

warmXtrophic Project: Greenup Analyses

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Script Details:

```
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_1000.csv'  
  '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' file contains  
  the following information:  
  - Date: The date at which the data was collected.  
  - Species: The species name.  
  - Spp_half_cover_date: The date at which 50% of the species max cover was reached (per plot, per year).  
  - State: Describes each treatment: warmed or ambient."))  
  
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 (per plot, per year)",  
  "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')

# 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"))
greenup <- greenup %>% select(-X) # get rid of 'X' column that shows up
greenupp <- read.csv(file.path(L2_dir, "greenup/final_greenup_plot_L2.csv"))
greenupp <- greenupp %>% select(-X) # get rid of 'X' column that shows up

# 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))
# check variable types
str(greenup)

```

```

## 'data.frame': 2026 obs. of 18 variables:
## $ site : chr "kbs" "kbs" "kbs" "kbs" ...
## $ plot : chr "A1" "A1" "A1" "A1" ...
## $ year : int 2016 2017 2018 2019 2020 2016 2017 2016 2017 2018 ...
## $ species : chr "Acmi" "Acmi" "Acmi" "Acmi" ...
## $ spp_half_cover_date: int 197 101 122 120 127 88 108 97 99 127 ...
## $ min_green_date : int 81 80 122 120 107 81 108 85 80 127 ...
## $ 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" ...

```

```

# 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"

```

```

greenupp$state <- as.factor(greenupp$state)
levels(greenupp$state)

```

```

## [1] "ambient" "warmed"

```

```
greenupp$state <- factor(greenupp$state, levels(greenupp$state)[c(2,
1)])
levels(greenupp$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
```

```
greenupp$year_factor[greenupp$year == 2016] <- 1
greenupp$year_factor[greenupp$year == 2017] <- 2
greenupp$year_factor[greenupp$year == 2018] <- 3
greenupp$year_factor[greenupp$year == 2019] <- 4
greenupp$year_factor[greenupp$year == 2020] <- 5
```

```
# 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(greenupp, site == "kbs")
green_umbsp <- subset(greenupp, site == "umbs")
```

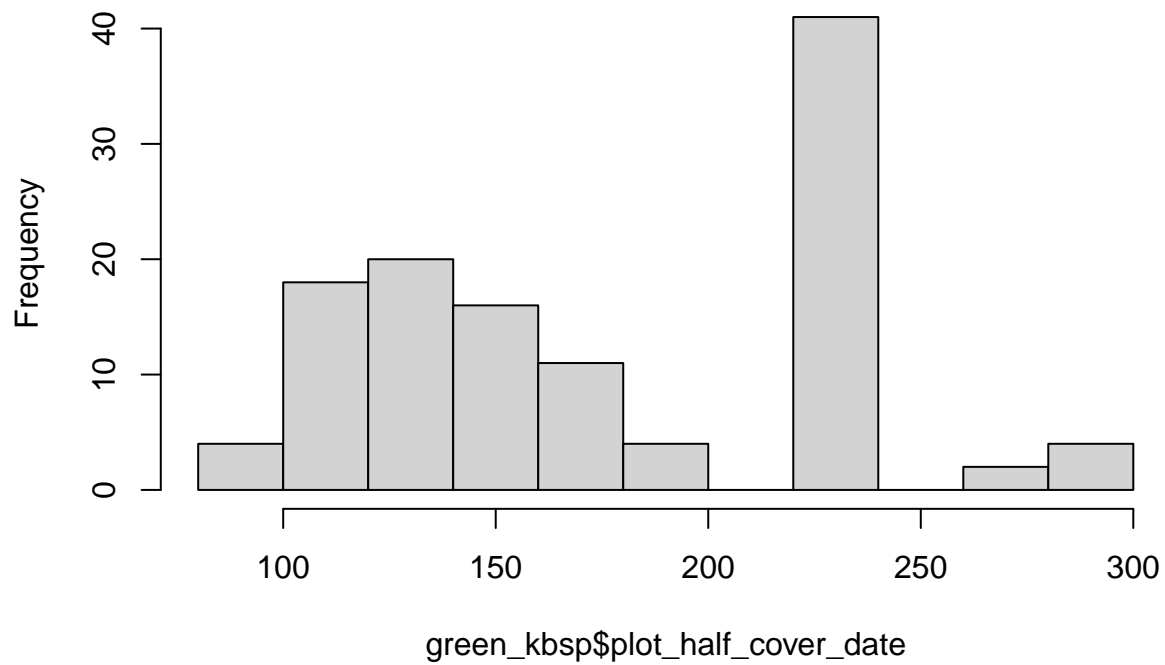
Data Exploration: are there differences between warmed vs. ambient plots when we account for species?

Starting with KBS

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.

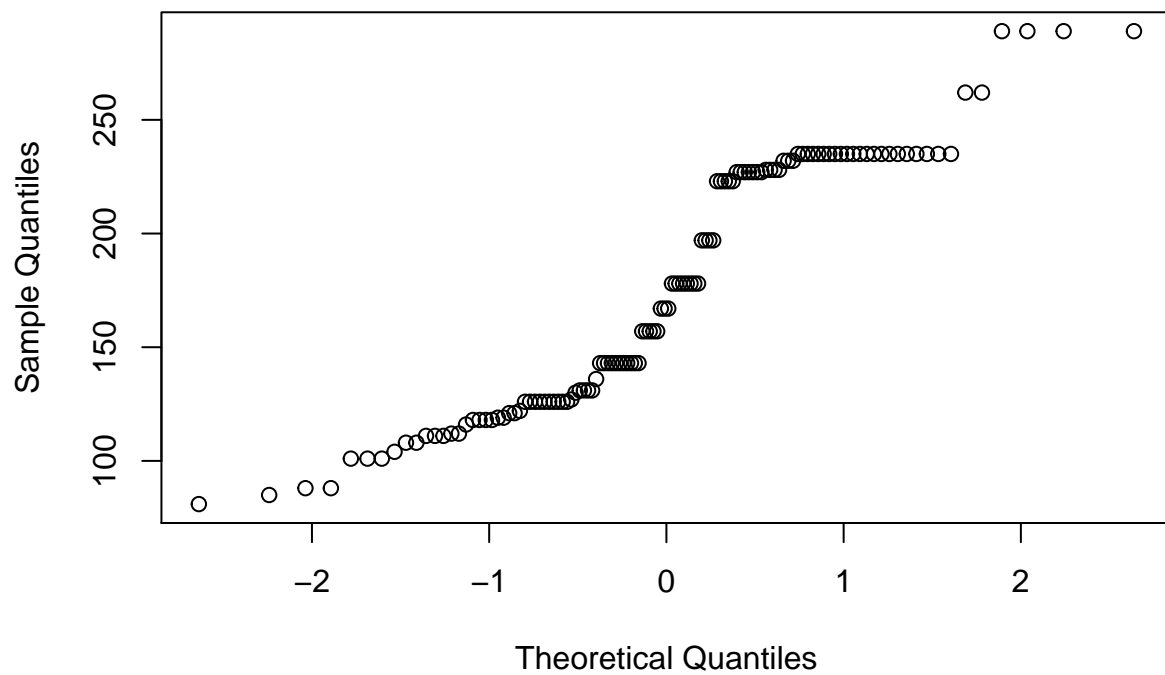
```
hist(green_kbsp$plot_half_cover_date)
```

Histogram of green_kbsp\$plot_half_cover_date



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

Normal Q-Q Plot



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

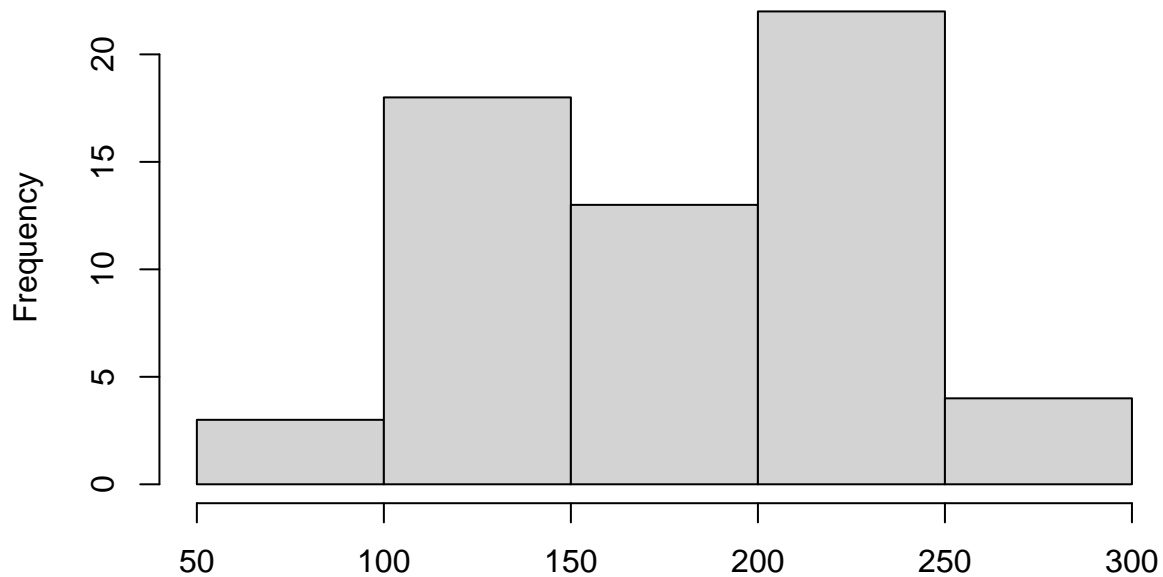
```
##
```

```
## Shapiro-Wilk normality test
##
## data: green_kbsp$plot_half_cover_date
## W = 0.90721, p-value = 4.673e-07
```

```
# histograms for each treatment separately
```

