# Carryover_CornResults

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3/4/2021

## Analysis Procedure

Prior to analysis I took the approach of plotting the response variables with box-plots to visualize treatment differences with soil management between locations. The intention of this was to visualize the differences between locations as well determine if I feel comfortable pooling things within a location (not testing for a site-year or year effect). This has been the desired direction to simplify results for publication. When I didn't feel the data allowed for this I tested for differences between site-years in a condensed model. This approach is up for more discussion, as it eliminates the potential to view anomalies in the data which might be insightful and scientifically interesting. We are assuming editors won't like complex findings.

I would also like to point out that for every linear-mixed-effects model I am testing to see that the model meets the visual assumptions for normal distribution of residual and evenly distributed variance. I will demonstrate for the first model, and only include it in the output for future analyses when it is suspected that transformations need to be made.

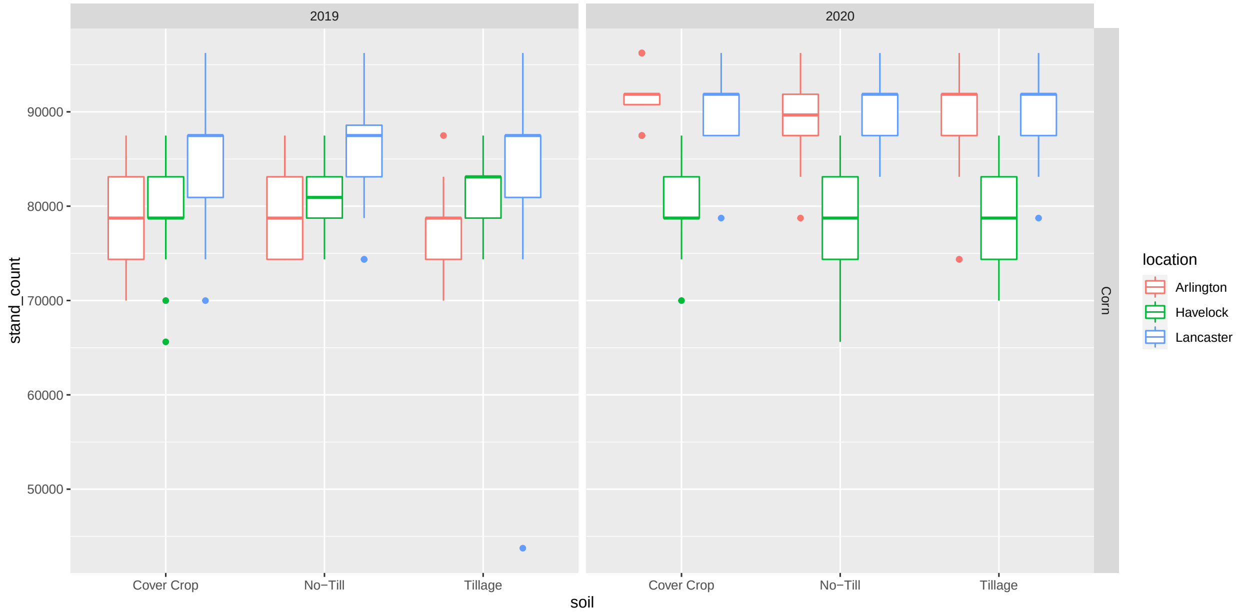
More analyses were made than are going to be included in this pdf. I chose not to include them all so as to condense the output to the approach and considerations that I think are most valuable for the publication.

### Removing the Arlington 2020 Site-year

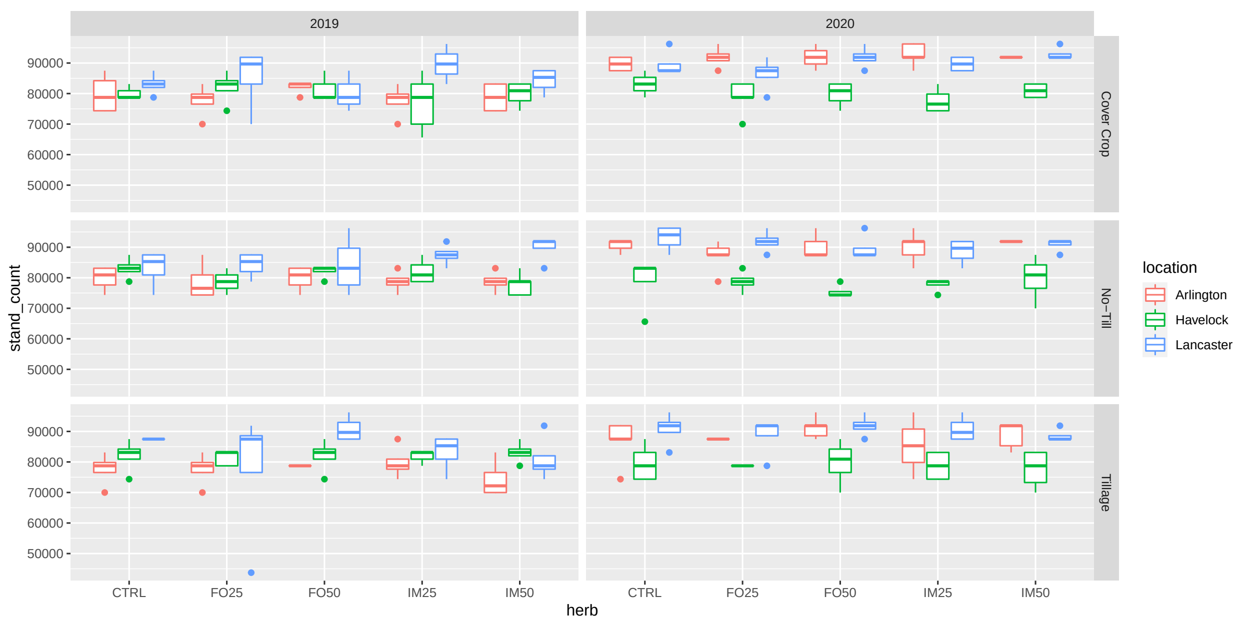
After some consideration and evaluating some analyses we decided to remove the Arlington 2020 site-year for corn from all analyses. There was an establishment issue with this site-year (Kolby used the wrong map to lay out herbicide treatments) and a suspected fertility misapplication that reduced yield for part of the trial.

## Early Season Stand Counts

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



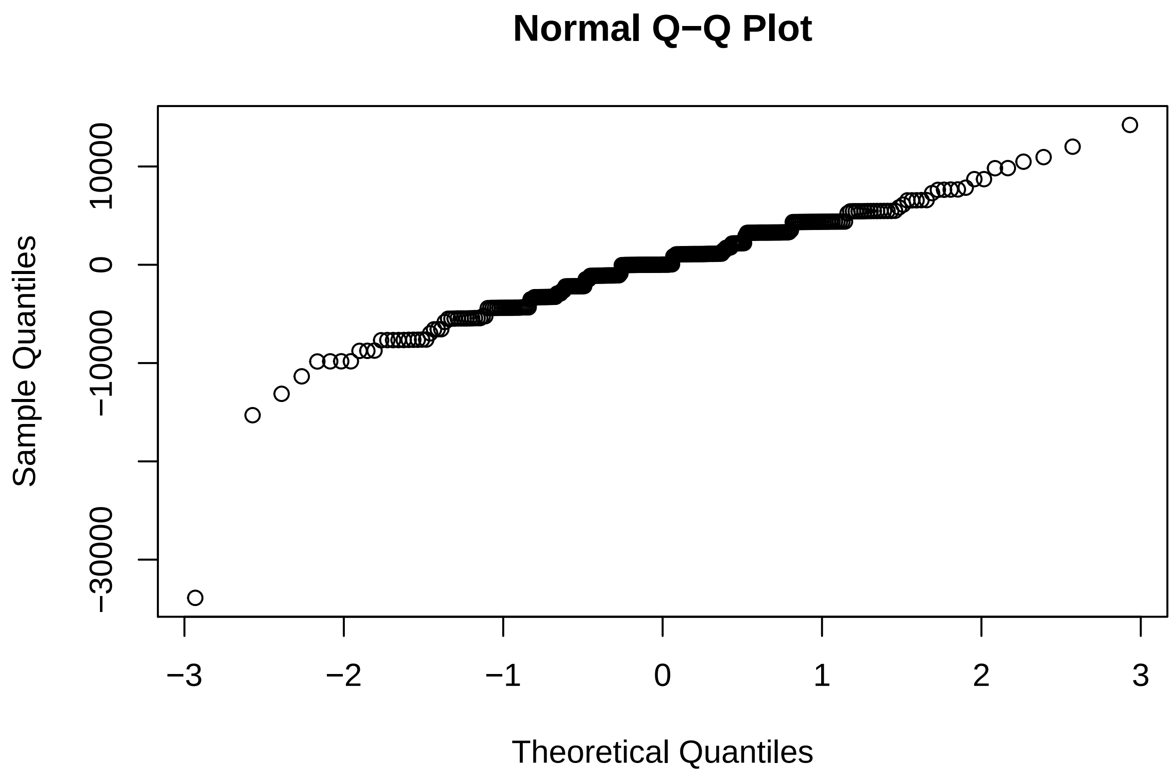

```r
Corn1 %>%
  ggplot(aes(x = herb, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(soil ~ year)
```



