

warmXtrophic Project: Greenup Analyses

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Script Details:

```
# this portion of the script won't knit, so its set to eval=F

script_tbl <- data.frame(Item = c("OVERVIEW", "COLLABORATORS",
  "REQUIRES", "DATA INPUT", "DATA OUTPUT", "NOTES"), Details = c("This script explores and analyses the  
Moriah Young, Mark Hammond, Pat Bills", "Prior to running this script, make sure plant_comp_clean_1  
Data imported as csv files from shared Google drive 'SpaCE_Lab_warmXtrophic' plant comp folder",  
"... a brief description of the data output from through the script, including what format it's in"  
"Each row in 'greenup' is the date at which spp_half_cover_date was recorded, per species. The 'greenup'"

kbl(script_tbl) %>% kable_paper(full_width = F) %>% column_spec(1,  
bold = T, border_right = T) %>% column_spec(2, width = "30em",  
background = "lightblue")

metadata_tbl <- data.frame(Variable = c("spp_half_cover_date",  
"plot_half_cover_date", "state"), Definition = c("date at which 50% of a species max cover was reached",  
"the date at which 50% of a plot's max cover was reached (per plot, per year)",  
"describes each treatment: warmed or ambient"))

kbl(metadata_tbl) %>% kable_paper(full_width = F) %>% column_spec(1,  
bold = T, border_right = T) %>% column_spec(2, width = "30em",  
background = "lightyellow")


# Clear all existing data
rm(list = ls())

# Load packages
library(tidyverse)
library(ggplot2)
library(lmerTest)
library(olsrr)
library(predictmeans)
library(car)
library(fitdistrplus)
library(ggpubr)
library(rstatix)
library(vegan)
library(interactions)
library(sjPlot)
library(effects)
library(glmmTMB)
```

```

library(bbmle)
library(emmeans)
# install.packages('TMB', type='source')

# Set ggplot2 plots to bw: see here for more options:
# http://www.sthda.com/english/wiki/ggplot2-themes-and-background-colors-the-3-elements
theme_set(theme_bw(base_size = 14))

# Get data
L1_dir <- Sys.getenv("L1DIR")
L2_dir <- Sys.getenv("L2DIR")
greenup <- read.csv(file.path(L2_dir, "greenup/final_greenup_species_L2.csv")) # spp level greenup data
greenup <- greenup %>% dplyr::select(-X) # get rid of 'X' column that shows up (could fix this in clean)
greenupp <- read.csv(file.path(L2_dir, "greenup/final_greenup_plot_L2.csv")) # plot level greenup data
greenupp <- greenupp %>% dplyr::select(-X) # get rid of 'X' column that shows up

# check variable types
str(greenup)

## 'data.frame': 2271 obs. of 18 variables:
## $ site : chr "kbs" "kbs" "kbs" "kbs" ...
## $ plot : chr "A1" "A1" "A1" "A1" ...
## $ year : int 2016 2017 2018 2019 2020 2021 2016 2017 2016 2017 ...
## $ species : chr "Acmi" "Acmi" "Acmi" "Acmi" ...
## $ spp_half_cover_date: int 104 101 122 120 223 257 88 108 101 99 ...
## $ min_green_date : int 81 80 122 120 107 92 81 108 85 80 ...
## $ treatment_key : chr "AO" "AO" "AO" "AO" ...
## $ state : chr "ambient" "ambient" "ambient" "ambient" ...
## $ insecticide : chr "no_insects" "no_insects" "no_insects" "no_insects" ...
## $ scientific_name : chr "Achillea millefolium" "Achillea millefolium" "Achillea millefolium" "A
## $ common_name : chr "common yarrow" "common yarrow" "common yarrow" "common yarrow" ...
## $ USDA_species : chr "ACMI2" "ACMI2" "ACMI2" "ACMI2" ...
## $ LTER_species : chr "ACHMI" "ACHMI" "ACHMI" "ACHMI" ...
## $ origin : chr "Native" "Native" "Native" "Native" ...
## $ group : chr "Dicot" "Dicot" "Dicot" "Dicot" ...
## $ family : chr "Fabaceae" "Fabaceae" "Fabaceae" "Fabaceae" ...
## $ duration : chr "Biennial" "Biennial" "Biennial" "Biennial" ...
## $ growth_habit : chr "Forb" "Forb" "Forb" "Forb" ...

str(greenupp)

## 'data.frame': 263 obs. of 8 variables:
## $ site : chr "kbs" "kbs" "kbs" "kbs" ...
## $ plot : chr "A1" "A1" "A1" "A1" ...
## $ year : int 2016 2017 2018 2019 2020 2021 2016 2017 2018 2019 ...
## $ treatment_key : chr "AO" "AO" "AO" "AO" ...
## $ state : chr "ambient" "ambient" "ambient" "ambient" ...
## $ insecticide : chr "no_insects" "no_insects" "no_insects" "no_insects" ...
## $ plot_half_cover_date: int 81 80 84 122 223 216 160 150 191 145 ...
## $ min_green_date : int 81 61 59 106 91 85 121 107 120 112 ...

# Order warm and ambient so that warm shows up first in
# plotting (and is default is red = warm; blue = ambient).
# First make it a factor.
greenup$state <- as.factor(greenup$state)

```

```

levels(greenup$state)

## [1] "ambient" "warmed"
greenup$state <- factor(greenup$state, levels(greenup$state)[c(2,
1)])
levels(greenup$state)

## [1] "warmed" "ambient"
greenup$state <- as.factor(greenup$state)
levels(greenup$state)

## [1] "ambient" "warmed"
greenup$state <- factor(greenup$state, levels(greenup$state)[c(2,
1)])
levels(greenup$state)

## [1] "warmed" "ambient"
# adding sequential year variable starting at 1: this is
# because 2016... are large numbers compare with other values
# in the dataset. We can always label axes with these real
# years.
greenup$year_factor[greenup$year == 2016] <- 1
greenup$year_factor[greenup$year == 2017] <- 2
greenup$year_factor[greenup$year == 2018] <- 3
greenup$year_factor[greenup$year == 2019] <- 4
greenup$year_factor[greenup$year == 2020] <- 5
greenup$year_factor[greenup$year == 2021] <- 6
greenup$year_factor <- as.factor(greenup$year_factor) # having year as numerical was messing with some

greenup$year_factor[greenup$year == 2016] <- 1
greenup$year_factor[greenup$year == 2017] <- 2
greenup$year_factor[greenup$year == 2018] <- 3
greenup$year_factor[greenup$year == 2019] <- 4
greenup$year_factor[greenup$year == 2020] <- 5
greenup$year_factor[greenup$year == 2021] <- 6
greenup$year_factor <- as.factor(greenup$year_factor)

# create dataframes for kbs and umbs - remember that these
# contain species within plots
green_kbs <- subset(greenup, site == "kbs")
green_umbs <- subset(greenup, site == "umbs")

green_kbsp <- subset(greenup, site == "kbs")
green_umbsp <- subset(greenup, site == "umbs")

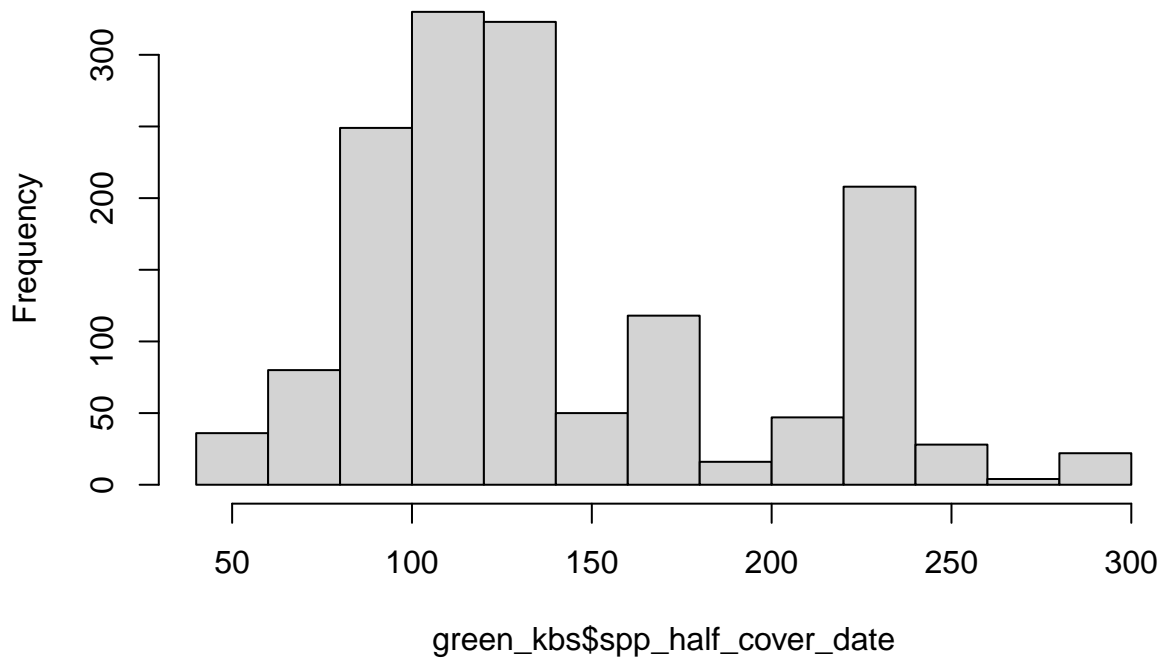
```

Data Exploration:

First, checking for normality in raw data. It's not going to tell you about normality once you fit a model to these data - that's when you really need to investigate the residuals.

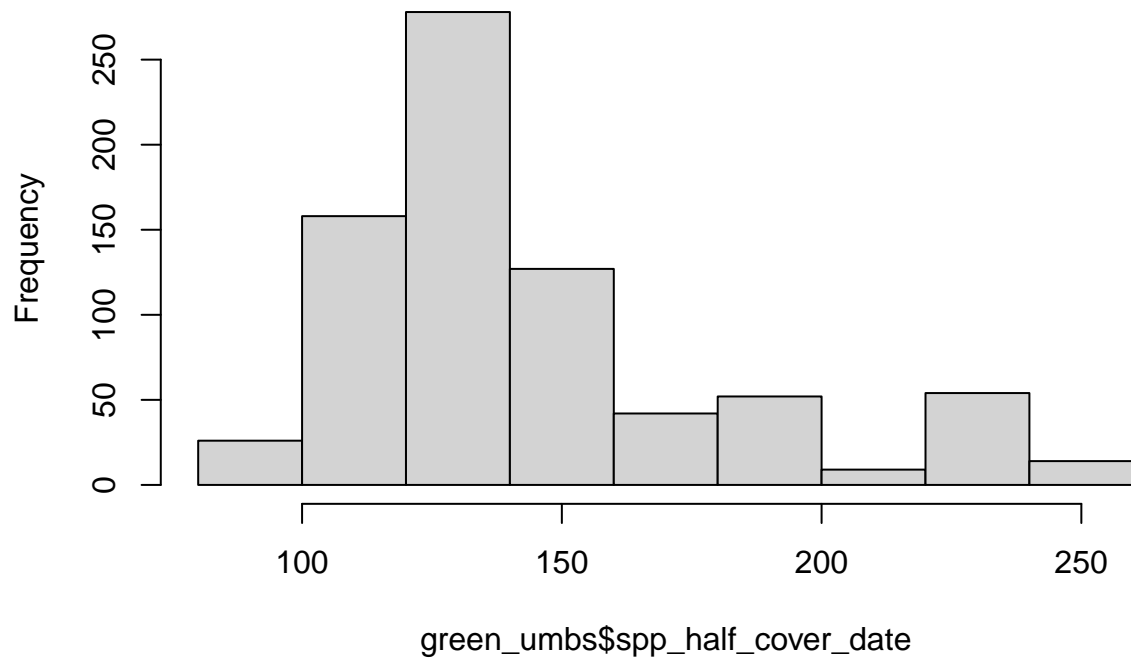
```
# species level  
hist(green_kbs$spp_half_cover_date)
```

Histogram of green_kbs\$spp_half_cover_date



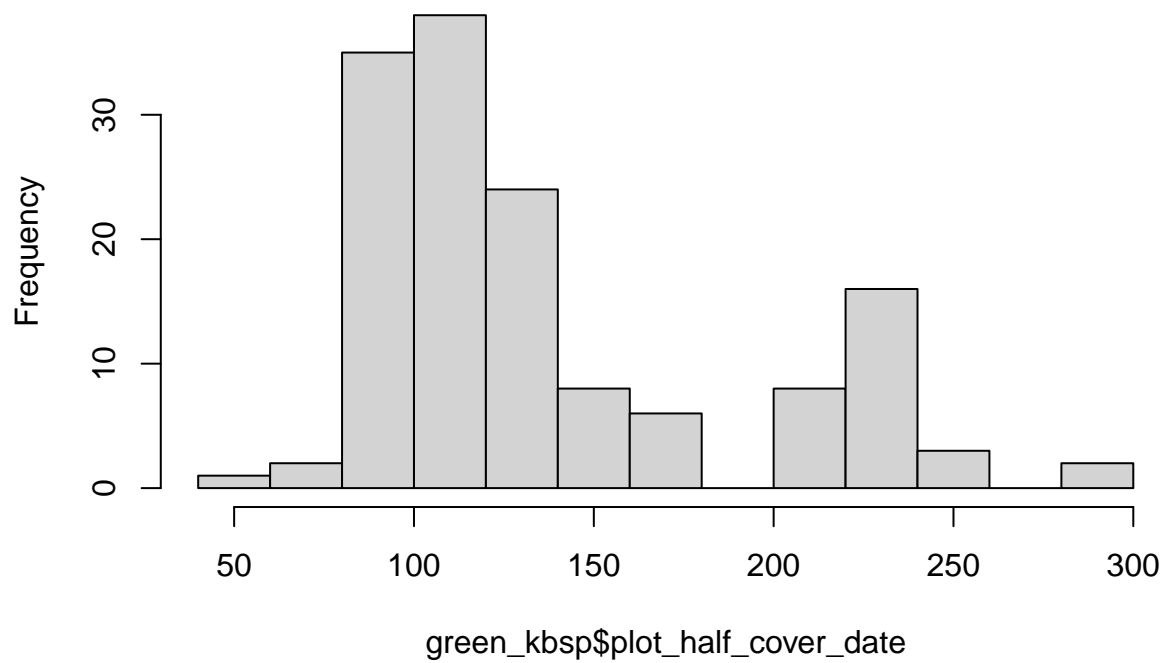
```
hist(green_umbs$spp_half_cover_date)
```

Histogram of green_umbs\$spp_half_cover_date

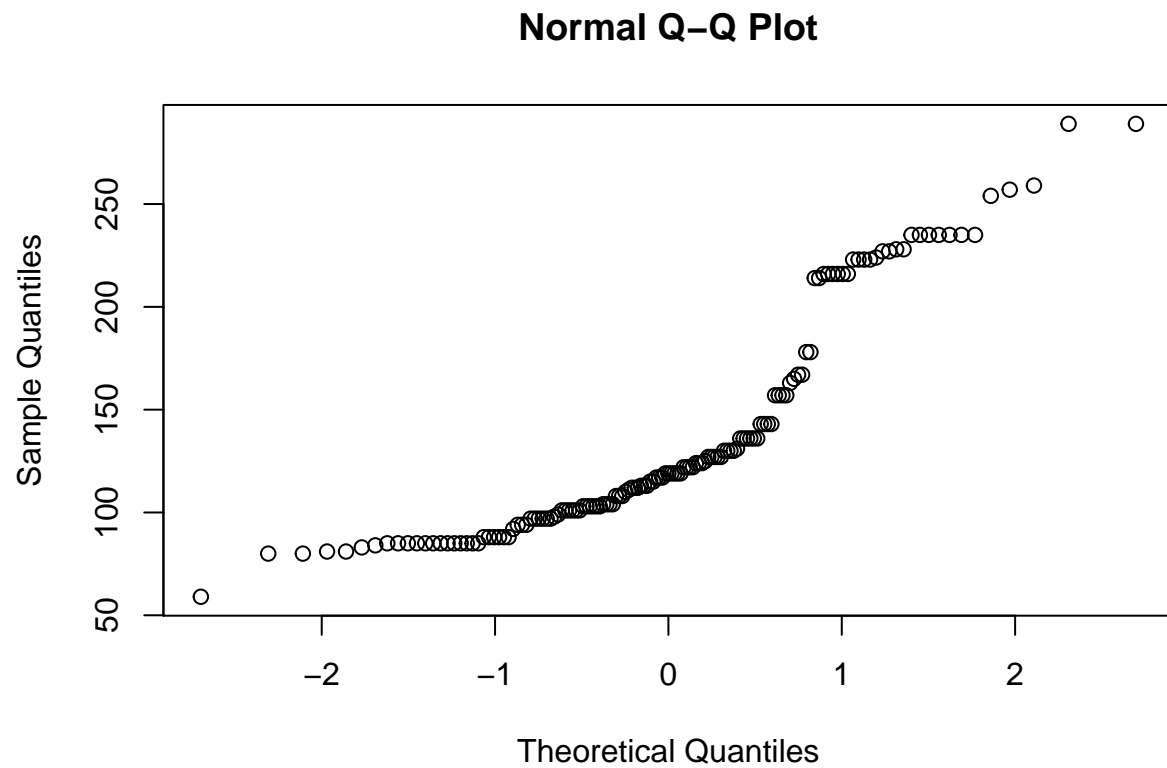


```
# plot level  
hist(green_kbsp$plot_half_cover_date)
```

Histogram of green_kbsp\$plot_half_cover_date



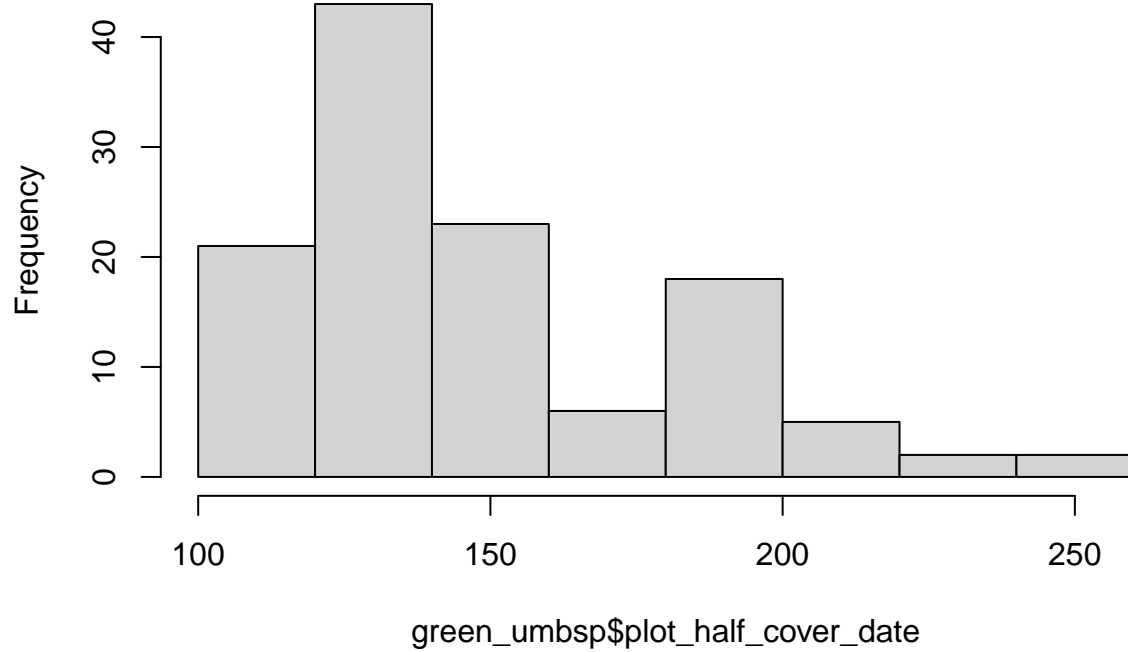
```
qqnorm(green_kbsp$plot_half_cover_date)
```



```
shapiro.test(green_kbsp$plot_half_cover_date)
```

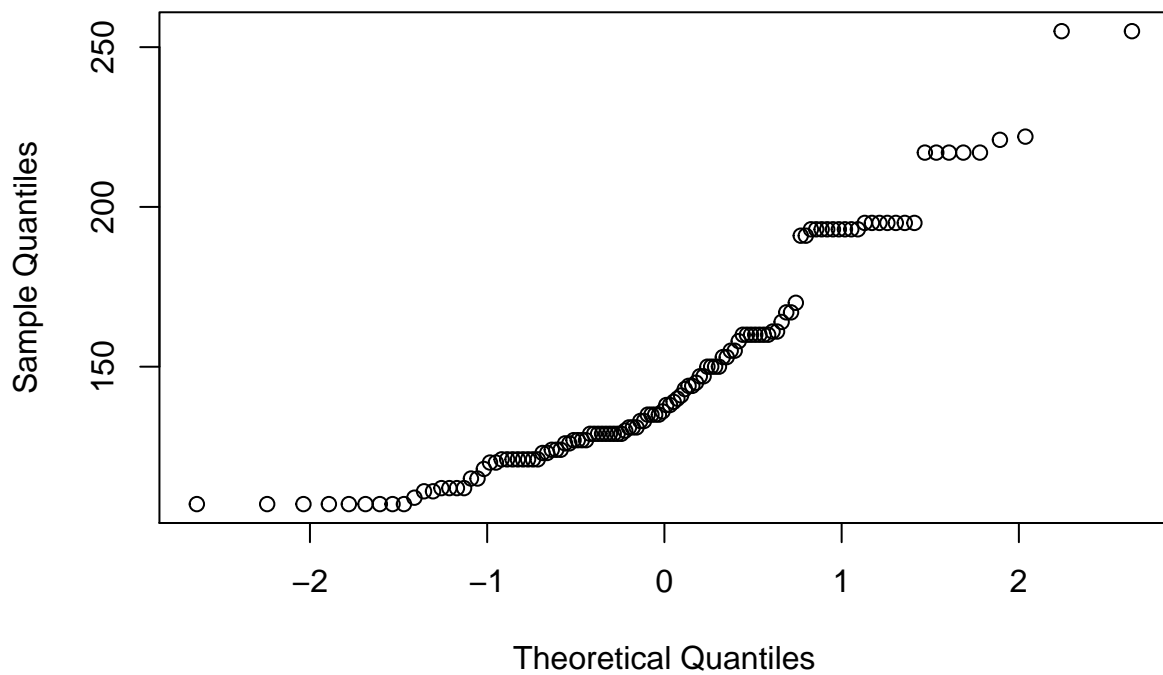
```
##  
##  Shapiro-Wilk normality test  
##  
## data:  green_kbsp$plot_half_cover_date  
## W = 0.84399, p-value = 5.136e-11  
hist(green_umbsp$plot_half_cover_date)
```

Histogram of green_umbasp\$plot_half_cover_date



```
qqnorm(green_umbasp$plot_half_cover_date)
```

Normal Q-Q Plot



```
shapiro.test(green_umbasp$plot_half_cover_date)
```

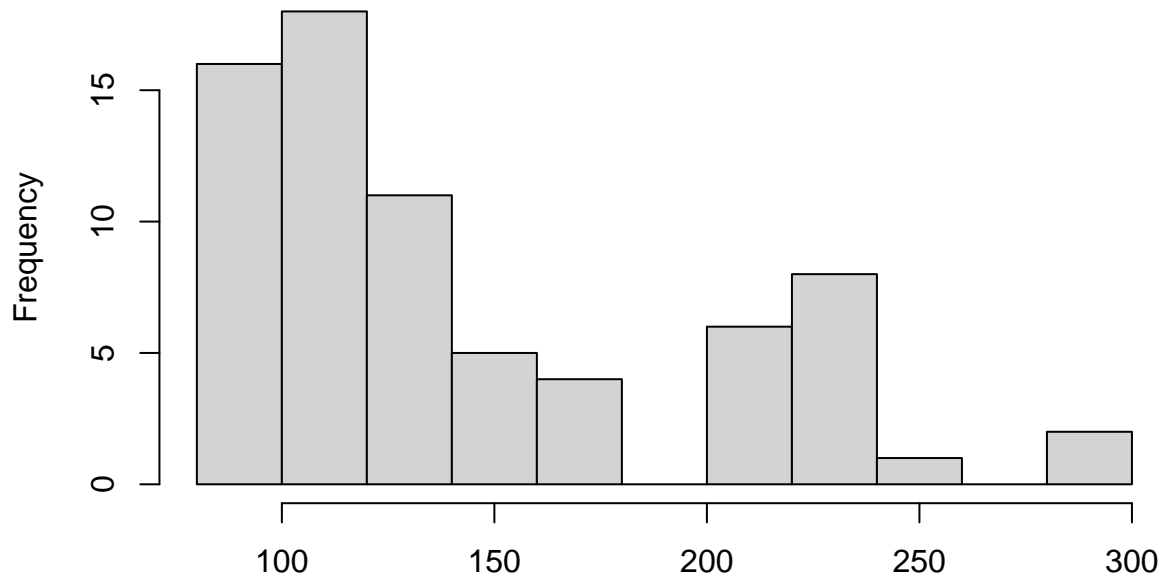
```
##
```

```
## Shapiro-Wilk normality test
##
## data: green_umbsp$plot_half_cover_date
## W = 0.89589, p-value = 1.217e-07
```

```
# histograms for each treatment separately - plot level
```

```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "ambient"])
```

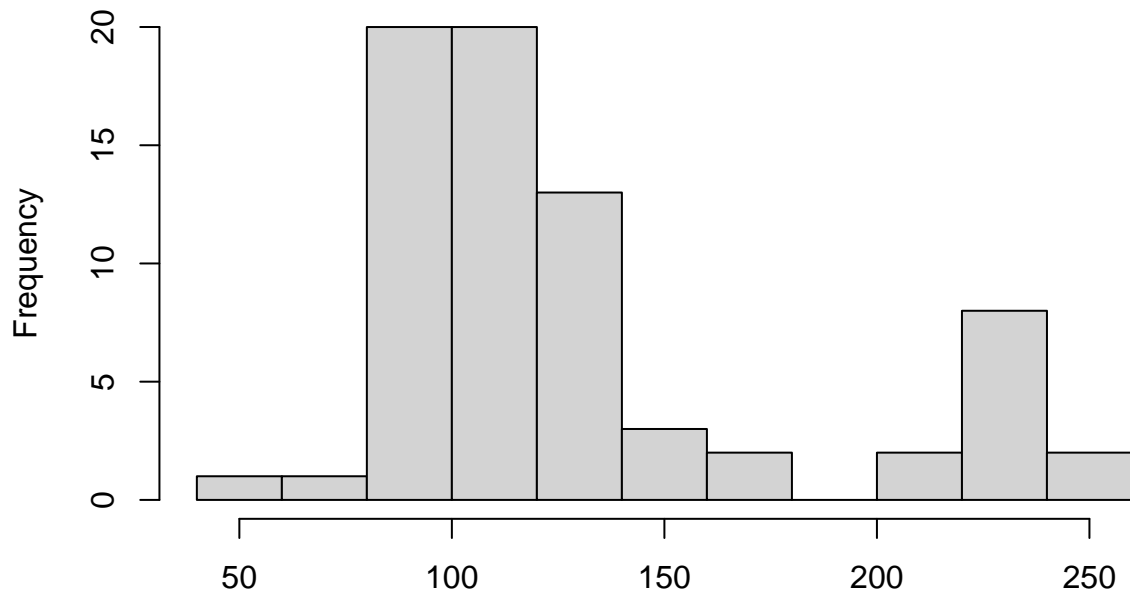
Histogram of green_kbsp\$plot_half_cover_date[green_kbsp\$state == "ambient"]



```
green_kbsp$plot_half_cover_date[green_kbsp$state == "ambient"]
```

```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "warmed"])
```

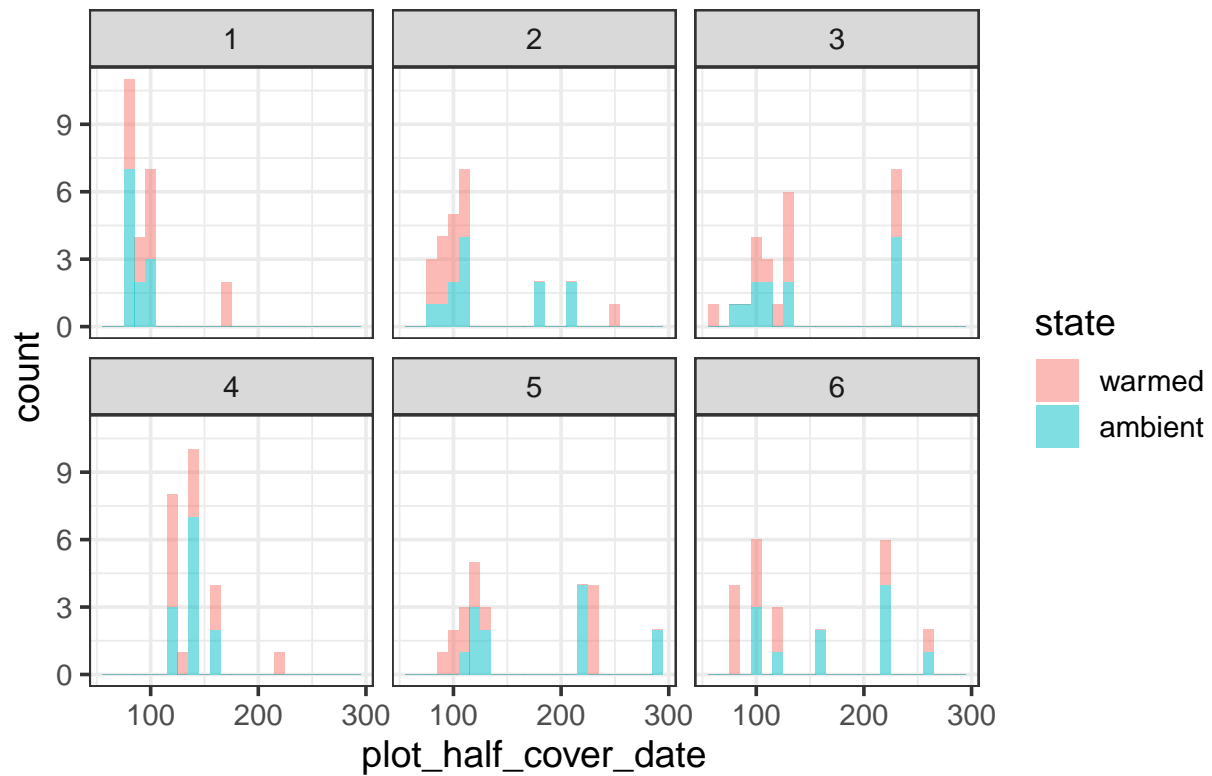

istogram of green_kbsp\$plot_half_cover_date[green_kbsp\$state == "wa



green_kbsp\$plot_half_cover_date[green_kbsp\$state == "warmed"]

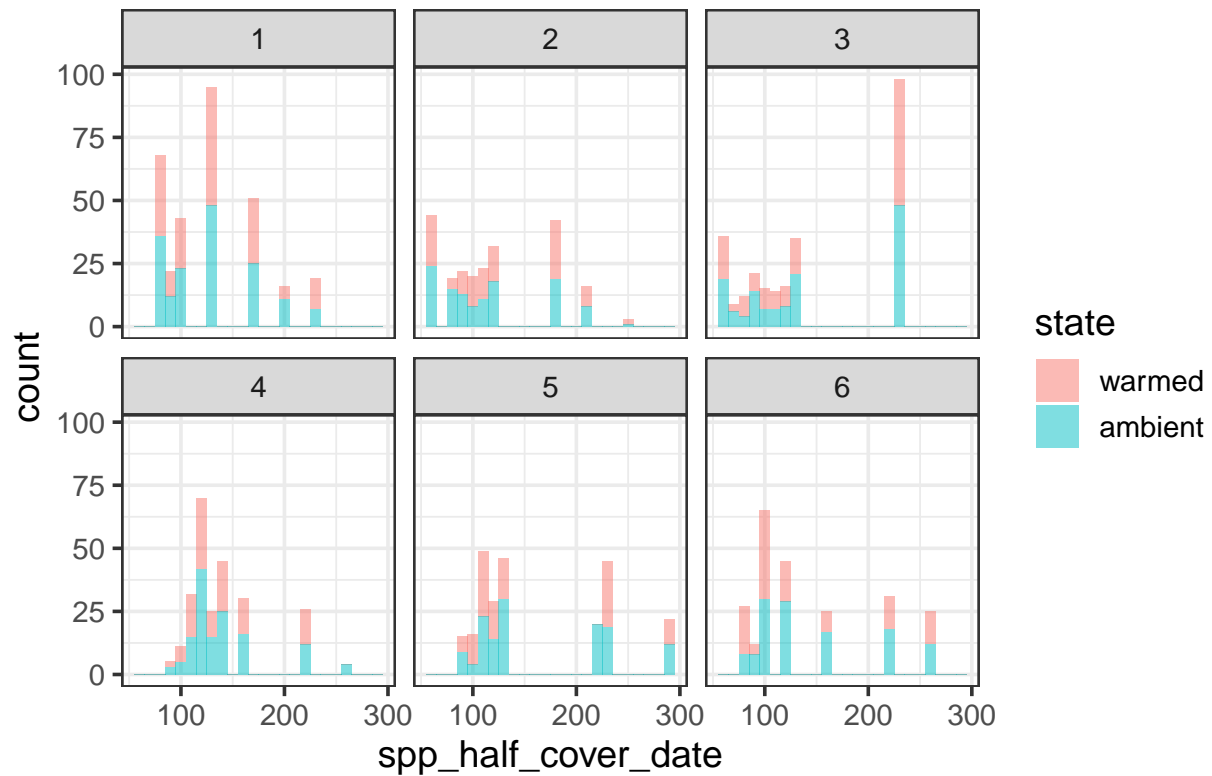
```
# histograms for each year - look at them together:
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
  fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```

Plot-level half cover date



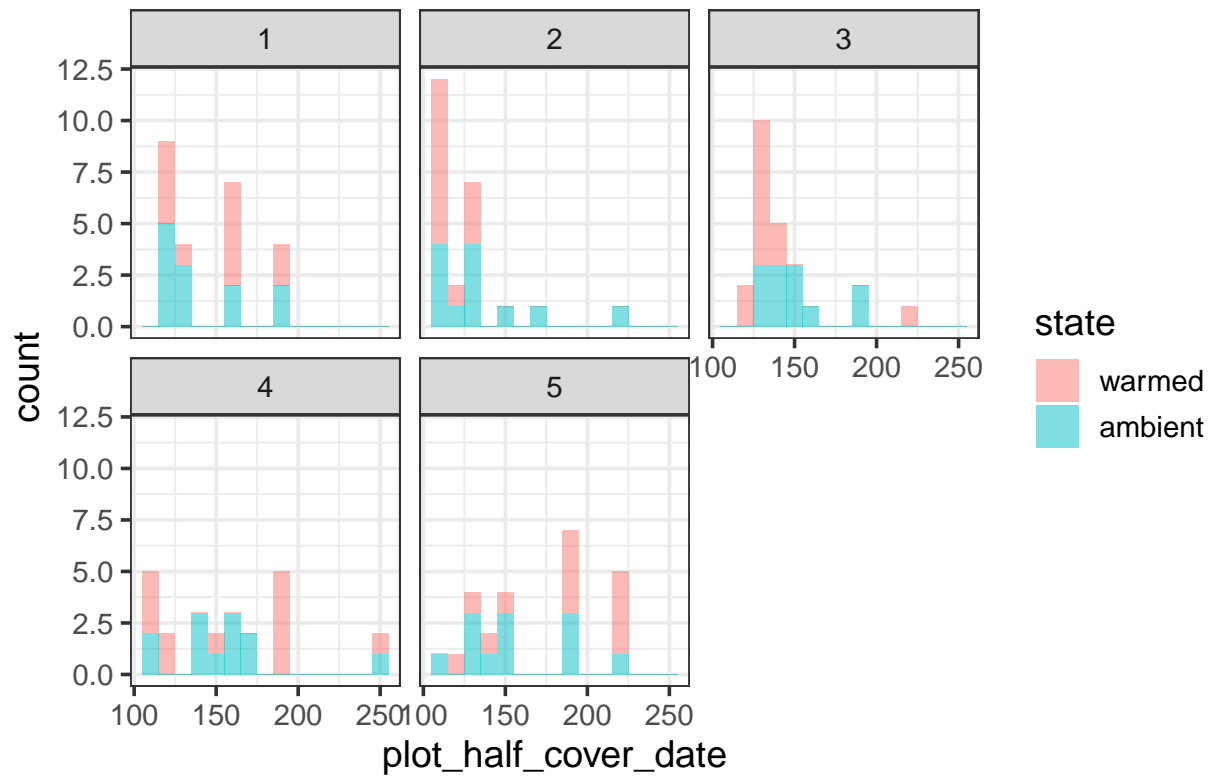
```
p1.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
  fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

Species-level half cover date



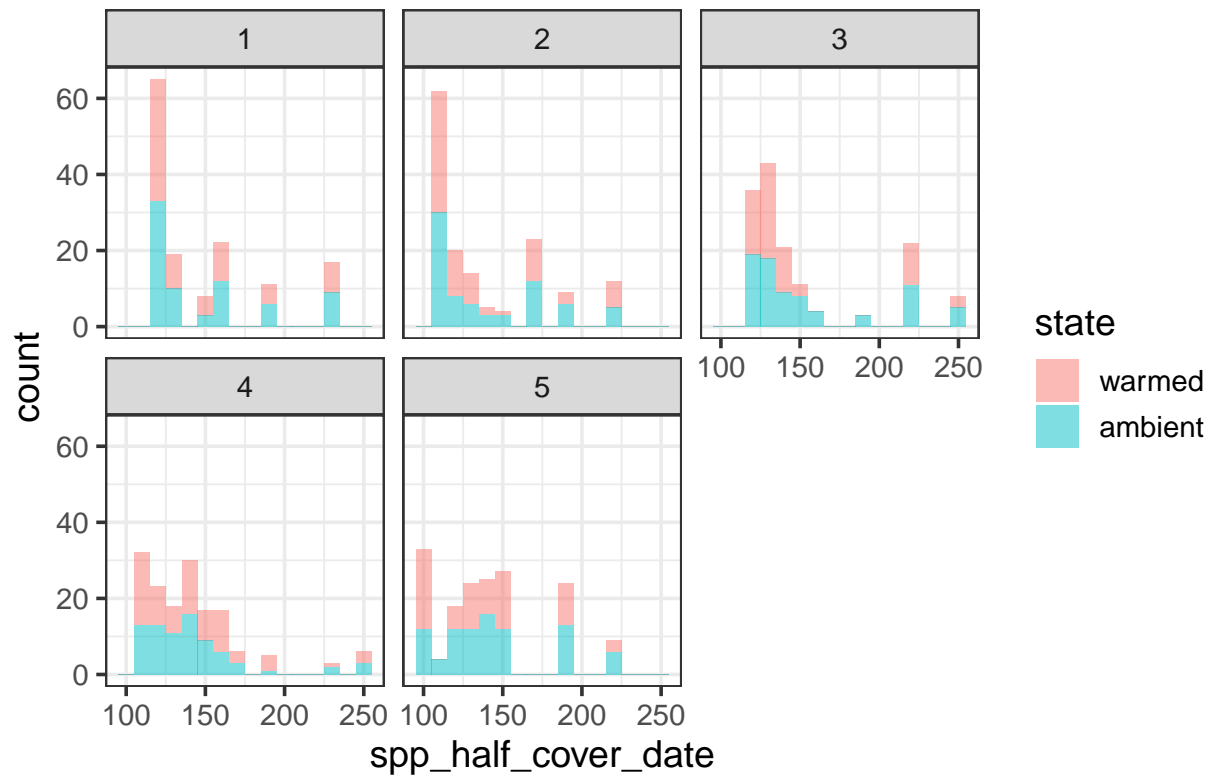
```
p1u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,  
  fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)  
p1u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```

Plot-level half cover date

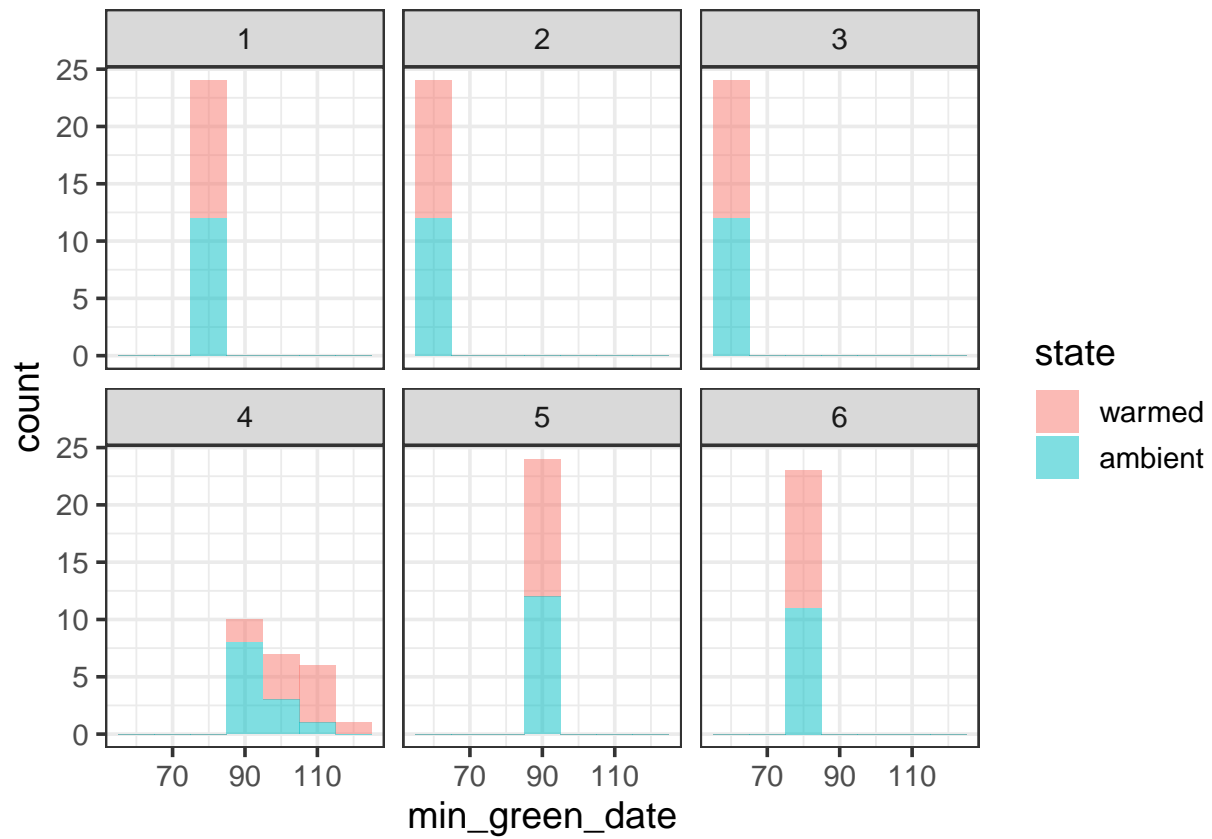


```
p1.2u <- ggplot(data = green_umbs, aes(x = spp_half_cover_date,
  fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2u + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

Species-level half cover date

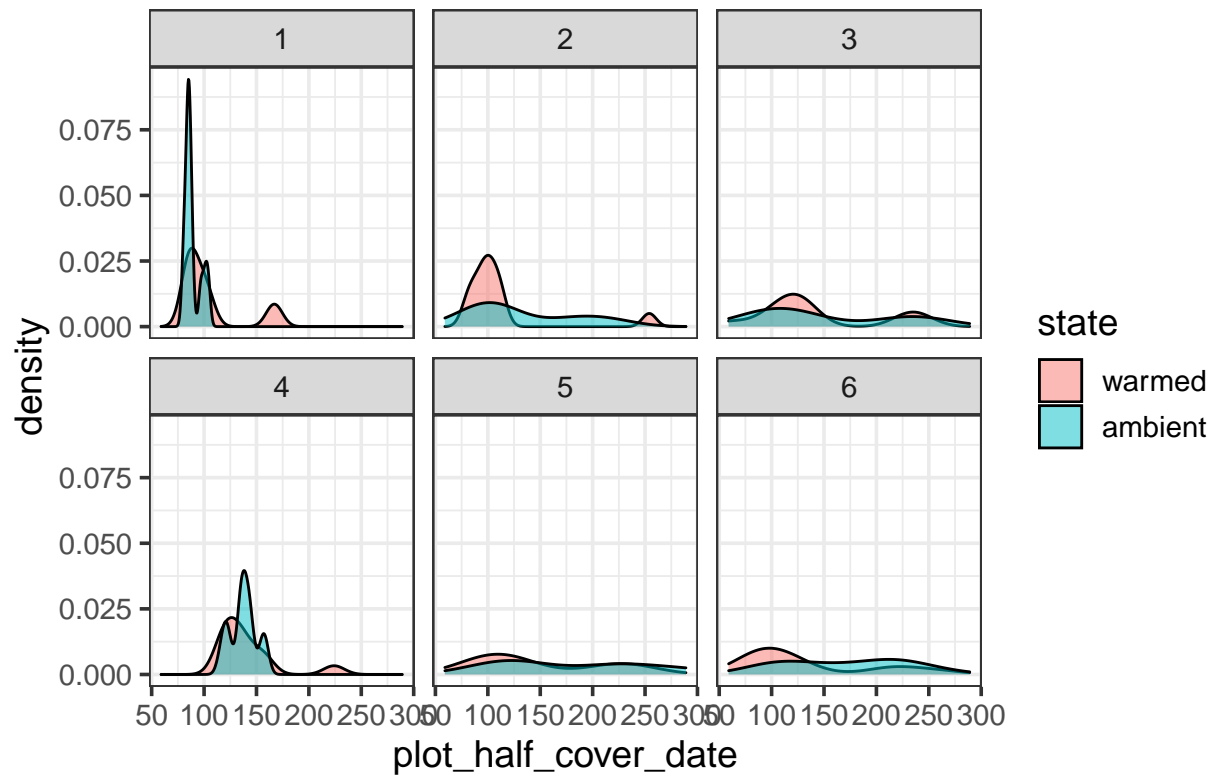


```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
  geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```



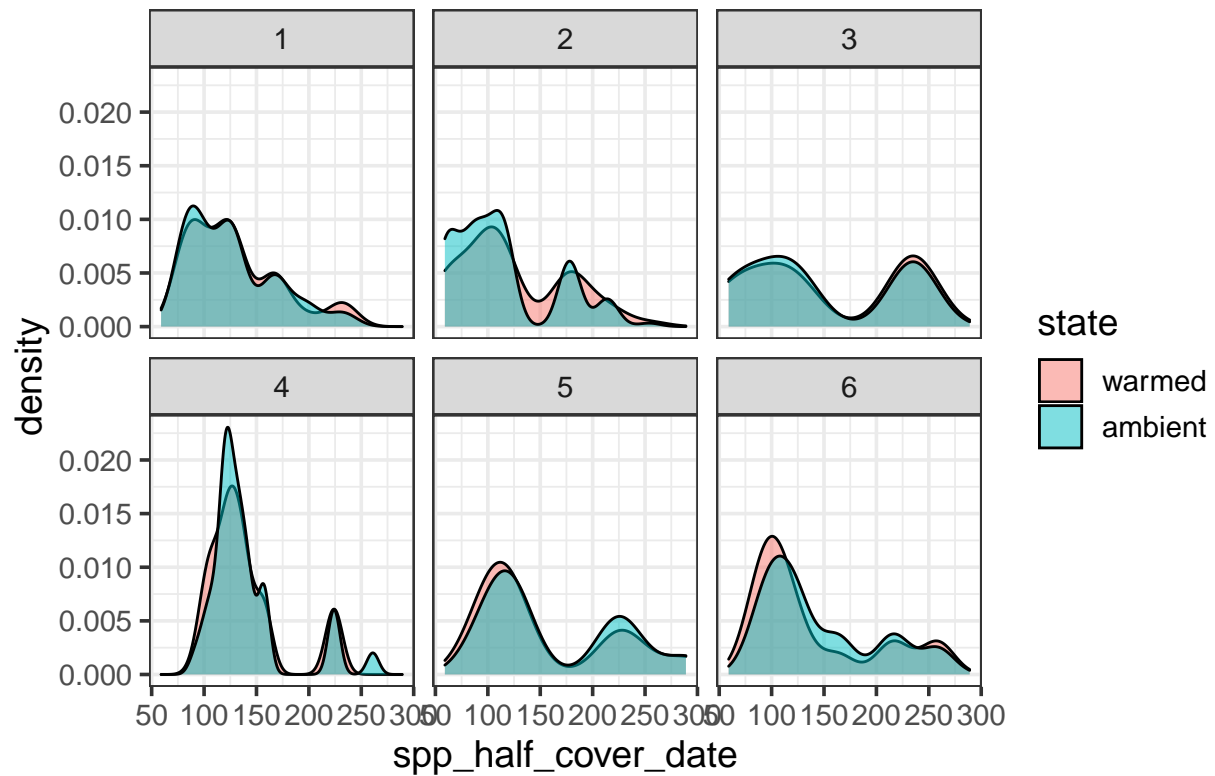
```
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
  fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```

