Carryover_CornResults

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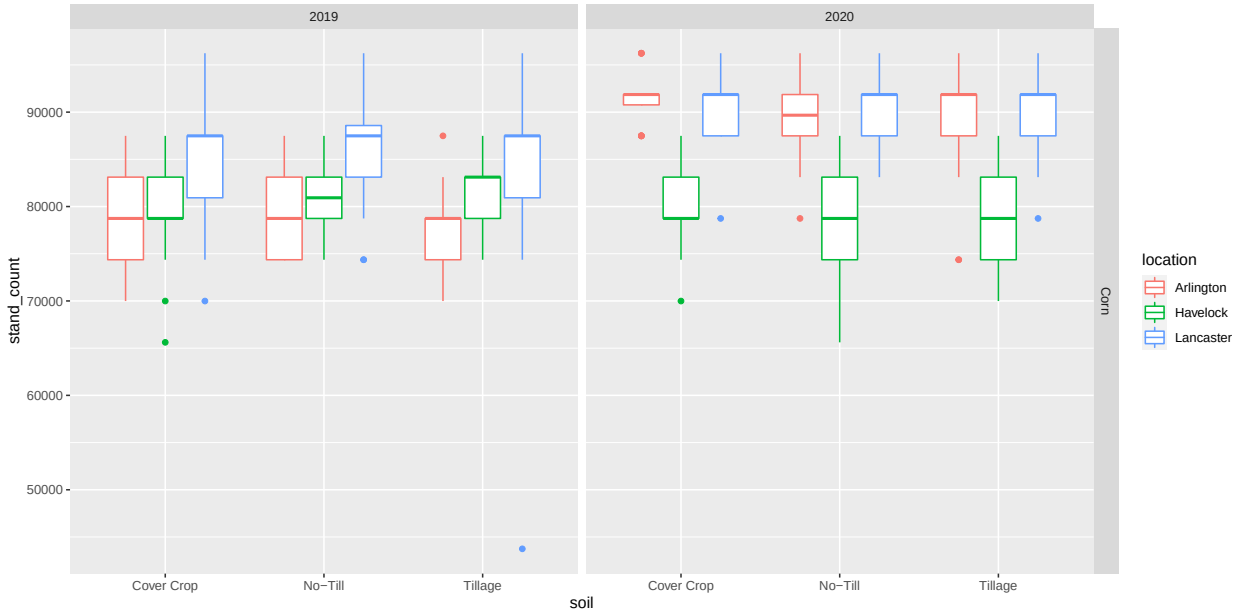
3/4/2021

Stand Counts

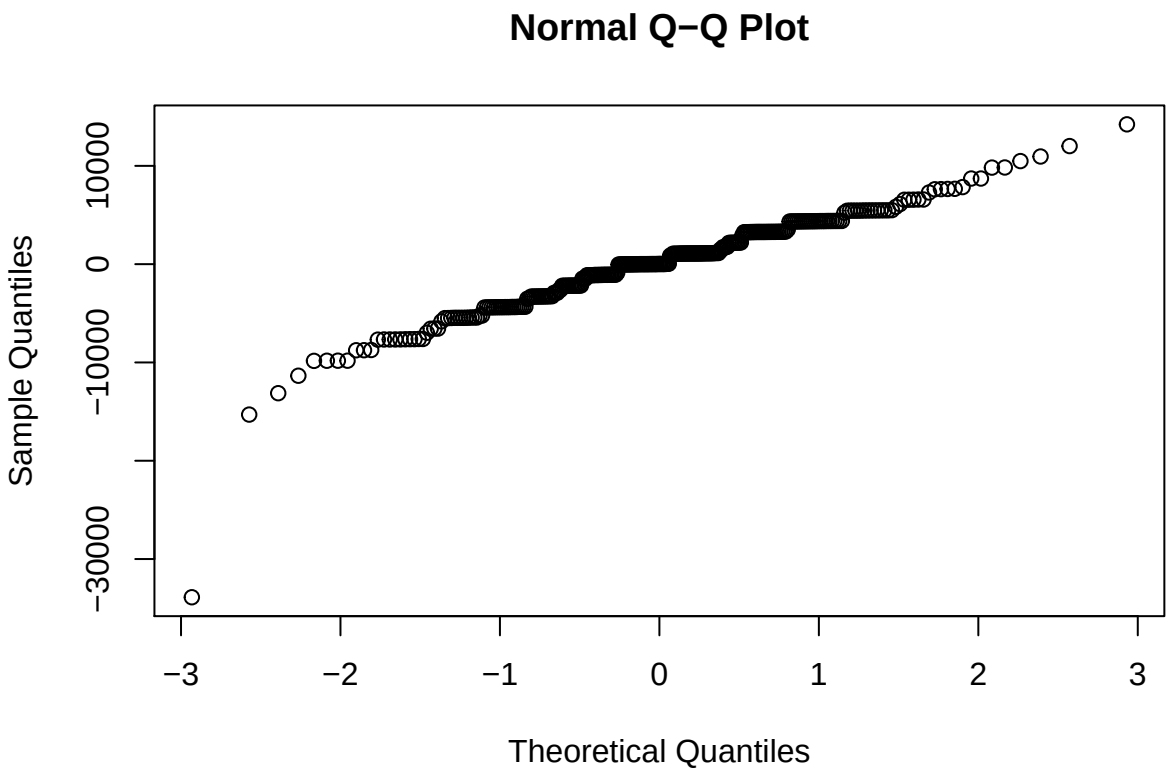
```
Corn1 %>%
  ggplot(aes(x = soil, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



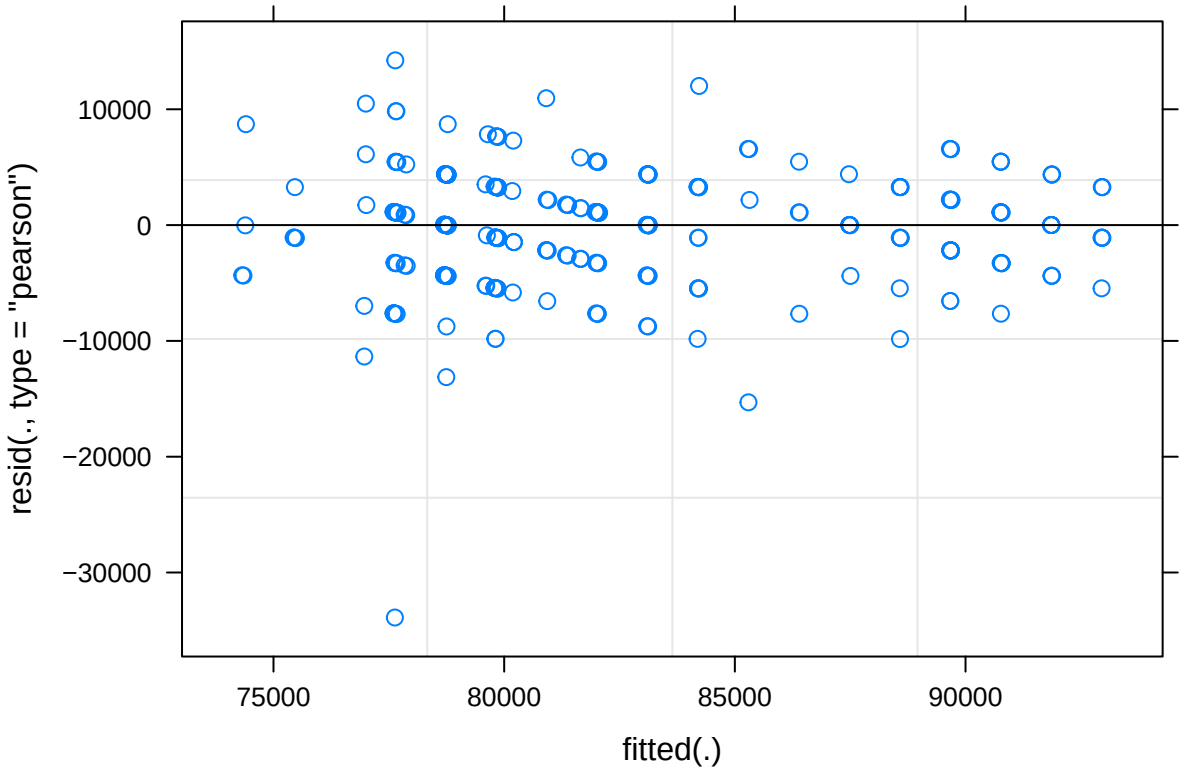

```
Corn1 %>%
  ggplot(aes(x = herb, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(soil ~ year)
```

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.

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

qqnorm(resid(cn_stand))
```




```
plot(cn_stand)
```

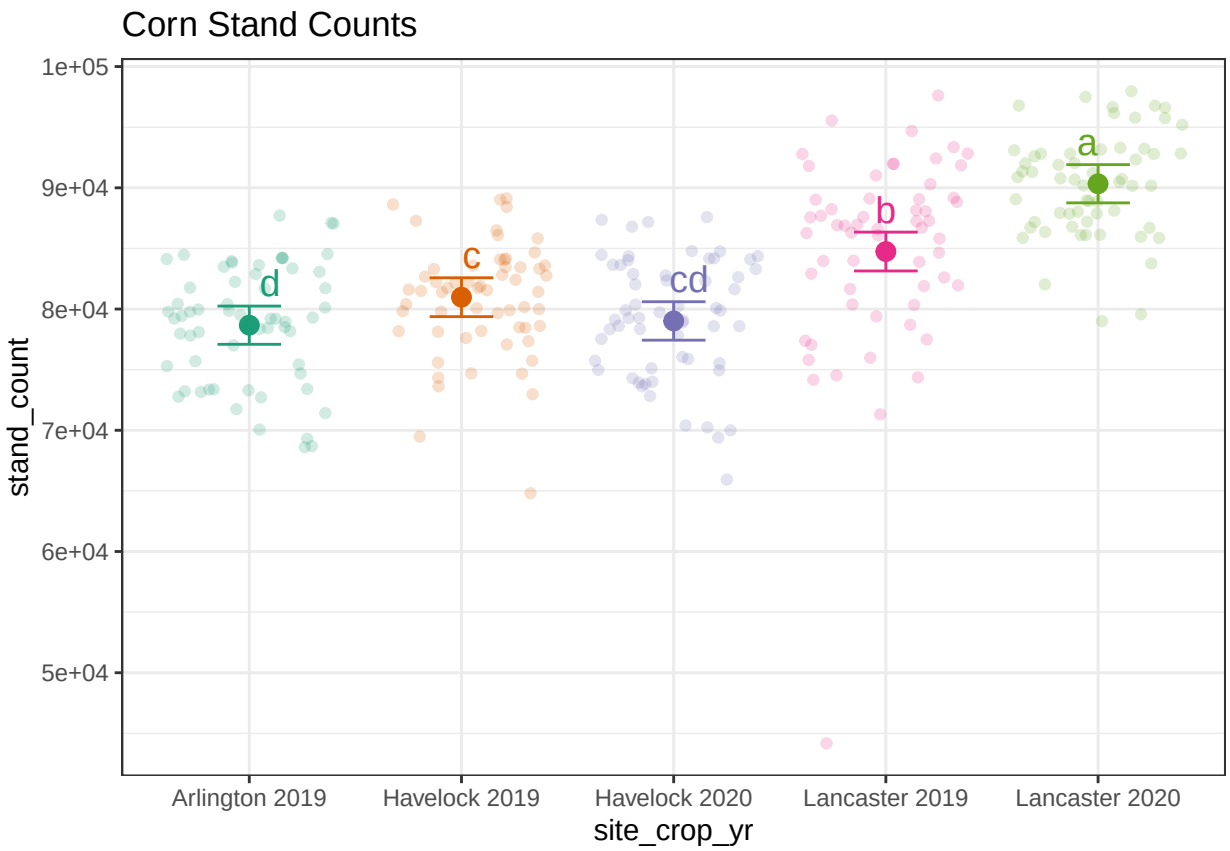



```
#assumptions met satisfactorily

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
```

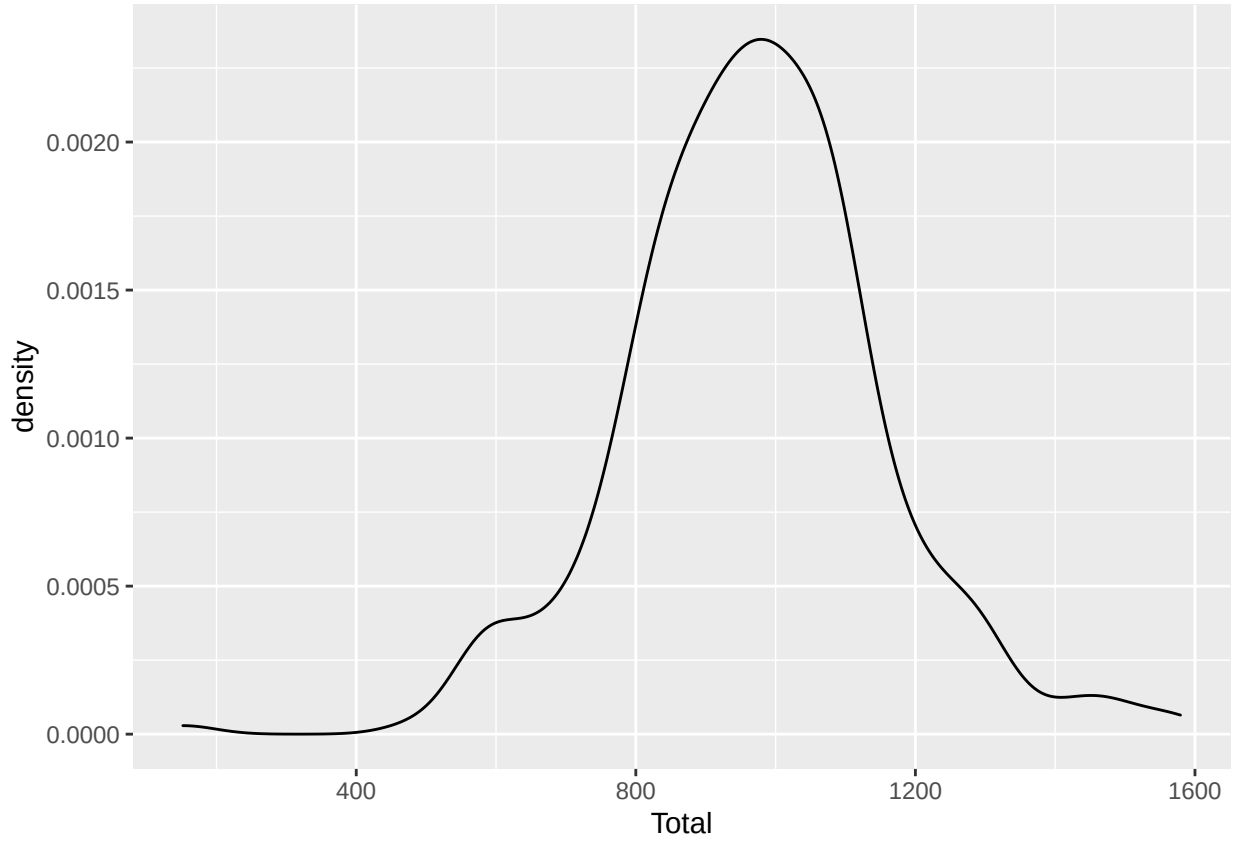
```
ggplot(cn_standCLD, aes(x= site_crop_yr, y= stand_count, color= site_crop_yr)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL, ymax= upper.CL), width= .3) +
  geom_text(aes(label = .group), nudge_y = 3500, size= 5) +
  geom_jitter(data = Corn1 ,mapping = aes(y = stand_count), alpha = 0.2) +
  #coord_flip() +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Corn Stand Counts")
```



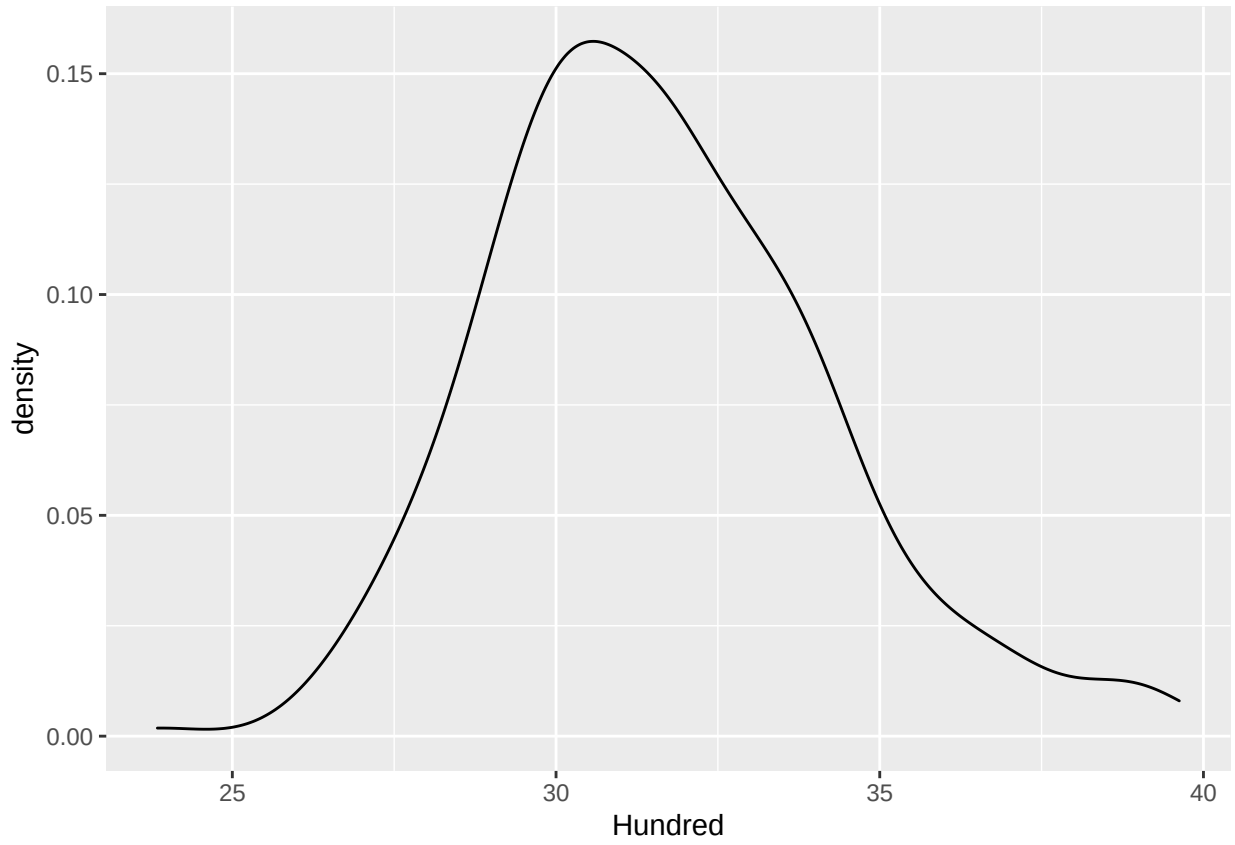
Lancaster Stand counts should be closer to 80,000 and Havelock should be closer to 79,000

