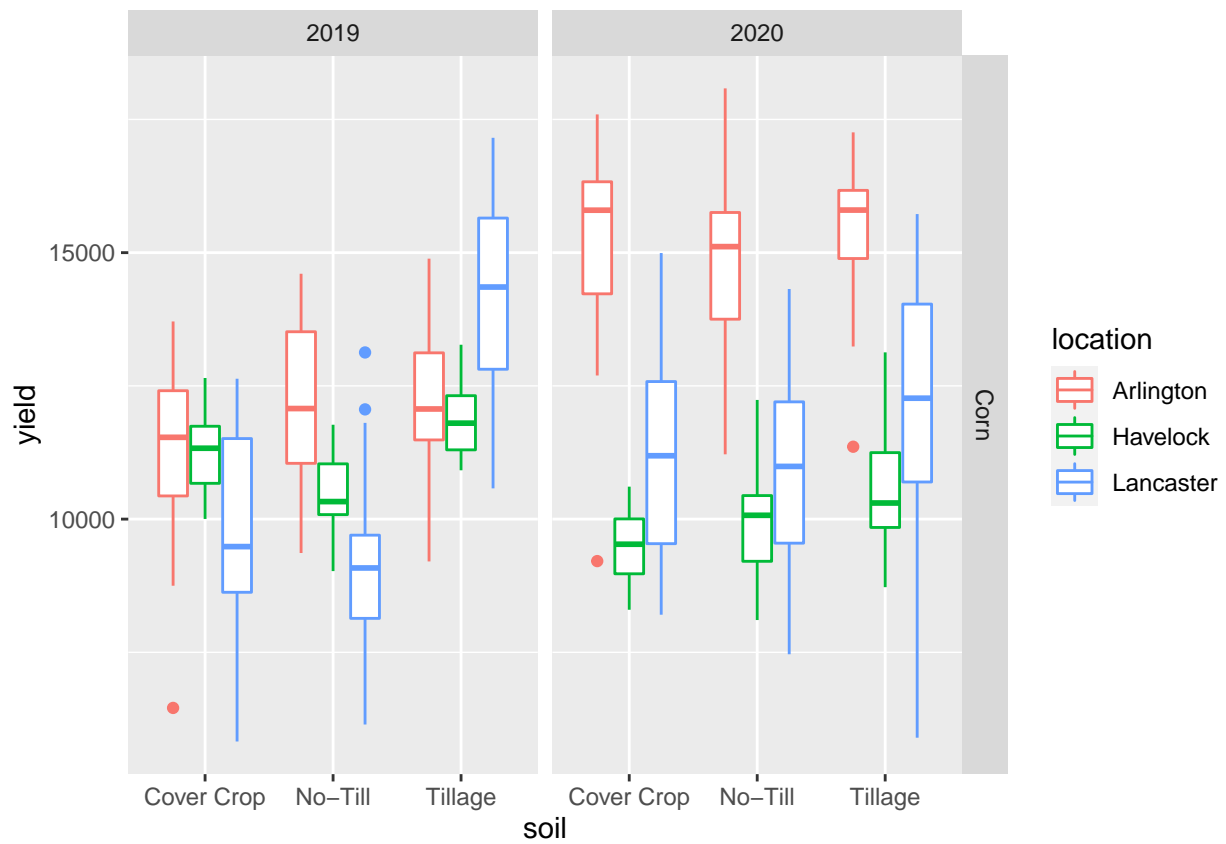


# Carryover 2.0

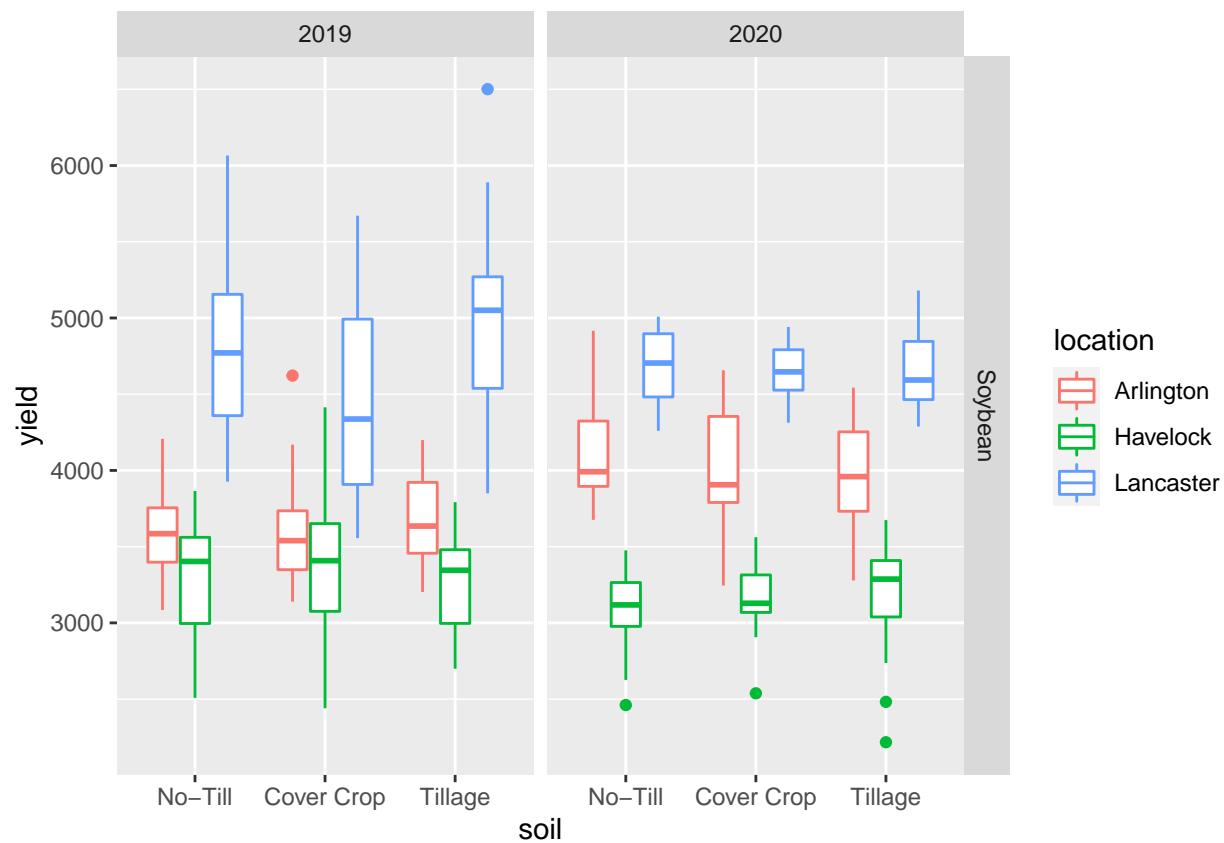
Kolby Grint

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)
```



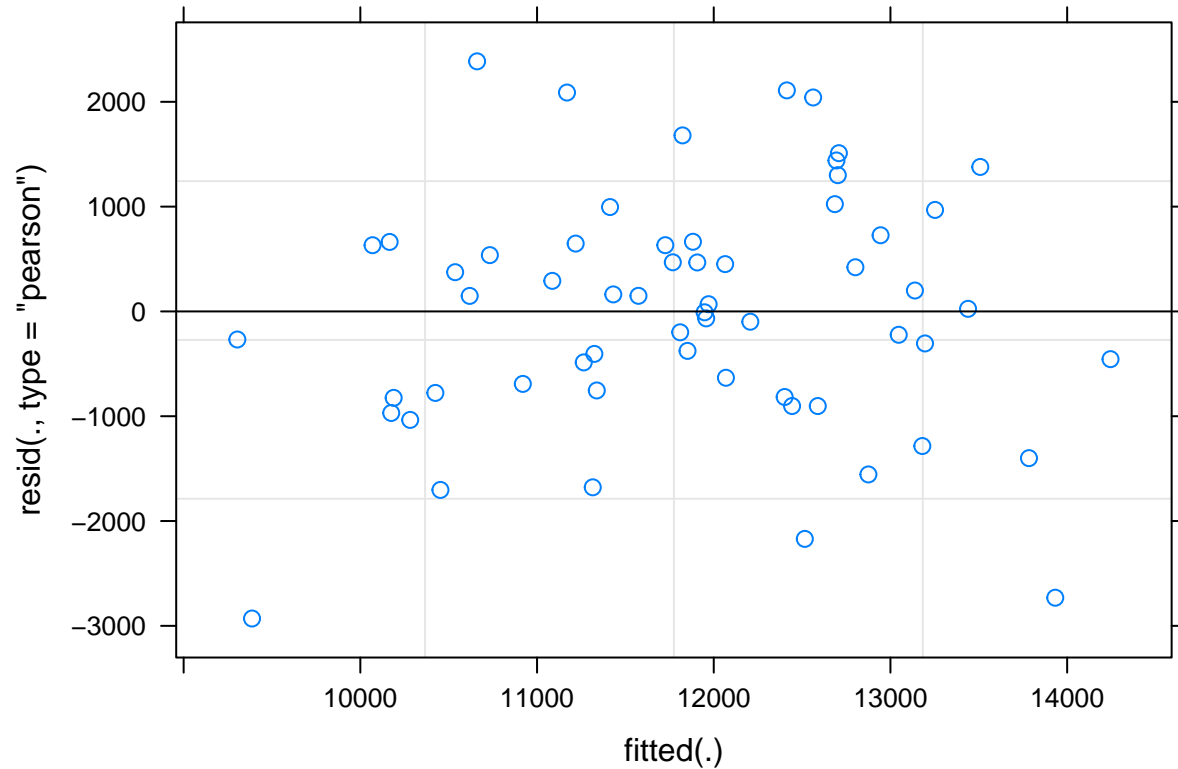
## Corn Yield

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

```
arlc_n_yield1 = lmer(yield ~ soil*herb + (1|rep:site_crop_yr), data = (filter(Corn1, site_crop_yr == "ARL_2019")))
qqnorm(resid(arlc_n_yield1))
```



```
plot(arlcn_yield1)
```



```
#assumptions look good
```

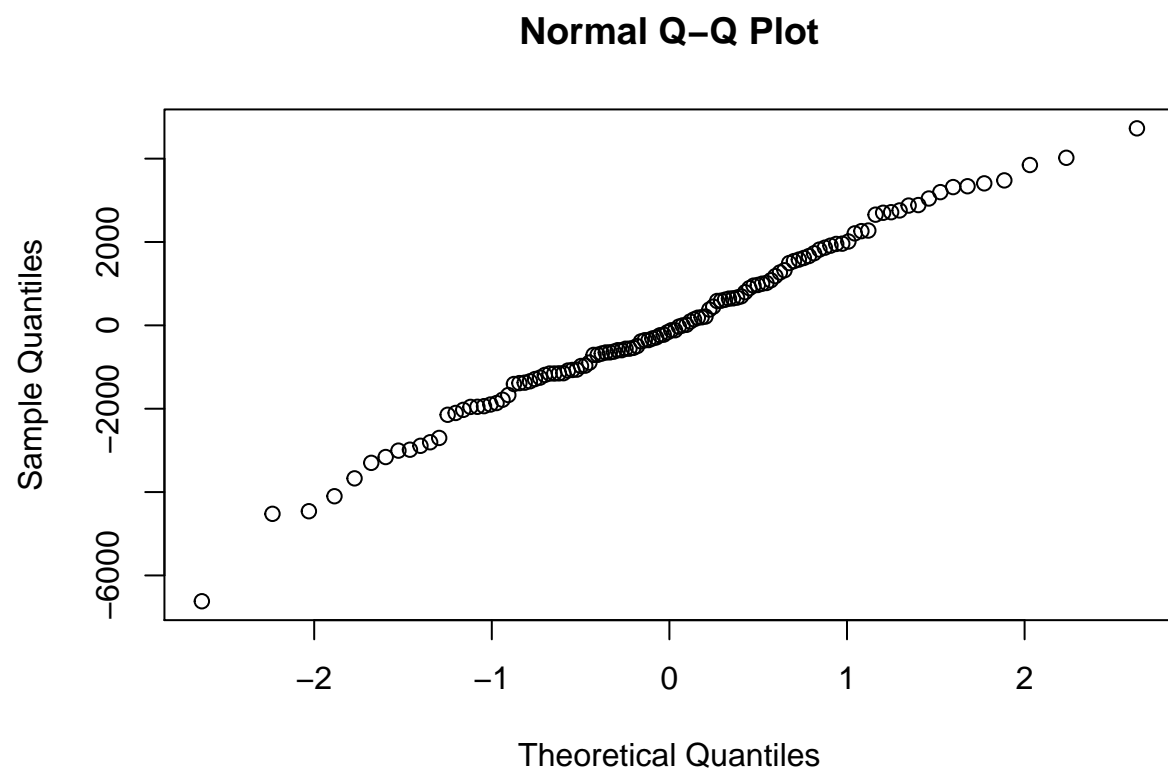
```
anova(arlcn_yield1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## soil      12799443  6399722      2    42  3.5104 0.03893 *
## herb       2171602   542900      4    42  0.2978 0.87774
## soil:herb  10675314 1334414      8    42  0.7320 0.66269
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

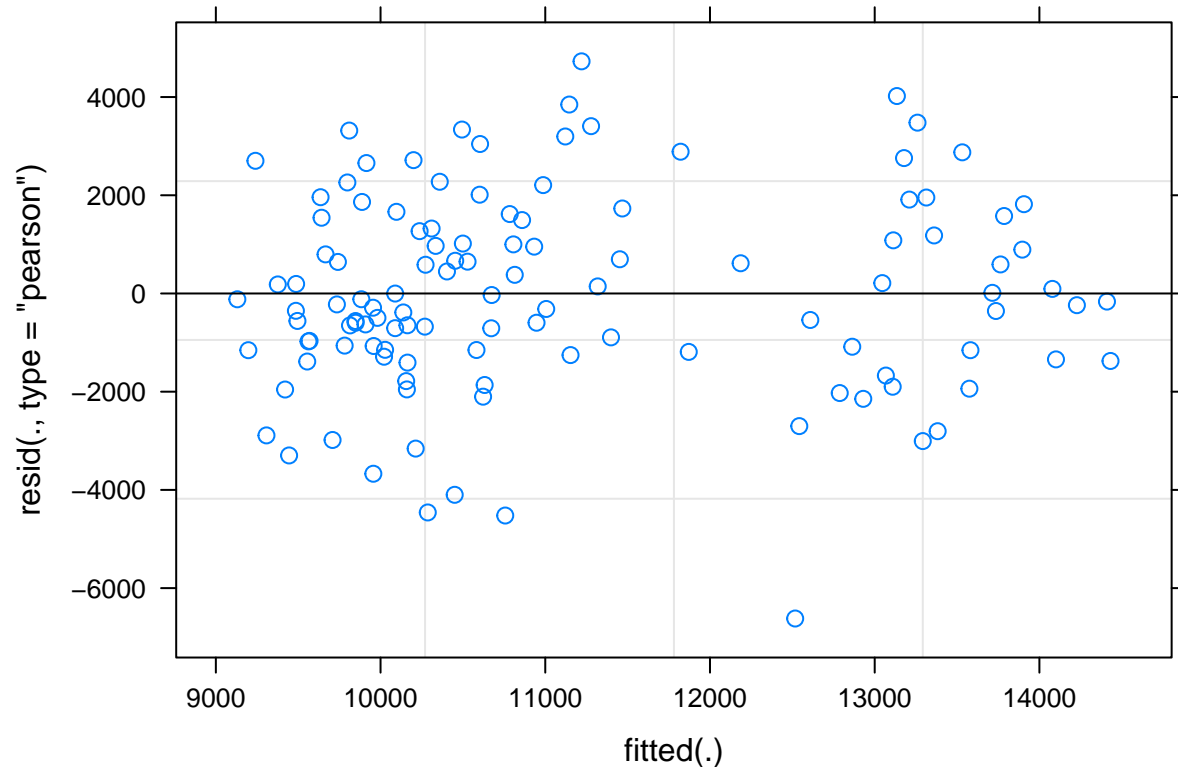
```
#soil managment fixed effect significant
```