Plot-level half cover date



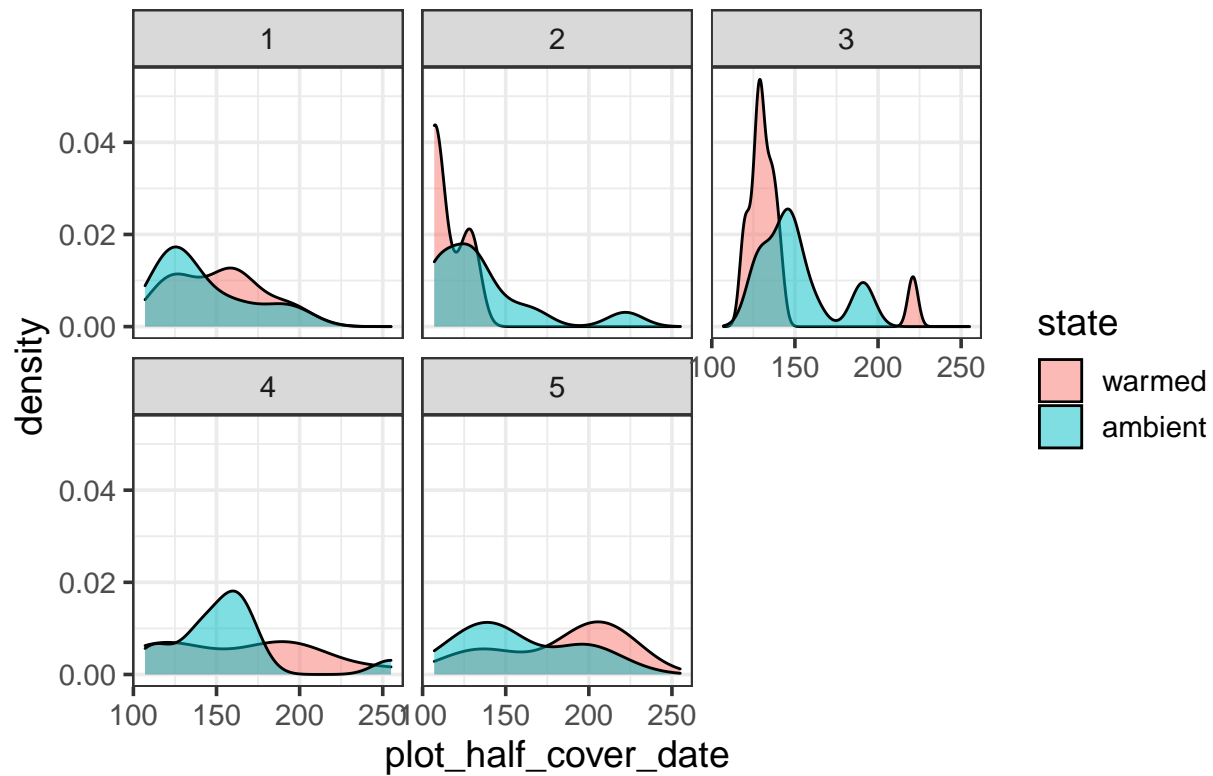
```
p3.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,  
  fill = state)) + geom_density(alpha = 0.5)  
p3.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

Species-level half cover date



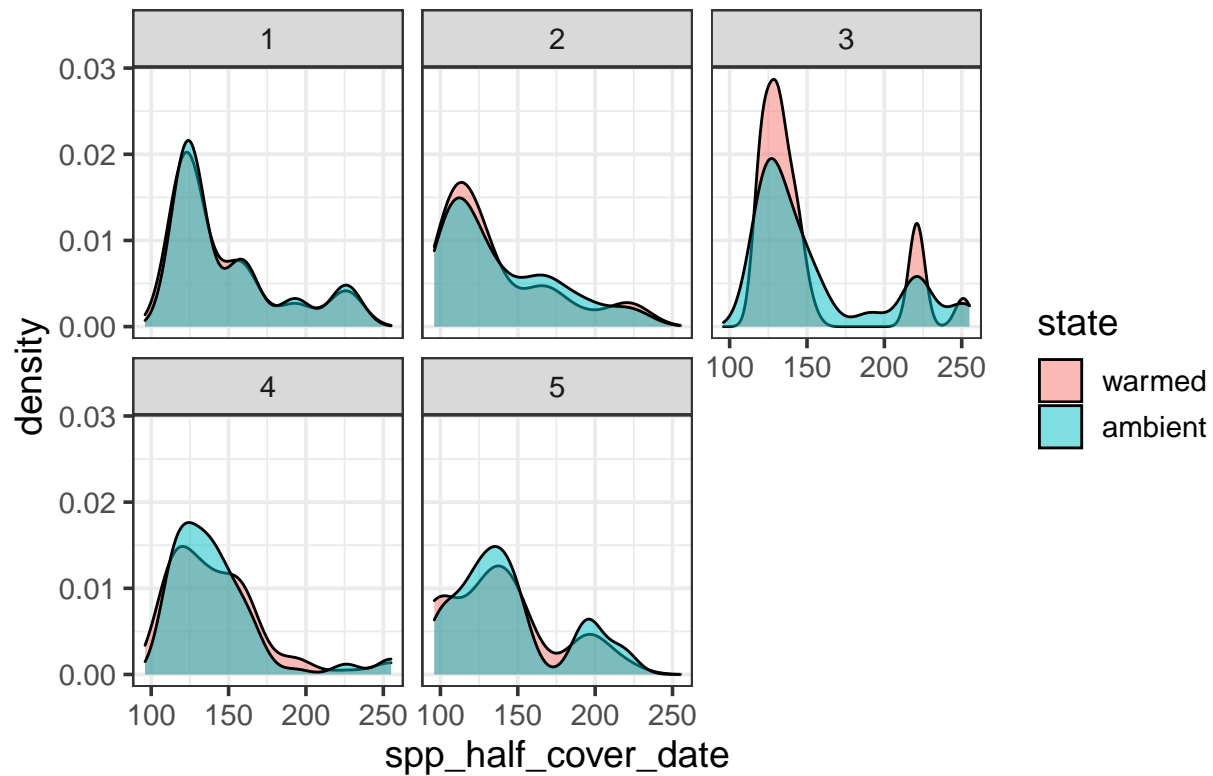
```
p3u <- ggplot(data = green_umbasp, aes(x = plot_half_cover_date,
  fill = state)) + geom_density(alpha = 0.5)
p3u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```


Plot-level half cover date

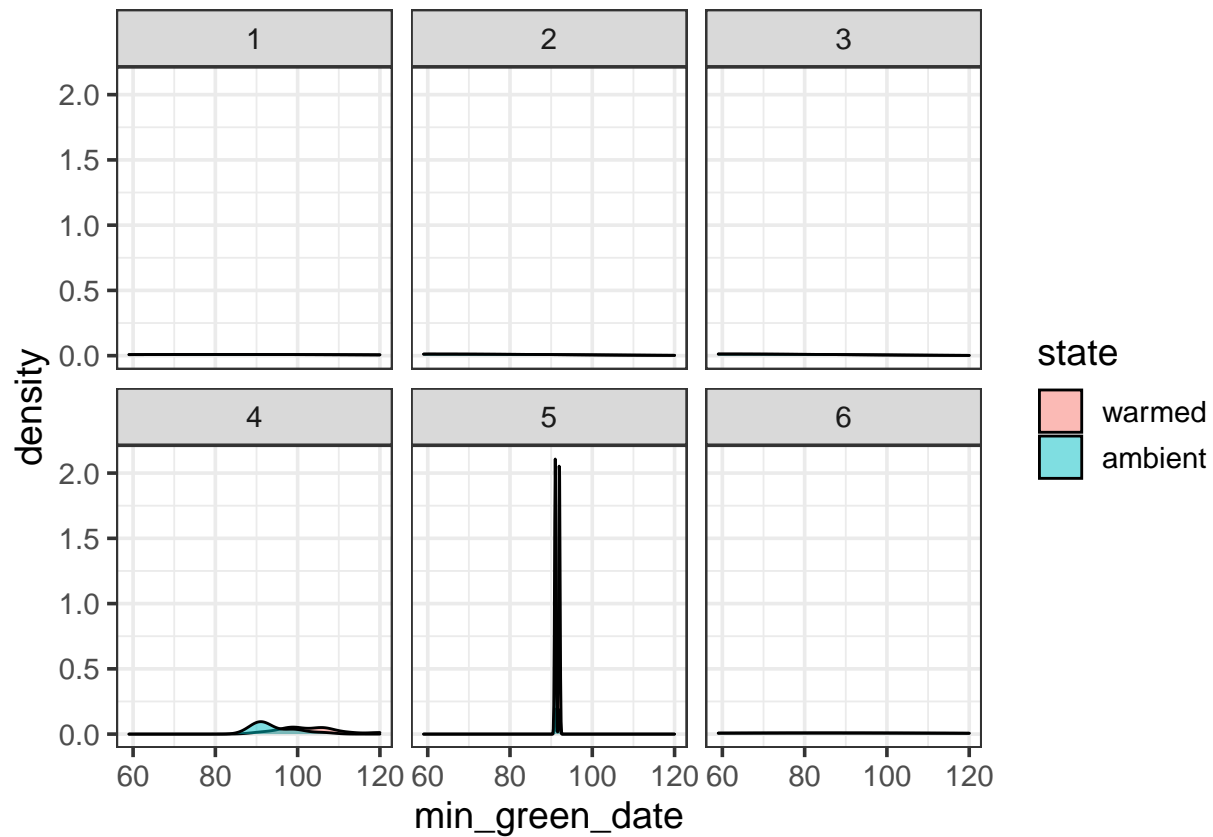


```
p3.2u <- ggplot(data = green_umbs, aes(x = spp_half_cover_date,
  fill = state)) + geom_density(alpha = 0.5)
p3.2u + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

Species-level half cover date



```
# this will just show sampling date artifact
p4 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
  geom_density(alpha = 0.5)
p4 + facet_wrap(~year_factor)
```



```
# KD: not sure what this code below was for code below won't
# run: Or try with tidyverse format
# green_kbsp.t<-as_tibble(green_kbsp) green_kbsp.t %>%
# gather(state, plot_half_cover_date, year_factor) %>%
# ggplot(aes(plot_half_cover_date, fill = state)) +
# geom_histogram() + facet_wrap(~year_factor)

# looks like the 225 spike is from 2018 and 2020 - what's
# going on here is that you are treating all species-plot
# records as independent observations, so the influence of
# species differences is likely coming through here.
kbs_2018 <- subset(green_kbs, year == 4) # many records on 235
kbs_2020 <- subset(green_kbs, year == 6) # records from 227 & 228
```

Leverage plots and detecting Outliers. <https://www.statmethods.net/stats/riagnostics.html>

These illustrate whether certain data points have more leverage (more influence), and thus could be outliers. It's a way of detecting outliers. Leverage plots can help identify whether a point has high or low influence, based on its leverage and residual and determining model fit with and without the point in question. Ultimately you decide whether the points are outliers or not, based on the knowledge of the system and how much it changes the model when included vs. excluded from the data used to fit the model. Here is a good overview of the combination of leverage and residual: scroll down to sections beginning at "13.3 Unusual Observations": <https://davidalpiaz.github.io/appliedstats/model-diagnostics.html>

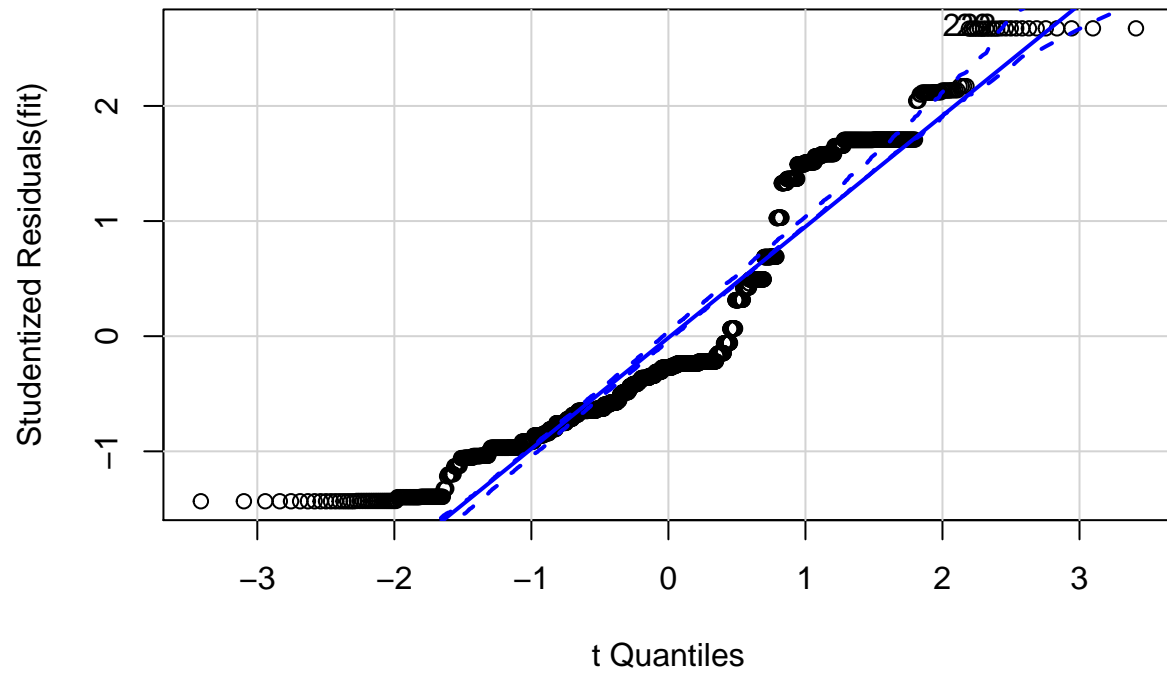
```
# checking fit for date as a function of state and species -  
# bringing in species here makes it obvious that that is  
# explaining some of the variation compared with the  
# state-only model you had previously.
```

```
# species-level data KBS State-only model  
fit <- lm(spp_half_cover_date ~ state, data = green_kbs)  
outlierTest(fit) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 29 2.673942          0.0075775          NA
```

```
qqPlot(fit, main = "QQ Plot")
```

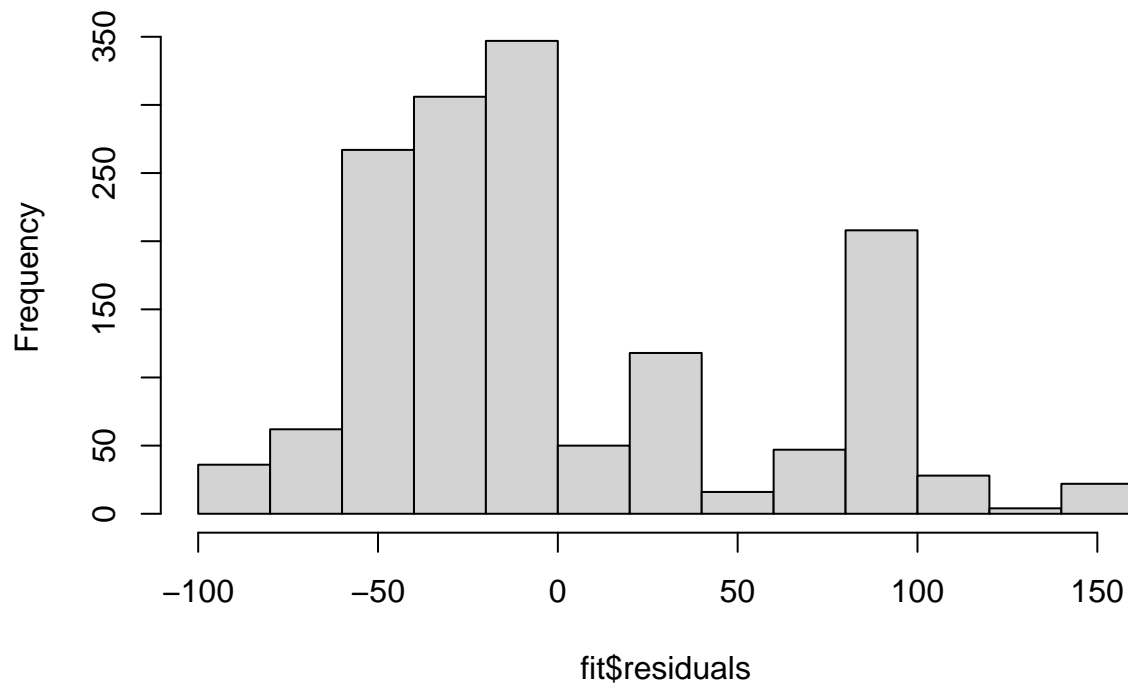
QQ Plot



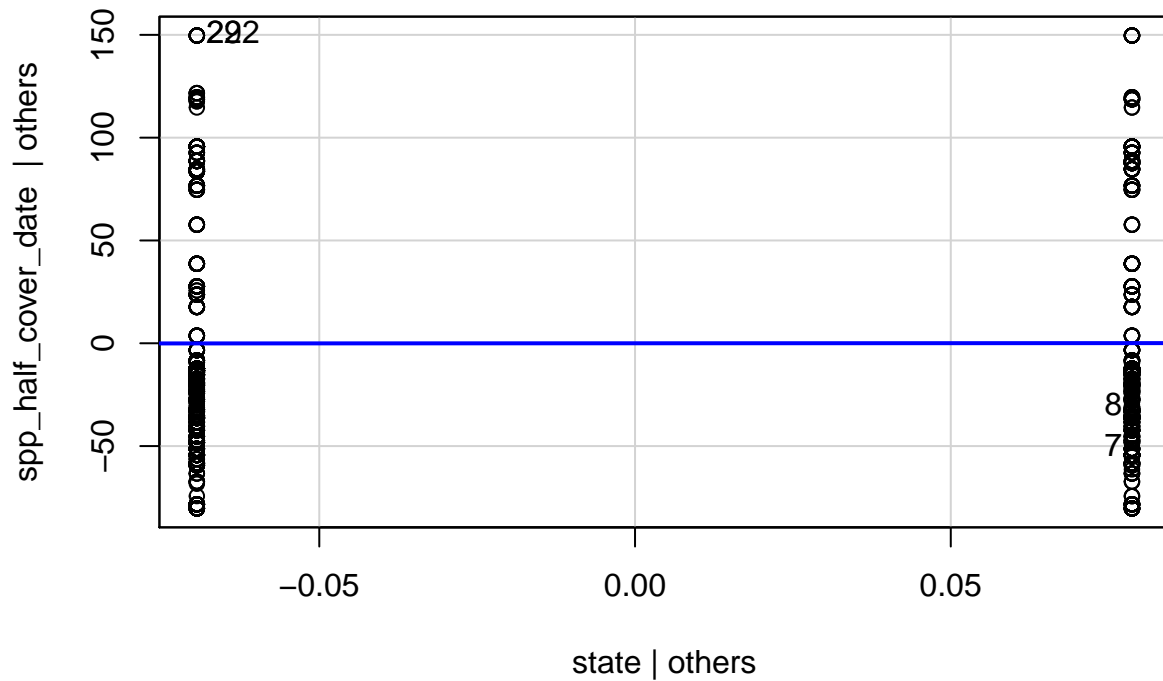
```
## 29 222  
## 29 195
```

```
hist(fit$residuals)
```

Histogram of fit\$residuals

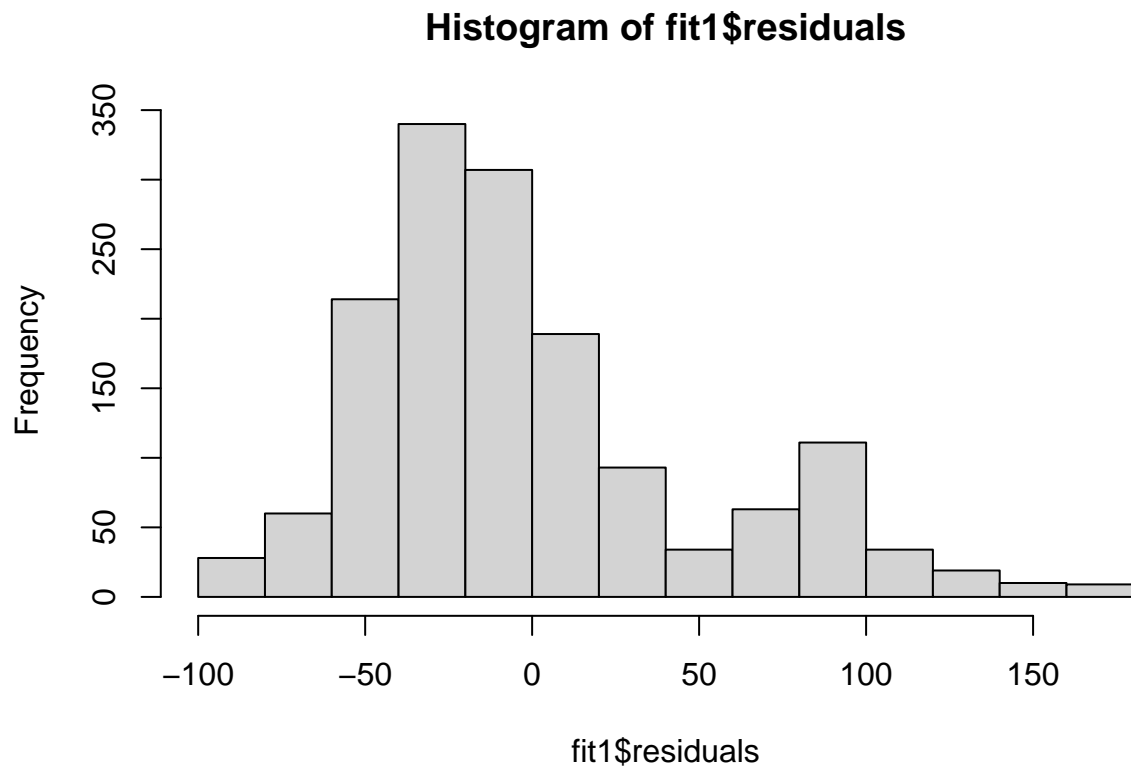


```
leveragePlots(fit)
```

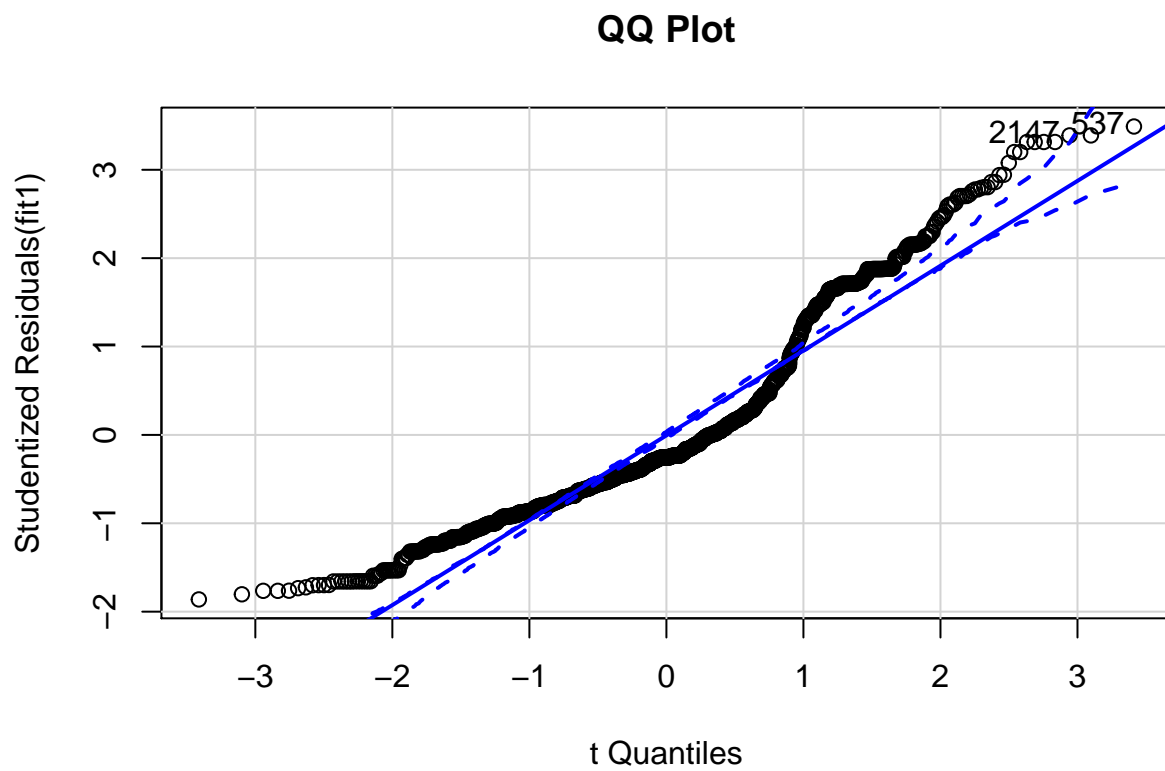


```
# KBS State and species model
fit1 <- lm(spp_half_cover_date ~ state + species, data = green_kbs)
outlierTest(fit1) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 537 3.489515      0.00049802      0.75251
hist(fit1$residuals)
```



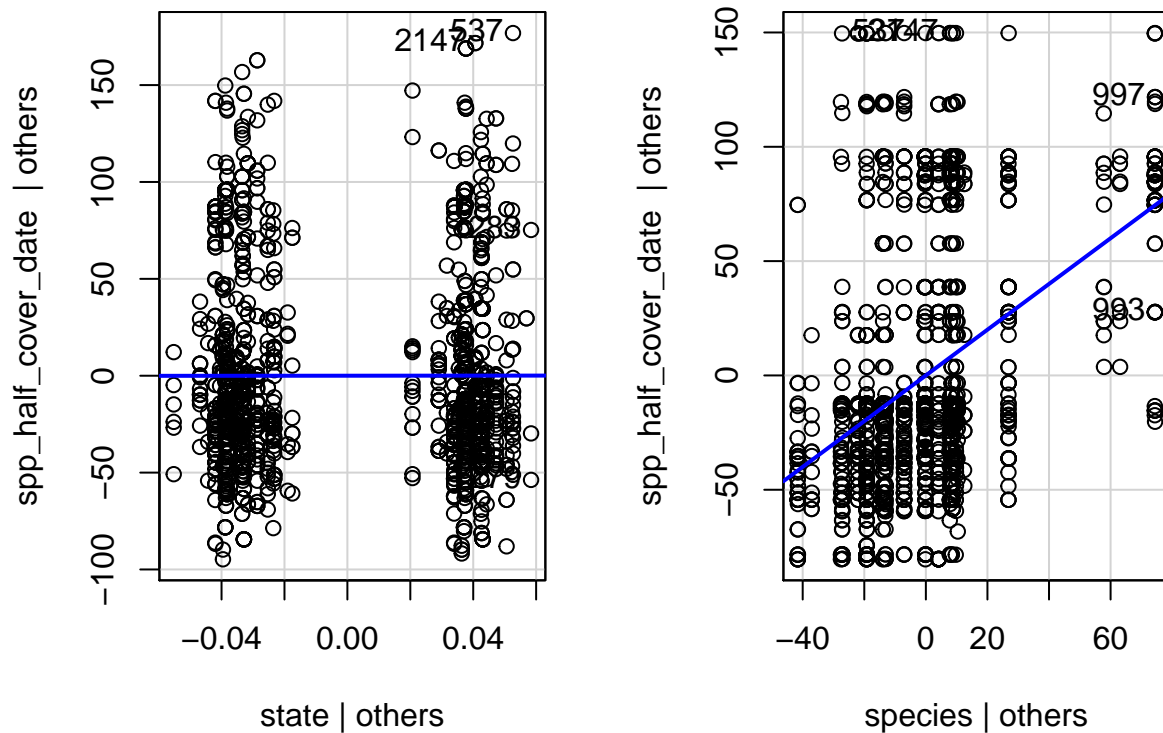
```
qqPlot(fit1, main = "QQ Plot")
```



```
## 537 2147
## 345 1387
```

```
leveragePlots(fit1)
```

Leverage Plots



```
ols_test_normality(fit1) # p < 0.05 for all, so data is normal (I think? Is this function useful?)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk          0.9143       0.0000
## Kolmogorov-Smirnov     0.1372       0.0000
## Cramer-von Mises      149.3847       0.0000
## Anderson-Darling       48.7735       0.0000
## -----
```

```
# UMBS State and species model
```

```
fitlumbs <- lm(spp_half_cover_date ~ state + species, data = green_umbs)
```

```
outlierTest(fitlumbs) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
```

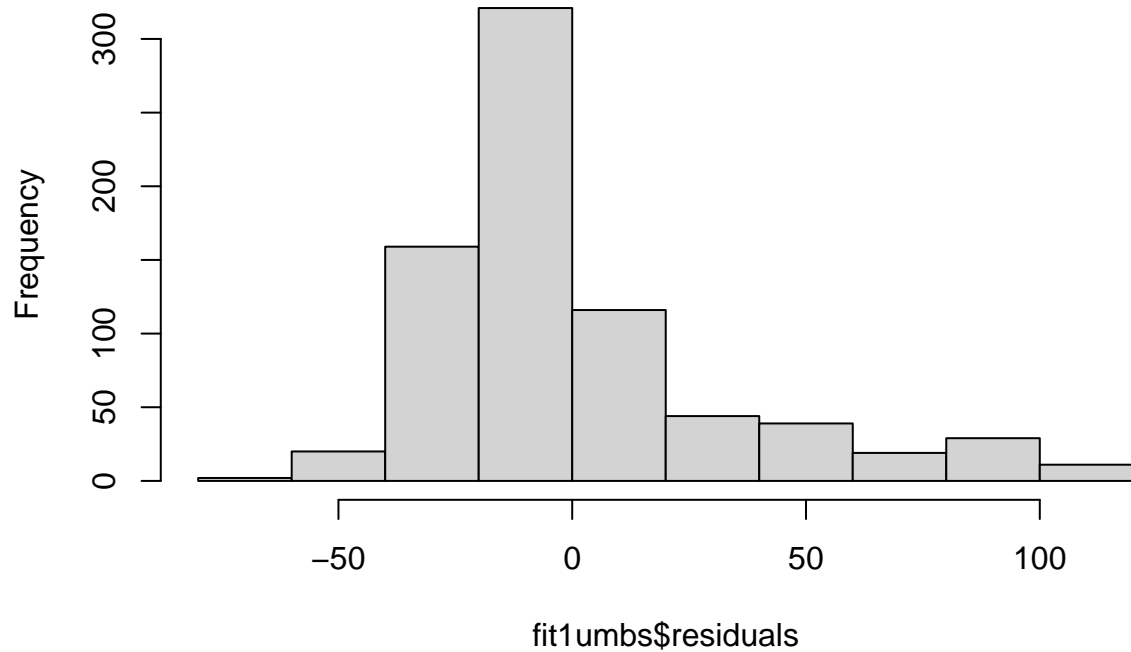
```
## Largest |rstudent|:
```

```
##      rstudent unadjusted p-value Bonferroni p
```

```
## 1906 3.595987      0.00034457      0.26187
```

```
hist(fitlumbs$residuals)
```

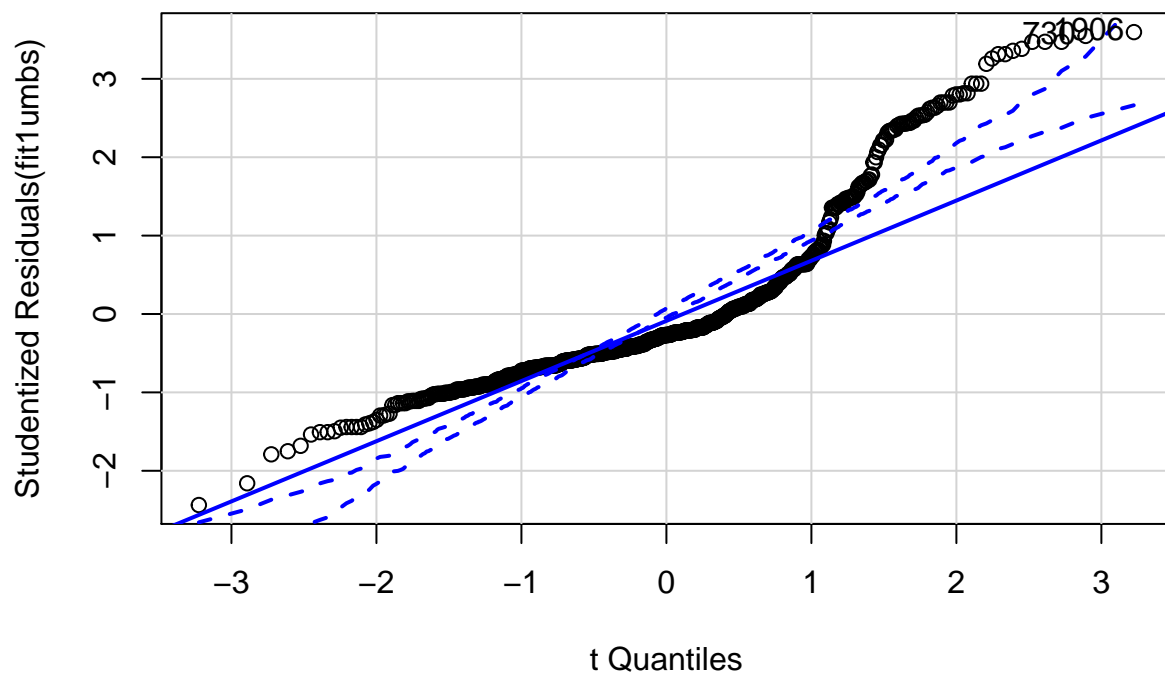

Histogram of fit1umbs\$residuals



```
qqPlot(fit1umbs, main = "QQ Plot")
```

```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :  
## 'rlm' failed to converge in 20 steps
```

QQ Plot

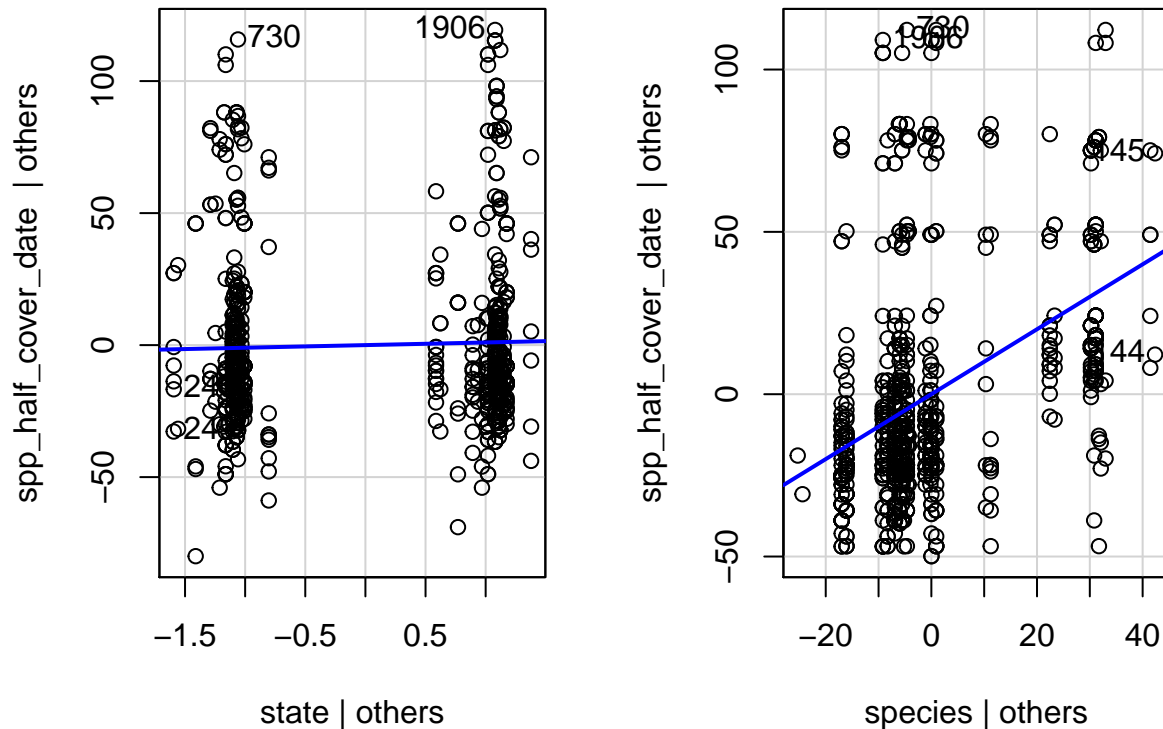


```
## 730 1906
```

```
## 269 668
```

```
leveragePlots(fit1umbs)
```

Leverage Plots



```
ols_test_normality(fit1umbs) # p < 0.05 for all, so data is normal (I think)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

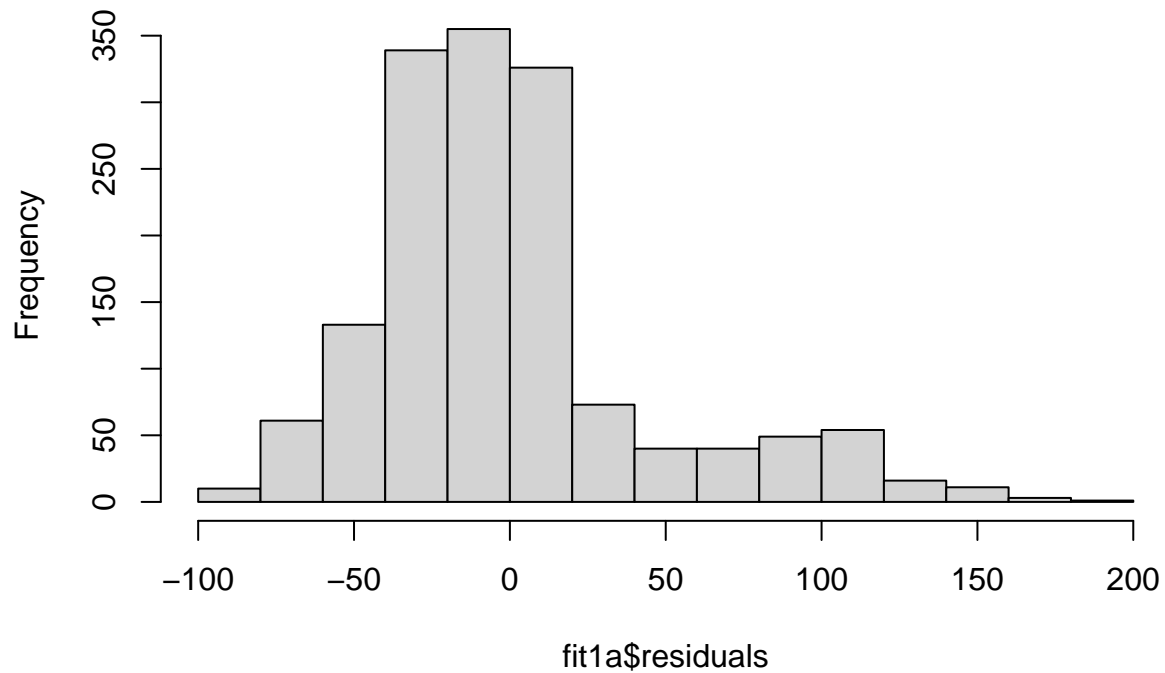
```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk         0.8532       0.0000
## Kolmogorov-Smirnov    0.172       0.0000
## Cramer-von Mises     83.0293       0.0000
## Anderson-Darling     39.6106       0.0000
## -----
```

```
fit1a <- lm(min_green_date ~ state + species, data = green_kbs)
outlierTest(fit1a) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 537 4.148749      3.5322e-05      0.053372
```

```
hist(fit1a$residuals)
```

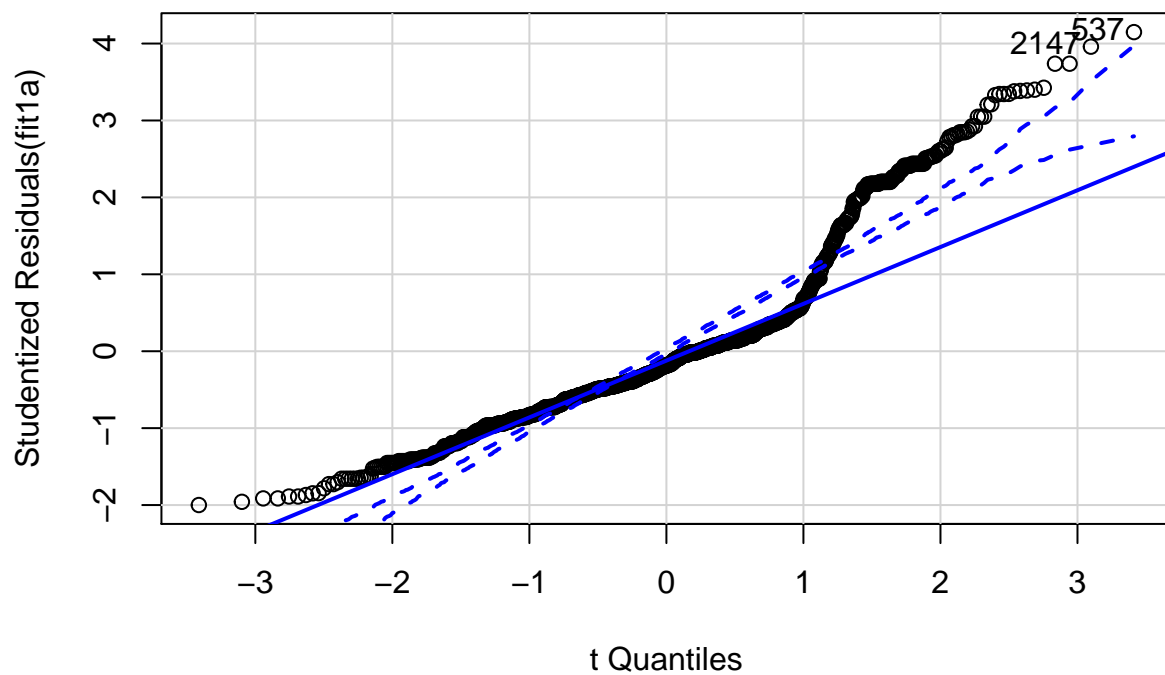
Histogram of fit1a\$residuals



```
qqPlot(fit1a, main = "QQ Plot")
```

```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :  
## 'rlm' failed to converge in 20 steps
```

QQ Plot

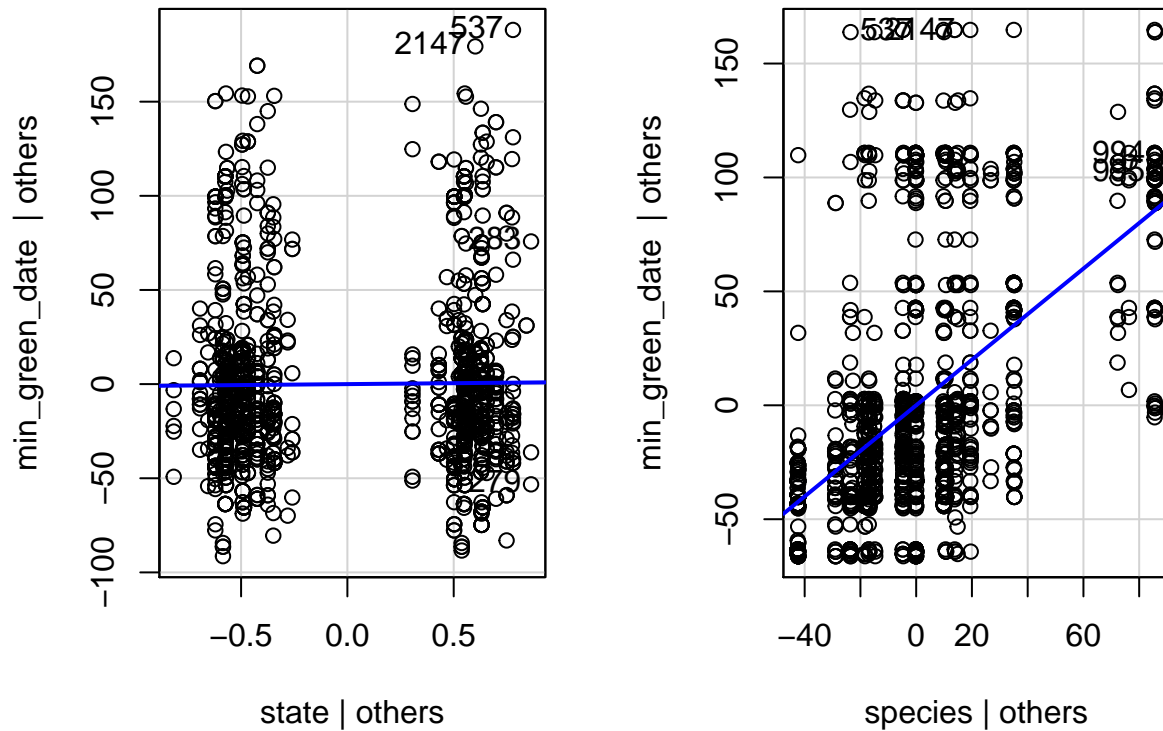


```
## 537 2147
```

```
## 345 1387
```

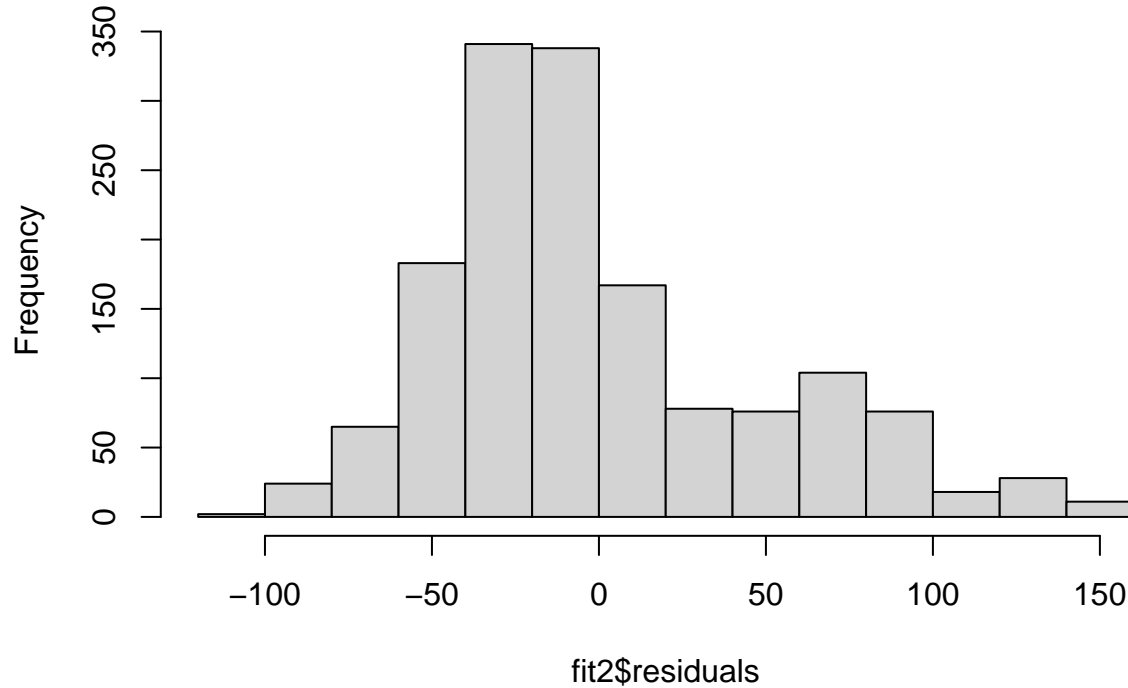
```
leveragePlots(fit1a)
```

Leverage Plots



```
# checking fit for date as a function of state and year
fit2 <- lm(spp_half_cover_date ~ state + species + year_factor,
  data = green_kbs)
hist(fit2$residuals)
```

