Survey

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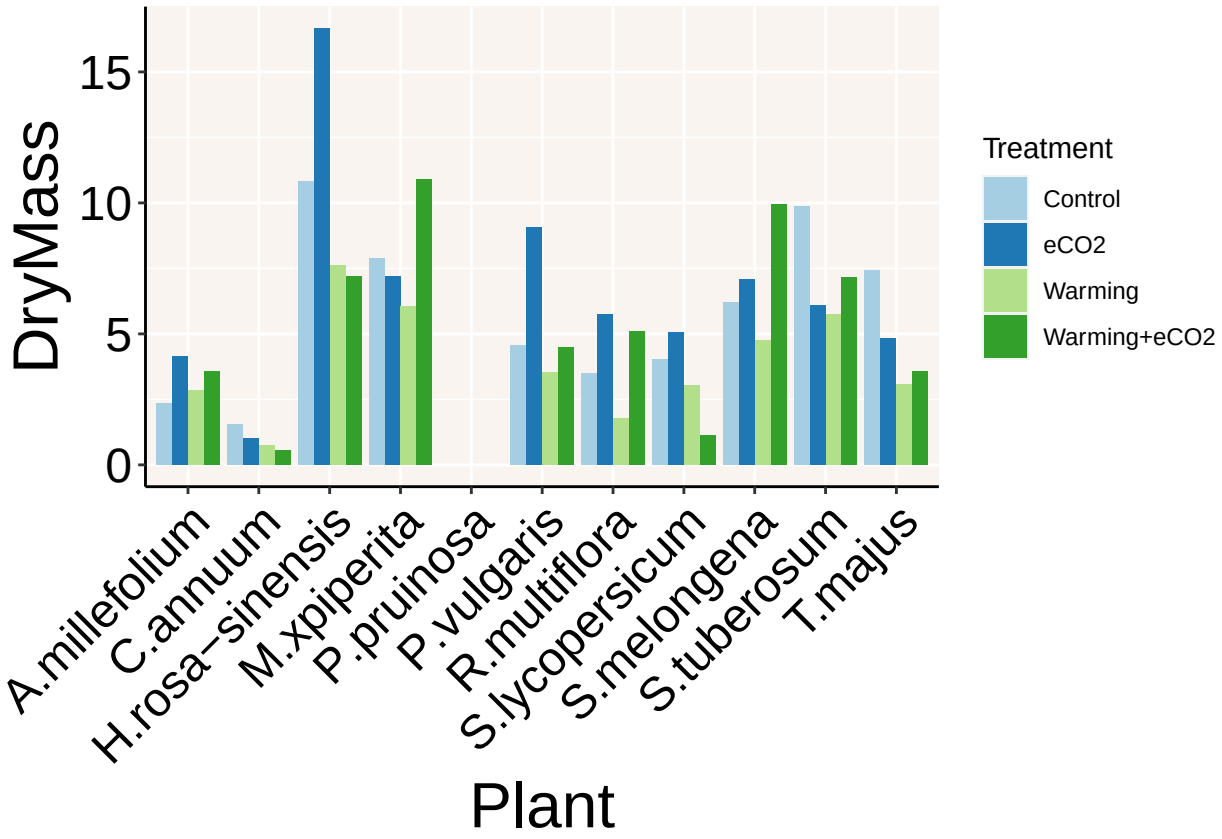
1/5/2023

Survey of species screened for plant responses to warming + eCO2 induced changes in leaf angle or leaf cupping/curling.

Import and subset the data by plant group. Filter to Angle and LCI groups. Compare treatments to ensure biomass decline with warming stress. Yarrow biomass did not decline at warming treatment, thus it was not stressed sufficiently. This may explain why there was no significant changes in yarrow morphology.

```
Survey<-read.csv('Leaf_Angle_Survey_Data.csv')
Survey$Treatment<-as.factor(Survey$Treatment)
Survey$Temp<-as.factor(Survey$Temp)
Survey$CO2<-as.factor(Survey$CO2)
SurveyAngle<-Survey[c(1:5,37,58)]
SurveyLCI<-Survey[c(1:5,56,58)]

ggplot(data=SurveyAngle, aes(x=Plant, y=DryMass, fill=Treatment)) +
  geom_bar(stat="identity", position=position_dodge())+
  scale_fill_brewer(palette="Paired")+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))
```

```
## Warning: Removed 31 rows containing missing values (geom_bar).
```




```
DryMassSummary<- group_by(SurveyAngle, Plant, Treatment) %>%
  summarise(Mass=mean(na.omit(DryMass)), Masssd=sd(na.omit(DryMass)), n=n())
```

```
## `summarise()` has grouped output by 'Plant'. You can override using the `.groups` argument.
```

```
bbeanAngle<-na.omit(filter(SurveyAngle, Plant =='P.vulgaris', preserve = TRUE))
tomatoAngle<-na.omit(filter(SurveyAngle, Plant =='S.lycopersicum', preserve = TRUE))
eggplantAngle<-na.omit(filter(SurveyAngle, Plant =='S.melongena', preserve = TRUE))
gcherryAngle<-filter(SurveyAngle, Plant =='P.pruinosa', preserve = TRUE)#dry mass values not available
gcherryAngle<-gcherryAngle[c(1:6)]
hibiscusAngle<-na.omit(filter(SurveyAngle, Plant =='H.rosa-sinensis', preserve = TRUE))
mintAngle<-na.omit(filter(SurveyAngle, Plant =='M.xpiperita', preserve = TRUE))
nasturtiumAngle<-na.omit(filter(SurveyAngle, Plant =='T.majus', preserve = TRUE))
pepperAngle<-na.omit(filter(SurveyAngle, Plant =='C.annuum', preserve = TRUE))
potatoAngle<-na.omit(filter(SurveyAngle, Plant =='S.tuberosum', preserve = TRUE))
yarrowAngle<-na.omit(filter(SurveyAngle, Plant =='A.millefolium', preserve = TRUE))
roseAngle<-na.omit(filter(SurveyAngle, Plant =='R.multiflora', preserve = TRUE))

bbeanLCI<-na.omit(filter(SurveyLCI, Plant =='P.vulgaris', preserve = TRUE))
tomatoLCI<-na.omit(filter(SurveyLCI, Plant =='S.lycopersicum', preserve = TRUE))
eggplantLCI<-na.omit(filter(SurveyLCI, Plant =='S.melongena', preserve = TRUE))
gcherryLCI<-filter(SurveyLCI, Plant =='P.pruinosa', preserve = TRUE)#dry mass values not available
gcherryLCI<-gcherryLCI[c(1:6)]
hibiscusLCI<-na.omit(filter(SurveyLCI, Plant =='H.rosa-sinensis', preserve = TRUE))
mintLCI<-na.omit(filter(SurveyLCI, Plant =='M.xpiperita', preserve = TRUE))
nasturtiumLCI<-na.omit(filter(SurveyLCI, Plant =='T.majus', preserve = TRUE))
pepperLCI<-na.omit(filter(SurveyLCI, Plant =='C.annuum', preserve = TRUE))
```

```
potatoLCI<-na.omit(filter(SurveyLCI, Plant =='S.tuberosum', preserve = TRUE))
yarrowLCI<-na.omit(filter(SurveyLCI, Plant =='A.millefolium', preserve = TRUE))
roseLCI<-na.omit(filter(SurveyLCI, Plant =='R.multiflora', preserve = TRUE))
```

examine data for normality and equal variance.

```
summary(SurveyAngle)
```

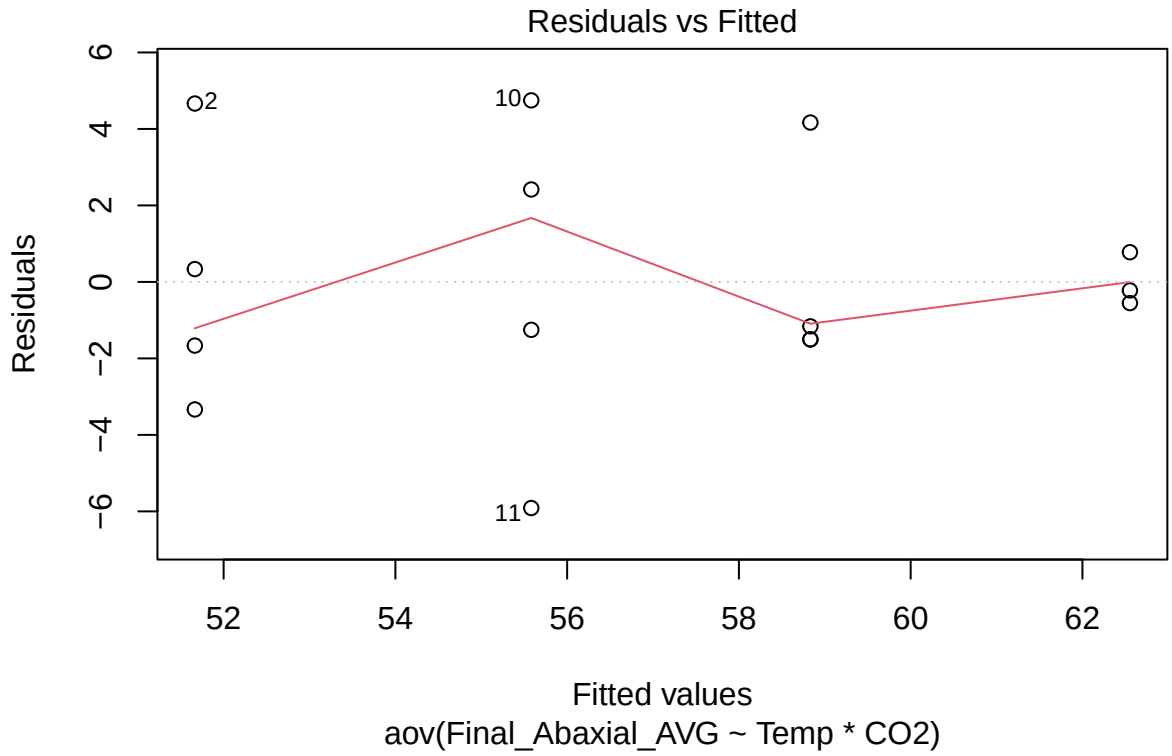
```
##    Plant.ID            Plant                Treatment       Temp     CO2
##  Length:190         Length:190         Control     :48   30     :43   400:96
##  Class :character   Class :character   eCO2        :47   38     :37   800:94
##  Mode  :character   Mode  :character   Warming     :48   28     :22
##                                        Warming+eCO2:47   36     :20
##                                                          29     :18
##                                                          37     :14
##                                                          (Other):36
##  Final_Abaxial_AVG    DryMass
##  Min.   :19.33     Min.   : 0.300
##  1st Qu.:35.41     1st Qu.: 2.105
##  Median :42.33     Median : 3.560
##  Mean   :44.16     Mean   : 4.182
##  3rd Qu.:51.88     3rd Qu.: 5.650
##  Max.   :88.33     Max.   :16.660
##  NA's   :39        NA's   :31
```

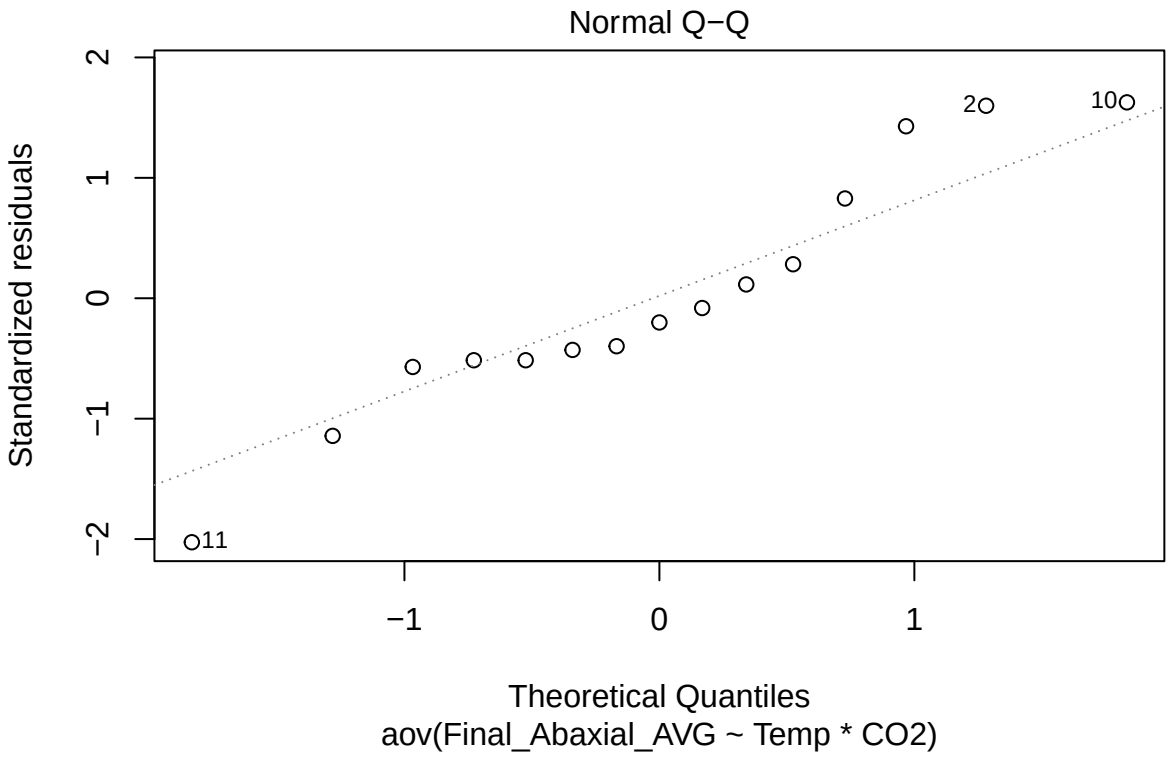
```
summary(SurveyLCI)
```

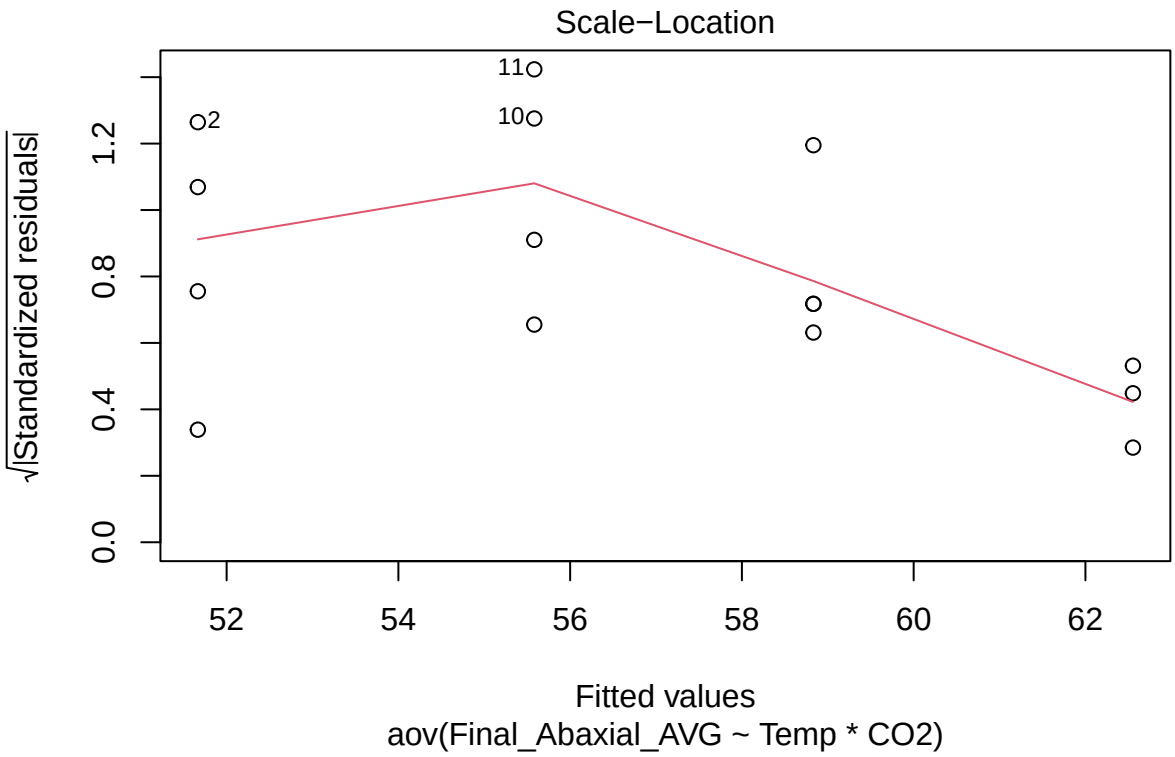
```
##    Plant.ID            Plant                Treatment       Temp     CO2
##  Length:190         Length:190         Control     :48   30     :43   400:96
##  Class :character   Class :character   eCO2        :47   38     :37   800:94
##  Mode  :character   Mode  :character   Warming     :48   28     :22
##                                        Warming+eCO2:47   36     :20
##                                                          29     :18
##                                                          37     :14
##                                                          (Other):36
##  Final_LCI_Avg       DryMass
##  Min.   :0.0000   Min.   : 0.300
##  1st Qu.:0.0500   1st Qu.: 2.105
##  Median :0.1700   Median : 3.560
##  Mean   :0.4859   Mean   : 4.182
##  3rd Qu.:0.6550   3rd Qu.: 5.650
##  Max.   :3.2300   Max.   :16.660
##  NA's   :139      NA's   :31
```

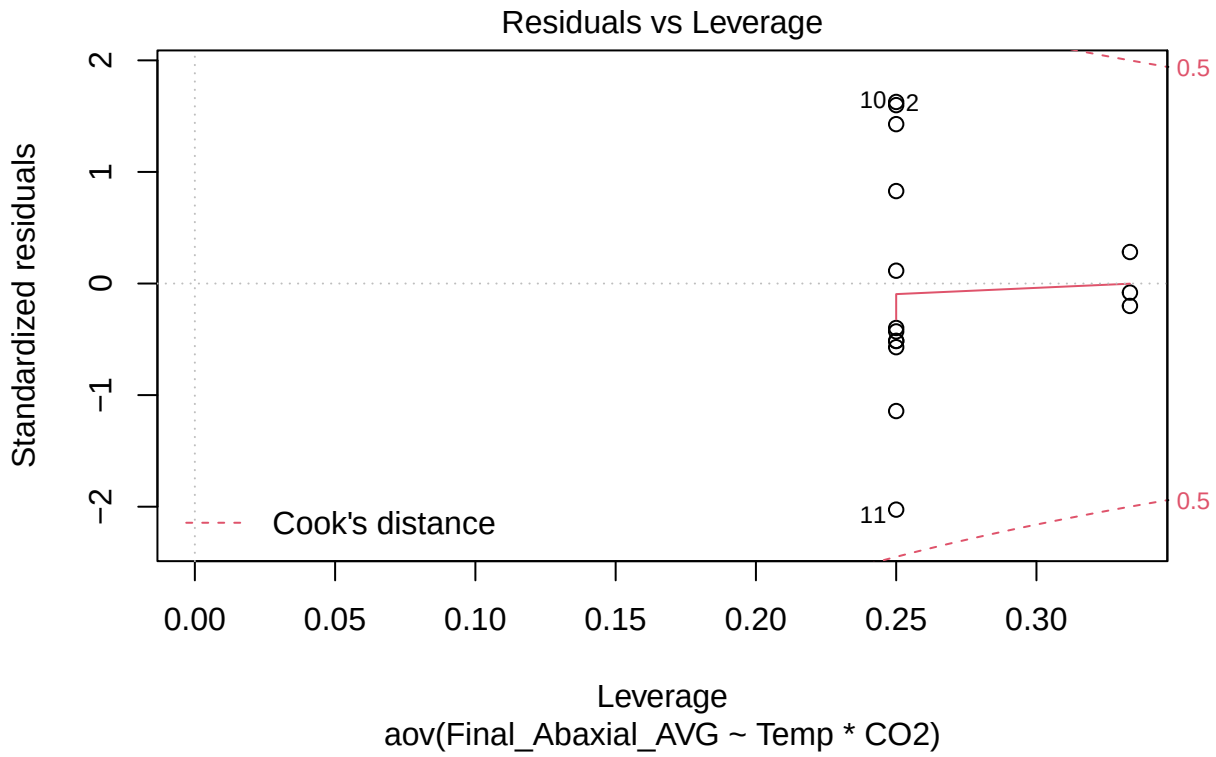
```
angle.bbean.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = bbeanAngle)
angle.tomato.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = tomatoAngle)
angle.eggplant.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = eggplantAngle)
angle.gcherry.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = gcherryAngle)
angle.hibiscus.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = hibiscusAngle)
#angle.mint.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = mintAngle)#no abaxial measure leaf curl more pr
angle.nasturtium.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = nasturtiumAngle)
angle.pepper.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = pepperAngle)
angle.potato.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = potatoAngle)
angle.yarrow.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = yarrowAngle)
#angle.rose.aov<-aov(Final_Abaxial_AVG~Temp*CO2, data = roseAngle)#no abaxial measure leaf curl more pr
```

```
LCI.bbean.aov<-aov(Final_LCI_Avg~Temp*CO2, data = bbeanLCI)
#LCI.tomato.aov<-aov(Final_LCI_Avg~Temp*CO2, data = tomatoLCI) no LCI
#LCI.eggplant.aov<-aov(Final_LCI_Avg~Temp*CO2, data = eggplantLCI) no LCI
#LCI.gcherry.aov<-aov(Final_LCI_Avg~Temp*CO2, data = gcherryLCI) no LCI
#LCI.hibiscus.aov<-aov(Final_LCI_Avg~Temp*CO2, data = hibiscusLCI) no LCI
LCI.mint.aov<-aov(Final_LCI_Avg~Temp*CO2, data = mintLCI)
#LCI.nasturtium.aov<-aov(Final_LCI_Avg~Temp*CO2, data = nasturtiumLCI) no LCI
#LCI.pepper.aov<-aov(Final_LCI_Avg~Temp*CO2, data = pepperLCI) no LCI
#LCI.potato.aov<-aov(Final_LCI_Avg~Temp*CO2, data = potatoLCI) no LCI
#LCI.yarrow.aov<-aov(Final_LCI_Avg~Temp*CO2, data = yarrowLCI) no LCI
LCI.rose.aov<-aov(Final_LCI_Avg~Temp*CO2, data = roseLCI)

#normality plot aov for qq plots.
plot(angle.bbean.aov)
```

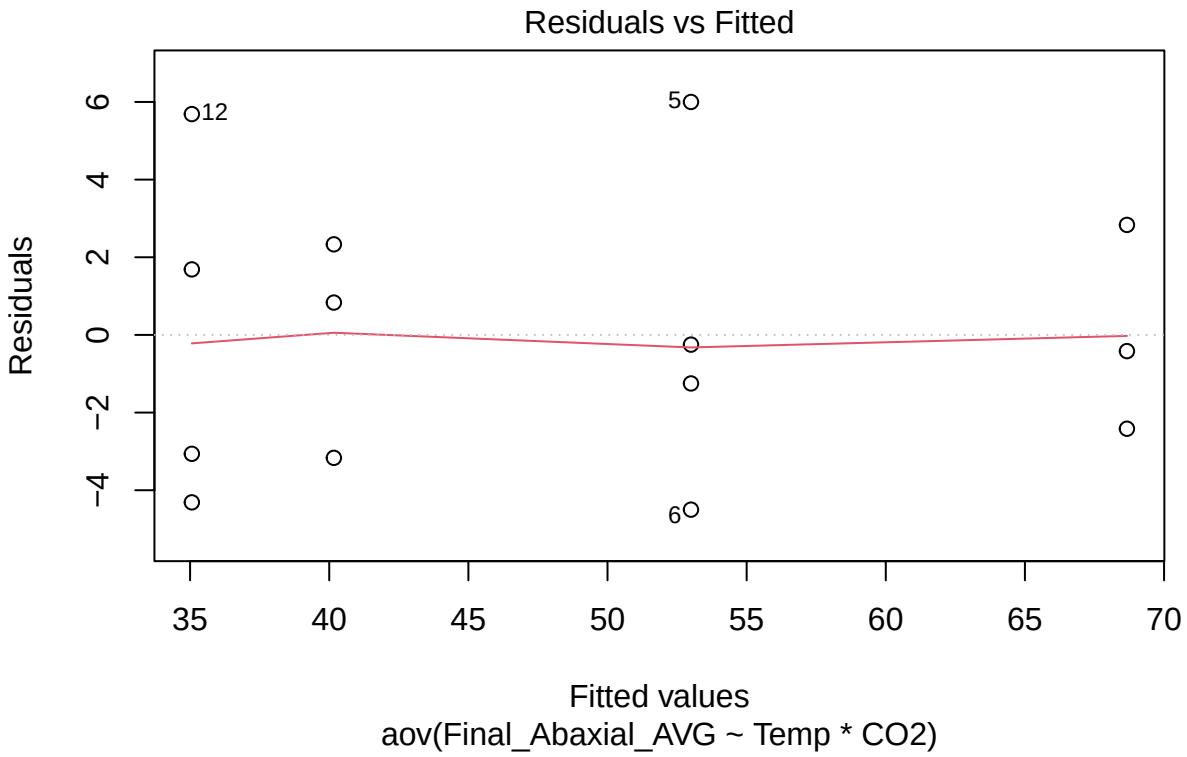


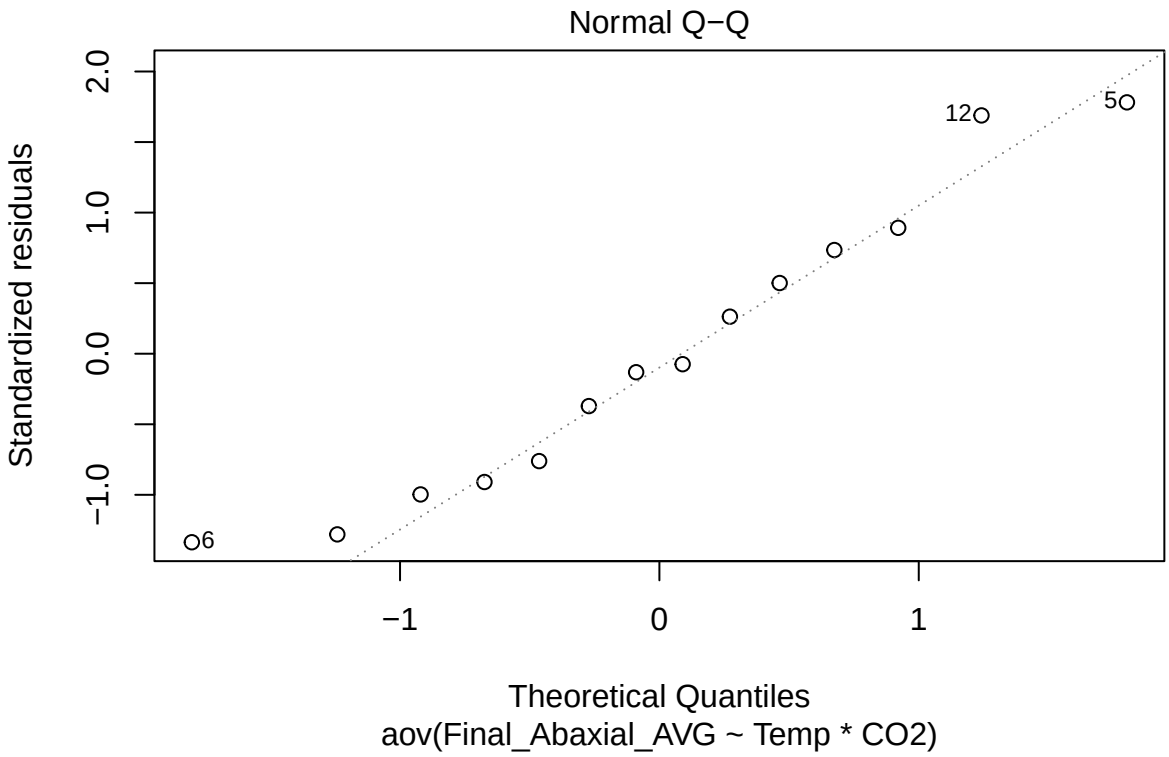

Normal Q−Q
Standardized residuals
2
1
0
−1
−2
11
2
10
−1
0
1
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

