

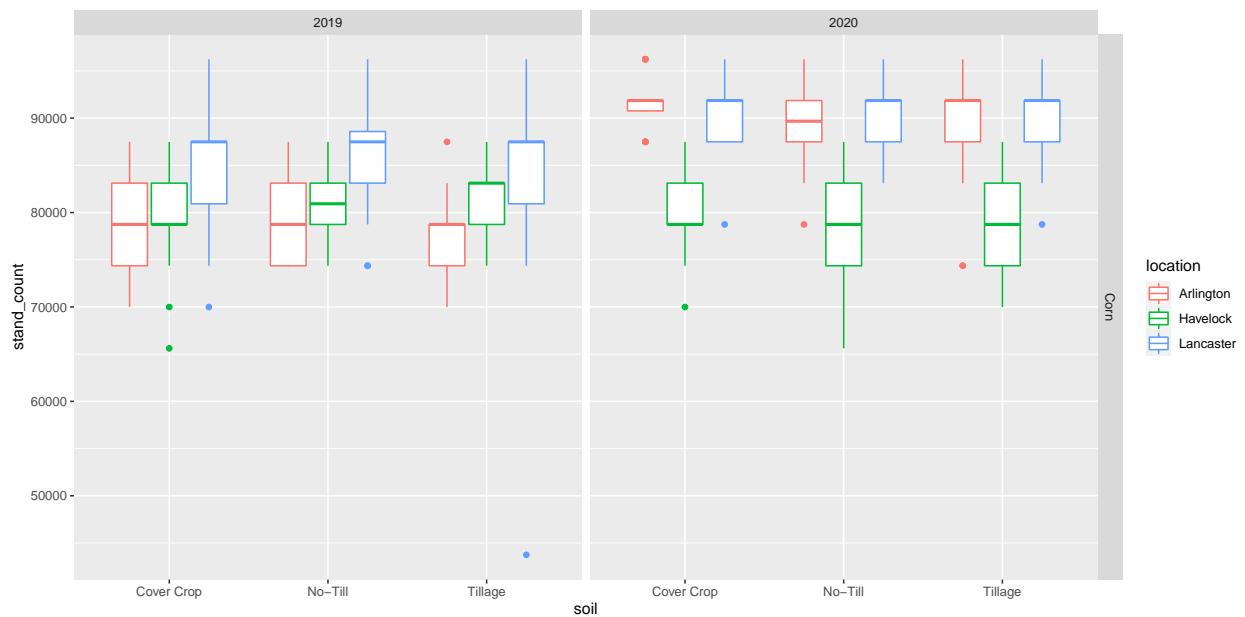
Carryover 2.0

Kolby Grint

11/20/2020

Stand Counts

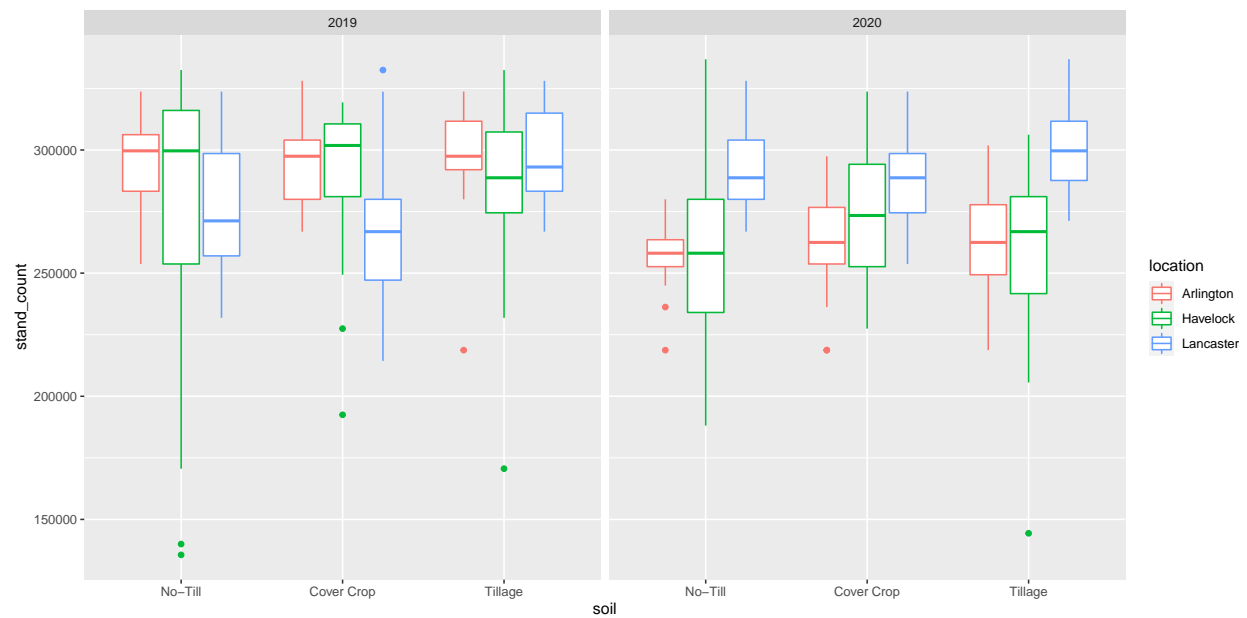
```
Corn1 %>%  
  ggplot(aes(x = soil, y = stand_count, color = location)) +  
  geom_boxplot() +  
  facet_grid(crop ~ year)
```



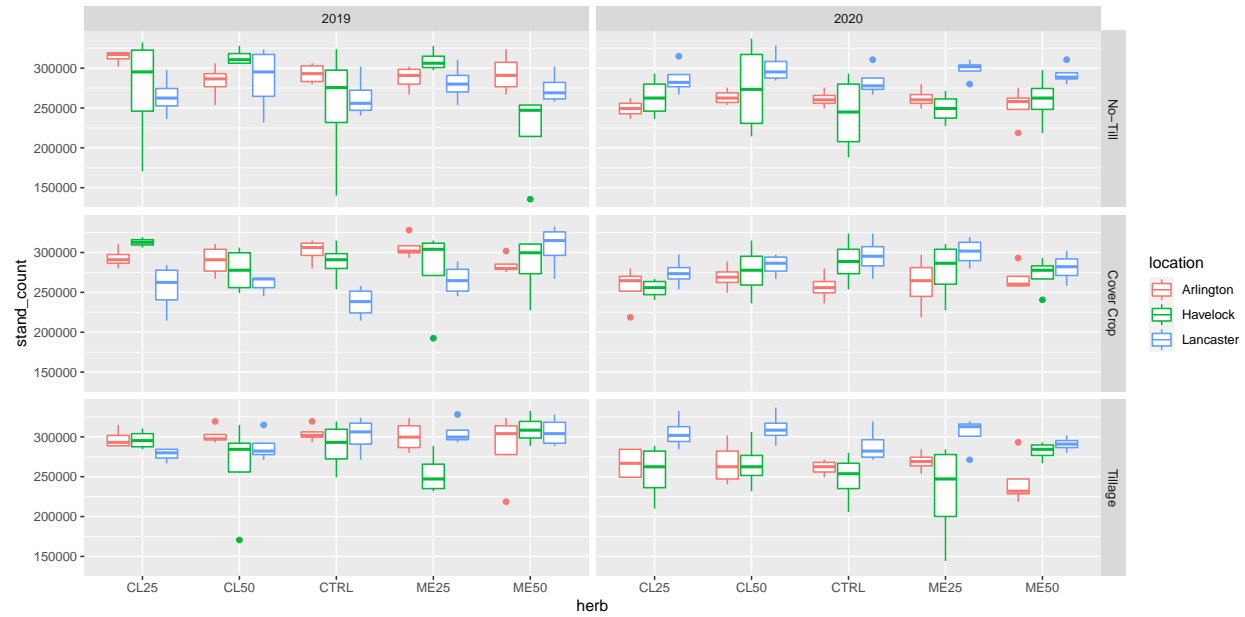
```
Corn1 %>%  
  ggplot(aes(x = herb, y = stand_count, color = location)) +  
  geom_boxplot() +  
  facet_grid(soil ~ year)
```



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



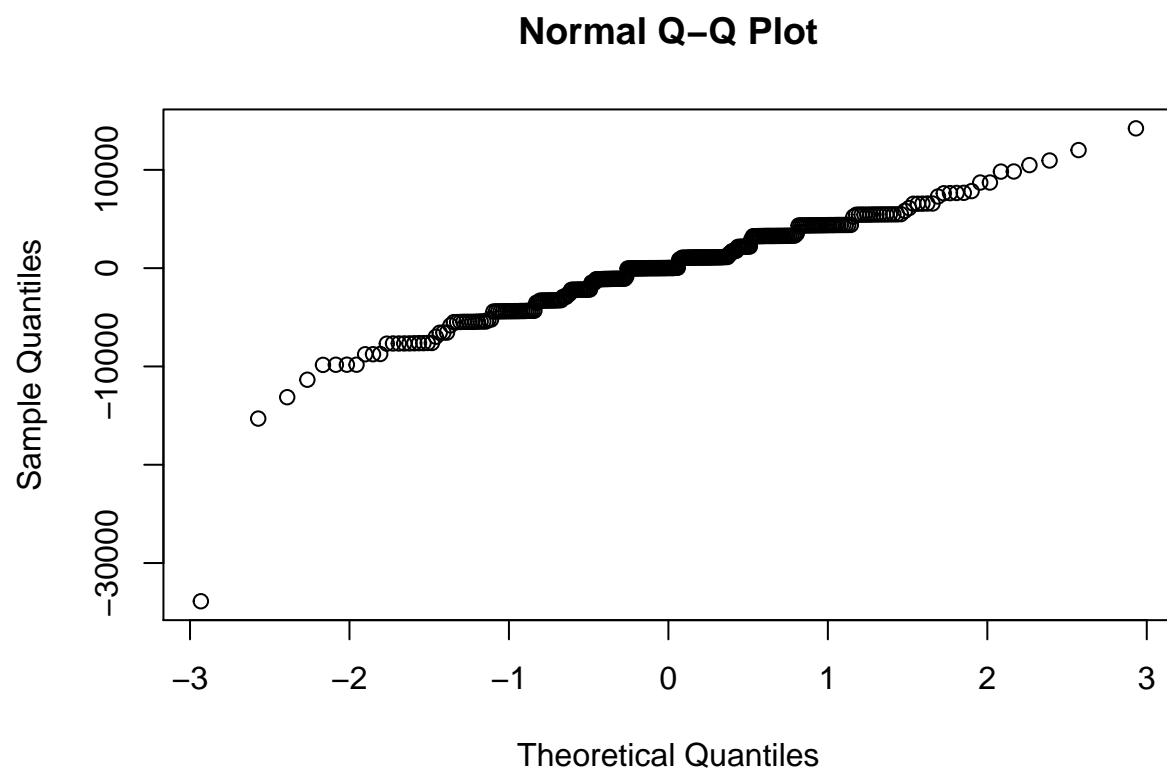
```
Soybean1 %>%
  ggplot(aes(x = herb, y = stand_count, color = location)) +
  geom_boxplot() +
  facet_grid(soil ~ year)
```



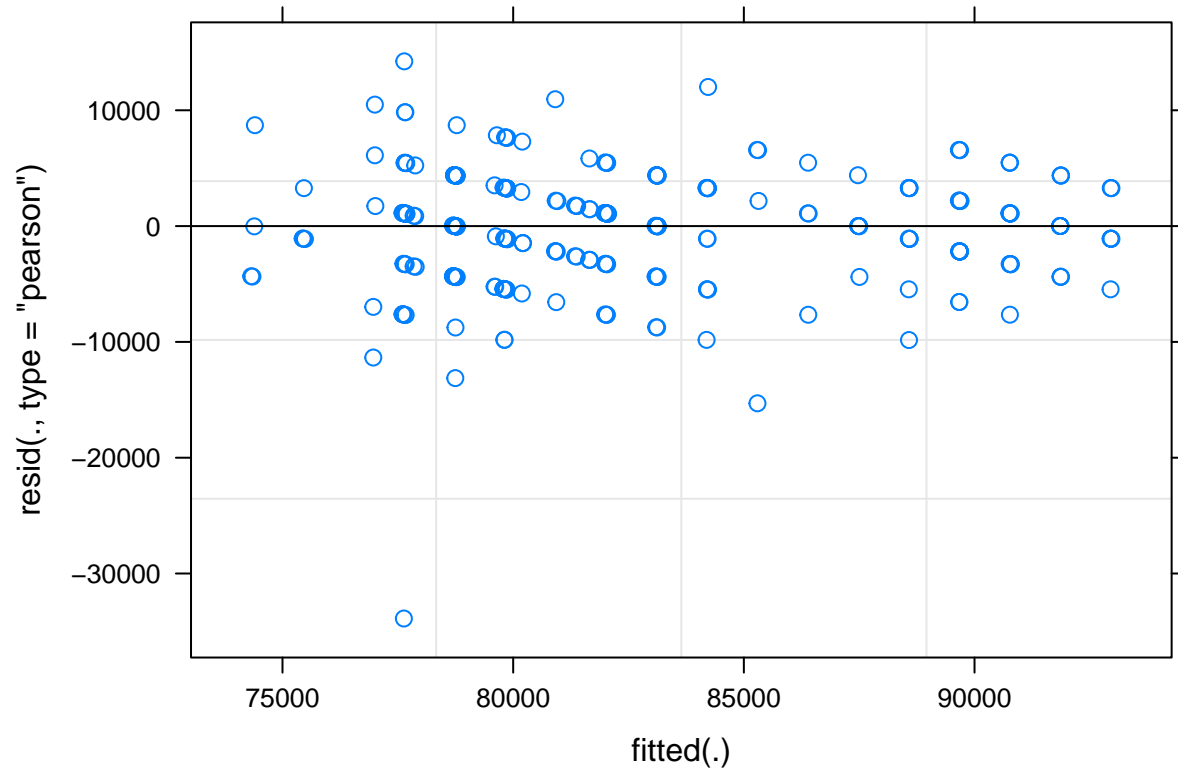
Based on these visual representations it doesn't appear to me that there are really any consistent patterns as a function of soil management, herbicide treatment, location, or year. There does appear to be differences in location across seasons. Therefore, I think it is best if we test for site-year 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
```

```
cn_cc_stand_lsmeans= lsmeans(cn_stand ,~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
cn_cc_standCLD<- CLD(cn_cc_stand_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, revers
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(cn_cc_stand_lsmeans, alpha = 0.05, Letters = letters, :
```