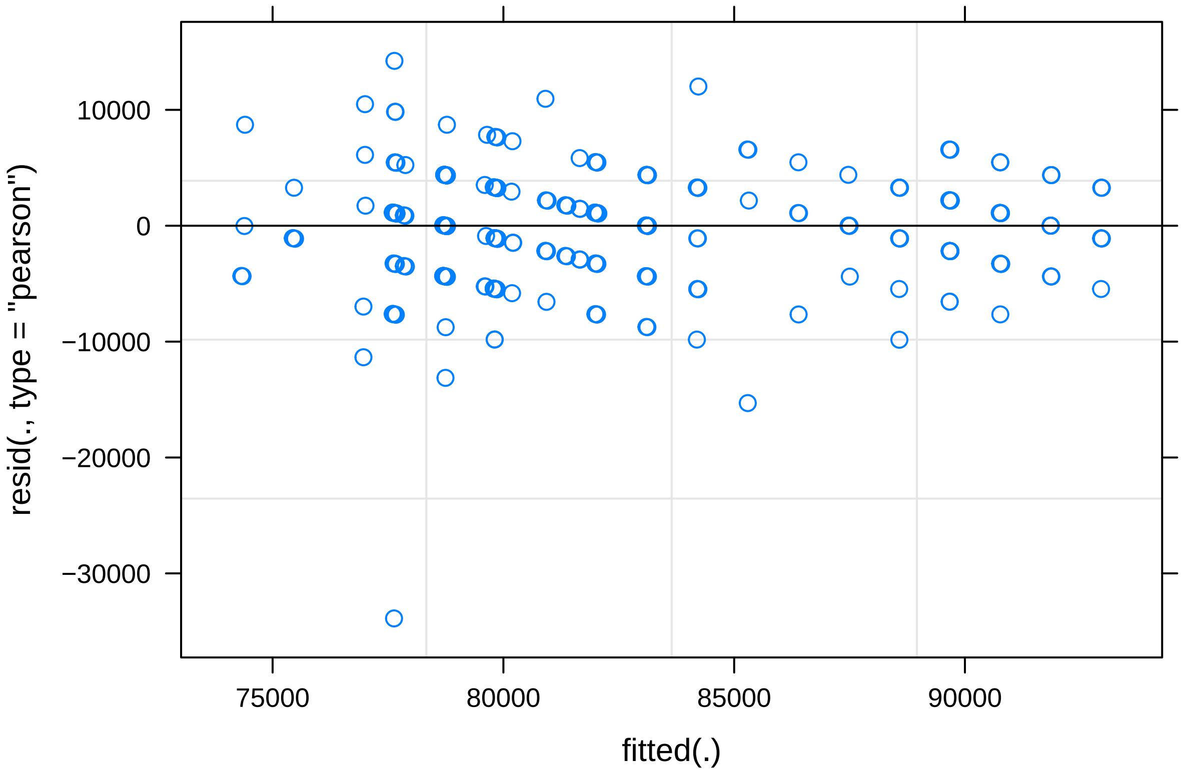

Based on these visual representations it doesn't appear to me that there are really any consistent patterns as a function of soil management, herbicide treatment, location, or year. There does appear to be differences in location across seasons. Therefore, I think it is best if we test for site-year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

### Condensed Stand Count Model

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

qqnorm(resid(cn_stand))
```




```
plot(cn_stand)
```

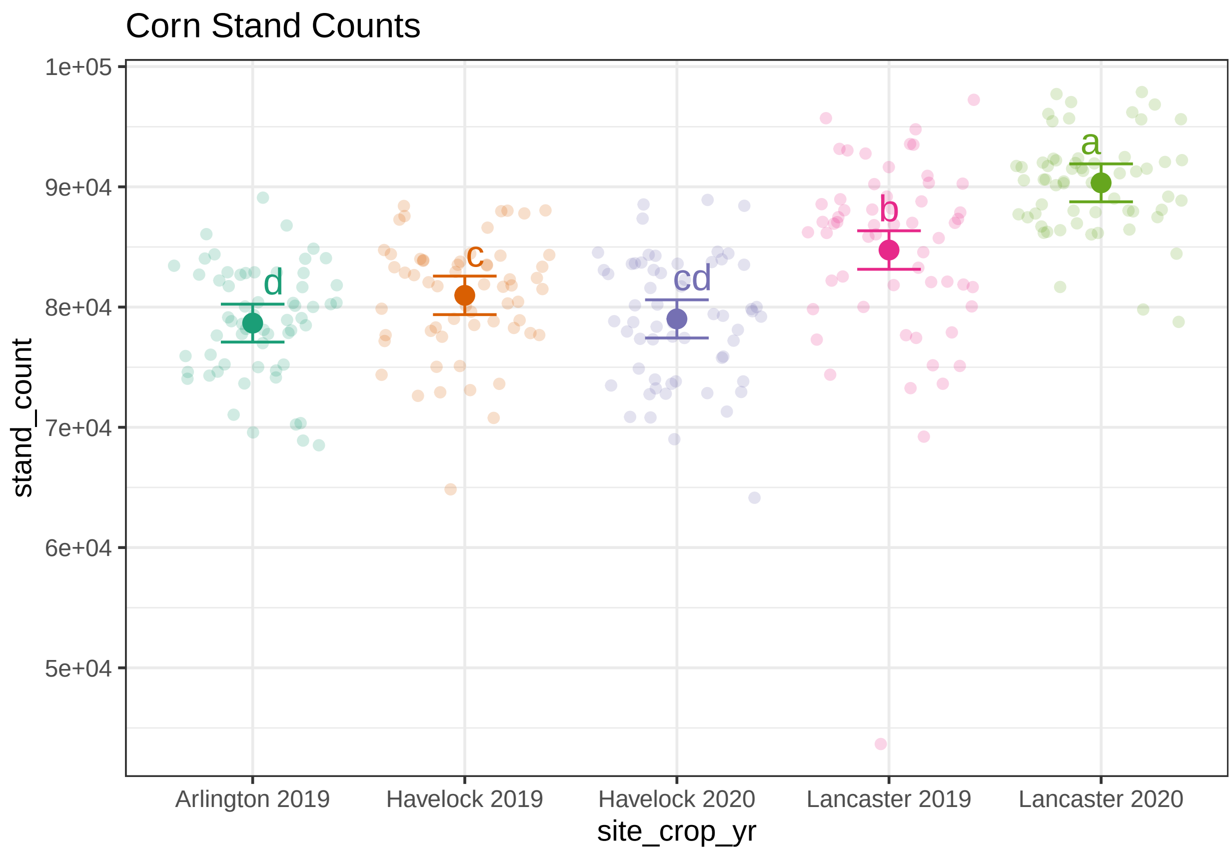



```r
#assumptions met satisfactorily

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
```

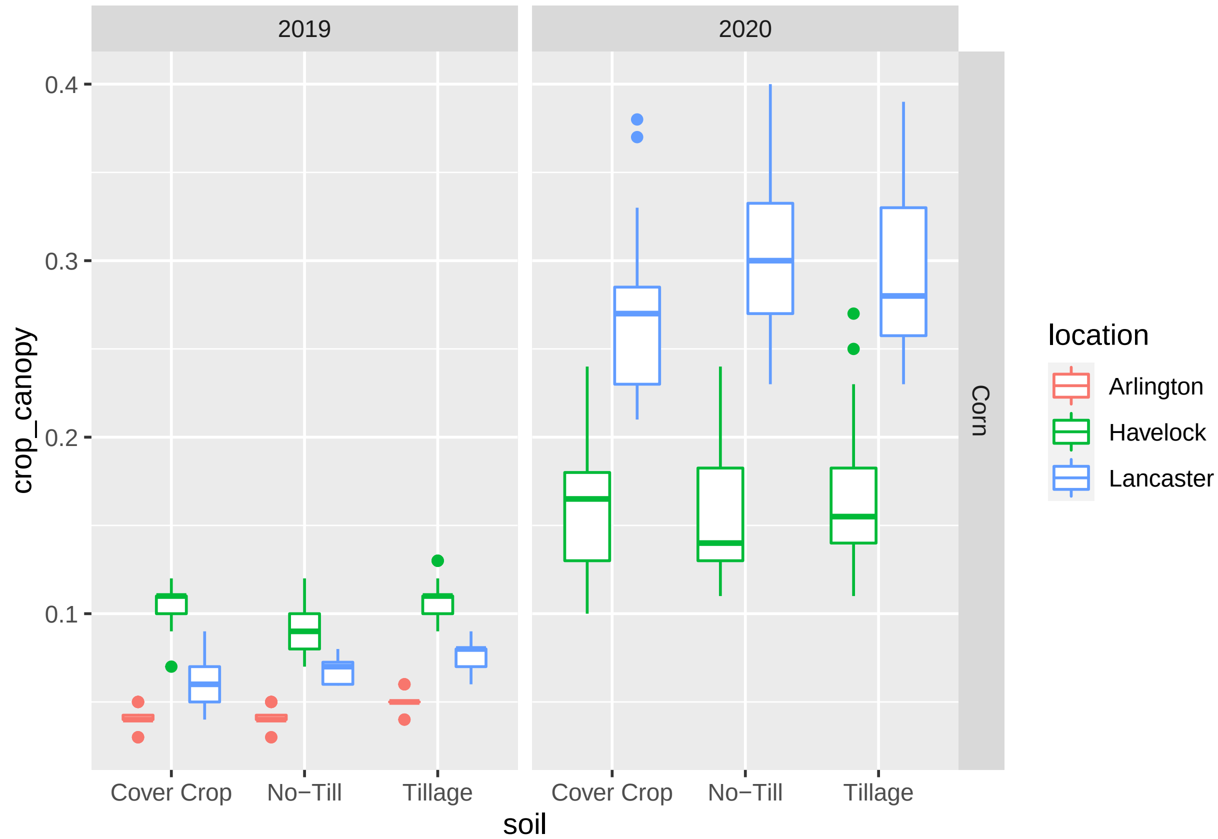
Herbicide carryover and soil management had no effect on early season stand counts in corn.




Wisconsin Stand counts should be closer to 80,000 and Havelock should be closer to 79,000

## Corn Canopy

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




Based on the variability in canopy coverage between cropping seasons within a location, I created a condensed model, similar to the stand count model, with site-year as a fixed effect.

I also decided to perform the analysis using a separate model for each site-year. The first model and figures resulting from this analysis will also be displayed.

### Condensed analysis

```
cn_canopy = glmmTMB(crop_canopy~ soil*herb*site_crop_yr + (1|rep:site_crop_yr), data= Corn1, beta_famil
#no assumptions to meet.

