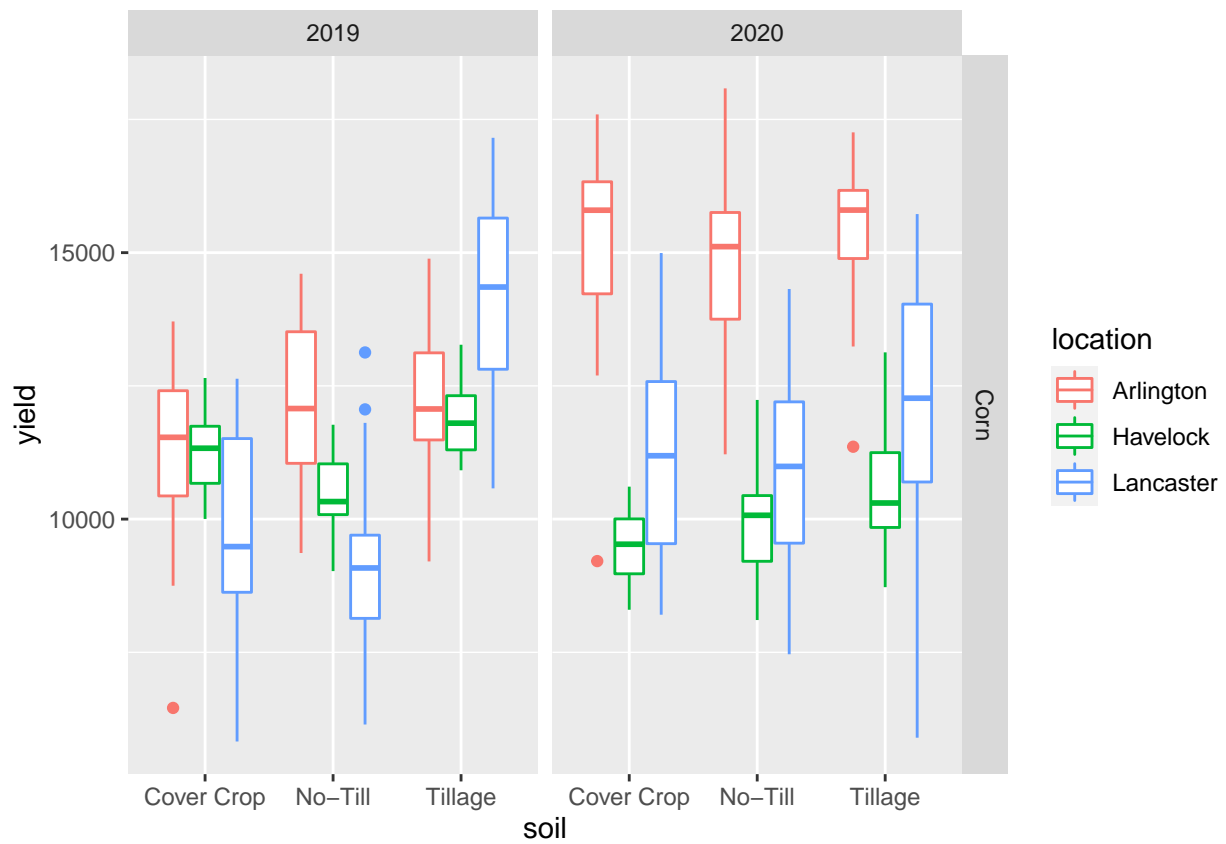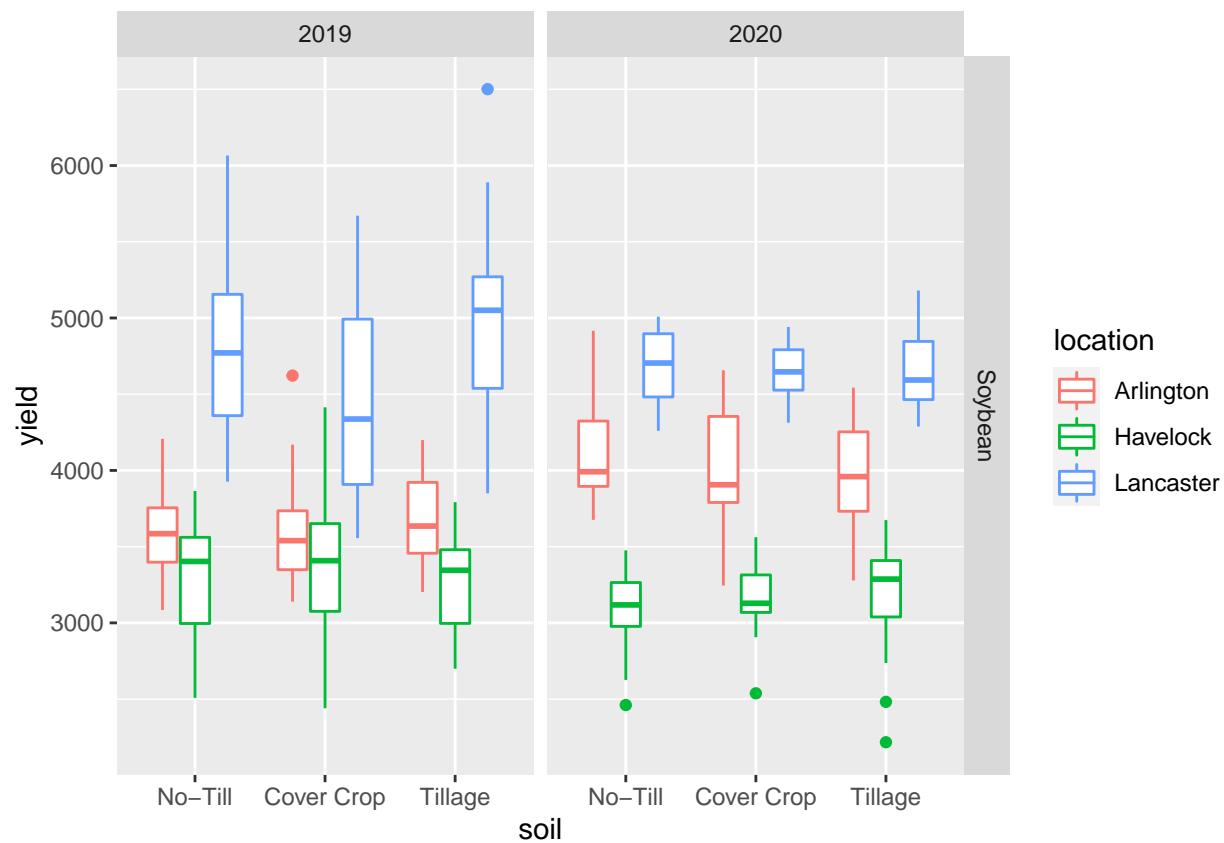# Carryover 2.0

Kolby Grint

11/20/2020

```
Corn1 %>%
  ggplot(aes(x = soil, y = yield, color = location)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```
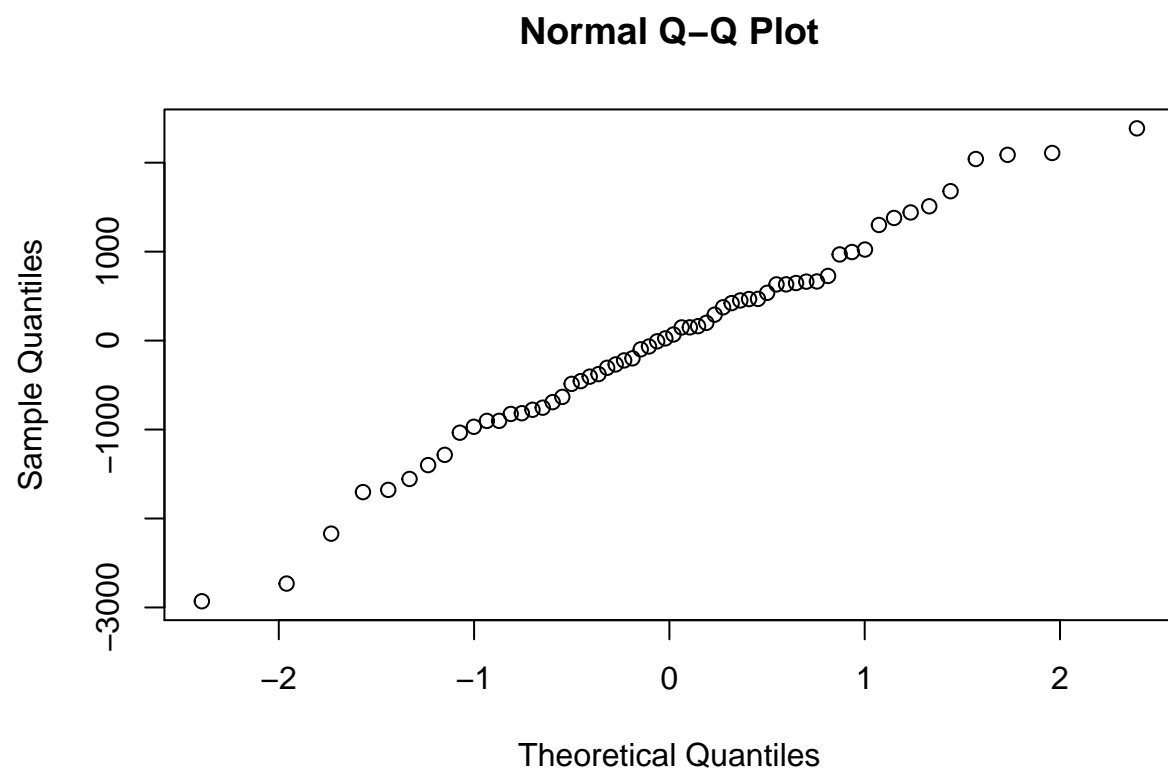


```
Soybean1 %>%
  ggplot(aes(x = soil, y = yield, color = location)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```
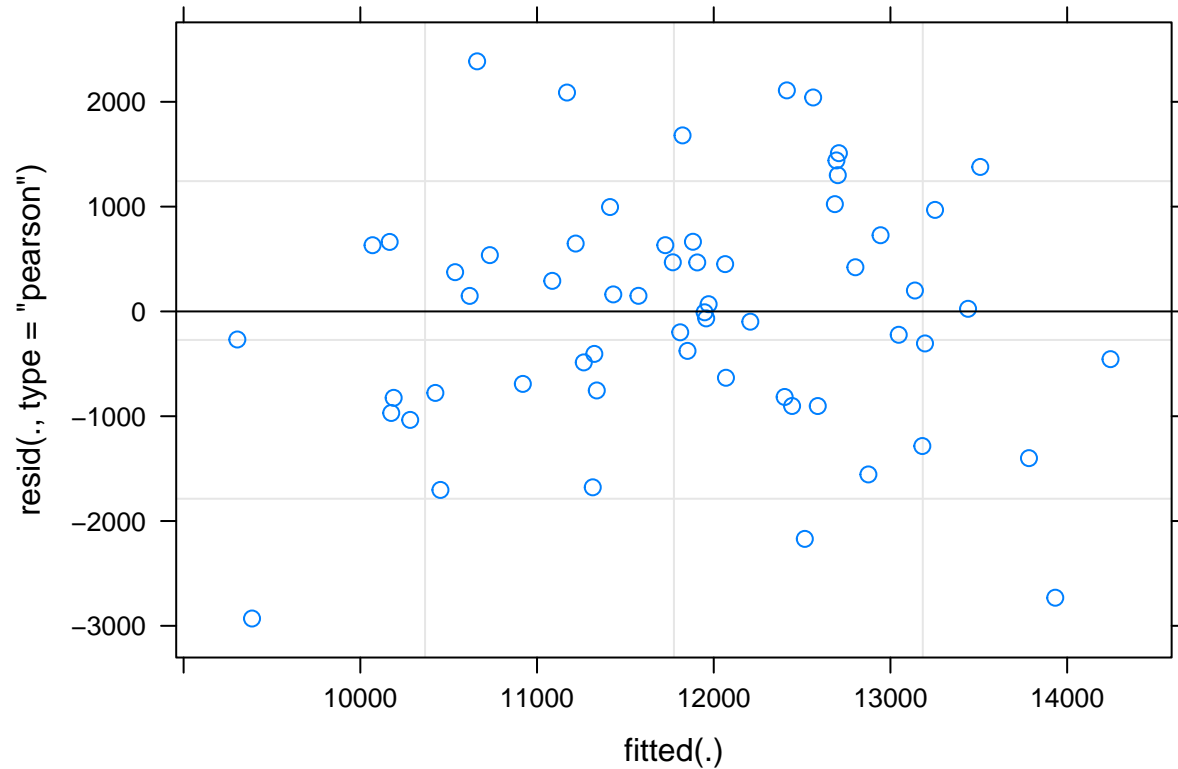
Corn Yield