Histogram of fit2\$residuals

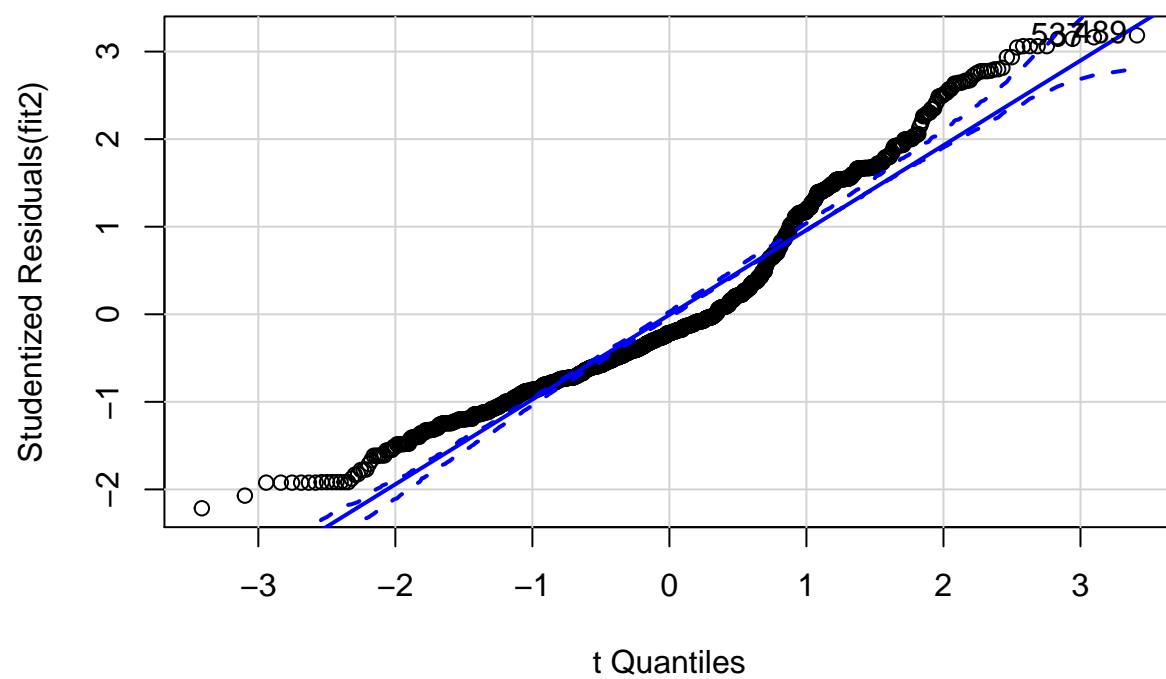


```
outlierTest(fit2) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 489 3.185508      0.0014751      NA
```

```
qqPlot(fit2, main = "QQ Plot")
```

QQ Plot

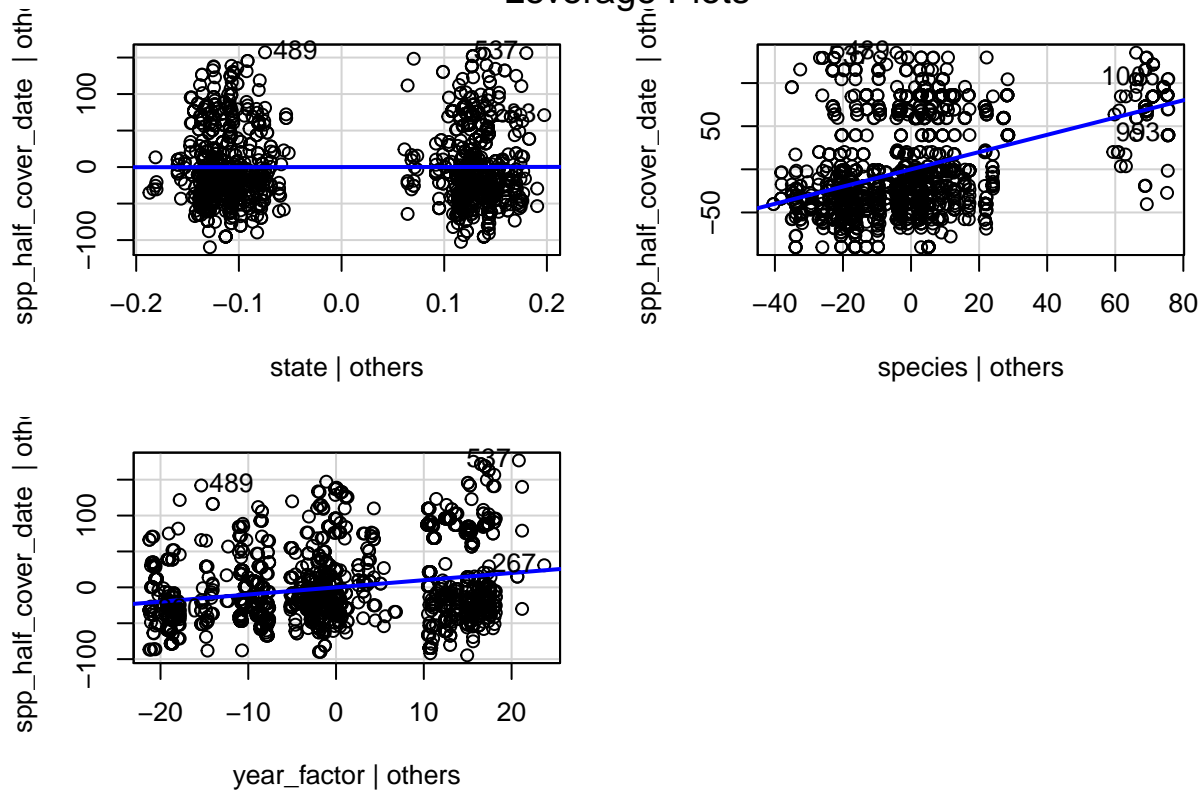


```
## 489 537
```

```
## 327 345
```

```
leveragePlots(fit2)
```

Leverage Plots



```
ols_test_normality(fit2) # p < 0.05 for all, so data is normal (I think)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk        0.9385        0.0000
## Kolmogorov-Smirnov   0.1351        0.0000
## Cramer-von Mises     151.8066      0.0000
## Anderson-Darling     35.3964      0.0000
## -----
```

```
# plot level data KBS State-only model
```

```
fitp <- lm(plot_half_cover_date ~ state, data = green_kbsp)
```

```
outlierTest(fitp) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
```

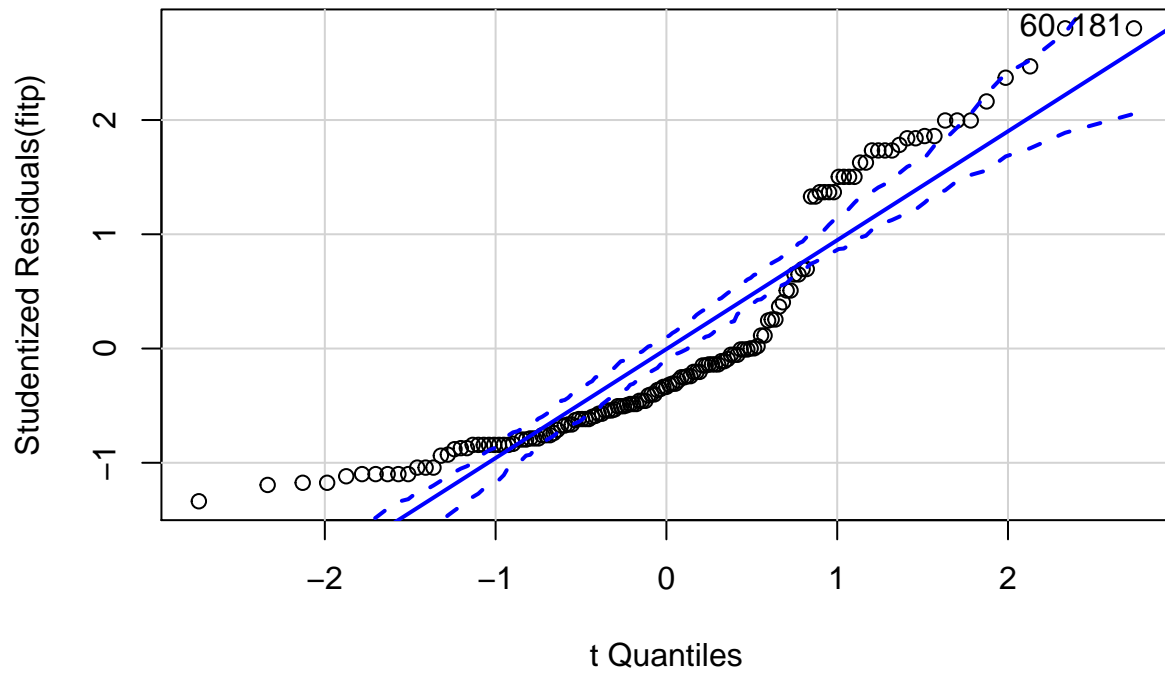
```
## Largest |rstudent|:
```

```
##      rstudent unadjusted p-value Bonferroni p
```

```
## 60 2.802256      0.0057943      0.82858
```

```
qqPlot(fitp, main = "QQ Plot")
```

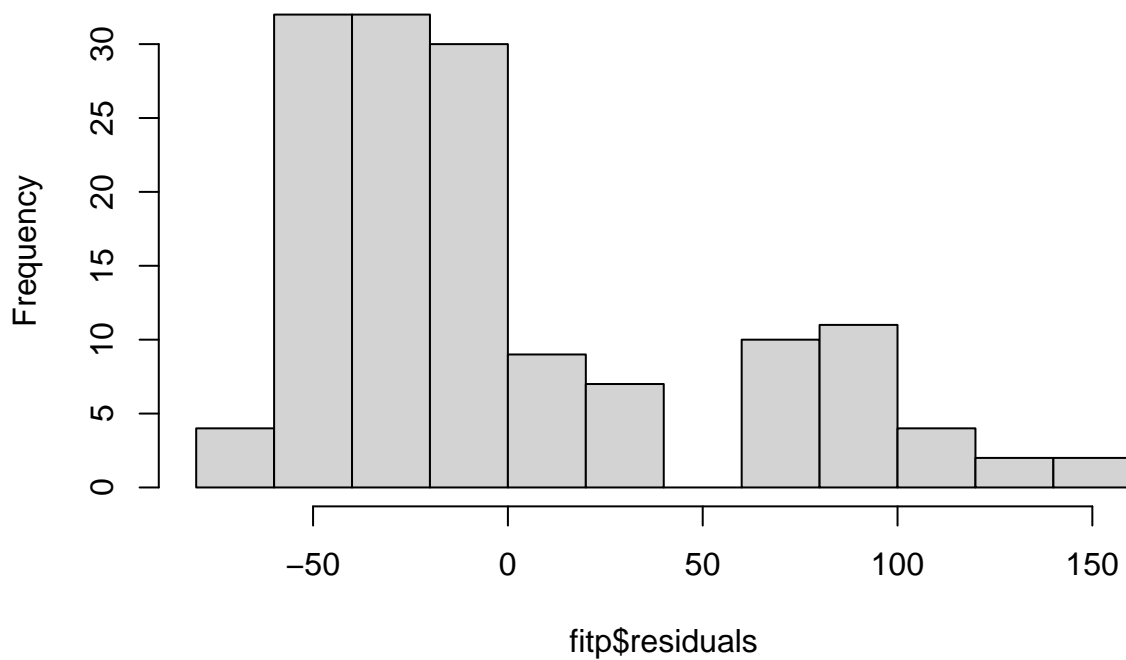
QQ Plot



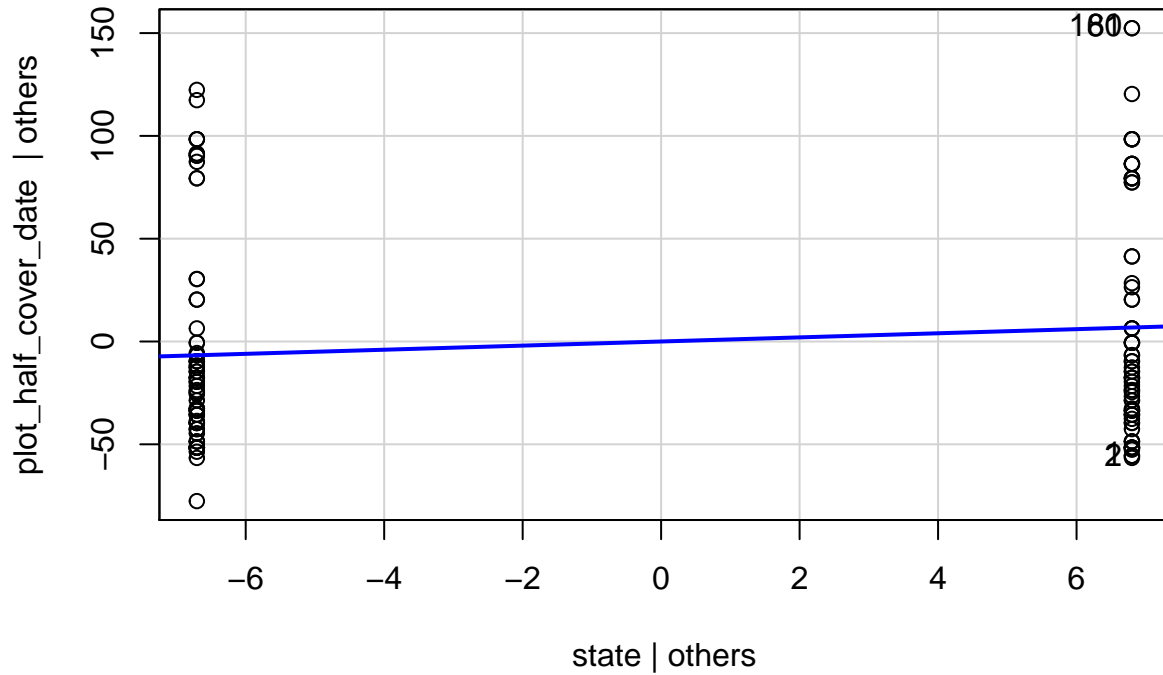
```
## 60 181  
## 35 101
```

```
hist(fitp$residuals)
```

Histogram of fitp\$residuals




```
leveragePlots(fitp)
```



```
ols_test_normality(fitp)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk         0.8578        0.0000
## Kolmogorov-Smirnov    0.1987        0.0000
## Cramer-von Mises     17.3799        0.0000
## Anderson-Darling      8.0711        0.0000
## -----
```

```
# UMBS State-only model
```

```
fitpu <- lm(plot_half_cover_date ~ state, data = green_umbsp)
outlierTest(fitpu) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
```

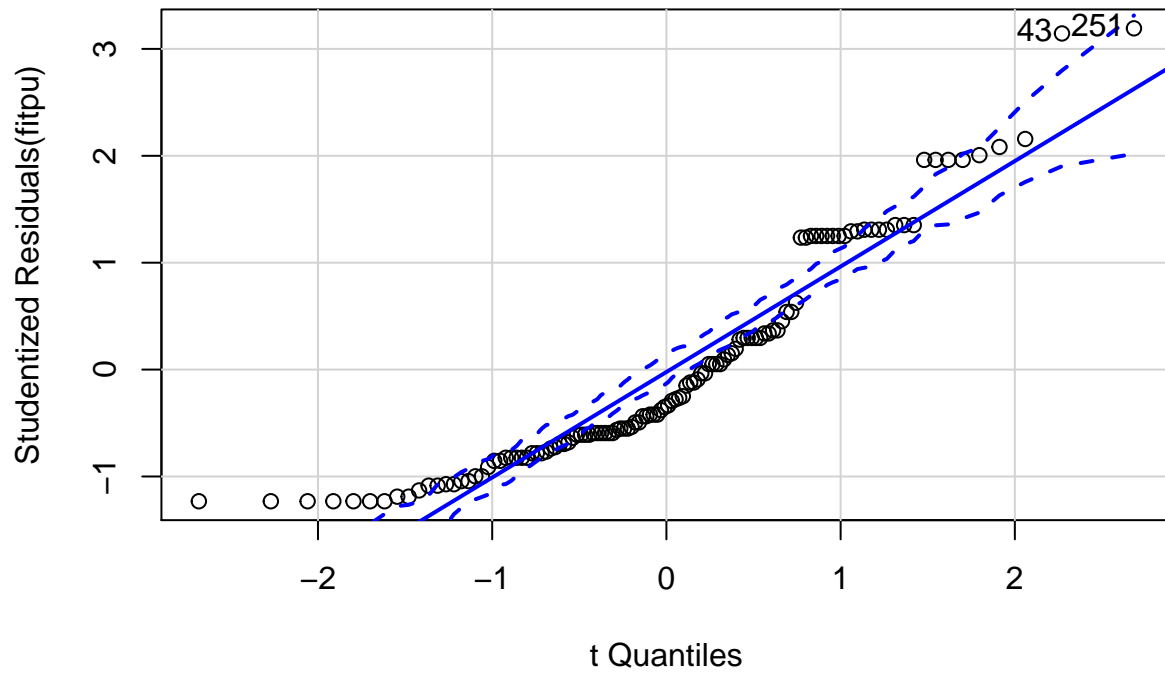
```
## Largest |rstudent|:
```

```
##      rstudent unadjusted p-value Bonferroni p
```

```
## 251 3.192341      0.0018128      0.21754
```

```
qqPlot(fitpu, main = "QQ Plot")
```

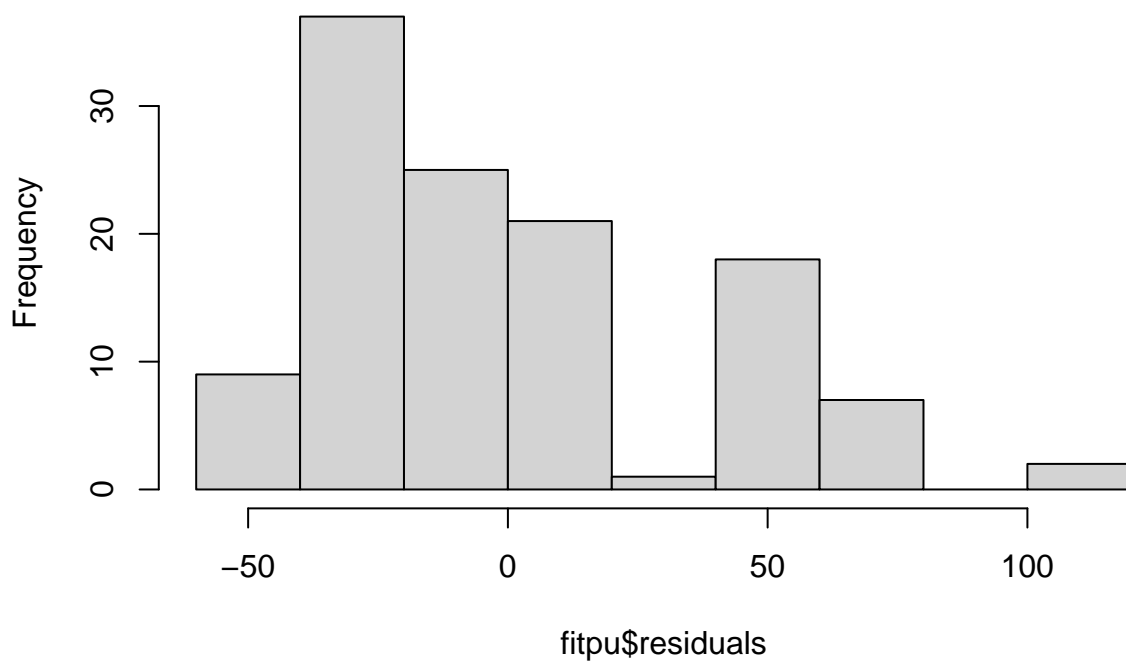
QQ Plot



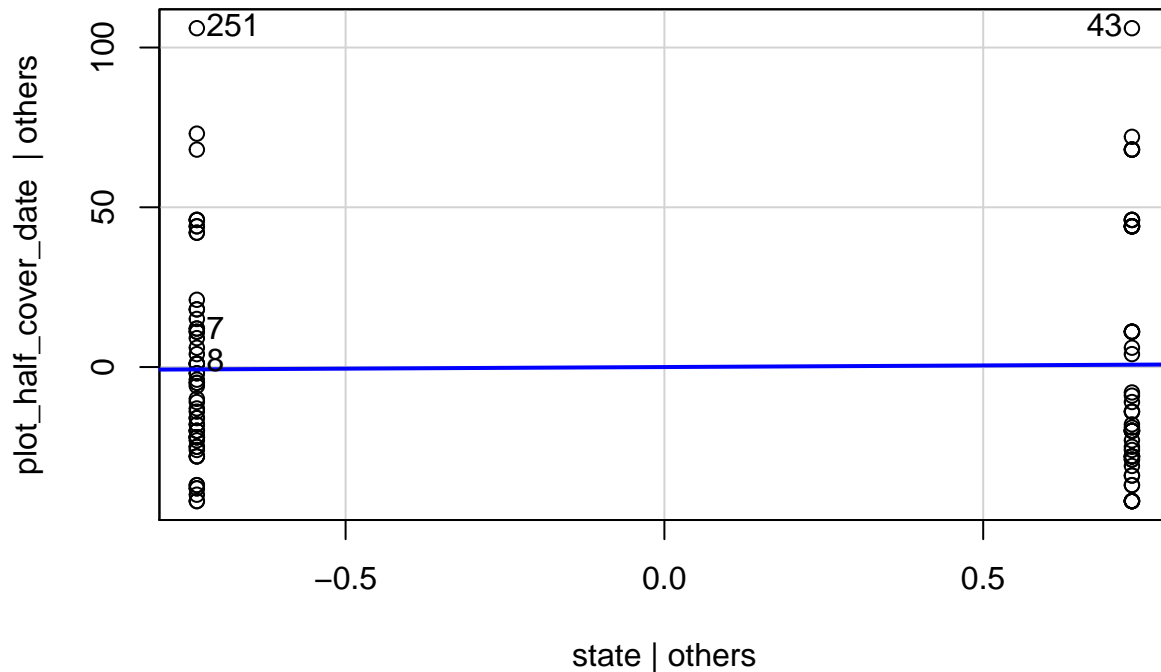
```
## 43 251  
## 19 114
```

```
hist(fitpu$residuals)
```

Histogram of fitpu\$residuals



```
leveragePlots(fitpu)
```



```
ols_test_normality(fitpu)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk         0.9001       0.0000
## Kolmogorov-Smirnov    0.1465       0.0116
## Cramer-von Mises     11.0083       0.0000
## Anderson-Darling      4.0679       0.0000
## -----
```

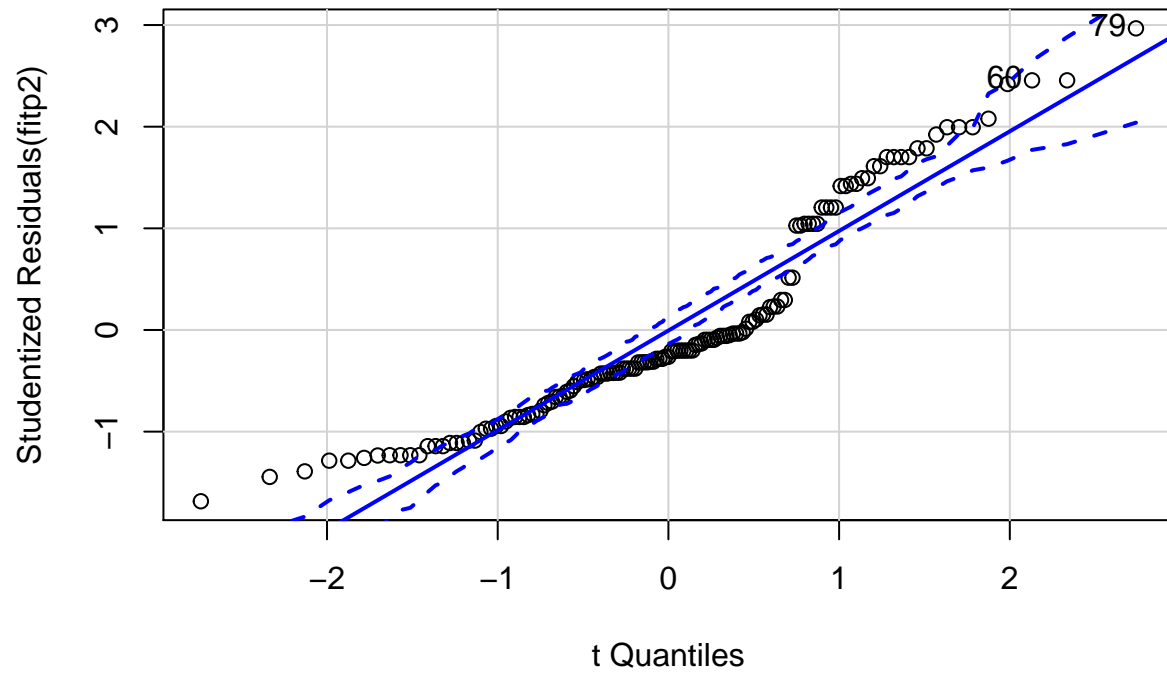
```
# KBS State and year model
```

```
fitp2 <- lm(plot_half_cover_date ~ state + year_factor, data = green_kbsp)
outlierTest(fitp2) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 79 2.967344      0.0035544      0.50827
```

```
qqPlot(fitp2, main = "QQ Plot")
```

QQ Plot

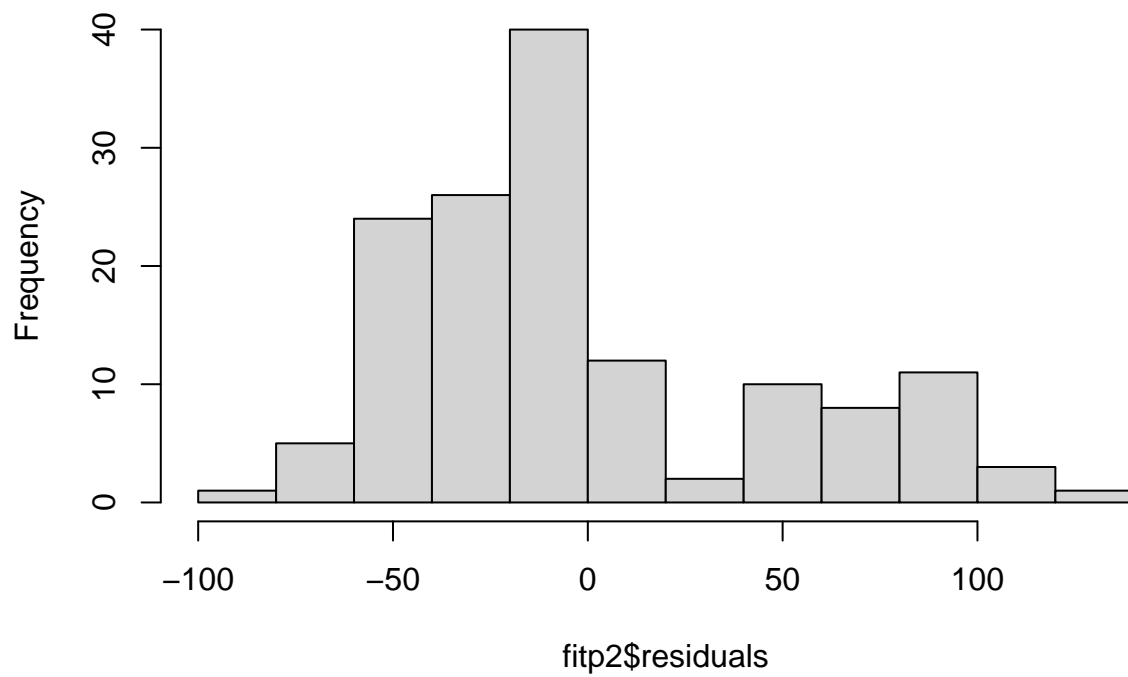


```
## 60 79
```

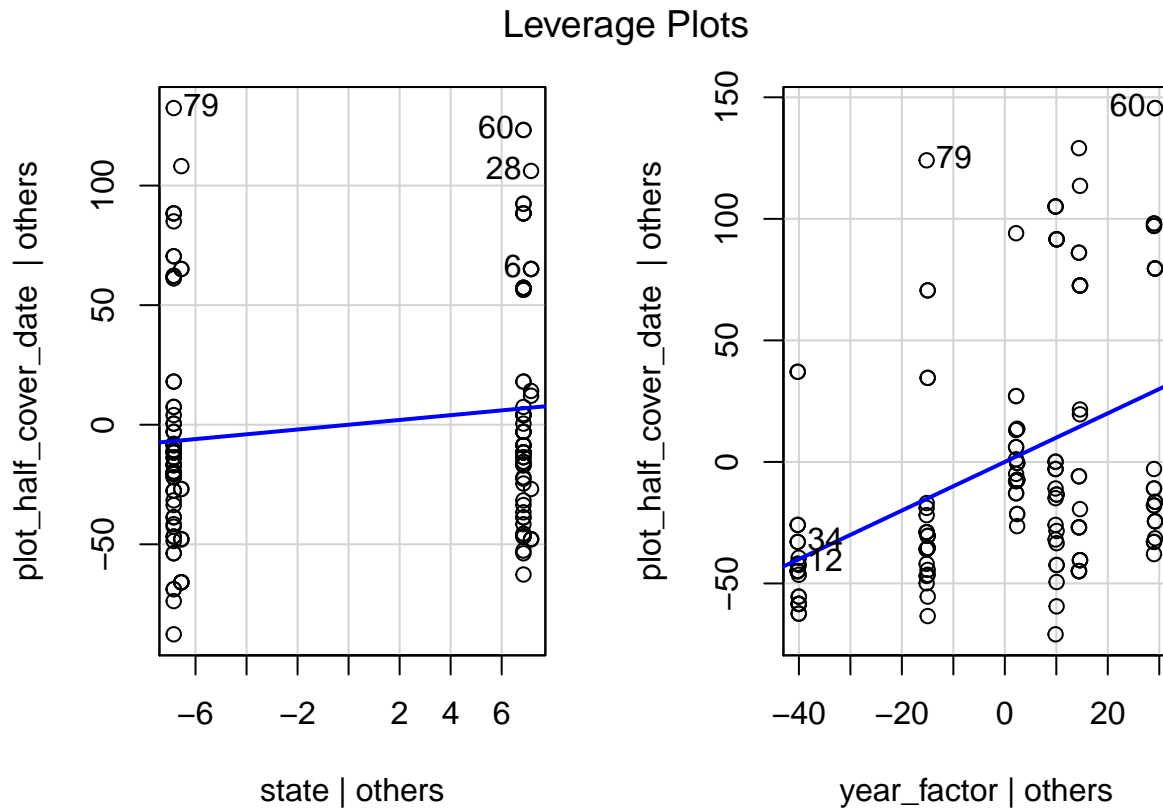
```
## 35 44
```

```
hist(fitp2$residuals)
```

Histogram of fitp2\$residuals



```
leveragePlots(fitp2)
```



```
ols_test_normality(fitp2)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk           0.91         0.0000
## Kolmogorov-Smirnov      0.1804        2e-04
## Cramer-von Mises       16.0135        0.0000
## Anderson-Darling        5.0934        0.0000
## -----
```

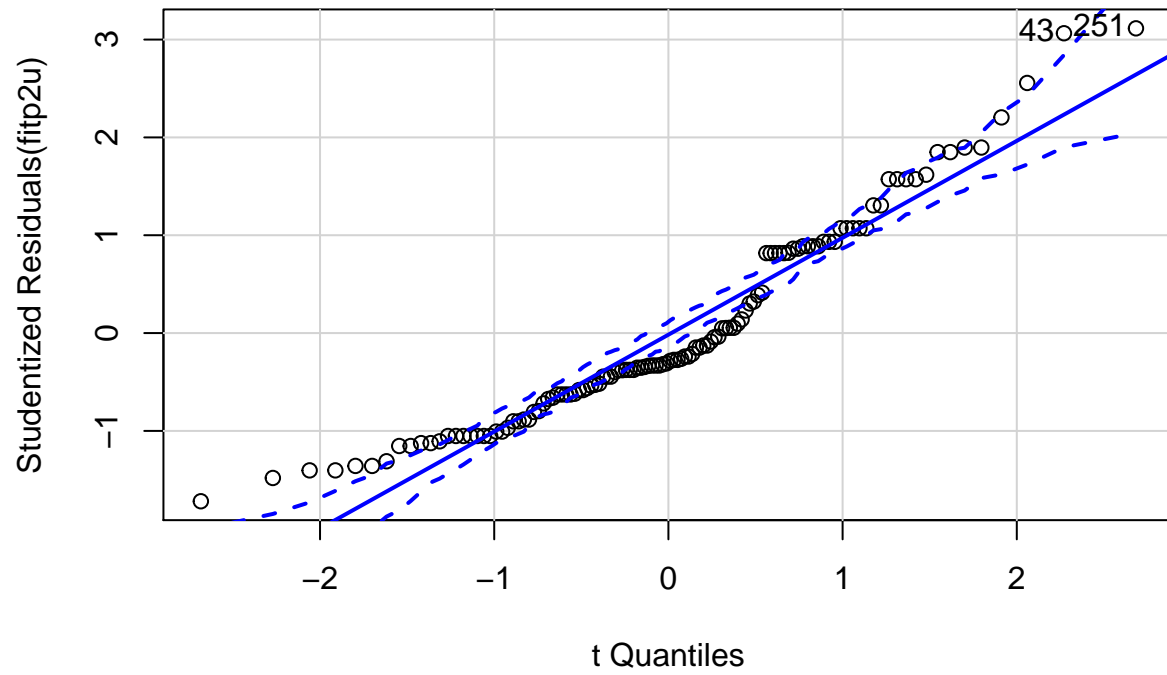
```
# UMBS State and year model
```

```
fitp2u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
outlierTest(fitp2u)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 251  3.11464      0.0023207      0.27849
```

```
qqPlot(fitp2u, main = "QQ Plot")
```

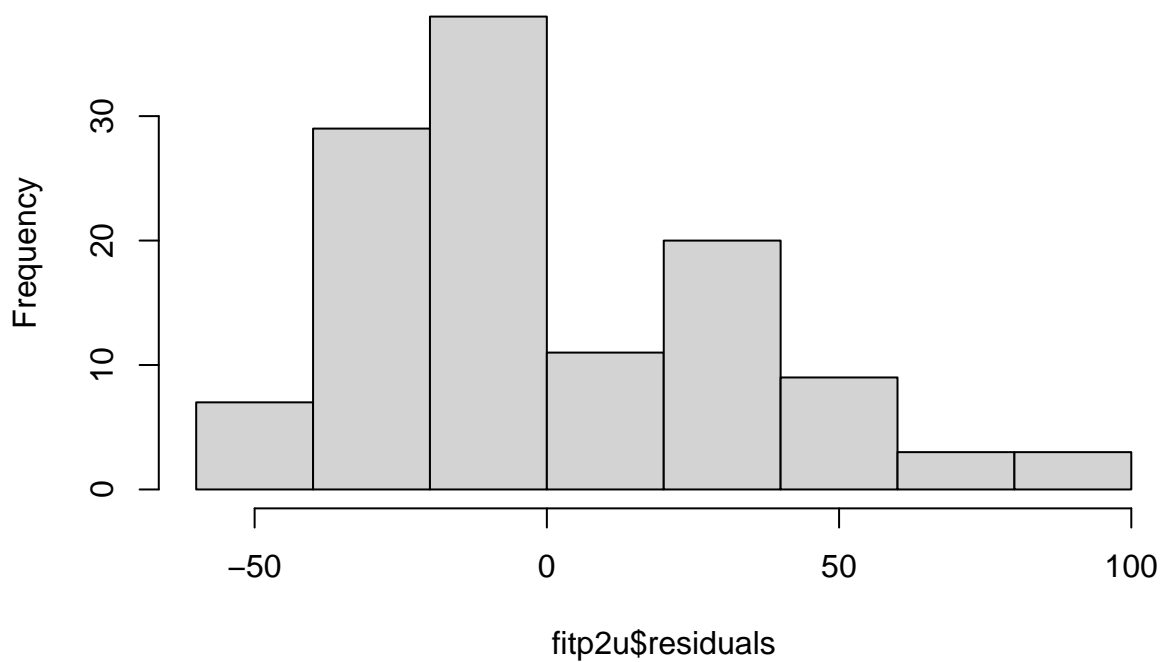
QQ Plot



```
## 43 251  
## 19 114
```

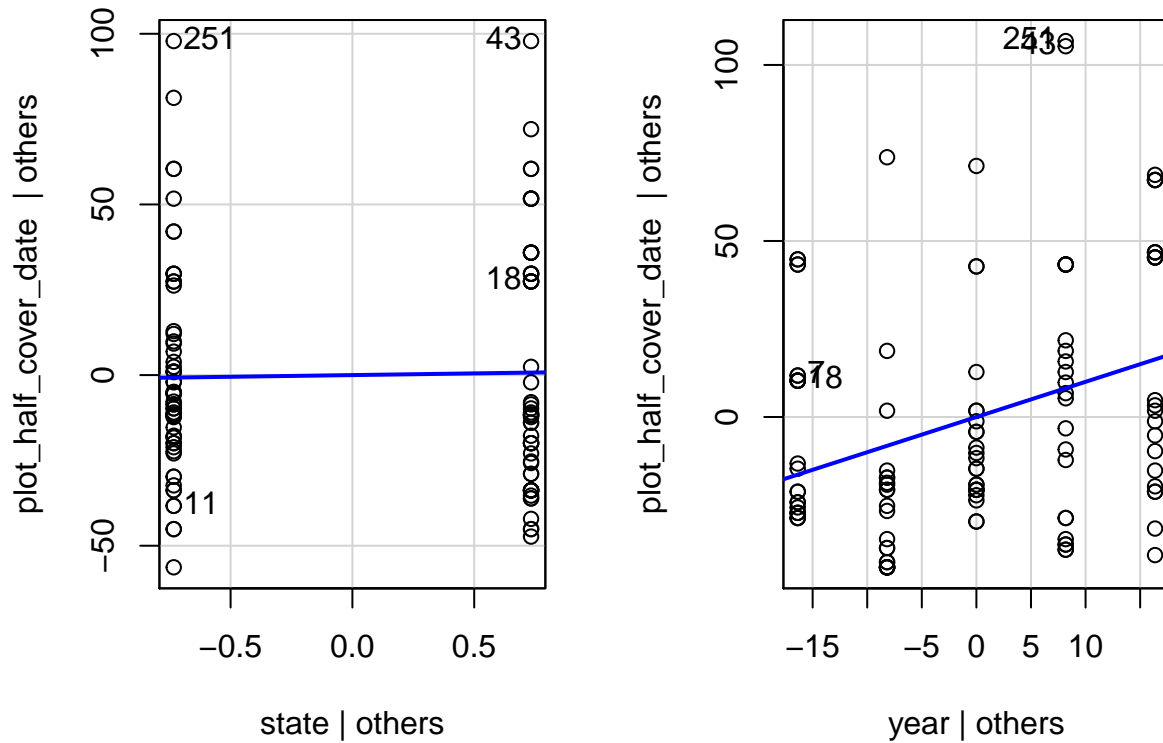
```
hist(fitp2u$residuals)
```

Histogram of fitp2u\$residuals



```
leveragePlots(fitp2u)
```

Leverage Plots



```
ols_test_normality(fitp2u)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

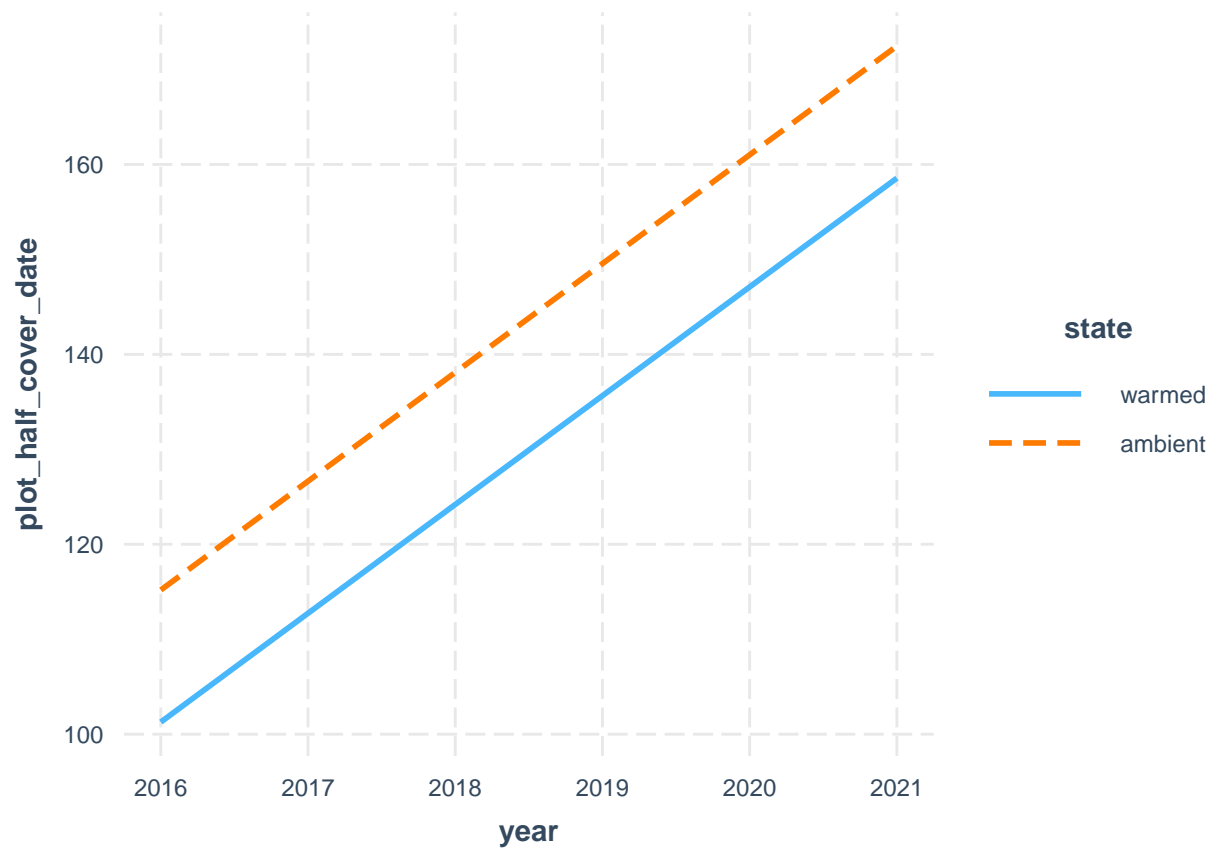
```
## -----
##      Test           Statistic      pvalue
## -----
## Shapiro-Wilk        0.9357        0.0000
## Kolmogorov-Smirnov   0.1443        0.0135
## Cramer-von Mises     11.6333        0.0000
## Anderson-Darling     2.6746        0.0000
## -----
```

Normal distribution after accounting for species and/or year for each site and model. Set up some linear mixed effects models to evaluate. From Ben Bolker: “The traditional view of random effects is as a way to do correct statistical tests when some observations are correlated. ... Random effects are especially useful when we have (1) lots of levels (e.g., many species or blocks), (2) relatively little data on each level (although we need multiple samples from most of the levels), and (3) uneven sampling across levels. People sometimes say that random effects are “factors that you aren’t interested in.” This is not always true. While it is often the case in ecological experiments (where variation among sites is usually just a nuisance), it is sometimes of great interest.” In our case, variation among plots is a nuisance, and not something we’re interested in. For some questions, variation among species is also a nuisance for us. It’s possible that variation among years is a nuisance if we only care about warm vs. ambient, but I think time is an interesting variable to consider with this study.

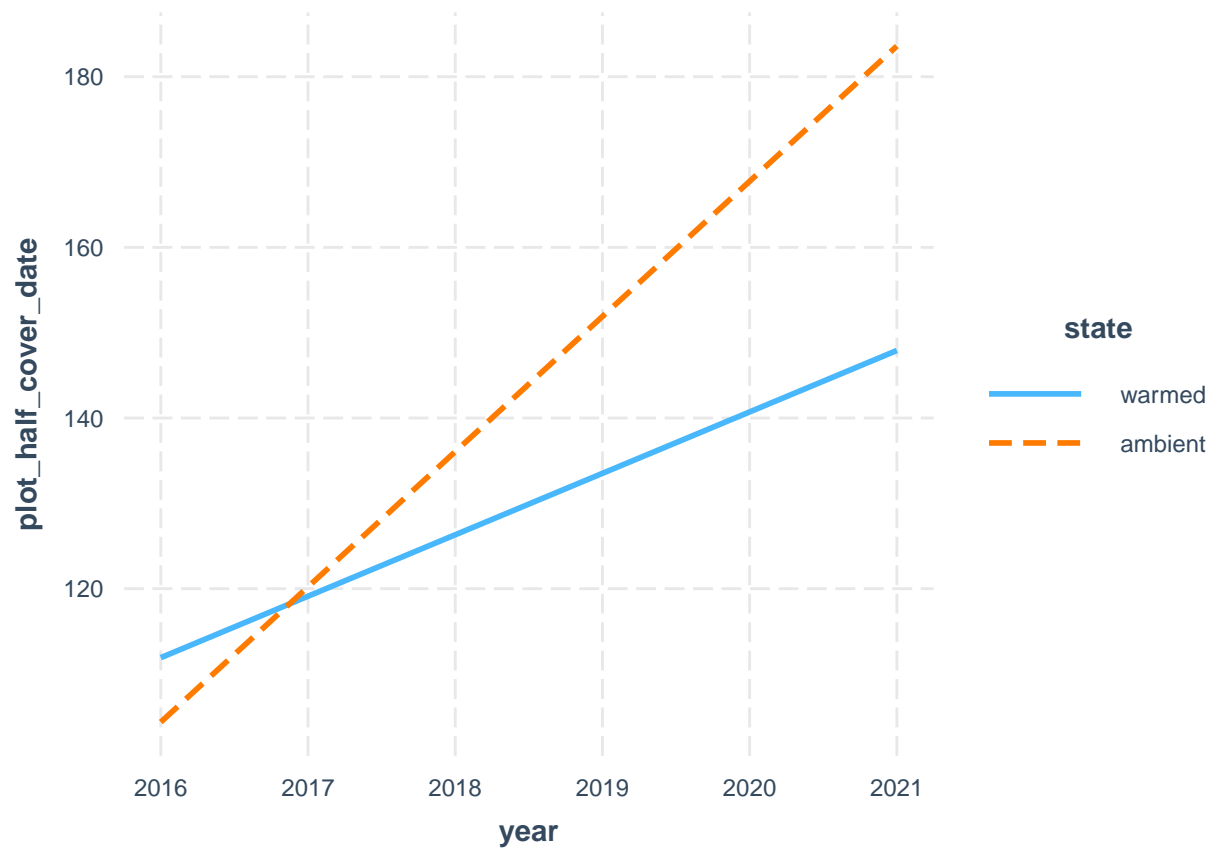
We should also think about how we’re treating year. Some of the models have a state * year interaction as a fixed effect, which means that the warming or ambient treatment could affect the half_cover_date differently over time (there would be a different slope for each state in the relationship between half_cover_date (y) and year (x)). If we just had state + year, the states would have the same slope, indicating that they have no interaction in their effect on half_cover_date (but they could still have different intercepts).