Anova(cn_canopy)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##                            Chisq Df Pr(>Chisq)
## soil                     17.1467  2  0.0001891 ***
## herb                     11.6068  4  0.0205277 *
## site_crop_yr           1502.0143  4  < 2.2e-16 ***
## soil:herb                 6.5237  8  0.5887809
## soil:site_crop_yr        29.6688  8  0.0002418 ***
## herb:site_crop_yr        19.5036 16  0.2434150
## soil:herb:site_crop_yr   24.0172 32  0.8437917
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#all 3 main fixed effects significant and the soil:site-year interaction
```

### Separated analysis for each site-year

Just showing the first one and then hiding later ones.

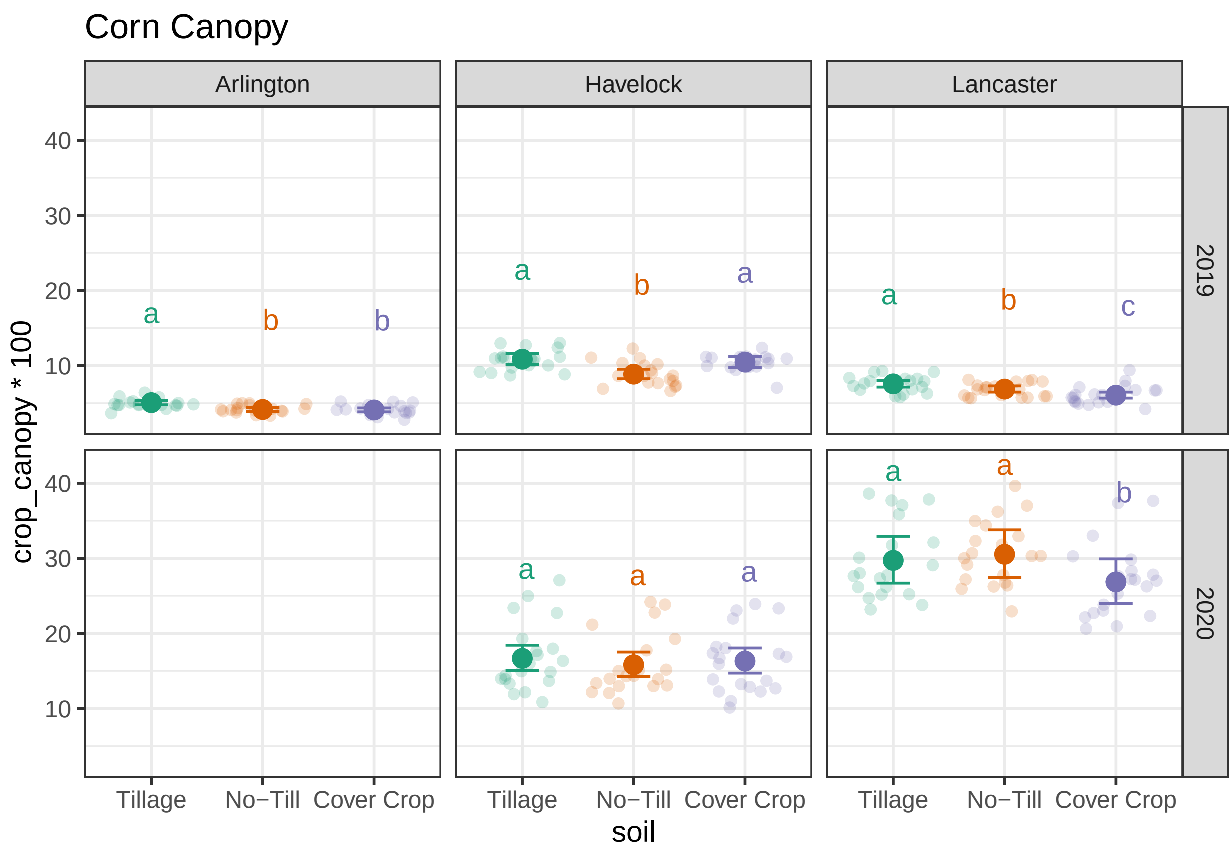
```
#begining of analysis with new model for each site-year
arl19_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_y