Arlington 2019 Analysis —- We decided to use only this site-year in the paper

```
arlcn_yield1= lmer(yield~ soil*herb + (1|rep:location), data= (filter(Corn1, site_crop_yr == "ARL_CN_19
qqnorm(resid(arlcn_yield1))
```

Normal Q–Q Plot


```
plot(arlcn_yield1)
```

```
#assumptions look good

anova(arlcn_yield1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## soil     12799443 6399722     2 41.999  3.5104 0.03893 *
## herb      2171602  542900     4 41.999  0.2978 0.87774
## soil:herb 10675314 1334414    8 41.999  0.7319 0.66271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#soil managment fixed effect significant
```

Lancaster Analysis

```
lancn_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Corn1, location == "Lancaster")))

qqnorm(resid(lancn_yield))
```

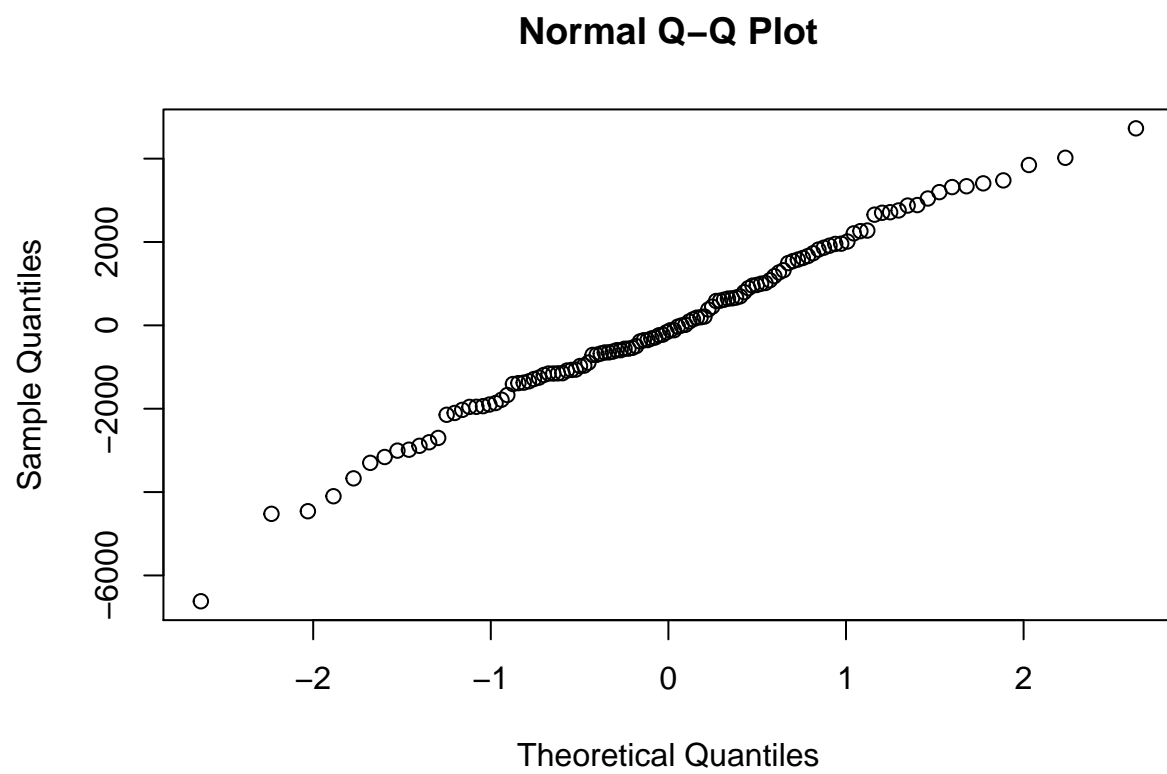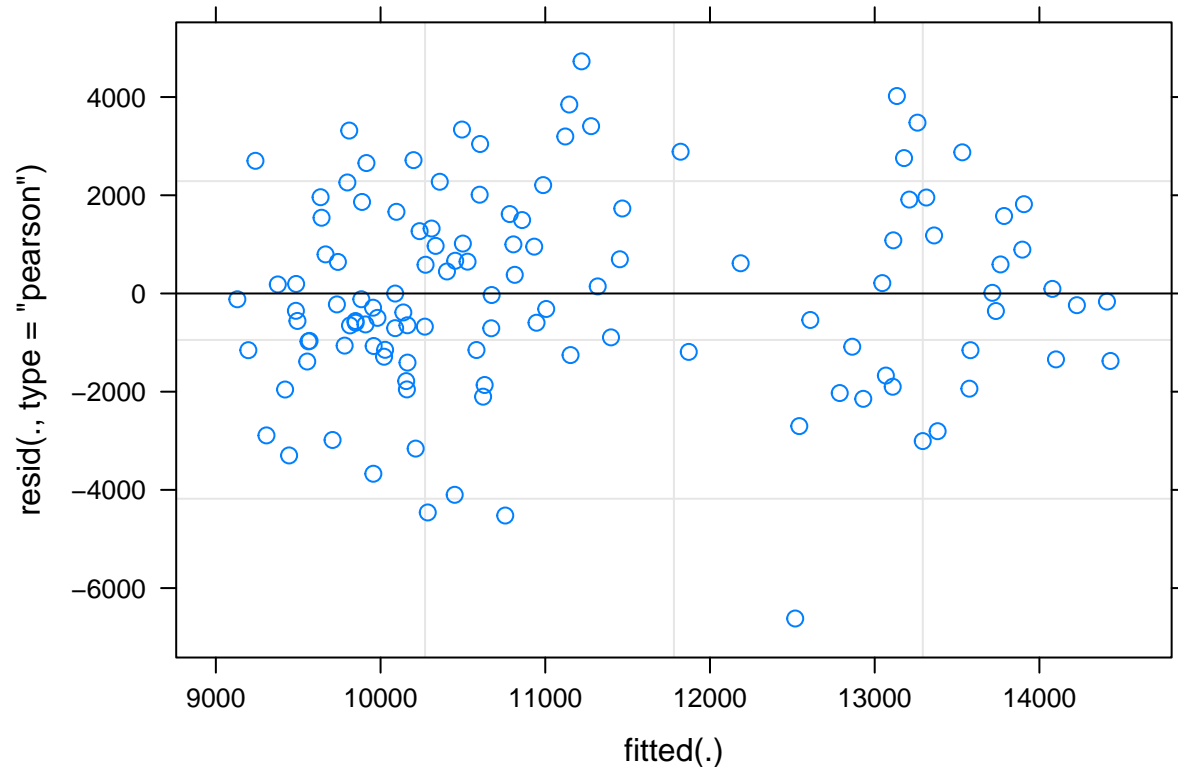## Normal Q–Q Plot


```
plot(lancn_yield)
```

```
anova(lancn_yield)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq   Mean Sq NumDF  DenDF F value   Pr(>F)
## soil      222731976 111365988     2 96.199 23.3190 5.53e-09 ***
## herb        3513660    878415     4 96.231  0.1839   0.9462
## soil:herb  22283004   2785375     8 96.271  0.5832   0.7895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
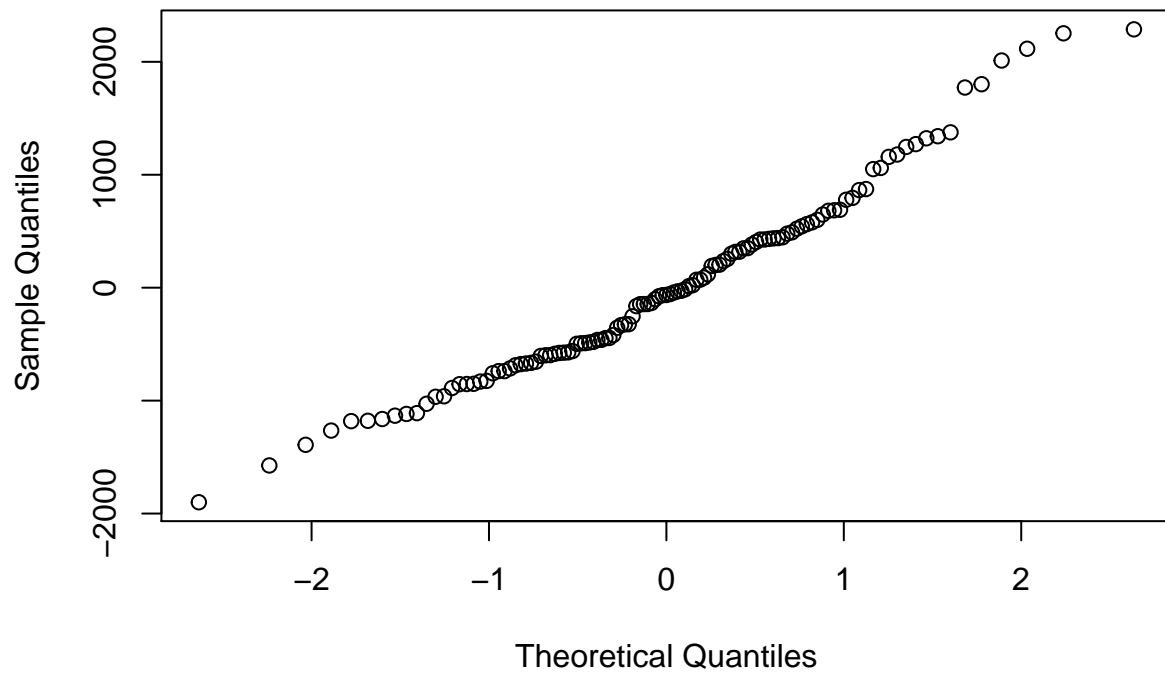
Havelock Analysis

```
havcn_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Corn1, location == "Havelock")))
```