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

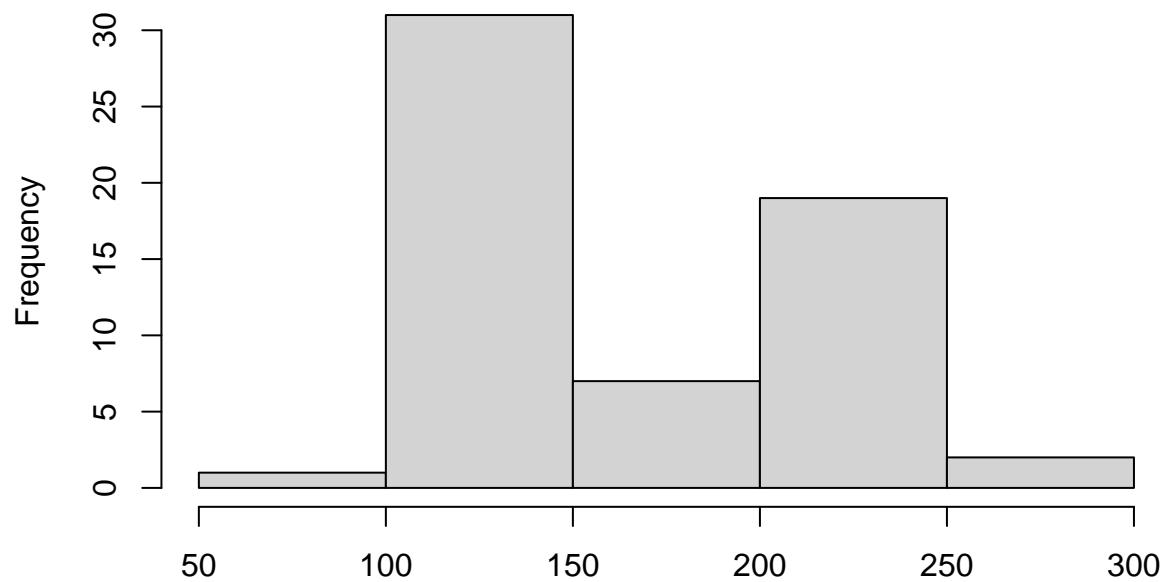
istogram of green_kbsp\$plot_half_cover_date[green_kbsp\$state == "ar



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

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

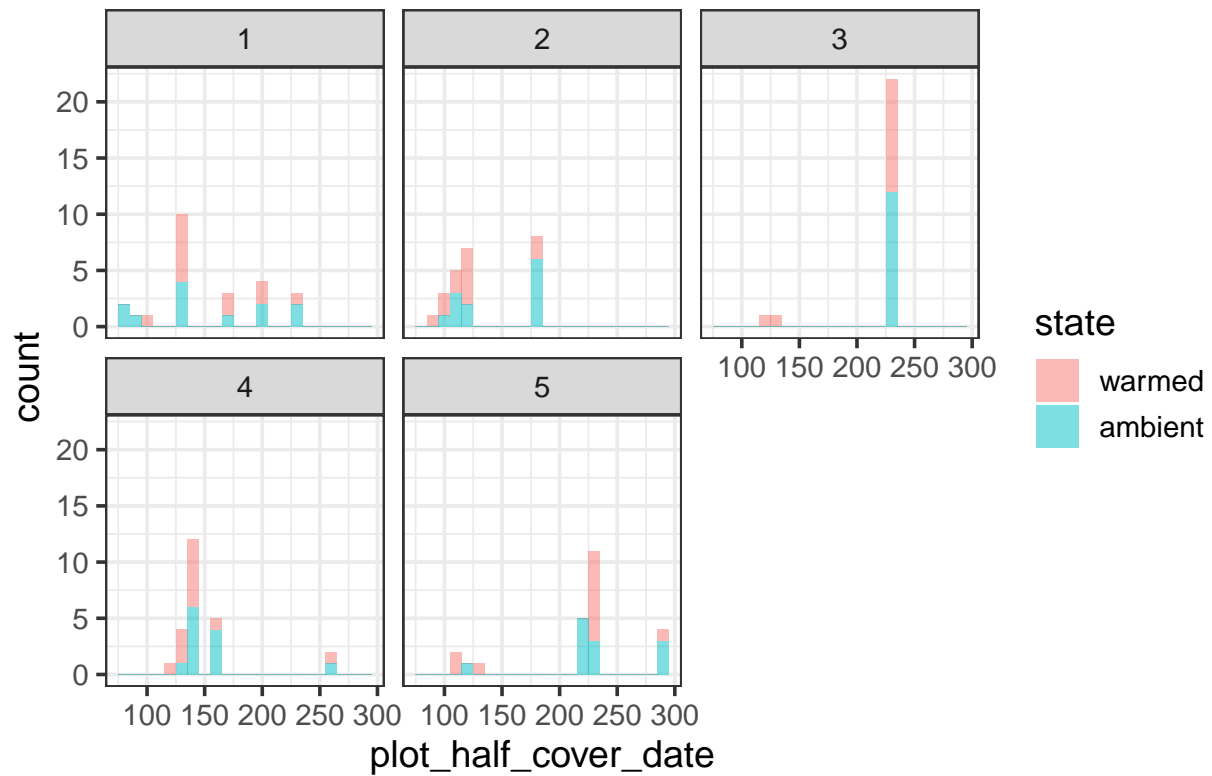
istogram of green_kbsp\$plot_half_cover_date[green_kbsp\$state == "wa



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

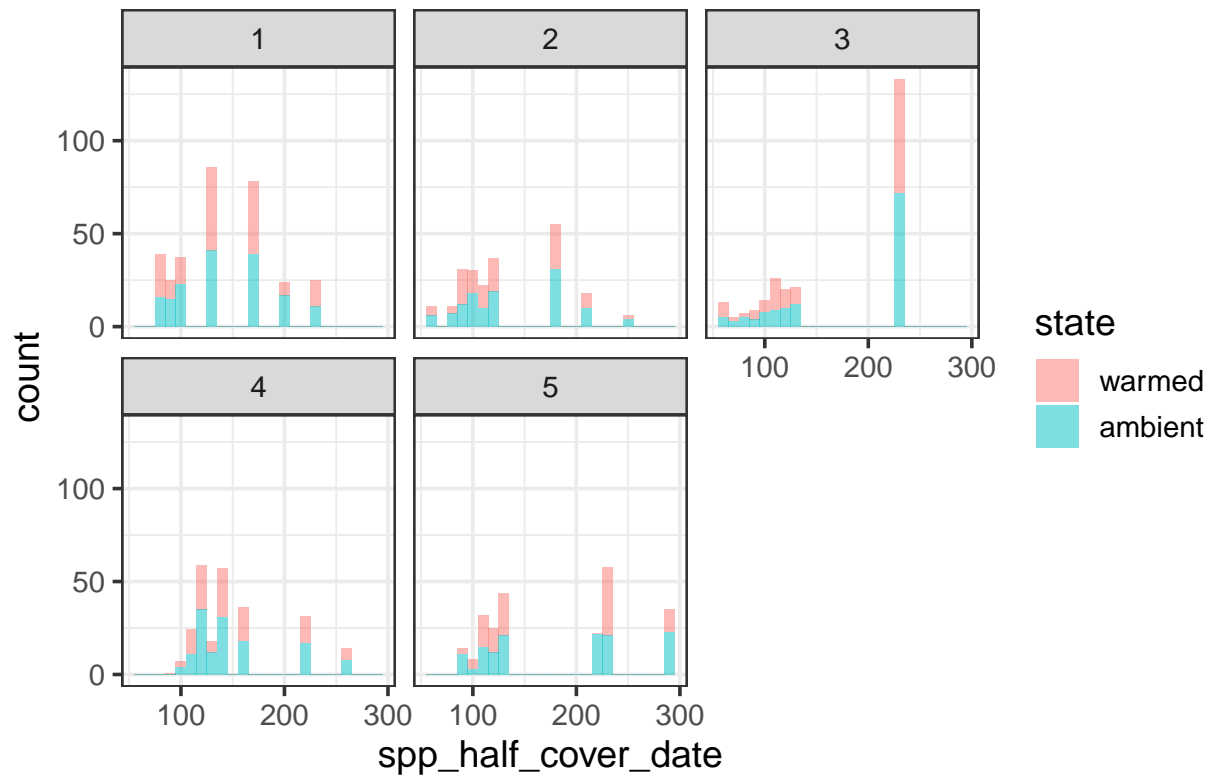
```
# histograms for each year - look at them together:  
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,  
  fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)  
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```

Plot-level half cover date

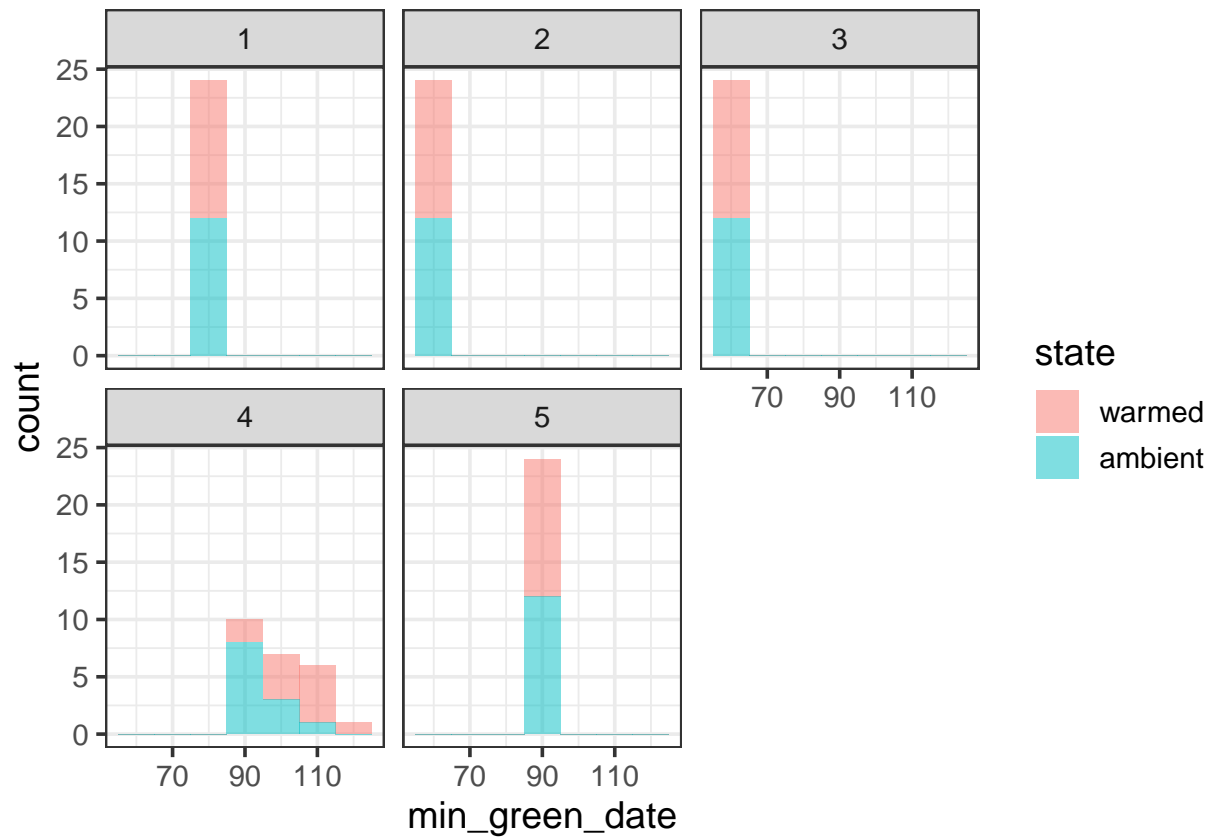