## Lancaster Analysis

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



```
plot(lancn_yield)
```



```
#assumptions look good
```

```
anova(lancn_yield)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq   Mean Sq NumDF  DenDF F value    Pr(>F)
## soil      222731977 111365989     2  96.199  23.3189 5.531e-09 ***
## herb       3513660    878415     4  96.230   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
```

```
#Soil management fixed effect significant
```

## Havelock Analysis

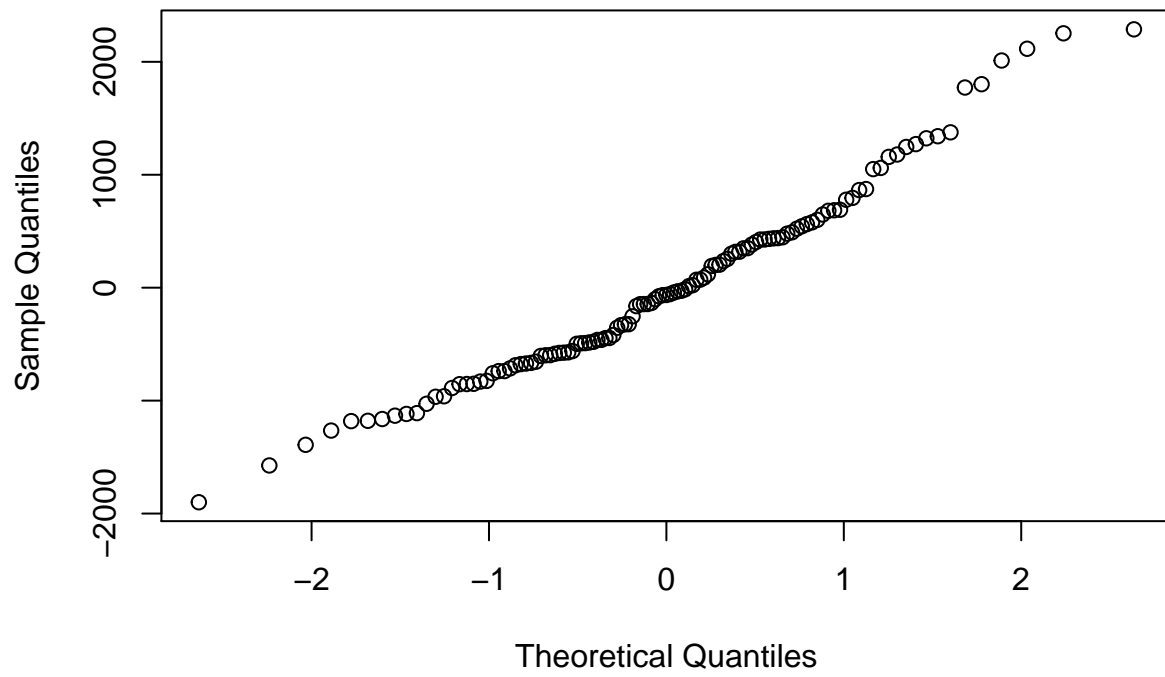
```
havcn_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Corn1, location == "Havelock")))
```

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

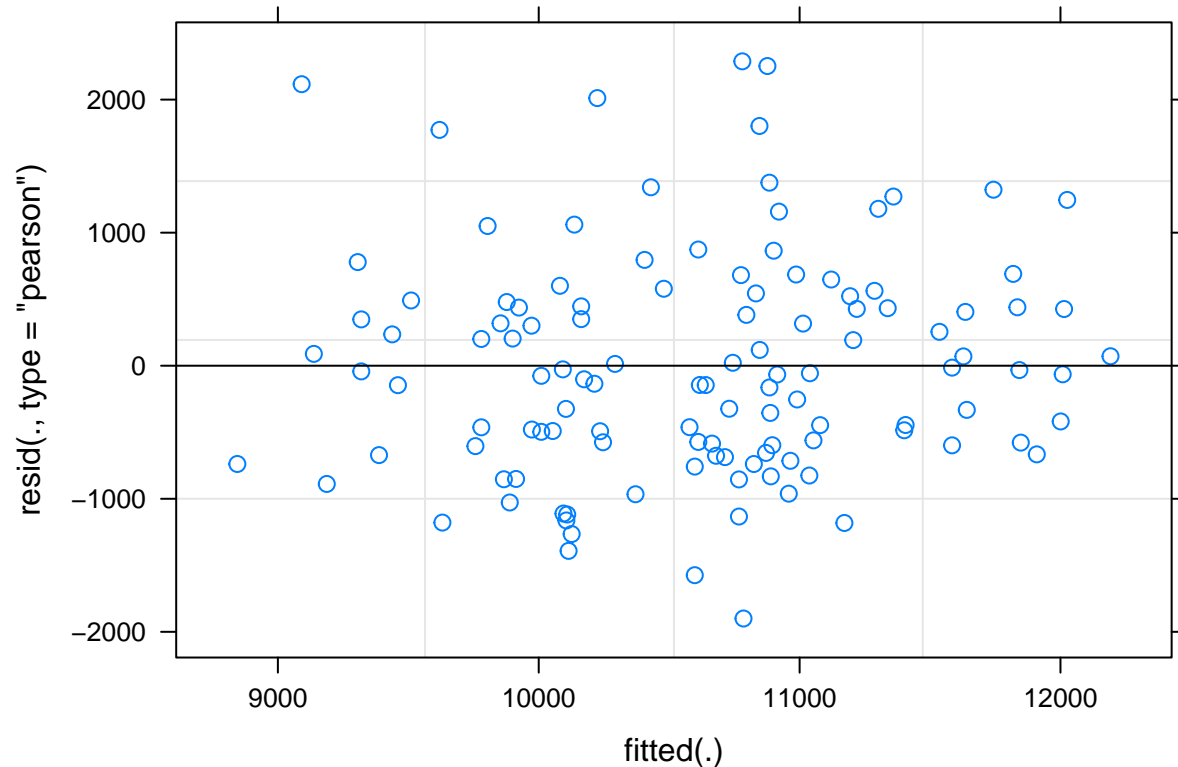
```
#from my understanding the "boundary (singular) fit: see ?isSingular" error means that the estimate of
```

```
qqnorm(resid(havcn_yield))
```

Normal Q-Q Plot



```
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      21547459 10773729     2  97.033 12.7752 1.188e-05 ***
## herb       884330   221082     4  97.065  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)
```

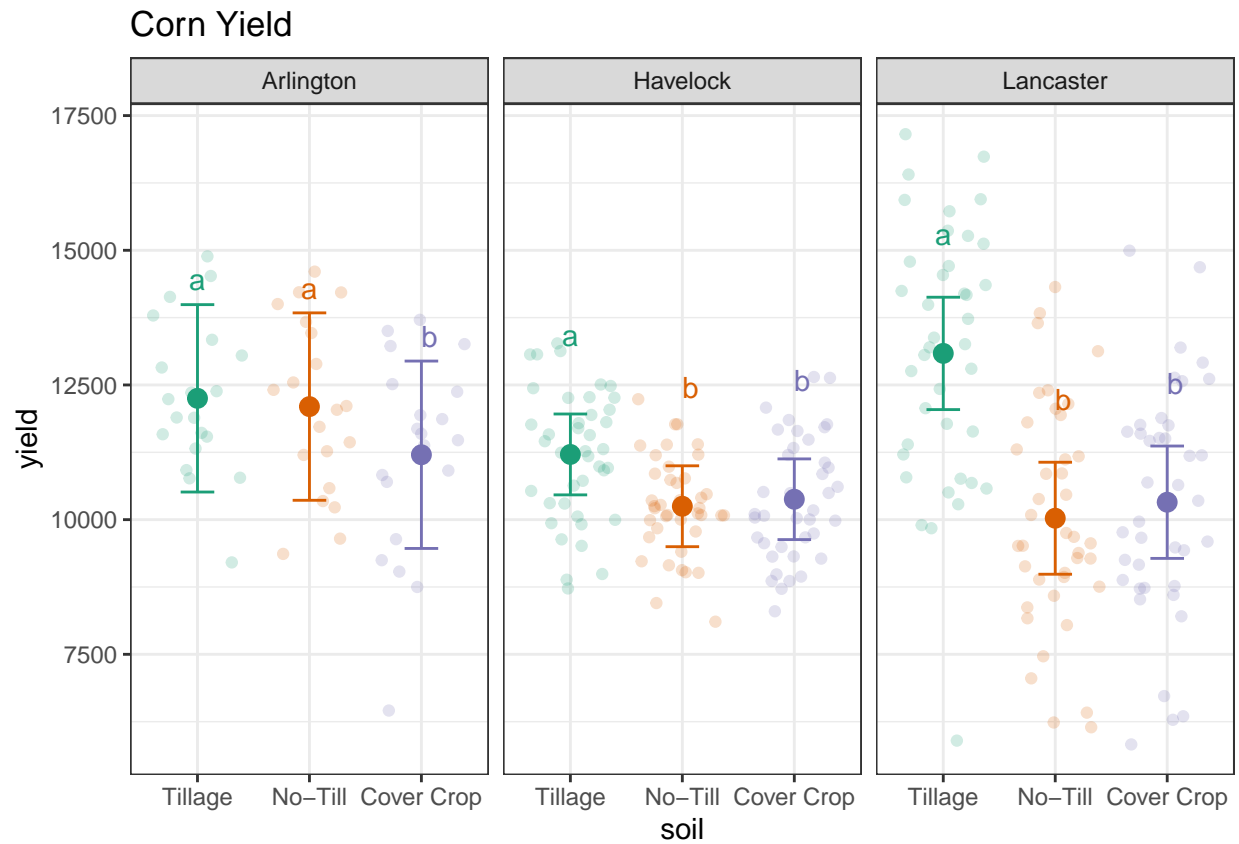
```
Corn1= Corn1 %>%
  filter(site_crop_yr != "ARL_CN_20")

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() +
```



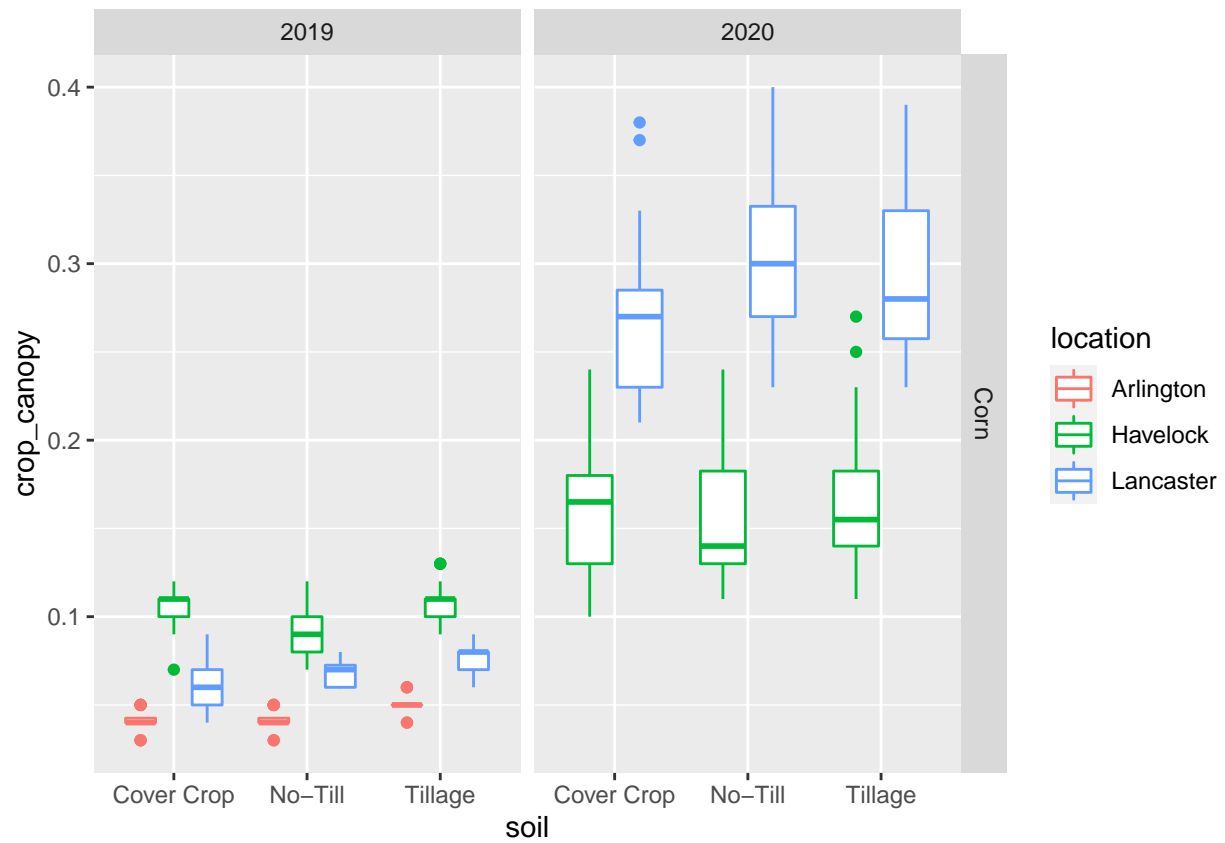
```
facet_grid(~location) +
theme_bw() +
scale_color_brewer(palette = "Dark2") +
theme(legend.position = "none") +
labs(title = "Corn Yield")
```