Corn Yield Components

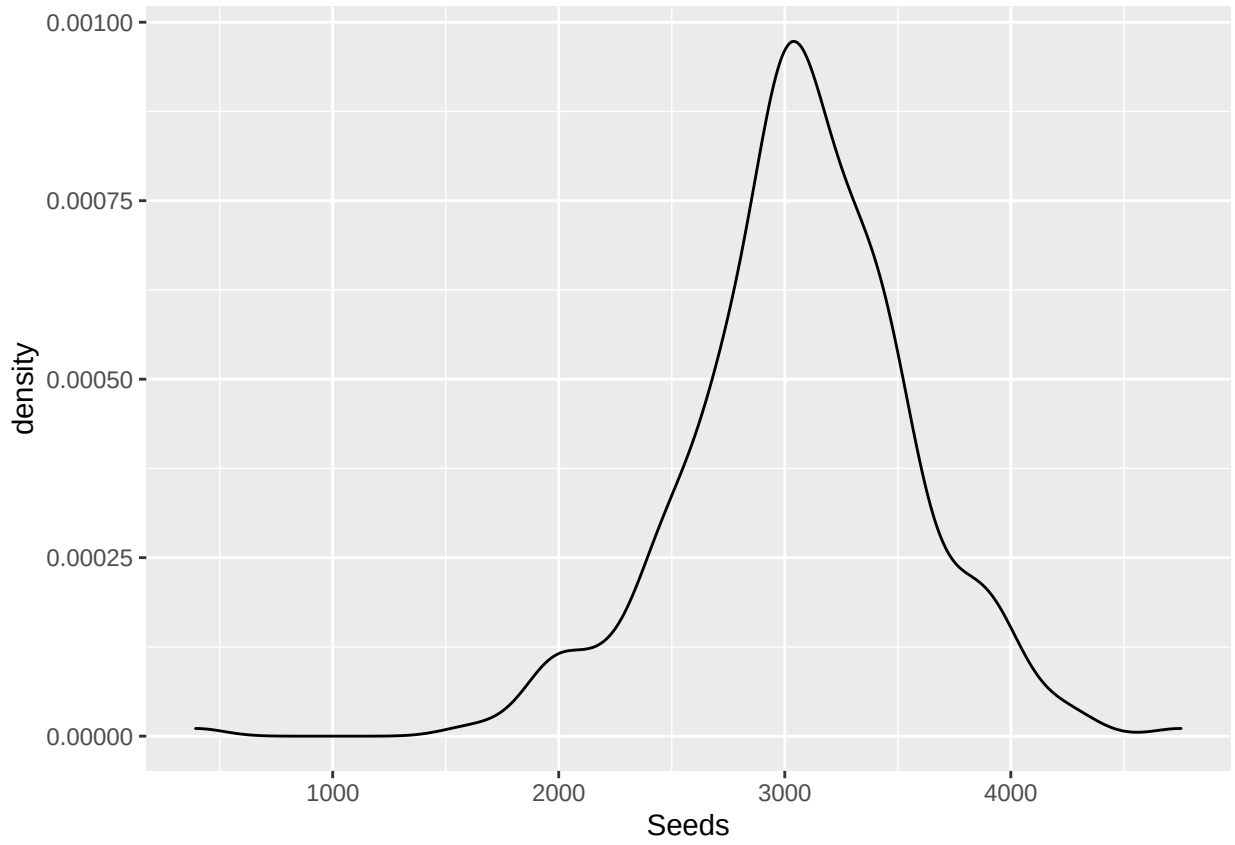
```
CornComp %>%
  ggplot(aes(x =Total)) +
  geom_density()
```



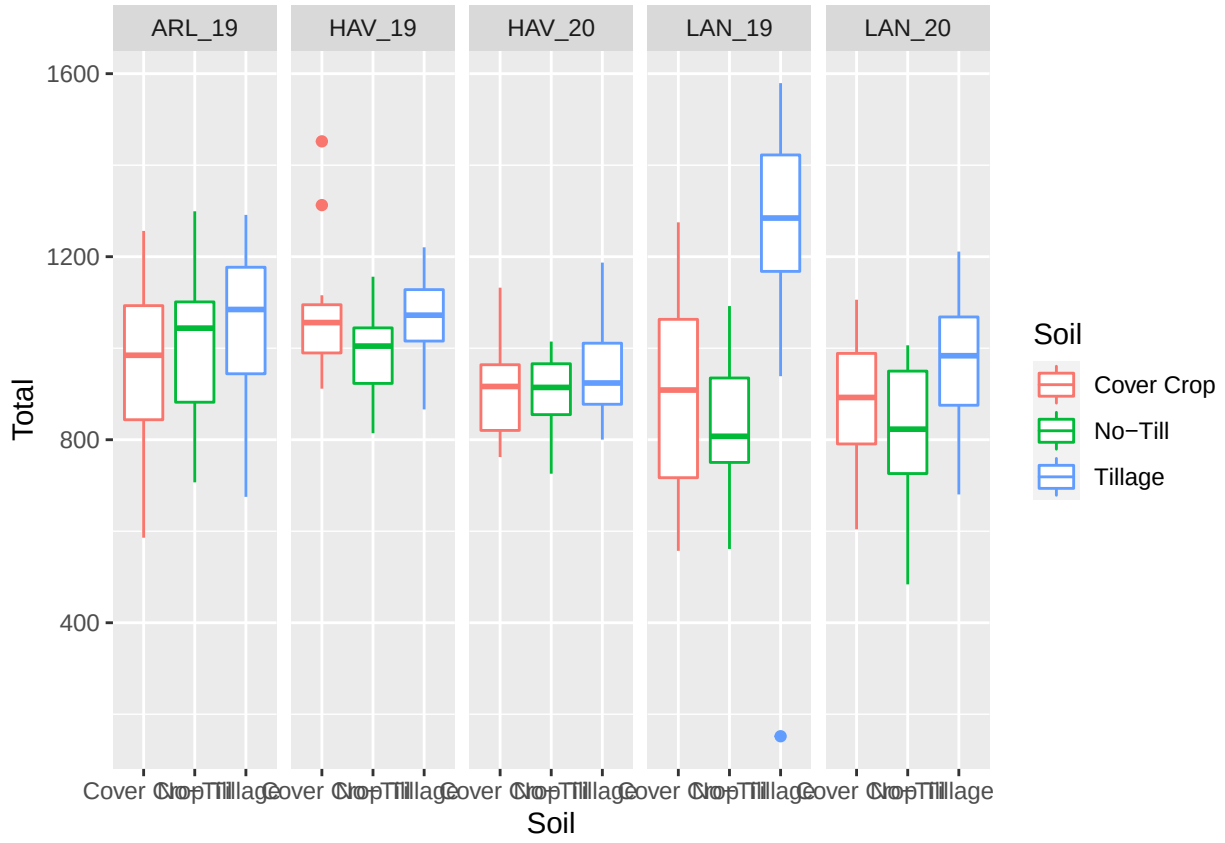

```
CornComp %>%
  ggplot(aes(x =Hundred)) +
  geom_density()
```



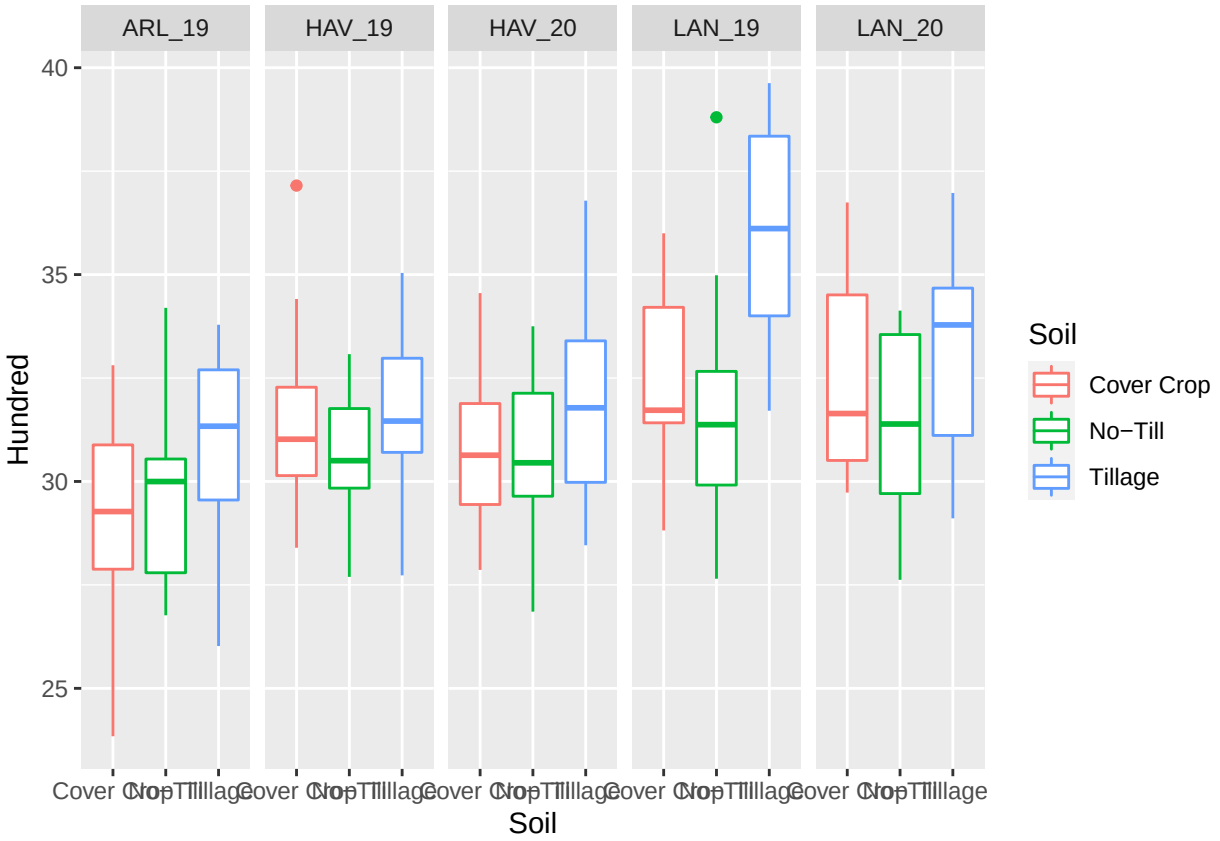

```
CornComp %>%
  ggplot(aes(x =Seeds)) +
  geom_density()
```



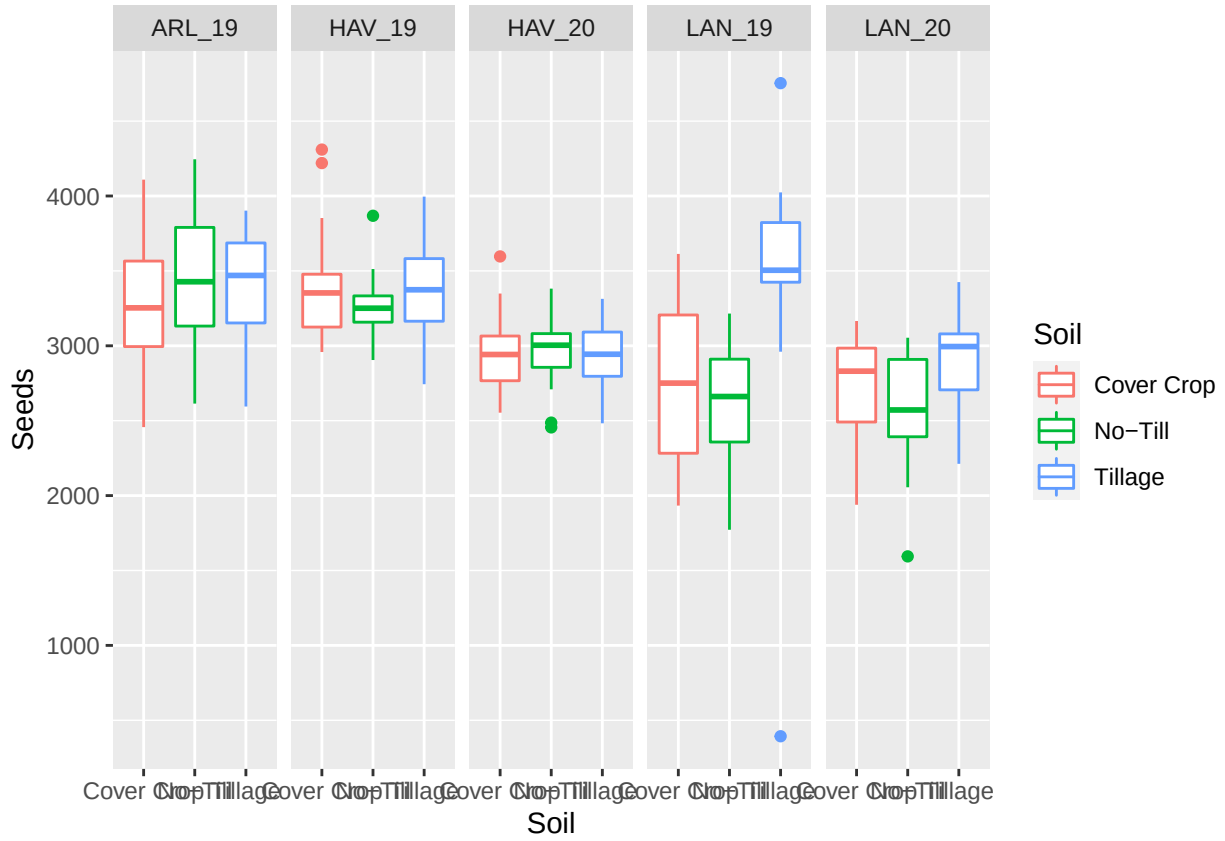

```
CornComp %>%
  ggplot(aes(x = Soil, y = Total, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```




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




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



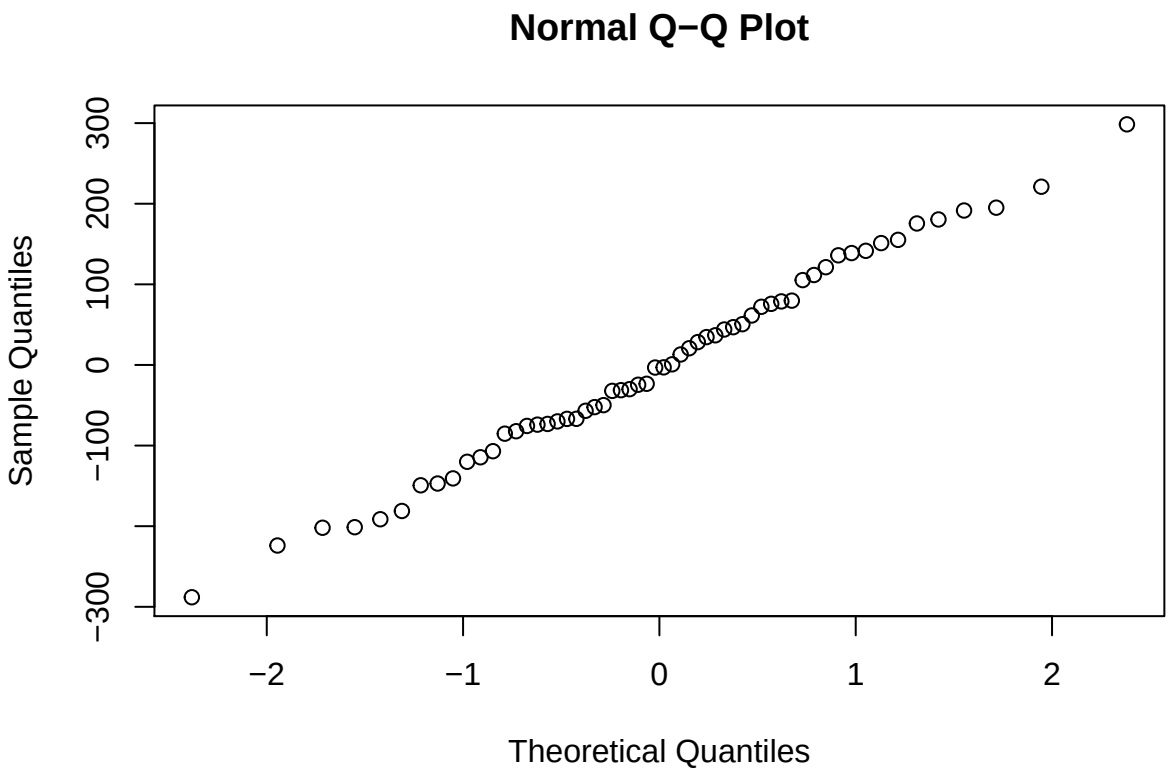
Based on these figures I think it would be appropriate to conduct analyses for each location separately.

Corn Total Sample Mass

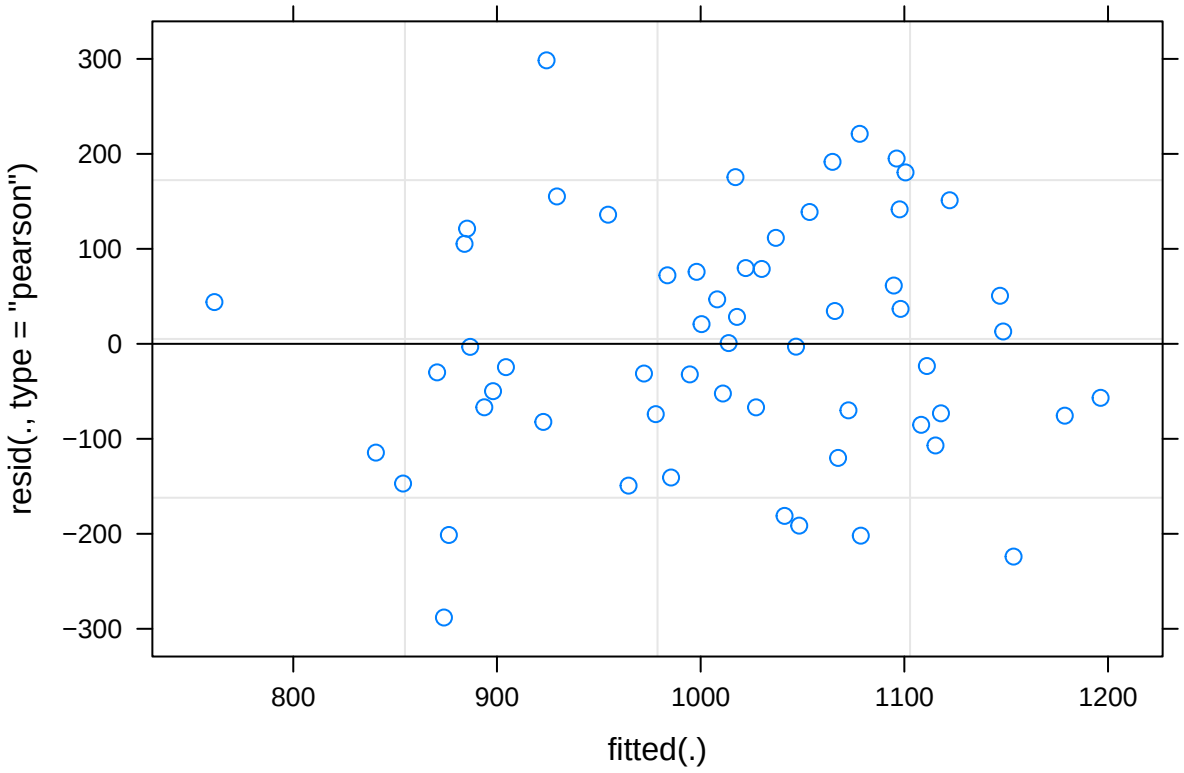
Analysis by Location

Arlington

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