```
## boundary (singular) fit: see ?isSingular
```
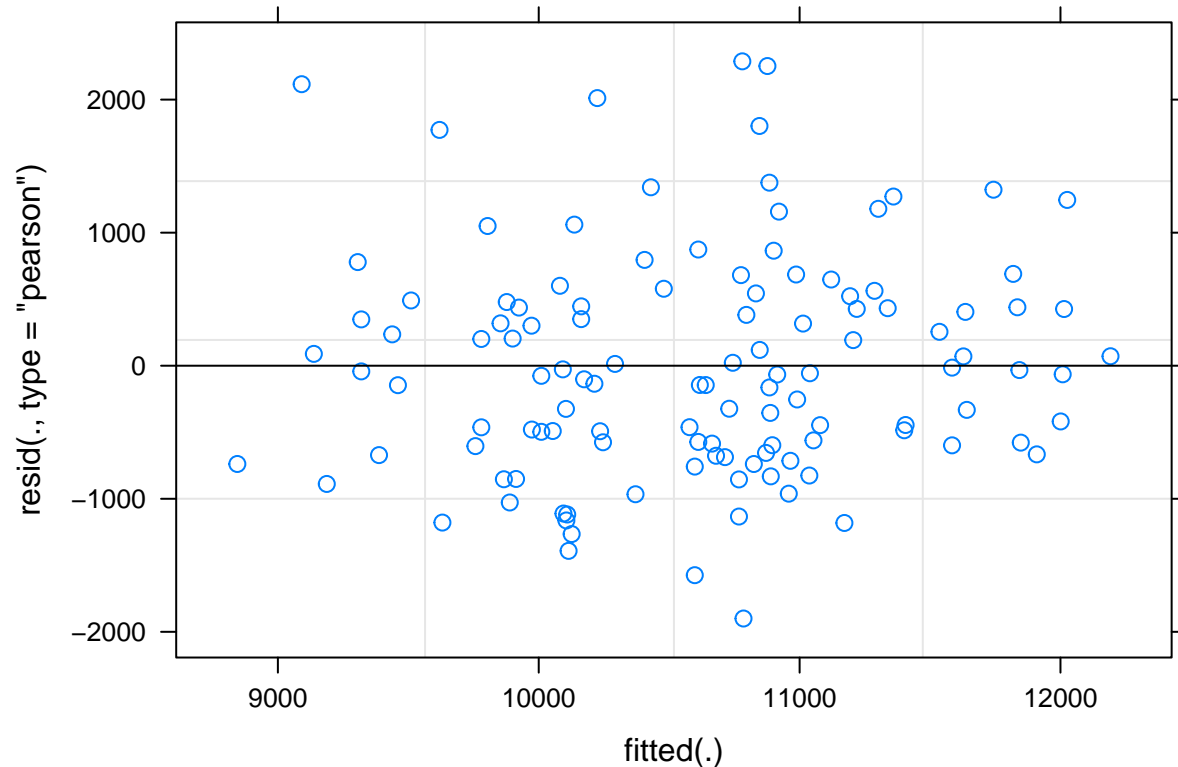
```
qqnorm(resid(havcn_yield))
```

Normal Q–Q Plot


```r
plot(havcn_yield)
```

```
#assumptions look good

anova(havcn_yield)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq  Mean Sq NumDF  DenDF F value    Pr(>F)
## soil       21547460 10773730     2 97.033 12.7752 1.188e-05 ***
## herb         884330   221083     4 97.064  0.2622    0.9016
## soil:herb   1679206   209901     8 97.404  0.2489    0.9800
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#soil management significant

#summary(havcn_yield)
```

```
Corn1= Corn1 %>%
 filter(site_crop_yr != "ARL_CN_20")

y1<- ggplot(cnyield, aes(x= soil, y= yield, color= soil)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL, ymax= upper.CL), width= .3) +
  geom_text(aes(label = .group), nudge_y = 2200) +
  geom_jitter(data = Corn1 ,mapping = aes(y = yield), alpha = 0.2) +
  #coord_flip() +
```

8

```
  facet_grid(~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Corn Yield")
```

```
y1
```
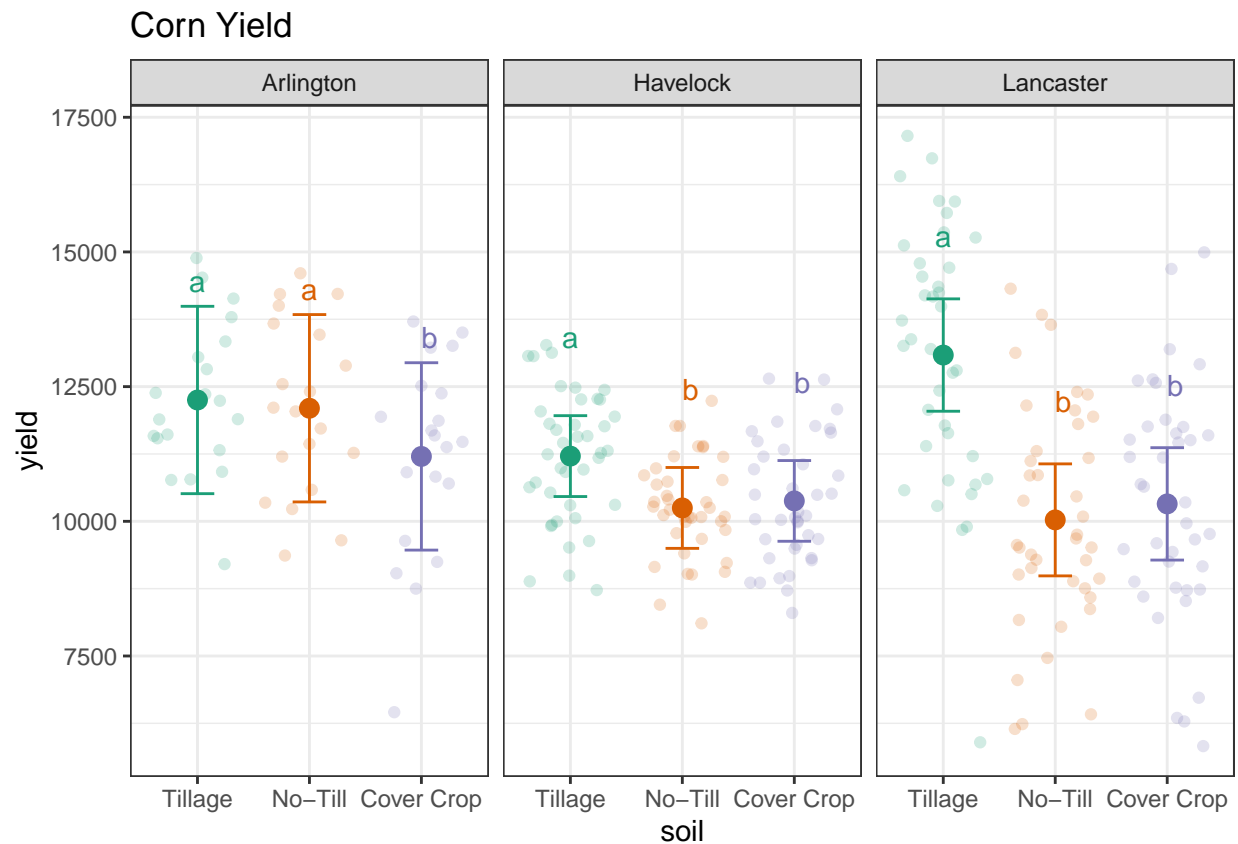

Soybean Yield

Arlington Analysis

```
arl_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Arlington")))
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00222375 (tol = 0.002, component 1)
```

```
summary(arl_sb_yield)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```
## Formula: yield ~ soil * herb + (1 | rep/year)
##    Data: (filter(Soybean1, location == "Arlington"))
##
## REML criterion at convergence: 1481.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8592 -0.6031 -0.0722  0.5465  3.3338
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  year:rep (Intercept) 106984   327.1
##  rep      (Intercept)  13525   116.3
##  Residual              45618   213.6
## Number of obs: 120, groups:  year:rep, 8; rep, 4
##
## Fixed effects:
##                            Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)                3841.125    149.855    5.135  25.632 1.28e-06 ***
## soilCover Crop             -201.625    106.792   97.997  -1.888   0.0620 .
## soilTillage                -101.875    106.792   97.997  -0.954   0.3425
## herbCL50                    -38.375    106.792   97.997  -0.359   0.7201
## herbControl                  81.000    106.792   97.997   0.758   0.4500
## herbME25                     82.375    106.792   97.997   0.771   0.4424
## herbME50                    -32.375    106.792   97.997  -0.303   0.7624
## soilCover Crop:herbCL50     267.500    151.027   97.997   1.771   0.0796 .
## soilTillage:herbCL50        176.750    151.027   97.997   1.170   0.2447
## soilCover Crop:herbControl  142.500    151.027   97.997   0.944   0.3477
## soilTillage:herbControl      69.750    151.027   97.997   0.462   0.6452
## soilCover Crop:herbME25     128.625    151.027   97.997   0.852   0.3965
## soilTillage:herbME25         49.125    151.027   97.997   0.325   0.7457
## soilCover Crop:herbME50     229.125    151.027   97.997   1.517   0.1325
## soilTillage:herbME50         56.250    151.027   97.997   0.372   0.7104
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it


## convergence code: 0
## Model failed to converge with max|grad| = 0.00222375 (tol = 0.002, component 1)
```
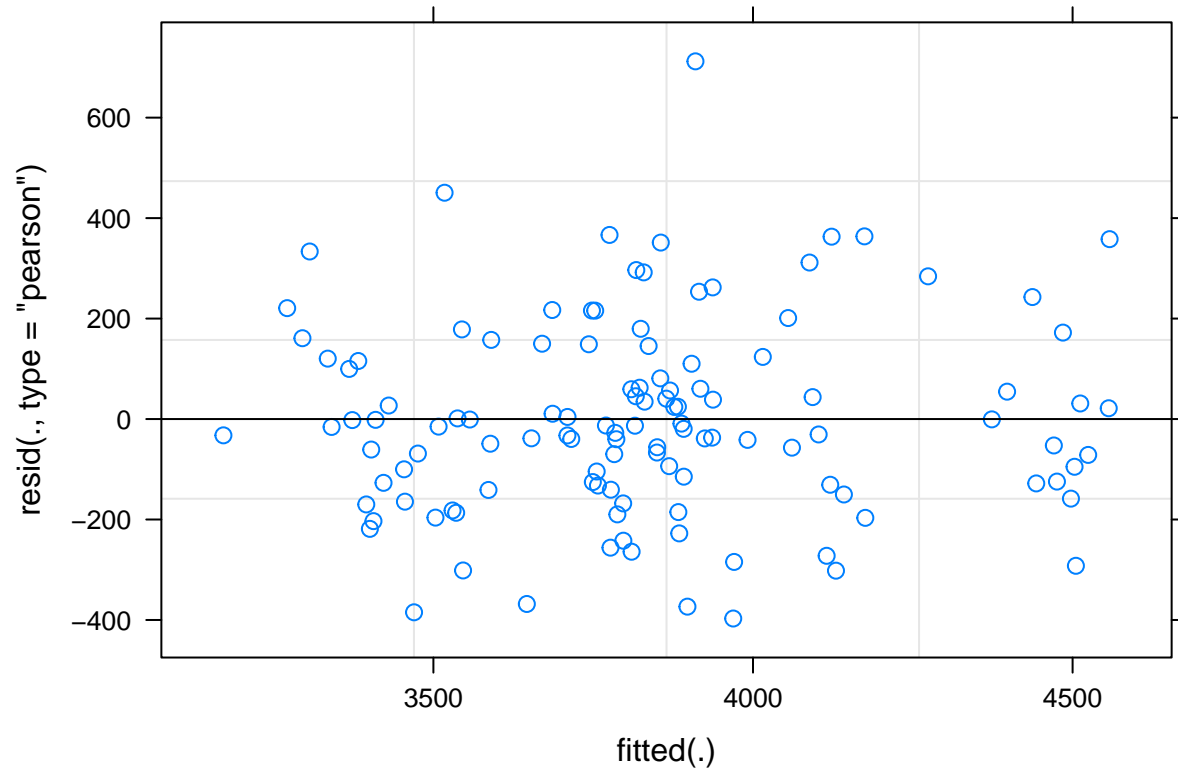
```
qqnorm(resid(arl_sb_yield))
```

Normal Q–Q Plot
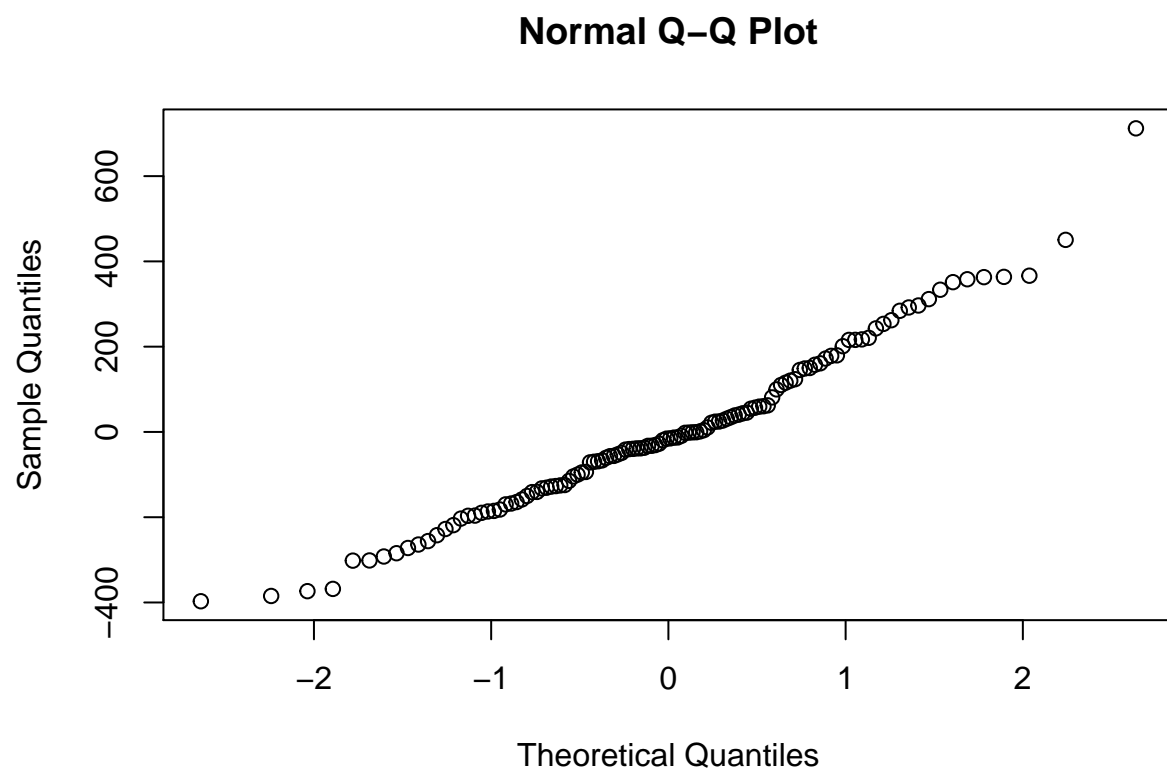

