

Host Response

2025-08-04

```
#Load in all packages  
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.3.3
```

```
library(nlme)
```

```
## Warning: package 'nlme' was built under R version 4.3.3
```

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 4.3.3
```

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

```
## Warning: package 'Matrix' was built under R version 4.3.3
```

```
##  
## Attaching package: 'lme4'
```

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

```
library(DAAG)
```

```
## Warning: package 'DAAG' was built under R version 4.3.3
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.3
```

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.3.3
```

```
##  
## Attaching package: 'dplyr'
```

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

```
## The following objects are masked from 'package:stats':  
##  
## filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
## intersect, setdiff, setequal, union
```

```
library(MuMIn)
```

```
## Warning: package 'MuMIn' was built under R version 4.3.3
```

```
library(car)
```

```
## Warning: package 'car' was built under R version 4.3.3
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 4.3.3
```

```
##  
## Attaching package: 'car'
```

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

```
## The following object is masked from 'package:DAAG':  
##  
## vif
```

```
library(viridis)
```

```
## Warning: package 'viridis' was built under R version 4.3.3
```

```
## Loading required package: viridisLite
```

```
library(DHARMA)
```

```
## Warning: package 'DHARMA' was built under R version 4.3.3
```

```
## This is DHARMA 0.4.7. For overview type '?DHARMA'. For recent changes, type news(package = 'DHARMA')
```

```
library(FSA)
```

```
## Warning: package 'FSA' was built under R version 4.3.3

## Registered S3 methods overwritten by 'FSA':
##   method      from
##   confint.boot car
##   hist.boot   car

## ## FSA v0.9.6. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related book.

##
## Attaching package: 'FSA'

## The following object is masked from 'package:car':
##
##   bootCase
```

```
library(emmeans)
```

```
## Warning: package 'emmeans' was built under R version 4.3.3

## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
library(ggpubr)
```

```
## Warning: package 'ggpubr' was built under R version 4.3.3
```

```
library(rstatix)
```

```
## Warning: package 'rstatix' was built under R version 4.3.3

##
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':
##
##   filter
```

```
library(glmmTMB)
```

```
## Warning: package 'glmmTMB' was built under R version 4.3.3
```

```
library(boot)
```

```
## Warning: package 'boot' was built under R version 4.3.3
```

```
##
```

```
## Attaching package: 'boot'
```

```
## The following object is masked from 'package:car':
```

```
##
```

```
##      logit
```

Import the dataset

```
#Import the dataset
data <- read.csv(file.path(
  "C:/Users/Joyalea/Documents/UBCO/Thesis",
  "Final_Files",
  "RQ2_HostResponse",
  "host_response_2024.csv"
))

#Add treatment group column
data <- data %>%
  mutate(treatment = ifelse(mesocosm_id %in% c(1:7), "Control",
    ifelse(mesocosm_id %in% c(8:14), "197198",
      ifelse(mesocosm_id %in% c(15:21), "240448",
        ifelse(mesocosm_id %in% c(22:28), "240720", NA))))),
    block = ifelse(mesocosm_id %in% c(15, 20, 22, 12, 11, 14, 24, 27, 19,
      21, 25, 3, 2, 7), "A",
      ifelse(mesocosm_id %in% c(4, 17, 9, 28, 6, 1, 5, 18, 8,
        26, 16, 23, 13, 10), "B", NA)))

#Review data import
head(data)
```

```
##   mesocosm_id   species biomass copies_uL copies_20uL copies_rxn      P
## 1           1    Bromus   14.39         0         0         0 0.428
## 2           1   Festuca   31.19         0         0         0 0.189
## 3           1 Gaillardia    6.69         0         0         0 0.232
## 4           1 Taraxacum   24.34         0         0         0 0.316
## 5           2    Bromus   26.19         0         0         0 0.412
## 6           2   Festuca   40.62         0         0         0 0.197
##   seed_weight date_bio_harvested date_roots_harvested number_plants treatment
## 1          NA          27-Aug          27-Aug          2      Control
## 2          NA          27-Aug          27-Aug          3      Control
## 3          NA          27-Aug          27-Aug          3      Control
## 4          NA          27-Aug          27-Aug          3      Control
## 5          NA          27-Aug          27-Aug          3      Control
## 6          NA          27-Aug          27-Aug          3      Control
##   block
## 1     B
```

```
## 2      B
## 3      B
## 4      B
## 5      A
## 6      A
```

```
str(data)
```

```
## 'data.frame':    112 obs. of  13 variables:
## $ mesocosm_id      : int  1 1 1 1 2 2 2 2 3 3 ...
## $ species          : chr  "Bromus" "Festuca" "Gaillardia" "Taraxacum" ...
## $ biomass          : num  14.39 31.19 6.69 24.34 26.19 ...
## $ copies_uL        : num  0 0 0 0 0 0 0 0 0 0 ...
## $ copies_20uL      : num  0 0 0 0 0 0 0 0 0 0 ...
## $ copies_rxn       : num  0 0 0 0 0 0 0 0 0 0 ...
## $ P                : num  0.428 0.189 0.232 0.316 0.412 0.197 0.244 0.299 NA NA ...
## $ seed_weight      : num  NA NA NA NA NA NA NA NA NA NA ...
## $ date_bio_harvested: chr  "27-Aug" "27-Aug" "27-Aug" "27-Aug" ...
## $ date_roots_havested: chr  "27-Aug" "27-Aug" "27-Aug" "27-Aug" ...
## $ number_plants    : int  2 3 3 3 3 3 3 3 2 3 ...
## $ treatment        : chr  "Control" "Control" "Control" "Control" ...
## $ block            : chr  "B" "B" "B" "B" ...
```

```
tail(data)
```

```
##      mesocosm_id  species biomass copies_uL copies_20uL copies_rxn      P
## 107          27 Gaillardia   13.09      0.56        11.2      12.32    NA
## 108          27  Taraxacum   24.22      0.22         4.4       4.84    NA
## 109          28    Bromus   23.48      0.00         0.0       0.00 0.366
## 110          28    Festuca   72.10      0.00         0.0       0.00 0.149
## 111          28 Gaillardia   12.99      0.50        10.0      11.00 0.210
## 112          28  Taraxacum   18.06      0.00         0.0       0.00 0.243
##      seed_weight date_bio_harvested date_roots_havested number_plants treatment
## 107    0.002060          28-Aug          04-Sep           3      240720
## 108         NA          28-Aug          04-Sep           3      240720
## 109         NA          28-Aug          05-Sep           2      240720
## 110         NA          28-Aug          05-Sep           3      240720
## 111    0.001730          28-Aug          05-Sep           3      240720
## 112    0.000505          28-Aug          05-Sep           3      240720
##      block
## 107      A
## 108      A
## 109      B
## 110      B
## 111      B
## 112      B
```

```
#Convert variables to appropriate form
#mesocosm id and species id as factors
data$mesocosm_id<-as.factor(data$mesocosm_id)
data$species<-as.factor(data$species)
data$treatment<-as.factor(data$treatment)
```

```

#biomass and seed weight as numeric
data$biomass<-as.numeric(data$biomass)
data$P<-as.numeric(data$P)

#summary of dataset
summary(data$mesocosm_id) #all mesocosms have four observations

```

```

## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
## 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
## 27 28
## 4 4

```

```

#Create data frames to view species independently
#view species independently
data_gaillardia<-data%>%
  filter(species=="Gaillardia")
data_taraxacum<-data%>%
  filter(species=="Taraxacum")
data_bromus<-data%>%
  filter(species=="Bromus")
data_festuca<-data%>%
  filter(species=="Festuca")

#By treatment
#197198
data_197198<-data%>%
  filter(treatment == "197198")
#240448
data_240448<-data%>%
  filter(treatment == "240448")
#240720
data_240720<-data%>%
  filter(treatment == "240720")
#control
data_control<-data%>%
  filter(treatment == "control")

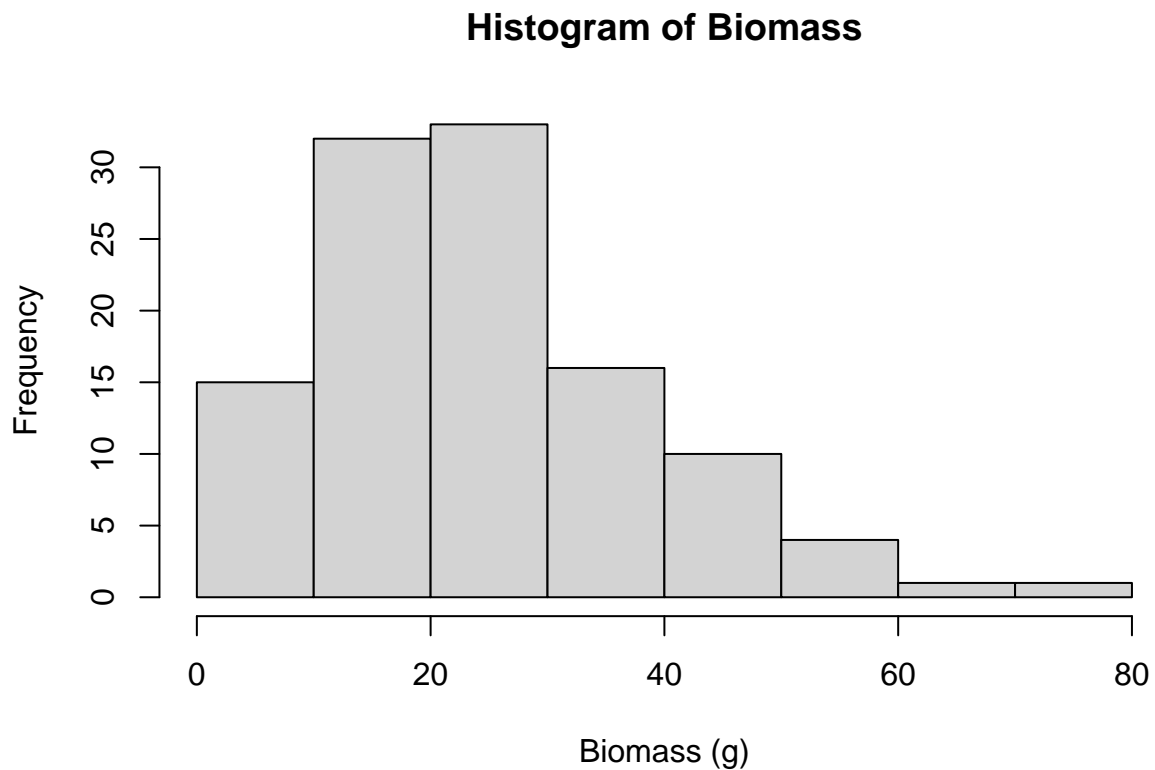
```

Visualisation and data exploration

```

#Histogram of all biomass values
hist(data$biomass,
      main = "Histogram of Biomass",
      xlab = "Biomass (g)")

```



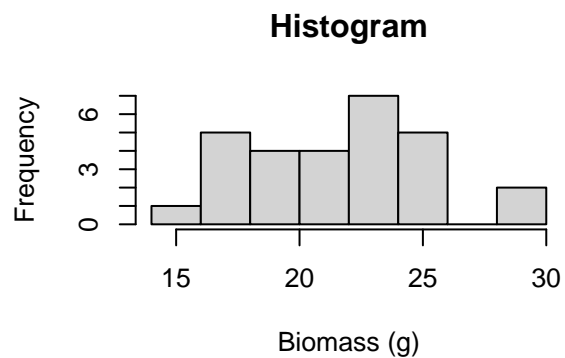
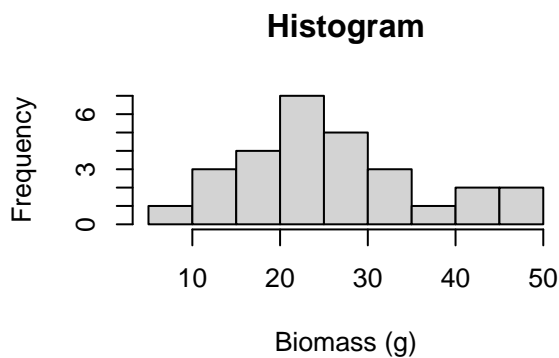
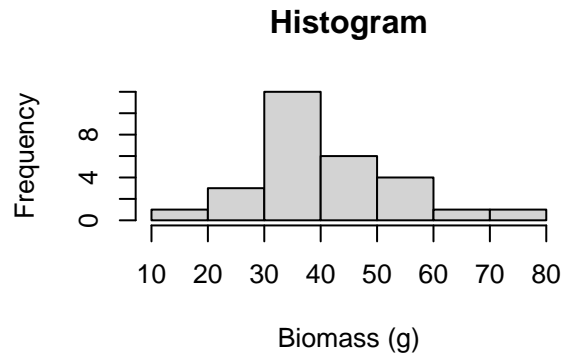
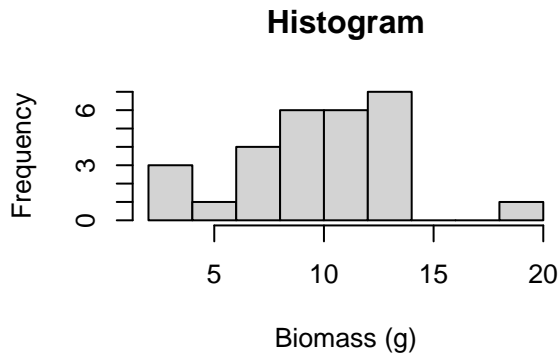
```
#near normal, slightly right skewed

par(mfrow = c(2, 2)) #2 rows, 2 columns

#View histogram by host species
#generate histogram of data distribution: GAILLARDIA
hist(data_gaillardia$biomass,
      main="Histogram",
      xlab="Biomass (g)")
#generate histogram of data distribution: FESTUCA
hist(data_festuca$biomass,
      main="Histogram",
      xlab="Biomass (g)")

#generate histogram of data distribution: BROMUS
hist(data_bromus$biomass,
      main="Histogram",
      xlab="Biomass (g)")

#generate histogram of data distribution: TARAXACUM
hist(data_taraxacum$biomass,
      main="Histogram",
      xlab="Biomass (g)")
```



```
#Skewed histogram driven by slight differences in species group density centres

par(mfrow = c(1,1)) #return plot view to default

#Create custom function to bootstrap 95% confidence intervals
mean_cl_boot <- function(x, conf = 0.95, R = 999) {
  boot_mean <- function(x, i) mean(x[i])
  boot_out <- boot(x, boot_mean, R = R)
  ci <- boot.ci(boot_out, type = "perc", conf = conf)$percent[4:5]
  data.frame(y = mean(x), ymin = ci[1], ymax = ci[2])
}

#Create species labels for plots
species_labels <- c(
  "Bromus" = expression(italic("B. tectorum")),
  "Taraxacum" = expression(italic("T. officinale")),
  "Festuca" = expression(italic("F. idahoensis")),
  "Gaillardia" = expression(italic("G. aristata"))
)

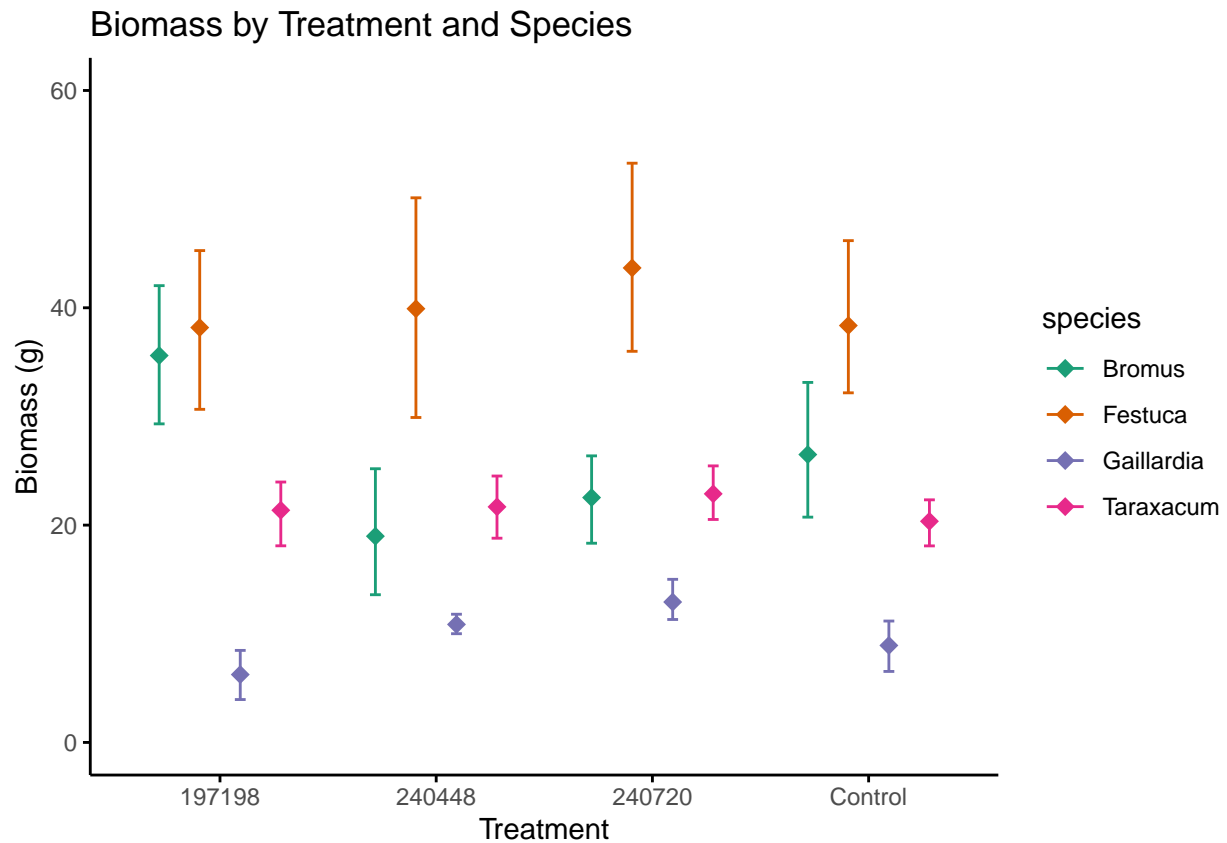
#Plot biomass by treatment and species (boxplot and bootstrapped mean)
print(plot_mean_biomass <- ggplot(data, aes(x = treatment, y = biomass, color = species)) +
  stat_summary(fun.data = mean_cl_boot, geom = "errorbar",
    position = position_dodge(0.75), width = 0.2) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 3,
    position = position_dodge(0.75)) +
```



```

labs(title = "Biomass by Treatment and Species",
      x = "Treatment",
      y = "Biomass (g)") +
coord_cartesian(ylim = c(0, 60)) +
scale_colour_brewer(palette = "Dark2") +
theme_minimal() +
theme(panel.grid = element_blank(),
      axis.line = element_line(color = "black"),
      axis.ticks = element_line(color = "black"))

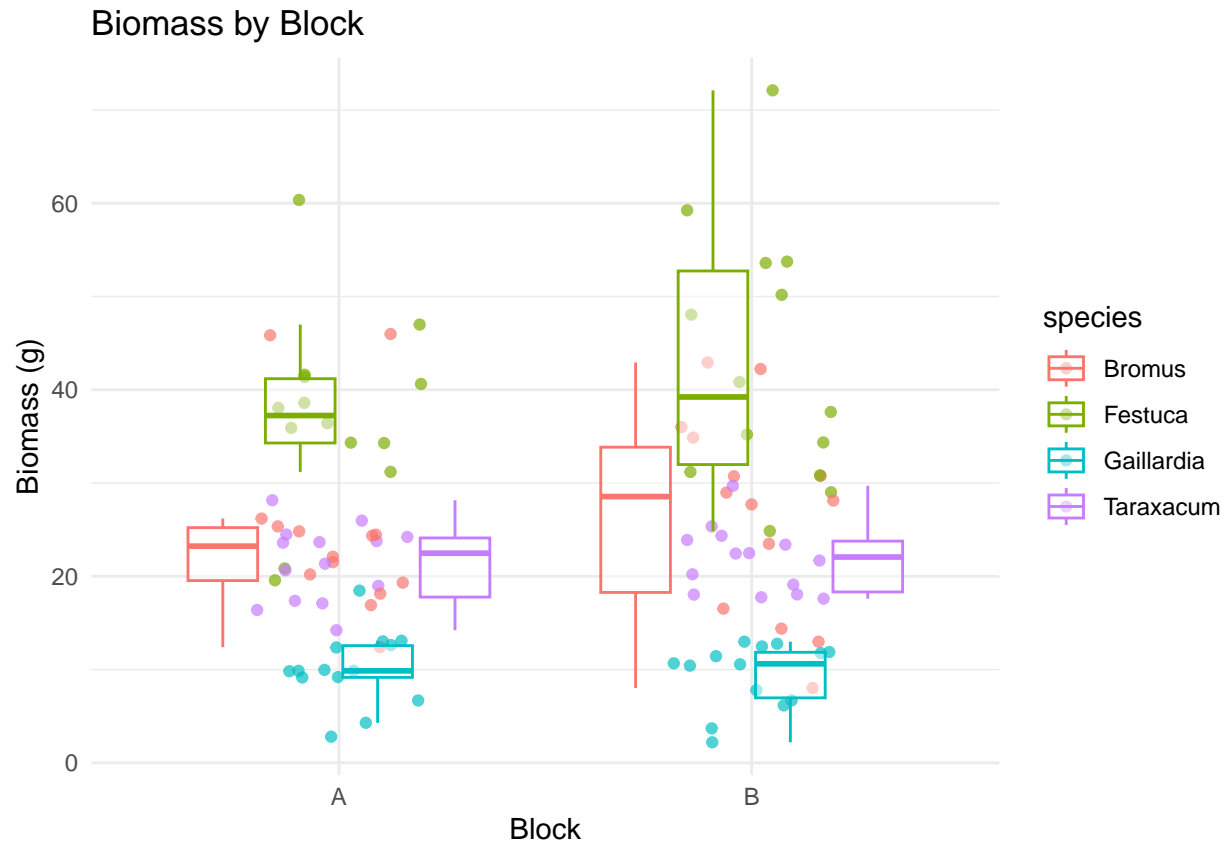
```



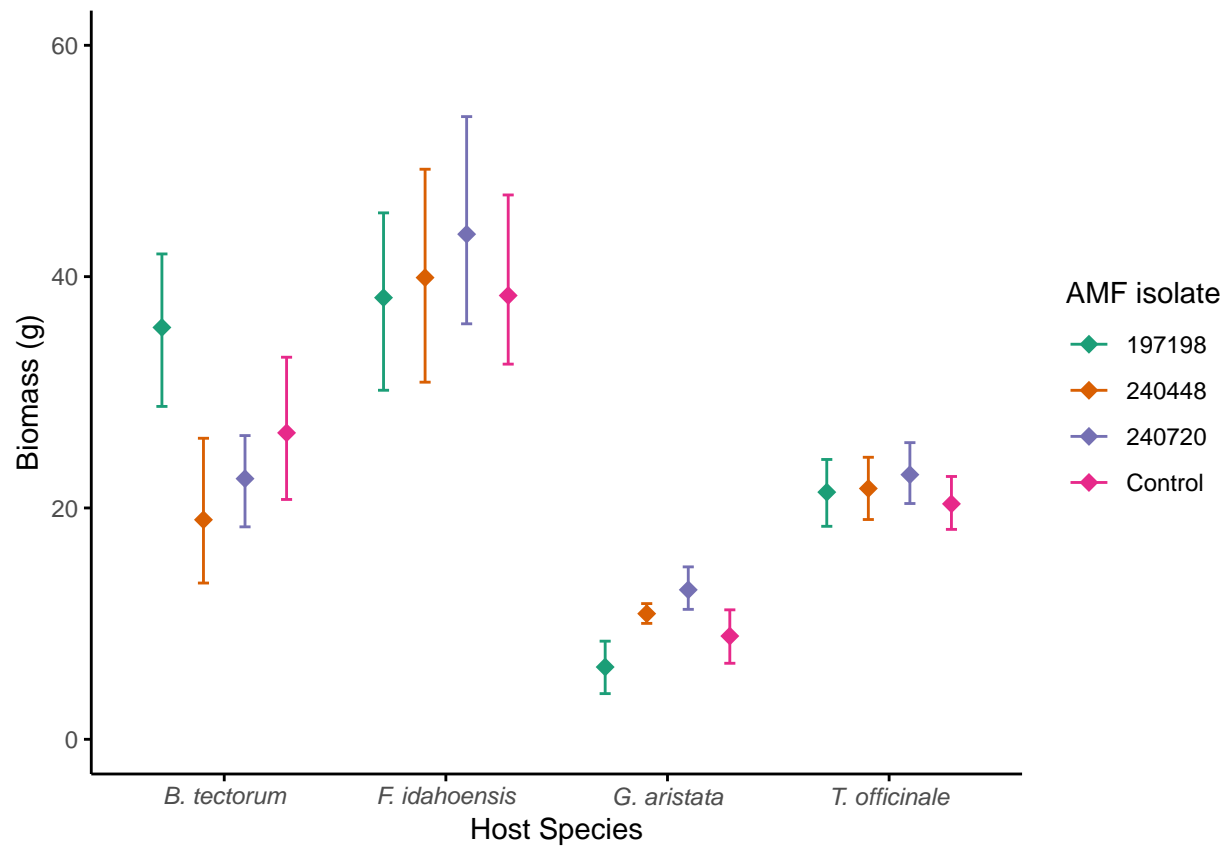
```

#Biomass by block and by species
print(biomass_by_block <- ggplot(data, aes(x = block, y = biomass, colour = species)) +
  geom_jitter(width = 0.2, alpha = 0.7) +
  geom_boxplot(alpha = 0.5, outlier.shape = NA) +
  labs(title = "Biomass by Block",
        x = "Block",
        y = "Biomass (g)") +
  theme_minimal())

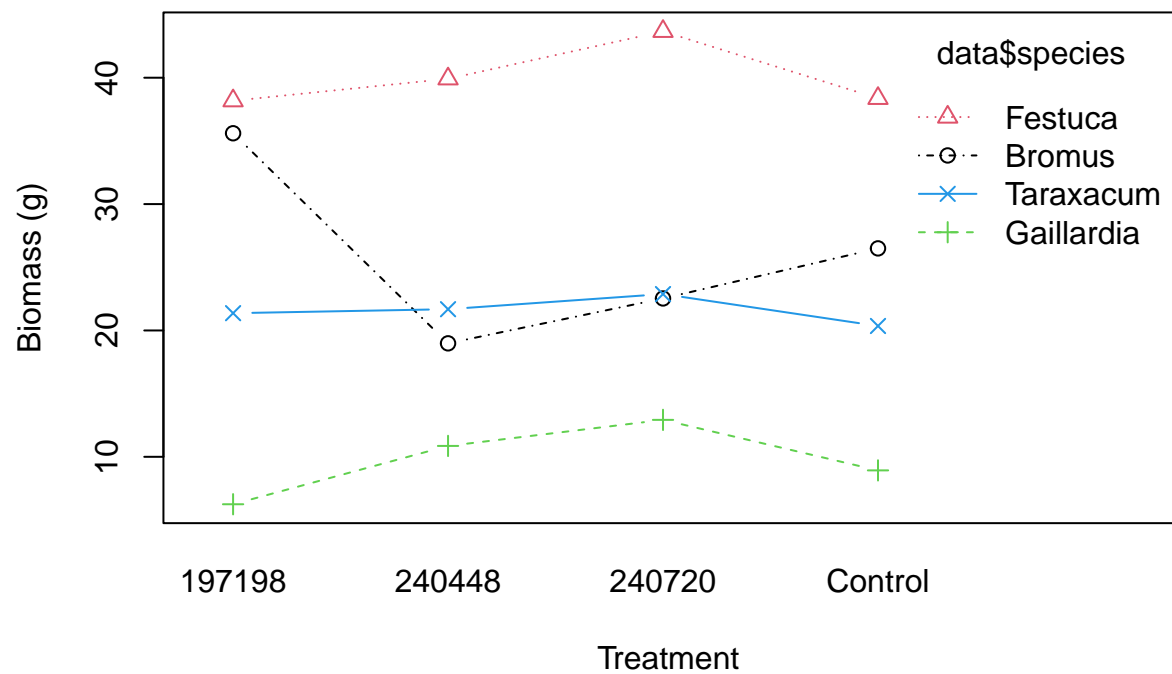
```



```
#Biomass by species
print(biomass_mean_species <- ggplot(data, aes(x = species, y = biomass, colour = treatment)) +
  stat_summary(fun.data = mean_cl_boot, geom = "errorbar",
    position = position_dodge(0.75), width = 0.2) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 3,
    position = position_dodge(0.75)) +
  labs(color = "AMF isolate",
    x = "Host Species",
    y = "Biomass (g)") +
  scale_colour_brewer(palette = "Dark2") +
  scale_x_discrete(labels = species_labels) +
  coord_cartesian(ylim = c(0, 60)) +
  theme_minimal() +
  theme(panel.grid = element_blank(),
    axis.line = element_line(color = "black"),
    axis.ticks = element_line(color = "black")))
```



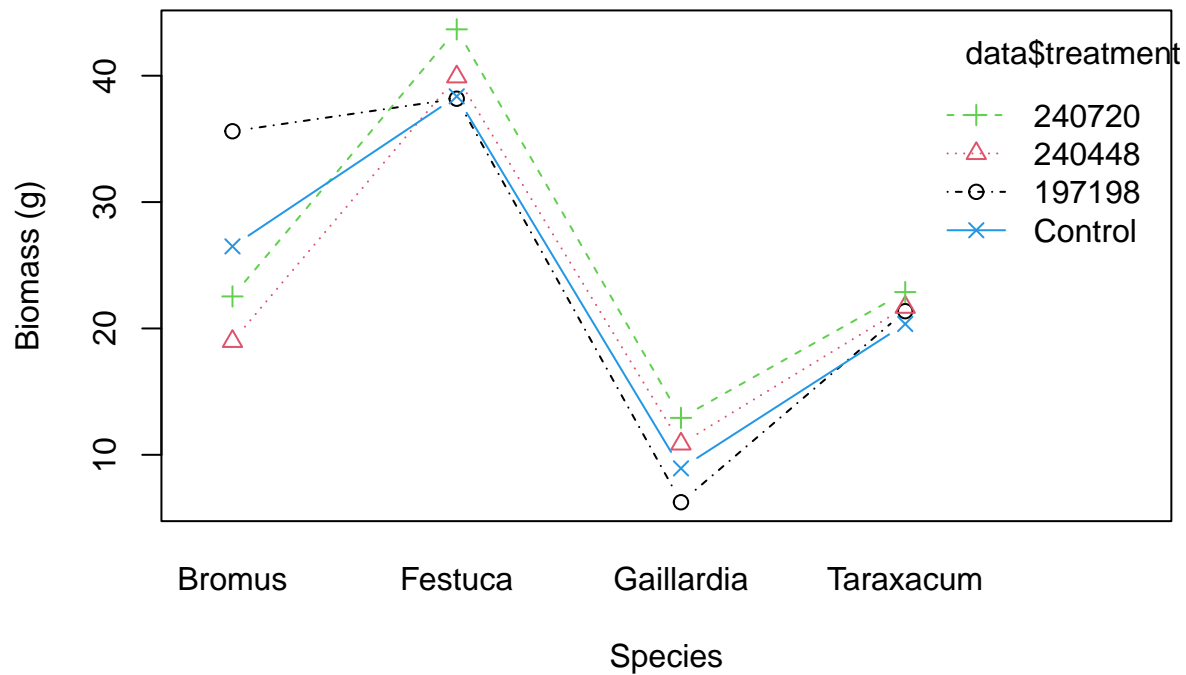
```
#Interaction plots
interaction.plot(data$treatment, data$species, data$biomass,
  xlab = "Treatment", ylab = "Biomass (g)",
  col = 1:length(unique(data$species)),
  pch = 1:length(unique(data$species)), type = "b")
```



*#Slopes are not the same between species, likely interaction between 197198 and
#bromus, 240720 and gaillardia*

#Flip axis

```
interaction.plot(data$species, data$treatment, data$biomass,
  xlab = "Species", ylab = "Biomass (g)",
  col = 1:length(unique(data$treatment)),
  pch = 1:length(unique(data$treatment)), type = "b")
```



*#Treatments follow roughly equivalent patterns within species (species identity
#has the strongest effect on biomass), excepting bromus * 197198,
#which remains equivalent to the biomass of festuca.*

