

Carryover_SoyResults

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#Analysis Procedure

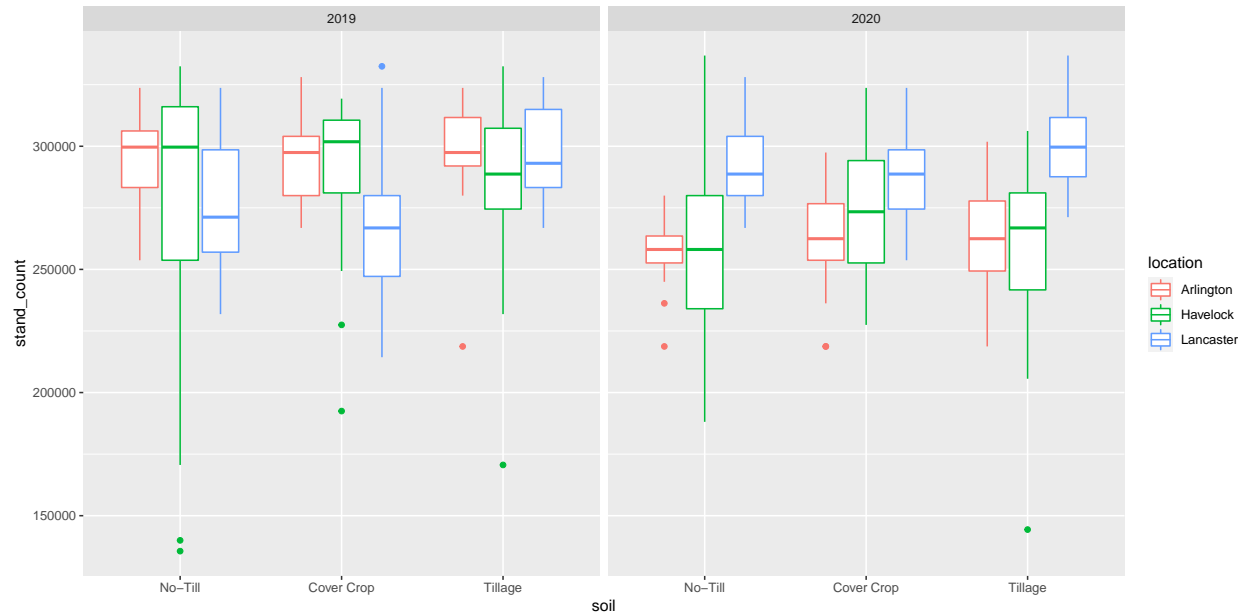
Prior to analysis I took the approach of plotting the response variables with box-plots to visualize treatment differences with soil management between locations. The intention of this was to visualize the differences between locations as well determine if I feel comfortable pooling things within a location (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.

Early seaston stand Counts Analysis

```
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)
```

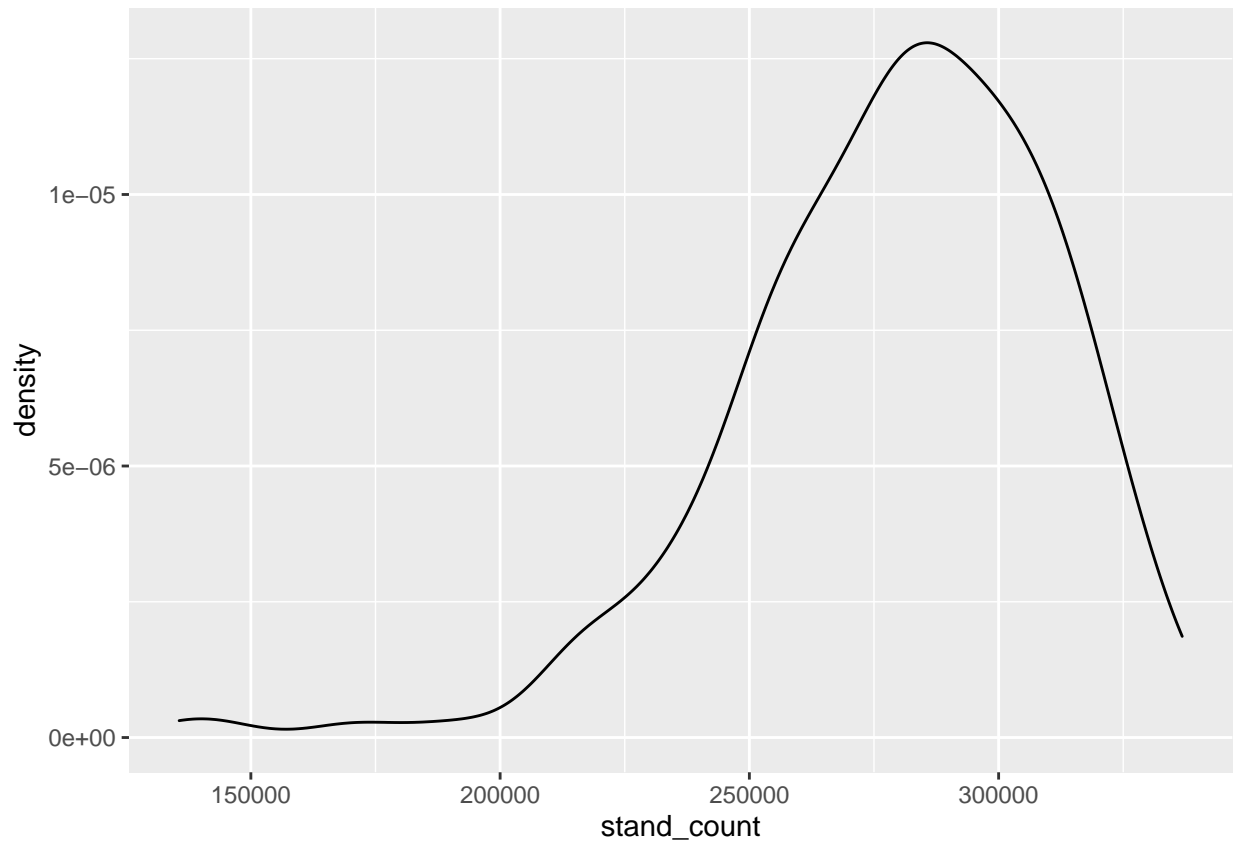


Based on these visual representations it doesn't appear to me that there are any consistent patterns as a function of soil management, herbicide treatment, location, or year. There does appear to be differences within a location across seasons. Therefore, I think it is best if we test for site-year differences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

Condensed Stand Count Model

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

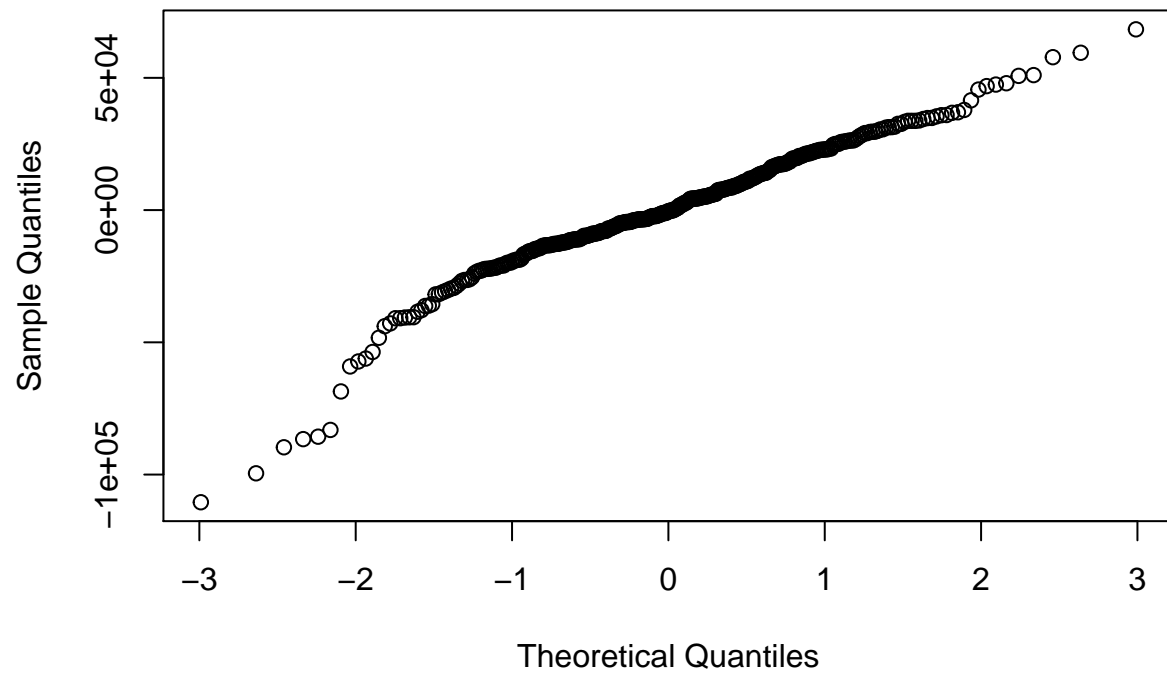
```
Soybean1 %>%  
  ggplot(aes(x = stand_count)) +  
  geom_density()
```