```
# Interaction plot (ignore for now the repeated measures with  
# species); see:  
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html  
# and: https://interactions.jacob-long.com/  
  
# KBS  
fit3 <- lm(plot_half_cover_date ~ state + year, data = green_kbsp)  
interact_plot(fit3, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the  
## model.
```

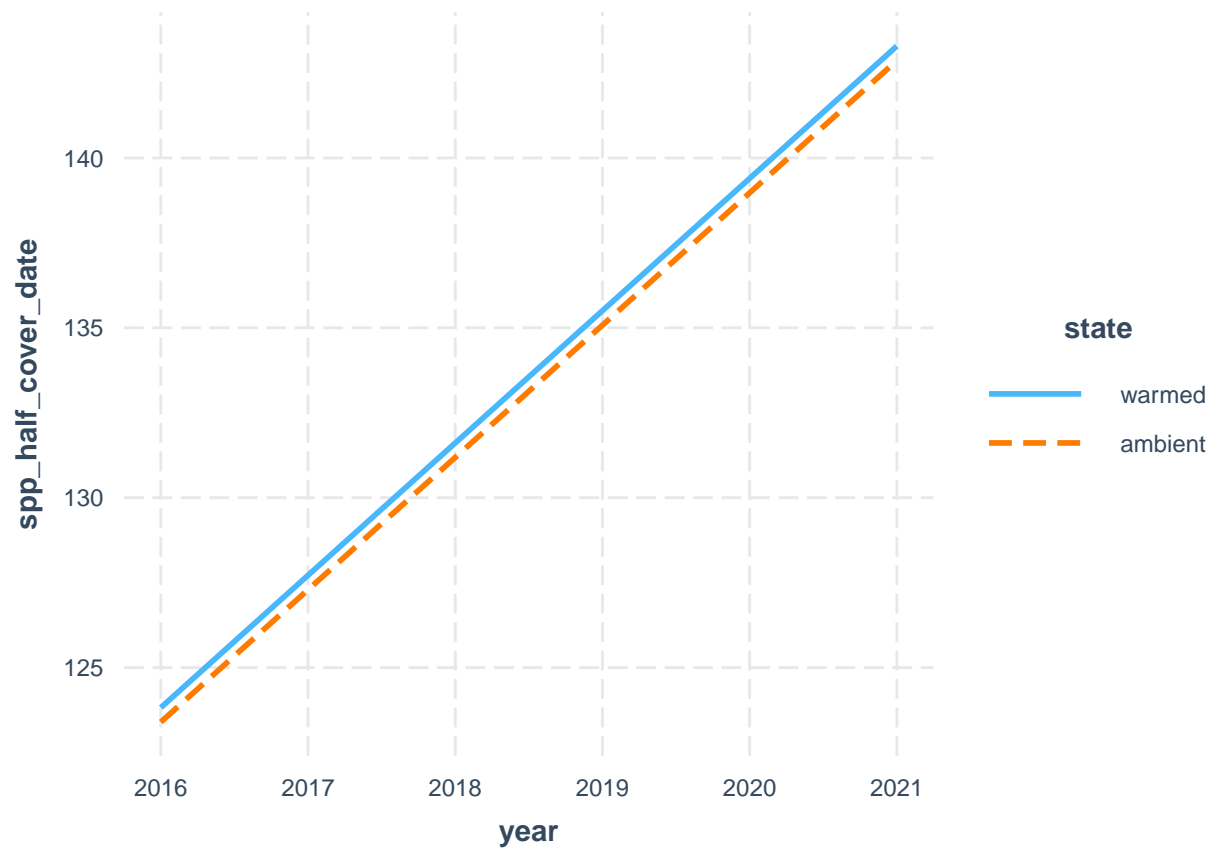



```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```



```
fit5 <- lm(spp_half_cover_date ~ state + year + species, data = green_kbs)
interact_plot(fit5, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the
## model.
```



```
fit6 <- lm(spp_half_cover_date ~ state * year + species, data = green_kbs)
interact_plot(fit6, pred = year, modx = state, mod2 = species)
```

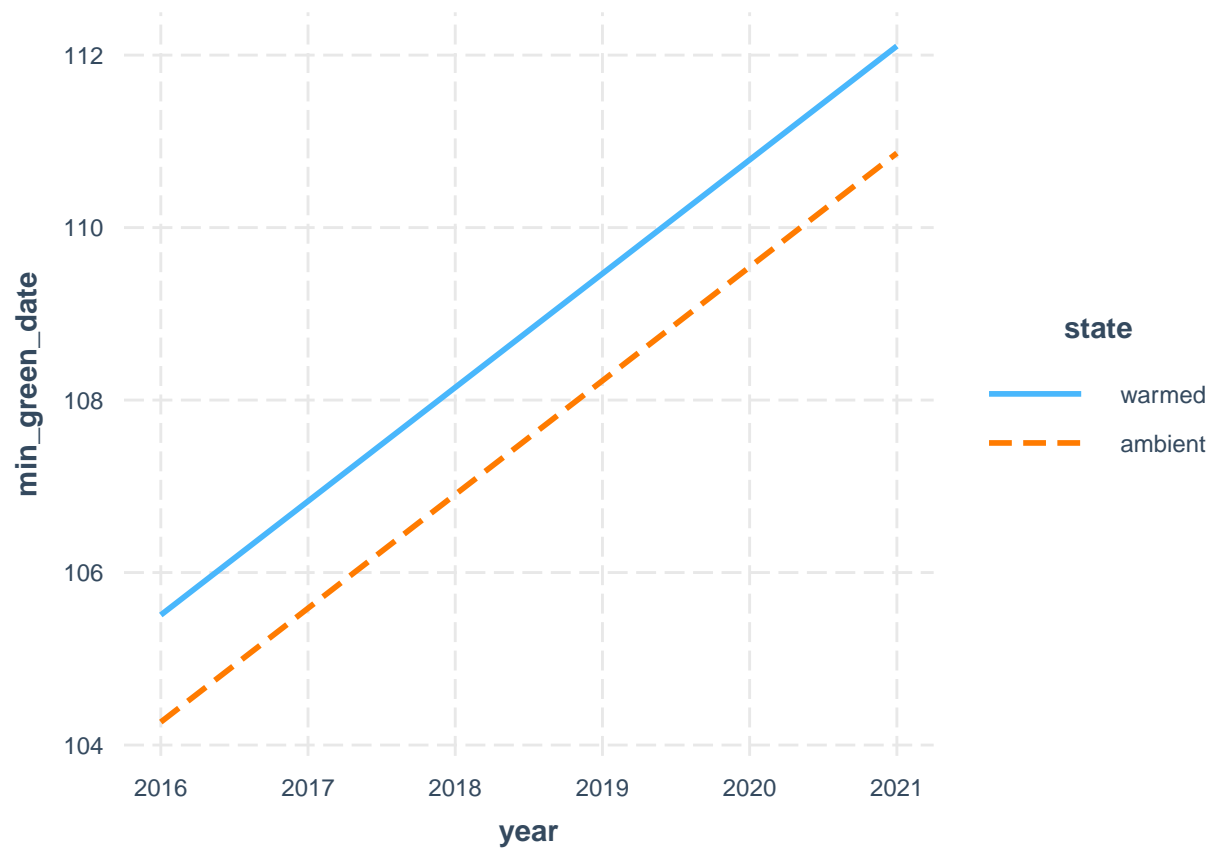
```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```



state — — — warmed ——— ambient

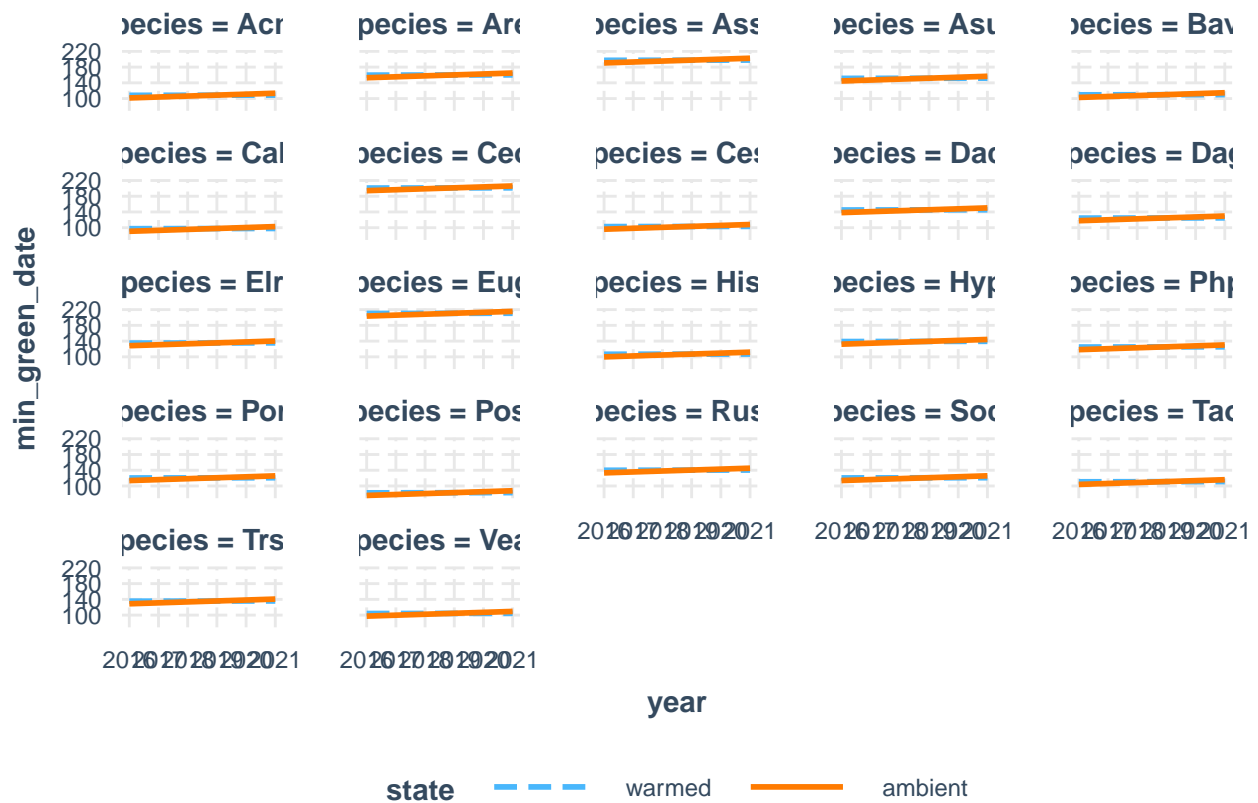
```
fit7 <- lm(min_green_date ~ state + year + species, data = green_kbs)
interact_plot(fit7, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the
## model.
```



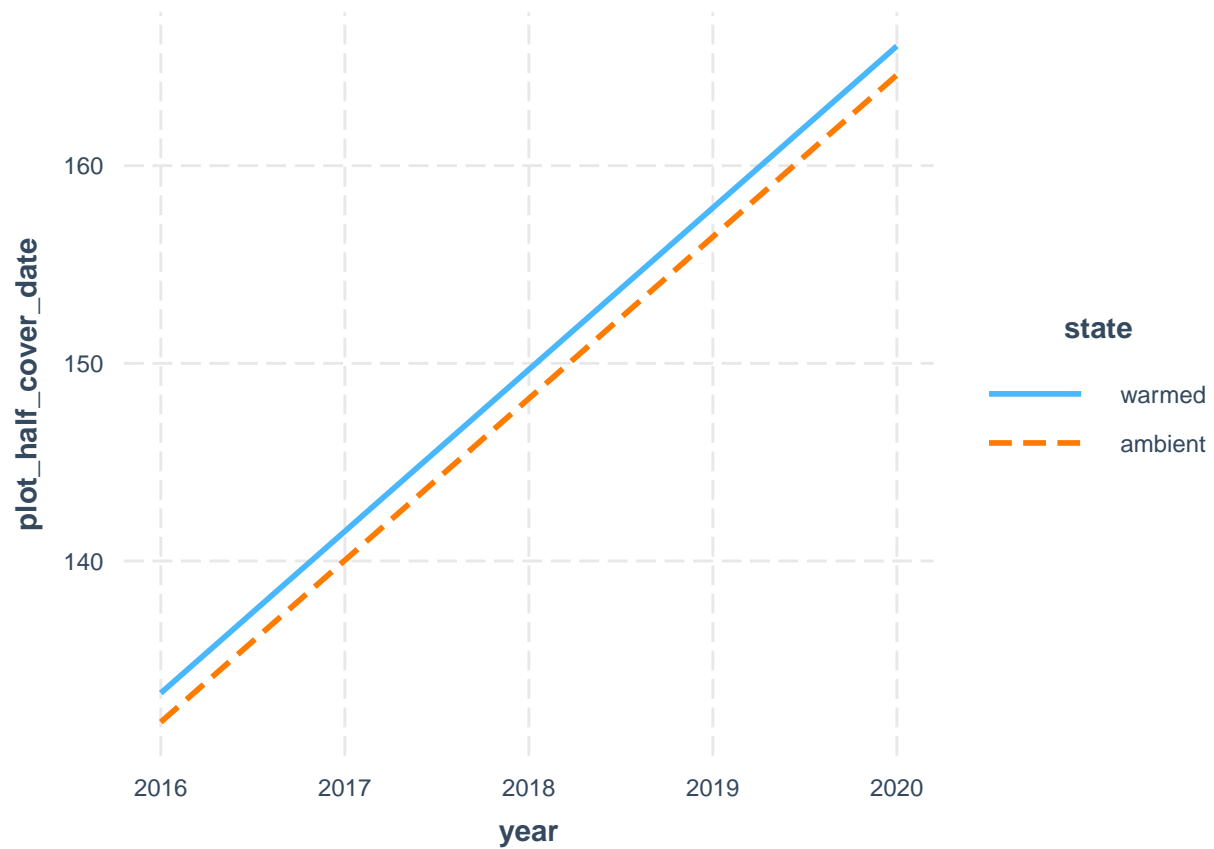
```
fit8 <- lm(min_green_date ~ state * year + species, data = green_kbs)
interact_plot(fit8, pred = year, modx = state, mod2 = species)
```

```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```

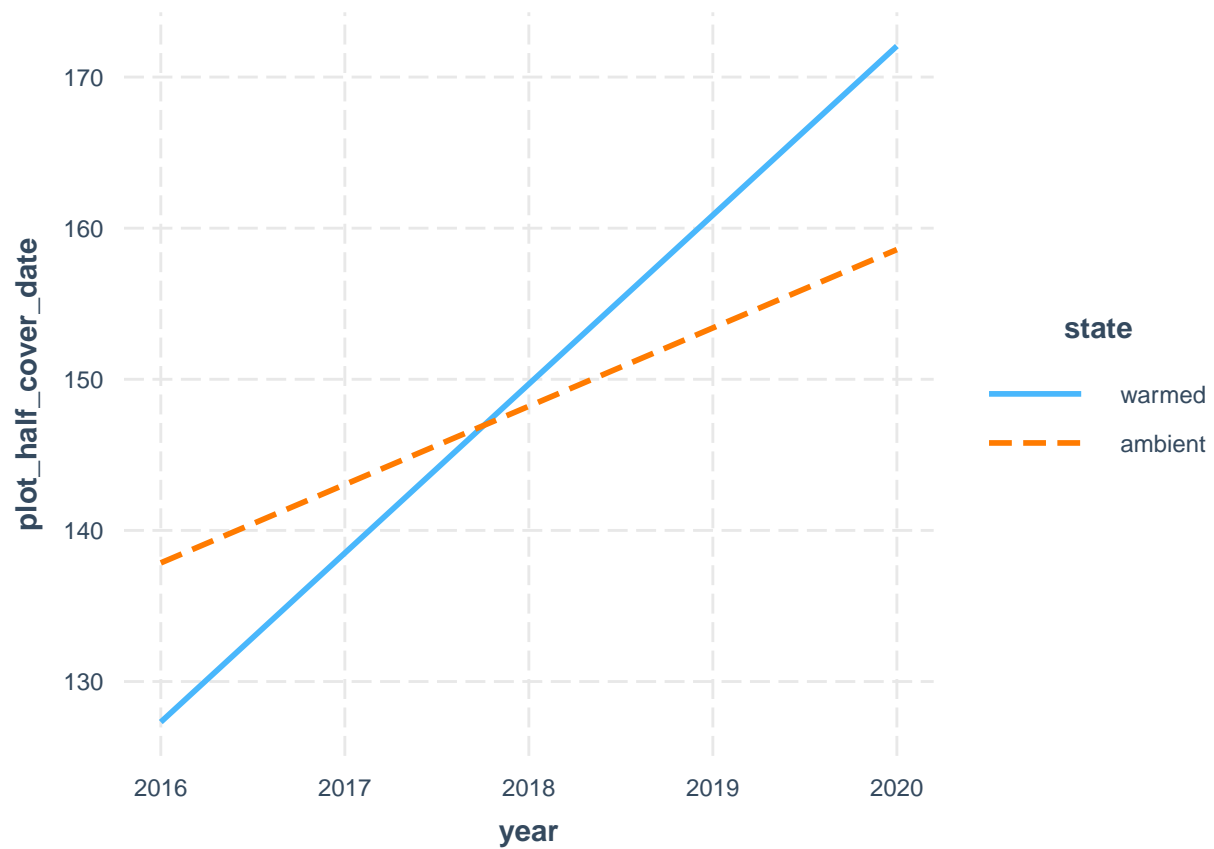


```
# UMBS
fit3u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
interact_plot(fit3u, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the
## model.
```

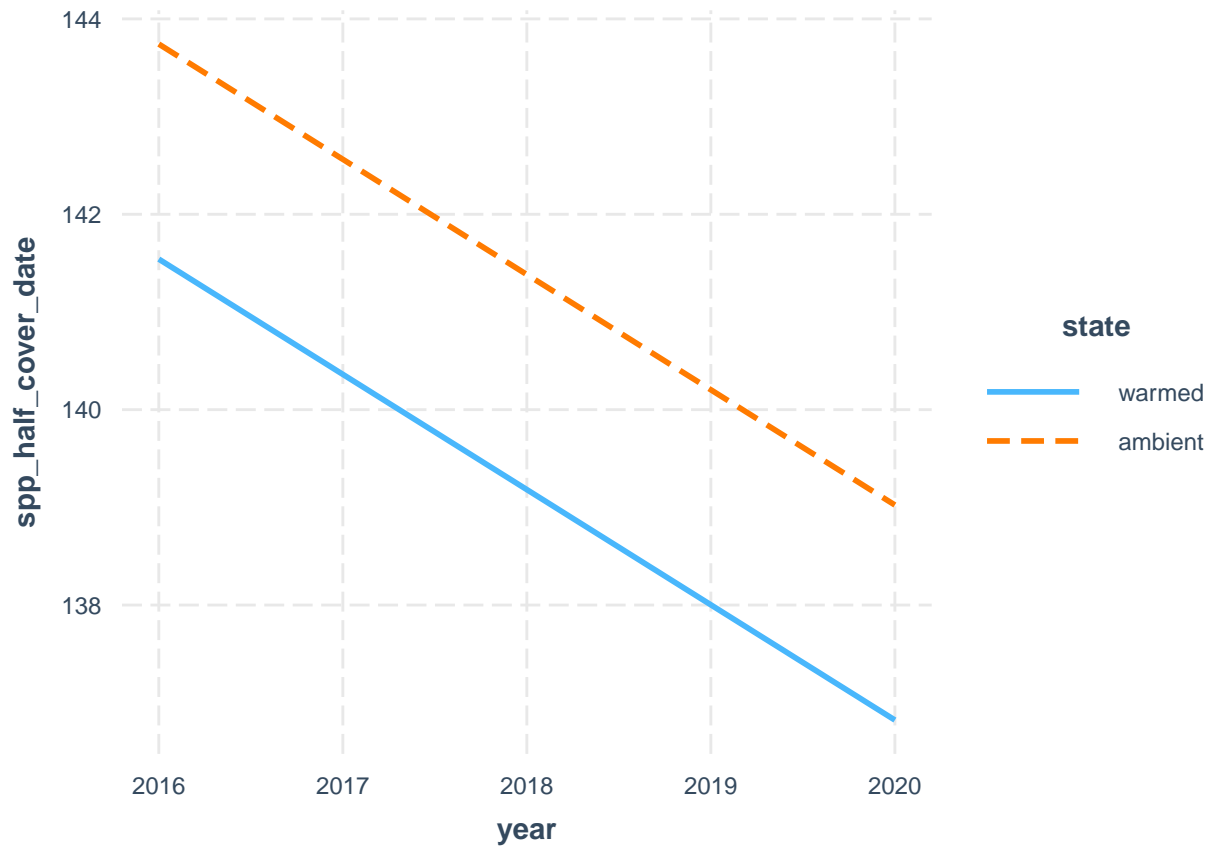


```
fit4u <- lm(plot_half_cover_date ~ state * year, data = green_umbsp)
interact_plot(fit4u, pred = year, modx = state)
```



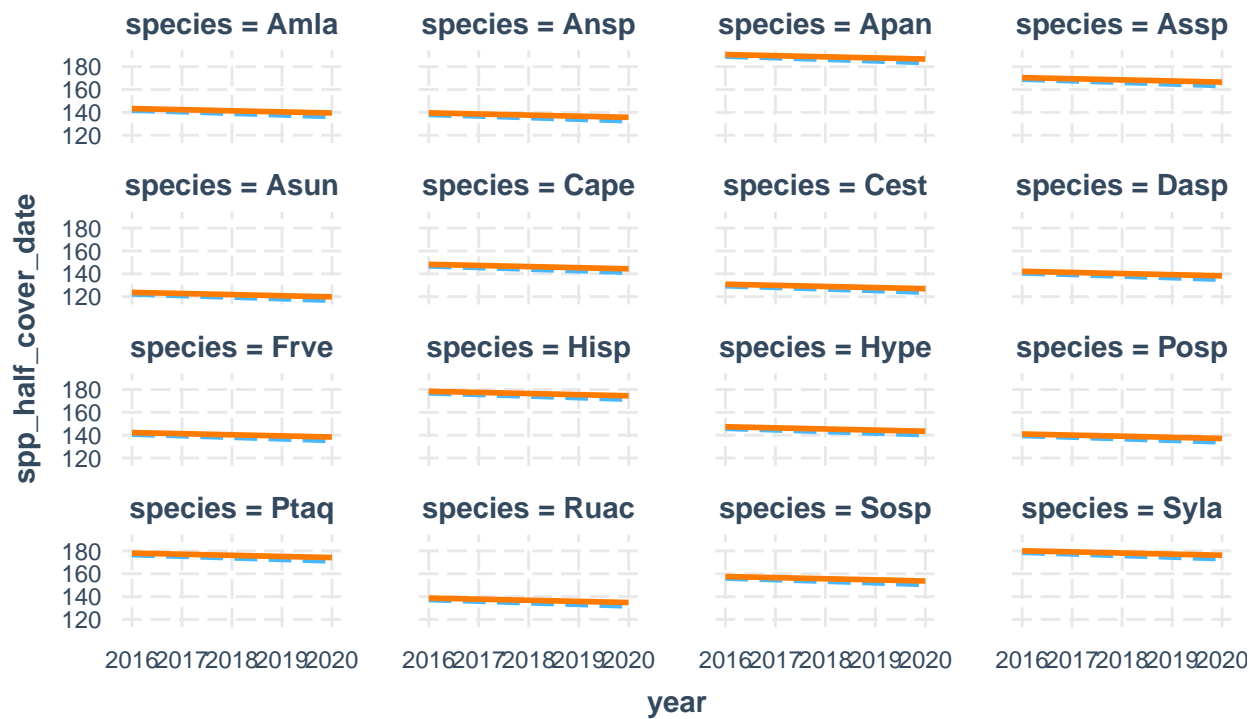
```
fit5u <- lm(spp_half_cover_date ~ state + year + species, data = green_umbs)
interact_plot(fit5u, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the
## model.
```

```
fit6u <- lm(spp_half_cover_date ~ state * year + species, data = green_umbs)
interact_plot(fit6u, pred = year, modx = state, mod2 = species)
```

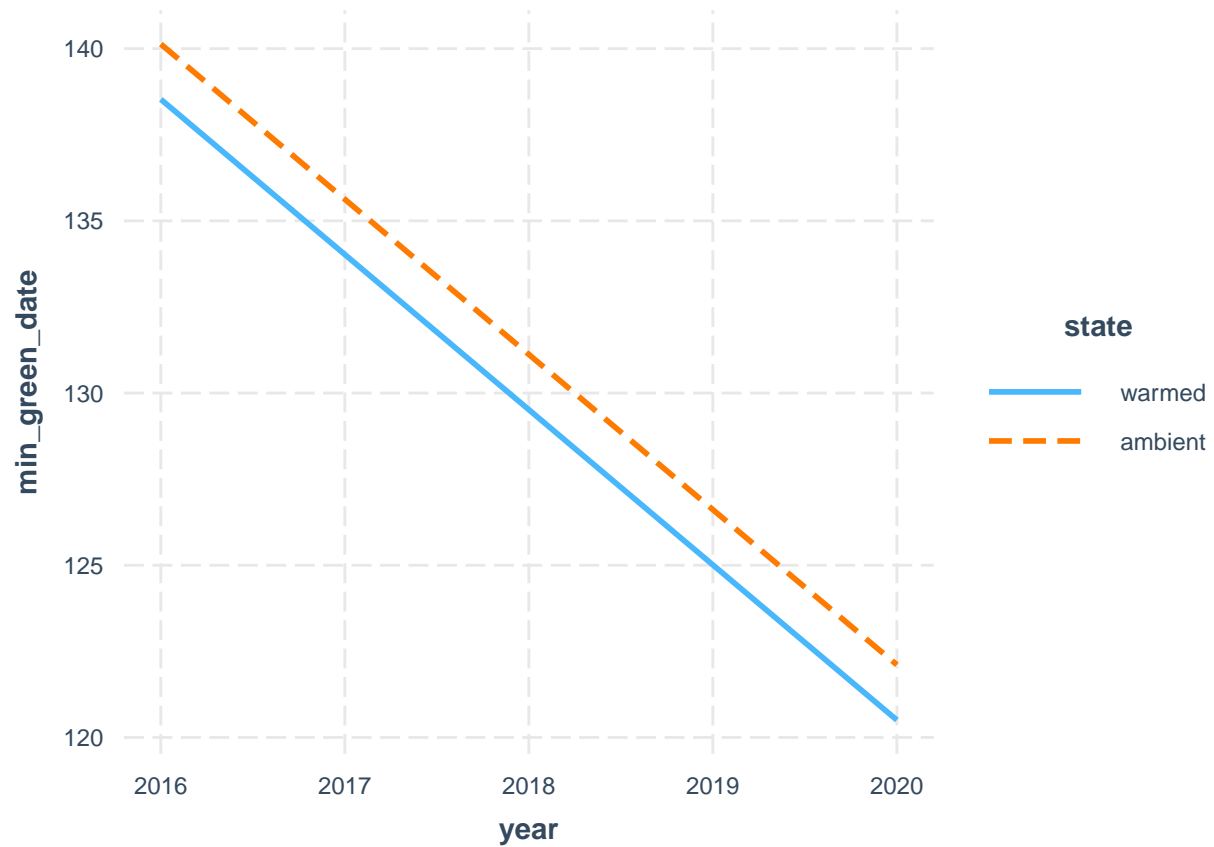
```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```



state — — — warmed — ambient

```
fit7u <- lm(min_green_date ~ state + year + species, data = green_umbs)
interact_plot(fit7u, pred = year, modx = state)
```

```
## Warning: year and state are not included in an interaction with one another in the
## model.
```



```
fit8u <- lm(min_green_date ~ state * year + species, data = green_umbs)
interact_plot(fit8u, pred = year, modx = state, mod2 = species)
```

```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```



KBS Species-level Mixed Effects Models:

```
# Start by replicating (almost) what we did in the Decologia
# 2018 paper. The only difference here is that we have
# multiple years, so we are also including year as a fixed
# effect and as an interactive term. Our goal here is to find
# a model that is the best fit to the data. We also want to
# find a model that is the most parsimonious (one that has
# the fewest parameters).
```

```
## Note: KD re-ran different models below, these are models by
## PLZ Do we need to include plot as a random effect with the
## KBS models?
```

```
mod1 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide *
  year_factor + (1 | species) + (1 | plot), green_kbs, REML = FALSE)
mod2 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide *
  year_factor + (1 | species), green_kbs, REML = FALSE)
# Run analysis of variance on each model (see this for more
# explanation on how anova on a linear mixed effects model is
# similar to an anova on a regular linear model:
# https://m-clark.github.io/docs/mixedModels/anovamixed.html)
anova(mod1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##
```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
## state	13	13	1	23.32	0.0051	0.9435
## year_factor	201178	40236	5	1481.69	16.3729	9.406e-16 ***
## insecticide	64	64	1	22.92	0.0260	0.8734

```

## state:year_factor      17353    3471     5 1476.94  1.4122    0.2168
## year_factor:insecticide 8290    1658     5 1476.73  0.6747    0.6427
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod2)

## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state                1         1      1 1494.6  0.0004    0.9834
## year_factor        201128    40226     5 1493.7 16.2373 1.272e-15 ***
## insecticide          38         38     1 1492.3  0.0153    0.9014
## state:year_factor    17392    3478     5 1488.7  1.4041    0.2198
## year_factor:insecticide 8167    1633     5 1489.1  0.6593    0.6544
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Run an ANOVA to test if 2 models to test whether the more
# complex model is significantly better at capturing the data
# than the simpler model. If the resulting p-value is
# sufficiently low (usually less than 0.05), we conclude that
# the more complex model is significantly better than the
# simpler model, and thus favor the more complex model. If
# the p-value is not sufficiently low (usually greater than
# 0.05), we should favor the simpler model.
# https://bookdown.org/ndphillips/YaRrr/comparing-regression-models-with-anova.html
anova(mod2, mod1) # favor mod 2

## Data: green_kbs
## Models:
## mod2: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod2:      (1 | species)
## mod1: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod1:      (1 | species) + (1 | plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2    20 16198 16304 -8078.9    16158
## mod1    21 16197 16309 -8077.7    16155 2.351  1    0.1252

summary(mod1)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
##      (1 | species) + (1 | plot)
##      Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 16197.4 16309.1 -8077.7 16155.4      1490
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1401 -0.6679 -0.2290  0.4939  3.2472
##
## Random effects:
##      Groups      Name              Variance Std.Dev.

```

```

## plot      (Intercept)   21.19   4.604
## species   (Intercept)  701.14  26.479
## Residual                2457.46  49.573
## Number of obs: 1511, groups: plot, 24; species, 22
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)    132.5912     7.7803   57.5190  17.042
## stateambient     -3.5259     5.9191  241.3907  -0.596
## year_factor2     -7.0774     7.7297 1472.4624  -0.916
## year_factor3     26.2075     7.3481 1474.5216   3.567
## year_factor4      6.7615     7.2793 1478.4970   0.929
## year_factor5     21.8553     7.3785 1478.4944   2.962
## year_factor6      9.2088     7.4941 1484.7880   1.229
## insecticideno_insects  3.7585     5.9185  241.1836   0.635
## stateambient:year_factor2 -4.5737     8.7486 1473.8850  -0.523
## stateambient:year_factor3 -1.1482     8.3975 1477.4538  -0.137
## stateambient:year_factor4  2.0347     8.5280 1480.6286   0.239
## stateambient:year_factor5 15.3518     8.5364 1475.4692   1.798
## stateambient:year_factor6 10.8806     8.7035 1481.9963   1.250
## year_factor2:insecticideno_insects -0.7372     8.7408 1474.0530  -0.084
## year_factor3:insecticideno_insects -7.7324     8.3948 1477.9488  -0.921
## year_factor4:insecticideno_insects  1.7398     8.5364 1478.9656   0.204
## year_factor5:insecticideno_insects -8.1151     8.5551 1473.6907  -0.949
## year_factor6:insecticideno_insects -10.8238     8.6939 1481.9730  -1.245
##
##              Pr(>|t|)
## (Intercept)    < 2e-16 ***
## stateambient    0.551948
## year_factor2    0.360025
## year_factor3    0.000373 ***
## year_factor4    0.353109
## year_factor5    0.003105 **
## year_factor6    0.219339
## insecticideno_insects 0.525995
## stateambient:year_factor2 0.601201
## stateambient:year_factor3 0.891264
## stateambient:year_factor4 0.811455
## stateambient:year_factor5 0.072319 .
## stateambient:year_factor6 0.211445
## year_factor2:insecticideno_insects 0.932801
## year_factor3:insecticideno_insects 0.357152
## year_factor4:insecticideno_insects 0.838529
## year_factor5:insecticideno_insects 0.342992
## year_factor6:insecticideno_insects 0.213330
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it
summary(mod2)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's

```

```

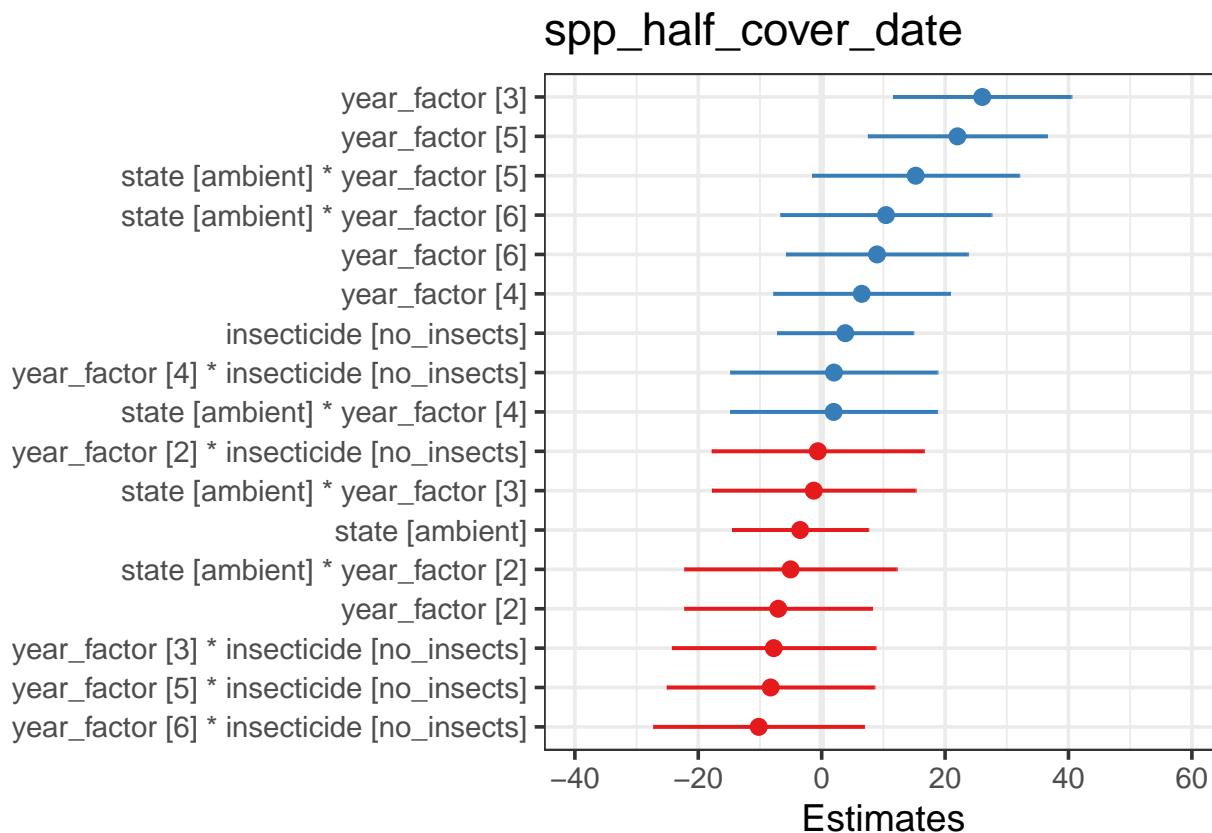
## method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## (1 | species)
## Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 16197.7 16304.2 -8078.9 16157.7    1491
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1987 -0.6827 -0.2261  0.4740  3.2316
##
## Random effects:
## Groups Name Variance Std.Dev.
## species (Intercept) 706.2 26.57
## Residual 2477.4 49.77
## Number of obs: 1511, groups: species, 22
##
## Fixed effects:
##
## Estimate Std. Error df t value
## (Intercept) 132.5308 7.6320 54.1583 17.365
## stateambient -3.4918 5.6309 1488.3923 -0.620
## year_factor2 -7.0395 7.7573 1490.0939 -0.907
## year_factor3 26.0247 7.3740 1491.7742 3.529
## year_factor4 6.4911 7.2996 1488.8786 0.889
## year_factor5 22.0036 7.4011 1491.2131 2.973
## year_factor6 8.9698 7.5120 1492.7434 1.194
## insecticideno_insects 3.8211 5.6302 1487.8702 0.679
## stateambient:year_factor2 -5.0420 8.7766 1487.9825 -0.574
## stateambient:year_factor3 -1.2774 8.4232 1490.1563 -0.152
## stateambient:year_factor4 1.9401 8.5506 1490.2157 0.227
## stateambient:year_factor5 15.2331 8.5623 1488.1527 1.779
## stateambient:year_factor6 10.4250 8.7228 1488.9871 1.195
## year_factor2:insecticideno_insects -0.6211 8.7688 1488.2688 -0.071
## year_factor3:insecticideno_insects -7.7677 8.4203 1490.4370 -0.923
## year_factor4:insecticideno_insects 1.9900 8.5618 1491.0238 0.232
## year_factor5:insecticideno_insects -8.2703 8.5830 1488.4535 -0.964
## year_factor6:insecticideno_insects -10.2006 8.7125 1488.4470 -1.171
##
## Pr(>|t|)
## (Intercept) < 2e-16 ***
## stateambient 0.535284
## year_factor2 0.364307
## year_factor3 0.000429 ***
## year_factor4 0.374017
## year_factor5 0.002996 **
## year_factor6 0.232640
## insecticideno_insects 0.497449
## stateambient:year_factor2 0.565731
## stateambient:year_factor3 0.879485
## stateambient:year_factor4 0.820540
## stateambient:year_factor5 0.075430 .
## stateambient:year_factor6 0.232222
## year_factor2:insecticideno_insects 0.943545

```

```
## year_factor3:insecticideno_insects 0.356417
## year_factor4:insecticideno_insects 0.816236
## year_factor5:insecticideno_insects 0.335420
## year_factor6:insecticideno_insects 0.241864
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

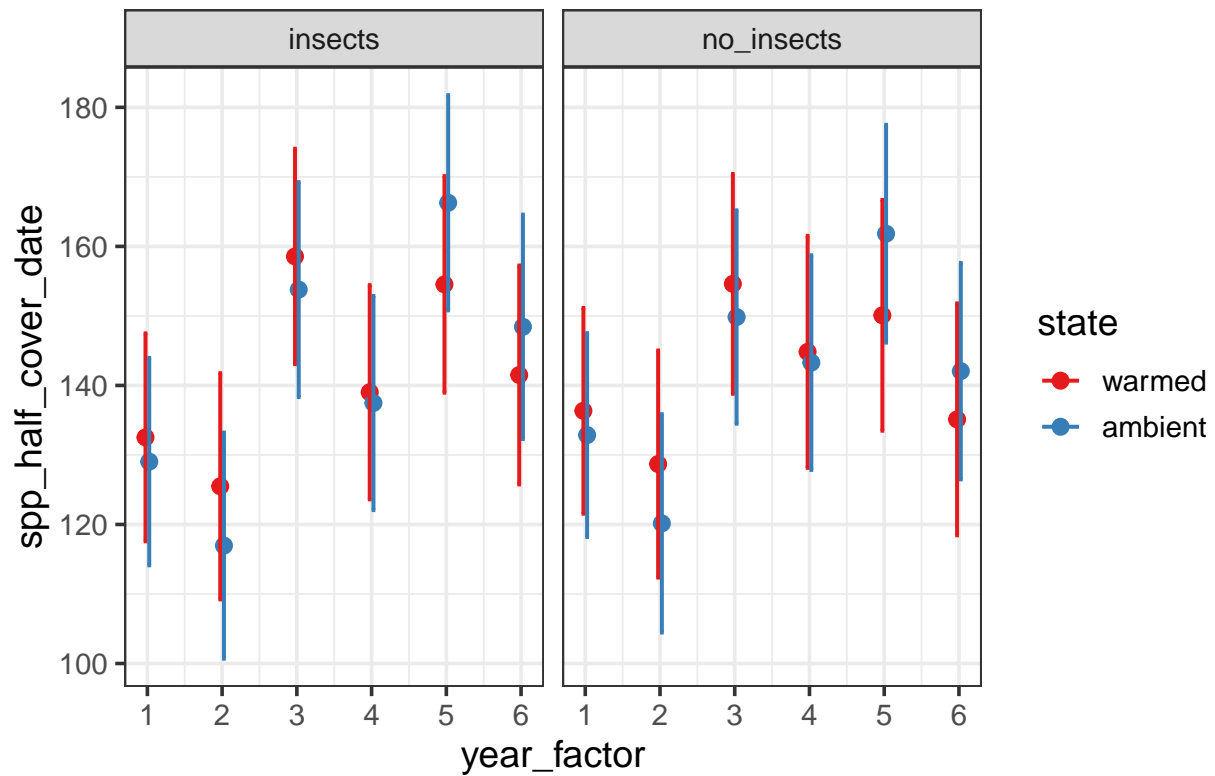
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it

# Next, plot the model. There are multiple variables but
# here's one way to do it based on this package sjPlot:
# https://strengjacke.github.io/sjPlot/articles/plot\_model\_estimates.html
# Annoyingly, this package somehow overwrites the factor
# order in its plotting so we will have to modify the code to
# get warmed = red. I haven't figured this out yet. It does
# seem to work on some of the plots. hmm. ?plot_model Plot
# the fixed effects estimates for different models these are
# the fixed effects estimates from summary(mod5)
plot_model(mod2, sort.est = TRUE)
```



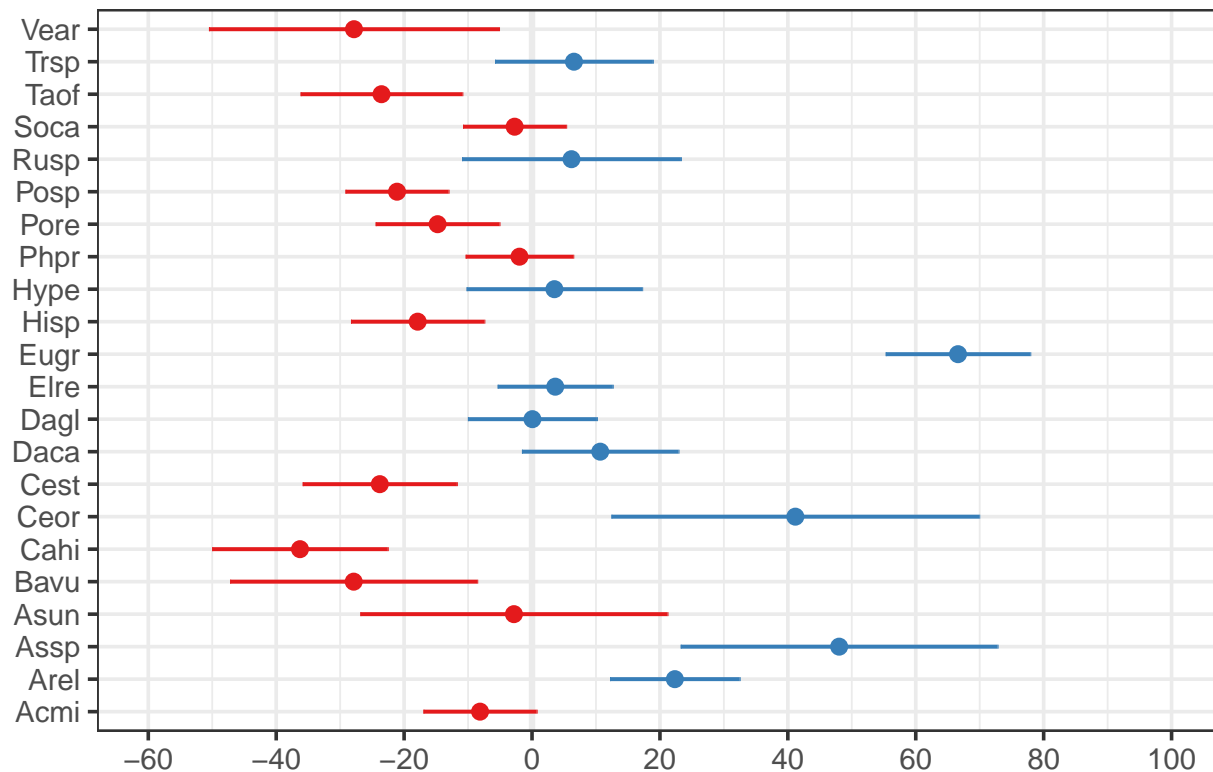
```
# these are the fixed predicted values:
plot_model(mod2, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```


Predicted values of spp_half_cover_date



```
# these are the random effects estimates  
plot_model(mod2, type = "re", terms = c("species"))
```

Random effects



Do we need to include insecticide?