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
```

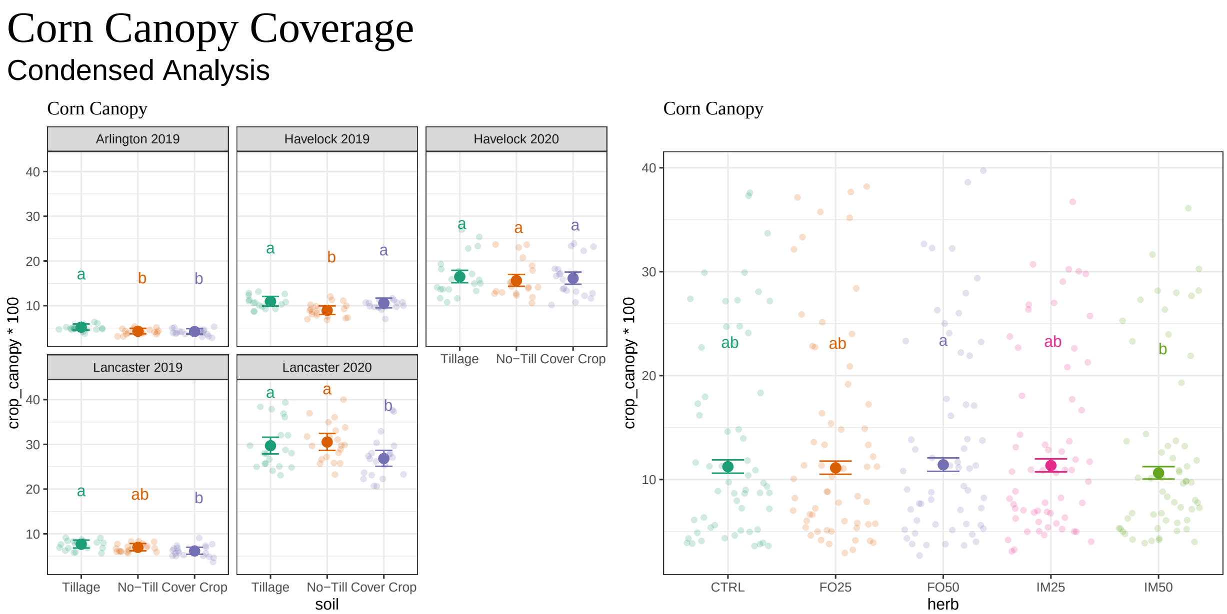
```
#Soil was significant
```

## Comparison of canopy coverage analysis approaches

### Separated



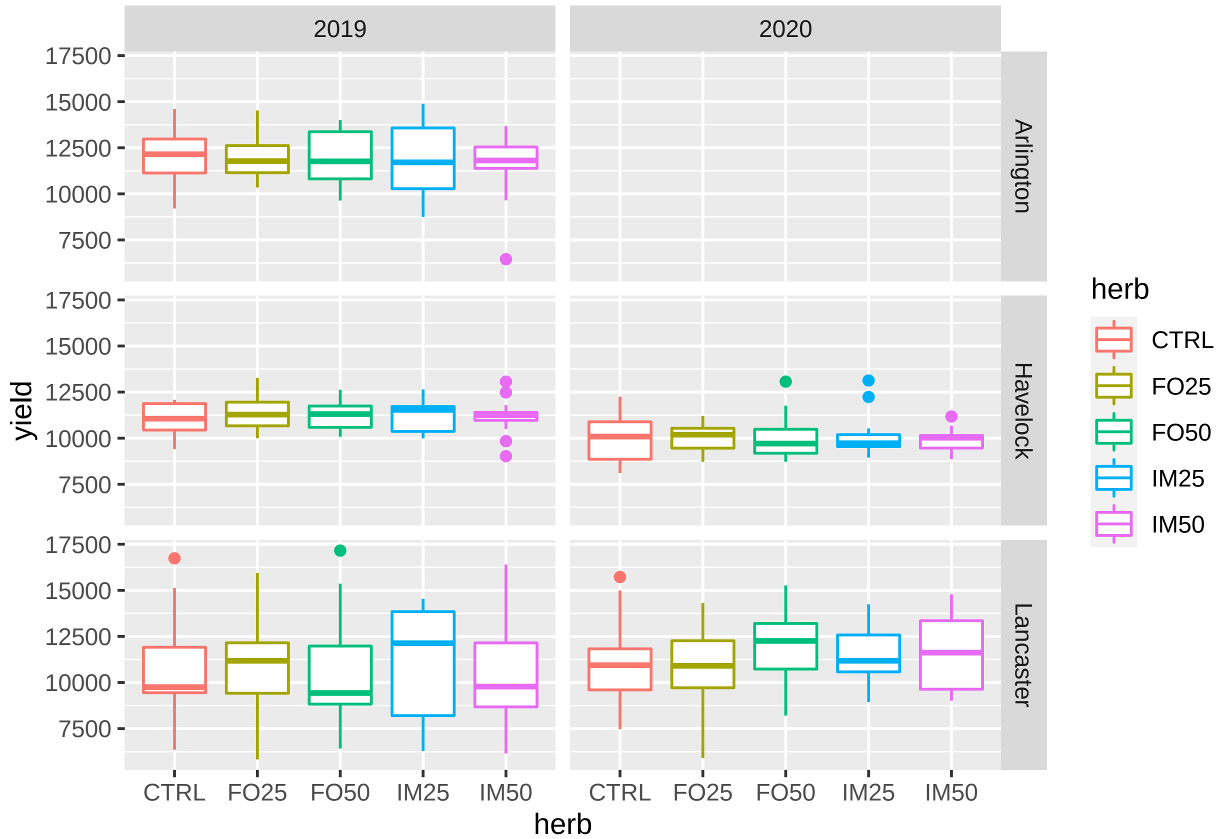
**Condensed**



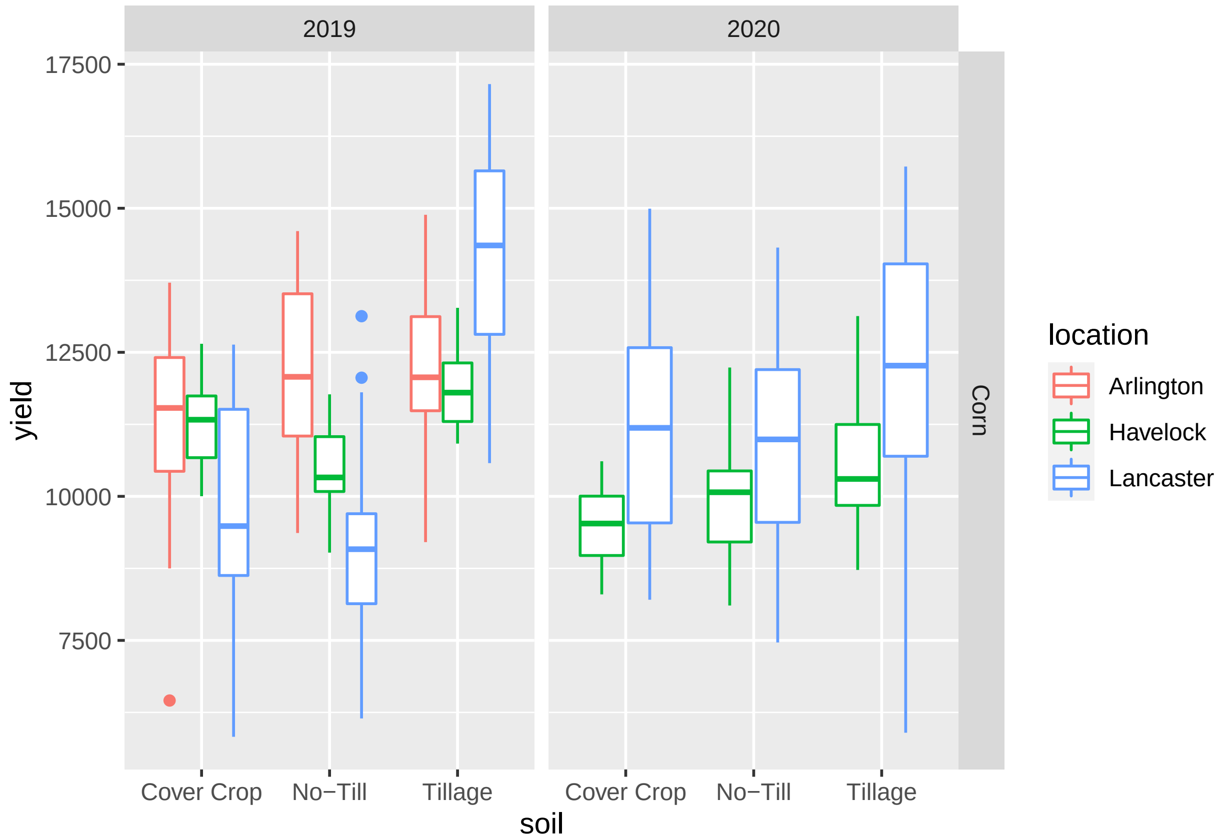

There were slight differences in the Lancaster 2019 site-year results between analysis approaches. The separated approach didn't show that herbicide treatment had a significant effect on canopy coverage but in the composite approach there was reduced coverage for the imazethapyr half-rate treatment, although not significantly different from the control treatment. I prefer the results from the composite approach, similar to my selection in soybean.

# Corn Yield

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




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




Doesn't appear as if herbicides are likely having any effect on corn yield. It does appear that there are similar trends and yield within a location across years. I will proceed with performing a separate analysis for each location.

**Arlington 2019 Analysis**

Only going to show the first model. Repeated for each location.

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

qqnorm(resid(arlcn_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
```

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

### Lancaster Analysis

```r
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
```

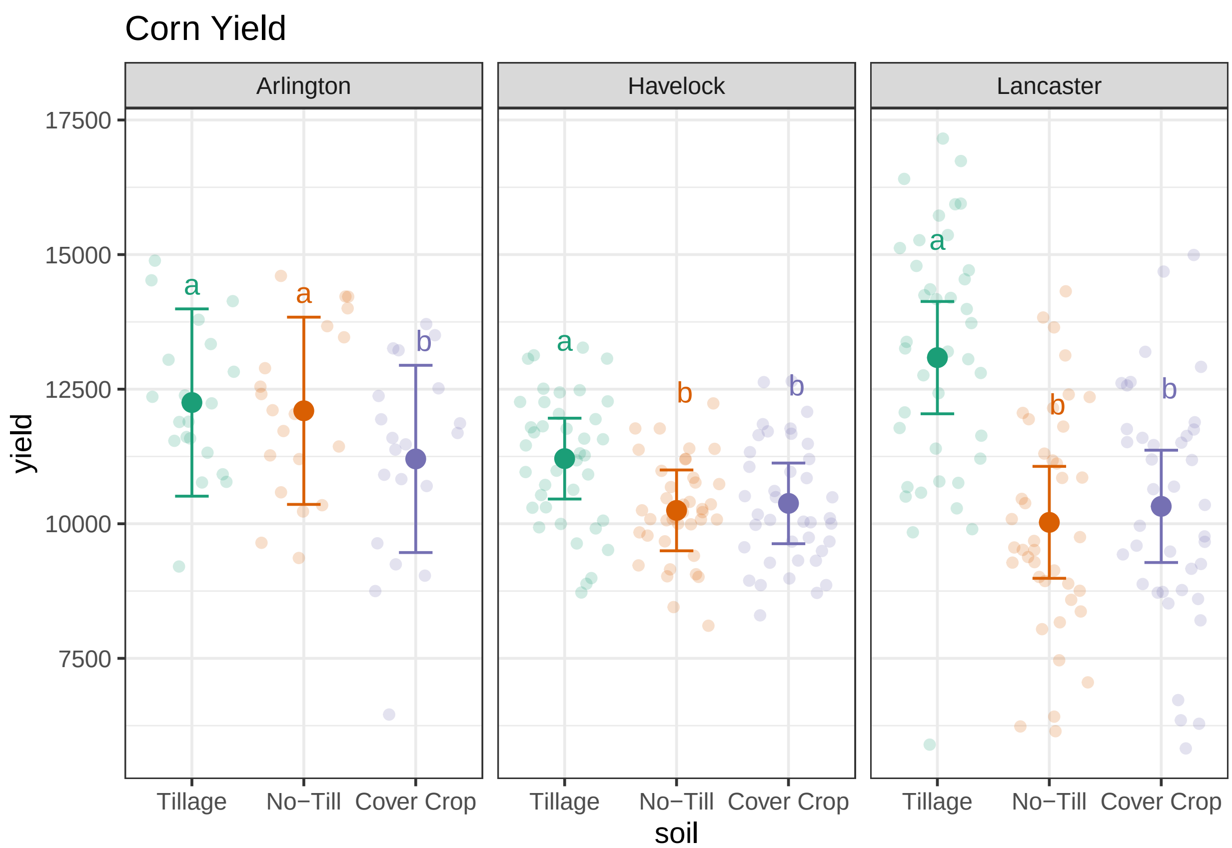
```r
#Soil management fixed effect significant
```

### Havelock Analysis

```r
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
```

```r
#soil management significant
```

