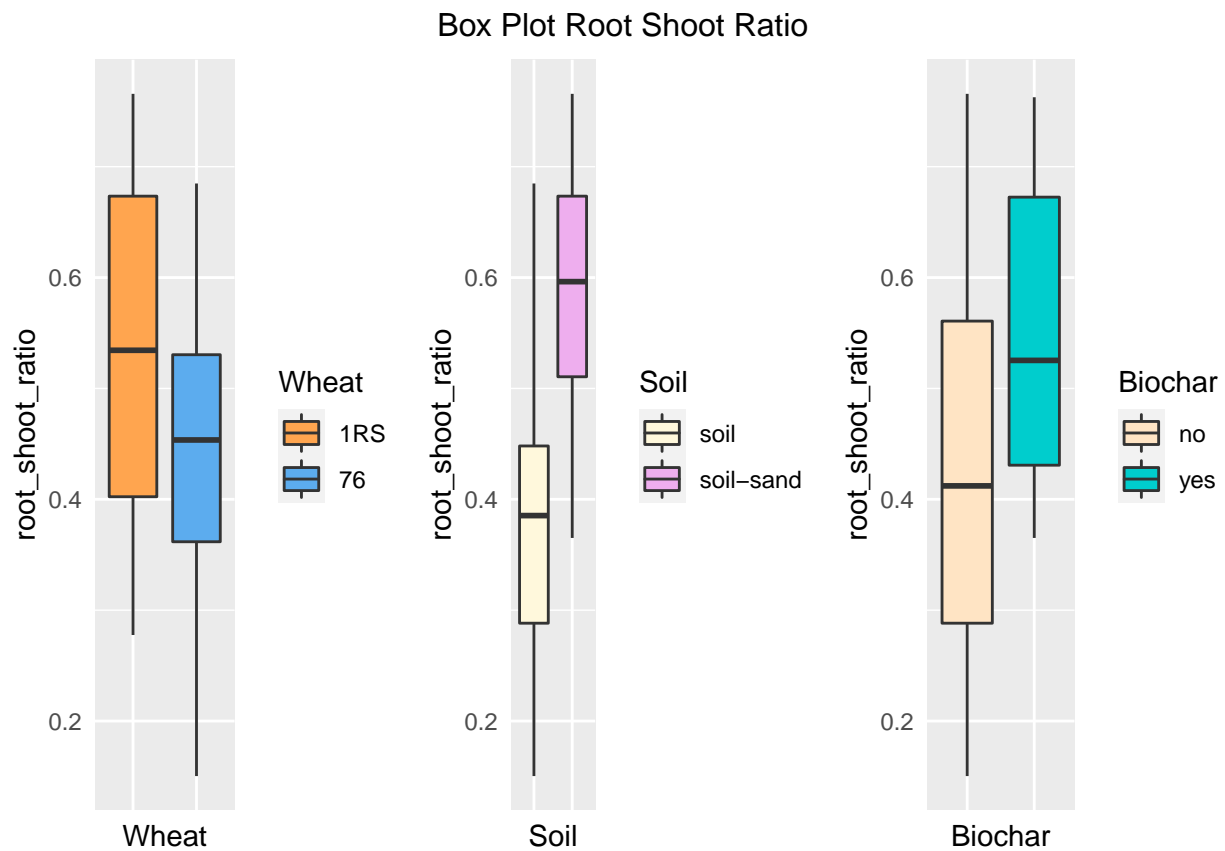
```
  scale_fill_manual(values=c("cornsilk", "plum2")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank()))
g3 <- gg_object +
  geom_boxplot(aes(x=Biochar, y=root_shoot_ratio, fill=Biochar)) +
  scale_fill_manual(values=c("bisque", "cyan3")) +
  theme(axis.text.x = element_blank(),axis.ticks = element_blank()))

grid.arrange(g1, g2, g3, nrow=1, top="Box Plot Root Shoot Ratio")
```


Box Plot Root Shoot Ratio

Fit Full Model

```
# fit full model
RSR_model <- aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biochar
```

Check Model Assumptions

```
# check assumptions
plot(RSR_model)
```

Residuals vs Fitted

Residuals

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Normal Q–Q

Theoretical Quantiles
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Scale–Location