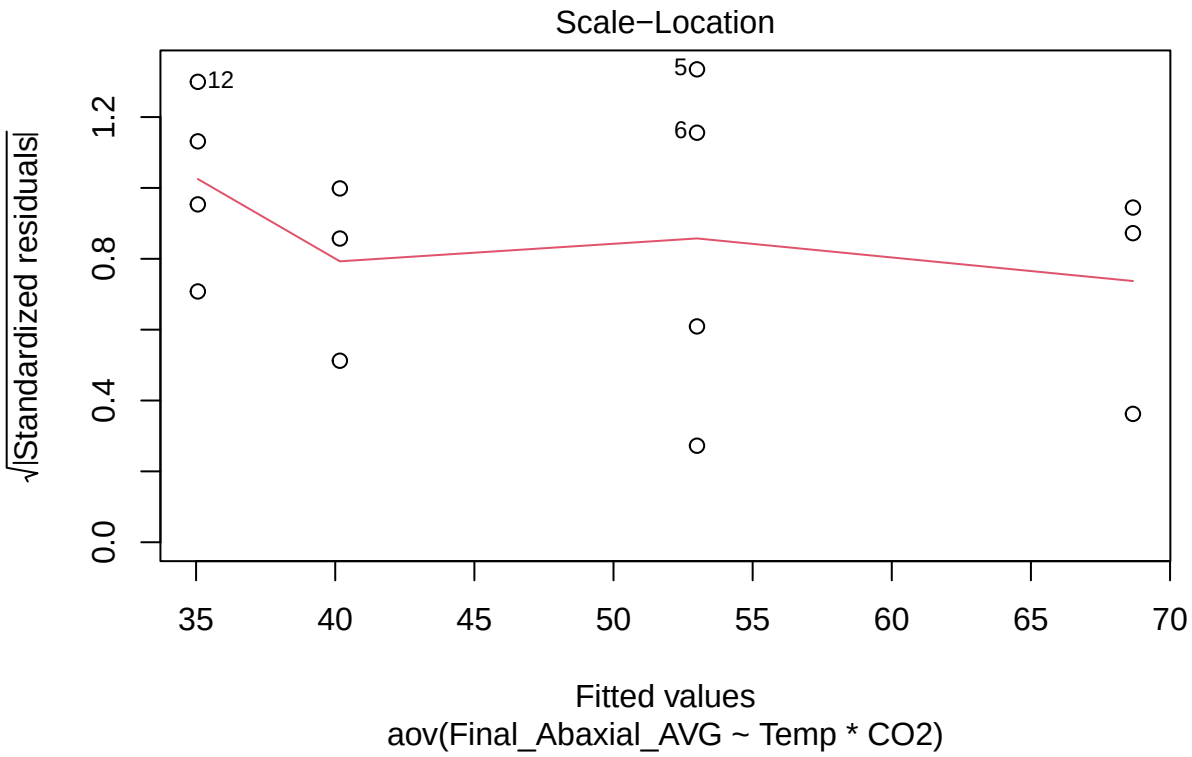

Scale−Location
√|Standardized residuals|
0.0
0.4
0.8
1.2
11
10
2
52
54
56
58
60
62
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

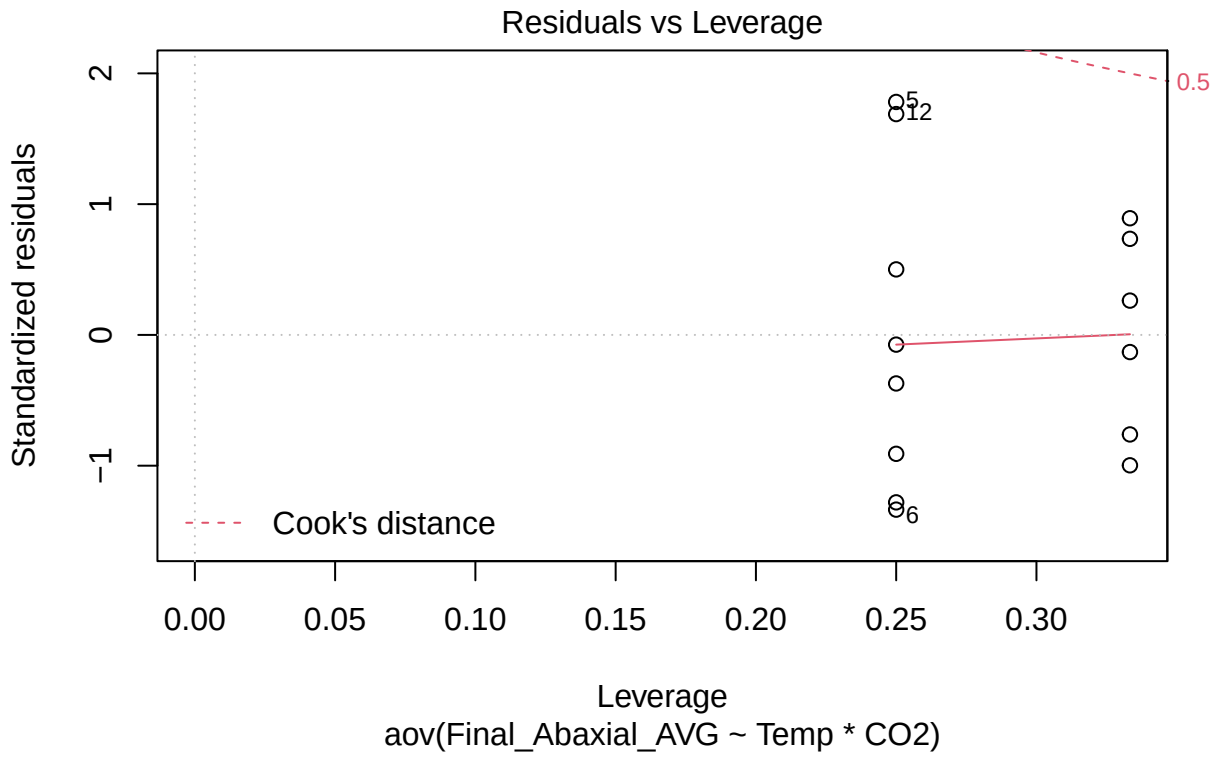



```
plot(angle.tomato.aov)
```

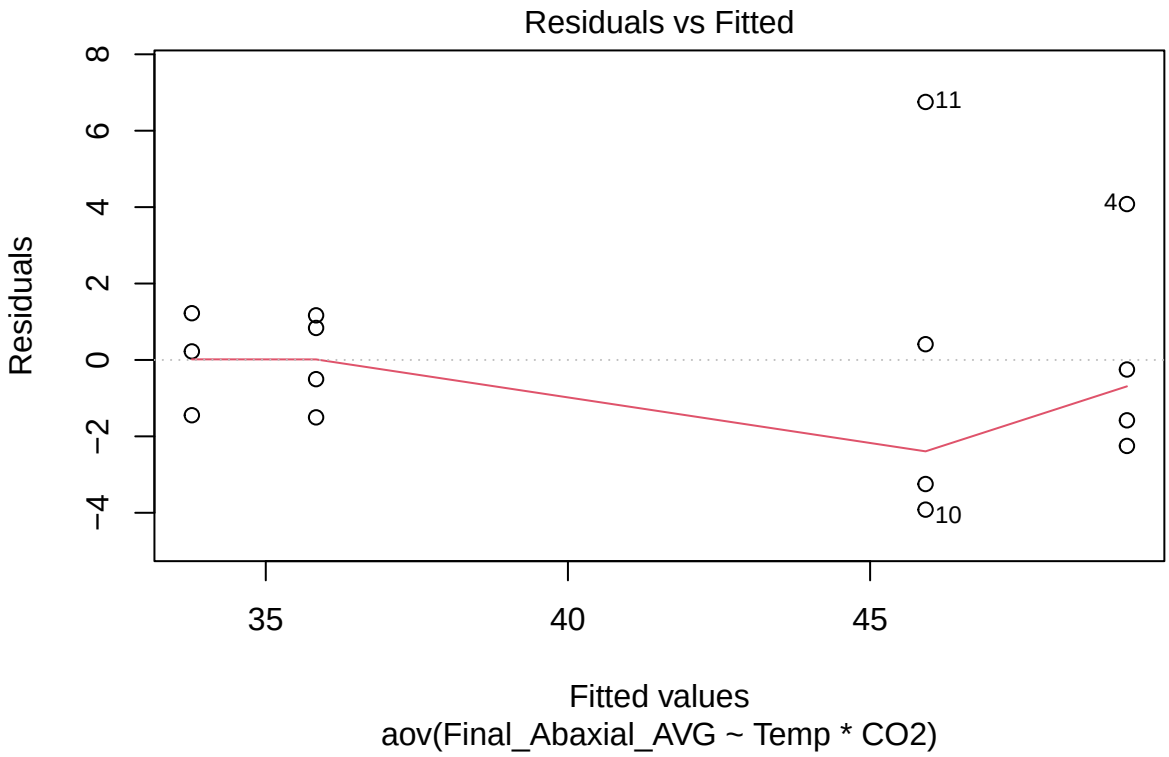

Residuals vs Fitted
Residuals
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)
12
5
6
−4
−2
0
2
4
6
35
40
45
50
55
60
65
70

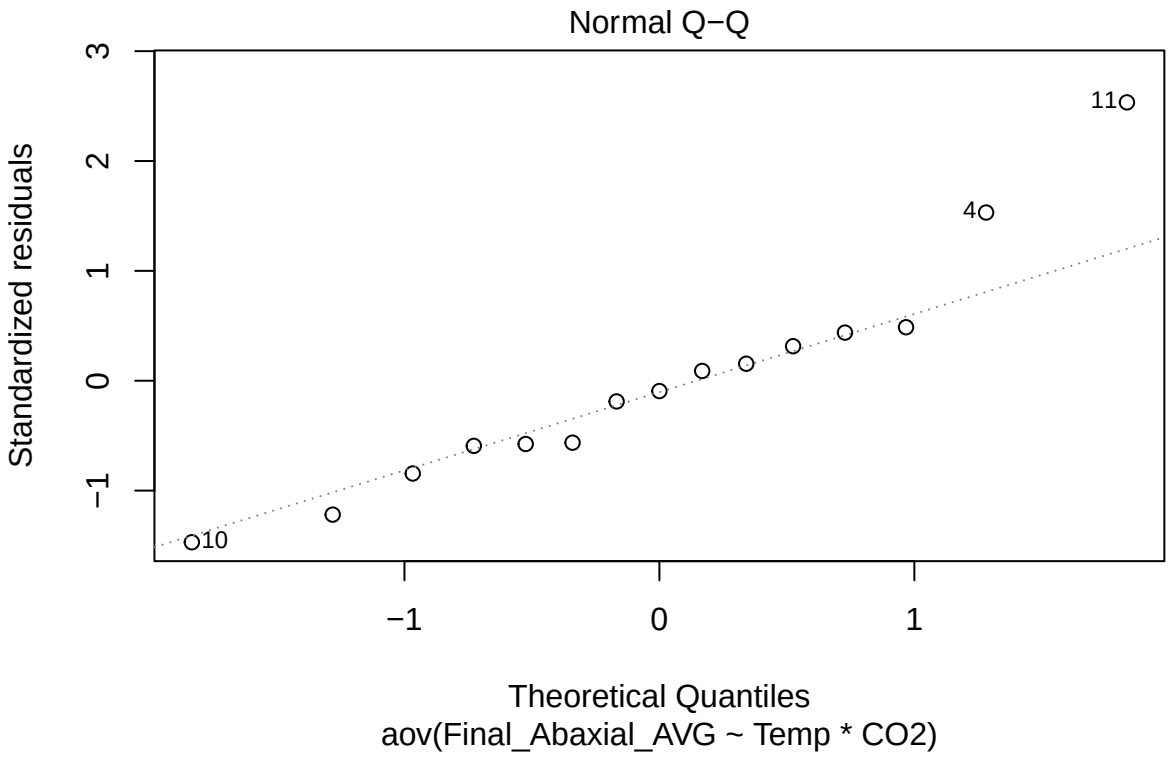

Normal Q−Q
Standardized residuals
2.0
1.0
0.0
−1.0
12
5
6
−1
0
1
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

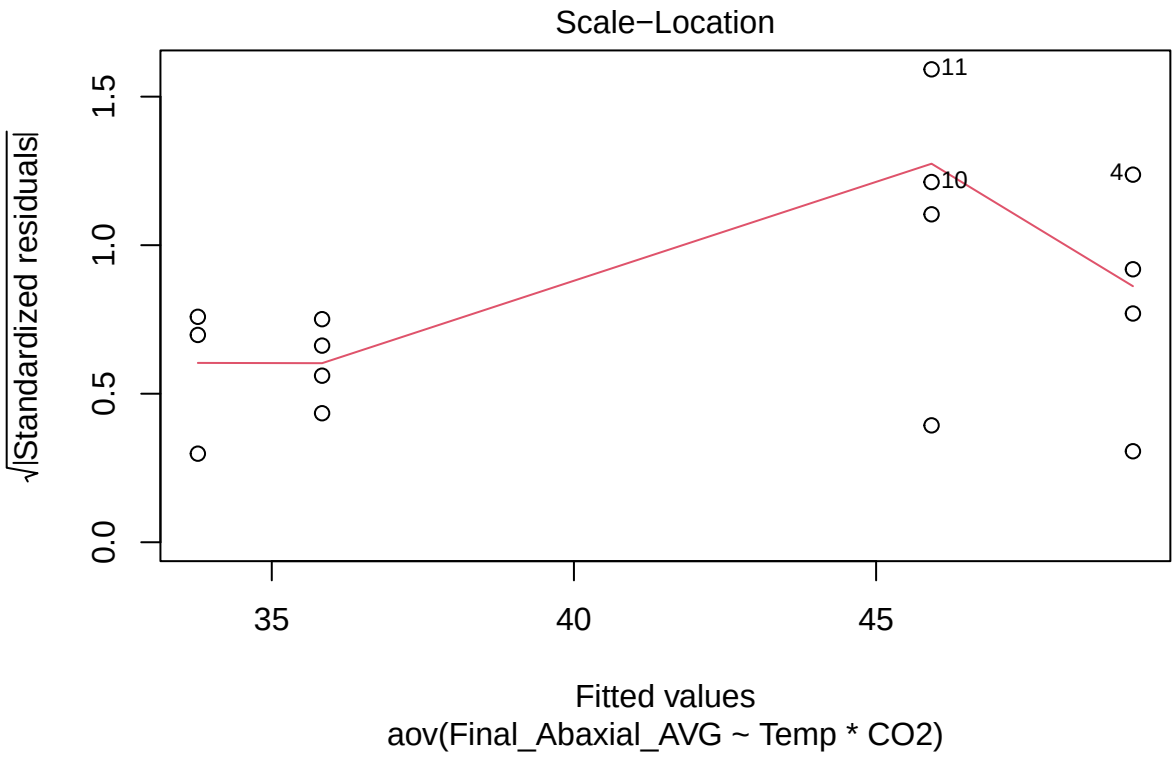

Scale−Location
√|Standardized residuals|
0.0
0.4
0.8
1.2
12
5
6
35
40
45
50
55
60
65
70
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

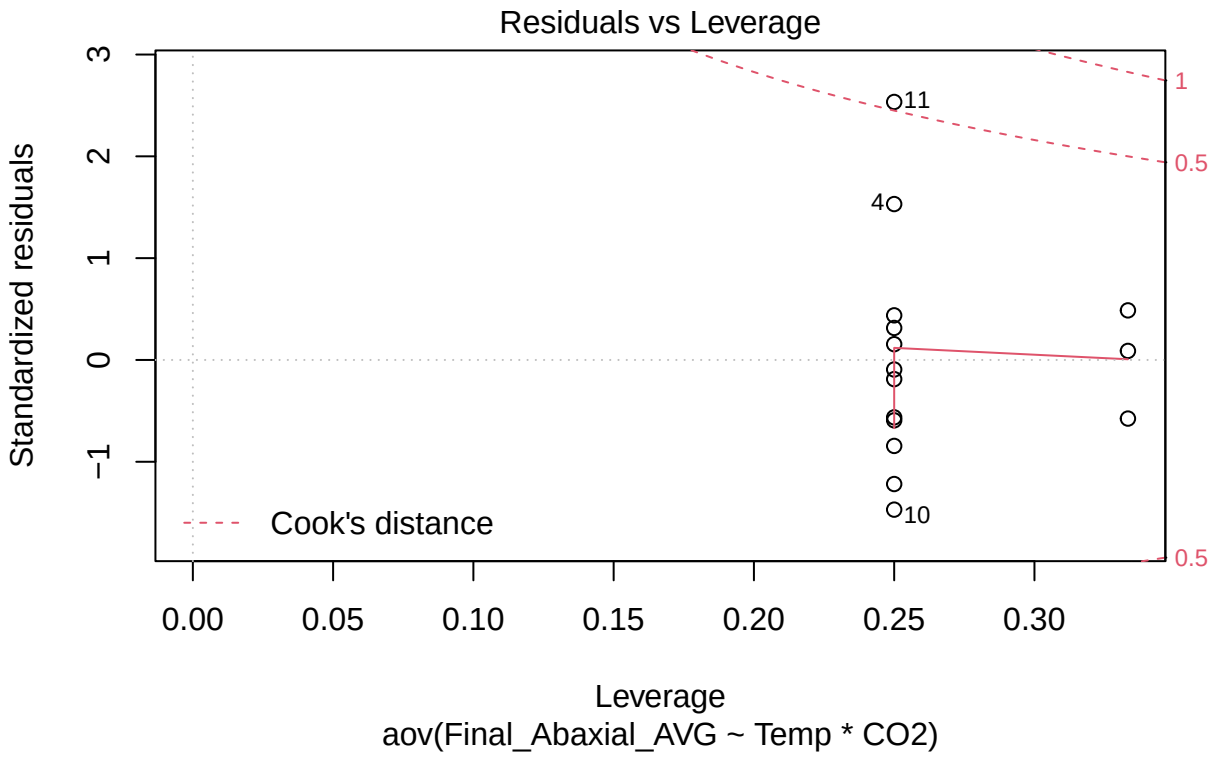



```
plot(angle.eggplant.aov)
```

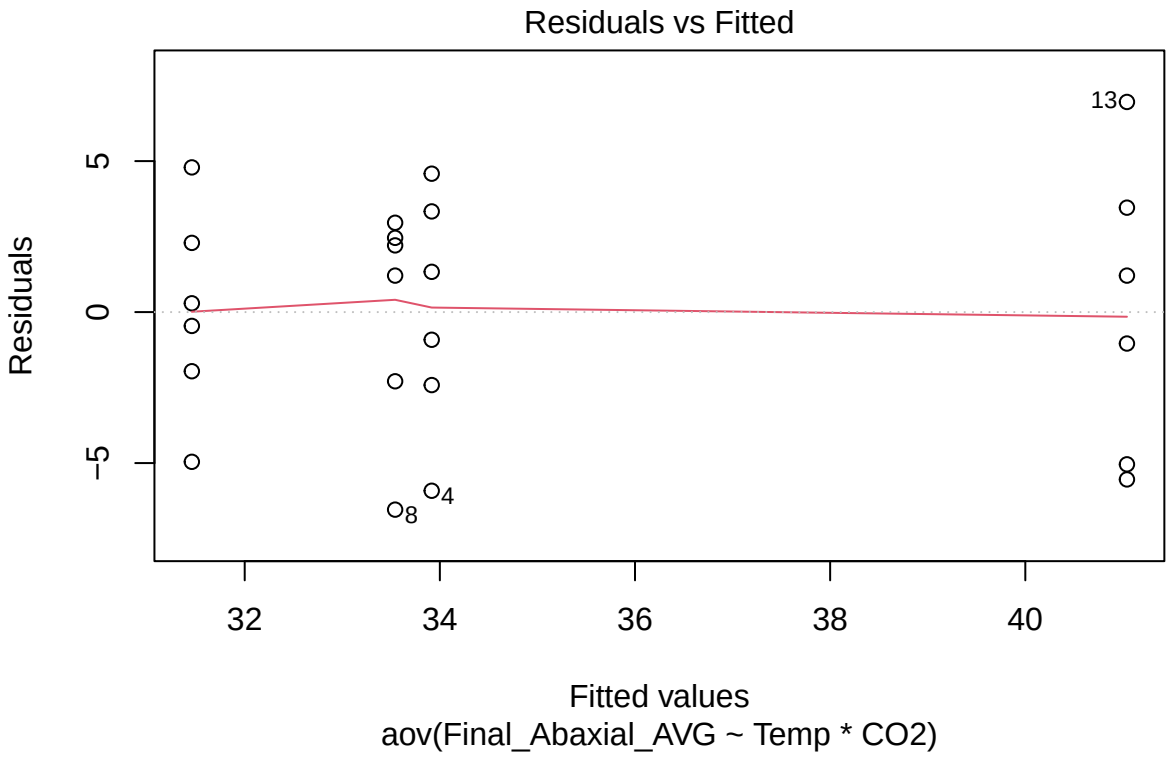

Residuals vs Fitted
Residuals
8
6
4
2
0
−2
−4
11
4
10
35
40
45
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

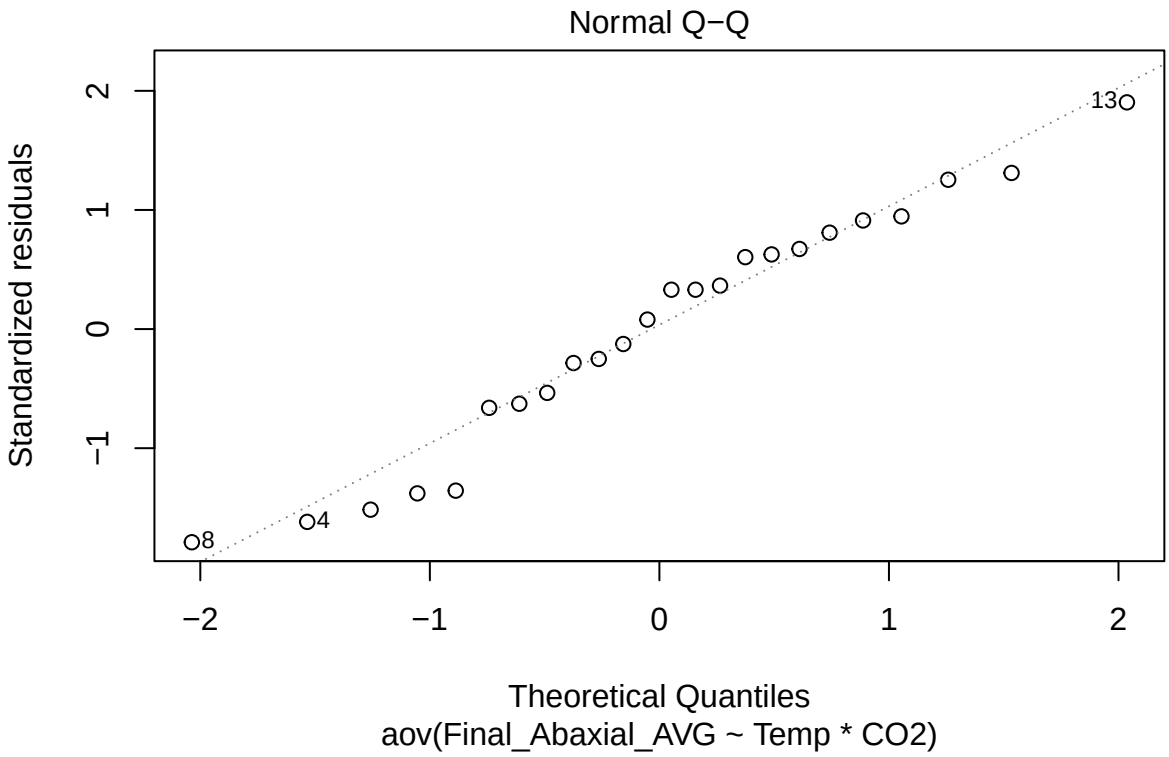

Normal Q−Q
Standardized residuals
3
2
1
0
−1
11
4
10
−1
0
1
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

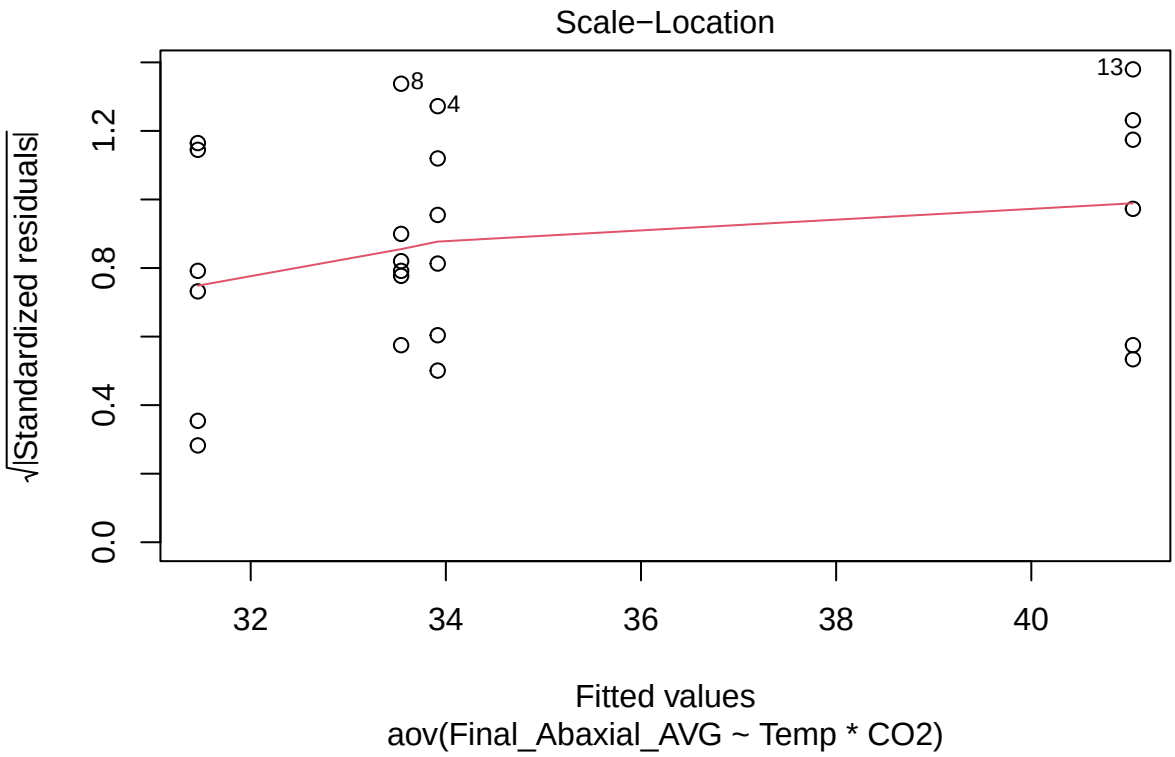

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
11
10
4
35
40
45
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