#Looks a little skewed left but good to see the distribution is one hump

```
qqnorm(resid(sb_stand))
```

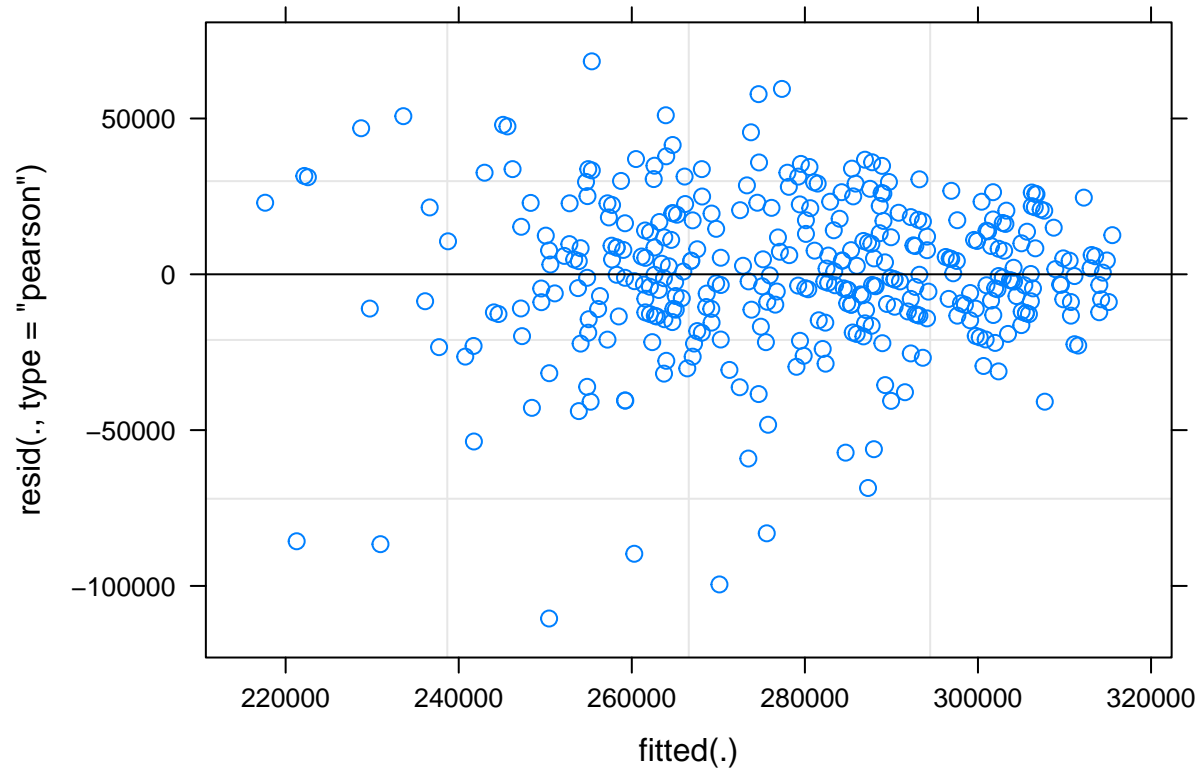
Normal Q-Q Plot



#Residuals are concentrated in a "straight" line.

#I am satisfied that this response variable is normally distributed

```
plot(sb_stand)
```



*#Residuals are spread out evenly verticall and horizontally.
#I am satisfied that this response variable has an evenly distributed variance.*

Stand count ANOVA

```
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.
```

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

Separation of means for each site-year based on soil management

Wasn't significant, done for fun (and to look at usefulness of means for yield later?)!

```
sb_cc_stand_soillsmeans= lsmeans(sb_stand ,~ soil|site_crop_yr, contr="pairwise", adjust="none", type="")
```

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

```
sb_cc_stand_SoilCLD<- CLD(sb_cc_stand_soillsmeans, alpha=0.05, Letters=letters, adjust="none", sort=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_stand_soillsmeans, 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_stand_SoilCLD
```

```
## site_crop_yr = Arlington 2019:
##   soil      lsmean    SE  df lower.CL upper.CL .group
## Tillage    298338 6591 102   285264   311412    a
## Cover Crop 295057 6591 102   281983   308131    a
## No-Till    294182 6591 102   281108   307256    a
##
## site_crop_yr = Arlington 2020:
##   soil      lsmean    SE  df lower.CL upper.CL .group
## Cover Crop 262467 6591 102   249393   275541    a
## Tillage    261592 6591 102   248518   274666    a
## No-Till    257874 6591 102   244800   270948    a
##
## site_crop_yr = Havelock 2019:
##   soil      lsmean    SE  df lower.CL upper.CL .group
## Cover Crop 288277 6591 102   275203   301350    a
## Tillage    282371 6591 102   269297   295445    a
## No-Till    274278 6591 102   261204   287352    a
##
## site_crop_yr = Havelock 2020:
##   soil      lsmean    SE  df lower.CL upper.CL .group
```

```
## Cover Crop 274060 6591 102 260986 287133 a
## No-Till 258093 6591 102 245019 271167 a
## Tillage 256562 6591 102 243488 269636 a
##
## site_crop_yr = Lancaster 2019:
## soil lsmean SE df lower.CL upper.CL .group
## Tillage 295713 6591 102 282639 308787 a
## No-Till 274060 6591 102 260986 287133 b
## Cover Crop 265193 6796 110 251724 278661 b
##
## site_crop_yr = Lancaster 2020:
## soil lsmean SE df lower.CL upper.CL .group
## Tillage 299869 6591 102 286795 312943 a
## No-Till 292213 6591 102 279140 305287 a
## Cover Crop 287183 6591 102 274109 300257 a
##
## Results are averaged over the levels of: herb
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
```

I wouldn't pay attention to the groupings since this interaction wasn't significant (although close). The reduced stand for soil management with a cover crop could help explain final grain yield.