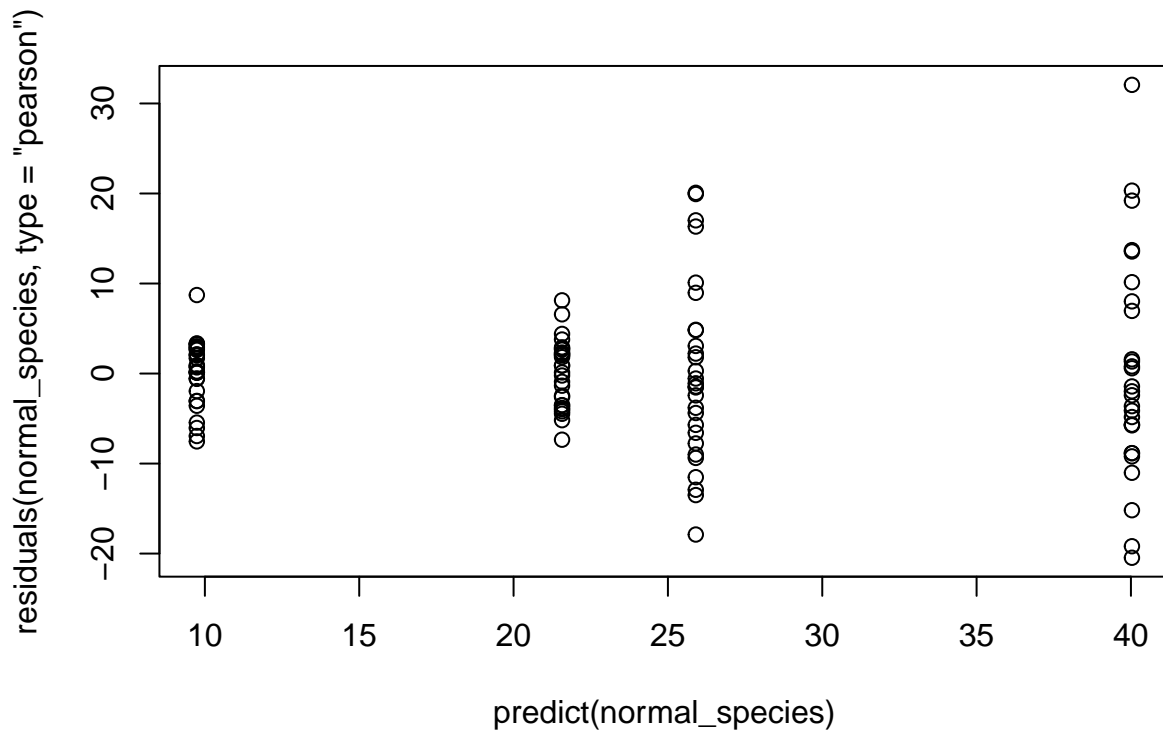
Model selection

```
#Start with the simplest model
#normal distribution with species as the predictor
normal_species<-glm(biomass~species,
                    family = gaussian(link="identity"),
                    data = data)
summary(normal_species)
```

```
##
## Call:
## glm(formula = biomass ~ species, family = gaussian(link = "identity"),
##      data = data)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    25.904     1.569  16.513  < 2e-16 ***
## speciesFestuca  14.129     2.218   6.369 4.76e-09 ***
## speciesGaillardia -16.164     2.218  -7.286 5.50e-11 ***
```

```
## speciesTaraxacum    -4.333      2.218  -1.953   0.0534 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 68.90103)
##
## Null deviance: 20589.0  on 111  degrees of freedom
## Residual deviance:  7441.3  on 108  degrees of freedom
## AIC: 797.83
##
## Number of Fisher Scoring iterations: 2
```

```
#Check heteroskedasticity
plot(predict(normal_species), residuals(normal_species, type = "pearson"))
```



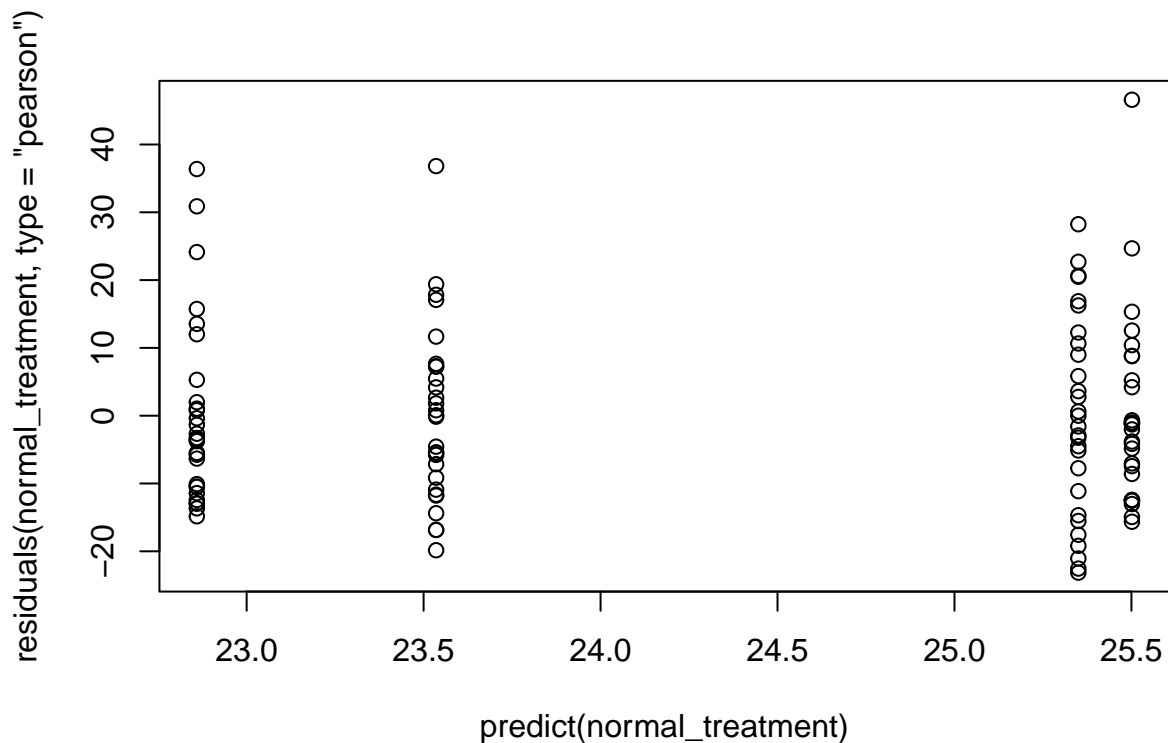
```
#Heteroskedastic residual variance

#normal distribution with treatment as the predictor
normal_treatment<-glm(biomass~treatment,
                      family = gaussian(link="identity"),
                      data = data)
summary(normal_treatment)
```

```
##
## Call:
```

```
## glm(formula = biomass ~ treatment, family = gaussian(link = "identity"),
##      data = data)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    25.3500     2.6001   9.750  <2e-16 ***
## treatment240448 -2.4907     3.6770  -0.677    0.500
## treatment240720  0.1514     3.6770   0.041    0.967
## treatmentControl -1.8146     3.6770  -0.494    0.623
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 189.2889)
##
## Null deviance: 20589  on 111  degrees of freedom
## Residual deviance: 20443  on 108  degrees of freedom
## AIC: 911.02
##
## Number of Fisher Scoring iterations: 2
```

```
#Check heteroskedasticity
plot(predict(normal_treatment), residuals(normal_treatment, type = "pearson"))
```



```
#Patterns in residual variance, large residual spread, less hetero. than species
#only model
```

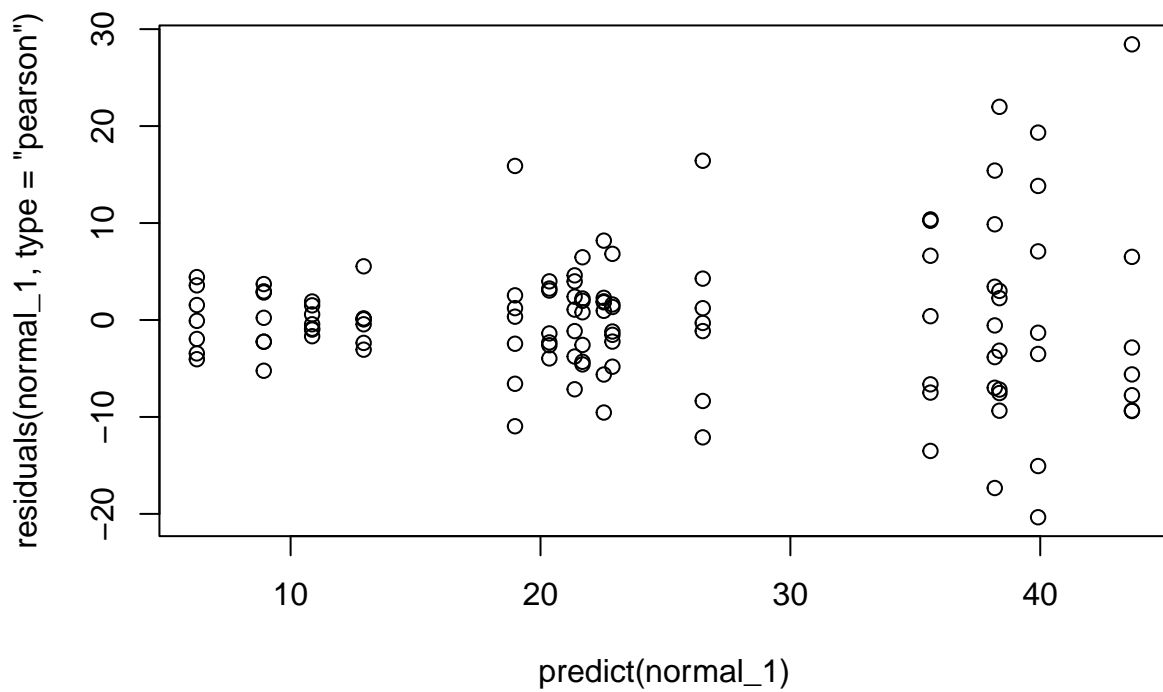
```

#Interaction model
normal_1<-glm(biomass~treatment*species,
              family = gaussian(link="identity"),
              data = data)
summary(normal_1)

##
## Call:
## glm(formula = biomass ~ treatment * species, family = gaussian(link = "identity"),
##      data = data)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      35.606      2.997  11.880 < 2e-16 ***
## treatment240448   -16.626      4.239   -3.923 0.000165 ***
## treatment240720   -13.071      4.239   -3.084 0.002668 **
## treatmentControl    -9.111      4.239   -2.150 0.034095 *
## speciesFestuca      2.574      4.239    0.607 0.545051
## speciesGaillardia  -29.359      4.239   -6.927 4.91e-10 ***
## speciesTaraxacum  -14.239      4.239   -3.359 0.001122 **
## treatment240448:speciesFestuca  18.360      5.994    3.063 0.002844 **
## treatment240720:speciesFestuca  18.561      5.994    3.097 0.002567 **
## treatmentControl:speciesFestuca   9.299      5.994    1.551 0.124130
## treatment240448:speciesGaillardia 21.240      5.994    3.543 0.000612 ***
## treatment240720:speciesGaillardia 19.747      5.994    3.294 0.001382 **
## treatmentControl:speciesGaillardia 11.790      5.994    1.967 0.052082 .
## treatment240448:speciesTaraxacum  16.940      5.994    2.826 0.005734 **
## treatment240720:speciesTaraxacum  14.583      5.994    2.433 0.016833 *
## treatmentControl:speciesTaraxacum   8.099      5.994    1.351 0.179849
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 62.87825)
##
##      Null deviance: 20589.0  on 111  degrees of freedom
## Residual deviance:  6036.3  on   96  degrees of freedom
## AIC: 798.39
##
## Number of Fisher Scoring iterations: 2

#Check heteroskedasticity
plot(predict(normal_1), residuals(normal_1, type = "pearson"))

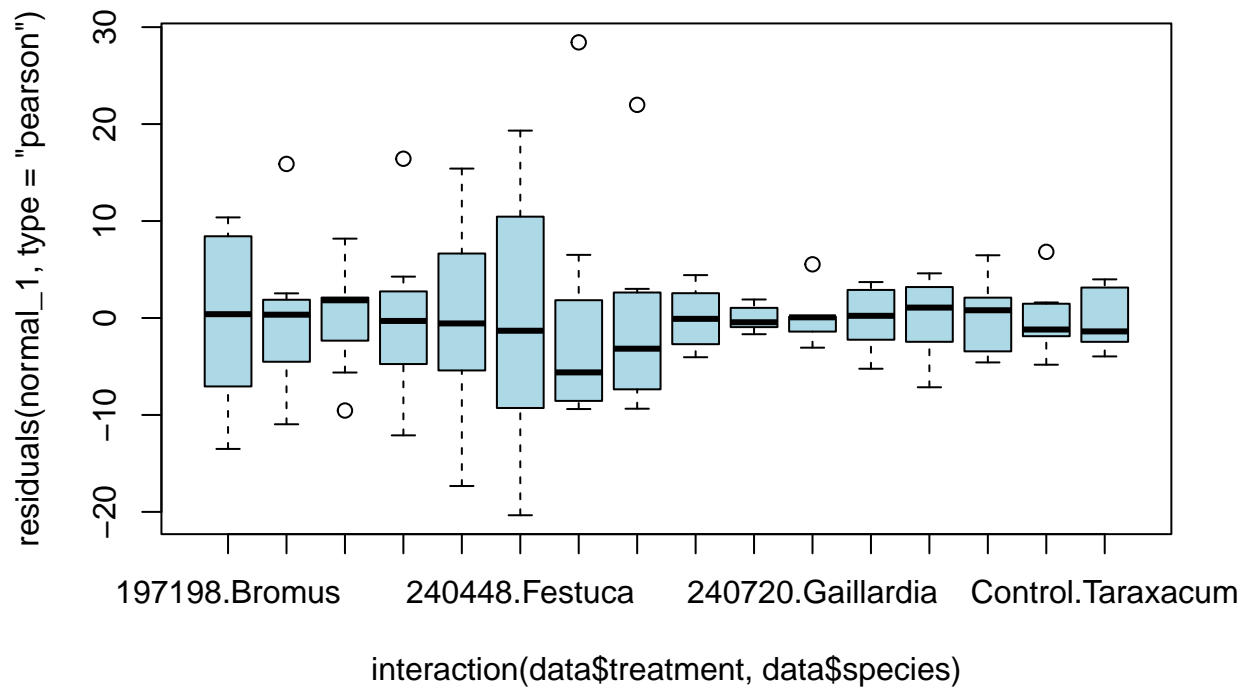
```

```
#Heteroskedastic residual variance
#Large y-axis spread and fan shape indicate variance is overdispersed
#heteroskedastic

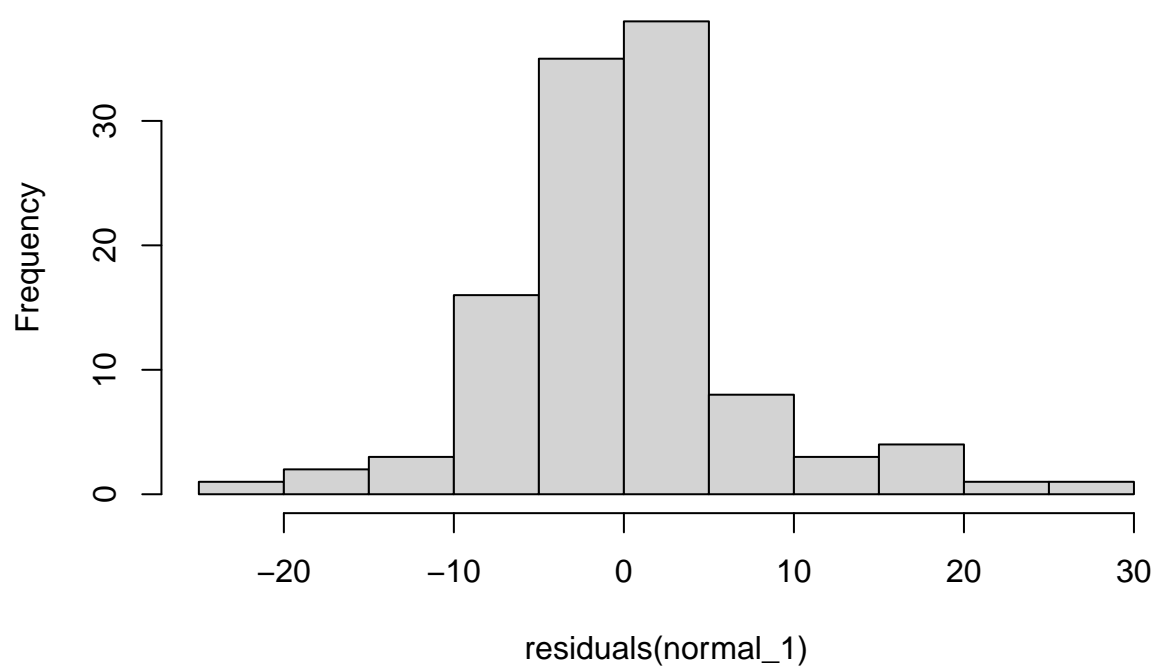
#Check spread of variance between treatments and species
boxplot(residuals(normal_1, type="pearson") ~ interaction(data$treatment,
                                                         data$species),
        main = "Boxplot of Residuals per Treatment",
        col = "lightblue")
```

Boxplot of Residuals per Treatment

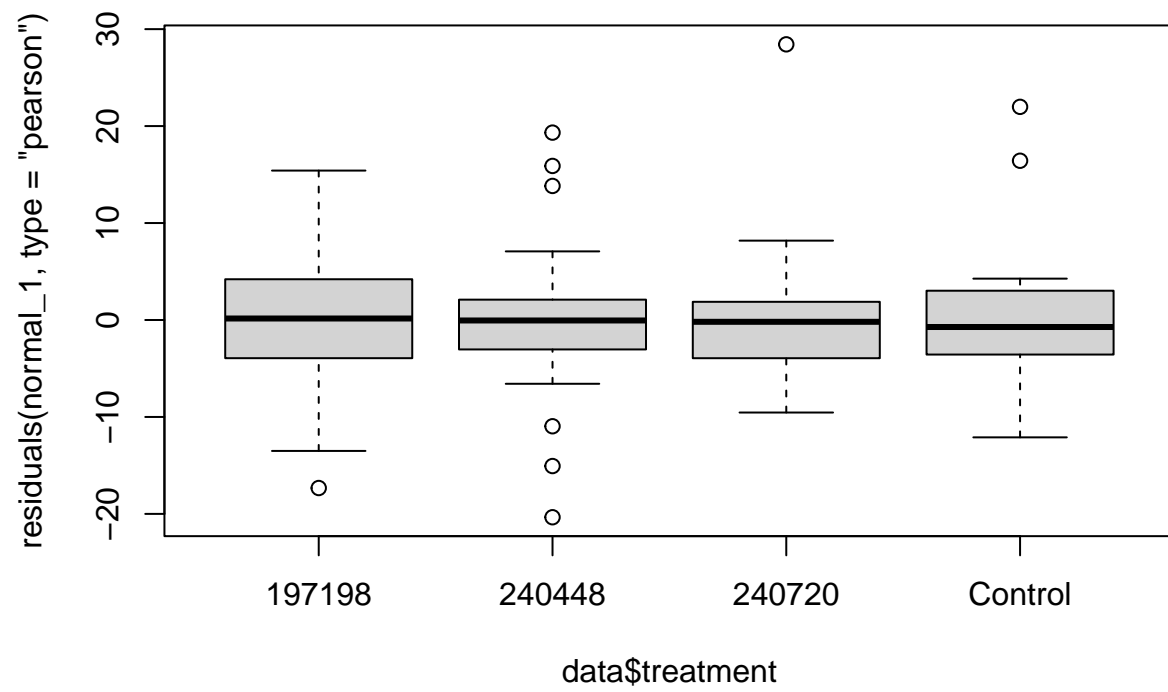


```
#Differences in residual variance between treatment*species interactions  
hist(residuals(normal_1))
```

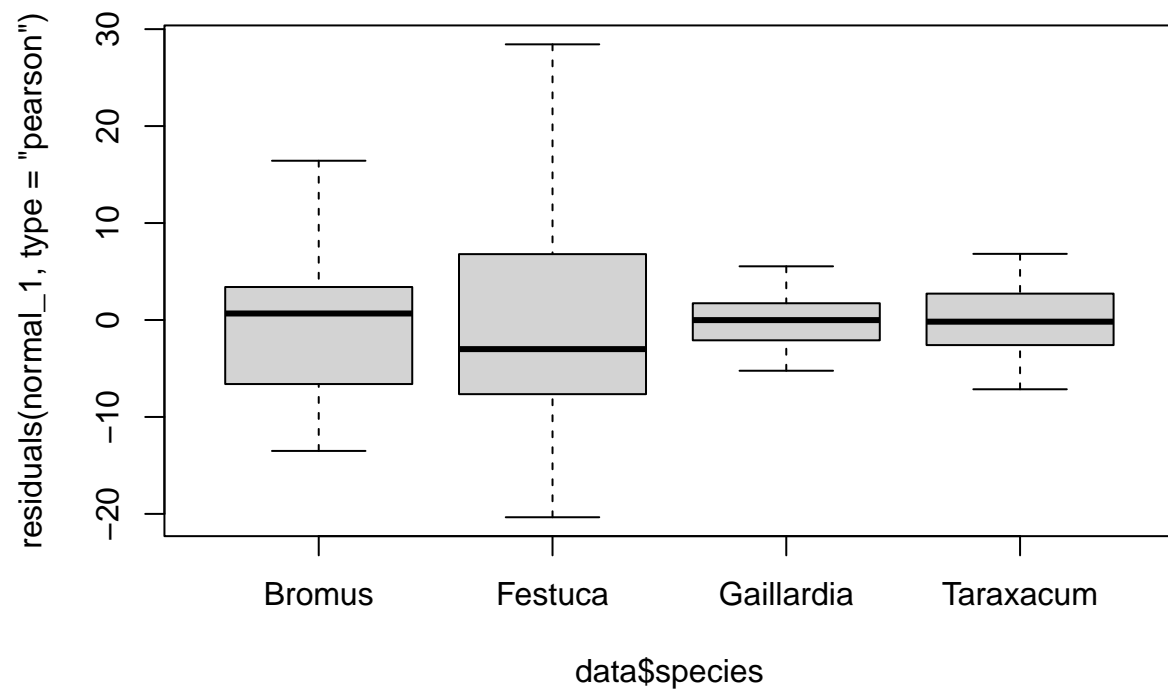
Histogram of residuals(normal_1)



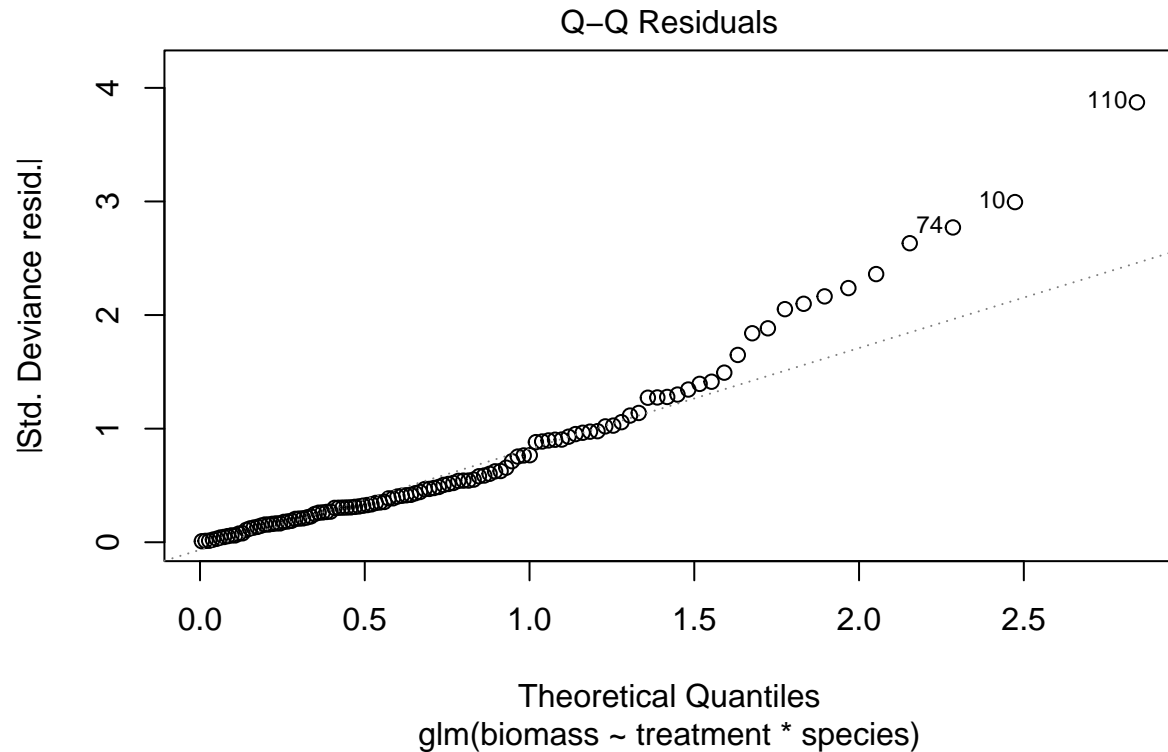
```
#Good histogram shape  
boxplot(residuals(normal_1, type = "pearson") ~ data$treatment) #Looks good
```



```
boxplot(residuals(normal_1, type = "pearson")~data$species)
```



```
#Variance between species  
#Check Q-Q residuals  
plot(normal_1, which = 2) #Struggles to predict higher values
```



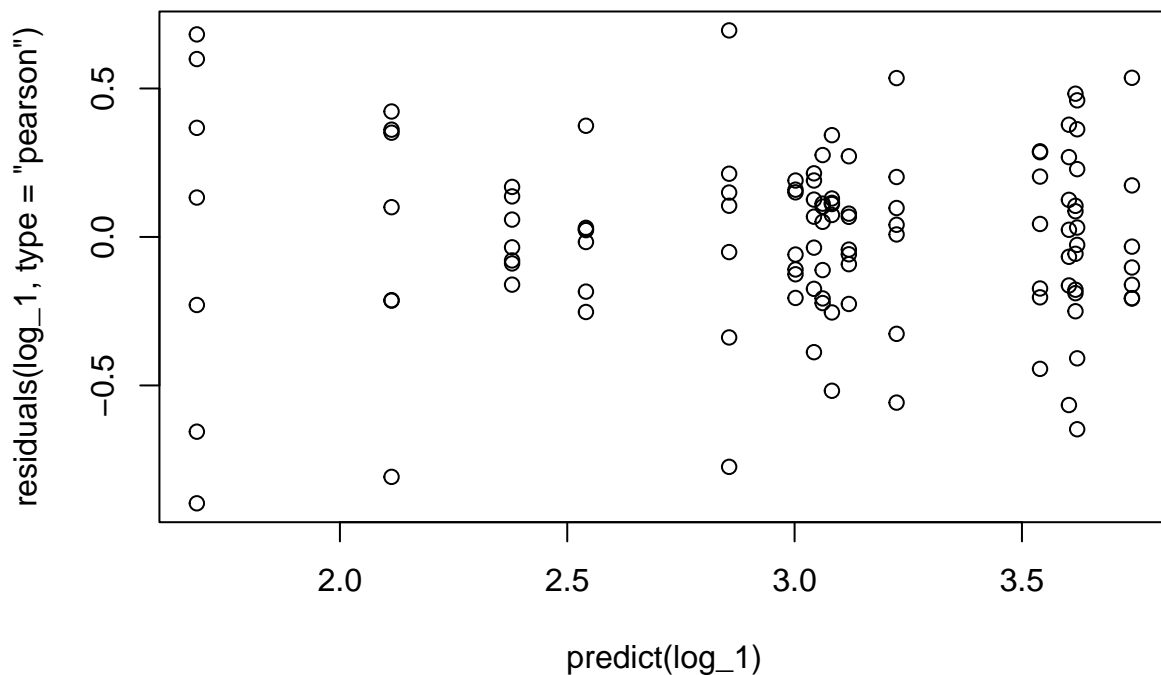
```
#Try a log transformation
data$log_biomass<-log(data$biomass)
```

```
#Model logged biomass with a normal distribution
log_1<-glm(log_biomass~species*treatment,
            family=gaussian(link="identity"),
            data=data)
summary(log_1)
```

```
##
## Call:
## glm(formula = log_biomass ~ species * treatment, family = gaussian(link = "identity"),
##      data = data)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.5398    0.1219  29.045 < 2e-16 ***
## speciesFestuca      0.0636    0.1724   0.369  0.71293
## speciesGaillardia  -1.8545    0.1724 -10.760 < 2e-16 ***
## speciesTaraxacum  -0.4972    0.1724  -2.885  0.00484 **
## treatment240448   -0.6837    0.1724  -3.967  0.00014 ***
## treatment240720   -0.4577    0.1724  -2.655  0.00928 **
## treatmentControl  -0.3155    0.1724  -1.830  0.07031 .
## speciesFestuca:treatment240448  0.7019    0.2437   2.880  0.00491 **
## speciesGaillardia:treatment240448 1.3771    0.2437   5.650 1.64e-07 ***
## speciesTaraxacum:treatment240448 0.7028    0.2437   2.883  0.00485 **
```

```
## speciesFestuca:treatment240720      0.5963      0.2437      2.446 0.01625 *
## speciesGaillardia:treatment240720    1.3135      0.2437      5.389 5.06e-07 ***
## speciesTaraxacum:treatment240720     0.5344      0.2437      2.193 0.03076 *
## speciesFestuca:treatmentControl       0.3298      0.2437      1.353 0.17915
## speciesGaillardia:treatmentControl    0.7437      0.2437      3.051 0.00295 **
## speciesTaraxacum:treatmentControl     0.2749      0.2437      1.128 0.26224
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1039667)
##
## Null deviance: 46.2342 on 111 degrees of freedom
## Residual deviance: 9.9808 on 96 degrees of freedom
## AIC: 81.045
##
## Number of Fisher Scoring iterations: 2
```

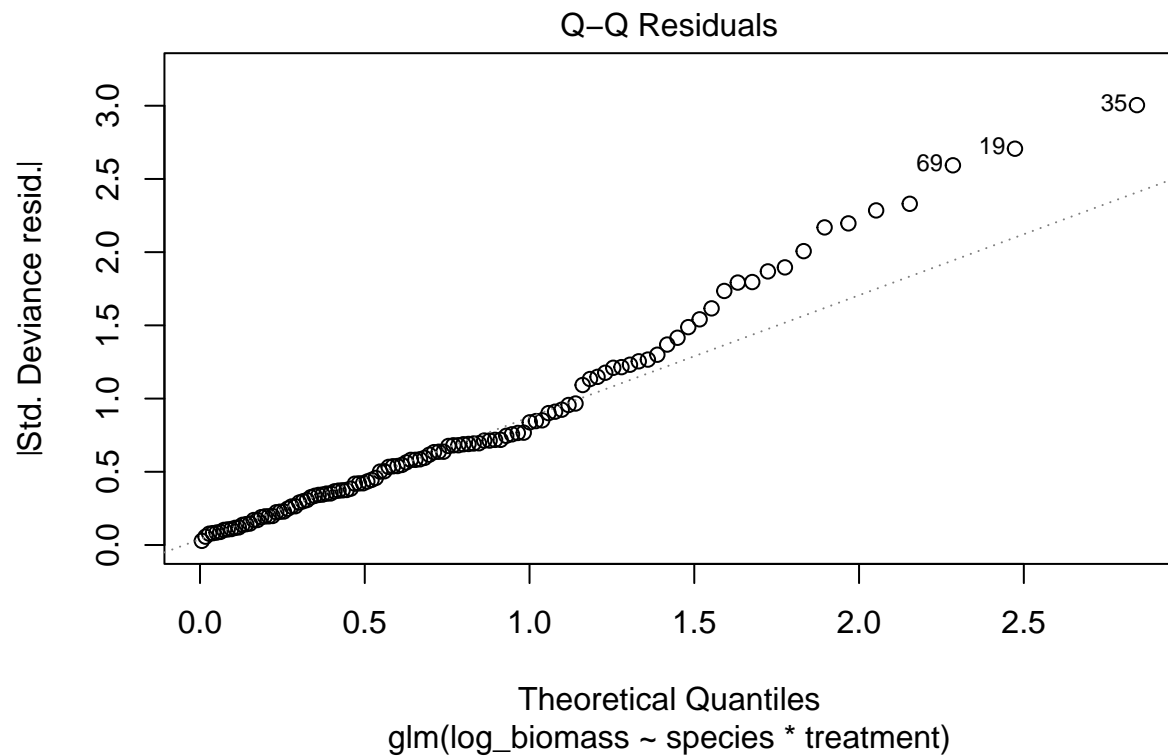
```
#Much better AIC
#Review residual diagnostics
res_log<-summary(residuals(log_1, type = "pearson"))
exp_res<-exp(res_log)
pred_log<-predict(log_1)
exp_pred<-exp(pred_log)
#Low variance in residuals,visually assess
plot(predict(log_1), residuals(log_1, type = "pearson"))
```



```

#Better residuals, but fan shaped, heteroskedastic residual variance persists
#Model is likely underdispersed. Residual spread expected between ~ -2 and 2
#with pearson residuals, log model has a spread of ~-0.5 to 0.5.
#Check Q-Q residuals
plot(log_1, which = 2)

