Focus of the preceding analyses:

While the original study looked primarily at community composition, I want to take a different approach and investigate whether or not the presence of clonal species acts as a form of stress on non-clonal species. I will use plant biomass as a predictor of perceived stress on behalf of the plant; biomass has been associated with a stress response in plants (support), and thus using this metric as a stress measurement has been supported in the past. Though I cannot take this study to the lengths I might like, I will follow it up with a discussion on how selection might act on the biomass of surviving plants within this experiment, and why this is important.

Below are the hypotheses I will be testing to address the following questions: 1) Does non-clonal plant biomass differ within each fertilizer plot by community? 2) Does clonal biomass have an effect on non-clonal biomass?

Hypothesis 1) Community type (presence of clonal vs no presence) has an effect on non-clonal plant biomass

Predictions: non-clonal plant biomass will be lower in the mixed community than in the non-mixed community

Biological Reasoning: clonal plants are effective at growing and usurping available resources and out-competing cohabitants.

Hypothesis 2) In the mixed community, clonal plant biomass will have an effect on non-clonal plant biomass

Predictions: There will be an overall decline in non-clonal plant biomass as clonal plant biomass increases; this declination will be more pronounced in small-patch fertilizer treatments based on the recruitment and foraging behavior of clonal plant species in such circumstances, as noted by the paper above

Biological Reasoning: clonal plants are effective at growing and usurping available resources and out-competing cohabitants.

Loading Required Packages:

```
library(tidyverse)
```

```
## -- Attaching packages ----------------------------------------------------------------------- tidyverse 1
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.1
## v tidyr   1.1.1     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts -------------------------------------------------------------------------- tidyverse_conflic
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(readxl)
library(nlme)
```

```
##
## Attaching package: 'nlme'
```

```
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack

##
## Attaching package: 'lme4'

## The following object is masked from 'package:nlme':
##
##     lmList
```

```
library(lattice)
library(grid)
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##     combine
```

```
library(car)
```

```
## Loading required package: carData

## Registered S3 methods overwritten by 'car':
##   method                          from
##   influence.merMod                lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod         lme4
##   dfbetas.influence.merMod        lme4

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```

Hypothesis 1: Community type and non-clonal plant biomass

1) Data processing

```
#The data
dat <- read_csv("~/Repos/School/BioStats/Lab6/Richness_and_Biomass_Lab6.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]

## Parsed with column specification:
## cols(
##   X1 = col_double(),
```

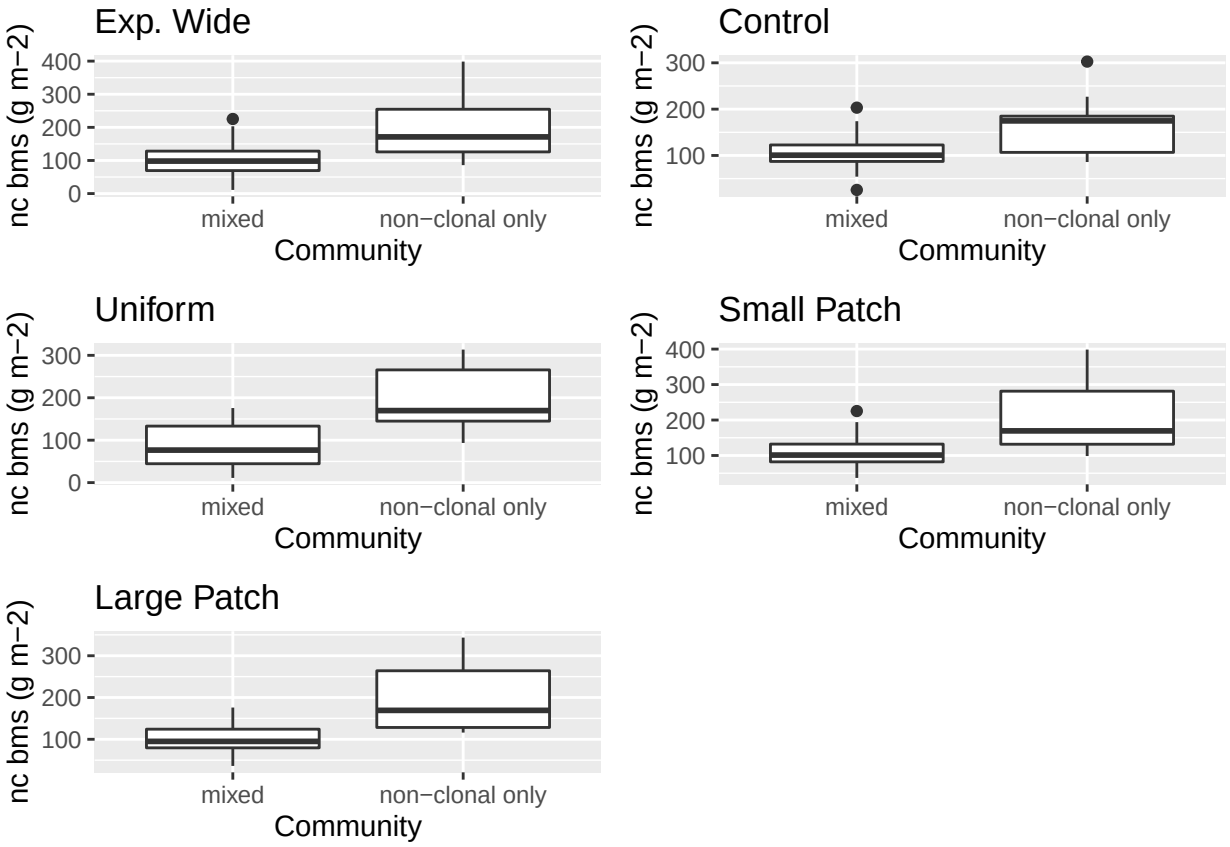
```
##   Year = col_double(),
##   Block = col_double(),
##   Community = col_character(),
##   FertilizerTreatment = col_character(),
##   TotalSppNum = col_double(),
##   NCSppNum = col_double(),
##   ClonSppNum = col_double(),
##   TotalBMS = col_double(),
##   NCBMS = col_double(),
##   ClonBMS = col_double()
## )
```