Separation of means by site-year based on ANOVA

I probably won't include mean separation for later analyses often, I just wanted to show you for the first one.

```
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
```

```
#Chris, you can ignore the warnings. It is just a suggestion!
```

```
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.
```

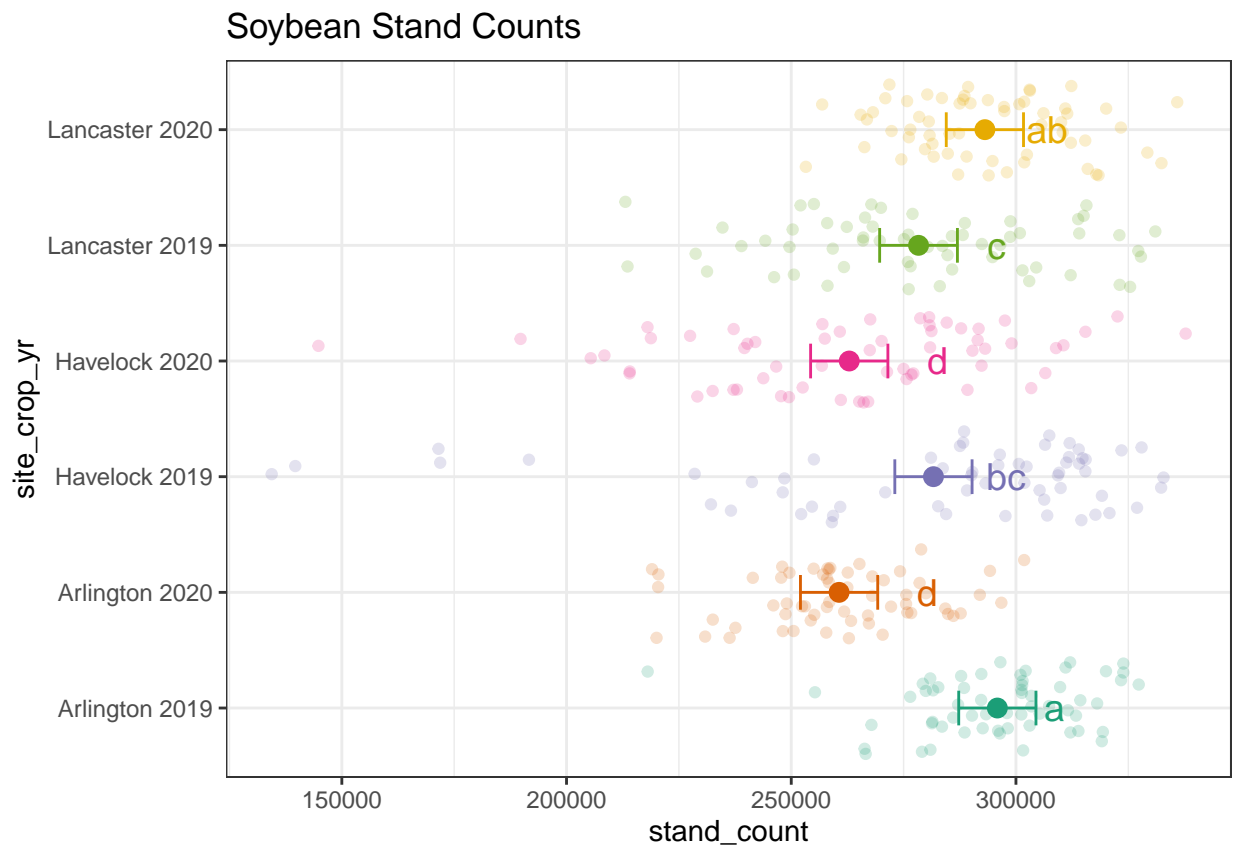
```
## Warning: 'CLD' will be deprecated. Its use is discouraged.
## See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
sb_cc_standCLD
```

```
## site_crop_yr lsmean SE df lower.CL upper.CL .group
## Arlington 2019 295859 4090 17.9 287262 304456 a
## Lancaster 2020 293088 4090 17.9 284492 301685 ab
```

```
## Havelock 2019 281642 4090 17.9 273045 290239 bc
## Lancaster 2019 278322 4127 18.5 269668 286976 c
## Havelock 2020 262905 4090 17.9 254308 271501 d
## Arlington 2020 260645 4090 17.9 252048 269241 d
##
## Results are averaged over the levels of: soil, herb
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
```

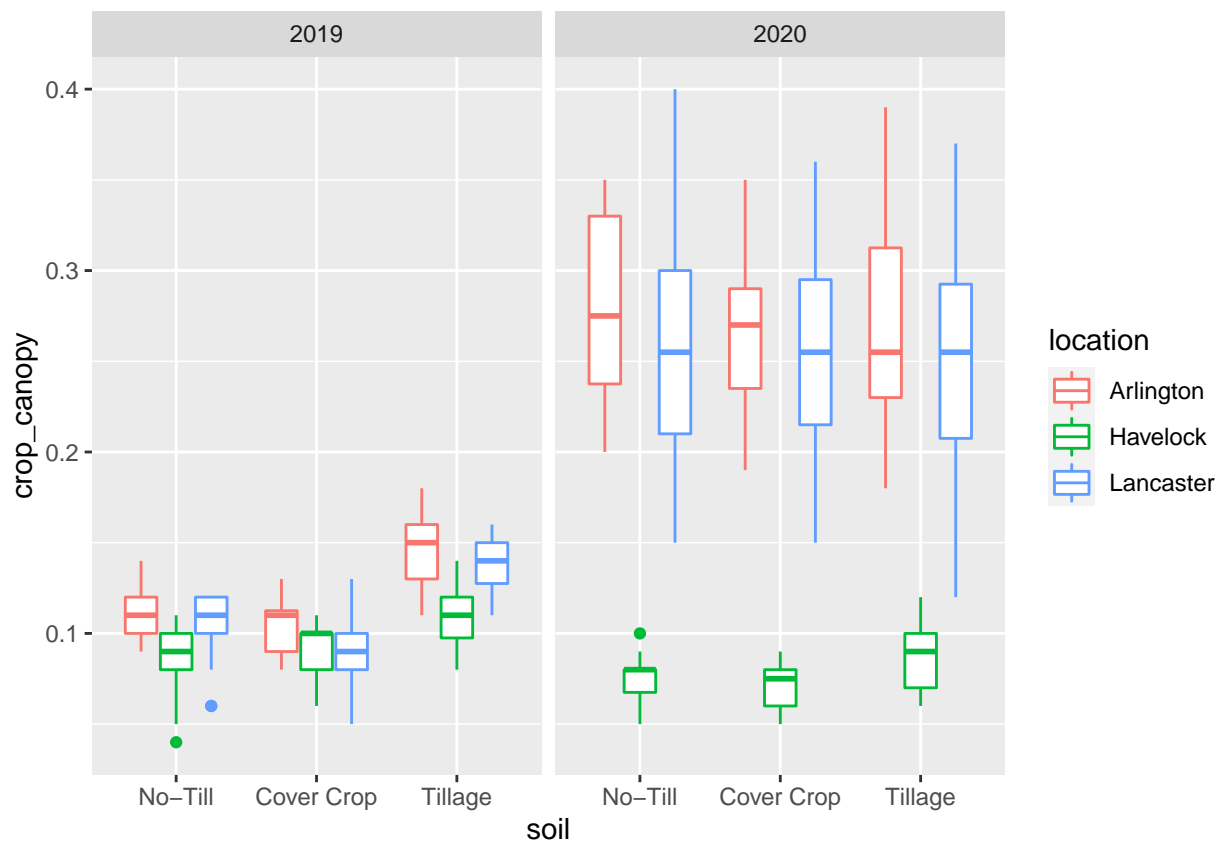
Stand Count figure – Not useful for paper but interesting



Soybean stand counts were planted at 370,000 seeds ha⁻¹ in NE and ~346,000 seeds ha⁻¹ in WI

Crop Canopy

```
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 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 Canopy model

a glmmTMB (generalized linear) model was used instead of a standard linear mixed-effects model because % canopy cover is a non-continuous variable. There are no assumption to meet for this type of 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

Means were separated for the Soil management:site-year interaction and herbicide treatment fixed effect separately. I delayed presenting the results until comparison to the separated analysis later on.

Separated analysis for each site-year

Only first model displayed

#Beginning of analysis for separate site-year models