√|Standardized residuals|

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...
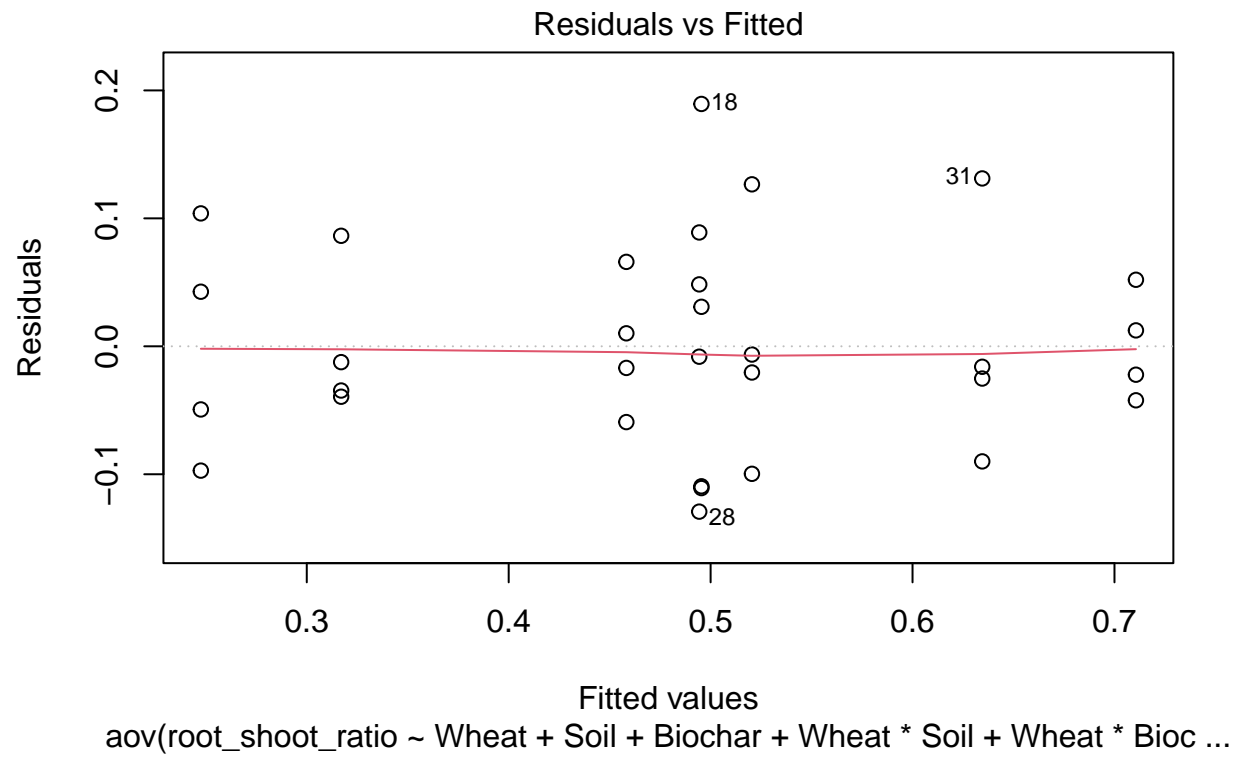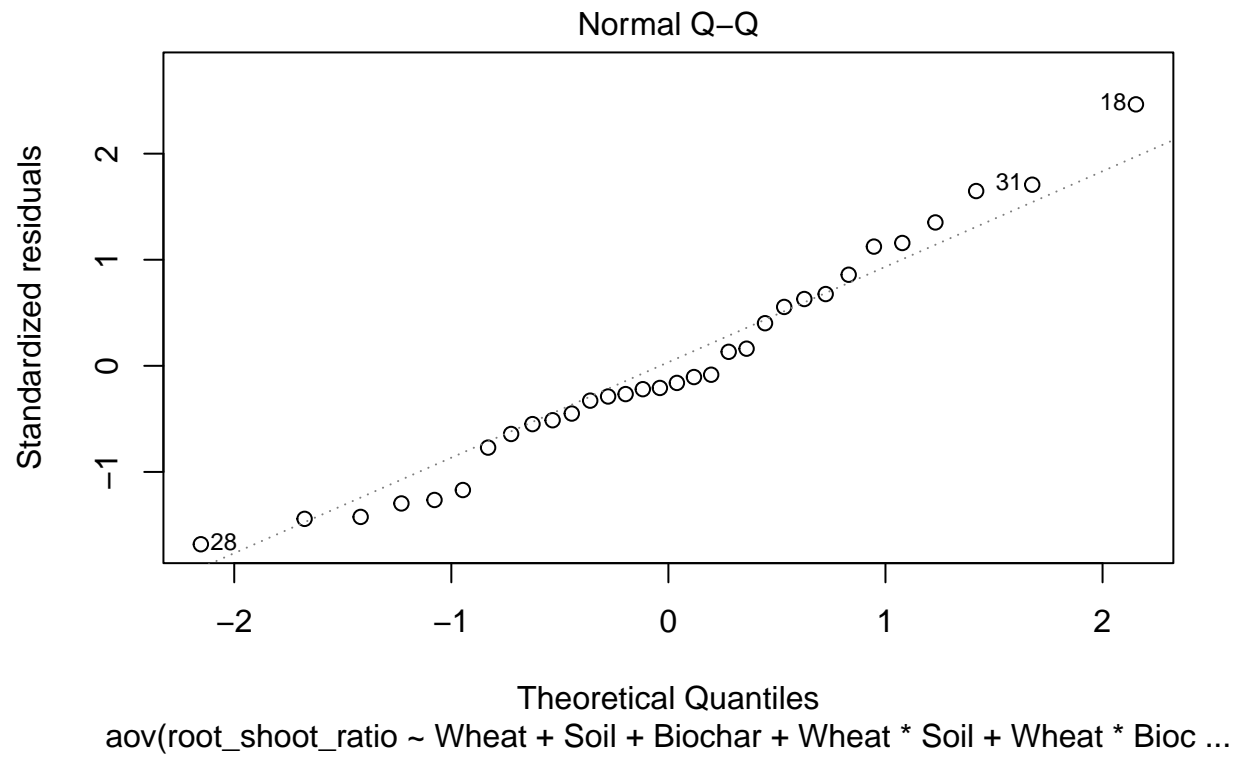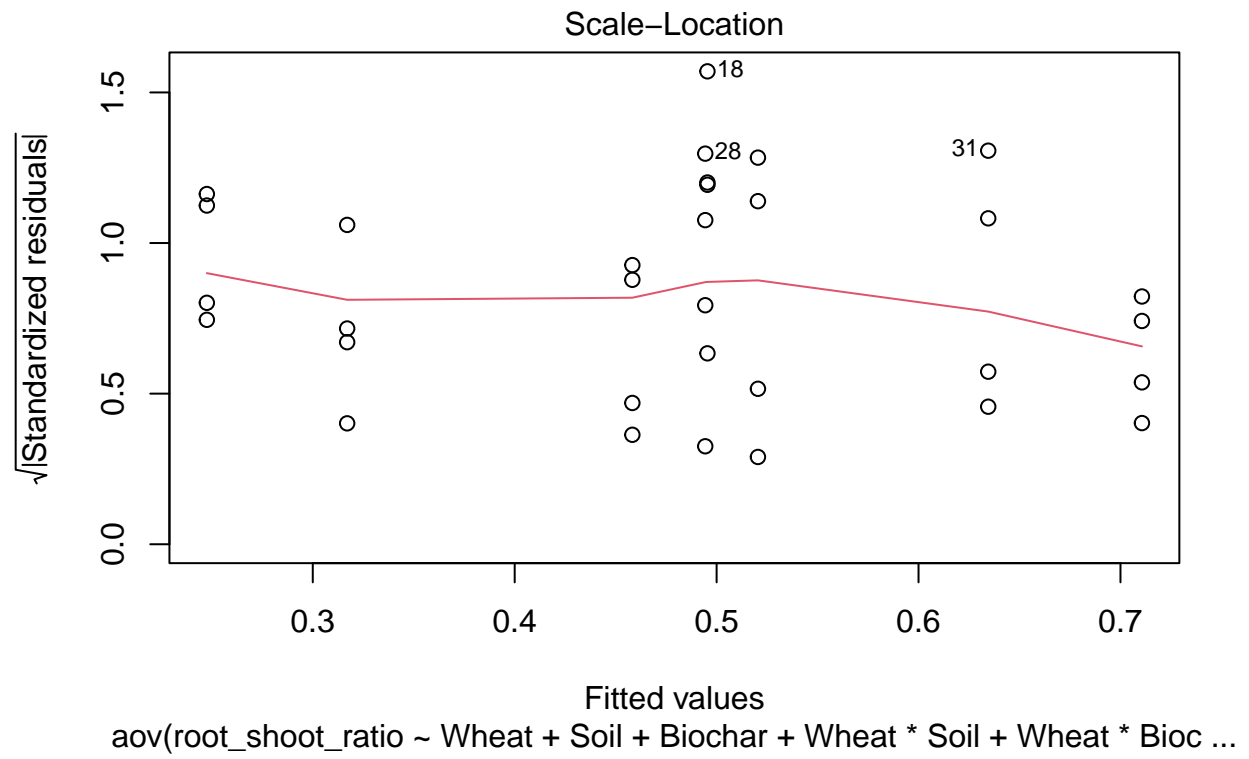
Check for 3-way Interactions

```
anova(RSR_model)
```

```
## Analysis of Variance Table
##
## Response: root_shoot_ratio
##                    Df  Sum Sq Mean Sq F value    Pr(>F)
## Wheat               1 0.06575 0.06575  8.3510  0.008050 **
## Soil                1 0.35424 0.35424 44.9928 6.145e-07 ***
## Biochar             1 0.09643 0.09643 12.2479  0.001844 **
## Wheat:Soil          1 0.04441 0.04441  5.6404  0.025889 *
## Wheat:Biochar       1 0.00001 0.00001  0.0013  0.971988
## Soil:Biochar        1 0.05750 0.05750  7.3030  0.012438 *
## Wheat:Soil:Biochar  1 0.02182 0.02182  2.7714  0.108963
## Residuals          24 0.18896 0.00787
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove 3 way interaction

Fit Model 2