```
plot(arl_sb_yield)
```

```
#assumptions look good
```

```
anova(arl_sb_yield)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## soil        47709   23855     2 97.997  0.5229 0.59443
## herb       375817   93954     4 97.997  2.0596 0.09194 .
## soil:herb  200215   25027     8 97.997  0.5486 0.81705
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
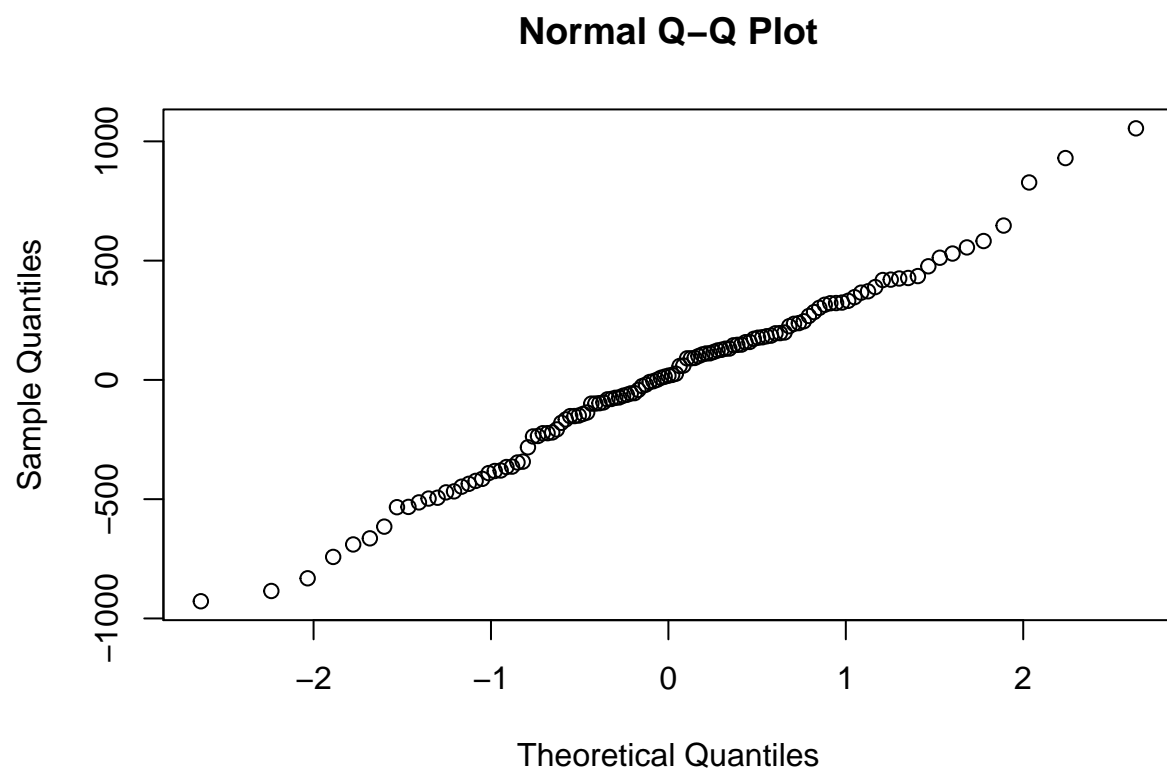
```
#Soil management fixed effect significant
```
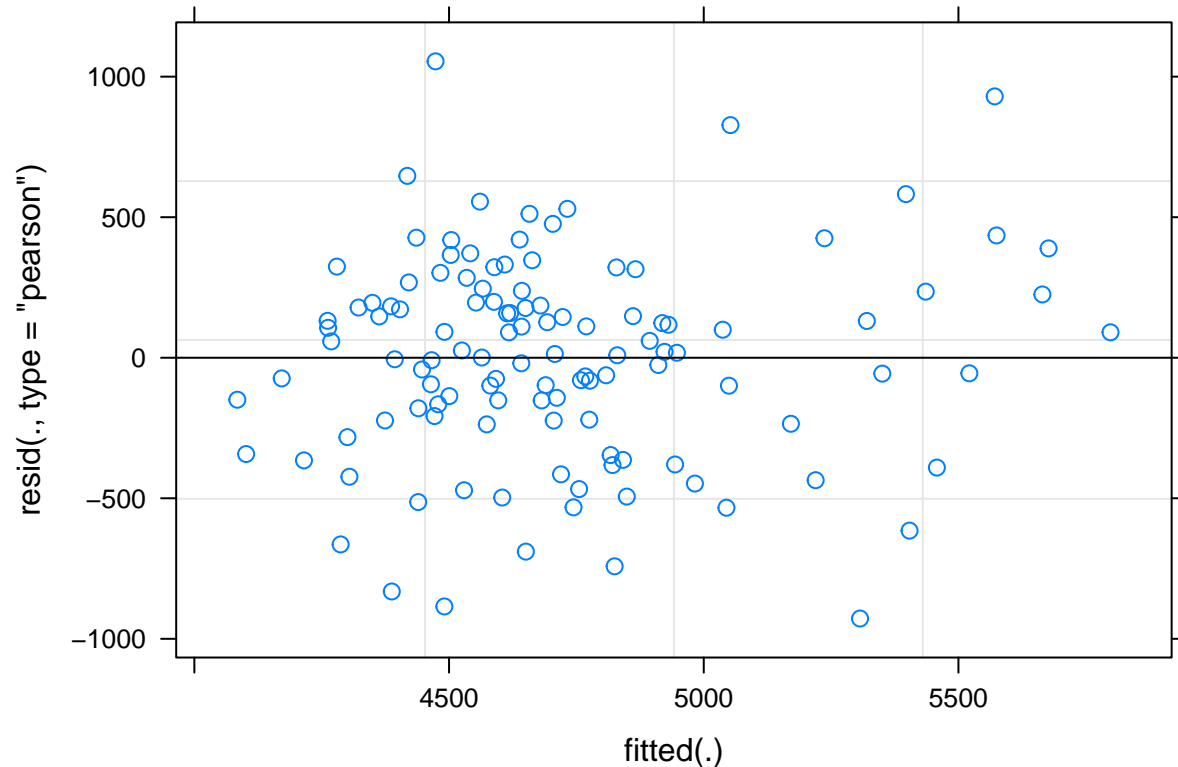
Lancaster Analysis

```
lan_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Lancaster")))
```

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

```
qqnorm(resid(lan_sb_yield))
```