```
## `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

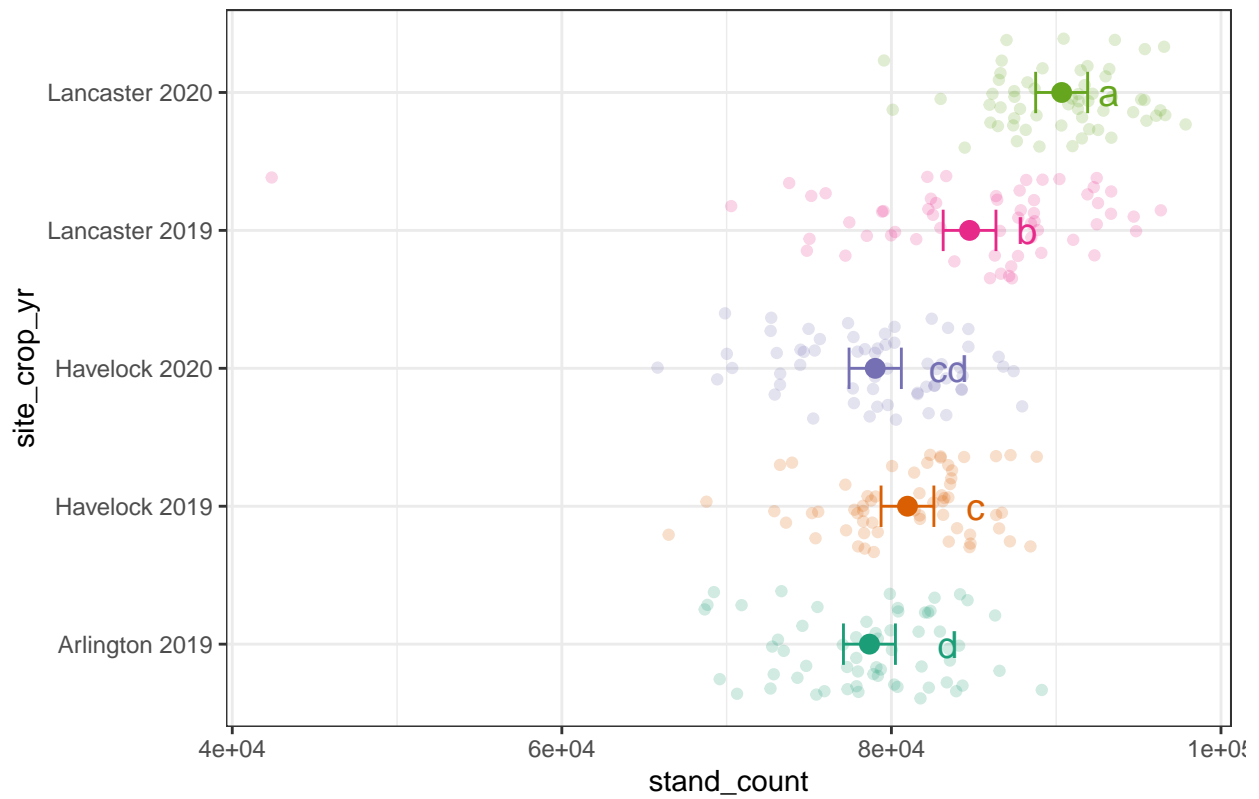
```
cn_cc_standCLD <- as_tibble(cn_cc_standCLD) %>%  
  rename(stand_count = lsmean) %>%  
  mutate(site_crop_yr = fct_recode(site_crop_yr,  
    "Arlington 2019" = "ARL_CN_19",  
    "Havelock 2019" = "HAV_CN_19",  
    "Havelock 2020" = "HAV_CN_20",  
    "Lancaster 2019" = "LAN_CN_19",  
    "Lancaster 2020" = "LAN_CN_20")) %>%  
  arrange(site_crop_yr)
```

```
## Warning: Unknown levels in `f`: ARL_CN_19, HAV_CN_19, HAV_CN_20, LAN_CN_19,
```

```
## LAN_CN_20
```

```
ggplot(cn_cc_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")
```

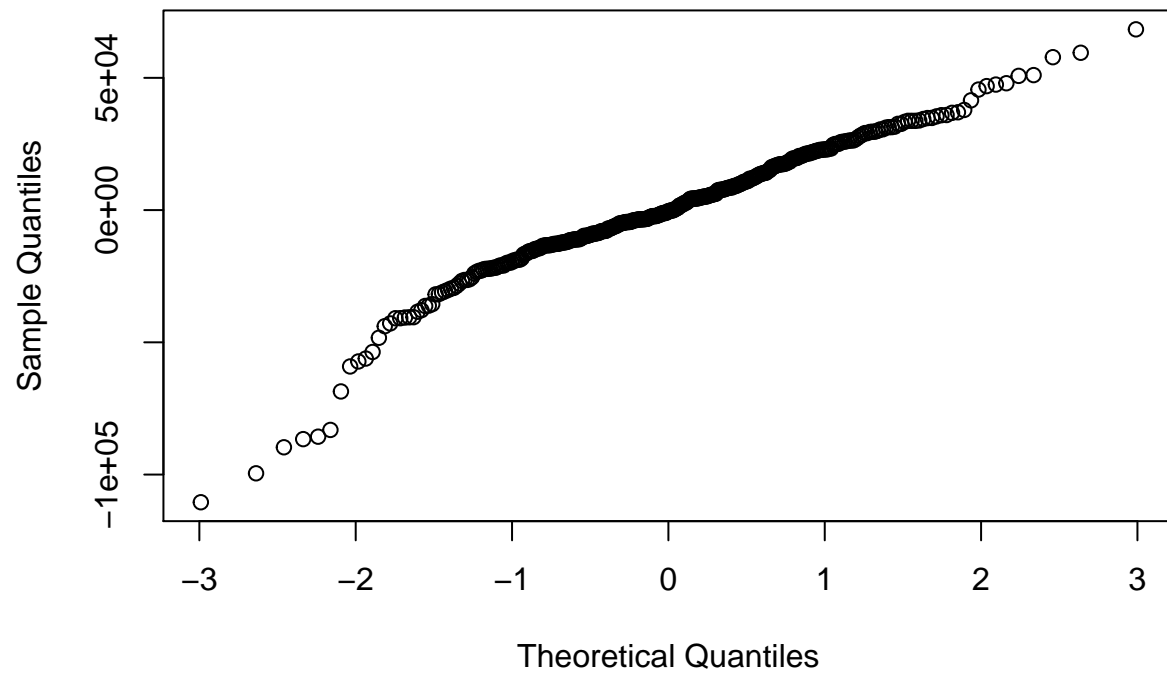
Corn Stand Counts



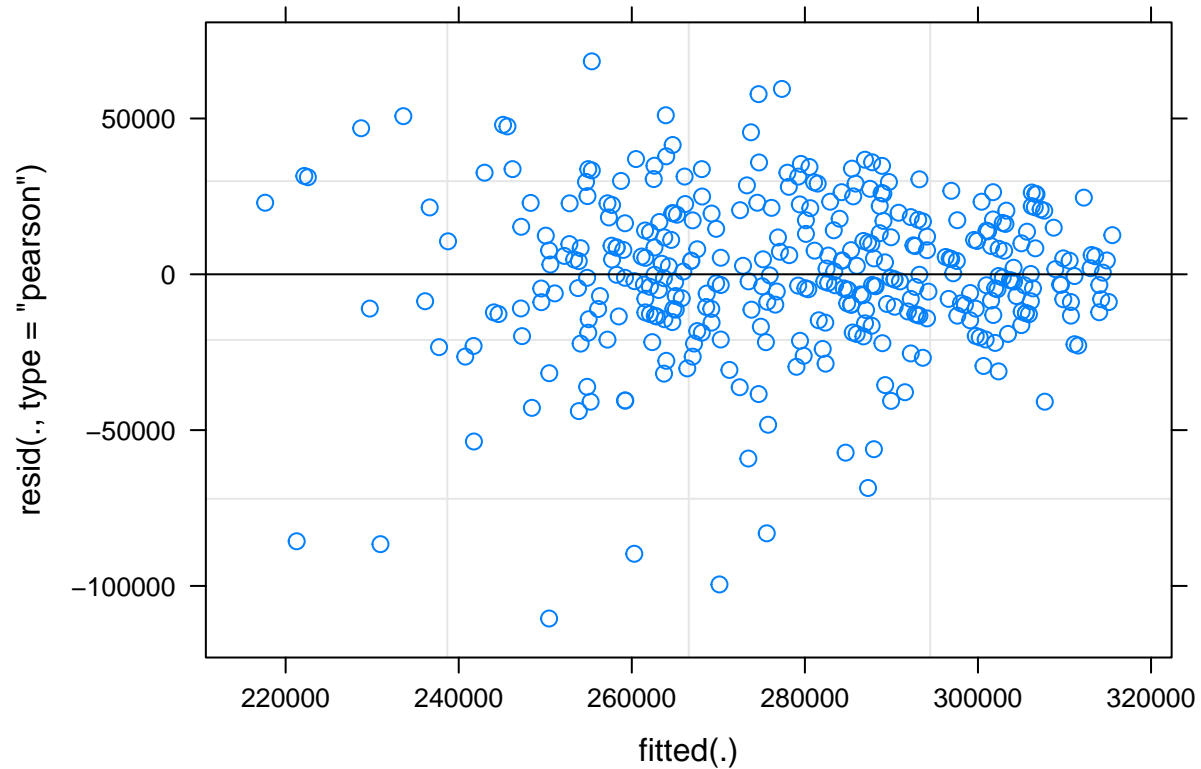
Soybean

```
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.
```

```
sb_cc_stand_lsmeans= lsmeans(sb_stand ,~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
sb_cc_standCLD<- CLD(sb_cc_stand_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, revers
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(sb_cc_stand_lsmeans, alpha = 0.05, Letters = letters, :
```

```
## `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

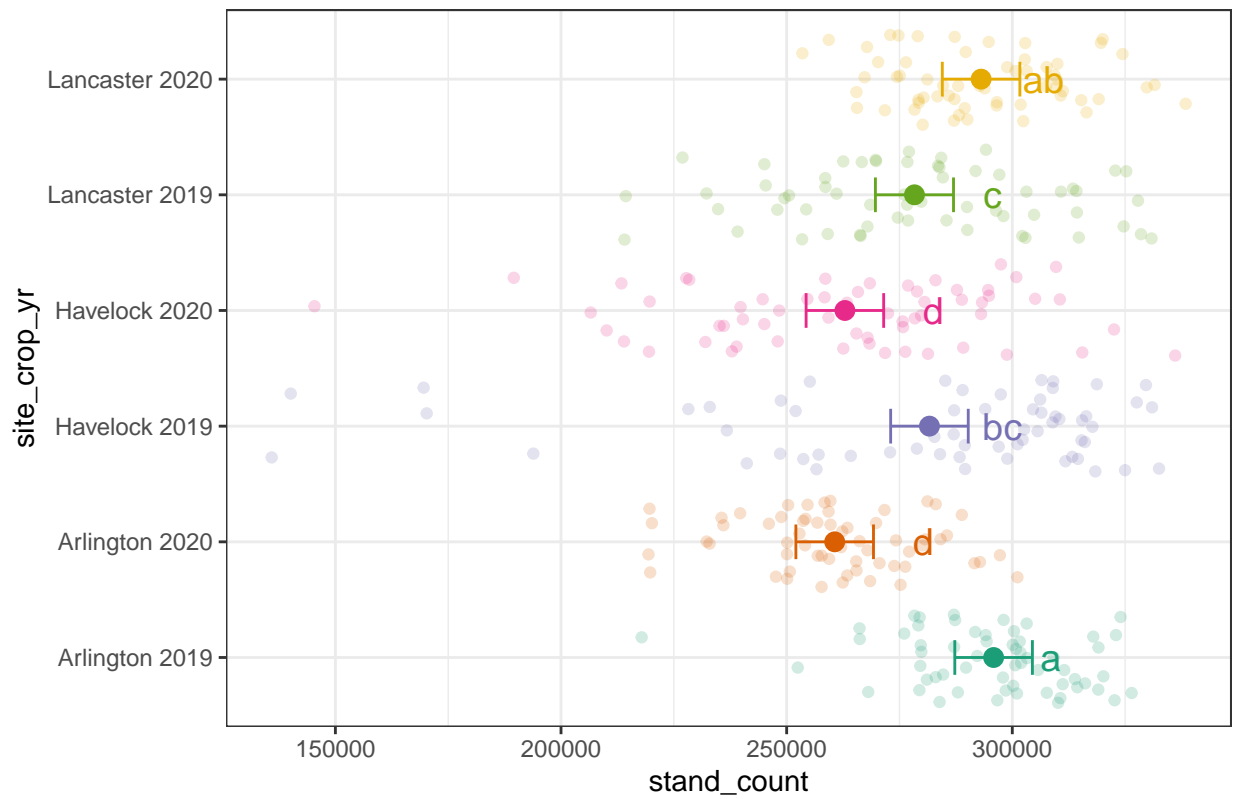
```
sb_cc_standCLD <- as_tibble(sb_cc_standCLD) %>%  
  rename(stand_count = lsmean) %>%  
  mutate(site_crop_yr = fct_recode(site_crop_yr,  
    "Arlington 2019" = "ARL_SB_19",  
    "Arlington 2020" = "ARL_SB_20",  
    "Havelock 2019" = "HAV_SB_19",  
    "Havelock 2020" = "HAV_SB_20",  
    "Lancaster 2019" = "LAN_SB_19",  
    "Lancaster 2020" = "LAN_SB_20")) %>%  
  arrange(site_crop_yr)
```

```
## Warning: Unknown levels in `f`: ARL_SB_19, ARL_SB_20, HAV_SB_19, HAV_SB_20,
```