```r
# fit full model
RSR_model_2 <- aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat*Soil + Wheat*Biochar + Soil*Biocha
```

Check Model Assumptions

```r
# check assumptions
plot(RSR_model_2)
```


Residuals vs Fitted

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Normal Q–Q

Theoretical Quantiles
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...

Scale–Location

√|Standardized residuals|

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Wheat * Bioc ...
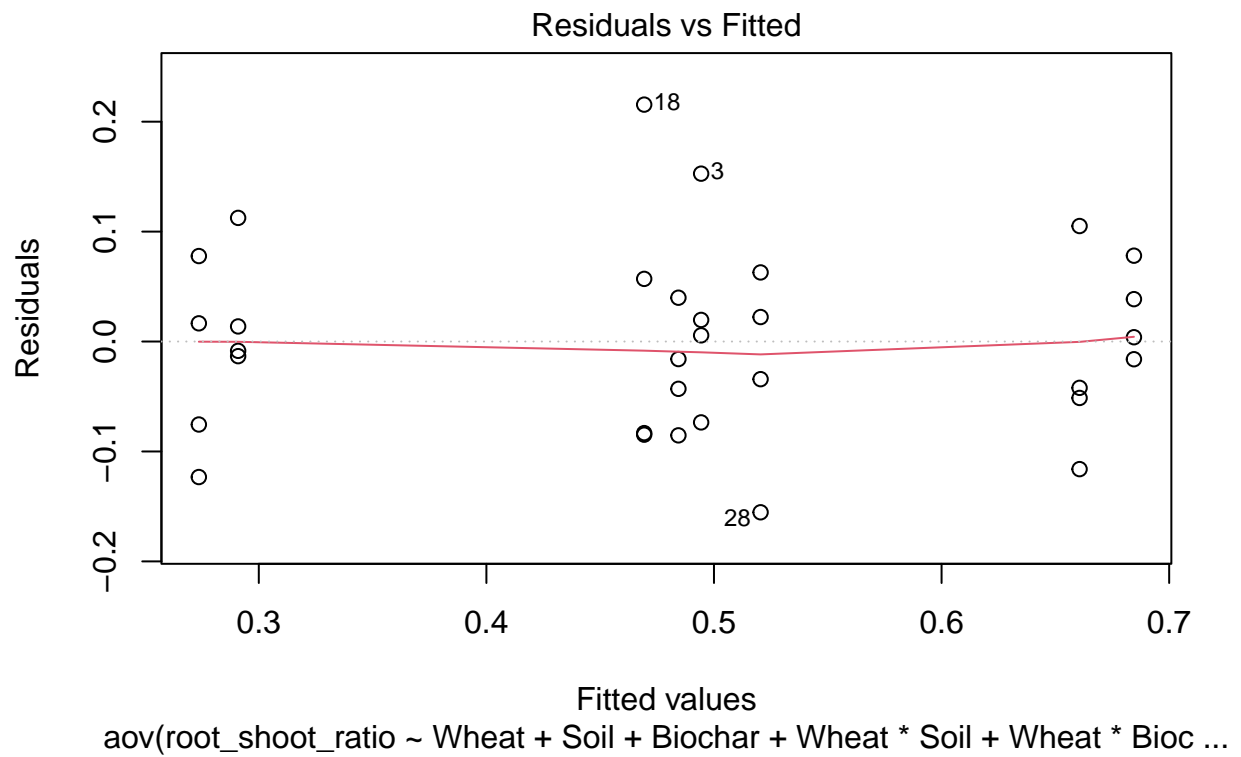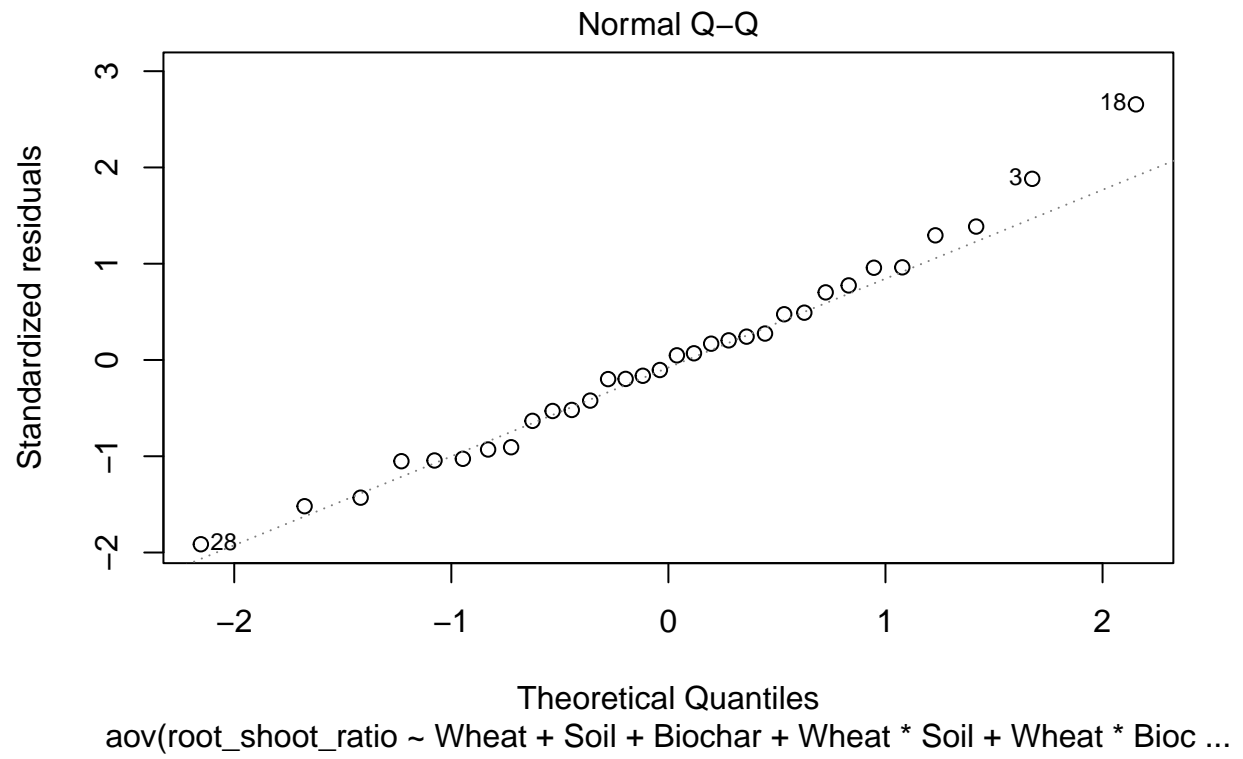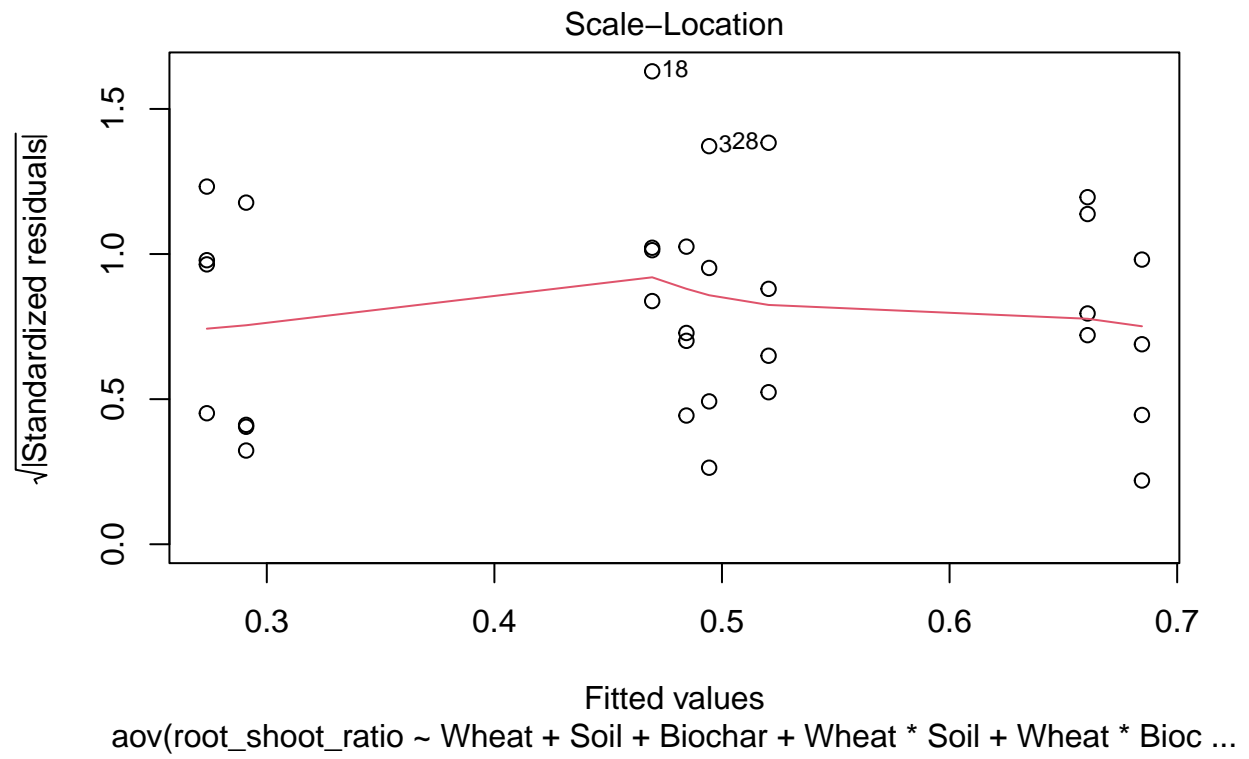
Check for Nonsignificant Interactions