y1

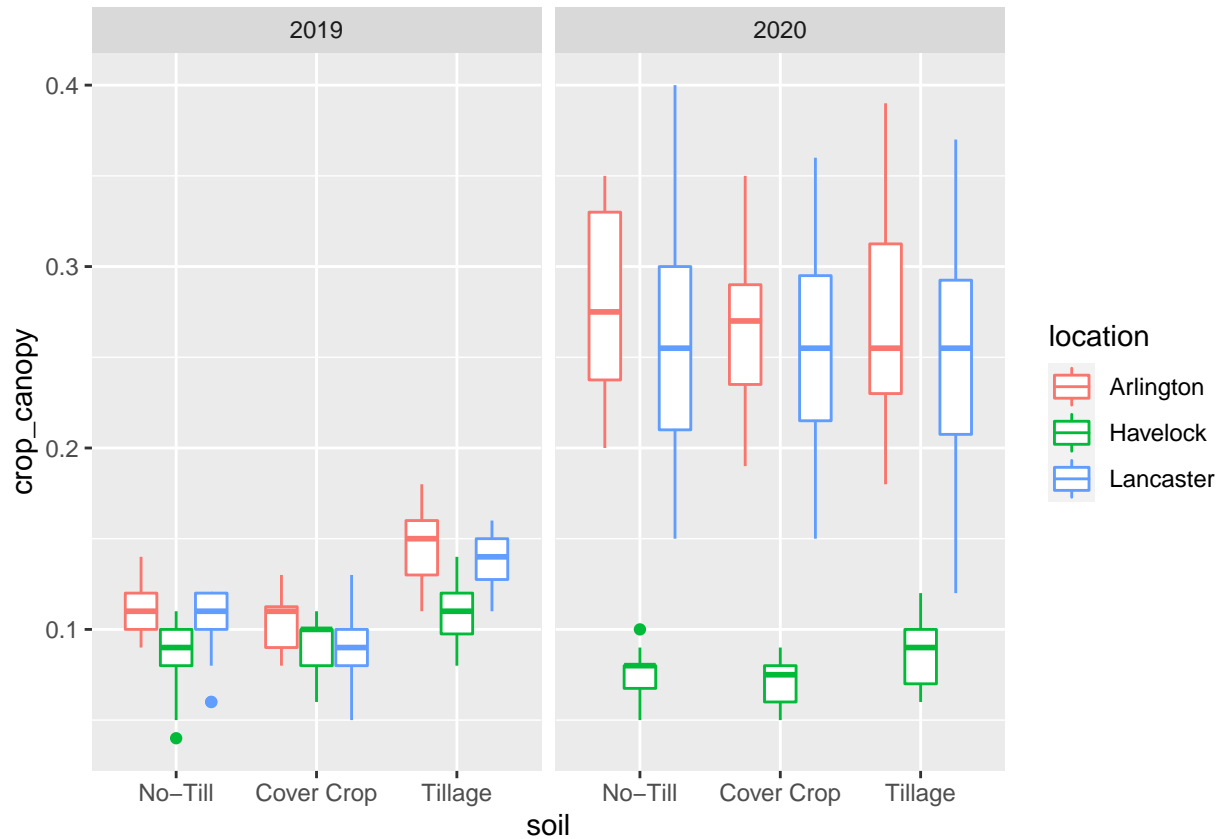


## Crop Canopy

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



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



Based on the variability in canopy coverage between cropping seasons for both crops, I will create separate models for each site-crop year

## Corn

### Arlington Corn Canopy

```
arl19_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_
Anova(arl19_corn_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil      42.0083  2 7.551e-10 ***
## herb       1.7739  4  0.7773
## soil:herb   6.0650  8  0.6399
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil was significant*

## Lancaster Corn Canopy

```
lan19_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_
Anova(lan19_corn_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil      23.9933  2  6.165e-06 ***
## herb       2.7502  4    0.6005
## soil:herb 12.5885  8    0.1268
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil was significant*

```
lan20_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_
Anova(lan20_corn_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil      11.8337  2  0.002694 **
## herb       6.6658  4  0.154641
## soil:herb  4.5791  8  0.801473
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil was significant*

## Havelock Corn Canopy

```
hav19_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_
Anova(hav19_corn_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil      41.3921  2  1.028e-09 ***
## herb       9.0449  4   0.05999 .
## soil:herb 14.3407  8   0.07331 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#soil management fixed effect was significant
```

```
hav20_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_
Anova(hav20_corn_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: crop_canopy
```

```
##           Chisq Df Pr(>Chisq)
```

```
## soil      0.5802  2    0.7482
```

```
## herb      6.7155  4    0.1517
```

```
## soil:herb 5.4463  8    0.7090
```

```
#nothing was significant
```

```
cn_canopy <- ggplot(cncanopy, aes(x= soil, y= crop_canopy*100, color= soil)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL*100, ymax= upper.CL*100), width= .3) +
  geom_text(aes(label = .group), nudge_y = 12) +
  geom_jitter(data = Corn1 ,mapping = aes(y = crop_canopy*100), alpha = 0.2) +
  #coord_flip() +
  facet_grid(year~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Corn Canopy")
```

## Soybean Yield

### Arlington Analysis

```
arl_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Arlington")))
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 -0.6032 -0.0721  0.5465  3.3338
```

```
##
```

```
## Random effects:
```

```
## Groups   Name              Variance Std.Dev.
```

```
## year:rep (Intercept) 107048   327.2
```

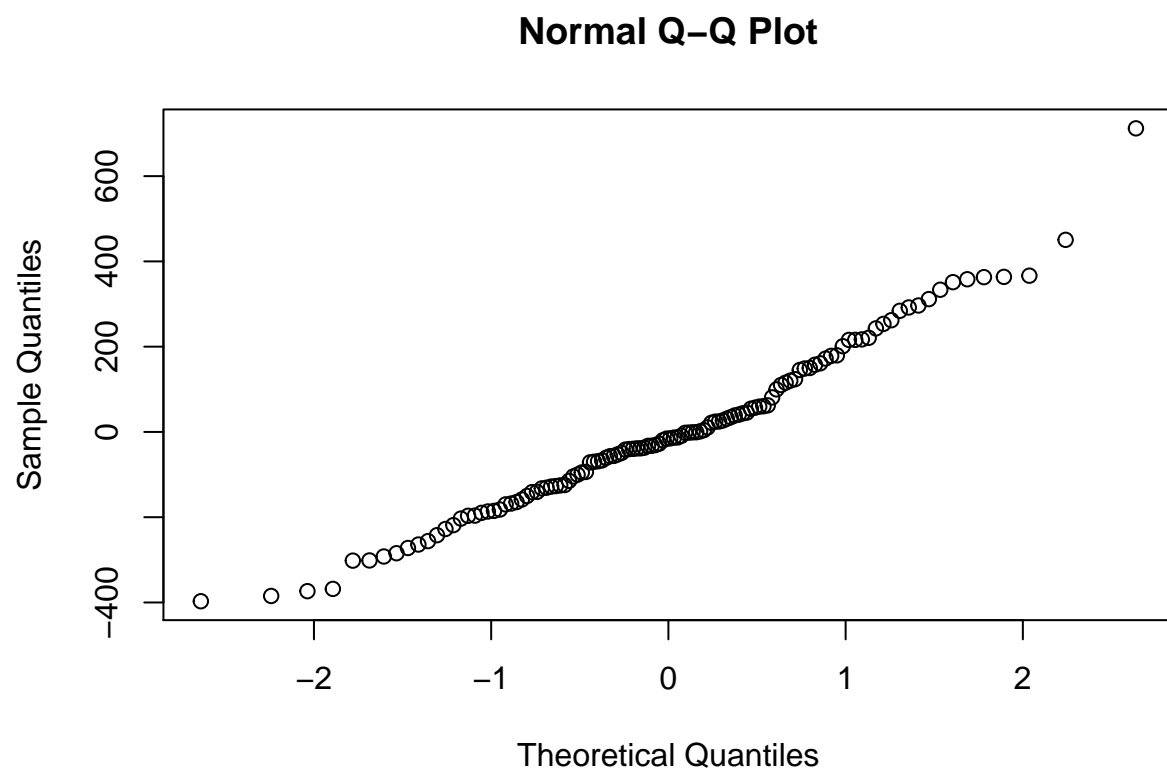
```

## rep      (Intercept) 13565  116.5
## Residual          45616  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    149.914     5.135  25.622 1.29e-06 ***
## soilCover Crop   -201.625    106.789    98.000   -1.888   0.0620 .
## soilTillage      -101.875    106.789    98.000   -0.954   0.3424
## herbCL50         -38.375    106.789    98.000   -0.359   0.7201
## herbCTRL          81.000    106.789    98.000    0.759   0.4500
## herbME25          82.375    106.789    98.000    0.771   0.4423
## herbME50        -32.375    106.789    98.000   -0.303   0.7624
## soilCover Crop:herbCL50 267.500    151.023    98.000    1.771   0.0796 .
## soilTillage:herbCL50   176.750    151.023    98.000    1.170   0.2447
## soilCover Crop:herbCTRL 142.500    151.023    98.000    0.944   0.3477
## soilTillage:herbCTRL   69.750    151.023    98.000    0.462   0.6452
## soilCover Crop:herbME25 128.625    151.023    98.000    0.852   0.3965
## soilTillage:herbME25   49.125    151.023    98.000    0.325   0.7457
## soilCover Crop:herbME50 229.125    151.023    98.000    1.517   0.1324
## soilTillage:herbME50   56.250    151.023    98.000    0.372   0.7104
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

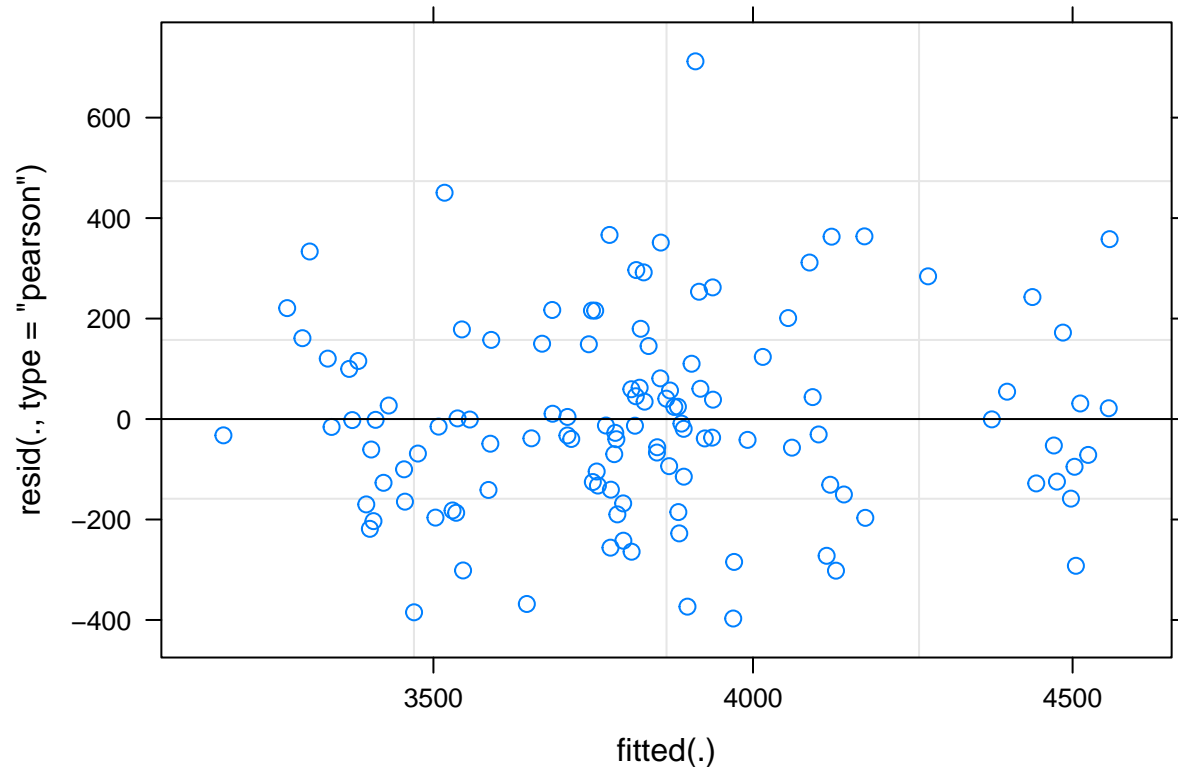
##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it