```
## LAN_SB_19, LAN_SB_20
```

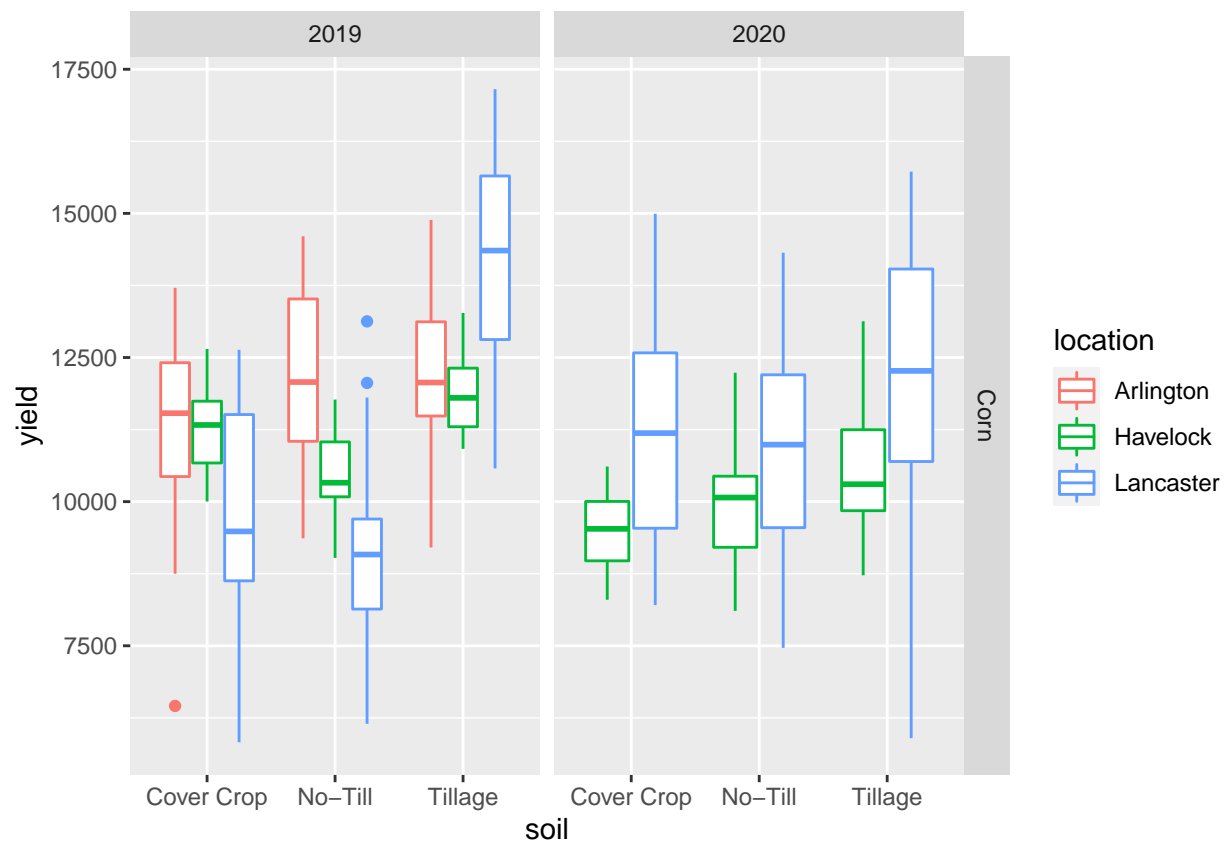
```
ggplot(sb_cc_standCLD, aes(x= site_crop_yr, y= stand_count, color= site_crop_yr)) +  
  geom_point(size= 3) +  
  geom_errorbar(aes(ymin= lower.CL, ymax= upper.CL), width= .3) +  
  geom_text(aes(label = .group), nudge_y = 15000, size= 5) +  
  geom_jitter(data = Soybean1 ,mapping = aes(y = stand_count), alpha = 0.2) +  
  coord_flip() +  
  theme_bw() +  
  scale_color_brewer(palette = "Dark2") +  
  theme(legend.position = "none") +  
  labs(title = "Soybean Stand Counts")
```

Soybean Stand Counts



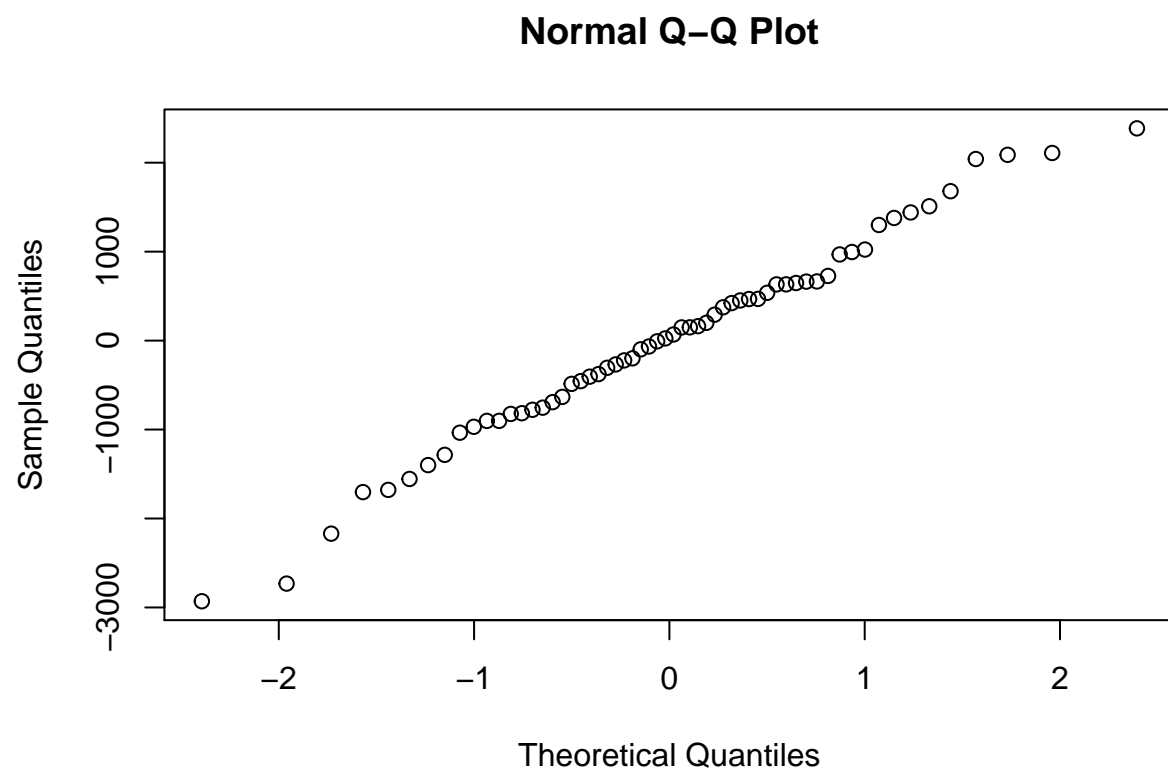
Corn Yield

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

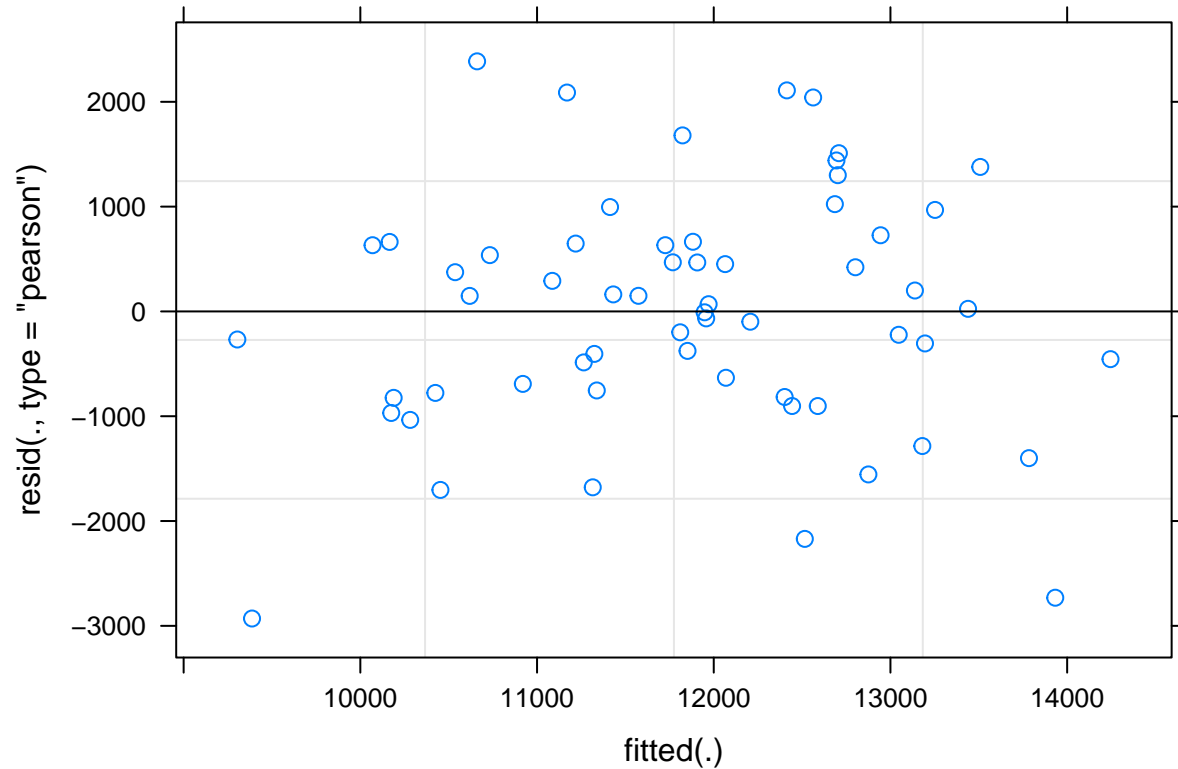


Arlington 2019 Analysis — We decided to use only this site-year in the paper

```
arlc_n_yield1 = lmer(yield ~ soil*herb + (1|rep):site_crop_yr, data = (filter(Corn1, site_crop_yr == "Arlington", year == 2019)))
qqnorm(resid(arlc_n_yield1))
```



```
plot(arlcn_yield1)
```



```
#assumptions look good
```

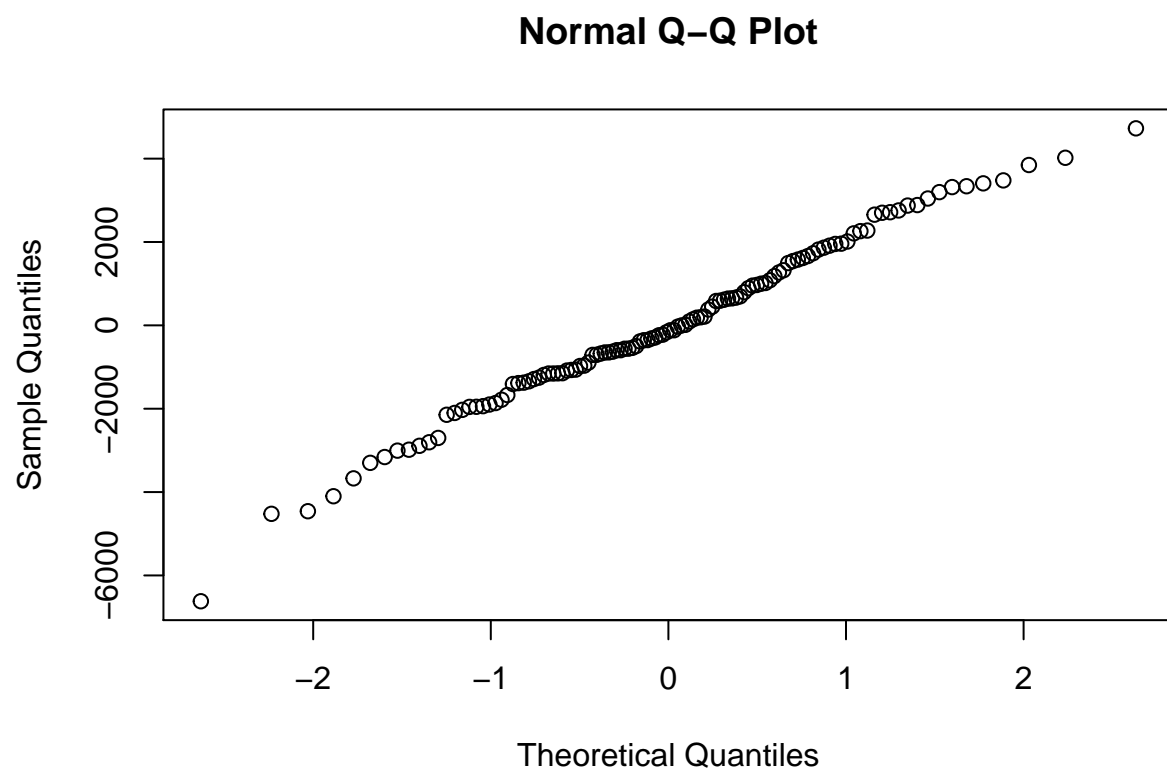
```
anova(arlcn_yield1)
```

```
## 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
```

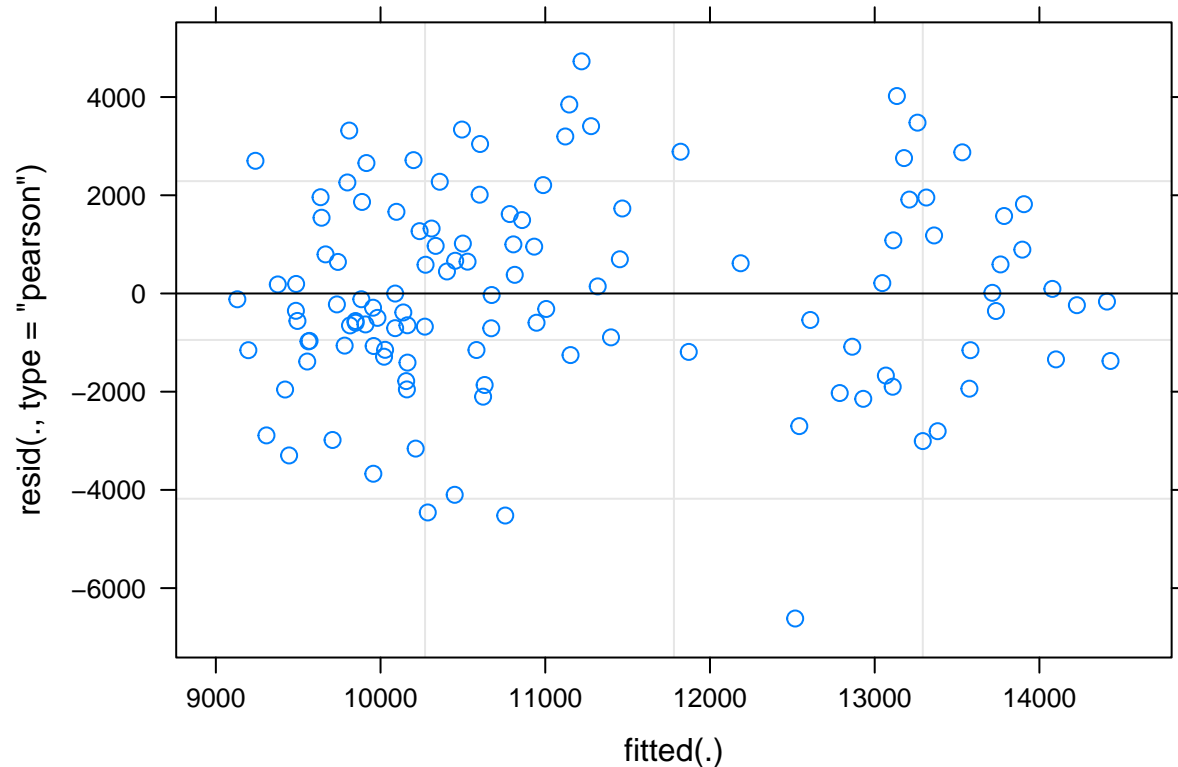
```
#soil managment fixed effect significant
```

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

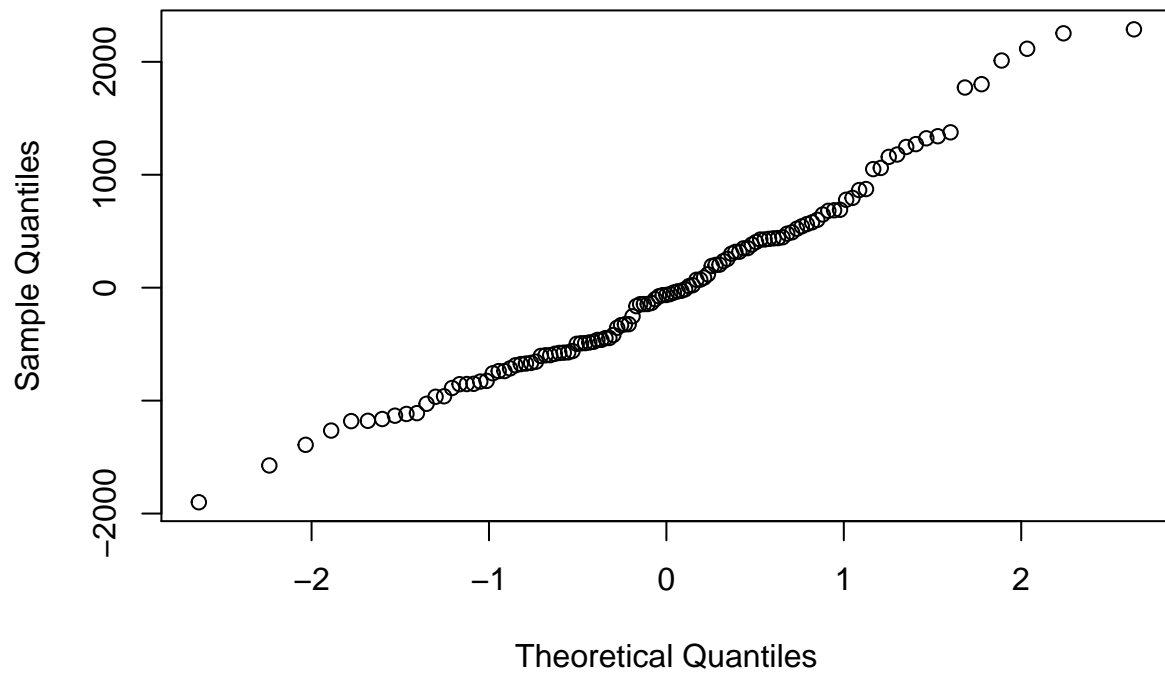
```
havcn_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Corn1, location == "Havelock")))
```

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

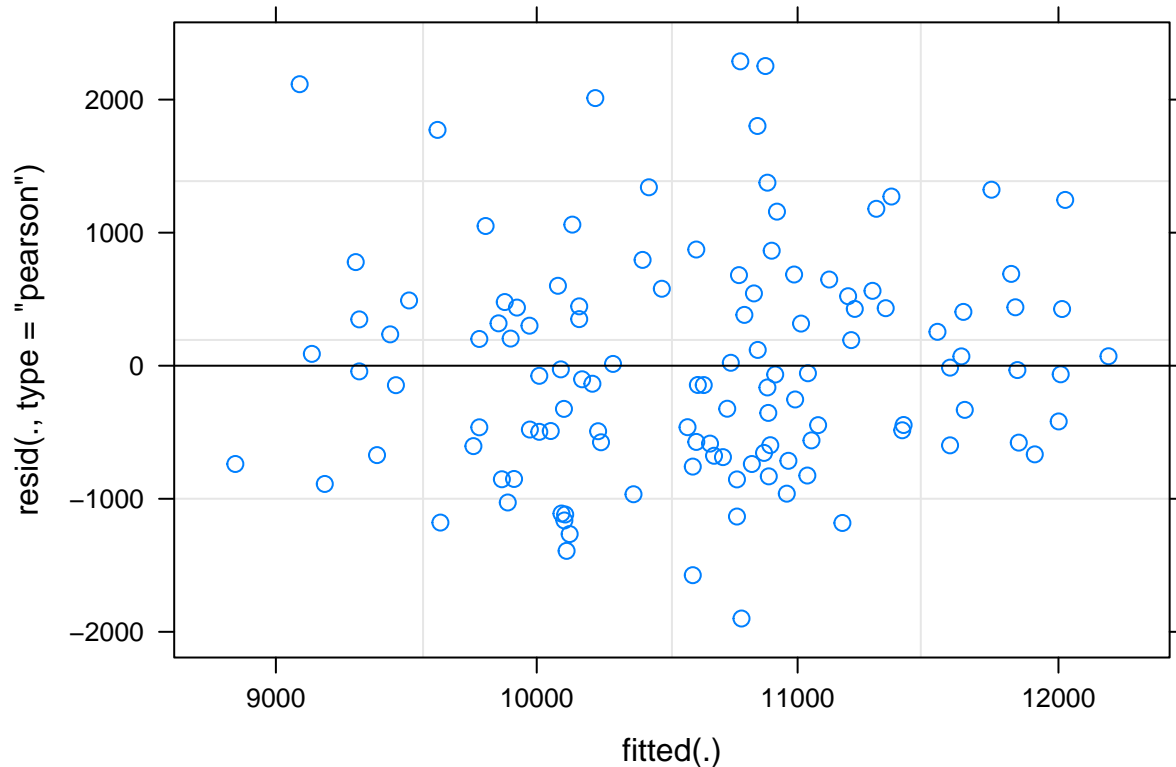
```
#from my understanding the "boundary (singular) fit: see ?isSingular" error means that the estimate of
```