```
plot(arl_CNTotal)
```



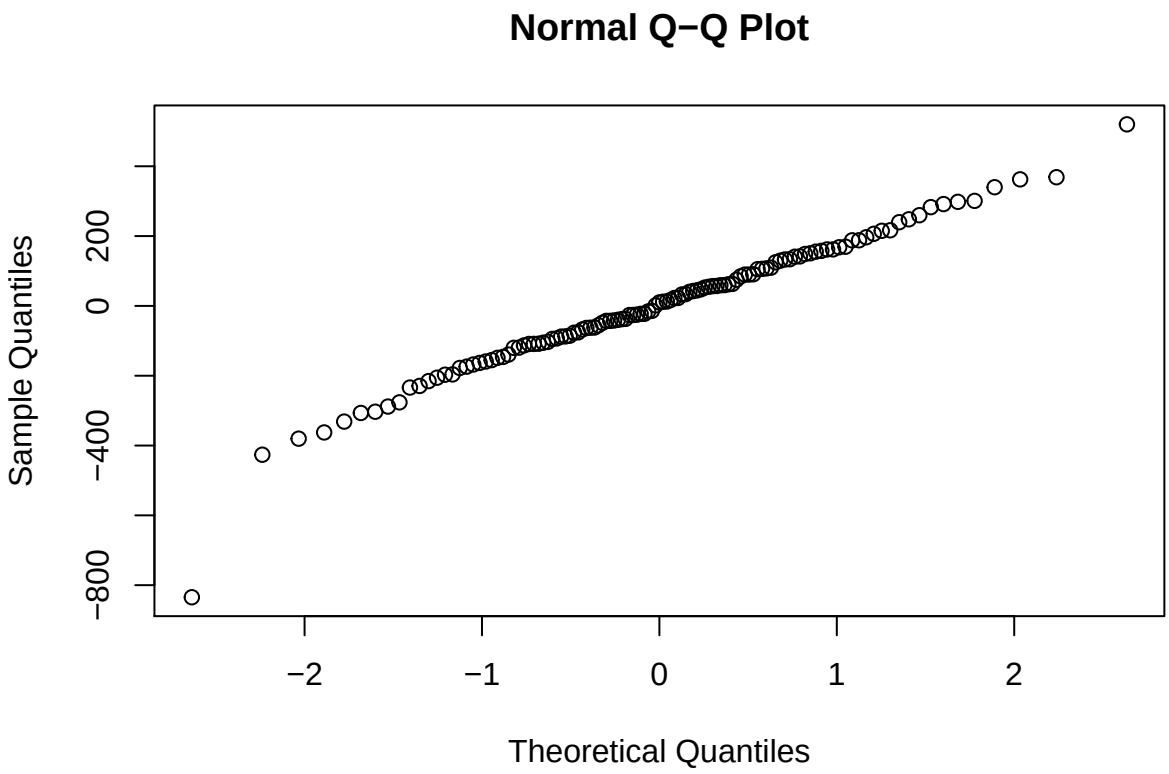

```
#Assumptions met

anova(arl_CNTotal)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Soil       69414   34707     2 40.055  1.5573 0.2232
## Herb        7475    1869     4 40.064  0.0839 0.9869
## Soil:Herb  60598    7575     8 40.072  0.3399 0.9450
```

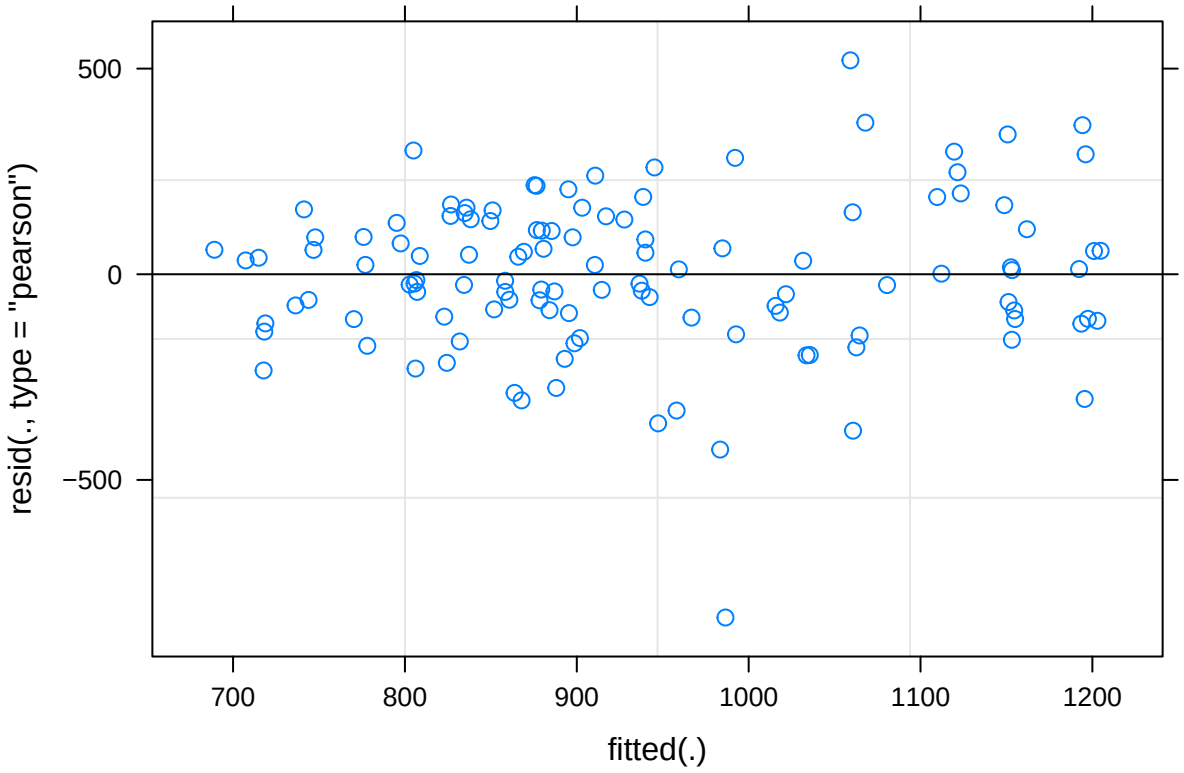
```
#Nothing significant
```

Lancaster

```
lan_CNTotal= lmer(Total~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Lancaster" )))
qqnorm(resid(lan_CNTotal))
```




```
plot(lan_CNTotal)
```




```
#Assumptions met

anova(lan_CNTotal)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value   Pr(>F)
## Soil      1800200  900100     2 97.091 21.5095 1.85e-08 ***
## Herb        32946    8236     4 97.090  0.1968   0.9395
## Soil:Herb  109535   13692     8 97.088  0.3272   0.9538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

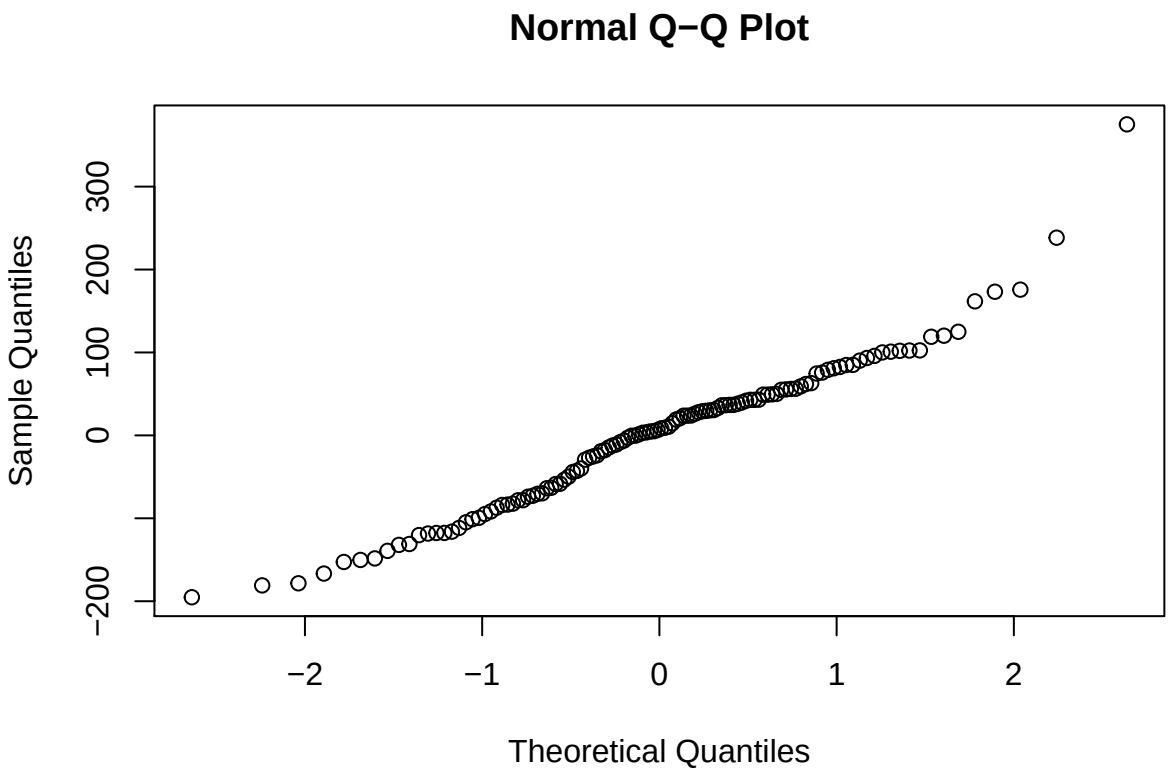
```
#Soil significant
```

Havelock

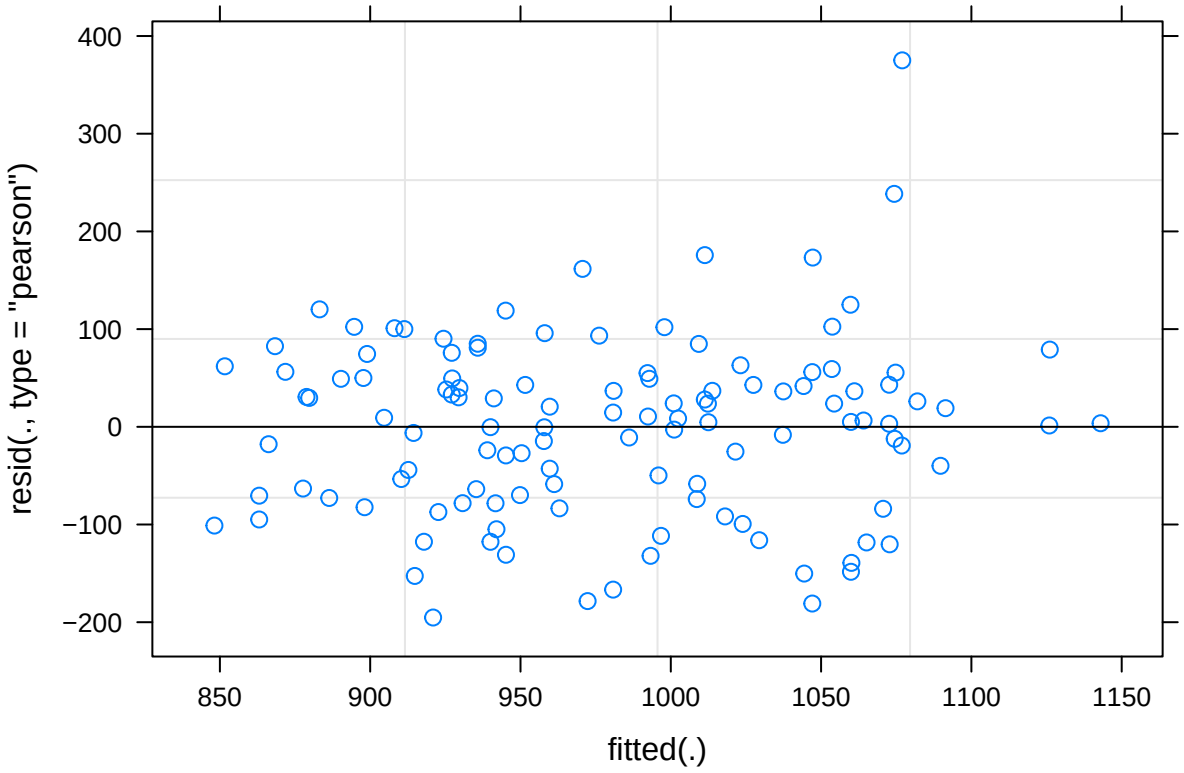
```
hav_CNTotal= lmer(Total~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Havelock" )))
```

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

```
qqnorm(resid(hav_CNTotal))
```




```
plot(hav_CNTotal)
```




```
#Assumptions met

anova(hav_CNTotal)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## Soil       55266 27633.1     2 98.017  2.7777 0.06708 .
## Herb       54989 13747.3     4 98.052  1.3819 0.24579
## Soil:Herb  44117  5514.6     8 98.455  0.5543 0.81259
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Nothing significant
```

Condensed analysis —- Not included in pdf

ANOVA of untransformed corn total sample mass model

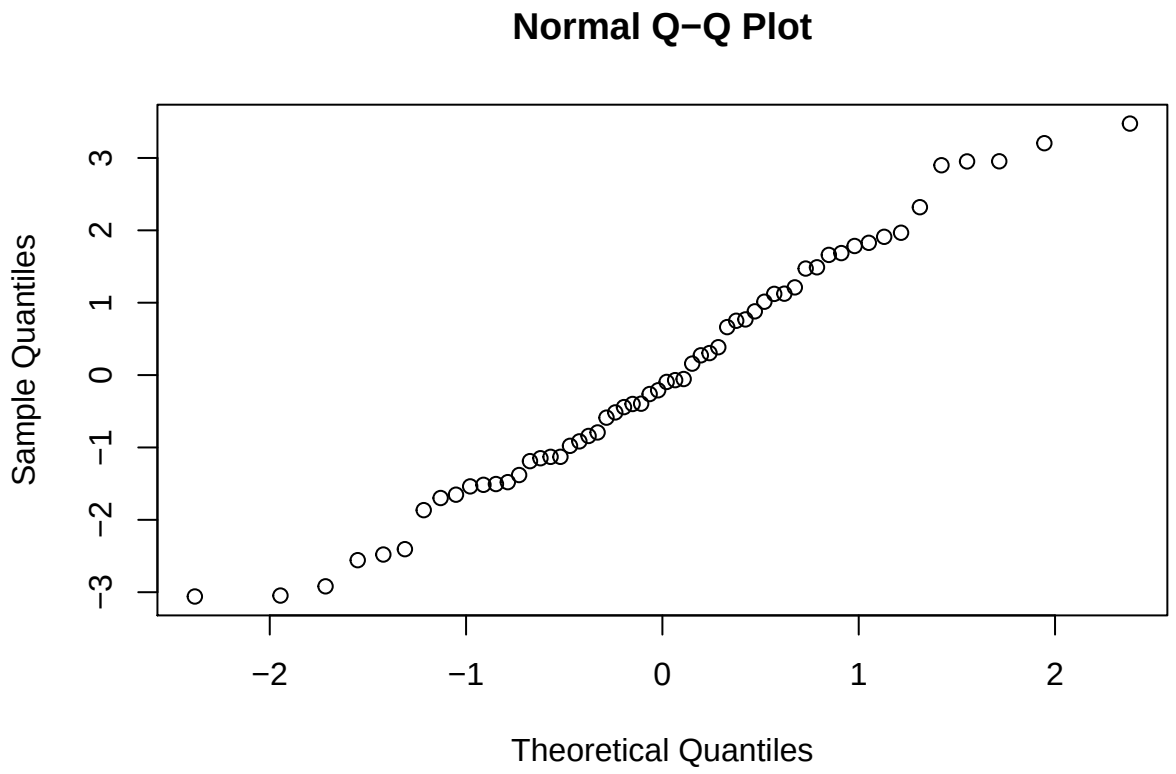
Corn total sample means comparison for Soil:Site-Year interaction

Corn Seed Density

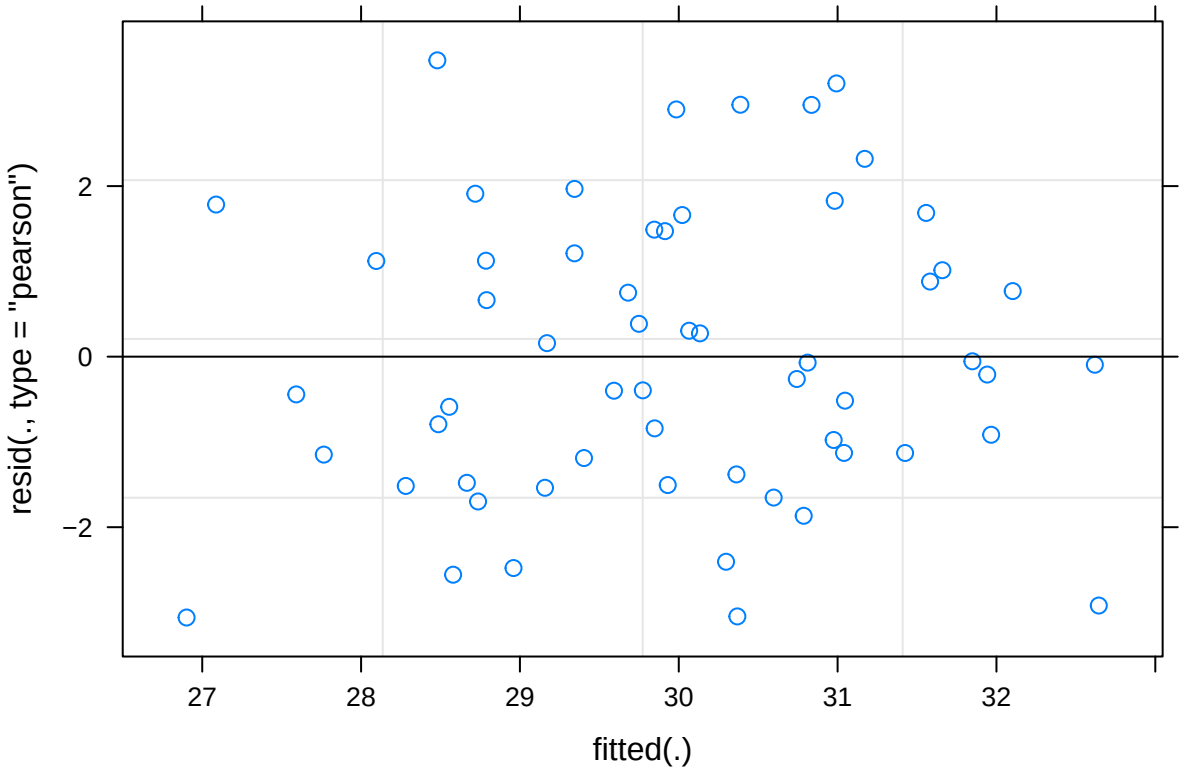
Analysis by Location

Arlington

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




```
plot(arl_CNHun)
```



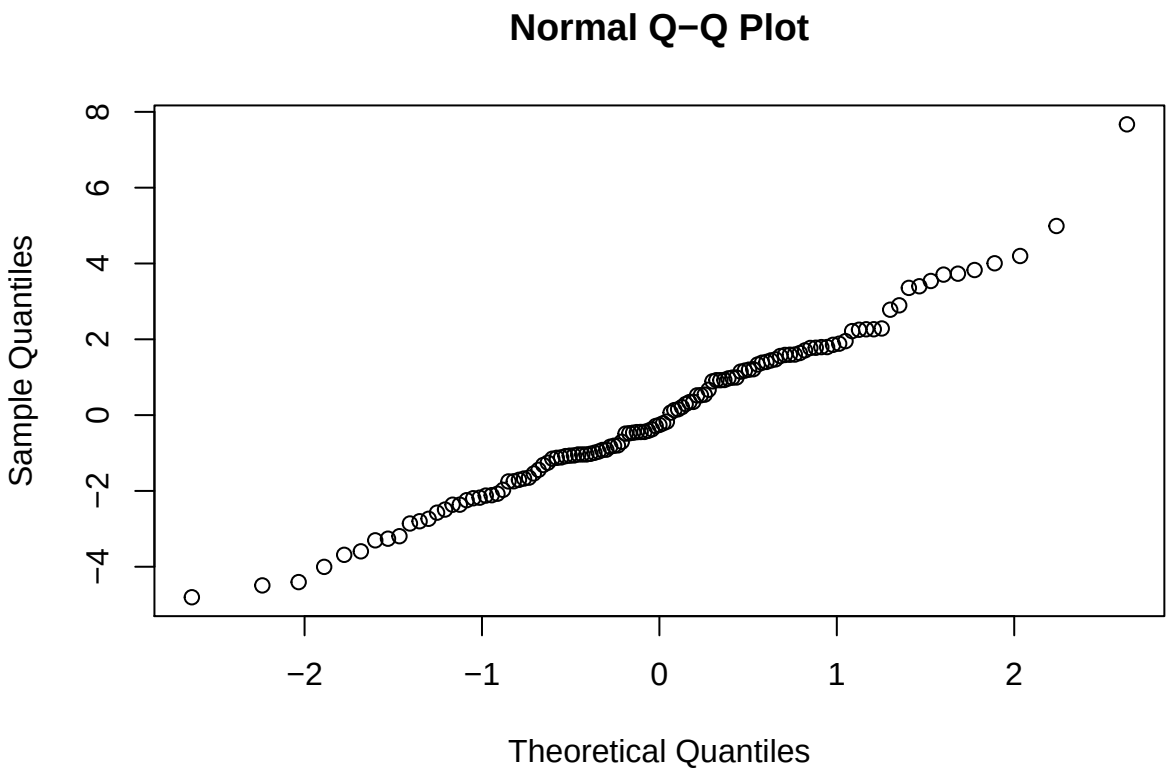

```
#Assumptions met

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
```