```
#Parsing
dat$Community <- as.factor(dat$Community)
dat$FertilizerTreatment <- as.factor(dat$FertilizerTreatment)

#Subsetting by fertilization treatment

#Control
controlDat <- dat %>%
  filter( FertilizerTreatment == "CO")
#Uniform Fert. Treatment
unDat <- dat %>%
  filter( FertilizerTreatment == "UN")
#Small Patch treatment
spDat <- dat %>%
  filter( FertilizerTreatment == "SP")
#Large Patch treatment
lpDat <- dat %>%
  filter( FertilizerTreatment == "LP")
```

2) Preliminary Visualizations

```
#Preliminary visualizations

#Quick prelim vis plotting function
prelimVisPlots <- function(d1,t1, d2, t2, d3, t3, d4, t4, d5, t5, ylab) {
  p1 <- ggplot(d1, aes(Community, NCBMS)) +
    geom_boxplot() +
    labs(y = ylab) +
    ggtitle(t1)
  p2 <- ggplot(d2, aes(Community, NCBMS)) +
    geom_boxplot() +
    labs(y = ylab) +
    ggtitle(t2)
  p3 <- ggplot(d3, aes(Community, NCBMS)) +
    geom_boxplot() +
    labs(y = ylab) +
    ggtitle(t3)
  p4 <- ggplot(d4, aes(Community, NCBMS)) +
    geom_boxplot() +
    labs(y = ylab) +
    ggtitle(t4)
  p5 <- ggplot(d5, aes(Community, NCBMS)) +
    geom_boxplot() +
```

```
    labs(y = ylab) +
    ggtitle(t5)

  gridPlot <- grid.arrange(p1, p2, p3, p4, p5)

  return(gridPlot)
}

#Vis
prelimVisPlots(dat, "Exp. Wide", controlDat, "Control", unDat, "Uniform", spDat, "Small Patch", lpDat,
```



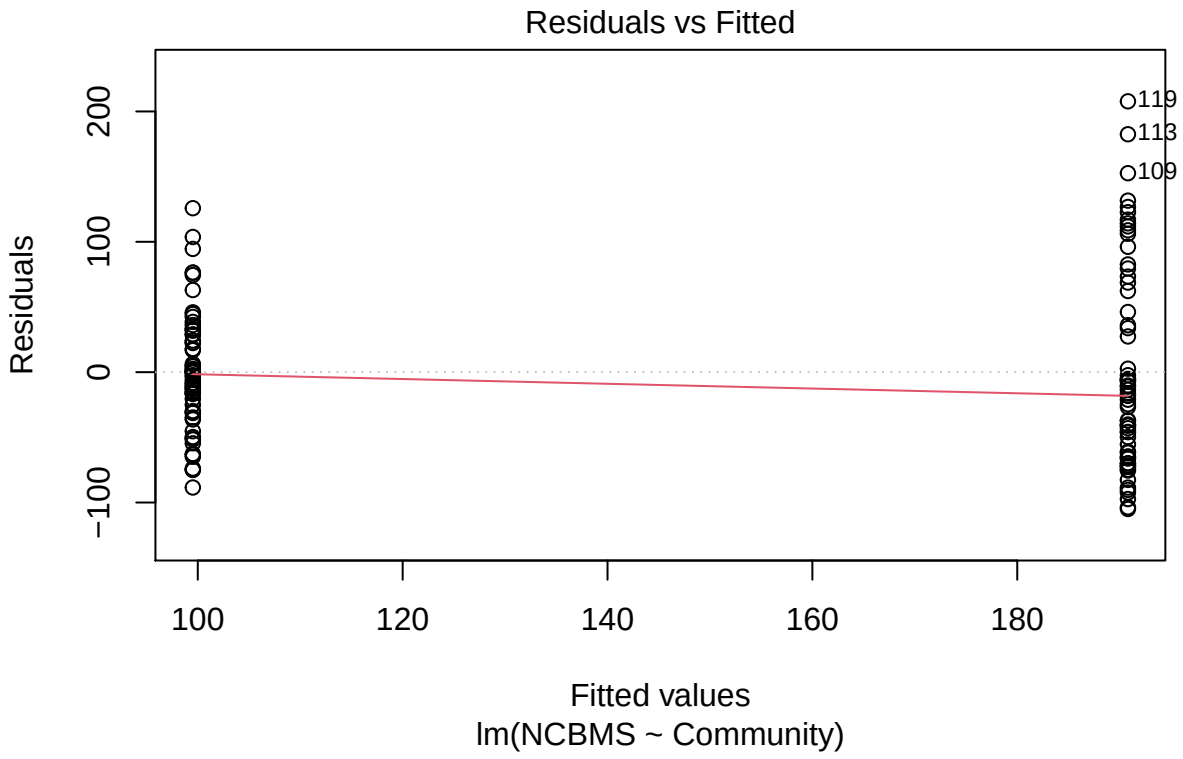