qqnorm(resid(arl_sb_yield))

```



```
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    98  0.5229 0.59442
## herb        375817   93954     4    98  2.0597 0.09193 .
## soil:herb  200215   25027     8    98  0.5486 0.81703
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Soil management fixed effect significant
```

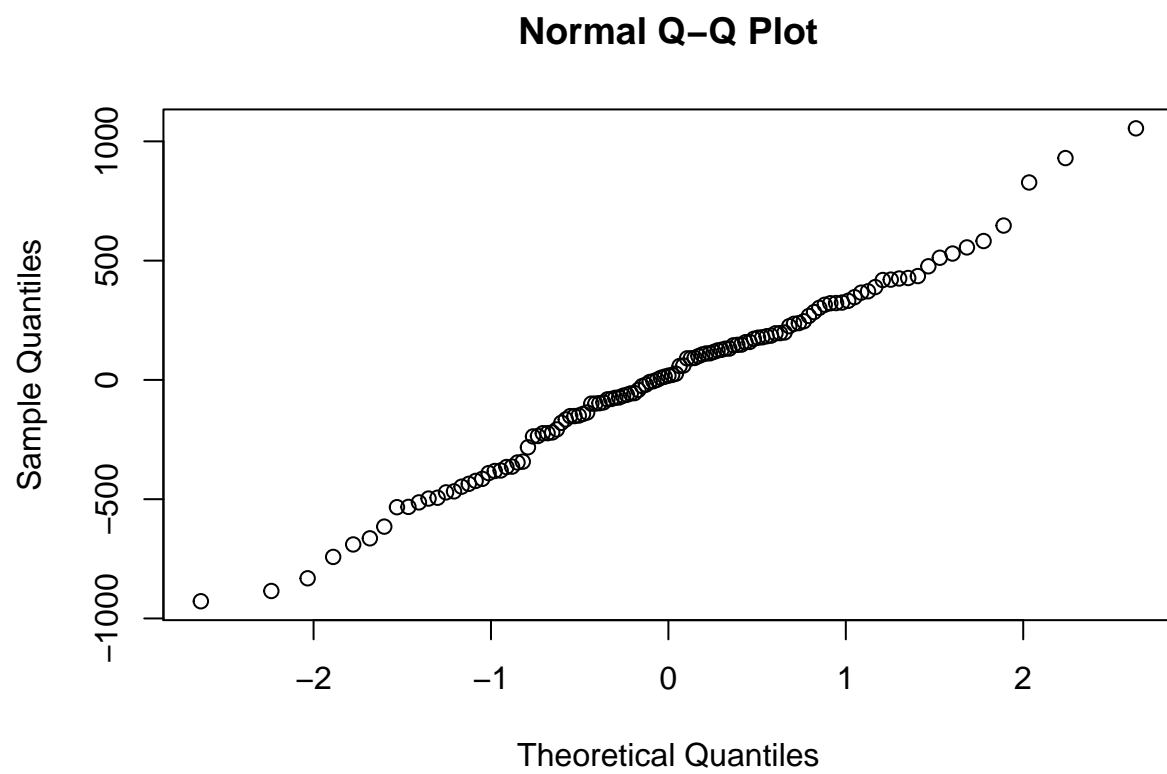
## Lancaster Analysis

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

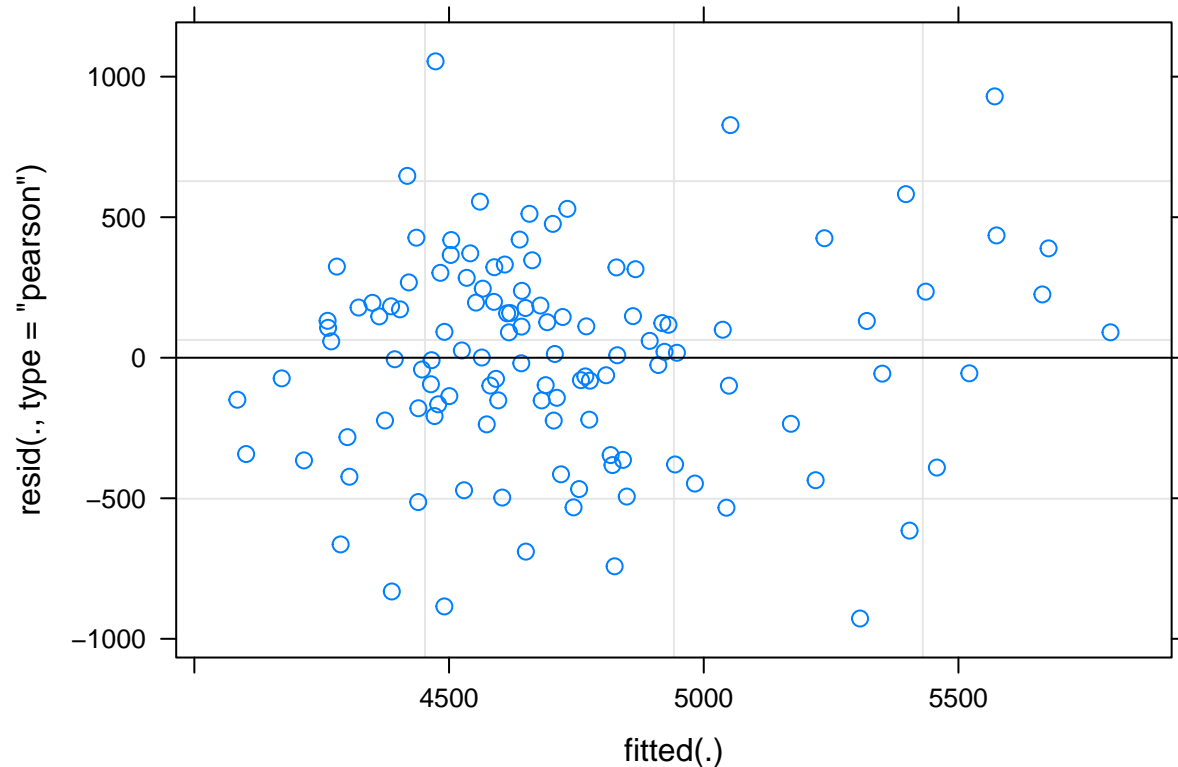
```
## boundary (singular) fit: see ?isSingular
```

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





```
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  767953      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
```

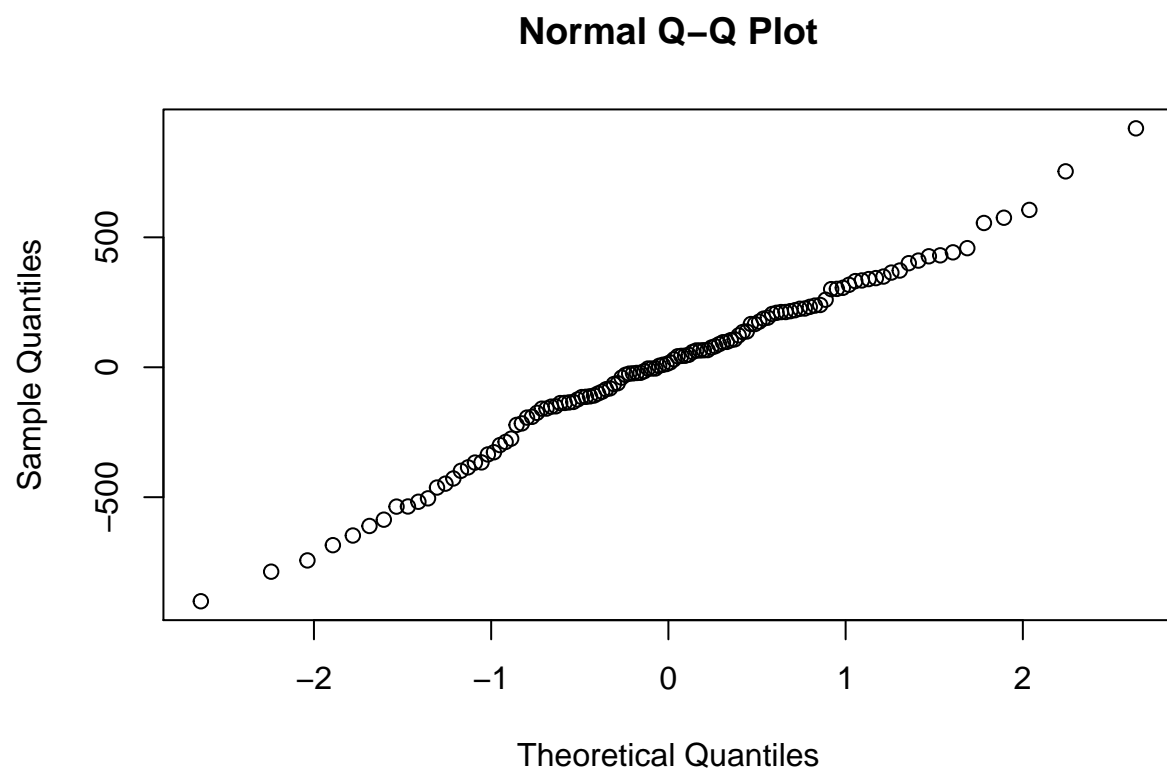
```
#Soil management fixed effect significant
```

## Havelock Analysis

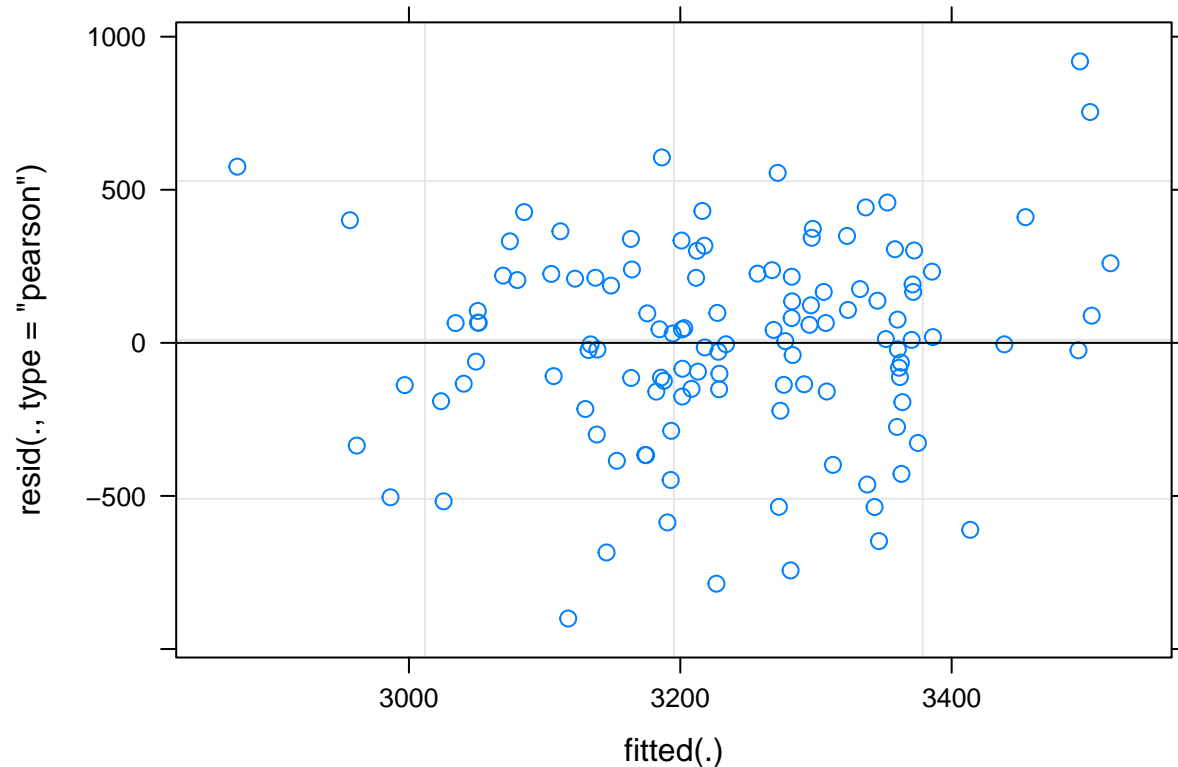
```
hav_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Havelock")))
```

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

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



```
plot(hav_sb_yield)
```



```
#assumptions look good
```

```
anova(hav_sb_yield)
```

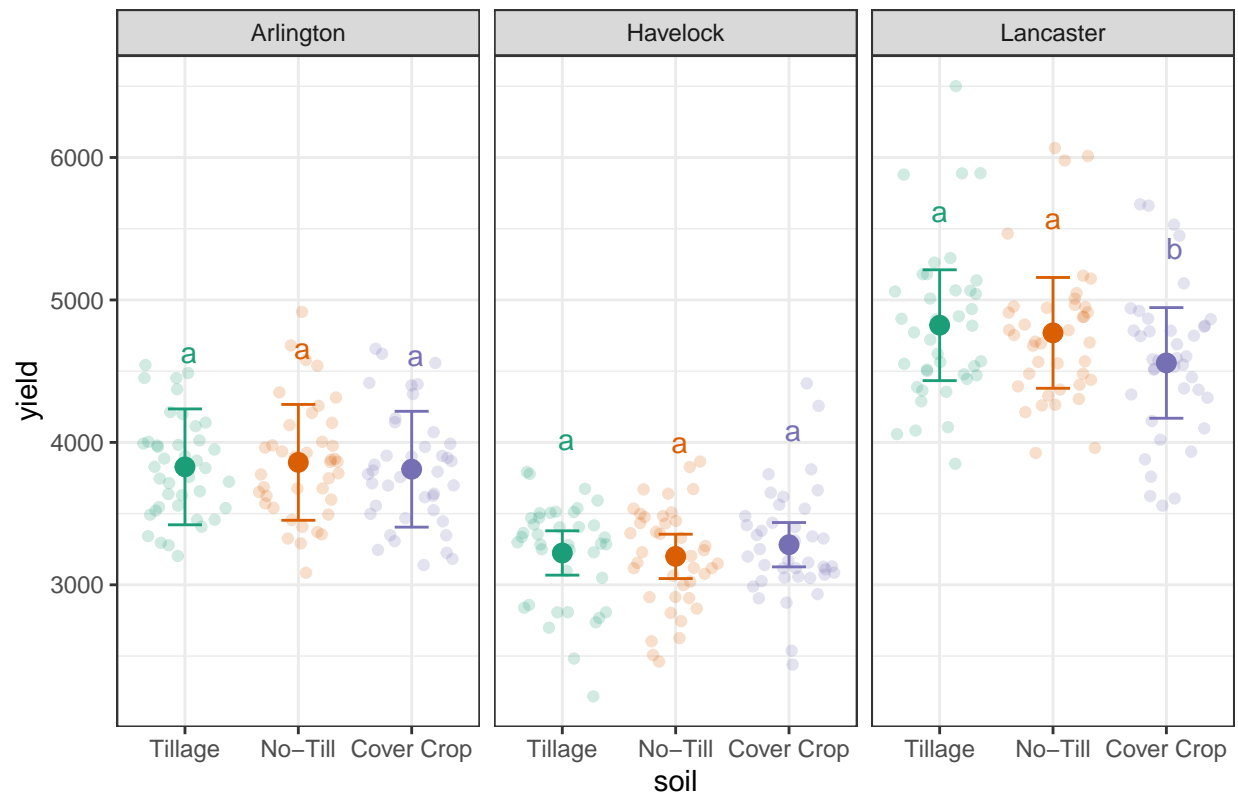
```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## soil      142276   71138     2    98  0.5747 0.5648
## herb      285685   71421     4    98  0.5770 0.6800
## soil:herb 656275   82034     8    98  0.6627 0.7230
```

```
#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



## Soybean Canopy

### Arlington Soy Canopy

```
arl19_soy_can = glmmTMB(crop_canopy ~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop == 'Arlington')),
                        Anova(arl19_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil      144.1446  2 < 2.2e-16 ***
## herb       18.5283  4 0.0009726 ***
## soil:herb   7.5376  8 0.4798878
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil and herb fixed effects significant*

```
arl20_soy_can = glmmTMB(crop_canopy ~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop == 'Arlington')),
                        Anova(arl20_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil        2.2723 2      0.3210
## herb        4.3798 4      0.3570
## soil:herb   7.9777 8      0.4357
```

*#nothing significant*

## Lancaster Soy Canopy

```
lan19_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop_yr==19)),
Anova(lan19_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil       74.9399 2    < 2e-16 ***
## herb       3.8951 4     0.42039
## soil:herb  14.9373 8     0.06038 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil was significant*

```
lan20_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop_yr==20)),
Anova(lan20_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil        0.3183 2      0.8529
## herb        1.6315 4      0.8031
## soil:herb   2.3403 8      0.9688
```

*#nothing significant*

## Havelock Soy Canopy

```
hav19_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop_yr==19)),
Anova(hav19_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil       29.681  2 3.588e-07 ***
## herb       10.719  4  0.02991 *
## soil:herb  11.192  8  0.19105
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil and herbicide fixed effects were significant*