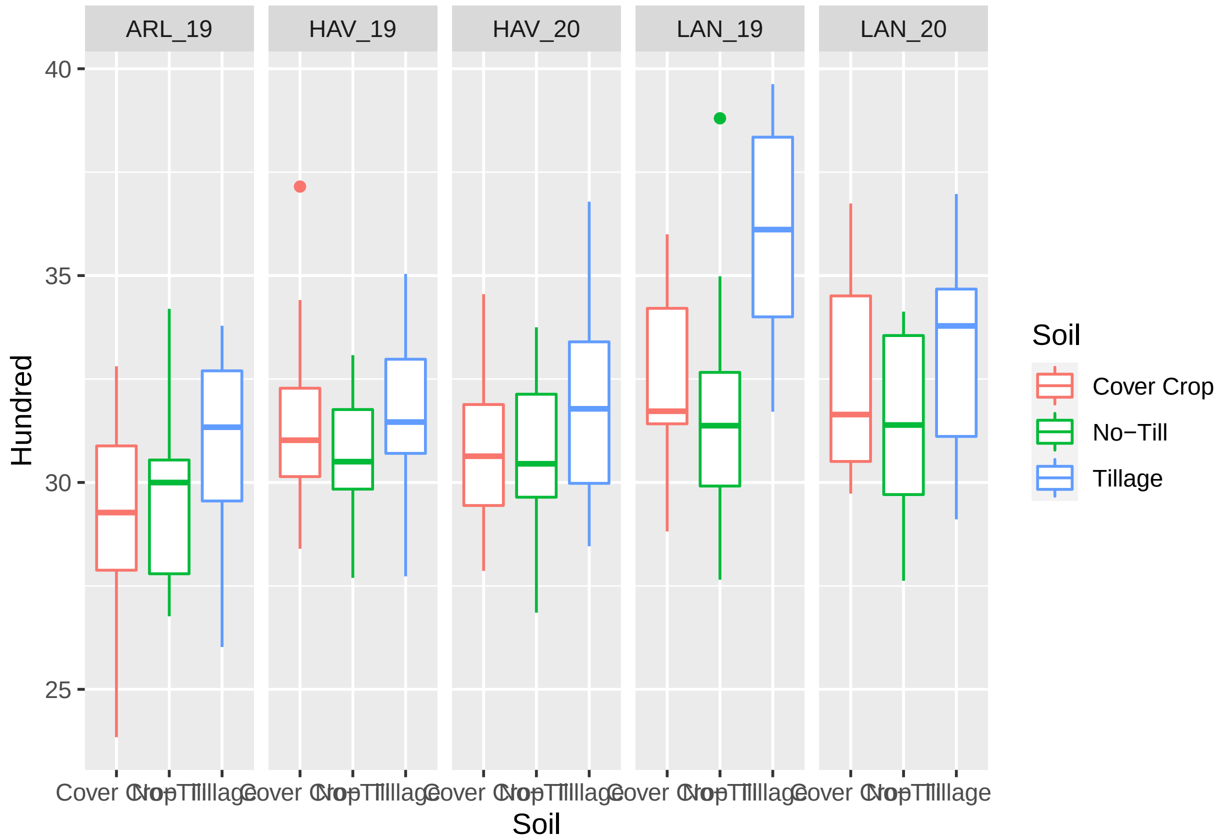



No impact on crop yield from herbicides. All three location had reduced yield for the CC treatment. Havelock and Lancaster showed reduced yield for the no-till treatment as well.

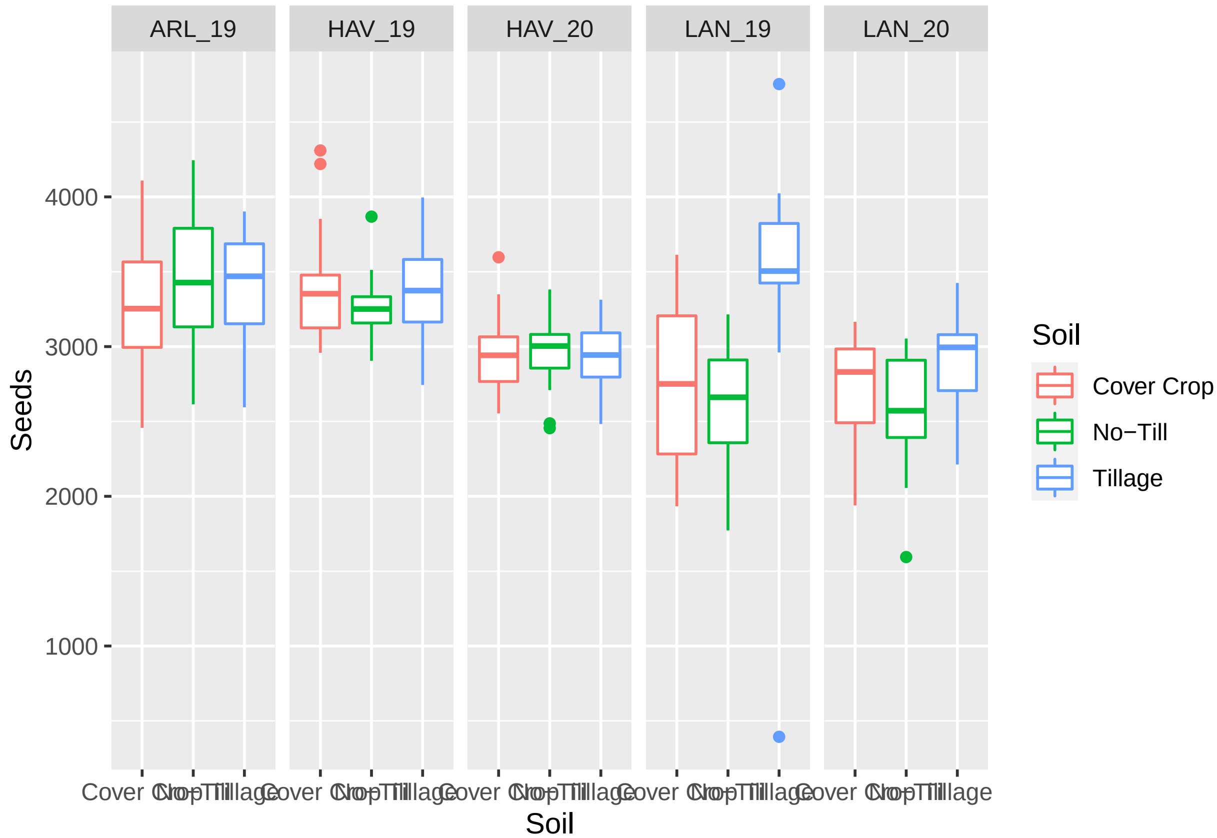
Now to see if the yield components explain more.

## Corn Yield Components

```
#CornComp %>%
  #ggplot(aes(x = Soil, y = Total, color = Soil)) +
  #geom_boxplot() +
  #facet_grid(~ Site_Yr)

#Plot of seed density
CornComp %>%
  ggplot(aes(x = Soil, y = Hundred, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```




```
#Plot of seed counts
CornComp %>%
  ggplot(aes(x = Soil, y = Seeds, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```




Based on these figures I think it would be appropriate to conduct analyses for each location separately similar to how yield was done.

**All yield component Figures will be included at the end of this section.**

## Corn Seed Density

### Arlington

Only chose to show the first model

```
arl_CNHun= lmer(Hundred~ Soil*Herb + (1|Rep) , data= (filter(CornComp, Location == "Arlington" )))
qqnorm(resid(arl_CNHun))
```

```
plot(arl_CNHun)
```

```
#Assumptions met
```

```
anova(arl_CNHun)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## Soil      31.525 15.7626     2 40.075  3.9809 0.02649 *
## Herb       2.254  0.5635     4 40.087  0.1423 0.96535
```

```
## Soil:Herb 28.057  3.5071     8 40.099  0.8857 0.53695
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Soil Significant
```

### Lancaster

```r
anova(lan_CNHun)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)    
## Soil      202.001 101.001     2 97.070 17.9829 2.272e-07 ***
## Herb        7.163   1.791     4 97.070  0.3188    0.8648    
## Soil:Herb  20.186   2.523     8 97.068  0.4493    0.8883    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Soil significant
```