```
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
```

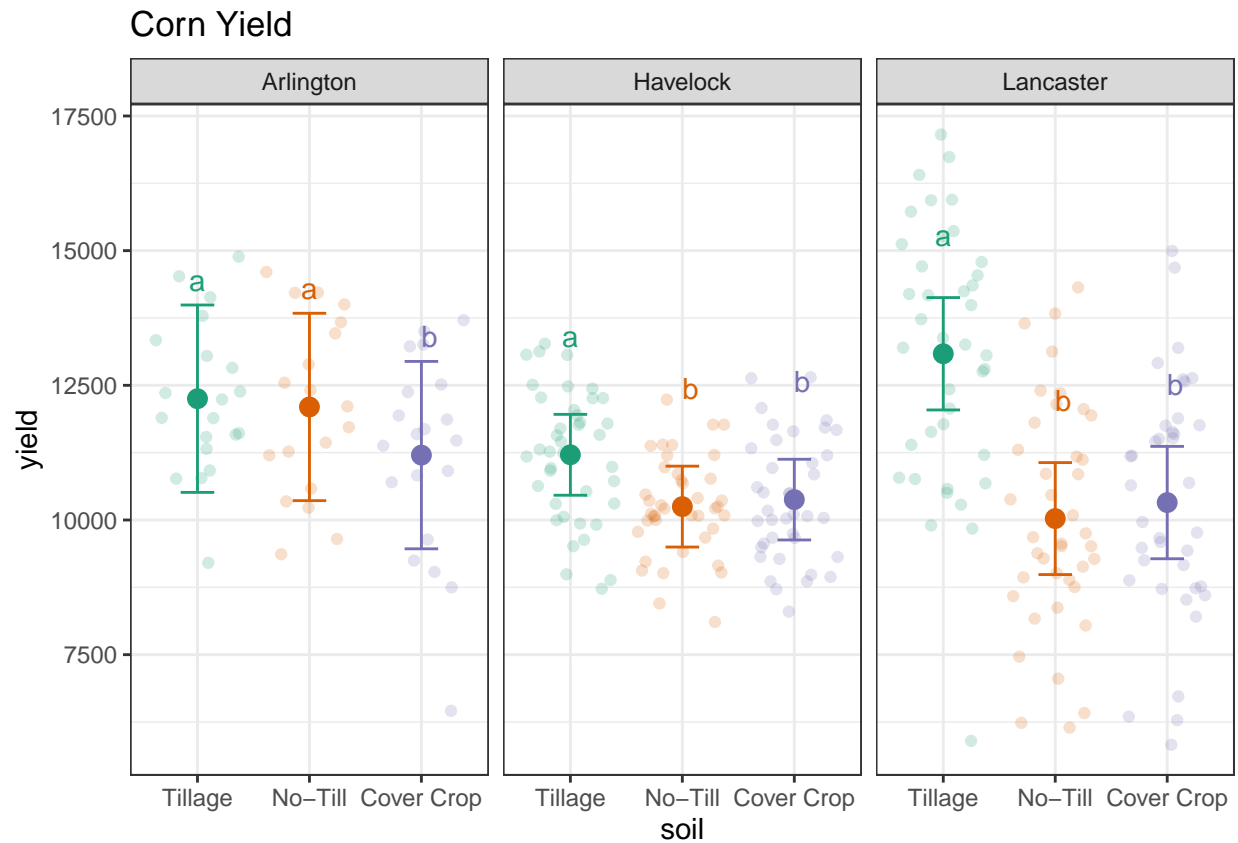
```
#soil management significant
```

```
#summary(havcn_yield)
```

```
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") +
```

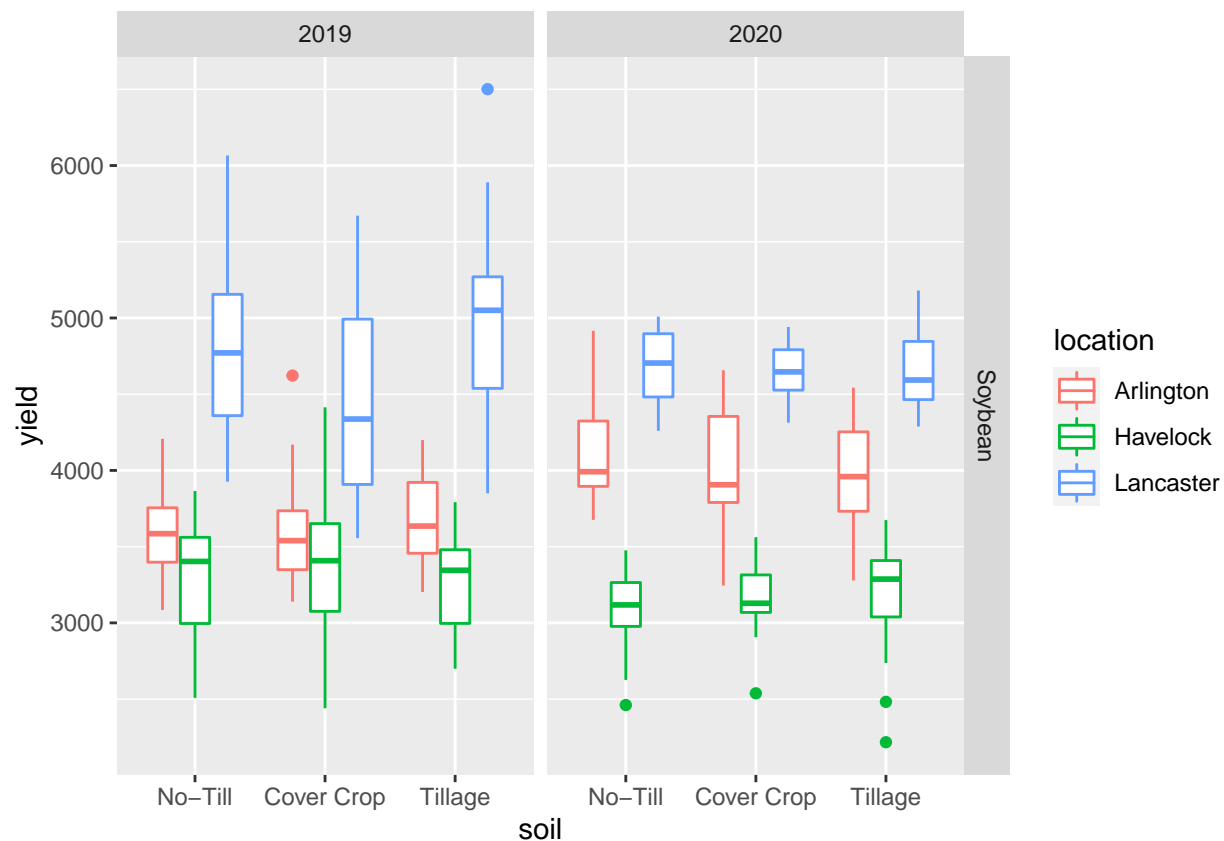
```
theme(legend.position = "none") +
labs(title = "Corn Yield")
```

y1



Soybean Yield

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



Arlington Analysis

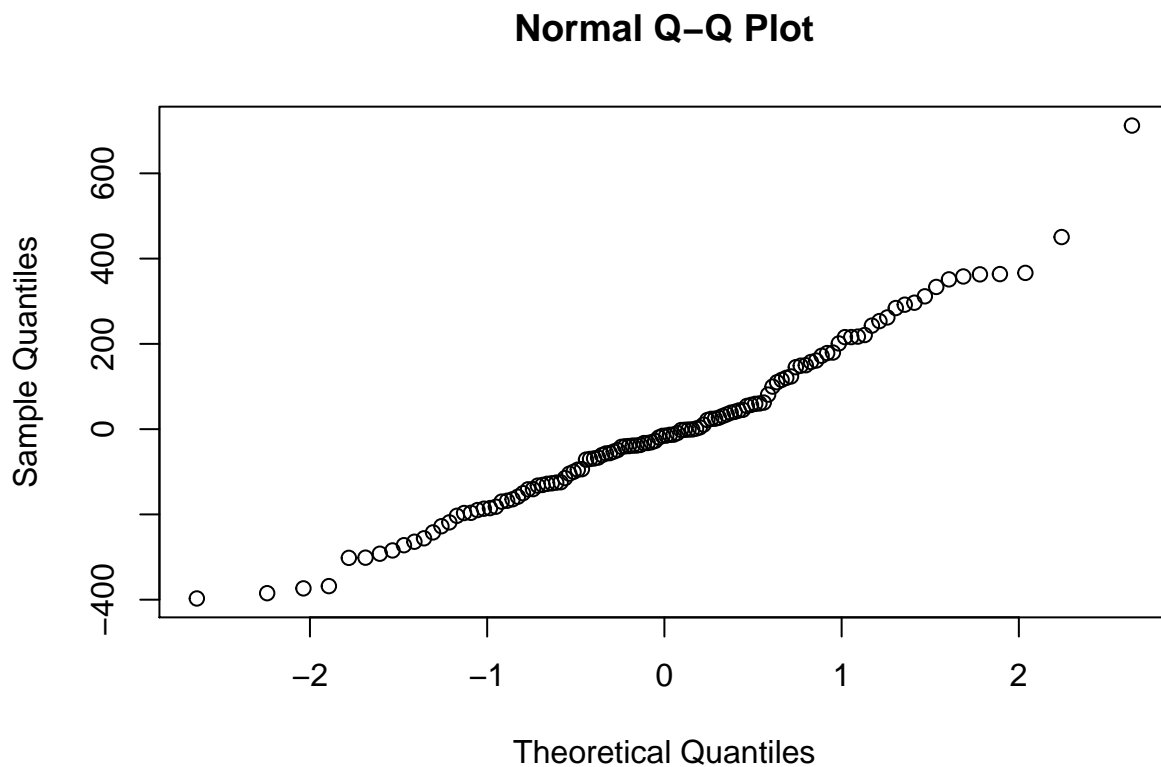
```
arl_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Arlington")))
summary(arl_sb_yield)
```

```
## 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:
```

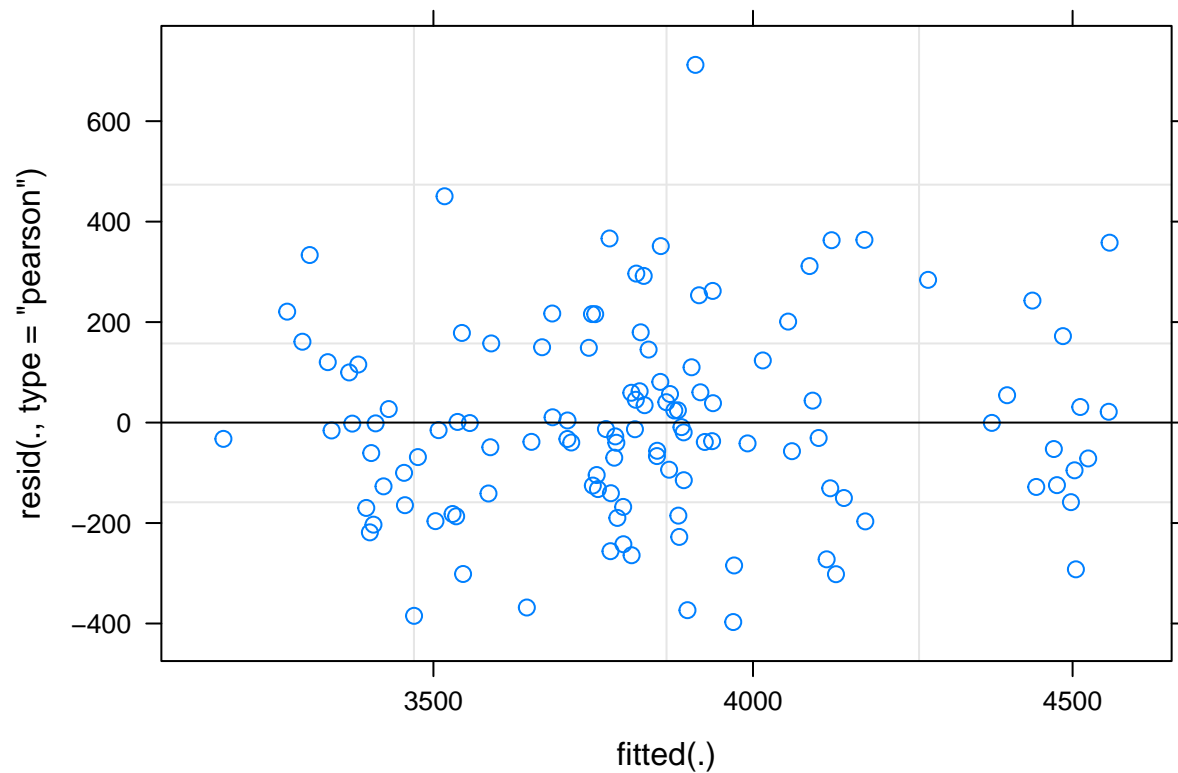
```
##               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      3841.125    149.914    5.135  25.622 1.29e-06 ***
## soilCover Crop      -201.625    106.789   98.000   -1.888   0.0620 .
## soilTillage         -101.875    106.789   98.000   -0.954   0.3424
## herbCL50            -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
```

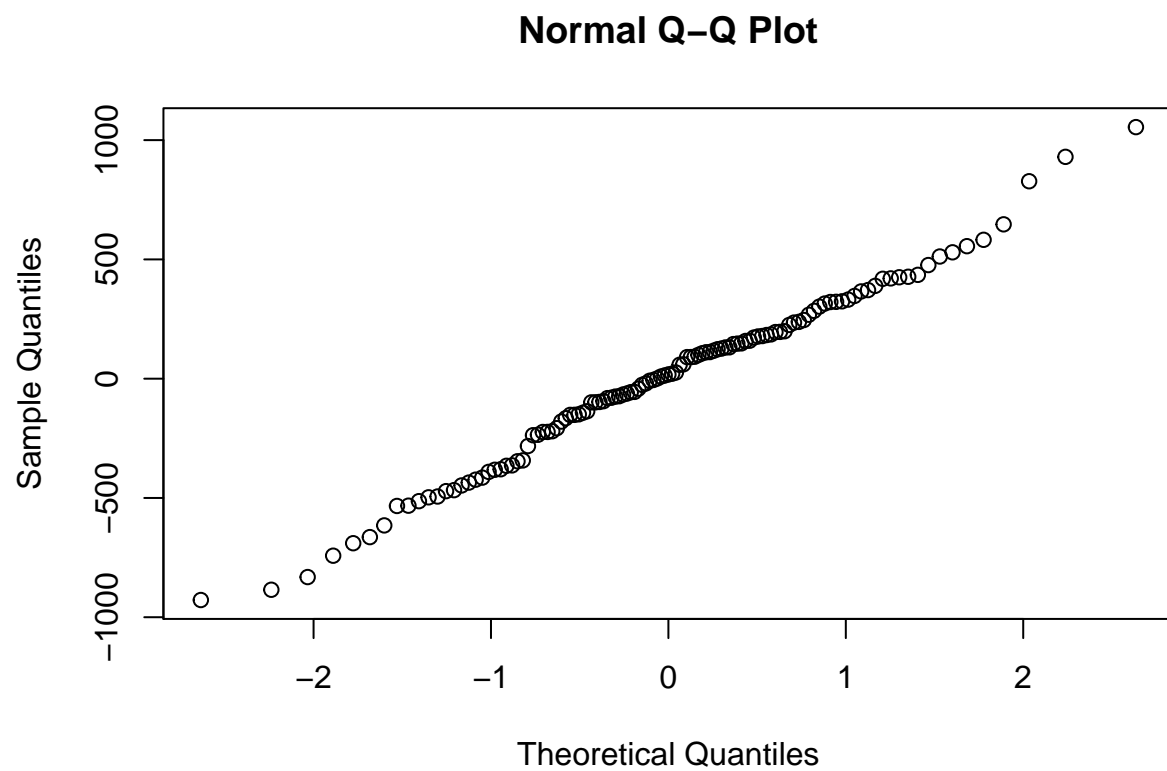
```
#Soil management fixed effect significant
```

Lancaster Analysis

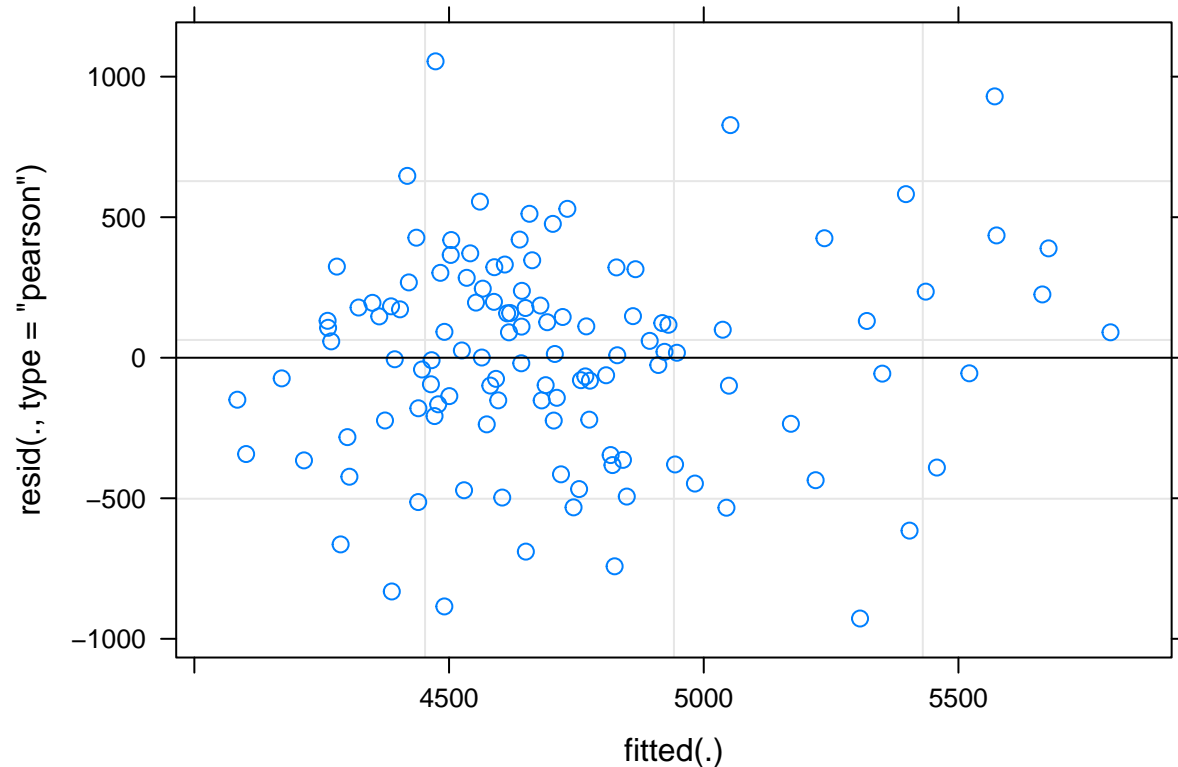
```
lan_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Lancaster")))
```