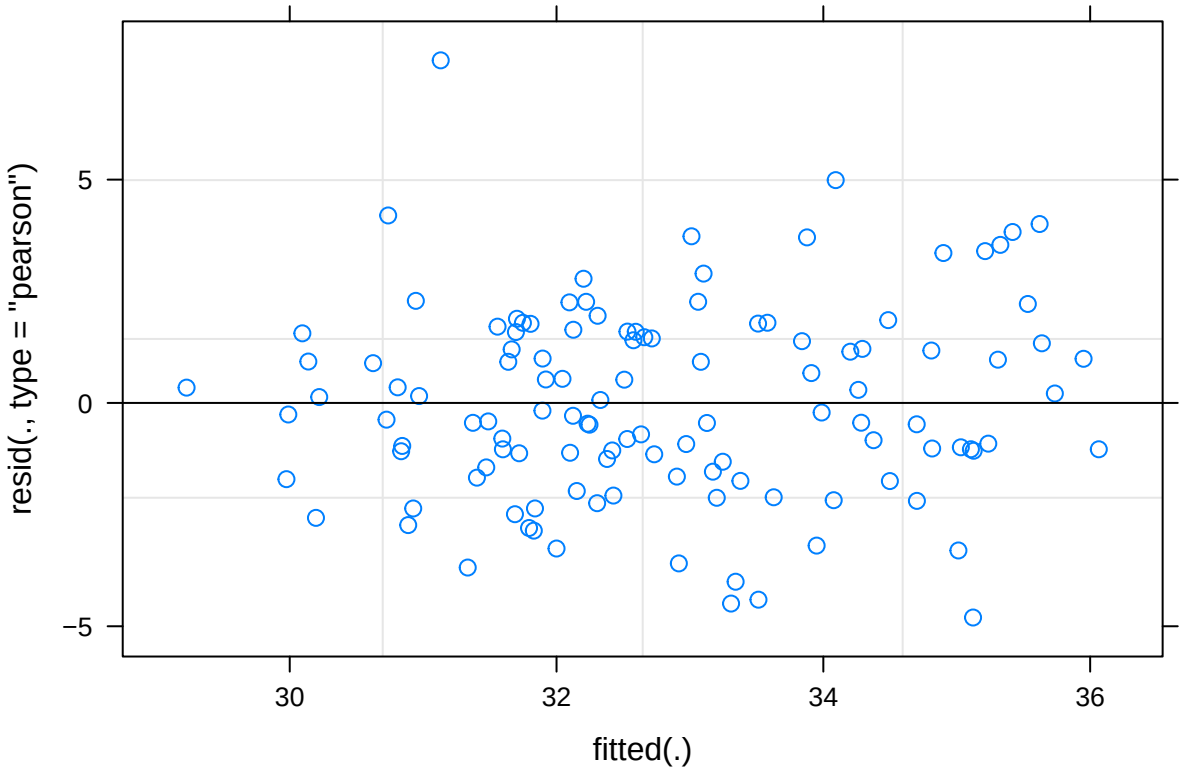
```
#Soil Significant
```

Lancaster

```
lan_CNHun= lmer(Hundred~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Lancaster" )))
qqnorm(resid(lan_CNHun))
```




```
plot(lan_CNHun)
```




```
#Assumptions met

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
```

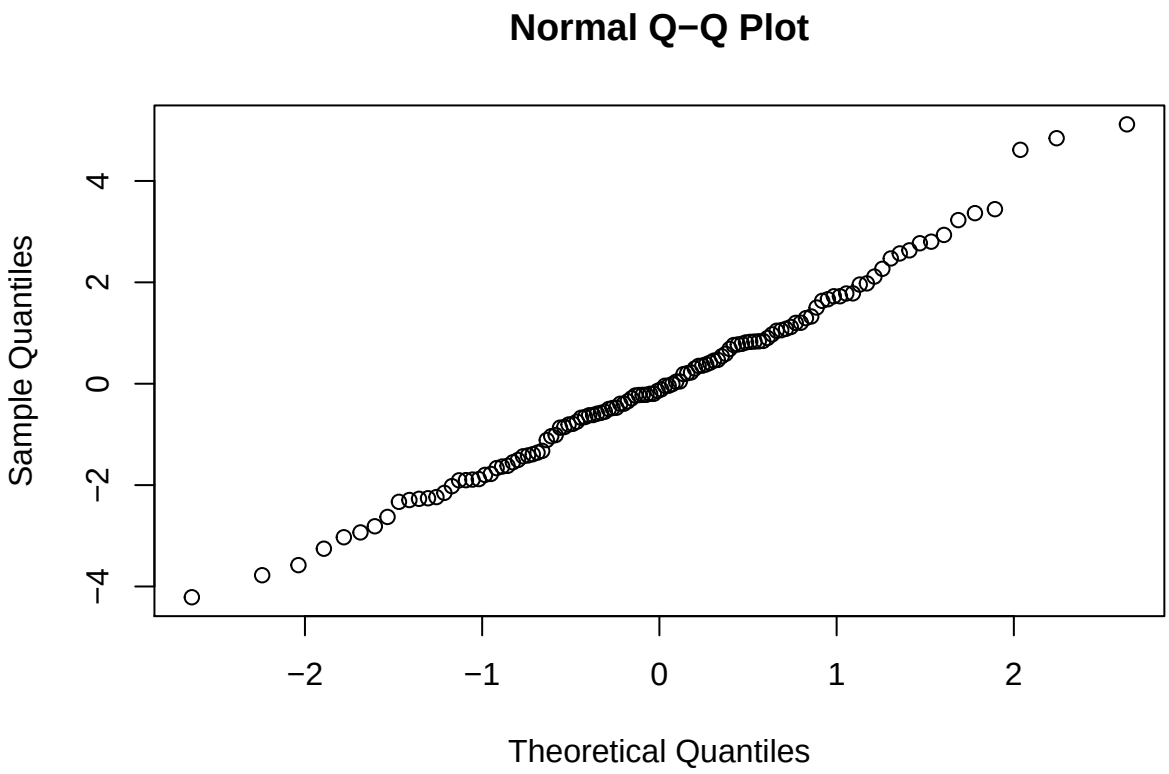
```
#Soil significant
```

Havelock

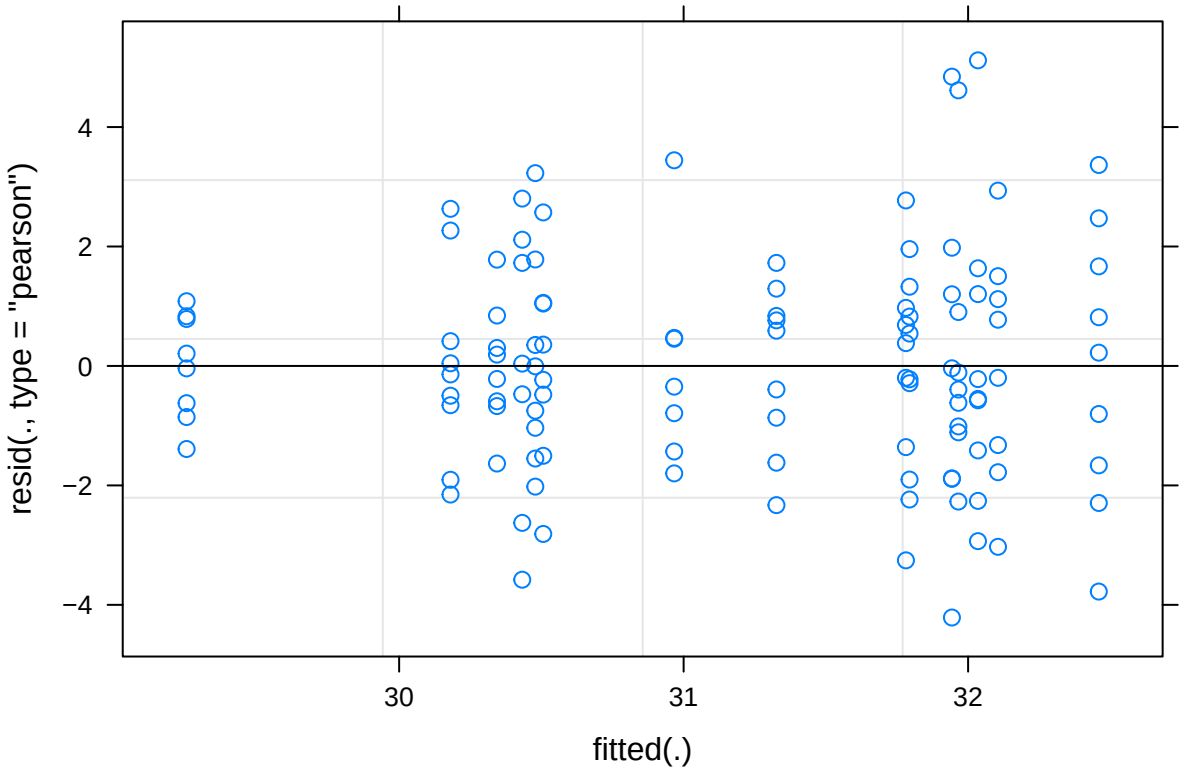
```
hav_CNHun= lmer(Hundred~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Havelock" )))
```

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

```
qqnorm(resid(hav_CNHun))
```




```
plot(hav_CNHun)
```




```
#Assumptions met

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
```

```
#Soil significant
```

Condensed Analysis—— not included in pdf

ANOVA of untransformed Corn Seed Density Model

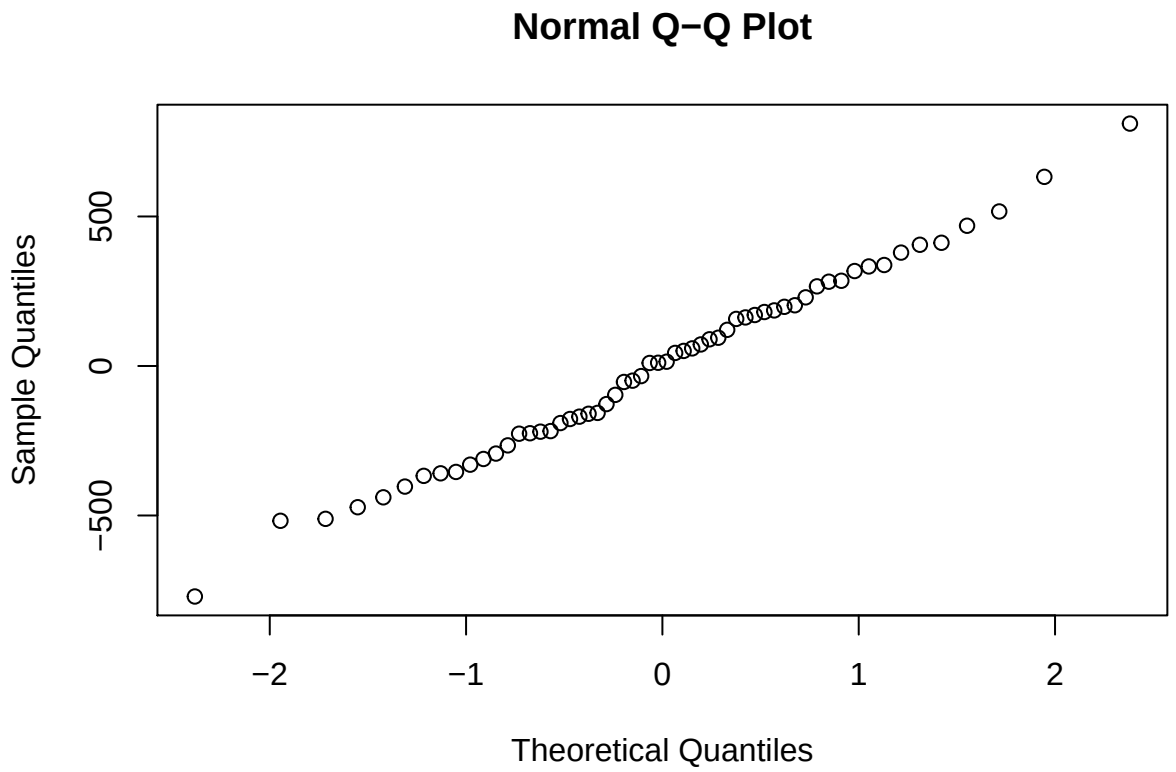
Corn total sample means comparison for Soil:Site-Year interaction

Corn Seed Count

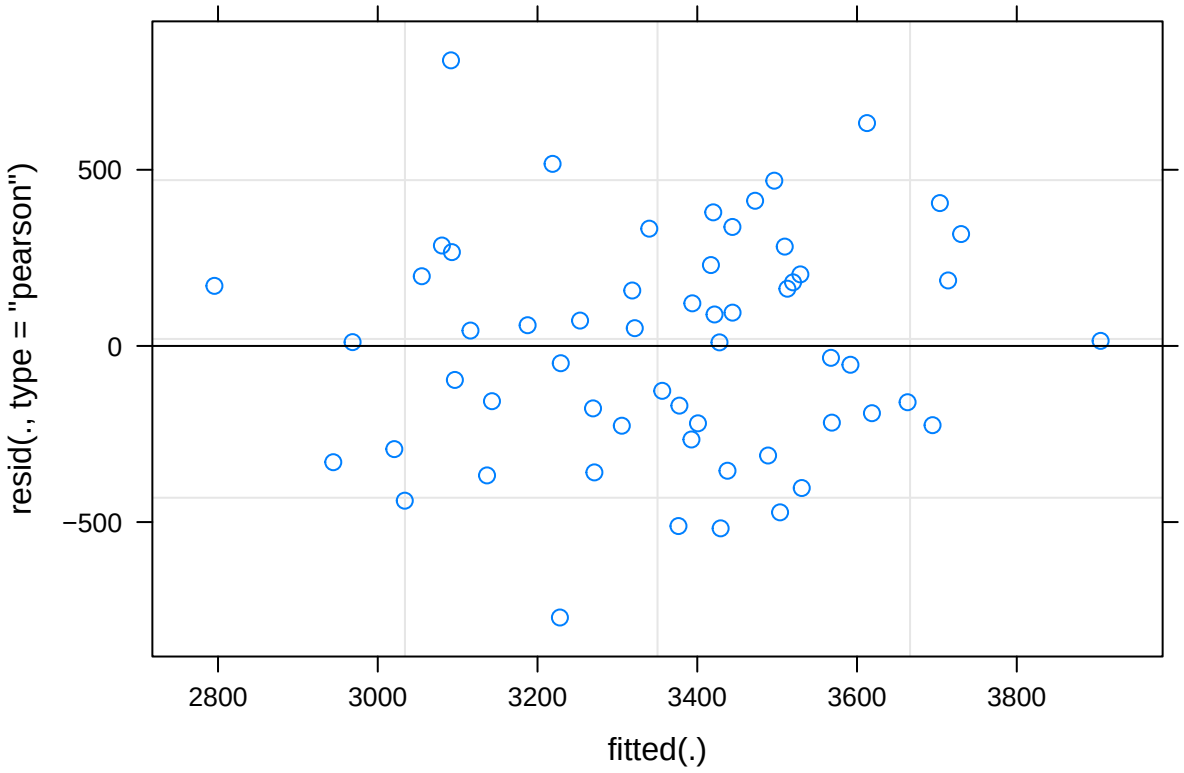
Analysis by Location

Arlington

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




```
plot(arl_Seeds)
```



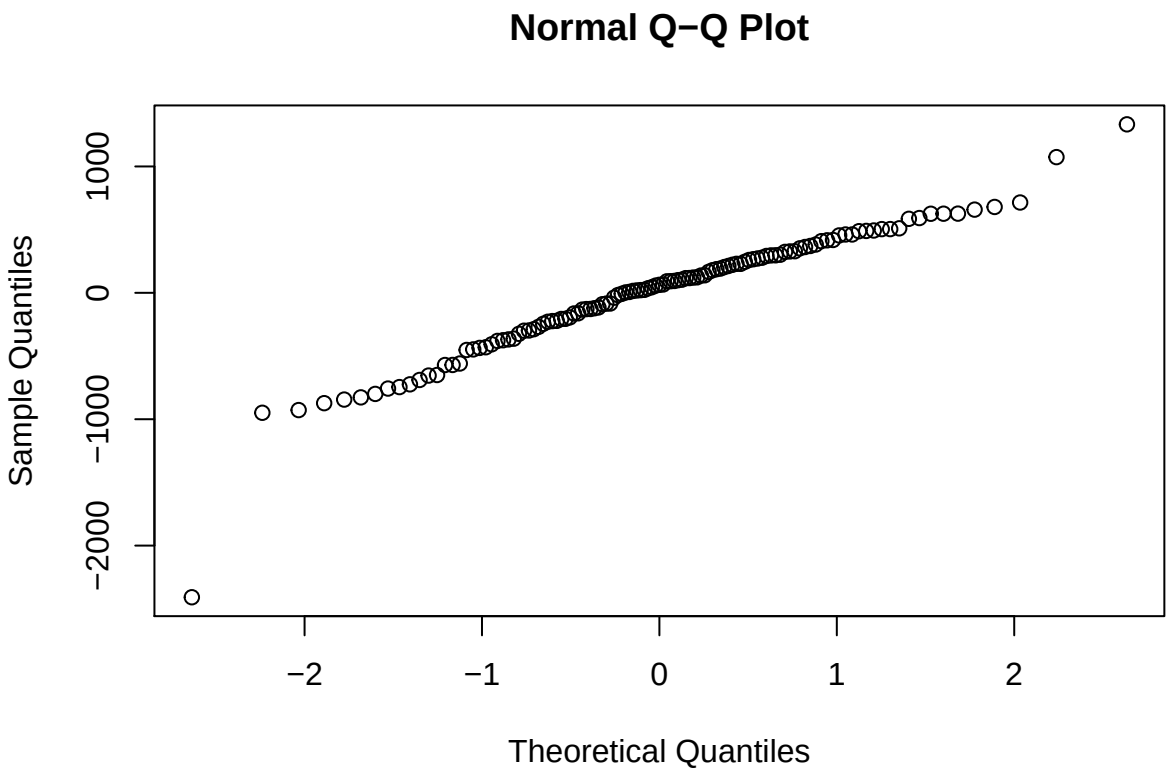

```
#Assumptions met

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
```