Normal Q−Q Plot


```
plot(lan_sb_yield)
```

```
#assumptions look good

anova(lan_sb_yield)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## soil      1535907  767954     2 97.005  4.7585 0.01068 *
## herb       434979  108745     4 97.005  0.6738 0.61172
## soil:herb 1222449  152806     8 97.005  0.9468 0.48214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
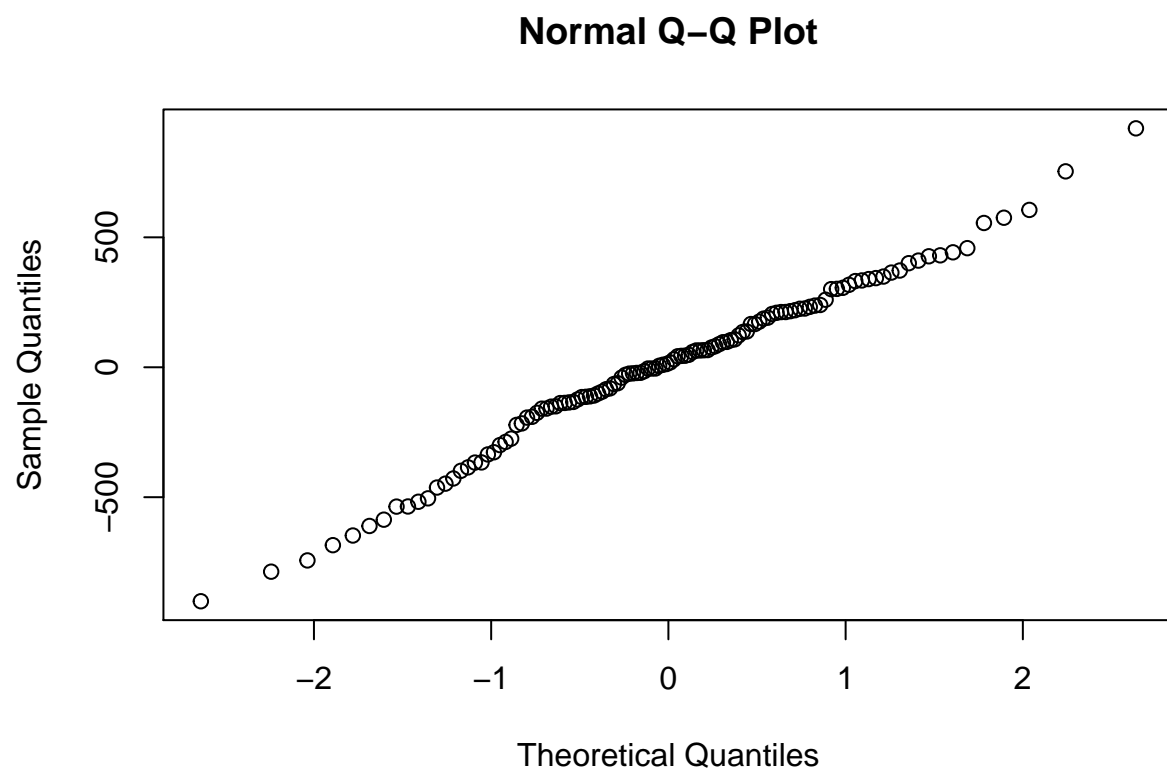
```
#Soil management fixed effect significant
```
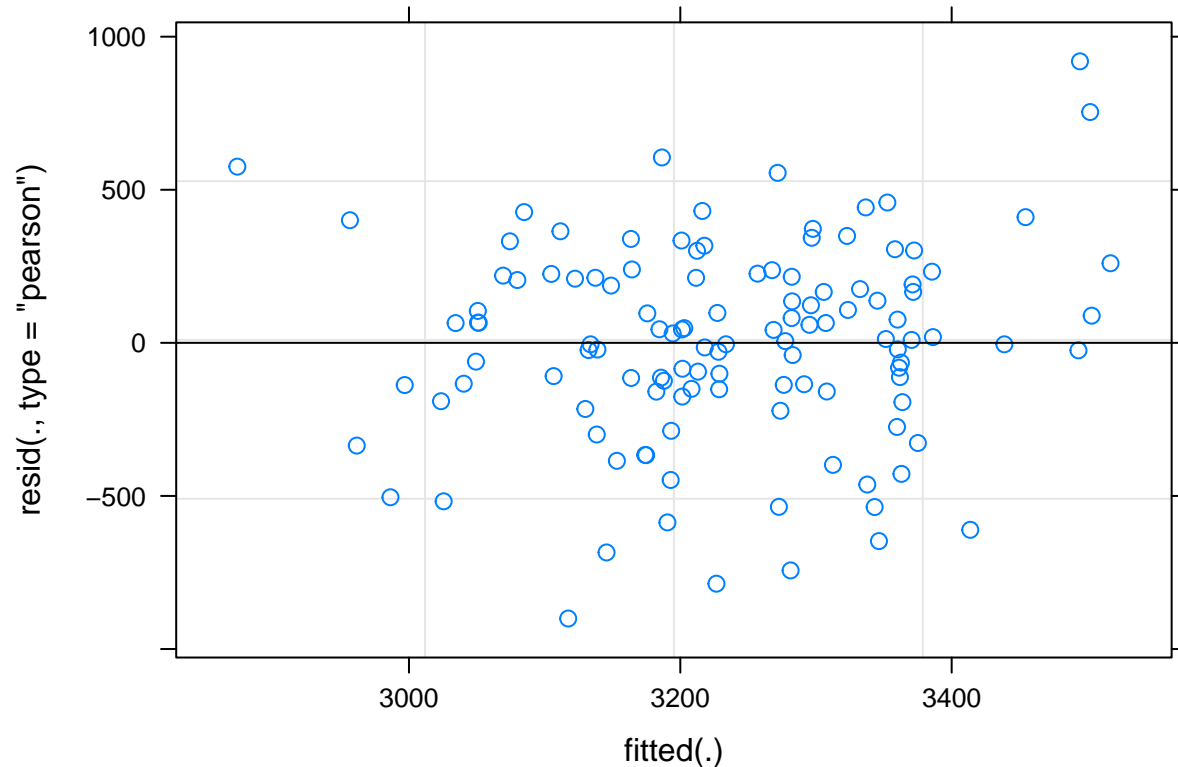
Havelock Analysis

```
hav_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Havelock")))
```

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

```
qqnorm(resid(hav_sb_yield))
```

Normal Q–Q Plot


```
plot(hav_sb_yield)
```

```
#assumptions look good

anova(hav_sb_yield)
```
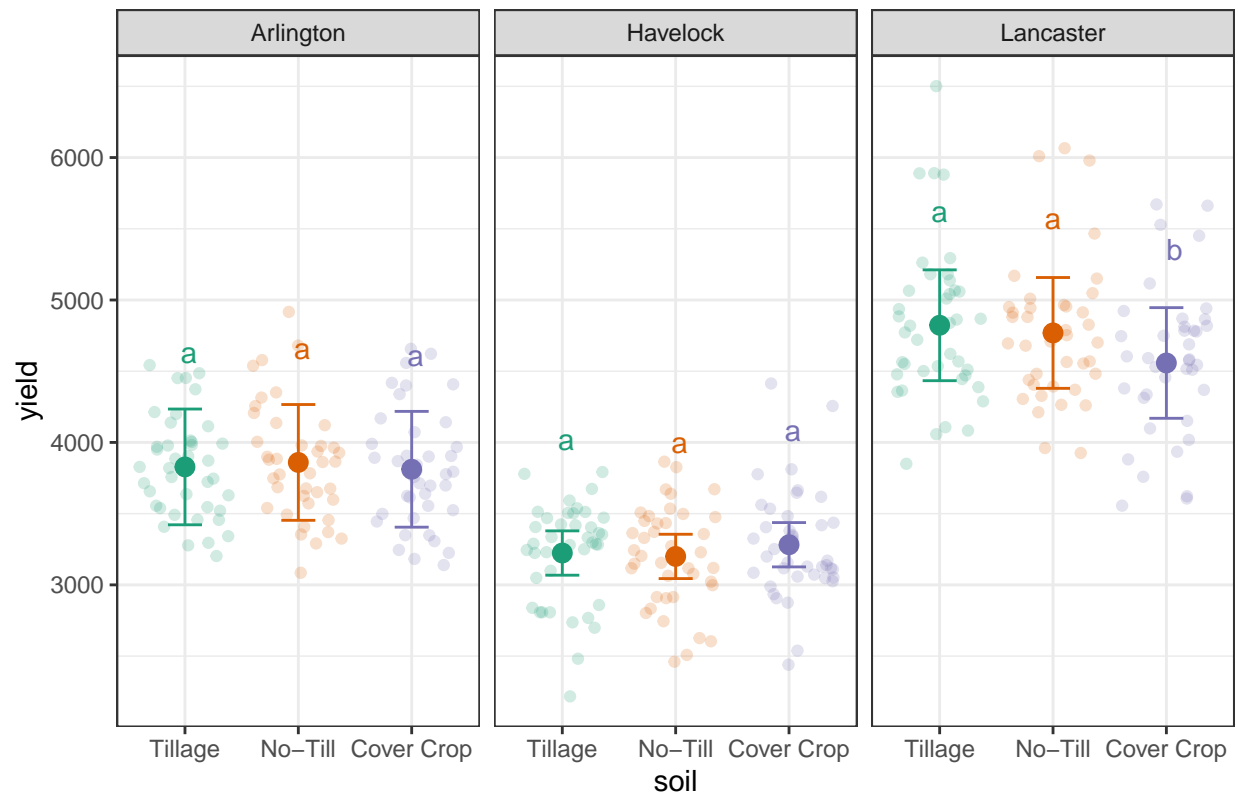
```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## soil       142276   71138     2 98.001  0.5747 0.5648
## herb       285685   71421     4 98.001  0.5770 0.6800
## soil:herb  656275   82034     8 98.001  0.6627 0.7229
```

```
#nothing significant
```

```
y2<- ggplot(sbyield, aes(x= soil, y= yield, color= soil)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL, ymax= upper.CL), width= .3) +
  geom_text(aes(label = .group), nudge_y = 800) +
  geom_jitter(data = Soybean1 ,mapping = aes(y = yield), alpha = 0.2) +
  #coord_flip() +
  facet_grid(~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Soybean Yield")

y2
```
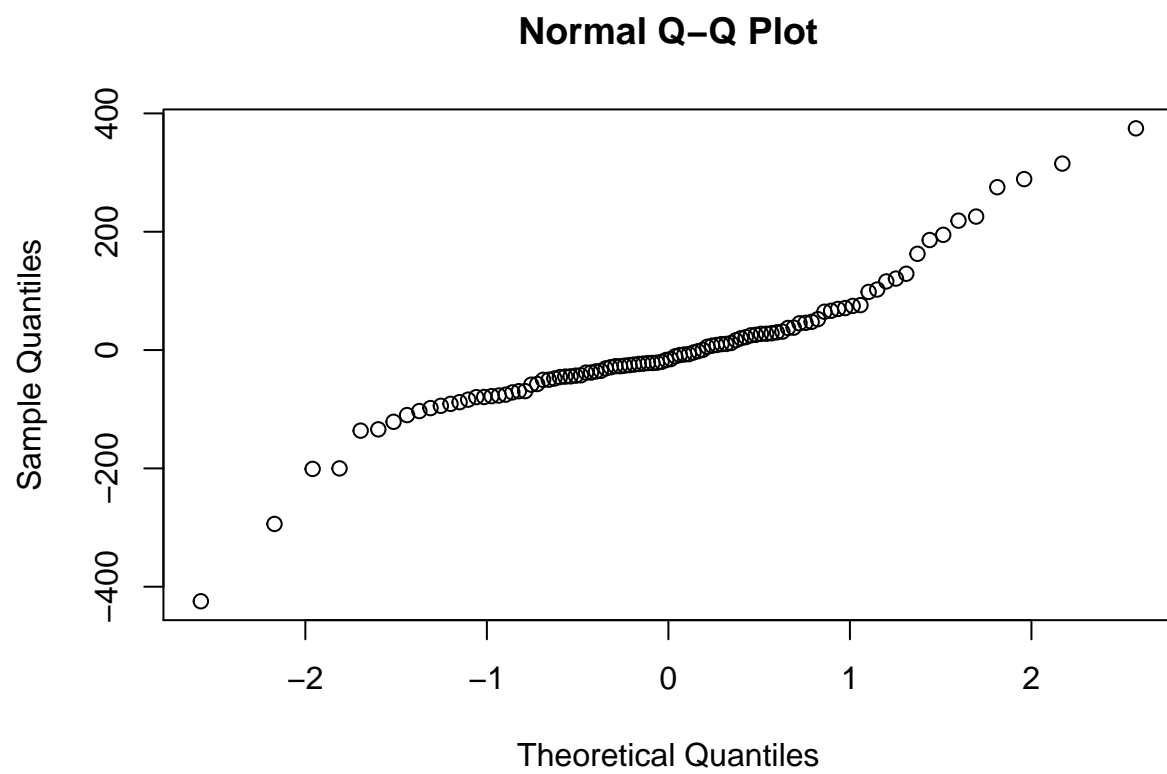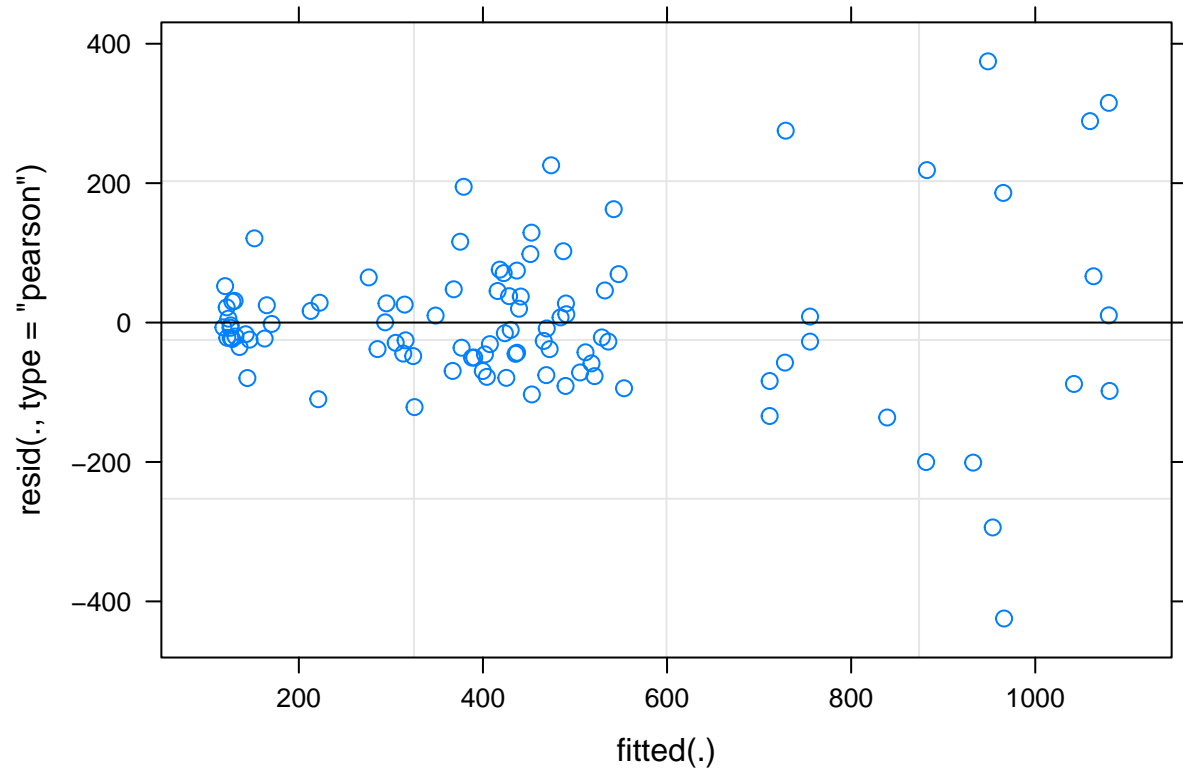
Soybean Yield

Cover Crop Biomass analysis

Corn