```
mod3 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |
  species), green_kbs, REML = FALSE)
anova(mod2, mod3)
```

Data: green_kbs

Models:

mod3: spp_half_cover_date ~ state * year_factor + (1 | species)

mod2: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +

mod2: (1 | species)

	npar	AIC	BIC	logLik	deviance	Chisq	Df	Pr(>Chisq)
## mod3	14	16189	16264	-8080.5	16161			
## mod2	20	16198	16304	-8078.9	16158	3.2951	6	0.771

AICctab(mod2, mod3, weights = T)

	dAICc	df	weight
## mod3	0	14	0.989
## mod2	9	20	0.011

Dont' need insecticide, continue with mod3

Does year need to be interactive with insecticide? -

already removed insecticide

```
mod4 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide +
  (1 | species) + (1 | plot), green_kbs, REML = FALSE)
anova(mod2, mod4)
```

Data: green_kbs

```
## Models:
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:   species) + (1 | plot)
## mod2: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod2:   (1 | species)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod4   16 16191 16276 -8079.4   16159
## mod2   20 16198 16304 -8078.9   16158 1.0182  4      0.907

## No, P>0.05 so insecticide*year doesn't strongly improve
## model fit so we will shift to mod4
anova(mod3, mod4)
```

```
## Data: green_kbs
## Models:
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:   species) + (1 | plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3   14 16189 16264 -8080.5   16161
## mod4   16 16191 16276 -8079.4   16159 2.2769  2      0.3203

# Still continue with no insecticide model 3

# Does year need to be interactive with state?
mod5 <- lmer(spp_half_cover_date ~ state + year_factor + (1 |
  species), green_kbs, REML = FALSE)
anova(mod3, mod5)
```

```
## Data: green_kbs
## Models:
## mod5: spp_half_cover_date ~ state + year_factor + (1 | species)
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5    9 16186 16233 -8083.8   16168
## mod3   14 16189 16264 -8080.5   16161 6.4803  5      0.2622

AICctab(mod3, mod5, weights = T)
```

```
##      dAICc df weight
## mod5  0.0  9  0.86
## mod3  3.7 14  0.14

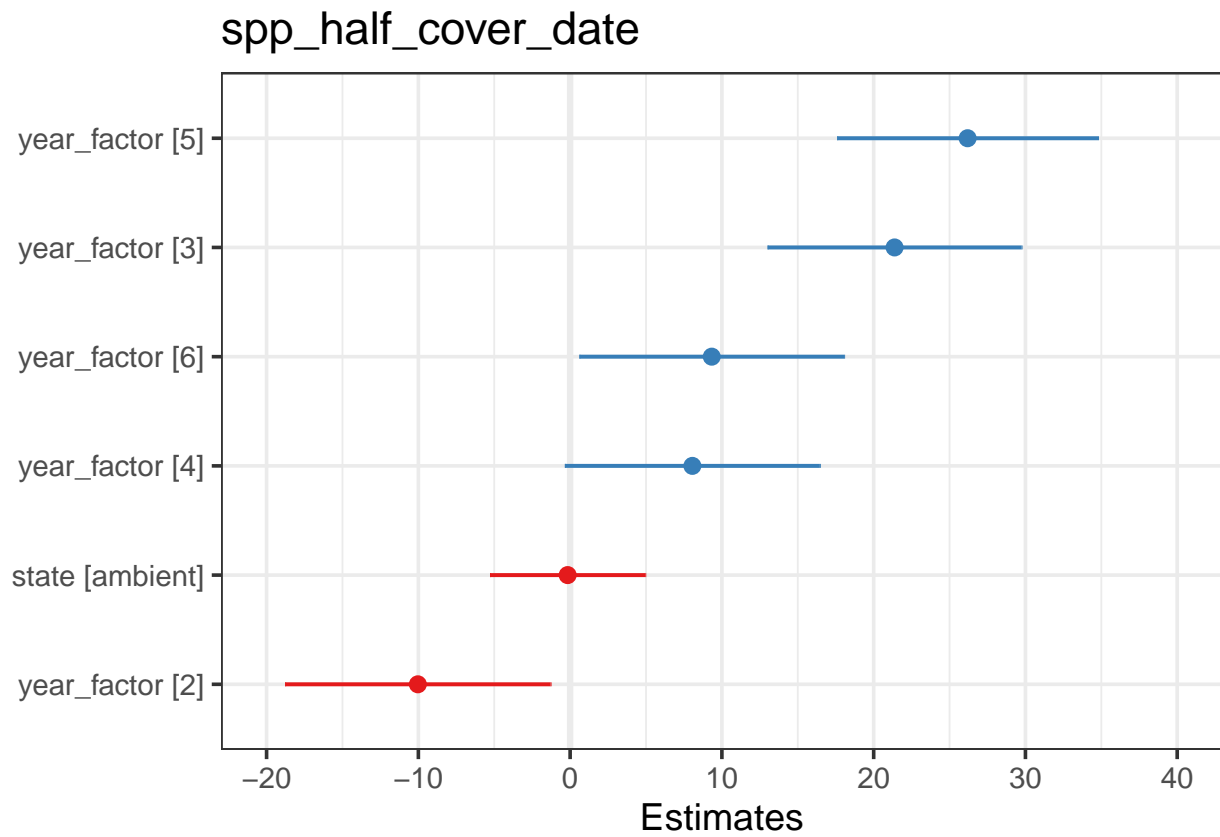
# state*year doesn't improve model fit so we could drop it
# and go with mod5
summary(mod5)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + (1 | species)
## Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 16185.5 16233.4 -8083.8 16167.5      1502
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

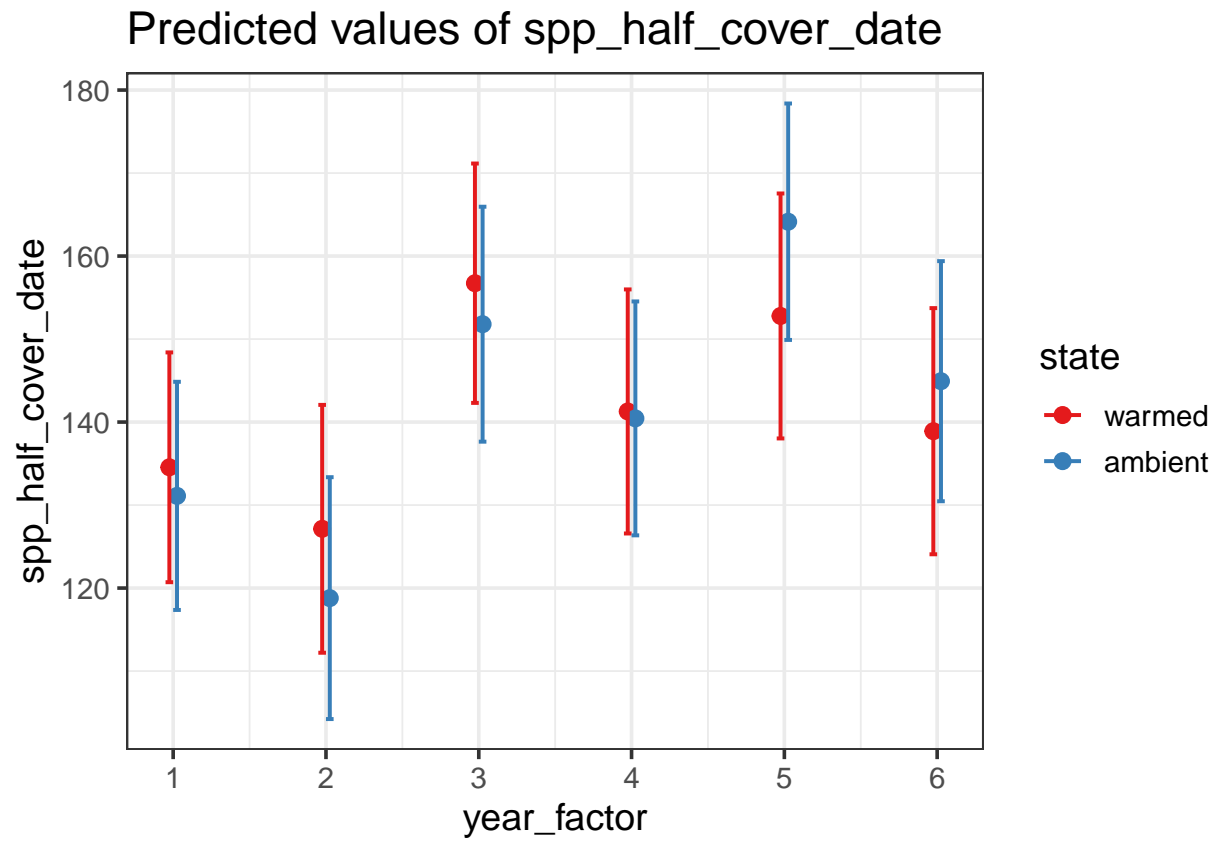
```

## -2.1336 -0.6860 -0.2278  0.4745  3.1191
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
## species (Intercept) 709.2    26.63
## Residual          2493.5    49.94
## Number of obs: 1511, groups: species, 22
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  132.8740    6.5879   29.8621  20.169 < 2e-16 ***
## stateambient  -0.1626    2.6097 1494.1996  -0.062  0.9503
## year_factor2 -10.0332    4.4619 1495.4833  -2.249  0.0247 *
## year_factor3  21.3776    4.2685 1498.0716   5.008 6.15e-07 ***
## year_factor4   8.0551    4.2861 1490.9749   1.879  0.0604 .
## year_factor5  26.1898    4.3838 1498.8556   5.974 2.88e-09 ***
## year_factor6   9.3321    4.4492 1498.6649   2.097  0.0361 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn yr_fc2 yr_fc3 yr_fc4 yr_fc5
## stateambint -0.203
## year_factr2 -0.273 -0.015
## year_factr3 -0.292 -0.008  0.437
## year_factr4 -0.283 -0.030  0.433  0.451
## year_factr5 -0.281 -0.024  0.433  0.454  0.451
## year_factr6 -0.277 -0.020  0.431  0.446  0.446  0.453
# these are the fixed effects estimates from summary(mod3)
plot_model(mod5, sort.est = TRUE)

```

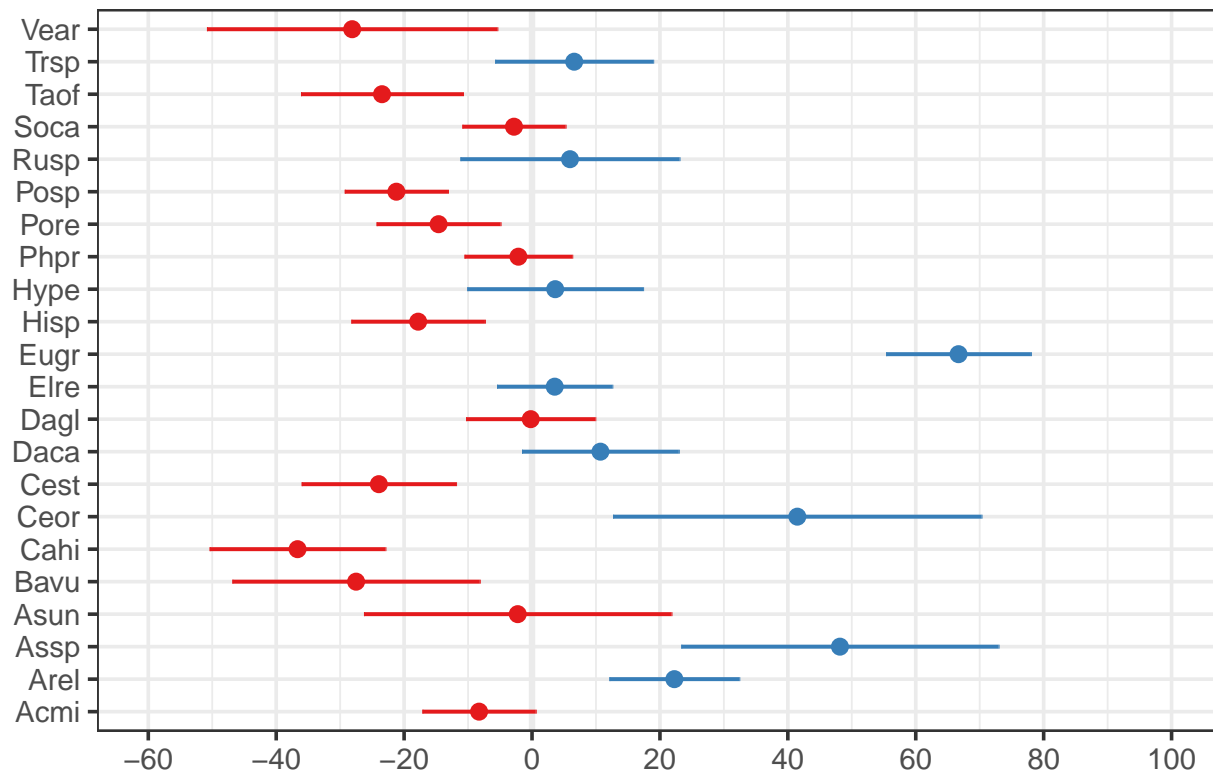


```
# these are the fixed predicted values:  
plot_model(mod3, type = "pred", terms = c("year_factor", "state"))
```



```
# these are the random effects estimates  
plot_model(mod3, type = "re", terms = c("species", "plot"))
```

Random effects



*# If we wanted to include plots nested within year it would
look like this:*

```
mod6 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |  
  species) + (1 + year | plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -7.0e+00
```

```
anova(mod5, mod6)
```

```
## Data: green_kbs
```

```
## Models:
```

```
## mod5: spp_half_cover_date ~ state + year_factor + (1 | species)
```

```
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +
```

```
## mod6:   year | plot)
```

```
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
```

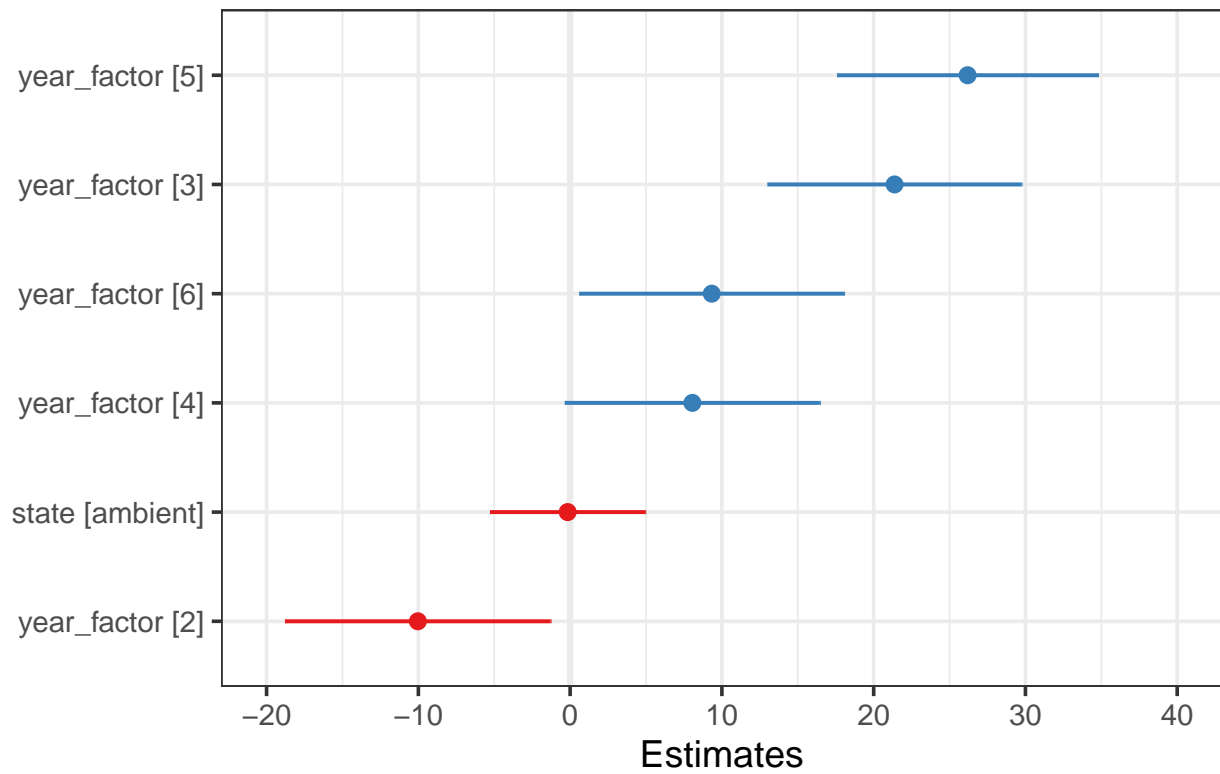
```
## mod5     9 16186 16233 -8083.8   16168
```

```
## mod6    17 16193 16283 -8079.4   16159 8.6671  8    0.3712
```

mod 5 still better fit

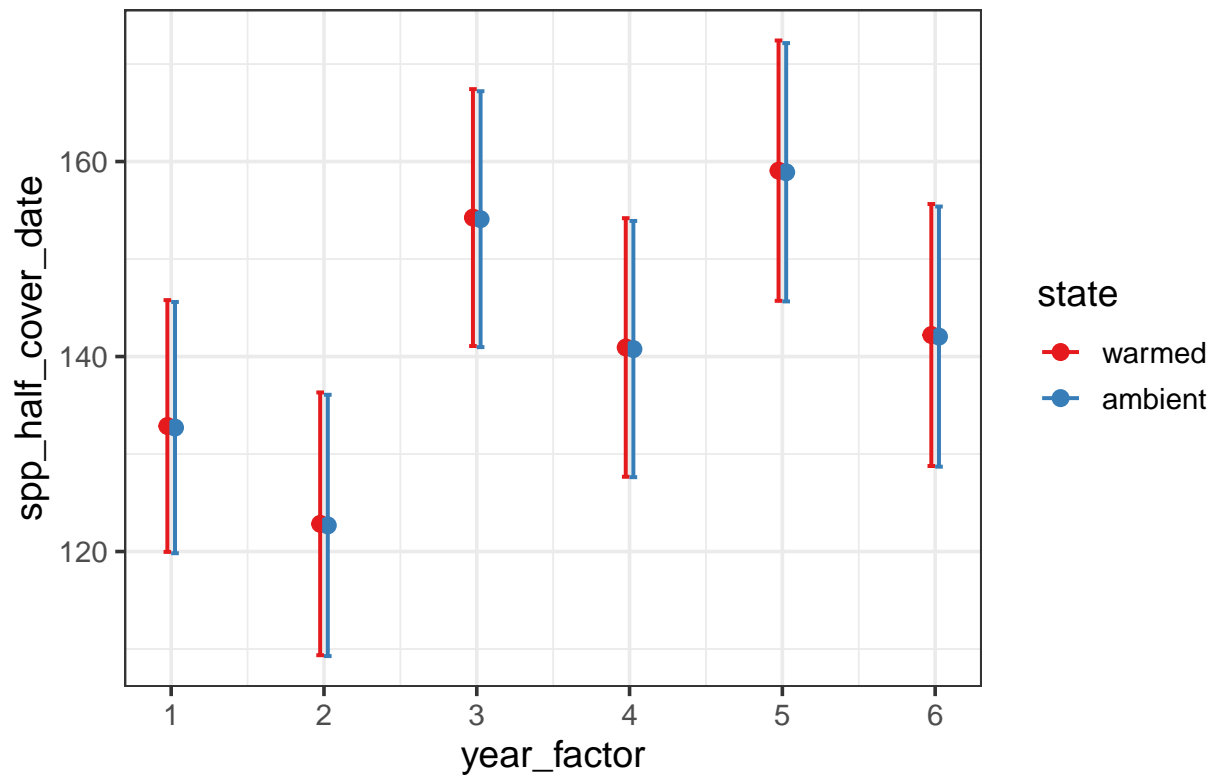
```
plot_model(mod5, sort.est = TRUE)
```

spp_half_cover_date



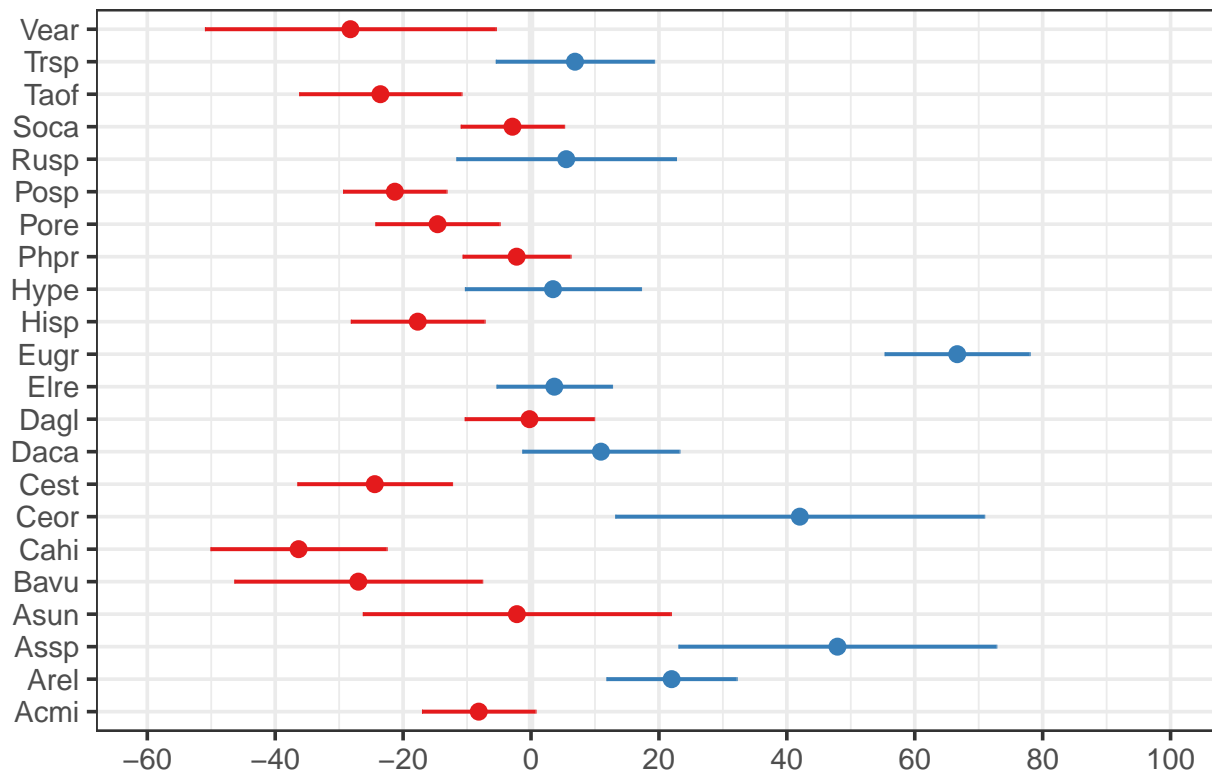
```
# these are the fixed predicted values:  
plot_model(mod5, type = "pred", terms = c("year_factor", "state"))
```


Predicted values of spp_half_cover_date



```
# these are the random effects estimates  
plot_model(mod5, type = "re", terms = c("species", "plot"))
```

Random effects



*# mod5 (and mod6) are pretty complex in terms of
interpretation (they actually don't have many parameters
though). We could consider an alternative model that's
simpler to understand and also one that provides more
insight about the species.*

including species as fixed effect

```
mod7 <- lmer(spp_half_cover_date ~ state + species + (1 + year_factor |  
  plot), green_kbs, REML = FALSE)
```

boundary (singular) fit: see ?isSingular

Warning: Model failed to converge with 1 negative eigenvalue: -3.2e+00

```
mod7a <- lmer(spp_half_cover_date ~ state + species + year_factor +  
  (1 | plot), green_kbs, REML = FALSE)
```

```
mod7b <- lmer(spp_half_cover_date ~ state * year_factor + species +  
  (1 | plot), green_kbs, REML = FALSE)
```

```
mod7c <- lmer(spp_half_cover_date ~ state + species + year_factor +  
  insecticide + (1 | plot), green_kbs, REML = FALSE)
```

```
anova(mod6, mod7) # model 7 is a better fit to data
```

Data: green_kbs

Models:

```
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +  
## mod6:   year | plot)
```

```
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
```

```
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
```

```
## mod6    17 16193 16283 -8079.4    16159
```

```

## mod7 45 16198 16437 -8054.0 16108 50.921 28 0.005095 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod7, mod7a) #mod 7a - but why is p = 1?

## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##      npar  AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a  30 16141 16301 -8040.6 16081
## mod7   45 16198 16437 -8054.0 16108 0 15 1

anova(mod7a, mod7b) #mod 7a

## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
##      npar  AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a  30 16141 16301 -8040.6 16081
## mod7b  35 16145 16331 -8037.3 16075 6.5812 5 0.2537

anova(mod7a, mod7c) #mod 7a

## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7c: spp_half_cover_date ~ state + species + year_factor + insecticide +
## mod7c: (1 | plot)
##      npar  AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a  30 16141 16301 -8040.6 16081
## mod7c  31 16143 16308 -8040.6 16081 0.002 1 0.964

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## Data: green_kbs
##
##      AIC      BIC logLik deviance df.resid
## 16141.1 16300.8 -8040.6 16081.1 1481
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1580 -0.6793 -0.2178  0.4667  3.1466
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 16.91 4.112
## Residual 2438.42 49.380
## Number of obs: 1511, groups: plot, 24
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)

```

```
## (Intercept) 124.6679 5.5355 658.1208 22.522 < 2e-16 ***
## stateambient -0.1218 3.0925 23.4606 -0.039 0.968910
## speciesArel 31.5237 6.9674 1502.0715 4.524 6.53e-06 ***
## speciesAssp 71.8944 15.0713 1504.7956 4.770 2.02e-06 ***
## speciesAsun 4.9822 14.5648 1497.4397 0.342 0.732343
## speciesBavu -21.9349 11.5623 1510.9007 -1.897 0.058004 .
## speciesCahi -30.8244 8.5743 1502.0958 -3.595 0.000335 ***
## speciesCeor 65.0746 18.2061 1473.6005 3.574 0.000362 ***
## speciesCest -17.7608 7.7939 1499.7908 -2.279 0.022819 *
## speciesDaca 20.4666 7.8568 1502.9399 2.605 0.009279 **
## speciesDagl 8.5034 6.9340 1501.4392 1.226 0.220267
## speciesElre 12.0669 6.5205 1496.9446 1.851 0.064424 .
## speciesEugr 78.4509 7.4574 1509.7734 10.520 < 2e-16 ***
## speciesHisp -10.1581 7.0897 1495.7777 -1.433 0.152123
## speciesHype 12.5225 8.5592 1510.9369 1.463 0.143660
## speciesPhpr 6.1822 6.2777 1493.4067 0.985 0.324886
## speciesPore -6.5550 6.7603 1499.9341 -0.970 0.332387
## speciesPosp -13.5300 6.1492 1491.2662 -2.200 0.027940 *
## speciesRusp 14.6457 10.3229 1478.7658 1.419 0.156182
## speciesSoca 5.3091 6.1492 1491.2662 0.863 0.388067
## speciesTaof -17.2928 8.0633 1510.5669 -2.145 0.032142 *
## speciesTrsp 15.8169 7.9265 1499.7857 1.995 0.046174 *
## speciesVear -25.8562 13.6356 1509.6798 -1.896 0.058121 .
## year_factor2 -10.0690 4.4226 1495.7614 -2.277 0.022943 *
## year_factor3 21.6909 4.2345 1498.3063 5.122 3.41e-07 ***
## year_factor4 7.9005 4.2476 1503.0642 1.860 0.063082 .
## year_factor5 25.8202 4.3513 1503.1515 5.934 3.67e-09 ***
## year_factor6 9.0605 4.4186 1507.1045 2.051 0.040484 *
```

```
## ---
```

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

```
##
```

```
## Correlation matrix not shown by default, as p = 28 > 12.
```

```
## Use print(x, correlation=TRUE) or
```

```
## vcov(x) if you need it
```

```
anova(mod7a) # investigates whether at least one of the levels within each factor is significantly dif
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
```

```
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state 4 4 1 23.46 0.0016 0.9689
## species 779402 37114 21 1501.43 15.2207 < 2.2e-16 ***
## year_factor 207080 41416 5 1499.58 16.9847 2.297e-16 ***
```

```
## ---
```

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

```
# Yes, at least one of the species is different (they do not
# all have the same half cover dates).
```

```
emmeans(mod7a, list(pairwise ~ state + year_factor), adjust = "tukey")
```

```
## $`emmeans of state, year_factor`
```

```
## state year_factor emmean SE df lower.CL upper.CL
## warmed 1 134 3.66 177 127 141
## ambient 1 134 3.63 176 127 141
## warmed 2 124 4.16 282 116 132
## ambient 2 124 4.09 271 116 132
```

```

## warmed 3          156 3.90 216          148          163
## ambient 3          155 3.85 214          148          163
## warmed 4          142 3.98 231          134          150
## ambient 4          142 3.86 216          134          149
## warmed 5          160 4.06 248          152          168
## ambient 5          160 3.97 237          152          167
## warmed 6          143 4.14 263          135          151
## ambient 6          143 4.05 256          135          151
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, year_factor`
## 1          estimate      SE      df t.ratio p.value
## warmed 1 - ambient 1      0.122 3.26   27.2  0.037  1.0000
## warmed 1 - warmed 2     10.069 4.46 1522.7  2.256  0.5088
## warmed 1 - ambient 2     10.191 5.49  226.9  1.855  0.7851
## warmed 1 - warmed 3    -21.691 4.27 1525.2 -5.075 <.0001
## warmed 1 - ambient 3   -21.569 5.36  207.8 -4.027  0.0044
## warmed 1 - warmed 4     -7.900 4.29 1530.2 -1.842  0.7942
## warmed 1 - ambient 4     -7.779 5.32  201.2 -1.463  0.9488
## warmed 1 - warmed 5    -25.820 4.39 1530.2 -5.877 <.0001
## warmed 1 - ambient 5   -25.698 5.42  214.8 -4.744  0.0002
## warmed 1 - warmed 6     -9.061 4.46 1534.3 -2.030  0.6725
## warmed 1 - ambient 6     -8.939 5.47  222.9 -1.633  0.8952
## ambient 1 - warmed 2      9.947 5.56  236.6  1.789  0.8225
## ambient 1 - ambient 2    10.069 4.46 1522.7  2.256  0.5088
## ambient 1 - warmed 3   -21.813 5.39  208.8 -4.044  0.0042
## ambient 1 - ambient 3   -21.691 4.27 1525.2 -5.075 <.0001
## ambient 1 - warmed 4     -8.022 5.45  214.9 -1.471  0.9468
## ambient 1 - ambient 4     -7.900 4.29 1530.2 -1.842  0.7942
## ambient 1 - warmed 5   -25.942 5.52  225.5 -4.697  0.0003
## ambient 1 - ambient 5   -25.820 4.39 1530.2 -5.877 <.0001
## ambient 1 - warmed 6     -9.182 5.58  229.3 -1.647  0.8897
## ambient 1 - ambient 6     -9.061 4.46 1534.3 -2.030  0.6725
## warmed 2 - ambient 2      0.122 3.26   27.2  0.037  1.0000
## warmed 2 - warmed 3   -31.760 4.64 1520.8 -6.851 <.0001
## warmed 2 - ambient 3   -31.638 5.68  259.3 -5.568 <.0001
## warmed 2 - warmed 4   -17.969 4.66 1523.0 -3.859  0.0066
## warmed 2 - ambient 4   -17.848 5.65  254.4 -3.157  0.0752
## warmed 2 - warmed 5   -35.889 4.71 1525.7 -7.617 <.0001
## warmed 2 - ambient 5   -35.767 5.71  262.1 -6.263 <.0001
## warmed 2 - warmed 6   -19.130 4.76 1533.4 -4.021  0.0035
## warmed 2 - ambient 6   -19.008 5.75  265.9 -3.305  0.0488
## ambient 2 - warmed 3   -31.882 5.65  250.0 -5.641 <.0001
## ambient 2 - ambient 3   -31.760 4.64 1520.8 -6.851 <.0001
## ambient 2 - warmed 4   -18.091 5.72  258.5 -3.166  0.0734
## ambient 2 - ambient 4   -17.969 4.66 1523.0 -3.859  0.0066
## ambient 2 - warmed 5   -36.011 5.75  263.0 -6.266 <.0001
## ambient 2 - ambient 5   -35.889 4.71 1525.7 -7.617 <.0001
## ambient 2 - warmed 6   -19.251 5.78  261.9 -3.329  0.0456
## ambient 2 - ambient 6   -19.130 4.76 1533.4 -4.021  0.0035
## warmed 3 - ambient 3      0.122 3.26   27.2  0.037  1.0000

```

```

## warmed 3 - warmed 4      13.790 4.48 1522.6  3.077 0.0888
## warmed 3 - ambient 4     13.912 5.49  227.6  2.532 0.3257
## warmed 3 - warmed 5     -4.129 4.52 1526.1 -0.913 0.9990
## warmed 3 - ambient 5     -4.008 5.54  232.5 -0.723 0.9999
## warmed 3 - warmed 6     12.630 4.60 1532.3  2.747 0.2046
## warmed 3 - ambient 6     12.752 5.60  241.3  2.275 0.4971
## ambient 3 - warmed 4     13.669 5.59  240.7  2.446 0.3797
## ambient 3 - ambient 4    13.790 4.48 1522.6  3.077 0.0888
## ambient 3 - warmed 5     -4.251 5.61  242.6 -0.758 0.9998
## ambient 3 - ambient 5     -4.129 4.52 1526.1 -0.913 0.9990
## ambient 3 - warmed 6     12.509 5.67  246.8  2.207 0.5463
## ambient 3 - ambient 6     12.630 4.60 1532.3  2.747 0.2046
## warmed 4 - ambient 4       0.122 3.26   27.2  0.037 1.0000
## warmed 4 - warmed 5     -17.920 4.54 1518.0 -3.950 0.0047
## warmed 4 - ambient 5     -17.798 5.60  244.3 -3.179 0.0710
## warmed 4 - warmed 6     -1.160 4.60 1526.3 -0.252 1.0000
## warmed 4 - ambient 6     -1.038 5.65  251.2 -0.184 1.0000
## ambient 4 - warmed 5     -18.042 5.57  241.2 -3.237 0.0602
## ambient 4 - ambient 5     -17.920 4.54 1518.0 -3.950 0.0047
## ambient 4 - warmed 6     -1.282 5.62  243.5 -0.228 1.0000
## ambient 4 - ambient 6     -1.160 4.60 1526.3 -0.252 1.0000
## warmed 5 - ambient 5       0.122 3.26   27.2  0.037 1.0000
## warmed 5 - warmed 6     16.760 4.62 1526.0  3.630 0.0154
## warmed 5 - ambient 6     16.882 5.65  252.2  2.986 0.1189
## ambient 5 - warmed 6     16.638 5.65  247.6  2.945 0.1321
## ambient 5 - ambient 6     16.760 4.62 1526.0  3.630 0.0154
## warmed 6 - ambient 6       0.122 3.26   27.2  0.037 1.0000
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 12 estimates
emmeans(mod7a, list(pairwise ~ year_factor), adjust = "tukey")

```

```

## $`emmeans of year_factor`
## year_factor emmean SE df lower.CL upper.CL
## 1           134 3.26 402      127      140
## 2           124 3.79 617      116      131
## 3           156 3.52 482      149      162
## 4           142 3.56 499      135      149
## 5           160 3.67 538      152      167
## 6           143 3.75 572      136      150
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
## 1 estimate SE df t.ratio p.value
## 1 - 2    10.07 4.46 1523  2.256 0.2130
## 1 - 3   -21.69 4.27 1525 -5.075 <.0001
## 1 - 4    -7.90 4.29 1530 -1.842 0.4387
## 1 - 5   -25.82 4.39 1530 -5.877 <.0001
## 1 - 6    -9.06 4.46 1534 -2.030 0.3255
## 2 - 3   -31.76 4.64 1521 -6.851 <.0001

```

```

## 2 - 4    -17.97 4.66 1523 -3.859 0.0017
## 2 - 5    -35.89 4.71 1526 -7.617 <.0001
## 2 - 6    -19.13 4.76 1533 -4.021 0.0009
## 3 - 4     13.79 4.48 1523  3.077 0.0259
## 3 - 5     -4.13 4.52 1526 -0.913 0.9432
## 3 - 6     12.63 4.60 1532  2.747 0.0670
## 4 - 5    -17.92 4.54 1518 -3.950 0.0011
## 4 - 6     -1.16 4.60 1526 -0.252 0.9999
## 5 - 6     16.76 4.62 1526  3.630 0.0040
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 6 estimates
emmeans(mod7a, list(pairwise ~ species), adjust = "tukey")

## $`emmeans of species`
##   species emmean    SE    df lower.CL upper.CL
##   Acmi      134  4.70 1009    124.5    143
##   Arel      165  5.40 1152    154.6    176
##   Assp      206 14.58 1507    177.0    234
##   Asun      139 14.01 1540    111.2    166
##   Bavu      112 10.79 1478     90.6    133
##   Cahi      103  7.42 1434     88.3    117
##   Ceor      199 17.88 1482    163.7    234
##   Cest      116  6.50 1358    103.2    129
##   Daca      154  6.57 1351    141.3    167
##   Dagl      142  5.36 1167    131.7    153
##   Elre      146  4.78 1047    136.4    155
##   Eugr      212  6.04 1213    200.3    224
##   Hisp      124  5.58 1226    112.6    134
##   Hype      146  7.40 1338    131.7    161
##   Phpr      140  4.46  936    131.1    149
##   Pore      127  5.15 1112    117.0    137
##   Posp      120  4.28  870    111.8    129
##   Rusp      148  9.43 1371    129.8    167
##   Soca      139  4.28  870    130.6    147
##   Taof      116  6.80 1337    103.0    130
##   Trsp      149  6.63 1378    136.5    163
##   Vear      108 13.04 1530     82.2    133
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of species`
##   1      estimate    SE    df t.ratio p.value
##   Acmi - Arel  -31.524  7.03 1529  -4.482 0.0016
##   Acmi - Assp  -71.894 15.25 1537  -4.714 0.0006
##   Acmi - Asun   -4.982 14.70 1524  -0.339 1.0000
##   Acmi - Bavu   21.935 11.69 1540   1.877 0.9612
##   Acmi - Cahi   30.824  8.66 1529   3.561 0.0567
##   Acmi - Ceor  -65.075 18.45 1510  -3.528 0.0629
##   Acmi - Cest   17.761  7.87 1527   2.258 0.8050
##   Acmi - Daca  -20.467  7.93 1530  -2.580 0.5690

```

##	Acmi - Dagl	-8.503	7.00	1529	-1.215	0.9999
##	Acmi - Elre	-12.067	6.58	1524	-1.834	0.9696
##	Acmi - Eugr	-78.451	7.53	1538	-10.413	<.0001
##	Acmi - Hisp	10.158	7.15	1523	1.420	0.9988
##	Acmi - Hype	-12.523	8.65	1540	-1.447	0.9984
##	Acmi - Phpr	-6.182	6.33	1520	-0.976	1.0000
##	Acmi - Pore	6.555	6.82	1527	0.961	1.0000
##	Acmi - Posp	13.530	6.20	1518	2.181	0.8493
##	Acmi - Rusp	-14.646	10.46	1516	-1.400	0.9990
##	Acmi - Soca	-5.309	6.20	1518	-0.856	1.0000
##	Acmi - Taof	17.293	8.15	1539	2.122	0.8786
##	Acmi - Trsp	-15.817	8.00	1527	-1.977	0.9351
##	Acmi - Vear	25.856	13.78	1537	1.877	0.9611
##	Arel - Assp	-40.371	15.50	1535	-2.605	0.5490
##	Arel - Asun	26.541	14.95	1527	1.775	0.9787
##	Arel - Bavu	53.459	11.98	1540	4.461	0.0018
##	Arel - Cahi	62.348	9.12	1537	6.837	<.0001
##	Arel - Ceor	-33.551	18.63	1514	-1.801	0.9749
##	Arel - Cest	49.285	8.37	1537	5.885	<.0001
##	Arel - Daca	11.057	8.39	1534	1.317	0.9996
##	Arel - Dagl	23.020	7.47	1531	3.080	0.2195
##	Arel - Elre	19.457	7.08	1531	2.748	0.4367
##	Arel - Eugr	-46.927	7.98	1540	-5.883	<.0001
##	Arel - Hisp	41.682	7.64	1531	5.456	<.0001
##	Arel - Hype	19.001	9.05	1540	2.100	0.8890
##	Arel - Phpr	25.341	6.87	1531	3.687	0.0373
##	Arel - Pore	38.079	7.33	1533	5.194	0.0001
##	Arel - Posp	45.054	6.76	1531	6.668	<.0001
##	Arel - Rusp	16.878	10.76	1529	1.568	0.9952
##	Arel - Soca	26.215	6.76	1531	3.880	0.0188
##	Arel - Taof	48.817	8.58	1538	5.693	<.0001
##	Arel - Trsp	15.707	8.44	1531	1.861	0.9645
##	Arel - Vear	57.380	14.05	1537	4.083	0.0087
##	Assp - Asun	66.912	20.25	1540	3.304	0.1226
##	Assp - Bavu	93.829	18.06	1538	5.195	0.0001
##	Assp - Cahi	102.719	16.25	1540	6.319	<.0001
##	Assp - Ceor	6.820	23.05	1519	0.296	1.0000
##	Assp - Cest	89.655	15.91	1537	5.635	<.0001
##	Assp - Daca	51.428	15.88	1540	3.239	0.1466
##	Assp - Dagl	63.391	15.48	1537	4.096	0.0083
##	Assp - Elre	59.827	15.28	1536	3.914	0.0166
##	Assp - Eugr	-6.557	15.69	1540	-0.418	1.0000
##	Assp - Hisp	82.052	15.56	1539	5.272	<.0001
##	Assp - Hype	59.372	16.29	1535	3.644	0.0432
##	Assp - Phpr	65.712	15.18	1537	4.329	0.0032
##	Assp - Pore	78.449	15.38	1539	5.100	0.0001
##	Assp - Posp	85.424	15.13	1536	5.646	<.0001
##	Assp - Rusp	57.249	17.27	1539	3.314	0.1191
##	Assp - Soca	66.585	15.13	1536	4.401	0.0023
##	Assp - Taof	89.187	16.02	1539	5.567	<.0001
##	Assp - Trsp	56.077	15.94	1540	3.518	0.0648
##	Assp - Vear	97.751	19.42	1533	5.033	0.0001
##	Asun - Bavu	26.917	17.65	1538	1.525	0.9967
##	Asun - Cahi	35.807	15.82	1528	2.264	0.8012

##	Asun - Ceor	-60.092	22.66	1536	-2.652	0.5117
##	Asun - Cest	22.743	15.34	1523	1.482	0.9977
##	Asun - Dac	-15.484	15.42	1527	-1.004	1.0000
##	Asun - Dagl	-3.521	14.92	1530	-0.236	1.0000
##	Asun - Elre	-7.085	14.73	1527	-0.481	1.0000
##	Asun - Eugr	-73.469	15.19	1530	-4.837	0.0003
##	Asun - Hisp	15.140	14.97	1524	1.011	1.0000
##	Asun - Hype	-7.540	15.77	1536	-0.478	1.0000
##	Asun - Phpr	-1.200	14.65	1527	-0.082	1.0000
##	Asun - Pore	11.537	14.85	1527	0.777	1.0000
##	Asun - Posp	18.512	14.58	1525	1.270	0.9998
##	Asun - Rusp	-9.663	16.83	1539	-0.574	1.0000
##	Asun - Soca	-0.327	14.58	1525	-0.022	1.0000
##	Asun - Taof	22.275	15.50	1530	1.437	0.9985
##	Asun - Trsp	-10.835	15.45	1527	-0.701	1.0000
##	Asun - Vear	30.838	19.11	1532	1.614	0.9931
##	Bavu - Cah	8.889	13.02	1539	0.683	1.0000
##	Bavu - Ceor	-87.010	20.91	1507	-4.161	0.0064
##	Bavu - Cest	-4.174	12.58	1539	-0.332	1.0000
##	Bavu - Dac	-42.402	12.58	1540	-3.371	0.1014
##	Bavu - Dagl	-30.438	11.97	1539	-2.543	0.5984
##	Bavu - Elre	-34.002	11.71	1538	-2.904	0.3249
##	Bavu - Eugr	-100.386	12.26	1539	-8.188	<.0001
##	Bavu - Hisp	-11.777	12.09	1539	-0.974	1.0000
##	Bavu - Hype	-34.457	13.00	1537	-2.651	0.5124
##	Bavu - Phpr	-28.117	11.59	1539	-2.425	0.6895
##	Bavu - Pore	-15.380	11.91	1537	-1.291	0.9997
##	Bavu - Posp	-8.405	11.53	1539	-0.729	1.0000
##	Bavu - Rusp	-36.581	14.28	1529	-2.562	0.5834
##	Bavu - Soca	-27.244	11.53	1539	-2.364	0.7346
##	Bavu - Taof	-4.642	12.73	1536	-0.365	1.0000
##	Bavu - Trsp	-37.752	12.61	1539	-2.994	0.2681
##	Bavu - Vear	3.921	16.89	1539	0.232	1.0000
##	Cahi - Ceor	-95.899	19.28	1529	-4.974	0.0002
##	Cahi - Cest	-13.064	9.70	1532	-1.347	0.9994
##	Cahi - Dac	-51.291	9.77	1528	-5.252	<.0001
##	Cahi - Dagl	-39.328	9.08	1535	-4.330	0.0032
##	Cahi - Elre	-42.891	8.76	1533	-4.897	0.0002
##	Cahi - Eugr	-109.275	9.47	1533	-11.540	<.0001
##	Cahi - Hisp	-20.666	9.16	1532	-2.256	0.8059
##	Cahi - Hype	-43.347	10.37	1536	-4.182	0.0058
##	Cahi - Phpr	-37.007	8.55	1531	-4.328	0.0032
##	Cahi - Pore	-24.269	8.93	1536	-2.718	0.4602
##	Cahi - Posp	-17.294	8.46	1531	-2.045	0.9114
##	Cahi - Rusp	-45.470	11.94	1535	-3.808	0.0245
##	Cahi - Soca	-36.134	8.46	1531	-4.273	0.0040
##	Cahi - Taof	-13.532	9.94	1538	-1.361	0.9993
##	Cahi - Trsp	-46.641	9.79	1524	-4.765	0.0004
##	Cahi - Vear	-4.968	14.84	1531	-0.335	1.0000
##	Ceor - Cest	82.835	18.96	1514	4.370	0.0027
##	Ceor - Dac	44.608	18.98	1516	2.350	0.7443
##	Ceor - Dagl	56.571	18.64	1509	3.036	0.2437
##	Ceor - Elre	53.008	18.47	1519	2.870	0.3481
##	Ceor - Eugr	-13.376	18.84	1506	-0.710	1.0000

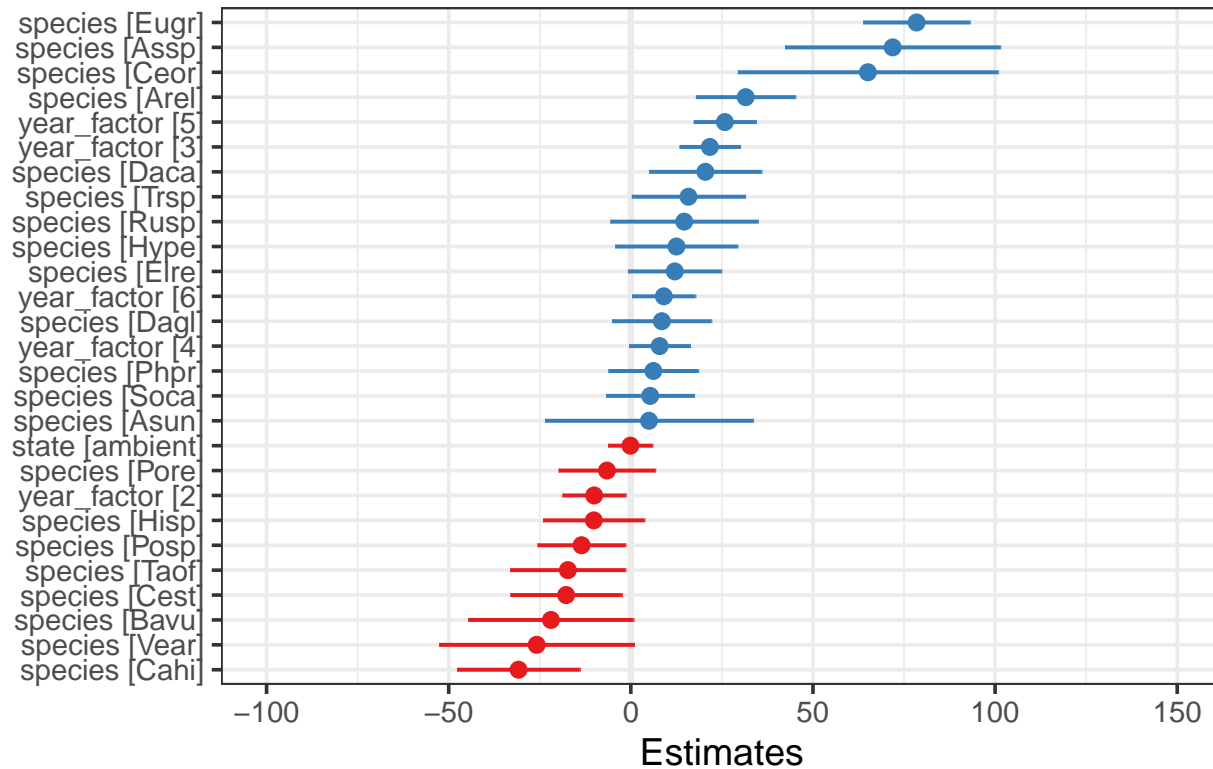
##	Ceor - Hisp	75.233	18.65	1518	4.035	0.0105
##	Ceor - Hype	52.552	19.35	1498	2.717	0.4612
##	Ceor - Phpr	58.892	18.40	1510	3.201	0.1619
##	Ceor - Pore	71.630	18.57	1505	3.858	0.0204
##	Ceor - Posp	78.605	18.34	1515	4.286	0.0038
##	Ceor - Rusp	50.429	20.14	1518	2.504	0.6293
##	Ceor - Soca	59.765	18.34	1515	3.259	0.1389
##	Ceor - Taof	82.367	19.05	1521	4.325	0.0032
##	Ceor - Trsp	49.258	18.97	1526	2.597	0.5559
##	Ceor - Vear	90.931	22.06	1525	4.123	0.0074
##	Cest - Dac	-38.227	9.06	1529	-4.219	0.0050
##	Cest - Dagl	-26.264	8.33	1535	-3.154	0.1829
##	Cest - Elre	-29.828	8.00	1530	-3.726	0.0326
##	Cest - Eugr	-96.212	8.79	1539	-10.942	<.0001
##	Cest - Hisp	-7.603	8.40	1523	-0.905	1.0000
##	Cest - Hype	-30.283	9.75	1540	-3.104	0.2069
##	Cest - Phpr	-23.943	7.77	1530	-3.082	0.2184
##	Cest - Pore	-11.206	8.14	1526	-1.377	0.9992
##	Cest - Posp	-4.231	7.66	1528	-0.552	1.0000
##	Cest - Rusp	-32.407	11.40	1508	-2.843	0.3666
##	Cest - Soca	-23.070	7.66	1528	-3.012	0.2574
##	Cest - Taof	-0.468	9.26	1537	-0.051	1.0000
##	Cest - Trsp	-33.578	9.13	1529	-3.678	0.0385
##	Cest - Vear	8.095	14.44	1538	0.561	1.0000
##	Daca - Dagl	11.963	8.37	1531	1.430	0.9986
##	Daca - Elre	8.400	8.04	1533	1.045	1.0000
##	Daca - Eugr	-57.984	8.82	1537	-6.574	<.0001
##	Daca - Hisp	30.625	8.48	1527	3.613	0.0479
##	Daca - Hype	7.944	9.80	1540	0.810	1.0000
##	Daca - Phpr	14.284	7.82	1531	1.827	0.9707
##	Daca - Pore	27.022	8.19	1527	3.297	0.1250
##	Daca - Posp	33.997	7.72	1532	4.406	0.0023
##	Daca - Rusp	5.821	11.41	1522	0.510	1.0000
##	Daca - Soca	15.158	7.72	1532	1.964	0.9390
##	Daca - Taof	37.759	9.34	1539	4.043	0.0102
##	Daca - Trsp	4.650	9.19	1525	0.506	1.0000
##	Daca - Vear	46.323	14.48	1534	3.200	0.1626
##	Dagl - Elre	-3.563	7.05	1524	-0.506	1.0000
##	Dagl - Eugr	-69.947	7.96	1539	-8.788	<.0001
##	Dagl - Hisp	18.661	7.61	1530	2.451	0.6705
##	Dagl - Hype	-4.019	9.03	1540	-0.445	1.0000
##	Dagl - Phpr	2.321	6.84	1523	0.340	1.0000
##	Dagl - Pore	15.058	7.30	1529	2.063	0.9045
##	Dagl - Posp	22.033	6.72	1526	3.277	0.1321
##	Dagl - Rusp	-6.142	10.75	1528	-0.571	1.0000
##	Dagl - Soca	3.194	6.72	1526	0.475	1.0000
##	Dagl - Taof	25.796	8.55	1537	3.017	0.2541
##	Dagl - Trsp	-7.314	8.43	1531	-0.868	1.0000
##	Dagl - Vear	34.360	14.05	1537	2.446	0.6739
##	Elre - Eugr	-66.384	7.58	1539	-8.761	<.0001
##	Elre - Hisp	22.225	7.24	1527	3.070	0.2248
##	Elre - Hype	-0.456	8.70	1539	-0.052	1.0000
##	Elre - Phpr	5.885	6.40	1517	0.920	1.0000
##	Elre - Pore	18.622	6.91	1527	2.695	0.4779

