

REX: T2 Wheat Height, Greenness & Biomass Analyses

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COLLABORATORS: Lisa Leonard, Grant Falvo (biomass data) DATA INPUT: csv from the shared Google drive

DATA OUTPUT: Code and Rmd are in the scripts folder in Github

PROJECT: REX

DESCRIPTION:

```
# Clear all existing data  
rm(list=ls())
```

```
# Load packages  
library(bbmle)
```

```
## Loading required package: stats4
```

```
library(lmerTest)
```

```
## Loading required package: lme4
```

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

```
##
```

```
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
```

```
##
```

```
##      lmer
```

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

```
##
```

```
##      step
```

```
library(fitdistrplus)
```

```
## Loading required package: MASS
```

```
## Loading required package: survival
```

```
library(sjPlot)
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
```

```
library(emmeans)
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3    v purrr  0.3.4
## v tibble  3.0.6    v dplyr  1.0.4
## v tidyr   1.1.2    v stringr 1.4.0
## v readr   1.4.0    v forcats 0.5.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x tidyr::pack()   masks Matrix::pack()
## x dplyr::recode() masks car::recode()
## x dplyr::select() masks MASS::select()
## x dplyr::slice()  masks bbmle::slice()
## x purrr::some()   masks car::some()
## x tidyr::unpack() masks Matrix::unpack()
```

```
library(ggpubr)
library(jtools) #summ
library(rstatix)
```

```
##
```

```
## Attaching package: 'rstatix'
```

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

```
##
```

```
##   select
```

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

```
##
```

```
##   filter
```

```

library(RColorBrewer)

## Warning: package 'RColorBrewer' was built under R version 4.0.5

library(plotrix) # std.error() function
library(olsrr) # ols_test_normality() function

##
## Attaching package: 'olsrr'

## The following object is masked from 'package:MASS':
##
##      cement

## The following object is masked from 'package:datasets':
##
##      rivers

# Set working directory from .Renviron
dir <- Sys.getenv("DATA_DIR")
list.files(dir)

## [1] "animal"
## [2] "Data Workshop Pre-Survey.gform"
## [3] "Falvo"
## [4] "GHG"
## [5] "Irrigation"
## [6] "lookup_tables"
## [7] "microbes"
## [8] "REX_Data_Management.gdoc"
## [9] "REX_Data_Template.gsheat"
## [10] "REX_meta_data.gsheat"
## [11] "REX_Microbial_sampling_IDs_complete.gsheat"
## [12] "REX_SampleArchive.gsheat"
## [13] "REX_stats_basics.Rmd"
## [14] "REX_template.csv"
## [15] "REX_warmx_metadata.csv"
## [16] "REX_warmx_metadata.xlsx"
## [17] "REX_warmx_Soca_ID_metadata_2021.csv"
## [18] "REX_warmX_taxon.csv"
## [19] "SamplingDemands_Plants.gsheat"
## [20] "SamplingDemands_Soil.xlsx"
## [21] "SamplingSchedule_T7Plants.gsheat"
## [22] "sensors"
## [23] "soil"
## [24] "T2_biomass_2022_L0.csv"
## [25] "T2_biomass_2022_L0.gsheat"
## [26] "T2_height_greenness_2022_L0.csv"
## [27] "T2_height_greenness_2022_L0.gsheat"
## [28] "T7_ANPP"
## [29] "T7_plant_comp"

```

```
## [30] "T7_plant_phenology"  
## [31] "T7_taxon_list.xlsx"  
## [32] "T7_warmx_insect"  
## [33] "T7_warmx_plant_traits"  
## [34] "T7_warmx_VOC"  
## [35] "weather"
```

```
# Read in data
```

```
wheat_data <- read.csv(file.path(dir, "T2_height_greenness_2022_L0.csv"))  
wheat_biomass <- read.csv(file.path(dir, "T2_biomass_2022_L0.csv"))
```

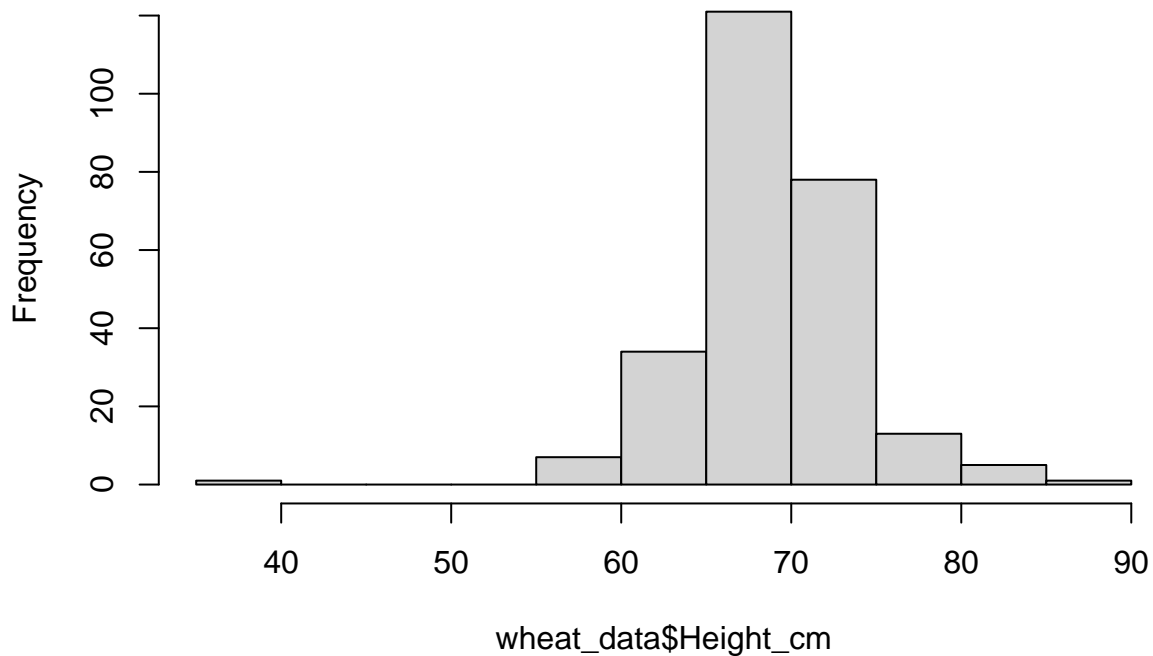
Data Exploration

```
# Height
```

```
# checking raw data
```

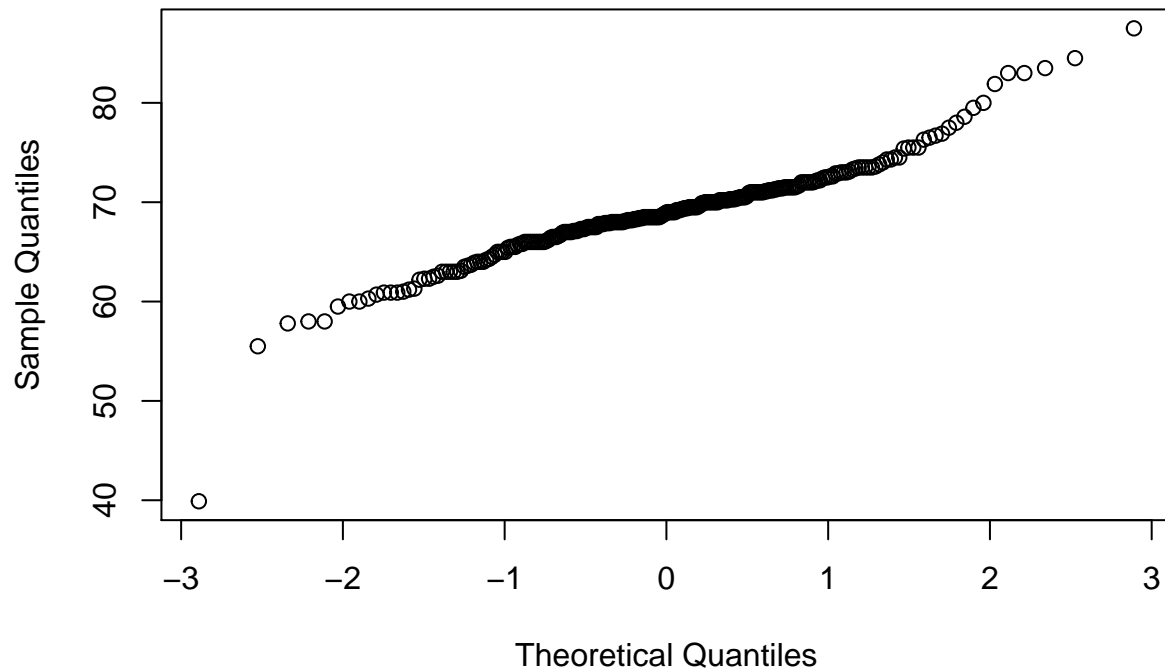
```
hist(wheat_data$Height_cm) # this looks pretty normal
```

Histogram of wheat_data\$Height_cm



```
qqnorm(wheat_data$Height_cm) # this looks ok
```