```
arl19_soy_can = glmmTMB(crop_canopy~ soil*herb + (1|rep:site_crop_yr), data= (filter(Soybean1, site_crop_yr==1991))
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
```

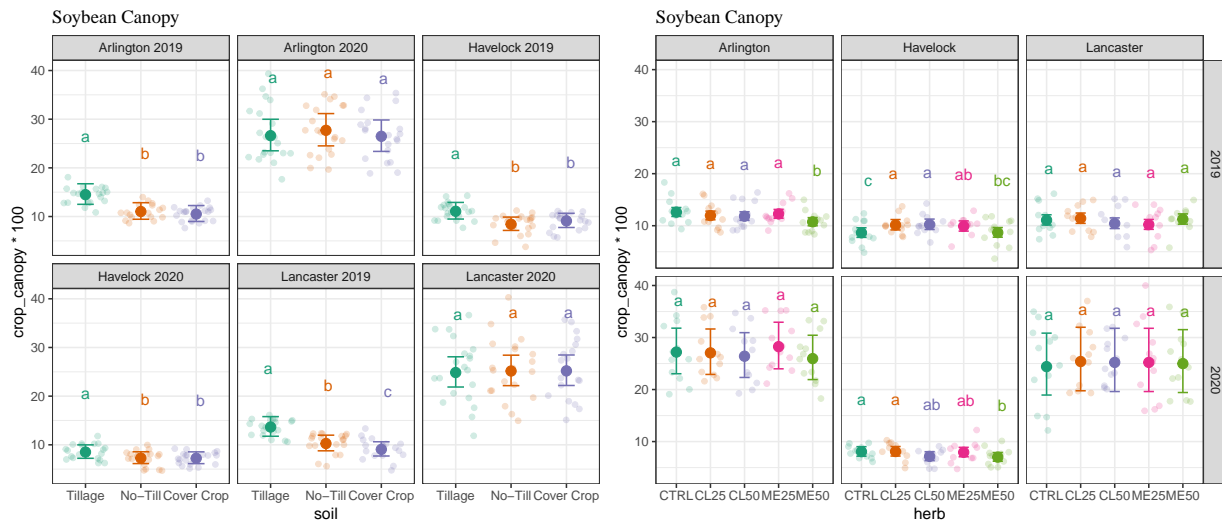
#Soil and herb fixed effects significant

Comparison of Canopy Coverage Analysis Approaches

Separated

separated

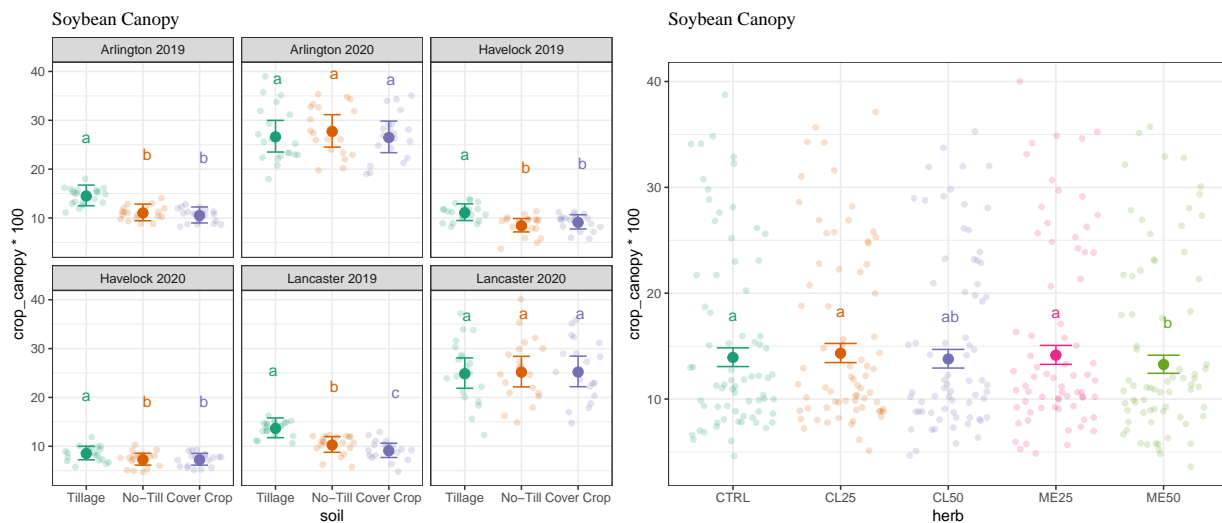
Soybean Canopy Coverage Separated Analysis



Composite

composite1

Soybean Canopy Coverage Composite Analysis



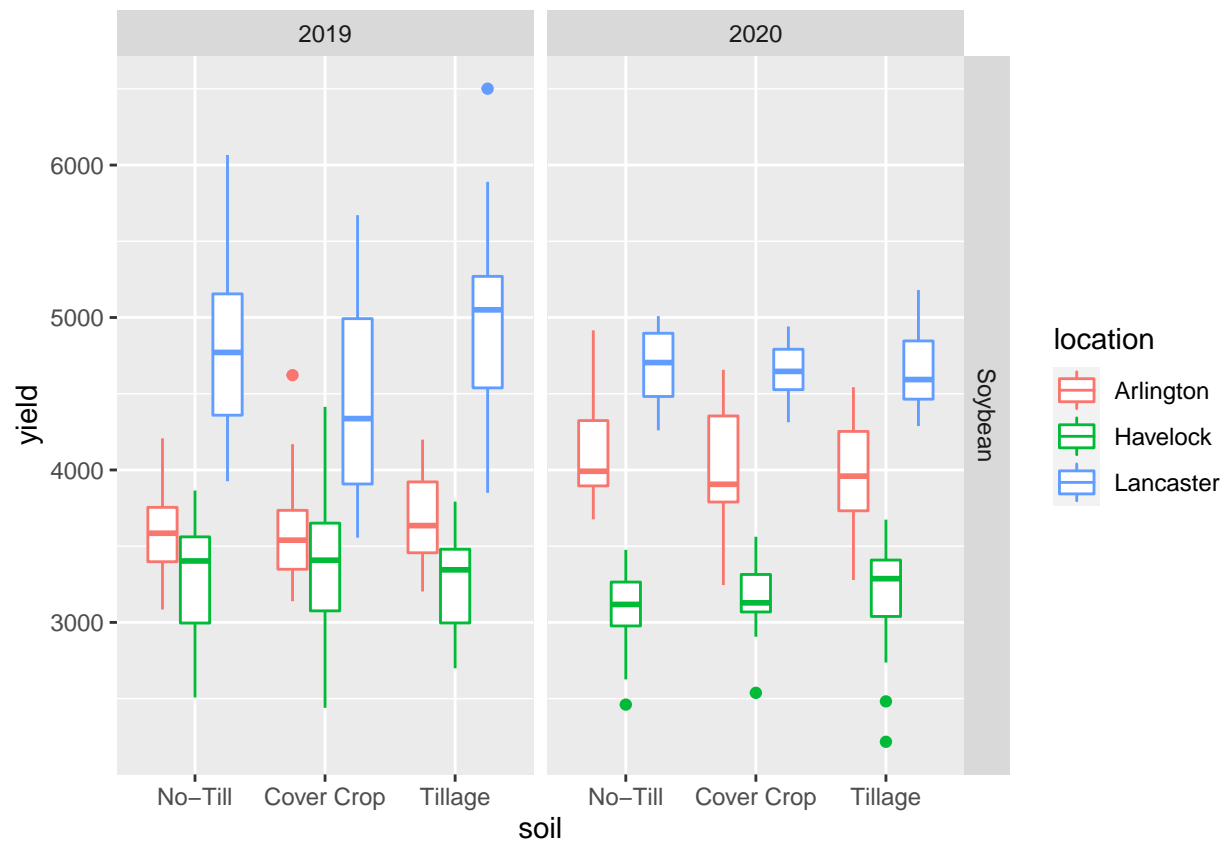
Results are very similar for all site-years with the soybean canopy models.

In the analysis with separate models for every site-year it seems weird that the control trt has 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, especially for the herbicide results.

Soybean Yield Analysis

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



It appears as if there are similar trends and yield within a location across years. I will proceed with performing a separate analysis for each location.

Arlington Analysis

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

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

```
#nothing significant
```

Lancaster Analysis

```
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

```
anova(hav_sb_yield)
```