##	Elre - Posp	25.597	6.27	1516	4.084	0.0087
##	Elre - Rusp	-2.579	10.48	1531	-0.246	1.0000
##	Elre - Soca	6.758	6.27	1516	1.078	1.0000
##	Elre - Taof	29.360	8.22	1536	3.572	0.0547
##	Elre - Trsp	-3.750	8.09	1529	-0.464	1.0000
##	Elre - Vear	37.923	13.86	1539	2.737	0.4454
##	Eugr - Hisp	88.609	8.10	1539	10.944	<.0001
##	Eugr - Hype	65.928	9.44	1539	6.984	<.0001
##	Eugr - Phpr	72.269	7.38	1538	9.792	<.0001
##	Eugr - Pore	85.006	7.82	1539	10.868	<.0001
##	Eugr - Posp	91.981	7.27	1539	12.646	<.0001
##	Eugr - Rusp	63.805	11.08	1537	5.758	<.0001
##	Eugr - Soca	73.142	7.27	1539	10.056	<.0001
##	Eugr - Taof	95.744	8.96	1537	10.681	<.0001
##	Eugr - Trsp	62.634	8.85	1536	7.080	<.0001
##	Eugr - Vear	104.307	14.29	1537	7.300	<.0001
##	Hisp - Hype	-22.681	9.16	1540	-2.476	0.6509
##	Hisp - Phpr	-16.340	7.02	1527	-2.328	0.7595
##	Hisp - Pore	-3.603	7.44	1522	-0.484	1.0000
##	Hisp - Posp	3.372	6.90	1524	0.489	1.0000
##	Hisp - Rusp	-24.804	10.88	1515	-2.279	0.7914
##	Hisp - Soca	-15.467	6.90	1524	-2.243	0.8140
##	Hisp - Taof	7.135	8.65	1535	0.825	1.0000
##	Hisp - Trsp	-25.975	8.50	1523	-3.057	0.2316
##	Hisp - Vear	15.698	14.06	1536	1.116	1.0000
##	Hype - Phpr	6.340	8.53	1540	0.744	1.0000
##	Hype - Pore	19.078	8.91	1539	2.140	0.8700
##	Hype - Posp	26.053	8.43	1540	3.089	0.2146
##	Hype - Rusp	-2.123	11.91	1521	-0.178	1.0000
##	Hype - Soca	7.213	8.43	1540	0.855	1.0000
##	Hype - Taof	29.815	9.95	1539	2.996	0.2669
##	Hype - Trsp	-3.294	9.83	1539	-0.335	1.0000
##	Hype - Vear	38.379	14.91	1536	2.575	0.5733
##	Phpr - Pore	12.737	6.67	1525	1.909	0.9539
##	Phpr - Posp	19.712	6.03	1515	3.271	0.1346
##	Phpr - Rusp	-8.463	10.34	1527	-0.818	1.0000
##	Phpr - Soca	0.873	6.03	1515	0.145	1.0000
##	Phpr - Taof	23.475	8.02	1538	2.927	0.3095
##	Phpr - Trsp	-9.635	7.87	1529	-1.223	0.9999
##	Phpr - Vear	32.038	13.71	1537	2.337	0.7535
##	Pore - Posp	6.975	6.55	1526	1.064	1.0000
##	Pore - Rusp	-21.201	10.65	1524	-1.991	0.9307
##	Pore - Soca	-11.864	6.55	1526	-1.810	0.9735
##	Pore - Taof	10.738	8.40	1537	1.279	0.9997
##	Pore - Trsp	-22.372	8.26	1527	-2.708	0.4680
##	Pore - Vear	19.301	13.93	1536	1.386	0.9991
##	Posp - Rusp	-28.176	10.27	1523	-2.744	0.4402
##	Posp - Soca	-18.839	5.89	1513	-3.198	0.1634
##	Posp - Taof	3.763	7.92	1538	0.475	1.0000
##	Posp - Trsp	-29.347	7.77	1528	-3.776	0.0274
##	Posp - Vear	12.326	13.65	1538	0.903	1.0000
##	Rusp - Soca	9.337	10.27	1523	0.909	1.0000
##	Rusp - Taof	31.939	11.50	1539	2.777	0.4153
##	Rusp - Trsp	-1.171	11.45	1534	-0.102	1.0000

```
## Rusp - Vear    40.502 16.03 1539    2.526 0.6121
## Soca - Taof    22.602  7.92 1538    2.855 0.3585
## Soca - Trsp   -10.508  7.77 1528   -1.352 0.9994
## Soca - Vear    31.165 13.65 1538    2.282 0.7895
## Taof - Trsp   -33.110  9.34 1536   -3.546 0.0595
## Taof - Vear     8.563 14.58 1538    0.587 1.0000
## Trsp - Vear    41.673 14.47 1534    2.881 0.3406
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 22 estimates
# using model 7a for overall species - level greenup model #

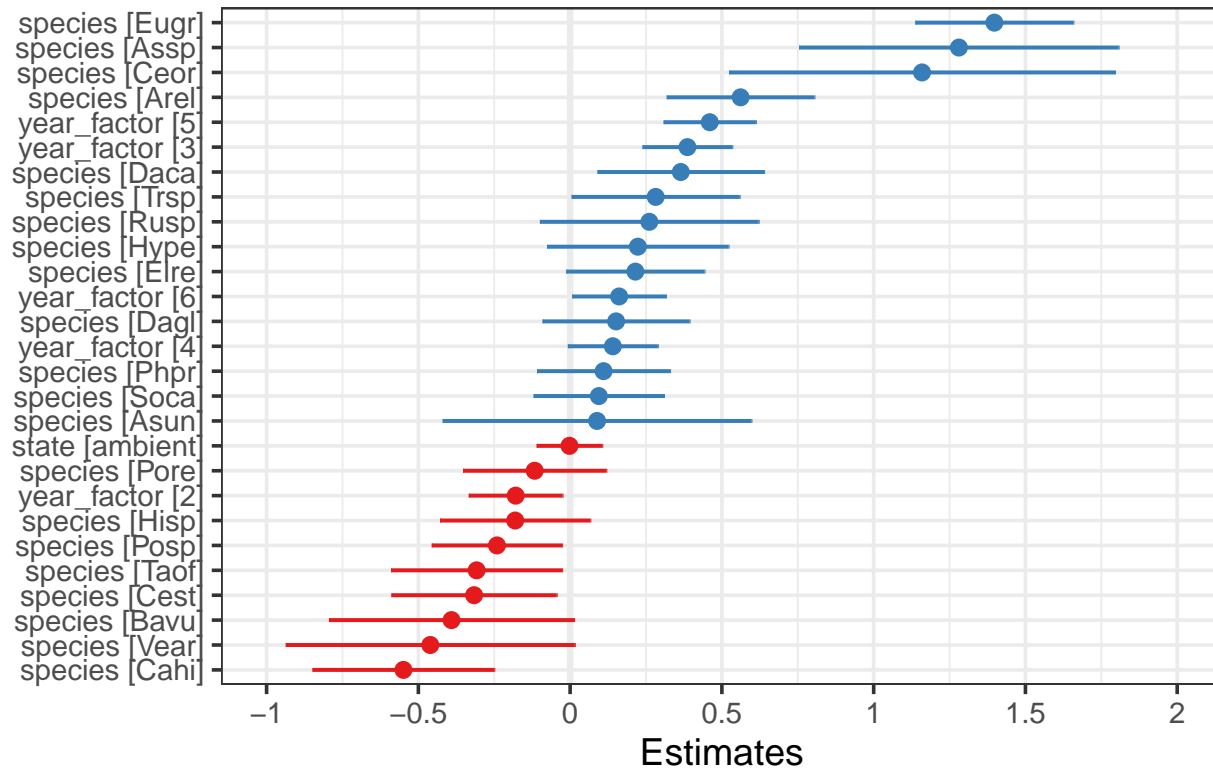
# Take a look at the estimates for each fixed effect. These
# are the estimates from summary(mod7a). You'll see that
# species vary a lot - and many of them are different from
# zero (meaning their half cover date is significantly
# different from zero).
plot_model(mod7a, sort.est = TRUE)
```

spp_half_cover_date



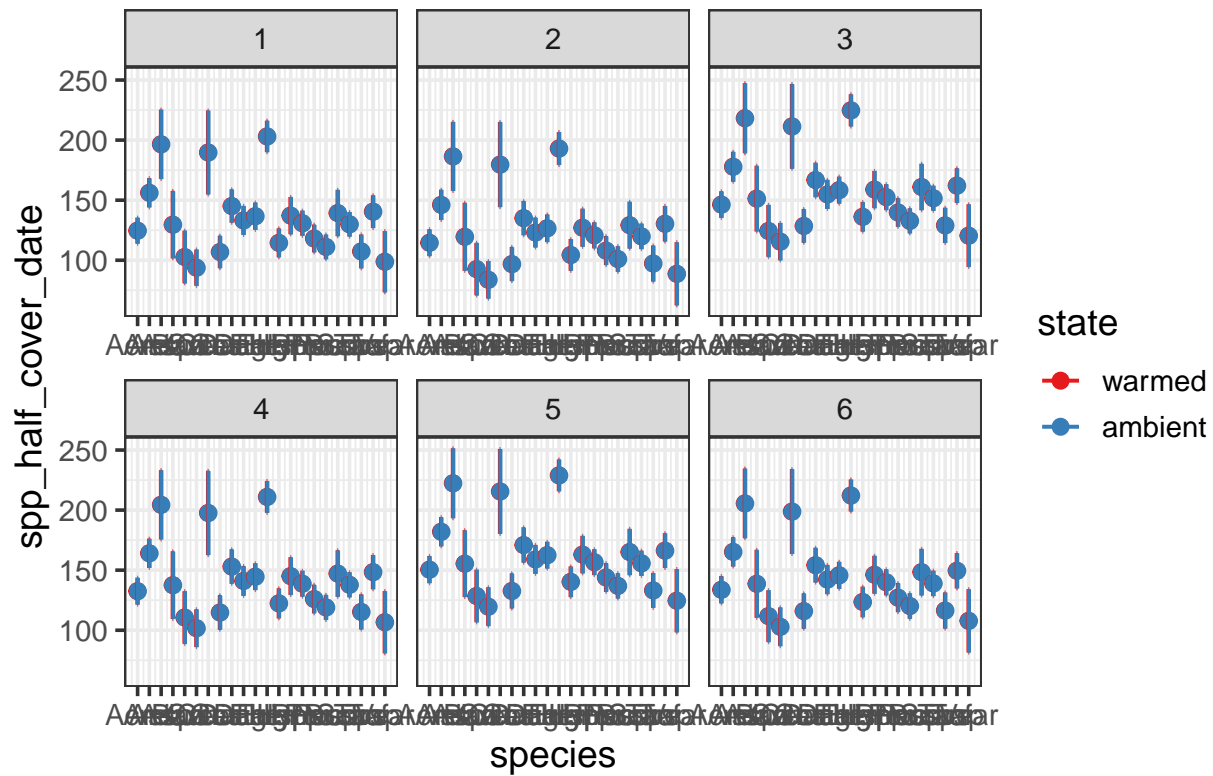
```
# if you want to standardize the estimates:
plot_model(mod7a, sort.est = TRUE, type = "std")
```

spp_half_cover_date



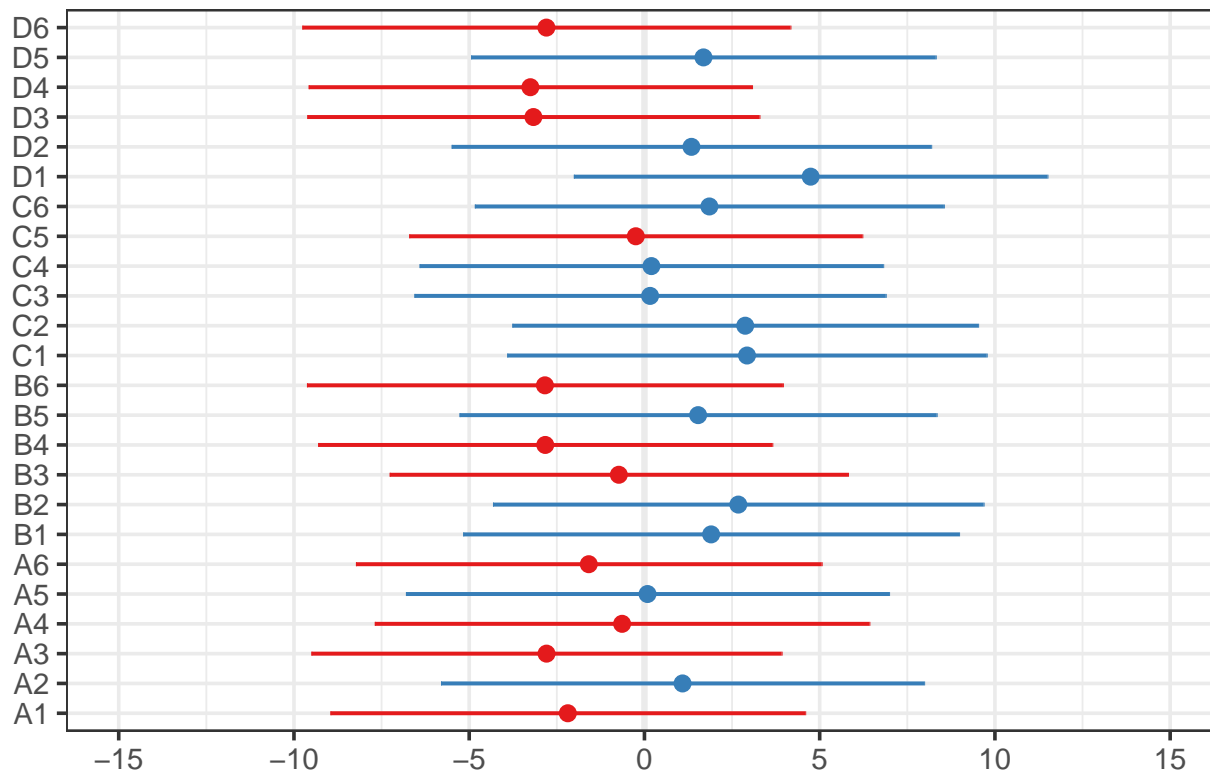
```
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7a, type = "pred", terms = c("species", "state",
      "year_factor"))
```

Predicted values of spp_half_cover_date



```
# these are the random effects estimates
plot_model(mod7a, type = "re")
```

Random effects



```
# Start KD models - listed out possible models all at once,
# then compared (some of these are duplicates of models
# above): KD: I did this just to sort out (in my mind) model
# formulation with diff combos of effects - not the best
# method here also, note all random effects are plot - I have
# diff models in plot-level section below
mod_kd1 <- lmer(spp_half_cover_date ~ state + (1 | plot), green_kbs,
  REML = FALSE)
mod_kd2 <- lmer(spp_half_cover_date ~ state + (1 | year_factor),
  green_kbs, REML = FALSE)
mod_kd3 <- lmer(spp_half_cover_date ~ state + (1 + year_factor |
  plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.1e+00
```

```
mod_kd4 <- lmer(spp_half_cover_date ~ state + year_factor + (1 |
  plot), green_kbs, REML = FALSE)
mod_kd4 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |
  plot), green_kbs, REML = FALSE)
mod_kd5 <- lmer(spp_half_cover_date ~ state + species + (1 |
  plot), green_kbs, REML = FALSE)
mod_kd6 <- lmer(spp_half_cover_date ~ state * species + (1 |
  plot), green_kbs, REML = FALSE)
mod_kd7 <- lmer(spp_half_cover_date ~ state + insecticide + (1 |
  plot), green_kbs, REML = FALSE)
mod_kd8 <- lmer(spp_half_cover_date ~ state * insecticide + (1 |
  plot), green_kbs, REML = FALSE)
```

```

mod_kd9 <- lmer(spp_half_cover_date ~ state + insecticide + species +
  (1 | plot), green_kbs, REML = FALSE)
mod_kd10 <- lmer(spp_half_cover_date ~ state + insecticide +
  year_factor + (1 | plot), green_kbs, REML = FALSE)
mod_kd11 <- lmer(spp_half_cover_date ~ state + year_factor +
  species + (1 | plot), green_kbs, REML = FALSE)
mod_kd12 <- lmer(spp_half_cover_date ~ state + year_factor +
  species + insecticide + (1 | plot), green_kbs, REML = FALSE)
mod_kd13 <- lmer(spp_half_cover_date ~ insecticide + (1 | plot),
  green_kbs, REML = FALSE)
AICctab(mod_kd1, mod_kd2, mod_kd3, mod_kd4, mod_kd5, mod_kd6,
  mod_kd7, mod_kd8, mod_kd9, mod_kd10, mod_kd11, mod_kd12,
  mod_kd13, weights = T)

##           dAICc df weight
## mod_kd11    0.0 30 0.74
## mod_kd12    2.1 31 0.26
## mod_kd5     72.2 25 <0.001
## mod_kd9     74.2 26 <0.001
## mod_kd6     95.3 46 <0.001
## mod_kd10   248.3 10 <0.001
## mod_kd4    251.2 14 <0.001
## mod_kd2    259.5  4 <0.001
## mod_kd3    311.3 24 <0.001
## mod_kd13   323.9  4 <0.001
## mod_kd1    323.9  4 <0.001
## mod_kd7    325.9  5 <0.001
## mod_kd8    327.9  6 <0.001

summary(mod_kd11) # same as model 7a - confirm this model as the best

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + species + (1 | plot)
## Data: green_kbs
##
##           AIC          BIC    logLik deviance df.resid
## 16141.1    16300.8   -8040.6   16081.1      1481
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1580 -0.6793 -0.2178  0.4667  3.1466
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## plot     (Intercept)         16.91    4.112
## Residual                    2438.42   49.380
## Number of obs: 1511, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  124.6679    5.5355   658.1208  22.522 < 2e-16 ***
## stateambient  -0.1218    3.0925    23.4606  -0.039 0.968910
## year_factor2 -10.0690    4.4226  1495.7614  -2.277 0.022943 *
```



```

## year_factor3    21.6909      4.2345 1498.3063    5.122 3.41e-07 ***
## year_factor4     7.9005      4.2476 1503.0642    1.860 0.063082 .
## year_factor5    25.8202      4.3513 1503.1515    5.934 3.67e-09 ***
## year_factor6     9.0605      4.4186 1507.1045    2.051 0.040484 *
## speciesArel     31.5237      6.9674 1502.0715    4.524 6.53e-06 ***
## speciesAssp     71.8944     15.0713 1504.7956    4.770 2.02e-06 ***
## speciesAsun      4.9822     14.5648 1497.4397    0.342 0.732343
## speciesBavu    -21.9349     11.5623 1510.9007   -1.897 0.058004 .
## speciesCahi    -30.8244      8.5743 1502.0958   -3.595 0.000335 ***
## speciesCeor     65.0746     18.2061 1473.6005    3.574 0.000362 ***
## speciesCest    -17.7608      7.7939 1499.7908   -2.279 0.022819 *
## speciesDaca     20.4666      7.8568 1502.9399    2.605 0.009279 **
## speciesDagl      8.5034      6.9340 1501.4392    1.226 0.220267
## speciesElre     12.0669      6.5205 1496.9446    1.851 0.064424 .
## speciesEugr     78.4509      7.4574 1509.7734   10.520 < 2e-16 ***
## speciesHisp    -10.1581      7.0897 1495.7777   -1.433 0.152123
## speciesHype     12.5225      8.5592 1510.9369    1.463 0.143660
## speciesPhpr      6.1822      6.2777 1493.4067    0.985 0.324886
## speciesPore     -6.5550      6.7603 1499.9341   -0.970 0.332387
## speciesPosp    -13.5300      6.1492 1491.2662   -2.200 0.027940 *
## speciesRusp     14.6457     10.3229 1478.7658    1.419 0.156182
## speciesSoca      5.3091      6.1492 1491.2662    0.863 0.388067
## speciesTaof    -17.2928      8.0633 1510.5669   -2.145 0.032142 *
## speciesTrsp     15.8169      7.9265 1499.7857    1.995 0.046174 *
## speciesVear    -25.8562     13.6356 1509.6798   -1.896 0.058121 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 28 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

# including native vs. exotic just swapped species out for
# origin, using the same model forms as above for species
green_kbs <- within(green_kbs, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
mod8 <- lmer(spp_half_cover_date ~ state * origin + (1 + year_factor |
  plot), green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 2 negative eigenvalues: -1.7e-02 -1.0e+00
mod9 <- lmer(spp_half_cover_date ~ state + origin + (1 + year_factor |
  plot), green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 2 negative eigenvalues: -3.7e-02 -3.1e+00
mod9a <- lmer(spp_half_cover_date ~ state + origin + factor(year_factor) +
  (1 | plot), green_kbs, REML = FALSE)
mod9b <- lmer(spp_half_cover_date ~ state + origin + insecticide +
  factor(year_factor) + (1 | plot), green_kbs, REML = FALSE)
anova(mod8, mod9) # model 9 is a better fit to data

## Data: green_kbs

```

```

## Models:
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## mod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9   27 16421 16564 -8183.3    16367
## mod8   30 16424 16583 -8181.8    16364 2.9482  3    0.3997

anova(mod9, mod9a) # mod 9a

## Data: green_kbs
## Models:
## mod9a: spp_half_cover_date ~ state + origin + factor(year_factor) +
## mod9a:      (1 | plot)
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9a   12 16357 16421 -8166.4    16333
## mod9    27 16421 16564 -8183.3    16367    0 15          1

anova(mod9a, mod9b) # mod 9a

## Data: green_kbs
## Models:
## mod9a: spp_half_cover_date ~ state + origin + factor(year_factor) +
## mod9a:      (1 | plot)
## mod9b: spp_half_cover_date ~ state + origin + insecticide + factor(year_factor) +
## mod9b:      (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9a   12 16357 16421 -8166.4    16333
## mod9b   13 16359 16428 -8166.3    16333 0.2202  1    0.6389

summary(mod9a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + factor(year_factor) +
##      (1 | plot)
## Data: green_kbs
##
##      AIC      BIC  logLik deviance df.resid
## 16356.8 16420.7 -8166.4 16332.8      1499
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7493 -0.7254 -0.3268  0.8091  2.7626
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## plot     (Intercept)         11.86    3.444
## Residual                    2886.39  53.725
## Number of obs: 1511, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   140.3973    4.4045 332.1637  31.876 < 2e-16 ***
## stateambient    -0.2628    3.1160  23.7557  -0.084 0.933483
## origin        -30.9606    5.2195 1493.6401  -5.932 3.72e-09 ***

```

```

## originBoth          -11.3637      4.9735 1509.7461 -2.285 0.022459 *
## originExotic         -15.2916      3.4880 1503.3942 -4.384 1.25e-05 ***
## factor(year_factor)2  -8.4820      4.7478 1497.7707 -1.786 0.074221 .
## factor(year_factor)3  22.4346      4.5361 1498.9553  4.946 8.44e-07 ***
## factor(year_factor)4  12.3891      4.5725 1502.6179  2.710 0.006815 **
## factor(year_factor)5  32.5549      4.6117 1500.3453  7.059 2.55e-12 ***
## factor(year_factor)6  15.8772      4.6777 1506.5918  3.394 0.000706 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn origin orgnBt orgnEx fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.352
## origin      -0.366 -0.002
## originBoth  -0.438 -0.023  0.334
## originExotc -0.577 -0.013  0.478  0.505
## fcctr(yr_f)2 -0.461 -0.009 -0.009  0.097  0.016
## fcctr(yr_f)3 -0.470 -0.006 -0.031  0.042  0.016  0.433
## fcctr(yr_f)4 -0.463 -0.021 -0.009  0.031  0.021  0.428  0.447
## fcctr(yr_f)5 -0.466 -0.015 -0.019  0.062  0.019  0.428  0.445  0.440
## fcctr(yr_f)6 -0.462 -0.010 -0.005  0.057  0.019  0.421  0.437  0.433  0.432
anova(mod9)

## Type III Analysis of Variance Table with Satterthwaite's method
##      Sum Sq Mean Sq NumDF    DenDF F value    Pr(>F)
## state    3019    3019      1    42.21  1.056    0.31
## origin 110931   36977      3   1470.01 12.934 2.43e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
emmeans(mod9a, list(pairwise ~ state + origin), adjust = "tukey")

## Warning in model.frame.default(formula, data = data, ...): variable
## 'year_factor' is not a factor

## $`emmeans of state, origin`
##   state   origin emmean    SE    df lower.CL upper.CL
## warmed Native    153 3.50 142.6    146    160
## ambient Native    153 3.47 143.4    146    159
## warmed          122 4.71 421.6    113    131
## ambient          122 4.67 426.4    112    131
## warmed Both     141 4.49 324.2    133    150
## ambient Both     141 4.38 310.6    133    150
## warmed Exotic   138 2.68  47.8    132    143
## ambient Exotic   137 2.57  41.7    132    143
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`
##   1 estimate    SE    df t.ratio p.value
## warmed Native - ambient Native    0.263 3.26   25.9  0.081  1.0000
## warmed Native - warmed          30.961 5.23 1501.6  5.914 <.0001
## warmed Native - ambient          31.223 6.17  325.2  5.065 <.0001

```

```
## warmed Native - warmed Both      11.364 4.99 1519.0  2.275  0.3080
## warmed Native - ambient Both      11.627 5.91  268.8  1.969  0.5052
## warmed Native - warmed Exotic     15.292 3.50 1511.8  4.369  0.0004
## warmed Native - ambient Exotic    15.554 4.76  121.8  3.270  0.0295
## ambient Native - warmed           30.698 6.17  328.4  4.972 <.0001
## ambient Native - ambient          30.961 5.23 1501.6  5.914 <.0001
## ambient Native - warmed Both      11.101 6.03  287.7  1.842  0.5920
## ambient Native - ambient Both      11.364 4.99 1519.0  2.275  0.3080
## ambient Native - warmed Exotic     15.029 4.82  130.2  3.121  0.0447
## ambient Native - ambient Exotic    15.292 3.50 1511.8  4.369  0.0004
## warmed - ambient                  0.263 3.26   25.9  0.081  1.0000
## warmed - warmed Both             -19.597 5.91 1517.6 -3.316  0.0209
## warmed - ambient Both             -19.334 6.70  409.8 -2.885  0.0783
## warmed - warmed Exotic           -15.669 4.71 1505.7 -3.329  0.0201
## warmed - ambient Exotic           -15.406 5.71  245.7 -2.699  0.1280
## ambient - warmed Both             -19.860 6.80  425.9 -2.920  0.0711
## ambient - ambient Both            -19.597 5.91 1517.6 -3.316  0.0209
## ambient - warmed Exotic           -15.932 5.75  254.7 -2.772  0.1069
## ambient - ambient Exotic          -15.669 4.71 1505.7 -3.329  0.0201
## warmed Both - ambient Both         0.263 3.26   25.9  0.081  1.0000
## warmed Both - warmed Exotic        3.928 4.42 1517.0  0.888  0.9871
## warmed Both - ambient Exotic       4.191 5.54  213.5  0.757  0.9950
## ambient Both - warmed Exotic       3.665 5.46  206.4  0.672  0.9976
## ambient Both - ambient Exotic      3.928 4.42 1517.0  0.888  0.9871
## warmed Exotic - ambient Exotic     0.263 3.26   25.9  0.081  1.0000
##
```

```
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

```
# including growth form - first with interaction term
green_kbs <- within(green_kbs, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
mod10 <- lmer(spp_half_cover_date ~ state * growth_habit + (1 +
  year_factor | plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 2 negative eigenvalues: -8.7e-02 -1.3e-01
```

```
mod11 <- lmer(spp_half_cover_date ~ state + growth_habit + (1 +
  year_factor | plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.0e+00
```

```
mod11a <- lmer(spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
  (1 | plot), green_kbs, REML = FALSE)
mod11b <- lmer(spp_half_cover_date ~ state + growth_habit + insecticide +
  factor(year_factor) + (1 | plot), green_kbs, REML = FALSE)
anova(mod10, mod11) # model 11 is a better fit to data
```

```
## Data: green_kbs
```

```
## Models:
```

```
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11: plot)
```

```

## mod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## mod10:      plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11  27 16450 16593 -8197.9    16396
## mod10  30 16454 16614 -8197.0    16394 1.7173  3    0.6331
anova(mod11, mod11a) # model 11a

## Data: green_kbs
## Models:
## mod11a: spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
## mod11a:      (1 | plot)
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11:      plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11a  12 16384 16448 -8180.1    16360
## mod11   27 16450 16593 -8197.9    16396    0 15      1
anova(mod11a, mod11b) # model 11a

## Data: green_kbs
## Models:
## mod11a: spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
## mod11a:      (1 | plot)
## mod11b: spp_half_cover_date ~ state + growth_habit + insecticide + factor(year_factor) +
## mod11b:      (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11a  12 16384 16448 -8180.1    16360
## mod11b  13 16386 16455 -8179.8    16360 0.4348  1    0.5096
summary(mod11a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
##      (1 | plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 16384.1 16448.0 -8180.1 16360.1      1499
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6850 -0.7388 -0.3369  0.7388  2.5016
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## plot     (Intercept)         3.749    1.936
## Residual                    2946.114  54.278
## Number of obs: 1511, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   127.2983     3.6569  215.2995  34.811 < 2e-16 ***
## stateambient    -0.5924     2.9167   23.4387  -0.203  0.840797
## growth_habit   -2.1183     4.4885 1505.1769  -0.472  0.637038

```

```
## growth_habitGraminoid    0.7180    3.0515 1510.8513    0.235 0.814020
## growth_habitVine         62.9345    19.3561 1421.6557    3.251 0.001175 **
## factor(year_factor)2     -8.6078    4.8090 1497.5236   -1.790 0.073668 .
## factor(year_factor)3     21.9800    4.5792 1500.4925    4.800 1.74e-06 ***
## factor(year_factor)4     12.1910    4.6253 1505.2357    2.636 0.008482 **
## factor(year_factor)5     32.2552    4.6818 1503.5078    6.889 8.21e-12 ***
## factor(year_factor)6     15.7438    4.7531 1509.5846    3.312 0.000947 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_V fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.409
## growth_habt -0.255 -0.030
## grwth_hbtGr -0.291  0.029  0.284
## grwth_hbtVn -0.062 -0.030  0.051  0.064
## fcctr(yr_f)2 -0.539 -0.015  0.099 -0.048  0.039
## fcctr(yr_f)3 -0.546 -0.007 -0.005 -0.051  0.020  0.431
## fcctr(yr_f)4 -0.532 -0.025  0.008 -0.065  0.003  0.429  0.447
## fcctr(yr_f)5 -0.518 -0.021  0.013 -0.115  0.017  0.429  0.445  0.443
## fcctr(yr_f)6 -0.515 -0.015  0.026 -0.113  0.016  0.424  0.438  0.437  0.438
```

```
anova(mod11a)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF    DenDF F value    Pr(>F)
## state              122      122      1    23.44  0.0413 0.84080
## growth_habit       32481   10827      3 1477.69  3.6750 0.01179 *
## factor(year_factor) 264166   52833      5 1502.21 17.9332 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod11a, list(pairwise ~ year_factor + growth_habit),
  adjust = "tukey")
```

```
## Warning in model.frame.default(formula, data = data, ...): variable
## 'year_factor' is not a factor
```

```
## $`emmeans of year_factor, growth_habit`
##   year_factor growth_habit emmean    SE    df lower.CL upper.CL
## 1          Forb           127  3.38  543      120      134
## 2          Forb           118  3.93  753      111      126
## 3          Forb           149  3.75  661      142      156
## 4          Forb           139  3.81  672      132      147
## 5          Forb           159  3.92  737      152      167
## 6          Forb           143  4.00  720      135      151
## 1          125  4.78 1082      116      134
## 2          116  5.58 1255      105      127
## 3          147  5.03 1128      137      157
## 4          137  5.13 1123      127      147
## 5          157  5.23 1155      147      167
## 6          141  5.34 1178      130      151
## 1          Graminoid       128  3.81  714      120      135
## 2          Graminoid       119  4.13  850      111      127
## 3          Graminoid       150  3.96  798      142      157
## 4          Graminoid       140  3.96  805      132      148
```

```

## 5      Graminoid      160  3.89  774      152      168
## 6      Graminoid      143  3.97  775      136      151
## 1      Vine          190 19.54 1420      152      228
## 2      Vine          181 19.81 1444      142      220
## 3      Vine          212 19.69 1435      173      251
## 4      Vine          202 19.63 1432      164      241
## 5      Vine          222 19.72 1422      184      261
## 6      Vine          206 19.72 1431      167      244
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor, growth_habit`
## 1      estimate      SE      df t.ratio p.value
## 1 Forb - 2 Forb      8.608  4.82 1506   1.784 0.9851
## 1 Forb - 3 Forb     -21.980  4.59 1509  -4.784 0.0005
## 1 Forb - 4 Forb     -12.191  4.64 1514  -2.626 0.05761
## 1 Forb - 5 Forb     -32.255  4.70 1512  -6.865 <.0001
## 1 Forb - 6 Forb     -15.744  4.77 1519  -3.298 0.01420
## 1 Forb - 1          2.118  4.50 1514   0.470 1.0000
## 1 Forb - 2          10.726  6.92 1509   1.550 0.09977
## 1 Forb - 3         -19.862  6.42 1509  -3.095 0.02382
## 1 Forb - 4         -10.073  6.49 1514  -1.551 0.09977
## 1 Forb - 5         -30.137  6.55 1515  -4.600 0.0011
## 1 Forb - 6         -13.626  6.65 1514  -2.050 0.09315
## 1 Forb - 1 Graminoid  -0.718  3.07 1521  -0.234 1.0000
## 1 Forb - 2 Graminoid   7.890  5.59 1508   1.411 0.09994
## 1 Forb - 3 Graminoid  -22.698  5.39 1504  -4.214 0.0060
## 1 Forb - 4 Graminoid  -12.909  5.39 1504  -2.396 0.07525
## 1 Forb - 5 Graminoid  -32.973  5.30 1506  -6.216 <.0001
## 1 Forb - 6 Graminoid  -16.462  5.37 1510  -3.066 0.02550
## 1 Forb - 1 Vine     -62.934 19.52 1444  -3.224 0.01732
## 1 Forb - 2 Vine     -54.327 20.28 1473  -2.679 0.05335
## 1 Forb - 3 Vine     -84.914 20.14 1466  -4.217 0.0060
## 1 Forb - 4 Vine     -75.126 20.07 1464  -3.743 0.0359
## 1 Forb - 5 Vine     -95.190 20.15 1455  -4.723 0.0006
## 1 Forb - 6 Vine     -78.678 20.16 1462  -3.902 0.0203
## 2 Forb - 3 Forb     -30.588  5.03 1505  -6.084 <.0001
## 2 Forb - 4 Forb     -20.799  5.06 1508  -4.110 0.0092
## 2 Forb - 5 Forb     -40.863  5.09 1508  -8.029 <.0001
## 2 Forb - 6 Forb     -24.352  5.15 1518  -4.725 0.0006
## 2 Forb - 1         -6.490  6.27 1510  -1.036 1.0000
## 2 Forb - 2          2.118  4.50 1514   0.470 1.0000
## 2 Forb - 3        -28.470  6.41 1507  -4.444 0.0023
## 2 Forb - 4        -18.681  6.48 1512  -2.884 0.03746
## 2 Forb - 5        -38.745  6.52 1513  -5.946 <.0001
## 2 Forb - 6        -22.233  6.61 1515  -3.365 0.01179
## 2 Forb - 1 Graminoid  -9.326  5.84 1517  -1.597 0.09965
## 2 Forb - 2 Graminoid  -0.718  3.07 1521  -0.234 1.0000
## 2 Forb - 3 Graminoid -31.306  5.88 1507  -5.321 <.0001
## 2 Forb - 4 Graminoid -21.517  5.88 1506  -3.662 0.0471
## 2 Forb - 5 Graminoid -41.581  5.78 1509  -7.196 <.0001
## 2 Forb - 6 Graminoid -25.070  5.83 1515  -4.297 0.0043

```

##	2	Forb	-	1	Vine	-71.542	19.93	1435	-3.589	0.0599
##	2	Forb	-	2	Vine	-62.934	19.52	1444	-3.224	0.1732
##	2	Forb	-	3	Vine	-93.522	20.07	1450	-4.660	0.0009
##	2	Forb	-	4	Vine	-83.733	20.00	1448	-4.186	0.0068
##	2	Forb	-	5	Vine	-103.797	20.08	1437	-5.170	0.0001
##	2	Forb	-	6	Vine	-87.286	20.08	1445	-4.346	0.0035
##	3	Forb	-	4	Forb	9.789	4.85	1507	2.016	0.9419
##	3	Forb	-	5	Forb	-10.275	4.90	1510	-2.098	0.9145
##	3	Forb	-	6	Forb	6.236	4.97	1516	1.255	0.9999
##	3	Forb	-	1		24.098	6.45	1513	3.735	0.0368
##	3	Forb	-	2		32.706	7.08	1511	4.621	0.0010
##	3	Forb	-	3		2.118	4.50	1514	0.470	1.0000
##	3	Forb	-	4		11.907	6.67	1513	1.786	0.9849
##	3	Forb	-	5		-8.157	6.71	1515	-1.215	1.0000
##	3	Forb	-	6		8.354	6.80	1514	1.228	0.9999
##	3	Forb	-	1	Graminoid	21.262	5.66	1520	3.759	0.0339
##	3	Forb	-	2	Graminoid	29.870	5.89	1516	5.068	0.0001
##	3	Forb	-	3	Graminoid	-0.718	3.07	1521	-0.234	1.0000
##	3	Forb	-	4	Graminoid	9.071	5.70	1511	1.590	0.9967
##	3	Forb	-	5	Graminoid	-10.993	5.62	1515	-1.958	0.9571
##	3	Forb	-	6	Graminoid	5.518	5.68	1517	0.972	1.0000
##	3	Forb	-	1	Vine	-40.955	19.97	1441	-2.051	0.9312
##	3	Forb	-	2	Vine	-32.347	20.24	1463	-1.598	0.9965
##	3	Forb	-	3	Vine	-62.934	19.52	1444	-3.224	0.1732
##	3	Forb	-	4	Vine	-53.146	20.04	1454	-2.652	0.5551
##	3	Forb	-	5	Vine	-73.210	20.12	1443	-3.639	0.0508
##	3	Forb	-	6	Vine	-56.698	20.12	1451	-2.817	0.4245
##	4	Forb	-	5	Forb	-20.064	4.93	1501	-4.073	0.0106
##	4	Forb	-	6	Forb	-3.553	5.00	1512	-0.711	1.0000
##	4	Forb	-	1		14.309	6.44	1513	2.221	0.8594
##	4	Forb	-	2		22.917	7.06	1509	3.245	0.1638
##	4	Forb	-	3		-7.671	6.58	1507	-1.166	1.0000
##	4	Forb	-	4		2.118	4.50	1514	0.470	1.0000
##	4	Forb	-	5		-17.946	6.69	1509	-2.682	0.5313
##	4	Forb	-	6		-1.435	6.78	1509	-0.211	1.0000
##	4	Forb	-	1	Graminoid	11.473	5.73	1521	2.001	0.9461
##	4	Forb	-	2	Graminoid	20.081	5.96	1519	3.370	0.1162
##	4	Forb	-	3	Graminoid	-10.507	5.78	1516	-1.818	0.9813
##	4	Forb	-	4	Graminoid	-0.718	3.07	1521	-0.234	1.0000
##	4	Forb	-	5	Graminoid	-20.782	5.68	1513	-3.660	0.0474
##	4	Forb	-	6	Graminoid	-4.271	5.74	1516	-0.744	1.0000
##	4	Forb	-	1	Vine	-50.743	20.05	1443	-2.530	0.6524
##	4	Forb	-	2	Vine	-42.136	20.33	1464	-2.073	0.9238
##	4	Forb	-	3	Vine	-72.723	20.19	1457	-3.602	0.0574
##	4	Forb	-	4	Vine	-62.934	19.52	1444	-3.224	0.1732
##	4	Forb	-	5	Vine	-82.999	20.20	1447	-4.109	0.0092
##	4	Forb	-	6	Vine	-66.487	20.21	1454	-3.290	0.1454
##	5	Forb	-	6	Forb	16.511	5.02	1512	3.290	0.1453
##	5	Forb	-	1		34.373	6.47	1511	5.316	<.0001
##	5	Forb	-	2		42.981	7.07	1509	6.082	<.0001
##	5	Forb	-	3		12.393	6.59	1508	1.879	0.9726
##	5	Forb	-	4		22.182	6.66	1506	3.331	0.1299
##	5	Forb	-	5		2.118	4.50	1514	0.470	1.0000
##	5	Forb	-	6		18.630	6.78	1508	2.747	0.4796

##	5	Forb - 1	Graminoid	31.537	5.90	1521	5.345	<.0001
##	5	Forb - 2	Graminoid	40.145	6.10	1518	6.581	<.0001
##	5	Forb - 3	Graminoid	9.557	5.94	1515	1.610	0.9961
##	5	Forb - 4	Graminoid	19.346	5.92	1508	3.266	0.1552
##	5	Forb - 5	Graminoid	-0.718	3.07	1521	-0.234	1.0000
##	5	Forb - 6	Graminoid	15.793	5.88	1514	2.686	0.5278
##	5	Forb - 1	Vine	-30.679	20.00	1453	-1.534	0.9980
##	5	Forb - 2	Vine	-22.071	20.27	1473	-1.089	1.0000
##	5	Forb - 3	Vine	-52.659	20.13	1466	-2.616	0.5846
##	5	Forb - 4	Vine	-42.870	20.06	1466	-2.137	0.8991
##	5	Forb - 5	Vine	-62.934	19.52	1444	-3.224	0.1732
##	5	Forb - 6	Vine	-46.423	20.14	1464	-2.304	0.8122
##	6	Forb - 1		17.862	6.48	1519	2.757	0.4716
##	6	Forb - 2		26.470	7.08	1518	3.741	0.0361
##	6	Forb - 3		-4.118	6.61	1516	-0.623	1.0000
##	6	Forb - 4		5.671	6.67	1516	0.850	1.0000
##	6	Forb - 5		-14.393	6.70	1517	-2.147	0.8948
##	6	Forb - 6		2.118	4.50	1514	0.470	1.0000
##	6	Forb - 1	Graminoid	15.026	5.96	1521	2.521	0.6600
##	6	Forb - 2	Graminoid	23.634	6.16	1521	3.840	0.0255
##	6	Forb - 3	Graminoid	-6.954	6.00	1520	-1.160	1.0000
##	6	Forb - 4	Graminoid	2.835	5.98	1516	0.474	1.0000
##	6	Forb - 5	Graminoid	-17.229	5.88	1518	-2.929	0.3428
##	6	Forb - 6	Graminoid	-0.718	3.07	1521	-0.234	1.0000
##	6	Forb - 1	Vine	-47.191	20.03	1444	-2.356	0.7791
##	6	Forb - 2	Vine	-38.583	20.29	1464	-1.902	0.9688
##	6	Forb - 3	Vine	-69.171	20.16	1458	-3.431	0.0974
##	6	Forb - 4	Vine	-59.382	20.09	1457	-2.956	0.3245
##	6	Forb - 5	Vine	-79.446	20.16	1447	-3.940	0.0177
##	6	Forb - 6	Vine	-62.934	19.52	1444	-3.224	0.1732
##	1	- 2		8.608	4.82	1506	1.784	0.9851
##	1	- 3		-21.980	4.59	1509	-4.784	0.0005
##	1	- 4		-12.191	4.64	1514	-2.626	0.5761
##	1	- 5		-32.255	4.70	1512	-6.865	<.0001
##	1	- 6		-15.744	4.77	1519	-3.298	0.1420
##	1	- 1	Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	1	- 2	Graminoid	5.772	6.28	1511	0.920	1.0000
##	1	- 3	Graminoid	-24.816	6.46	1509	-3.843	0.0251
##	1	- 4	Graminoid	-15.027	6.41	1506	-2.343	0.7880
##	1	- 5	Graminoid	-35.091	6.33	1506	-5.547	<.0001
##	1	- 6	Graminoid	-18.580	6.34	1515	-2.931	0.3415
##	1	- 1	Vine	-65.053	19.80	1467	-3.286	0.1472
##	1	- 2	Vine	-56.445	20.44	1488	-2.761	0.4681
##	1	- 3	Vine	-87.033	20.42	1484	-4.263	0.0049
##	1	- 4	Vine	-77.244	20.34	1483	-3.798	0.0295
##	1	- 5	Vine	-97.308	20.41	1475	-4.767	0.0005
##	1	- 6	Vine	-80.797	20.41	1480	-3.959	0.0164
##	2	- 3		-30.588	5.03	1505	-6.084	<.0001
##	2	- 4		-20.799	5.06	1508	-4.110	0.0092
##	2	- 5		-40.863	5.09	1508	-8.029	<.0001
##	2	- 6		-24.352	5.15	1518	-4.725	0.0006
##	2	- 1	Graminoid	-11.444	7.13	1515	-1.605	0.9963
##	2	- 2	Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	2	- 3	Graminoid	-33.424	7.18	1510	-4.654	0.0009

##	2	-	4	Graminoid	-23.635	7.14	1507	-3.312	0.1369
##	2	-	5	Graminoid	-43.699	7.04	1508	-6.206	<.0001
##	2	-	6	Graminoid	-27.188	7.05	1516	-3.857	0.0239
##	2	-	1	Vine	-73.661	20.31	1461	-3.626	0.0531
##	2	-	2	Vine	-65.053	19.80	1467	-3.286	0.1472
##	2	-	3	Vine	-95.641	20.45	1472	-4.676	0.0008
##	2	-	4	Vine	-85.852	20.37	1471	-4.214	0.0060
##	2	-	5	Vine	-105.916	20.44	1462	-5.181	0.0001
##	2	-	6	Vine	-89.404	20.44	1467	-4.375	0.0031
##	3	-	4		9.789	4.85	1507	2.016	0.9419
##	3	-	5		-10.275	4.90	1510	-2.098	0.9145
##	3	-	6		6.236	4.97	1516	1.255	0.9999
##	3	-	1	Graminoid	19.144	6.65	1518	2.879	0.3785
##	3	-	2	Graminoid	27.752	6.53	1515	4.249	0.0052
##	3	-	3	Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	3	-	4	Graminoid	6.953	6.67	1509	1.043	1.0000
##	3	-	5	Graminoid	-13.111	6.57	1511	-1.995	0.9478
##	3	-	6	Graminoid	3.400	6.58	1517	0.516	1.0000
##	3	-	1	Vine	-43.073	20.24	1464	-2.129	0.9026
##	3	-	2	Vine	-34.465	20.40	1481	-1.689	0.9926
##	3	-	3	Vine	-65.053	19.80	1467	-3.286	0.1472
##	3	-	4	Vine	-55.264	20.30	1475	-2.723	0.4985
##	3	-	5	Vine	-75.328	20.37	1466	-3.698	0.0418
##	3	-	6	Vine	-58.817	20.36	1471	-2.888	0.3718
##	4	-	5		-20.064	4.93	1501	-4.073	0.0106
##	4	-	6		-3.553	5.00	1512	-0.711	1.0000
##	4	-	1	Graminoid	9.355	6.76	1521	1.385	0.9996
##	4	-	2	Graminoid	17.963	6.63	1519	2.709	0.5099
##	4	-	3	Graminoid	-12.625	6.81	1517	-1.853	0.9767
##	4	-	4	Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	4	-	5	Graminoid	-22.900	6.67	1512	-3.434	0.0966
##	4	-	6	Graminoid	-6.389	6.68	1518	-0.956	1.0000
##	4	-	1	Vine	-52.862	20.34	1465	-2.599	0.5976
##	4	-	2	Vine	-44.254	20.50	1481	-2.159	0.8895
##	4	-	3	Vine	-74.842	20.48	1476	-3.655	0.0482
##	4	-	4	Vine	-65.053	19.80	1467	-3.286	0.1472
##	4	-	5	Vine	-85.117	20.47	1468	-4.159	0.0075
##	4	-	6	Vine	-68.606	20.46	1473	-3.353	0.1221
##	5	-	6		16.511	5.02	1512	3.290	0.1453
##	5	-	1	Graminoid	29.419	6.91	1520	4.255	0.0051
##	5	-	2	Graminoid	38.027	6.78	1518	5.612	<.0001
##	5	-	3	Graminoid	7.439	6.96	1517	1.069	1.0000
##	5	-	4	Graminoid	17.228	6.91	1510	2.493	0.6812
##	5	-	5	Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	5	-	6	Graminoid	13.675	6.82	1518	2.006	0.9449
##	5	-	1	Vine	-32.798	20.29	1474	-1.617	0.9959
##	5	-	2	Vine	-24.190	20.44	1488	-1.183	1.0000
##	5	-	3	Vine	-54.778	20.42	1484	-2.682	0.5311
##	5	-	4	Vine	-44.989	20.34	1484	-2.212	0.8642
##	5	-	5	Vine	-65.053	19.80	1467	-3.286	0.1472
##	5	-	6	Vine	-48.541	20.40	1481	-2.379	0.7640
##	6	-	1	Graminoid	12.908	7.00	1521	1.843	0.9782
##	6	-	2	Graminoid	21.515	6.86	1520	3.134	0.2169
##	6	-	3	Graminoid	-9.072	7.05	1518	-1.287	0.9999

##	6	- 4 Graminoid	0.717	7.00	1513	0.102	1.0000
##	6	- 5 Graminoid	-19.348	6.90	1513	-2.805	0.4339
##	6	- 6 Graminoid	-2.836	4.67	1519	-0.607	1.0000
##	6	- 1 Vine	-49.309	20.33	1467	-2.426	0.7311
##	6	- 2 Vine	-40.701	20.48	1482	-1.987	0.9499
##	6	- 3 Vine	-71.289	20.46	1478	-3.484	0.0832
##	6	- 4 Vine	-61.500	20.38	1478	-3.018	0.2843
##	6	- 5 Vine	-81.564	20.45	1470	-3.989	0.0147
##	6	- 6 Vine	-65.053	19.80	1467	-3.286	0.1472
##	1	Graminoid - 2 Graminoid	8.608	4.82	1506	1.784	0.9851
##	1	Graminoid - 3 Graminoid	-21.980	4.59	1509	-4.784	0.0005
##	1	Graminoid - 4 Graminoid	-12.191	4.64	1514	-2.626	0.5761
##	1	Graminoid - 5 Graminoid	-32.255	4.70	1512	-6.865	<.0001
##	1	Graminoid - 6 Graminoid	-15.744	4.77	1519	-3.298	0.1420
##	1	Graminoid - 1 Vine	-62.217	19.56	1451	-3.181	0.1935
##	1	Graminoid - 2 Vine	-53.609	20.35	1478	-2.634	0.5698
##	1	Graminoid - 3 Vine	-84.197	20.21	1470	-4.165	0.0074
##	1	Graminoid - 4 Vine	-74.408	20.16	1468	-3.691	0.0428
##	1	Graminoid - 5 Vine	-94.472	20.28	1460	-4.659	0.0009
##	1	Graminoid - 6 Vine	-77.960	20.29	1467	-3.843	0.0252
##	2	Graminoid - 3 Graminoid	-30.588	5.03	1505	-6.084	<.0001
##	2	Graminoid - 4 Graminoid	-20.799	5.06	1508	-4.110	0.0092
##	2	Graminoid - 5 Graminoid	-40.863	5.09	1508	-8.029	<.0001
##	2	Graminoid - 6 Graminoid	-24.352	5.15	1518	-4.725	0.0006
##	2	Graminoid - 1 Vine	-70.824	19.94	1442	-3.552	0.0673
##	2	Graminoid - 2 Vine	-62.217	19.56	1451	-3.181	0.1935
##	2	Graminoid - 3 Vine	-92.804	20.11	1455	-4.615	0.0011
##	2	Graminoid - 4 Vine	-83.015	20.05	1453	-4.140	0.0082
##	2	Graminoid - 5 Vine	-103.080	20.16	1444	-5.112	0.0001
##	2	Graminoid - 6 Vine	-86.568	20.17	1450	-4.291	0.0044
##	3	Graminoid - 4 Graminoid	9.789	4.85	1507	2.016	0.9419
##	3	Graminoid - 5 Graminoid	-10.275	4.90	1510	-2.098	0.9145
##	3	Graminoid - 6 Graminoid	6.236	4.97	1516	1.255	0.9999
##	3	Graminoid - 1 Vine	-40.237	19.97	1449	-2.015	0.9423
##	3	Graminoid - 2 Vine	-31.629	20.28	1470	-1.560	0.9975
##	3	Graminoid - 3 Vine	-62.217	19.56	1451	-3.181	0.1935
##	3	Graminoid - 4 Vine	-52.428	20.09	1460	-2.610	0.5892
##	3	Graminoid - 5 Vine	-72.492	20.20	1451	-3.588	0.0600
##	3	Graminoid - 6 Vine	-55.980	20.21	1458	-2.770	0.4613
##	4	Graminoid - 5 Graminoid	-20.064	4.93	1501	-4.073	0.0106
##	4	Graminoid - 6 Graminoid	-3.553	5.00	1512	-0.711	1.0000
##	4	Graminoid - 1 Vine	-50.026	20.05	1451	-2.495	0.6794
##	4	Graminoid - 2 Vine	-41.418	20.35	1471	-2.035	0.9363
##	4	Graminoid - 3 Vine	-72.005	20.22	1464	-3.561	0.0654
##	4	Graminoid - 4 Vine	-62.217	19.56	1451	-3.181	0.1935
##	4	Graminoid - 5 Vine	-82.281	20.27	1454	-4.058	0.0112
##	4	Graminoid - 6 Vine	-65.769	20.28	1461	-3.243	0.1651
##	5	Graminoid - 6 Graminoid	16.511	5.02	1512	3.290	0.1453
##	5	Graminoid - 1 Vine	-29.961	19.96	1460	-1.501	0.9986
##	5	Graminoid - 2 Vine	-21.354	20.26	1479	-1.054	1.0000
##	5	Graminoid - 3 Vine	-51.941	20.13	1471	-2.581	0.6125
##	5	Graminoid - 4 Vine	-42.152	20.07	1471	-2.101	0.9137
##	5	Graminoid - 5 Vine	-62.217	19.56	1451	-3.181	0.1935
##	5	Graminoid - 6 Vine	-45.705	20.18	1469	-2.264	0.8359