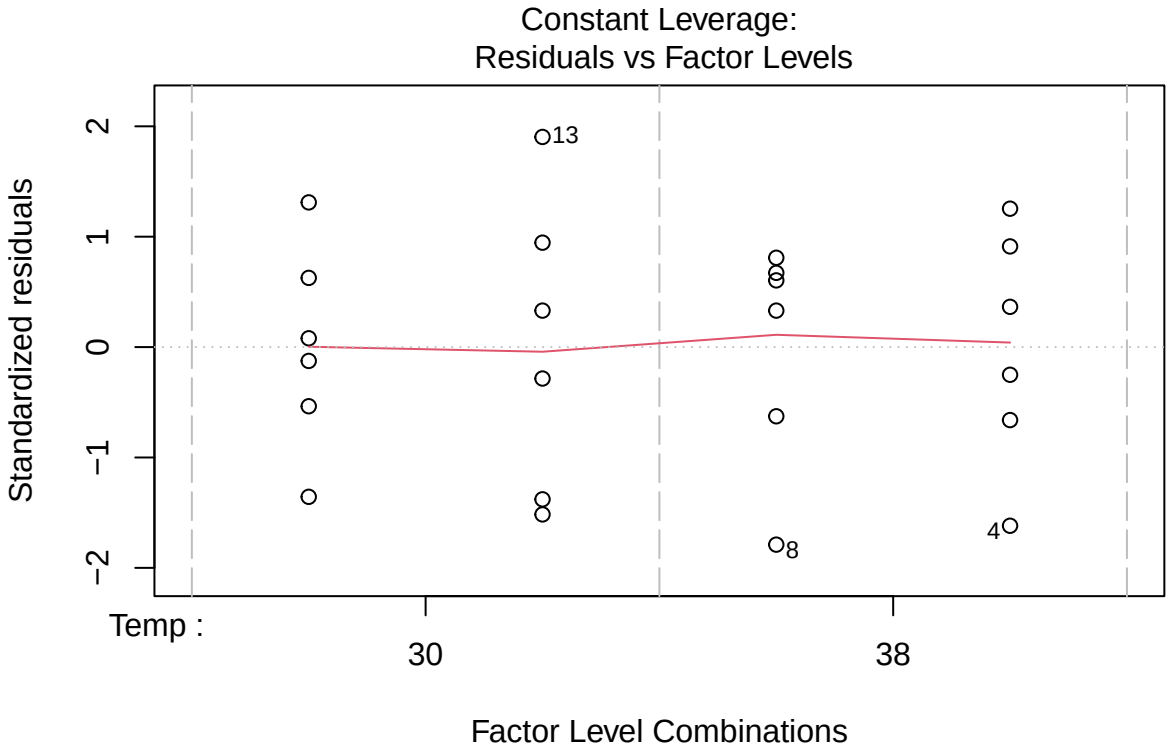



```
plot(angle.gcherry.aov)
```

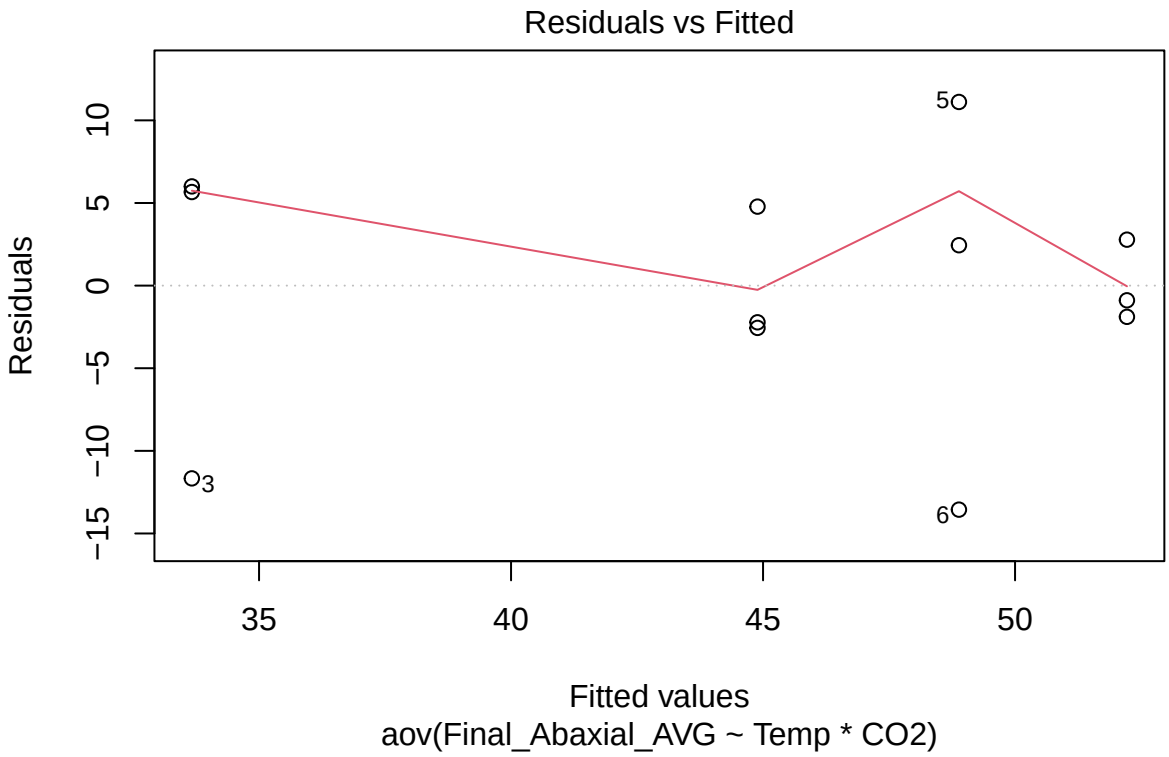

Residuals vs Fitted
Residuals
5
0
−5
13
4
8
32
34
36
38
40
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

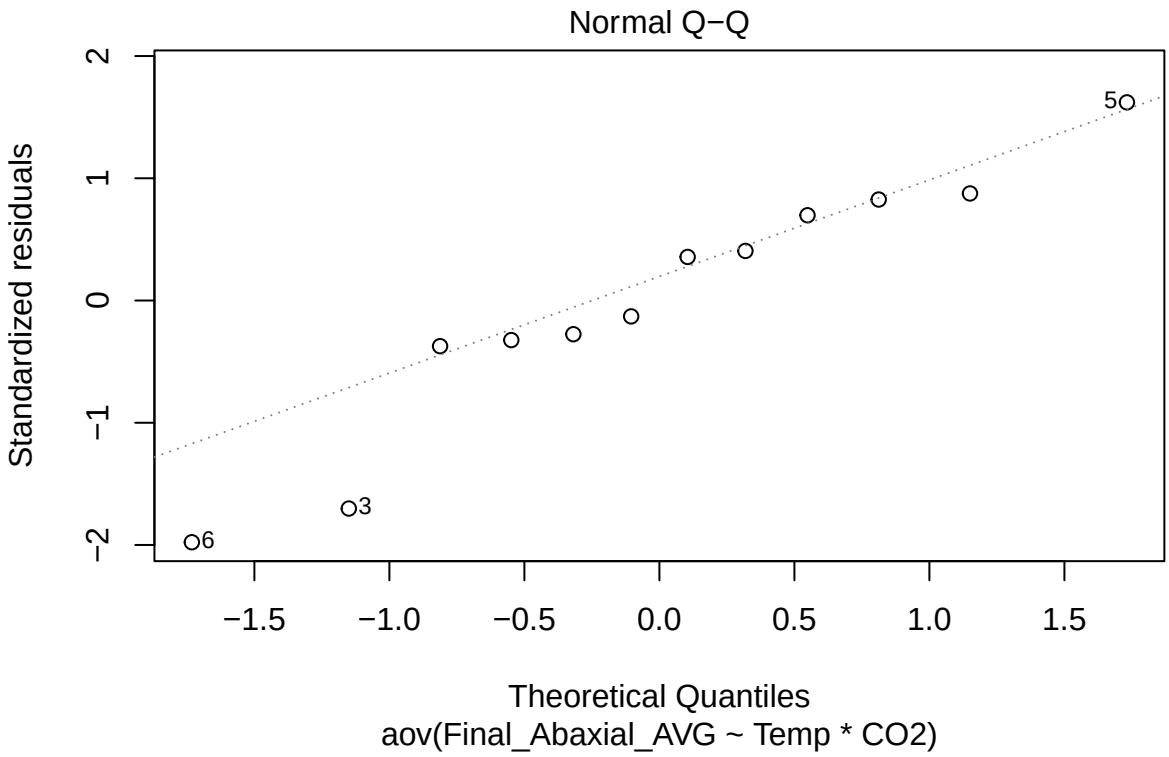

Normal Q−Q
Standardized residuals
2
1
0
−1
13
8
4
−2
−1
0
1
2
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

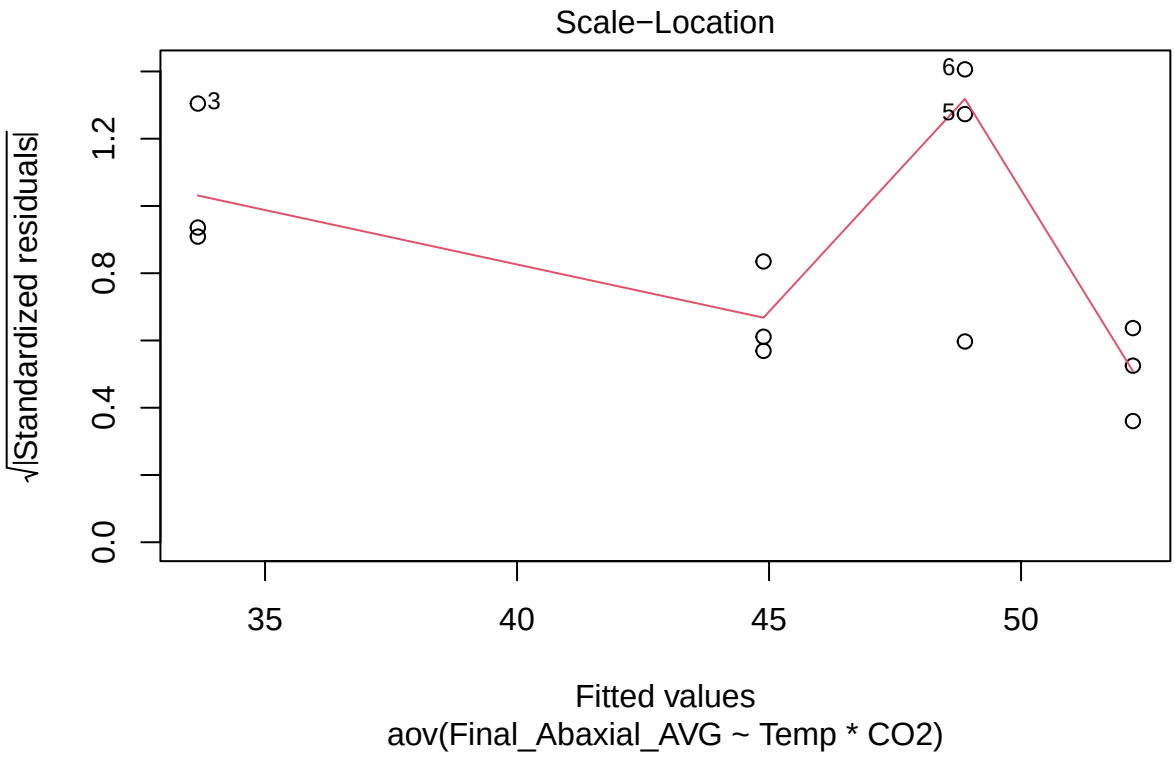

Scale−Location
√|Standardized residuals|
0.0
0.4
0.8
1.2
8
4
13
32
34
36
38
40
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

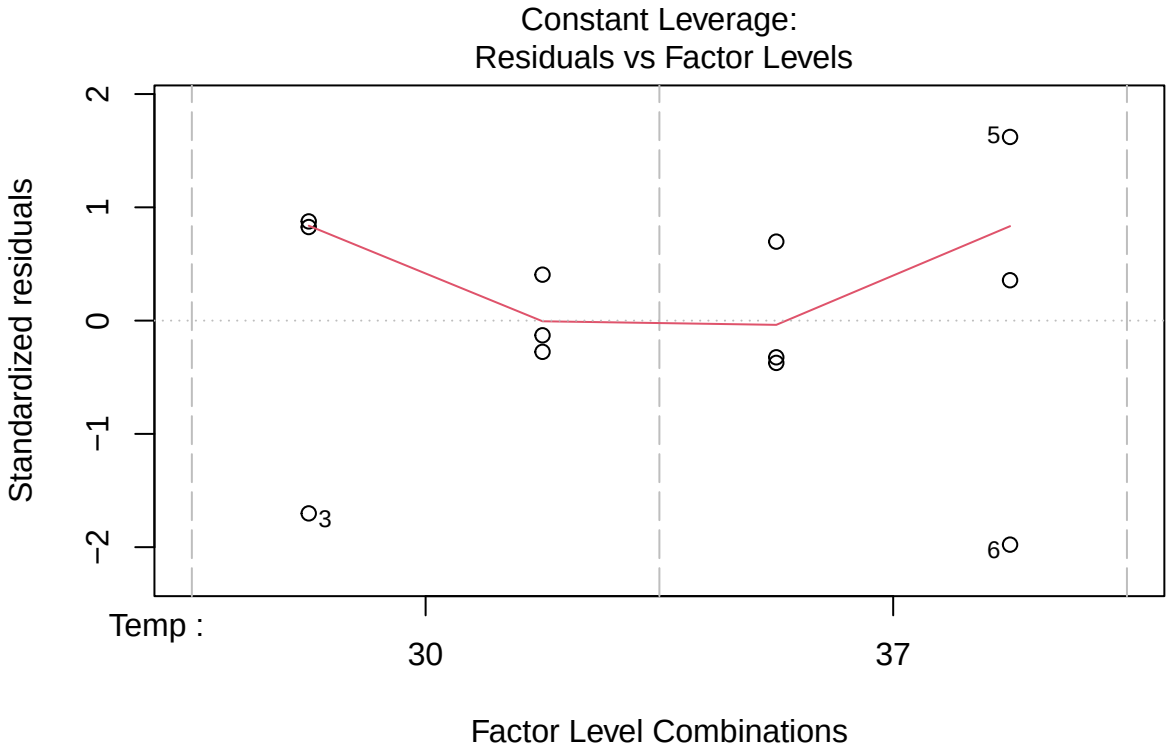



```
plot(angle.hibiscus.aov)
```

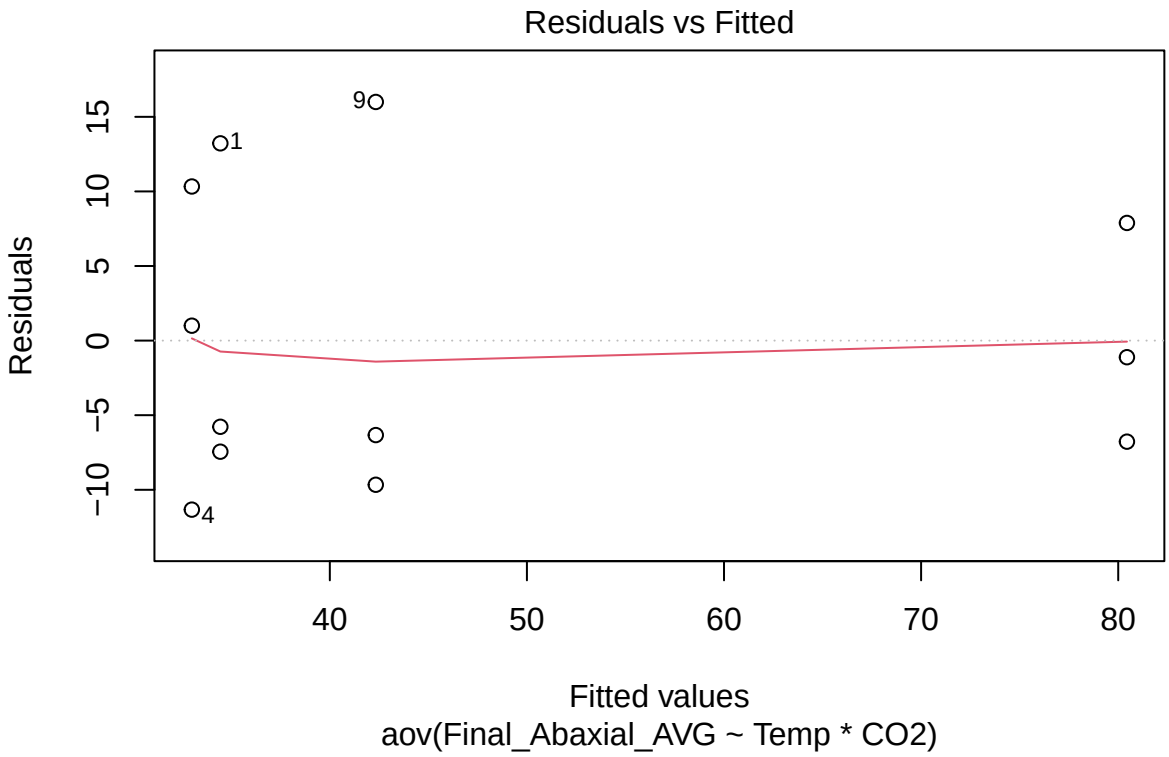

Residuals vs Fitted
Residuals
10
5
0
−5
−10
−15
35
40
45
50
5
3
6
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

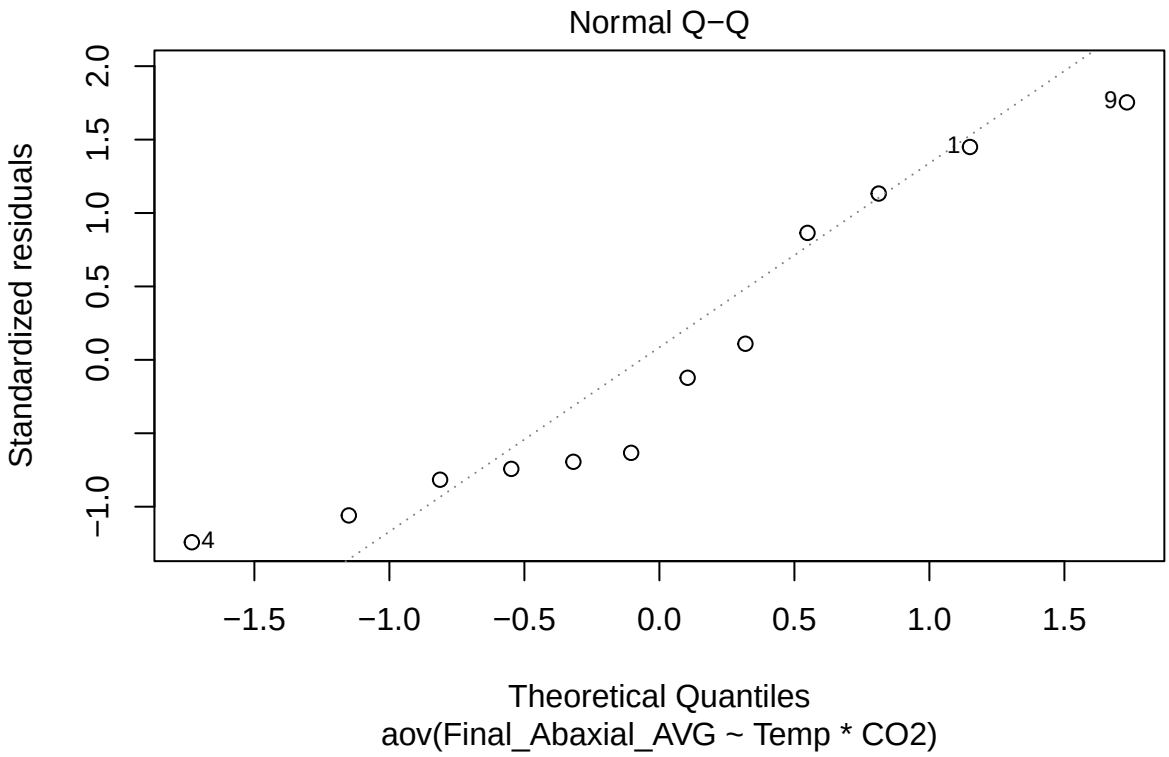

Normal Q−Q
Standardized residuals
2
1
0
−1
−2
5
3
6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

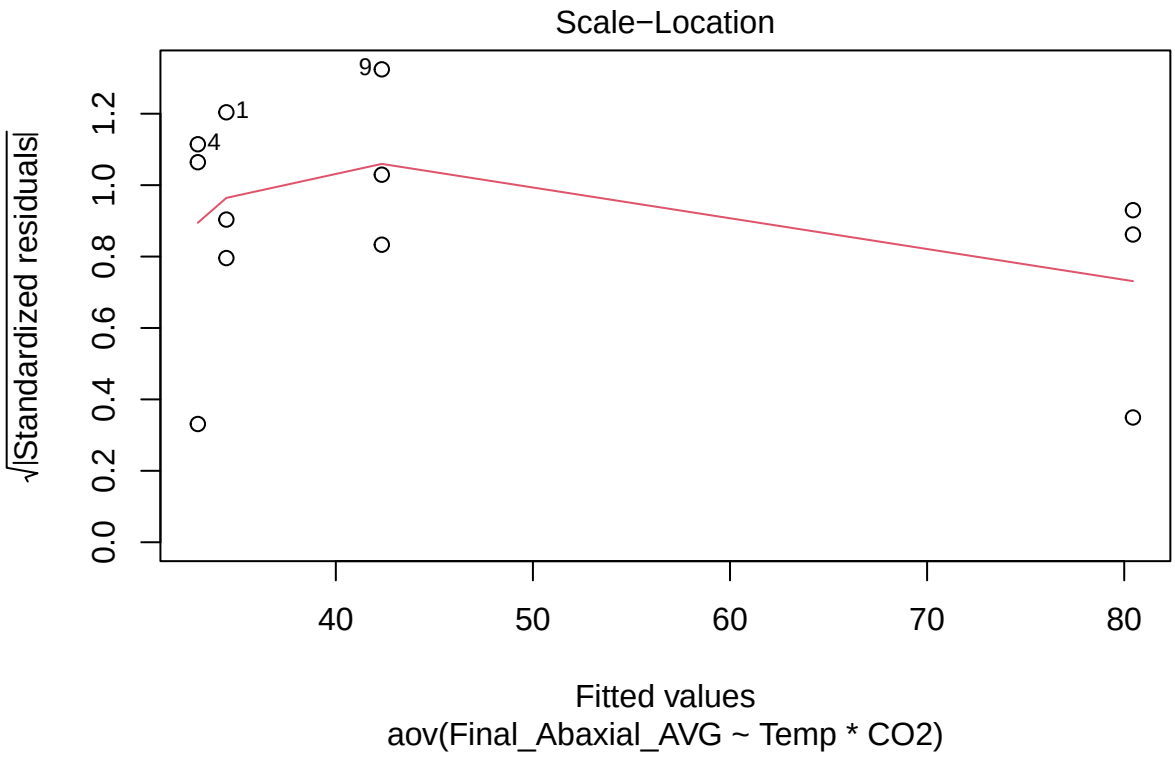

Scale−Location
√|Standardized residuals|
0.0
0.4
0.8
1.2
3
6
5
35
40
45
50
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

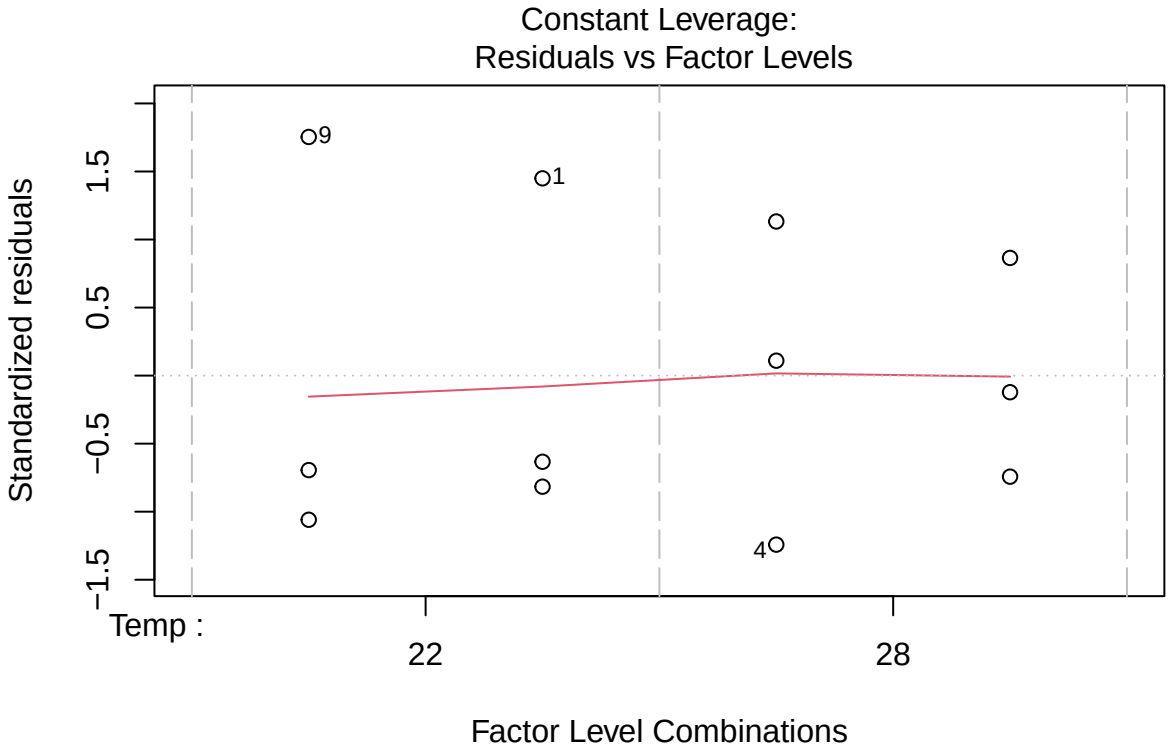



```
#plot(angle.mint.aov)
plot(angle.nasturtium.aov)
```

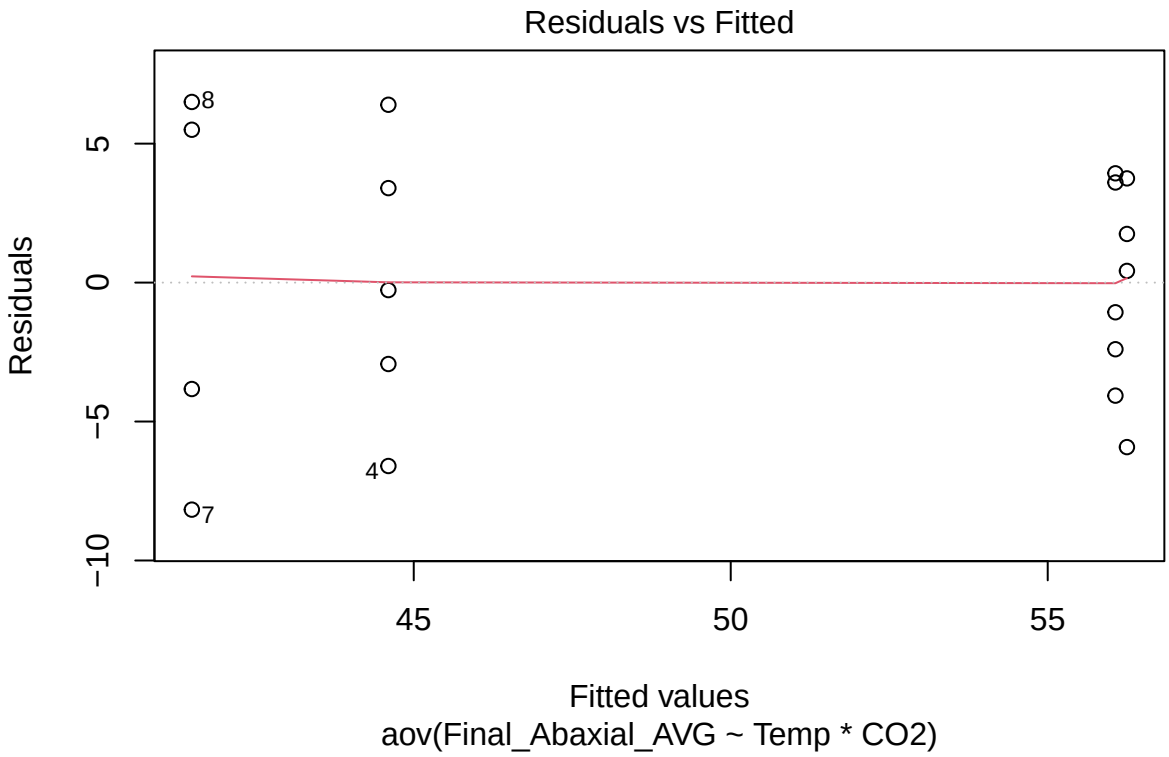

Residuals vs Fitted
Residuals
15
10
5
0
−5
−10
9
1
4
40
50
60
70
80
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