```
## TableGrob (3 x 2) "arrange": 5 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (2-2,1-1) arrange gtable[layout]
## 4 4 (2-2,2-2) arrange gtable[layout]
## 5 5 (3-3,1-1) arrange gtable[layout]
```

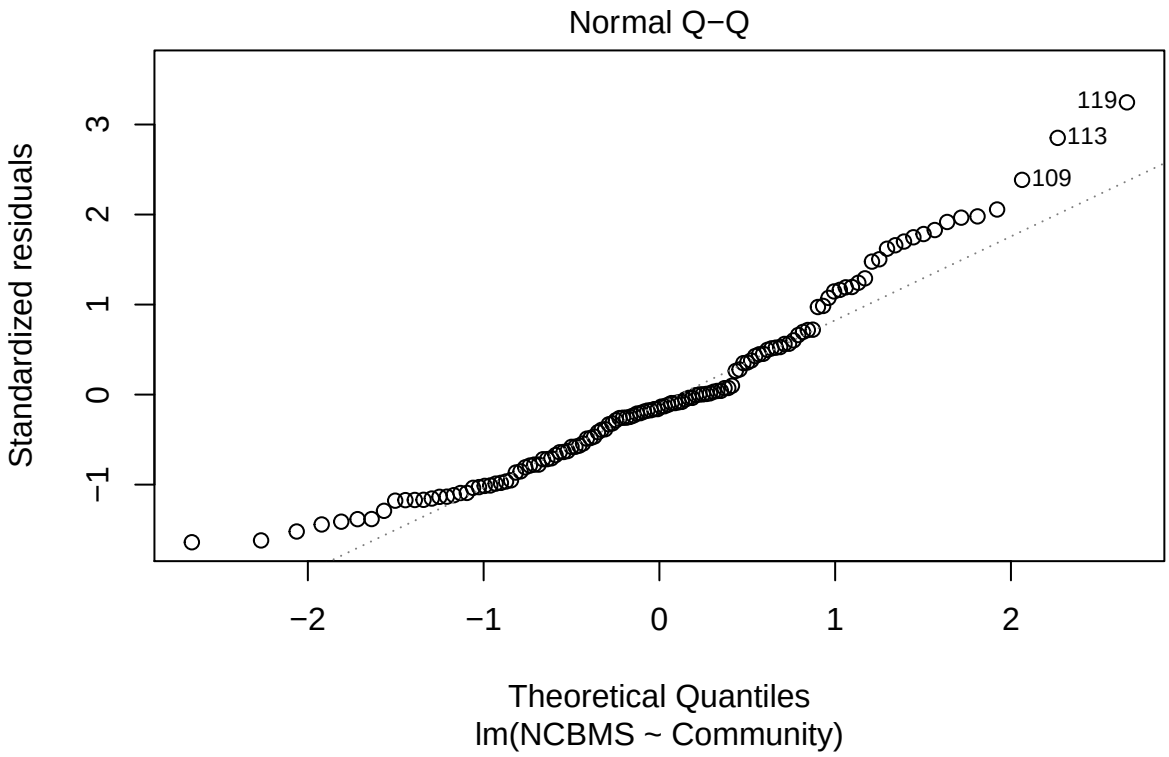