```
## 6 Graminoid - 1 Vine      -46.473 19.98 1452 -2.326 0.7990
## 6 Graminoid - 2 Vine      -37.865 20.28 1471 -1.867 0.9746
## 6 Graminoid - 3 Vine      -68.453 20.15 1464 -3.397 0.1078
## 6 Graminoid - 4 Vine      -58.664 20.09 1462 -2.920 0.3495
## 6 Graminoid - 5 Vine      -78.728 20.20 1454 -3.897 0.0207
## 6 Graminoid - 6 Vine      -62.217 19.56 1451 -3.181 0.1935
## 1 Vine - 2 Vine           8.608 4.82 1506 1.784 0.9851
## 1 Vine - 3 Vine          -21.980 4.59 1509 -4.784 0.0005
## 1 Vine - 4 Vine          -12.191 4.64 1514 -2.626 0.5761
## 1 Vine - 5 Vine          -32.255 4.70 1512 -6.865 <.0001
## 1 Vine - 6 Vine          -15.744 4.77 1519 -3.298 0.1420
## 2 Vine - 3 Vine          -30.588 5.03 1505 -6.084 <.0001
## 2 Vine - 4 Vine          -20.799 5.06 1508 -4.110 0.0092
## 2 Vine - 5 Vine          -40.863 5.09 1508 -8.029 <.0001
## 2 Vine - 6 Vine          -24.352 5.15 1518 -4.725 0.0006
## 3 Vine - 4 Vine           9.789 4.85 1507 2.016 0.9419
## 3 Vine - 5 Vine          -10.275 4.90 1510 -2.098 0.9145
## 3 Vine - 6 Vine           6.236 4.97 1516 1.255 0.9999
## 4 Vine - 5 Vine          -20.064 4.93 1501 -4.073 0.0106
## 4 Vine - 6 Vine          -3.553 5.00 1512 -0.711 1.0000
## 5 Vine - 6 Vine          16.511 5.02 1512 3.290 0.1453
##
```

Results are averaged over the levels of: state

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 24 estimates

You could now run some post hoc tests on these (see:

<https://stats.stackexchange.com/questions/169543/output-of-fixed-effects-summary-in-lmertest-in-r-and>

Here are some other options for plotting these plots above:

<https://stackoverflow.com/questions/31075407/plot-mixed-effects-model-in-ggplot>

Here's another approach:

<https://stats.stackexchange.com/questions/98958/plots-to-illustrate-results-of-linear-mixed-effect-mo>

Not quite working yet: newdat <-

expand.grid(state=unique(green_kbs\$state),

year=c(min(green_kbs\$year), max(green_kbs\$year)),

insecticide=unique(green_kbs\$insecticide)) p <-

ggplot(green_kbs, aes(x=year, y=spp_half_cover_date,

colour=state, shape=insecticide)) + geom_point(size=3) +

geom_line(aes(y=predict(mod5), group=species,

size='species')) + geom_line(data=newdat,

aes(y=predict(mod5, level=0, newdata=newdat),

size='Population')) + scale_size_manual(name='Predictions',

values=c('species'=0.5, 'Population'=3)) +

#facet_wrap(~insecticide) + theme_bw(base_size=22) print(p)

KD note: these models are included below in plot-level

section New version of our model incorporating interaction

term and species within year so that there is a separate

intercept and slope for each species. The issue here is

that there are some species that are not found each year.

Easiest to remove those from another version of this

dataframe before running below. Otherwise, it's not a

```
# balanced design. updated mod4 mod12 <-
# lmer(spp_half_cover_date ~ state * year + (1+year/species),
# green_kbs)

# So another version of this model would include the
# interaction but not include the nesting (and thus would
# assume that species aren't observed ea yr) updated mod5
# mod13 <- lmer(spp_half_cover_date ~ state * year +
# (1/species), green_kbs)
```

KBS Plot-level Mixed Effects Models:

```
# plot-level models using the species summarized data frame
# with specific random effects
mod1ps <- lmer(spp_half_cover_date ~ state + (1 | plot/species),
  green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod2ps <- lmer(spp_half_cover_date ~ state + insecticide + (1 |
  plot/species), green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod3ps <- lmer(spp_half_cover_date ~ state + insecticide + year_factor +
  (1 | plot/species), green_kbs, REML = FALSE)
mod4ps <- lmer(spp_half_cover_date ~ state + year_factor + (1 |
  plot/species), green_kbs, REML = FALSE)
mod5ps <- lmer(spp_half_cover_date ~ state + year_factor + (1 |
  species) + (1 | plot), green_kbs, REML = FALSE)
mod6ps <- lmer(spp_half_cover_date ~ state + year_factor + insecticide +
  (1 | species) + (1 | plot), green_kbs, REML = FALSE)
mod7ps <- lmer(spp_half_cover_date ~ state + year_factor + insecticide +
  (1 | species), green_kbs, REML = FALSE)

anova(mod1ps, mod2ps) #1

## Data: green_kbs
## Models:
## mod1ps: spp_half_cover_date ~ state + (1 | plot/species)
## mod2ps: spp_half_cover_date ~ state + insecticide + (1 | plot/species)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod1ps    5 16435 16462 -8212.6    16425
## mod2ps    6 16437 16469 -8212.6    16425 0.005  1    0.9438

anova(mod1ps, mod3ps) #3

## Data: green_kbs
## Models:
## mod1ps: spp_half_cover_date ~ state + (1 | plot/species)
## mod3ps: spp_half_cover_date ~ state + insecticide + year_factor + (1 |
## mod3ps:      plot/species)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod1ps    5 16435 16462 -8212.6    16425
## mod3ps   11 16357 16416 -8167.6    16335 89.898  6 < 2.2e-16 ***
```

```

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

anova(mod4ps, mod3ps) #4

## Data: green_kbs
## Models:
## mod4ps: spp_half_cover_date ~ state + year_factor + (1 | plot/species)
## mod3ps: spp_half_cover_date ~ state + insecticide + year_factor + (1 |
## mod3ps: plot/species)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod4ps   10 16355 16408 -8167.7    16335
## mod3ps   11 16357 16416 -8167.6    16335 0.0966  1    0.7559

anova(mod4ps, mod5ps) #5

## Data: green_kbs
## Models:
## mod4ps: spp_half_cover_date ~ state + year_factor + (1 | plot/species)
## mod5ps: spp_half_cover_date ~ state + year_factor + (1 | species) + (1 |
## mod5ps: plot)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod4ps   10 16355 16408 -8167.7    16335
## mod5ps   10 16185 16238 -8082.6    16165 170.07  0 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod6ps, mod5ps) #5

## Data: green_kbs
## Models:
## mod5ps: spp_half_cover_date ~ state + year_factor + (1 | species) + (1 |
## mod5ps: plot)
## mod6ps: spp_half_cover_date ~ state + year_factor + insecticide + (1 |
## mod6ps: species) + (1 | plot)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5ps   10 16185 16238 -8082.6    16165
## mod6ps   11 16187 16246 -8082.6    16165 0.0012  1    0.9728

anova(mod5ps, mod7ps) # the same...?

## Data: green_kbs
## Models:
## mod5ps: spp_half_cover_date ~ state + year_factor + (1 | species) + (1 |
## mod5ps: plot)
## mod7ps: spp_half_cover_date ~ state + year_factor + insecticide + (1 |
## mod7ps: species)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5ps   10 16185 16238 -8082.6    16165
## mod7ps   10 16188 16241 -8083.8    16168      0  0          1

AICctab(mod1ps, mod2ps, mod3ps, mod4ps, mod5ps, mod6ps, mod7ps,
weights = T)

##      dAICc df weight
## mod5ps   0.0 10 0.59
## mod6ps   2.0 11 0.22
## mod7ps   2.3 10 0.19

```

```

## mod4ps 170.1 10 <0.001
## mod3ps 172.0 11 <0.001
## mod1ps 249.8 5 <0.001
## mod2ps 251.8 6 <0.001

summary(mod5ps)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + (1 | species) + (1 |
## plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 16185.3 16238.5 -8082.6 16165.3     1501
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0732 -0.6728 -0.2247  0.4880  3.0894
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 20.82 4.563
## species (Intercept) 703.44 26.522
## Residual 2473.98 49.739
## Number of obs: 1511, groups: plot, 24; species, 22
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 132.81518 6.69607 32.07361 19.835 < 2e-16 ***
## stateambient -0.02241 3.21024 22.66365 -0.007 0.9945
## year_factor2 -9.87350 4.44828 1481.72440 -2.220 0.0266 *
## year_factor3 21.64648 4.25645 1486.48707 5.086 4.13e-07 ***
## year_factor4 8.26986 4.27638 1483.88468 1.934 0.0533 .
## year_factor5 26.18114 4.37381 1491.54199 5.986 2.69e-09 ***
## year_factor6 9.48743 4.44228 1495.06929 2.136 0.0329 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn yr_fc2 yr_fc3 yr_fc4 yr_fc5
## stateambint -0.244
## year_factr2 -0.267 -0.012
## year_factr3 -0.286 -0.007 0.437
## year_factr4 -0.277 -0.025 0.434 0.452
## year_factr5 -0.275 -0.020 0.433 0.454 0.453
## year_factr6 -0.271 -0.018 0.431 0.446 0.447 0.454

anova(mod4ps)

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state          25      25      1 23.74 0.0096 0.9227
## year_factor 239106 47821      5 1261.53 18.5120 <2e-16 ***
## ---

```

```

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

# plot-level models using the re-summarized data frame
mod1p <- lmer(plot_half_cover_date ~ state + (1 | plot), green_kbsp,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod2p <- lmer(plot_half_cover_date ~ insecticide + (1 | plot),
  green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod3p <- lmer(plot_half_cover_date ~ insecticide + state + (1 |
  plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod4p <- lmer(plot_half_cover_date ~ insecticide * state + (1 |
  plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod5p <- lmer(plot_half_cover_date ~ state + year_factor + (1 |
  plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod6p <- lmer(plot_half_cover_date ~ state + year_factor + insecticide +
  (1 | plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod7p <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
  plot), green_kbsp, REML = FALSE)
mod8p <- lmer(plot_half_cover_date ~ state * year_factor + insecticide +
  (1 | plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod9p <- lmer(plot_half_cover_date ~ state * insecticide + year_factor +
  (1 | plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod10p <- lmer(plot_half_cover_date ~ state + insecticide * year_factor +
  (1 | plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
mod11p <- lmer(plot_half_cover_date ~ state * year_factor * insecticide +
  (1 | plot), green_kbsp, REML = FALSE)

## boundary (singular) fit: see ?isSingular
AICctab(mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p, mod8p,
  mod9p, mod10p, mod11p, weights = T) # 5p or 6p

##      dAICc df weight
## mod5p   0.0   9  0.364
## mod6p   0.0  10  0.358
## mod9p   1.0  11  0.223

```



```

## mod7p    6.0  14 0.019
## mod8p    6.0  15 0.018
## mod10p   6.0  15 0.018
## mod1p   16.8  4 <0.001
## mod3p   17.2  5 <0.001
## mod2p   17.4  4 <0.001
## mod4p   18.3  6 <0.001
## mod11p  24.6 26 <0.001

anova(mod5p, mod6p) #5p - used this model in results section

## Data: green_kbsp
## Models:
## mod5p: plot_half_cover_date ~ state + year_factor + (1 | plot)
## mod6p: plot_half_cover_date ~ state + year_factor + insecticide + (1 |
## mod6p:    plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5p     9 1532.5 1559.2 -757.25   1514.5
## mod6p    10 1532.2 1561.8 -756.11   1512.2 2.2764  1    0.1314

summary(mod5p)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + year_factor + (1 | plot)
## Data: green_kbsp
##
##      AIC      BIC   logLik deviance df.resid
##  1532.5   1559.2   -757.2   1514.5      134
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6738 -0.6830 -0.2646  0.2966  2.8861
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 2.149e-11 4.635e-06
## Residual 2.329e+03 4.826e+01
## Number of obs: 143, groups: plot, 24
##
## Fixed effects:
##      Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)  89.687    10.645 143.000   8.425 3.47e-14 ***
## stateambient  13.709     8.072 143.000   1.698 0.091620 .
## year_factor2  25.042    13.930 143.000   1.798 0.074340 .
## year_factor3  50.083    13.930 143.000   3.595 0.000445 ***
## year_factor4  42.417    13.930 143.000   3.045 0.002771 **
## year_factor5  69.208    13.930 143.000   4.968 1.90e-06 ***
## year_factor6  54.626    14.082 143.000   3.879 0.000159 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn yr_fc2 yr_fc3 yr_fc4 yr_fc5
## stateambint -0.379

```

```

## year_factor2 -0.654 0.000
## year_factor3 -0.654 0.000 0.500
## year_factor4 -0.654 0.000 0.500 0.500
## year_factor5 -0.654 0.000 0.500 0.500 0.500
## year_factor6 -0.652 0.012 0.495 0.495 0.495 0.495
## convergence code: 0
## boundary (singular) fit: see ?isSingular

anova(mod5p)

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state          6716  6716.3      1   143  2.8843  0.09162 .
## year_factor   71742 14348.3      5   143  6.1619 3.344e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod5p, list(pairwise ~ state + year_factor), adjust = "tukey")

## $`emmeans of state, year_factor`
## state year_factor emmean SE df lower.CL upper.CL
## warmed 1          89.7 10.9 138    68.0    111
## ambient 1         103.4 10.9 138    81.8    125
## warmed 2         114.7 10.9 138    93.1    136
## ambient 2         128.4 10.9 138   106.8    150
## warmed 3         139.8 10.9 138   118.1    161
## ambient 3         153.5 10.9 138   131.8    175
## warmed 4         132.1 10.9 138   110.5    154
## ambient 4         145.8 10.9 138   124.2    167
## warmed 5         158.9 10.9 138   137.3    181
## ambient 5         172.6 10.9 138   151.0    194
## warmed 6         144.3 11.1 138   122.4    166
## ambient 6         158.0 11.2 139   135.8    180
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, year_factor`
## 1 estimate SE df t.ratio p.value
## warmed 1 - ambient 1 -13.709 8.42 26 -1.628 0.8830
## warmed 1 - warmed 2 -25.042 14.24 124 -1.759 0.8365
## warmed 1 - ambient 2 -38.750 16.54 144 -2.343 0.4517
## warmed 1 - warmed 3 -50.083 14.24 124 -3.518 0.0287
## warmed 1 - ambient 3 -63.792 16.54 144 -3.857 0.0091
## warmed 1 - warmed 4 -42.417 14.24 124 -2.979 0.1273
## warmed 1 - ambient 4 -56.125 16.54 144 -3.393 0.0406
## warmed 1 - warmed 5 -69.208 14.24 124 -4.861 0.0002
## warmed 1 - ambient 5 -82.917 16.54 144 -5.013 0.0001
## warmed 1 - warmed 6 -54.626 14.40 125 -3.794 0.0118
## warmed 1 - ambient 6 -68.335 16.77 145 -4.075 0.0042
## ambient 1 - warmed 2 -11.333 16.54 144 -0.685 0.9999
## ambient 1 - ambient 2 -25.042 14.24 124 -1.759 0.8365
## ambient 1 - warmed 3 -36.375 16.54 144 -2.199 0.5529
## ambient 1 - ambient 3 -50.083 14.24 124 -3.518 0.0287
## ambient 1 - warmed 4 -28.708 16.54 144 -1.736 0.8486

```

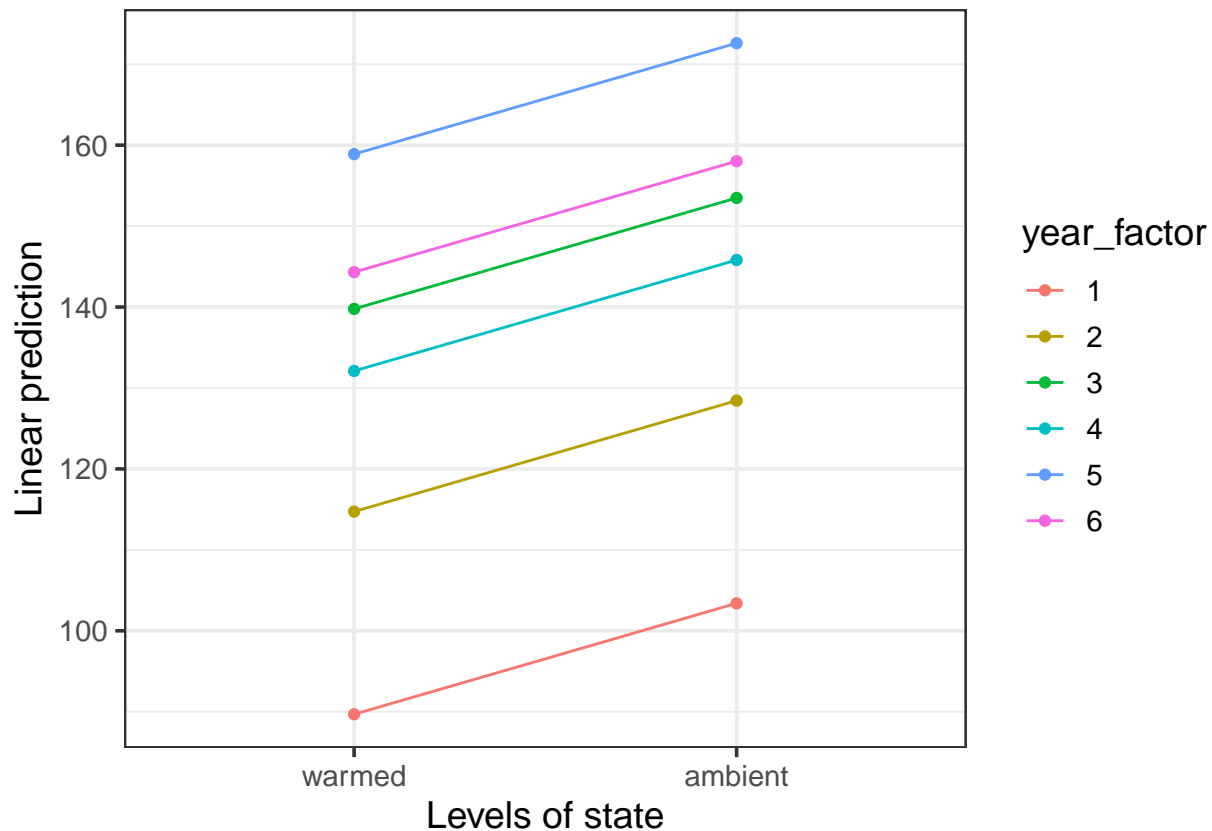
```

## ambient 1 - ambient 4 -42.417 14.24 124 -2.979 0.1273
## ambient 1 - warmed 5 -55.500 16.54 144 -3.356 0.0454
## ambient 1 - ambient 5 -69.208 14.24 124 -4.861 0.0002
## ambient 1 - warmed 6 -40.917 16.59 144 -2.467 0.3692
## ambient 1 - ambient 6 -54.626 14.40 125 -3.794 0.0118
## warmed 2 - ambient 2 -13.709 8.42 26 -1.628 0.8830
## warmed 2 - warmed 3 -25.042 14.24 124 -1.759 0.8365
## warmed 2 - ambient 3 -38.750 16.54 144 -2.343 0.4517
## warmed 2 - warmed 4 -17.375 14.24 124 -1.220 0.9864
## warmed 2 - ambient 4 -31.084 16.54 144 -1.879 0.7699
## warmed 2 - warmed 5 -44.167 14.24 124 -3.102 0.0935
## warmed 2 - ambient 5 -57.875 16.54 144 -3.499 0.0295
## warmed 2 - warmed 6 -29.584 14.40 125 -2.055 0.6552
## warmed 2 - ambient 6 -43.293 16.77 145 -2.582 0.3000
## ambient 2 - warmed 3 -11.333 16.54 144 -0.685 0.9999
## ambient 2 - ambient 3 -25.042 14.24 124 -1.759 0.8365
## ambient 2 - warmed 4 -3.666 16.54 144 -0.222 1.0000
## ambient 2 - ambient 4 -17.375 14.24 124 -1.220 0.9864
## ambient 2 - warmed 5 -30.458 16.54 144 -1.842 0.7922
## ambient 2 - ambient 5 -44.167 14.24 124 -3.102 0.0935
## ambient 2 - warmed 6 -15.876 16.59 144 -0.957 0.9983
## ambient 2 - ambient 6 -29.584 14.40 125 -2.055 0.6552
## warmed 3 - ambient 3 -13.709 8.42 26 -1.628 0.8830
## warmed 3 - warmed 4 7.667 14.24 124 0.539 1.0000
## warmed 3 - ambient 4 -6.042 16.54 144 -0.365 1.0000
## warmed 3 - warmed 5 -19.125 14.24 124 -1.343 0.9715
## warmed 3 - ambient 5 -32.834 16.54 144 -1.985 0.7026
## warmed 3 - warmed 6 -4.543 14.40 125 -0.316 1.0000
## warmed 3 - ambient 6 -18.251 16.77 145 -1.088 0.9948
## ambient 3 - warmed 4 21.375 16.54 144 1.292 0.9789
## ambient 3 - ambient 4 7.667 14.24 124 0.539 1.0000
## ambient 3 - warmed 5 -5.416 16.54 144 -0.327 1.0000
## ambient 3 - ambient 5 -19.125 14.24 124 -1.343 0.9715
## ambient 3 - warmed 6 9.166 16.59 144 0.553 1.0000
## ambient 3 - ambient 6 -4.543 14.40 125 -0.316 1.0000
## warmed 4 - ambient 4 -13.709 8.42 26 -1.628 0.8830
## warmed 4 - warmed 5 -26.792 14.24 124 -1.882 0.7680
## warmed 4 - ambient 5 -40.500 16.54 144 -2.449 0.3810
## warmed 4 - warmed 6 -12.209 14.40 125 -0.848 0.9994
## warmed 4 - ambient 6 -25.918 16.77 145 -1.546 0.9250
## ambient 4 - warmed 5 -13.083 16.54 144 -0.791 0.9997
## ambient 4 - ambient 5 -26.792 14.24 124 -1.882 0.7680
## ambient 4 - warmed 6 1.499 16.59 144 0.090 1.0000
## ambient 4 - ambient 6 -12.209 14.40 125 -0.848 0.9994
## warmed 5 - ambient 5 -13.709 8.42 26 -1.628 0.8830
## warmed 5 - warmed 6 14.582 14.40 125 1.013 0.9972
## warmed 5 - ambient 6 0.874 16.77 145 0.052 1.0000
## ambient 5 - warmed 6 28.291 16.59 144 1.706 0.8628
## ambient 5 - ambient 6 14.582 14.40 125 1.013 0.9972
## warmed 6 - ambient 6 -13.709 8.42 26 -1.628 0.8830
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 12 estimates

```

```
mod5p.emm <- emmeans(mod5p, ~state + year_factor) # why are the comparisons the same for each year?
contrast(mod5p.emm, "consec", simple = "each", combine = F, adjust = "mvt")
```

```
## $`simple contrasts for state`
## year_factor = 1:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## year_factor = 2:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## year_factor = 3:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## year_factor = 4:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## year_factor = 5:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## year_factor = 6:
## contrast      estimate    SE df t.ratio p.value
## ambient - warmed      13.7 8.42 26 1.628   0.1155
##
## Degrees-of-freedom method: kenward-roger
##
## $`simple contrasts for year_factor`
## state = warmed:
## contrast estimate    SE  df t.ratio p.value
## 2 - 1      25.04 14.2 124  1.759 0.3060
## 3 - 2      25.04 14.2 124  1.759 0.3060
## 4 - 3      -7.67 14.2 124 -0.539 0.9789
## 5 - 4      26.79 14.2 124  1.882 0.2440
## 6 - 5     -14.58 14.4 125 -1.013 0.7937
##
## state = ambient:
## contrast estimate    SE  df t.ratio p.value
## 2 - 1      25.04 14.2 124  1.759 0.3060
## 3 - 2      25.04 14.2 124  1.759 0.3063
## 4 - 3      -7.67 14.2 124 -0.539 0.9789
## 5 - 4      26.79 14.2 124  1.882 0.2440
## 6 - 5     -14.58 14.4 125 -1.013 0.7938
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: mvt method for 5 tests
emmip(mod5p, year_factor ~ state)
```



Analyses for species who reached half cover within the green-up observation window

```
# Selecting species (these were determined in the
# half_cover_kbs dataframe made in the phenology_dates_L2.R
# script)
species_kbs <- subset(green_kbs, species == "Taof") # can change/add more species
mod_spp <- lmer(spp_half_cover_date ~ state + factor(year_factor) +
  (1 | plot), species_kbs, REML = FALSE)
mod_spp2 <- lmer(min_green_date ~ state + factor(year_factor) +
  (1 | plot), species_kbs, REML = FALSE)
summary(mod_spp)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + factor(year_factor) + (1 | plot)
## Data: species_kbs
##
##      AIC      BIC    logLik deviance df.resid
##    567.7    585.9   -274.8    549.7      47
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3148 -0.5539 -0.1129  0.2388  4.0379
##
## Random effects:
```

```

## Groups Name Variance Std.Dev.
## plot (Intercept) 155.9 12.49
## Residual 941.5 30.68
## Number of obs: 56, groups: plot, 21
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 120.052 9.287 45.084 12.927 <2e-16 ***
## stateambient -18.032 10.395 20.860 -1.735 0.0975 .
## factor(year_factor)2 -6.455 15.941 50.140 -0.405 0.6872
## factor(year_factor)3 1.826 13.289 49.205 0.137 0.8913
## factor(year_factor)4 14.201 12.850 51.489 1.105 0.2742
## factor(year_factor)5 29.594 11.545 47.823 2.563 0.0136 *
## factor(year_factor)6 -23.750 19.956 52.047 -1.190 0.2394
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.576
## fcctr(yr_f)2 -0.317 -0.033
## fcctr(yr_f)3 -0.372 -0.053 0.277
## fcctr(yr_f)4 -0.460 0.054 0.282 0.330
## fcctr(yr_f)5 -0.446 -0.038 0.295 0.347 0.358
## fcctr(yr_f)6 -0.317 0.066 0.190 0.207 0.240 0.242
summary(mod_spp2)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: min_green_date ~ state + factor(year_factor) + (1 | plot)
## Data: species_kbs
##
## AIC BIC logLik deviance df.resid
## 544.5 562.7 -263.2 526.5 47
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -0.9957 -0.4769 -0.1362 0.4147 5.9393
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 49.15 7.011
## Residual 663.65 25.762
## Number of obs: 56, groups: plot, 21
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 114.371 7.359 48.916 15.542 <2e-16 ***
## stateambient -13.709 7.846 22.356 -1.747 0.0943 .
## factor(year_factor)2 -8.624 13.188 52.518 -0.654 0.5160
## factor(year_factor)3 4.476 11.021 51.089 0.406 0.6864
## factor(year_factor)4 8.045 10.614 52.700 0.758 0.4518
## factor(year_factor)5 12.390 9.599 49.693 1.291 0.2028
## factor(year_factor)6 -16.684 16.441 54.211 -1.015 0.3147

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.555
## fcctr(yr_f)2 -0.340 -0.037
## fcctr(yr_f)3 -0.399 -0.058  0.264
## fcctr(yr_f)4 -0.485  0.055  0.269  0.317
## fcctr(yr_f)5 -0.475 -0.040  0.290  0.343  0.353
## fcctr(yr_f)6 -0.336  0.075  0.178  0.201  0.227  0.233
```

UMBS Mixed Effects Models

```
# umod4 (and umod6) are pretty complex in terms of
# interpretation (they actually don't have many parameters
# though). We could consider an alternative umodel that's
# simpler to understand and also one that provides more
# insight about the species. That would be something like
# this:
```

```
umod7 <- lmer(spp_half_cover_date ~ state + species + (1 + year_factor |
  plot), green_umbs, REML = FALSE)
```

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

```
umod7a <- lmer(spp_half_cover_date ~ state + species + year_factor +
  (1 | plot), green_umbs, REML = FALSE)
```

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

```
umod7b <- lmer(spp_half_cover_date ~ state * year_factor + species +
  (1 | plot), green_umbs, REML = FALSE)
```

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

```
umod7c <- lmer(spp_half_cover_date ~ state + species + year_factor +
  insecticide + (1 | plot), green_umbs, REML = FALSE)
```

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

```
# anova(umod6, umod7) # umodel 7 is a better fit to data
anova(umod7, umod7a) #umod 7a
```

```
## Data: green_umbs
```

```
## Models:
```

```
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
```

```
## umod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
```

```
##          npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
```

```
## umod7a    23 7488.0 7594.6 -3721.0   7442.0
```

```
## umod7     33 7520.8 7673.7 -3727.4   7454.8    0 10          1
```

```
anova(umod7a, umod7b) #umod 7a
```

```
## Data: green_umbs
```

```
## Models:
```

```
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
```

```
## umod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
```

```

##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod7a    23 7488.0 7594.6 -3721.0 7442.0
## umod7b    27 7495.2 7620.3 -3720.6 7441.2 0.8269 4 0.9348
anova(umod7a, umod7c) #umod 7a

## Data: green_umbs
## Models:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7c: spp_half_cover_date ~ state + species + year_factor + insecticide +
## umod7c: (1 | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod7a    23 7488.0 7594.6 -3721.0 7442.0
## umod7c    24 7489.5 7600.7 -3720.8 7441.5 0.4787 1 0.489

summary(umod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## Data: green_umbs
##
##          AIC      BIC logLik deviance df.resid
## 7488.0 7594.6 -3721.0 7442.0 737
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5078 -0.6474 -0.3215  0.3286  3.7096
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 1.355e-15 3.681e-08
## Residual 1.048e+03 3.237e+01
## Number of obs: 760, groups: plot, 24
##
## Fixed effects:
##          Estimate Std. Error    df t value Pr(>|t|)
## (Intercept) 139.979 12.710 760.000 11.013 < 2e-16 ***
## stateambient 1.966 2.368 760.000 0.830 0.406703
## speciesAnsp 1.372 15.298 760.000 0.090 0.928553
## speciesApan 49.085 17.312 760.000 2.835 0.004700 **
## speciesAssp 30.149 13.823 760.000 2.181 0.029484 *
## speciesAsun -15.656 26.053 760.000 -0.601 0.548067
## speciesCape 8.110 12.802 760.000 0.634 0.526588
## speciesCest -8.827 12.630 760.000 -0.699 0.484806
## speciesDasp 2.626 12.689 760.000 0.207 0.836116
## speciesFrve 2.859 14.110 760.000 0.203 0.839478
## speciesHisp 45.946 14.722 760.000 3.121 0.001871 **
## speciesHype 6.646 13.009 760.000 0.511 0.609570
## speciesPosp 1.469 12.643 760.000 0.116 0.907536
## speciesPtaq 38.902 12.826 760.000 3.033 0.002503 **
## speciesRuac -1.207 12.744 760.000 -0.095 0.924578
## speciesSosp 19.100 14.394 760.000 1.327 0.184928
## speciesSyla 39.296 16.337 760.000 2.405 0.016395 *
## year_factor2 -12.789 3.865 760.000 -3.309 0.000979 ***

```



```

## year_factor3      5.802      3.837 760.000    1.512 0.130919
## year_factor4     -5.806      3.802 760.000   -1.527 0.127098
## year_factor5     -8.756      3.757 760.000   -2.330 0.020042 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
##
## convergence code: 0
## boundary (singular) fit: see ?isSingular

summary(umod7b)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
## Data: green_umbs
##
##      AIC      BIC    logLik deviance df.resid
##  7495.2   7620.3  -3720.6   7441.2     733
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4663 -0.6362 -0.3359  0.3265  3.7578
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 0 0.00
## Residual 1046 32.35
## Number of obs: 760, groups: plot, 24
##
## Fixed effects:
##
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 140.5620 12.9411 760.0000 10.862 < 2e-16 ***
## stateambient 0.6241 5.4437 760.0000 0.115 0.90875
## year_factor2 -13.1905 5.4177 760.0000 -2.435 0.01513 *
## year_factor3 4.0237 5.4915 760.0000 0.733 0.46396
## year_factor4 -5.0481 5.3544 760.0000 -0.943 0.34609
## year_factor5 -10.8472 5.3966 760.0000 -2.010 0.04478 *
## speciesAnsp 1.6138 15.3082 760.0000 0.105 0.91607
## speciesApan 48.7495 17.3073 760.0000 2.817 0.00498 **
## speciesAssp 30.2132 13.8203 760.0000 2.186 0.02911 *
## speciesAsun -15.5265 26.0408 760.0000 -0.596 0.55119
## speciesCape 8.1910 12.8000 760.0000 0.640 0.52242
## speciesCest -8.6955 12.6273 760.0000 -0.689 0.49127
## speciesDasp 2.6976 12.6862 760.0000 0.213 0.83166
## speciesFrve 2.8462 14.1063 760.0000 0.202 0.84015
## speciesHisp 46.0680 14.7350 760.0000 3.126 0.00184 **
## speciesHype 6.7780 13.0066 760.0000 0.521 0.60243
## speciesPosp 1.5913 12.6401 760.0000 0.126 0.89985
## speciesPtaq 39.0395 12.8232 760.0000 3.044 0.00241 **
## speciesRuac -1.1021 12.7409 760.0000 -0.086 0.93109
## speciesSosp 19.1724 14.3985 760.0000 1.332 0.18341

```

```

## speciesSyla          39.5456    16.3453 760.0000    2.419  0.01578 *
## stateambient:year_factor2  0.7435     7.6547 760.0000    0.097  0.92265
## stateambient:year_factor3  3.4439     7.6289 760.0000    0.451  0.65181
## stateambient:year_factor4 -1.5988     7.5098 760.0000   -0.213  0.83147
## stateambient:year_factor5  4.0002     7.4386 760.0000    0.538  0.59089
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 25 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

## convergence code: 0
## boundary (singular) fit: see ?isSingular

summary(umod7c)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year_factor + insecticide +
## (1 | plot)
## Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
## 7489.5   7600.7 -3720.8   7441.5      736
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4938 -0.6497 -0.3250  0.3196  3.6825
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## plot      (Intercept)    0      0.00
## Residual              1047     32.36
## Number of obs: 760, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    140.643    12.742 760.000   11.038 < 2e-16 ***
## stateambient      1.981     2.367 760.000    0.837 0.402935
## speciesAnsp       1.577    15.296 760.000    0.103 0.917905
## speciesApan       50.024    17.360 760.000    2.882 0.004068 **
## speciesAssp       29.894    13.823 760.000    2.163 0.030884 *
## speciesAsun      -15.543    26.045 760.000   -0.597 0.550835
## speciesCape       8.247    12.799 760.000    0.644 0.519551
## speciesCest      -8.697    12.627 760.000   -0.689 0.491206
## speciesDasp       2.750    12.686 760.000    0.217 0.828422
## speciesFrve       3.067    14.108 760.000    0.217 0.827980
## speciesHisp      46.420    14.733 760.000    3.151 0.001693 **
## speciesHype       6.846    13.008 760.000    0.526 0.598833
## speciesPosp       1.584    12.640 760.000    0.125 0.900295
## speciesPtaq      39.098    12.825 760.000    3.048 0.002380 **
## speciesRuac      -1.012    12.743 760.000   -0.079 0.936716
## speciesSosp      19.628    14.409 760.000    1.362 0.173552
## speciesSyla      39.516    16.335 760.000    2.419 0.015792 *

```

```

## year_factor2          -12.782      3.863 760.000  -3.309 0.000982 ***
## year_factor3           5.833      3.836 760.000   1.521 0.128764
## year_factor4          -5.766      3.801 760.000  -1.517 0.129641
## year_factor5          -8.724      3.756 760.000  -2.323 0.020457 *
## insecticideno_insects  -1.648      2.382 760.000  -0.692 0.489163
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

## convergence code: 0
## boundary (singular) fit: see ?isSingular

anova(umod7a) # investigates whether at least one of the levels within each factor is significantly di.