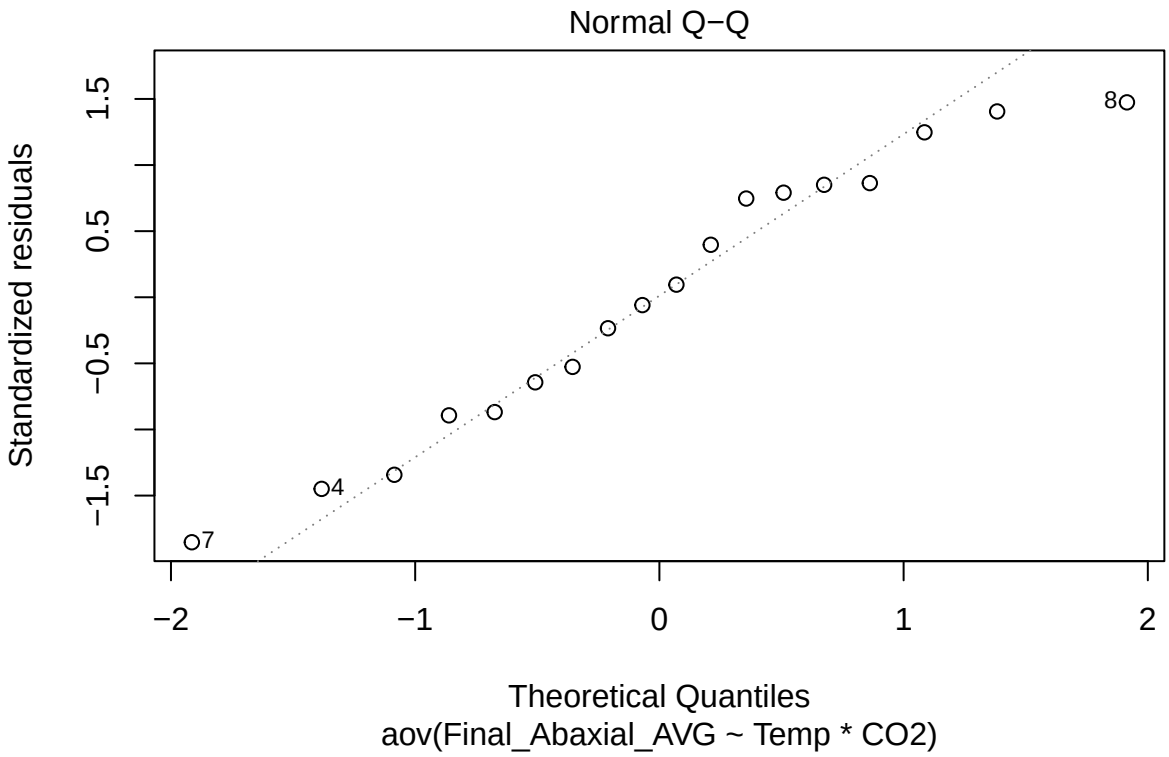

Normal Q−Q
Standardized residuals
2.0
1.5
1.0
0.5
0.0
−1.0
9
1
4
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

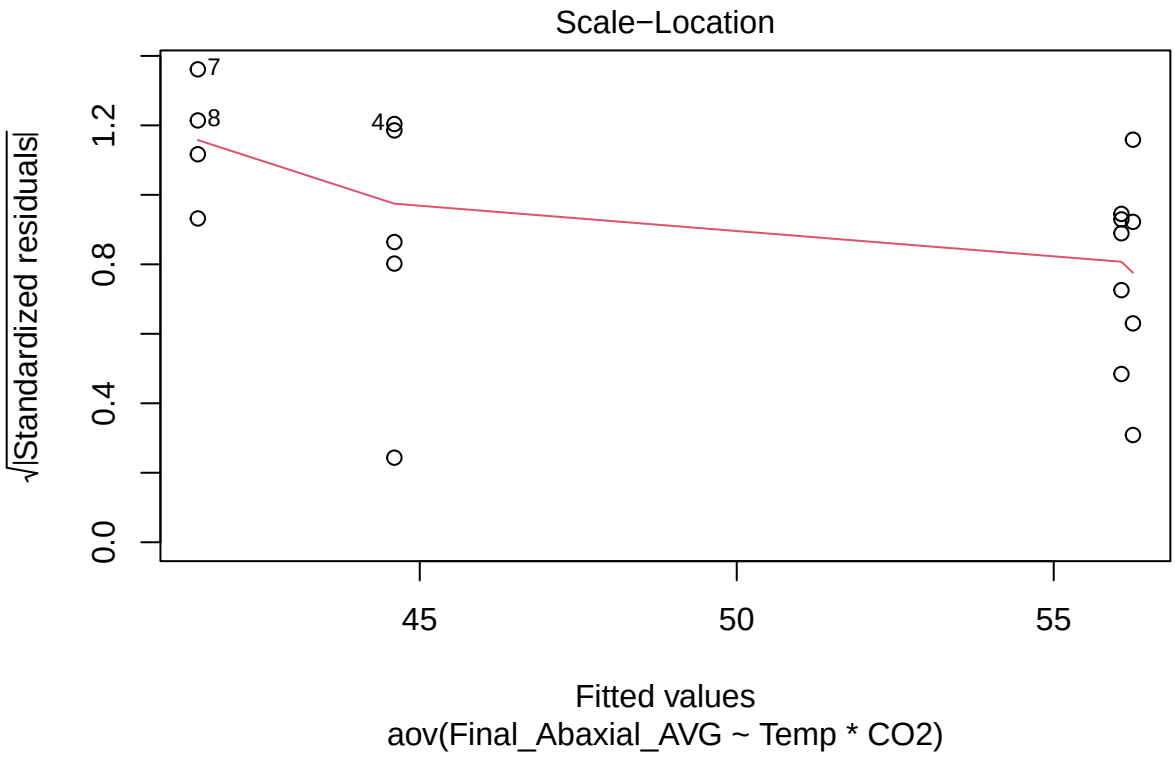

Scale−Location
√|Standardized residuals|
0.0
0.2
0.4
0.6
0.8
1.0
1.2
9
1
4
40
50
60
70
80
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

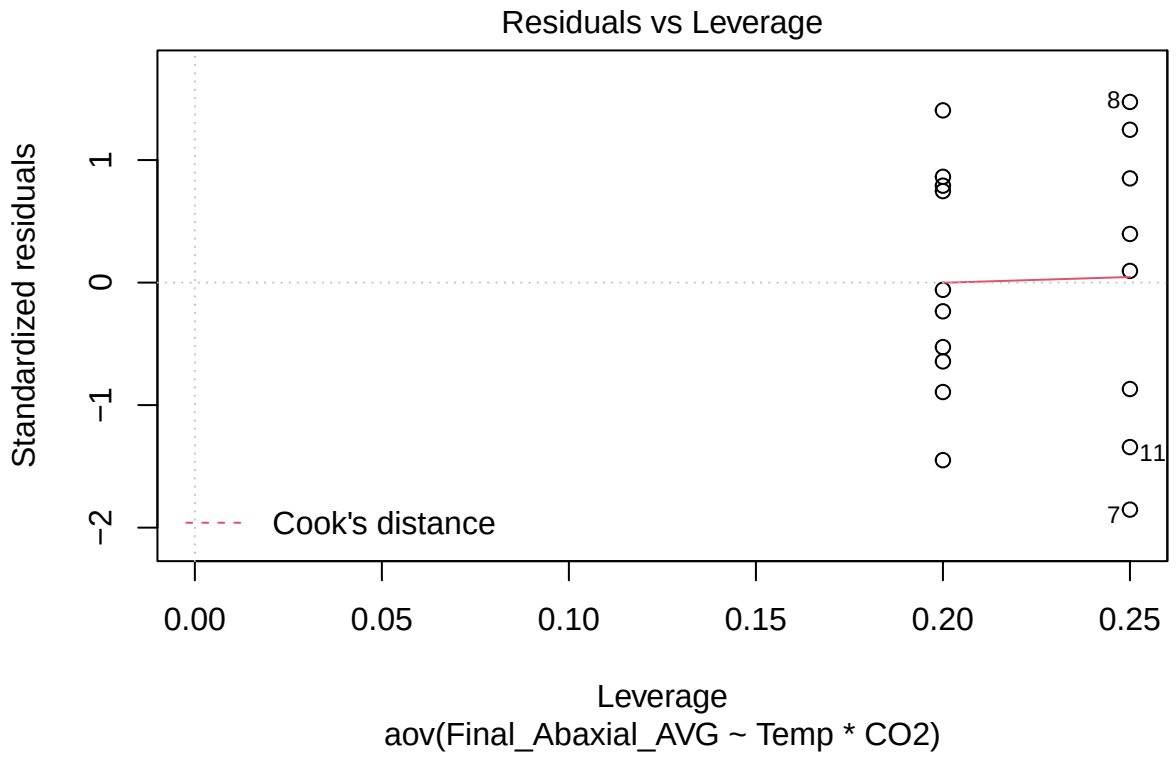



```
plot(angle.pepper.aov)
```

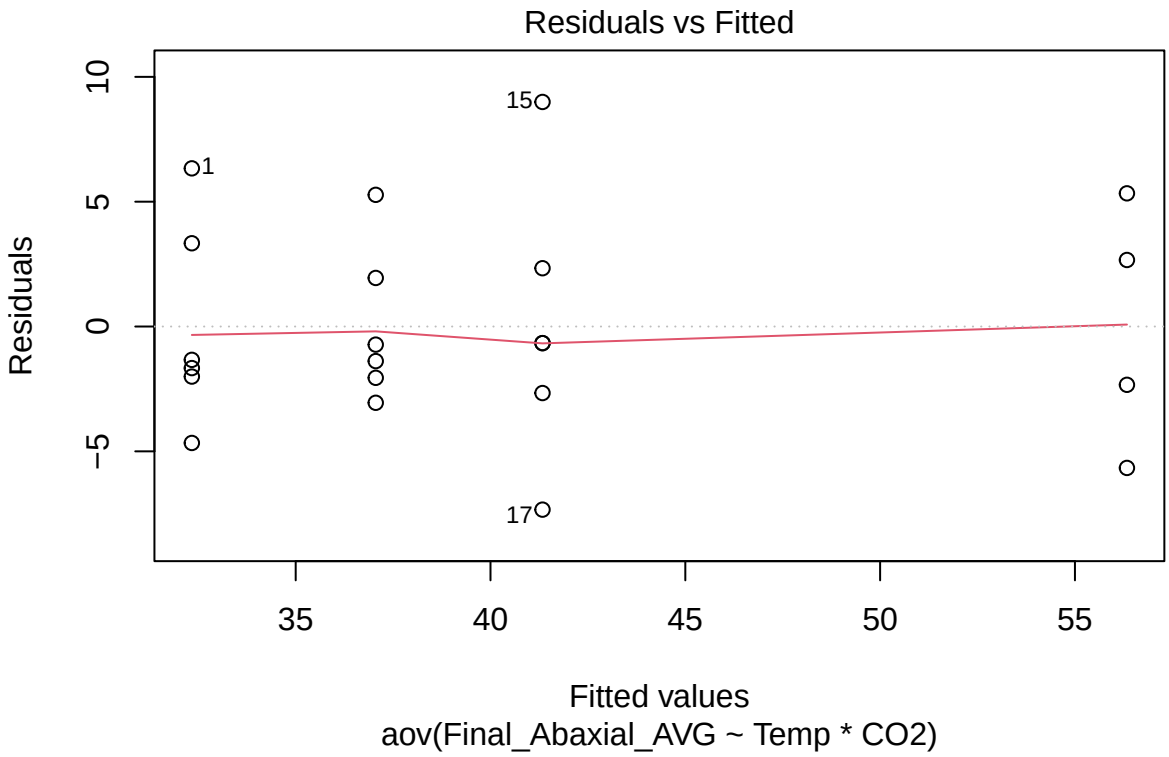

Residuals vs Fitted
Residuals
5
0
−5
−10
8
4
7
45
50
55
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

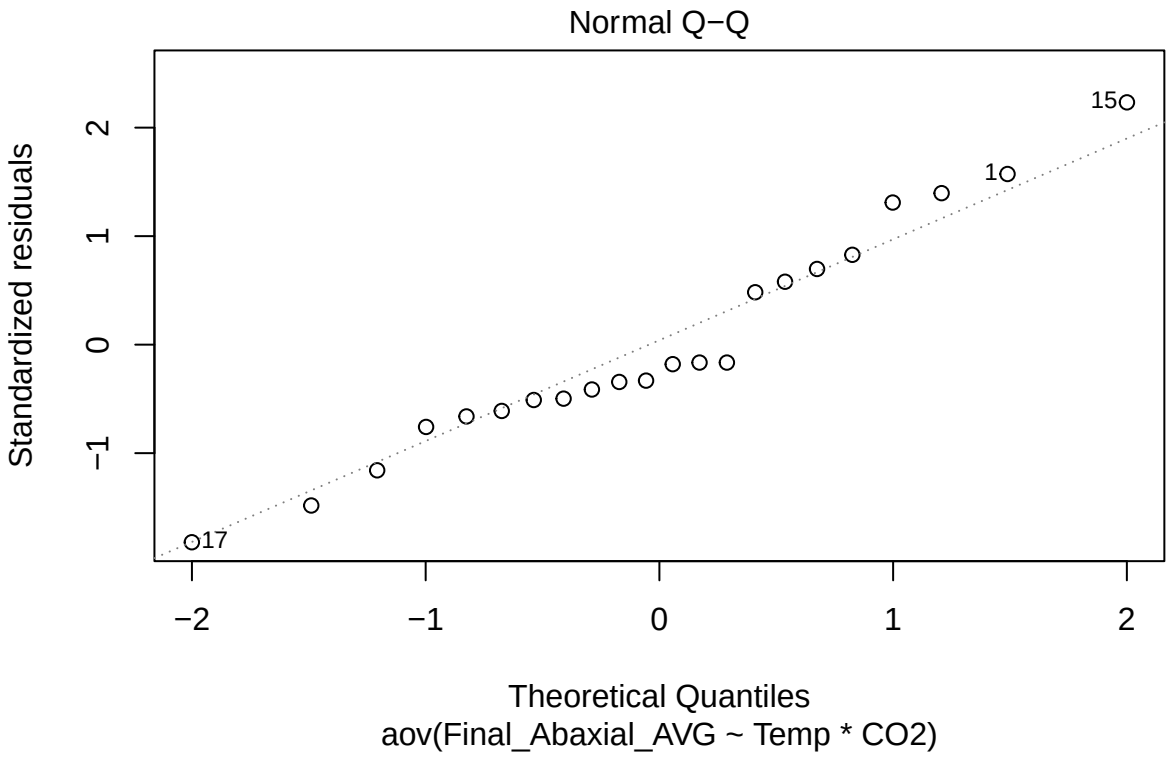

Normal Q−Q
Standardized residuals
1.5
0.5
−0.5
−1.5
8
4
7
−2
−1
0
1
2
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)

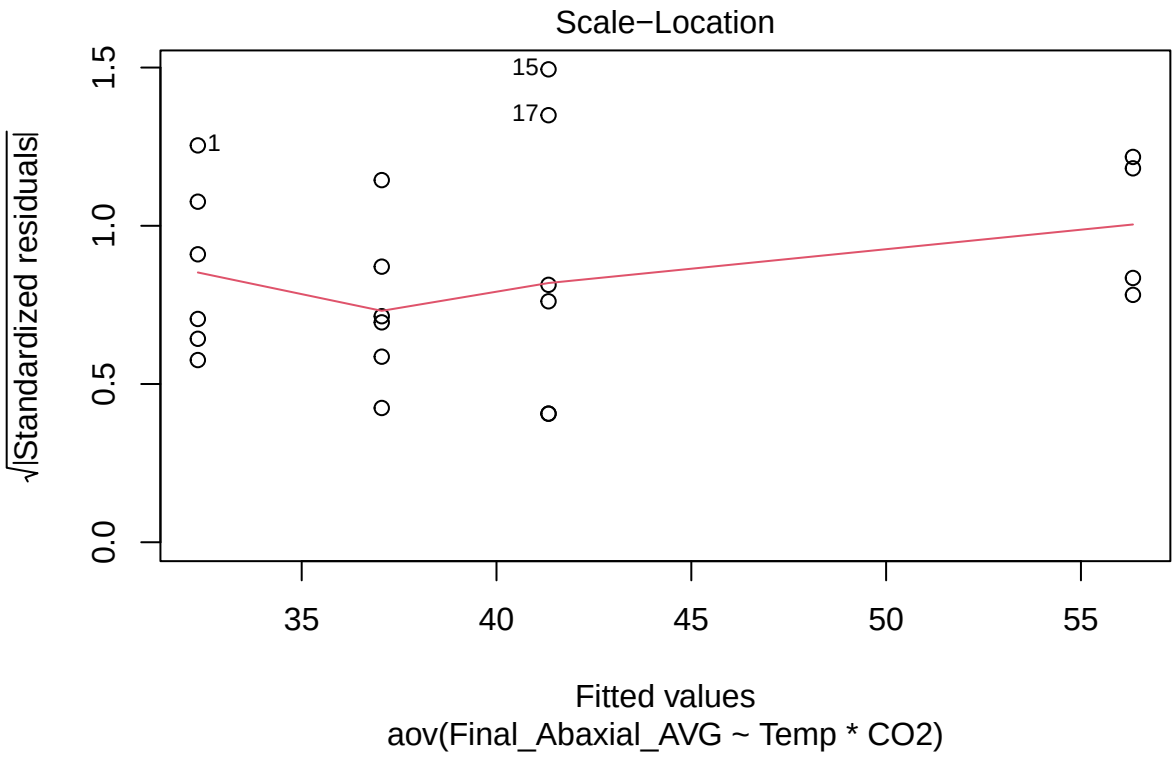

Scale−Location
√|Standardized residuals|
0.0
0.4
0.8
1.2
7
8
4
45
50
55
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

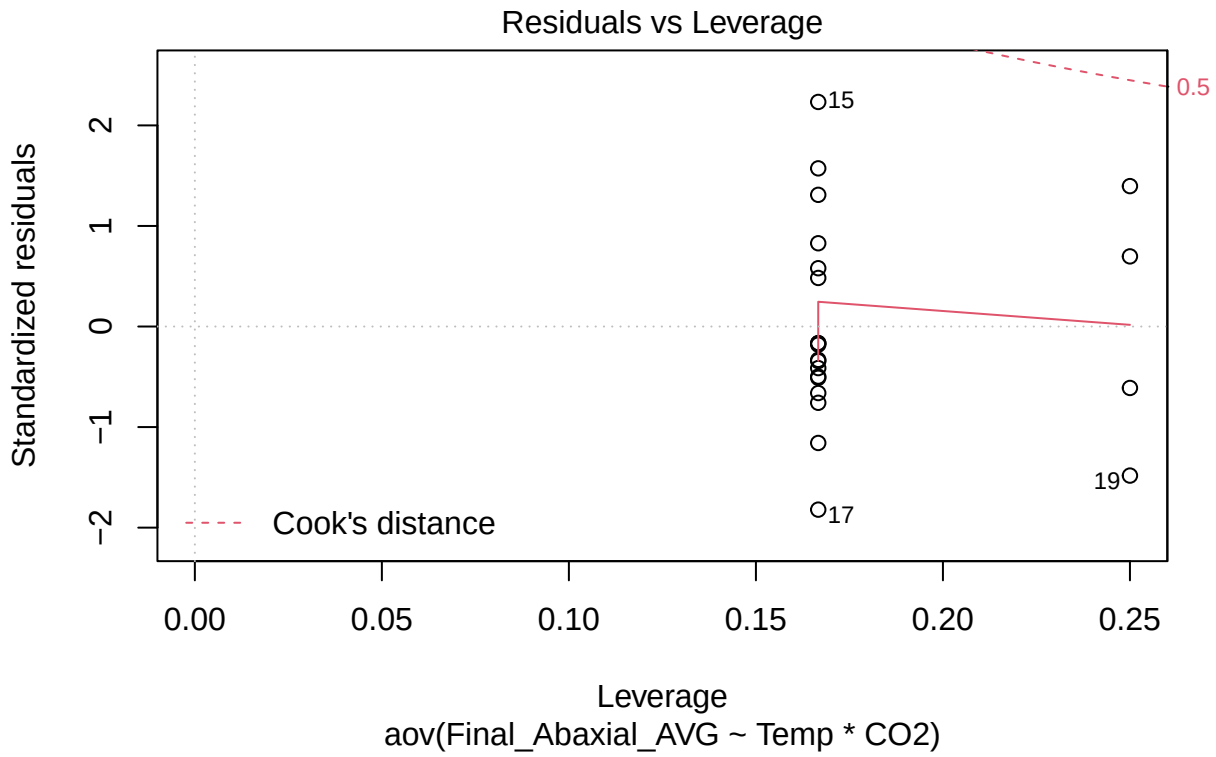



```
plot(angle.potato.aov)
```

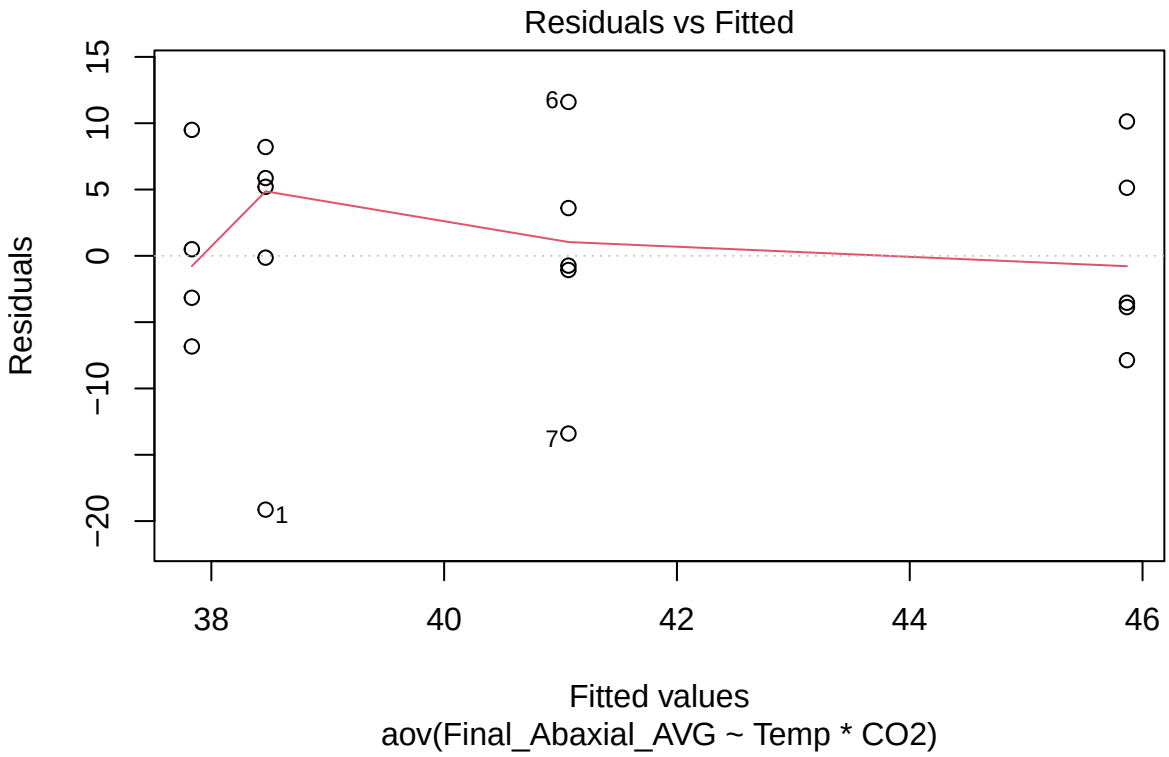

Residuals vs Fitted
Residuals
10
5
0
−5
15
1
17
35
40
45
50
55
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

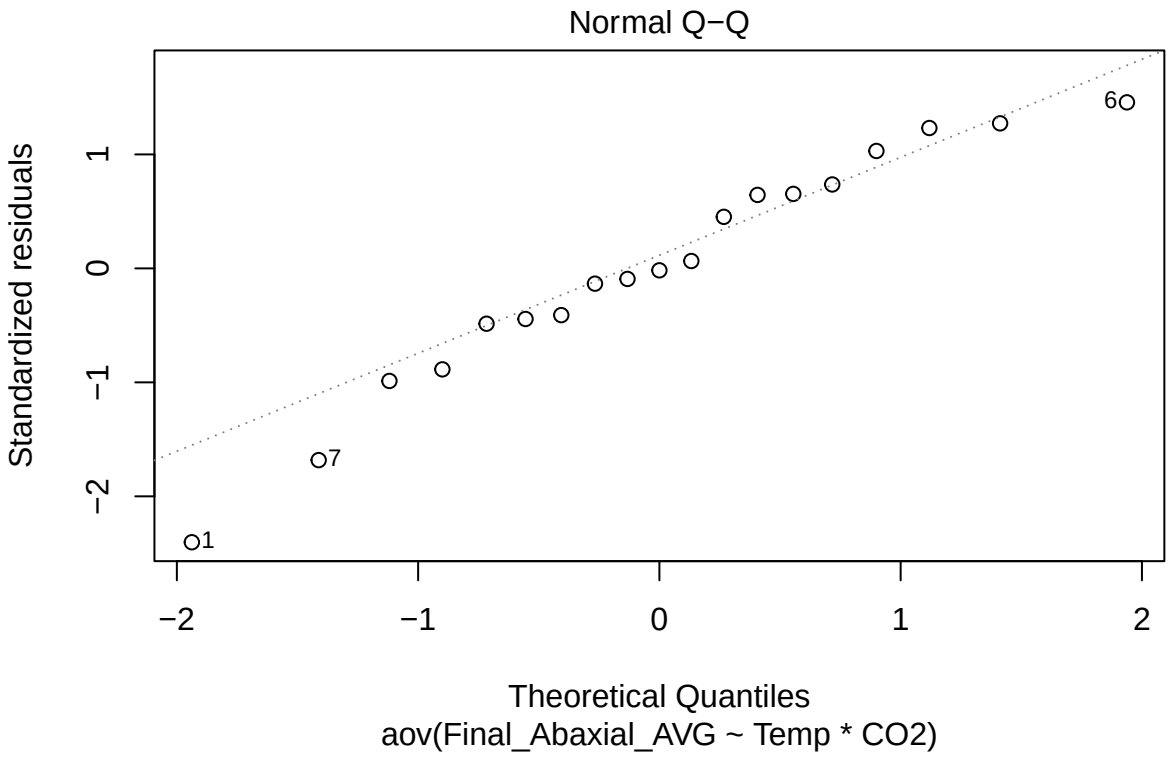

Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)
15
1
17
−2
−1
0
1
2

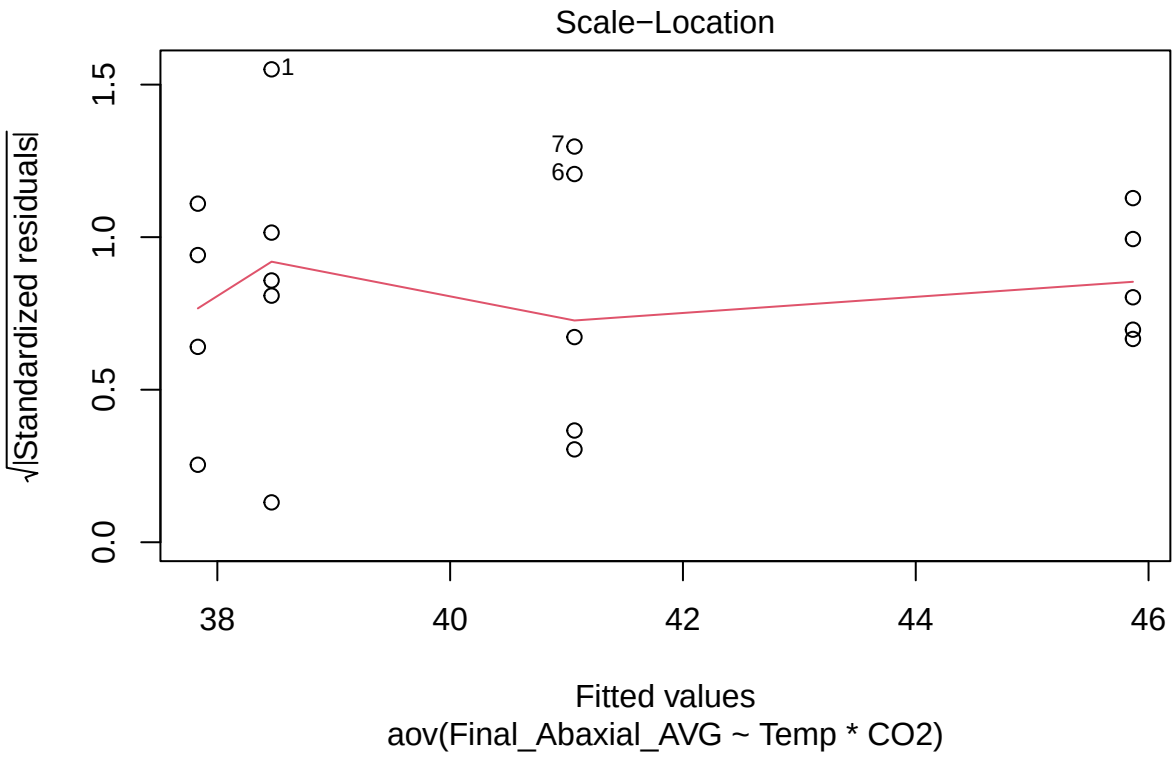

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
15
17
1
35
40
45
50
55
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