```
## 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
```

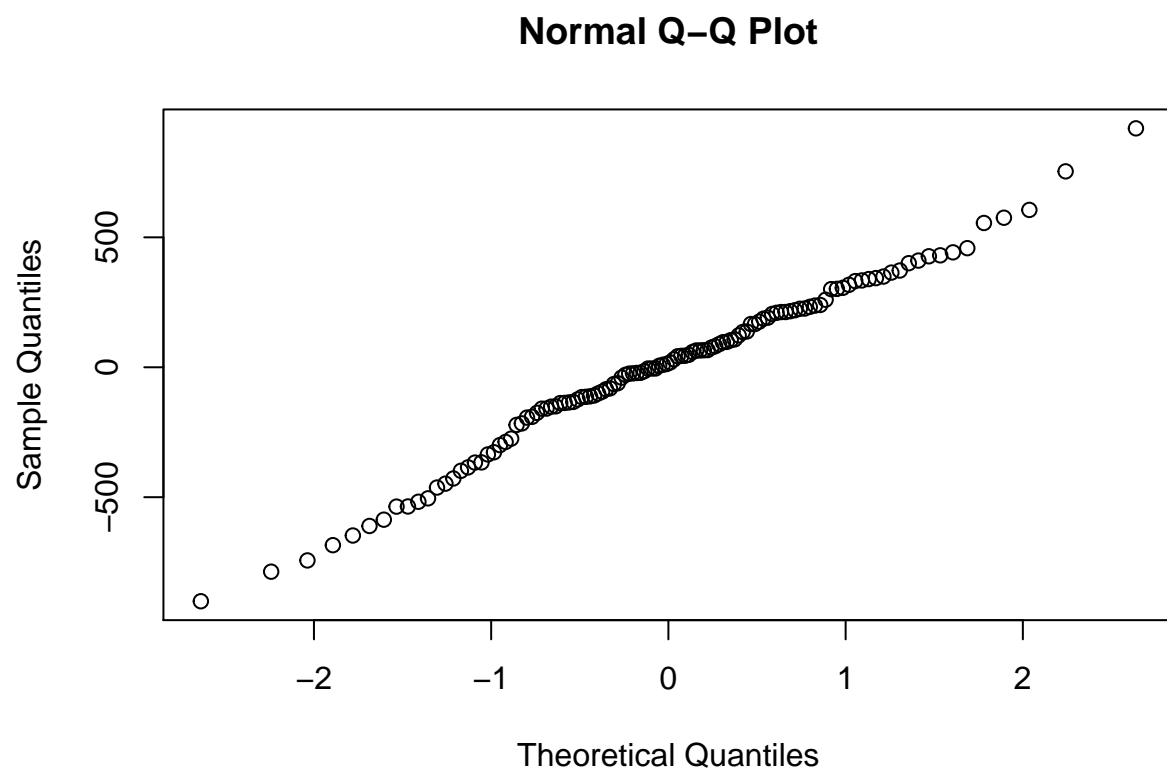
```
#Soil management fixed effect significant
```

Havelock Analysis

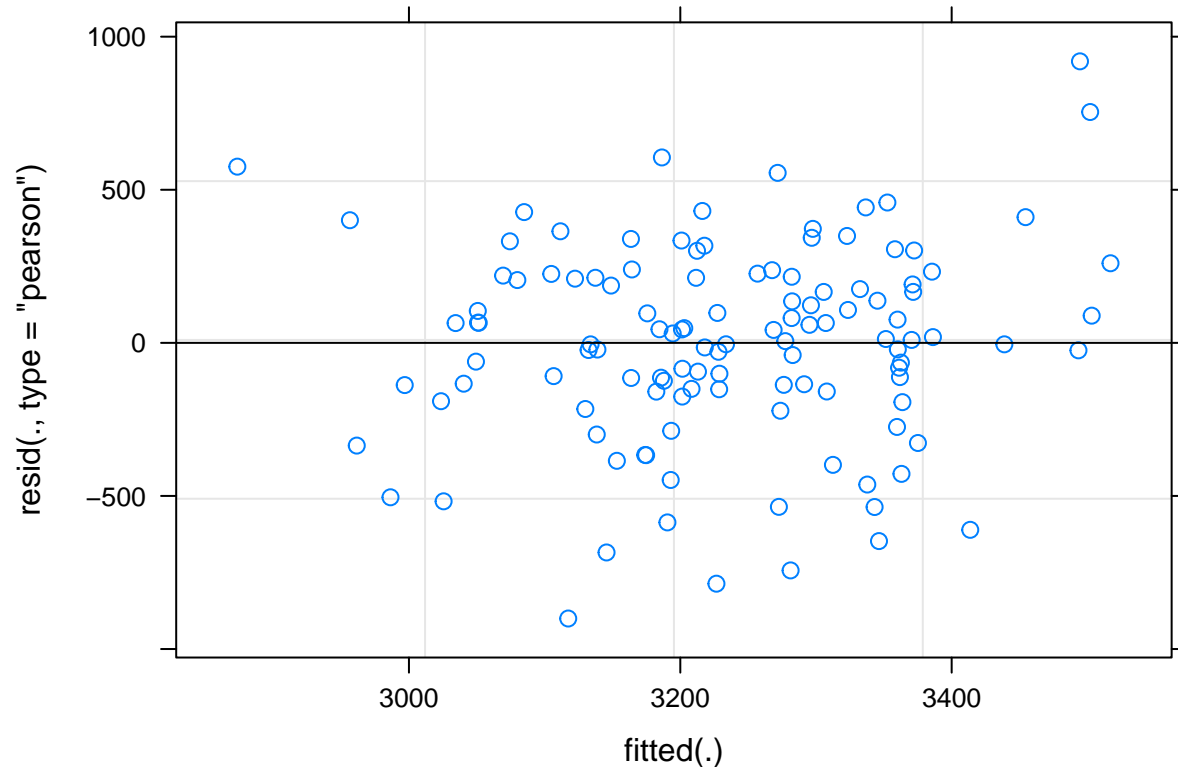
```
hav_sb_yield= lmer(yield~ soil*herb + (1|rep/year), data= (filter(Soybean1, location == "Havelock")))
```

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

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

```
plot(hav_sb_yield)
```



```
#assumptions look good
```

```
anova(hav_sb_yield)
```

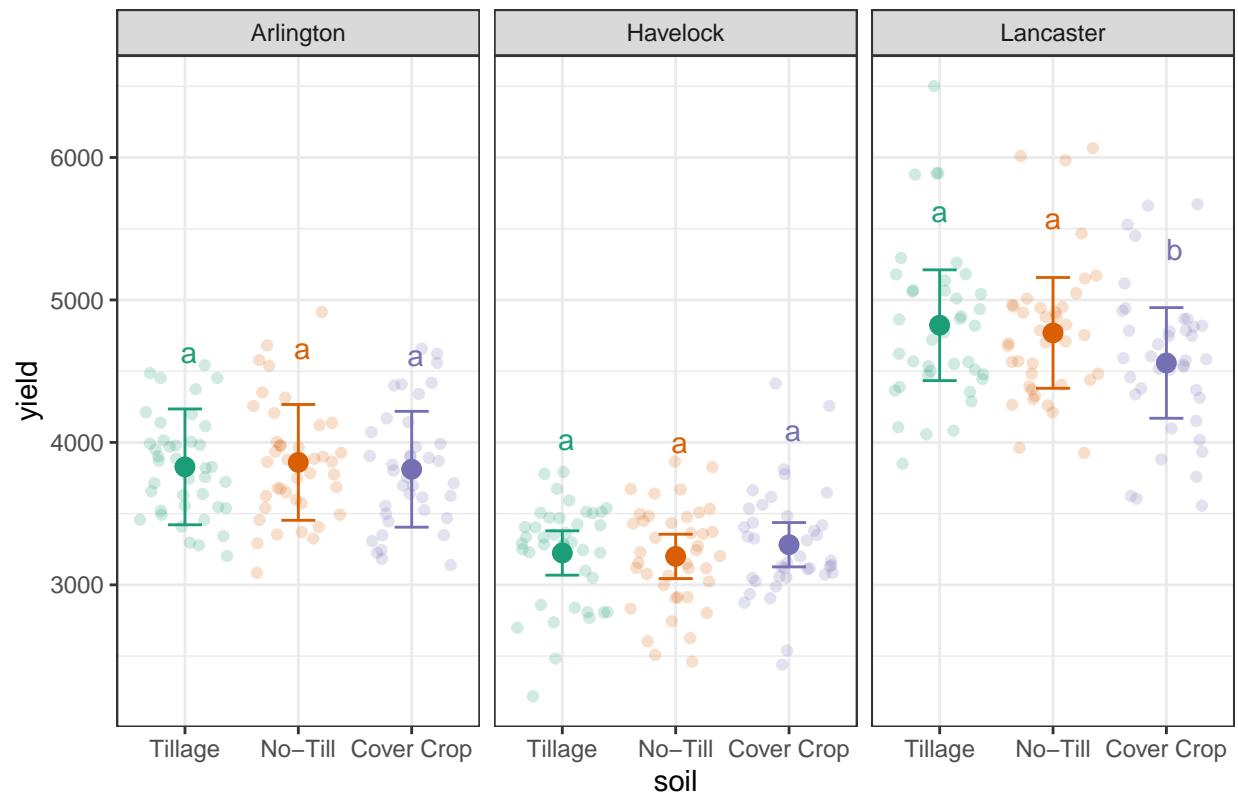
```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## soil      142276   71138     2    98  0.5747 0.5648
## herb      285685   71421     4    98  0.5770 0.6800
## soil:herb 656275   82034     8    98  0.6627 0.7230
```