Graphically, there seems to be a clear difference in non-clonal biomass in each community experiment wide and within each fertilizer treatment

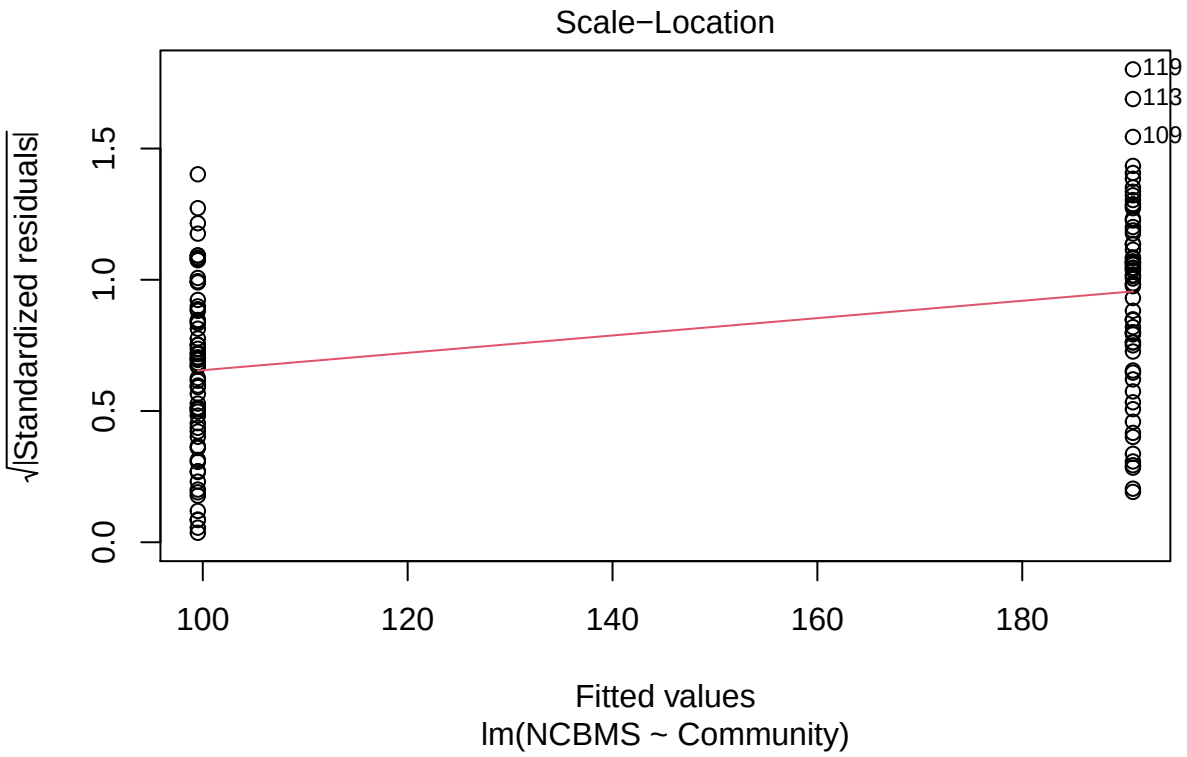
3) Modeling

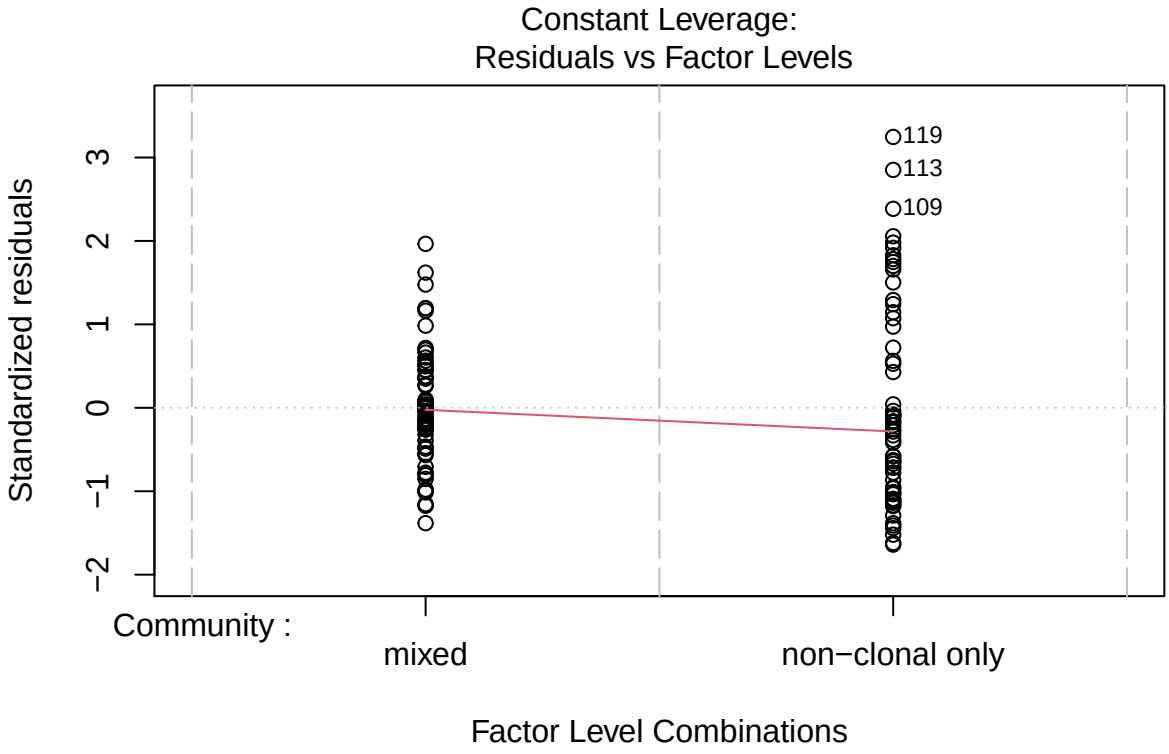
Experiment Wide: Community