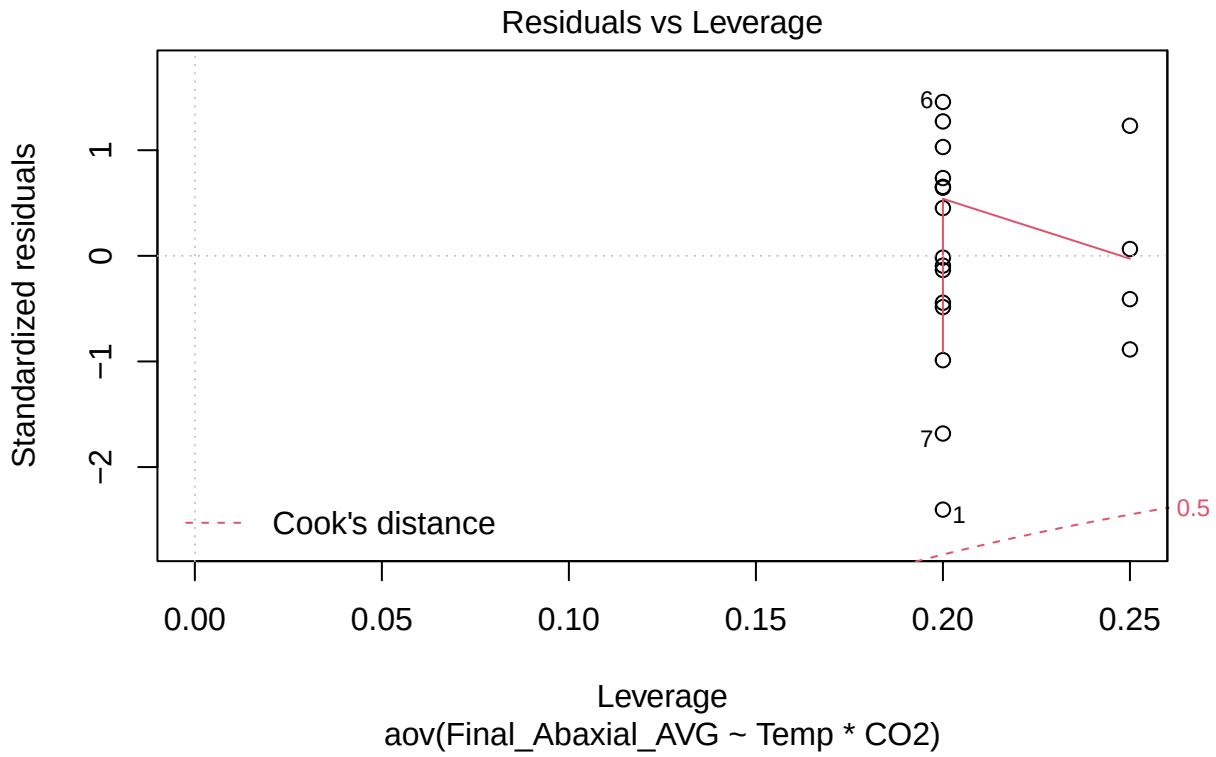



```
plot(angle.yarrow.aov)
```

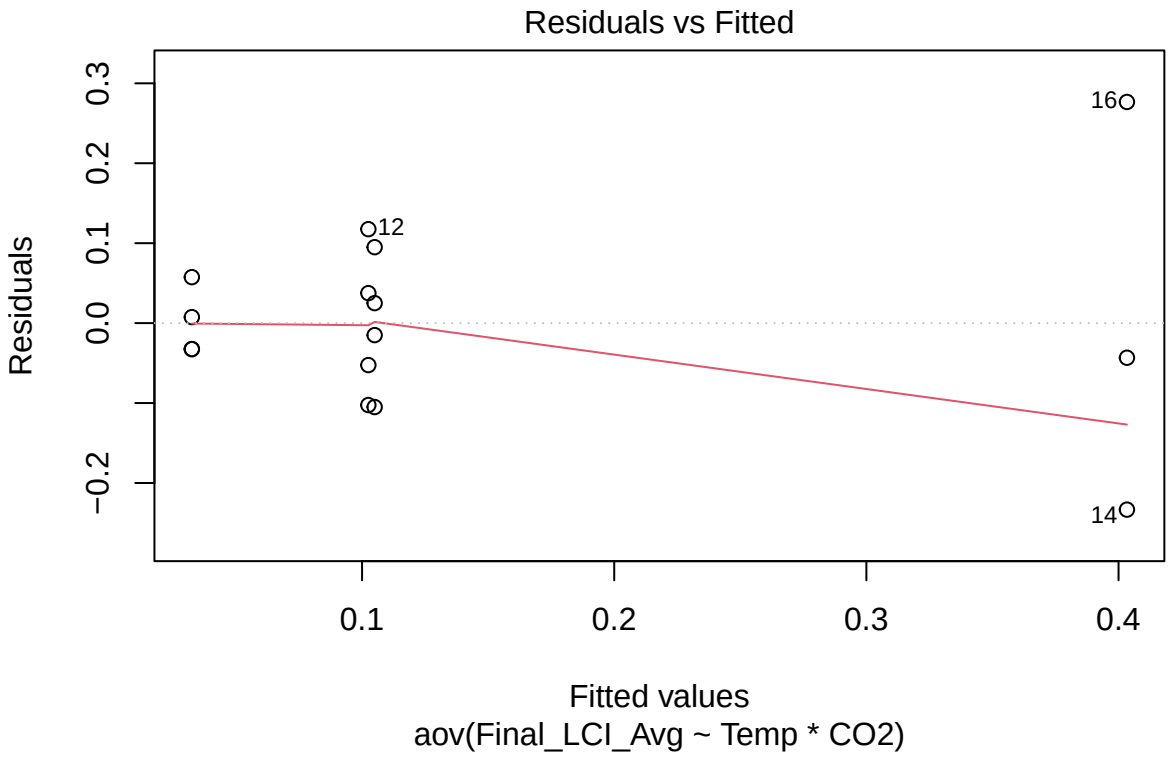

Residuals vs Fitted
Residuals
15
10
5
0
−10
−20
38
40
42
44
46
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)
6
7
1

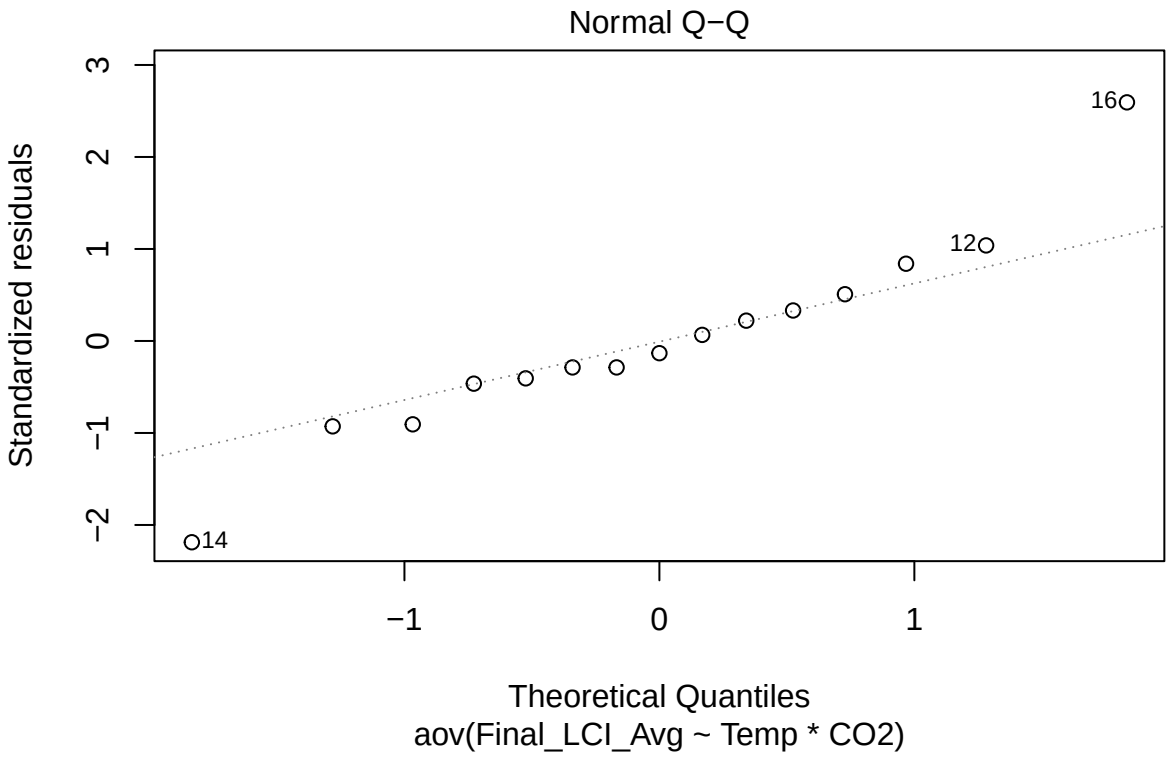

Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(Final_Abaxial_AVG ~ Temp * CO2)
1
6
7

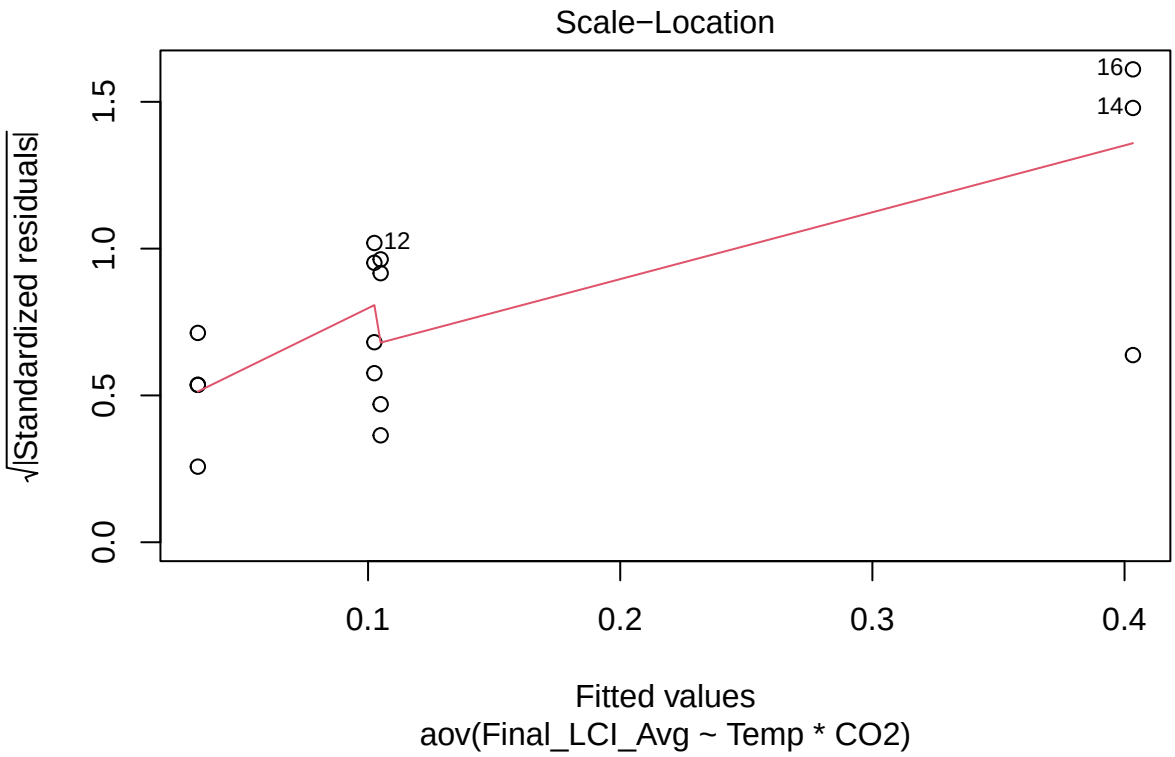

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
1
7
6
38
40
42
44
46
Fitted values
aov(Final_Abaxial_AVG ~ Temp * CO2)

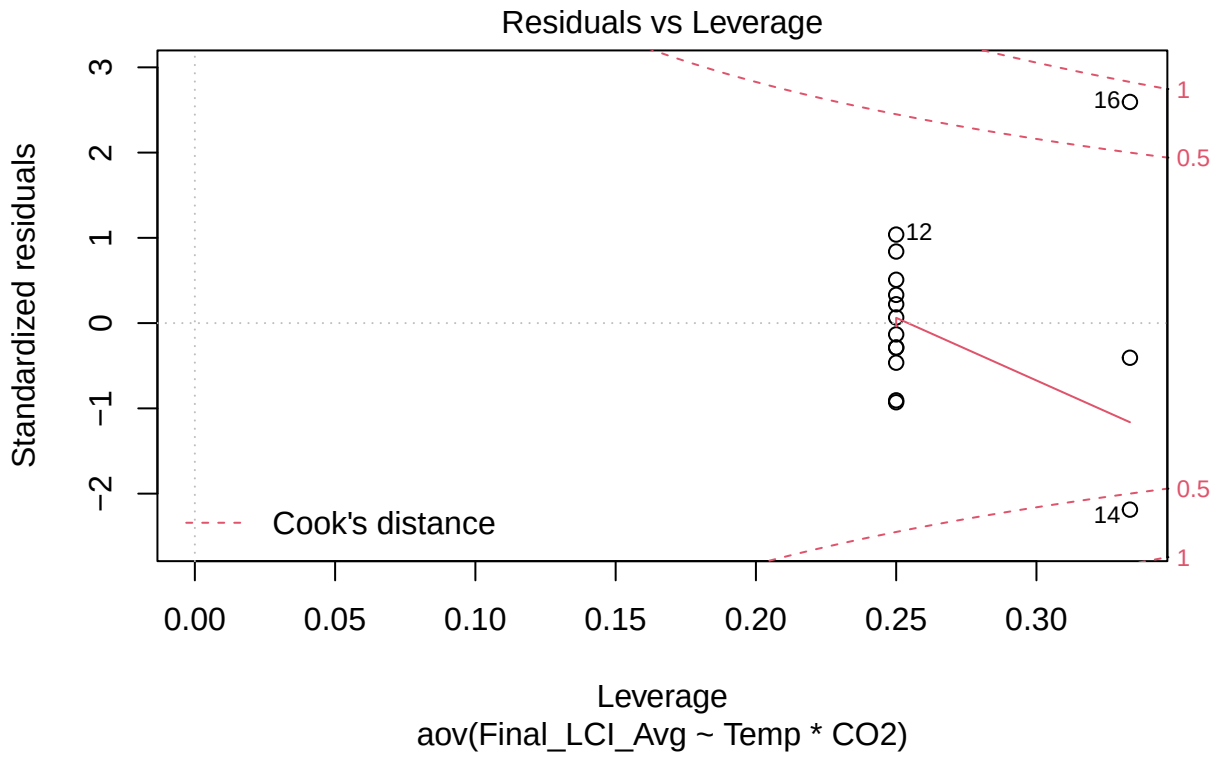



```
#plot(angle.rose.aov)

plot(LCI.bbean.aov)
```

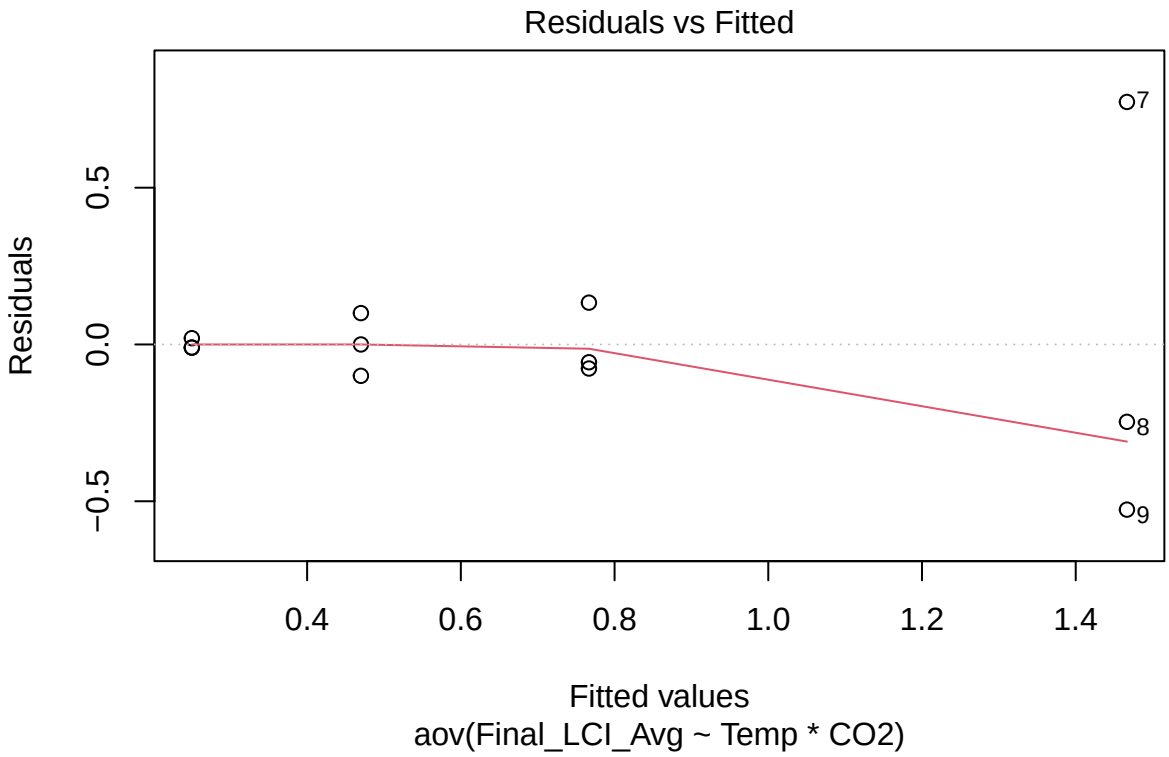

Residuals vs Fitted
Residuals
0.3
0.2
0.1
0.0
−0.2
16
12
14
0.1
0.2
0.3
0.4
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)

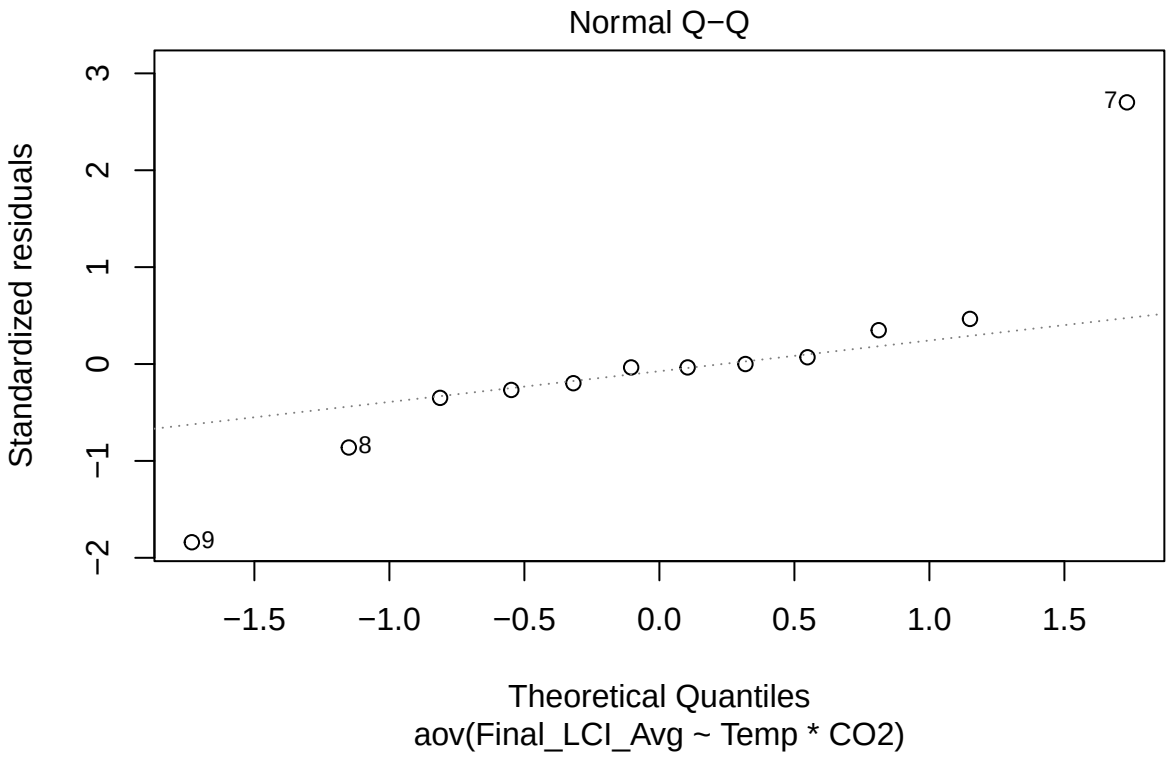

Normal Q−Q
Standardized residuals
3
2
1
0
−1
−2
16
12
14
−1
0
1
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)

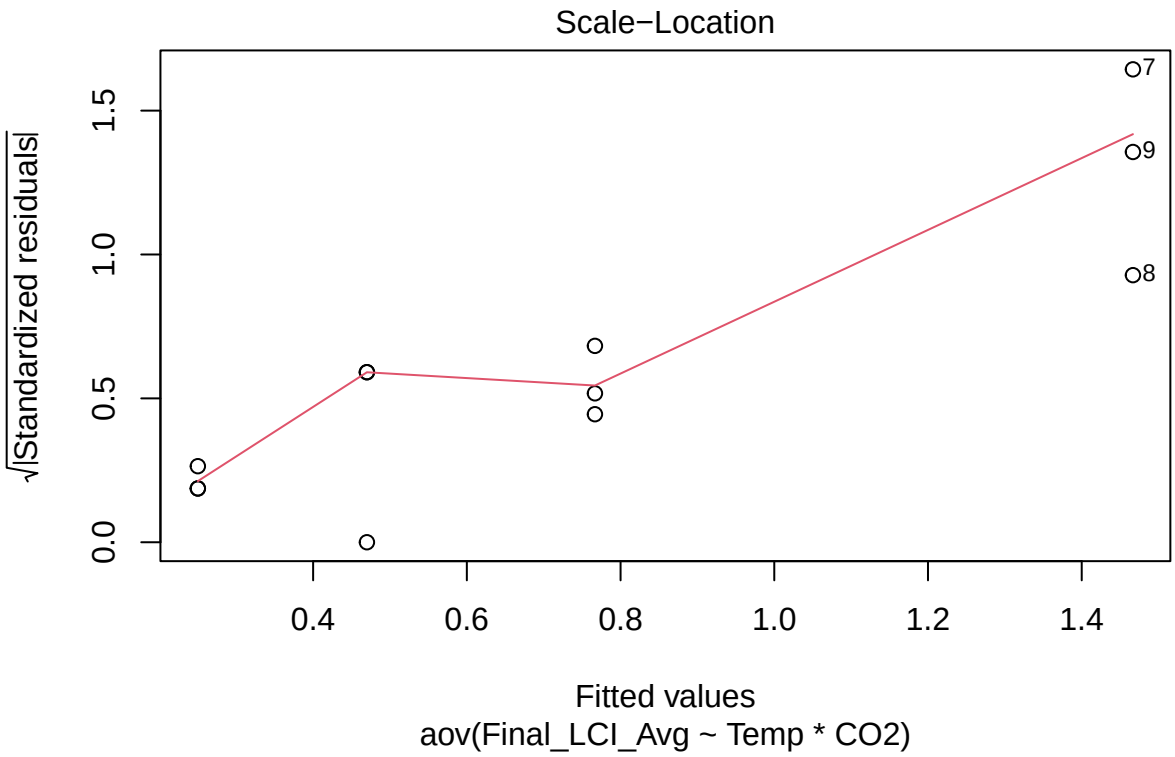

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
16
14
12
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)