```

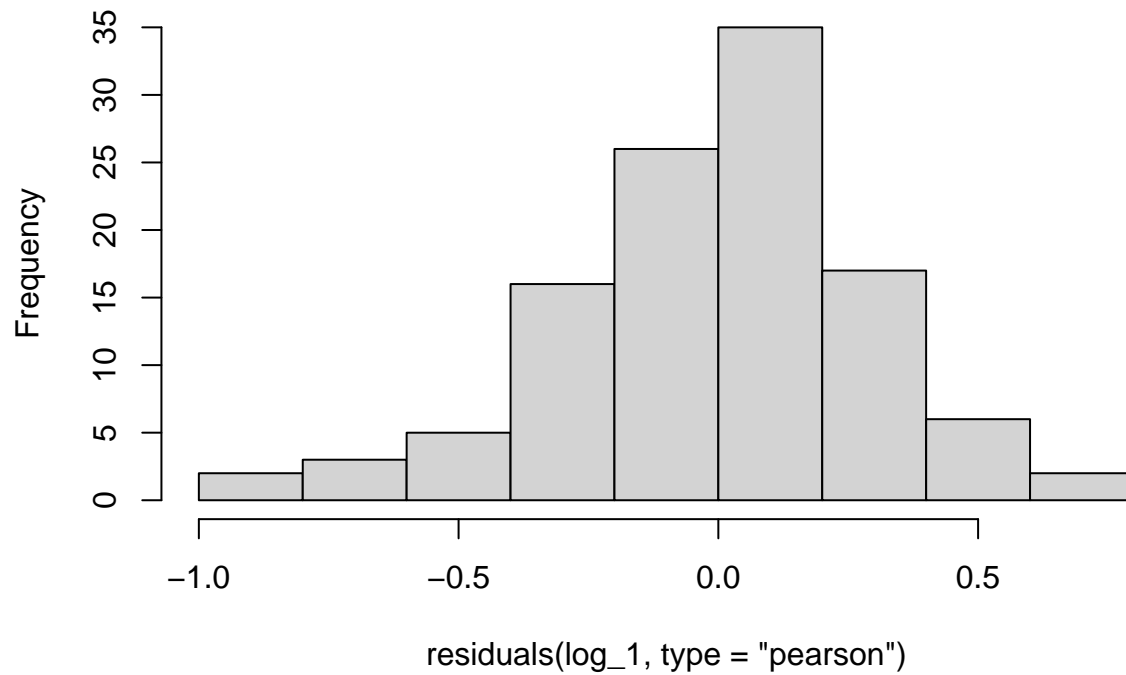


```

#Model struggles to predict higher values
#Check histogram of residuals
hist(residuals(log_1, type = "pearson")) #Compressed residual variance

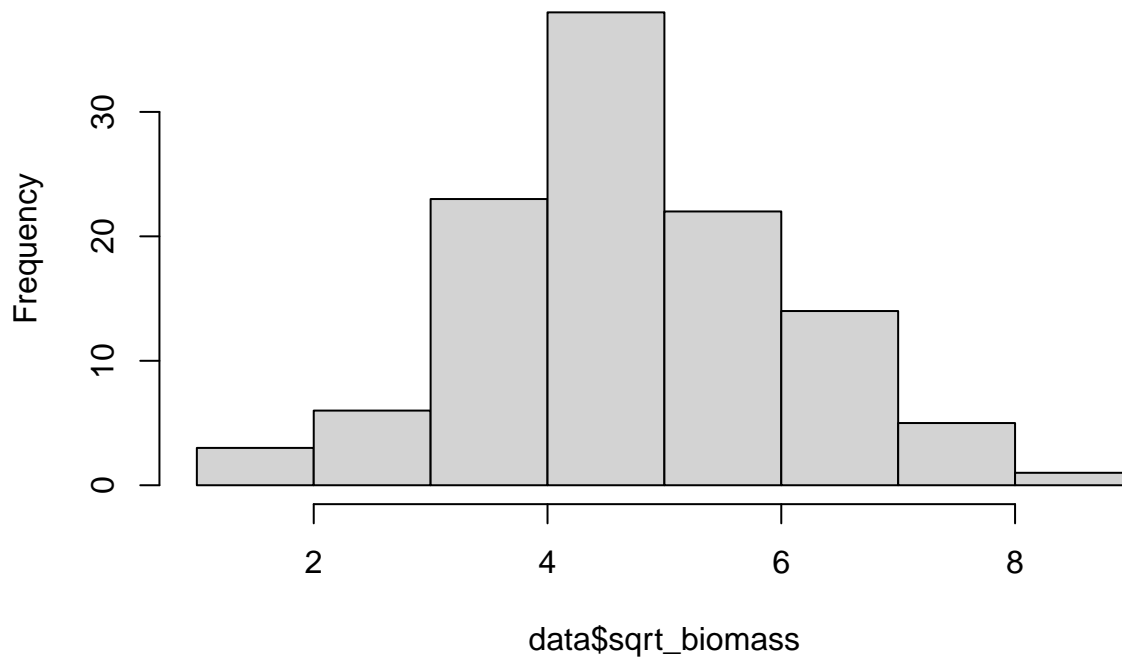
```


Histogram of residuals(log_1, type = "pearson")



```
#Square root transformation  
data$sqrt_biomass<-sqrt(data$biomass)  
  
#Create the histogram  
hist(data$sqrt_biomass) #Looks good
```

Histogram of data\$sqrt_biomass



```
#Create the model
sqrt_1<-glm(sqrt_biomass~species*treatment,
             family=gaussian(link="identity"),
             data=data)
summary(sqrt_1)
```

```
##
## Call:
## glm(formula = sqrt_biomass ~ species * treatment, family = gaussian(link = "identity"),
##      data = data)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.9194    0.2733  21.656 < 2e-16 ***
## speciesFestuca      0.2017    0.3866   0.522 0.602947
## speciesGaillardia  -3.5050    0.3866  -9.067 1.50e-14 ***
## speciesTaraxacum   -1.3185    0.3866  -3.411 0.000948 ***
## treatment240448    -1.6547    0.3866  -4.281 4.41e-05 ***
## treatment240720    -1.2098    0.3866  -3.130 0.002319 **
## treatmentControl   -0.8385    0.3866  -2.169 0.032538 *
## speciesFestuca:treatment240448  1.7533    0.5467   3.207 0.001821 **
## speciesGaillardia:treatment240448  2.5305    0.5467   4.629 1.15e-05 ***
## speciesTaraxacum:treatment240448  1.6930    0.5467   3.097 0.002564 **
## speciesFestuca:treatment240720    1.6372    0.5467   2.995 0.003492 **
## speciesGaillardia:treatment240720  2.3738    0.5467   4.342 3.50e-05 ***
## speciesTaraxacum:treatment240720  1.3790    0.5467   2.522 0.013298 *
```

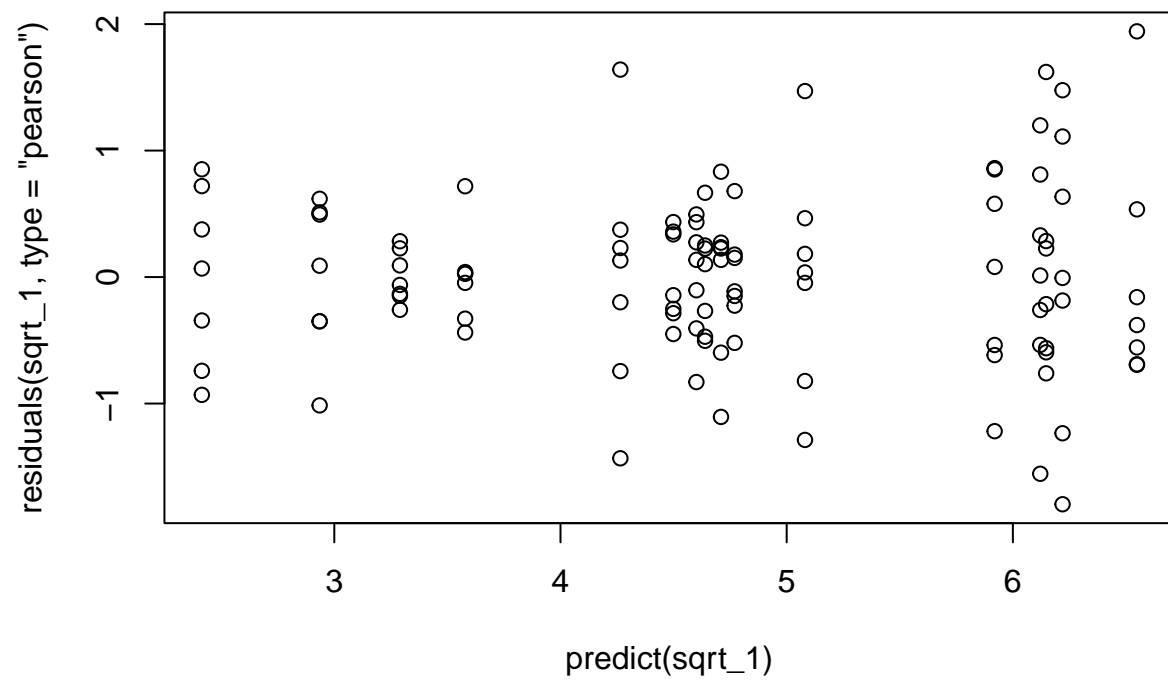
```
## speciesFestuca:treatmentControl      0.8645      0.5467      1.581 0.117080
## speciesGaillardia:treatmentControl    1.3593      0.5467      2.487 0.014624 *
## speciesTaraxacum:treatmentControl     0.7365      0.5467      1.347 0.181078
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.5229848)
##
##      Null deviance: 213.216  on 111  degrees of freedom
## Residual deviance:  50.207  on  96  degrees of freedom
## AIC: 261.98
##
## Number of Fisher Scoring iterations: 2
```

```
#Better AIC fit than no transformation, worse than log,
#but better dispersion. Underdispersion (dispersion parameter ~0.5) persists
#but may be acceptable
summary(residuals(sqrt_1, type = "pearson")) #Residual spread of pearson
```

```
##      Min.   1st Qu.   Median     Mean  3rd Qu.     Max.
## -1.79594 -0.41386  0.02776  0.00000  0.36289  1.94251
```

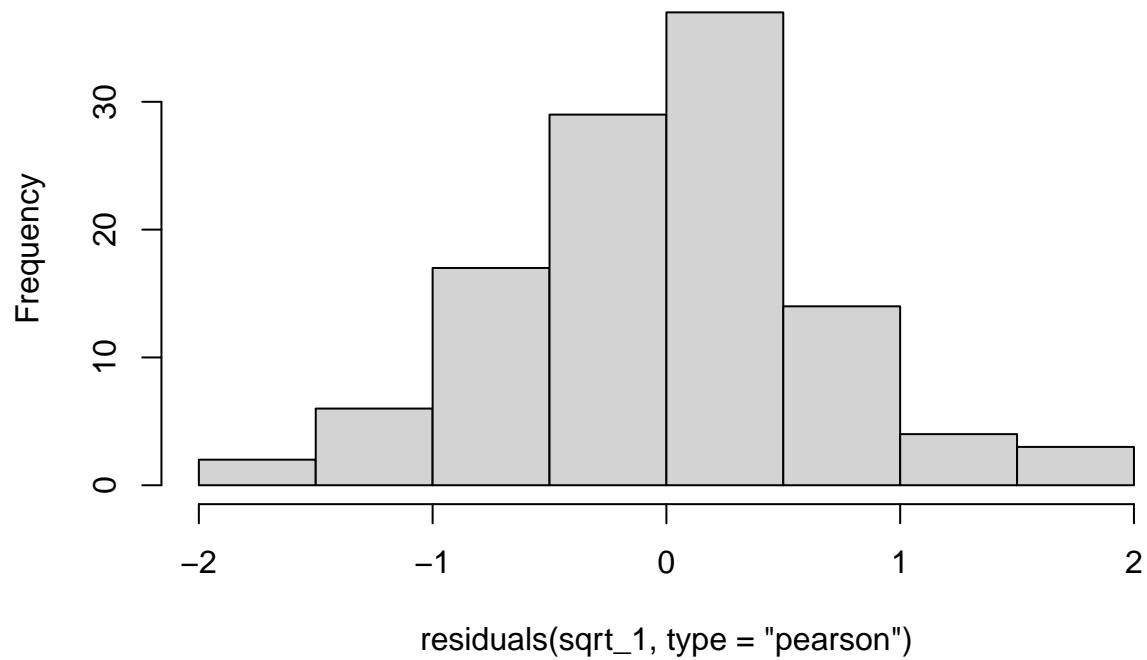
```
#residuals expected between -2 and 2 for a normally distributed model, this
#residual spread looks good
```

```
#Plot residuals
#predict vs. residuals
plot(predict(sqrt_1), residuals(sqrt_1, type = "pearson"))
```

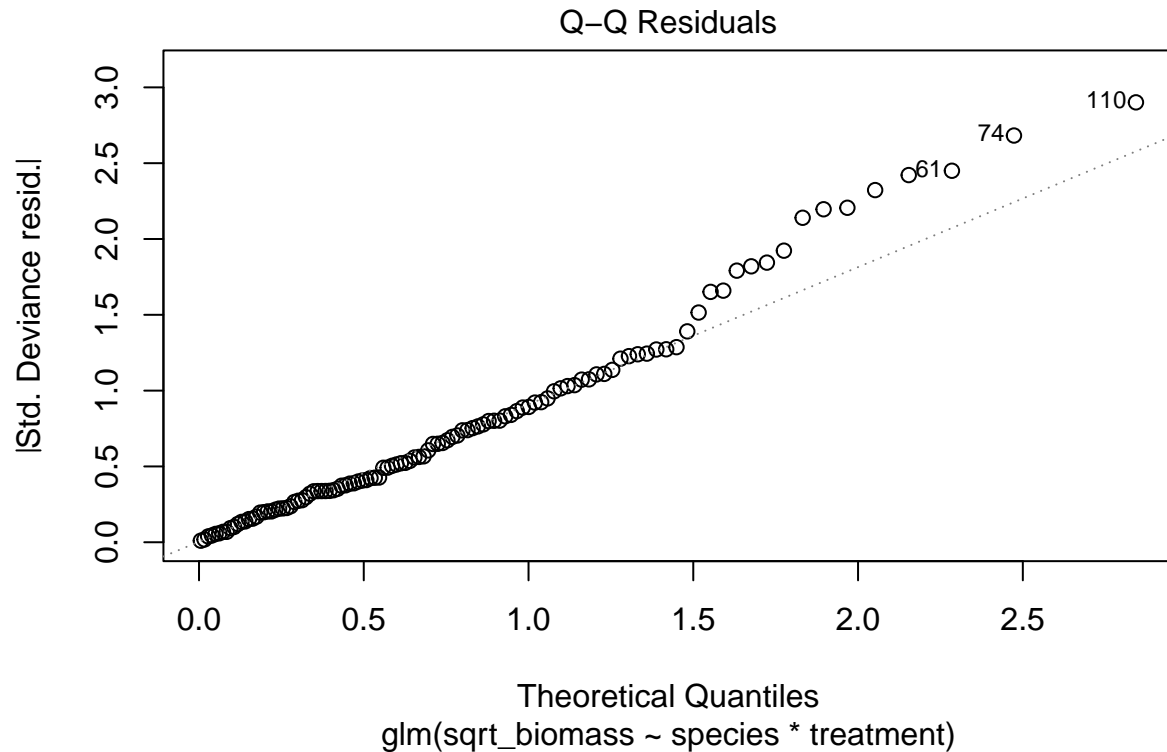


```
#Looks okay, slightly underdispersed. Persistence of heteroskedastic fan shape.  
#Check histogram  
hist(residuals(sqrt_1, type="pearson"))
```

Histogram of residuals(sqrt_1, type = "pearson")

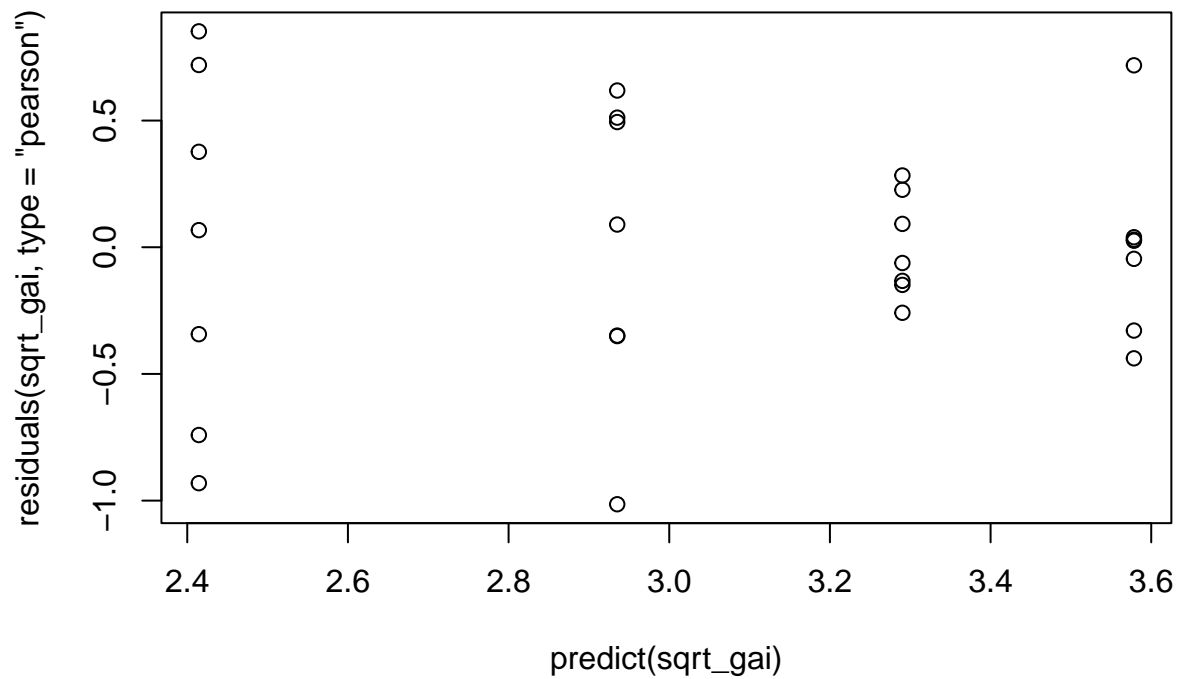


```
#looks good  
#Check QQplot  
plot(sqrt_1, which =2) #struggles to predict on higher biomass
```



```
#Try analysing the data by species to account for heterogeneity of variance
#Add the sqrt transformation to species groups
data_gaillardia<-data%>%
  filter(species=="Gaillardia")
data_taraxacum<-data%>%
  filter(species=="Taraxacum")
data_bromus<-data%>%
  filter(species=="Bromus")
data_festuca<-data%>%
  filter(species=="Festuca")

#Model diagnostics for each species (sqrt transformed)
#GAILLARDIA
sqrt_gai<-glm(sqrt_biomass~treatment,
  family=gaussian(link="identity"),
  data=data_gaillardia)
#Check heteroskedasticity
plot(predict(sqrt_gai), residuals(sqrt_gai, type = "pearson"))
```



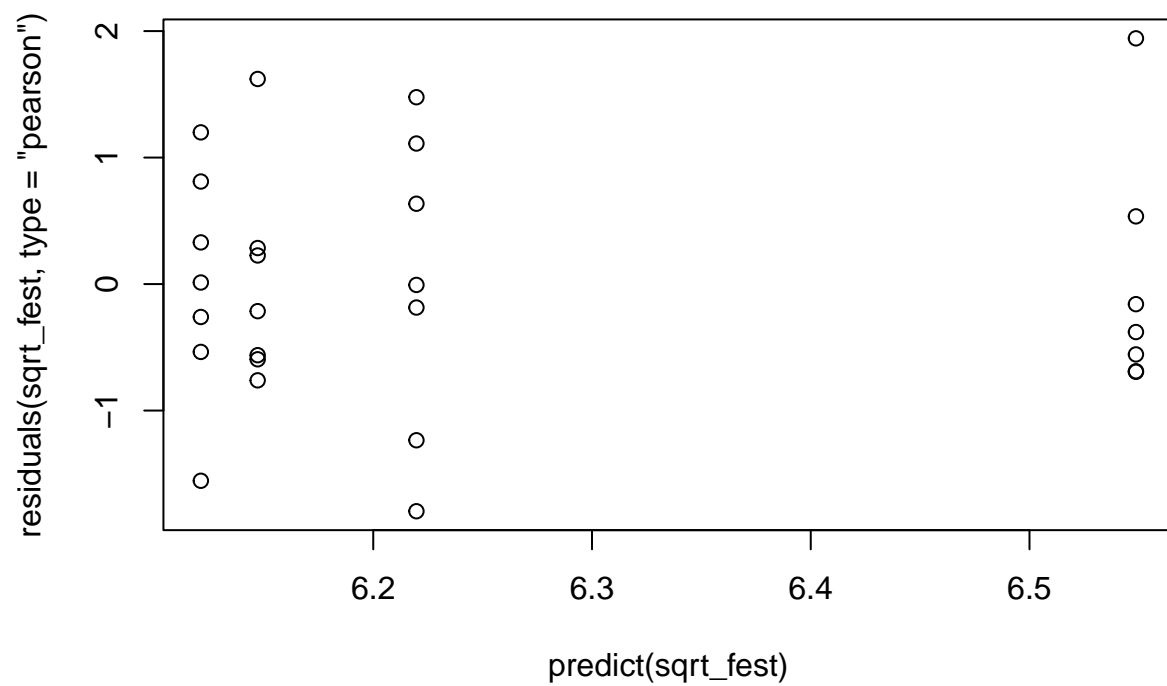
```
#Compressed residual variance
```

```
#FESTUCA
```

```
sqrt_fest<-glm(sqrt_biomass~treatment,  
               family=gaussian(link="identity"),  
               data=data_festuca)
```

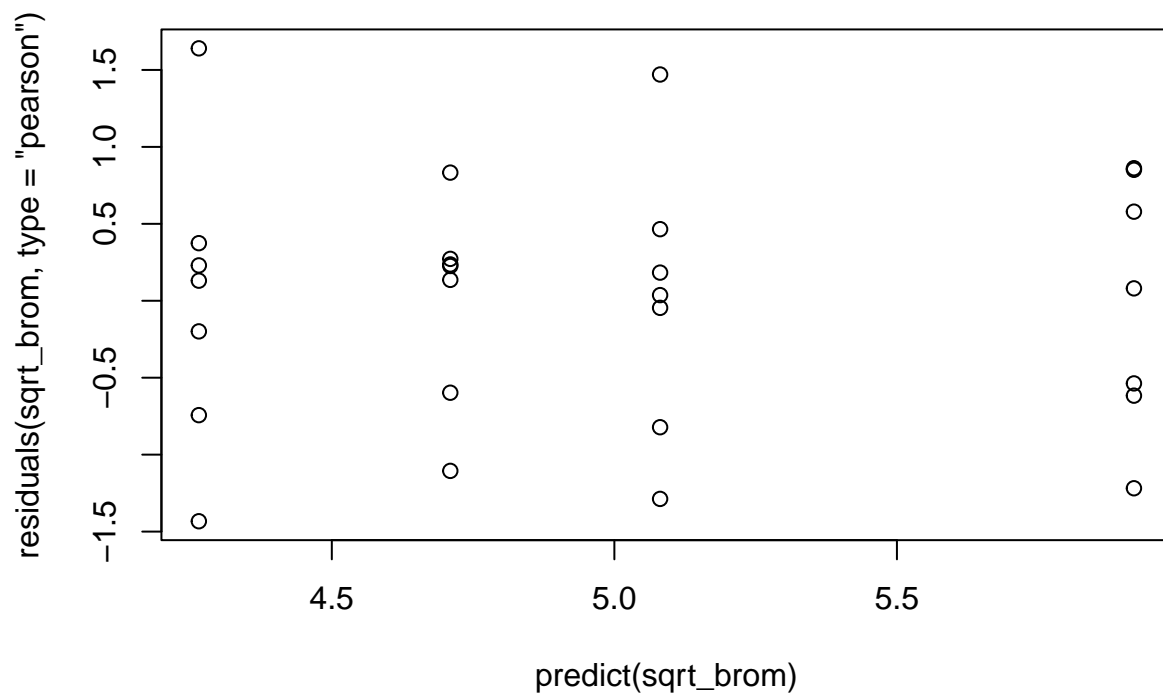
```
#Check heteroskedasticity
```

```
plot(predict(sqrt_fest), residuals(sqrt_fest, type = "pearson"))
```



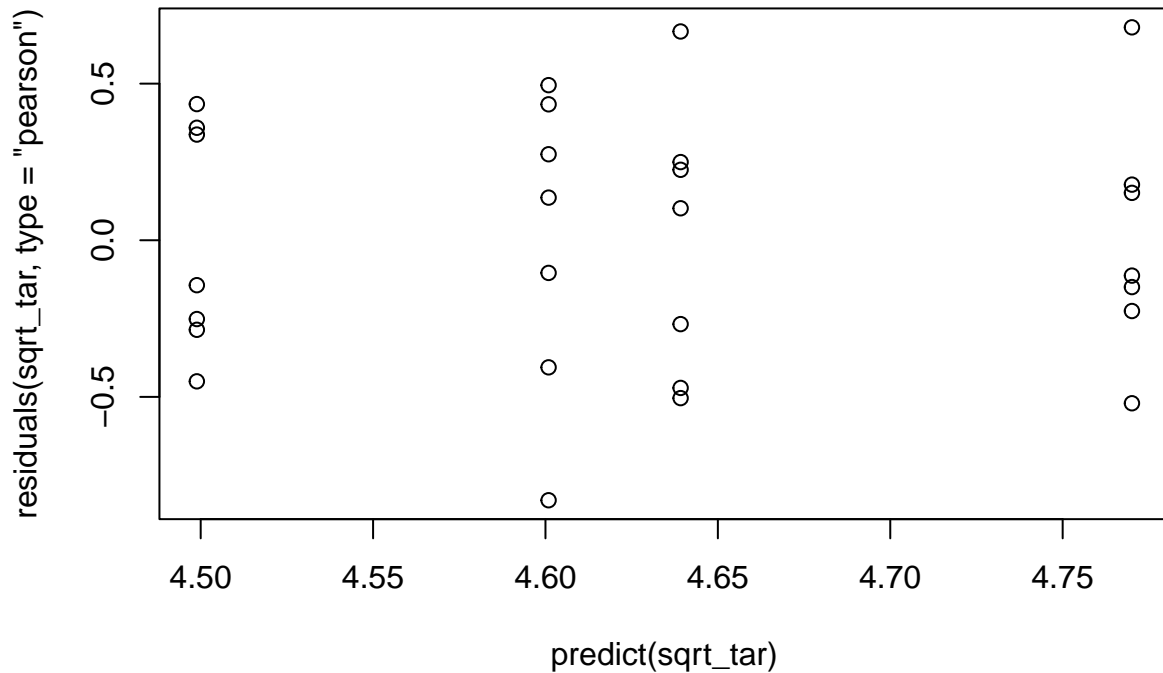
```
#Okay

#BROMUS
sqrt_brom<-glm(sqrt_biomass~treatment,
               family=gaussian(link="identity"),
               data=data_bromus)
#Check heteroskedasticity
plot(predict(sqrt_brom), residuals(sqrt_brom, type = "pearson"))
```

```
#Okay

#TARAXACUM
sqrt_tar<-glm(sqrt_biomass~treatment,
              family=gaussian(link="identity"),
              data=data_taraxacum)
#Check heteroskedasticity
plot(predict(sqrt_tar), residuals(sqrt_tar, type = "pearson"))
```



```
#Compressed residual variance (underdispersed residuals, overfit model)

#Variation within species groups does not allow for all data to be transformed
#or not trasnfored (i.e. variance is underdispersed when transformed
#for taraxacum and gaillardia)

#Try a generalised least square (GLS) model that allows variance to differ
#between species groups

#No variance structure
gls_no_var <- gls(biomass ~ treatment * species,
                  data = data)
summary(gls_no_var)

## Generalized least squares fit by REML
## Model: biomass ~ treatment * species
## Data: data
##      AIC      BIC   logLik
## 735.126 778.7199 -350.563
##
## Coefficients:
##
##              Value Std.Error   t-value p-value
## (Intercept)    35.60571   2.997100  11.880056  0.0000
## treatment240448 -16.62571   4.238539  -3.922511  0.0002
## treatment240720 -13.07143   4.238539  -3.083947  0.0027
```

```

## treatmentControl          -9.11143  4.238539 -2.149662  0.0341
## speciesFestuca            2.57429  4.238539  0.607352  0.5451
## speciesGaillardia        -29.35857  4.238539 -6.926578  0.0000
## speciesTaraxacum         -14.23857  4.238539 -3.359311  0.0011
## treatment240448:speciesFestuca 18.36000  5.994200  3.062961  0.0028
## treatment240720:speciesFestuca 18.56143  5.994200  3.096565  0.0026
## treatmentControl:speciesFestuca  9.29857  5.994200  1.551262  0.1241
## treatment240448:speciesGaillardia 21.24000  5.994200  3.543426  0.0006
## treatment240720:speciesGaillardia 19.74714  5.994200  3.294375  0.0014
## treatmentControl:speciesGaillardia 11.79000  5.994200  1.966901  0.0521
## treatment240448:speciesTaraxacum 16.94000  5.994200  2.826065  0.0057
## treatment240720:speciesTaraxacum 14.58286  5.994200  2.432828  0.0168
## treatmentControl:speciesTaraxacum  8.09857  5.994200  1.351068  0.1798
##
## Correlation:
##                               (Intr) tr240448 tr240720 trtmnC spcsFs
## treatment240448             -0.707
## treatment240720             -0.707  0.500
## treatmentControl             -0.707  0.500  0.500
## speciesFestuca               -0.707  0.500  0.500  0.500
## speciesGaillardia            -0.707  0.500  0.500  0.500  0.500
## speciesTaraxacum             -0.707  0.500  0.500  0.500  0.500
## treatment240448:speciesFestuca  0.500 -0.707 -0.354 -0.354 -0.707
## treatment240720:speciesFestuca  0.500 -0.354 -0.707 -0.354 -0.707
## treatmentControl:speciesFestuca  0.500 -0.354 -0.354 -0.707 -0.707
## treatment240448:speciesGaillardia 0.500 -0.707 -0.354 -0.354 -0.354
## treatment240720:speciesGaillardia 0.500 -0.354 -0.707 -0.354 -0.354
## treatmentControl:speciesGaillardia 0.500 -0.354 -0.354 -0.707 -0.354
## treatment240448:speciesTaraxacum 0.500 -0.707 -0.354 -0.354 -0.354
## treatment240720:speciesTaraxacum 0.500 -0.354 -0.707 -0.354 -0.354
## treatmentControl:speciesTaraxacum 0.500 -0.354 -0.354 -0.707 -0.354
##                               spcsGl spcsTr t240448:F t240720:F trtC:F
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum           0.500
## treatment240448:speciesFestuca -0.354 -0.354
## treatment240720:speciesFestuca -0.354 -0.354  0.500
## treatmentControl:speciesFestuca -0.354 -0.354  0.500  0.500
## treatment240448:speciesGaillardia -0.707 -0.354  0.500  0.250  0.250
## treatment240720:speciesGaillardia -0.707 -0.354  0.250  0.500  0.250
## treatmentControl:speciesGaillardia -0.707 -0.354  0.250  0.250  0.500
## treatment240448:speciesTaraxacum -0.354 -0.707  0.500  0.250  0.250
## treatment240720:speciesTaraxacum -0.354 -0.707  0.250  0.500  0.250
## treatmentControl:speciesTaraxacum -0.354 -0.707  0.250  0.250  0.500
##                               t240448:G t240720:G trtC:G t240448:T
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum