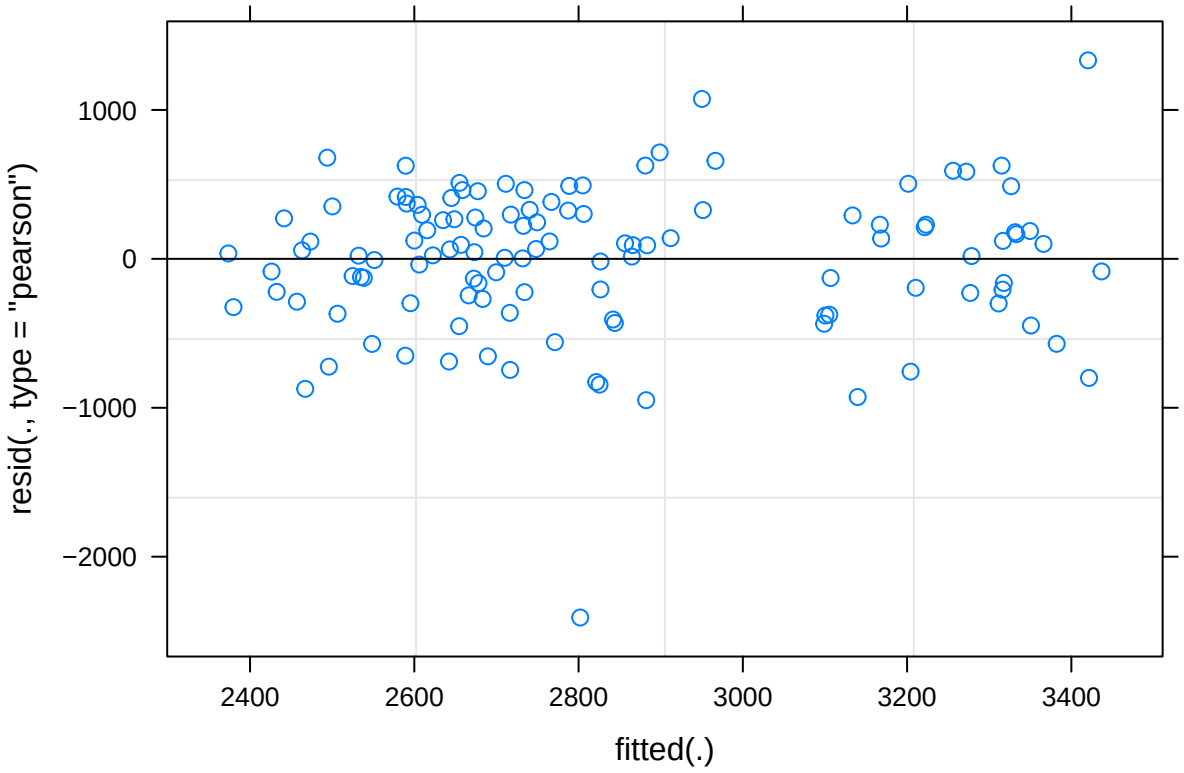
```
#Nothing Significant
```

Lancaster

```
lan_Seeds= lmer(Seeds~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Lancaster" )))
qqnorm(resid(lan_Seeds))
```




```
plot(lan_Seeds)
```




```
#Normality slightly questionable, Equal variance good

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
```

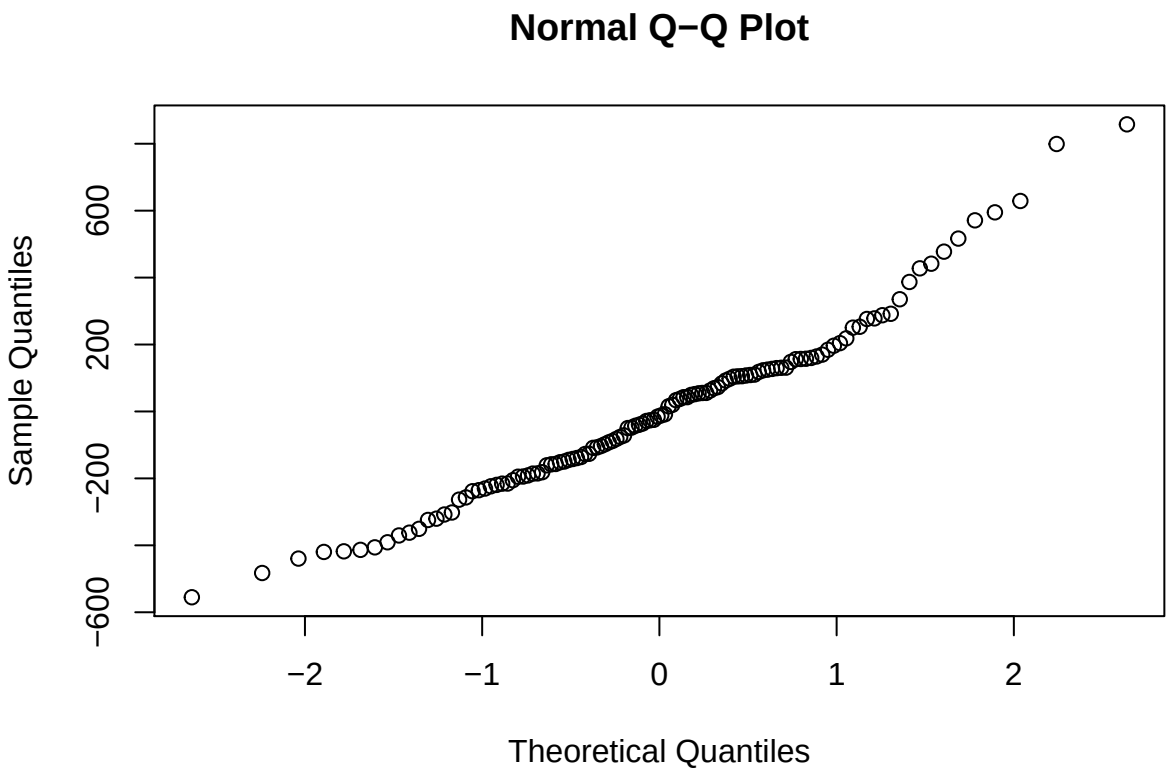
```
#Soil significant
```

Havelock

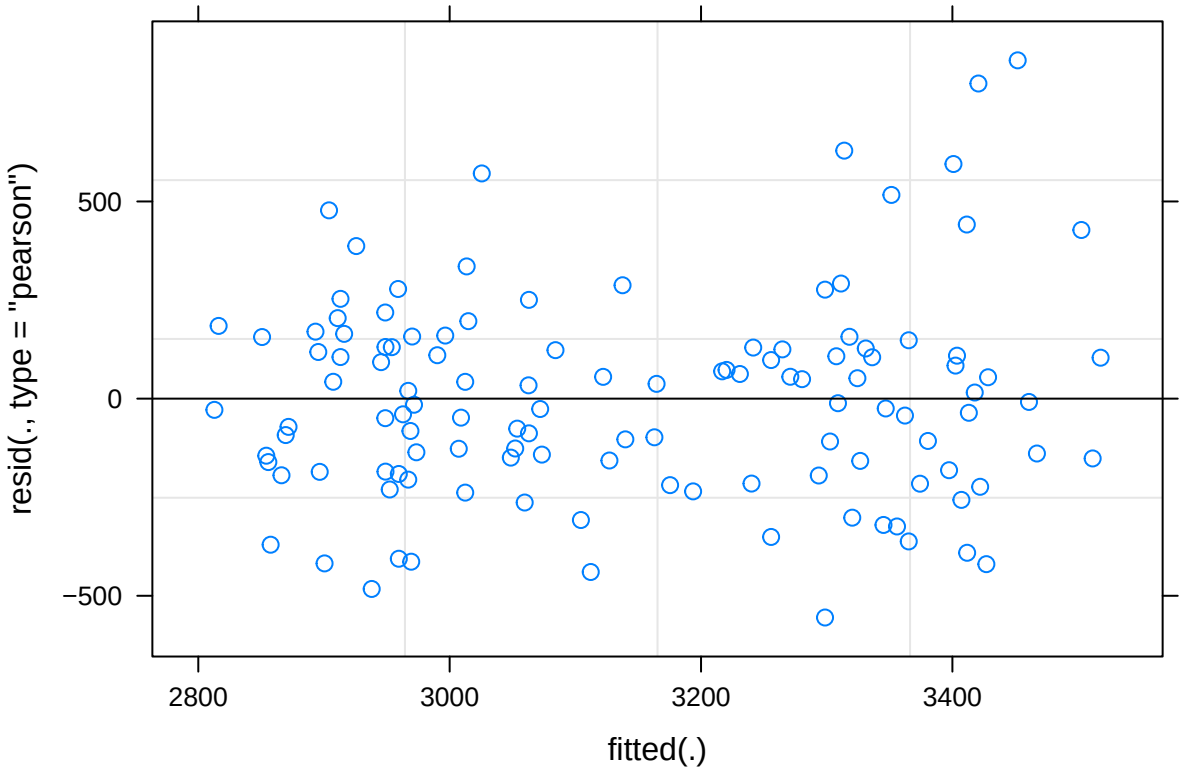
```
hav_Seeds= lmer(Seeds~ Soil*Herb + (1|Rep/Year) , data= (filter(CornComp, Location == "Havelock" )))
```

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

```
qqnorm(resid(hav_Seeds))
```




```
plot(hav_Seeds)
```




```
#Assumptions met

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
```

```
#Nothing significant
```

Condensed Analysis——- Not included in pdf

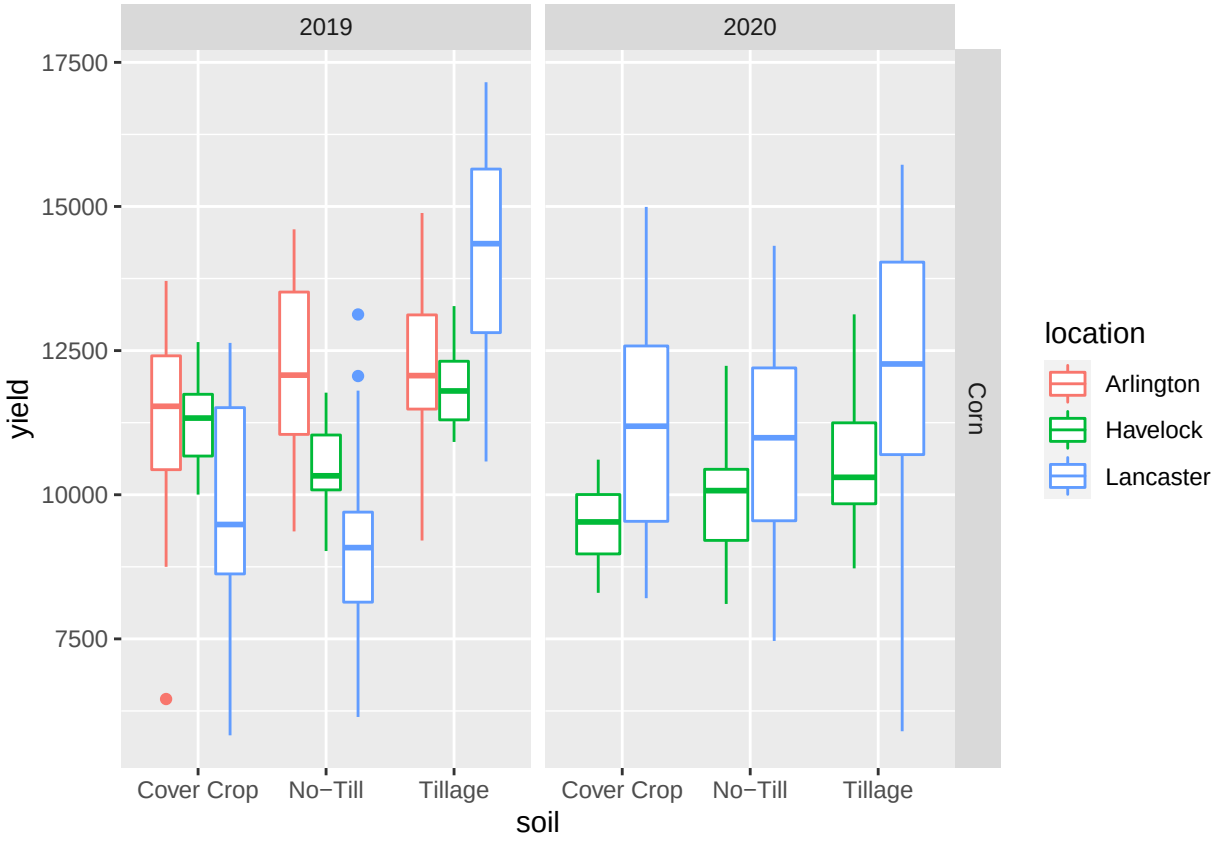
ANOVA of untransformed Corn Seed Count Model

Corn seed count means comparison for Soil:Site-Year interaction

Corn Yield Component Figures

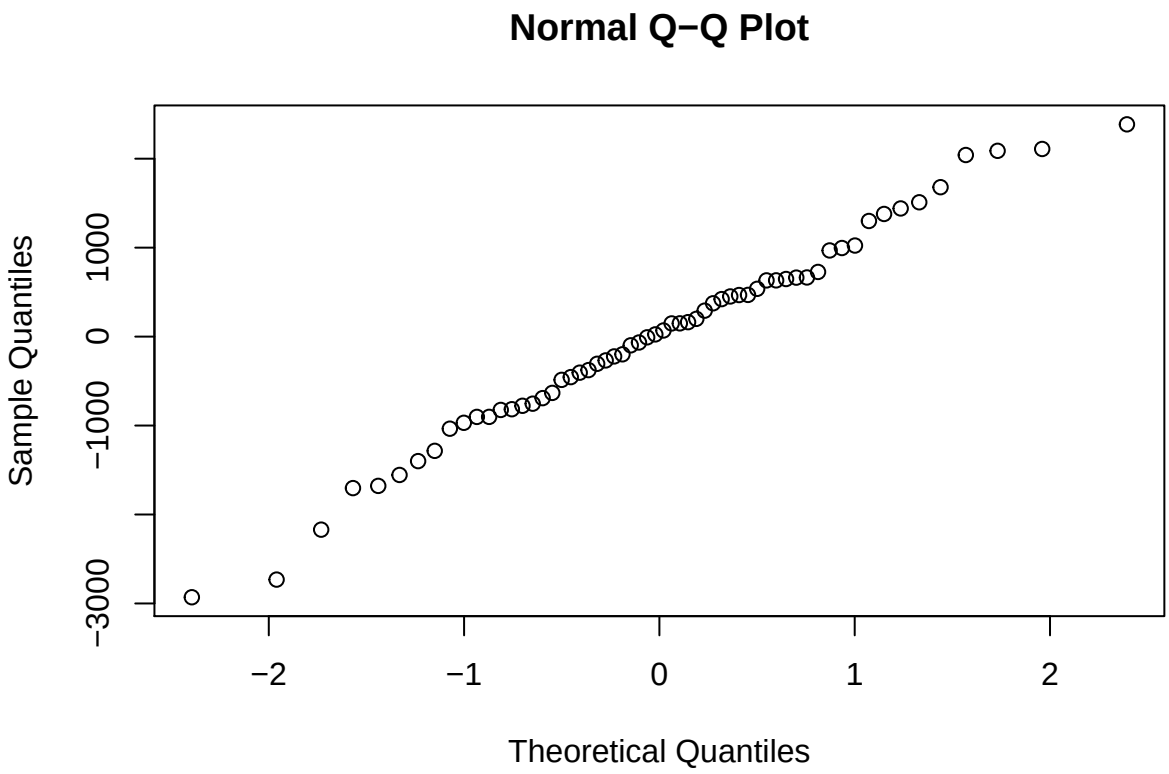
Corn Yield

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

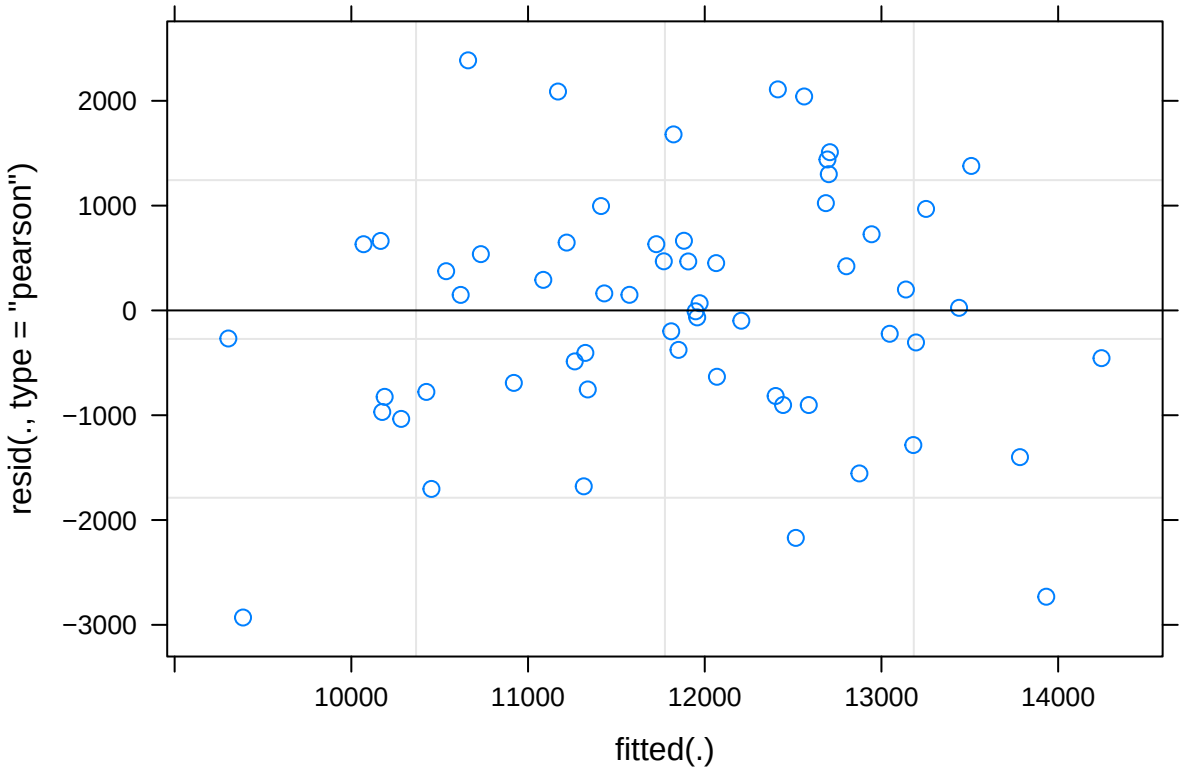


Arlington 2019 Analysis —- We decided to use only this site-year in the paper

```
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)
```



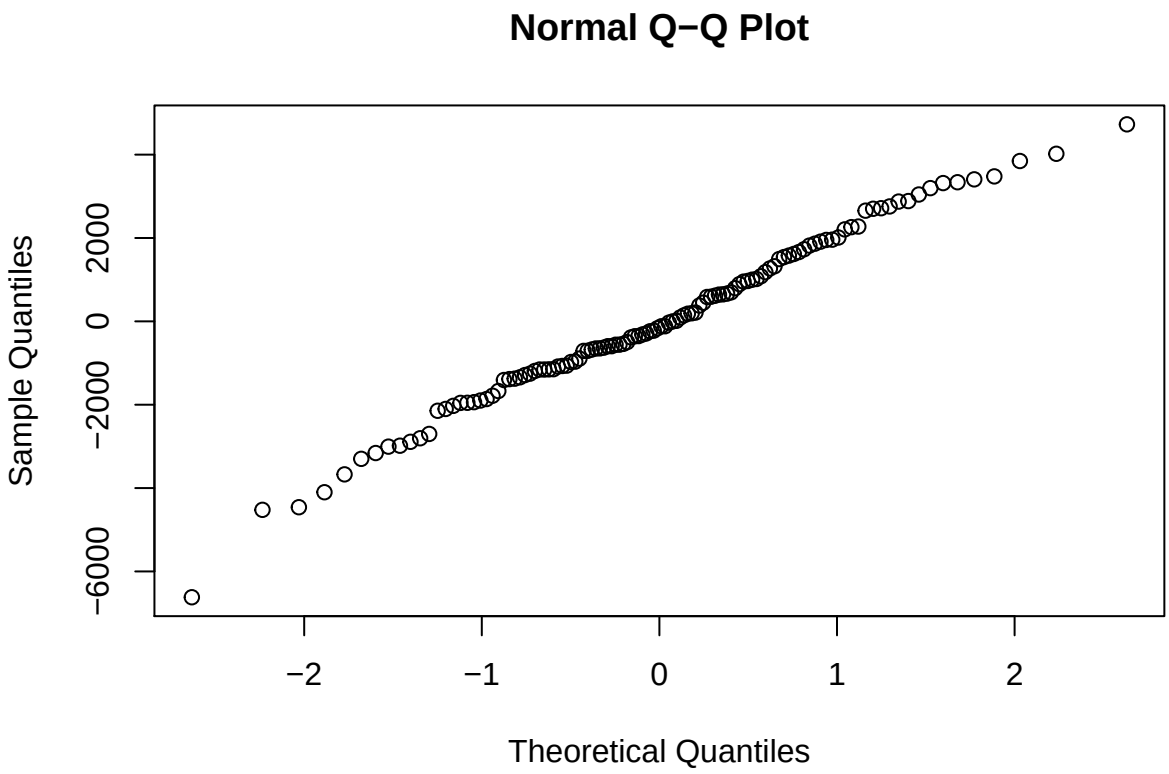

```
#assumptions look good

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
```