```
hav20_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop_yr==2019)))
Anova(hav20_soy_can)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##           Chisq Df Pr(>Chisq)
## soil       16.2868  2 0.0002907 ***
## herb       10.4300  4 0.0337757 *
## soil:herb   6.7152  8 0.5676475
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Soil and herbicide fixed effects were significant*

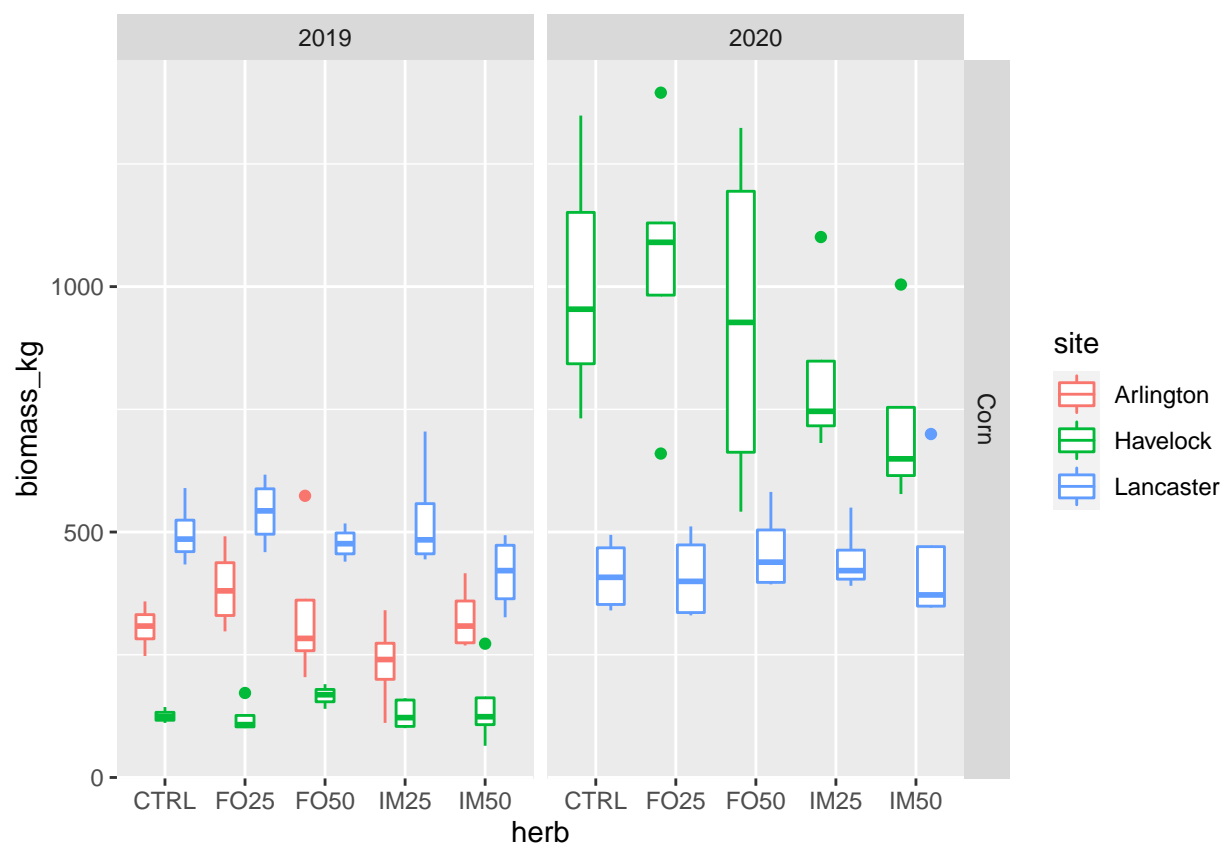
```
sb_canopy <- ggplot(sbc canopy, aes(x= soil, y= crop_canopy*100, color= soil)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL*100, ymax= upper.CL*100), width= .3) +
  geom_text(aes(label = .group), nudge_y = 10) +
  geom_jitter(data = Soybean1 ,mapping = aes(y = crop_canopy*100), alpha = 0.2) +
  #coord_flip() +
  facet_grid(year~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Soybean Canopy")
```

```
sb_canopyherb <- ggplot(sbc canopy2, aes(x= herb, y= crop_canopy*100, color= herb)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL*100, ymax= upper.CL*100), width= .3) +
  geom_text(aes(label = .group), nudge_y = 10) +
  geom_jitter(data = Soybean1 ,mapping = aes(y = crop_canopy*100), alpha = 0.2) +
  #coord_flip() +
  facet_grid(year~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Soybean Canopy")
```

Seems odd that the Ctrl treatment had reduced canopy cover at Havelock 2019. I double checked the herbicide treatments for the EUs and they seem to match.

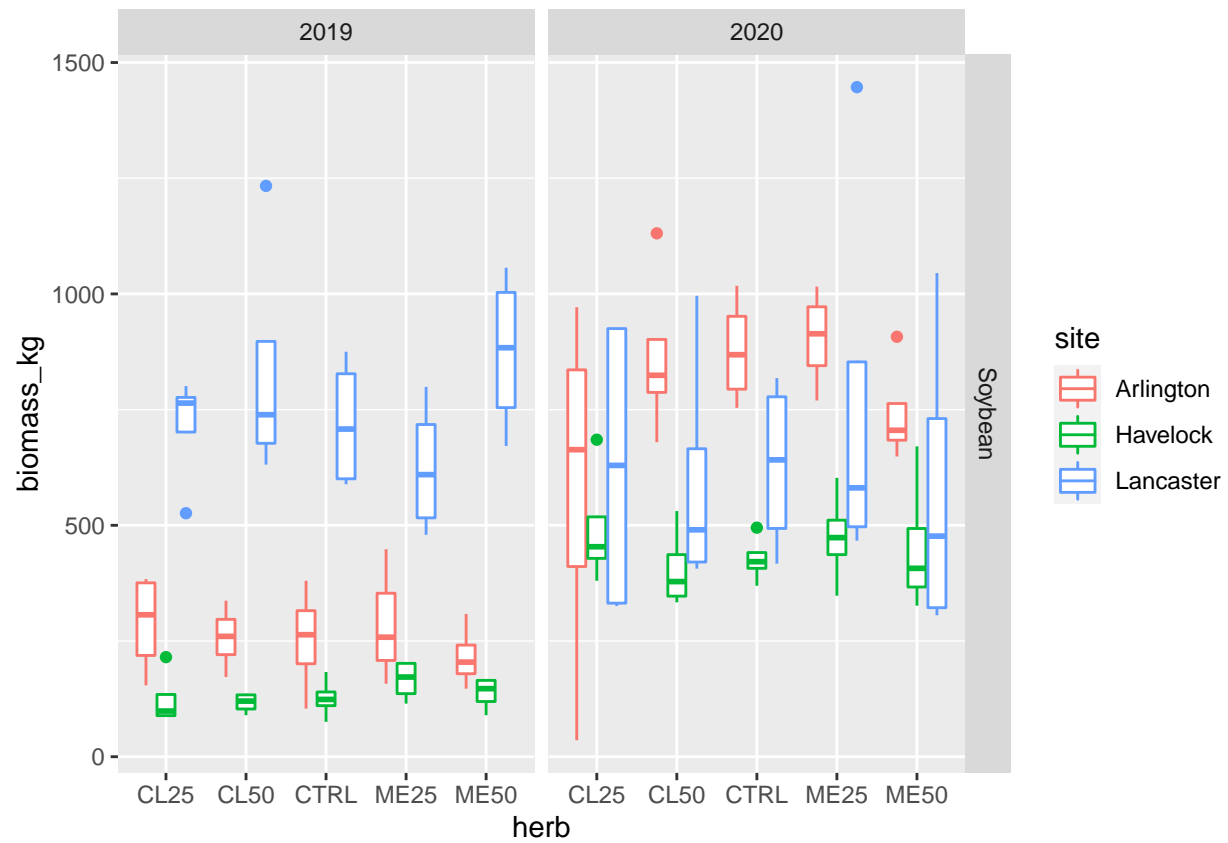
## Cover Crop Biomass analysis

```
CornCC %>%
  ggplot(aes(x = herb, y = biomass_kg, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



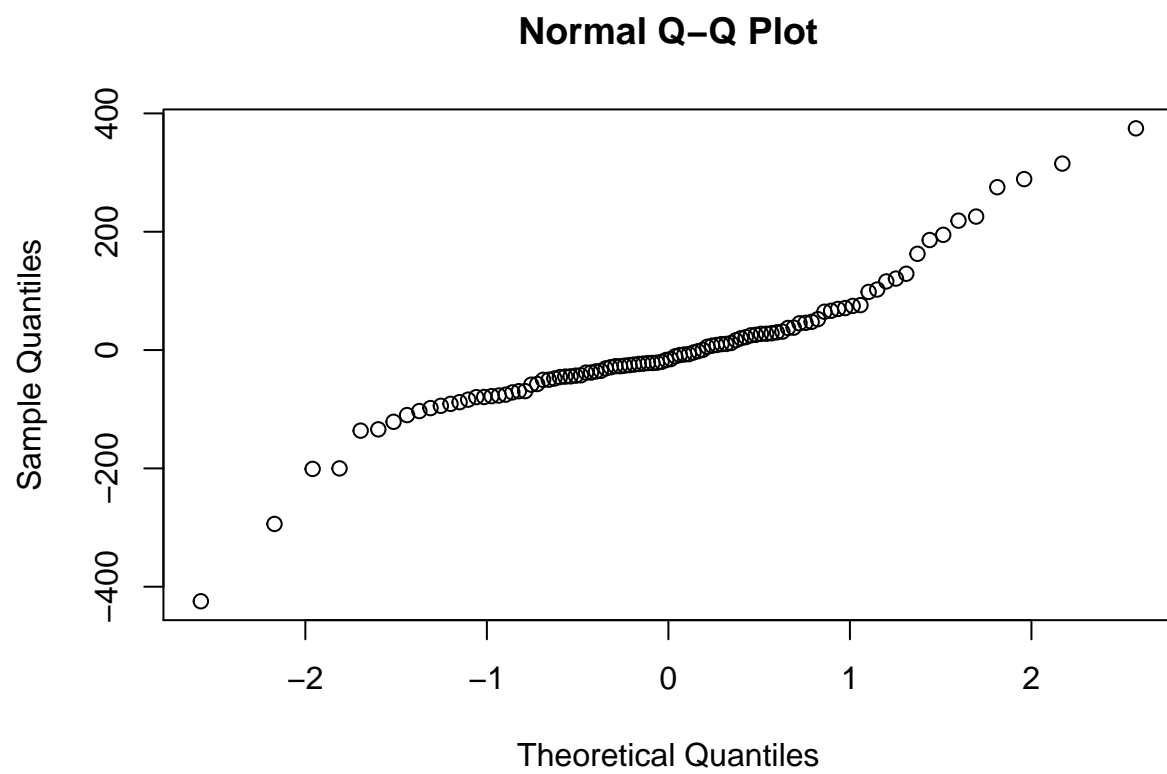
```
SBCC %>%
  ggplot(aes(x = herb, y = biomass_kg, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