```
p1 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date, fill = state)) +
  geom_histogram(alpha = 0.5, binwidth = 10)
p1 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

Species-level half cover date

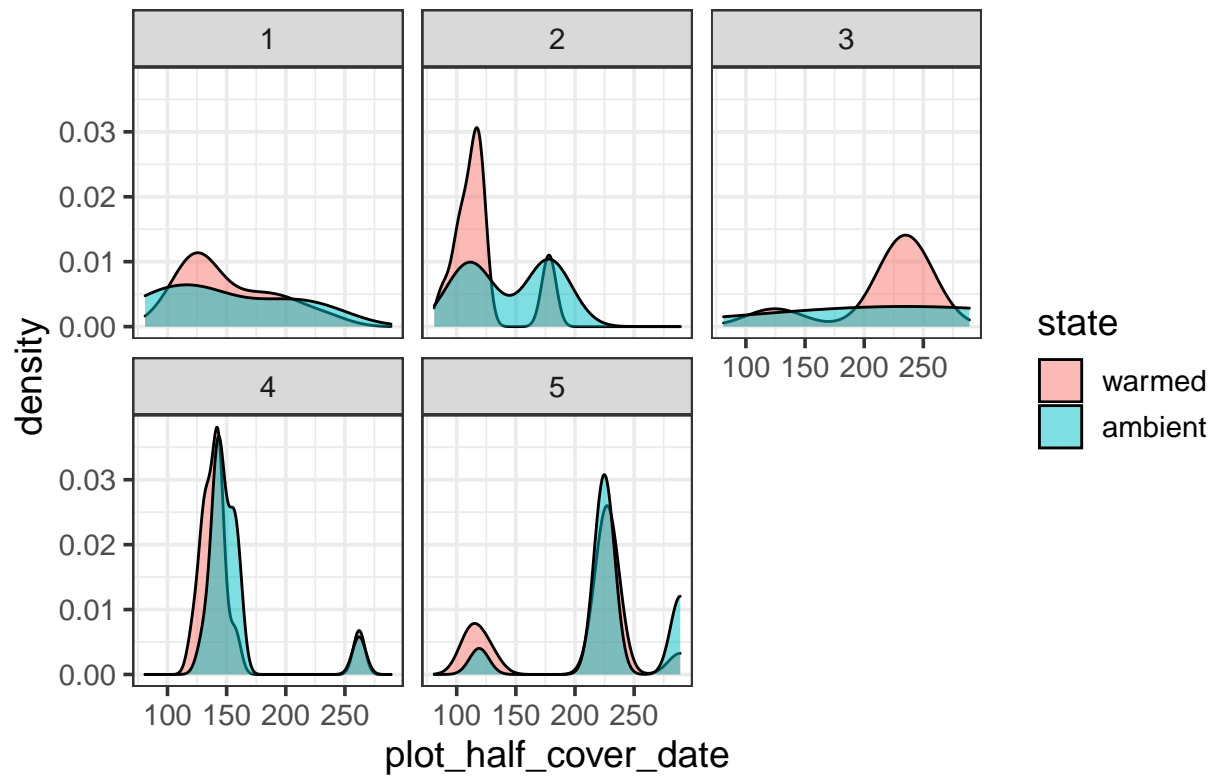


```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
  geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```

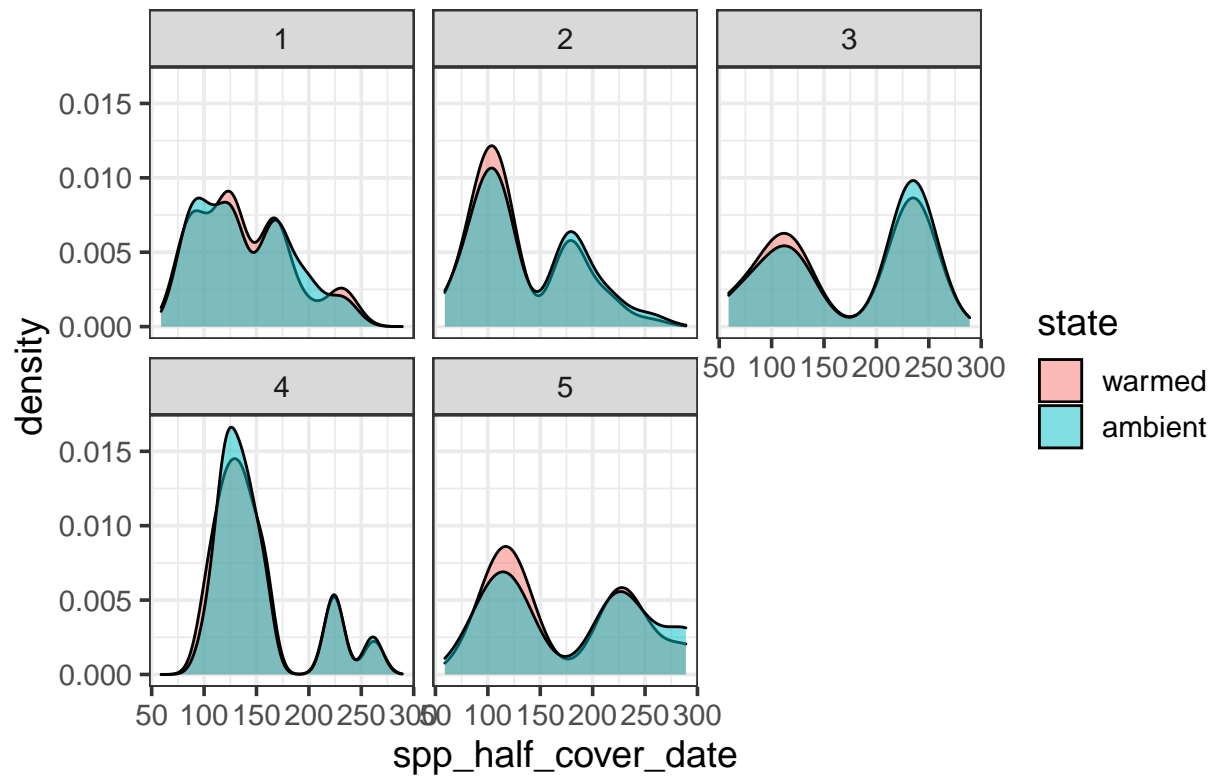
```
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
  fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```