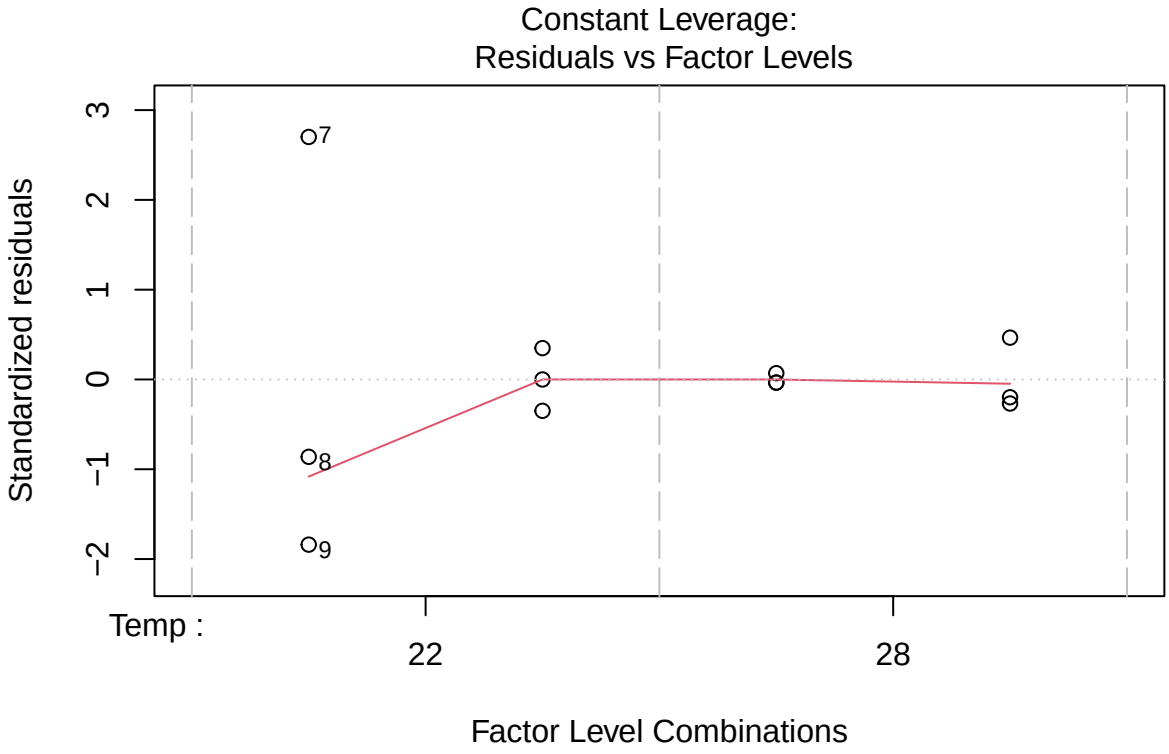



```
#plot(angle.tomato.aov)
#plot(angle.eggplant.aov)
#plot(angle.gcherry.aov)
#plot(angle.hibiscus.aov)
plot(LCI.mint.aov)
```

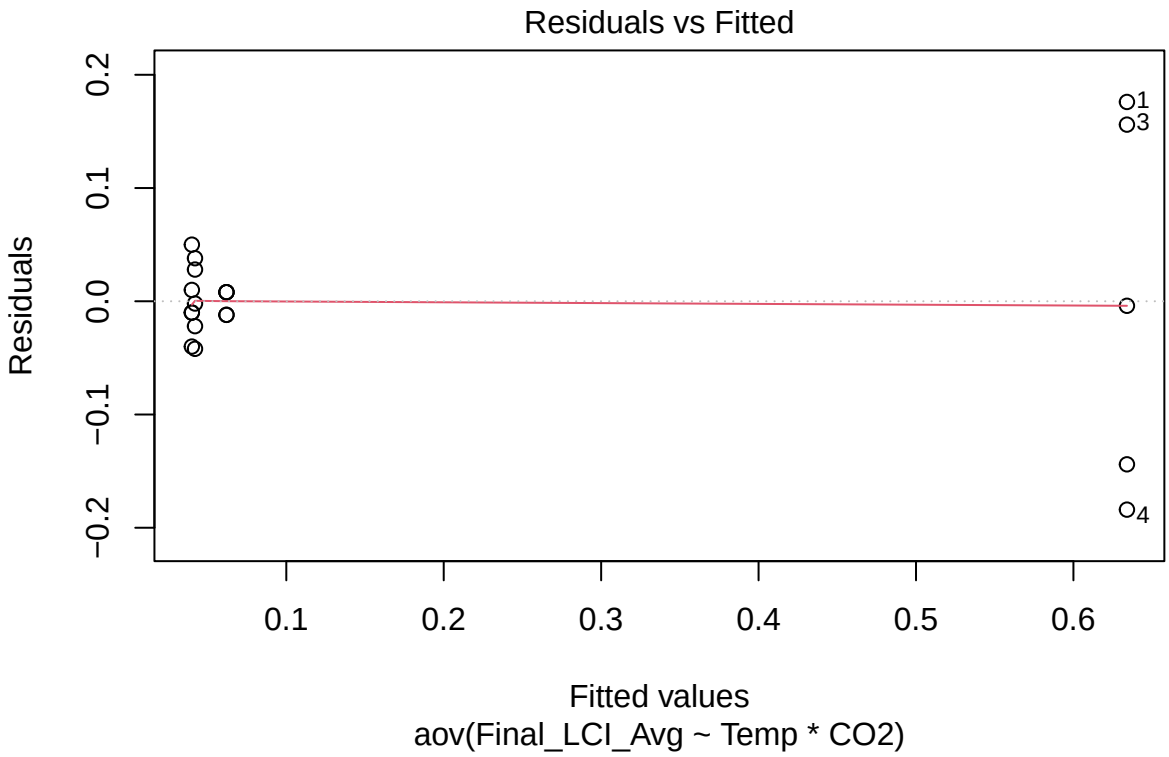

Residuals vs Fitted
Residuals
0.5
0.0
−0.5
7
8
9
0.4
0.6
0.8
1.0
1.2
1.4
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)

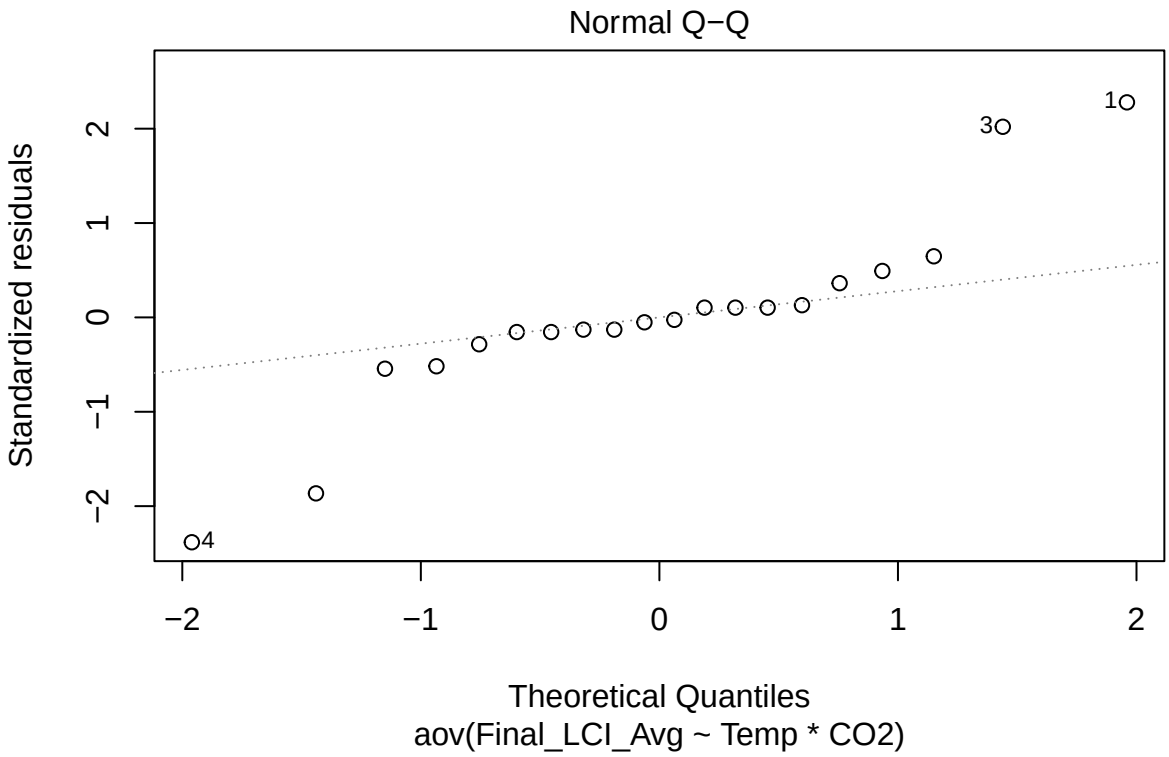

Normal Q−Q
Standardized residuals
3
2
1
0
−1
−2
7
8
9
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)

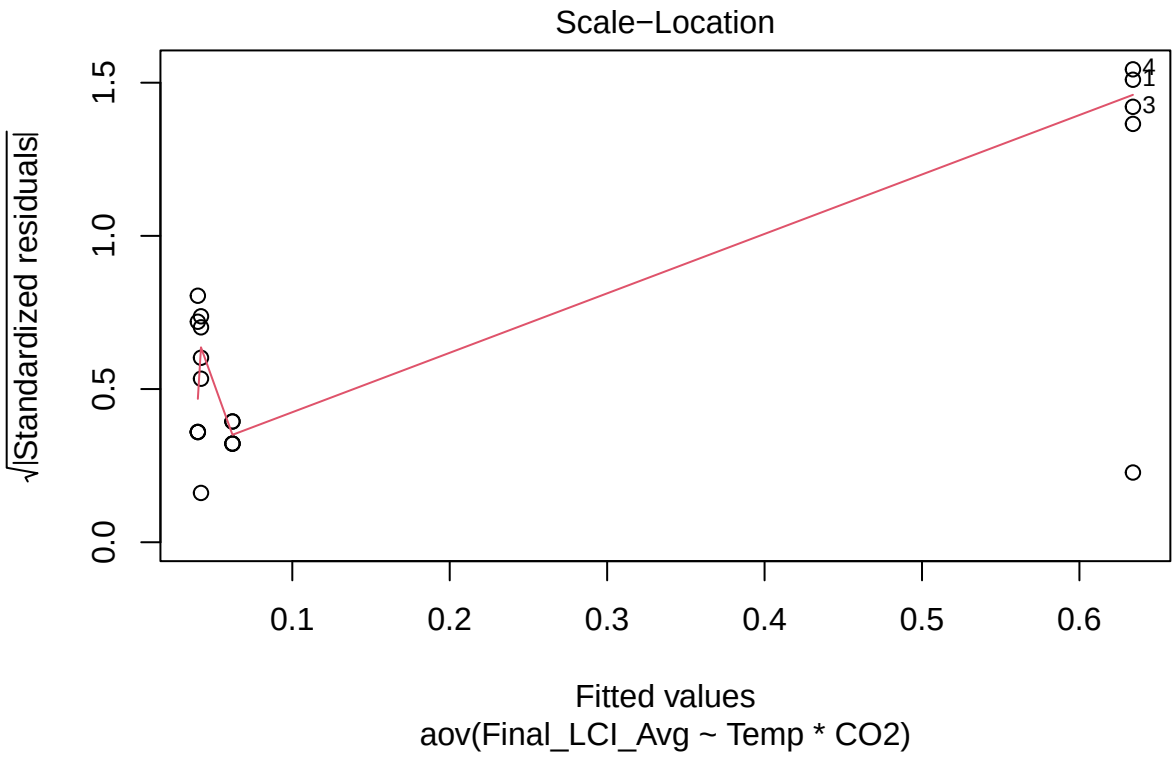

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.4
0.6
0.8
1.0
1.2
1.4
7
9
8
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)

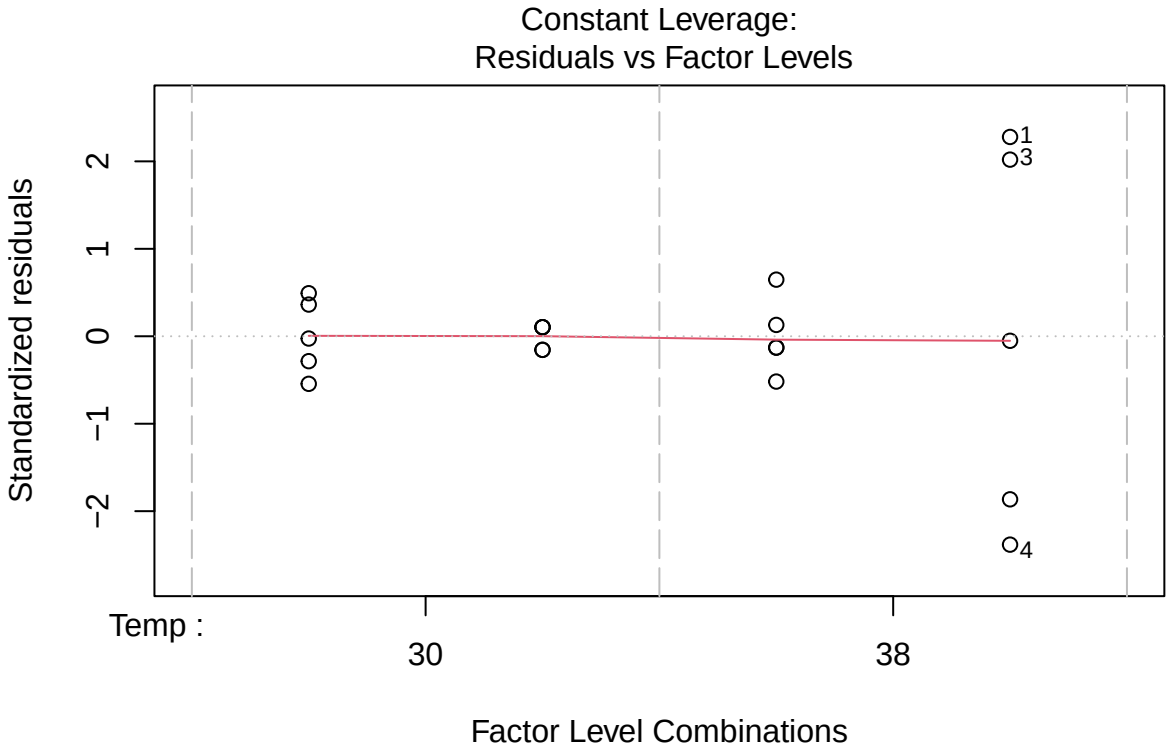



```
#plot(angle.nasturtium.aov)
#plot(angle.pepper.aov)
#plot(angle.potato.aov)
#plot(angle.yarrow.aov)
plot(LCI.rose.aov)
```


Residuals vs Fitted
Residuals
0.2
0.1
0.0
−0.1
−0.2
1
3
4
0.1
0.2
0.3
0.4
0.5
0.6
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)


Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)
1
3
4
−2
−1
0
1
2


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
0.5
0.6
4
1
3
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)




```
#plots all relatively normal, with the exception of small sample size in hibiscus.

#test for equal variance.

bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = bbeanAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 4.6631, df = 3, p-value = 0.1982
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = tomatoAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 0.9077, df = 3, p-value = 0.8236
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = eggplantAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 5.5958, df = 3, p-value = 0.133
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = gcherryAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 0.71124, df = 3, p-value = 0.8706
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = hibiscusAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 4.4681, df = 3, p-value = 0.2151
```

```
#bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = mintAngle)#empty response column
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = nasturtiumAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 0.63221, df = 3, p-value = 0.889
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = pepperAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 1.6654, df = 3, p-value = 0.6447
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = potatoAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 1.5366, df = 3, p-value = 0.6739
```

```
bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = yarrowAngle)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Final_Abaxial_AVG by interaction(Temp, CO2)
## Bartlett's K-squared = 0.90612, df = 3, p-value = 0.824
```

```
#bartlett.test(Final_Abaxial_AVG~interaction(Temp,CO2), data = roseAngle)#empty resposne column

#all angle data pass bartlett test with no significant differences found in variance.
```

LCI non-parametric test and post hoc

```
#bartlett.test(Final_LCI_Avg~interaction(Temp,CO2), data = bbeanLCI)

#bartlett.test(Final_LCI_Avg~interaction(Temp,CO2), data = mintLCI)
```

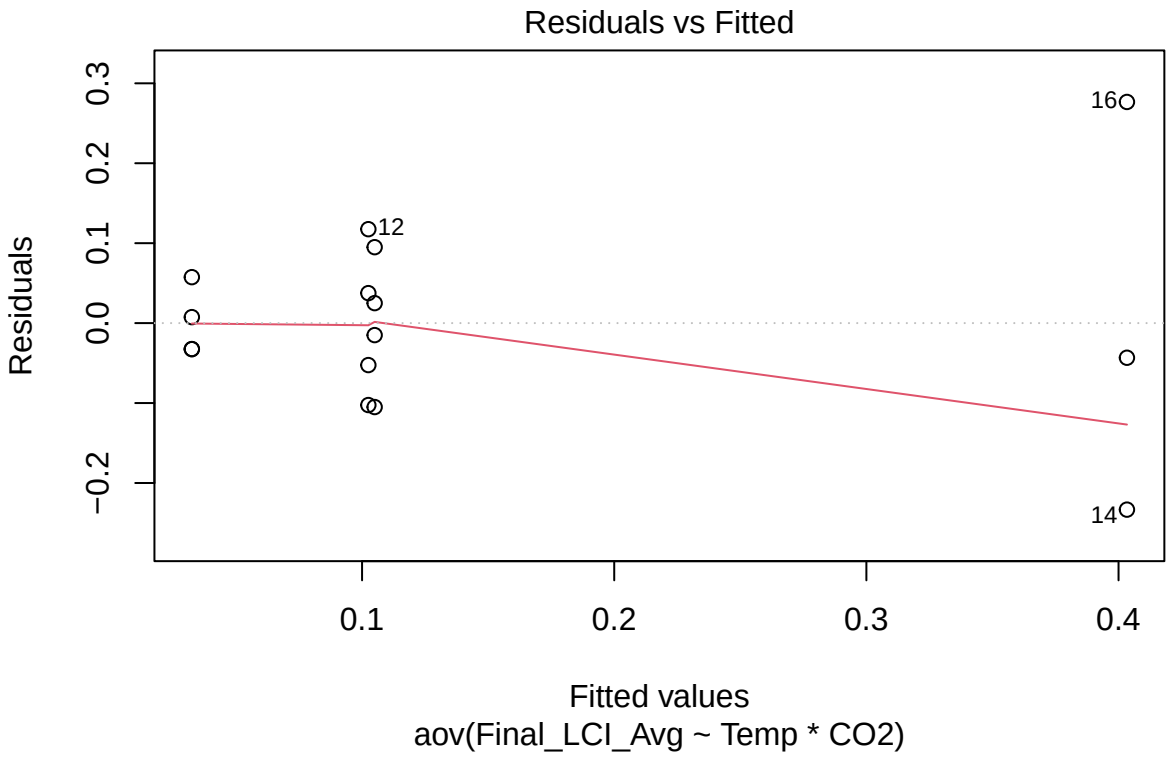
```
#bartlett.test(Final_LCI_Avg~interaction(Temp,CO2), data = roseLCI)

aovLCIbbean<-aov(Final_LCI_Avg~Temp*CO2, data = bbeanLCI)
summary(aovLCIbbean)
```

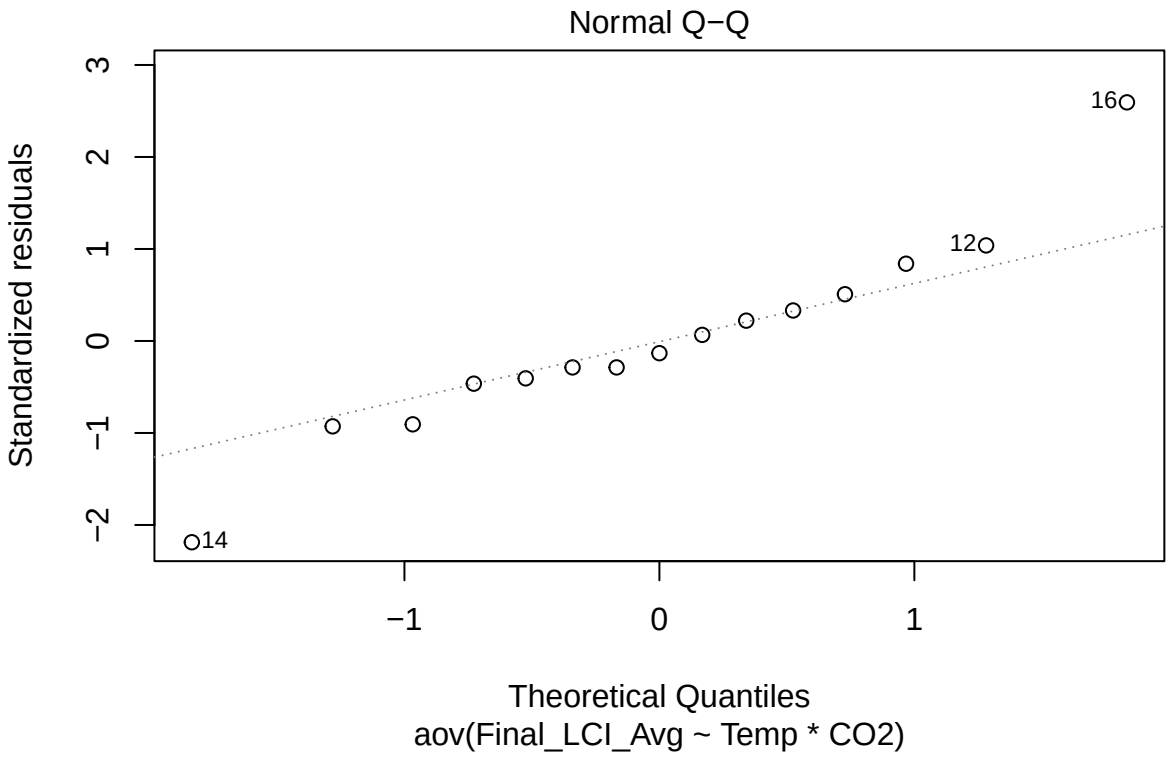
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Temp         1 0.0287 0.02870   1.682 0.2212
## CO2          1 0.1071 0.10710   6.276 0.0292 *
## Temp:CO2     1 0.1287 0.12866   7.539 0.0190 *
## Residuals   11 0.1877 0.01707
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

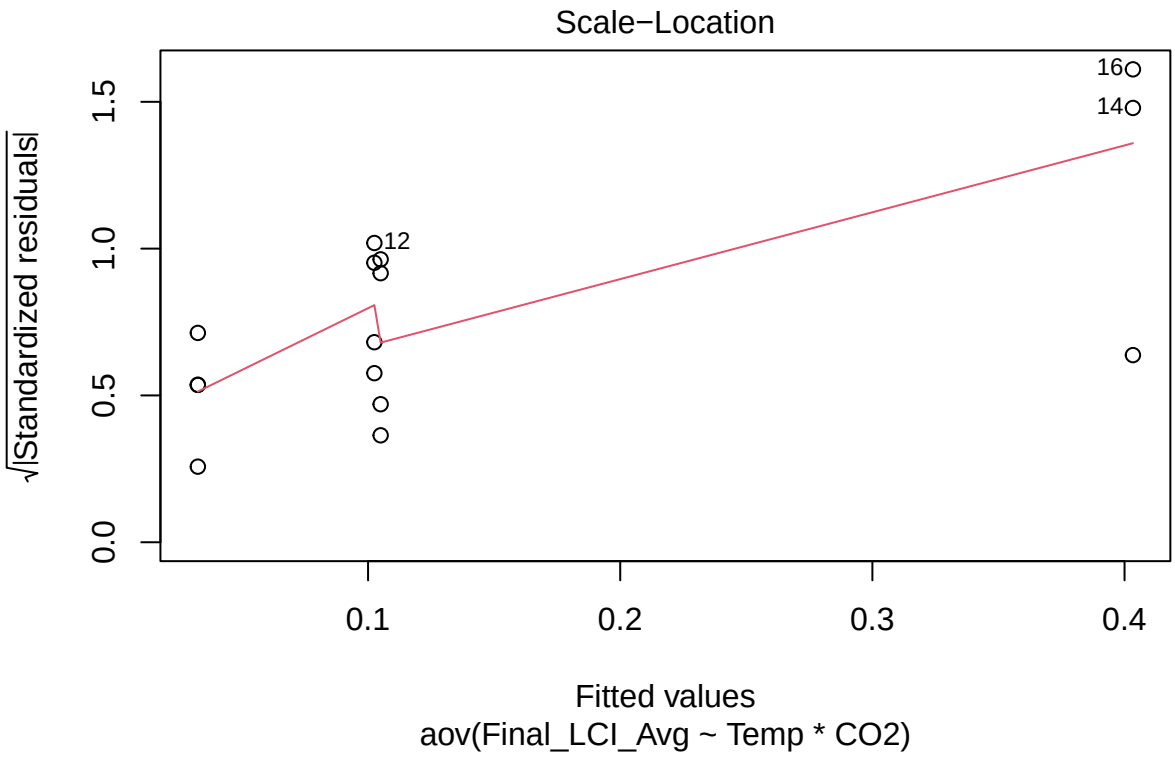
```
TukeyHSD(aovLCIbbean)
```

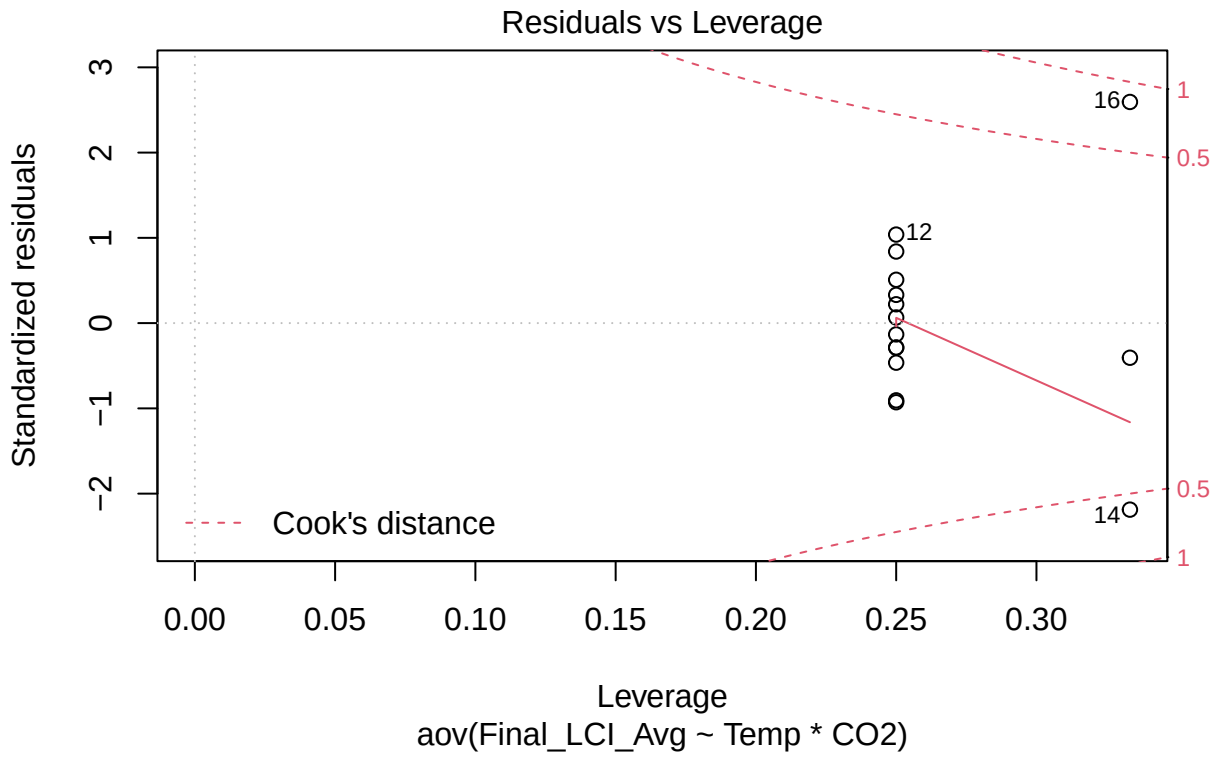
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Final_LCI_Avg ~ Temp * CO2, data = bbeanLCI)
##
## $Temp
##             diff         lwr       upr     p adj
## 37-29 0.08767857 -0.06112858 0.2364857 0.2212285
##
## $CO2
##              diff        lwr       upr     p adj
## 800-400 0.1689413 0.02013418 0.3177485 0.0295701
##
## $`Temp:CO2`
##                      diff           lwr       upr     p adj
## 37:400-29:400 -0.0725000 -0.3504977789 0.2054978 0.8597811
## 29:800-29:400 -0.0025000 -0.2804977789 0.2754978 0.9999924
## 37:800-29:400  0.2983333 -0.0019385866 0.5986053 0.0516408
## 29:800-37:400  0.0700000 -0.2079977789 0.3479978 0.8715111
## 37:800-37:400  0.3708333  0.0705614134 0.6711053 0.0153337
## 37:800-29:800  0.3008333  0.0005614134 0.6011053 0.0495344
```