Normal Q-Q Plot

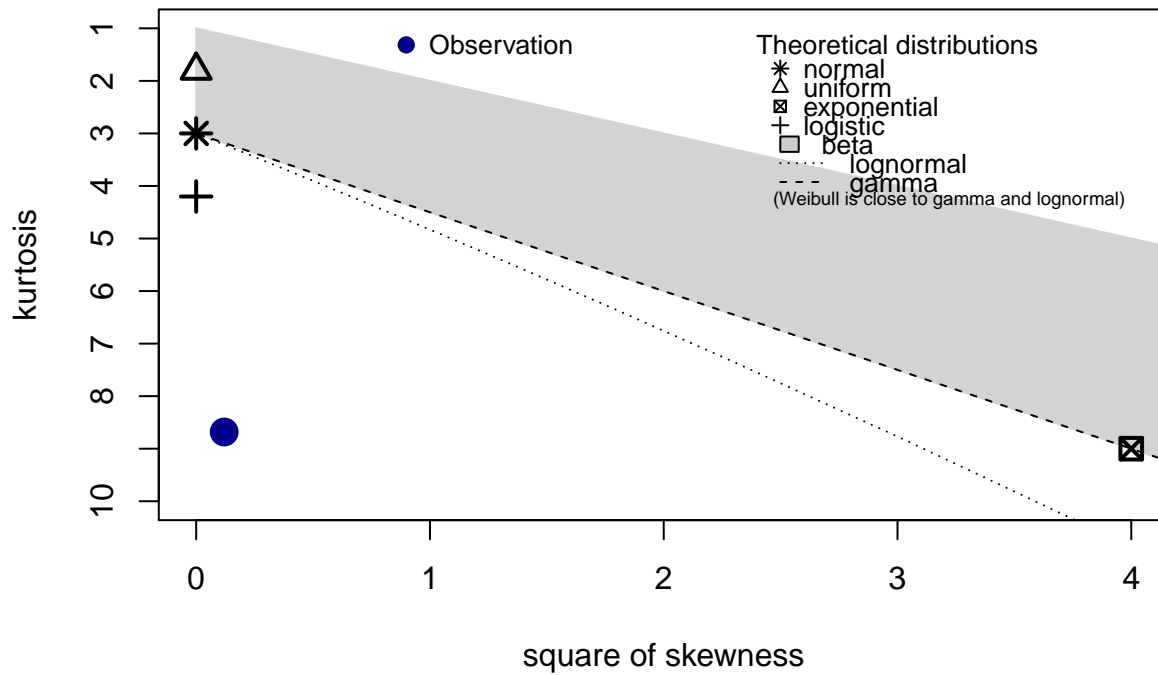


```
shapiro.test(wheat_data$Height_cm) # pvalue is < 0.05 so we reject the null hypothesis that the data is
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  wheat_data$Height_cm  
## W = 0.93023, p-value = 1.007e-09
```

```
# Exploring distributions for these right-skewed data:  
descdist(wheat_data$Height_cm, discrete = FALSE)
```

Cullen and Frey graph



```
## summary statistics
## -----
## min: 39.9   max: 87.5
## median: 68.95
## mean: 68.92962
## estimated sd: 4.906438
## estimated skewness: -0.3461397
## estimated kurtosis: 8.682389
```

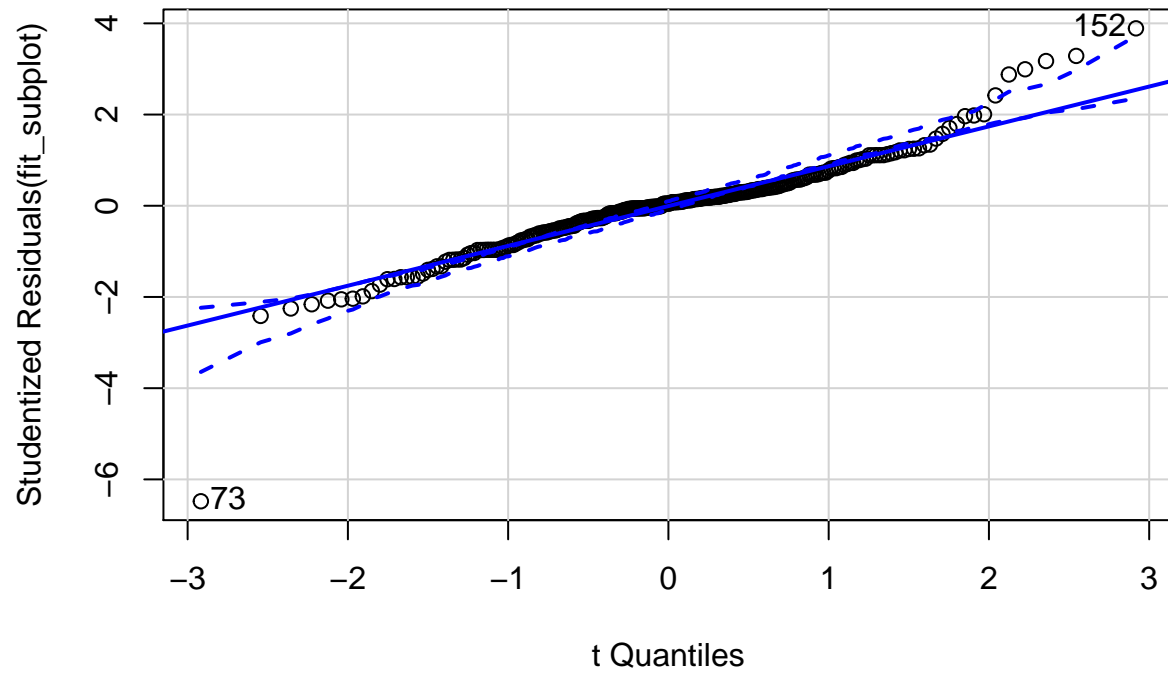
*# Leverage plots and detecting Outliers. <https://www.statmethods.net/stats/riagnostics.html>
These illustrate whether certain data points have more leverage (more influence), and thus could be o*

```
# species level data
# UMBS State-only model
fit_subplot <- lm(Height_cm ~ Subplot_Descriptions, data = wheat_data)
outlierTest(fit_subplot) # outliers in row 73 and 152
```

```
##      rstudent unadjusted p-value Bonferroni p
## 73 -6.479564      4.8001e-10  1.2480e-07
## 152 3.890653      1.2800e-04  3.3281e-02
```

```
qqPlot(fit_subplot, main="QQ Plot")
```

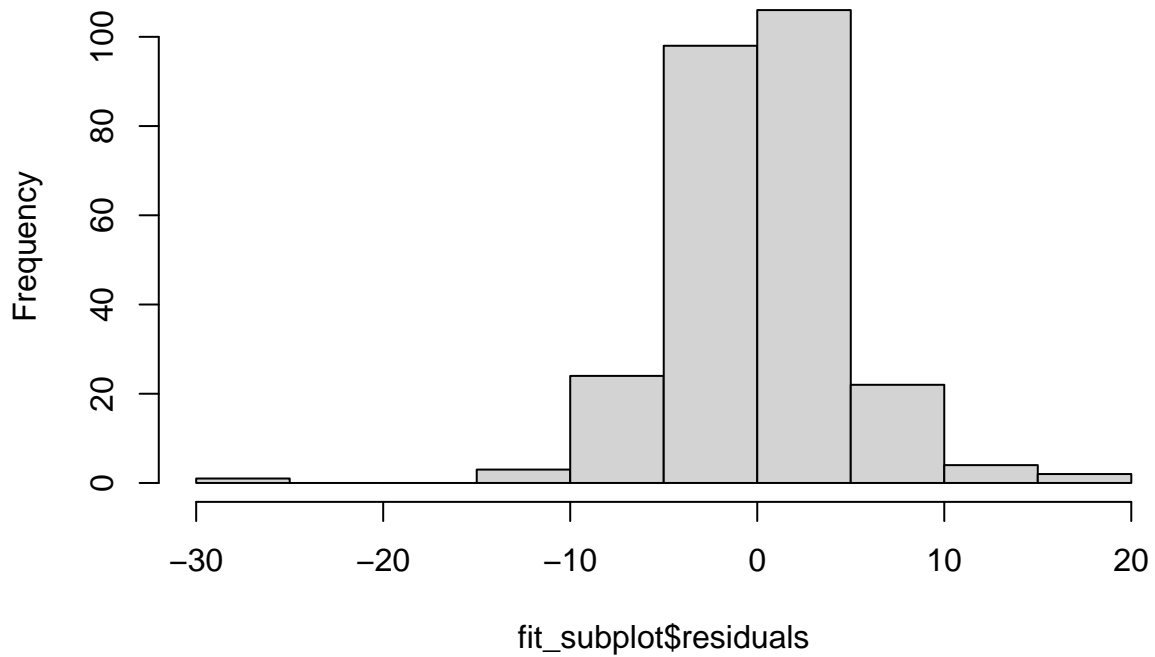
QQ Plot



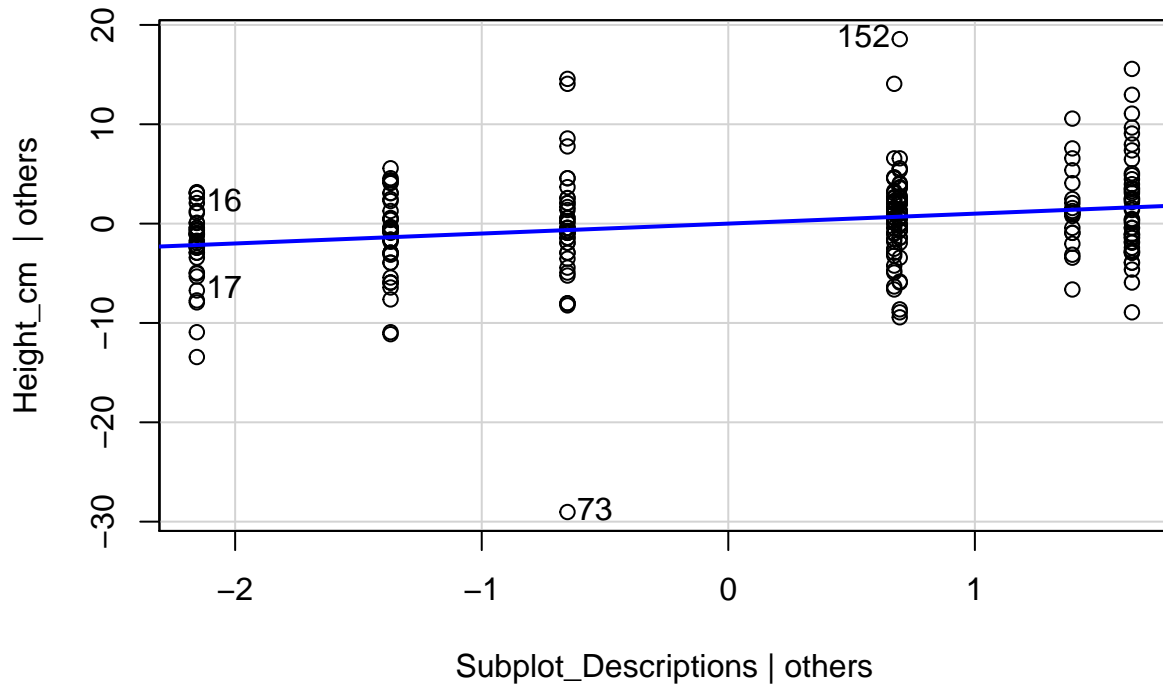
```
## [1] 73 152
```

```
hist(fit_subplot$residuals)
```