Plot-level half cover date

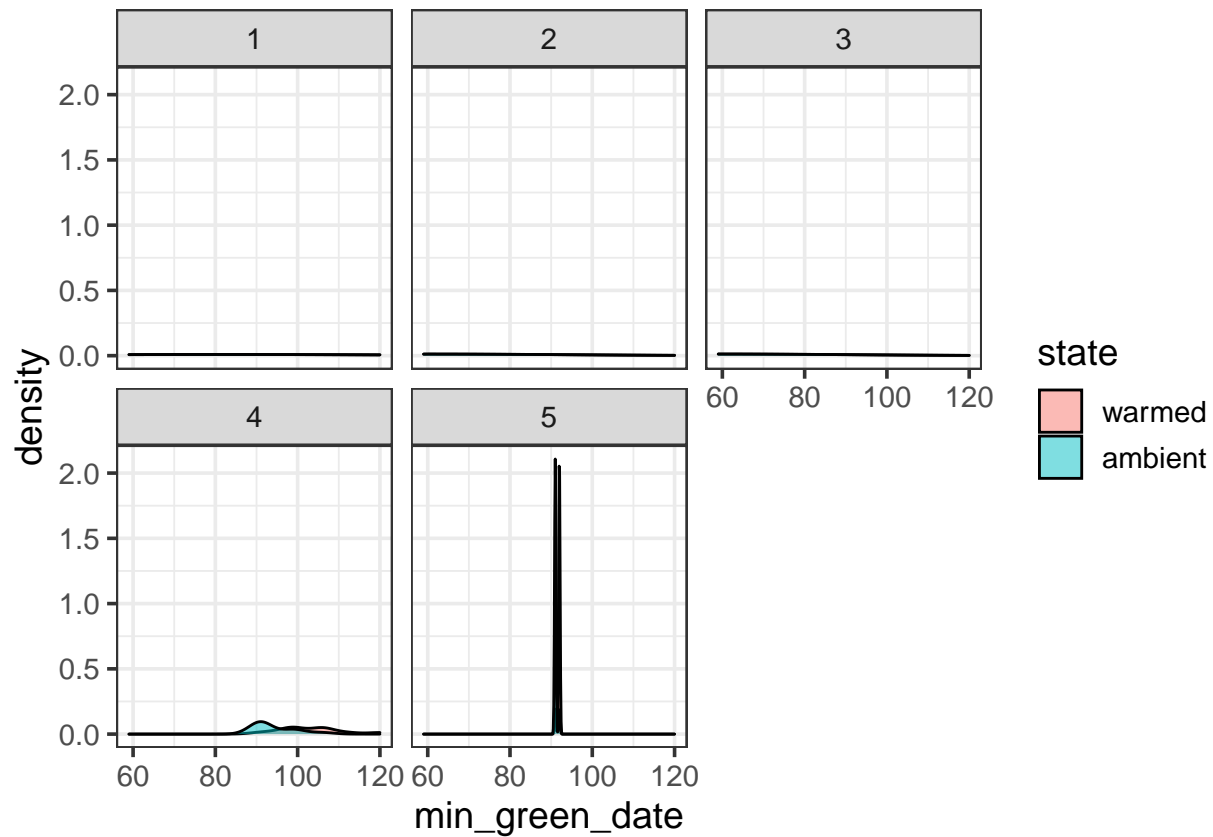


```
p3 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date, fill = state)) +
  geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```

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)
```



```
# 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>

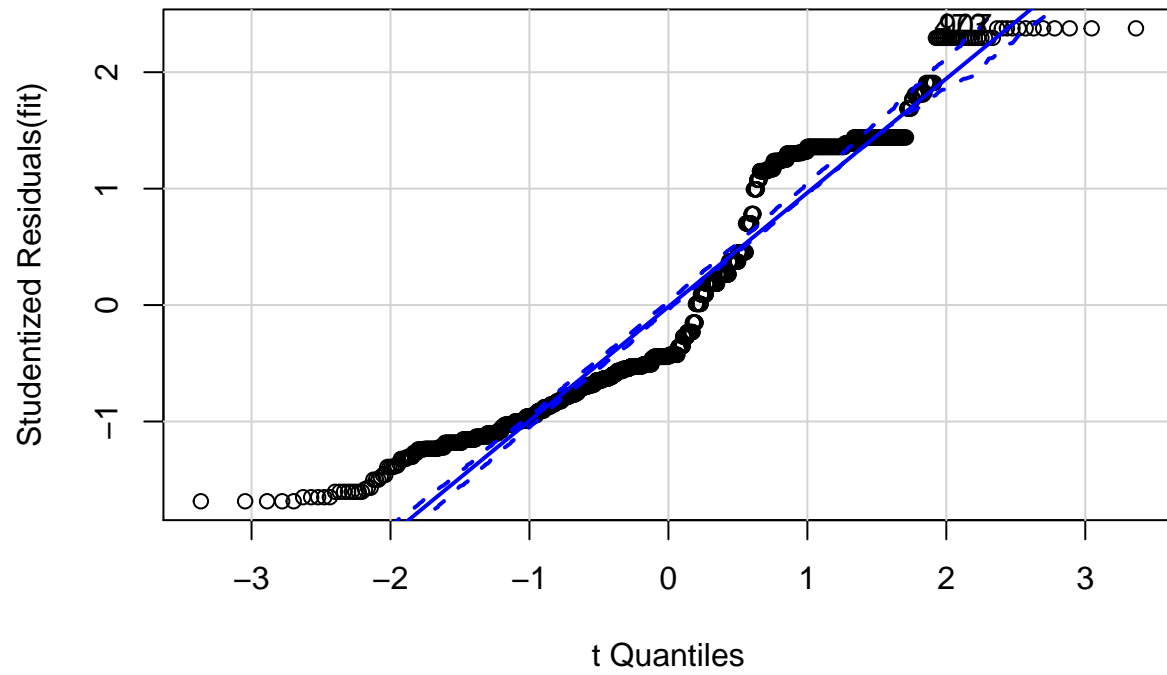
These illustrate whether certain data points have more leverage (more influence), and thus could be outliers. It's a way of detecting outliers. Leverage plots can help identify whether a point has high or low influence, based on its leverage and residual and determining model fit with and without the 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.
```

```
# 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  
## 473 2.376821      0.017611      NA  
qqPlot(fit, main = "QQ Plot")
```