```
plot(aovLCIbbean)
```


Residuals vs Fitted
Residuals
0.3
0.2
0.1
0.0
−0.2
16
12
14
0.1
0.2
0.3
0.4
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)


Normal Q−Q
Standardized residuals
3
2
1
0
−1
−2
16
12
14
−1
0
1
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
16
14
12
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)




```
aovLCImint<-aov(Final_LCI_Avg~Temp*CO2, data = mintLCI)
summary(aovLCImint)
```

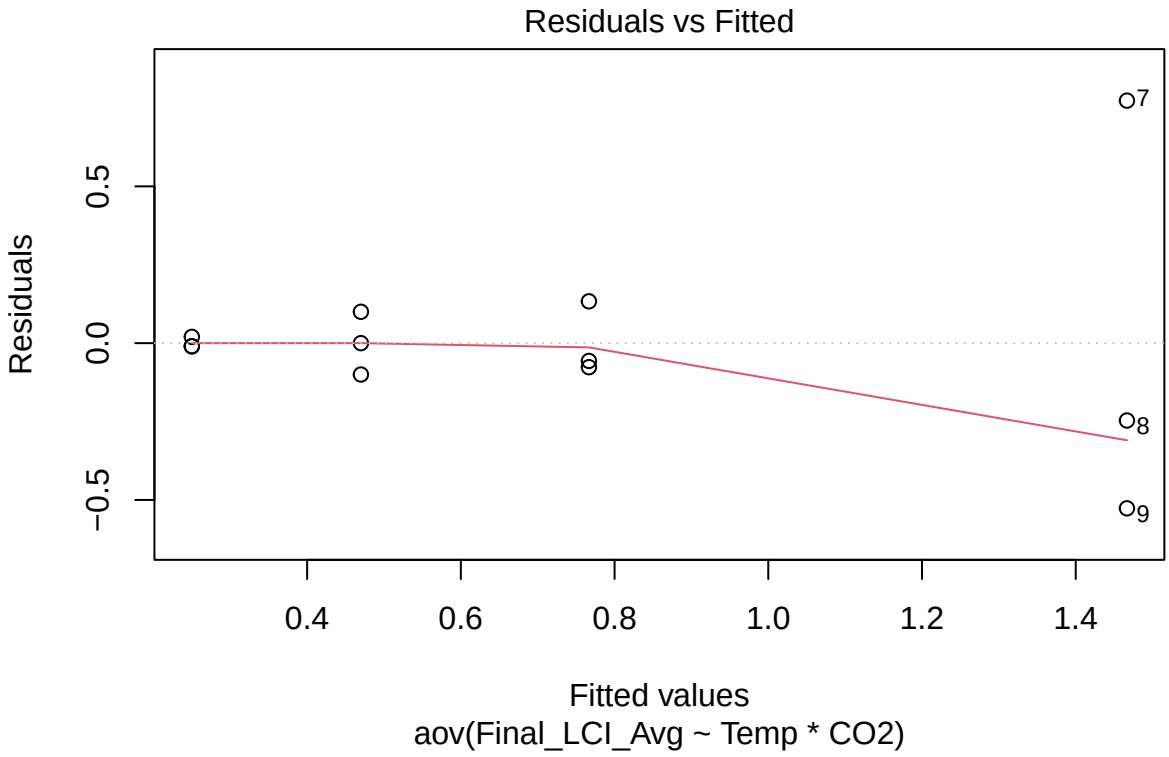
```
##             Df Sum Sq Mean Sq F value  Pr(>F)
## Temp         1 0.6348  0.6348   5.162 0.05272 .
## CO2          1 0.1728  0.1728   1.405 0.26986
## Temp:CO2     1 1.7176  1.7176  13.968 0.00573 **
## Residuals    8 0.9837  0.1230
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

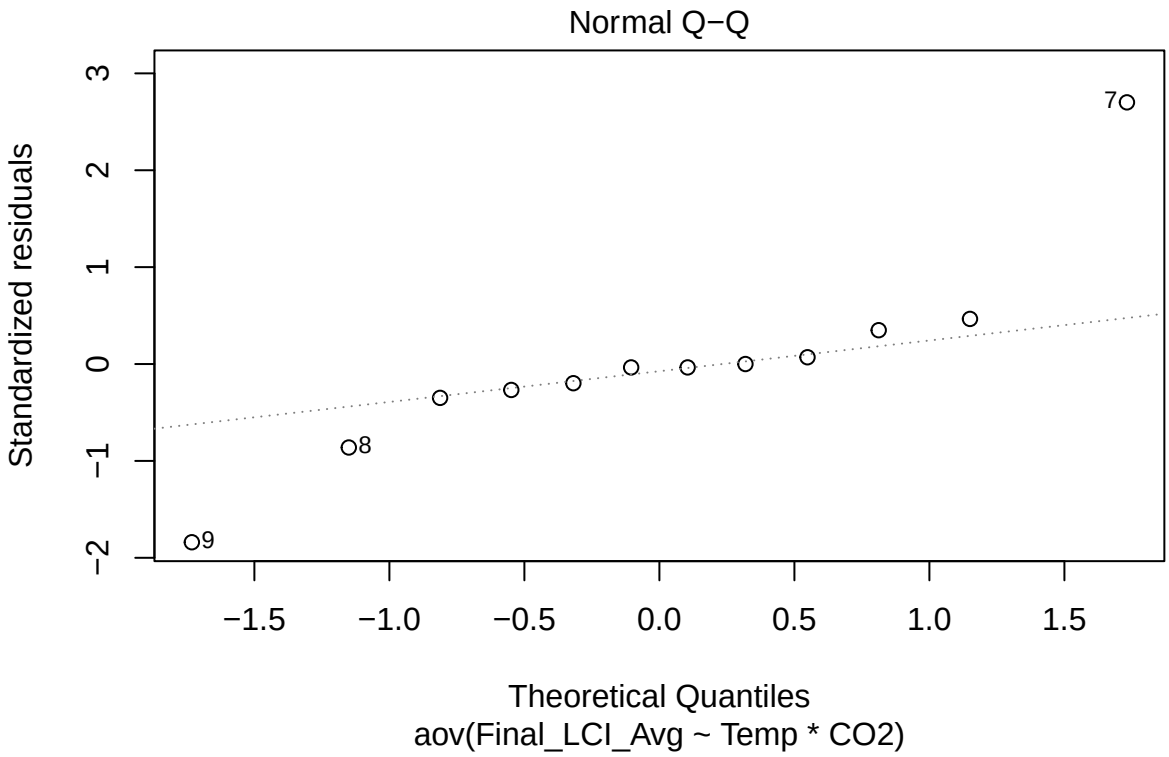
```
TukeyHSD(aovLCImint)
```

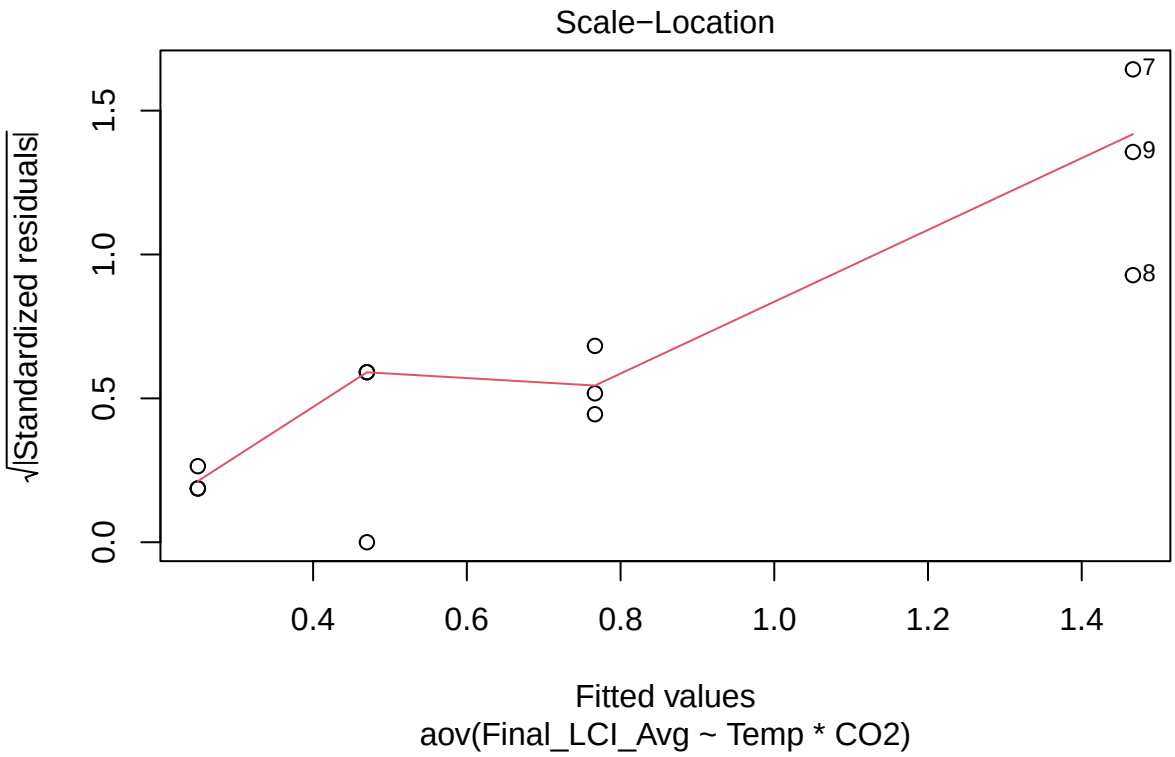
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Final_LCI_Avg ~ Temp * CO2, data = mintLCI)
##
## $Temp
##        diff       lwr         upr     p adj
## 28-22 -0.46 -0.926867 0.006866977 0.0527185
##
## $CO2
##          diff       lwr      upr   p adj
## 800-400 -0.24 -0.706867 0.226867 0.26986
##
## $`Temp:CO2`
```

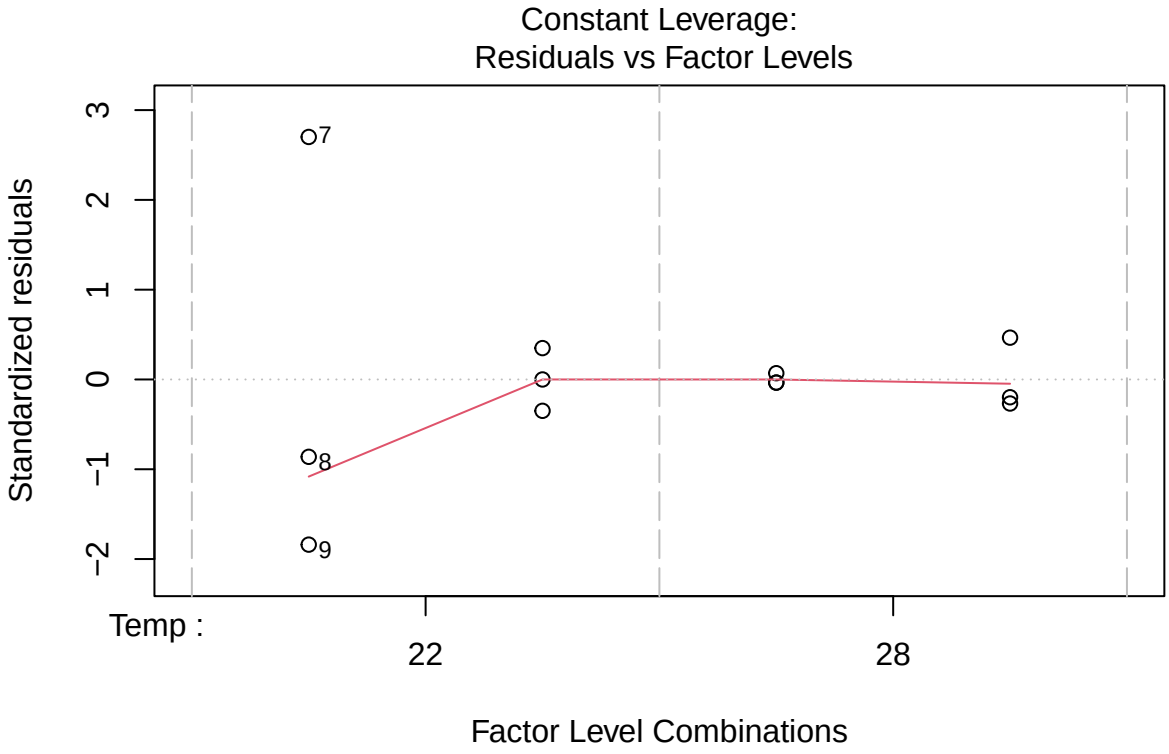
```
##                       diff        lwr         upr     p adj
## 28:400-22:400 -1.2166667 -2.1335565 -0.29977687 0.0119626
## 22:800-22:400 -0.9966667 -1.9135565 -0.07977687 0.0338564
## 28:800-22:400 -0.7000000 -1.6168898  0.21688979 0.1451162
## 22:800-28:400  0.2200000 -0.6968898  1.13688979 0.8664742
## 28:800-28:400  0.5166667 -0.4002231  1.43355646 0.3378131
## 28:800-22:800  0.2966667 -0.6202231  1.21355646 0.7344324
```

```
plot(aovLCImint)
```




Normal Q−Q
Standardized residuals
3
2
1
0
−1
−2
7
8
9
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.4
0.6
0.8
1.0
1.2
1.4
7
9
8
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)




```
aovLCIrose<-aov(Final_LCI_Avg~Temp*CO2, data = roseLCI)
summary(aovLCIrose)
```

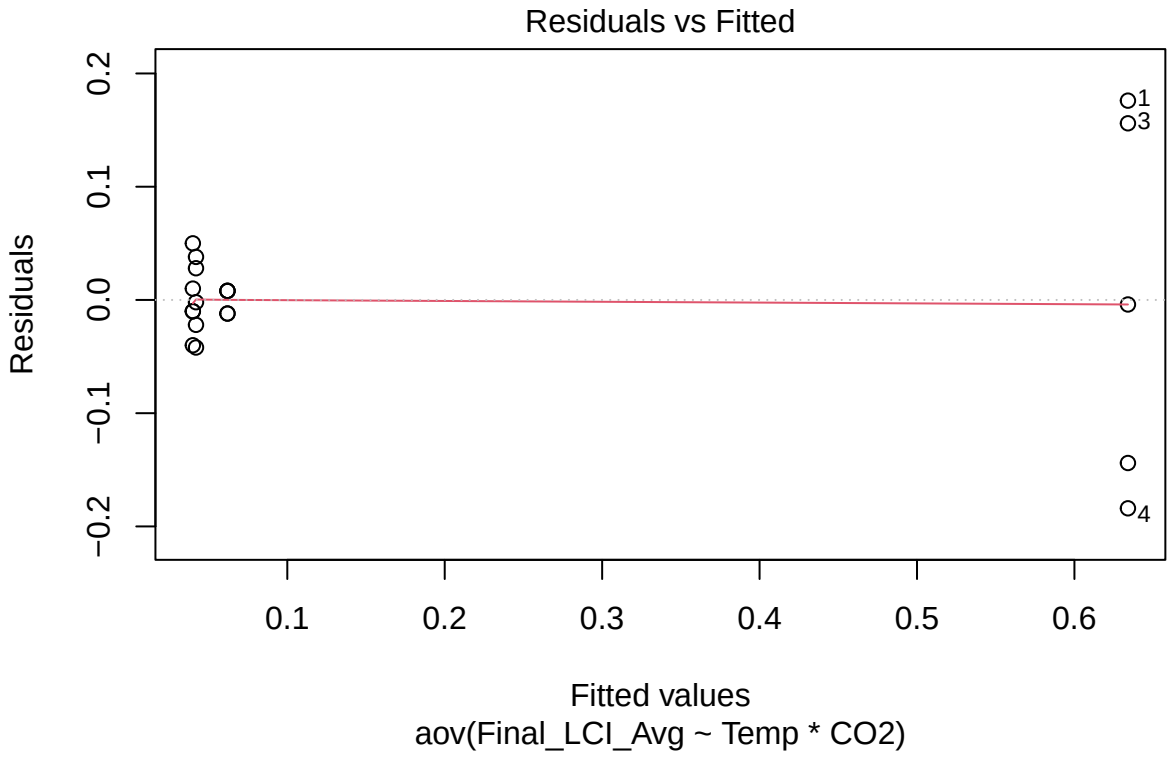
```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Temp         1 0.4061  0.4061   54.48 1.55e-06 ***
## CO2          1 0.4712  0.4712   63.21 6.01e-07 ***
## Temp:CO2     1 0.4118  0.4118   55.24 1.42e-06 ***
## Residuals   16 0.1193  0.0075
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

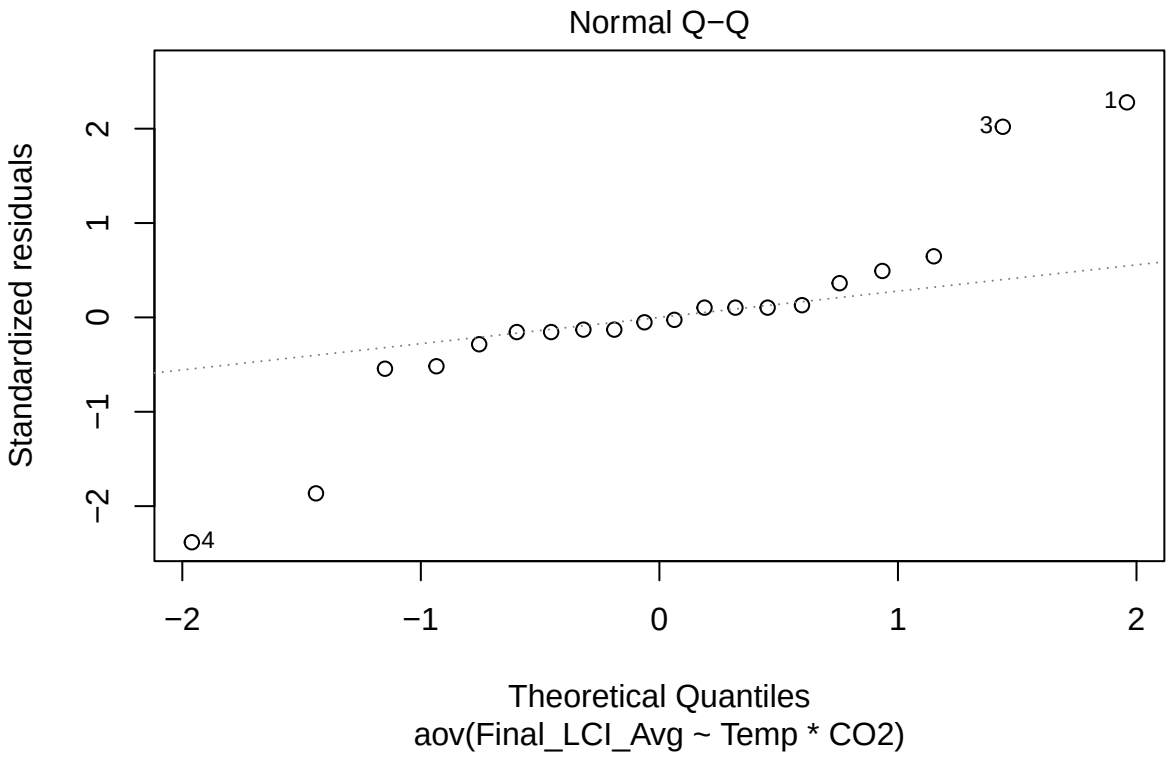
```
TukeyHSD(aovLCIrose)
```

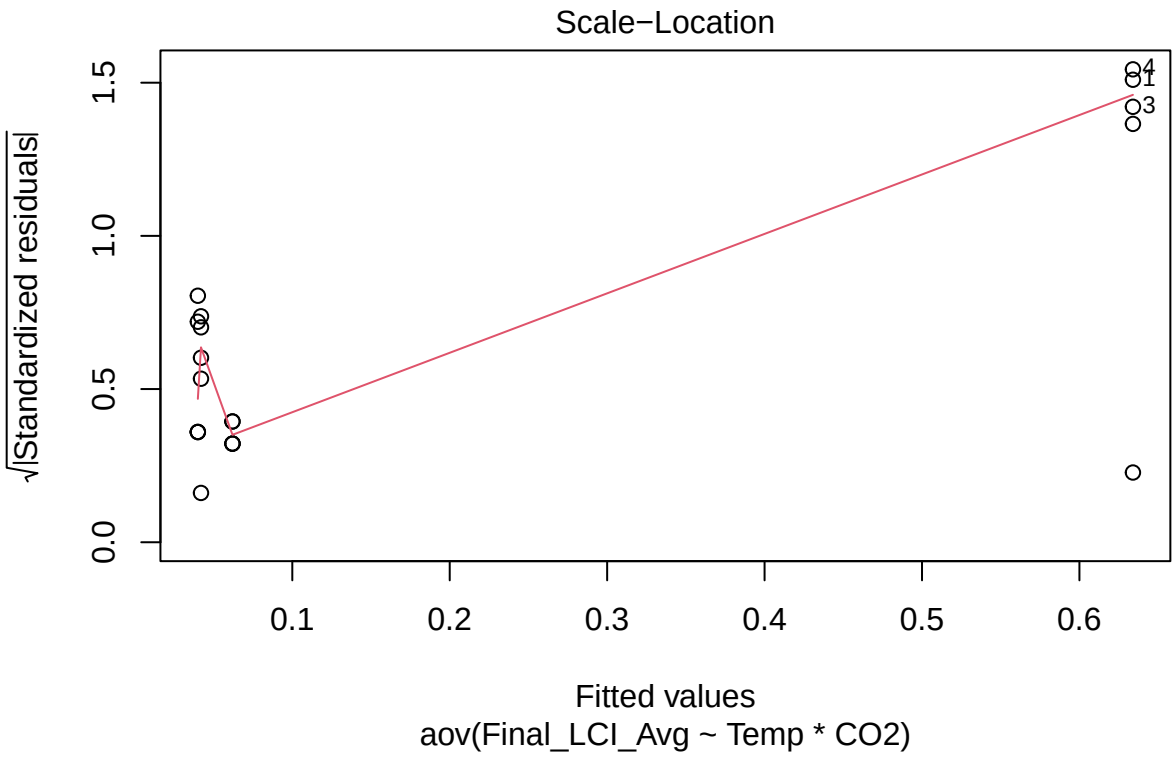
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Final_LCI_Avg ~ Temp * CO2, data = roseLCI)
##
## $Temp
##        diff       lwr       upr   p adj
## 38-30 0.285 0.2031431 0.3668569 1.6e-06
##
## $CO2
##          diff       lwr       upr p adj
## 800-400 0.307 0.2251431 0.3888569 6e-07
##
## $`Temp:CO2`
```

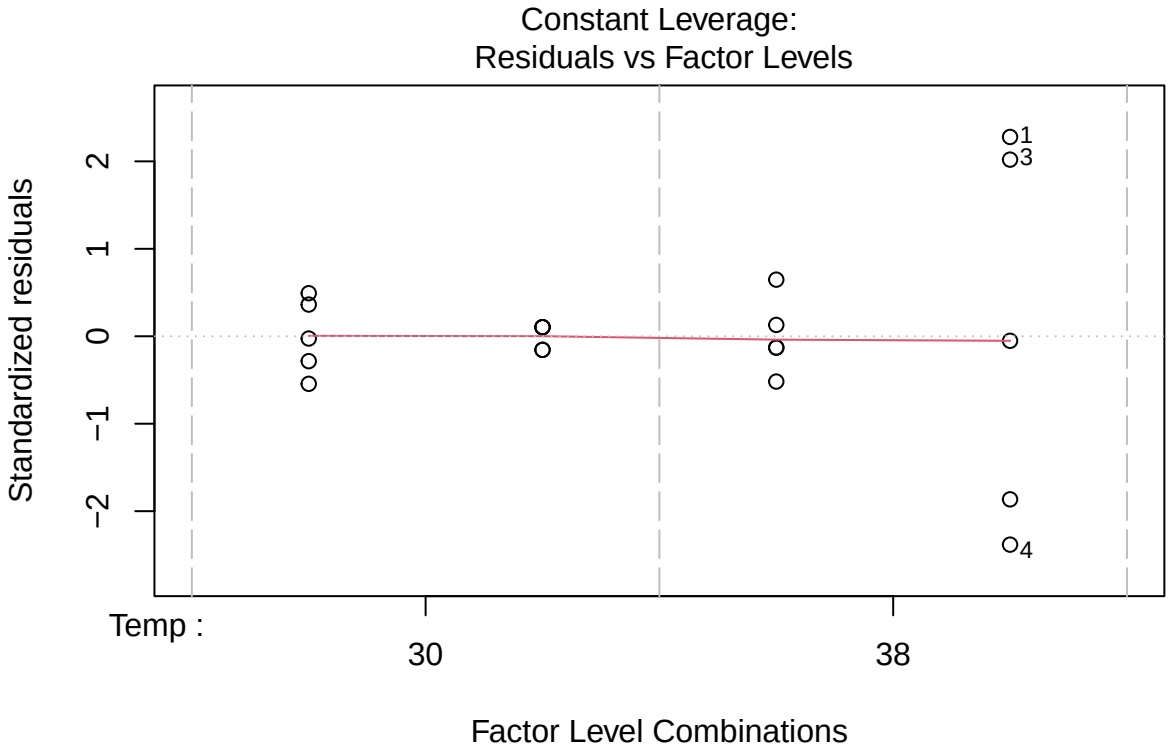
```
##                  diff        lwr       upr     p adj
## 38:400-30:400 -0.002 -0.1582337 0.1542337 0.9999816
## 30:800-30:400  0.020 -0.1362337 0.1762337 0.9826019
## 38:800-30:400  0.592  0.4357663 0.7482337 0.0000000
## 30:800-38:400  0.022 -0.1342337 0.1782337 0.9771254
## 38:800-38:400  0.594  0.4377663 0.7502337 0.0000000
## 38:800-30:800  0.572  0.4157663 0.7282337 0.0000001
```

```
plot(aovLCIrose)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(Final_LCI_Avg ~ Temp * CO2)
1
3
4
−2
−1
0
1
2


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
0.5
0.6
4
1
3
Fitted values
aov(Final_LCI_Avg ~ Temp * CO2)




```
#no LCI data pass bartlett test, suggesting unequal variance between treatment groups. ANOVA is not app

bbean.kruskal<-kruskal.test(Final_LCI_Avg ~ interaction(Temp,CO2), data = bbeanLCI)

mint.kruskal<-kruskal.test(Final_LCI_Avg ~ interaction(Temp,CO2), data = mintLCI)

rose.kruskal<-kruskal.test(Final_LCI_Avg ~ interaction(Temp,CO2), data = roseLCI)
```