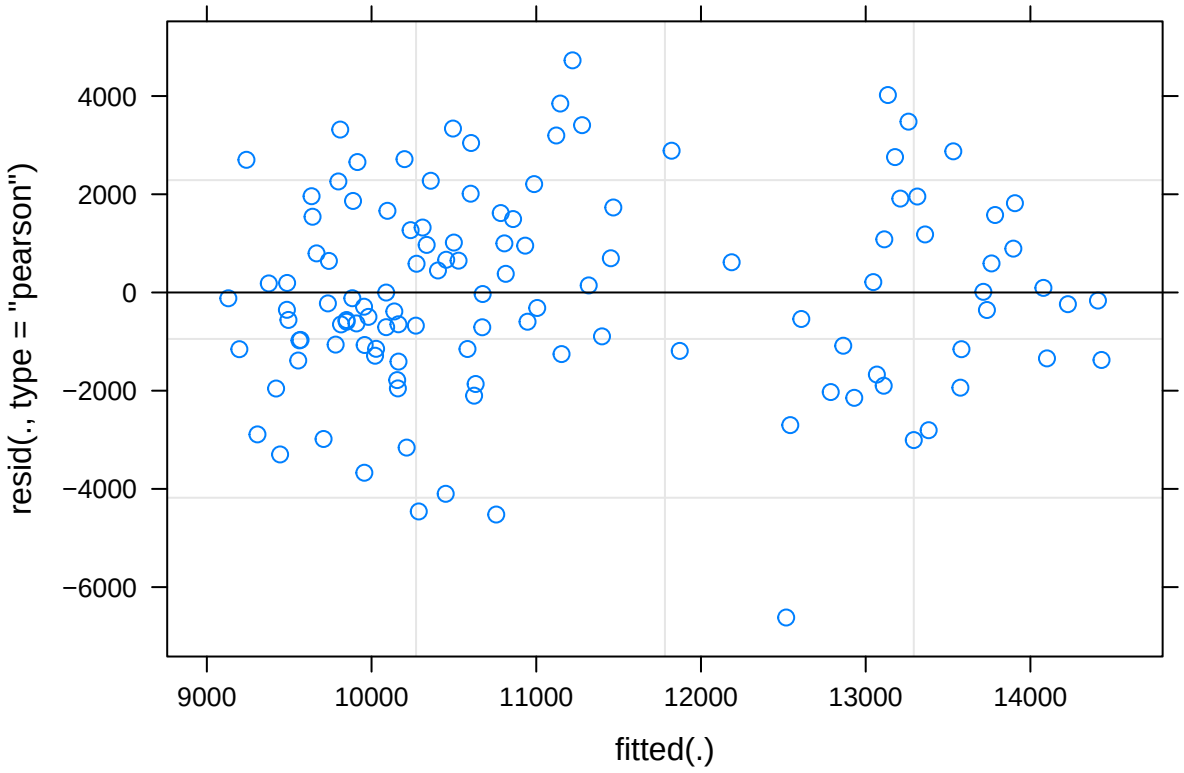
```
#soil managment fixed effect significant
```

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
```

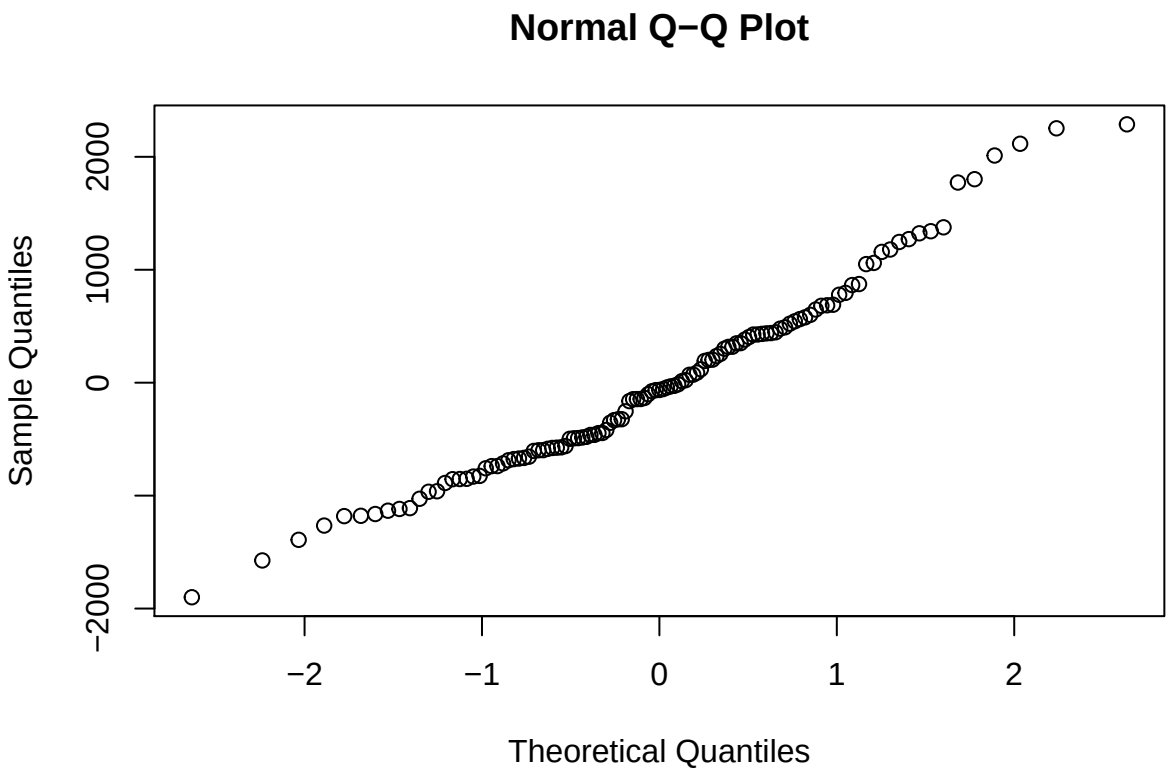
```
#Soil management fixed effect significant
```

Havelock Analysis

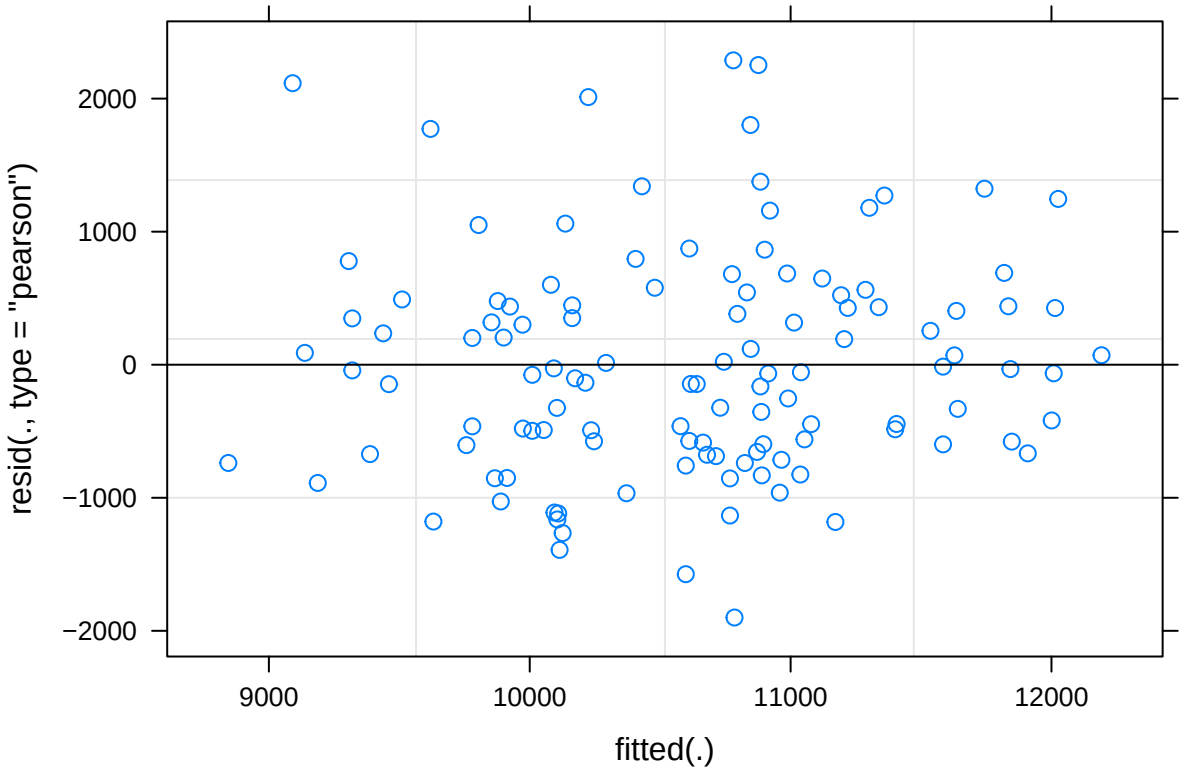
```
havcn_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Corn1, location == "Havelock")))
```

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

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

qqnorm(resid(havcn_yield))
```




```
plot(havcn_yield)
```



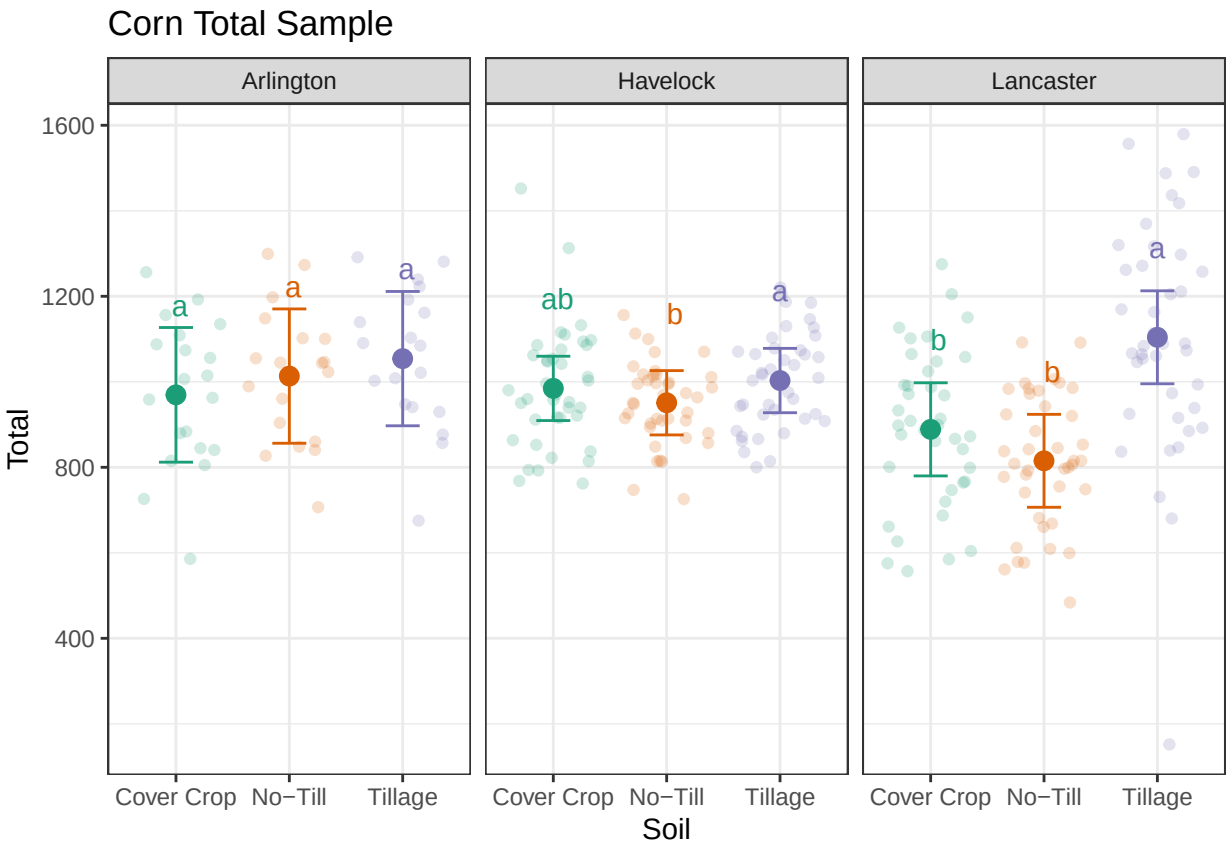

```
#assumptions look good

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
```

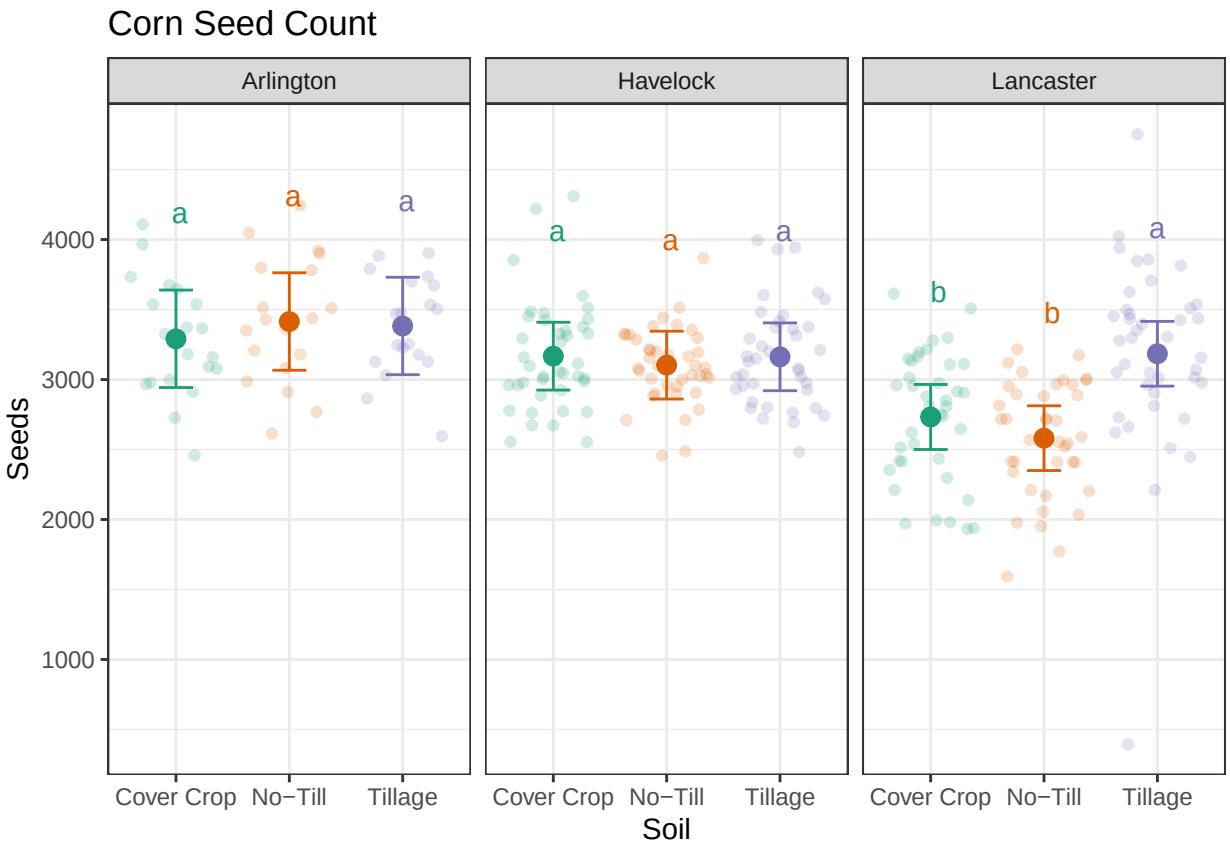
```
#soil management significant

#summary(havcn_yield)
```

Corn Yield Component Figures

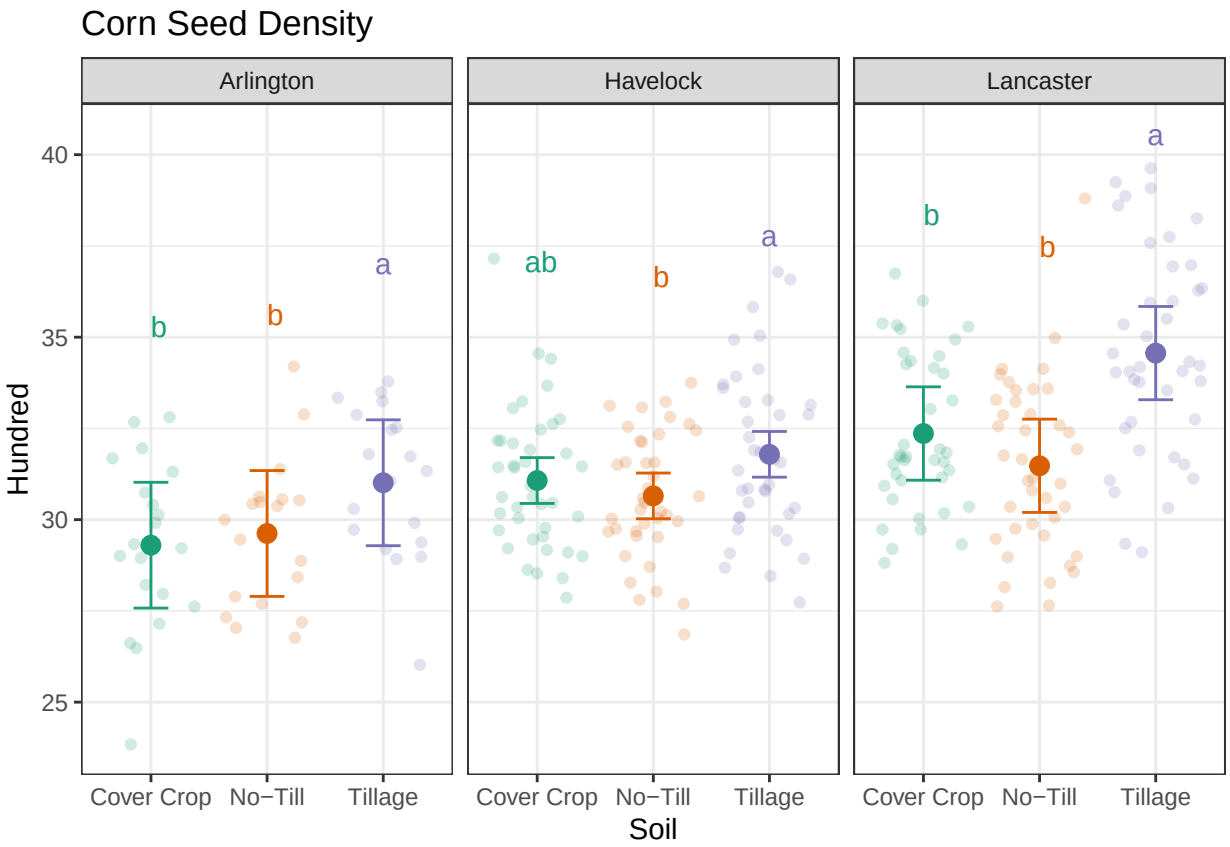
```
CNTotal_site
```




```
CNSeeds_site
```