```
#Experiment wide modeling: testing to see if non-clonal plant biomass in each fertilizer treatmebent di

#model
expLM <- lm(NCBMS ~ Community, data = dat)
#diagnostics plot
plot(expLM)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(NCBMS ~ Community)
119
113
109
−2
−1
0
1
2
−1
0
1
2
3


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
100
120
140
160
180
119
113
109
Fitted values
lm(NCBMS ~ Community)



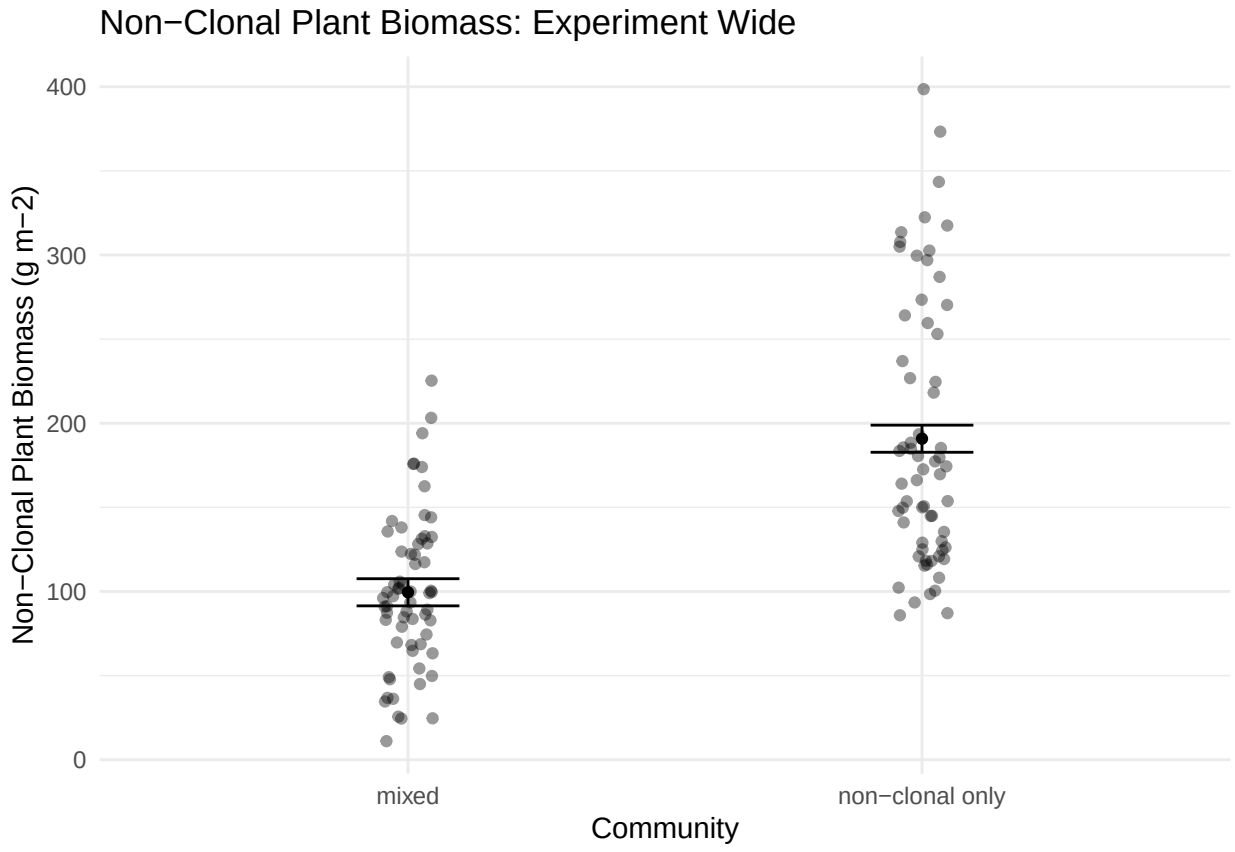
diagnostics seem fine to me

```
summary_expLM <- summary(expLM)
summary_expLM
```

```
##
## Call:
## lm(formula = NCBMS ~ Community, data = dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -104.955  -46.894   -9.439   33.470  207.765
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  99.517      8.064  12.342  < 2e-16 ***
## Communitynon-clonal only     91.291     11.404   8.005 6.76e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 64.51 on 126 degrees of freedom
## Multiple R-squared:  0.3371, Adjusted R-squared:  0.3319
## F-statistic: 64.09 on 1 and 126 DF,  p-value: 6.757e-13
```

The above model suggests that mean non-clonal biomass in the unmixed community is significantly different than that of the mixed community, where the effect size of presence of clonal species is a 91.3g/m^2 decrease in mean non-clonal plant biomass (p<.001, t = 8.0, DF = 1)