```

```

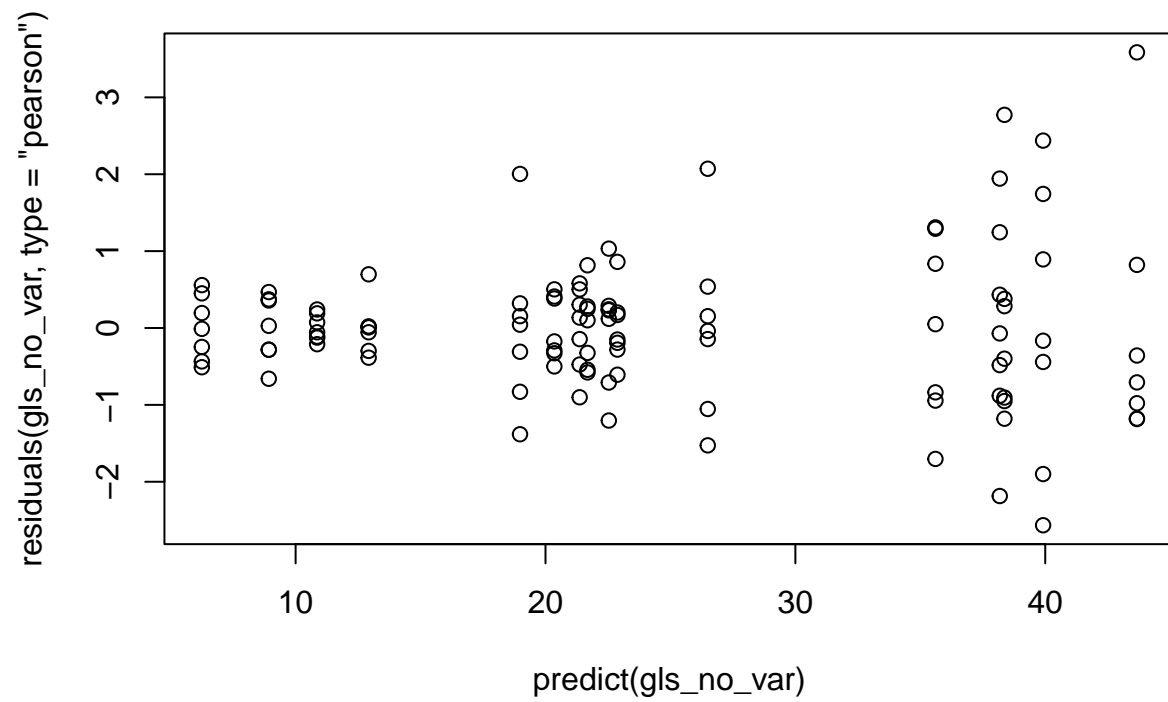
## treatment240448:speciesFestuca
## treatment240720:speciesFestuca
## treatmentControl:speciesFestuca
## treatment240448:speciesGaillardia
## treatment240720:speciesGaillardia    0.500
## treatmentControl:speciesGaillardia    0.500    0.500
## treatment240448:speciesTaraxacum    0.500    0.250    0.250
## treatment240720:speciesTaraxacum    0.250    0.500    0.250    0.500
## treatmentControl:speciesTaraxacum    0.250    0.250    0.500    0.500
##
##                               t240720:T
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum
## treatment240448:speciesFestuca
## treatment240720:speciesFestuca
## treatmentControl:speciesFestuca
## treatment240448:speciesGaillardia
## treatment240720:speciesGaillardia
## treatmentControl:speciesGaillardia
## treatment240448:speciesTaraxacum
## treatment240720:speciesTaraxacum
## treatmentControl:speciesTaraxacum    0.500
##
## Standardized residuals:
##           Min           Q1           Med           Q3           Max
## -2.56561939 -0.47705640 -0.02468154  0.37409653  3.58530942
##
## Residual standard error: 7.929581
## Degrees of freedom: 112 total; 96 residual

```

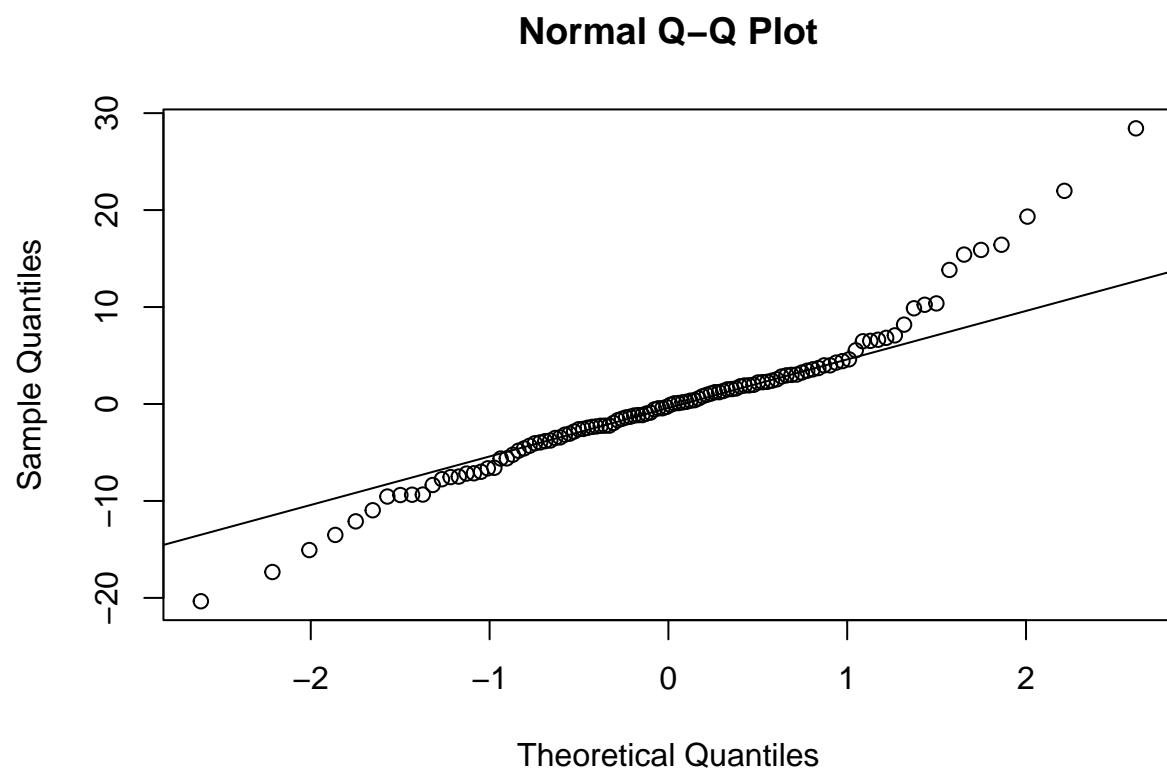
```

#Check residuals
plot(predict(gls_no_var), residuals(gls_no_var, type = "pearson"))

```

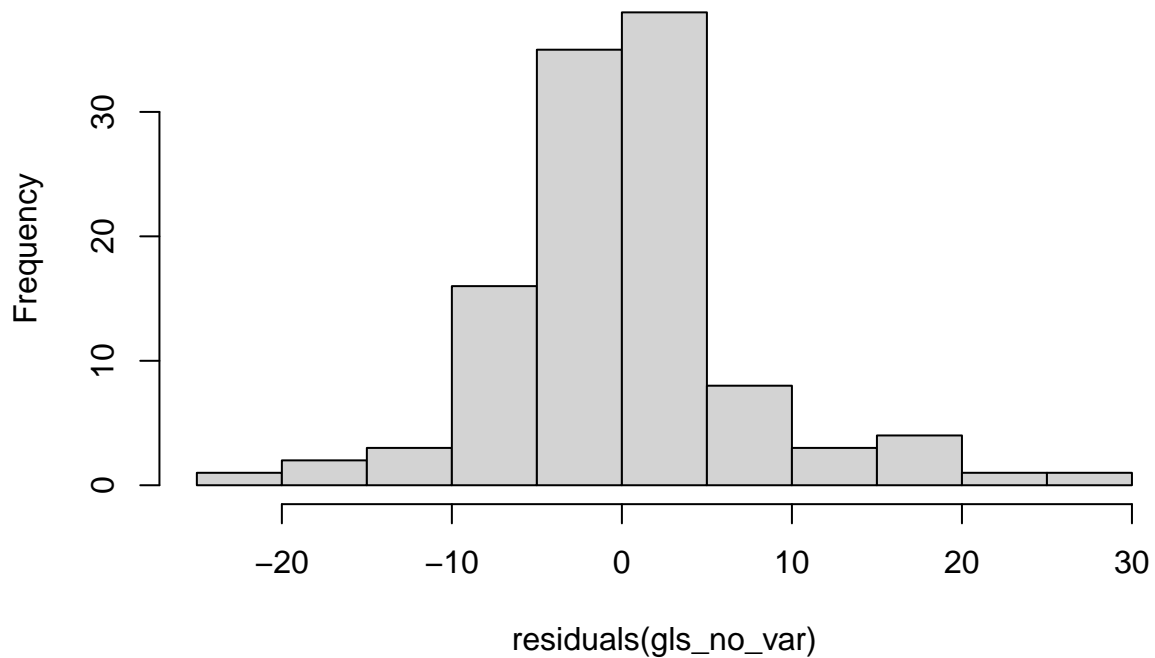


```
qqnorm(residuals(gls_no_var)); qqline(residuals(gls_no_var))
```



```
hist(residuals(gls_no_var))
```

Histogram of residuals(gls_no_var)



```
#Heteroskedastic
```

```
#additive model
```

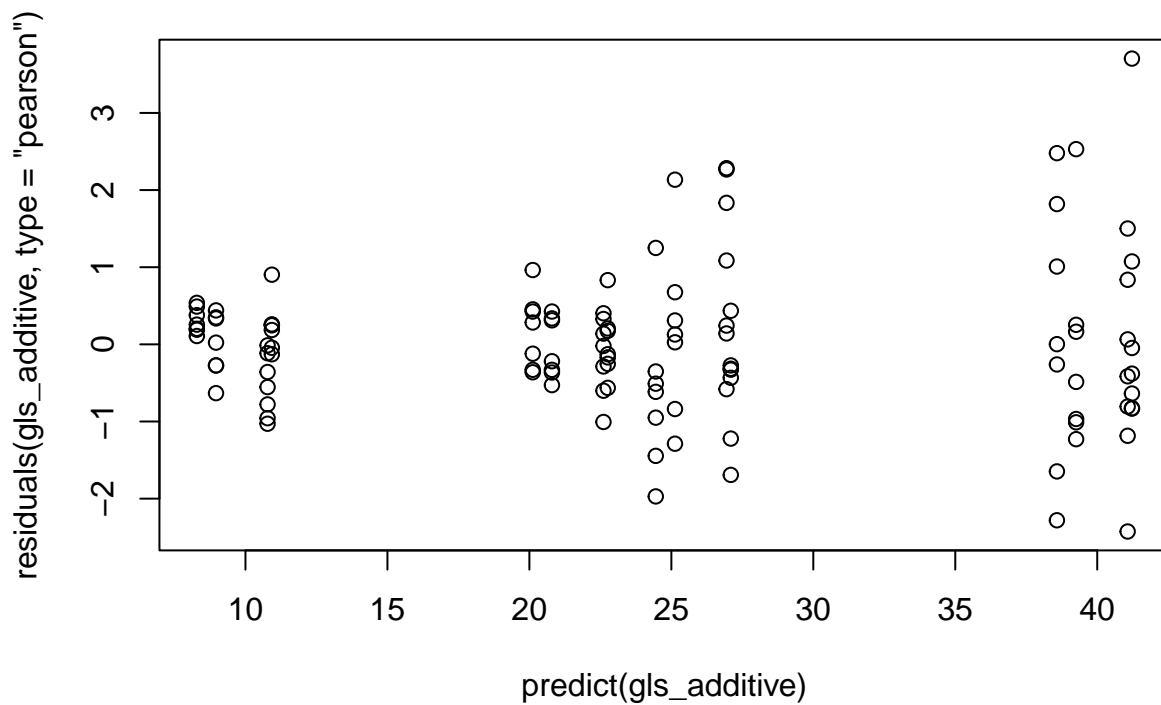
```
gls_additive <- gls(biomass ~ treatment + species,
                    data = data)
summary(gls_additive)
```

```
## Generalized least squares fit by REML
## Model: biomass ~ treatment + species
## Data: data
##      AIC      BIC    logLik
## 781.2275 802.4592 -382.6137
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  26.942054  2.083888  12.928743  0.0000
## treatment240448 -2.490714  2.227770  -1.118030  0.2661
## treatment240720  0.151429  2.227770  0.067973  0.9459
## treatmentControl -1.814643  2.227770 -0.814556  0.4172
## speciesFestuca  14.129286  2.227770  6.342345  0.0000
## speciesGaillardia -16.164286  2.227770 -7.255814  0.0000
## speciesTaraxacum -4.333214  2.227770 -1.945090  0.0544
##
## Correlation:
##              (Intr) t24044 t24072 trtmnC spcsFs spcsGl
## treatment240448 -0.535
```

```
## treatment240720 -0.535 0.500
## treatmentControl -0.535 0.500 0.500
## speciesFestuca -0.535 0.000 0.000 0.000
## speciesGaillardia -0.535 0.000 0.000 0.000 0.500
## speciesTaraxacum -0.535 0.000 0.000 0.000 0.500 0.500
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.42591473 -0.53476831 -0.03227355 0.33993805 3.70428147
##
## Residual standard error: 8.335552
## Degrees of freedom: 112 total; 105 residual
```

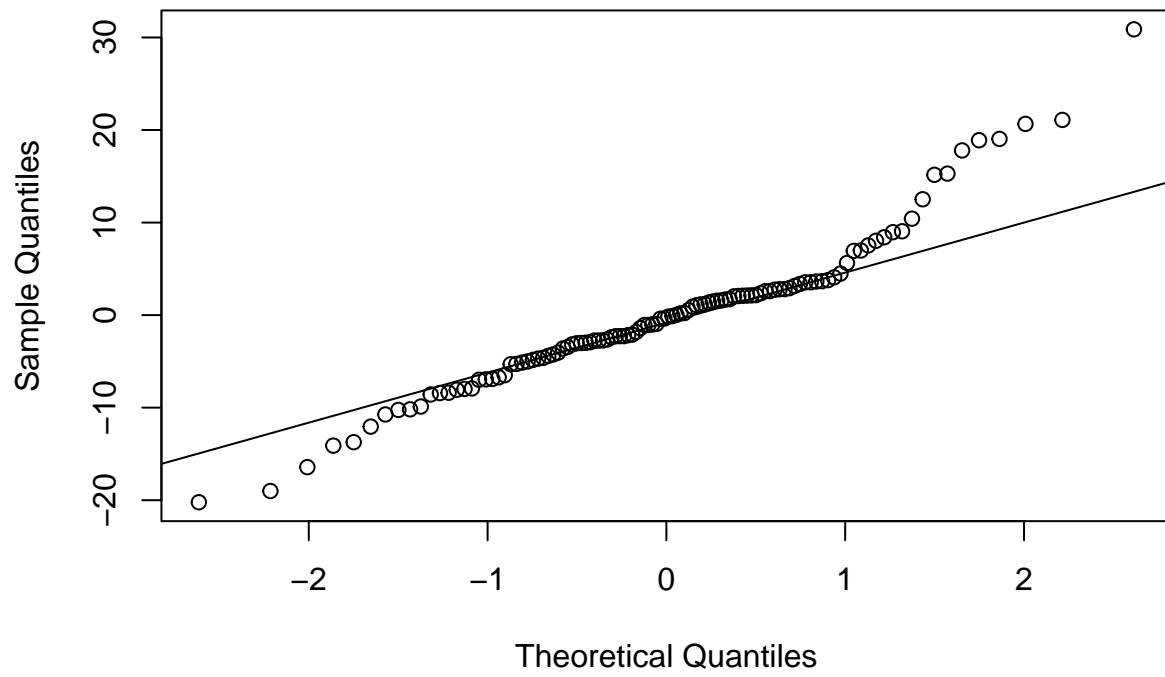
```
#Check residuals
```

```
plot(predict(gls_additive), residuals(gls_additive, type = "pearson"))
```



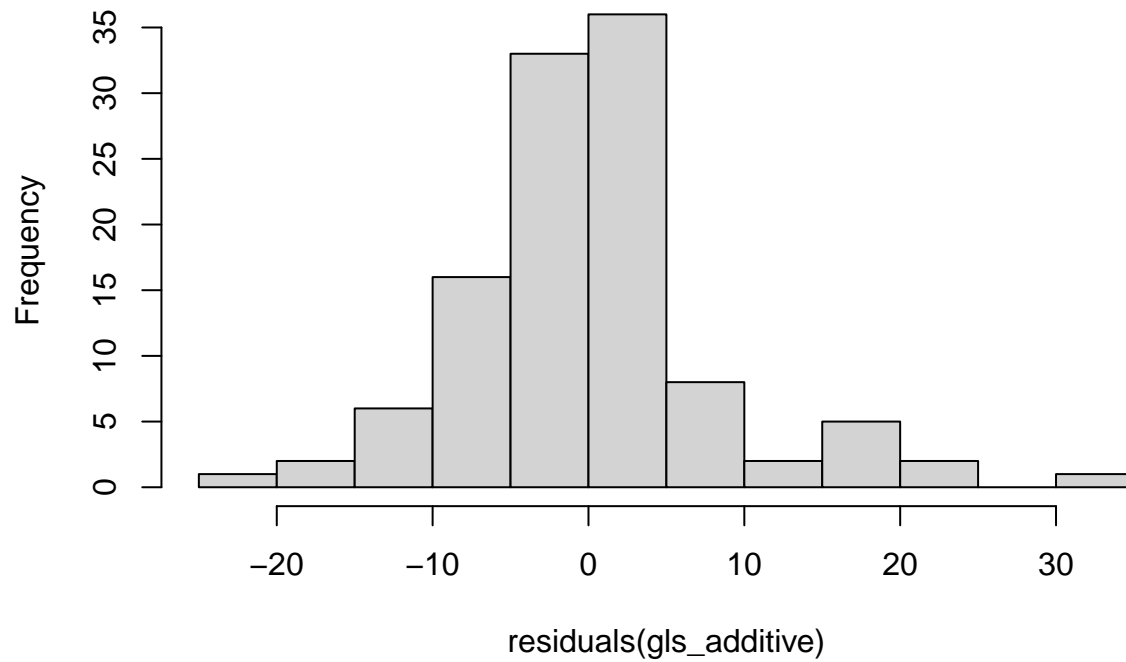
```
qqnorm(residuals(gls_additive)); qqline(residuals(gls_additive))
```


Normal Q-Q Plot



```
hist(residuals(gls_additive))
```

Histogram of residuals(gls_additive)



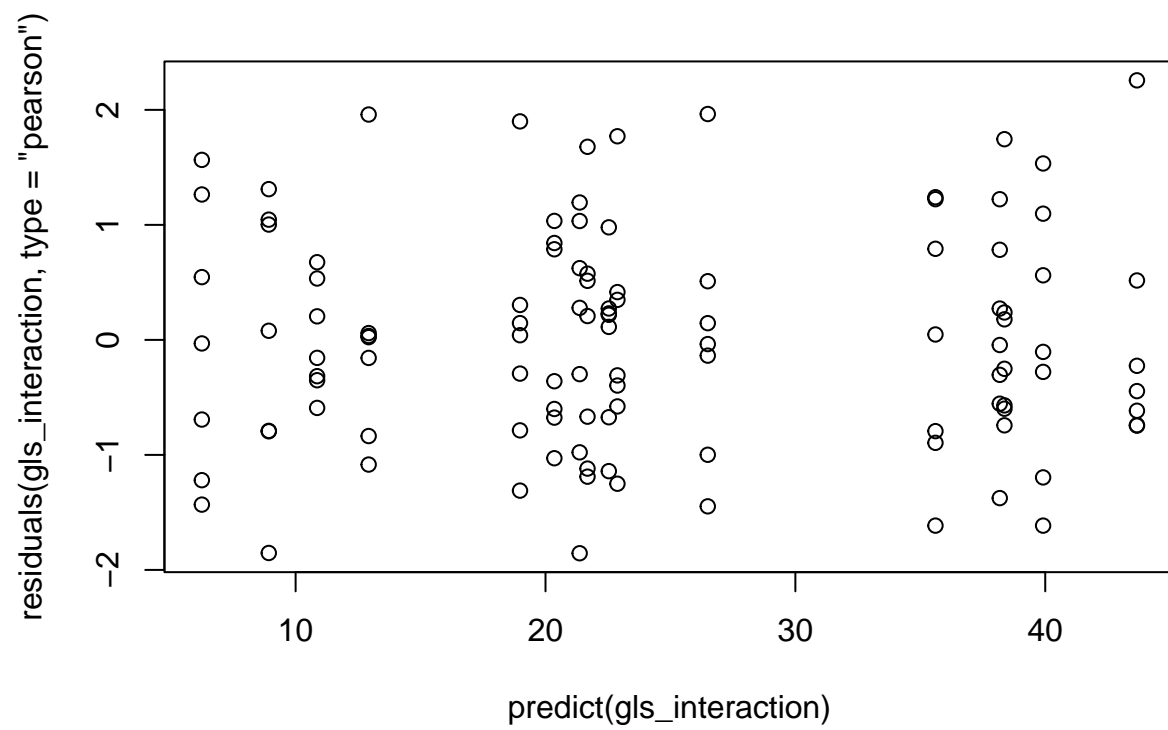
```
#Heteroskedastic
```

```
#Fit GLS model with species-specific variance structure
```

```
gls_interaction <- gls(biomass ~ treatment * species,  
  data = data,  
  weights = varIdent(form = ~ 1 | species))
```

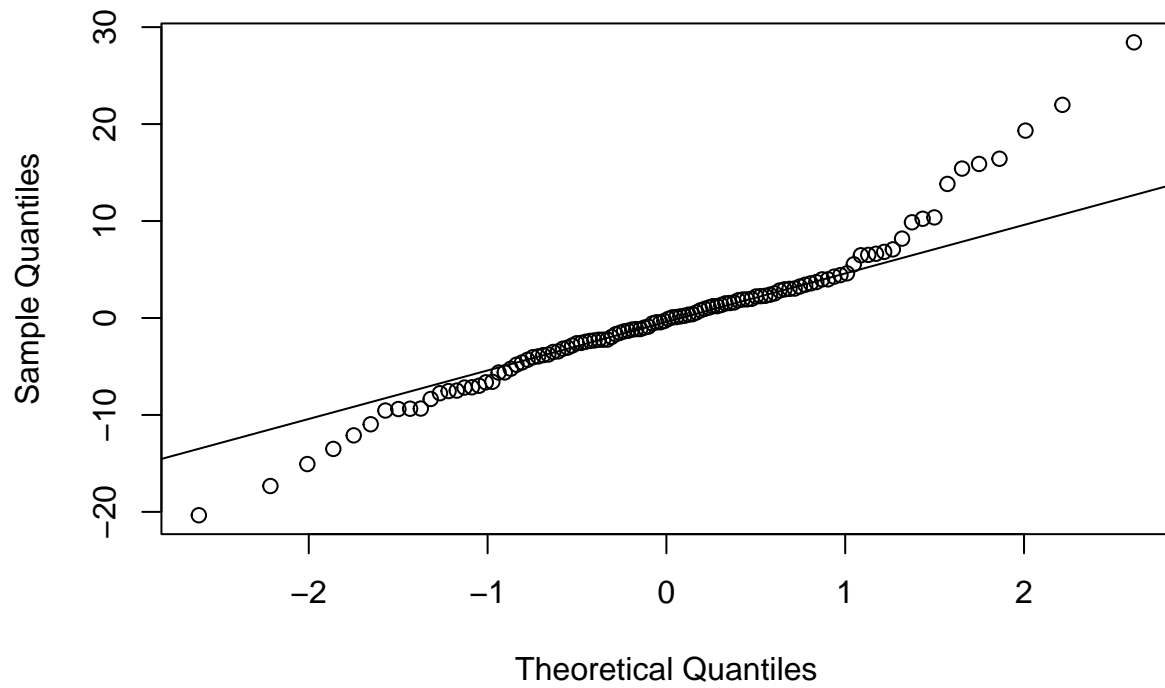
```
#Check residuals
```

```
plot(predict(gls_interaction), residuals(gls_interaction, type = "pearson"))
```



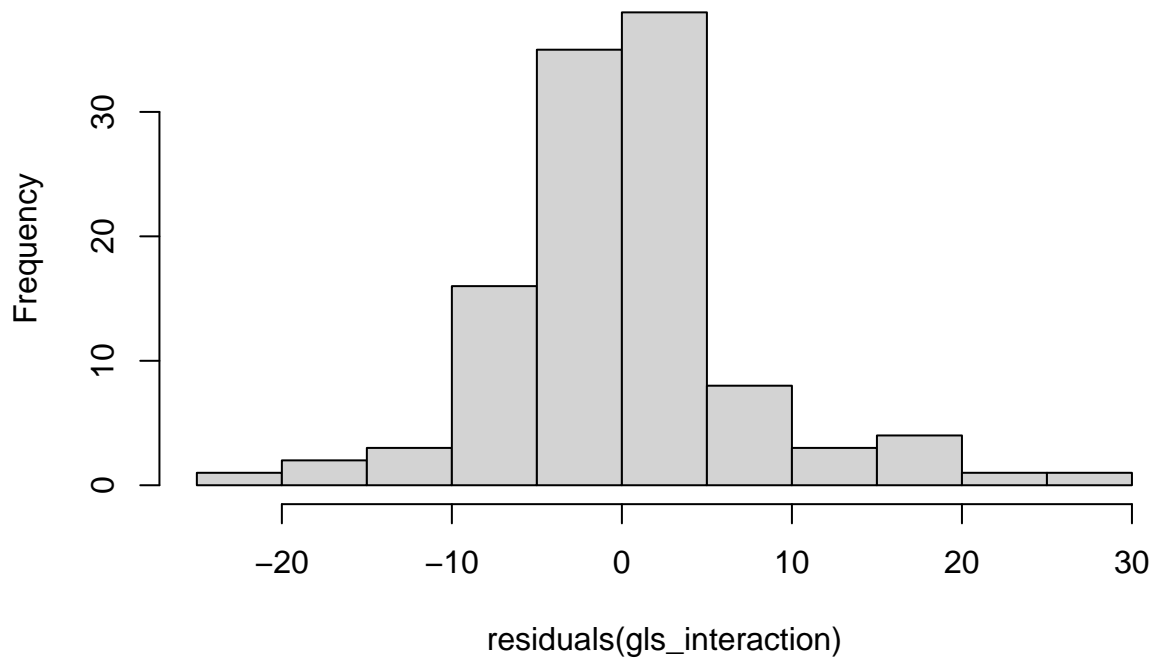
```
qqnorm(residuals(gls_interaction)); qqline(residuals(gls_interaction))
```

Normal Q-Q Plot



```
#Struggles to predicat at higher and lower values  
hist(residuals(gls_interaction))
```

Histogram of residuals(gls_interaction)



#Good

`summary(gls_interaction)`

```
## Generalized least squares fit by REML
##   Model: biomass ~ treatment * species
##   Data: data
##       AIC      BIC    logLik
##  681.7433 733.0302 -320.8716
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | species
## Parameter estimates:
##      Bromus      Festuca Gaillardia  Taraxacum
##  1.0000000  1.5063050  0.3378848  0.4606768
##
## Coefficients:
##                               Value Std.Error   t-value p-value
## (Intercept)                35.60571   3.161265  11.263121  0.0000
## treatment240448            -16.62571   4.470704  -3.718813  0.0003
## treatment240720            -13.07143   4.470704  -2.923796  0.0043
## treatmentControl             -9.11143   4.470704  -2.038030  0.0443
## speciesFestuca               2.57429   5.715647   0.450393  0.6534
## speciesGaillardia           -29.35857   3.336844  -8.798304  0.0000
## speciesTaraxacum            -14.23857   3.480585  -4.090856  0.0001
## treatment240448:speciesFestuca  18.36000   8.083146   2.271393  0.0254
```

```

## treatment240720:speciesFestuca      18.56143  8.083146  2.296312  0.0238
## treatmentControl:speciesFestuca      9.29857  8.083146  1.150365  0.2529
## treatment240448:speciesGaillardia    21.24000  4.719010  4.500944  0.0000
## treatment240720:speciesGaillardia    19.74714  4.719010  4.184594  0.0001
## treatmentControl:speciesGaillardia    11.79000  4.719010  2.498405  0.0142
## treatment240448:speciesTaraxacum     16.94000  4.922291  3.441487  0.0009
## treatment240720:speciesTaraxacum     14.58286  4.922291  2.962616  0.0038
## treatmentControl:speciesTaraxacum      8.09857  4.922291  1.645285  0.1032
##
## Correlation:
##
## (Intr) tr240448 tr240720 trtmnC spcsFs
## treatment240448      -0.707
## treatment240720      -0.707  0.500
## treatmentControl      -0.707  0.500  0.500
## speciesFestuca        -0.553  0.391  0.391  0.391
## speciesGaillardia     -0.947  0.670  0.670  0.670  0.524
## speciesTaraxacum      -0.908  0.642  0.642  0.642  0.502
## treatment240448:speciesFestuca  0.391 -0.553 -0.277 -0.277 -0.707
## treatment240720:speciesFestuca  0.391 -0.277 -0.553 -0.277 -0.707
## treatmentControl:speciesFestuca  0.391 -0.277 -0.277 -0.553 -0.707
## treatment240448:speciesGaillardia 0.670 -0.947 -0.474 -0.474 -0.371
## treatment240720:speciesGaillardia 0.670 -0.474 -0.947 -0.474 -0.371
## treatmentControl:speciesGaillardia 0.670 -0.474 -0.474 -0.947 -0.371
## treatment240448:speciesTaraxacum 0.642 -0.908 -0.454 -0.454 -0.355
## treatment240720:speciesTaraxacum 0.642 -0.454 -0.908 -0.454 -0.355
## treatmentControl:speciesTaraxacum 0.642 -0.454 -0.454 -0.908 -0.355
##
## spcsGl spcsTr t240448:F t240720:F trtC:F
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum      0.860
## treatment240448:speciesFestuca -0.371 -0.355
## treatment240720:speciesFestuca -0.371 -0.355 0.500
## treatmentControl:speciesFestuca -0.371 -0.355 0.500 0.500
## treatment240448:speciesGaillardia -0.707 -0.608 0.524 0.262 0.262
## treatment240720:speciesGaillardia -0.707 -0.608 0.262 0.524 0.262
## treatmentControl:speciesGaillardia -0.707 -0.608 0.262 0.262 0.524
## treatment240448:speciesTaraxacum -0.608 -0.707 0.502 0.251 0.251
## treatment240720:speciesTaraxacum -0.608 -0.707 0.251 0.502 0.251
## treatmentControl:speciesTaraxacum -0.608 -0.707 0.251 0.251 0.502
##
## t240448:G t240720:G trtC:G t240448:T
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum
## treatment240448:speciesFestuca
## treatment240720:speciesFestuca
## treatmentControl:speciesFestuca
## treatment240448:speciesGaillardia
## treatment240720:speciesGaillardia 0.500

```

```
## treatmentControl:speciesGaillardia 0.500 0.500
## treatment240448:speciesTaraxacum 0.860 0.430 0.430
## treatment240720:speciesTaraxacum 0.430 0.860 0.430 0.500
## treatmentControl:speciesTaraxacum 0.430 0.430 0.860 0.500
##
## t240720:T
## treatment240448
## treatment240720
## treatmentControl
## speciesFestuca
## speciesGaillardia
## speciesTaraxacum
## treatment240448:speciesFestuca
## treatment240720:speciesFestuca
## treatmentControl:speciesFestuca
## treatment240448:speciesGaillardia
## treatment240720:speciesGaillardia
## treatmentControl:speciesGaillardia
## treatment240448:speciesTaraxacum
## treatment240720:speciesTaraxacum
## treatmentControl:speciesTaraxacum 0.500
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.8549239 -0.6800594 -0.0336082 0.5651681 2.2565967
##
## Residual standard error: 8.363922
## Degrees of freedom: 112 total; 96 residual
```

```
AIC(gls_no_var)
```

```
## [1] 735.126
```

```
AIC(gls_additive) #Worse fit
```

```
## [1] 781.2275
```

```
AIC(gls_interaction) #Best fit (delta AIC>50)
```

```
## [1] 681.7433
```

```
#Check GLS by species group (simpler models for n=7 sample size)
```

```
#Gaillardia
```

```
gls_gaillardia <- gls(biomass ~ treatment,
                      data = data_gaillardia)
summary(gls_gaillardia)
```

```
## Generalized least squares fit by REML
```

```
## Model: biomass ~ treatment
```

```
## Data: data_gaillardia
```

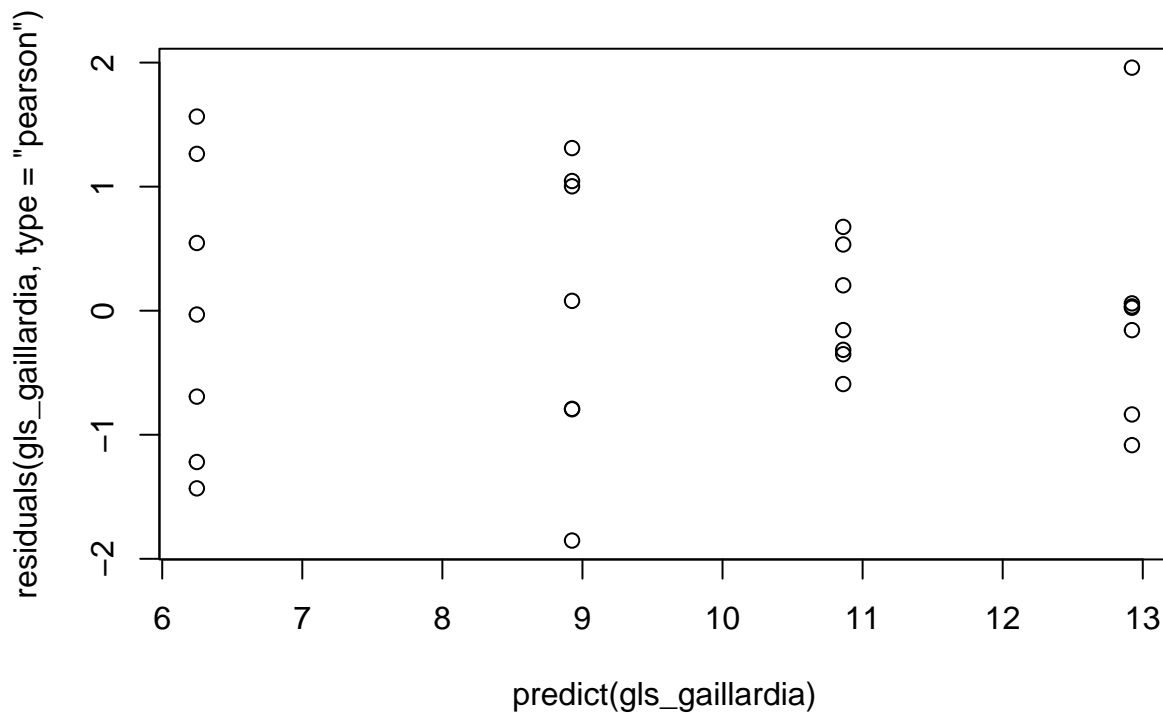
```
## AIC BIC logLik
```

```
## 135.7588 141.6491 -62.8794
```