QQ Plot

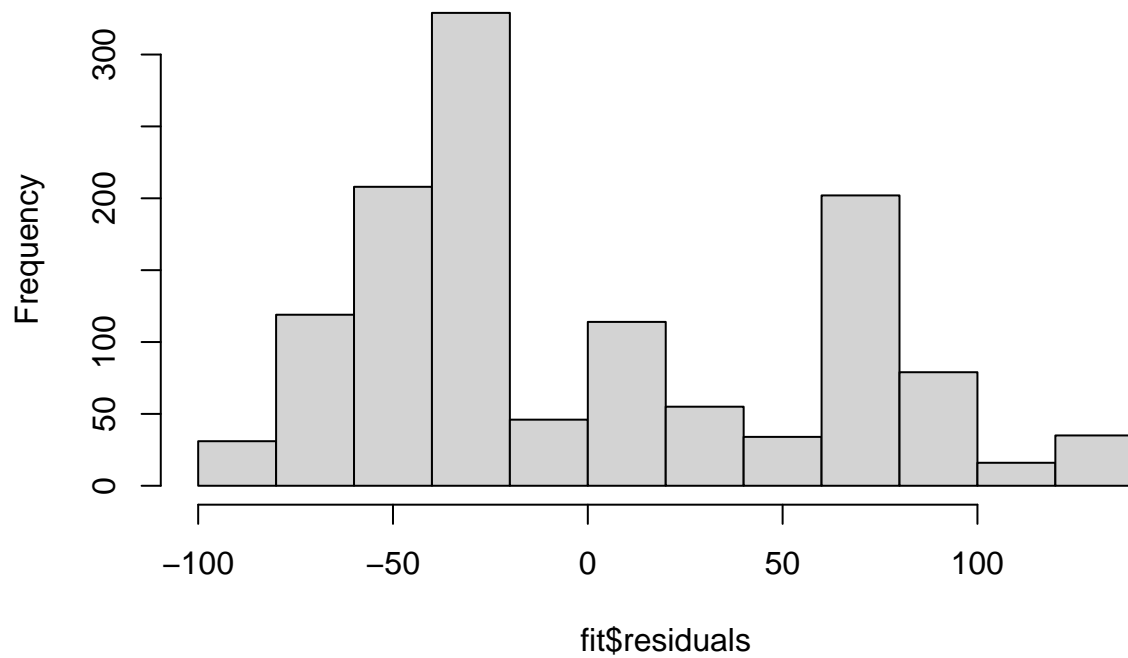


```
## 473 907
```

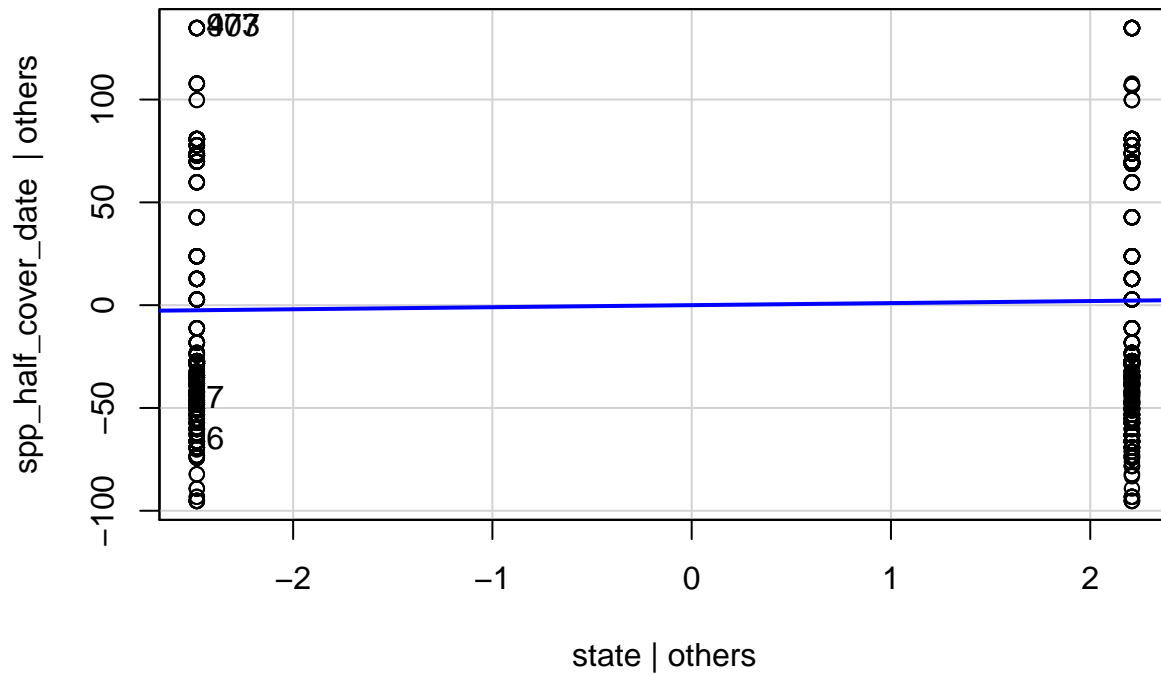
```
## 283 552
```

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

Histogram of fit\$residuals



```
leveragePlots(fit)
```



```
# 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
```

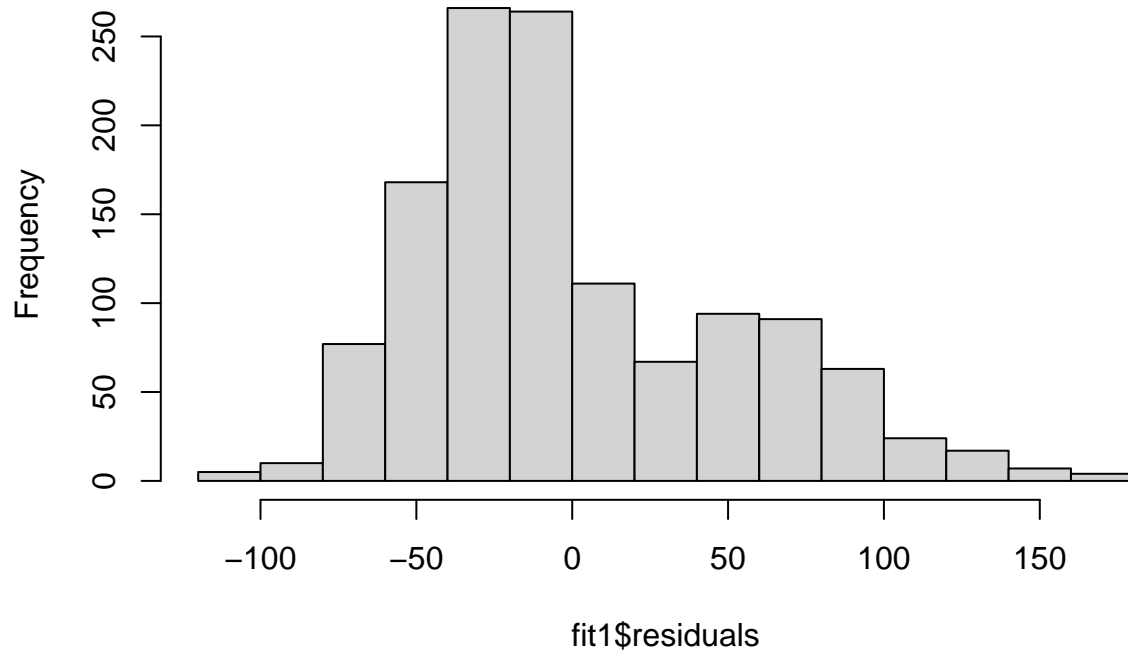
```
## Largest |rstudent|:
```

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

```
## 1910 3.455976      0.00056677      0.71866
```

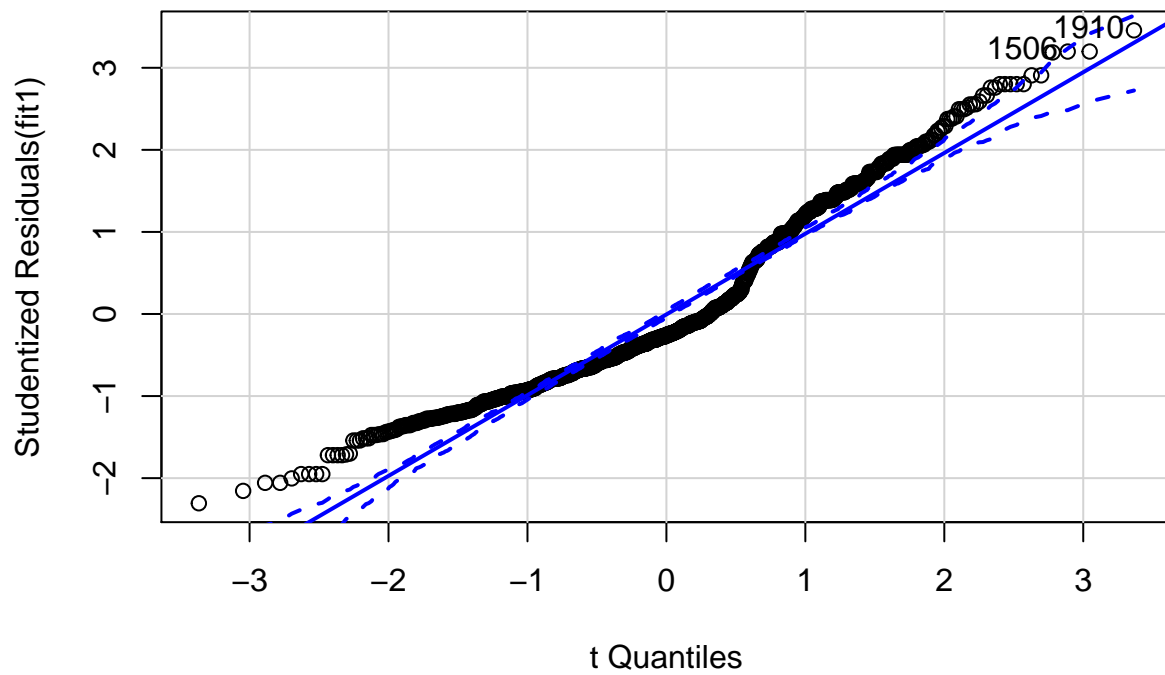
```
hist(fit1$residuals)
```

Histogram of fit1\$residuals



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

QQ Plot

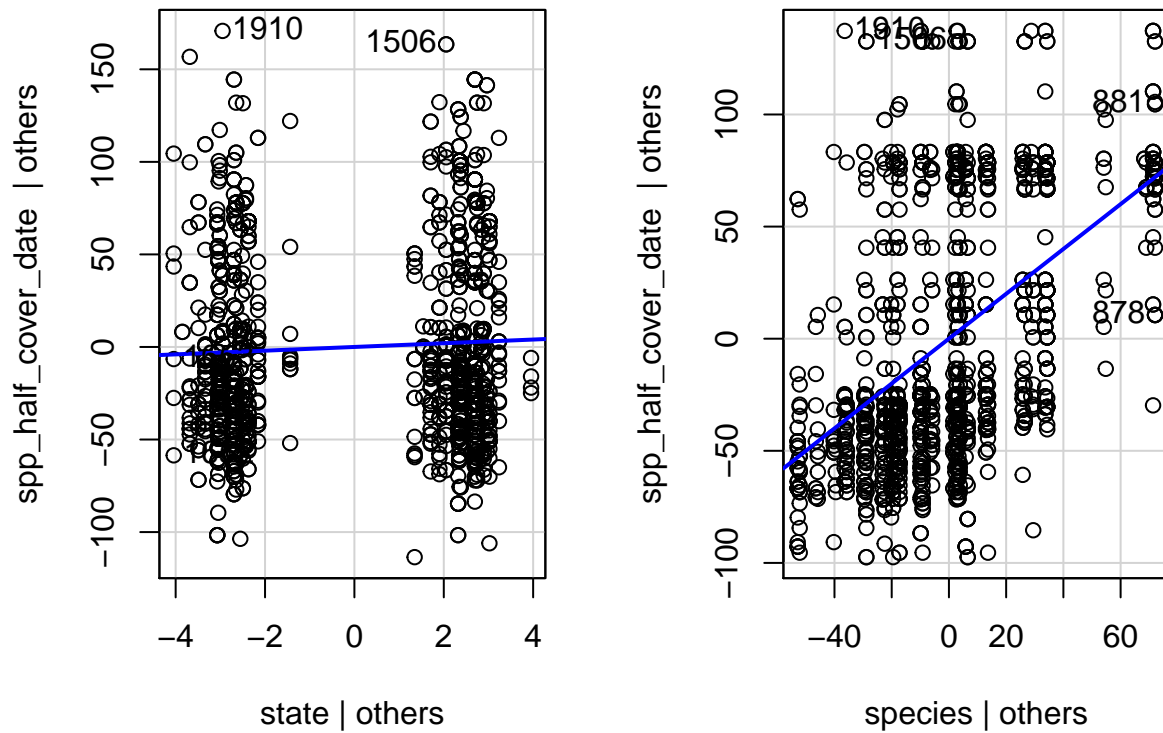


```
## 1506 1910  
## 943 1152
```



```
leveragePlots(fit1)
```