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state           722   722.0     1   760  0.6892    0.4067
## species       185793 12386.2    15   760 11.8233 < 2.2e-16 ***
## year_factor    31128  7781.9     4   760  7.4283 7.169e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Yes, at least one of the species is different (they do not
# all have the same half cover dates).
emmmeans(umod7a, list(pairwise ~ year_factor), adjust = "tukey")

## $`emmmeans of year_factor`
##   year_factor emmean   SE  df lower.CL upper.CL
## 1             155 3.50 450     148     162
## 2             142 3.42 454     135     149
## 3             161 3.40 416     154     167
## 4             149 3.25 350     143     155
## 5             146 3.30 401     139     152
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
##   1      estimate   SE  df t.ratio p.value
## 1 - 2      12.79 3.92 767   3.262 0.0101
## 1 - 3      -5.80 3.89 764  -1.491 0.5686
## 1 - 4       5.81 3.86 768   1.505 0.5592
## 1 - 5       8.76 3.81 765   2.298 0.1466
## 2 - 3     -18.59 3.90 764  -4.763 <.0001
## 2 - 4      -6.98 3.86 764  -1.809 0.3690
## 2 - 5      -4.03 3.81 767  -1.058 0.8280
## 3 - 4      11.61 3.78 762   3.068 0.0189
## 3 - 5      14.56 3.74 763   3.897 0.0010
## 4 - 5       2.95 3.68 763   0.801 0.9301
##
## Results are averaged over the levels of: state, species

```

```
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 5 estimates
emmeans(umod7a, list(pairwise ~ species), adjust = "tukey")
```

```
## $`emmeans of species`
## species emmean SE df lower.CL upper.CL
## Amla      137 12.56 715    112.0    161
## Ansp      138  9.20 776    120.0    156
## Apan      186 12.55 739    161.1    210
## Assp      167  6.52 655    154.0    180
## Asun      121 23.40 782     75.1    167
## Cape      145  3.77 606    137.4    152
## Cest      128  3.00 508    121.9    134
## Dasp      139  3.21 545    133.0    146
## Frve      140  7.09 618    125.6    153
## Hisp      183  8.17 769    166.6    199
## Hype      143  4.48 652    134.5    152
## Posp      138  3.08 527    132.1    144
## Ptaq      176  3.74 575    168.2    183
## Ruac      135  3.50 551    128.6    142
## Sosp      156  7.63 628    140.8    171
## Syla      176 11.09 645    154.2    198
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of species`
## 1 estimate SE df t.ratio p.value
## Amla - Ansp -1.3722 15.63 749 -0.088 1.0000
## Amla - Apan -49.0845 17.66 770 -2.779 0.2833
## Amla - Assp -30.1488 14.17 700 -2.128 0.7464
## Amla - Asun 15.6560 26.48 779 0.591 1.0000
## Amla - Cape -8.1101 13.09 735 -0.619 1.0000
## Amla - Cest 8.8274 12.91 742 0.684 1.0000
## Amla - Dasp -2.6258 12.97 743 -0.202 1.0000
## Amla - Frve -2.8590 14.46 709 -0.198 1.0000
## Amla - Hisp -45.9457 15.02 774 -3.059 0.1475
## Amla - Hype -6.6464 13.29 756 -0.500 1.0000
## Amla - Posp -1.4689 12.93 744 -0.114 1.0000
## Amla - Ptaq -38.9021 13.10 754 -2.969 0.1850
## Amla - Ruac 1.2068 13.02 751 0.093 1.0000
## Amla - Sosp -19.0996 14.70 763 -1.300 0.9959
## Amla - Syla -39.2963 16.68 771 -2.357 0.5812
## Ansp - Apan -47.7124 15.60 779 -3.059 0.1477
## Ansp - Assp -28.7766 11.28 781 -2.552 0.4346
## Ansp - Asun 17.0282 25.22 782 0.675 1.0000
## Ansp - Cape -6.7379 9.97 782 -0.676 1.0000
## Ansp - Cest 10.1995 9.67 781 1.055 0.9996
## Ansp - Dasp -1.2536 9.72 781 -0.129 1.0000
## Ansp - Frve -1.4869 11.58 779 -0.128 1.0000
## Ansp - Hisp -44.5736 12.21 781 -3.651 0.0247
## Ansp - Hype -5.2742 10.27 780 -0.513 1.0000
## Ansp - Posp -0.0967 9.70 781 -0.010 1.0000
```

##	Ansp	- Ptaq	-37.5299	9.93	781	-3.778	0.0158
##	Ansp	- Ruac	2.5790	9.83	778	0.262	1.0000
##	Ansp	- Sosp	-17.7274	11.92	755	-1.487	0.9838
##	Ansp	- Syla	-37.9241	14.44	724	-2.627	0.3812
##	Apan	- Assp	18.9358	14.13	725	1.340	0.9943
##	Apan	- Asun	64.7405	26.55	780	2.439	0.5186
##	Apan	- Cape	40.9745	13.07	755	3.134	0.1212
##	Apan	- Cest	57.9119	12.90	760	4.490	0.0009
##	Apan	- Dasp	46.4588	12.96	762	3.585	0.0310
##	Apan	- Frve	46.2255	14.45	712	3.200	0.1014
##	Apan	- Hisp	3.1388	15.00	772	0.209	1.0000
##	Apan	- Hype	42.4382	13.27	770	3.198	0.1018
##	Apan	- Posp	47.6156	12.91	758	3.687	0.0219
##	Apan	- Ptaq	10.1825	13.08	771	0.778	1.0000
##	Apan	- Ruac	50.2914	13.01	767	3.866	0.0115
##	Apan	- Sosp	29.9850	14.73	750	2.036	0.8041
##	Apan	- Syla	9.7883	16.74	725	0.585	1.0000
##	Assp	- Asun	45.8047	24.27	781	1.887	0.8815
##	Assp	- Cape	22.0387	7.52	743	2.930	0.2027
##	Assp	- Cest	38.9761	7.17	759	5.434	<.0001
##	Assp	- Dasp	27.5230	7.26	769	3.790	0.0152
##	Assp	- Frve	27.2897	9.59	745	2.846	0.2457
##	Assp	- Hisp	-15.7970	10.45	778	-1.511	0.9812
##	Assp	- Hype	23.5024	7.89	767	2.978	0.1809
##	Assp	- Posp	28.6799	7.21	759	3.978	0.0075
##	Assp	- Ptaq	-8.7533	7.51	767	-1.166	0.9988
##	Assp	- Ruac	31.3556	7.39	762	4.245	0.0026
##	Assp	- Sosp	11.0492	10.04	734	1.100	0.9994
##	Assp	- Syla	-9.1475	12.82	732	-0.714	1.0000
##	Asun	- Cape	-23.7661	23.69	782	-1.003	0.9998
##	Asun	- Cest	-6.8286	23.59	781	-0.289	1.0000
##	Asun	- Dasp	-18.2818	23.63	781	-0.774	1.0000
##	Asun	- Frve	-18.5150	24.42	780	-0.758	1.0000
##	Asun	- Hisp	-61.6017	24.78	778	-2.486	0.4834
##	Asun	- Hype	-22.3024	23.79	781	-0.937	0.9999
##	Asun	- Posp	-17.1249	23.60	781	-0.726	1.0000
##	Asun	- Ptaq	-54.5581	23.69	780	-2.303	0.6216
##	Asun	- Ruac	-14.4491	23.66	781	-0.611	1.0000
##	Asun	- Sosp	-34.7555	24.56	772	-1.415	0.9900
##	Asun	- Syla	-54.9523	25.75	759	-2.134	0.7427
##	Cape	- Cest	16.9374	4.81	774	3.522	0.0381
##	Cape	- Dasp	5.4843	4.95	779	1.107	0.9993
##	Cape	- Frve	5.2511	8.03	736	0.654	1.0000
##	Cape	- Hisp	-37.8357	9.01	781	-4.200	0.0031
##	Cape	- Hype	1.4637	5.82	780	0.251	1.0000
##	Cape	- Posp	6.6412	4.85	774	1.368	0.9929
##	Cape	- Ptaq	-30.7920	5.30	782	-5.805	<.0001
##	Cape	- Ruac	9.3169	5.13	778	1.815	0.9108
##	Cape	- Sosp	-10.9895	8.53	719	-1.288	0.9962
##	Cape	- Syla	-31.1862	11.71	676	-2.663	0.3571
##	Cest	- Dasp	-11.4531	4.39	763	-2.611	0.3927
##	Cest	- Frve	-11.6864	7.69	728	-1.520	0.9801
##	Cest	- Hisp	-54.7731	8.69	782	-6.300	<.0001
##	Cest	- Hype	-15.4738	5.38	781	-2.874	0.2305

```

## Cest - Posp -10.2963  4.29 759 -2.398  0.5493
## Cest - Ptaq -47.7295  4.79 779 -9.972  <.0001
## Cest - Ruac  -7.6205  4.60 775 -1.658  0.9568
## Cest - Sosp -27.9269  8.20 724 -3.408  0.0550
## Cest - Syla -48.1236 11.48 693 -4.191  0.0032
## Dasp - Frve  -0.2333  7.77 727 -0.030  1.0000
## Dasp - Hisp -43.3200  8.76 781 -4.945  0.0001
## Dasp - Hype  -4.0206  5.51 780 -0.729  1.0000
## Dasp - Posp   1.1569  4.45 764  0.260  1.0000
## Dasp - Ptaq -36.2763  4.92 778 -7.376  <.0001
## Dasp - Ruac   3.8326  4.74 773  0.809  1.0000
## Dasp - Sosp -16.4738  8.27 722 -1.992  0.8290
## Dasp - Syla -36.6705 11.54 697 -3.178  0.1078
## Frve - Hisp -43.0867 10.77 782 -4.001  0.0069
## Frve - Hype  -3.7874  8.39 740 -0.452  1.0000
## Frve - Posp   1.3901  7.73 734  0.180  1.0000
## Frve - Ptaq -36.0431  8.00 721 -4.505  0.0008
## Frve - Ruac   4.0659  7.89 733  0.515  1.0000
## Frve - Sosp -16.2405 10.38 740 -1.565  0.9739
## Frve - Syla -36.4372 13.10 749 -2.782  0.2817
## Hisp - Hype  39.2994  9.35 777  4.204  0.0030
## Hisp - Posp  44.4768  8.71 781  5.104  <.0001
## Hisp - Ptaq   7.0437  8.97 781  0.785  1.0000
## Hisp - Ruac  47.1526  8.88 779  5.313  <.0001
## Hisp - Sosp  26.8462 11.12 778  2.415  0.5367
## Hisp - Syla   6.6495 13.75 772  0.484  1.0000
## Hype - Posp   5.1775  5.42 781  0.955  0.9999
## Hype - Ptaq -32.2557  5.82 782 -5.539  <.0001
## Hype - Ruac   7.8532  5.66 779  1.388  0.9918
## Hype - Sosp -12.4532  8.87 717 -1.403  0.9908
## Hype - Syla -32.6499 11.94 714 -2.735  0.3103
## Posp - Ptaq -37.4332  4.84 780 -7.734  <.0001
## Posp - Ruac   2.6757  4.65 776  0.575  1.0000
## Posp - Sosp -17.6307  8.23 727 -2.143  0.7364
## Posp - Syla -37.8274 11.50 695 -3.288  0.0788
## Ptaq - Ruac  40.1089  5.11 781  7.852  <.0001
## Ptaq - Sosp  19.8025  8.48 733  2.335  0.5979
## Ptaq - Syla  -0.3942 11.68 720 -0.034  1.0000
## Ruac - Sosp -20.3064  8.39 731 -2.420  0.5326
## Ruac - Syla -40.5031 11.61 710 -3.489  0.0426
## Sosp - Syla -20.1967 13.35 782 -1.513  0.9810
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 16 estimates
# including native vs. exotic - first with interaction term
green_umbs <- within(green_umbs, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
umod8 <- lmer(spp_half_cover_date ~ state * origin + (1 + year_factor |
  plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

umod9 <- lmer(spp_half_cover_date ~ state + origin + (1 + year_factor |
  plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
umod9a <- lmer(spp_half_cover_date ~ state + origin + factor(year_factor) +
  (1 | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
anova(umod8, umod9) # umodel 9 is a better fit to data

## Data: green_umbs
## Models:
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## umod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## umod9    21 7587.0 7684.3 -3772.5   7545.0
## umod8    24 7586.3 7697.5 -3769.1   7538.3 6.7095  3    0.08176 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(umod9, umod9a) # umod 9a?

## Data: green_umbs
## Models:
## umod9a: spp_half_cover_date ~ state + origin + factor(year_factor) +
## umod9a:      (1 | plot)
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## umod9a    11 7551.8 7602.8 -3764.9   7529.8
## umod9     21 7587.0 7684.3 -3772.5   7545.0      0 10      1
summary(umod9a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + factor(year_factor) +
##      (1 | plot)
## Data: green_umbs
##
##      AIC      BIC  logLik deviance df.resid
##  7551.8   7602.8 -3764.9   7529.8      749
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1289 -0.6741 -0.3268  0.3574  3.5490
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## plot     (Intercept)          0      0.00
## Residual                    1176     34.29
## Number of obs: 760, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    154.708     3.394 760.000  45.577 < 2e-16 ***

```

```

## stateambient          1.513      2.501 760.000    0.605 0.545403
## origin                -13.916     3.696 760.000   -3.765 0.000179 ***
## originBoth            21.376     5.601 760.000    3.816 0.000146 ***
## originExotic         -18.139     2.822 760.000   -6.428 2.28e-10 ***
## factor(year_factor)2  -12.593     4.038 760.000   -3.119 0.001884 **
## factor(year_factor)3    5.639     4.032 760.000    1.398 0.162392
## factor(year_factor)4   -4.780     3.976 760.000   -1.202 0.229641
## factor(year_factor)5   -7.080     3.935 760.000   -1.799 0.072387 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn origin orgnBt orgnEx fc(_)2 fc(_)3 fc(_)4
## stateambint -0.375
## origin      -0.247  0.006
## originBoth  -0.120 -0.090  0.169
## originExotc -0.345  0.006  0.336  0.218
## fcctr(yr_f)2 -0.603  0.022 -0.035 -0.081  0.002
## fcctr(yr_f)3 -0.589 -0.005 -0.038  0.001 -0.032  0.509
## fcctr(yr_f)4 -0.604  0.015 -0.043 -0.015 -0.031  0.518  0.518
## fcctr(yr_f)5 -0.601 -0.008 -0.030 -0.033 -0.032  0.524  0.523  0.531
## convergence code: 0
## boundary (singular) fit: see ?isSingular
anova(umod9)

## Type III Analysis of Variance Table with Satterthwaite's method
##      Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state      633    632.6      1 198.48  0.5449    0.4613
## origin  83070 27690.0      3 721.14 23.8496 1.004e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
emmeans(umod9a, list(pairwise ~ state + origin), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## Warning in model.frame.default(formula, data = data, ...): variable
## 'year_factor' is not a factor

## $`emmeans of state, origin`
##   state origin emmean SE    df lower.CL upper.CL
## warmed Native    151 2.27  53.7     146      156
## ambient Native    152 2.27  51.3     148      157
## warmed          137 3.44 253.6     130      144
## ambient          139 3.46 255.1     132      145
## warmed Both     172 5.60 502.7     161      183
## ambient Both     174 5.38 417.5     163      184
## warmed Exotic    133 2.47  75.9     128      138
## ambient Exotic    134 2.48  77.3     129      139
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`

```



```
## 1
## estimate SE df t.ratio p.value
## warmed Native - ambient Native -1.51 2.53 21.4 -0.598 0.9985
## warmed Native - warmed 13.92 3.72 760.5 3.739 0.0049
## warmed Native - ambient 12.40 4.51 188.2 2.749 0.1147
## warmed Native - warmed Both -21.38 5.66 760.6 -3.777 0.0042
## warmed Native - ambient Both -22.89 6.00 304.4 -3.816 0.0040
## warmed Native - warmed Exotic 18.14 2.85 769.0 6.374 <.0001
## warmed Native - ambient Exotic 16.63 3.82 102.5 4.358 0.0008
## ambient Native - warmed 15.43 4.49 179.8 3.438 0.0163
## ambient Native - ambient 13.92 3.72 760.5 3.739 0.0049
## ambient Native - warmed Both -19.86 6.39 414.0 -3.107 0.0420
## ambient Native - ambient Both -21.38 5.66 760.6 -3.777 0.0042
## ambient Native - warmed Exotic 19.65 3.80 96.9 5.173 <.0001
## ambient Native - ambient Exotic 18.14 2.85 769.0 6.374 <.0001
## warmed - ambient -1.51 2.53 21.4 -0.598 0.9985
## warmed - warmed Both -35.29 6.23 762.0 -5.664 <.0001
## warmed - ambient Both -36.80 6.53 363.0 -5.635 <.0001
## warmed - warmed Exotic 4.22 3.85 759.0 1.097 0.9573
## warmed - ambient Exotic 2.71 4.60 199.4 0.589 0.9990
## ambient - warmed Both -33.78 6.91 472.3 -4.887 <.0001
## ambient - ambient Both -35.29 6.23 762.0 -5.664 <.0001
## ambient - warmed Exotic 5.74 4.61 199.4 1.244 0.9175
## ambient - ambient Exotic 4.22 3.85 759.0 1.097 0.9573
## warmed Both - ambient Both -1.51 2.53 21.4 -0.598 0.9985
## warmed Both - warmed Exotic 39.51 5.76 760.2 6.863 <.0001
## warmed Both - ambient Exotic 38.00 6.49 426.9 5.860 <.0001
## ambient Both - warmed Exotic 41.03 6.09 309.6 6.742 <.0001
## ambient Both - ambient Exotic 39.51 5.76 760.2 6.863 <.0001
## warmed Exotic - ambient Exotic -1.51 2.53 21.4 -0.598 0.9985
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
# including growth form - first with interaction term
green_umbs <- within(green_umbs, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
umod10 <- lmer(spp_half_cover_date ~ state * growth_habit + (1 +
  year_factor | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 1 negative eigenvalue: -4.1e+00
umod11 <- lmer(spp_half_cover_date ~ state + growth_habit + (1 +
  year_factor | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
umod11a <- lmer(spp_half_cover_date ~ state + growth_habit +
  year_factor + (1 | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
anova(umod10, umod11) # umodel 11 is a better fit to data

## Data: green_umbs
```

```

## Models:
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## umod11:      plot)
## umod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## umod10:      plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod11    21 7638.3 7735.6 -3798.2   7596.3
## umod10    24 7643.7 7754.9 -3797.8   7595.7 0.6019  3      0.896
anova(umod11, umod11a)

## Data: green_umbs
## Models:
## umod11a: spp_half_cover_date ~ state + growth_habit + year_factor + (1 |
## umod11a:      plot)
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## umod11:      plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod11a   11 7603.7 7654.6 -3790.8   7581.7
## umod11    21 7638.3 7735.6 -3798.2   7596.3      0 10      1
summary(umod11a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + growth_habit + year_factor + (1 |
##      plot)
##      Data: green_umbs
##
##      AIC      BIC logLik deviance df.resid
## 7603.7 7654.6 -3790.8   7581.7      749
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.1301 -0.7142 -0.3160  0.3951  3.3161
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
##      plot      (Intercept)      0      0.00
##      Residual      1259      35.48
## Number of obs: 760, groups: plot, 24
##
## Fixed effects:
##
##      Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    149.370     3.406 760.000  43.854 < 2e-16 ***
## stateambient      2.462     2.579 760.000   0.955 0.339962
## growth_habit     30.012     8.473 760.000   3.542 0.000421 ***
## growth_habitGraminoid -5.851     2.672 760.000  -2.190 0.028852 *
## growth_habitTree    -9.415    13.564 760.000  -0.694 0.487806
## year_factor2    -13.306     4.219 760.000  -3.154 0.001676 **
## year_factor3      4.810     4.179 760.000   1.151 0.250182
## year_factor4     -6.179     4.121 760.000  -1.500 0.134151
## year_factor5     -7.802     4.074 760.000  -1.915 0.055899 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_T yr_fc2 yr_fc3 yr_fc4
## stateambint -0.392
## growth_habt -0.021 -0.043
## grwth_hbtGr -0.290  0.008  0.131
## grwth_hbtTr -0.019 -0.011  0.019  0.081
## year_facr2 -0.615  0.022 -0.164 -0.036 -0.004
## year_facr3 -0.611 -0.003 -0.005 -0.035 -0.068  0.504
## year_facr4 -0.630  0.017 -0.056 -0.029 -0.045  0.520  0.518
## year_facr5 -0.630 -0.008 -0.040 -0.020 -0.042  0.522  0.524  0.532
## convergence code: 0
## boundary (singular) fit: see ?isSingular

anova(umod11)

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state           1475      1475      1 210.85  1.1866 0.2772663
## growth_habit    20940      6980      3 715.19  5.6150 0.0008296 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(umod11a, list(pairwise ~ state + growth_habit), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## $`emmeans of state, growth_habit`
##   state growth_habit emmean    SE    df lower.CL upper.CL
## warmed  Forb         145  2.17  38.9      140      149
## ambient  Forb         147  2.15  34.1      143      152
## warmed           175  8.54 689.8      158      192
## ambient           177  8.42 679.2      161      194
## warmed  Graminoid     139  2.45  66.9      134      144
## ambient  Graminoid     141  2.45  67.7      137      146
## warmed    Tree       135 13.73 666.1      108      162
## ambient    Tree       138 13.69 677.0      111      165
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, growth_habit`
##   1 estimate    SE    df t.ratio p.value
## warmed Forb - ambient Forb      -2.46  2.61  20.8 -0.944  0.9776
## warmed Forb - warmed           -30.01  8.55 768.9 -3.511  0.0111
## warmed Forb - ambient          -32.47  8.83 611.8 -3.677  0.0062
## warmed Forb - warmed Graminoid    5.85  2.70 767.4  2.169  0.3718
## warmed Forb - ambient Graminoid    3.39  3.76  85.9  0.901  0.9853
## warmed Forb - warmed Tree    9.42 13.75 724.9  0.685  0.9974
## warmed Forb - ambient Tree    6.95 13.96 654.1  0.498  0.9997
## ambient Forb - warmed          -27.55  9.04 625.2 -3.047  0.0492
## ambient Forb - ambient          -30.01  8.55 768.9 -3.511  0.0111
## ambient Forb - warmed Graminoid    8.31  3.74  76.3  2.221  0.3510
## ambient Forb - ambient Graminoid    5.85  2.70 767.4  2.169  0.3718
## ambient Forb - warmed Tree   11.88 14.03 627.4  0.846  0.9903
```

```
## ambient Forb - ambient Tree          9.42 13.75 724.9  0.685  0.9974
## warmed  - ambient                    -2.46  2.61  20.8 -0.944  0.9776
## warmed  - warmed Graminoid           35.86  8.63 766.7  4.154  0.0009
## warmed  - ambient Graminoid           33.40  9.13 603.1  3.660  0.0066
## warmed  - warmed Tree                 39.43 16.04 759.8  2.458  0.2153
## warmed  - ambient Tree                 36.96 16.28 727.5  2.271  0.3112
## ambient  - warmed Graminoid           38.32  8.91 574.9  4.302  0.0005
## ambient  - ambient Graminoid           35.86  8.63 766.7  4.154  0.0009
## ambient  - warmed Tree                 41.89 16.22 710.8  2.582  0.1642
## ambient  - ambient Tree                 39.43 16.04 759.8  2.458  0.2153
## warmed Graminoid - ambient Graminoid  -2.46  2.61  20.8 -0.944  0.9776
## warmed Graminoid - warmed Tree         3.56 13.80 716.5  0.258  1.0000
## warmed Graminoid - ambient Tree        1.10 14.01 641.1  0.079  1.0000
## ambient Graminoid - warmed Tree        6.03 14.09 619.6  0.428  0.9999
## ambient Graminoid - ambient Tree       3.56 13.80 716.5  0.258  1.0000
## warmed Tree - ambient Tree             -2.46  2.61  20.8 -0.944  0.9776
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

UMBS Plot-level Mixed Effects Models:

```
mod1pu <- lmer(plot_half_cover_date ~ state + (1 | plot), green_umbsp,
  REML = FALSE)
```

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

```
mod2pu <- lmer(plot_half_cover_date ~ state + factor(year_factor) +
  (1 | plot), green_umbsp, REML = FALSE)
```

```
mod3pu <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
  plot), green_umbsp, REML = FALSE)
```

```
anova(mod1pu, mod2pu, mod3pu) #mod2pu
```

```
## Data: green_umbsp
```

```
## Models:
```

```
## mod1pu: plot_half_cover_date ~ state + (1 | plot)
```

```
## mod2pu: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
```

```
## mod3pu: plot_half_cover_date ~ state * year_factor + (1 | plot)
```

```
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
```

```
## mod1pu      4 1200.0 1211.1 -595.98   1192.0
```

```
## mod2pu      8 1181.9 1204.2 -582.97   1165.9 26.024  4  3.13e-05 ***
```

```
## mod3pu     12 1181.3 1214.7 -578.65   1157.3  8.642  4  0.0707 .
```

```
## ---
```

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

```
summary(mod2pu)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
```

```
## method [lmerModLmerTest]
```

```
## Formula: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
```

```
## Data: green_umbsp
```

```
##
```

```
##      AIC      BIC    logLik deviance df.resid
```

```
## 1181.9 1204.2 -583.0 1165.9      112
```

```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8579 -0.6259 -0.2222  0.5474  3.0755
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   plot     (Intercept) 30.97    5.565
##   Residual             941.80   30.689
## Number of obs: 120, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      147.150      7.048 102.011   20.879 < 2e-16 ***
## stateambient       -1.467      6.046  24.000   -0.243  0.81039
## factor(year_factor)2 -21.500      8.859  96.000   -2.427  0.01709 *
## factor(year_factor)3  -2.583      8.859  96.000   -0.292  0.77122
## factor(year_factor)4   13.167      8.859  96.000    1.486  0.14049
## factor(year_factor)5   23.583      8.859  96.000    2.662  0.00911 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4
## stateambint -0.429
## fcctr(yr_f)2 -0.629  0.000
## fcctr(yr_f)3 -0.629  0.000  0.500
## fcctr(yr_f)4 -0.629  0.000  0.500  0.500
## fcctr(yr_f)5 -0.629  0.000  0.500  0.500  0.500
```

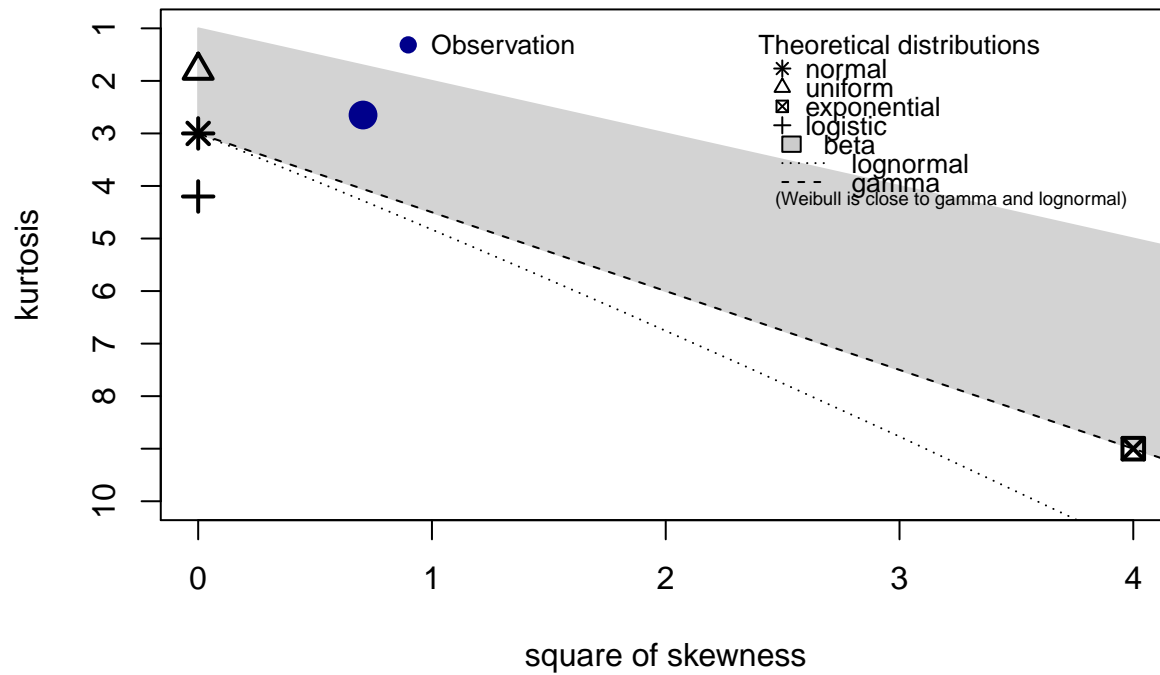
ORIGINAL CODE BELOW; not edited by Phoebe

can pretty much ignore everything below!

Seeing what other distribution could fit

```
descdist(green_kbs$spp_half_cover_date, discrete = FALSE)
```

Cullen and Frey graph

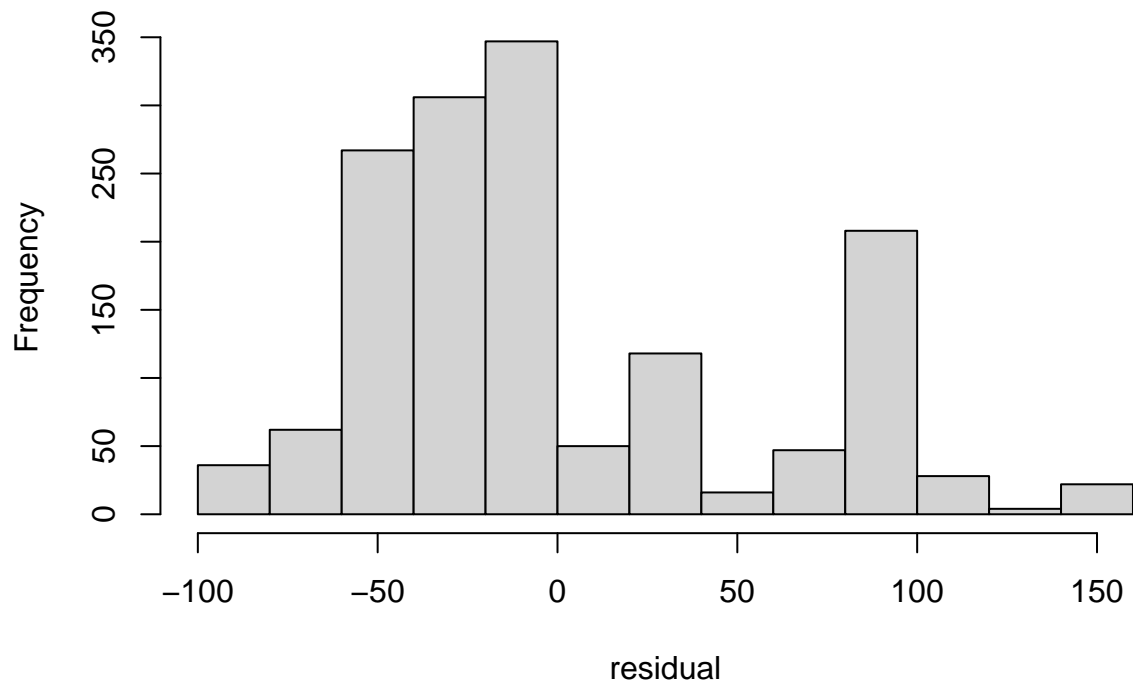


```
## summary statistics
## -----
## min: 59    max: 289
## median: 124
## mean: 139.3309
## estimated sd: 56.12957
## estimated skewness: 0.8397458
## estimated kurtosis: 2.650025
```

While uniform looks the closest, I'll try poisson

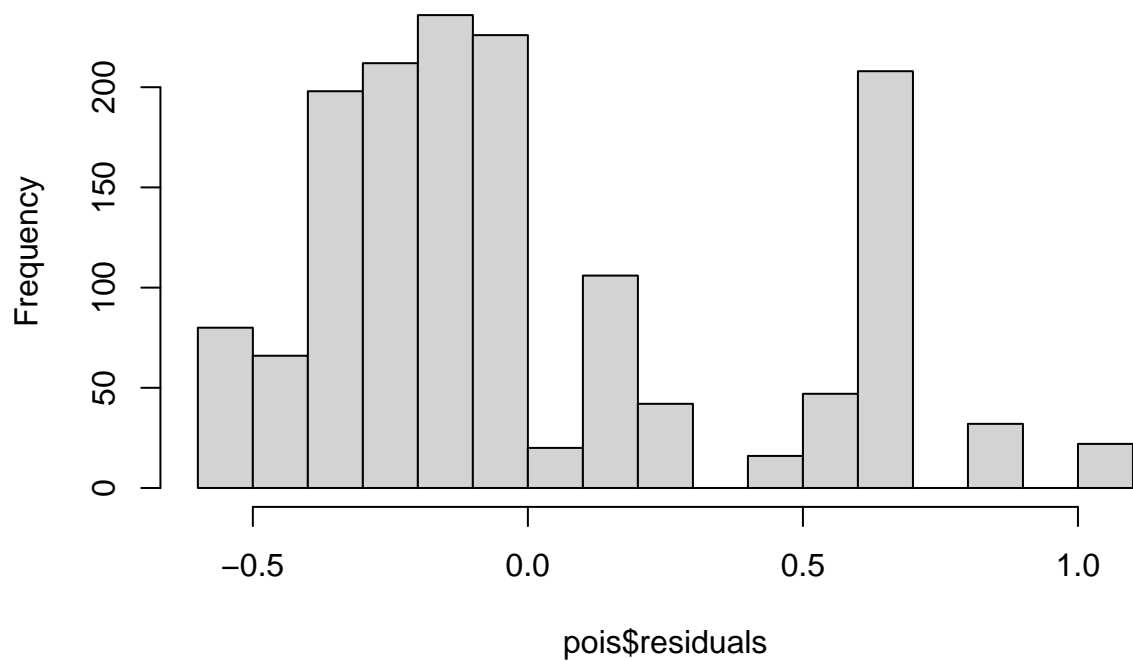
```
fit <- lm(spp_half_cover_date ~ state, data = green_kbs)
residual <- fit$residuals
hist(residual, main = "Raw residuals")
```

Raw residuals



```
pois <- glm(spp_half_cover_date ~ state, data = green_kbs, family = "poisson")  
hist(pois$residuals, main = "Poisson glm residuals")
```

Poisson glm residuals



Below I try a few different generalized linear models with poisson distribution:

An interaction between state and year, plus insecticide as a fixed effect and species and plot as random effects

```
moda <- glmer(spp_half_cover_date ~ state * year + insecticide +
  (1 | species) + (1 | plot), data = green_kbs, family = poisson)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0107867 (tol = 0.002, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?

summary(moda)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## (1 | plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 35773.3 35810.5 -17879.6 35759.3     1504
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -7.563 -2.897 -1.147  1.916 15.309
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 0.003081 0.0555
## species (Intercept) 0.035562 0.1886
## Number of obs: 1511, groups: plot, 24; species, 22
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -28.182598   3.682645  -7.653 1.97e-14 ***
## stateambient    -43.588658   4.908873  -8.880 < 2e-16 ***
## year              0.016413   0.001824   8.996 < 2e-16 ***
## insecticideno_insects -0.006946   0.023099  -0.301 0.764
## stateambient:year   0.021595   0.002432   8.880 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year  insct_
## stateambint -0.701
## year        -1.000 0.701
```



```
## insctcdn_ns -0.017  0.009  0.014
## statmbnt:yr  0.701 -1.000 -0.701 -0.009
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model failed to converge with max|grad| = 0.0107867 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

No interaction between state and year, but with state and insecticide as fixed effects and species and plot as random effects

```
modb <- glmer(spp_half_cover_date ~ state + year + insecticide +
  (1 | species) + (1 | plot), data = green_kbs, family = poisson)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00446952 (tol = 0.002, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

```
summary(modb)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: spp_half_cover_date ~ state + year + insecticide + (1 | species) +
## (1 | plot)
## Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 35843.8 35875.7 -17915.9 35831.8      1505
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -7.541 -2.891 -1.142  1.953 14.948
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 0.003069 0.0554
## species (Intercept) 0.035936 0.1896
## Number of obs: 1511, groups: plot, 24; species, 22
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.122e+01  2.628e+00 -19.493  <2e-16 ***
## stateambient    -4.661e-04  2.306e-02  -0.020    0.984
## year            2.783e-02  1.302e-03  21.378  <2e-16 ***
## insecticideno_insects -5.141e-03  2.306e-02  -0.223    0.824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year
## stateambint  0.003
## year        -1.000 -0.007
## insctcdn_ns -0.016 -0.003  0.011
## convergence code: 0
## Model failed to converge with max|grad| = 0.00446952 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

State and insecticide as fixed effects & year, species and plot as random effects

```
modc <- glmer(spp_half_cover_date ~ state + insecticide + (1 |  
  year) + (1 | species) + (1 | plot), data = green_kbs, family = poisson)  
summary(modc)
```

Because no distributions seems to match well, I'll try a Friedman's test

```
# friedman_kbs <- green_kbs %>%  
# friedman_test(spp_half_cover_date ~ state)
```

Error: Must extract column with a single valid subscript. x Subscript var can't be NA

Can't figure out what this means

If I include the blocks portion of the formula (from the documentation) I get this error

```
# friedman_kbs <- green_kbs %>%  
# friedman_test(spp_half_cover_date ~ state | plot)
```

Error in friedman.test.default(c(141L, 202L, 122L, 101L, 127L, 120L, 197L, : not an unreplicated complete block design

Permanova?

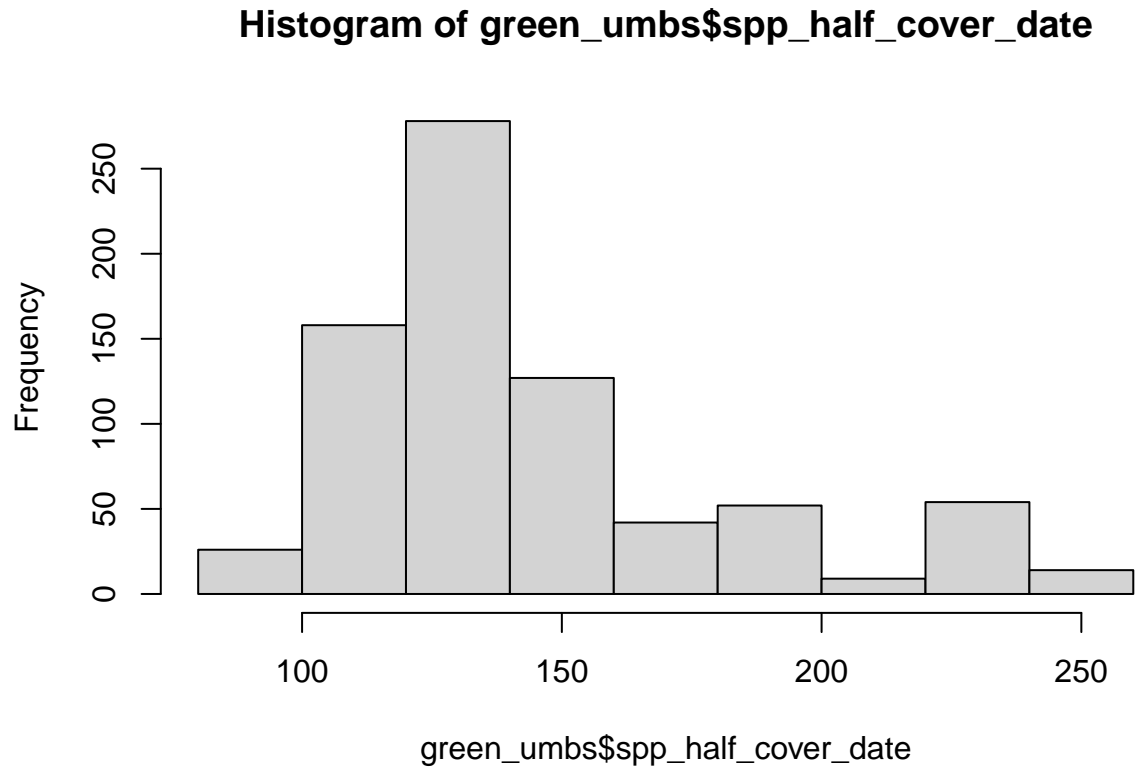
```
per1 <- adonis2(green_kbs$spp_half_cover_date ~ state * year +  
  insecticide, data = green_kbs)  
per1  
per2 <- adonis(formula = green_kbs$spp_half_cover_date ~ state *  
  year + insecticide, strata = green_kbs$plot, data = green_kbs)  
per2
```

With per2, when controlling for “plot”, there is a difference btwn treatments

UMBS

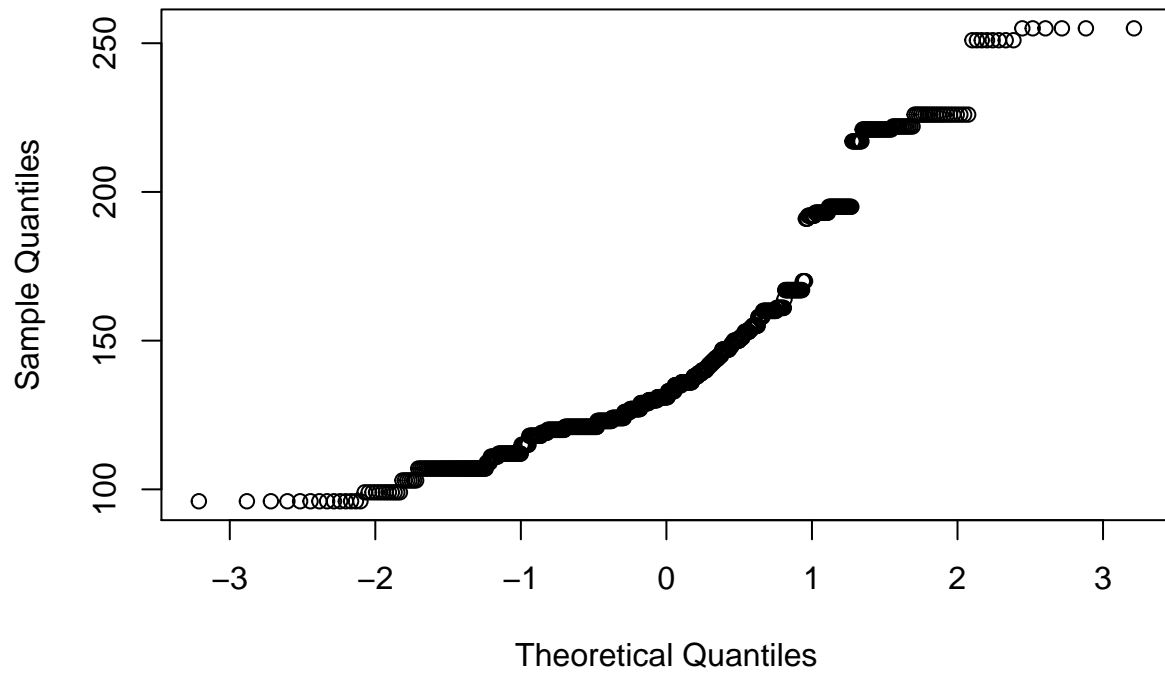
Checking for normality

```
hist(green_umbs$spp_half_cover_date)
```



```
qqnorm(green_umbs$spp_half_cover_date)
```

Normal Q-Q Plot

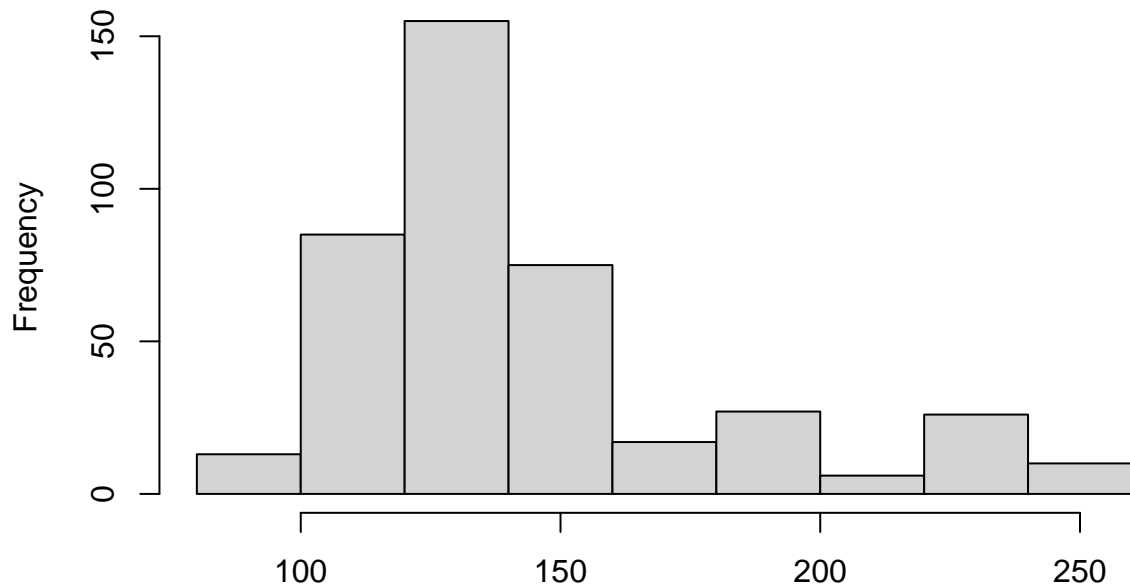


```
shapiro.test(green_umbs$spp_half_cover_date)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  green_umbs$spp_half_cover_date  
## W = 0.8651, p-value < 2.2e-16
```

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "ambient"])
```

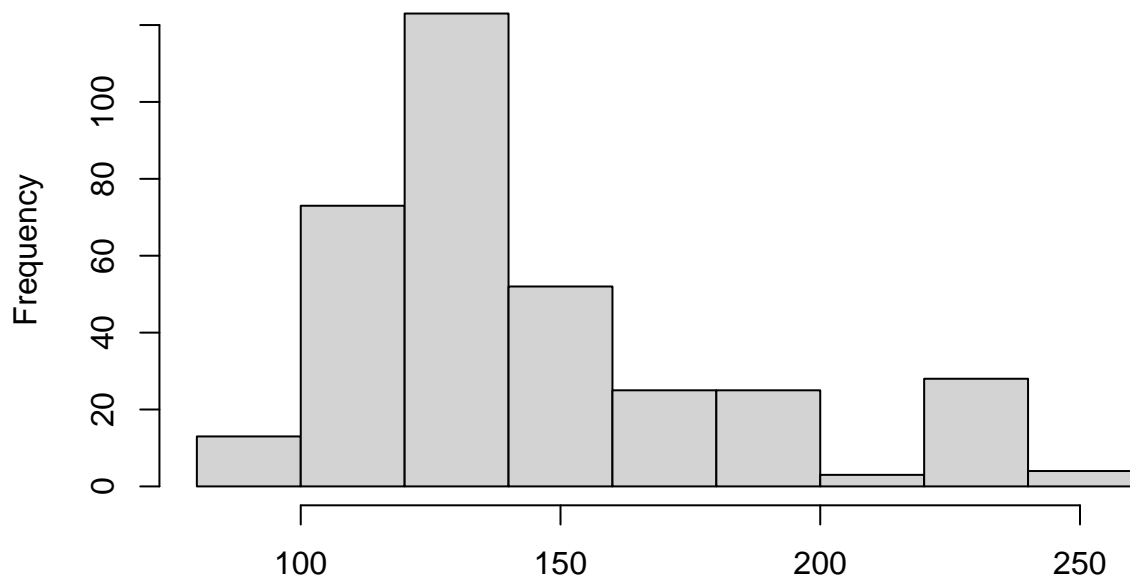
istogram of green_umbs\$spp_half_cover_date[green_kbs\$state == "am



green_umbs\$spp_half_cover_date[green_kbs\$state == "ambient"]

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "warmed"])
```

istogram of green_umbs\$spp_half_cover_date[green_kbs\$state == "wa

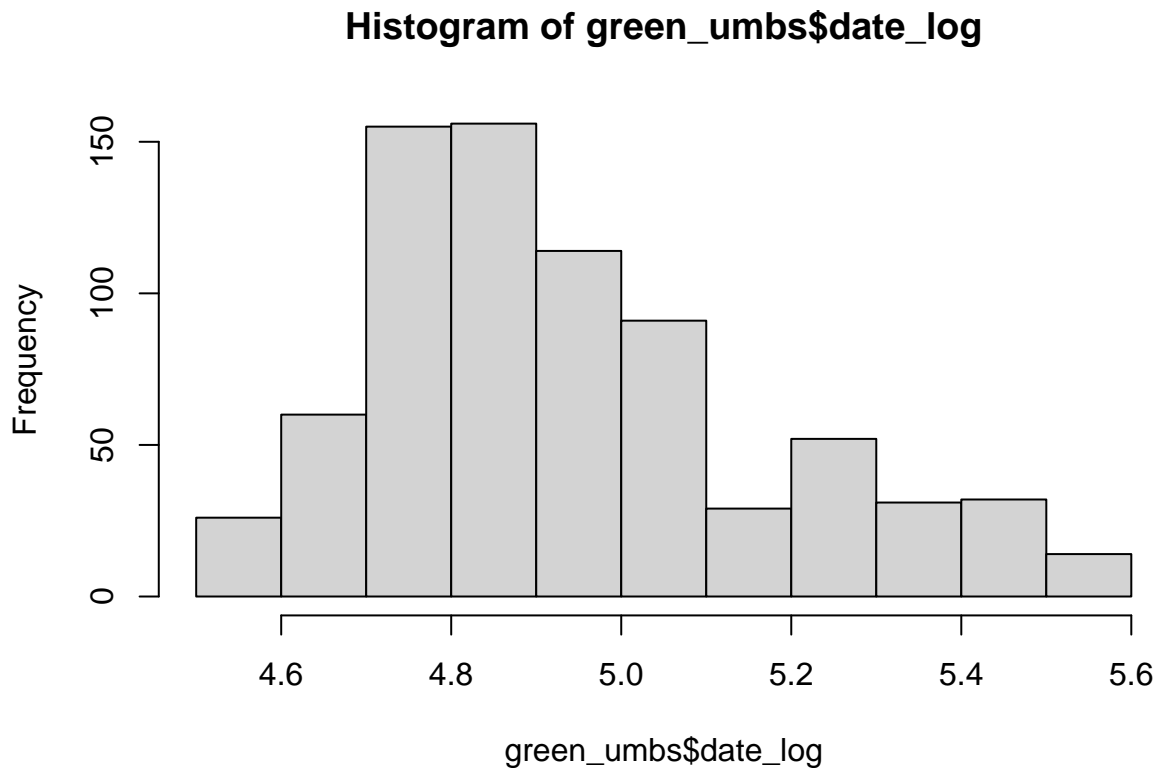


green_umbs\$spp_half_cover_date[green_kbs\$state == "warmed"]

These look pretty good

Trying log transformation

```
green_umbs$date_log <- log(green_umbs$spp_half_cover_date)
hist(green_umbs$date_log)
```



```
shapiro.test(green_umbs$date_log)
```

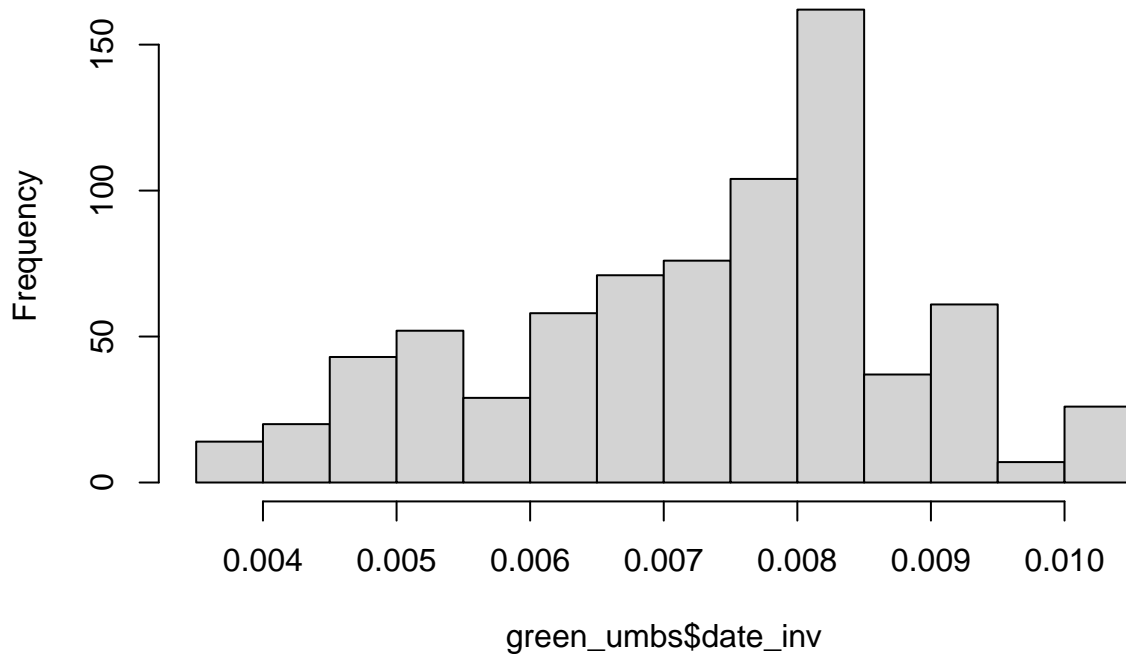
```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_log
## W = 0.92667, p-value < 2.2e-16
```

I think this looks good but shapiro-wilk is lower than 0.05

Trying inverse tranformation

```
green_umbs$date_inv <- 1/(green_umbs$spp_half_cover_date)
hist(green_umbs$date_inv)
```

Histogram of green_umbs\$date_inv



```
shapiro.test(green_umbs$date_inv)

##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_inv
## W = 0.96547, p-value = 2.083e-12
```

This also looks good but is also still low for shapiro-wilk