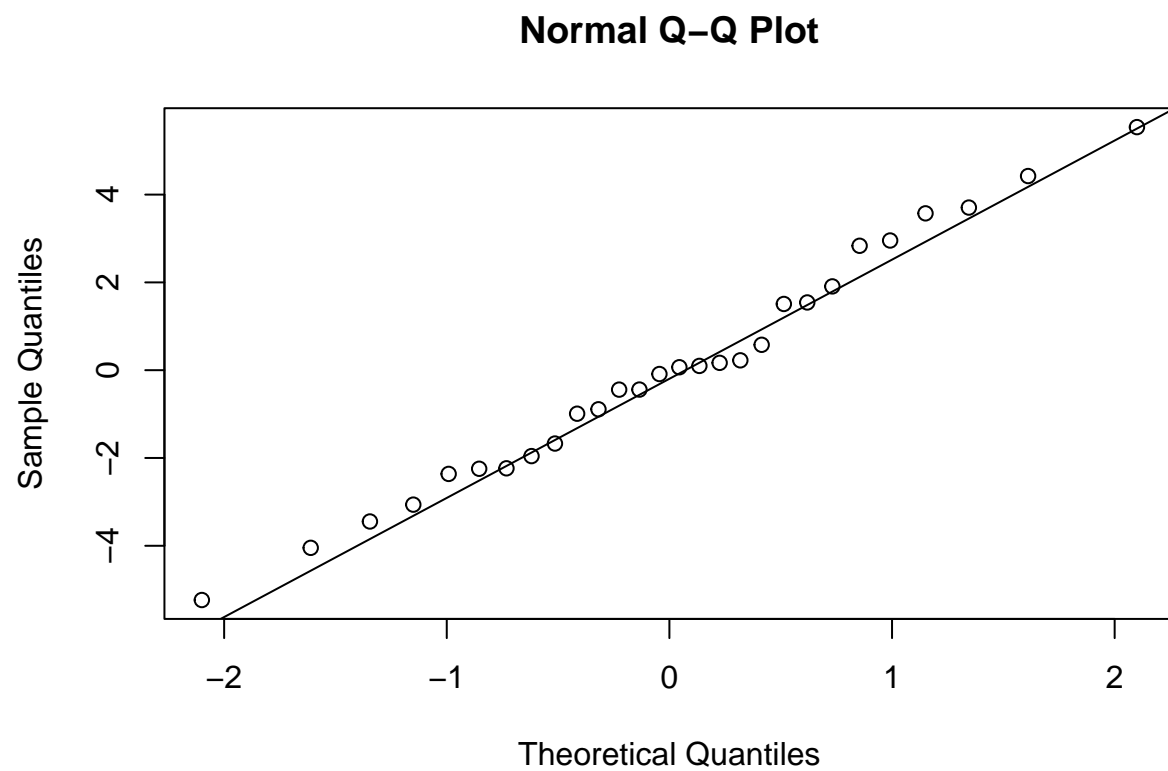
```
##
## Coefficients:
##              Value Std.Error  t-value p-value
## (Intercept)   6.247143  1.068143  5.848599  0.0000
## treatment240448 4.614286  1.510583  3.054639  0.0054
## treatment240720 6.675714  1.510583  4.419296  0.0002
## treatmentControl 2.678571  1.510583  1.773204  0.0889
##
## Correlation:
##              (Intr) t24044 t24072
## treatment240448  -0.707
## treatment240720  -0.707  0.500
## treatmentControl -0.707  0.500  0.500
##
## Standardized residuals:
##              Min           Q1           Med           Q3           Max
## -1.852666730 -0.717181698 -0.003538518  0.578294881  1.959327761
##
## Residual standard error: 2.826042
## Degrees of freedom: 28 total; 24 residual
```

```
#Check residuals
```

```
plot(predict(gls_gaillardia), residuals(gls_gaillardia, type = "pearson"))
```

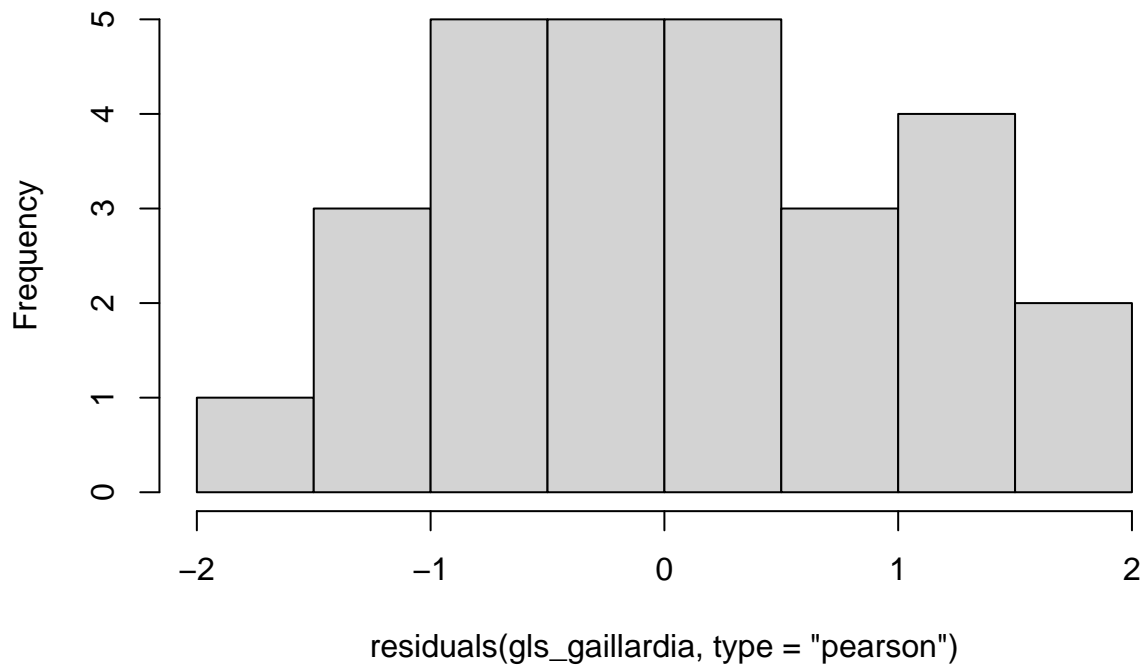



```
qqnorm(residuals(gls_gaillardia)); qqline(residuals(gls_gaillardia)) #God
```



```
hist(residuals(gls_gaillardia, type = "pearson")) #Okay
```

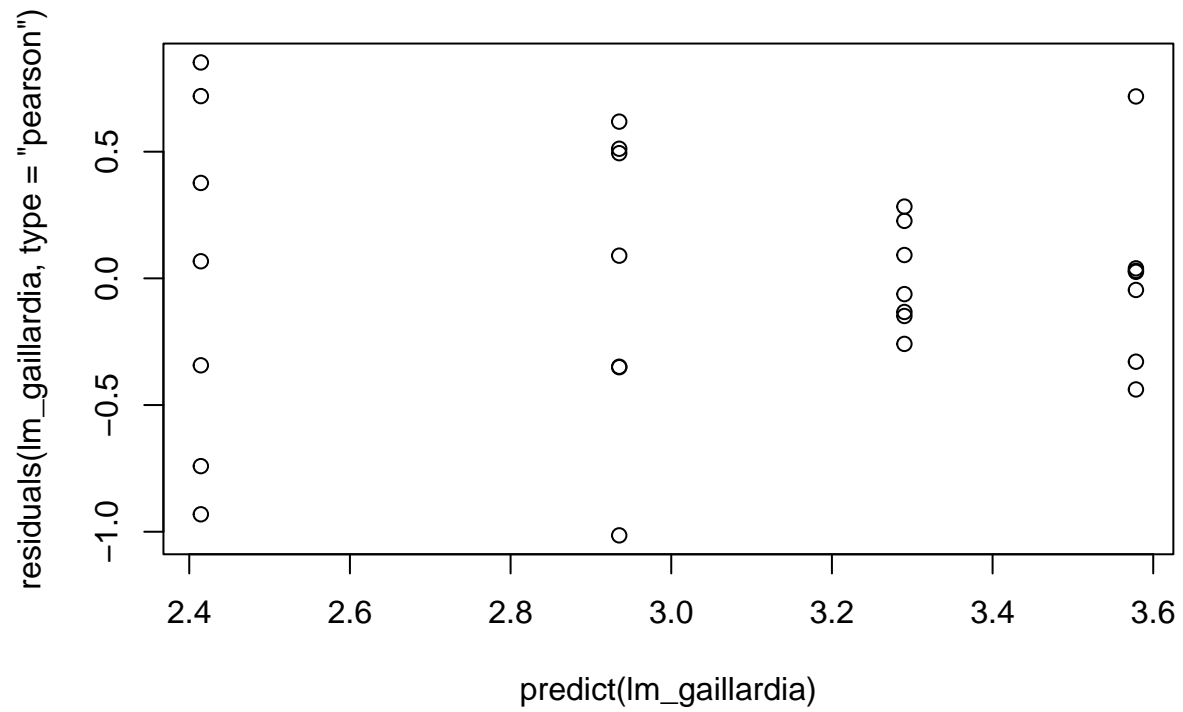
Histogram of residuals(gls_gaillardia, type = "pearson")



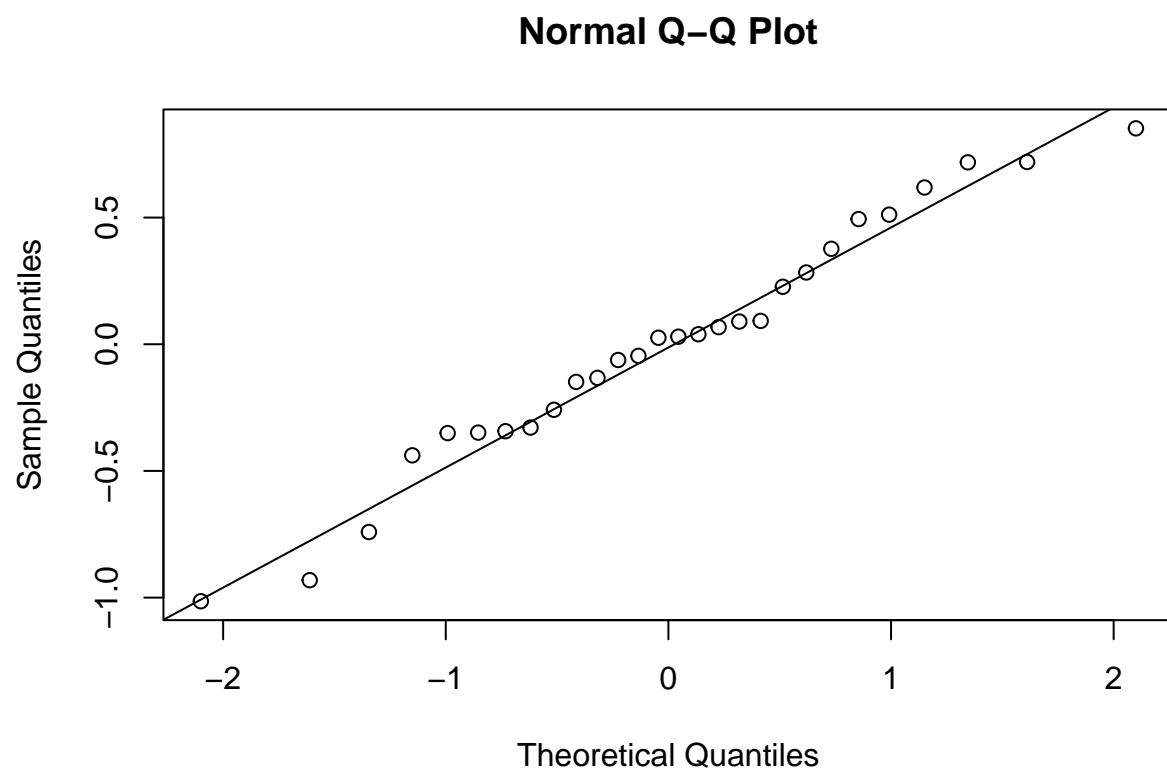
```
#Gaillardia
lm_gaillardia <- lm(sqrt_biomass ~ treatment,
                    data = data_gaillardia)
summary(lm_gaillardia)

##
## Call:
## lm(formula = sqrt_biomass ~ treatment, data = data_gaillardia)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.01432 -0.33245  0.02776  0.30662  0.85207
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.4144     0.1916  12.603  4.5e-12 ***
## treatment240448    0.8758     0.2709   3.233 0.003548 **
## treatment240720    1.1641     0.2709   4.297 0.000248 ***
## treatmentControl    0.5208     0.2709   1.922 0.066498 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5069 on 24 degrees of freedom
## Multiple R-squared:  0.4612, Adjusted R-squared:  0.3939
## F-statistic: 6.849 on 3 and 24 DF,  p-value: 0.001708
```

```
#Check residuals  
plot(predict(lm_gaillardia), residuals(lm_gaillardia, type = "pearson"))
```

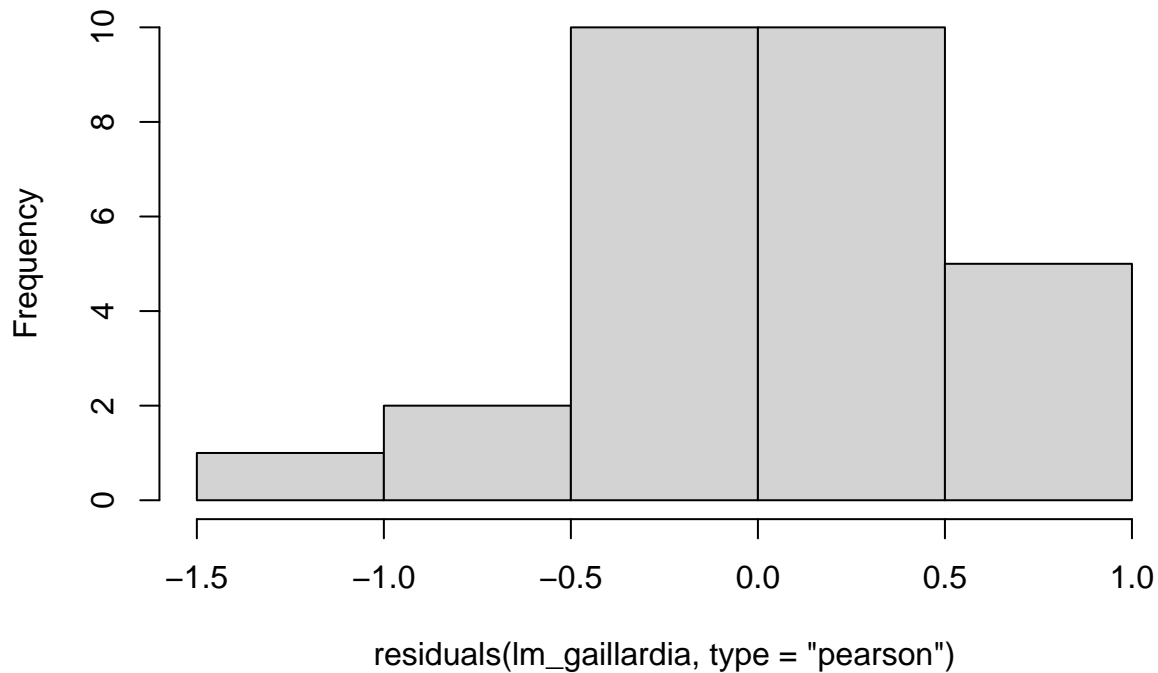


```
qqnorm(residuals(lm_gaillardia)); qqline(residuals(lm_gaillardia)) #God
```



```
hist(residuals(lm_gaillardia, type = "pearson"))
```

Histogram of residuals(lm_gaillardia, type = "pearson")



#GLS is a better fit for gaillardia based on residual diagnostics

#FESTUCA

```
gls_festuca <- gls(biomass ~ treatment,
                  data = data_festuca)
summary(gls_festuca)
```

Generalized least squares fit by REML

Model: biomass ~ treatment

Data: data_festuca

AIC BIC logLik

207.5049 213.3951 -98.75244

##

Coefficients:

Value Std.Error t-value p-value

(Intercept) 38.18000 4.761830 8.017926 0.0000

treatment240448 1.73429 6.734244 0.257532 0.7990

treatment240720 5.49000 6.734244 0.815236 0.4230

treatmentControl 0.18714 6.734244 0.027790 0.9781

##

Correlation:

(Intr) t24044 t24072

treatment240448 -0.707

treatment240720 -0.707 0.500

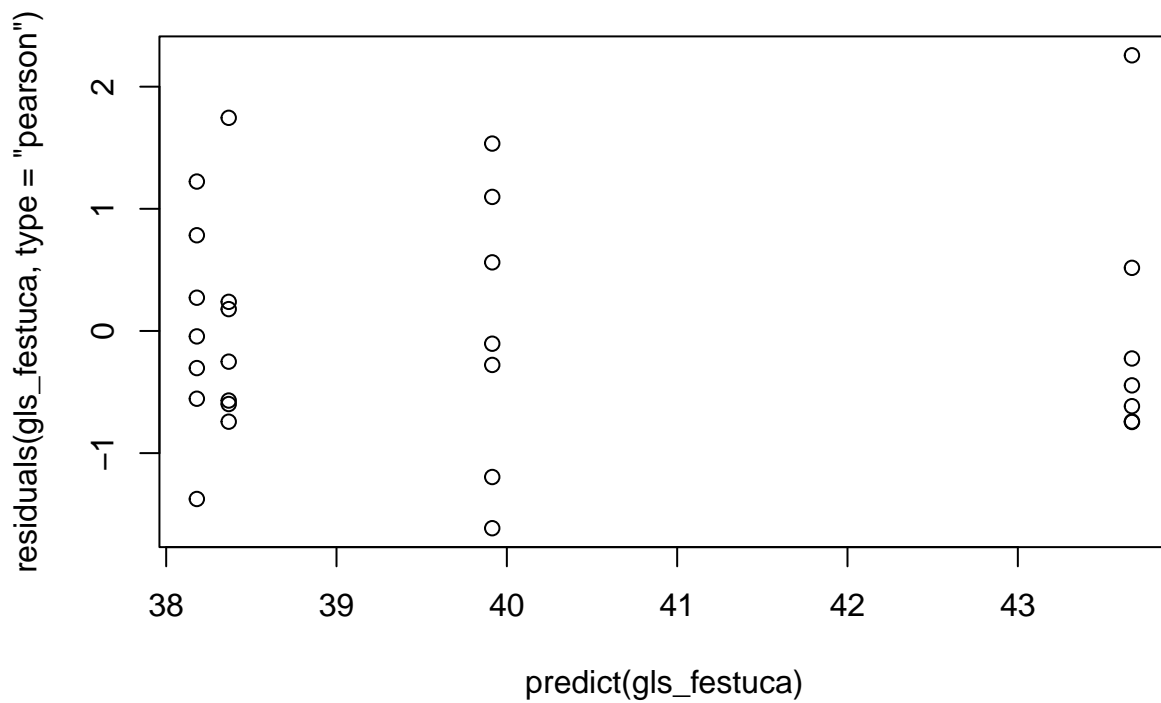
treatmentControl -0.707 0.500 0.500

##

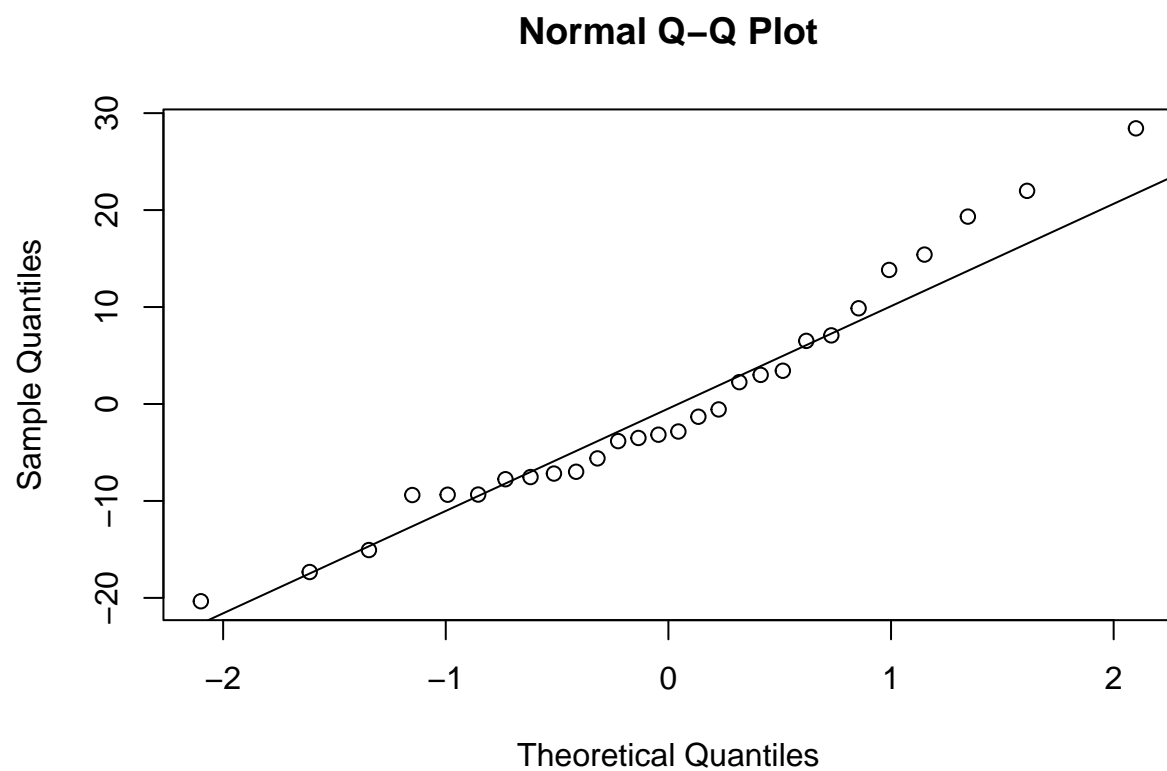
```
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.6148030 -0.6026738 -0.2384048  0.5279491  2.2565967
##
## Residual standard error: 12.59862
## Degrees of freedom: 28 total; 24 residual
```

```
#Check residuals
```

```
plot(predict(gls_festuca), residuals(gls_festuca, type = "pearson"))
```

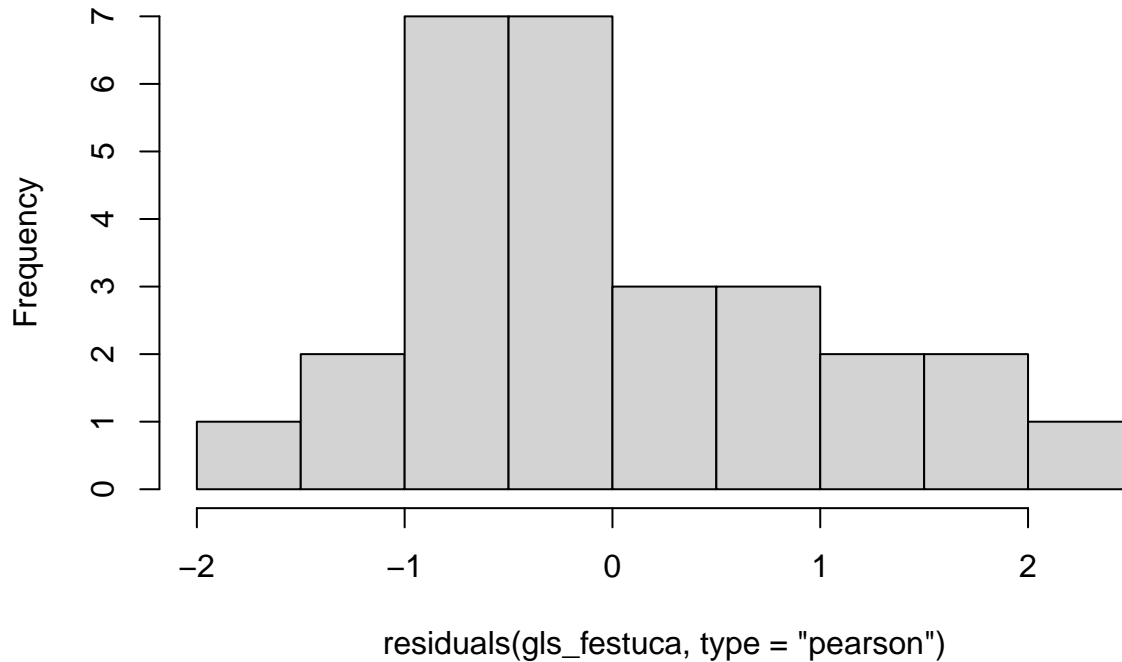


```
qqnorm(residuals(gls_festuca)); qqline(residuals(gls_festuca)) #okay
```



```
hist(residuals(gls_festuca, type = "pearson")) #Okay, slight left tail
```

Histogram of residuals(gls_festuca, type = "pearson")

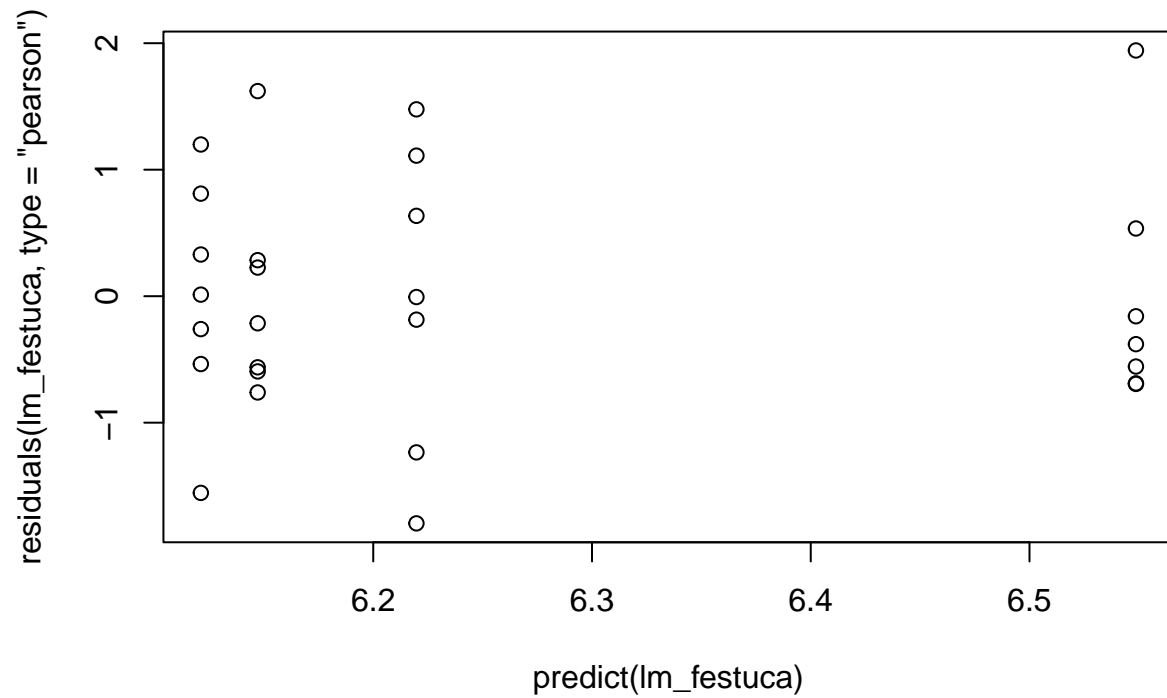


```
#Without block effect
lm_festuca <- lm(sqrt_biomass ~ treatment,
                  data = data_festuca)
summary(lm_festuca)

##
## Call:
## lm(formula = sqrt_biomass ~ treatment, data = data_festuca)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7959 -0.5705 -0.1722  0.5601  1.9425
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    6.12118    0.37107   16.496 1.35e-14 ***
## treatment240448  0.09855    0.52477    0.188   0.853
## treatment240720  0.42748    0.52477    0.815   0.423
## treatmentControl  0.02599    0.52477    0.050   0.961
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9818 on 24 degrees of freedom
## Multiple R-squared:  0.03418,    Adjusted R-squared:  -0.08655
## F-statistic: 0.2831 on 3 and 24 DF,  p-value: 0.8371
```

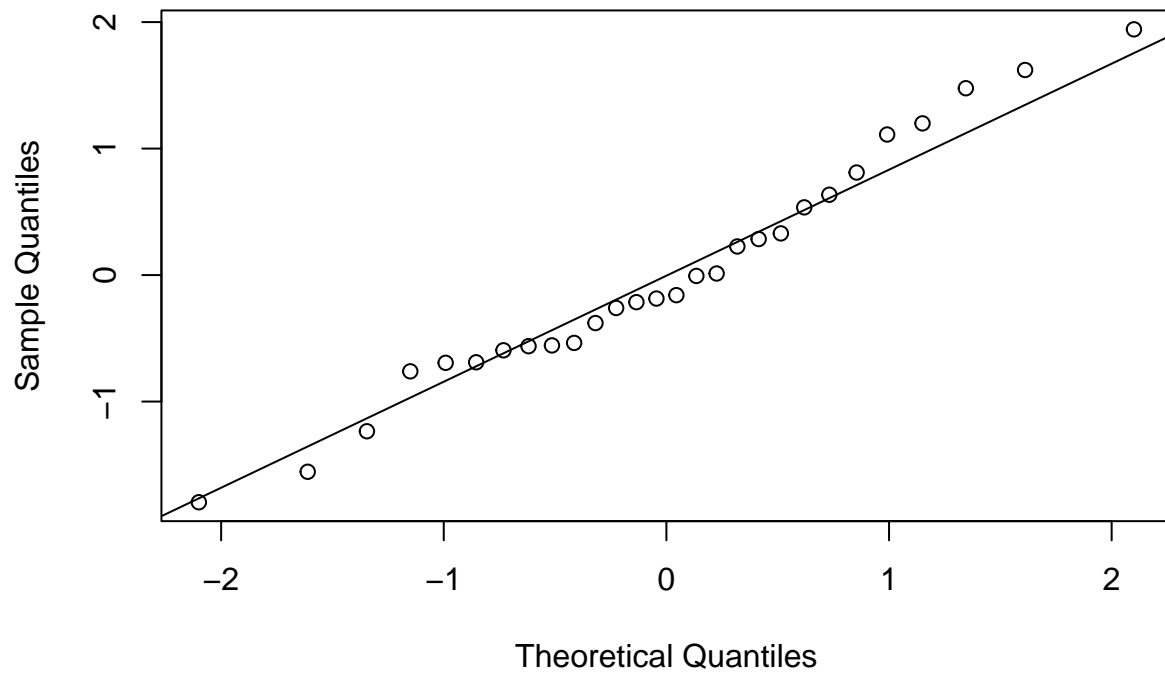


```
#Check residuals  
plot(predict(lm_festuca), residuals(lm_festuca, type = "pearson"))
```