Histogram of fit_subplot\$residuals



```
leveragePlots(fit_subplot)
```



```
ols_test_normality(fit_subplot) # pvalues are < 0.05 so we can reject the null that the errors are not
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

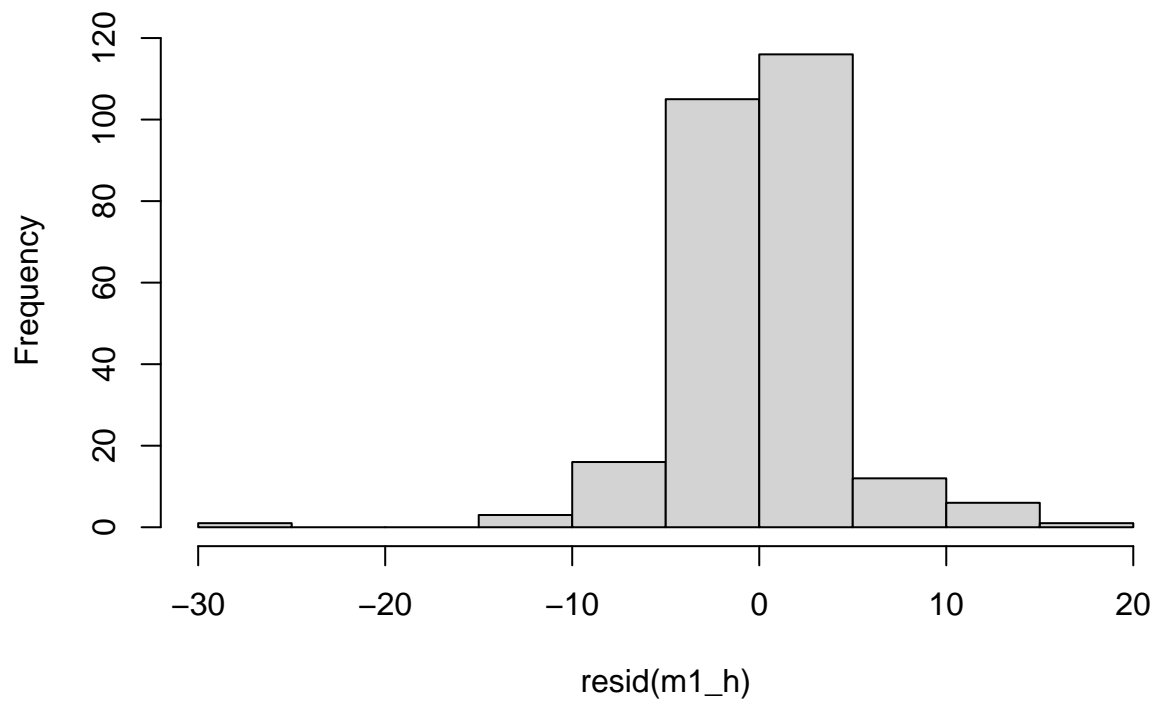
```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk         0.9306        0.0000
## Kolmogorov-Smirnov    0.0882        0.0351
## Cramer-von Mises     15.9243        0.0000
## Anderson-Darling      3.4896        0.0000
## -----
```

```
m1_h <- lmer((Height_cm) ~ Subplot_Descriptions + (1|Replicate/Footprint), data = wheat_data, REML=F)
```

```
## boundary (singular) fit: see ?isSingular
```

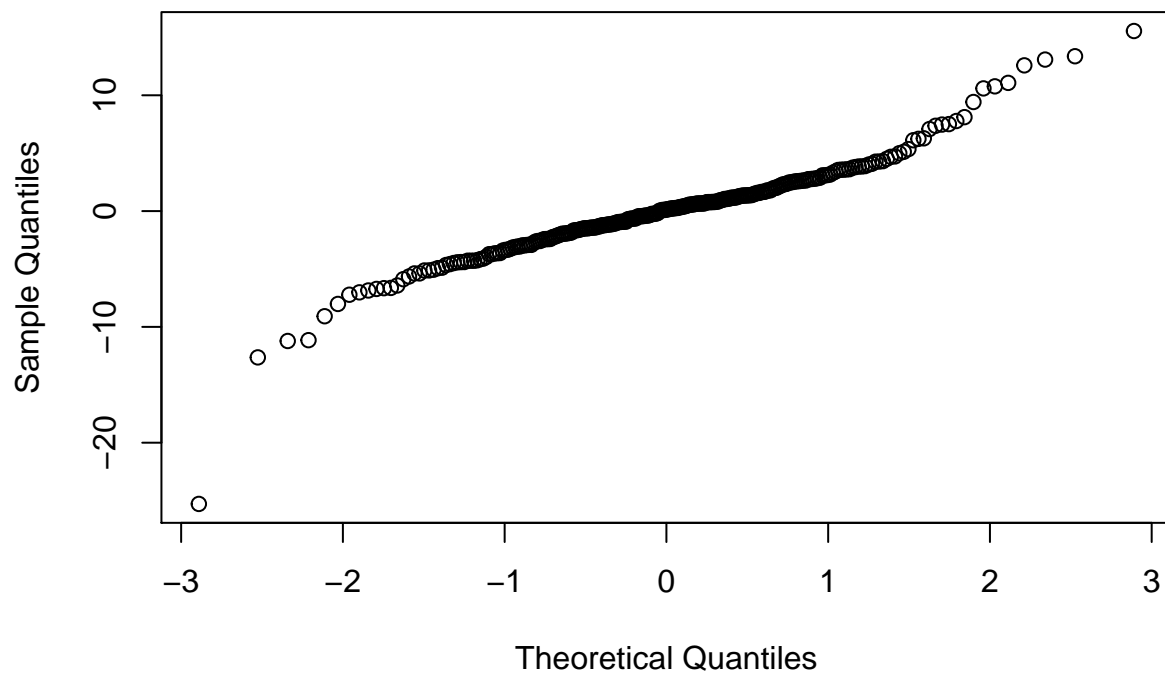
```
hist(resid(m1_h))
```


Histogram of resid(m1_h)

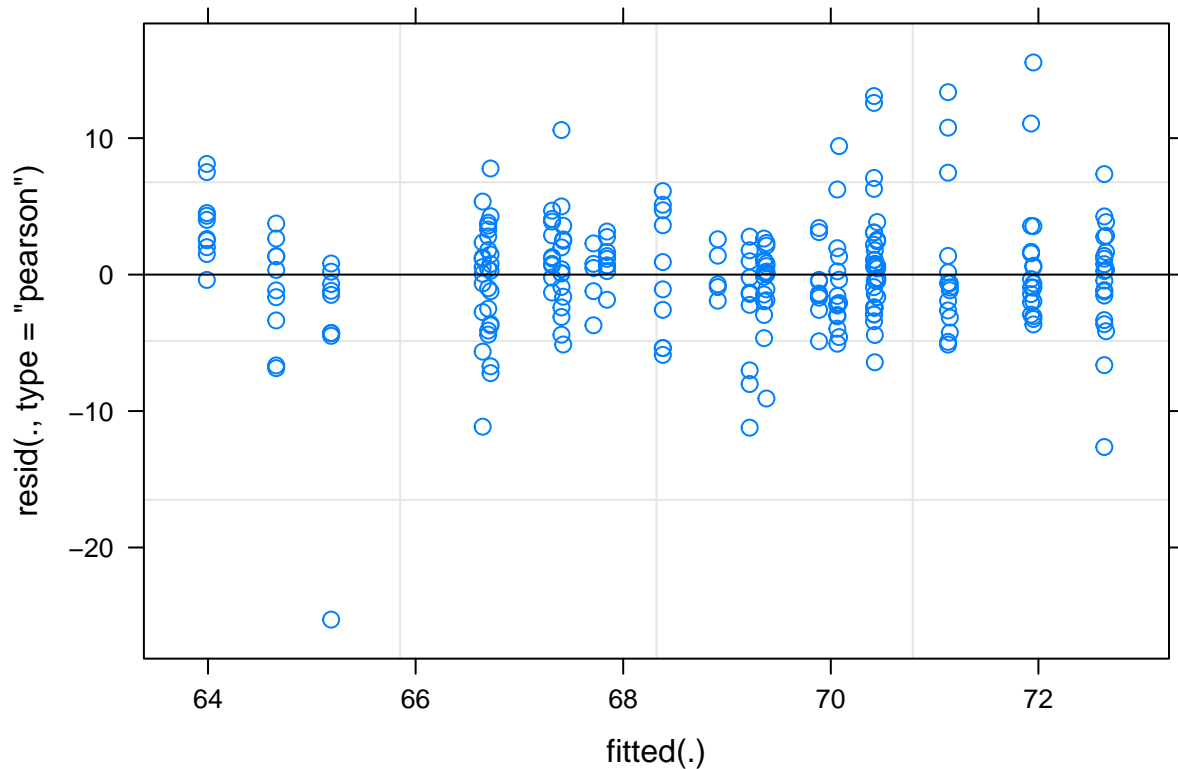