```
anova(RSR_model_2)
```

```
## Analysis of Variance Table
##
## Response: root_shoot_ratio
##                Df  Sum Sq Mean Sq F value     Pr(>F)
## Wheat           1 0.06575 0.06575  7.7985   0.009880 **
## Soil            1 0.35424 0.35424 42.0157 8.668e-07 ***
## Biochar         1 0.09643 0.09643 11.4374   0.002371 **
## Wheat:Soil      1 0.04441 0.04441  5.2671   0.030399 *
## Wheat:Biochar   1 0.00001 0.00001  0.0012   0.972919
## Soil:Biochar    1 0.05750 0.05750  6.8198   0.015027 *
## Residuals      25 0.21078 0.00843
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove Wheat:Biochar interaction

Fit Model 3

```
# fit full model
RSR_model_3 <- aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat*Soil + Soil*Biochar, data=bc_data)
```

Check Model Assumptions

```
# check assumptions
plot(RSR_model_3)
```

Residuals vs Fitted

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioch ...

Normal Q–Q

Standardized residuals

Theoretical Quantiles
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioch ...

Scale–Location

Fitted values
aov(root_shoot_ratio ~ Wheat + Soil + Biochar + Wheat * Soil + Soil * Bioch ...
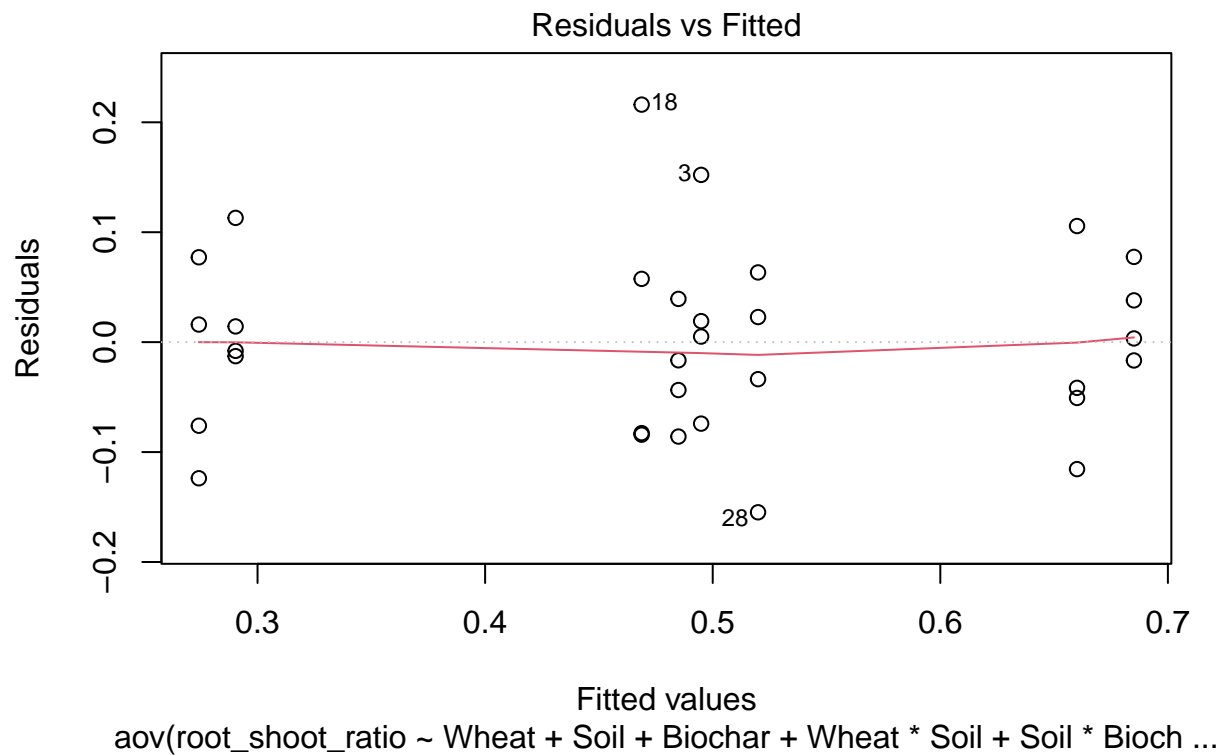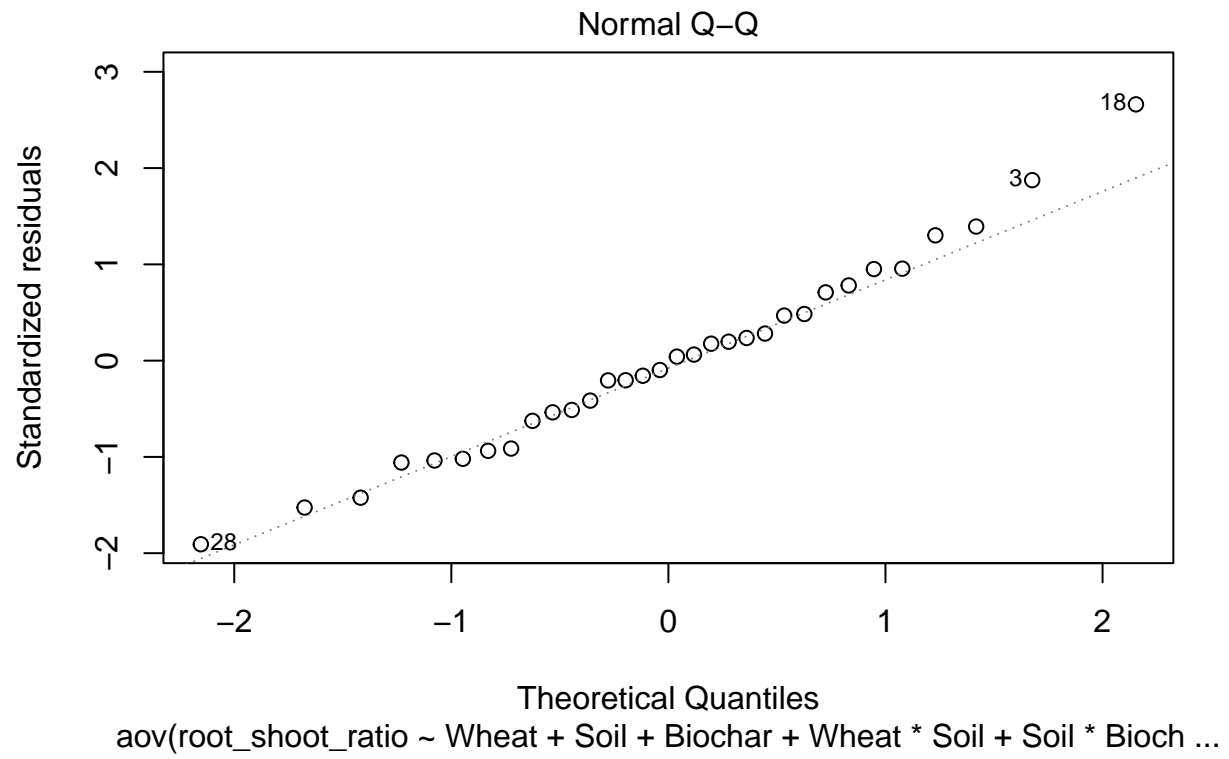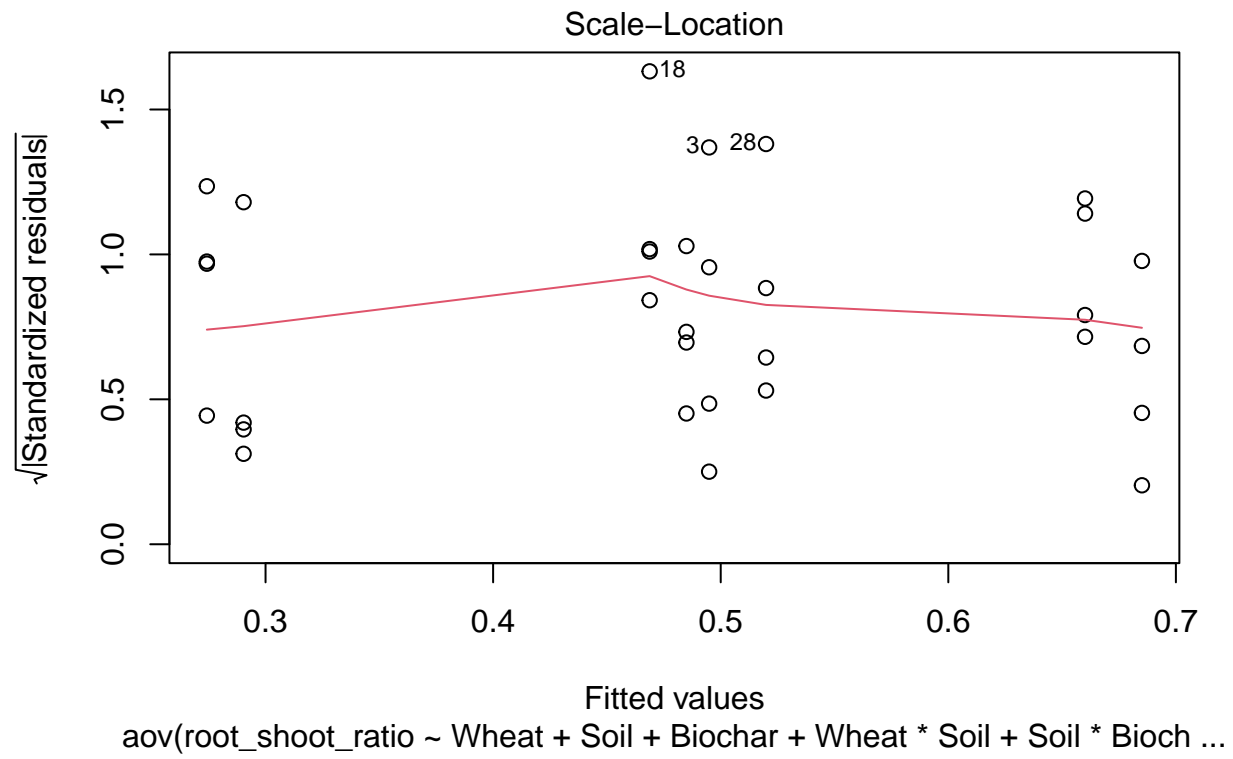
Check for Nonsignificant Interactions

```
anova(RSR_model_3)
```

```