Leverage Plots



```
fit1a <- lm(min_green_date ~ state + species, data = green_kbs)
```

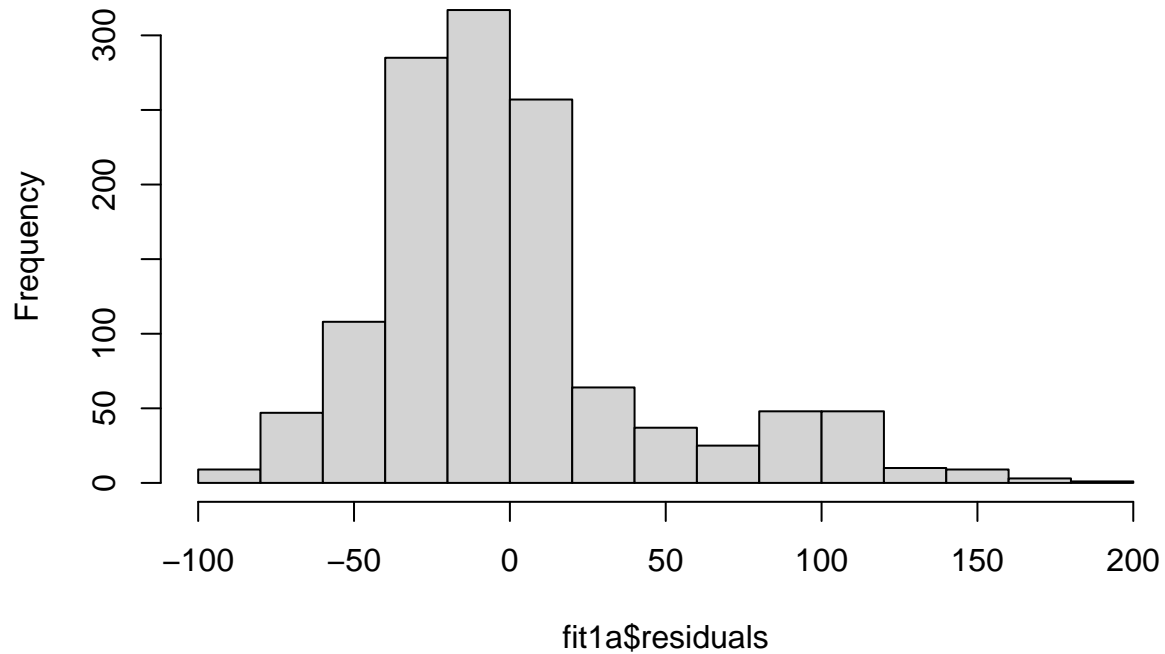
```
outlierTest(fit1a) # record 473 is an outlier, could probably ignore since we aren't using min date as
```

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

```
## 473 4.211351      2.7212e-05      0.034505
```

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

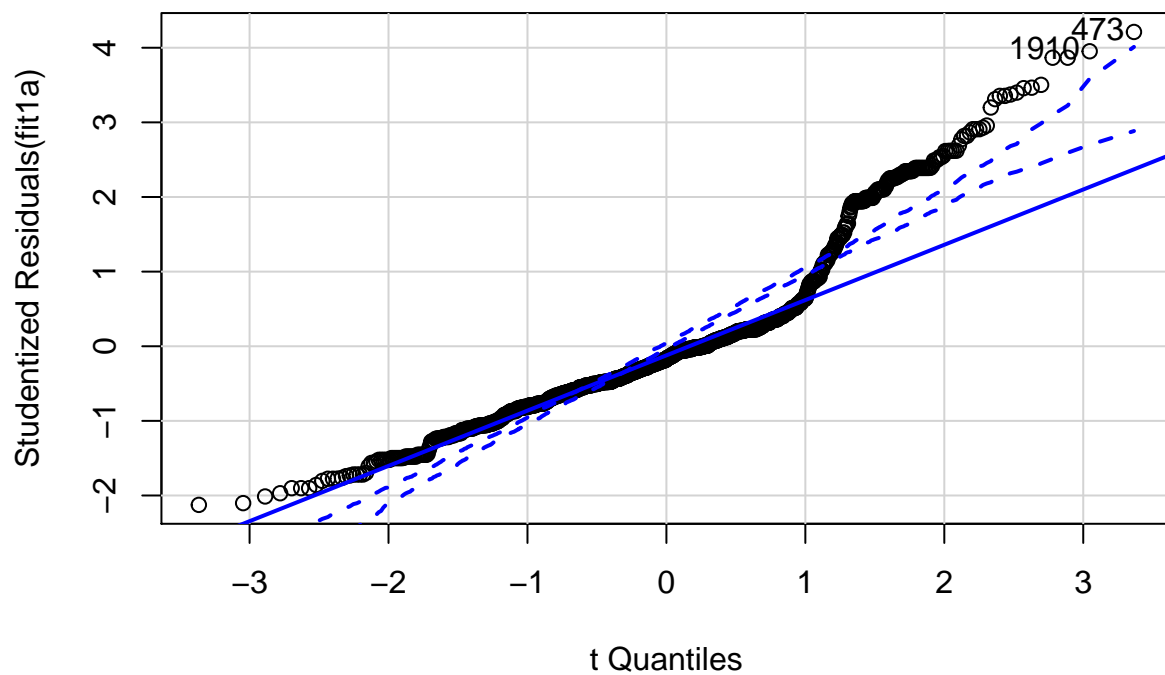
Histogram of fit1a\$residuals



```
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

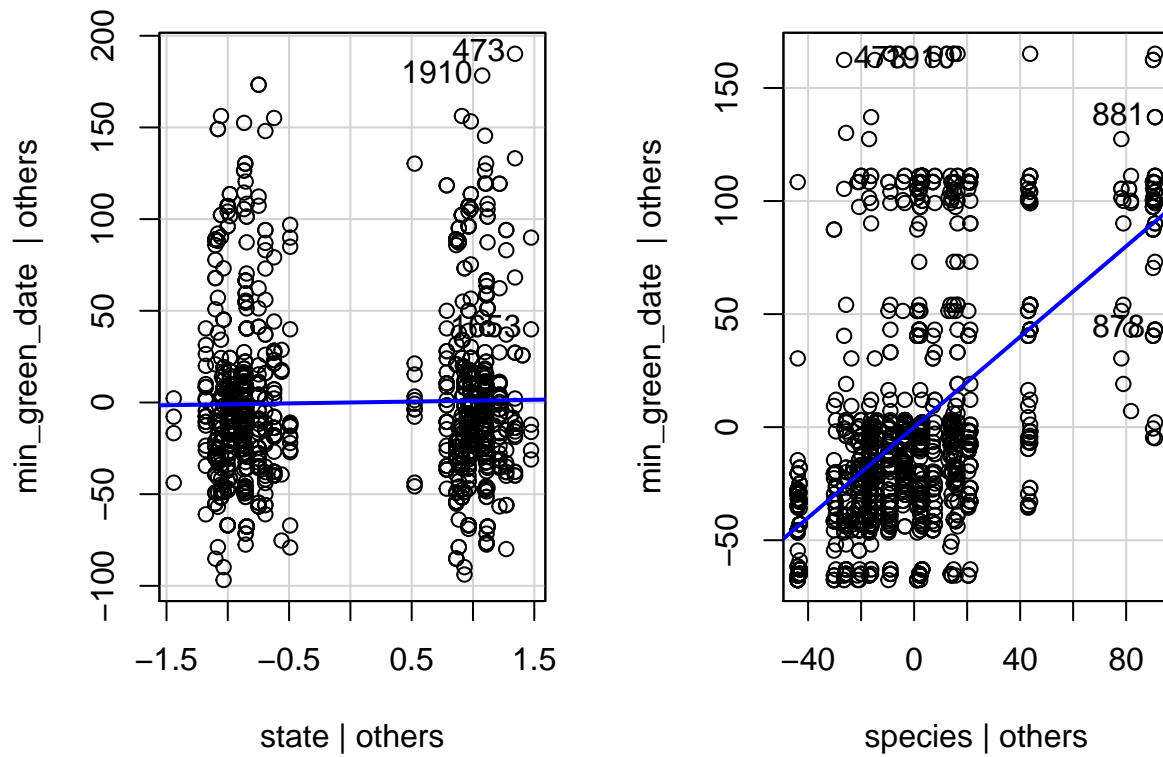