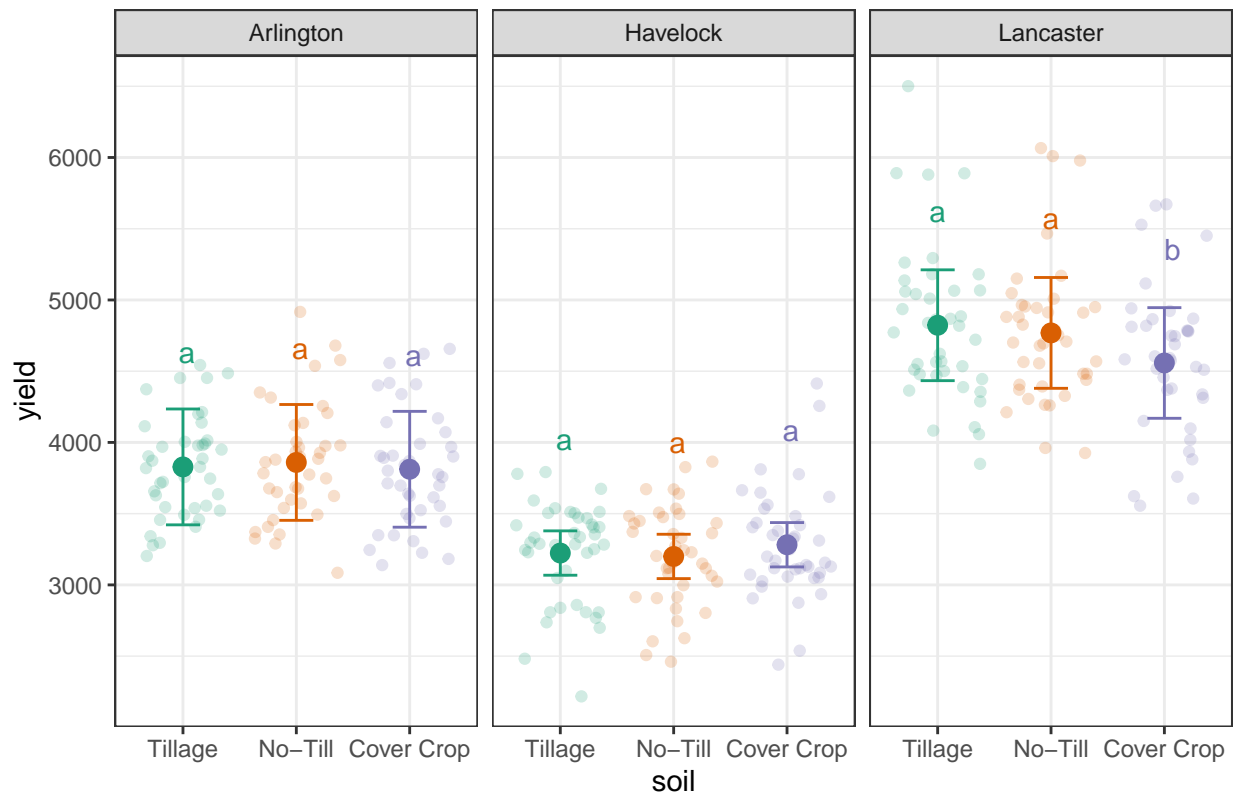
```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## soil     142276   71138     2    98  0.5747 0.5648
## herb     285685   71421     4    98  0.5770 0.6800
## soil:herb 656275   82034     8    98  0.6627 0.7230
```

```
#nothing significant
```

Soybean Yield Figure

```
y2
```

Soybean Yield



Lancaster had reduced yield for the cover crop soil management treatment. If you look back to the analysis we did on stand counts you can see that this treatment had the lowest mean early-season stand count at Lancaster both years.

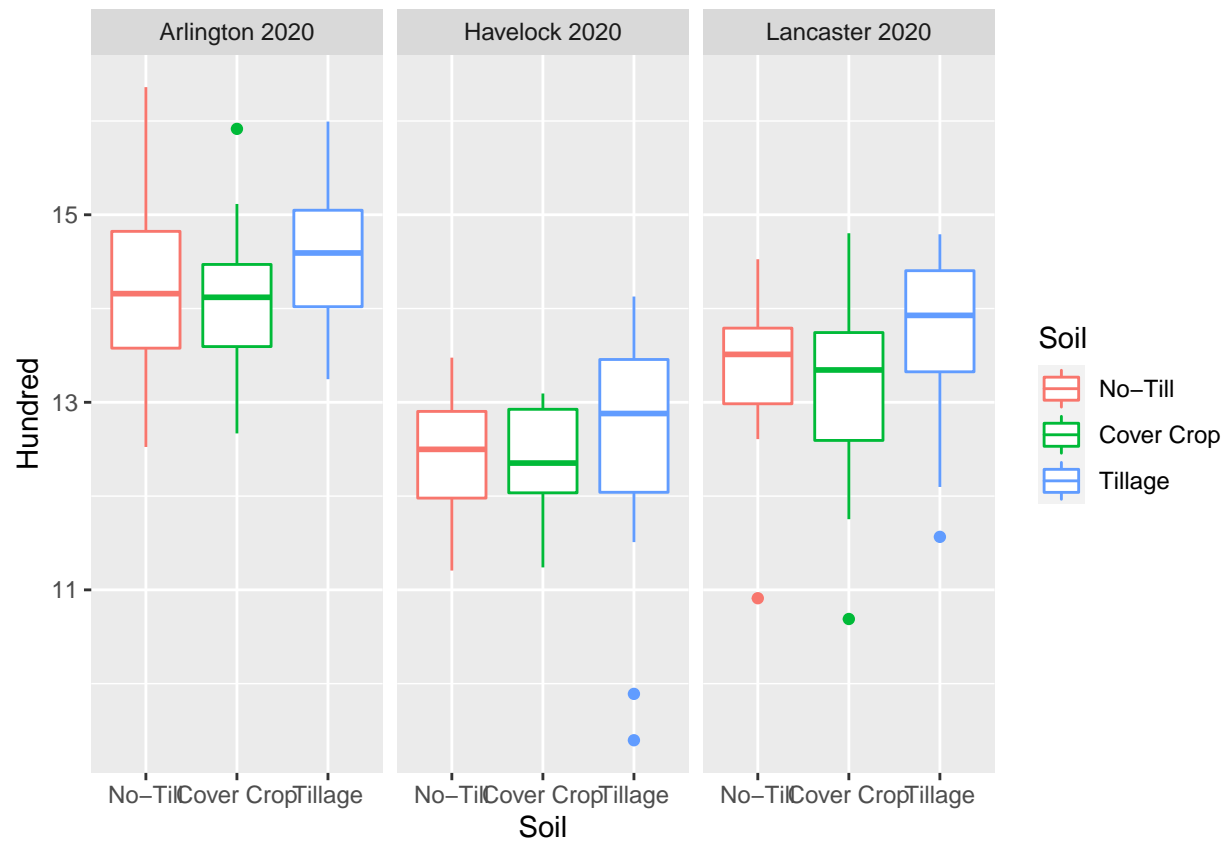
Now to see if the yield components explain more.