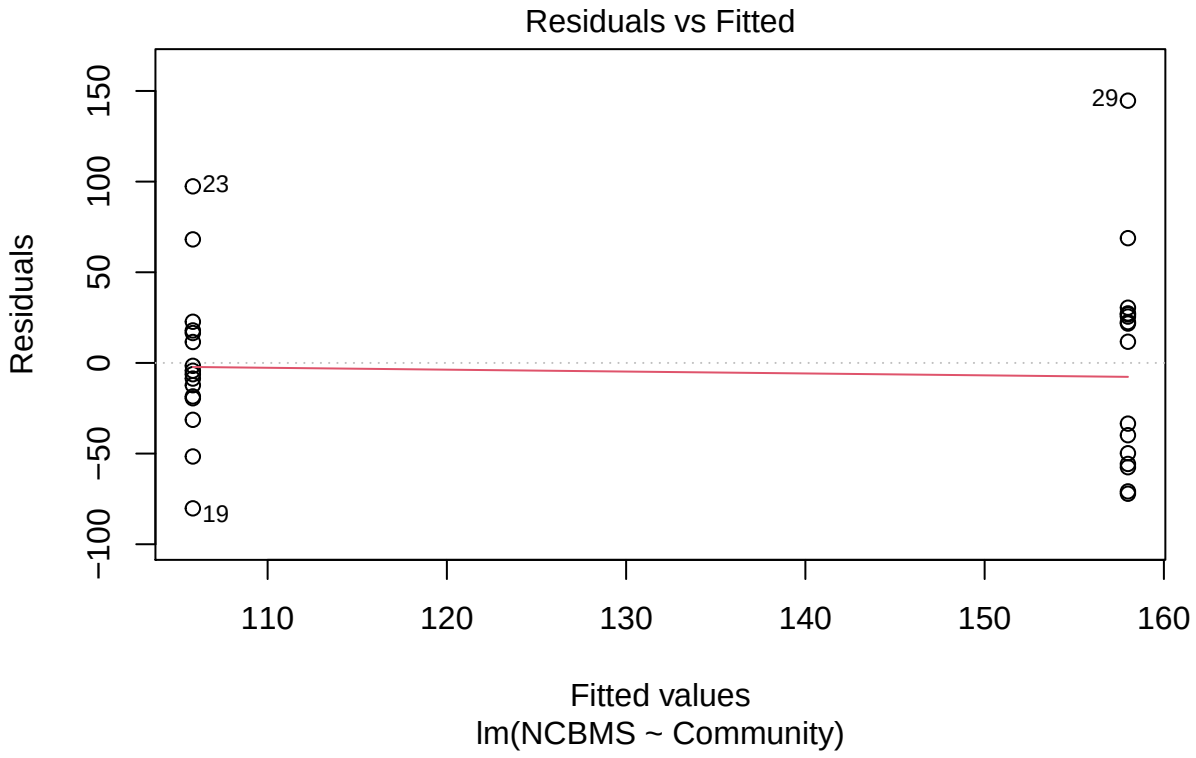
```r
#Plotting

#creating data frame with important statistics (mean, se)
explLM_ni <- lm(NCBMS ~ 0 + Community, data = dat)
summary_expLM_ni <- summary(explLM_ni)

expLM_output_df <- data.frame(cat_mean_noint = summary_expLM_ni$coefficients[, "Estimate"],
                              cat_se_noint = summary_expLM_ni$coefficients[,"Std. Error"],
                              trt_cat = levels(dat$Community))
#Creating the plot
expHyp1_plot <- ggplot(expLM_output_df, aes(trt_cat, cat_mean_noint)) +
  geom_point() +
  geom_errorbar(aes(ymin=cat_mean_noint-cat_se_noint, ymax=cat_mean_noint+cat_se_noint), width = 0.2) +
  geom_jitter(data = dat, aes(Community, NCBMS), width = .05, alpha = .4) +
  labs(x = "Community",
       y = "Non-Clonal Plant Biomass (g m-2)") +
  ggtitle(label = "Non-Clonal Plant Biomass: Experiment Wide") +
  theme_minimal()
expHyp1_plot
```