```
#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")
```

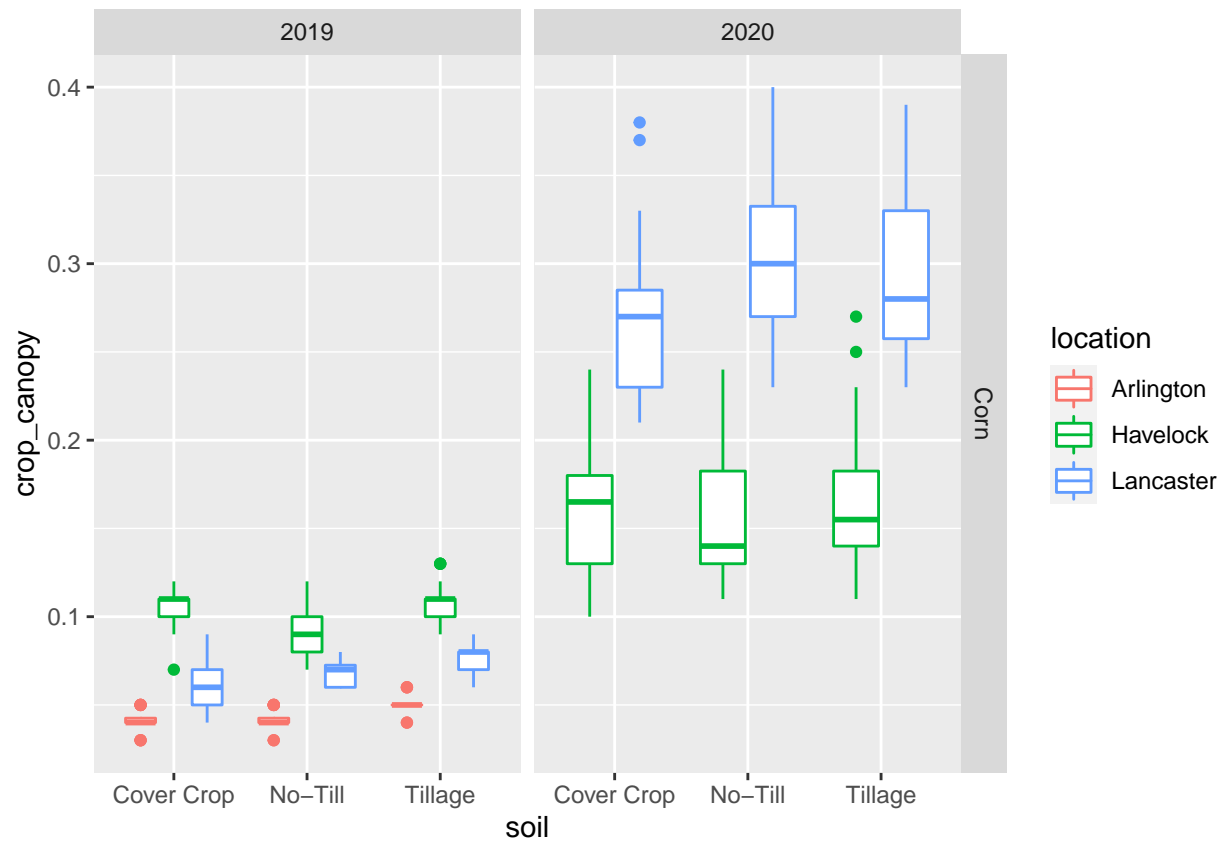
```
y2
```

Soybean Yield

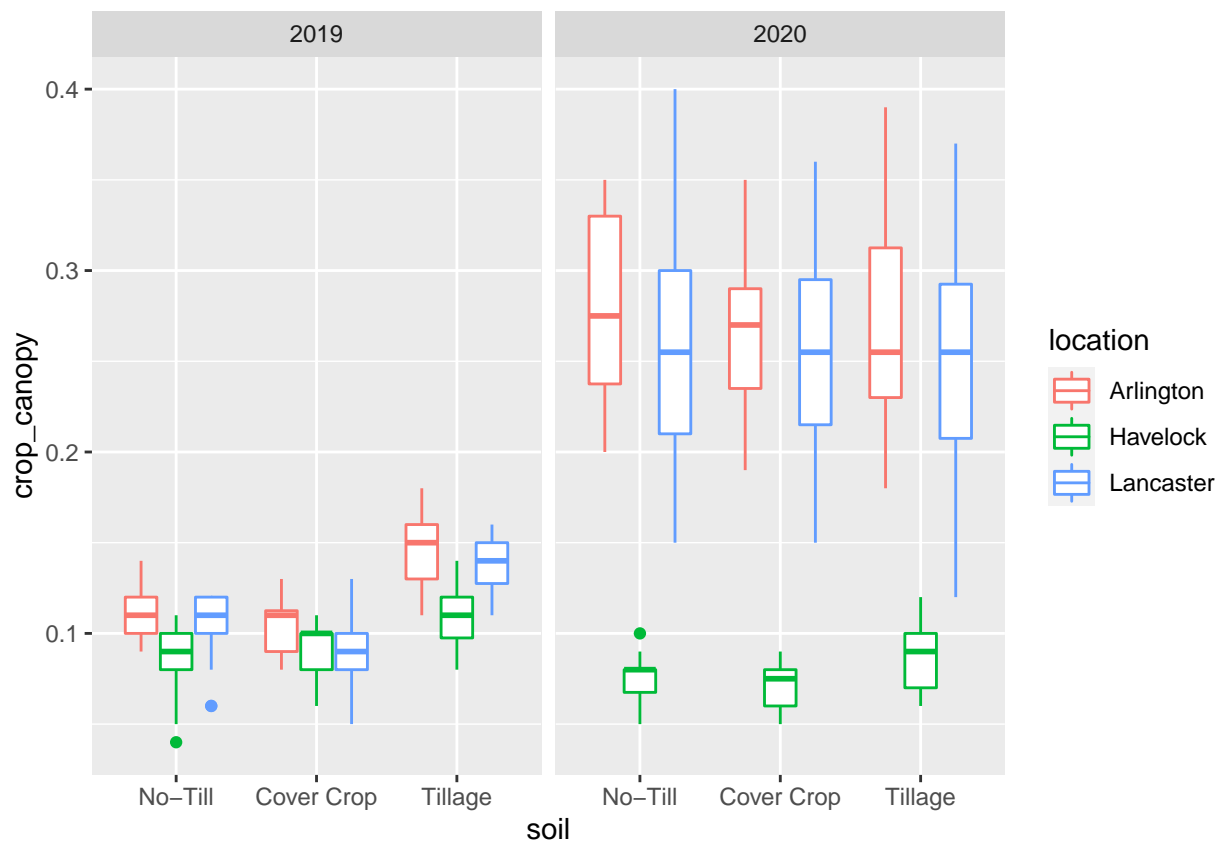


Crop Canopy

```
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 a simplified model with for all of them and then separating means with this model as well as models for each site-crop year.

Corn Canopy

Simplified model

```
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_herbemmeans = emmeans(cn_canopy, ~ herb, contr= "pairwise", adjust= "none", type= "response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
cn_canopy_herbCLD = CLD(cn_canopy_herbemmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, r
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(cn_canopy_herbemmeans, alpha = 0.05, Letters =
```

```
## letters, : `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
cn_canopy_soilemmeans = emmeans(cn_canopy, ~ soil|site_crop_yr, contr= "pairwise", adjust= "none", type
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
cn_canopy_soilCLD = CLD(cn_canopy_soilemmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, r
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(cn_canopy_soilemmeans, alpha = 0.05, Letters =
```

```
## letters, : `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
cn_canopy_soilCLD <- as_tibble(cn_canopy_soilCLD) %>%  
  rename(crop_canopy = response) %>%  
  mutate(soil= factor(soil, levels= order)) %>%  
  arrange(soil)
```

Arlington Corn Canopy

```
arl19_corn_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Corn1, site_crop_yr_2019 == 1))  
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(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")
```

```
cn_canopy1 <- 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")
```

The analysis with a separate model for each analysis increased the separation in the Lancaster 2019 site-year

Soybean Canopy

Simplified model

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

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: crop_canopy
##               Chisq Df Pr(>Chisq)
## soil           81.473  2    < 2e-16 ***
## herb           11.097  4    0.02549 *
## site_crop_yr   281.821  5    < 2e-16 ***
## soil:herb       10.305  8    0.24428
## soil:site_crop_yr 123.079 10   < 2e-16 ***
## herb:site_crop_yr  29.434 20   0.07956 .
## soil:herb:site_crop_yr 41.907 40   0.38810
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
sb_canopy_herbemmeans = emmeans(sb_canopy, ~ herb, contr= "pairwise", adjust= "none", type= "response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
sb_canopy_herbCLD = CLD(sb_canopy_herbemmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, r
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(sb_canopy_herbemmeans, alpha = 0.05, Letters =
```

```
## letters, : `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
sb_canopy_soilemmeans = emmeans(sb_canopy, ~ soil|site_crop_yr, contr= "pairwise", adjust= "none", type=
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
sb_canopy_soilCLD = CLD(sb_canopy_soilemmmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, r
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.

## Warning in CLD.emm_list(sb_canopy_soilemmmeans, alpha = 0.05, Letters =
## letters, : `CLD()` called with a list of 2 objects. Only the first one was used.

## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
sb_canopy_herbCLD <- as_tibble(sb_canopy_herbCLD) %>%
  rename(crop_canopy = response) %>%
  mutate(herb= factor(herb, levels= order2)) %>%
  arrange(herb)

sb_canopy_soilCLD <- as_tibble(sb_canopy_soilCLD) %>%
  rename(crop_canopy = response) %>%
  mutate(soil= factor(soil, levels= order)) %>%
  arrange(soil)
```

Arlington Soy Canopy

```
arl19_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop
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
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(sb_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 = Soybean1 ,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 = "Soybean Canopy")
```

```
sb_canopy1 <- 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")
```

Results are very similar for all site-years with the soybean canopy models.

```
sb_canopyherb <- ggplot(sb_canopy_herbCLD, 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 = 4) +  
  geom_jitter(data = Soybean1 ,mapping = aes(y = crop_canopy*100), alpha = 0.2) +  
  #coord_flip() +  
  #facet_grid(year~location) +  
  theme_bw() +
```

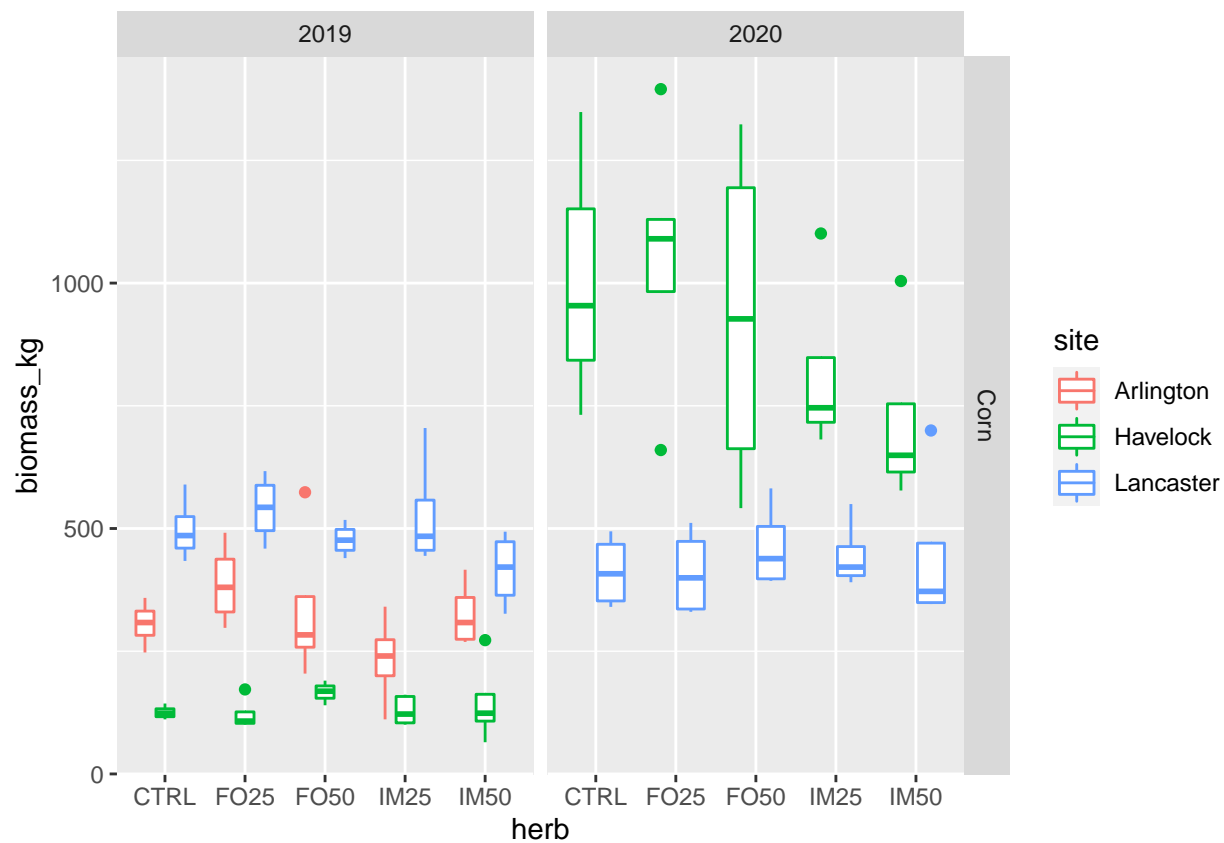
```
scale_color_brewer(palette = "Dark2") +
theme(legend.position = "none") +
labs(title = "Soybean Canopy")
```