Soybean Yield Components

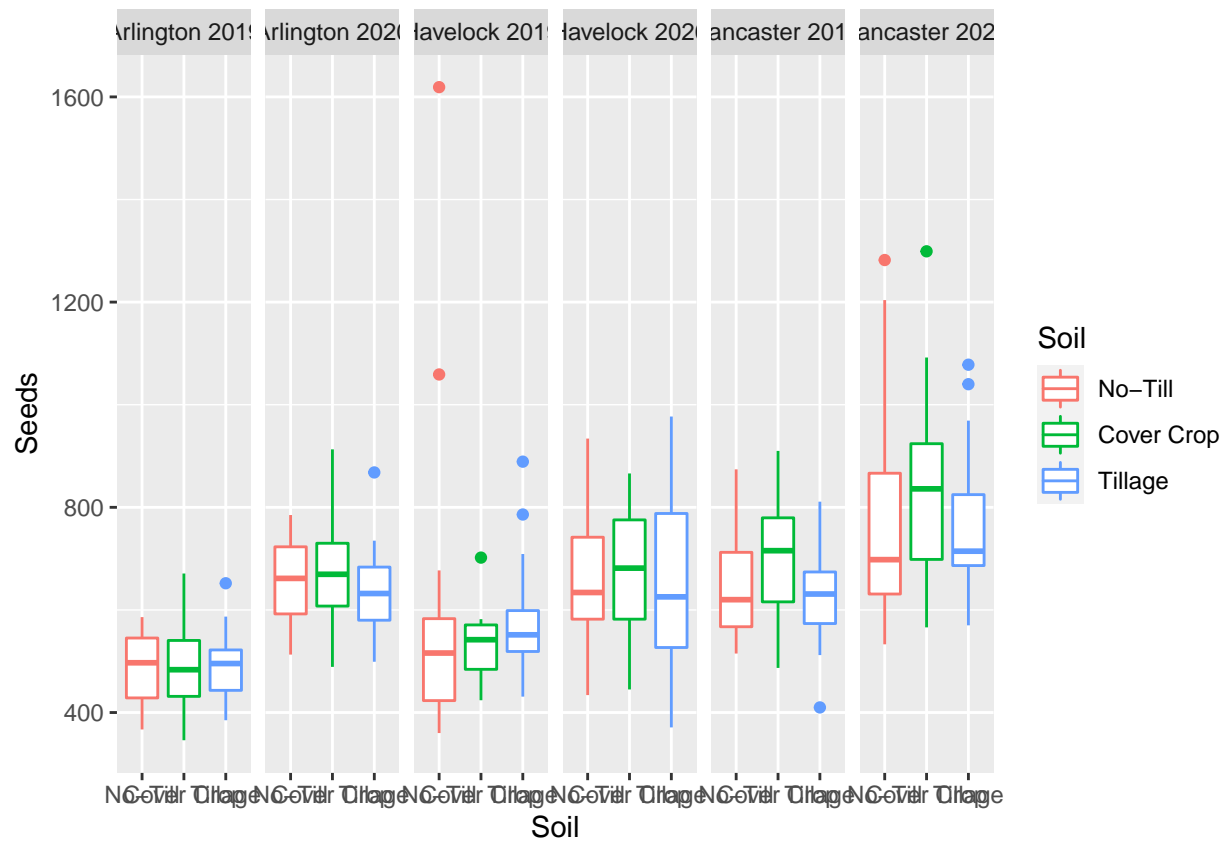
Based on issues with storage and seed damage in 2019, the only data I feel comfortable with using for 2019 yield components are the pod counts. Even the seed counts seem suspiciously low for 2019 so seeds per pod is probably useless for 2019.

```
#SoybeanComp1 %>%
  #ggplot(aes(x = Soil, y = Total, color = Soil)) +
  #geom_boxplot() +
  #facet_grid(~ Site_Yr)

#Plot of Soybean seed density (Hundred weight)
SoybeanComp1 %>%
  ggplot(aes(x = Soil, y = Hundred, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```



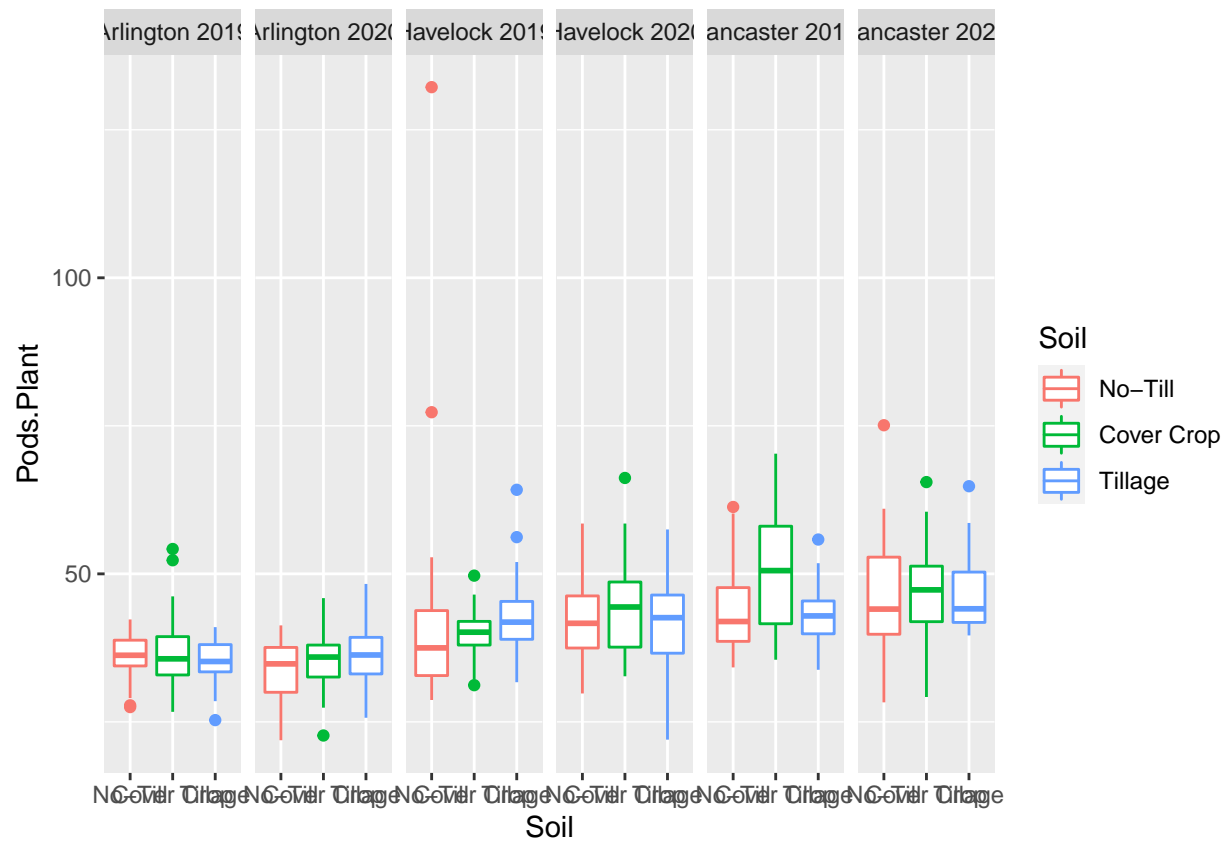
```
#Plot of Soybean seed counts
SoybeanComp %>%
  ggplot(aes(x = Soil, y = Seeds, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```



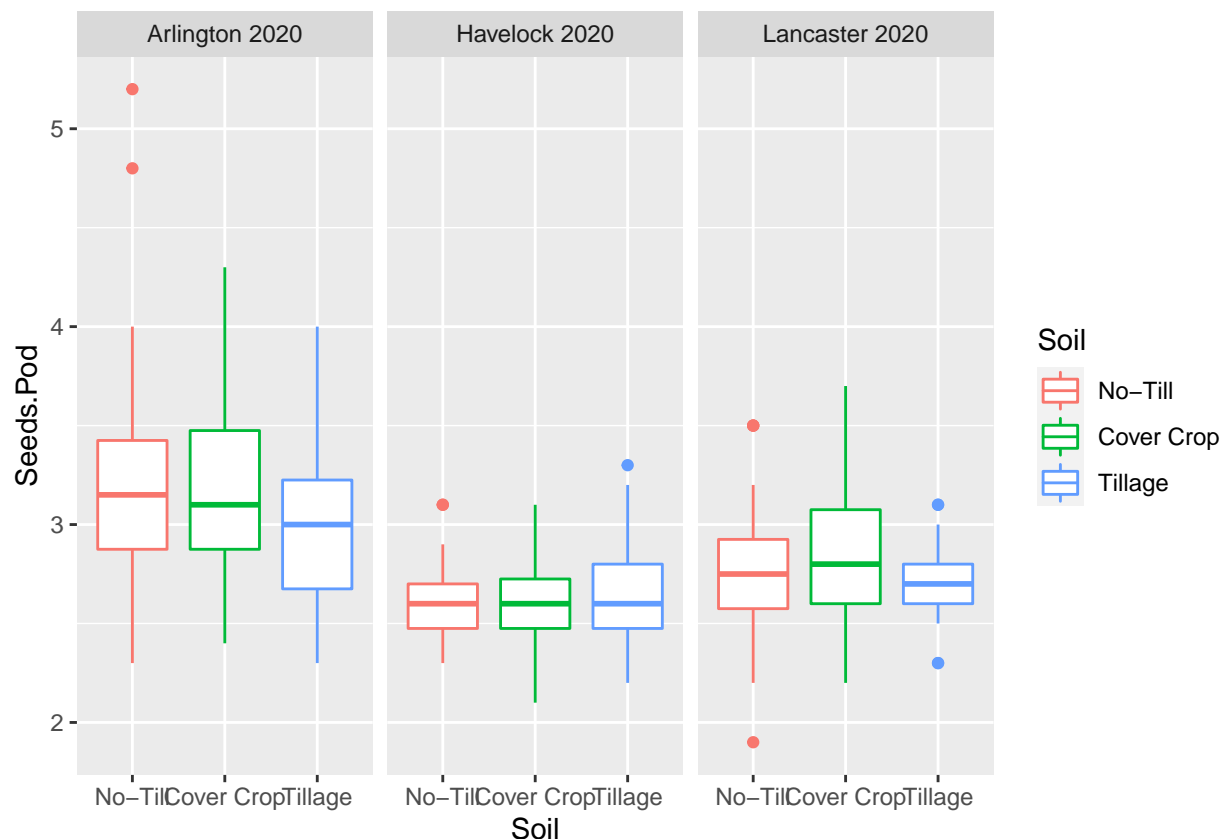
#All of the 2019 data is lower, I am not confident in using it.