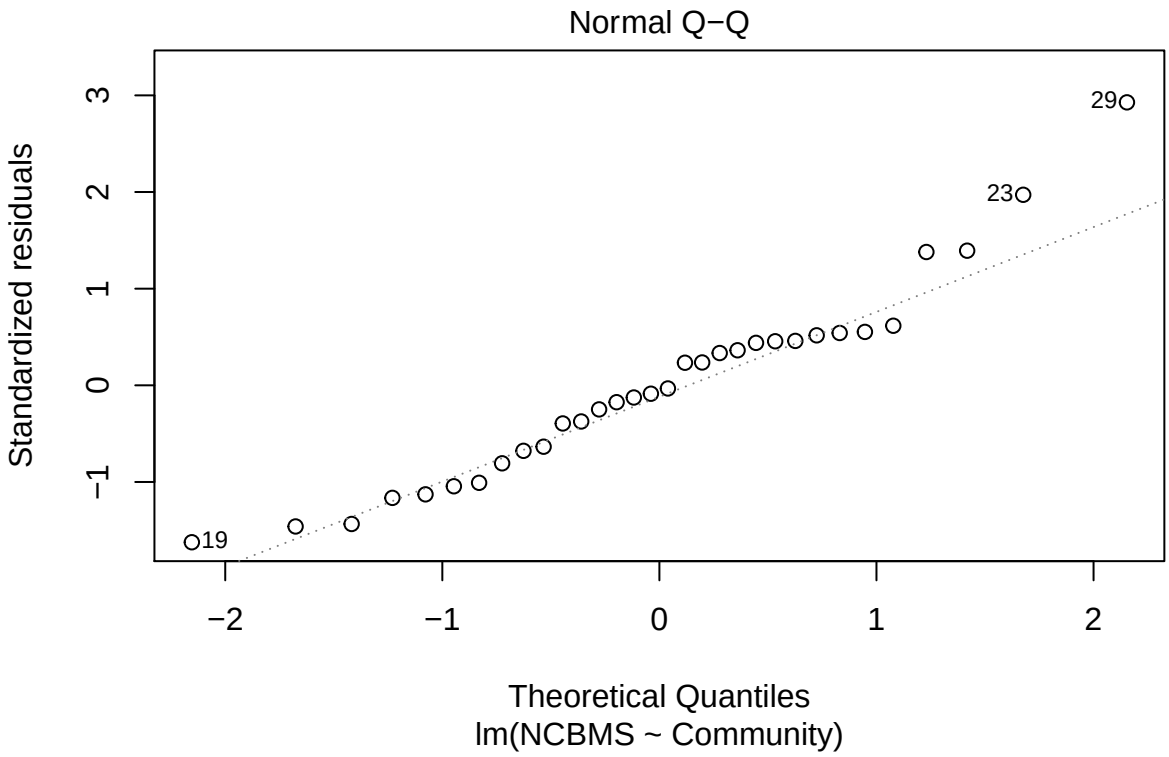


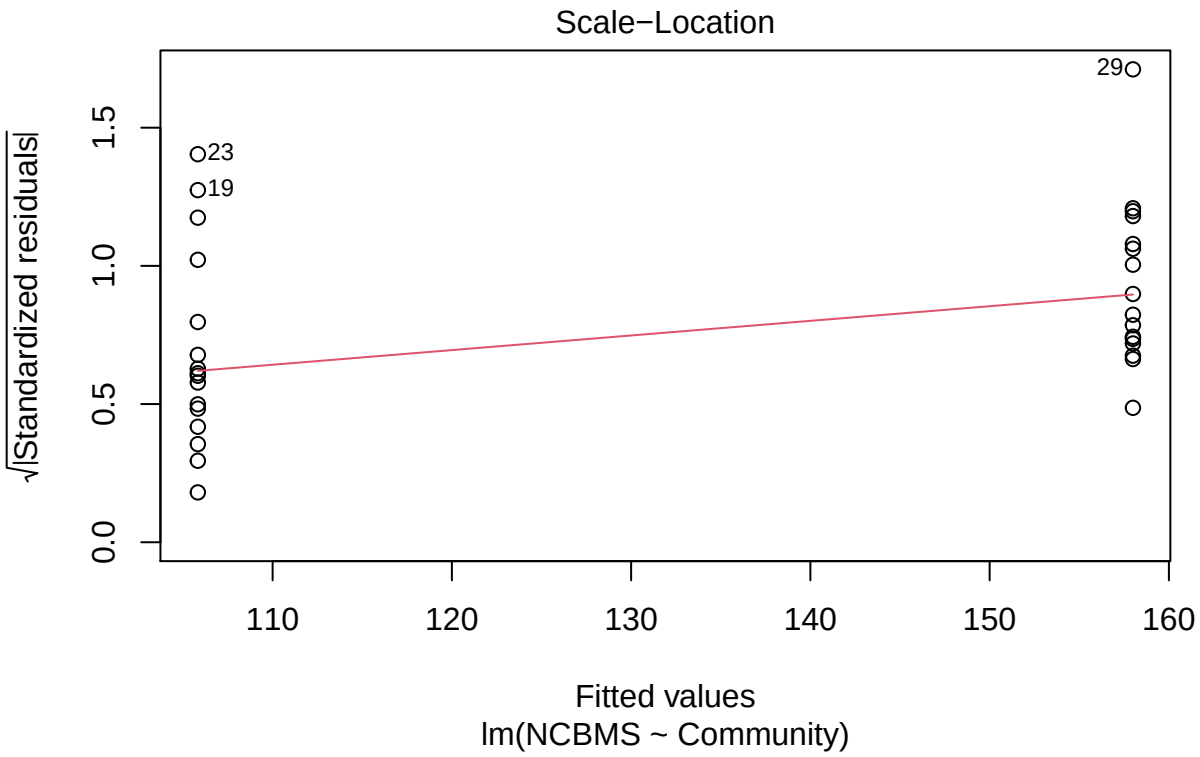
By Control: Community

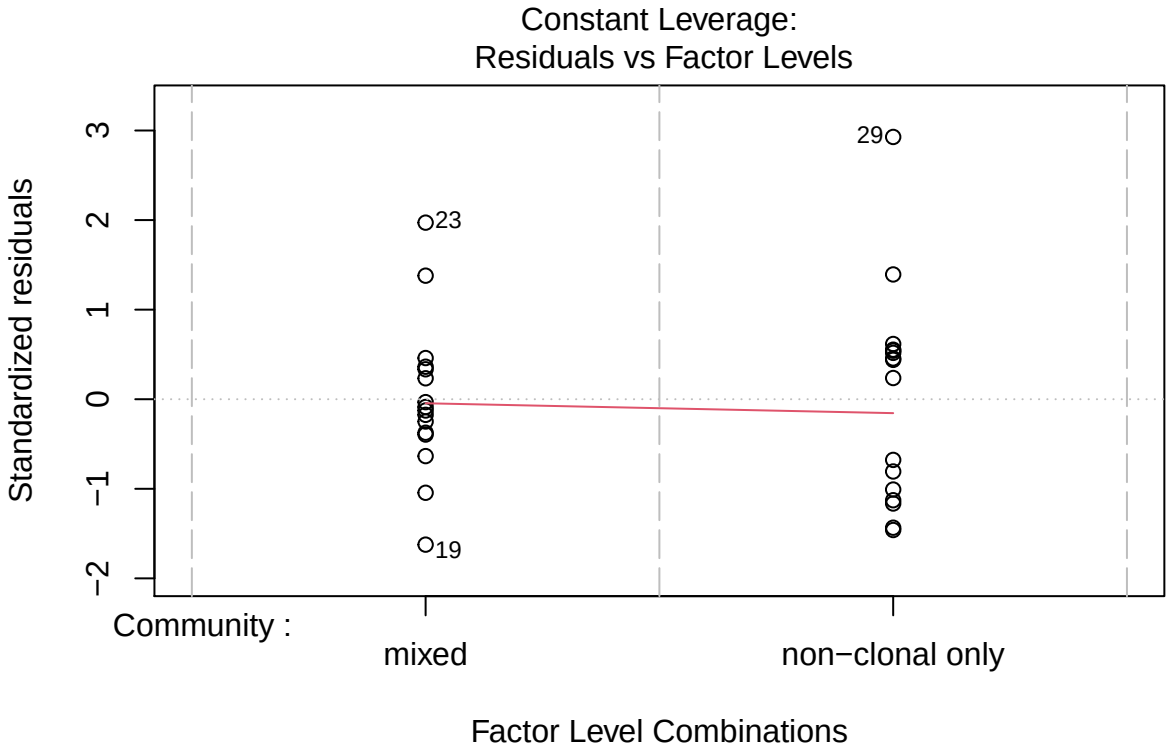
```r
#model
controlLM <- lm(NCBMS ~ Community, data = controlDat)
```

```r
#diagnostics
plot(controlLM)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(NCBMS ~ Community)
29
23
19
−2
−1
0
1
2
−1
0
1
2
3


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
23
19
29
110
120
130
140
150
160
Fitted values
lm(NCBMS ~ Community)



Diagnostics look fine to me; assumptions of normalcy met

```
summary_controlLM <- summary(controlLM)
summary_controlLM
```

```
##
## Call:
## lm(formula = NCBMS ~ Community, data = controlDat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -80.201 -35.073  -2.951  23.417 144.637
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 105.83      12.76   8.296 2.92e-09 ***
## Communitynon-clonal only     52.17      18.04   2.892  0.00706 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 51.02 on 30 degrees of freedom
## Multiple R-squared:  0.218,  Adjusted R-squared:  0.1919
## F-statistic: 8.363 on 1 and 30 DF,  p-value: 0.00706
```