```
qqnorm(resid(m1_h))
```

Normal Q-Q Plot



```
plot(m1_h)
```



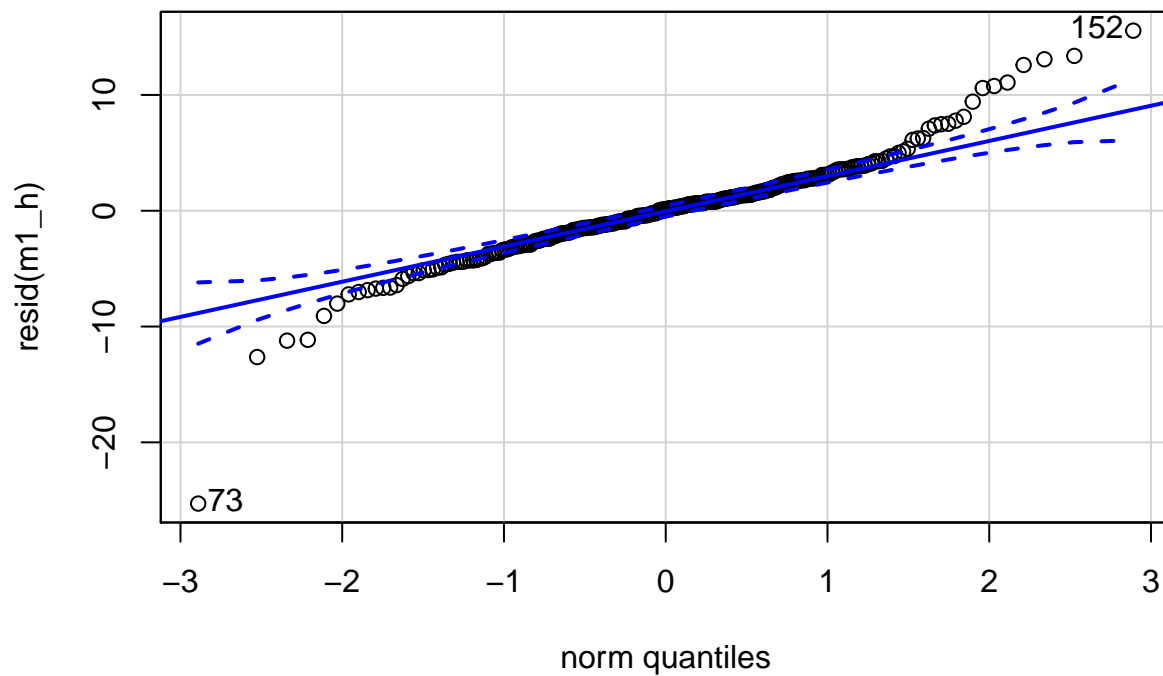
```
# Check for homogeneity of variances (true if p>0.05). If the result is not significant, the assumption
# *****Levene's Test - tests whether or not the variance among two or more groups is equal - If the p-value
```

```
# homogeneity of variance? yes, p > 0.05 (no significant difference between the group variances)
leveneTest(residuals(m1_h) ~ wheat_data$Subplot_Descriptions) # Assumption met
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  6  0.7064 0.6447
##      253
```

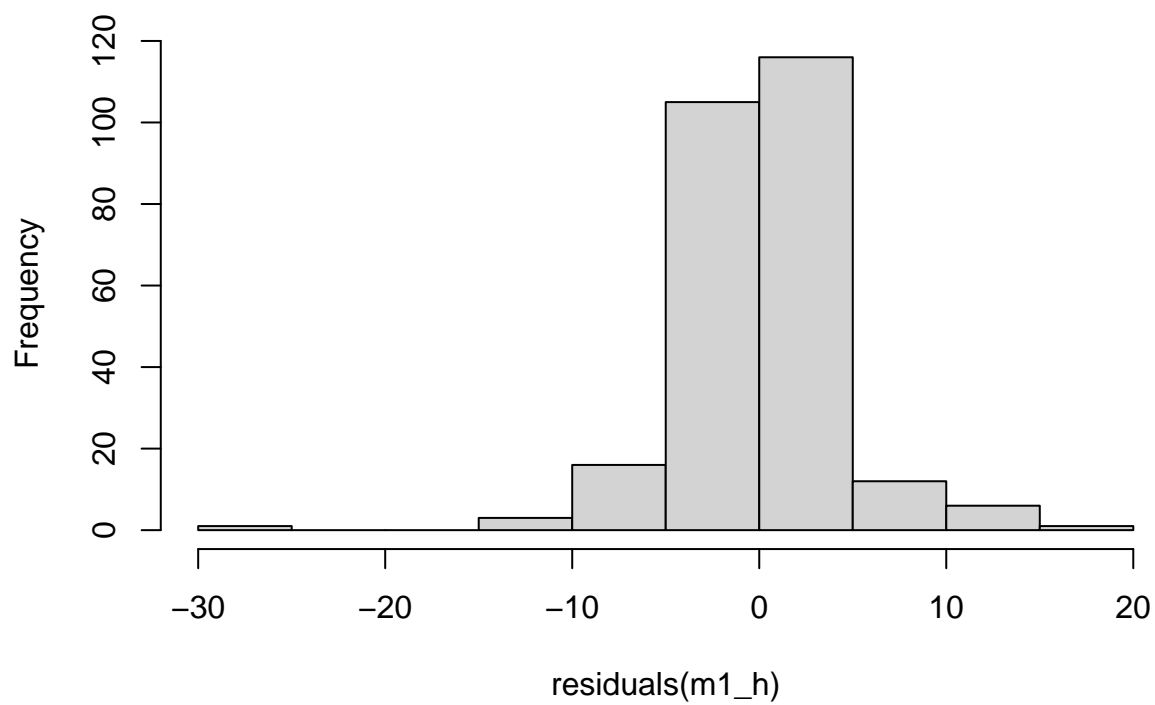
```
# Normality of error term: need to check by histogram, QQplot of residuals, could do Kolmogorov-Smirnov
# Check for normal residuals
qqPlot(resid(m1_h))
```



```
## [1] 73 152
```

```
hist(residuals(m1_h))
```

Histogram of residuals(m1_h)



```
shapiro.test(resid(m1_h)) # not normally distributed resids bc p<0.05
```

```
##
## Shapiro-Wilk normality test
##
## data: resid(m1_h)
## W = 0.92756, p-value = 5.855e-10

outlierTest(m1_h) # row 73 outlier

##      rstudent unadjusted p-value Bonferroni p
## 73 -6.041023      5.5462e-09      1.442e-06

summary(m1_h)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: (Height_cm) ~ Subplot_Descriptions + (1 | Replicate/Footprint)
## Data: wheat_data
##
##      AIC      BIC   logLik deviance df.resid
## 1522.7   1558.3   -751.3   1502.7      250
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -5.9312 -0.4927  0.0309  0.4689  3.6470
##
## Random effects:
## Groups              Name             Variance Std.Dev.
## Footprint:Replicate (Intercept)  0.000   0.000
## Replicate           (Intercept)  3.908   1.977
## Residual                        18.176   4.263
## Number of obs: 260, groups: Footprint:Replicate, 16; Replicate, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df
## (Intercept)      68.0894    1.1999   7.5783
## Subplot_Descriptionscontrol_fungicide    -1.1977    0.9881 256.1151
## Subplot_Descriptionsdrought_control     -0.5294    0.9577 256.3718
## Subplot_Descriptionsdrought_corn_control    2.2356    1.1712 256.2589
## Subplot_Descriptionsdrought_fungicide     1.5356    0.9577 256.3718
## Subplot_Descriptionsdrought_legacy_control  1.5131    0.9577 256.3718
## Subplot_Descriptionsdrought_legacy_fungicide 2.2188    0.9285 256.2020
##
##              t value Pr(>|t|)
## (Intercept)    56.746 3.06e-11 ***
## Subplot_Descriptionscontrol_fungicide    -1.212   0.2266
## Subplot_Descriptionsdrought_control     -0.553   0.5809
## Subplot_Descriptionsdrought_corn_control    1.909   0.0574 .
## Subplot_Descriptionsdrought_fungicide     1.603   0.1101
## Subplot_Descriptionsdrought_legacy_control  1.580   0.1154
## Subplot_Descriptionsdrought_legacy_fungicide 2.390   0.0176 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
```

```
##          (Intr) Sbplt_Dscrptnsc_ Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsc_          -0.386
## Sbplt_Dscrptnsdrght_c     -0.403  0.484
## Sbplt_Dscrptnsdrght_c_     -0.329  0.395          0.413
## Sbplt_Dscrptnsdrght_f     -0.403  0.484          0.505
## Sbplt_Dscrptnsdrght_lgcy_c -0.403  0.484          0.505
## Sbplt_Dscrptnsdrght_lgcy_f -0.412  0.496          0.517
##          Sbplt_Dscrptnsdrght_c_ Sbplt_Dscrptnsdrght_f
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_c_
## Sbplt_Dscrptnsdrght_f      0.413
## Sbplt_Dscrptnsdrght_lgcy_c 0.413          0.505
## Sbplt_Dscrptnsdrght_lgcy_f 0.422          0.517
##          Sbplt_Dscrptnsdrght_lgcy_c
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_c_
## Sbplt_Dscrptnsdrght_f
## Sbplt_Dscrptnsdrght_lgcy_c
## Sbplt_Dscrptnsdrght_lgcy_f 0.517
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
emmeans(m1_h, list(pairwise ~ Subplot_Descriptions), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