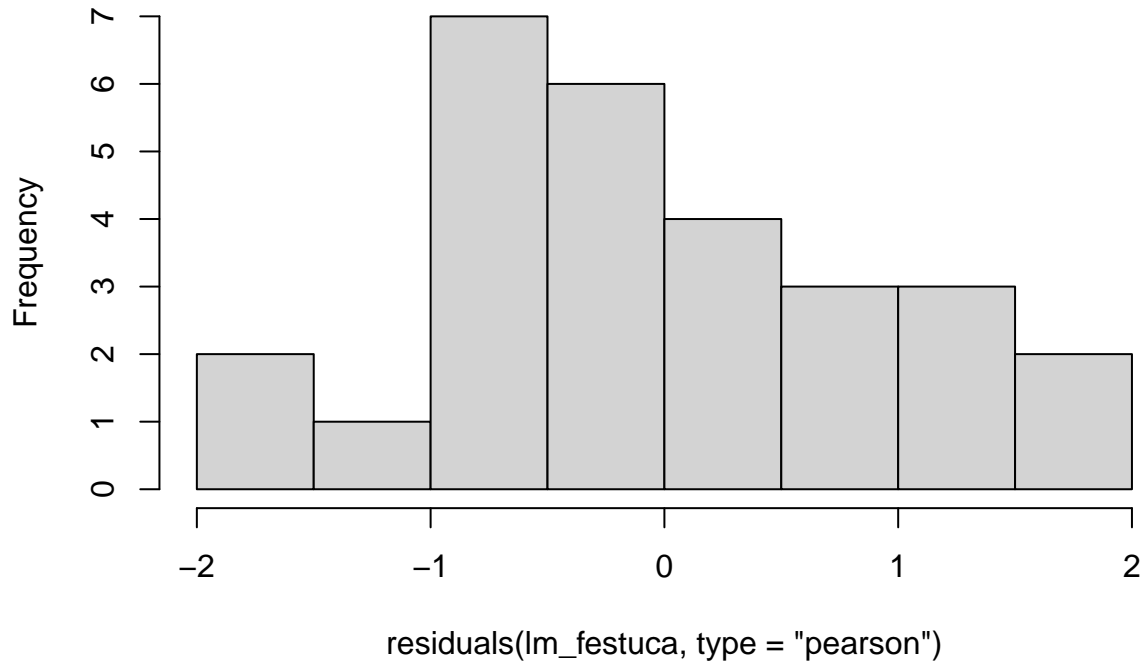
```
qqnorm(residuals(lm_festuca)); qqline(residuals(lm_festuca)) #okay
```

Normal Q-Q Plot



```
hist(residuals(lm_festuca, type = "pearson"))
```

Histogram of residuals(lm_festuca, type = "pearson")



#GLS is a better fit for festuca based on residual diagnostics

#BROMUS

```
gls_bromus<- gls(biomass ~ treatment,  
                 data = data_bromus)  
summary(gls_bromus)
```

Generalized least squares fit by REML

Model: biomass ~ treatment

Data: data_bromus

AIC BIC logLik

187.8412 193.7315 -88.9206

##

Coefficients:

	Value	Std.Error	t-value	p-value
--	-------	-----------	---------	---------

## (Intercept)	35.60571	3.161265	11.263121	0.0000
----------------	----------	----------	-----------	--------

## treatment240448	-16.62571	4.470705	-3.718813	0.0011
--------------------	-----------	----------	-----------	--------

## treatment240720	-13.07143	4.470705	-2.923796	0.0074
--------------------	-----------	----------	-----------	--------

## treatmentControl	-9.11143	4.470705	-2.038030	0.0527
---------------------	----------	----------	-----------	--------

##

Correlation:

	(Intr)	t24044	t24072
--	--------	--------	--------

## treatment240448	-0.707		
--------------------	--------	--	--

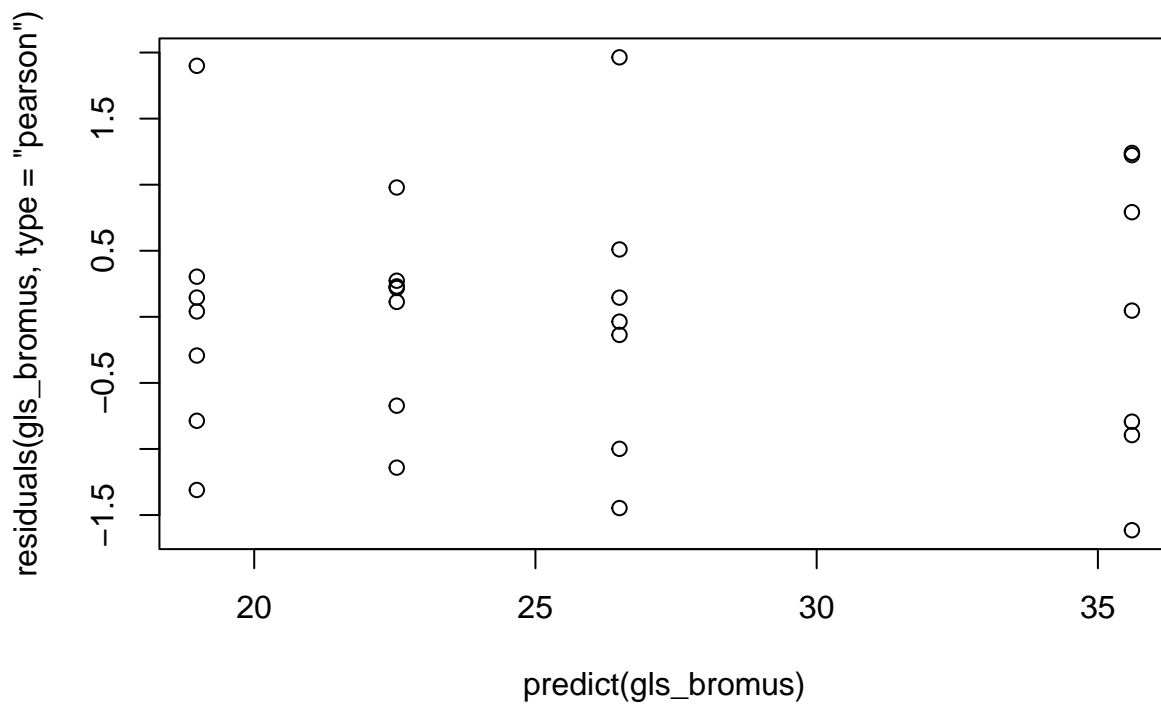
## treatment240720	-0.707	0.500	
--------------------	--------	-------	--

## treatmentControl	-0.707	0.500	0.500
---------------------	--------	-------	-------

##

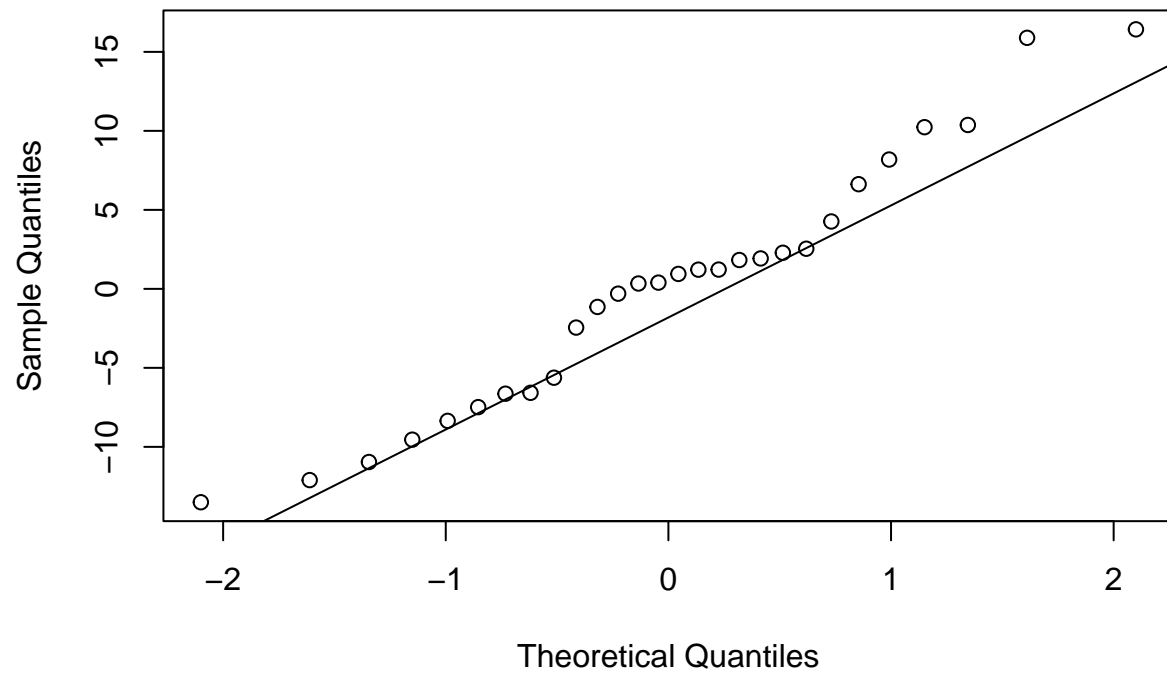
```
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.61475846 -0.78837755  0.08010596  0.35526736  1.96387696
##
## Residual standard error: 8.363922
## Degrees of freedom: 28 total; 24 residual
```

```
#check residuals
plot(predict(gls_bromus), residuals(gls_bromus, type = "pearson")) #Okay residual
```



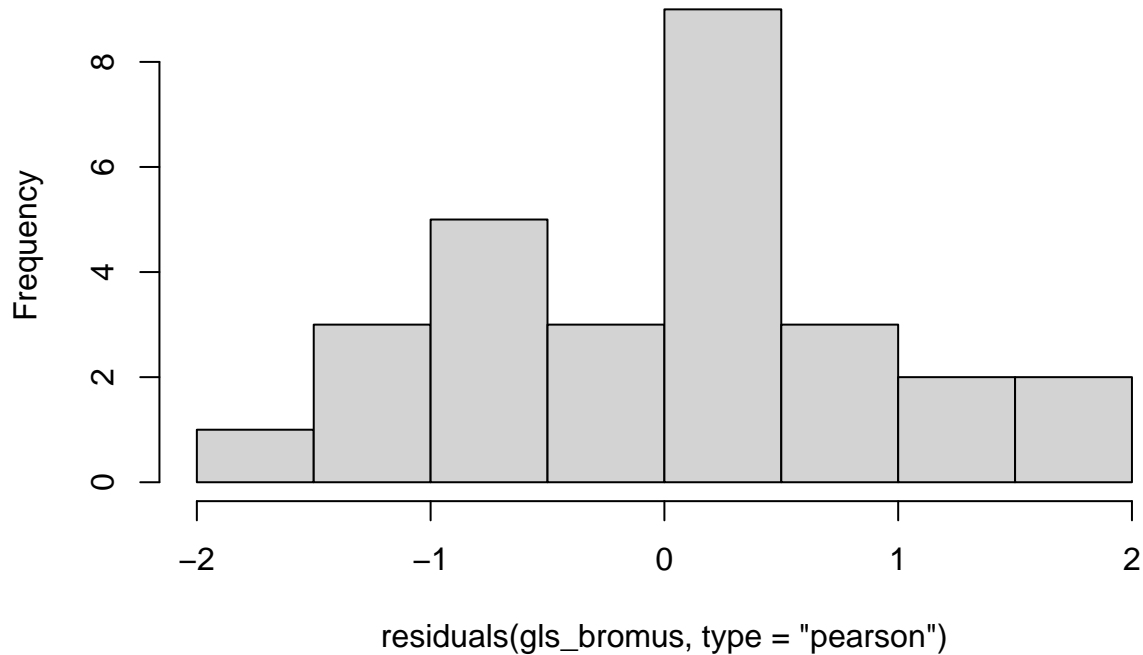
```
#spread
qqnorm(residuals(gls_bromus)); qqline(residuals(gls_bromus)) #okay
```

Normal Q-Q Plot



```
hist(residuals(gls_bromus, type="pearson")) #Okay
```

Histogram of residuals(gls_bromus, type = "pearson")

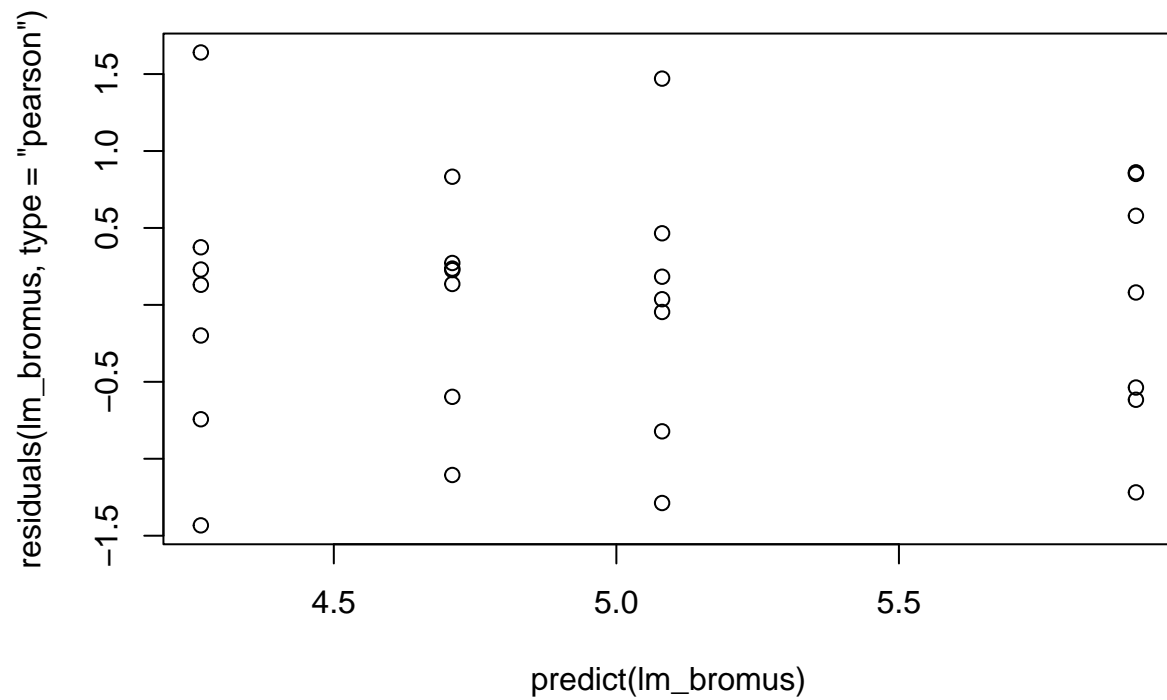


#residuals still centered around 0

```
lm_bromus <- lm(sqrt_biomass ~ treatment,
  data = data_bromus)
summary(lm_bromus)
```

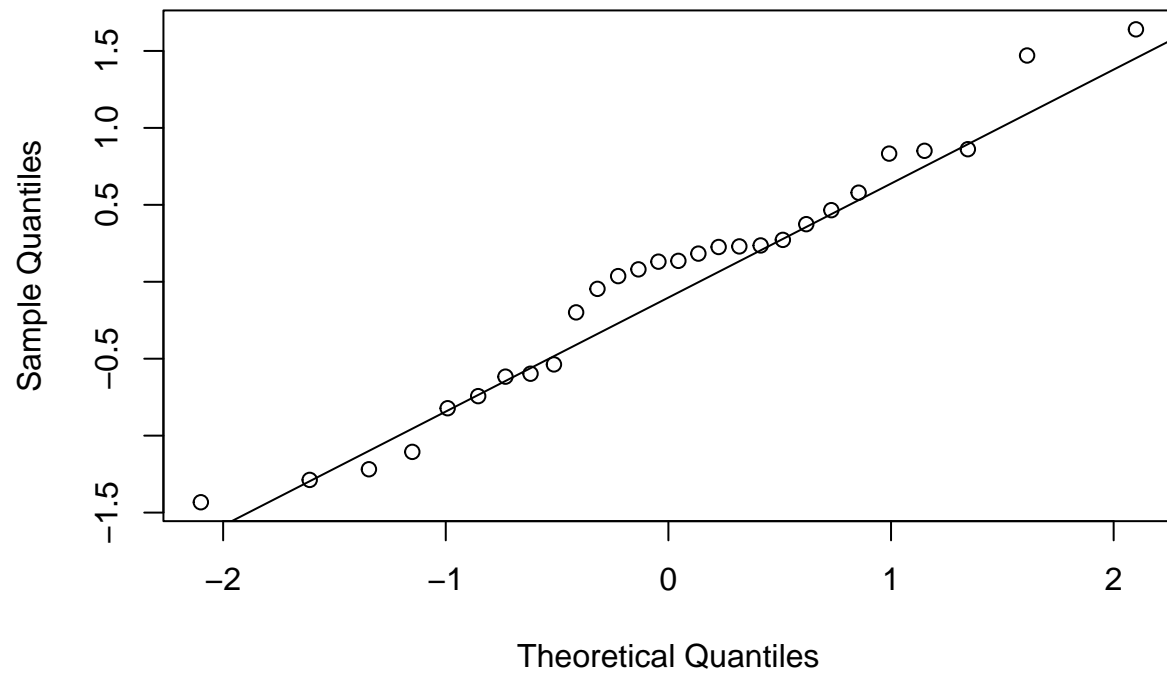
```
##
## Call:
## lm(formula = sqrt_biomass ~ treatment, data = data_bromus)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4327 -0.6023  0.1333  0.3970  1.6404
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.9194     0.3155  18.759 7.62e-16 ***
## treatment240448  -1.6547     0.4463  -3.708  0.0011 **
## treatment240720  -1.2098     0.4463  -2.711  0.0122 *
## treatmentControl -0.8385     0.4463  -1.879  0.0724 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8349 on 24 degrees of freedom
## Multiple R-squared:  0.3819, Adjusted R-squared:  0.3047
## F-statistic: 4.944 on 3 and 24 DF, p-value: 0.008196
```

```
#Check residuals
plot(predict(lm_bromus), residuals(lm_bromus, type = "pearson"))
```



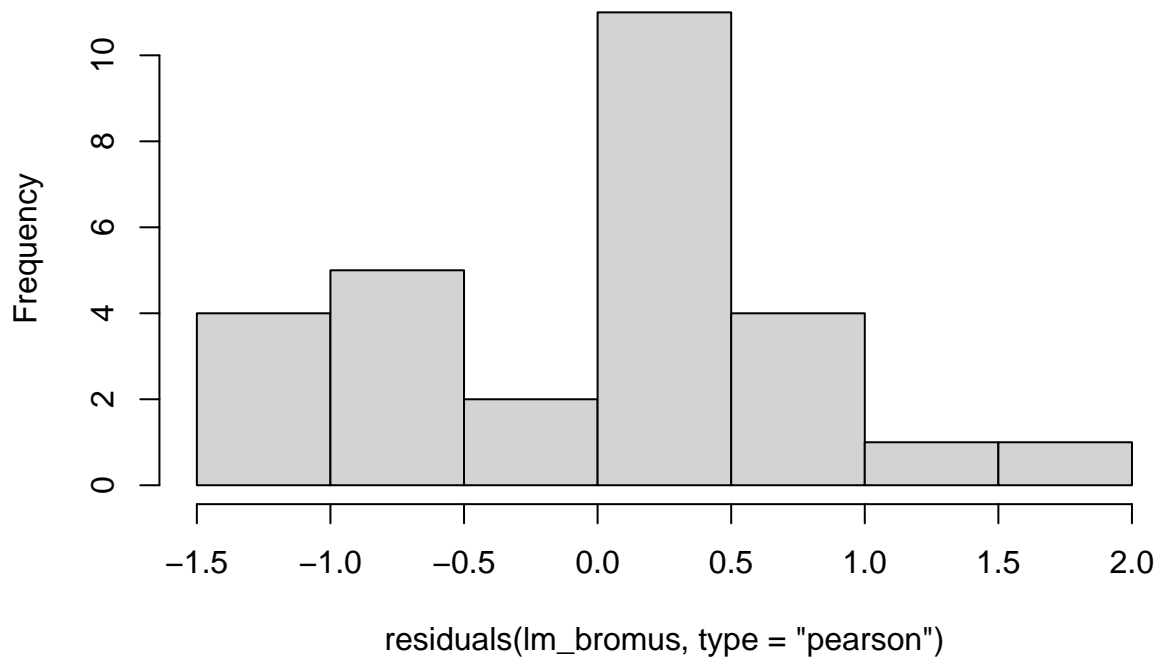
```
qqnorm(residuals(lm_bromus)); qqline(residuals(lm_bromus)) #meh
```

Normal Q-Q Plot



```
hist(residuals(lm_bromus, type = "pearson")) #Does not fit expected distribution, bimodal
```


Histogram of residuals(lm_bromus, type = "pearson")



#GLS is a better fit based on residual diagnostics

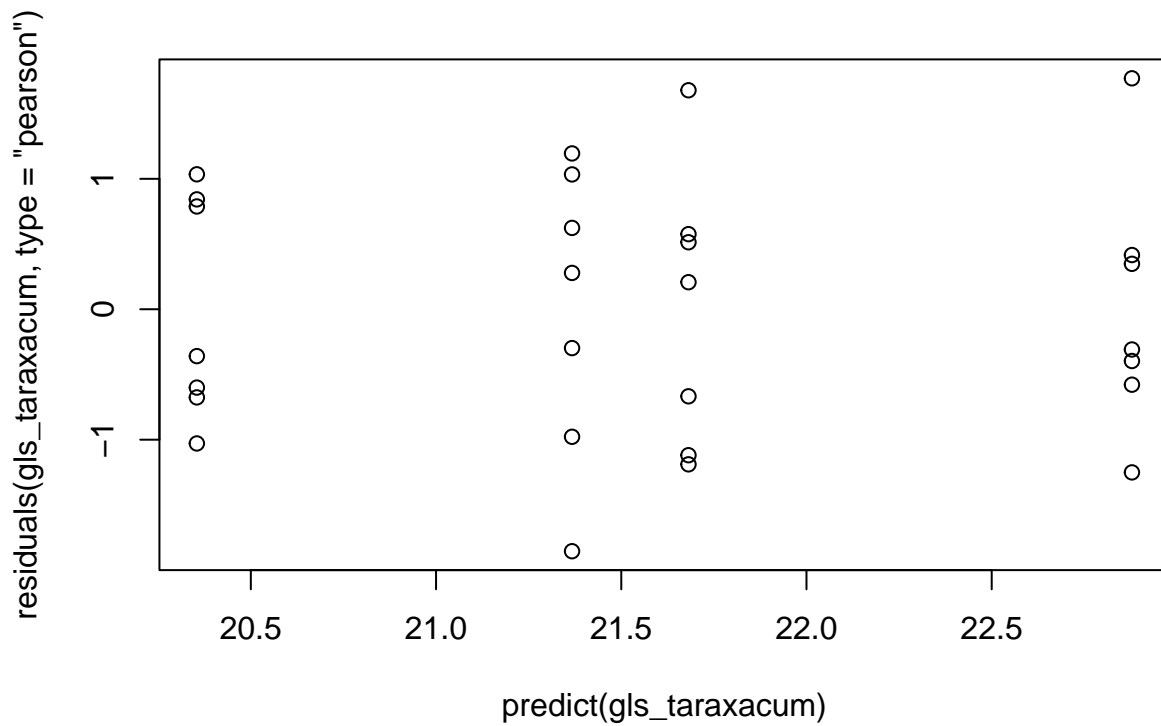
#TARAXACUM

```
gls_taraxacum <- gls(biomass ~ treatment,
                     data = data_taraxacum)
summary(gls_taraxacum)
```

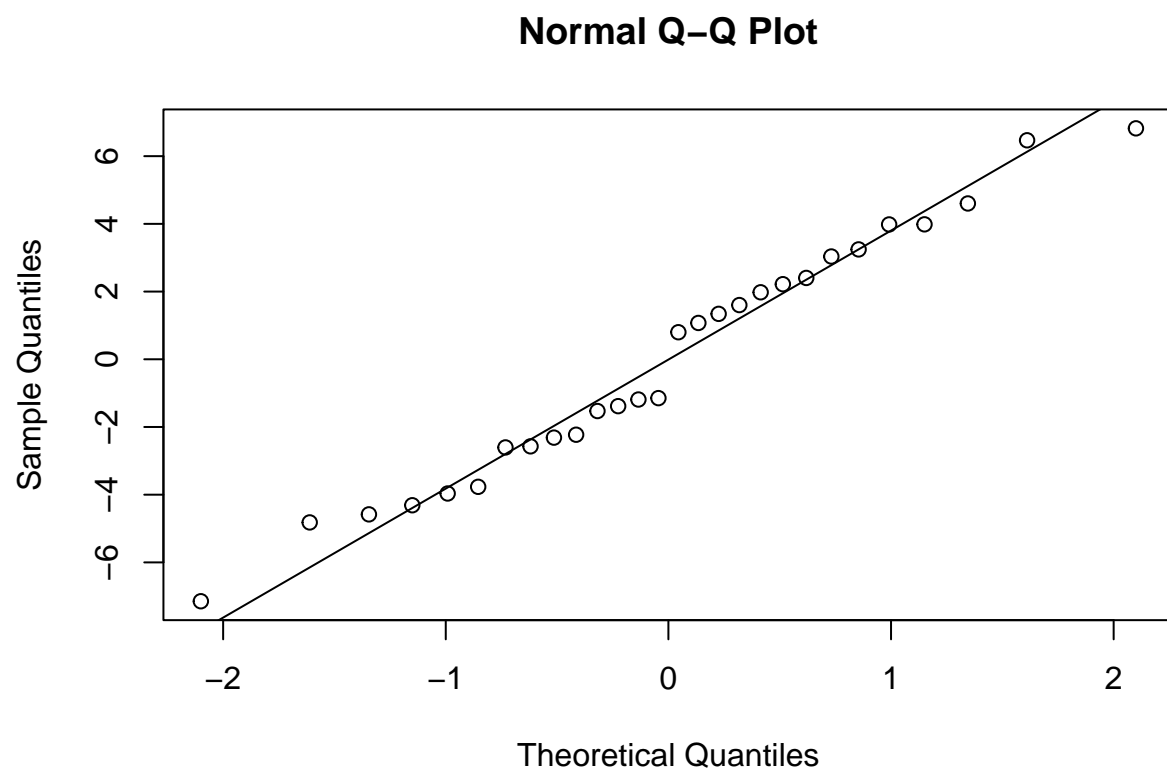
```
## Generalized least squares fit by REML
## Model: biomass ~ treatment
## Data: data_taraxacum
##      AIC      BIC    logLik
## 150.6384 156.5287 -70.3192
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  21.367143  1.456322  14.671993  0.0000
## treatment240448  0.314286  2.059550  0.152599  0.8800
## treatment240720  1.511429  2.059550  0.733863  0.4701
## treatmentControl -1.012857  2.059550 -0.491786  0.6273
##
## Correlation:
##              (Intr) t24044 t24072
## treatment240448 -0.707
## treatment240720 -0.707  0.500
## treatmentControl -0.707  0.500  0.500
##
```

```
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.8549239 -0.6695041 -0.0452330  0.6646842  1.7703901
##
## Residual standard error: 3.853065
## Degrees of freedom: 28 total; 24 residual
```

```
#Check residuals
plot(predict(gls_taraxacum), residuals(gls_taraxacum, type = "pearson"))
```

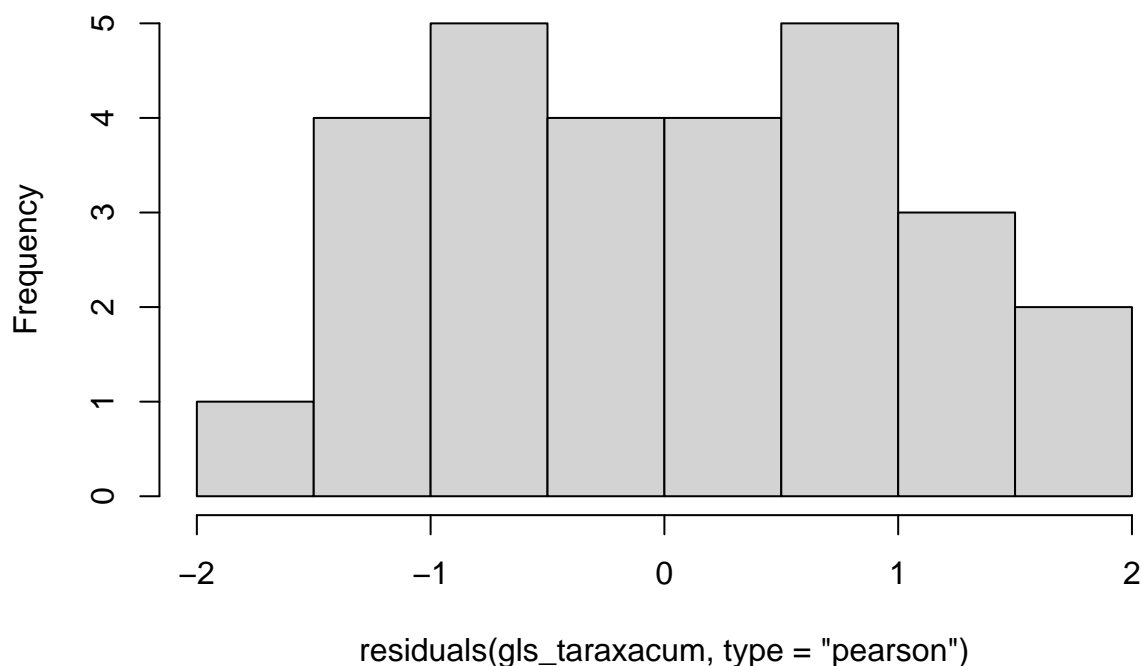


```
#Okay, possible heteroskedasticity
qqnorm(residuals(gls_taraxacum)); qqline(residuals(gls_taraxacum)) #okay
```



```
hist(residuals(gls_taraxacum, type = "pearson")) #Residuals centered around 0
```

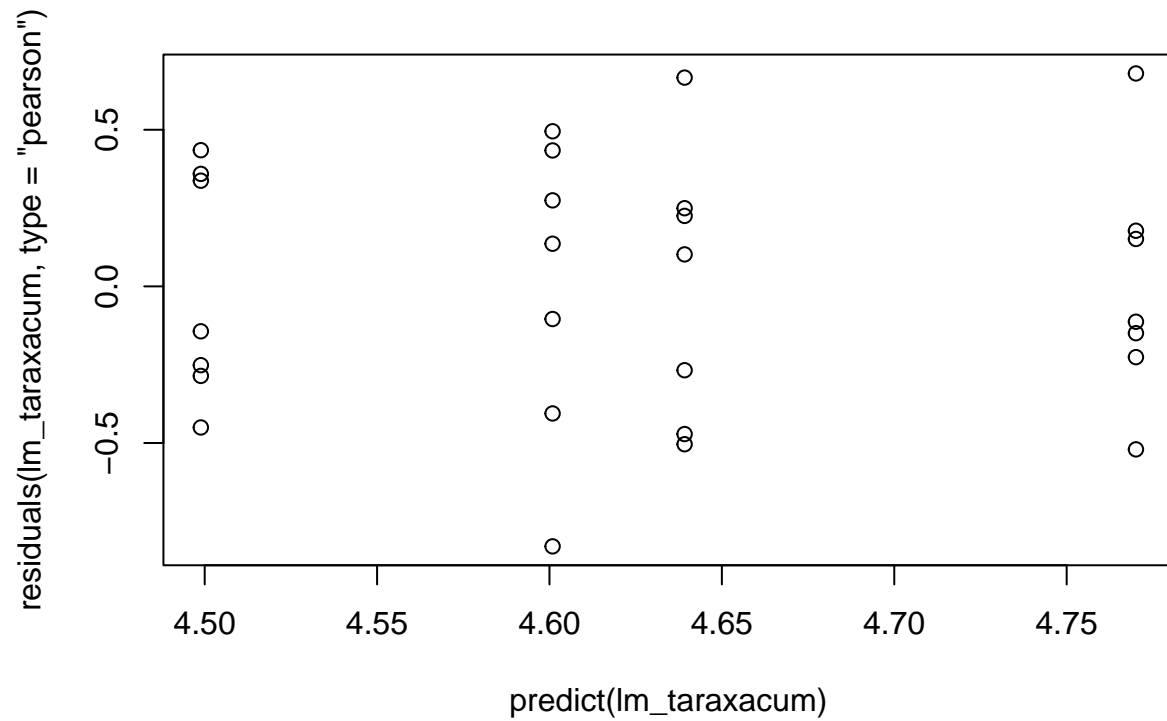
Histogram of residuals(gls_taraxacum, type = "pearson")