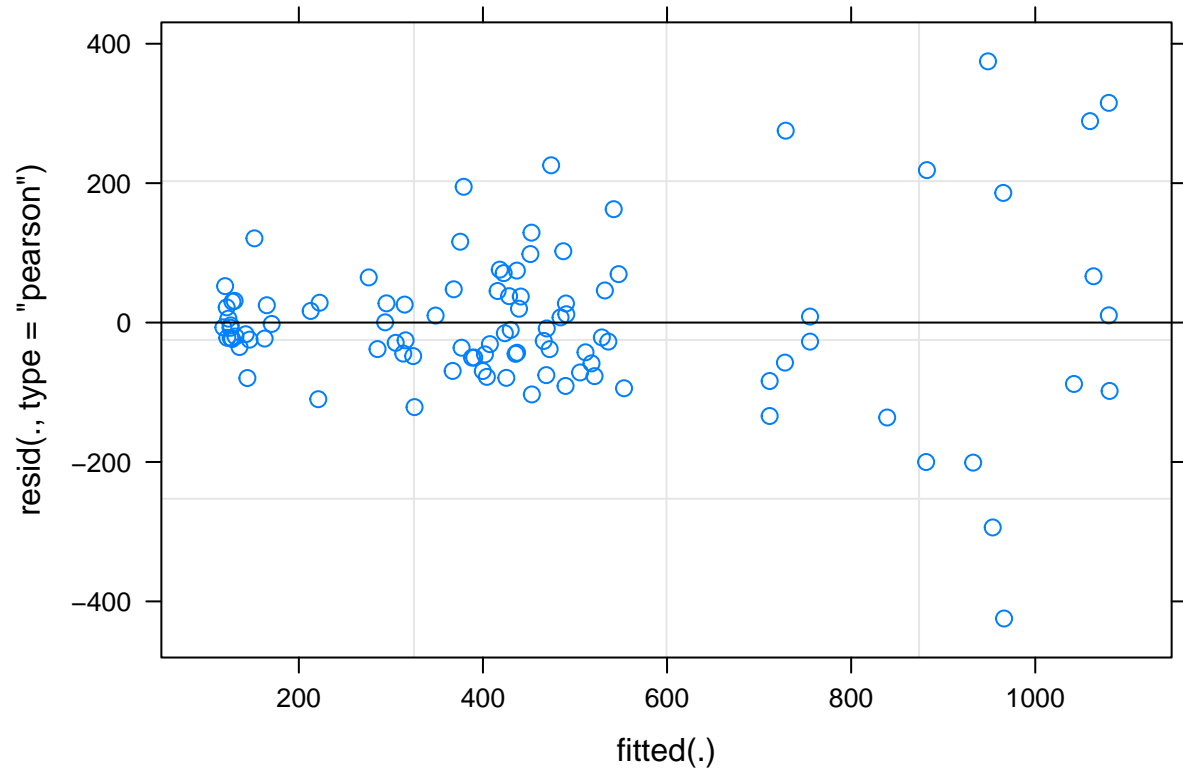


Corn

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



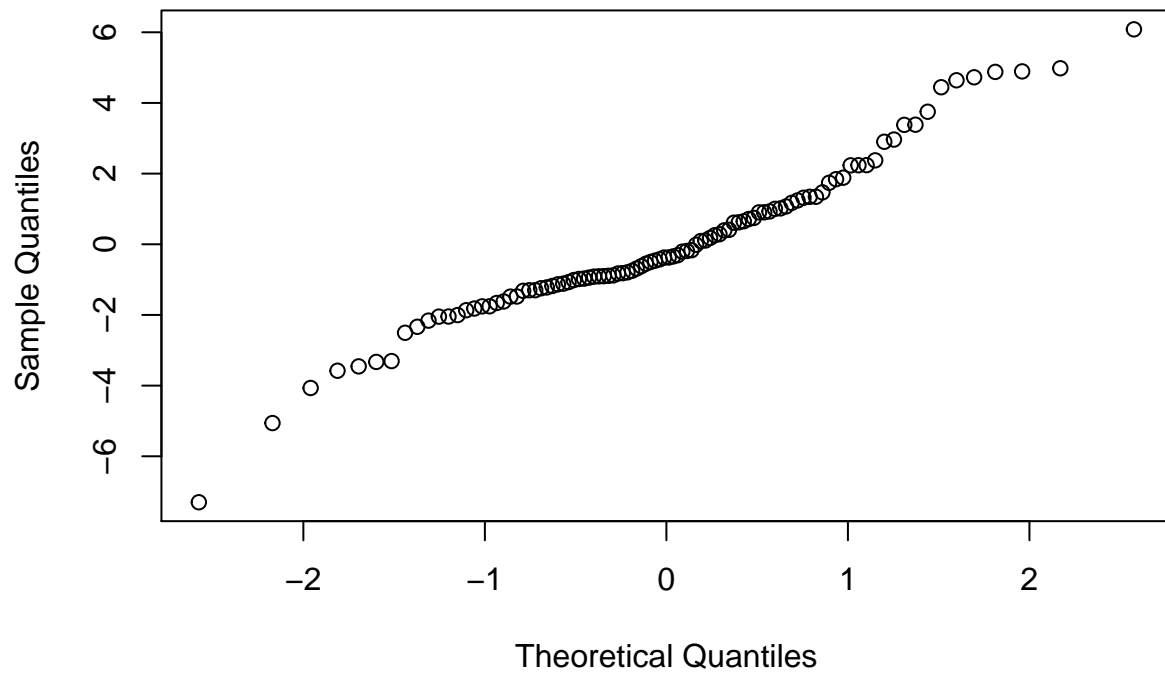
```
plot(cn_cc_bio)
```



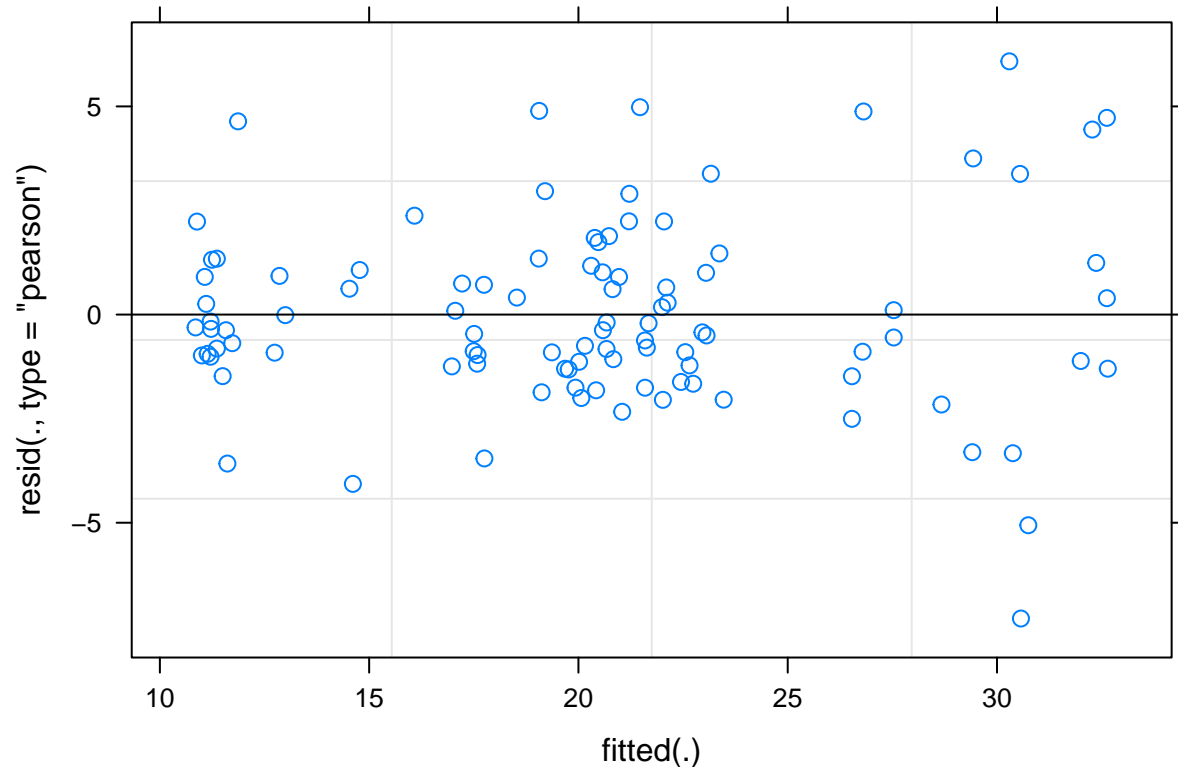
*#Assumption for equal variance not met*

```
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)
```



*#assumptions improved. Use this one!*

```
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*

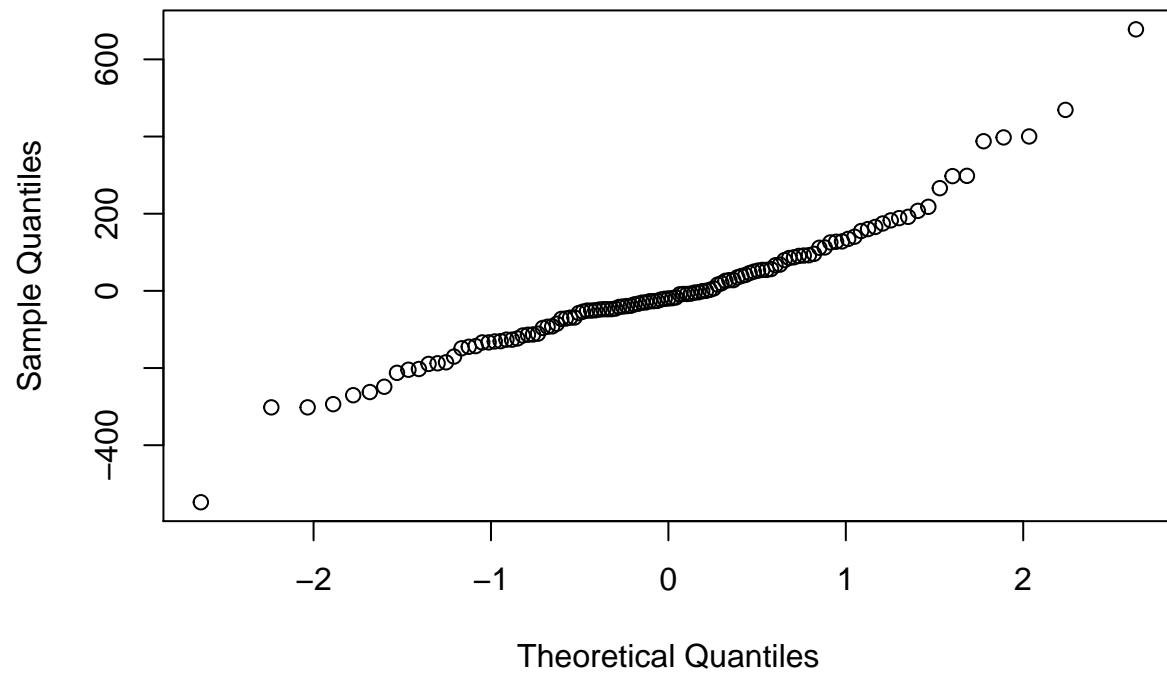
Soybean

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

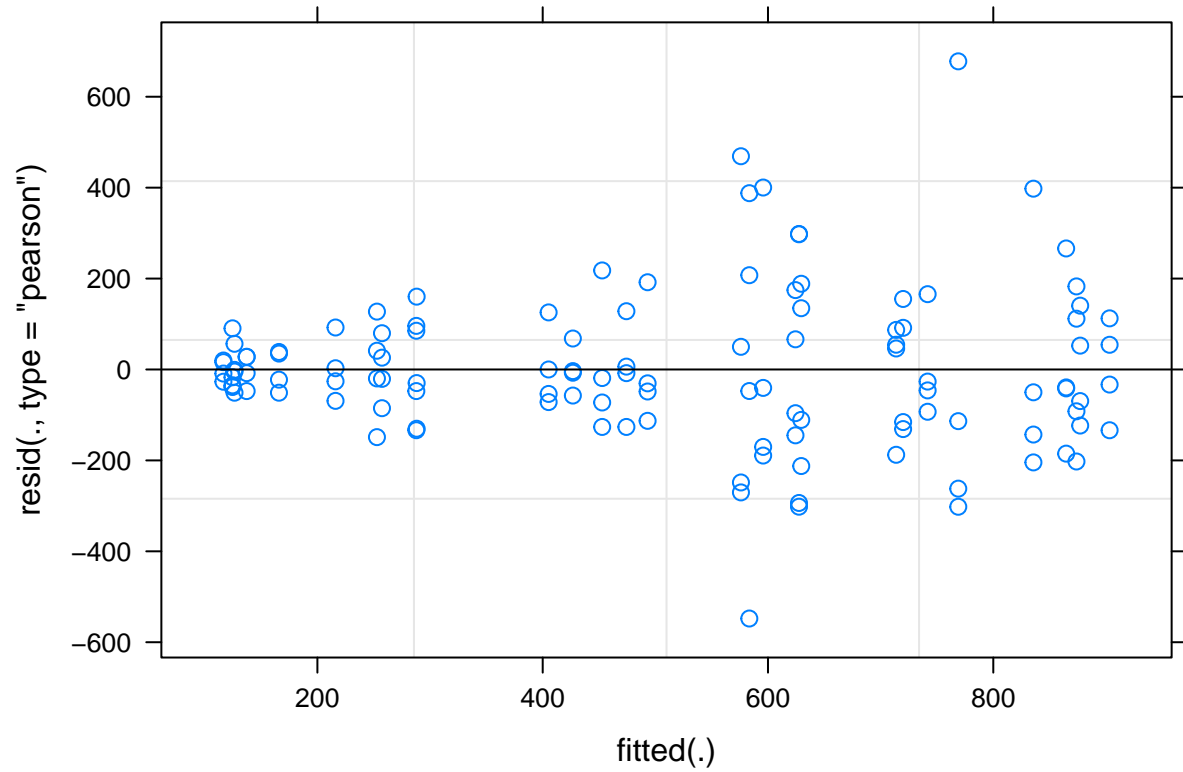
```
## boundary (singular) fit: see ?isSingular
```