Run Tukey test and assign Tukey comparison letters to a list, for use in summary table

```
bbean.tukey<-TukeyHSD(angle.bbean.aov)
bbean.HSD<-multcompLetters4(angle.bbean.aov,bbean.tukey)
bbean.Tukey<-as.data.frame.list(bbean.HSD$`Temp:CO2`)
bbean.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Warming', 'eCO2', 'Control'))

tomato.tukey<-TukeyHSD(angle.tomato.aov)
tomato.HSD<-multcompLetters4(angle.tomato.aov,tomato.tukey)
tomato.Tukey<-as.data.frame.list(tomato.HSD$`Temp:CO2`)
tomato.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Warming', 'eCO2', 'Control'))

eggplant.tukey<-TukeyHSD(angle.eggplant.aov)
eggplant.HSD<-multcompLetters4(angle.eggplant.aov,eggplant.tukey)
eggplant.Tukey<-as.data.frame.list(eggplant.HSD$`Temp:CO2`)
eggplant.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Warming', 'eCO2', 'Control'))

gcherry.tukey<-TukeyHSD(angle.gcherry.aov)
gcherry.HSD<-multcompLetters4(angle.gcherry.aov,gcherry.tukey)
```

```
gcherry.Tukey<-as.data.frame.list(gcherry.HSD$`Temp:CO2`)
gcherry.Tukey$Treatment<-as.factor(c('eCO2','Warming+eCO2', 'Warming', 'Control'))

hibiscus.tukey<-TukeyHSD(angle.hibiscus.aov)
hibiscus.HSD<-multcompLetters4(angle.hibiscus.aov,hibiscus.tukey)
hibiscus.Tukey<-as.data.frame.list(hibiscus.HSD$`Temp:CO2`)
hibiscus.Tukey$Treatment<-as.factor(c( 'eCO2','Warming+eCO2', 'Warming', 'Control'))

#TukeyHSD(angle.mint.aov)

nasturtium.tukey<-TukeyHSD(angle.nasturtium.aov)
nasturtium.HSD<-multcompLetters4(angle.nasturtium.aov,nasturtium.tukey)
nasturtium.Tukey<-as.data.frame.list(nasturtium.HSD$`Temp:CO2`)
nasturtium.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Control' , 'eCO2','Warming'))

pepper.tukey<-TukeyHSD(angle.pepper.aov)
pepper.HSD<-multcompLetters4(angle.pepper.aov,pepper.tukey)
pepper.Tukey<-as.data.frame.list(pepper.HSD$`Temp:CO2`)
pepper.Tukey$Treatment<-as.factor(c( 'eCO2', 'Warming','Control', 'Warming+eCO2'))

potato.tukey<-TukeyHSD(angle.potato.aov)
potato.HSD<-multcompLetters4(angle.potato.aov,potato.tukey)
potato.Tukey<-as.data.frame.list(potato.HSD$`Temp:CO2`)
potato.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Warming', 'eCO2', 'Control'))

yarrow.tukey<-TukeyHSD(angle.yarrow.aov)
yarrow.HSD<-multcompLetters4(angle.yarrow.aov,yarrow.tukey)
yarrow.Tukey<-as.data.frame.list(yarrow.HSD$`Temp:CO2`)
yarrow.Tukey$Treatment<-as.factor(c('Control', 'Warming', 'eCO2', 'Warming+eCO2'))

#TukeyHSD(angle.rose.aov)

bbeanLCI.tukey<-TukeyHSD(aovLCIbbean)
bbeanLCI.HSD<-multcompLetters4(aovLCIbbean,bbeanLCI.tukey)
bbeanLCI.Tukey<-as.data.frame.list(bbeanLCI.HSD$`Temp:CO2`)
bbeanLCI.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'Control', 'eCO2', 'Warming'))

mintLCI.tukey<-TukeyHSD(aovLCImint)
mintLCI.HSD<-multcompLetters4(aovLCImint,mintLCI.tukey)
mintLCI.Tukey<-as.data.frame.list(mintLCI.HSD$`Temp:CO2`)
mintLCI.Tukey$Treatment<-as.factor(c('Control','Warming+eCO2' , 'eCO2', 'Warming'))

roseLCI.tukey<-TukeyHSD(aovLCIrose)
roseLCI.HSD<-multcompLetters4(aovLCIrose,roseLCI.tukey)
roseLCI.Tukey<-as.data.frame.list(roseLCI.HSD$`Temp:CO2`)
roseLCI.Tukey$Treatment<-as.factor(c('Warming+eCO2', 'eCO2', 'Warming', 'Control'))

bbean.dunn<-dunnTest(Final_LCI_Avg ~ interaction(Temp,CO2),
         data=bbeanLCI,
         method="bonferroni")
mint.dunn<-dunnTest(Final_LCI_Avg ~ interaction(Temp,CO2),
         data=mintLCI,
         method="bonferroni")
```

```
rose.dunn<-dunnTest(Final_LCI_Avg ~ interaction(Temp,CO2),
         data=roseLCI,
         method="bonferroni")
```

analysis summary tables

```
bbean.summary<- group_by(bbeanAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
bbean.summary<-merge(x = bbean.summary, y = bbean.Tukey, by = "Treatment", all.x=T, all.y=T)

tomato.summary<- group_by(tomatoAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
tomato.summary<-merge(x = tomato.summary, y = tomato.Tukey, by = "Treatment", all.x=T, all.y=T)

eggplant.summary<- group_by(eggplantAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
eggplant.summary<-merge(x = eggplant.summary, y = eggplant.Tukey, by = "Treatment", all.x=T, all.y=T)

gcherry.summary<- group_by(gcherryAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
gcherry.summary<-merge(x = gcherry.summary, y = gcherry.Tukey, by = "Treatment", all.x=T, all.y=T)

hibiscus.summary<- group_by(hibiscusAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
hibiscus.summary<-merge(x = hibiscus.summary, y = hibiscus.Tukey, by = "Treatment", all.x=T, all.y=T)


#mint.summary<- group_by(mintAngle, Temp, CO2, Treatment, Plant) %>%
#  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), #n=n())


nasturtium.summary<- group_by(nasturtiumAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
nasturtium.summary<-merge(x = nasturtium.summary, y = nasturtium.Tukey, by = "Treatment", all.x=T, all.y

pepper.summary<- group_by(pepperAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
pepper.summary<-merge(x = pepper.summary, y = pepper.Tukey, by = "Treatment", all.x=T, all.y=T)

potato.summary<- group_by(potatoAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
potato.summary<-merge(x = potato.summary, y = potato.Tukey, by = "Treatment", all.x=T, all.y=T)

yarrow.summary<- group_by(yarrowAngle, Temp, CO2, Treatment, Plant) %>%
  summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
yarrow.summary<-merge(x = yarrow.summary, y = yarrow.Tukey, by = "Treatment", all.x=T, all.y=T)

#rose.summary<- group_by(roseAngle, Temp, CO2, Treatment, Plant) %>%
 # summarise(angle=mean(na.omit(Final_Abaxial_AVG)), anglesd=sd(na.omit(Final_Abaxial_AVG)), #n=n())

bbeanLCI.summary<- group_by(bbeanLCI, Temp, CO2, Treatment, Plant) %>%
  summarise(LCI=mean(na.omit(Final_LCI_Avg)), LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
bbeanLCI.summary<-merge(x = bbeanLCI.summary, y = bbeanLCI.Tukey, by = "Treatment", all.x=T, all.y=T)

mintLCI.summary<- group_by(mintLCI, Temp, CO2, Treatment, Plant) %>%
  summarise(LCI=mean(na.omit(Final_LCI_Avg)), LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
mintLCI.summary<-merge(x = mintLCI.summary, y = mintLCI.Tukey, by = "Treatment", all.x=T, all.y=T)

roseLCI.summary<- group_by(roseLCI, Temp, CO2, Treatment, Plant) %>%
  summarise(LCI=mean(na.omit(Final_LCI_Avg)),
  LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
```

```
## `summarise()` has grouped output by 'Temp', 'CO2', 'Treatment'. You can override using the `.groups`
```

```
roseLCI.summary<-merge(x = roseLCI.summary, y = roseLCI.Tukey, by = "Treatment", all.x=T, all.y=T)

#manually entered "PostHoc" values from on Dunn test
#bbeanLCI.summary<- group_by(bbeanLCI, Temp, CO2, Treatment) %>%
#  summarise(LCI=mean(na.omit(Final_LCI_Avg)),
#            LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
#bbeanLCI.summary$PostHoc<-c("ab", "ab", "b", "a")
#mintLCI.summary<- group_by(mintLCI, Temp, CO2, Treatment) %>%
#  summarise(LCI=mean(na.omit(Final_LCI_Avg)),
#            LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
#mintLCI.summary$PostHoc<-c("a", "ab", "b", "ab")
#bbean.summary<-merge(x = bbean.summary, y = bbean.Tukey, by = "Treatment", all.x=T, all.y=T)
#roseLCI.summary<-group_by(roseLCI, Temp, CO2, Treatment) %>%
#  summarise(LCI=mean(na.omit(Final_LCI_Avg)),
#            LCIsd=sd(na.omit(Final_LCI_Avg)), n=n())
#roseLCI.summary$PostHoc<-c("b","ab","b","a")

bbean.summary
```

```
##      Treatment Temp CO2      Plant    angle   anglesd n Letters
## 1      Control   29 400 P.vulgaris 51.66500 3.4529649 4       b
## 2         eCO2   29 800 P.vulgaris 55.58250 4.6515042 4      ab
## 3      Warming   37 400 P.vulgaris 58.83250 2.7829526 4      ab
## 4 Warming+eCO2   37 800 P.vulgaris 62.55333 0.6925557 3       a
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 b          FALSE           TRUE
## 2                ab           TRUE           TRUE
## 3                ab           TRUE           TRUE
## 4                 a           TRUE          FALSE
```

```
tomato.summary
```

```
##      Treatment Temp CO2          Plant    angle  anglesd n Letters
## 1      Control   30 400 S.lycopersicum 35.06250 4.588822 4       c
## 2         eCO2   30 800 S.lycopersicum 40.16667 2.843120 3       c
## 3      Warming   38 400 S.lycopersicum 53.00000 4.392228 4       b
## 4 Warming+eCO2   38 800 S.lycopersicum 68.66667 2.649686 3       a
##   monospacedLetters LetterMatrix.a LetterMatrix.b LetterMatrix.c
## 1                 c          FALSE          FALSE           TRUE
## 2                 c          FALSE          FALSE           TRUE
## 3                 b          FALSE           TRUE          FALSE
## 4                 a           TRUE          FALSE          FALSE
```

```
eggplant.summary
```

```
##      Treatment Temp CO2       Plant    angle  anglesd n Letters
## 1      Control   30 400 S.melongena 33.77667 1.348938 3       b
## 2         eCO2   30 800 S.melongena 35.83250 1.234838 4       b
## 3      Warming   38 400 S.melongena 45.91750 4.887381 4       a
## 4 Warming+eCO2   38 800 S.melongena 49.25000 2.844164 4       a
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 b          FALSE           TRUE
## 2                 b          FALSE           TRUE
## 3                 a           TRUE          FALSE
## 4                 a           TRUE          FALSE
```

```
gcherry.summary
```

```
##      Treatment Temp CO2      Plant    angle  anglesd n Letters
## 1      Control   30 400 P.pruinosa 31.45833 3.374228 6       b
## 2         eCO2   30 800 P.pruinosa 41.04167 4.879592 6       a
## 3      Warming   38 400 P.pruinosa 33.54167 3.719599 6       b
## 4 Warming+eCO2   38 800 P.pruinosa 33.91667 3.888016 6       b
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 b          FALSE           TRUE
## 2                 a           TRUE          FALSE
## 3                 b          FALSE           TRUE
## 4                 b          FALSE           TRUE
```

```
hibiscus.summary
```

```
##      Treatment Temp CO2           Plant    angle   anglesd n Letters    a
## 1      Control   30 400 H.rosa-sinensis 33.66667 10.105060 3       a TRUE
## 2         eCO2   30 800 H.rosa-sinensis 52.22000  2.458923 3       a TRUE
## 3      Warming   37 400 H.rosa-sinensis 44.89000  4.143091 3       a TRUE
## 4 Warming+eCO2   37 800 H.rosa-sinensis 48.88667 12.515176 3       a TRUE
```

```
nasturtium.summary
```

```
##      Treatment Temp CO2   Plant    angle   anglesd n Letters monospacedLetters
## 1      Control   22 400 T.majus 42.33333 13.953216 3       b                 b
## 2         eCO2   22 800 T.majus 34.44667 11.482144 3       b                 b
## 3      Warming   28 400 T.majus 33.00000 10.864571 3       b                 b
## 4 Warming+eCO2   28 800 T.majus 80.44333  7.393141 3       a                 a
##   LetterMatrix.a LetterMatrix.b
## 1          FALSE           TRUE
## 2          FALSE           TRUE
## 3          FALSE           TRUE
## 4           TRUE          FALSE
```

```
pepper.summary
```

```
##      Treatment Temp CO2    Plant  angle  anglesd n Letters monospacedLetters
## 1      Control   28 400 C.annuum 44.600 5.117074 5       b                 b
## 2         eCO2   28 800 C.annuum 56.250 4.177232 4       a                 a
## 3      Warming   36 400 C.annuum 56.068 3.601204 5       a                 a
## 4 Warming+eCO2   36 800 C.annuum 41.500 7.162816 4       b                 b
##   LetterMatrix.a LetterMatrix.b
## 1          FALSE           TRUE
## 2           TRUE          FALSE
## 3           TRUE          FALSE
## 4          FALSE           TRUE
```

```
potato.summary
```

```
##      Treatment Temp CO2       Plant  angle  anglesd n Letters monospacedLetters
## 1      Control   24 400 S.tuberosum 32.335 4.039583 6       c                 c
## 2         eCO2   24 800 S.tuberosum 37.055 3.085727 6      bc                bc
## 3      Warming   32 400 S.tuberosum 41.335 5.443366 6       b                 b
## 4 Warming+eCO2   32 800 S.tuberosum 56.335 4.936561 4       a                 a
##   LetterMatrix.a LetterMatrix.b LetterMatrix.c
## 1          FALSE          FALSE           TRUE
## 2          FALSE           TRUE           TRUE
## 3          FALSE           TRUE          FALSE
## 4           TRUE          FALSE          FALSE
```

```
bbeanLCI.summary
```

```
##      Treatment Temp CO2      Plant       LCI      LCIsd n Letters
## 1      Control   29 400 P.vulgaris 0.1050000 0.08346656 4      ab
## 2         eCO2   29 800 P.vulgaris 0.1025000 0.09742518 4       b
## 3      Warming   37 400 P.vulgaris 0.0325000 0.04272002 4       b
## 4 Warming+eCO2   37 800 P.vulgaris 0.4033333 0.25774665 3       a
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                ab           TRUE           TRUE
## 2                 b          FALSE           TRUE
## 3                 b          FALSE           TRUE
## 4                a            TRUE          FALSE
```

```
mintLCI.summary
```

```
##      Treatment Temp CO2       Plant       LCI      LCIsd n Letters
## 1      Control   22 400 M.xpiperita 1.4666667 0.68420270 3       a
## 2         eCO2   22 800 M.xpiperita 0.4700000 0.10000000 3       b
```

```
## 3      Warming   28 400 M.xpiperita 0.2500000 0.01732051 3       b
## 4 Warming+eCO2   28 800 M.xpiperita 0.7666667 0.11590226 3      ab
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 a            TRUE          FALSE
## 2                 b           FALSE           TRUE
## 3                 b           FALSE           TRUE
## 4                ab            TRUE           TRUE
```

```
roseLCI.summary
```

```
##      Treatment Temp CO2        Plant   LCI      LCIsd n Letters
## 1      Control   30 400 R.multiflora 0.042 0.03346640 5       b
## 2         eCO2   30 800 R.multiflora 0.062 0.01095445 5       b
## 3      Warming   38 400 R.multiflora 0.040 0.03316625 5       b
## 4 Warming+eCO2   38 800 R.multiflora 0.634 0.16577093 5       a
##   monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 b           FALSE           TRUE
## 2                 b           FALSE           TRUE
## 3                 b           FALSE           TRUE
## 4                 a            TRUE          FALSE
```

Graphing

```
My_cols<-c("#93CCC3FF","#881D18FF","#E3604CFF","#E4D1C2FF","F9F4F0FF")

bbeanplot<-ggplot(bbean.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

tomatoplot<-ggplot(tomato.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
```

```
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

eggplantplot<-ggplot(eggplant.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

gcherryplot<-ggplot(gcherry.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

hibiscusplot<-ggplot(hibiscus.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 18, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))
```

```
#mint.plot<-ggplot(mint.summary, aes(x=Treatment, y=angle, fill = TRUE))+
#  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
#  scale_fill_manual(values = My_cols)+
#  labs(x = "Treatment", y = "Leaf Angle (°)")+
#  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
#  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 13)+
#  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
#        plot.background = element_rect(fill = "#F9F4F0FF"),
#        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
#        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
#        axis.line=element_line(colour="black"),
#        axis.title.x = element_text(size = 42),
#        axis.text.x = element_text(size = 36, colour = 'black'),
#        axis.title.y = element_text(size = 42),
#        axis.text.y = element_text(size = 36, colour = 'black'))

nasturtiumplot<-ggplot(nasturtium.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 20, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

pepperplot<-ggplot(pepper.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

potatoplot<-ggplot(potato.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
```

```
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

yarrowplot<-ggplot(yarrow.summary, aes(x=Treatment, y=angle, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "Leaf Angle (°)")+
  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 15, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

# geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
#  scale_fill_manual(values = My_cols)+
#  labs(x = "Treatment", y = "Leaf Angle (°)")+
#  geom_errorbar(aes(ymin = angle-anglesd, ymax = angle+anglesd), width = 0.2)+
#  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = 10, size = 13)+
#  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
#        plot.background = element_rect(fill = "#F9F4F0FF"),
#        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
#        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
#        axis.line=element_line(colour="black"),
#        axis.title.x = element_text(size = 42),
#        axis.text.x = element_text(size = 36, colour = 'black'),
#        axis.title.y = element_text(size = 42),
#        axis.text.y = element_text(size = 36, colour = 'black'))
```

LCI Graphs

```
My_cols<-c("#93CCC3FF","#881D18FF","#E3604CFF","#E4D1C2FF","F9F4F0FF")

bbeanLCIplot<-ggplot(bbeanLCI.summary, aes(x=Treatment, y=LCI, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "LCI")+
```

```
  geom_errorbar(aes(ymin = LCI-LCIsd, ymax = LCI+LCIsd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = .5, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

mintLCIplot<-ggplot(mintLCI.summary, aes(x=Treatment, y=LCI, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "LCI")+
  geom_errorbar(aes(ymin = LCI-LCIsd, ymax = LCI+LCIsd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = .5, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))

roseLCIplot<-ggplot(roseLCI.summary, aes(x=Treatment, y=LCI, fill = TRUE))+
  geom_bar(stat='identity', color = "black", width = 0.8, show.legend = FALSE)+
  scale_fill_manual(values = My_cols)+
  labs(x = "Treatment", y = "LCI")+
  geom_errorbar(aes(ymin = LCI-LCIsd, ymax = LCI+LCIsd), width = 0.2)+
  geom_text(aes(label = Letters), nudge_x = 0, nudge_y = .5, size = 8)+
  theme(panel.background = element_rect(fill = "#F9F4F0FF", color = "#F9F4F0FF"),
        plot.margin = margin(1.5,.5,1,0.5, "cm"),
        plot.background = element_rect(fill = "#F9F4F0FF"),
        panel.grid.major = element_line(color = "#E3604CFF", linetype = 'dotted'),
        panel.grid.minor = element_line(color ="#E3604CFF", linetype = 'dotted'),
        axis.line=element_line(colour="black"),
        axis.title.x = element_text(size = 24),
        axis.text.x = element_text(size = 18, colour = 'black', angle= 45, hjust=1),
        axis.title.y = element_text(size = 24),
        axis.text.y = element_text(size = 18, colour = 'black'))
```

Layout for data visualization

Layout

```
Angle.Poster<-ggarrange(bbeanplot, tomatoplot, eggplantplot, gcherryplot, hibiscusplot, nasturtiumplot,
    labels = c('Bush Bean', 'Tomato', 'Eggplant', 'Ground Cherry', 'Hibiscus', 'Nasturtium', 'Pepper',
    font.label= list(size = 20, color = 'black'),
    label.x = 0,
```

```
    label.y = 1,
    align = 'hv',
    ncol=3,nrow=4)
png(file="Angle.Poster.png", height = 5*320, width = 2.5*320)
Angle.Poster
dev.off()
```

```
## pdf
##   2
```

```
SummaryAngle<-bind_rows(bbean.summary, tomato.summary, eggplant.summary, gcherry.summary, hibiscus.summa

SummaryLCI<-bind_rows(bbeanLCI.summary, mintLCI.summary, roseLCI.summary)

DryMassSummary<- group_by(SurveyAngle, Plant, Treatment) %>%
  summarise(Mass=mean(na.omit(DryMass)), Masssd=sd(na.omit(DryMass)), n=n())
```

```
## `summarise()` has grouped output by 'Plant'. You can override using the `.groups` argument.
```

```
SummaryAngle
```

```
##       Treatment Temp CO2           Plant    angle    anglesd n Letters
## 1       Control   29 400      P.vulgaris 51.66500  3.4529649 4       b
## 2          eCO2   29 800      P.vulgaris 55.58250  4.6515042 4      ab
## 3       Warming   37 400      P.vulgaris 58.83250  2.7829526 4      ab
## 4  Warming+eCO2   37 800      P.vulgaris 62.55333  0.6925557 3       a
## 5       Control   30 400  S.lycopersicum 35.06250  4.5888225 4       c
## 6          eCO2   30 800  S.lycopersicum 40.16667  2.8431204 3       c
## 7       Warming   38 400  S.lycopersicum 53.00000  4.3922280 4       b
## 8  Warming+eCO2   38 800  S.lycopersicum 68.66667  2.6496855 3       a
## 9       Control   30 400     S.melongena 33.77667  1.3489379 3       b
## 10         eCO2   30 800     S.melongena 35.83250  1.2348380 4       b
## 11      Warming   38 400     S.melongena 45.91750  4.8873809 4       a
## 12 Warming+eCO2   38 800     S.melongena 49.25000  2.8441636 4       a
## 13      Control   30 400      P.pruinosa 31.45833  3.3742283 6       b
## 14         eCO2   30 800      P.pruinosa 41.04167  4.8795919 6       a
## 15      Warming   38 400      P.pruinosa 33.54167  3.7195990 6       b
## 16 Warming+eCO2   38 800      P.pruinosa 33.91667  3.8880158 6       b
## 17      Control   30 400 H.rosa-sinensis 33.66667 10.1050598 3       a
## 18         eCO2   30 800 H.rosa-sinensis 52.22000  2.4589225 3       a
## 19      Warming   37 400 H.rosa-sinensis 44.89000  4.1430906 3       a
## 20 Warming+eCO2   37 800 H.rosa-sinensis 48.88667 12.5151761 3       a
## 21      Control   22 400         T.majus 42.33333 13.9532159 3       b
## 22         eCO2   22 800         T.majus 34.44667 11.4821441 3       b
## 23      Warming   28 400         T.majus 33.00000 10.8645709 3       b
## 24 Warming+eCO2   28 800         T.majus 80.44333  7.3931410 3       a
## 25      Control   28 400        C.annuum 44.60000  5.1170744 5       b
## 26         eCO2   28 800        C.annuum 56.25000  4.1772319 4       a
## 27      Warming   36 400        C.annuum 56.06800  3.6012040 5       a
## 28 Warming+eCO2   36 800        C.annuum 41.50000  7.1628160 4       b
## 29      Control   24 400     S.tuberosum 32.33500  4.0395829 6       c
## 30         eCO2   24 800     S.tuberosum 37.05500  3.0857268 6      bc
## 31      Warming   32 400     S.tuberosum 41.33500  5.4433657 6       b
## 32 Warming+eCO2   32 800     S.tuberosum 56.33500  4.9365609 4       a
##    monospacedLetters LetterMatrix.a LetterMatrix.b LetterMatrix.c    a
```

```
## 1                  b          FALSE           TRUE             NA   NA
## 2                 ab           TRUE           TRUE             NA   NA
## 3                 ab           TRUE           TRUE             NA   NA
## 4                  a           TRUE          FALSE             NA   NA
## 5                  c          FALSE          FALSE           TRUE   NA
## 6                  c          FALSE          FALSE           TRUE   NA
## 7                  b          FALSE           TRUE          FALSE   NA
## 8                  a           TRUE          FALSE          FALSE   NA
## 9                  b          FALSE           TRUE             NA   NA
## 10                 b          FALSE           TRUE             NA   NA
## 11                 a           TRUE          FALSE             NA   NA
## 12                 a           TRUE          FALSE             NA   NA
## 13                 b          FALSE           TRUE             NA   NA
## 14                 a           TRUE          FALSE             NA   NA
## 15                 b          FALSE           TRUE             NA   NA
## 16                 b          FALSE           TRUE             NA   NA
## 17              <NA>             NA             NA             NA TRUE
## 18              <NA>             NA             NA             NA TRUE
## 19              <NA>             NA             NA             NA TRUE
## 20              <NA>             NA             NA             NA TRUE
## 21                 b          FALSE           TRUE             NA   NA
## 22                 b          FALSE           TRUE             NA   NA
## 23                 b          FALSE           TRUE             NA   NA
## 24                 a           TRUE          FALSE             NA   NA
## 25                 b          FALSE           TRUE             NA   NA
## 26                 a           TRUE          FALSE             NA   NA
## 27                 a           TRUE          FALSE             NA   NA
## 28                 b          FALSE           TRUE             NA   NA
## 29                 c          FALSE          FALSE           TRUE   NA
## 30                bc          FALSE           TRUE           TRUE   NA
## 31                 b          FALSE           TRUE          FALSE   NA
## 32                 a           TRUE          FALSE          FALSE   NA
```

```
SummaryLCI
```

```
##       Treatment Temp CO2        Plant       LCI      LCIsd n Letters
## 1       Control   29 400   P.vulgaris 0.1050000 0.08346656 4      ab
## 2          eCO2   29 800   P.vulgaris 0.1025000 0.09742518 4       b
## 3       Warming   37 400   P.vulgaris 0.0325000 0.04272002 4       b
## 4  Warming+eCO2   37 800   P.vulgaris 0.4033333 0.25774665 3       a
## 5       Control   22 400  M.xpiperita 1.4666667 0.68420270 3       a
## 6          eCO2   22 800  M.xpiperita 0.4700000 0.10000000 3       b
## 7       Warming   28 400  M.xpiperita 0.2500000 0.01732051 3       b
## 8  Warming+eCO2   28 800  M.xpiperita 0.7666667 0.11590226 3      ab
## 9       Control   30 400 R.multiflora 0.0420000 0.03346640 5       b
## 10         eCO2   30 800 R.multiflora 0.0620000 0.01095445 5       b
## 11      Warming   38 400 R.multiflora 0.0400000 0.03316625 5       b
## 12 Warming+eCO2   38 800 R.multiflora 0.6340000 0.16577093 5       a
##    monospacedLetters LetterMatrix.a LetterMatrix.b
## 1                 ab           TRUE           TRUE
## 2                  b          FALSE           TRUE
## 3                  b          FALSE           TRUE
## 4                  a           TRUE          FALSE
## 5                  a           TRUE          FALSE
## 6                  b          FALSE           TRUE
```

```
## 7                   b          FALSE           TRUE
## 8                  ab           TRUE           TRUE
## 9                   b          FALSE           TRUE
## 10                  b          FALSE           TRUE
## 11                  b          FALSE           TRUE
## 12                 a            TRUE          FALSE
```

```
DryMassSummary
```

```
## # A tibble: 44 x 5
## # Groups:   Plant [11]
##    Plant           Treatment      Mass Masssd     n
##    <chr>           <fct>         <dbl>  <dbl> <int>
##  1 A.millefolium   Control       1.87   0.293     5
##  2 A.millefolium   eCO2          3.23   0.719     5
##  3 A.millefolium   Warming       2.34   0.746     5
##  4 A.millefolium   Warming+eCO2  2.42   1.22      5
##  5 C.annuum        Control       0.978  0.330     5
##  6 C.annuum        eCO2          0.838  0.224     5
##  7 C.annuum        Warming       0.506  0.195     5
##  8 C.annuum        Warming+eCO2  0.438  0.131     5
##  9 H.rosa-sinensis Control      10.2    1.08      3
## 10 H.rosa-sinensis eCO2         16.2    0.414     3
## # ... with 34 more rows
```

```
write.csv(SummaryAngle, "SummaryAngle.csv", row.names=FALSE)
write.csv(SummaryLCI, "SummaryLCI.csv", row.names=FALSE)
write.csv(DryMassSummary, "SummaryDryMass.csv", row.names=FALSE)
```