#Plot of Soybean pods per plant

```
SoybeanComp %>%
  ggplot(aes(x = Soil, y = Pods.Plant, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```

```
#Plot of Soybean seeds per pod
SoybeanComp1 %>%
  ggplot(aes(x = Soil, y = Seeds.Pod, color = Soil)) +
  geom_boxplot() +
  facet_grid(~ Site_Yr)
```



I decided to only analyse models for the lancaster location. I have done more analysis on these yield components looking at site-year but they aren't really useful if we can't compare them to yield so I am not sharing them with this document. Remember, we are trying to explain reduced yield from soil management with a cover crop at Lancaster. I made models for all locations for fun though.

Pods per plant

```
lan_SBPods_Plant= lmer(Pods.Plant~Soil*Herb+ (1|Rep/Year) , data= (filter(SoybeanComp, Location == "Lancaster") %>%
qnorm(resid(lan_SBPods_Plant)))
```

```
plot(lan_SBPods_Plant)
```

```
#assumptions met
```

```
anova(lan_SBPods_Plant)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Soil       410.06  205.029     2    98  2.9104 0.05918 .
## Herb       157.05   39.263     4    98  0.5573 0.69415
## Soil:Herb  480.23   60.028     8    98  0.8521 0.55955
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#nothing significant, soil almost significant
```

```
lan_pod_plantlsmeans<- lsmeans(lan_SBPods_Plant, ~ Soil, contr="pairwise", adjust="none")
```

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

```
lan_pod_plantcld <- cld(lan_pod_plantlsmeans$lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=
```

```
lan_pod_plantcld <- as_tibble(lan_pod_plantcld) %>%  
  rename(Pods.Plant = lsmean) %>%  
  mutate(Soil= factor(Soil, levels= order)) %>%  
  arrange(Soil)
```

```
lan_pod_plantcld
```

```
## # A tibble: 3 x 7  
##   Soil      Pods.Plant    SE    df lower.CL upper.CL .group  
##   <fct>          <dbl> <dbl> <dbl>   <dbl>   <dbl> <chr>  
## 1 Tillage         44.9  1.62  9.68    41.3    48.5 " b"  
## 2 No-Till         45.8  1.62  9.68    42.1    49.4 " ab"  
## 3 Cover Crop      49.2  1.62  9.68    45.6    52.8 " a "
```

Seed density

```
lan_dens= lmer(Hundred~Soil*Herb+ (1|Rep) , data= (filter(SoybeanComp1, Location == "Lancaster")))
```

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

```
qqnorm(resid(lan_dens))
```

```
plot(lan_dens)
```

```
#assumptions met
```

```
anova(lan_dens)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method  
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)  
## Soil       2.8546  1.42732     2    45  1.7856 0.1794  
## Herb       2.4815  0.62037     4    45  0.7761 0.5466  
## Soil:Herb  8.6961  1.08702     8    45  1.3599 0.2400
```

```
#nothing significant
```

```
lan_denslsmeans<- lsmeans(lan_dens, ~ Soil, contr="pairwise", adjust="none")
```

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

```
lan_denscld <- cld(lan_denslsmeans$lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=FALSE)

lan_denscld <- as_tibble(lan_denscld) %>%
  rename(Hundred = lsmean) %>%
  mutate(Soil= factor(Soil, levels= order)) %>%
  arrange(Soil)

lan_denscld
```

```
## # A tibble: 3 x 7
##   Soil      Hundred    SE    df lower.CL upper.CL .group
##   <fct>      <dbl> <dbl> <dbl>   <dbl>   <dbl> <chr>
## 1 Tillage      13.7 0.200   21.    13.3    14.1 " a"
## 2 No-Till      13.4 0.200   21.    13.0    13.8 " a"
## 3 Cover Crop   13.2 0.200   21.    12.8    13.6 " a"
```

Seed Counts

```
lan_seeds= lmer(Seeds~Soil*Herb+ (1|Rep) , data= (filter(SoybeanComp1, Location == "Lancaster")))
qqnorm(resid(lan_seeds))
```

```
plot(lan_seeds)
```

```
#assumptions met
```

```
anova(lan_seeds)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## Soil           53474    26737     2    42  1.1154 0.3373
## Herb           98239    24560     4    42  1.0246 0.4058
## Soil:Herb    336683    42085     8    42  1.7557 0.1137
```

```
#nothing significant
```

```
lan_seedslsmeans<- lsmeans(lan_seeds, ~ Soil, contr="pairwise", adjust="none")
```

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

```
lan_seedsclld <- cld(lan_seedslsmeans$lsmeans, alpha=0.05, Letters=letters, adjust="none", sort=TRUE, reverse=FALSE)

lan_seedsclld <- as_tibble(lan_seedsclld) %>%
  rename(Seeds = lsmean) %>%
  mutate(Soil= factor(Soil, levels= order)) %>%
  arrange(Soil)

lan_seedsclld
```

```
## # A tibble: 3 x 7
##   Soil      Seeds    SE    df lower.CL upper.CL .group
##   <fct>      <dbl> <dbl> <dbl>   <dbl>   <dbl> <chr>
## 1 Tillage    764.  47.7  6.97    651.    877. " a"
## 2 No-Till    781.  47.7  6.97    668.    894. " a"
## 3 Cover Crop 834.  47.7  6.97    721.    947. " a"
```

Soybean Seeds/Pod

```
lan_seeds_pod= lmer(Seeds.Pod~Soil*Herb+ (1|Rep) , data= (filter(SoybeanComp1, Location == "Lancaster"))
qqnorm(resid(lan_seeds_pod))
```

```
plot(lan_seeds_pod)
```

```
#assumptions met
```

```
anova(lan_seeds_pod)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## Soil      0.51433  0.257167     2    42  1.8673 0.1671
## Herb      0.26267  0.065667     4    42  0.4768 0.7525
## Soil:Herb 0.93733  0.117167     8    42  0.8507 0.5645
```

```
#nothing significant
```

```
lan_seeds_podlsmmeans<- lsmeans(lan_seeds_pod, ~ Soil, contr="pairwise", adjust="none")
```

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

```
lan_seeds_podcld <- cld(lan_seeds_podlsmmeans$lsmmeans, alpha=0.05, Letters=letters, adjust="none", sort=
```

```
lan_seeds_podcld <- as_tibble(lan_seeds_podcld) %>%
  rename(Seeds = lsmean) %>%
  mutate(Soil= factor(Soil, levels= order)) %>%
  arrange(Soil)
```