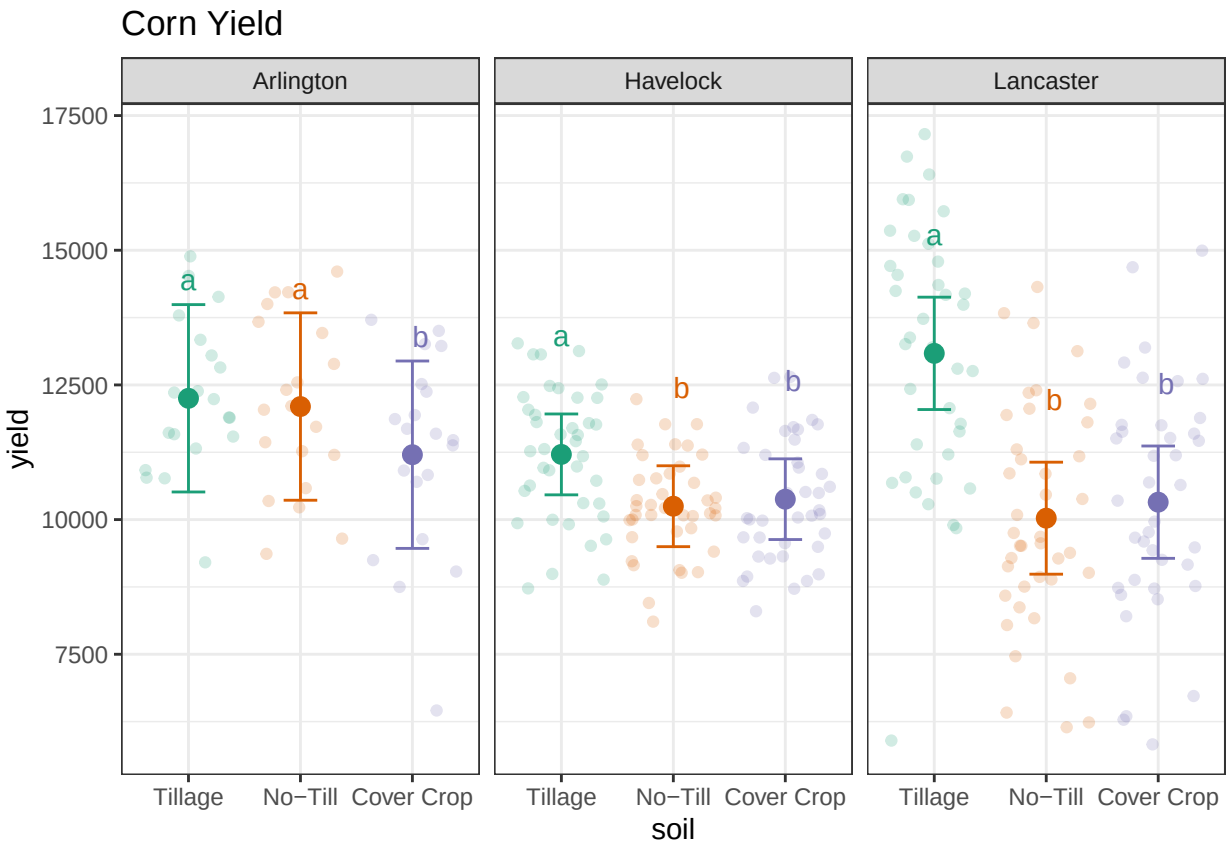



```
CNHundred_site
```



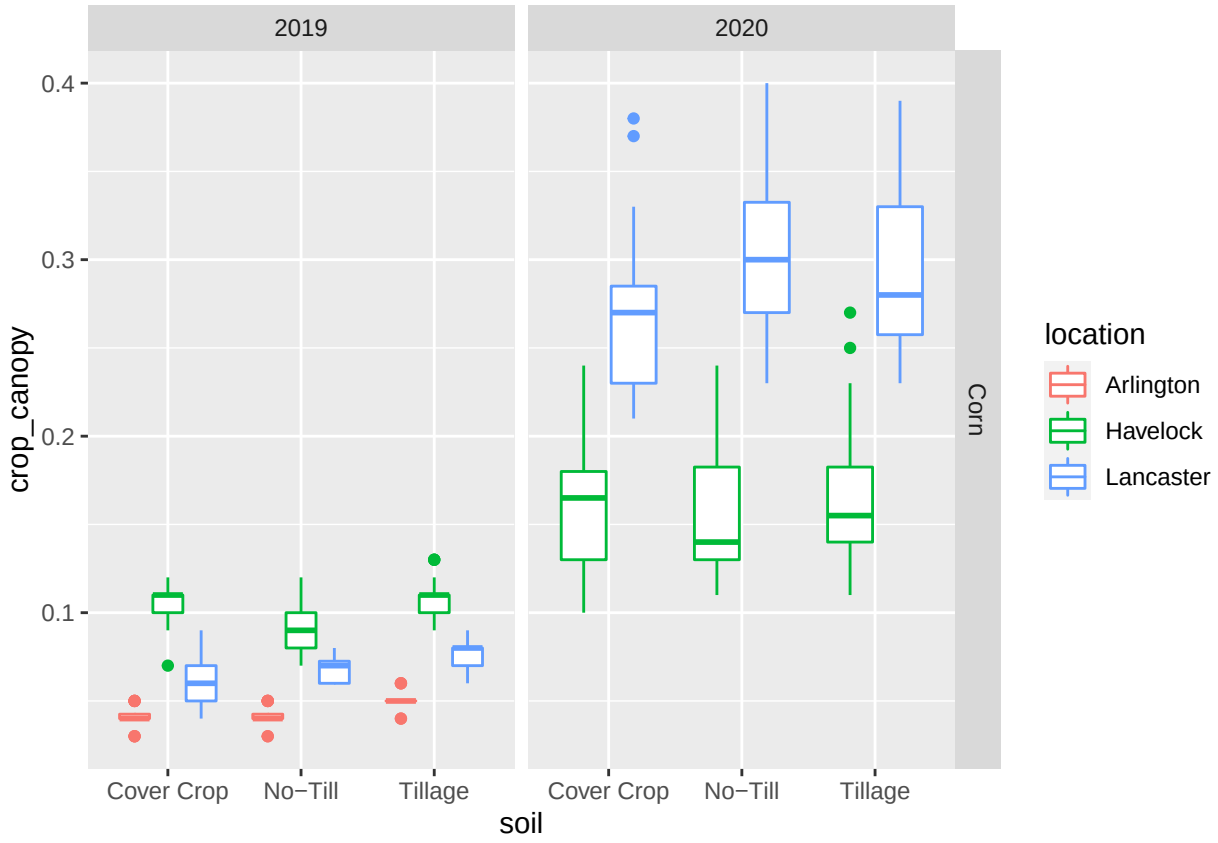
Corn Yield Figure

```
y1
```



Corn Canopy

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



Condensed analysis

```
cn_canopy = glmmTMB(crop_canopy~ soil*herb*site_crop_yr + (1|rep:site_crop_yr), data= Corn1, beta_family

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
```

```
cn_canopy <- ggplot(cn_canopy_soilCLD, 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_wrap(~site_crop_yr) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Corn Canopy")
```

Figure with Soil:site-Years

```
cn_canopy
```

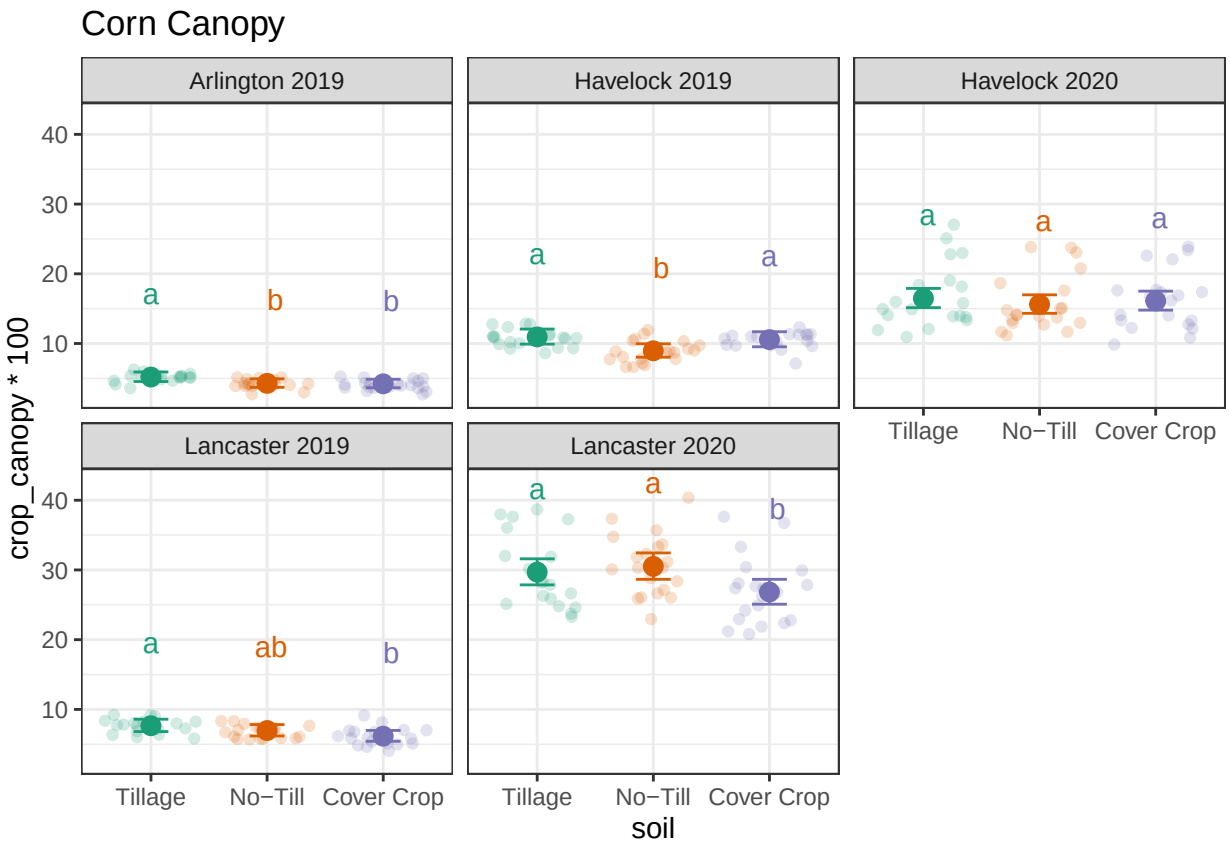
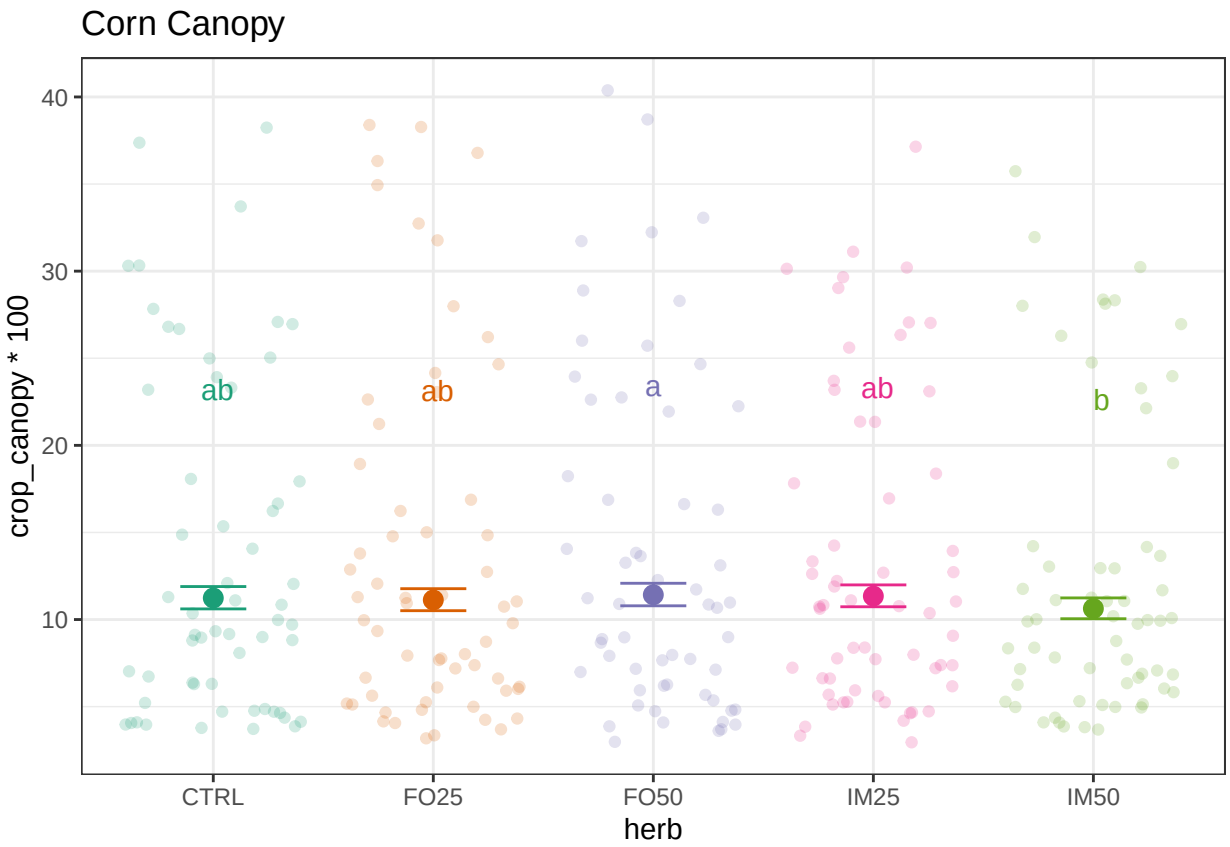