### Havelock

```r
anova(hav_CNHun)
```

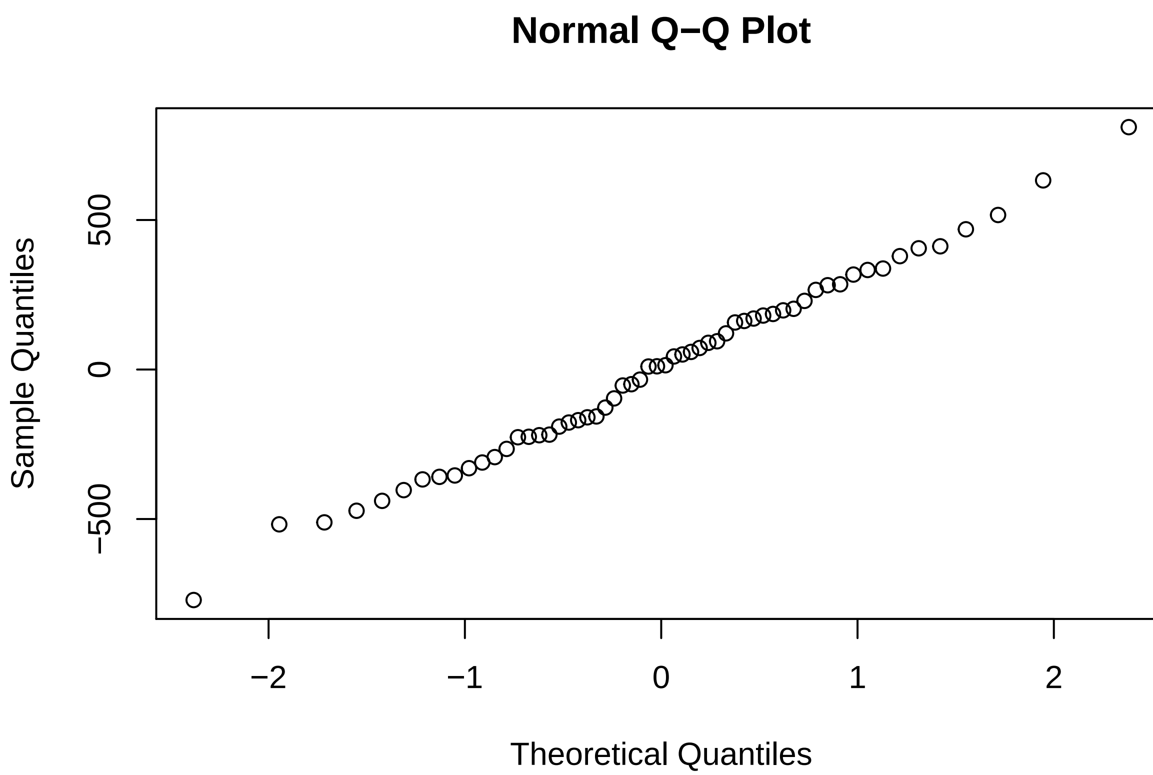
```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)  
## Soil      26.356 13.1780     2   105  3.6167 0.03027 *
## Herb      25.971  6.4928     4   105  1.7820 0.13795  
## Soil:Herb 43.752  5.4690     8   105  1.5009 0.16565  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Soil significant
```

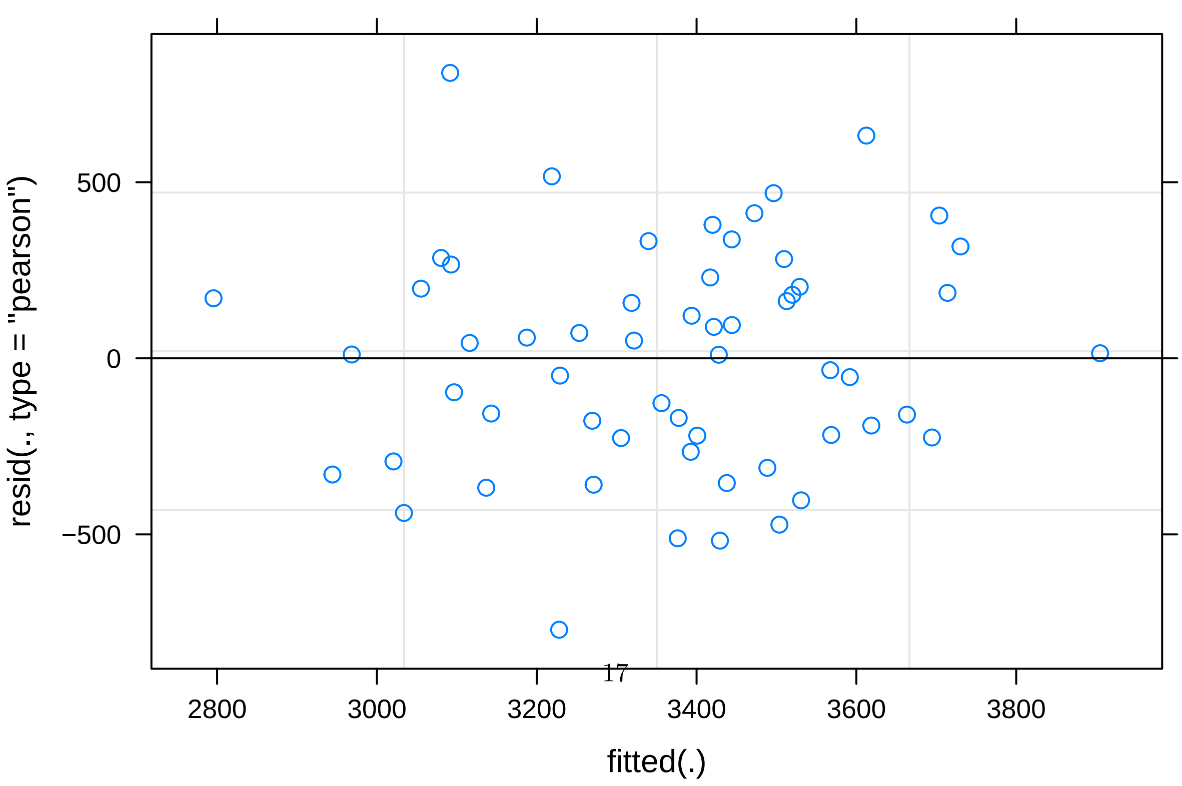
## Corn Seed Count

## Analysis by Location

### Arlington




Showing first model only



```r
anova(arl_Seeds)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Soil      159990   79995     2 40.071  0.5652 0.5727
## Herb      129497   32374     4 40.082  0.2287 0.9207
## Soil:Herb 852129  106516     8 40.092  0.7526 0.6454
```

```r
#Nothing Significant
```

### Lancaster

```r
anova(lan_Seeds)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Soil      7863046 3931523     2 97.145 14.3403 3.491e-06 ***
## Herb       325624   81406     4 97.144  0.2969    0.8793
## Soil:Herb  994778  124347     8 97.140  0.4536    0.8855
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Soil significant
```

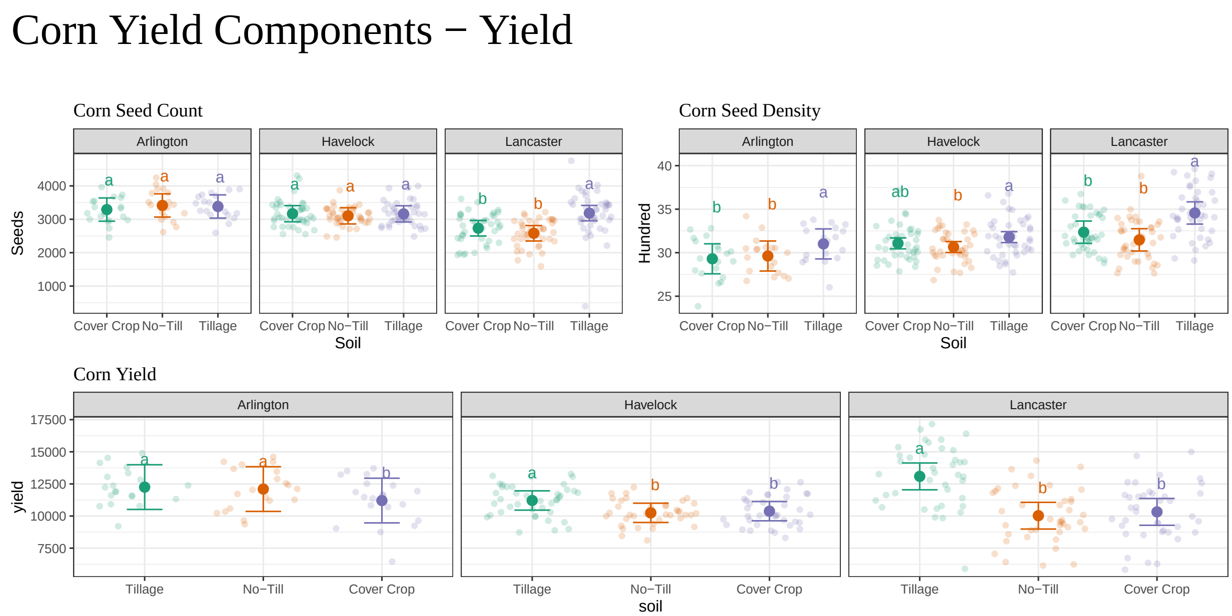
### Havelock

```r
anova(hav_Seeds)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Soil      100933   50467     2 98.005  0.6196 0.5403
## Herb      137558   34390     4 98.034  0.4222 0.7923
## Soil:Herb 252556   31569     8 98.360  0.3876 0.9249
```

```r
#Nothing significant
```

## Corn Yield Components to Yield comparison




### Arlington

When final grain yield was lowest for the cover crop soil management treatment, there was reduced seed density (also reduced density for the no-till treatment).