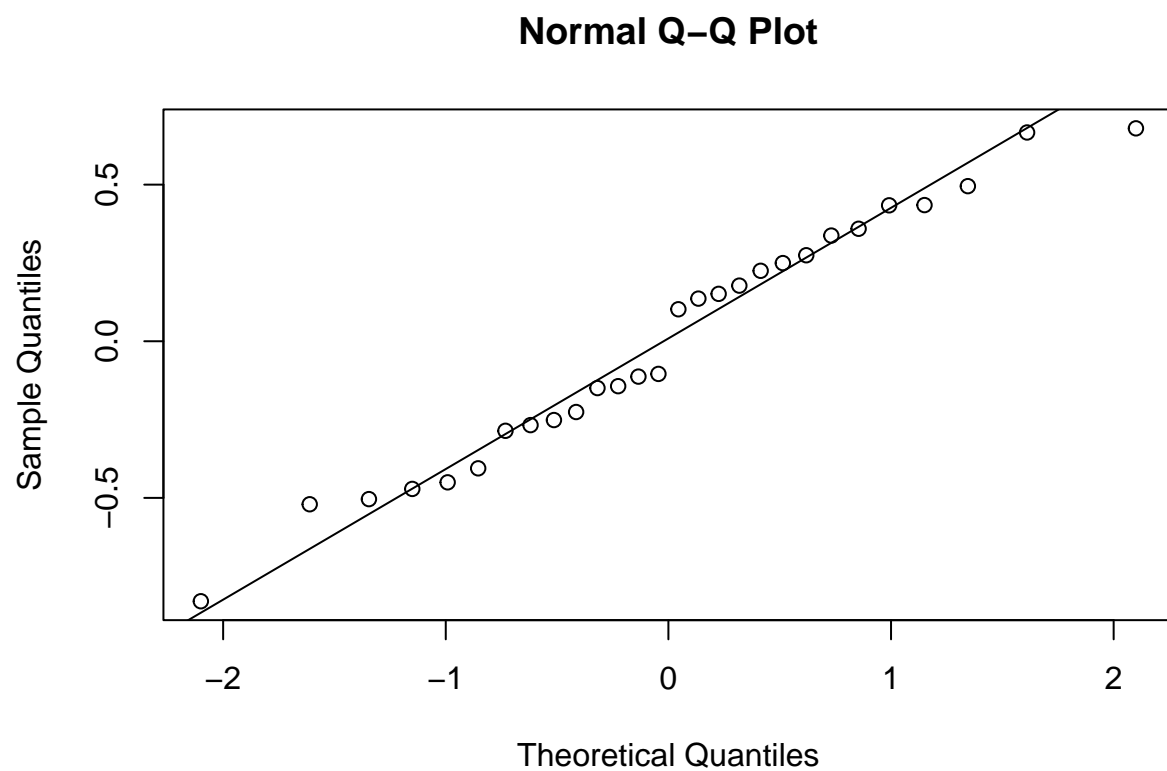
```
#okay
lm_taraxacum <- lm(sqrt_biomass ~ treatment,
                    data = data_taraxacum)
summary(lm_taraxacum)
```

```
##
## Call:
## lm(formula = sqrt_biomass ~ treatment, data = data_taraxacum)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82996 -0.27222 -0.00106  0.29027  0.67967
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.60090    0.15775   29.166  <2e-16 ***
## treatment240448  0.03828    0.22309    0.172    0.865
## treatment240720  0.16919    0.22309    0.758    0.456
## treatmentControl -0.10202    0.22309   -0.457    0.652
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4174 on 24 degrees of freedom
## Multiple R-squared:  0.0594, Adjusted R-squared:  -0.05817
## F-statistic: 0.5052 on 3 and 24 DF, p-value: 0.6823
```

```
#Check residuals  
plot(predict(lm_taraxacum), residuals(lm_taraxacum, type = "pearson"))
```

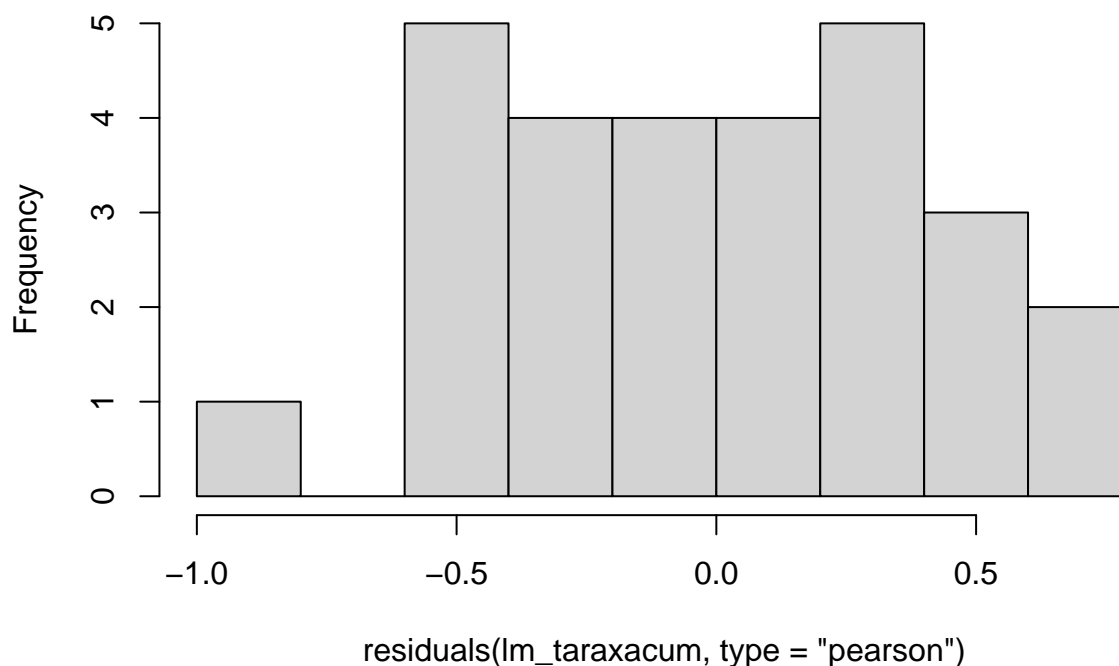


```
qqnorm(residuals(lm_taraxacum)); qqline(residuals(lm_taraxacum)) #okay
```



```
hist(residuals(lm_taraxacum, type = "pearson"))
```

Histogram of residuals(lm_taraxacum, type = "pearson")



#GLS is a better fit than lm models based on residual diagnostics

Extract estimated marginal means

```
#Compute estimated marginal means
#infer = (c(TRUE,FALSE)) includes confidence intervals, excludes
#p vlaues testing significant difference form 0
#Gaillardia
emm_gaillardia <- emmeans(gls_gaillardia, ~ treatment, mode = "df.error")
summary(emm_gaillardia)
```

```
## treatment emmean SE df lower.CL upper.CL
## 197198      6.25 1.07 24      4.04      8.45
## 240448     10.86 1.07 24      8.66     13.07
## 240720     12.92 1.07 24     10.72     15.13
## Control      8.93 1.07 24      6.72     11.13
##
## Degrees-of-freedom method: df.error
## Confidence level used: 0.95
```

```
pairs(emm_gaillardia, adjust = "tukey")
```

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

```
## 197198 - 240448      -4.61 1.51 24  -3.055 0.0261
## 197198 - 240720      -6.68 1.51 24  -4.419 0.0010
## 197198 - Control     -2.68 1.51 24  -1.773 0.3102
## 240448 - 240720      -2.06 1.51 24  -1.365 0.5327
## 240448 - Control      1.94 1.51 24   1.281 0.5831
## 240720 - Control      4.00 1.51 24   2.646 0.0634
##
## Degrees-of-freedom method: df.error
## P value adjustment: tukey method for comparing a family of 4 estimates
```

#Festuca

```
emm_festuca <- emmeans(gls_festuca, ~ treatment, mode = "df.error")
summary(emm_festuca)
```

```
## treatment emmean SE df lower.CL upper.CL
## 197198      38.2 4.76 24    28.4    48.0
## 240448      39.9 4.76 24    30.1    49.7
## 240720      43.7 4.76 24    33.8    53.5
## Control     38.4 4.76 24    28.5    48.2
##
## Degrees-of-freedom method: df.error
## Confidence level used: 0.95
```

```
pairs(emm_festuca, adjust = "tukey")
```

```
## contrast      estimate SE df t.ratio p.value
## 197198 - 240448   -1.734 6.73 24  -0.258 0.9938
## 197198 - 240720   -5.490 6.73 24  -0.815 0.8467
## 197198 - Control  -0.187 6.73 24  -0.028 1.0000
## 240448 - 240720   -3.756 6.73 24  -0.558 0.9435
## 240448 - Control    1.547 6.73 24   0.230 0.9956
## 240720 - Control    5.303 6.73 24   0.787 0.8594
##
## Degrees-of-freedom method: df.error
## P value adjustment: tukey method for comparing a family of 4 estimates
```

#Bromus

```
emm_bromus <- emmeans(gls_bromus, ~ treatment, mode = "df.error")
summary(emm_bromus)
```

```
## treatment emmean SE df lower.CL upper.CL
## 197198      35.6 3.16 24    29.1    42.1
## 240448      19.0 3.16 24    12.5    25.5
## 240720      22.5 3.16 24    16.0    29.1
## Control     26.5 3.16 24    20.0    33.0
##
## Degrees-of-freedom method: df.error
## Confidence level used: 0.95
```

```
pairs(emm_bromus, adjust = "tukey")
```



```
## contrast      estimate    SE df t.ratio p.value
## 197198 - 240448      16.63 4.47 24   3.719  0.0055
## 197198 - 240720      13.07 4.47 24   2.924  0.0349
## 197198 - Control       9.11 4.47 24   2.038  0.2024
## 240448 - 240720      -3.55 4.47 24  -0.795  0.8560
## 240448 - Control      -7.51 4.47 24  -1.681  0.3553
## 240720 - Control      -3.96 4.47 24  -0.886  0.8122
##
## Degrees-of-freedom method: df.error
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
# Taraxacum
emm_taraxacum <- emmeans(gls_taraxacum, ~ treatment, mode = "df.error")
summary(emm_taraxacum)
```

```
## treatment emmean    SE df lower.CL upper.CL
## 197198      21.4 1.46 24     18.4     24.4
## 240448      21.7 1.46 24     18.7     24.7
## 240720      22.9 1.46 24     19.9     25.9
## Control     20.4 1.46 24     17.3     23.4
##
## Degrees-of-freedom method: df.error
## Confidence level used: 0.95
```

```
pairs(emm_taraxacum, adjust = "tukey")
```

```
## contrast      estimate    SE df t.ratio p.value
## 197198 - 240448    -0.314 2.06 24  -0.153  0.9987
## 197198 - 240720    -1.511 2.06 24  -0.734  0.8825
## 197198 - Control    1.013 2.06 24   0.492  0.9602
## 240448 - 240720    -1.197 2.06 24  -0.581  0.9368
## 240448 - Control    1.327 2.06 24   0.644  0.9165
## 240720 - Control    2.524 2.06 24   1.226  0.6171
##
## Degrees-of-freedom method: df.error
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Total phosphorous analysis (exploration and model selection)

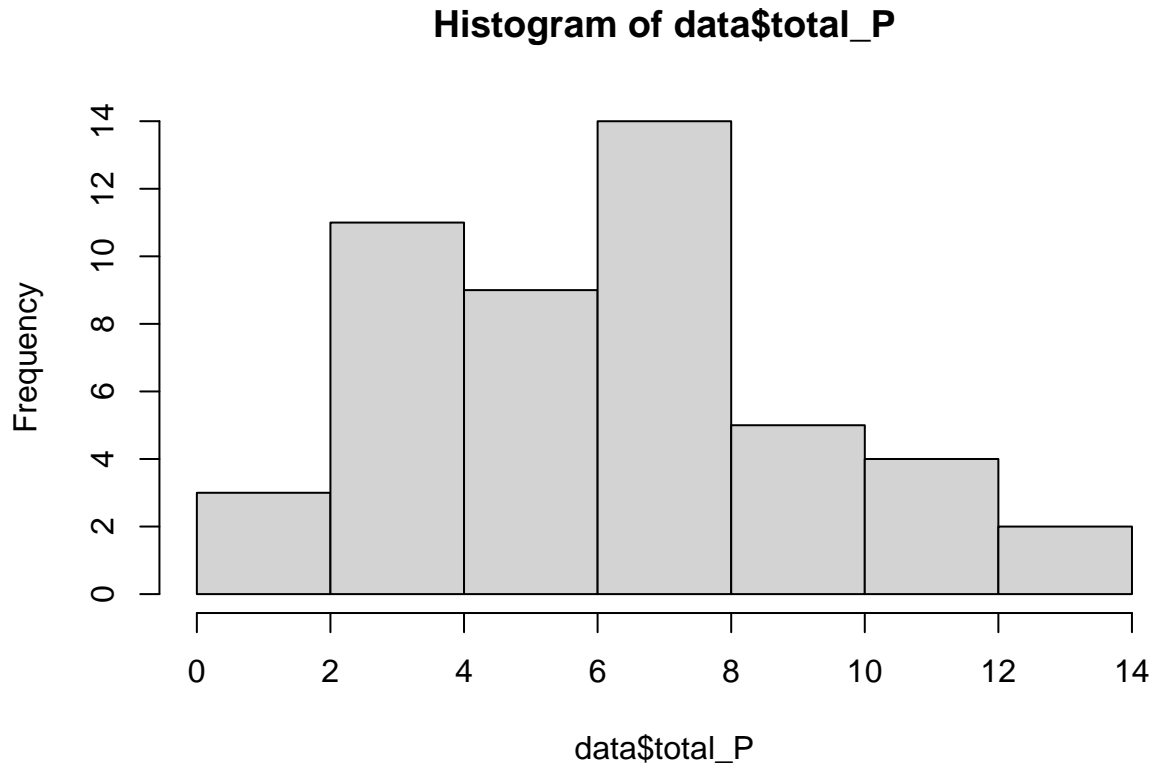
```
#Convert % P to total P per species
data$total_P<-data$P*data$biomass
str(data$biomass)
```

```
## num [1:112] 14.39 31.19 6.69 24.34 26.19 ...
```

```
#Add total phosphorous to the species datasets
data_gaillardia<-data%>%
  filter(species=="Gaillardia")
data_taraxacum<-data%>%
  filter(species=="Taraxacum")
```

```
data_bromus<-data%>%
  filter(species=="Bromus")
data_festuca<-data%>%
  filter(species=="Festuca")

#Histogram of P distribution
hist(data$total_P) #near approximation of a normal distribtuion. May be bimodal
```



```
#Visualise total P within species groups/treatment
print(total_P_median_species <- ggplot(data,
  aes(x = species,
    y = total_P,
    fill = treatment)) +

  # Boxplot per species x treatment
  geom_boxplot(position = position_dodge(width = 0.75),
    width = 0.6, alpha = 0.8,
    outlier.shape = NA) + # Hide default outlier points
  labs(title = "Total P by Species and Treatment",
    x = "Species",
    y = "Total P (g)") +
  scale_fill_brewer(palette = "Dark2") +
  scale_colour_brewer(palette = "Dark2") +
  scale_x_discrete(labels = species_labels) +
  theme_minimal() +
  theme(
```

```

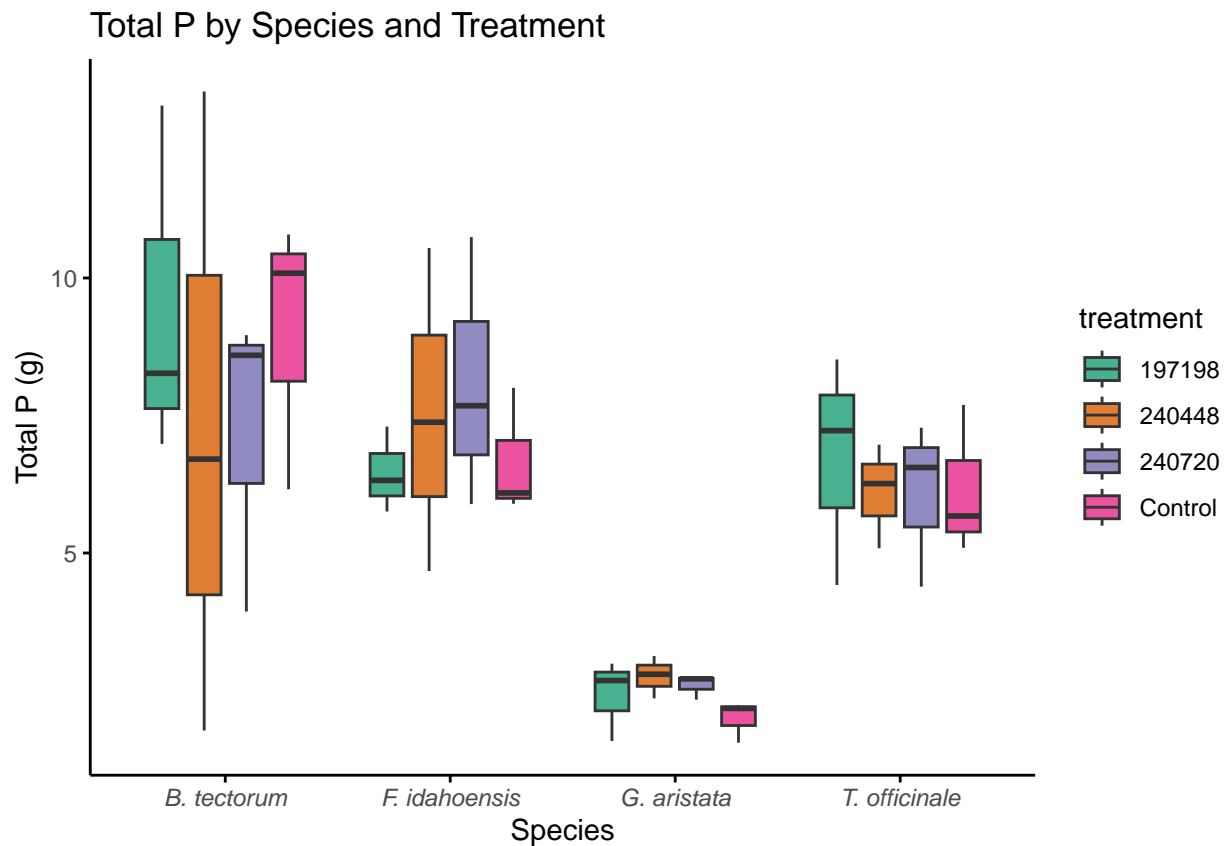
panel.grid = element_blank(),
axis.line = element_line(color = "black"),
axis.ticks = element_line(color = "black")
))

```

```

## Warning: Removed 64 rows containing non-finite outside the scale range
## ('stat_boxplot()').

```



```

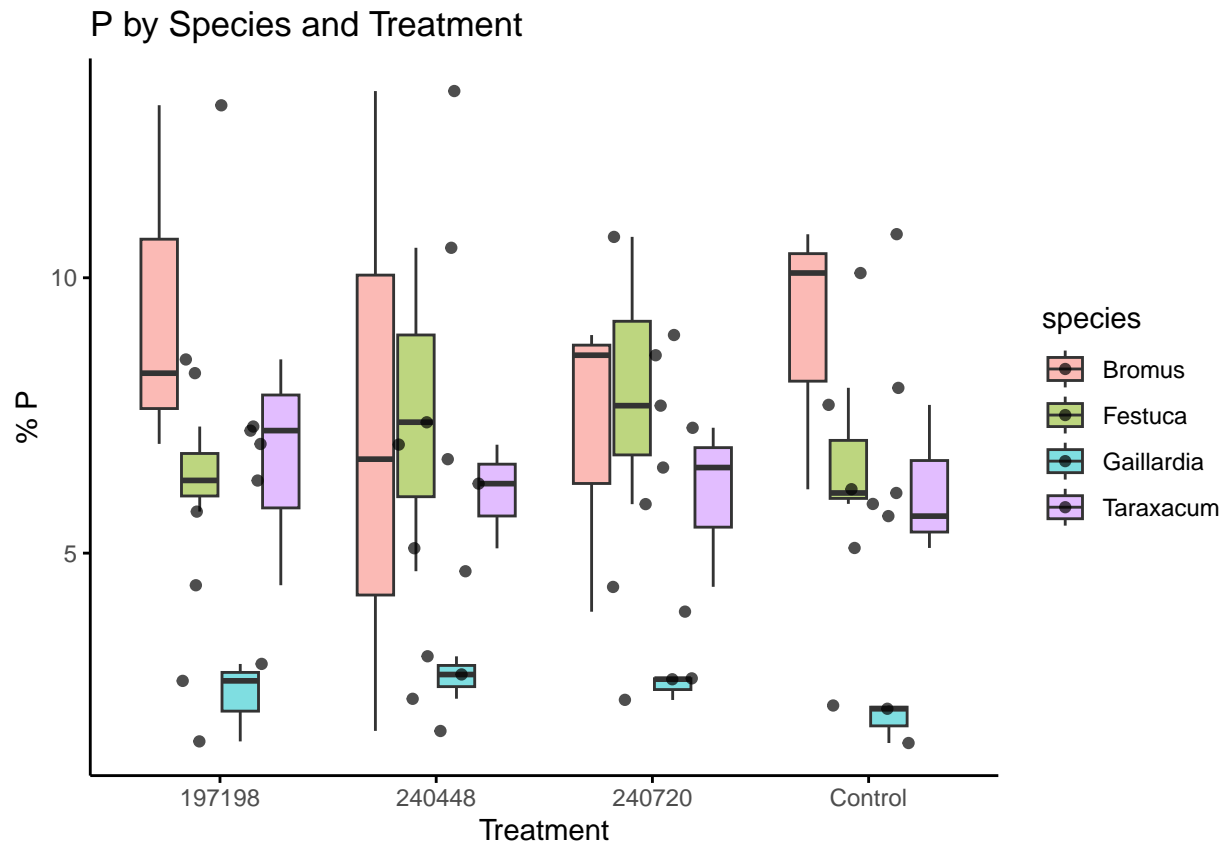
#Median
print(total_P_median<-ggplot(data, aes(x = treatment, y = total_P, fill = species)) +
  geom_boxplot(outlier.shape = NA, alpha = 0.5) +
  geom_jitter(width = 0.2, alpha = 0.7, color = "black") +
  labs(title = "Gaillardia Phosphorus by Treatment",
        x = "Treatment",
        y = "Phosphorus (% total foliar biomass)") +
  labs(title = "P by Species and Treatment",
        x = "Treatment",
        y = "% P") +
  scale_colour_brewer(palette = "Dark2") +
  scale_x_discrete(labels = species_labels) +
  theme_minimal() +
  theme(
    panel.grid = element_blank(), #Removes all grid lines
    axis.line = element_line(color = "black"), #Adds black x and y axis lines

```

```
axis.ticks = element_line(color = "black") #show tick marks
))
```

```
## Warning: Removed 64 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

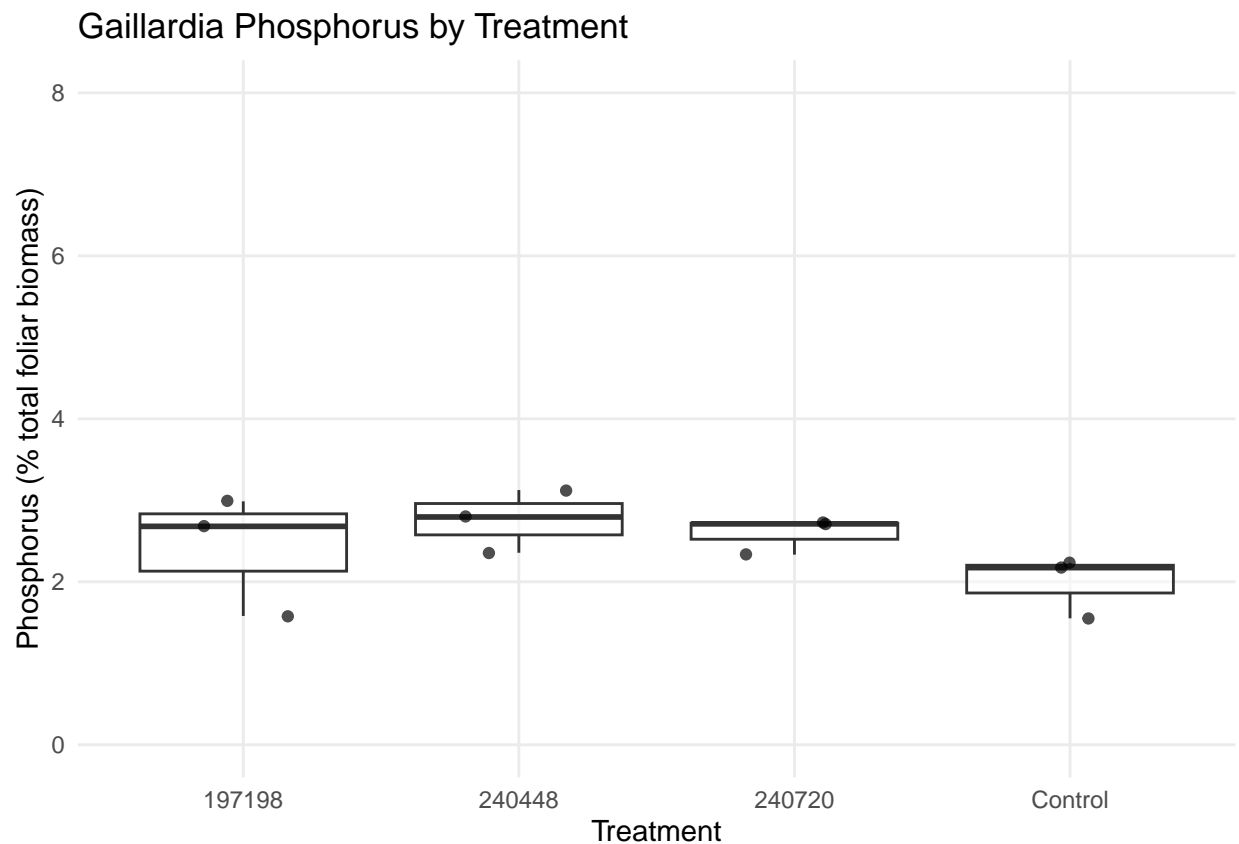
```
## Warning: Removed 64 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#Median with individual points by species group
#GAILLARDIA
print(total_P_gaillardia<-ggplot(data_gaillardia, aes(x = treatment, y = total_P,)) +
  geom_boxplot(outlier.shape = NA, alpha = 0.5) +
  geom_jitter(width = 0.2, alpha = 0.7, color = "black") +
  labs(title = "Gaillardia Phosphorus by Treatment",
    x = "Treatment",
    y = "Phosphorus (% total foliar biomass)") +
  scale_y_continuous(limits = c(0,8))+
  theme_minimal() +
  theme(panel.grid.minor = element_blank()))
```

```
## Warning: Removed 16 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

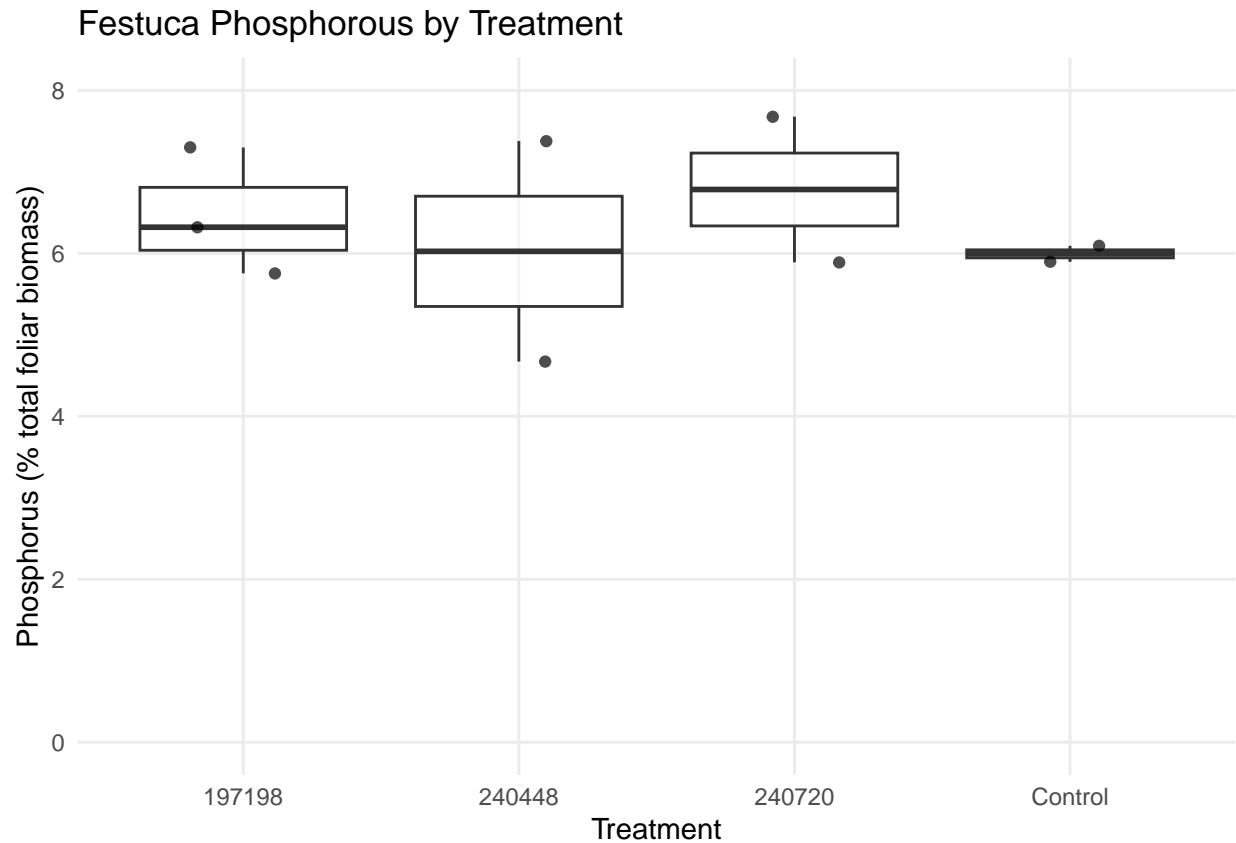
```
## Warning: Removed 16 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#FESTUCA
print(total_P_festuca<-ggplot(data_festuca, aes(x = treatment, y = total_P,)) +
  geom_boxplot(outlier.shape = NA, alpha = 0.5) +
  geom_jitter(width = 0.2, alpha = 0.7, color = "black") +
  labs(title = "Festuca Phosphorous by Treatment",
        x = "Treatment",
        y = "Phosphorus (% total foliar biomass)") +
  scale_y_continuous(limits = c(0,8))+
  theme_minimal() +
  theme(panel.grid.minor = element_blank()))
```

```
## Warning: Removed 19 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

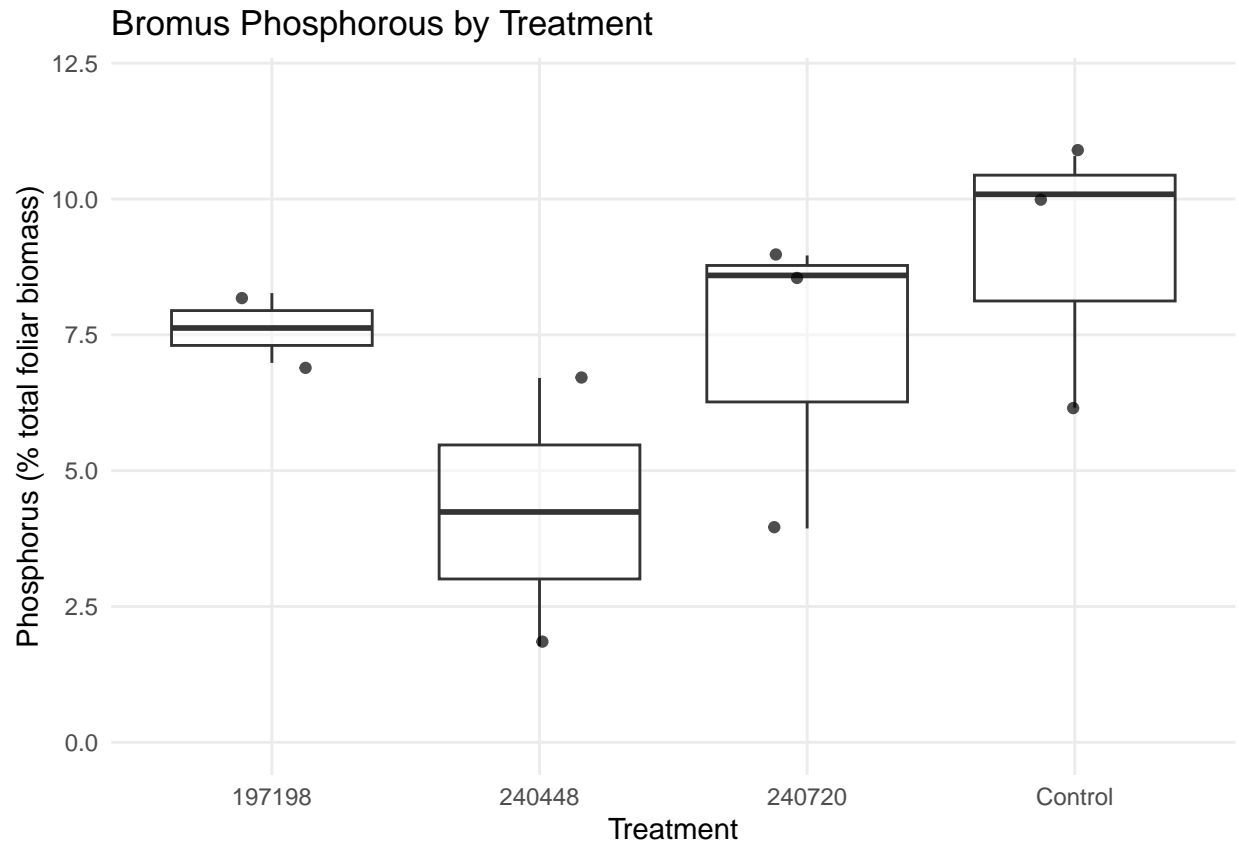
```
## Warning: Removed 19 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#BROMUS
print(total_P_bromus<-ggplot(data_bromus, aes(x = treatment, y = total_P,)) +
  geom_boxplot(outlier.shape = NA, alpha = 0.5) +
  geom_jitter(width = 0.2, alpha = 0.7, color = "black") +
  labs(title = "Bromus Phosphorous by Treatment",
        x = "Treatment",
        y = "Phosphorus (% total foliar biomass)") +
  scale_y_continuous(limits = c(0,12
  )) +
  theme_minimal() +
  theme(panel.grid.minor = element_blank()))
```

```
## Warning: Removed 18 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

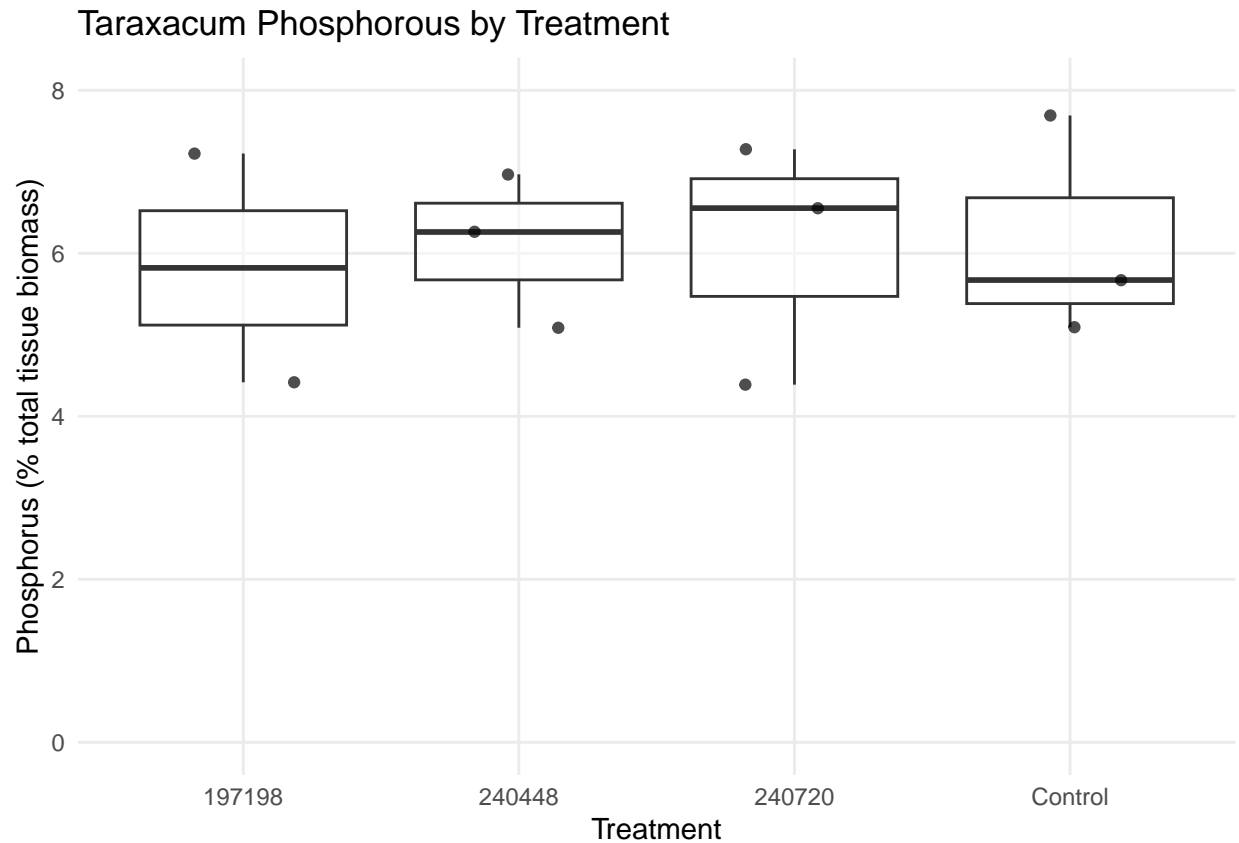
```
## Warning: Removed 18 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#TARAXACUM
print(total_P_taraxacum<-ggplot(data_taraxacum, aes(x = treatment, y = total_P,)) +
  geom_boxplot(outlier.shape = NA, alpha = 0.5) +
  geom_jitter(width = 0.2, alpha = 0.7, color = "black") +
  labs(title = "Taraxacum Phosphorous by Treatment",
        x = "Treatment",
        y = "Phosphorus (% total tissue biomass)") +
  scale_y_continuous(limits = c(0,8)) +
  theme_minimal() +
  theme(panel.grid.minor = element_blank()))
```

```
## Warning: Removed 17 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 17 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#Arrange species plots together in a single figure (mean)
multi_figure_total_P <- ggarrange(total_P_bromus, total_P_festuca,
                                   total_P_gaillardia, total_P_taraxacum,
                                   ncol = 2, nrow = 2,
                                   labels = c("a", "b", "c", "d"))

## Warning: Removed 18 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 18 rows containing missing values or values outside the scale range
## ('geom_point()').