```
sb_canopyherb1 <- ggplot(sbcanopy2, 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")
```

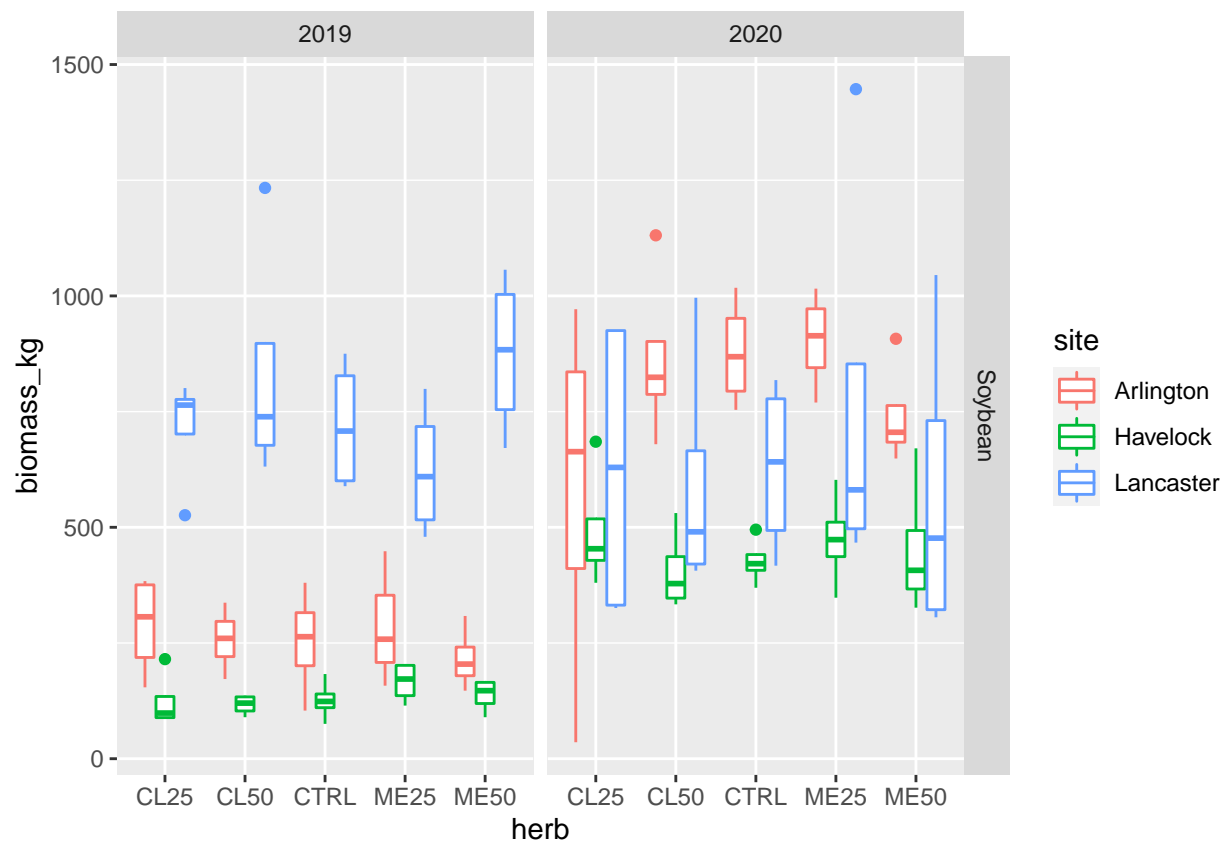
In the analysis with separate models for every site-year it seems weird that the control trt ends up with a lower canopy coverage compared to some of the herbicide trts at Havelock 2019. Personally I prefer the simplified analyses with one model for all site-years to keep things straightforward.

Cover Crop Biomass analysis

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



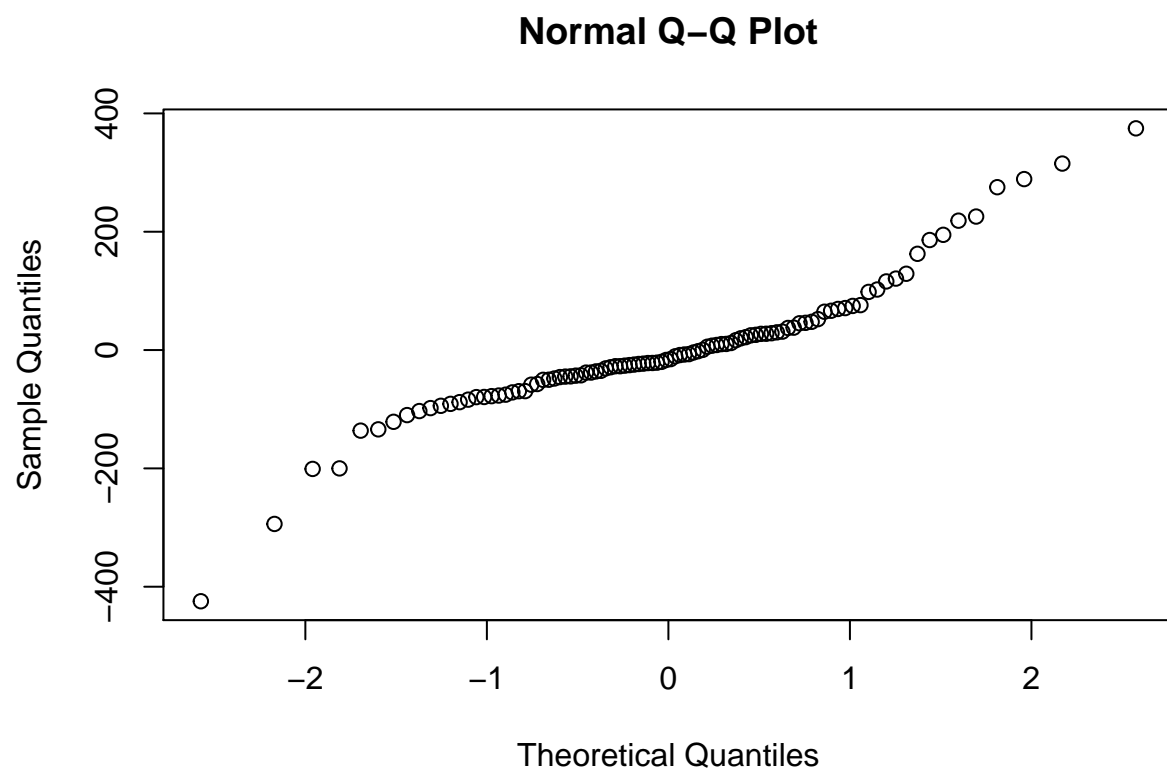
```
SBCC %>%
  ggplot(aes(x = herb, y = biomass_kg, color = site)) +
  geom_boxplot() +
  facet_grid(crop ~ year)
```



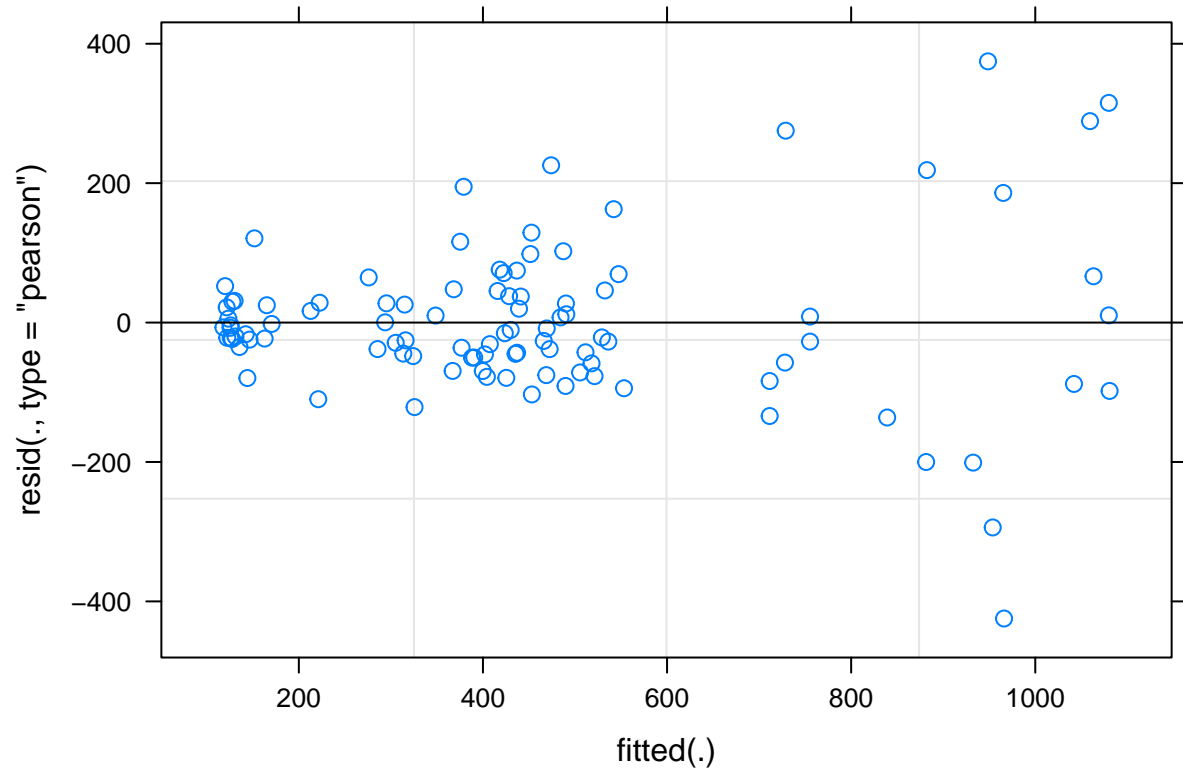
based on separations between locations and across years, I think it is appropriate to look for significant differences between site-years and separate means accordingly in CC biomass models.

Corn

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



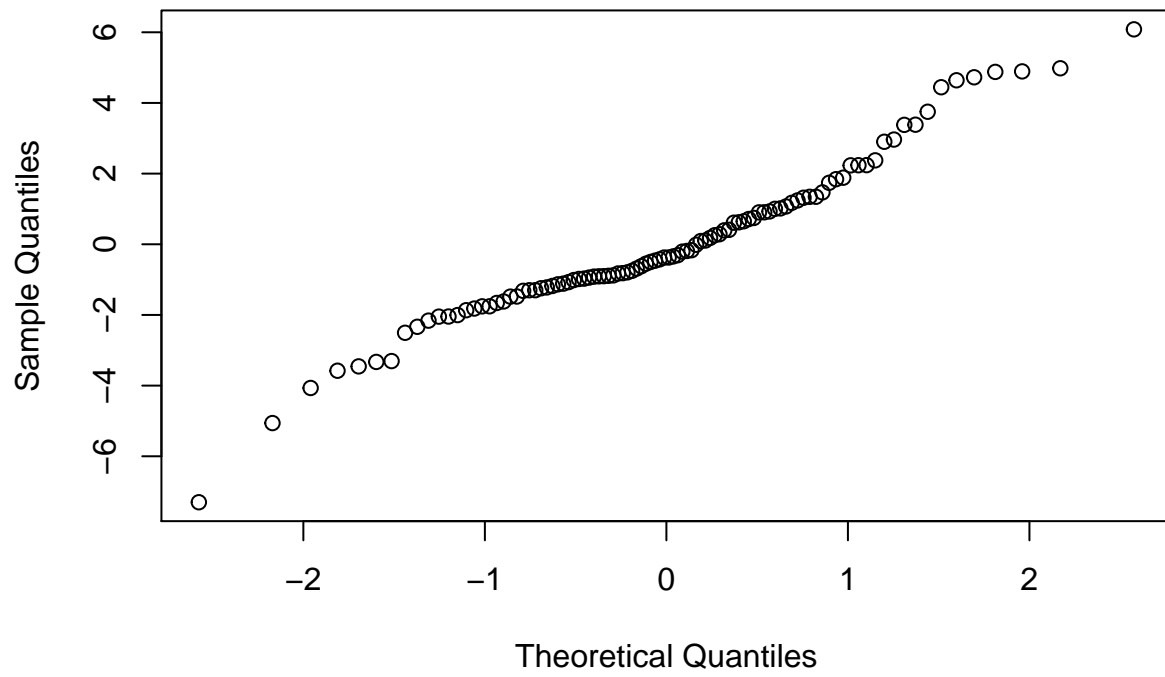
```
plot(cn_cc_bio)
```

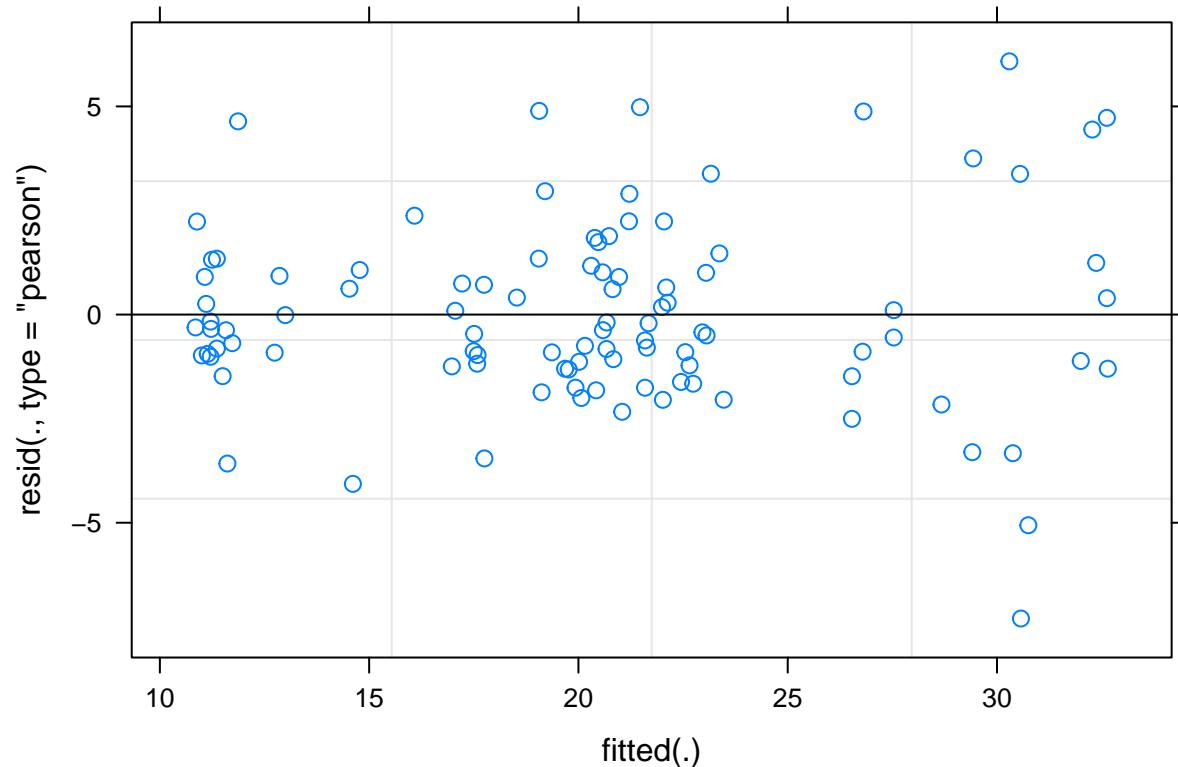
#Assumption for equal variance not met

```
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

```
cn_cc_lsmeans= emmeans(cn_cc_bio1 ,~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

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

```
cn_ccCLD<- CLD(cn_cc_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(cn_cc_lsmeans, alpha = 0.05, Letters = letters, :
## `CLD()` called with a list of 2 objects. Only the first one was used.

## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.

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

```
cn_ccCLD <- as_tibble(cn_ccCLD) %>%
  rename(biomass_kg = response)
```

```
Corn_CCbio= ggplot(cn_ccCLD, aes(x= site_crop_yr, y= biomass_kg, 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 = 150, size= 5) +
  geom_jitter(data = CornCC ,mapping = aes(y = biomass_kg), alpha = 0.2) +
  coord_flip() +
  #facet_grid(year~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Corn")
```

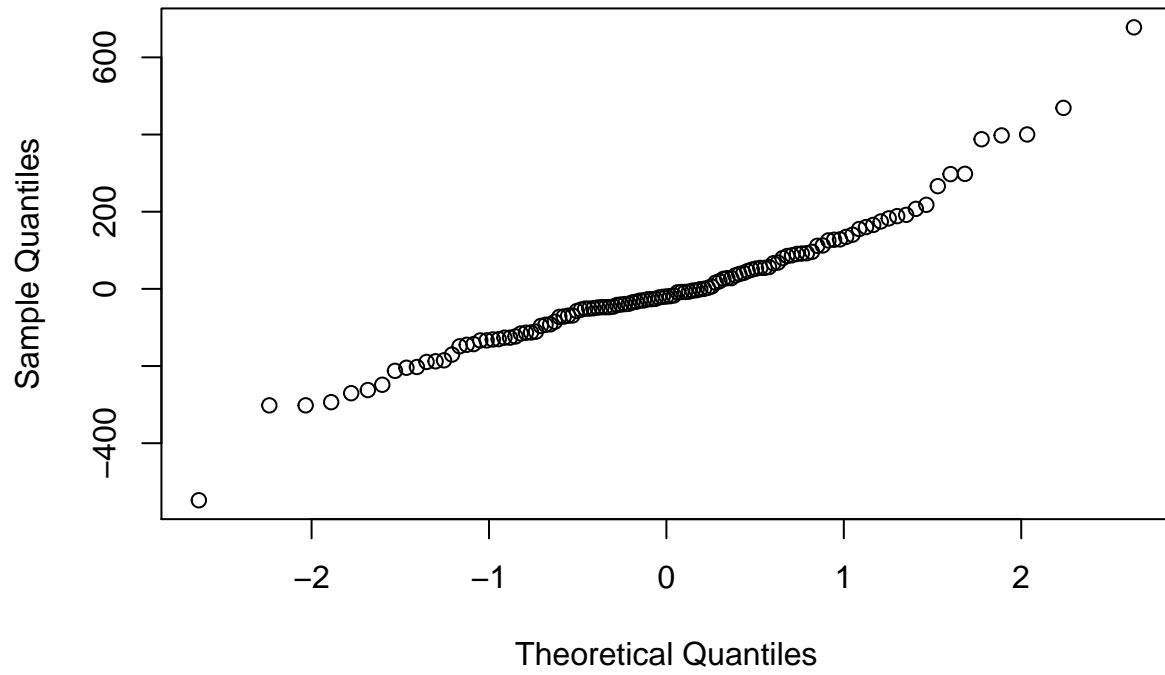
Soybean

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

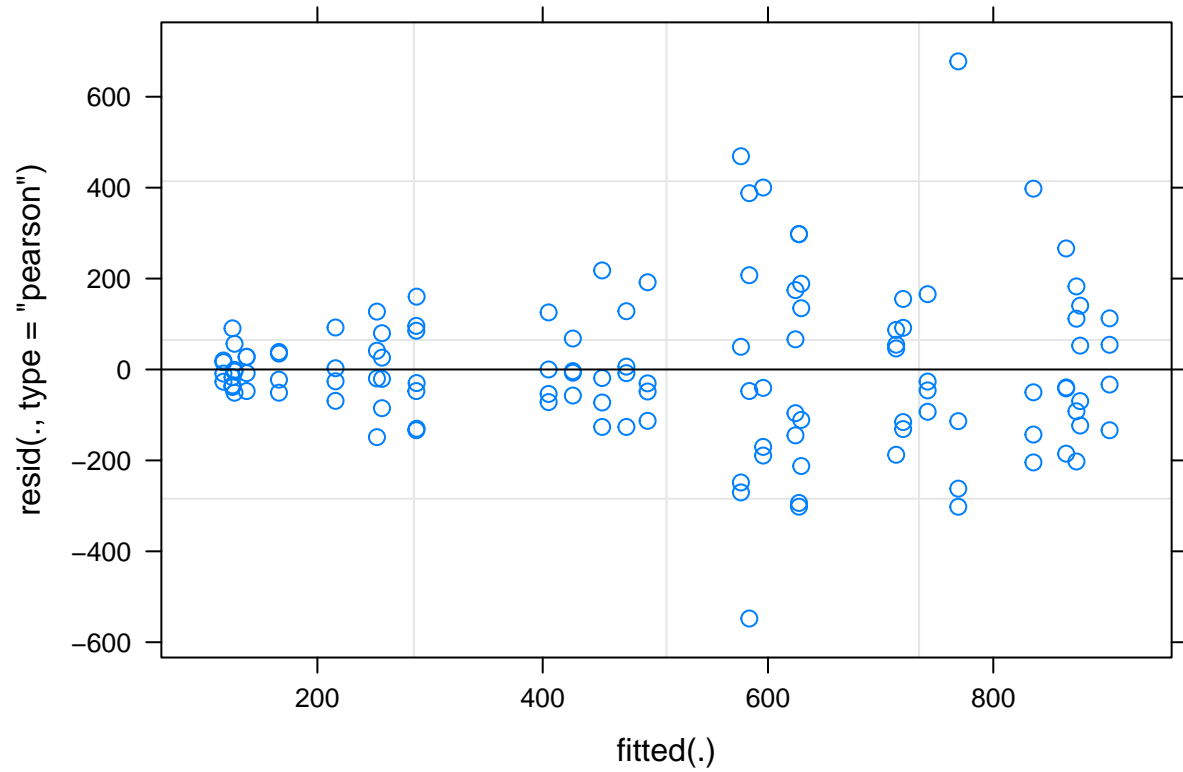
```
## boundary (singular) fit: see ?isSingular
```