```
## 473 1910
```

```
## 283 1152
```

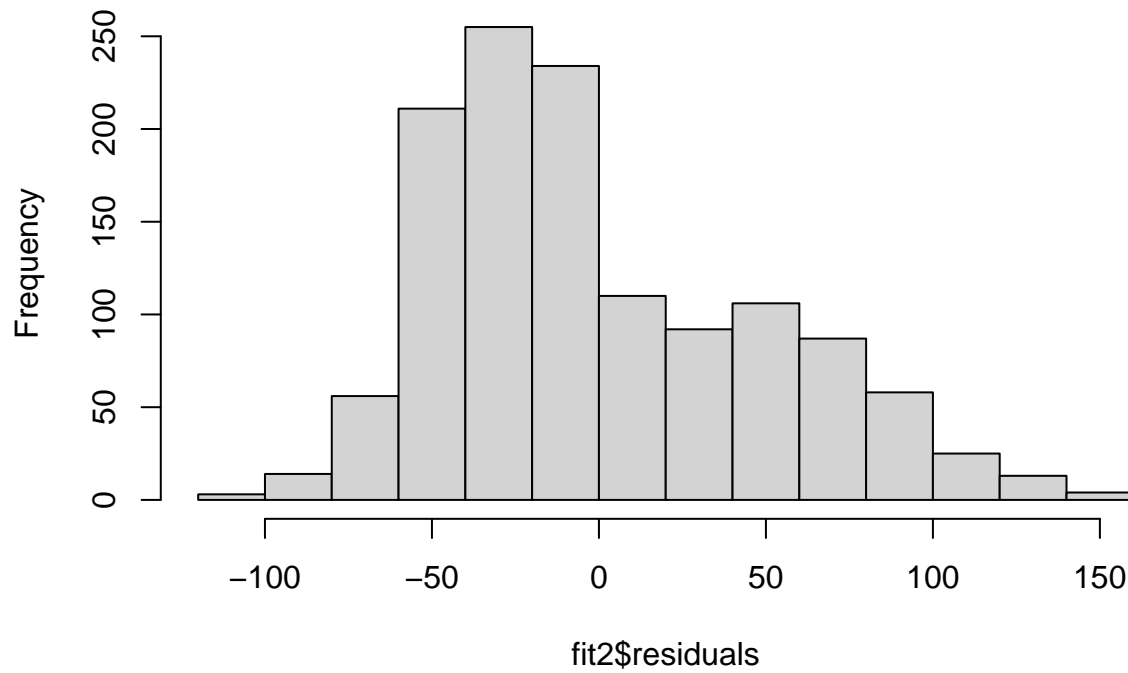
```
leveragePlots(fit1a)
```

Leverage Plots



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

Histogram of fit2\$residuals

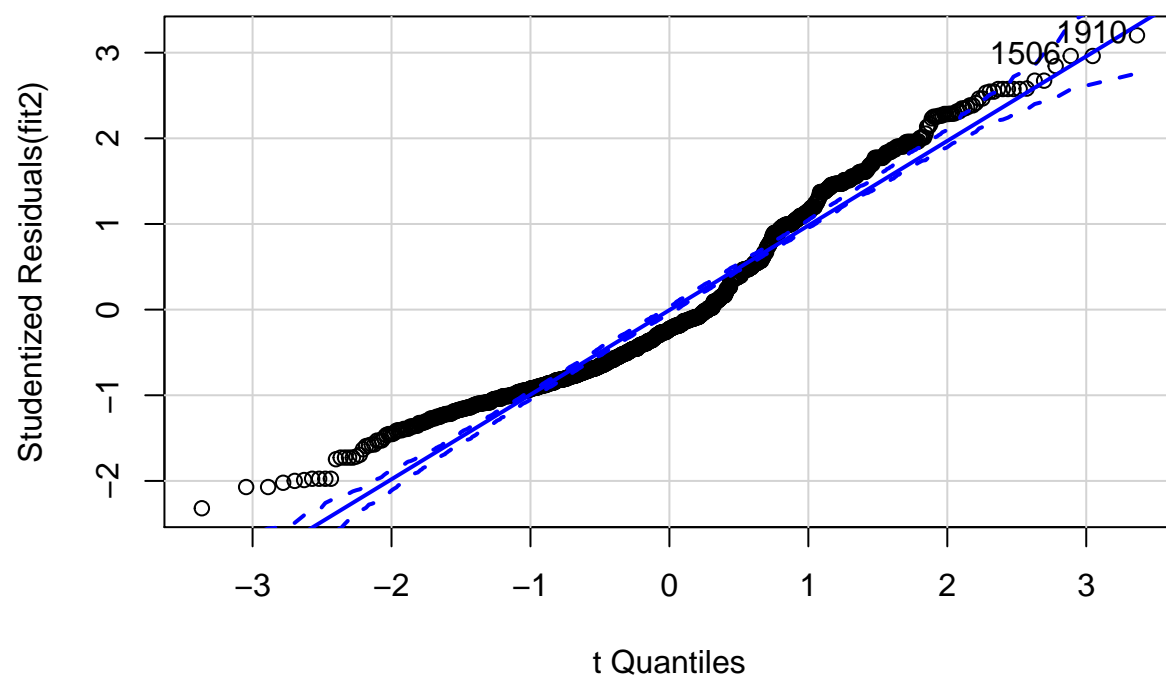


```
outlierTest(fit2) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 1910 3.202366      0.0013976      NA
```

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

QQ Plot

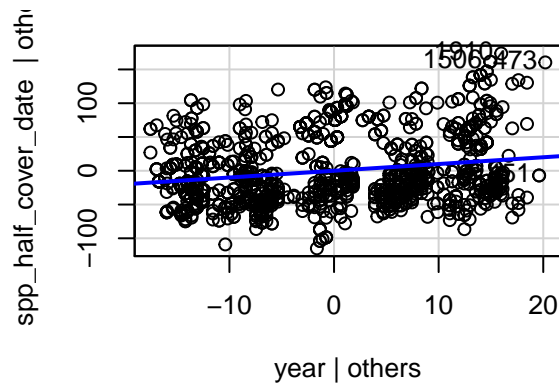
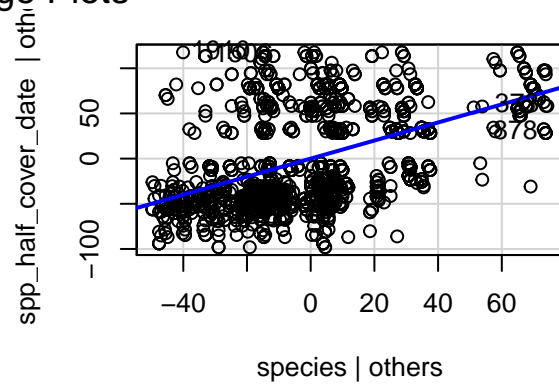
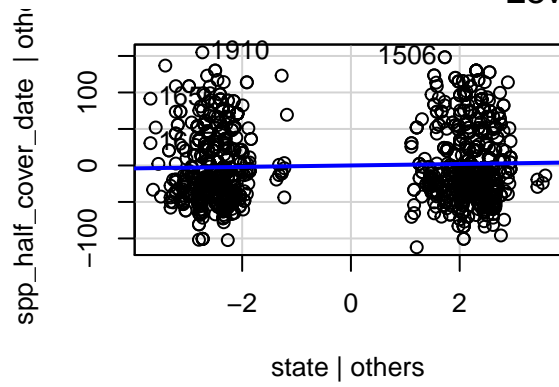