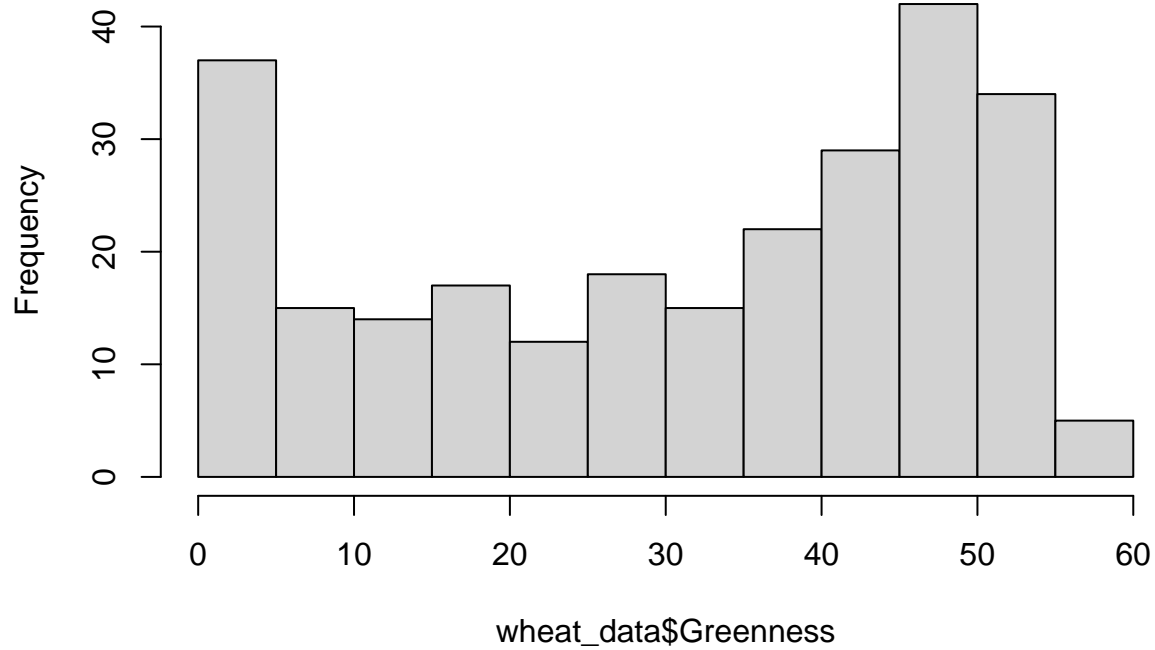
```
## Note: Use 'contrast(regrid(object), ...)' to obtain contrasts of back-transformed estimates
```

```
## $'emmeans of Subplot_Descriptions'
## Subplot_Descriptions      emmean   SE    df lower.CL upper.CL
## control                   68.1 1.35  9.91    65.1    71.1
## control_fungicide         66.9 1.37 10.66    63.9    69.9
## drought_control           67.6 1.34  9.74    64.6    70.6
## drought_corn_control       70.3 1.50 16.69    67.2    73.5
## drought_fungicide          69.6 1.34  9.74    66.6    72.6
## drought_legacy_control      69.6 1.34  9.80    66.6    72.6
## drought_legacy_fungicide    70.3 1.33  9.08    67.3    73.3
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the ( (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of Subplot_Descriptions'
## 1                estimate    SE    df t.ratio
## control - control_fungicide    1.1977 1.004 260.4  1.193
## control - drought_control      0.5294 0.977  30.6  0.542
## control - drought_corn_control -2.2356 1.192  62.8 -1.876
## control - drought_fungicide    -1.5356 0.977  30.6 -1.571
## control - drought_legacy_control -1.5131 0.995  54.8 -1.520
## control - drought_legacy_fungicide -2.2188 0.971  36.7 -2.285
## control_fungicide - drought_control -0.6683 1.014  28.1 -0.659
```

```
## control_fungicide - drought_corn_control      -3.4333 1.222 56.3 -2.810
## control_fungicide - drought_fungicide         -2.7333 1.014 28.1 -2.696
## control_fungicide - drought_legacy_control    -2.7108 1.027 42.9 -2.639
## control_fungicide - drought_legacy_fungicide  -3.4165 1.023 24.6 -3.340
## drought_control - drought_corn_control        -2.7650 1.181 53.9 -2.340
## drought_control - drought_fungicide           -2.0650 0.965 253.9 -2.141
## drought_control - drought_legacy_control       -2.0425 0.973 29.0 -2.099
## drought_control - drought_legacy_fungicide    -2.7482 0.953 22.5 -2.885
## drought_corn_control - drought_fungicide      0.7000 1.181 53.9 0.592
## drought_corn_control - drought_legacy_control  0.7225 1.188 60.2 0.608
## drought_corn_control - drought_legacy_fungicide 0.0168 1.172 49.5 0.014
## drought_fungicide - drought_legacy_control     0.0225 0.973 29.0 0.023
## drought_fungicide - drought_legacy_fungicide  -0.6832 0.953 22.5 -0.717
## drought_legacy_control - drought_legacy_fungicide -0.7057 0.960 250.6 -0.735
## p.value
## 0.8964
## 0.9979
## 0.5037
## 0.7008
## 0.7318
## 0.2783
## 0.9938
## 0.0914
## 0.1364
## 0.1397
## 0.0371
## 0.2445
## 0.3322
## 0.3797
## 0.1011
## 0.9968
## 0.9963
## 1.0000
## 1.0000
## 0.9901
## 0.9903
##
## Note: contrasts are still on the ( scale
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 7 estimates
```

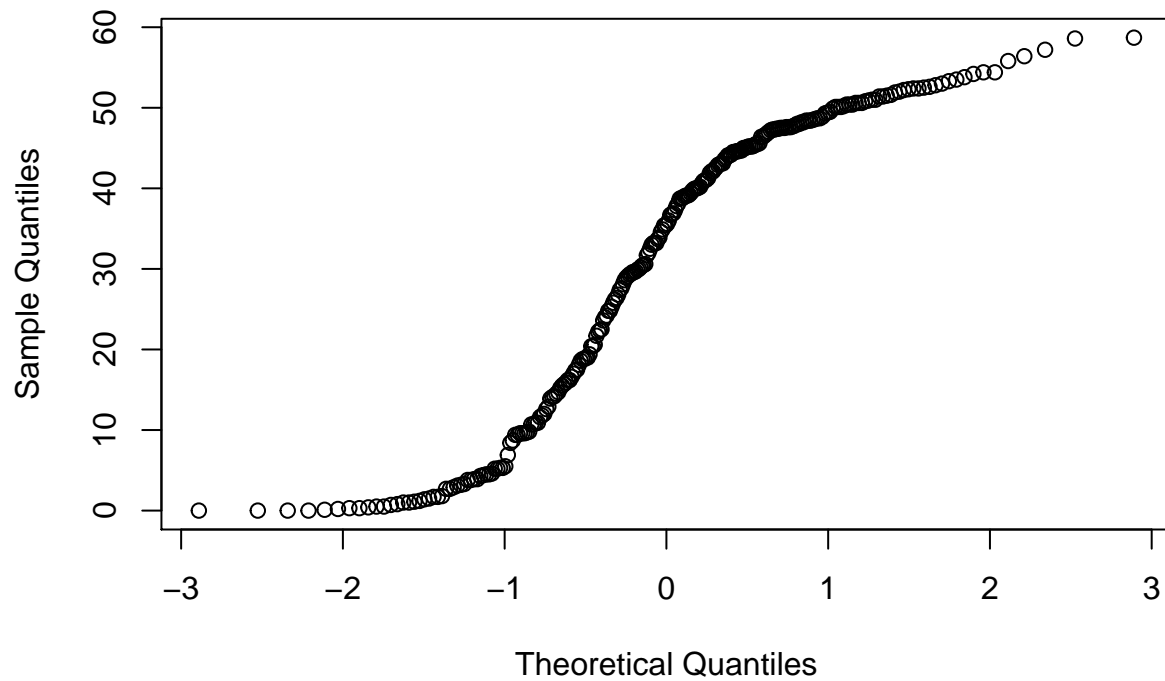
```
# Greenness
# checking raw data
hist(wheat_data$Greenness) # this looks pretty normal
```

Histogram of wheat_data\$Greenness



```
qqnorm(wheat_data$Greenness) # this looks ok
```

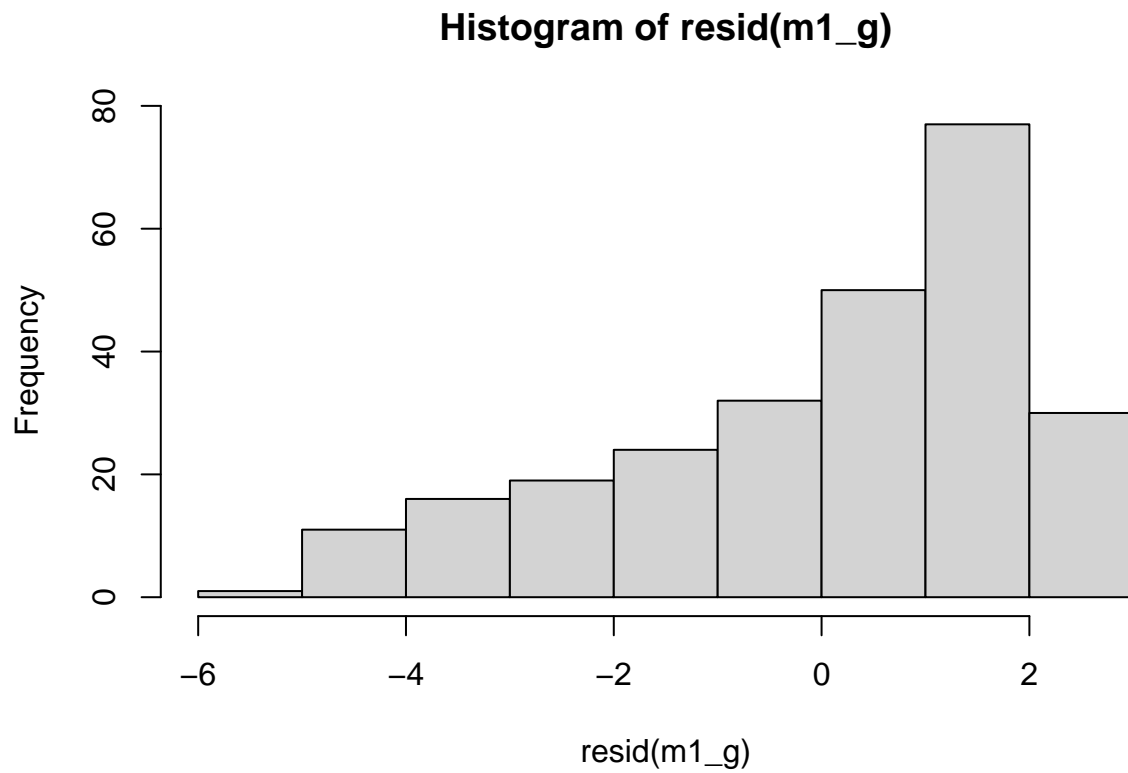
Normal Q-Q Plot



```
m1_g <- lmer(sqrt(Greenness) ~ Subplot_Descriptions + (1|Replicate/Footprint), data = wheat_data, REML=1)
```