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

Normal Q-Q Plot



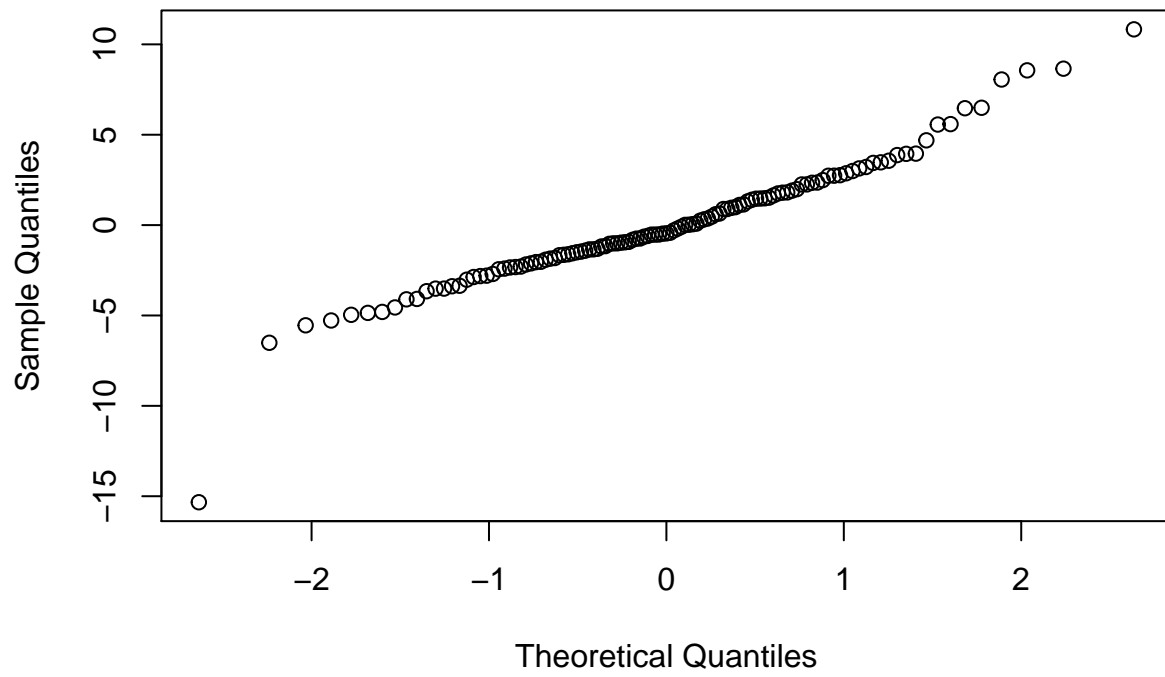
```
plot(sb_cc_bio)
```



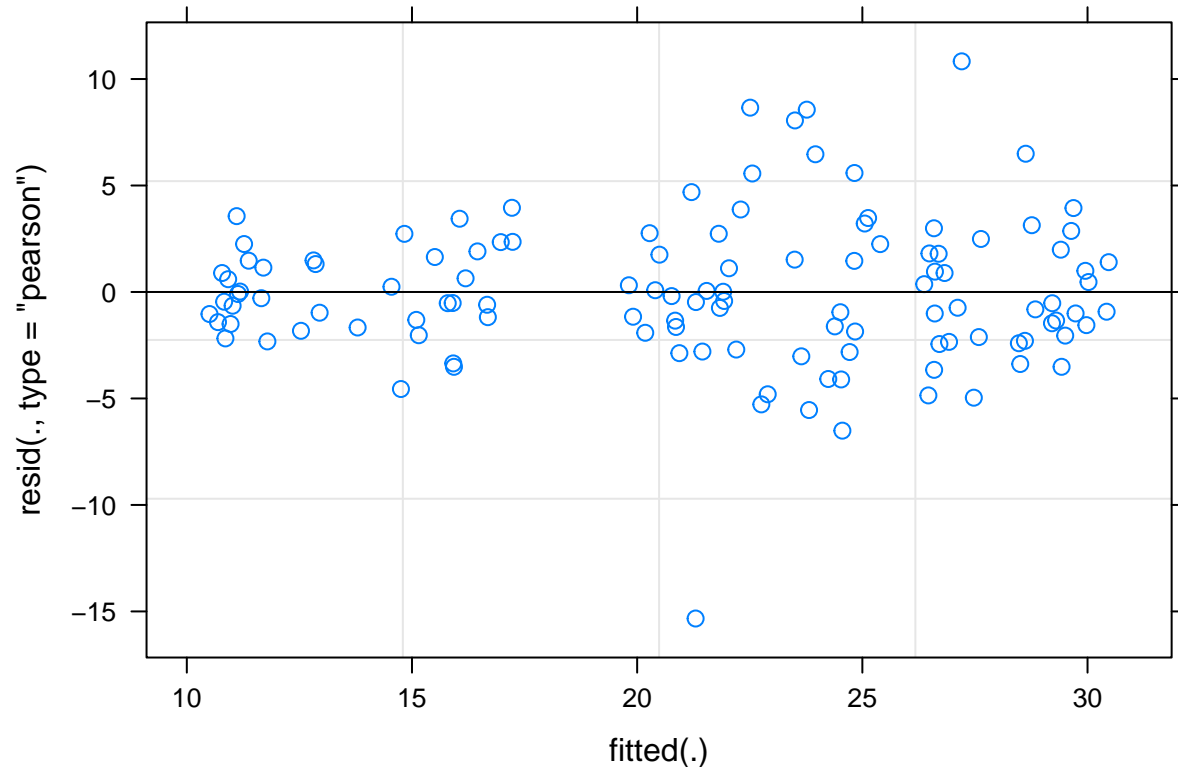
#assumptions for equal variance not met

```
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
```

```
sb_cc_lsmeans= emmeans(sb_cc_bio1 ,~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

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

```
sb_ccCLD<- CLD(sb_cc_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```



```
## Warning in CLD.emm_list(sb_cc_lsmeans, alpha = 0.05, Letters = letters, :
## `CLD()` called with a list of 2 objects. Only the first one was used.

## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.

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

```
sb_ccCLD <- as_tibble(sb_ccCLD) %>%
  rename(biomass_kg = response)
```

```
Soy_CCbio= ggplot(sb_ccCLD, aes(x= site_crop_yr, y= biomass_kg, 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 = 150, size= 5) +
  geom_jitter(data = SBCC ,mapping = aes(y = biomass_kg), alpha = 0.2) +
  coord_flip() +
  #facet_grid(year~location) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  theme(legend.position = "none") +
  labs(title = "Soybean")
```

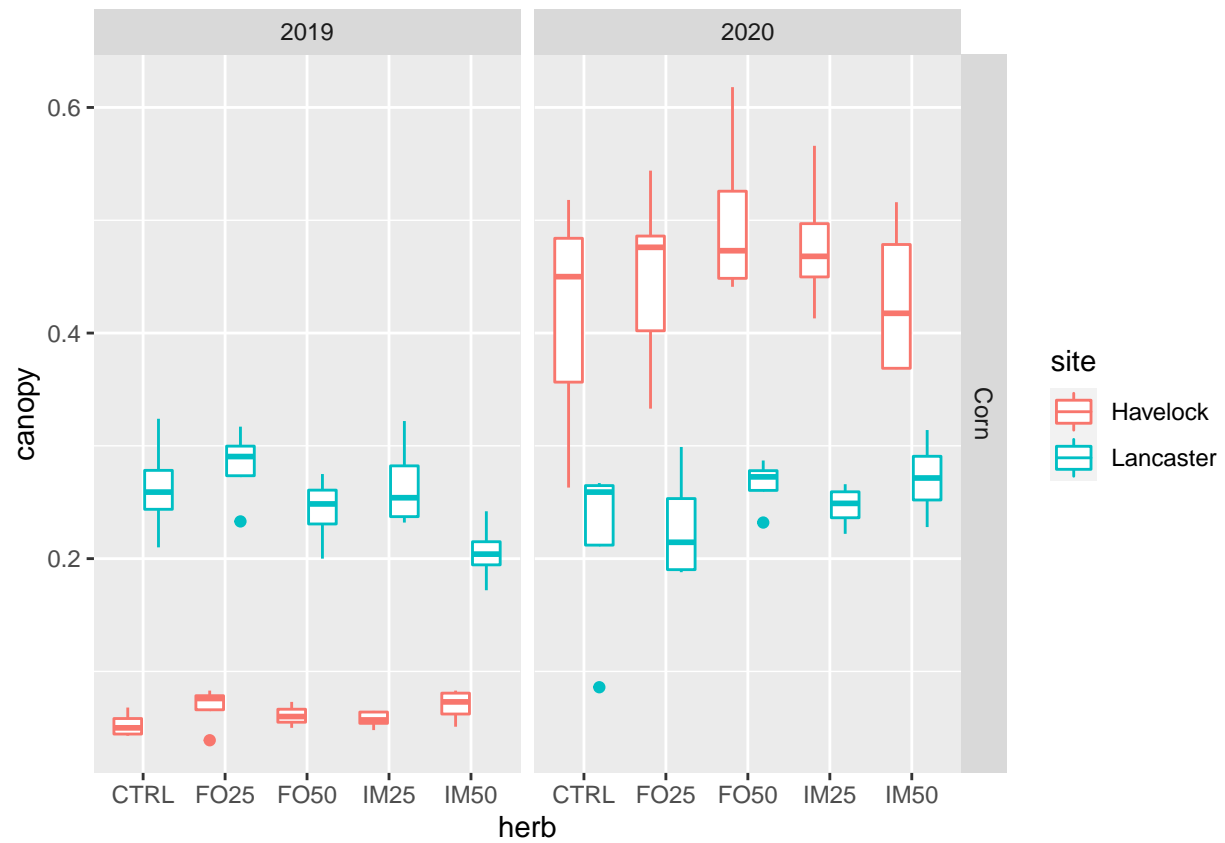
Cover Crop Canopy

Corn

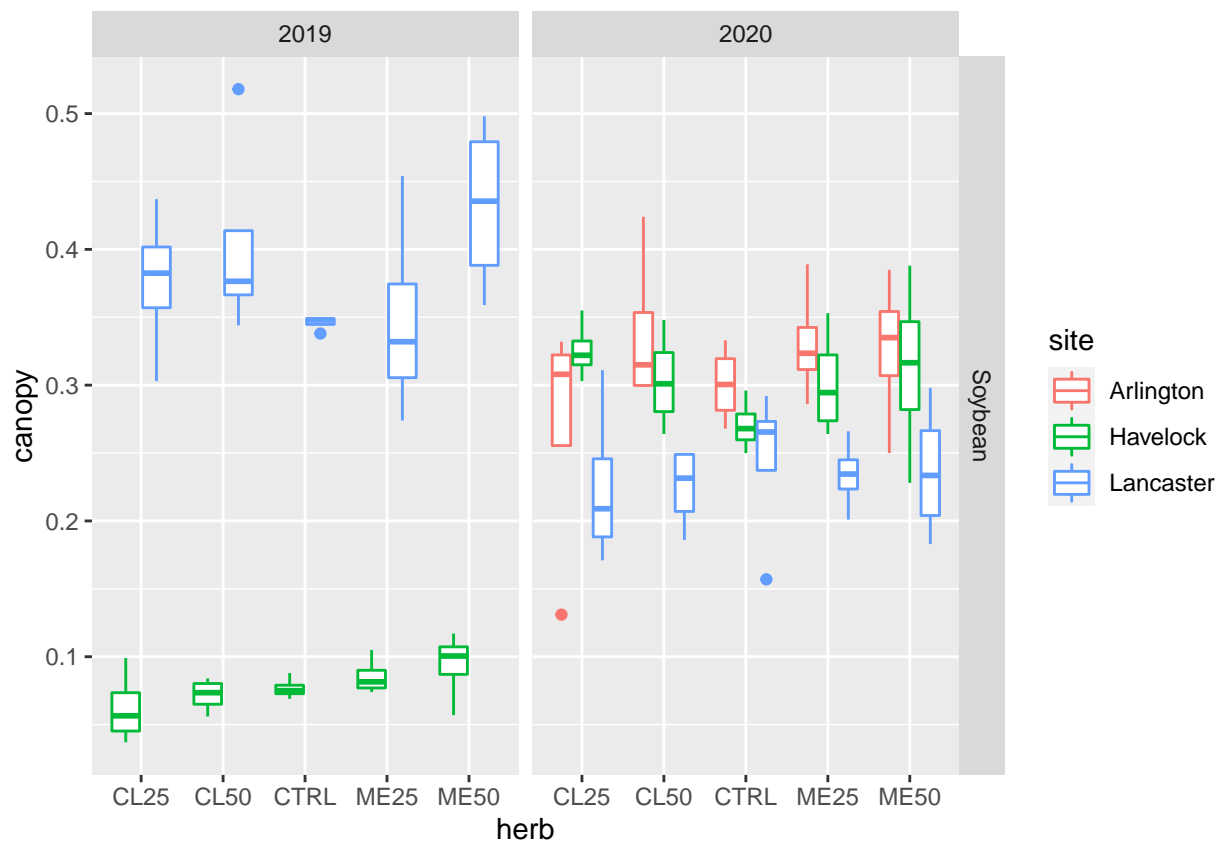
```
CornCC1 <- CornCC %>%
  filter(!is.na(canopy))
```

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

```
cn_cc_can_lsmeans= emmeans(cn_cc_can ,~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

NOTE: Results may be misleading due to involvement in interactions

```
cn_cc_canCLD<- CLD(cn_cc_can_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(cn_cc_can_lsmeans, alpha = 0.05, Letters = letters, :
## `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
cn_cc_canCLD <- as_tibble(cn_cc_canCLD) %>%
  rename(canopy = response)
```

```
Corn_CCcan= ggplot(cn_cc_canCLD, aes(x= site_crop_yr, y= canopy*100, color= site_crop_yr)) +
  geom_point(size= 3) +
  geom_errorbar(aes(ymin= lower.CL*100, ymax= upper.CL*100), width= .3) +
  geom_text(aes(label = .group), nudge_y = 5, size= 5) +
  geom_jitter(data = CornCC1,mapping = aes(y = 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")
```

Soybean

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

```
sb_cc_can= 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: biomass_kg
##              Chisq Df Pr(>Chisq)
## site_crop_yr    196.8051  5    <2e-16 ***
## herb             1.4513  4     0.8352
## site_crop_yr:herb 14.3036 20     0.8148
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Site-Year significant
```

```
sb_cc_can_lsmeans= emmeans(sb_cc_can , ~ site_crop_yr, contr="pairwise", adjust="none", type="response")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
sb_cc_canCLD<- CLD(sb_cc_can_lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=TRUE)
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
## Warning in CLD.emm_list(sb_cc_can_lsmeans, alpha = 0.05, Letters = letters, :
```

```
## `CLD()` called with a list of 2 objects. Only the first one was used.
```

```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
```

```
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
sb_cc_canCLD <- as_tibble(sb_cc_canCLD) %>%  
  rename(canopy = response)
```

```
Soy_CCcan= ggplot(sb_cc_canCLD, aes(x= site_crop_yr, y= canopy*100, color= site_crop_yr)) +  
  geom_point(size= 3) +  
  geom_errorbar(aes(ymin= lower.CL*100, ymax= upper.CL*100), width= .3) +  
  geom_text(aes(label = .group), nudge_y = 5, size= 5) +  
  geom_jitter(data = SBCC1 ,mapping = aes(y = 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")
```