### Havelock

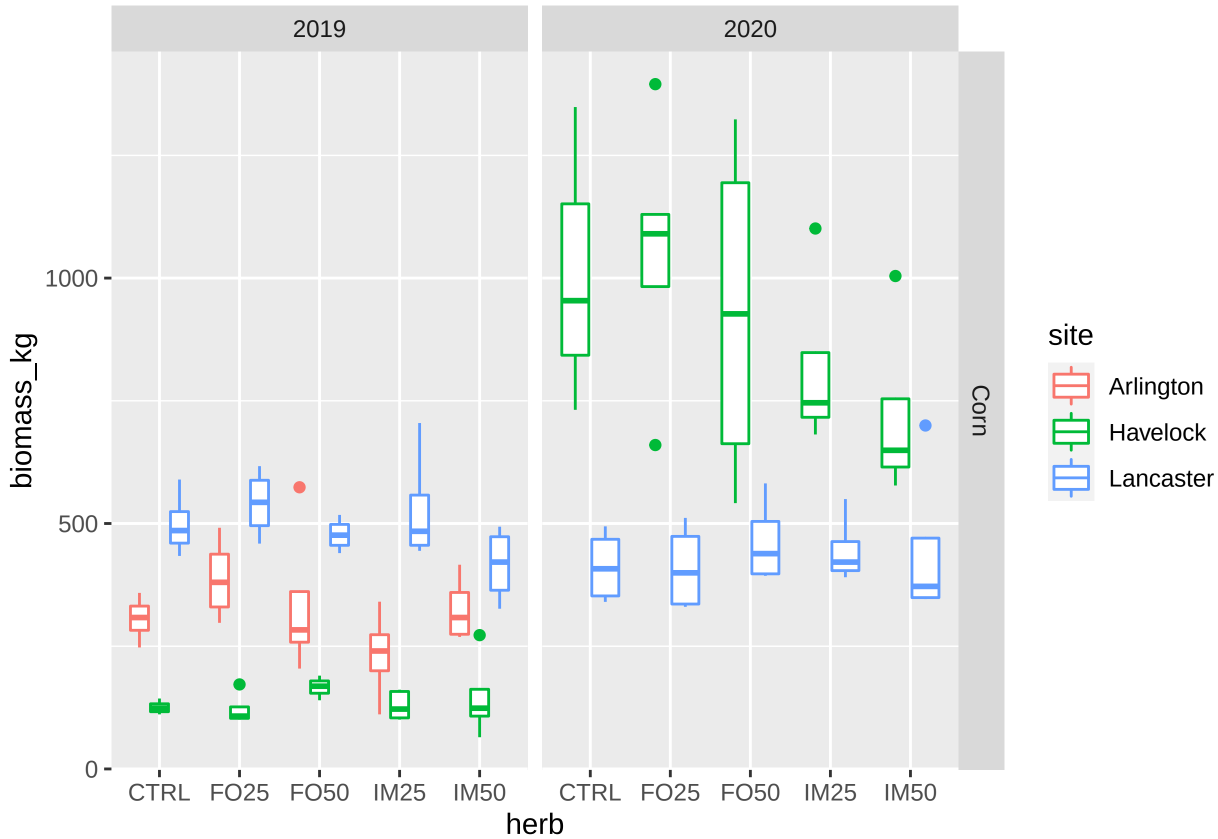
For the reduced final grain yield for the no-till and cover crop treatments, there was significantly lower seed density for the no-till treatment and (not significantly reduced) mean grain density for the cover crop treatment

### Lancaster

For the reduced final grain yield for the no-till and cover crop treatments, there was significantly lower seed density for the no-till and cover crop treatments as well as significantly lower seed counts.

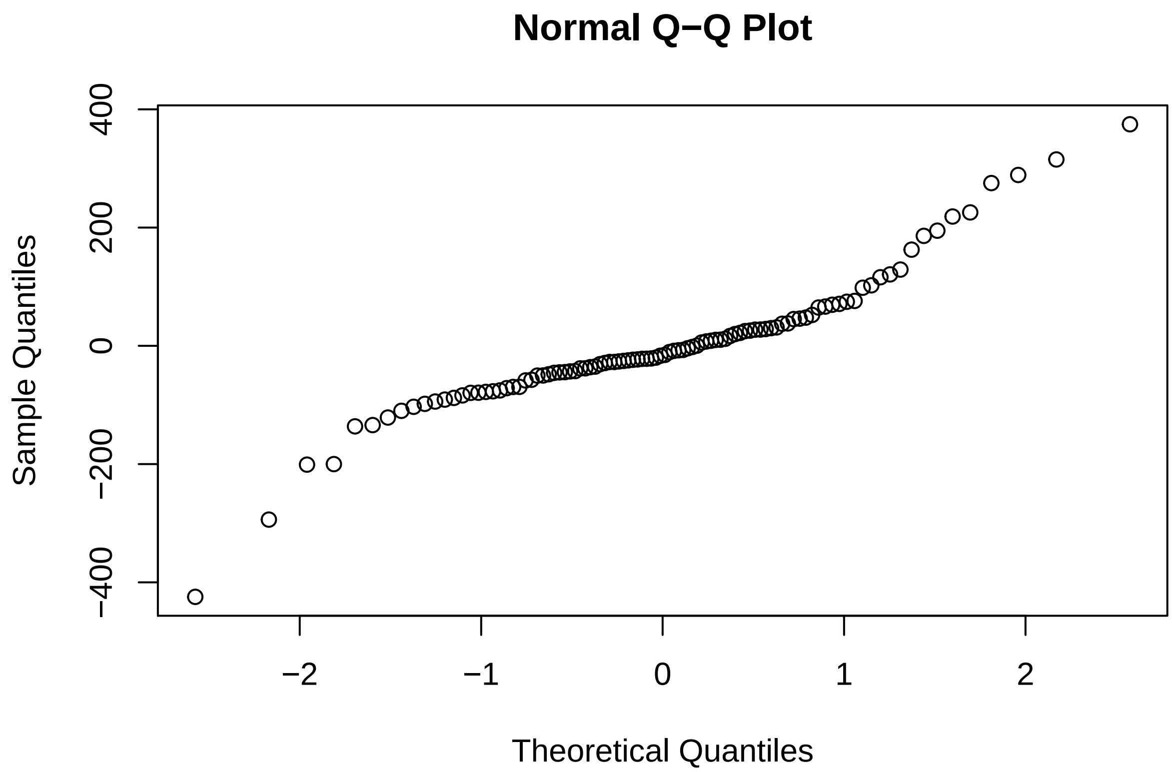
## Cover Crop Biomass analysis

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

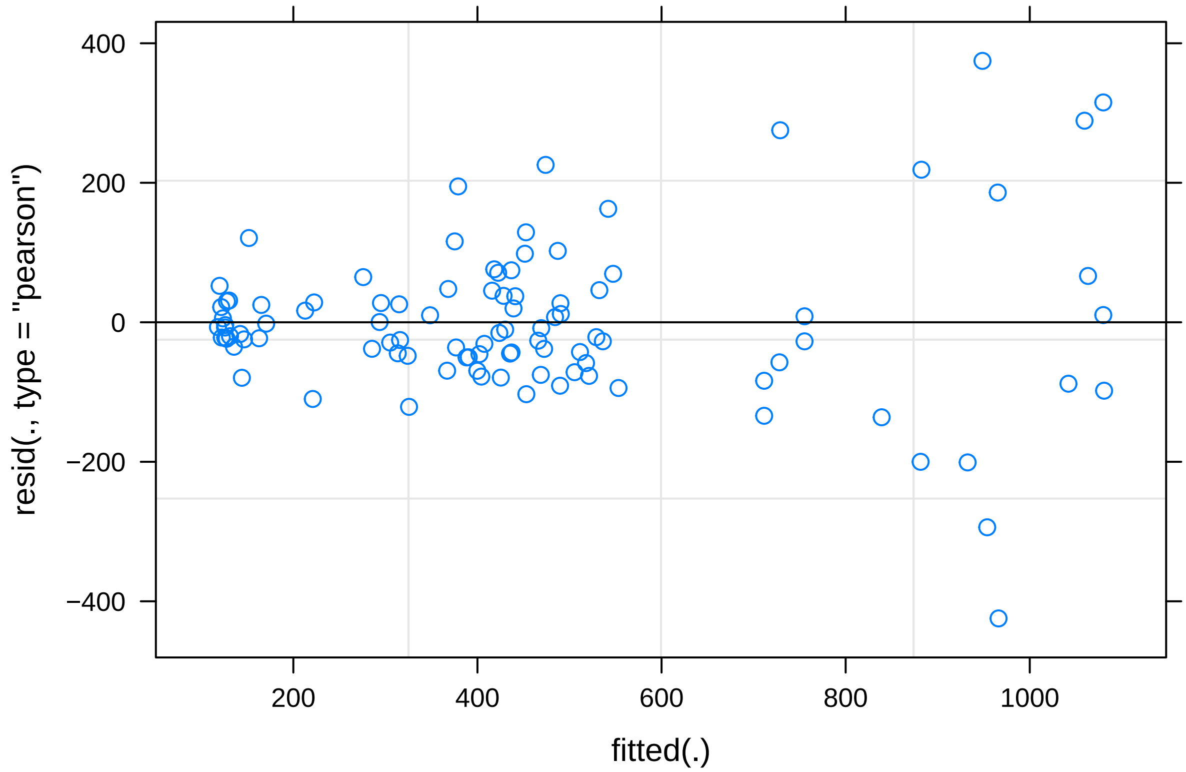



based on separations between locations and across years, I think it is appropriate to look for significant differences between site-years and separate means accordingly in CC biomass models.