the above model suggests that, within the control, non-clonal plant biomass differes significantly between communities; mean non-clonal plant mass in the unmixed community is approximately 52g/m^2 greater than that of the mixed community ($p<.01$, $DF = 2$, $T = 2.892$)

```r
#Plotting

#creating data frame with important statistics (mean, se)
controlLM_ni <- controlLM <- lm(NCBMS ~ 0 + Community, data = controlDat)
summary_controlLM_ni <- summary(controlLM_ni)

controlLM_output_df <- data.frame(cat_mean_noint = summary_controlLM_ni$coefficients[, "Estimate"],
                                  cat_se_noint = summary_controlLM_ni$coefficients[,"Std. Error"],
                                  trt_cat = levels(controlDat$Community))
#Creating the plot
controlHyp1_plot <- ggplot(controlLM_output_df, aes(trt_cat, cat_mean_noint)) +
  geom_point() +
  geom_errorbar(aes(ymin=cat_mean_noint-cat_se_noint, ymax=cat_mean_noint+cat_se_noint), width = 0.2) +
  geom_jitter(data = controlDat, aes(Community, NCBMS), width = .05, alpha = .4) +
  labs(x = "Community",
       y = "Non-Clonal Plant Biomass (g m-2)") +
  ggtitle(label = "Non-Clonal Plant Biomass: Control Treatment") +
  theme_minimal()
controlHyp1_plot
```