```
cn_cc_bio= lmer(biomass_kg~ site_crop_yr * herb + (1|site_crop_yr:rep), data=CornCC)

qqnorm(resid(cn_cc_bio))
```
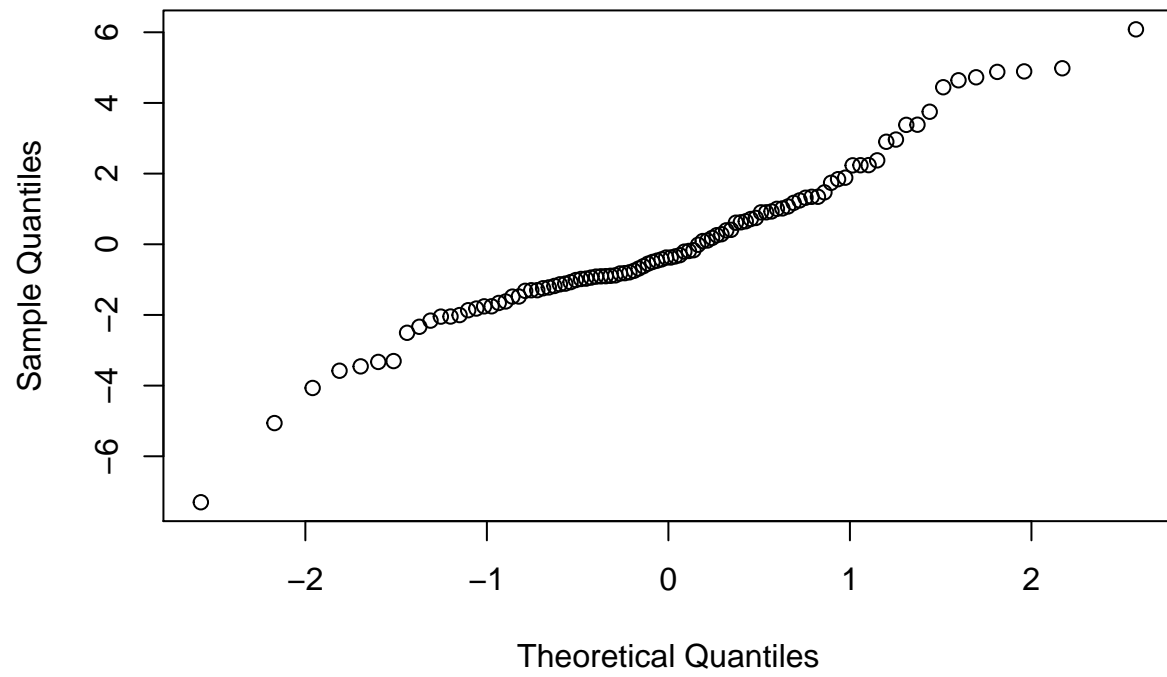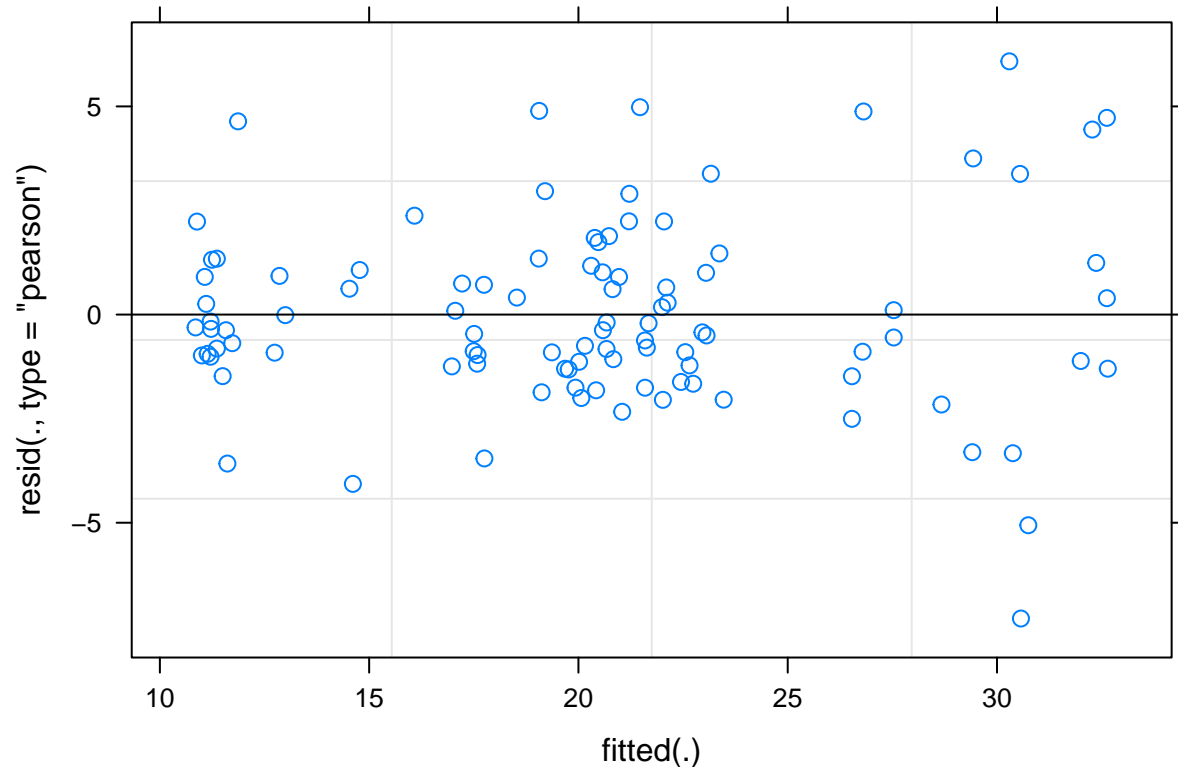
Normal Q–Q Plot


```
plot(cn_cc_bio)
```

```
#Assumption for equal variance not met

cn_cc_bio1= lmer(sqrt(biomass_kg)~ site_crop_yr * herb + (1|site_crop_yr:rep), data=CornCC)