## Warning: Removed 19 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 19 rows containing missing values or values outside the scale range
## ('geom_point()').

## Warning: Removed 16 rows containing non-finite outside the scale range
## ('stat_boxplot()').

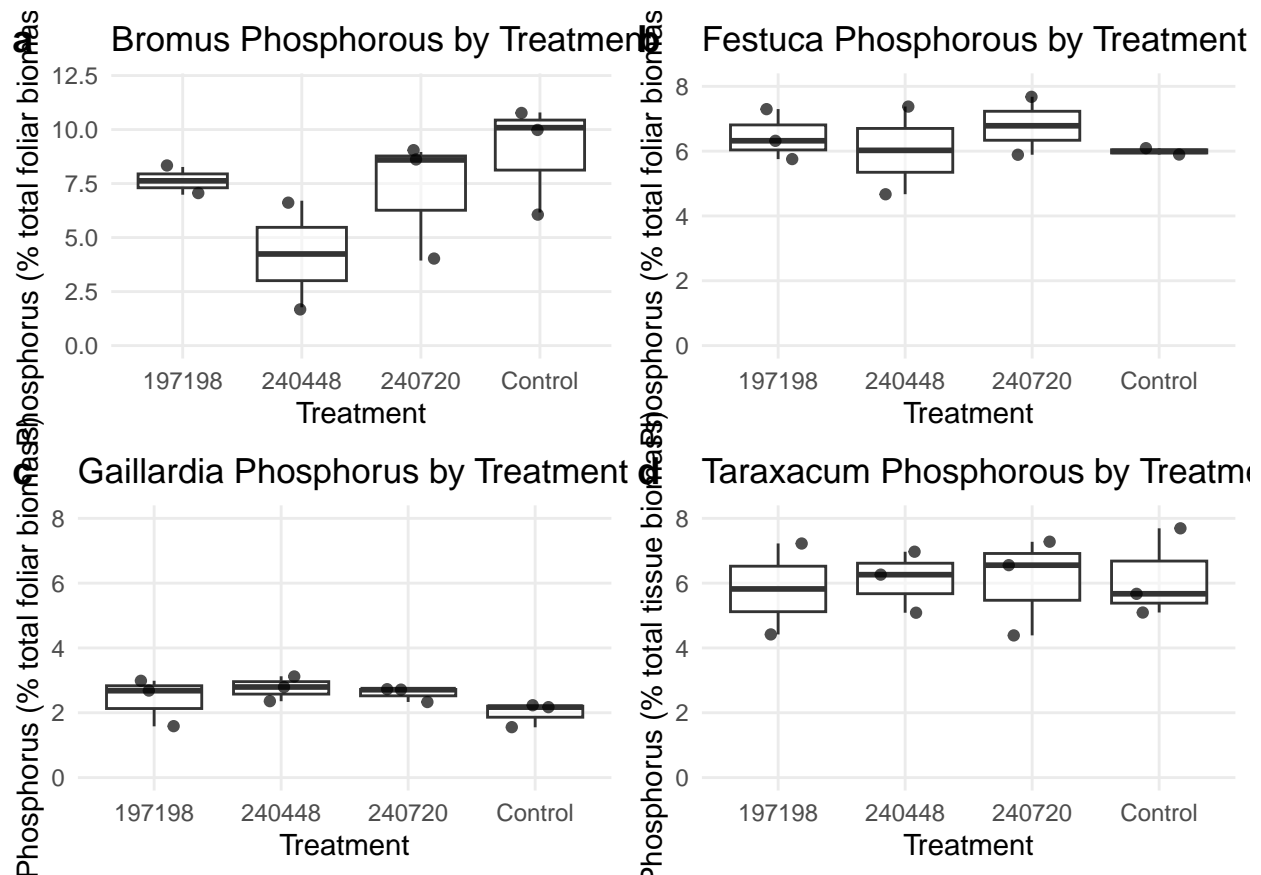
## Warning: Removed 16 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
## Warning: Removed 17 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 17 rows containing missing values or values outside the scale range
## ('geom_point()').
```

```
#Display the combined figure
print(multi_figure_total_P)
```



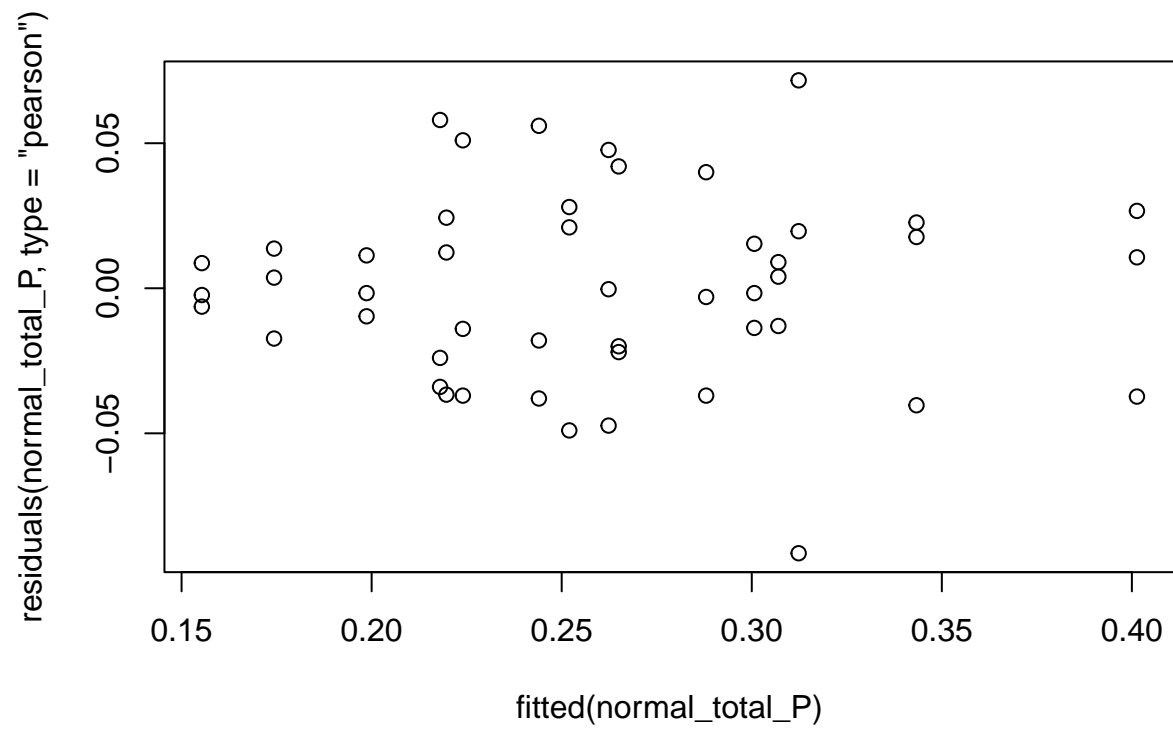
```
#####
#MODEL SELECTION: Total P
#####

#Start with the simplest model
#fit of a normal distribution
normal_total_P<-glm(P~treatment*species,
                    family=gaussian(link="identity"),
                    data=data)
summary(normal_total_P)
```

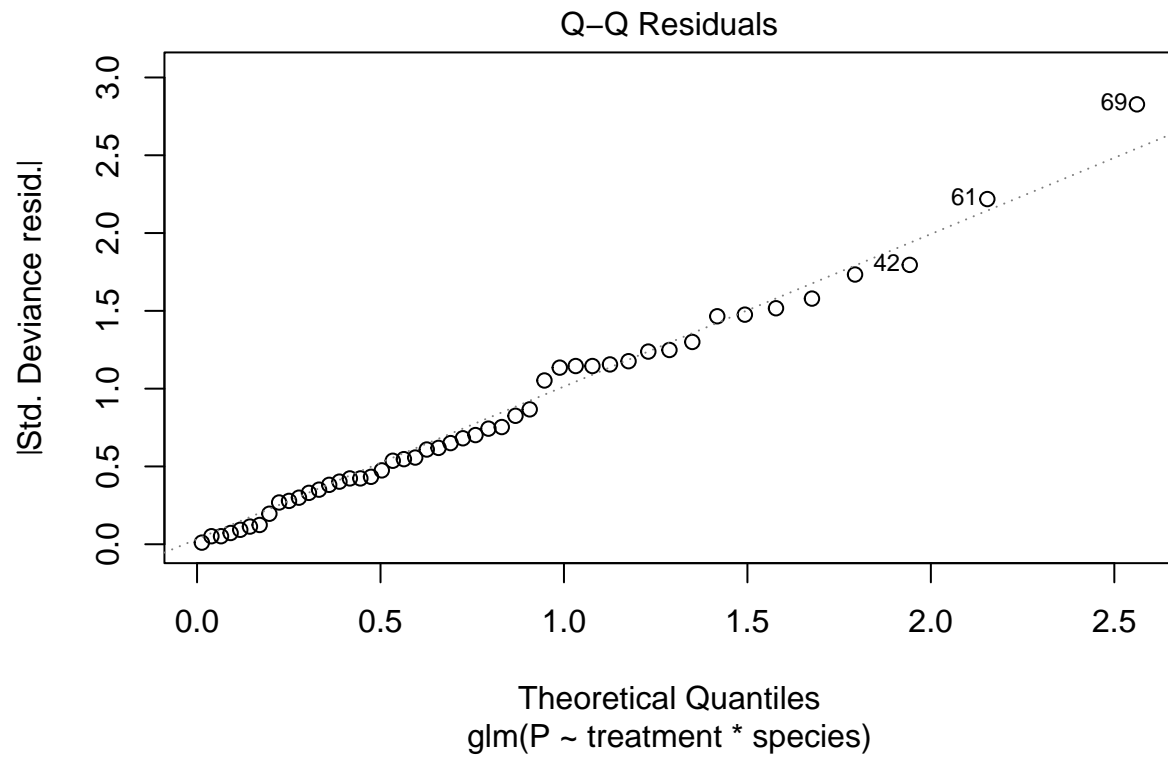
```
##
## Call:
## glm(formula = P ~ treatment * species, family = gaussian(link = "identity"),
##      data = data)
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.307000   0.022843  13.440 1.05e-14 ***
## treatment240448    0.005333   0.032305   0.165  0.86991
## treatment240720    0.036333   0.032305   1.125  0.26908
## treatmentControl    0.094333   0.032305   2.920  0.00636 **
## speciesFestuca     -0.089000   0.032305  -2.755  0.00960 **
## speciesGaillardia  -0.055000   0.032305  -1.703  0.09835 .
## speciesTaraxacum   -0.019000   0.032305  -0.588  0.56056
## treatment240448:speciesFestuca -0.049000   0.045686  -1.073  0.29150
## treatment240720:speciesFestuca -0.099000   0.045686  -2.167  0.03779 *
## treatmentControl:speciesFestuca -0.113667   0.045686  -2.488  0.01824 *
## treatment240448:speciesGaillardia -0.013333   0.045686  -0.292  0.77228
## treatment240720:speciesGaillardia -0.064333   0.045686  -1.408  0.16872
## treatmentControl:speciesGaillardia -0.126667   0.045686  -2.773  0.00920 **
## treatment240448:speciesTaraxacum -0.031000   0.045686  -0.679  0.50230
## treatment240720:speciesTaraxacum -0.059333   0.045686  -1.299  0.20332
## treatmentControl:speciesTaraxacum -0.081667   0.045686  -1.788  0.08332 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.001565375)
##
## Null deviance: 0.234279 on 47 degrees of freedom
## Residual deviance: 0.050092 on 32 degrees of freedom
## (64 observations deleted due to missingness)
## AIC: -159.31
##
## Number of Fisher Scoring iterations: 2
```

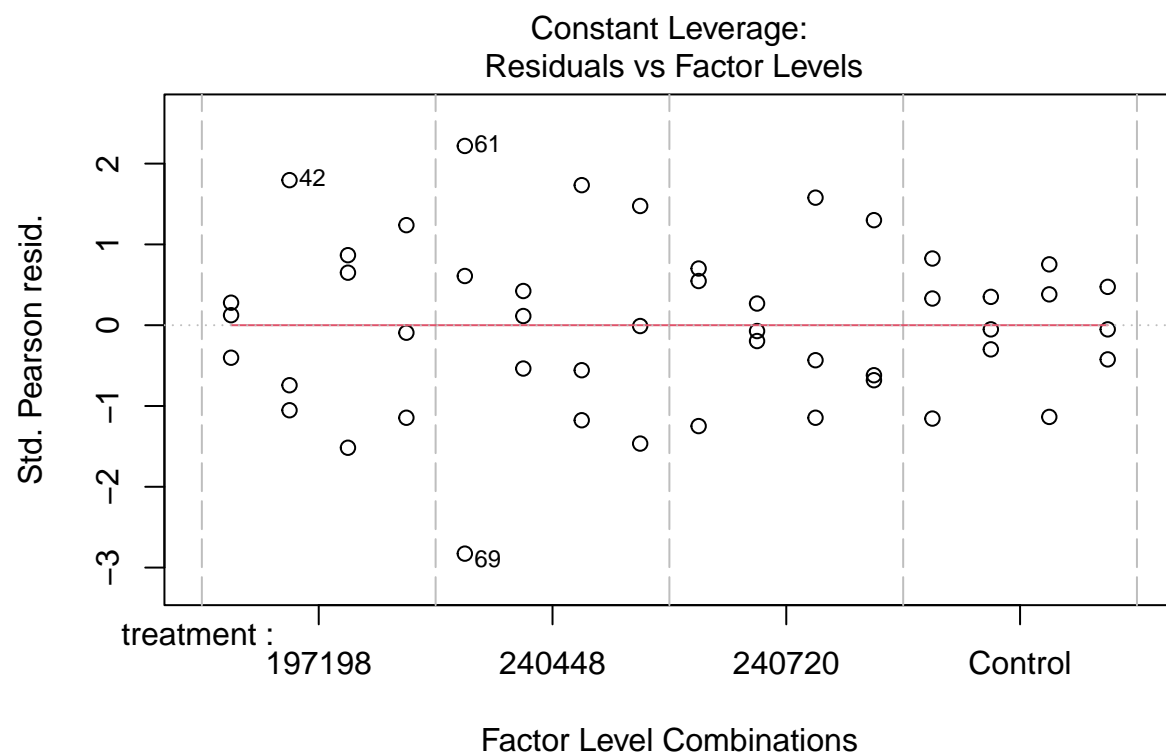
```
#Residual diagnostics
#Fitted vs. residuals
plot(fitted(normal_total_P), residuals(normal_total_P, type = "pearson"))
```



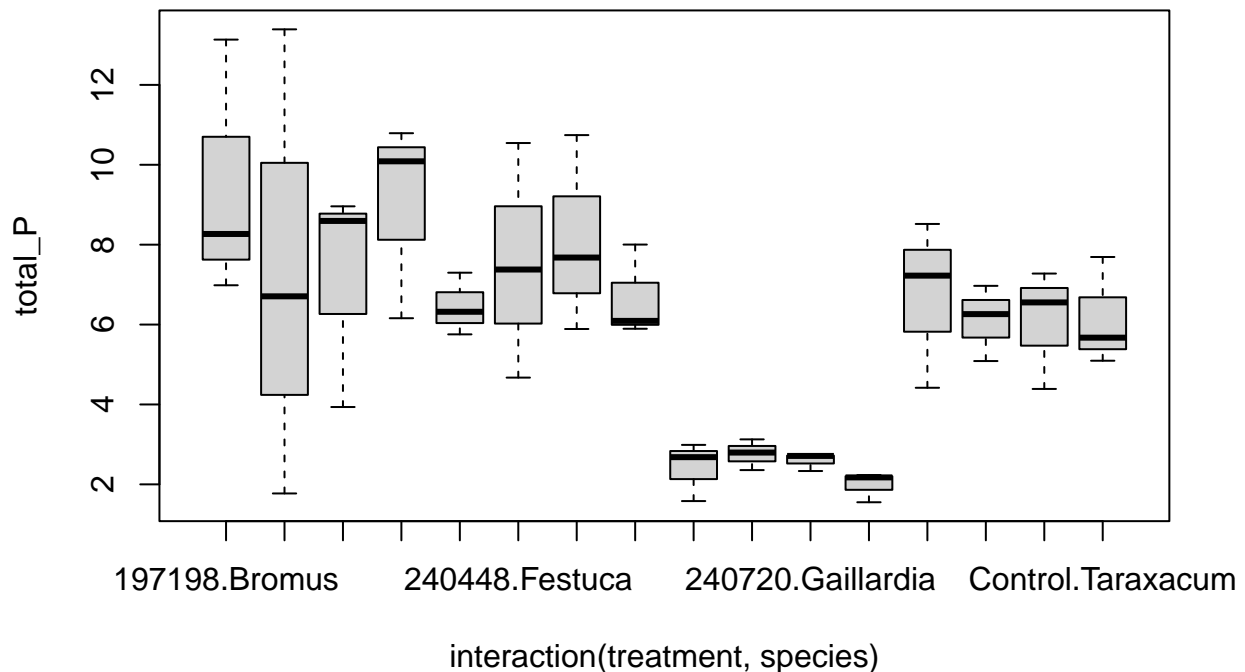
```
#some heteroskedasticity  
#qqplot  
plot(normal_total_P, which = 2) #Looks good
```



```
#Residuals by factor level  
plot(normal_total_P, which =5) #Looks good, decrease in residual variance
```



```
#within control
#Check variance between groups
boxplot(total_P~interaction(treatment,species),
        data=data)
```



*#There are difference in variation between species and within treatment groups,
 #try accounting for variance structure. There are only 3 observations/group,
 #modelling a variance structure is too complex for the number
 #of observations. Use Welch's ANOVA (rstatix package) to account for group
 #variance. Welch's ANOVA must be run on each species group independently as it
 #does not account for interactions. Games-Howell (rstatix package) is the posthoc test for Welch's ANOV.
 #https://search.r-project.org/CRAN/refmans/rstatix/html/games_howell_test.html*

#GAILLARDIA

```
print(gaillardia_welch_P<-oneway.test(total_P ~ treatment, data = data_gaillardia,
                                     var.equal = FALSE) )
```

##

One-way analysis of means (not assuming equal variances)

##

data: total_P and treatment

F = 1.8844, num df = 3.0000, denom df = 4.1762, p-value = 0.2685

#Not significant

#FESTUCA

#Run Welch's one way comparisons (to account for variance between groups)

```
print(festuca_welch_P<-oneway.test(total_P ~ treatment, data = data_festuca,
                                   var.equal = FALSE) )
```

##

```
## One-way analysis of means (not assuming equal variances)
##
## data: total_P and treatment
## F = 0.37683, num df = 3.0000, denom df = 4.0602, p-value = 0.7755
```

#Not significant

#TARAXACUM

#Run Welch's one way comparisons (to account for variance between groups)

```
print(taraxacum_welch_P<-oneway.test(total_P ~ treatment, data = data_taraxacum,
                                     var.equal = FALSE) )
```

```
##
## One-way analysis of means (not assuming equal variances)
##
## data: total_P and treatment
## F = 0.059325, num df = 3.0000, denom df = 4.2941, p-value = 0.9787
```

#Not significant

#BROMUS

#Run Welch's one way comparisons (to account for variance between groups)

```
print(bromus_welch_P<-oneway.test(total_P ~ treatment, data = data_bromus,
                                   var.equal = FALSE) )
```

```
##
## One-way analysis of means (not assuming equal variances)
##
## data: total_P and treatment
## F = 0.3046, num df = 3.000, denom df = 4.338, p-value = 0.8218
```

#Not significant

Seed production data

#Can not statistically compare seed weight or seed head count, visualise.

#Create a new dataframe that subset the treatments

#Add seed count data

```
data$seed_count<-data$seed_weight>0
data$seed_count<-as.numeric(data$seed_count)
```

#Do descriptive statistics and show plots of seed weight

#Summarize seed count

```
seed_summary <- data %>%
  group_by(species, treatment) %>%
  summarize(total_seed_count = sum(seed_count, na.rm = TRUE), .groups = "drop")
```

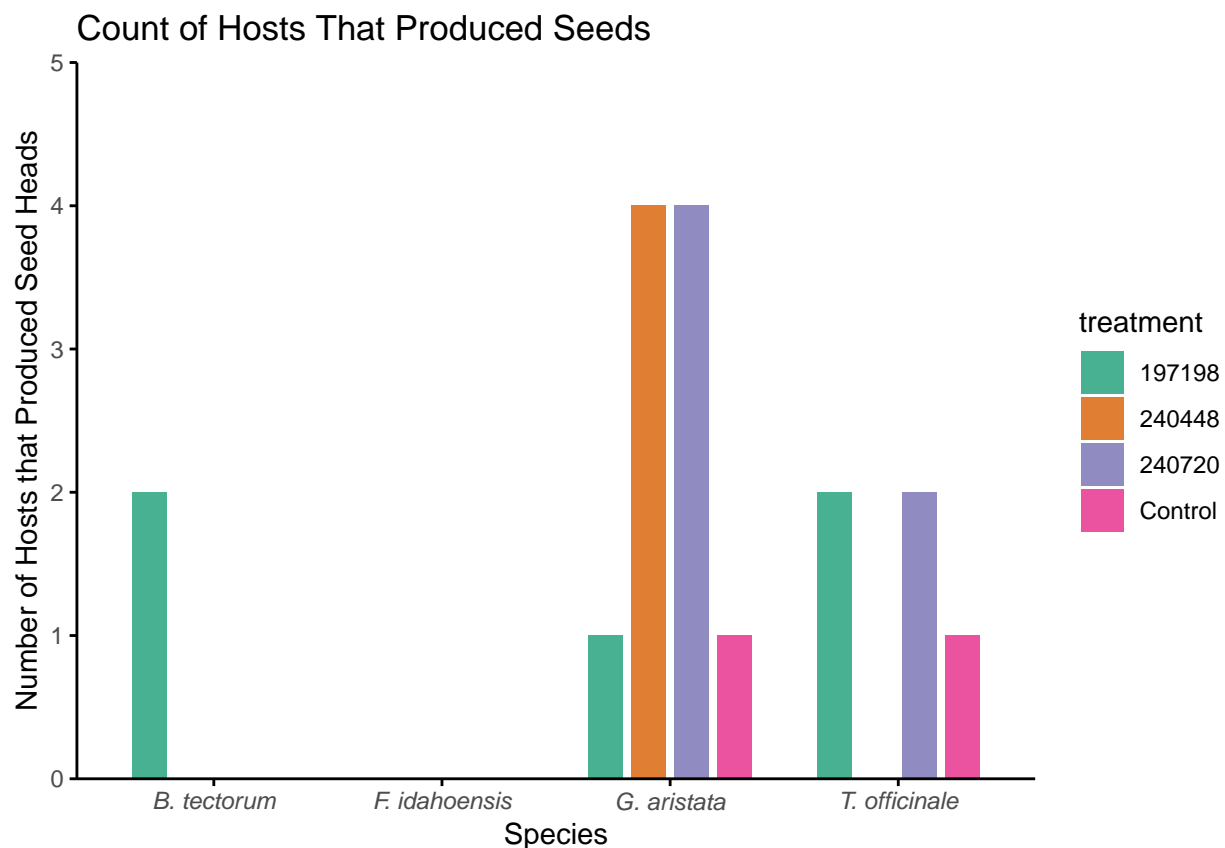
#Plot

```
seed_count<-ggplot(seed_summary, aes(x = species, y = total_seed_count, fill = treatment)) +
  geom_col(position = position_dodge(width = 0.75), width = 0.6, alpha = 0.8) +
```

```

labs(title = "Count of Hosts That Produced Seeds",
     x = "Species",
     y = "Number of Hosts that Produced Seed Heads") +
scale_y_continuous(limits = c(0, 5), expand = c(0, 0)) + # Removes space on x-axis
scale_fill_brewer(palette = "Dark2") +
scale_x_discrete(labels = species_labels) +
theme_minimal() +
theme(
  panel.grid = element_blank(),
  axis.line = element_line(color = "black"),
  axis.ticks = element_line(color = "black")
)
print(seed_count)

```



```

#View seed count by mesocosm
#Summarize seed count
seed_summary <- data %>%
  group_by(species, treatment, mesocosm_id) %>%
  summarize(total_seed_count = sum(seed_count, na.rm = TRUE), .groups = "drop")

#Plot
seed_count_meso <- ggplot(seed_summary, aes(x = mesocosm_id, y = total_seed_count,
                                           fill = species)) +
  geom_col(position = position_dodge(width = 0.75), width = 0.6, alpha = 0.8) +
  labs(title = "Count of Hosts That Produced Seeds",

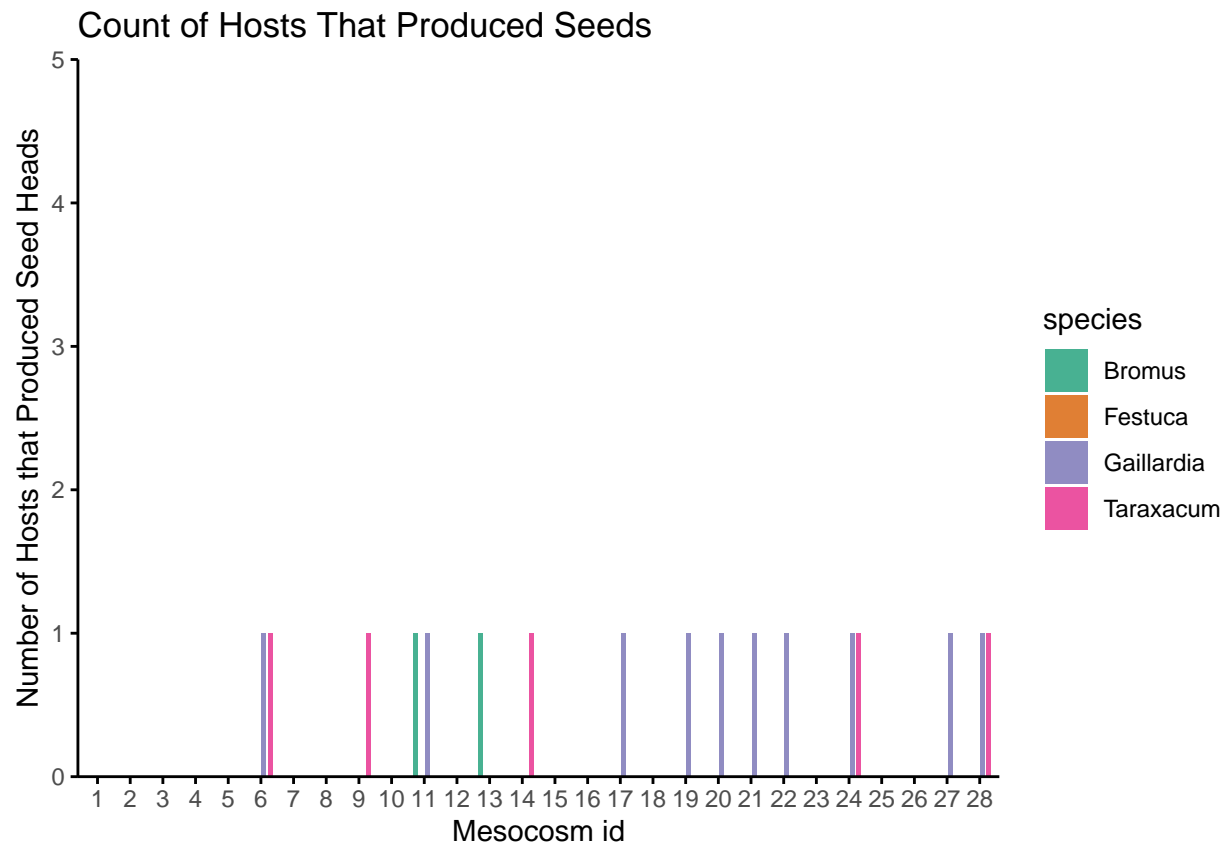
```



```

x = "Mesocosm id",
y = "Number of Hosts that Produced Seed Heads" +
scale_y_continuous(limits = c(0, 5), expand = c(0, 0)) + # Removes space on x-axis
scale_fill_brewer(palette = "Dark2") +
scale_x_discrete(labels = species_labels) +
theme_minimal() +
theme(
  panel.grid = element_blank(),
  axis.line = element_line(color = "black"),
  axis.ticks = element_line(color = "black")
)
print(seed_count_meso)

```



```

#Alternative reasons variation in seed production could be observed:
#Not enough growing time
#Nested within mesocosms (mesocosm specific)

```