```
qqnorm(resid(sb_cc_bio))
```

Normal Q-Q Plot



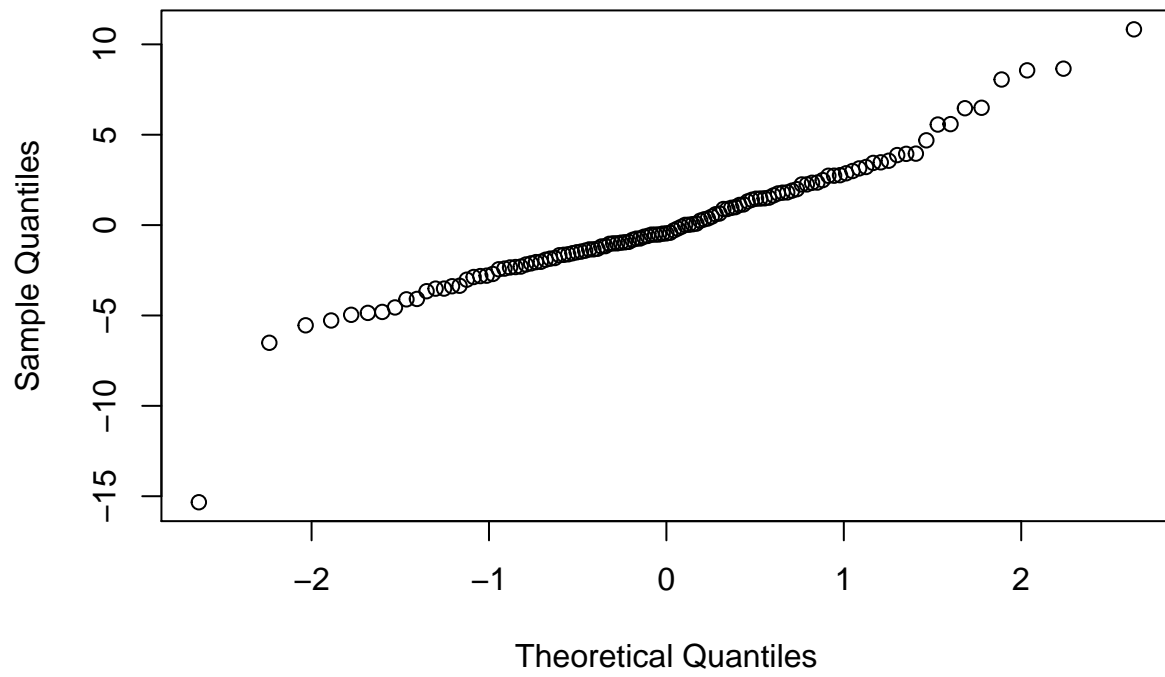
```
plot(sb_cc_bio)
```



*#assumptions for equal variance not met*

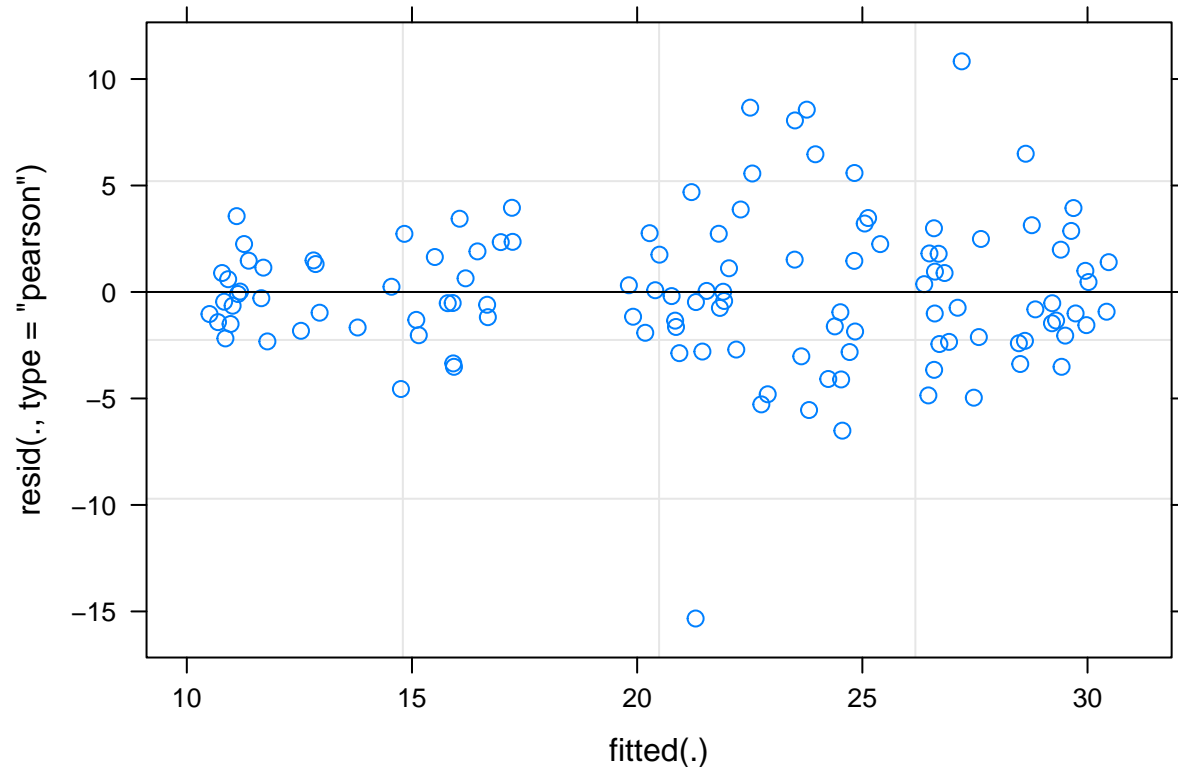
```
sb_cc_bio1= lmer(sqrt(biomass_kg)~ site_crop_yr * herb + (1|site_crop_yr:rep), data=SBCC)
qqnorm(resid(sb_cc_bio1))
```

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    3372.1   674.43     5 18.042 42.2749 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*

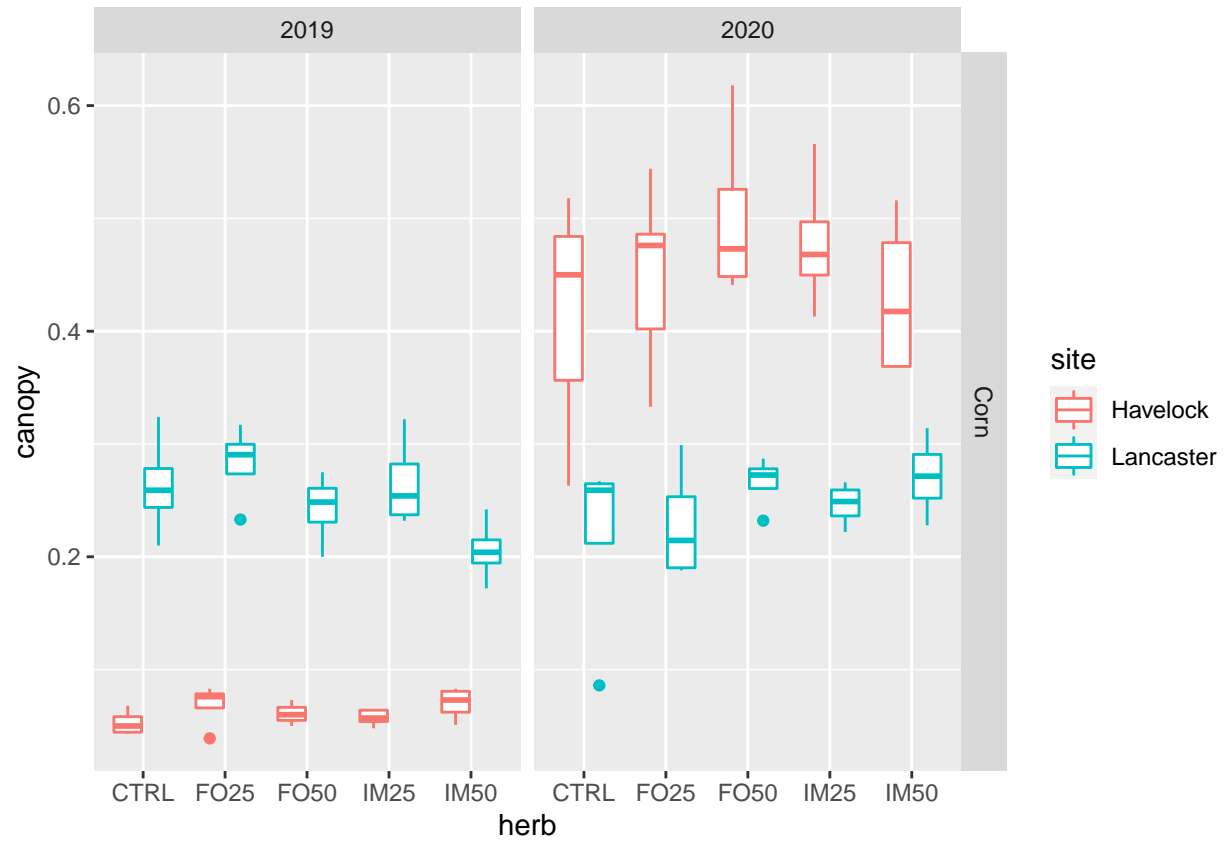
## Cover Crop Canopy

### Corn

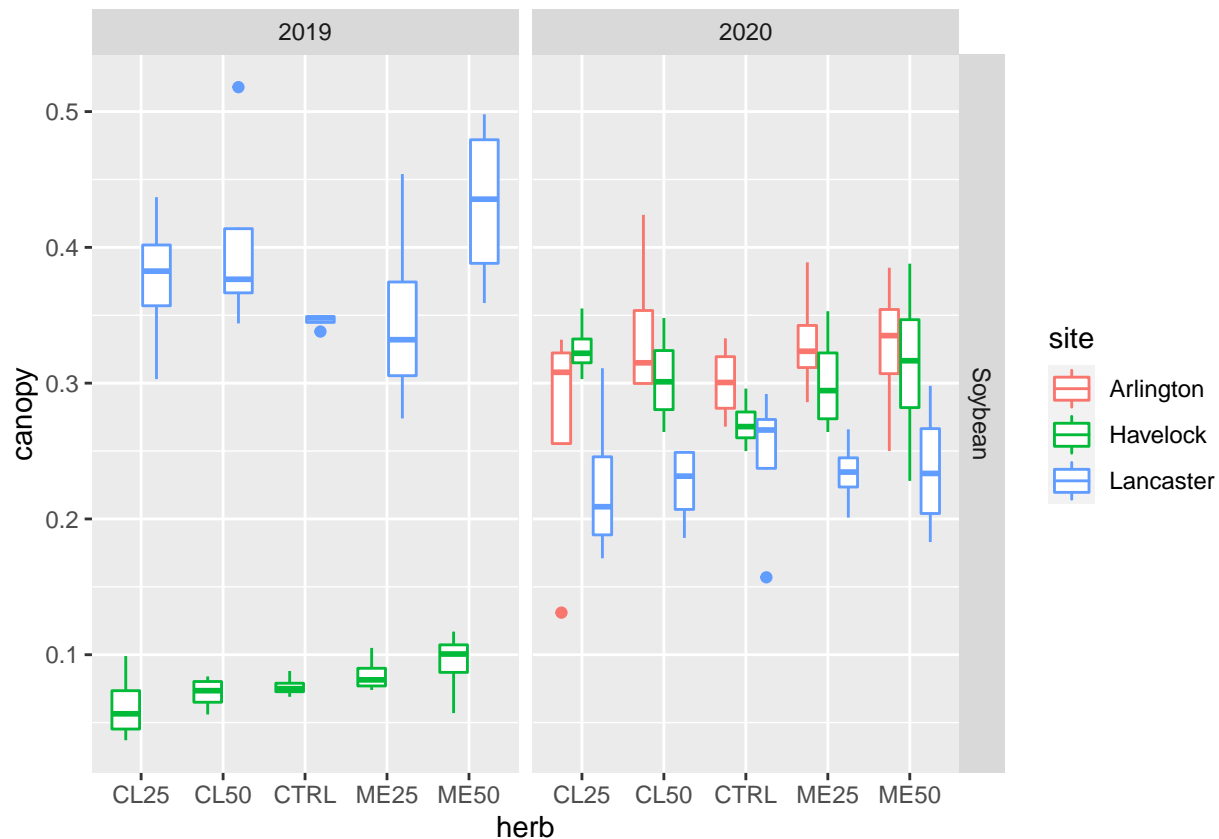
```
CornCC1 <- CornCC %>%
  filter(!is.na(canopy))

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

```
CornCC1 %>%
  ggplot(aes(x = herb, y = canopy, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



```
SBCC1 %>%
  ggplot(aes(x = herb, y = canopy, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



Based on differences between location across growing seasons I thought it was best to proceed with testing site-year as a fixed effect.

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

```
Anova(cn_cc_bio)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: canopy
```

```
##
```

```
## site_crop_yr      Chisq Df Pr(>Chisq)
```

```
## 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))
```

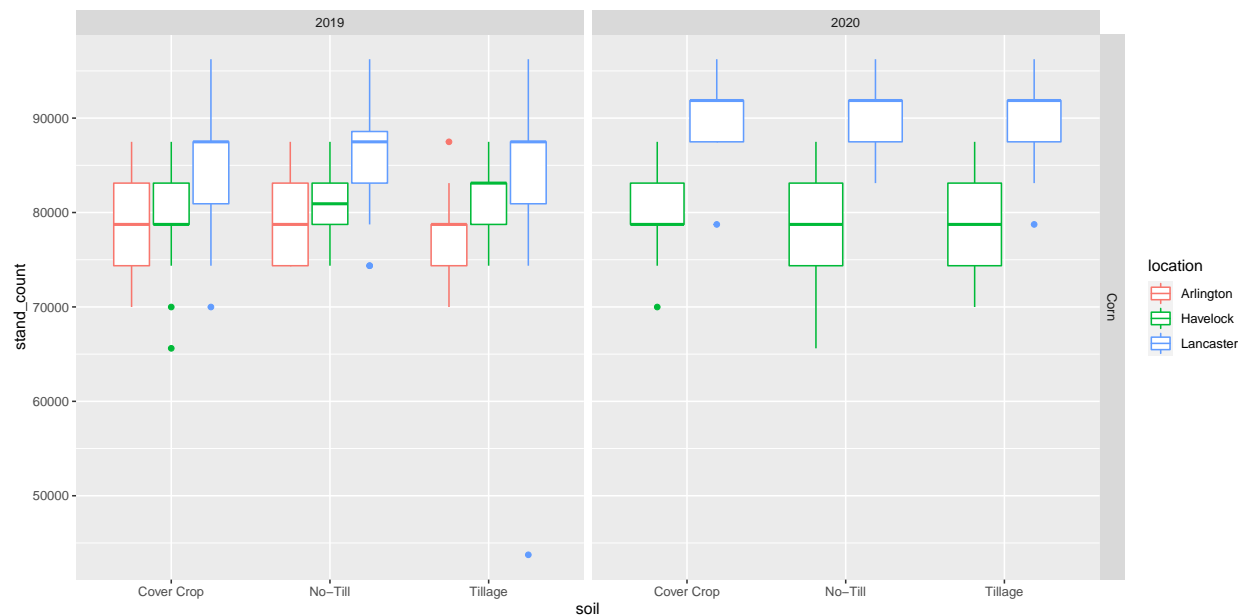
```
sb_cc_bio= glmmTMB(canopy~ site_crop_yr*herb + (1|site_crop_yr:rep), data=SBCC, beta_family(link="logit")
Anova(sb_cc_bio)
```

```
## 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

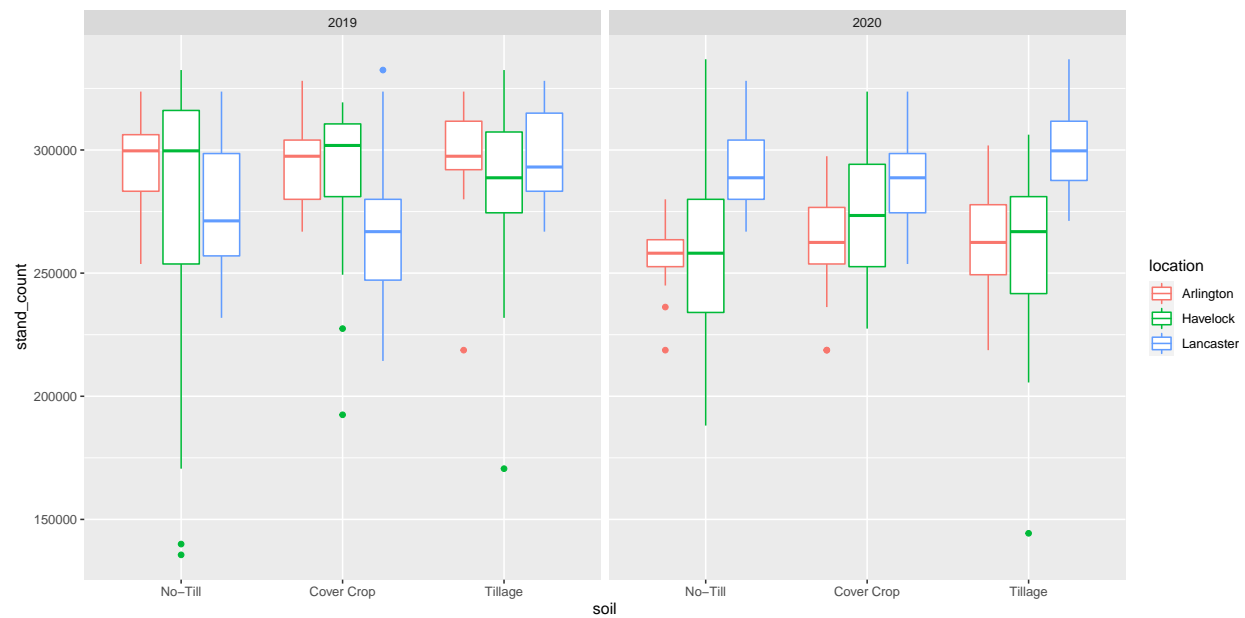
```
Corn1 %>%
  ggplot(aes(x = soil, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