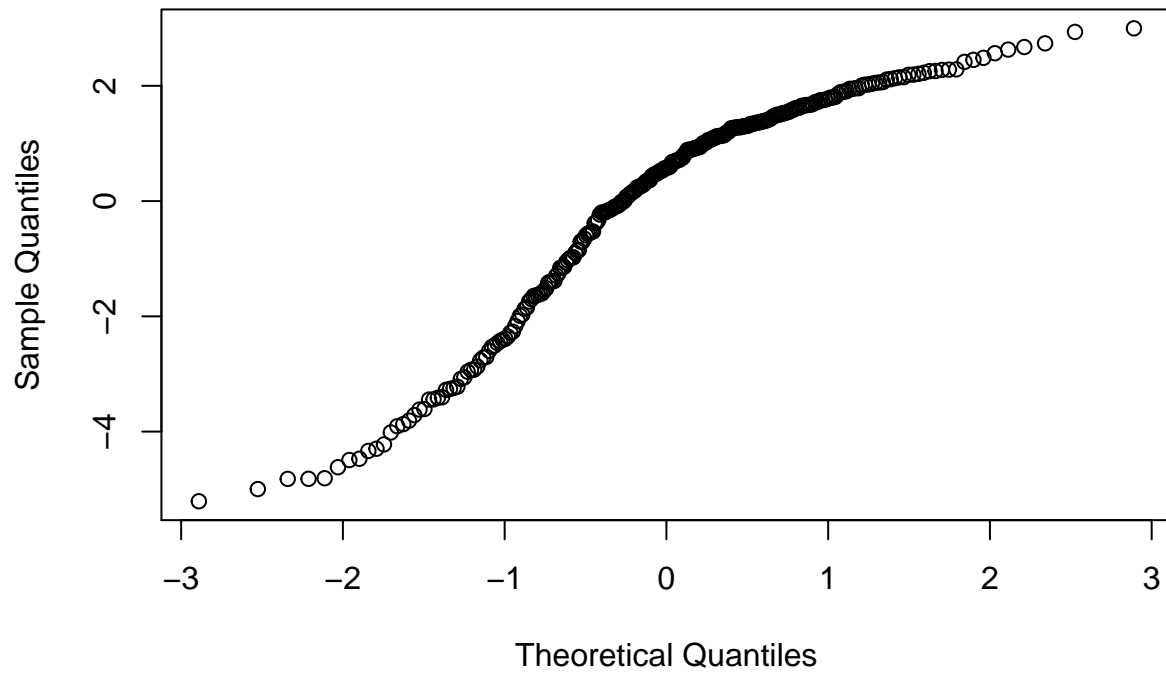
```
## boundary (singular) fit: see ?isSingular
```

```
hist(resid(m1_g))
```

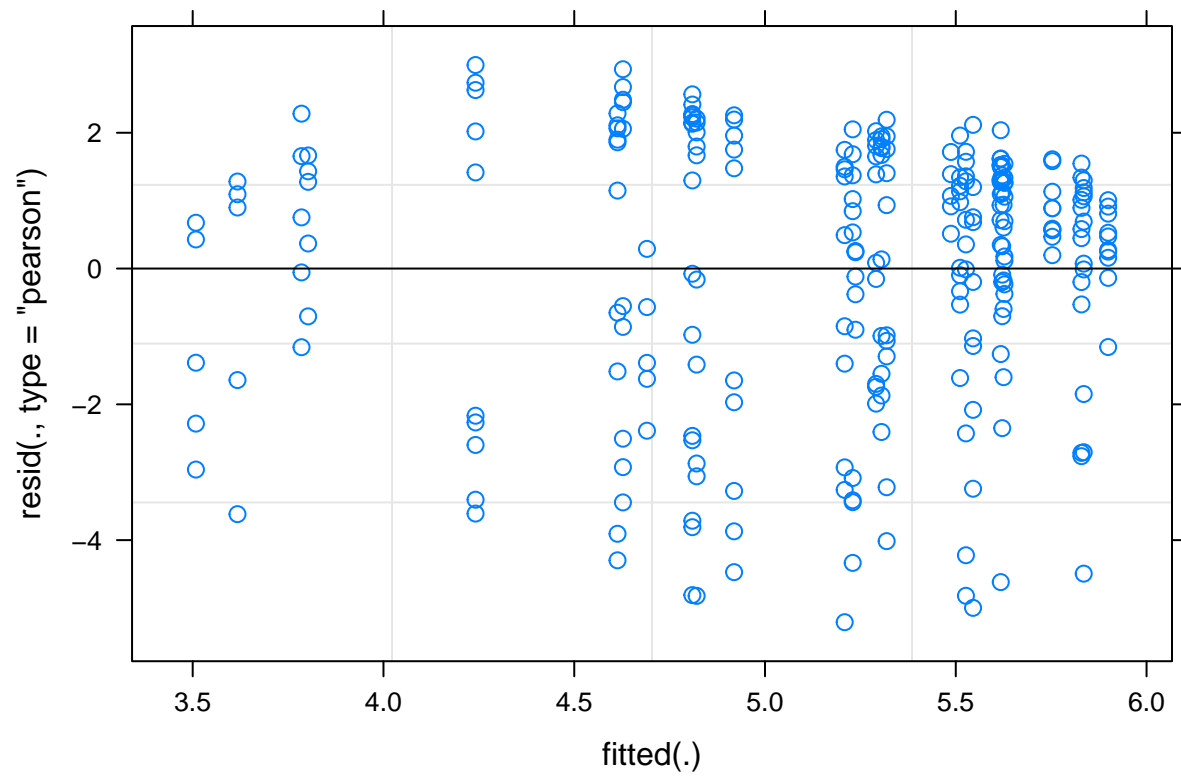


```
qqnorm(resid(m1_g))
```


Normal Q-Q Plot



```
plot(m1_g)
```



```
# homogeneity of variance? yes, p >0.05 (no significant difference between the group variances)
leveneTest(residuals(m1_g) ~ wheat_data$Subplot_Descriptions)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value  Pr(>F)
## group  6  3.2614 0.00417 **
##      253
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m1_g)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: sqrt(Greenness) ~ Subplot_Descriptions + (1 | Replicate/Footprint)
## Data: wheat_data
##
##      AIC      BIC    logLik deviance df.resid
##  1115.4   1151.1   -547.7   1095.4      250
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6506 -0.6451  0.2933  0.7537  1.5253
##
## Random effects:
## Groups              Name                Variance Std.Dev.
## Footprint:Replicate (Intercept) 0.1187   0.3446
## Replicate           (Intercept) 0.0000   0.0000
## Residual                        3.8619   1.9652
## Number of obs: 260, groups: Footprint:Replicate, 16; Replicate, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df
## (Intercept)      5.2903    0.3475  49.8833
## Subplot_Descriptionscontrol_fungicide      0.3881    0.4566 252.5377
## Subplot_Descriptionsdrought_control      0.2381    0.4970  40.1940
## Subplot_Descriptionsdrought_corn_control    -1.6118    0.5861  72.0601
## Subplot_Descriptionsdrought_fungicide      0.4458    0.4970  40.1940
## Subplot_Descriptionsdrought_legacy_control   -0.1301    0.4781  86.5954
## Subplot_Descriptionsdrought_legacy_fungicide -0.8078    0.4727  65.3323
##
##              t value Pr(>|t|)
## (Intercept)    15.225 < 2e-16 ***
## Subplot_Descriptionscontrol_fungicide      0.850  0.39615
## Subplot_Descriptionsdrought_control      0.479  0.63451
## Subplot_Descriptionsdrought_corn_control   -2.750  0.00753 **
## Subplot_Descriptionsdrought_fungicide      0.897  0.37500
## Subplot_Descriptionsdrought_legacy_control  -0.272  0.78616
## Subplot_Descriptionsdrought_legacy_fungicide -1.709  0.09220 .
## ---
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sbplt_Dscrptnsc_ Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsc_      -0.598
## Sbplt_Dscrptnsdrght_c -0.699  0.418
## Sbplt_Dscrptnsdrght_c_ -0.593  0.355      0.415
## Sbplt_Dscrptnsdrght_f -0.699  0.418      0.609
## Sbplt_Dscrptnsdrght_lgcy_c -0.687  0.428      0.480
## Sbplt_Dscrptnsdrght_lgcy_f -0.700  0.422      0.490
##              Sbplt_Dscrptnsdrght_c_ Sbplt_Dscrptnsdrght_f
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_c_
## Sbplt_Dscrptnsdrght_f      0.415
## Sbplt_Dscrptnsdrght_lgcy_c  0.407      0.480
## Sbplt_Dscrptnsdrght_lgcy_f  0.415      0.490
##              Sbplt_Dscrptnsdrght_lgcy_c
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_c_
## Sbplt_Dscrptnsdrght_f
## Sbplt_Dscrptnsdrght_lgcy_c
## Sbplt_Dscrptnsdrght_lgcy_f  0.587
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

emmeans(m1_g, list(pairwise ~ Subplot_Descriptions), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## Note: Use 'contrast(regrid(object), ...)' to obtain contrasts of back-transformed estimates

## $'emmeans of Subplot_Descriptions'
## Subplot_Descriptions      emmean      SE    df lower.CL upper.CL
## control                   5.29 0.382 59.8    4.53    6.06
## control_fungicide         5.68 0.413 58.6    4.85    6.51
## drought_control           5.53 0.390 42.3    4.74    6.31
## drought_corn_control       3.68 0.500 65.7    2.68    4.68
## drought_fungicide          5.74 0.390 42.3    4.95    6.52
## drought_legacy_control     5.16 0.382 60.4    4.40    5.92
## drought_legacy_fungicide   4.48 0.379 44.6    3.72    5.25
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the sqrt (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of Subplot_Descriptions'
##      1              estimate      SE    df t.ratio
## control - control_fungicide    -0.3881 0.462 255.6 -0.840
## control - drought_control      -0.2381 0.546  37.9 -0.436
## control - drought_corn_control  1.6118 0.629  48.8  2.561
## control - drought_fungicide    -0.4458 0.546  37.9 -0.817