qqnorm(resid(cn_cc_bio1))
```

Normal Q–Q Plot


```
plot(cn_cc_bio1)
```

```r
anova(cn_cc_bio1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## site_crop_yr      2155.06  538.77     4 13.964 75.2804 2.725e-09 ***
## herb                42.79   10.70     4 60.805  1.4949    0.2149
## site_crop_yr:herb  123.04    7.69    16 60.528  1.0745    0.3982
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Site-year significant
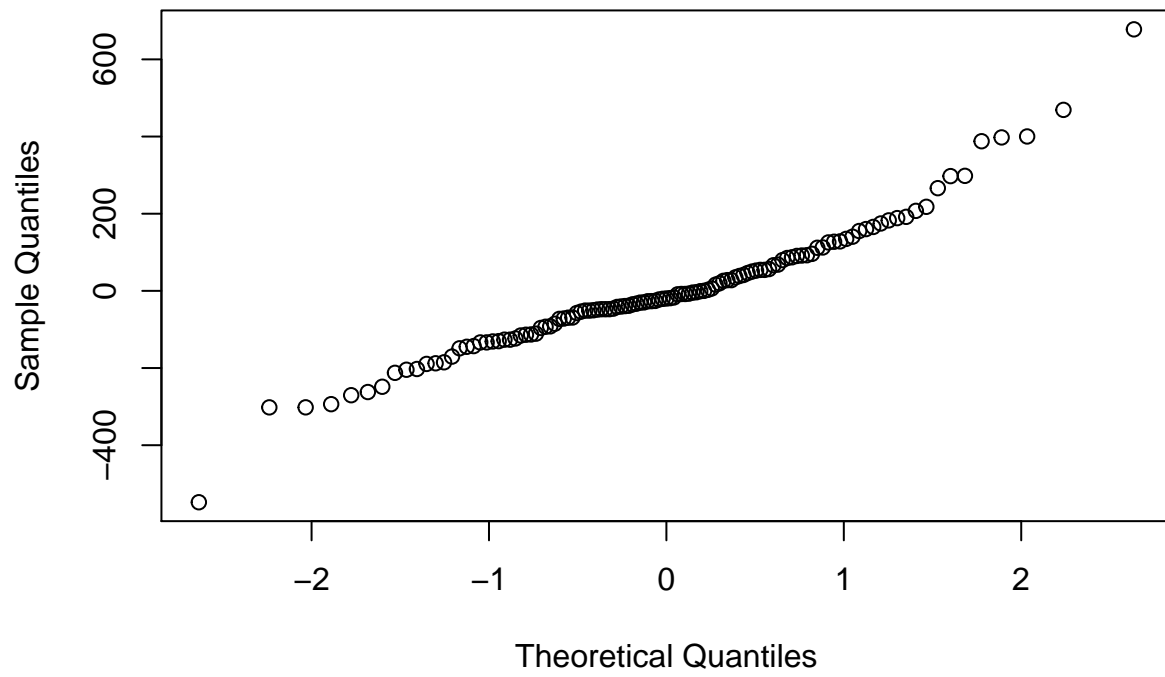
Soybean

```r
sb_cc_bio= lmer(biomass_kg~ site_crop_yr * herb + (1|site_crop_yr:rep), data=SBCC)
```
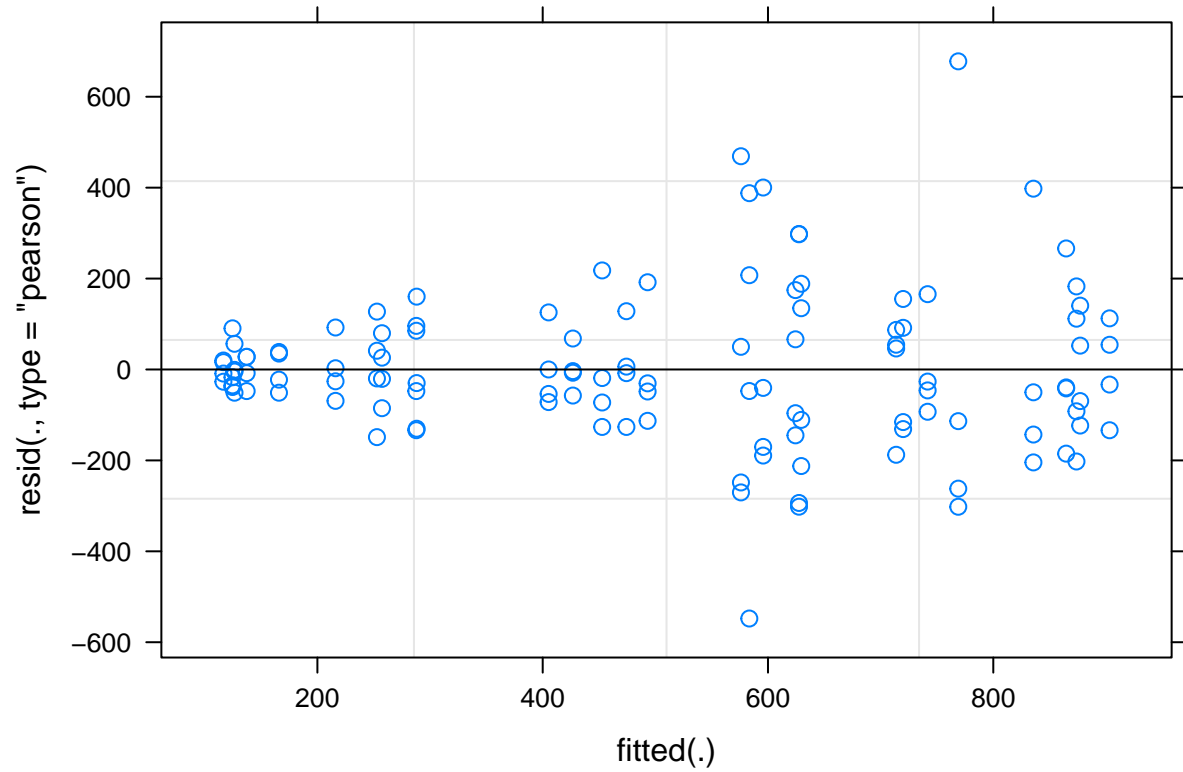
```
## boundary (singular) fit: see ?isSingular
```

```r
qqnorm(resid(sb_cc_bio))
```
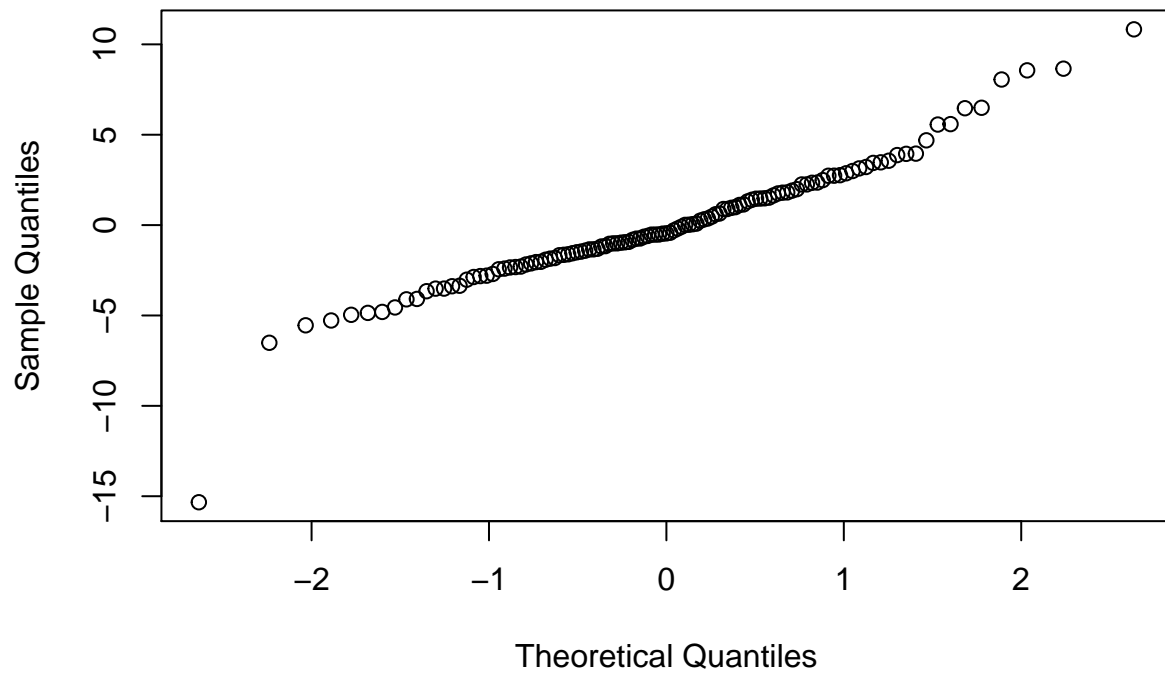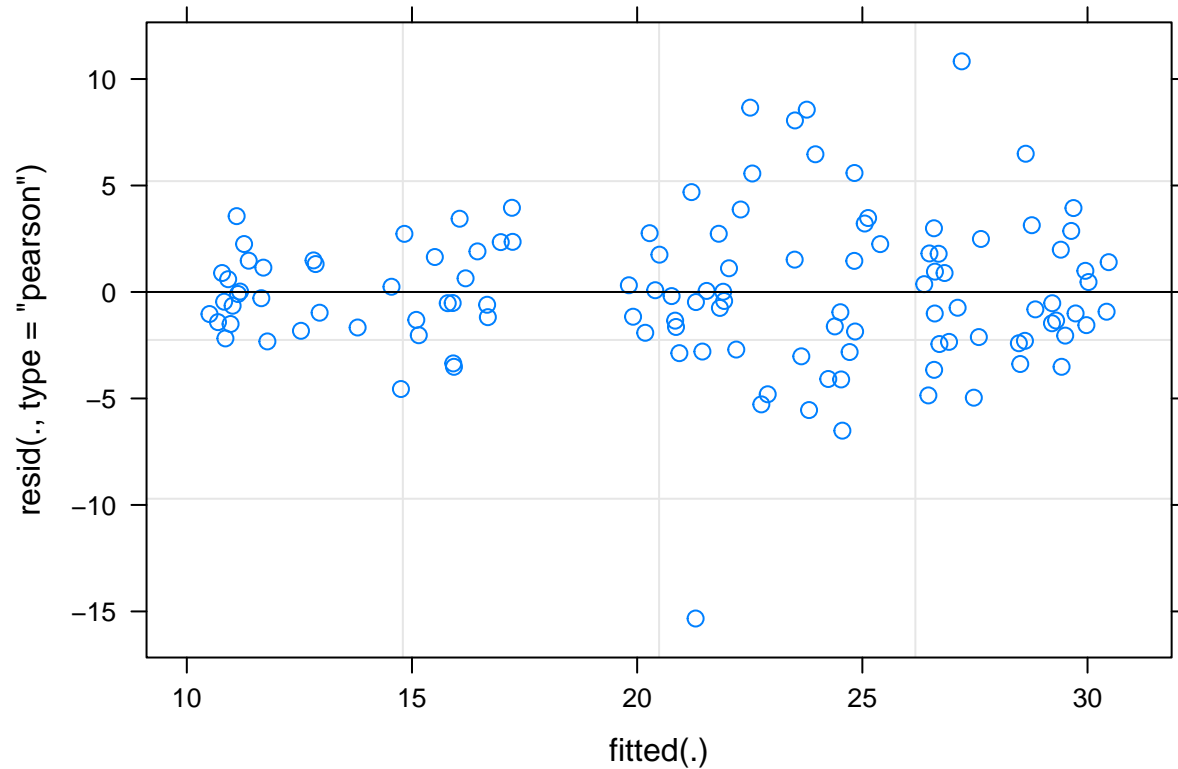
Normal Q–Q Plot


```
plot(sb_cc_bio)
```

```
#assumptions for equal variance not met

sb_cc_bio1= lmer(sqrt(biomass_kg)~ site_crop_yr * herb + (1|site_crop_yr:rep), data=SBCC)

qqnorm(resid(sb_cc_bio1))
```

Normal Q–Q Plot


```
plot(sb_cc_bio1)
```

```
#assumption improved. Maybe clean datapoint
```

```
anova(sb_cc_bio1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## site_crop_yr     3372.2  674.43     5 18.042 42.2751 2.417e-09 ***
## herb               34.9    8.72     4 71.375  0.5467    0.7020
## site_crop_yr:herb 253.8   12.69    20 71.325  0.7955    0.7103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Site-year significant
```

Cover Crop Canopy

Corn

```
CornCC1 <- CornCC %>%
  filter(!is.na(canopy))
```

```
cn_cc_bio= glmmTMB(canopy~ site_crop_yr*herb + (1|site_crop_yr:rep), data=CornCC1, beta_family(link="lo
```

```
Anova(cn_cc_bio)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: canopy
##                   Chisq Df Pr(>Chisq)
## site_crop_yr    612.4325  3    <2e-16 ***
## herb              6.4557  4    0.1676
## site_crop_yr:herb 15.1064 12   0.2357
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Site-year significant
```

Soybean

```
SBCC1 <- SBCC %>%
  filter(!is.na(canopy))
```

```
sb_cc_bio= glmmTMB(canopy~ site_crop_yr*herb + (1|site_crop_yr:rep), data=SBCC, beta_family(link="logit
```

```
Anova(sb_cc_bio)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: canopy
##                   Chisq Df Pr(>Chisq)
## site_crop_yr    407.8495  4   < 2e-16 ***
## herb              9.2482  4   0.05519 .
## site_crop_yr:herb 19.8632 16   0.22645
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Site-Year significant
```
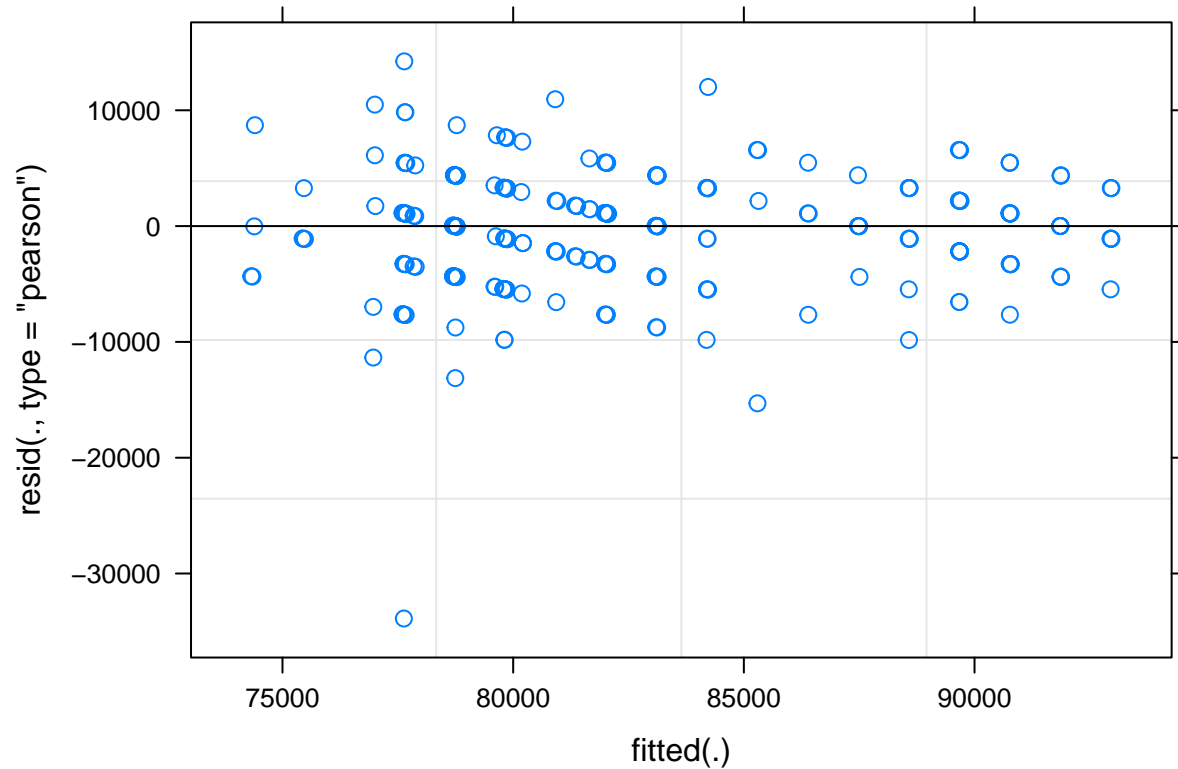
Stand Counts