Figure with herbicide

```
cn_canopyherb
```



Canopy by Location ——— Chose to go with Condensed analysis

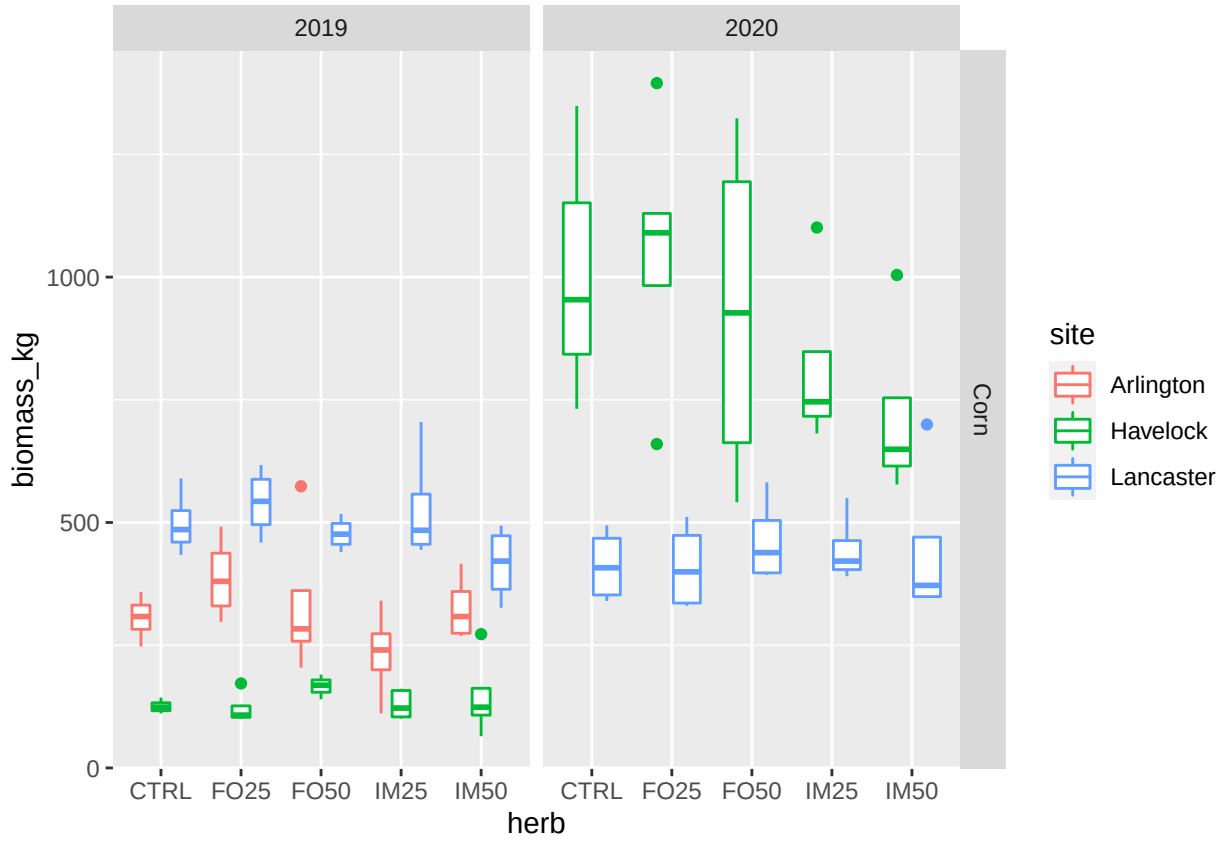
Arlington Corn Canopy

Lancaster Corn Canopy

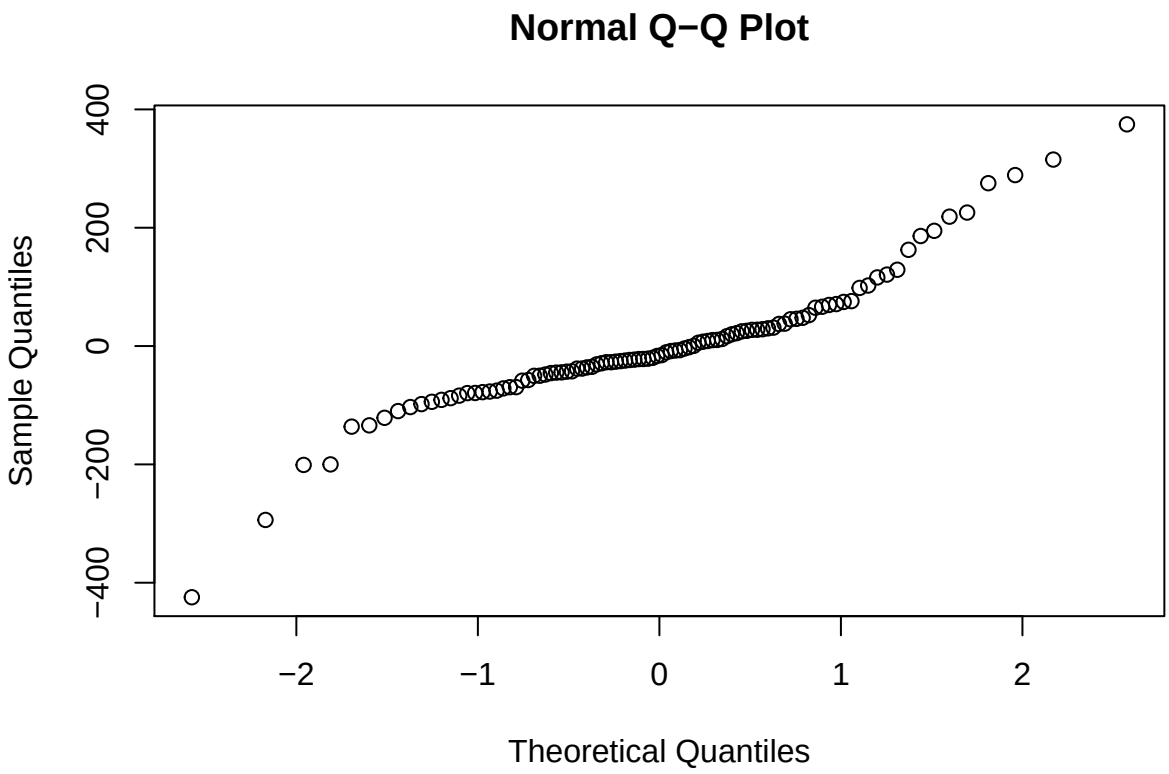
Havelock Corn Canopy

Cover Crop Biomass analysis

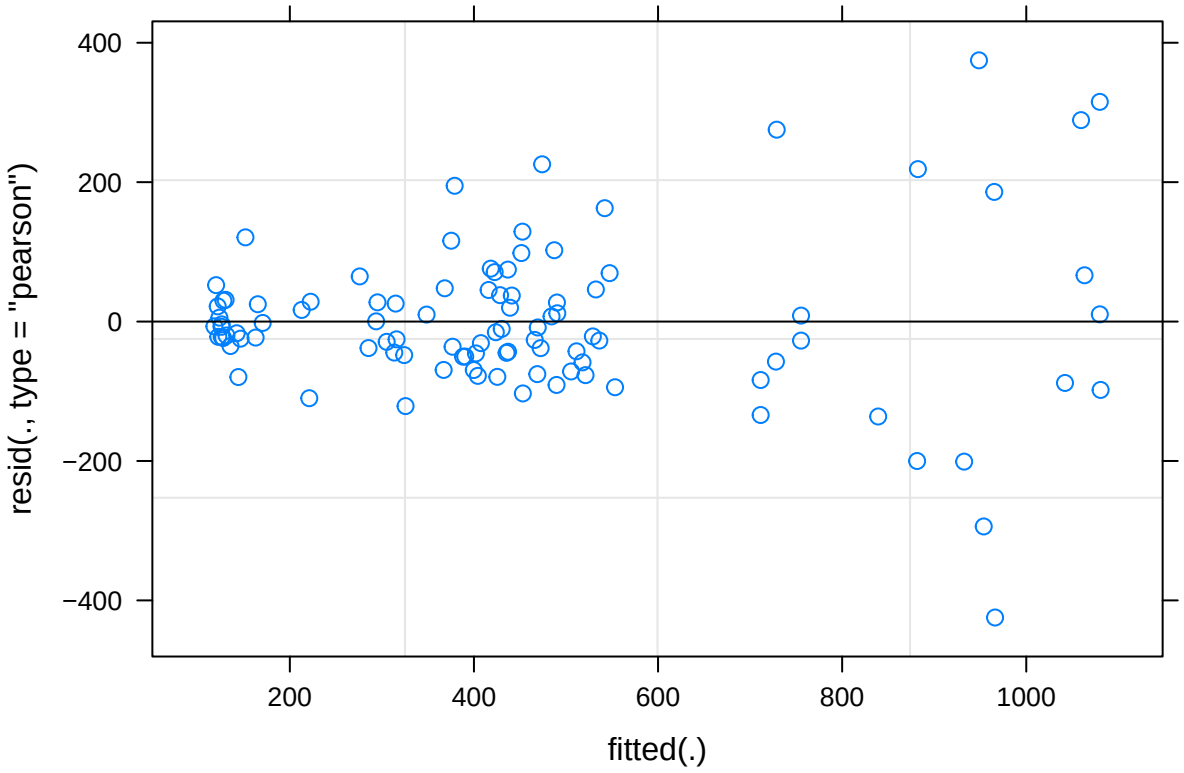
```
CornCC %>%
  ggplot(aes(x = herb, y = biomass_kg, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



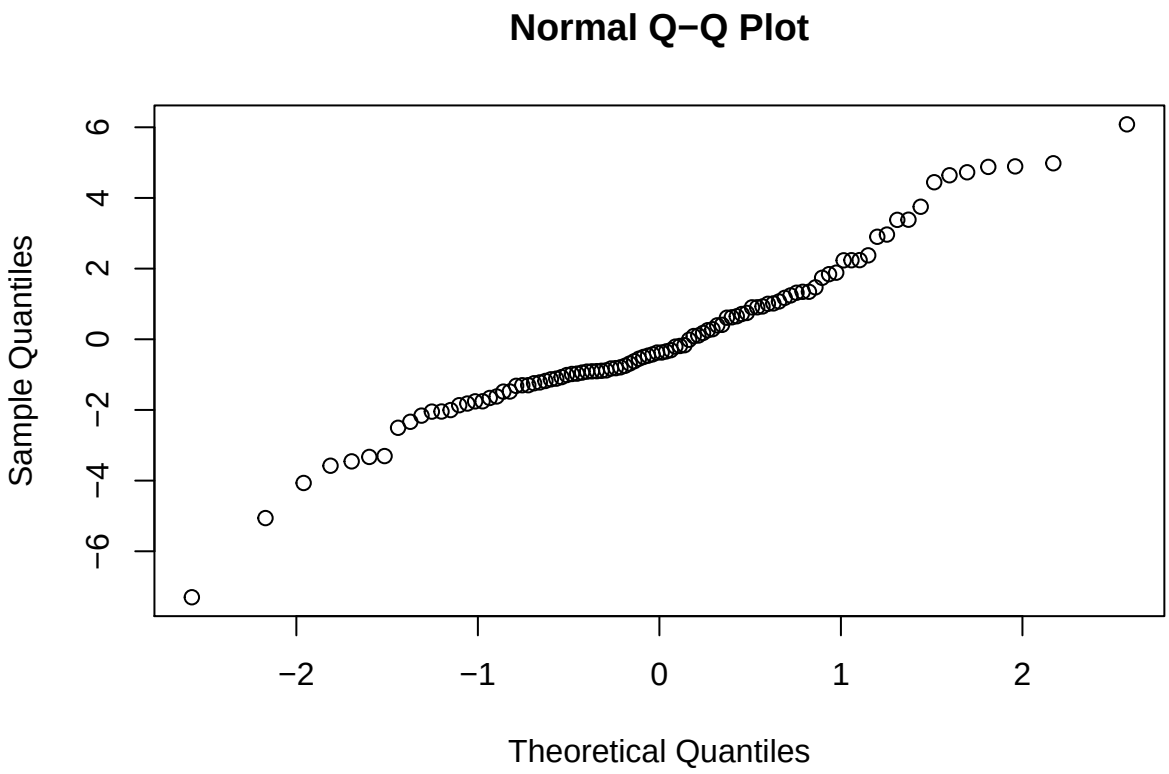

```
cn_cc_bio= lmer(biomass_kg~ site_crop_yr * herb + (1|site_crop_yr:rep), data=CornCC)

qqnorm(resid(cn_cc_bio))
```



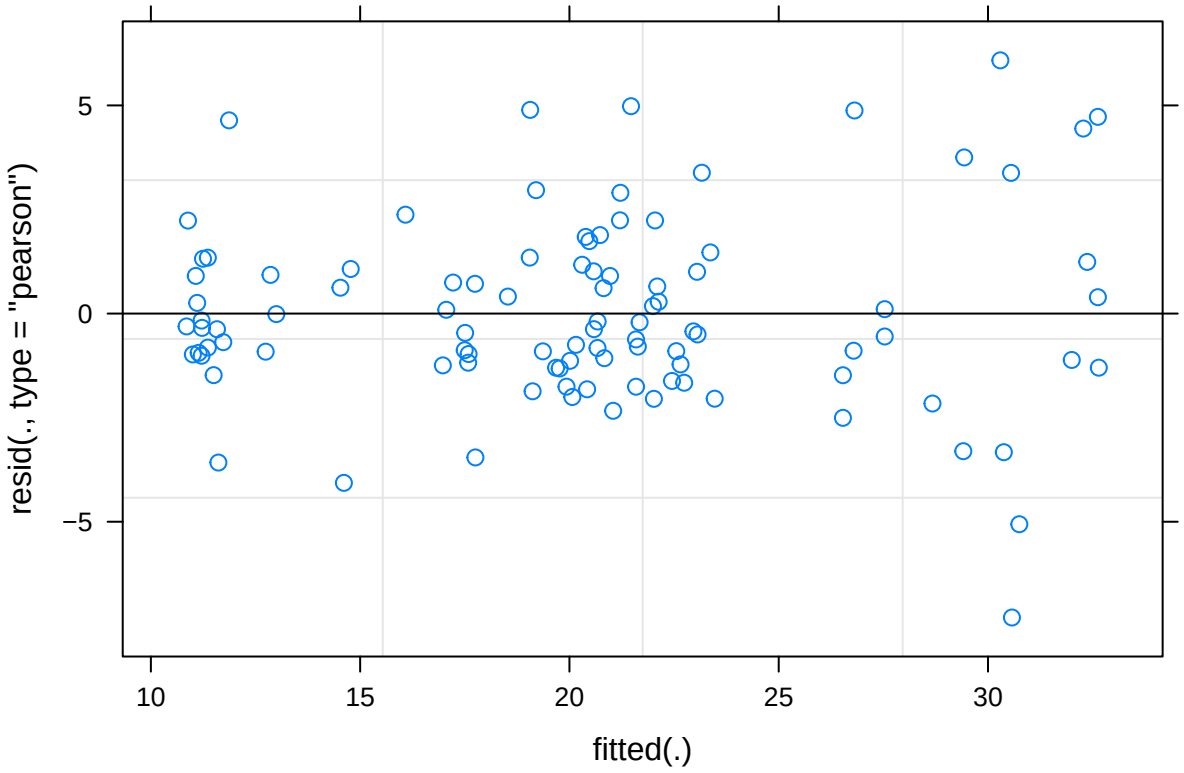

```
plot(cn_cc_bio)
```




```
#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))
```




```
plot(cn_cc_bio1)
```

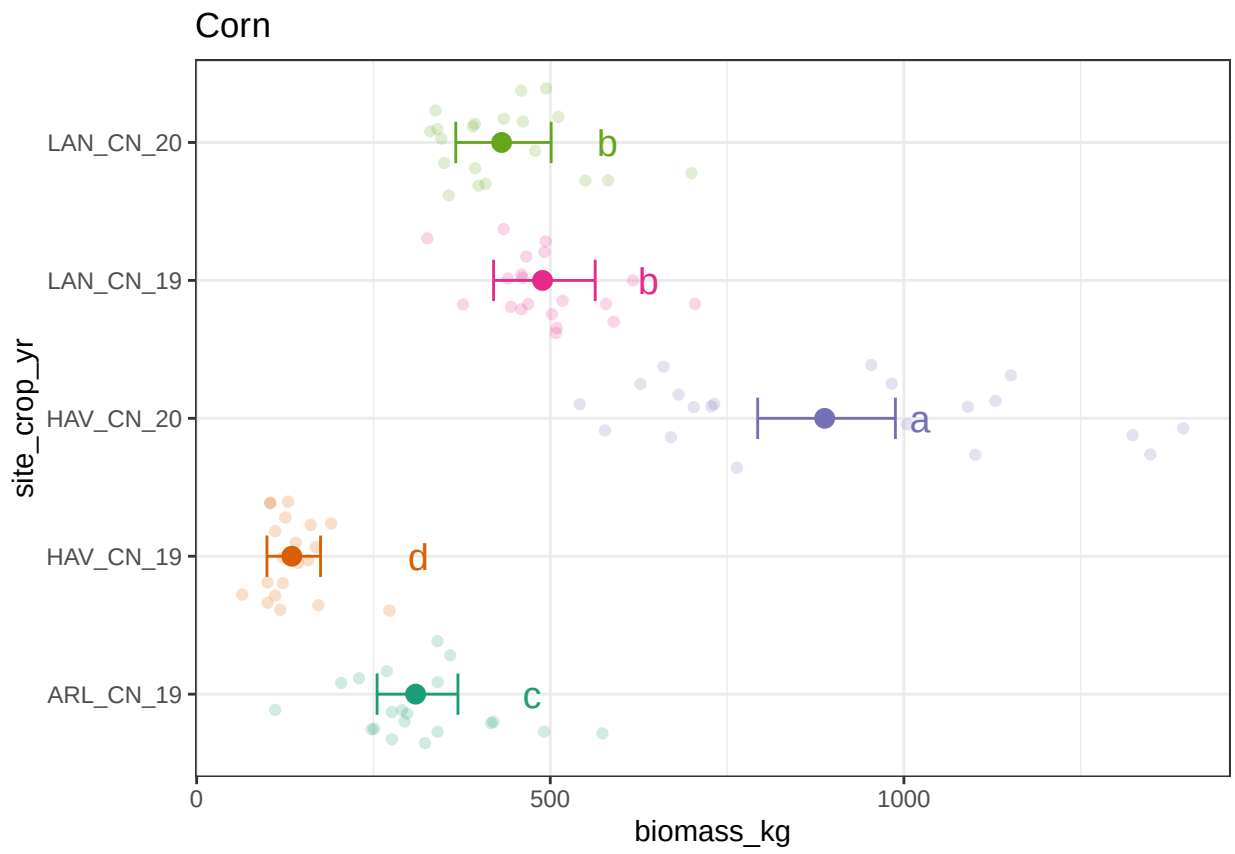



```
#assumptions improved. Use this one!

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
```

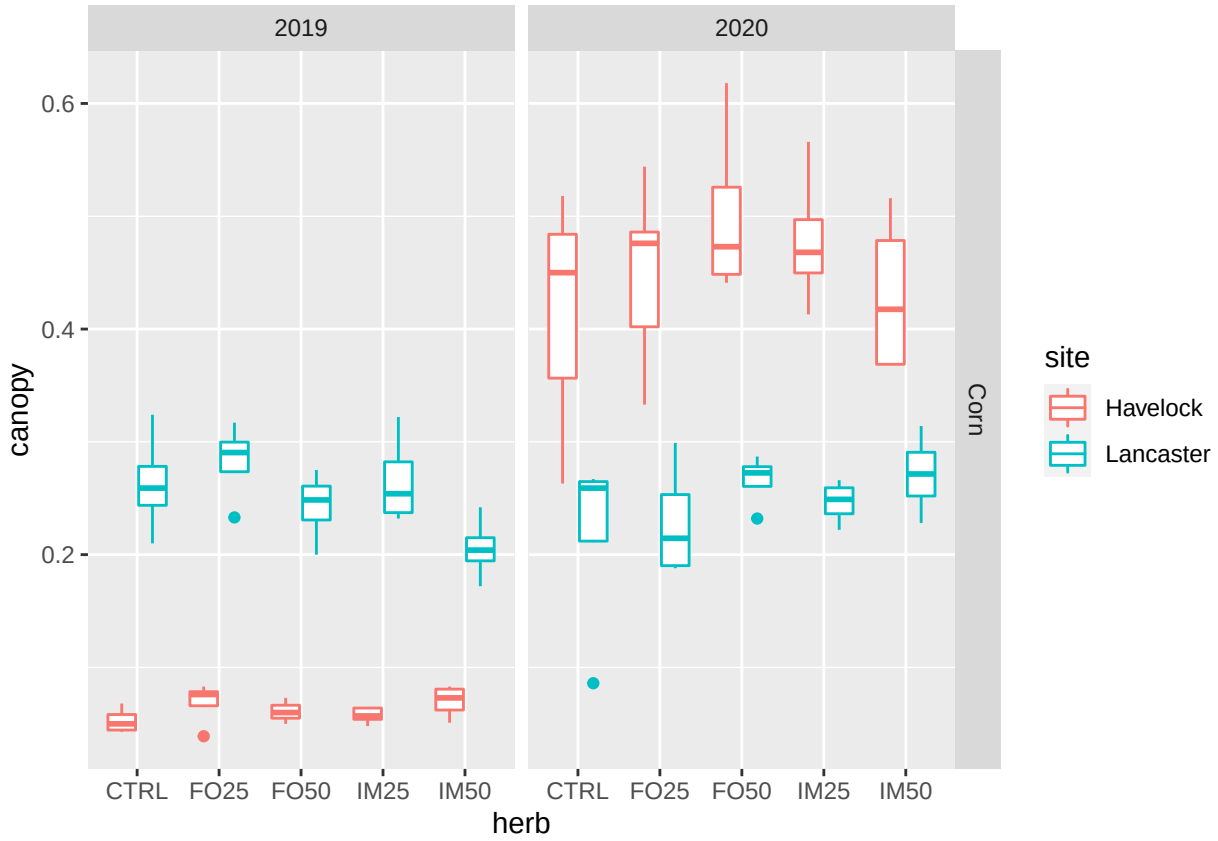
```
Corn_CCbio
```



Cover Crop Canopy

Corn

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



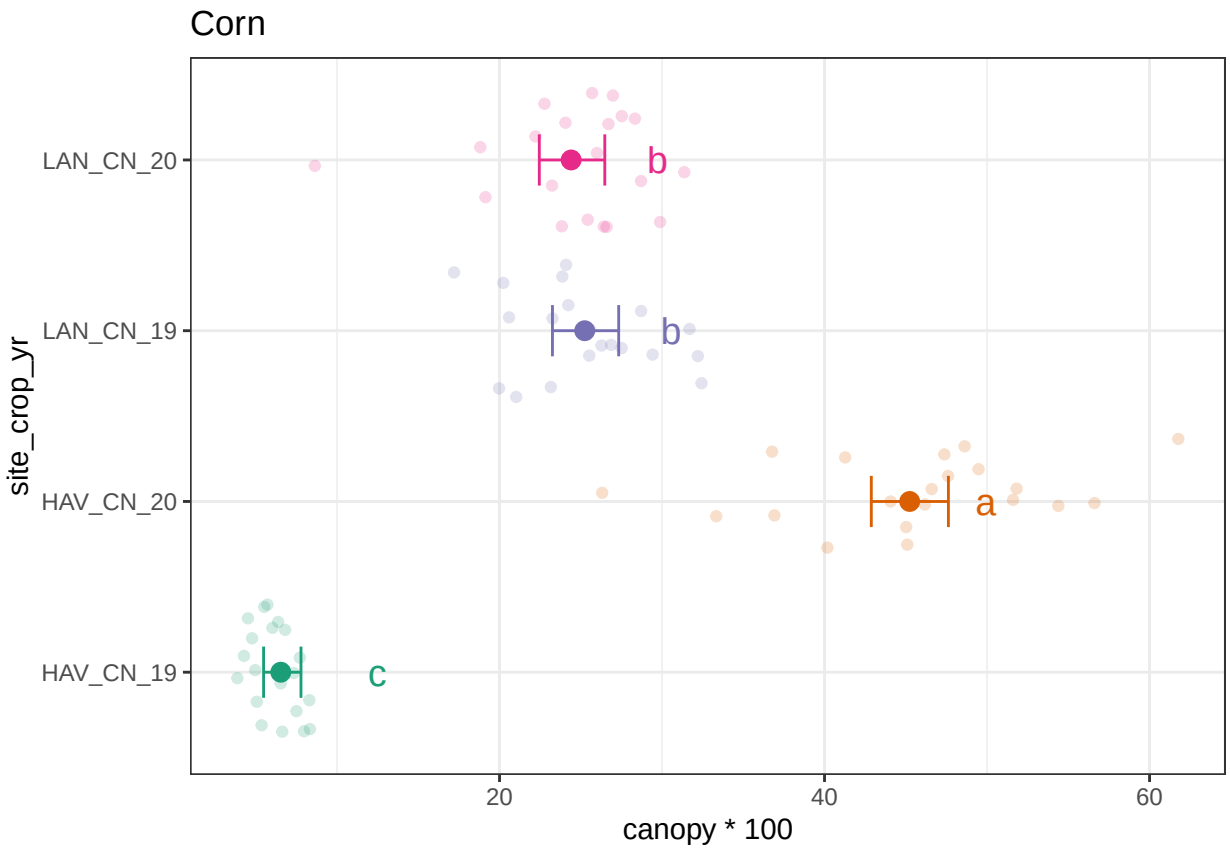
Based on differences between location across growing seasons I thought it was best to proceed with testing site-year as a fixed effect.

```
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
```

```
Corn_CCcan
```


Corn
LAN_CN_20
LAN_CN_19
HAV_CN_20
HAV_CN_19
site_crop_yr
b
b
a
c
20
40
60
canopy * 100