```

```

## control - drought_legacy_control          0.1301 0.524 82.1 0.248
## control - drought_legacy_fungicide         0.8078 0.525 62.0 1.539
## control_fungicide - drought_control        0.1500 0.568 37.1 0.264
## control_fungicide - drought_corn_control   1.9999 0.648 47.2 3.084
## control_fungicide - drought_fungicide      -0.0578 0.568 37.1 -0.102
## control_fungicide - drought_legacy_control 0.5182 0.553 66.2 0.937
## control_fungicide - drought_legacy_fungicide 1.1959 0.563 48.5 2.125
## drought_control - drought_corn_control     1.8499 0.634 41.3 2.919
## drought_control - drought_fungicide        -0.2078 0.443 249.0 -0.469
## drought_control - drought_legacy_control    0.3682 0.546 37.3 0.675
## drought_control - drought_legacy_fungicide 1.0458 0.544 32.0 1.924
## drought_corn_control - drought_fungicide   -2.0577 0.634 41.3 -3.247
## drought_corn_control - drought_legacy_control -1.4817 0.629 48.2 -2.355
## drought_corn_control - drought_legacy_fungicide -0.8041 0.627 42.9 -1.282
## drought_fungicide - drought_legacy_control 0.5760 0.546 37.3 1.055
## drought_fungicide - drought_legacy_fungicide 1.2536 0.544 32.0 2.306
## drought_legacy_control - drought_legacy_fungicide 0.6777 0.441 262.5 1.536
## p.value
## 0.9805
## 0.9994
## 0.1608
## 0.9817
## 1.0000
## 0.7202
## 1.0000
## 0.0494
## 1.0000
## 0.9650
## 0.3550
## 0.0763
## 0.9992
## 0.9933
## 0.4802
## 0.0346
## 0.2400
## 0.8564
## 0.9370
## 0.2722
## 0.7227
##
## Note: contrasts are still on the sqrt scale
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 7 estimates

```

```

# Biomass
# checking raw data
hist(wheat_biomass$anpp) # this looks normal

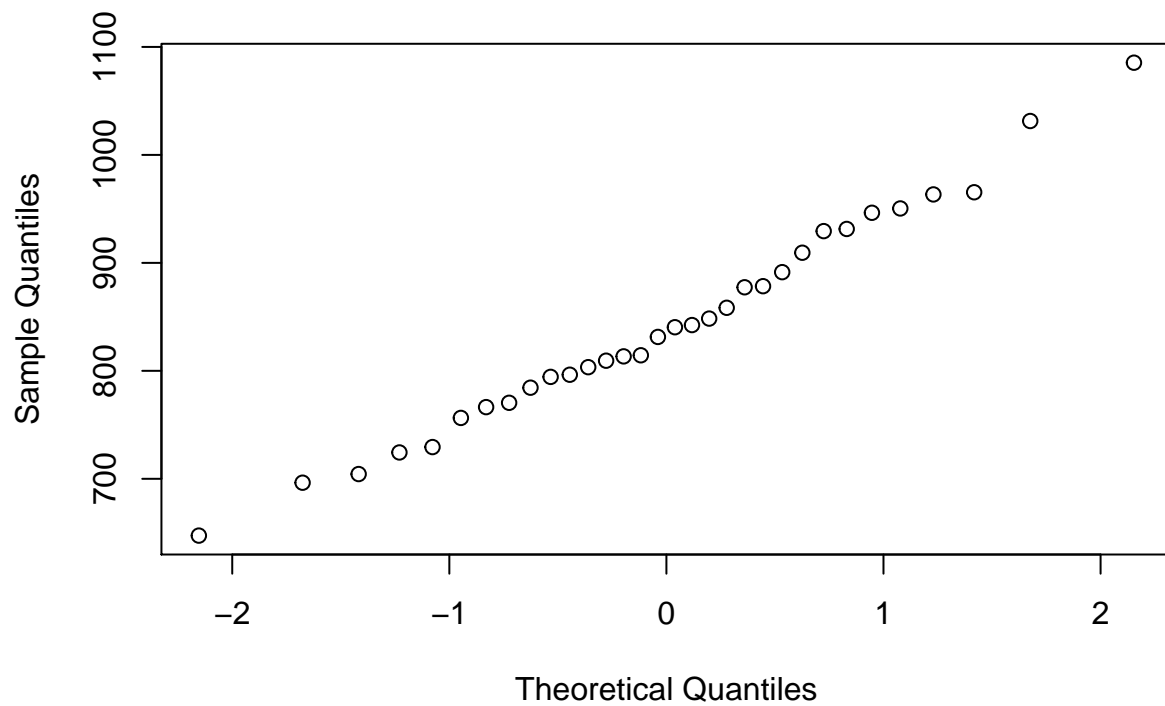
```

Histogram of wheat_biomass\$anpp



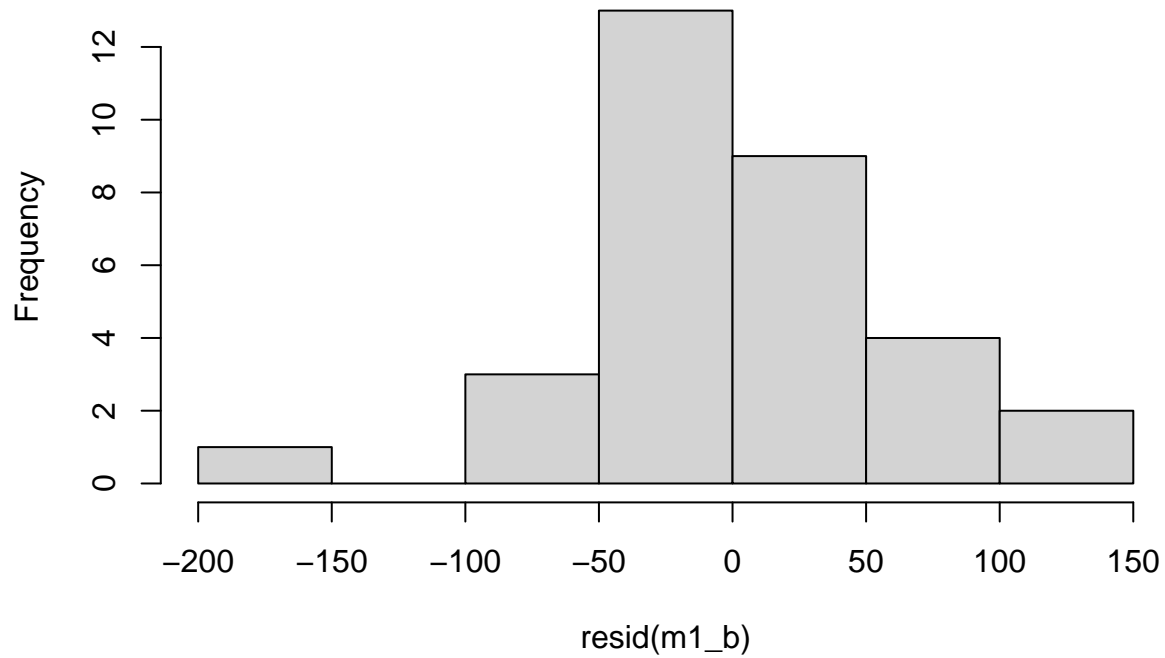
```
qqnorm(wheat_biomass$anpp) # this looks ok
```

Normal Q-Q Plot



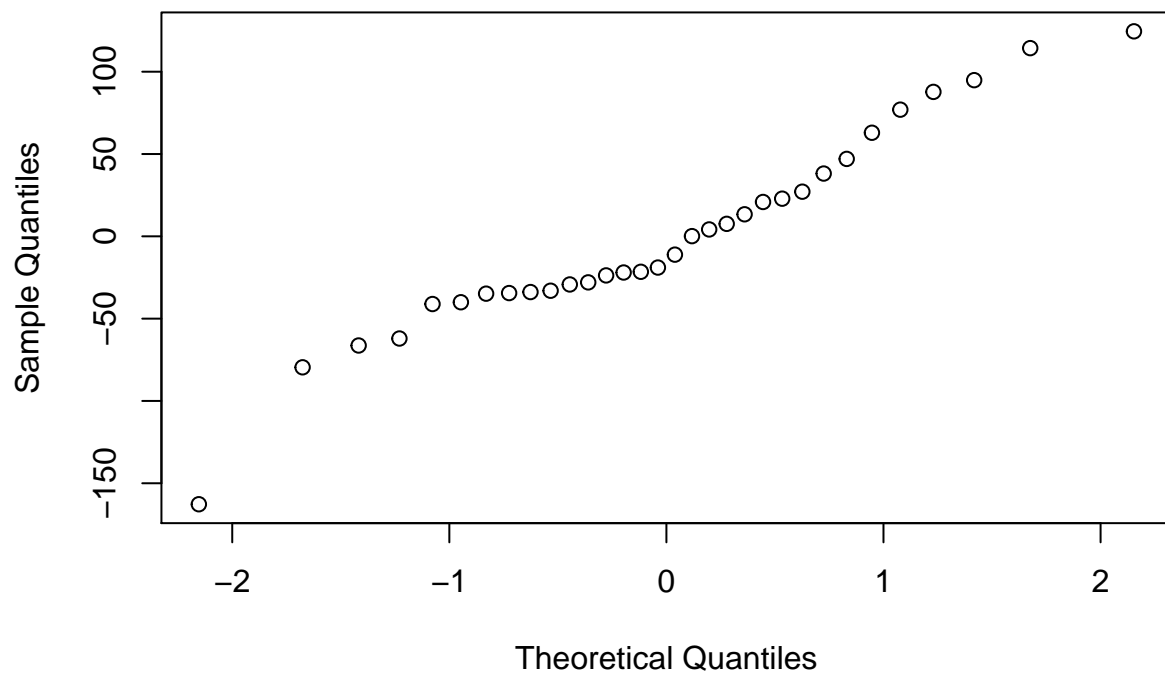
```
m1_b <- lmer(anpp ~ Subplot_Descriptions + (1|Replicate/Footprint), data = wheat_biomass, REML=F)
hist(resid(m1_b))
```

Histogram of resid(m1_b)