Corn

```
cn_stand= lmer(stand_count~ site_crop_yr*soil*herb + (1|site_crop_yr:rep), data= (filter(Corn1, !site_c
```

```
qqnorm(resid(cn_stand))
```

Normal Q–Q Plot
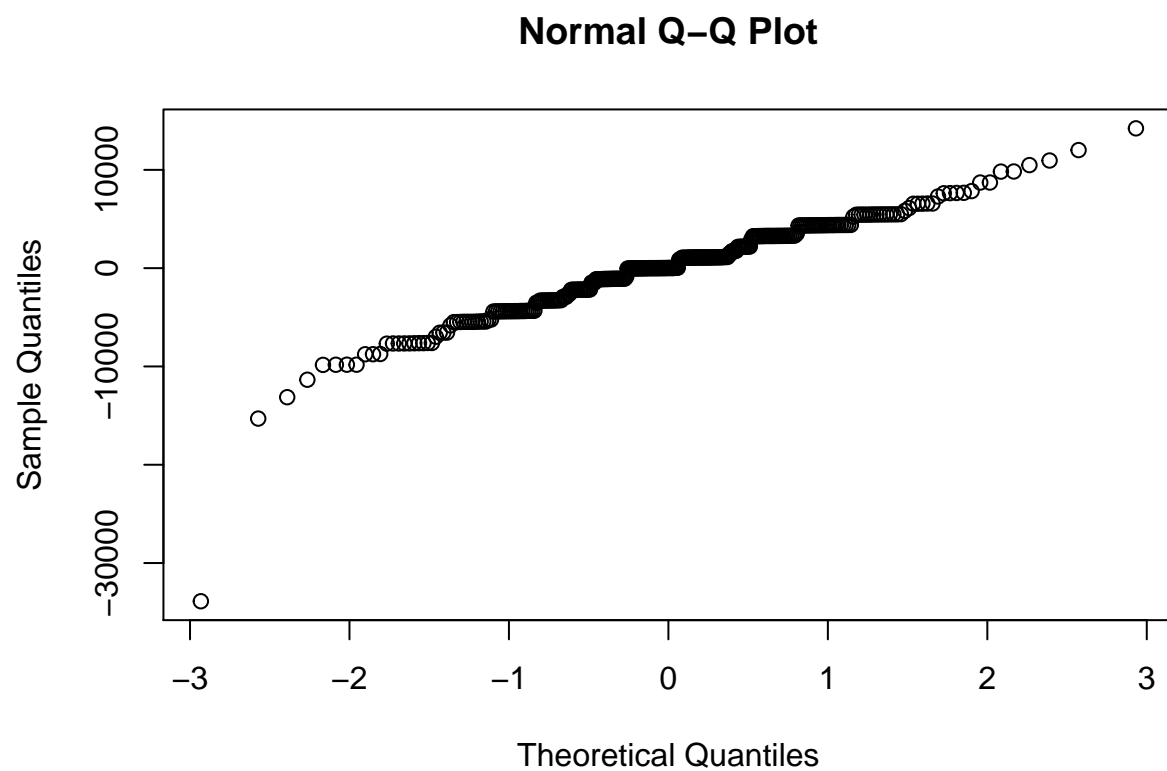

```r
plot(cn_stand)
```

```
#assumptions met satisfactorily

anova(cn_stand)
```
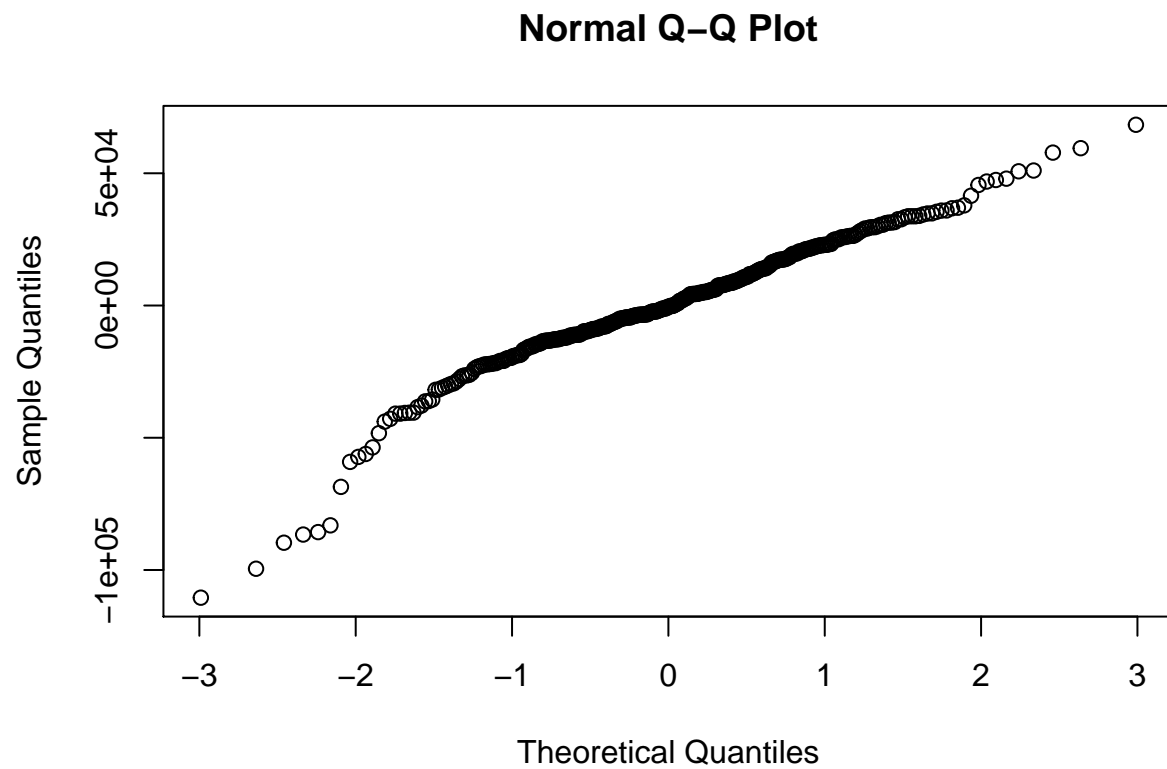
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                              Sum Sq    Mean Sq NumDF   DenDF F value    Pr(>F)
## site_crop_yr            5594122358 1398530589     4  14.702 43.6973 5.367e-08
## soil                       6890560    3445280     2 207.315  0.1076    0.8980
## herb                     105594857   26398714     4 207.613  0.8248    0.5107
## site_crop_yr:soil        135486319   16935790     8 207.310  0.5292    0.8338
## site_crop_yr:herb        189233011   11827063    16 207.594  0.3695    0.9878
## soil:herb                165394950   20674369     8 210.009  0.6460    0.7384
## site_crop_yr:soil:herb   836954876   26154840    32 209.495  0.8172    0.7471
##
## site_crop_yr           ***
## soil
## herb
## site_crop_yr:soil
## site_crop_yr:herb
## soil:herb
## site_crop_yr:soil:herb
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
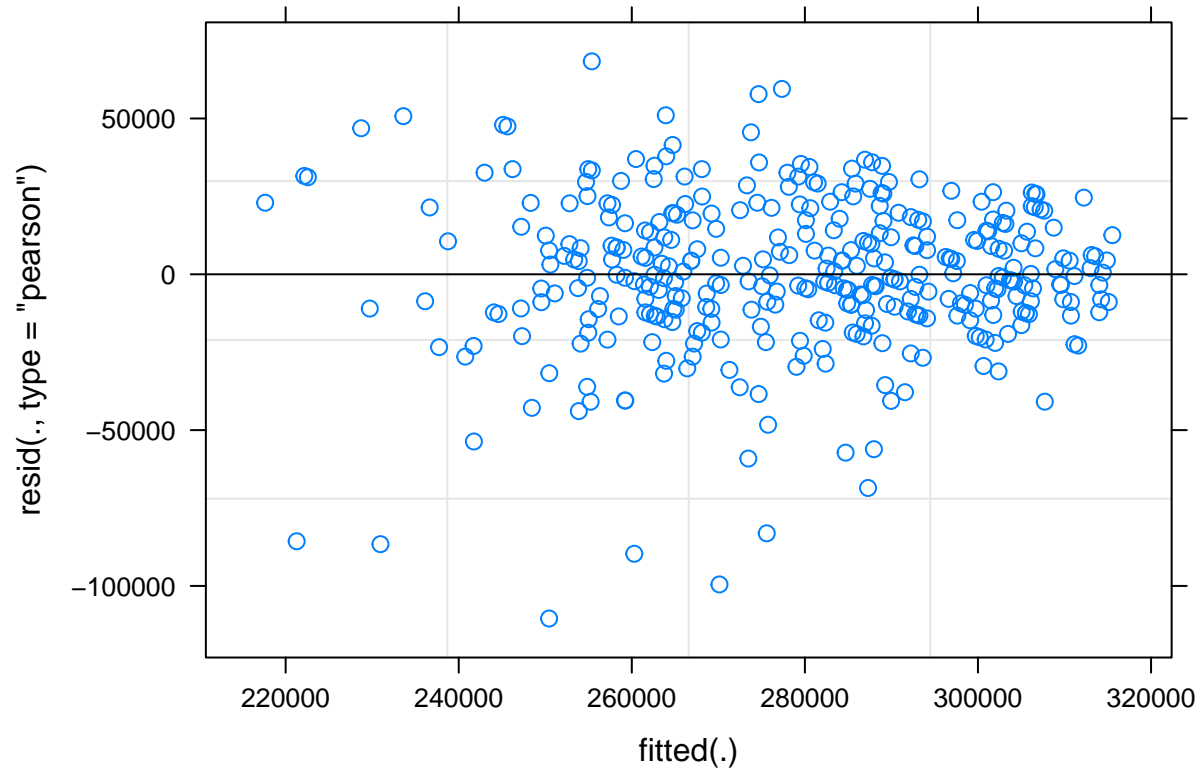
```
#nothing significant
```

Soybean

```
sb_stand= lmer(stand_count~ site_crop_yr*soil*herb + (1|site_crop_yr:rep), data= Soybean1)

qqnorm(resid(sb_stand))
```

Normal Q–Q Plot


```
plot(sb_stand)
```

```
#assumptions satisfactorily met

anova(sb_stand)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                          Sum Sq    Mean Sq NumDF   DenDF F value   Pr(>F)
## site_crop_yr         5.2018e+10 1.0404e+10     5  18.088 12.9796 1.858e-05
## soil                 3.1896e+09 1.5948e+09     2 251.196  1.9897  0.13889
## herb                 1.7474e+09 4.3686e+08     4 251.195  0.5450  0.70281
## site_crop_yr:soil    1.4241e+10 1.4241e+09    10 251.193  1.7767  0.06522
## site_crop_yr:herb    1.7159e+10 8.5794e+08    20 251.188  1.0704  0.38141
## soil:herb            8.9429e+09 1.1179e+09     8 251.194  1.3946  0.19911
## site_crop_yr:soil:herb 4.5032e+10 1.1258e+09  40 251.182  1.4046  0.06374
##
## site_crop_yr           ***
## soil
## herb
## site_crop_yr:soil       .
## site_crop_yr:herb
## soil:herb
## site_crop_yr:soil:herb .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#site-year fixed effect significant.
```