## Analysis of Variance Table
##
## Response: root_shoot_ratio
##              Df  Sum Sq Mean Sq F value    Pr(>F)
## Wheat         1 0.06575 0.06575  8.1100  0.008488 **
## Soil          1 0.35424 0.35424 43.6942 5.199e-07 ***
## Biochar       1 0.09643 0.09643 11.8944  0.001931 **
## Wheat:Soil    1 0.04441 0.04441  5.4776  0.027209 *
## Soil:Biochar  1 0.05750 0.05750  7.0922  0.013110 *
## Residuals    26 0.21079 0.00811
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
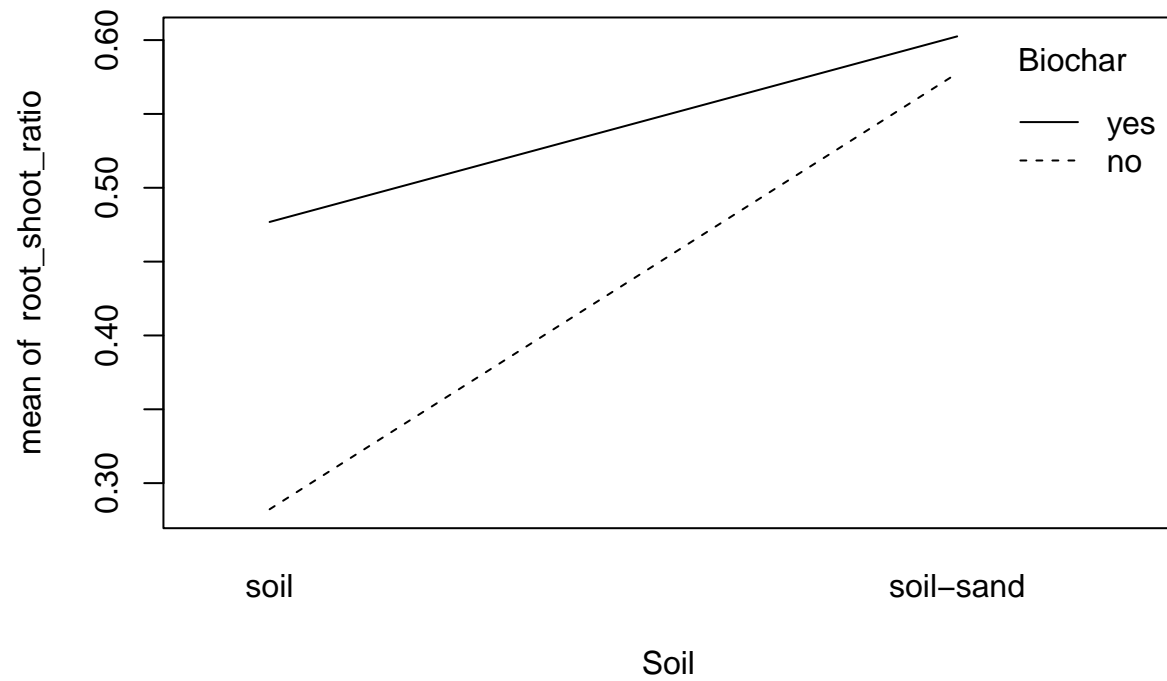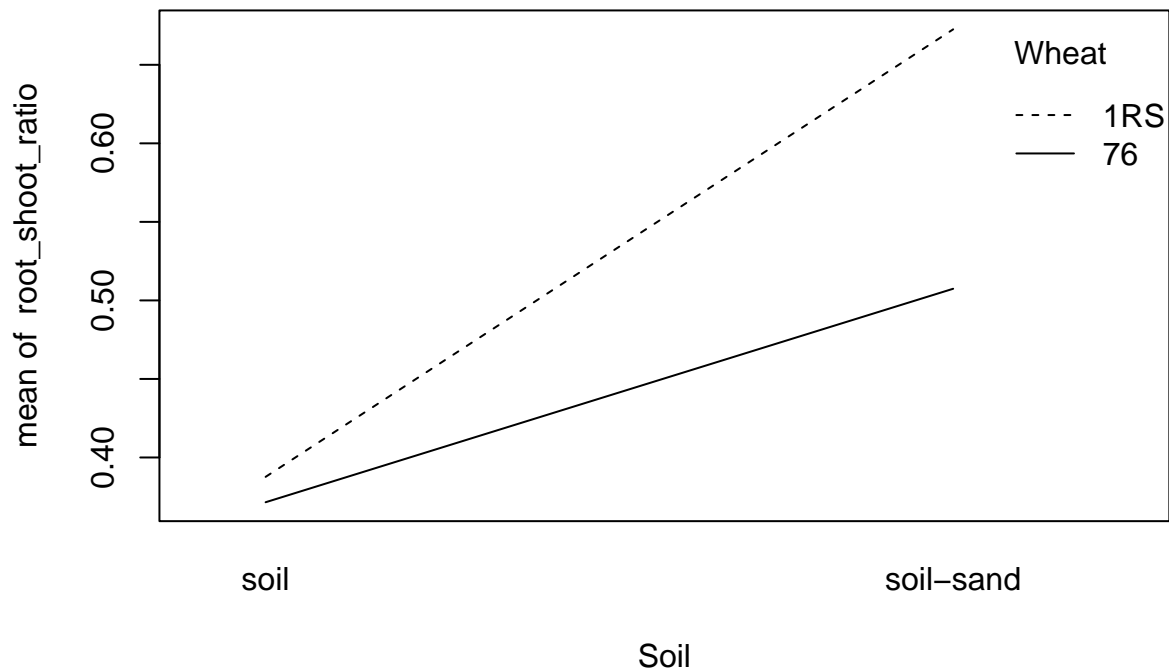
Final Model: 2-way with 2 interaction effect

Final Model: Root Shoot Ratio = Wheat + Soil + Biochar + Wheat:Soil + Soil:Biochar