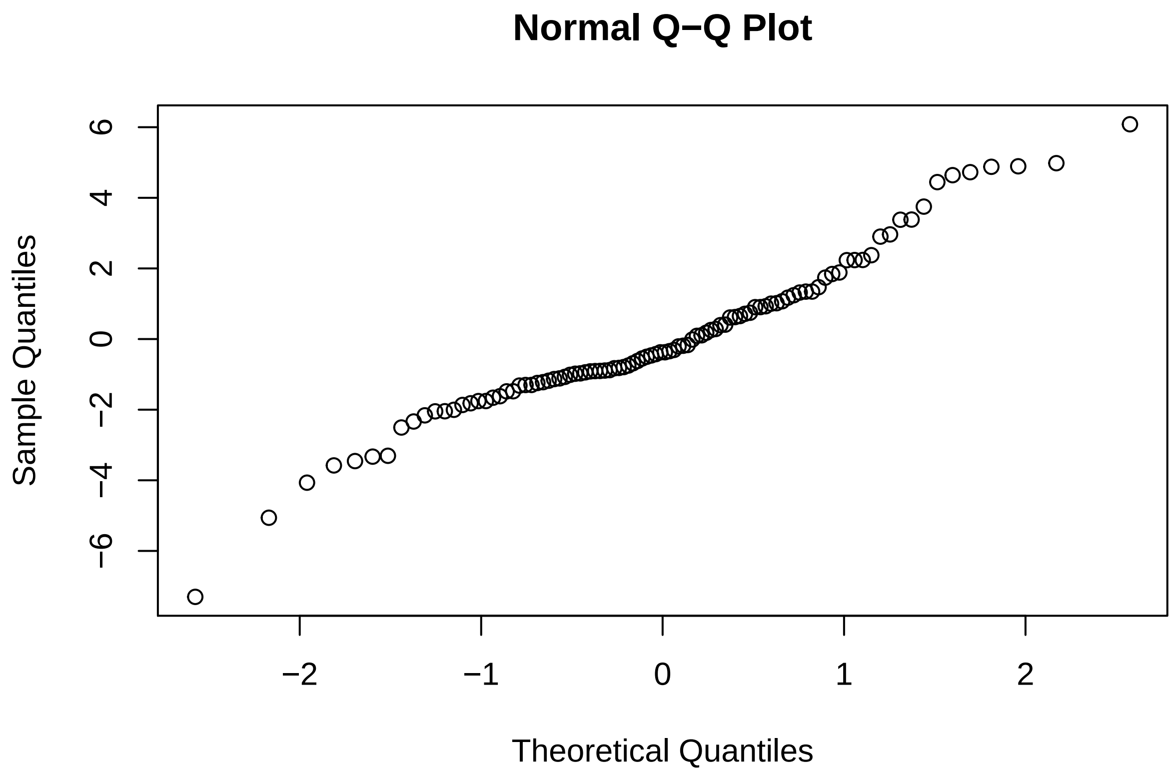
```
cn_cc_bio= lmer(biomass_kg~ site_crop_yr * herb + (1|site_crop_yr:rep), data=CornCC)

qqnorm(resid(cn_cc_bio))
```



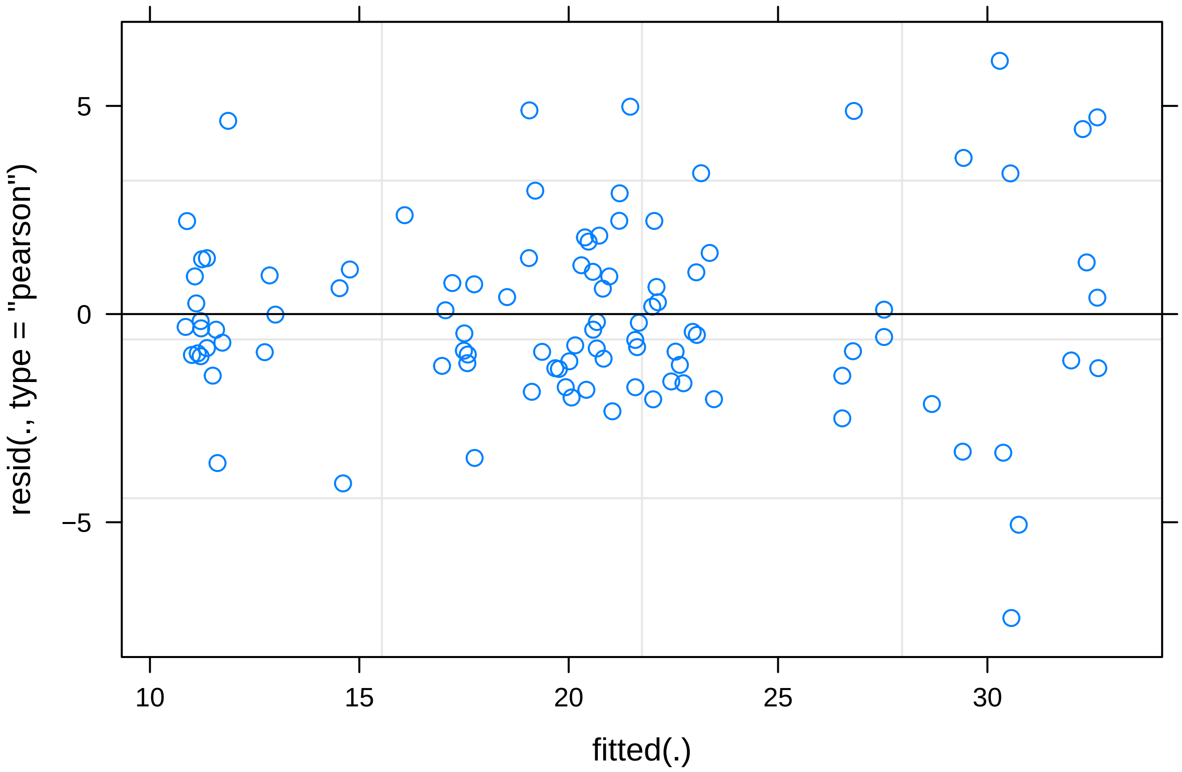

```r
plot(cn_cc_bio)
```




```r
#Assumption for equal variance not met

#Proceeded with a square-root transformation
cn_cc_bio1= lmer(sqrt(biomass_kg)~ site_crop_yr * herb + (1|site_crop_yr:rep), data=CornCC)

qqnorm(resid(cn_cc_bio1))
```




```r
plot(cn_cc_bio1)
```




```r
#assumptions improved. Use this one!

anova(cn_cc_bio1)
```

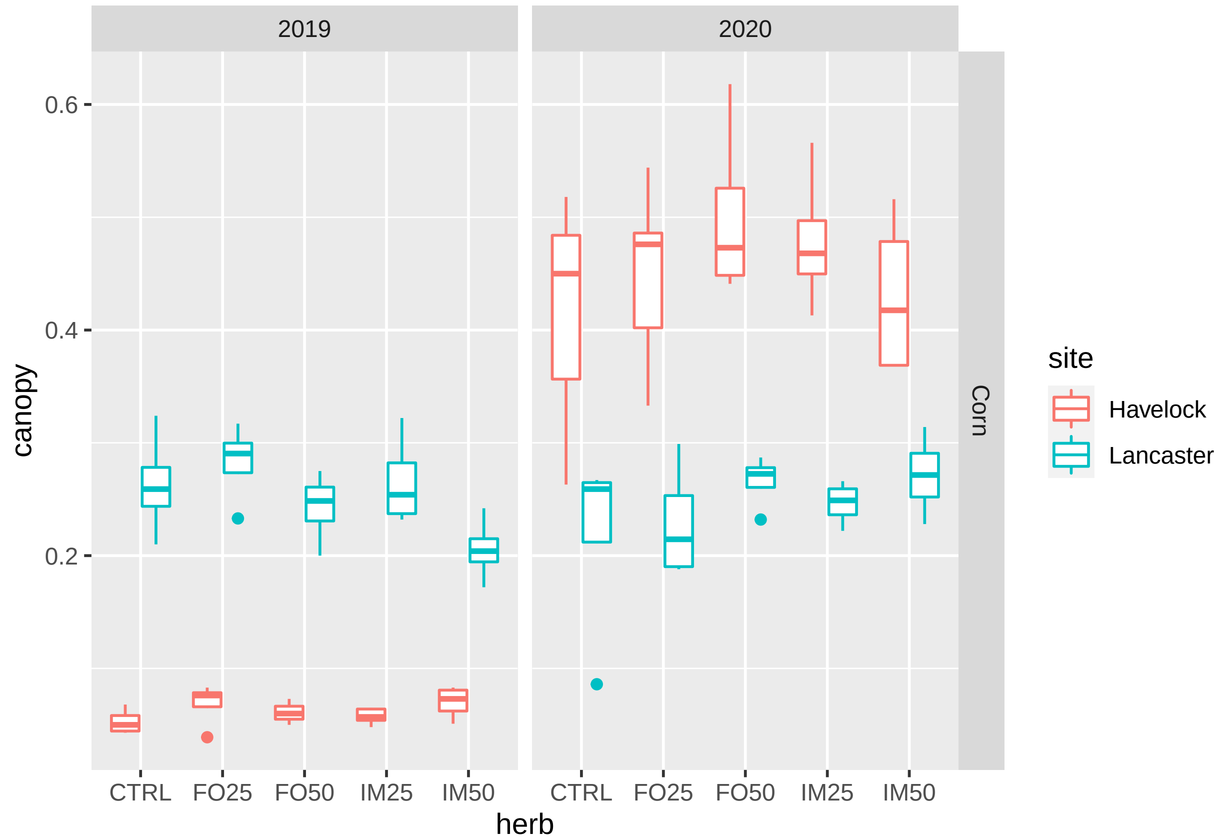
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## site_crop_yr      2155.06  538.77     4 13.964 75.2804 2.725e-09 ***
## herb                42.79   10.70     4 60.805  1.4949    0.2149
## site_crop_yr:herb 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

```r
#Site-year significant
```

There is no evidence that herbicide treatment influenced cover crop biomass.

## Cover Crop Canopy

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

Anova(cn_cc_can)
```

```
## 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
```

There is no evidence that herbicide treatment influenced cover crop biomass.