```
lan_seeds_podcld
```

```
## # A tibble: 3 x 7
##   Soil      Seeds    SE    df lower.CL upper.CL .group
##   <fct>      <dbl> <dbl> <dbl>   <dbl>   <dbl> <chr>
## 1 Tillage    2.72  0.106  8.26    2.48    2.97 " a"
## 2 No-Till    2.77  0.106  8.26    2.53    3.01 " a"
## 3 Cover Crop 2.94  0.106  8.26    2.70    3.18 " a"
```

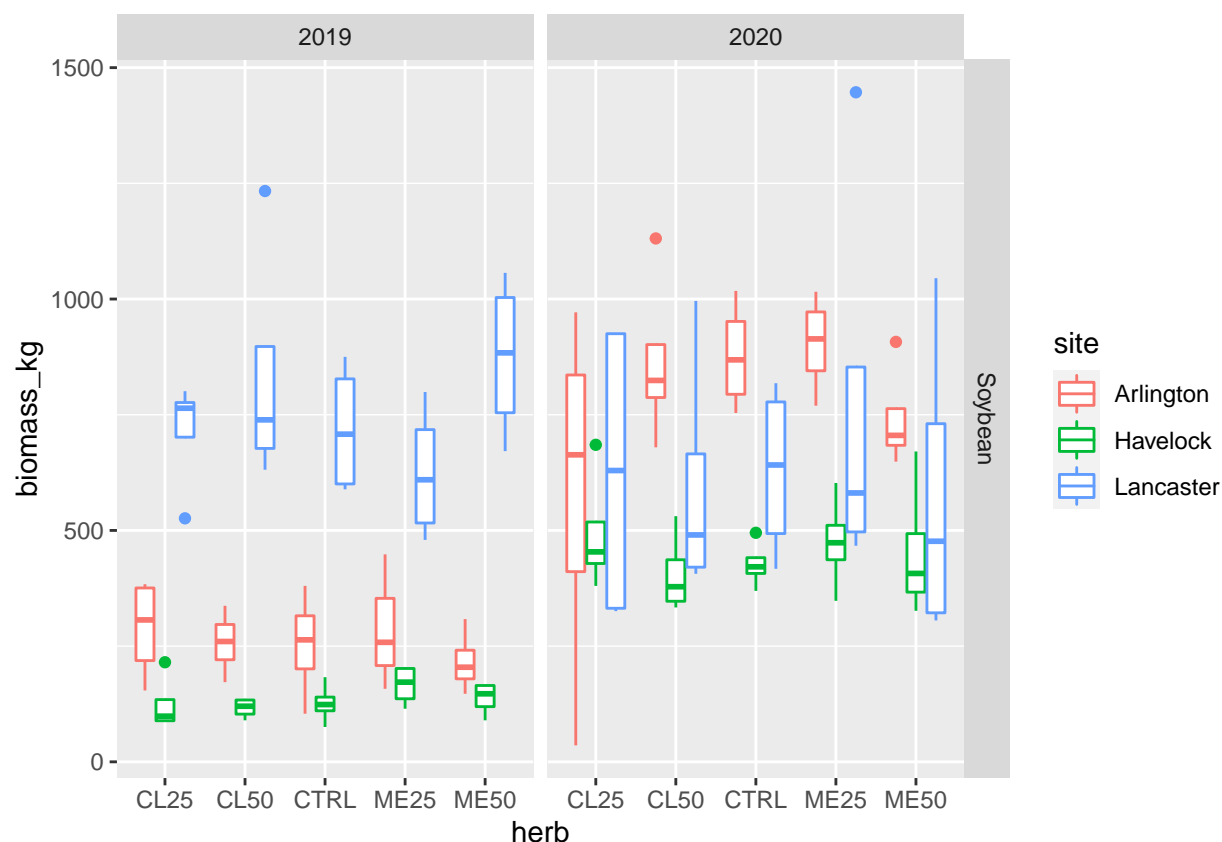
Summary of yield components analysis

There weren't any useful yield components to explain what we saw at Lancaster with reduced yield for the cover crop soil management treatment. I think the lowest mean stand count early-season is our best explanation. Only having 2020 data for most yield components didn't help this and if you look at the boxplots generated prior to the yield analysis the reduced yield appears to have occurred in 2019. There was also reduced canopy cover for this treatment in 2019.

Cover crop analysis

Biomass analysis

```
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.

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))
```

```
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))
```

```
plot(sb_cc_bio1)
```

```
#assumption improved.
```

```
anova(sb_cc_bio1)
```

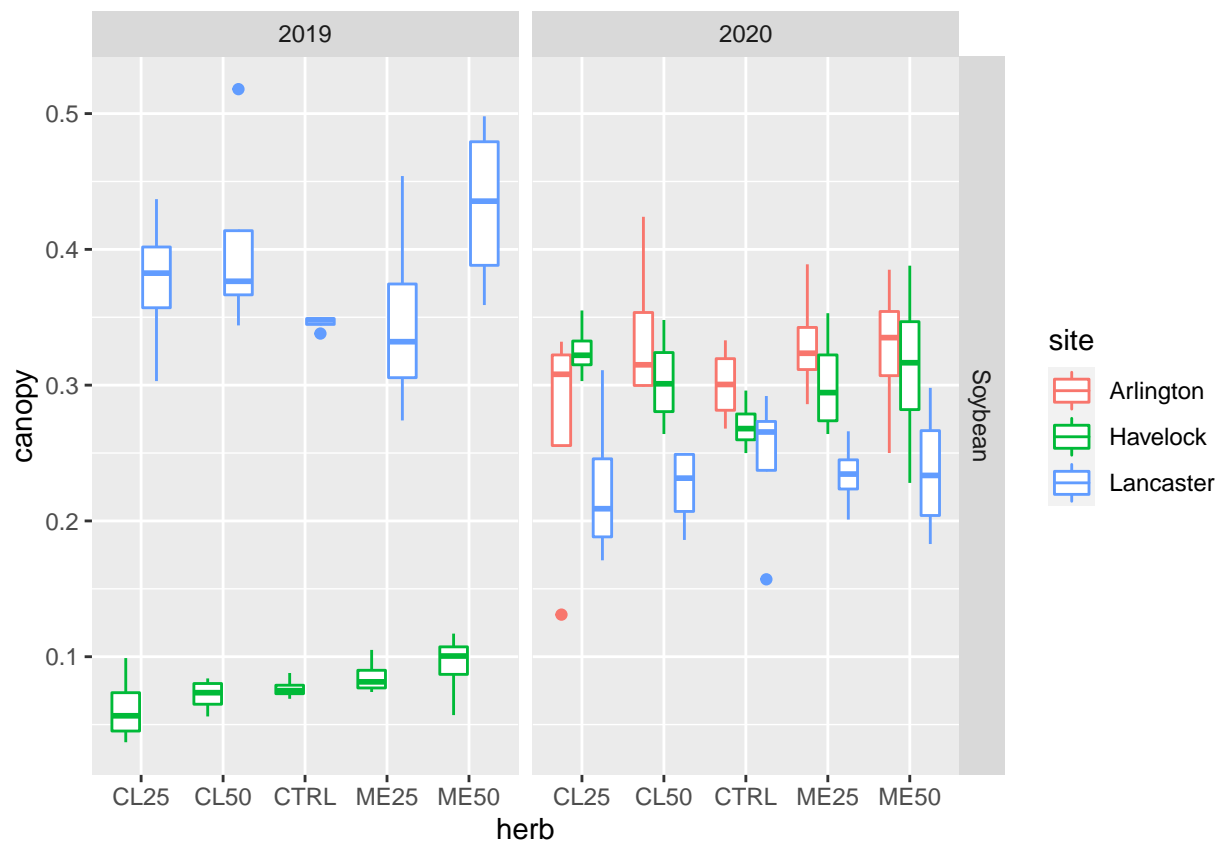
```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## site_crop_yr   3372.1   674.43     5  18.042  42.2749 2.417e-09 ***
## herb           34.9     8.72     4  71.375   0.5467   0.7020
## site_crop_yr:herb 253.8   12.69    20  71.325   0.7955   0.7103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Site-year significant
```

There is no evidence that herbicide carryover reduced CC biomass.

Cover Crop Canopy

```
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.

```
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
```

There is no evidence that herbicide carryover influenced cover crop canopy