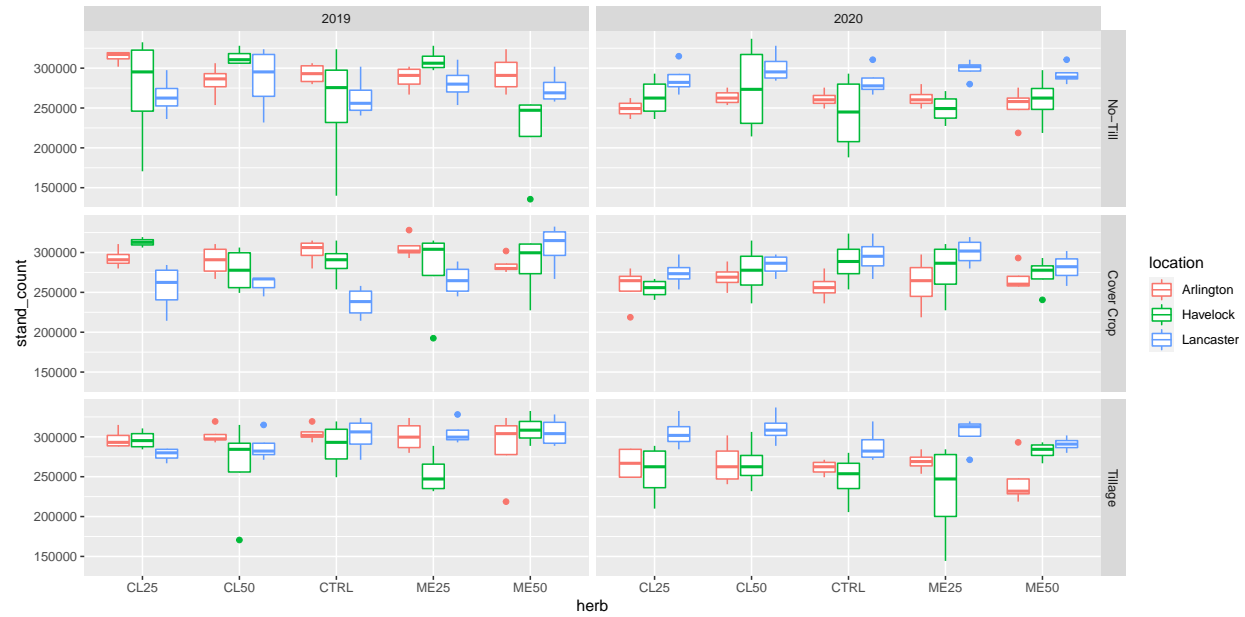
```
Corn1 %>%
  ggplot(aes(x = herb, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(soil ~ year)
```



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



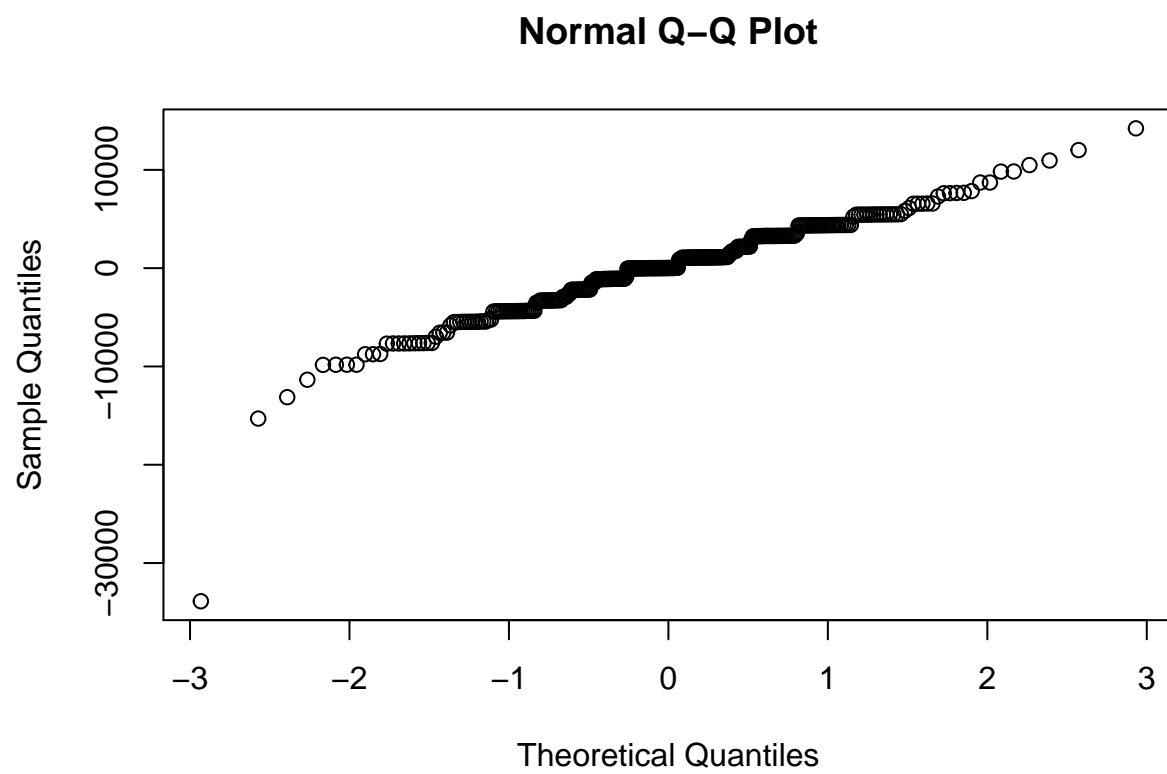
```
Soybean1 %>%
  ggplot(aes(x = herb, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(soil ~ year)
```



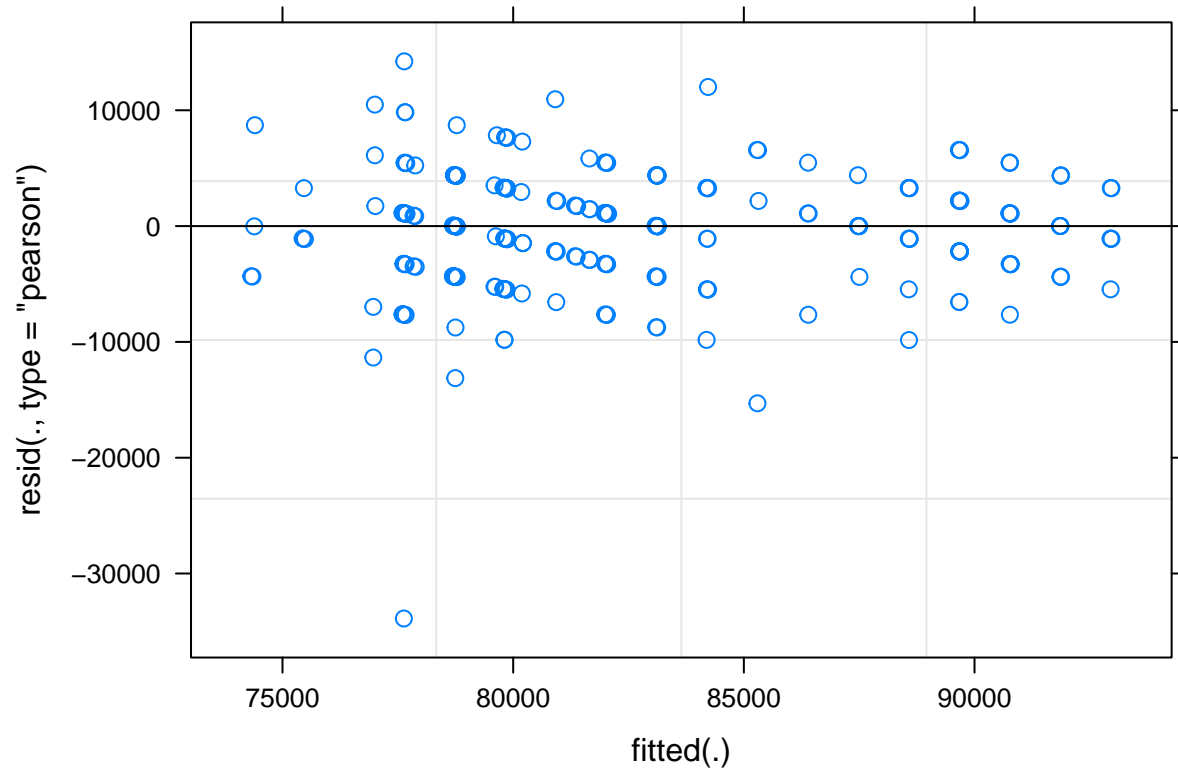
Based on these visual representations it doesn't appear to me that there are really any consistent patterns as a function of soil management, herbicide treatment, location, or year. There does appear to be differences in location across seasons. Therefore, I think it is best if we test for site-year differences as a fixed effect in models for our initial approach and separate means by site-year where appropriate.

## Corn

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



```
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	5594185266	1398546317	4	14.697	43.6977	5.387e-08
## soil	6890561	3445280	2	207.310	0.1076	0.8980
## herb	105594808	26398702	4	207.608	0.8248	0.5107
## site_crop_yr:soil	135486393	16935799	8	207.305	0.5292	0.8338
## site_crop_yr:herb	189233105	11827069	16	207.589	0.3695	0.9878
## soil:herb	165394906	20674363	8	210.005	0.6460	0.7384
## site_crop_yr:soil:herb	836955171	26154849	32	209.491	0.8172	0.7471

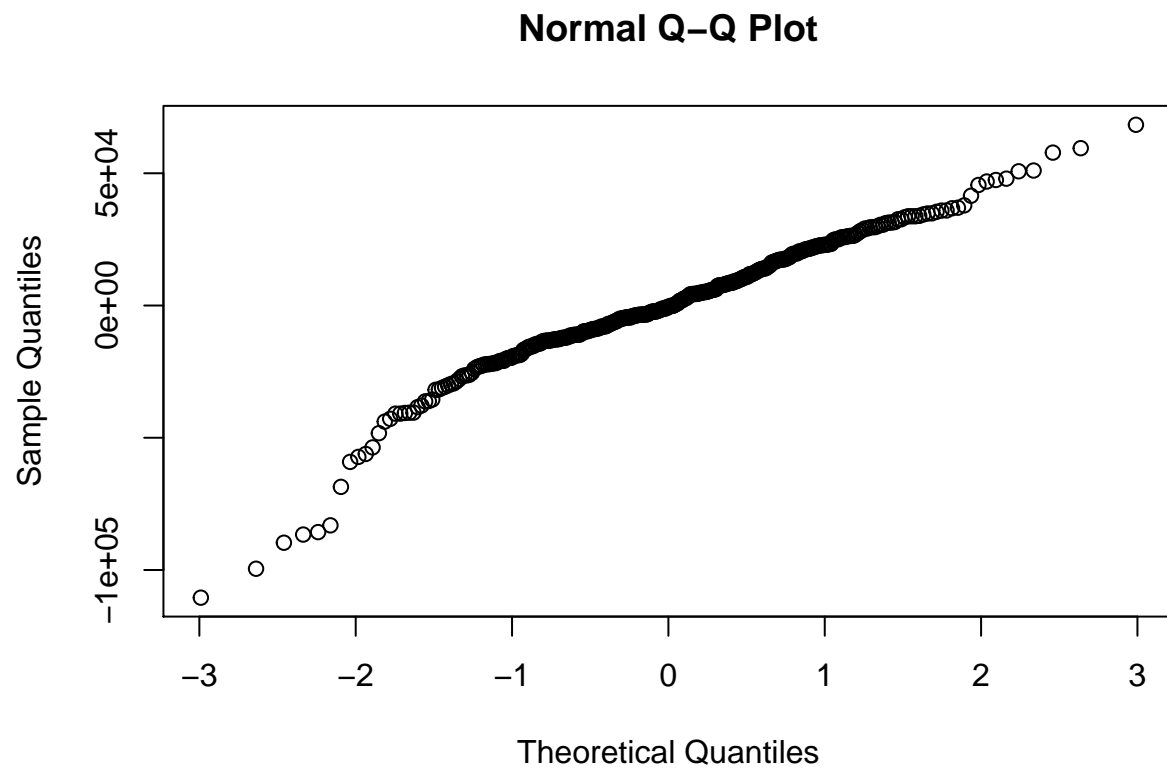
```
##
## site_crop_yr      ***
## soil
## herb
## site_crop_yr:soil
## site_crop_yr:herb
## soil:herb
## site_crop_yr:soil:herb
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



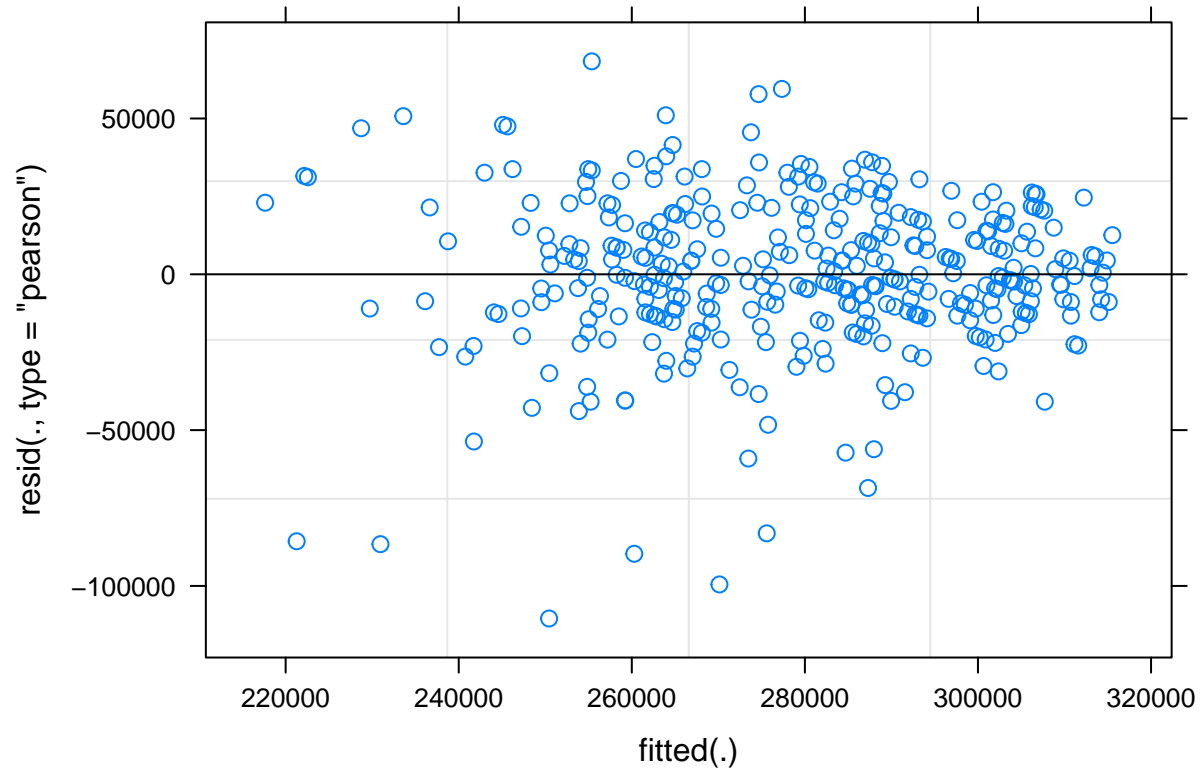
```
#site-year significant
```

Soybean

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



```
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.*