```
interaction.plot(Soil, Biochar, root_shoot_ratio)
```



```
interaction.plot(Soil, Wheat, root_shoot_ratio)
```

Multiple Comparison

```r
# compare the effect of Wheat at each level of Soil
emmeans(RSR_model_3, list(pairwise ~ Wheat|Soil))
```

```
## $`emmeans of Wheat | Soil`
## Soil = soil:
##  Wheat emmean     SE df lower.CL upper.CL
##  1RS    0.388 0.0318 26    0.322    0.453
##  76     0.371 0.0318 26    0.306    0.437
##
## Soil = soil-sand:
##  Wheat emmean     SE df lower.CL upper.CL
##  1RS    0.673 0.0318 26    0.607    0.738
##  76     0.507 0.0318 26    0.442    0.573
##
## Results are averaged over the levels of: Biochar
## Confidence level used: 0.95
##
## $`pairwise differences of Wheat | Soil`
## Soil = soil:
##  2        estimate    SE df t.ratio p.value
##  1RS - 76   0.0162 0.045 26   0.359  0.7227
##
```

```
## Soil = soil-sand:
##  2         estimate   SE df t.ratio p.value
##  1RS - 76   0.1652 0.045 26 3.669   0.0011
##
## Results are averaged over the levels of: Biochar
```

- The effect of Wheat is significant when Soil type is "soil-sand" (p-value = 0.0011 < 0.05) in terms of root shoot ratio.

```
# compare the effect of Soil at each level of Wheat
emmeans(RSR_model_3, list(pairwise ~ Soil|Wheat))
```

```
## $`emmeans of Soil | Wheat`
## Wheat = 1RS:
##  Soil      emmean      SE df lower.CL upper.CL
##  soil       0.388 0.0318 26    0.322    0.453
##  soil-sand  0.673 0.0318 26    0.607    0.738
##
## Wheat = 76:
##  Soil      emmean      SE df lower.CL upper.CL
##  soil       0.371 0.0318 26    0.306    0.437
##  soil-sand  0.507 0.0318 26    0.442    0.573
##
## Results are averaged over the levels of: Biochar
## Confidence level used: 0.95
##
## $`pairwise differences of Soil | Wheat`
## Wheat = 1RS:
##  2                  estimate   SE df t.ratio p.value
##  soil - (soil-sand)   -0.285 0.045 26 -6.329  <.0001
##
## Wheat = 76:
##  2                  estimate   SE df t.ratio p.value
##  soil - (soil-sand)   -0.136 0.045 26 -3.019  0.0056
##
## Results are averaged over the levels of: Biochar
```

- The effect of Soil is significant at each level of Wheat type (both p-value < 0.05) in terms of root shoot ratio.

```
# compare the effect of Wheat at each level of Soil
emmeans(RSR_model_3, list(pairwise ~ Soil|Biochar))
```

```
## $`emmeans of Soil | Biochar`
## Biochar = no:
##  Soil      emmean      SE df lower.CL upper.CL
##  soil       0.282 0.0318 26    0.217    0.348
##  soil-sand  0.577 0.0318 26    0.512    0.643
##
## Biochar = yes:
##  Soil      emmean      SE df lower.CL upper.CL
##  soil       0.477 0.0318 26    0.411    0.542
```

```
##  soil-sand  0.603 0.0318 26    0.537    0.668
##
## Results are averaged over the levels of: Wheat
## Confidence level used: 0.95
##
## $`pairwise differences of Soil | Biochar`
## Biochar = no:
##  2                  estimate    SE df t.ratio p.value
##  soil - (soil-sand)   -0.295 0.045 26 -6.557  <.0001
##
## Biochar = yes:
##  2                  estimate    SE df t.ratio p.value
##  soil - (soil-sand)   -0.126 0.045 26 -2.791  0.0097
##
## Results are averaged over the levels of: Wheat
```

- The effect of Soil is significant when at each level of Biochar treatment (both p-value < 0.05) in terms of root shoot ratio.

```
# compare the effect of Soil at each level of Wheat
emmeans(RSR_model_3, list(pairwise ~ Biochar|Soil))
```

```
## $`emmeans of Biochar | Soil`
## Soil = soil:
##  Biochar emmean     SE df lower.CL upper.CL
##  no       0.282 0.0318 26    0.217    0.348
##  yes      0.477 0.0318 26    0.411    0.542
##
## Soil = soil-sand:
##  Biochar emmean     SE df lower.CL upper.CL
##  no       0.577 0.0318 26    0.512    0.643
##  yes      0.603 0.0318 26    0.537    0.668
##
## Results are averaged over the levels of: Wheat
## Confidence level used: 0.95
##
## $`pairwise differences of Biochar | Soil`
## Soil = soil:
##  2       estimate    SE df t.ratio p.value
##  no - yes   -0.195 0.045 26 -4.322  0.0002
##
## Soil = soil-sand:
##  2       estimate    SE df t.ratio p.value
##  no - yes   -0.025 0.045 26 -0.556  0.5832
##
## Results are averaged over the levels of: Wheat
```

- The effect of Biochar is significant when Soil type is "soil" (p-value = 0.0002 < 0.05) in terms of root shoot ratio.