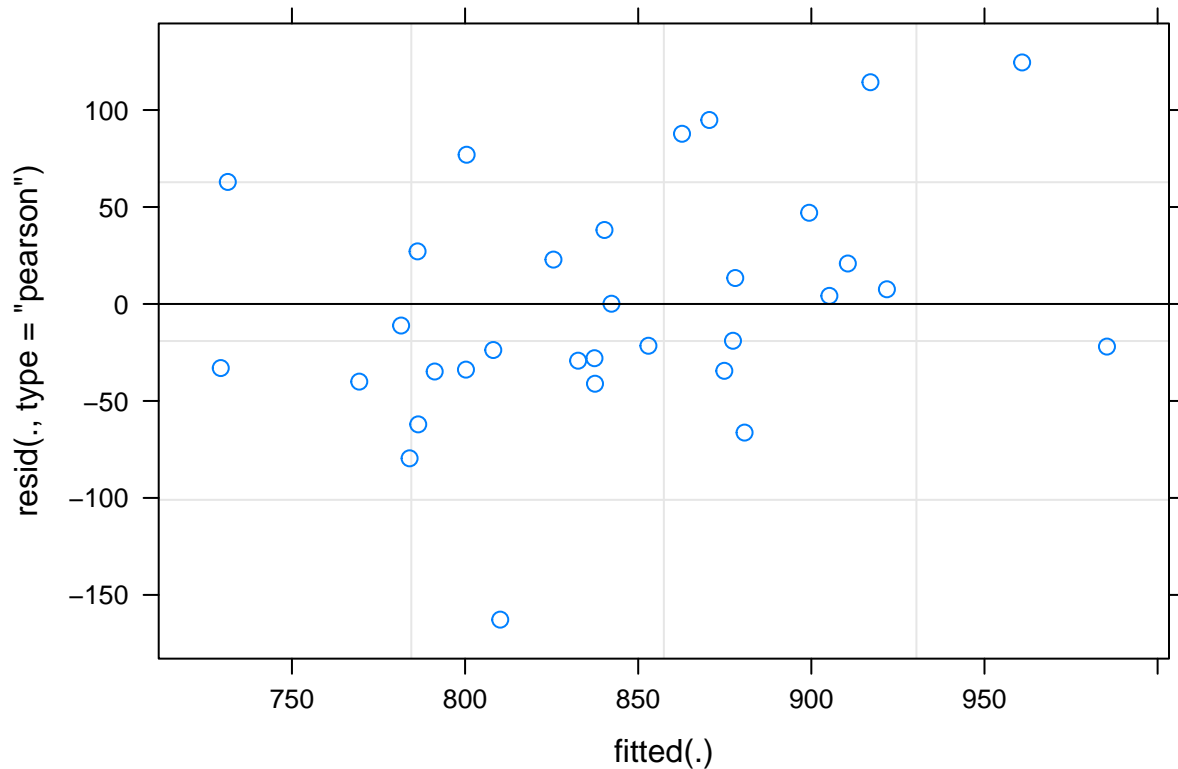


```
qqnorm(resid(m1_b))
```

Normal Q-Q Plot



```
plot(m1_b)
```



```
# homogeneity of variance? yes, p > 0.05 (no significant difference between the group variances)
leveneTest(residuals(m1_b) ~ wheat_biomass$Subplot_Descriptions)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  7  0.4223 0.8787
##      24
```

```
summary(m1_b)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: anpp ~ Subplot_Descriptions + (1 | Replicate/Footprint)
## Data: wheat_biomass
##
##      AIC      BIC   logLik deviance df.resid
##    396.6    412.7   -187.3   374.6      21
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3611 -0.4934 -0.2183  0.4335  1.8066
```

```

##
## Random effects:
##   Groups          Name          Variance Std.Dev.
## Footprint:Replicate (Intercept) 1645      40.56
## Replicate          (Intercept) 2049      45.27
## Residual              4751      68.93
## Number of obs: 32, groups: Footprint:Replicate, 16; Replicate, 4
##
## Fixed effects:
##               Estimate Std. Error    df t value
## (Intercept)         844.40      45.95  20.72  18.376
## Subplot_Descriptionscontrol_fungicide -52.50      48.74  16.00  -1.077
## Subplot_Descriptionsdrought_control -35.00      56.55  24.07  -0.619
## Subplot_Descriptionsdrought_corn_control -13.75      56.55  24.07  -0.243
## Subplot_Descriptionsdrought_corn_fungicide -9.00      56.55  24.07  -0.159
## Subplot_Descriptionsdrought_fungicide  5.00      56.55  24.07   0.088
## Subplot_Descriptionsdrought_legacy_control  61.25      56.55  24.07   1.083
## Subplot_Descriptionsdrought_legacy_fungicide  36.75      56.55  24.07   0.650
##               Pr(>|t|)
## (Intercept)         2.67e-14 ***
## Subplot_Descriptionscontrol_fungicide  0.297
## Subplot_Descriptionsdrought_control  0.542
## Subplot_Descriptionsdrought_corn_control  0.810
## Subplot_Descriptionsdrought_corn_fungicide  0.875
## Subplot_Descriptionsdrought_fungicide  0.930
## Subplot_Descriptionsdrought_legacy_control  0.290
## Subplot_Descriptionsdrought_legacy_fungicide  0.522
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##               (Intr) Sbplt_Dscrptnsc_ Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsc_ -0.530
## Sbplt_Dscrptnsdrght_c -0.615  0.431
## Sbplt_Dscrptnsdrght_crn_c -0.615  0.431  0.500
## Sbplt_Dscrptnsdrght_crn_f -0.615  0.431  0.500
## Sbplt_Dscrptnsdrght_f -0.615  0.431  0.629
## Sbplt_Dscrptnsdrght_lgcy_c -0.615  0.431  0.500
## Sbplt_Dscrptnsdrght_lgcy_f -0.615  0.431  0.500
##               Sbplt_Dscrptnsdrght_crn_c Sbplt_Dscrptnsdrght_crn_f
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_crn_c
## Sbplt_Dscrptnsdrght_crn_f  0.629
## Sbplt_Dscrptnsdrght_f  0.500  0.500
## Sbplt_Dscrptnsdrght_lgcy_c  0.500  0.500
## Sbplt_Dscrptnsdrght_lgcy_f  0.500  0.500
##               Sbplt_Dscrptnsdrght_f Sbplt_Dscrptnsdrght_lgcy_c
## Sbplt_Dscrptnsc_
## Sbplt_Dscrptnsdrght_c
## Sbplt_Dscrptnsdrght_crn_c
## Sbplt_Dscrptnsdrght_crn_f
## Sbplt_Dscrptnsdrght_f
## Sbplt_Dscrptnsdrght_lgcy_c  0.500

```



```
## Sbplt_Dscrptnsdrght_lgcy_f 0.500 0.629
```

```
emmeans(m1_b, list(pairwise ~ Subplot_Descriptions), adjust = "tukey")
```

```
## $'emmeans of Subplot_Descriptions'
```

## Subplot_Descriptions	emmean	SE	df	lower.CL	upper.CL
## control	844	53.1	27.6	736	953
## control_fungicide	792	53.1	27.6	683	901
## drought_control	809	53.1	27.6	701	918
## drought_corn_control	831	53.1	27.6	722	939
## drought_corn_fungicide	835	53.1	27.6	727	944
## drought_fungicide	849	53.1	27.6	741	958
## drought_legacy_control	906	53.1	27.6	797	1014
## drought_legacy_fungicide	881	53.1	27.6	772	990

```
##
```

```
## Degrees-of-freedom method: kenward-roger
```

```
## Confidence level used: 0.95
```

```
##
```

```
## $'pairwise differences of Subplot_Descriptions'
```

## 1	estimate	SE	df	t.ratio
## control - control_fungicide	52.50	56.3	21.3	0.933
## control - drought_control	35.00	65.3	32.1	0.536
## control - drought_corn_control	13.75	65.3	32.1	0.211
## control - drought_corn_fungicide	9.00	65.3	32.1	0.138
## control - drought_fungicide	-5.00	65.3	32.1	-0.077
## control - drought_legacy_control	-61.25	65.3	32.1	-0.938
## control - drought_legacy_fungicide	-36.75	65.3	32.1	-0.563
## control_fungicide - drought_control	-17.50	65.3	32.1	-0.268
## control_fungicide - drought_corn_control	-38.75	65.3	32.1	-0.593
## control_fungicide - drought_corn_fungicide	-43.50	65.3	32.1	-0.666
## control_fungicide - drought_fungicide	-57.50	65.3	32.1	-0.881
## control_fungicide - drought_legacy_control	-113.75	65.3	32.1	-1.742
## control_fungicide - drought_legacy_fungicide	-89.25	65.3	32.1	-1.367
## drought_control - drought_corn_control	-21.25	65.3	32.1	-0.325
## drought_control - drought_corn_fungicide	-26.00	65.3	32.1	-0.398
## drought_control - drought_fungicide	-40.00	56.3	21.3	-0.711
## drought_control - drought_legacy_control	-96.25	65.3	32.1	-1.474
## drought_control - drought_legacy_fungicide	-71.75	65.3	32.1	-1.099
## drought_corn_control - drought_corn_fungicide	-4.75	56.3	21.3	-0.084
## drought_corn_control - drought_fungicide	-18.75	65.3	32.1	-0.287
## drought_corn_control - drought_legacy_control	-75.00	65.3	32.1	-1.149
## drought_corn_control - drought_legacy_fungicide	-50.50	65.3	32.1	-0.773
## drought_corn_fungicide - drought_fungicide	-14.00	65.3	32.1	-0.214
## drought_corn_fungicide - drought_legacy_control	-70.25	65.3	32.1	-1.076
## drought_corn_fungicide - drought_legacy_fungicide	-45.75	65.3	32.1	-0.701
## drought_fungicide - drought_legacy_control	-56.25	65.3	32.1	-0.861
## drought_fungicide - drought_legacy_fungicide	-31.75	65.3	32.1	-0.486
## drought_legacy_control - drought_legacy_fungicide	24.50	56.3	21.3	0.435

```
## p.value
```

```
## 0.9790
```

```
## 0.9993
```

```
## 1.0000
```

```
## 1.0000
```

```
## 1.0000
```

```
## 0.9797
## 0.9991
## 1.0000
## 0.9987
## 0.9974
## 0.9858
## 0.6612
## 0.8653
## 1.0000
## 0.9999
## 0.9957
## 0.8151
## 0.9524
## 1.0000
## 1.0000
## 0.9404
## 0.9934
## 1.0000
## 0.9574
## 0.9964
## 0.9875
## 0.9997
## 0.9998
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```