```
## 1506 1910
```

```
## 943 1152
```

```
leveragePlots(fit2)
```

Leverage Plots



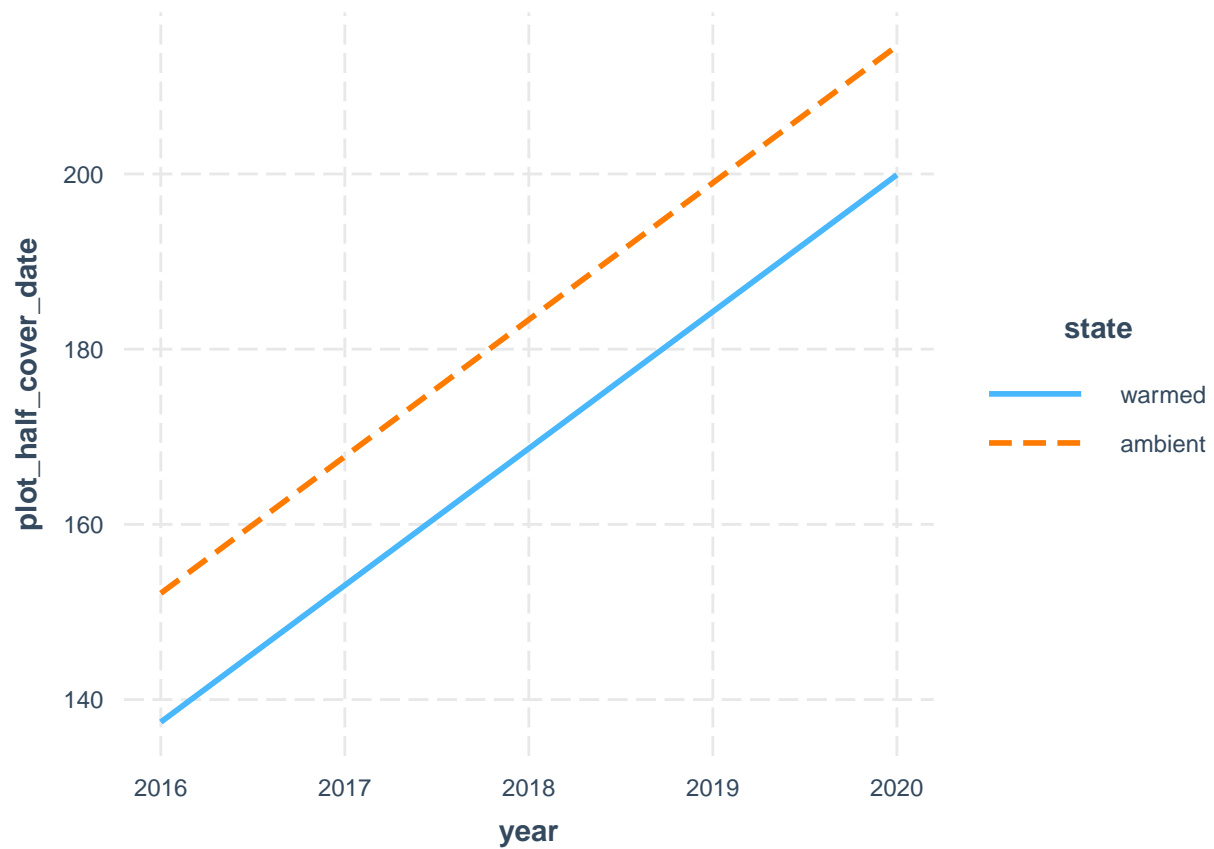
Normal distribution after accounting for species - we will be using species as a random effect to account for their variation. Set up some linear mixed effects models to evaluate. From Ben Bolker: “The traditional view of random effects is as a way to do correct statistical tests when some observations 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).

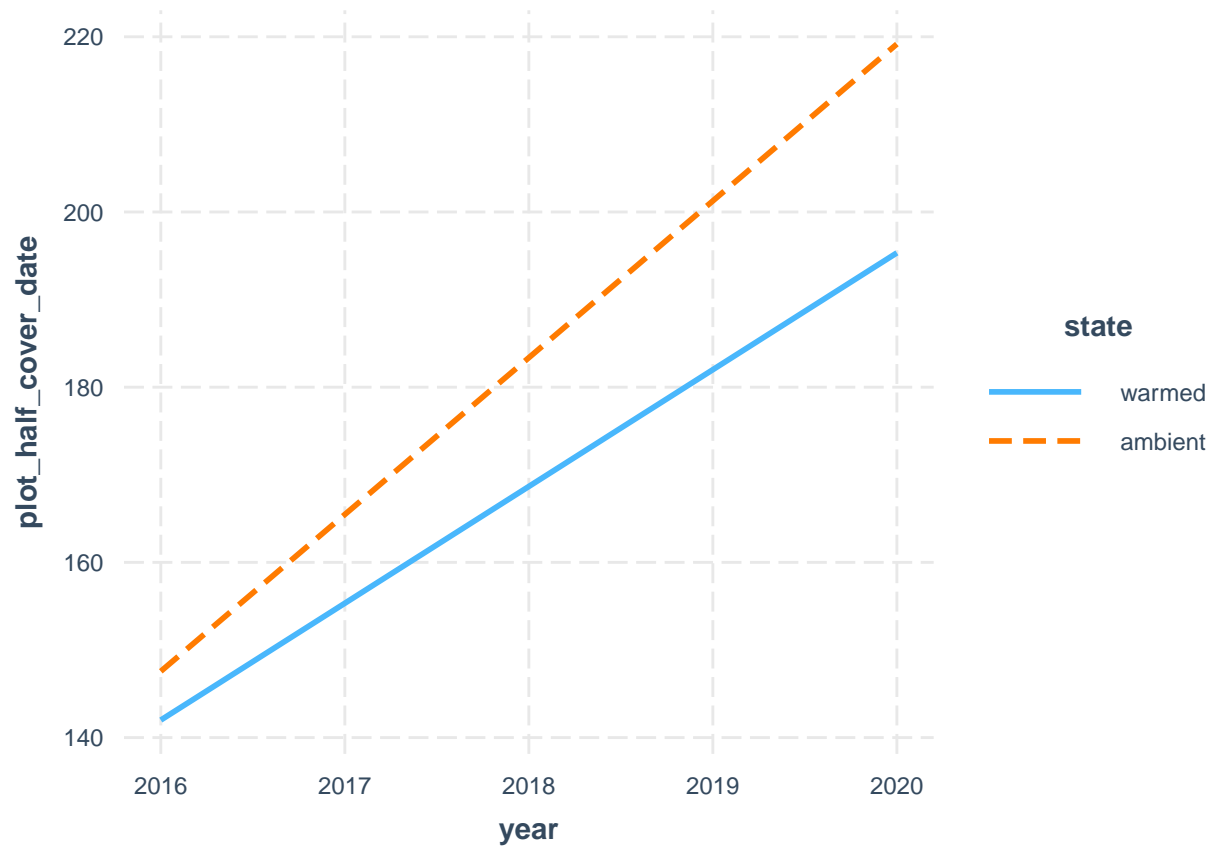
```
# Interaction plot (ignore for now the repeated measures with
# species); see:
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html
# and: https://interactions.jacob-long.com/

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.
```

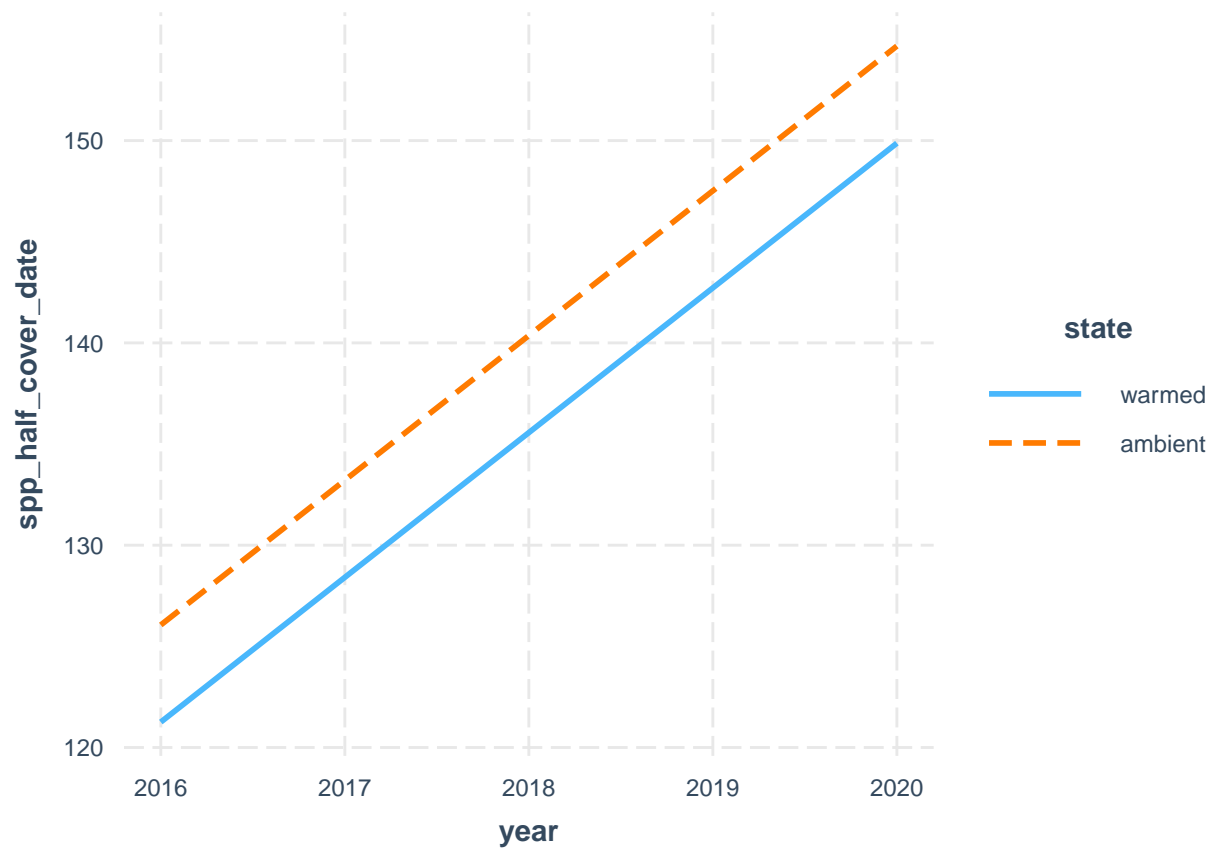


```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```

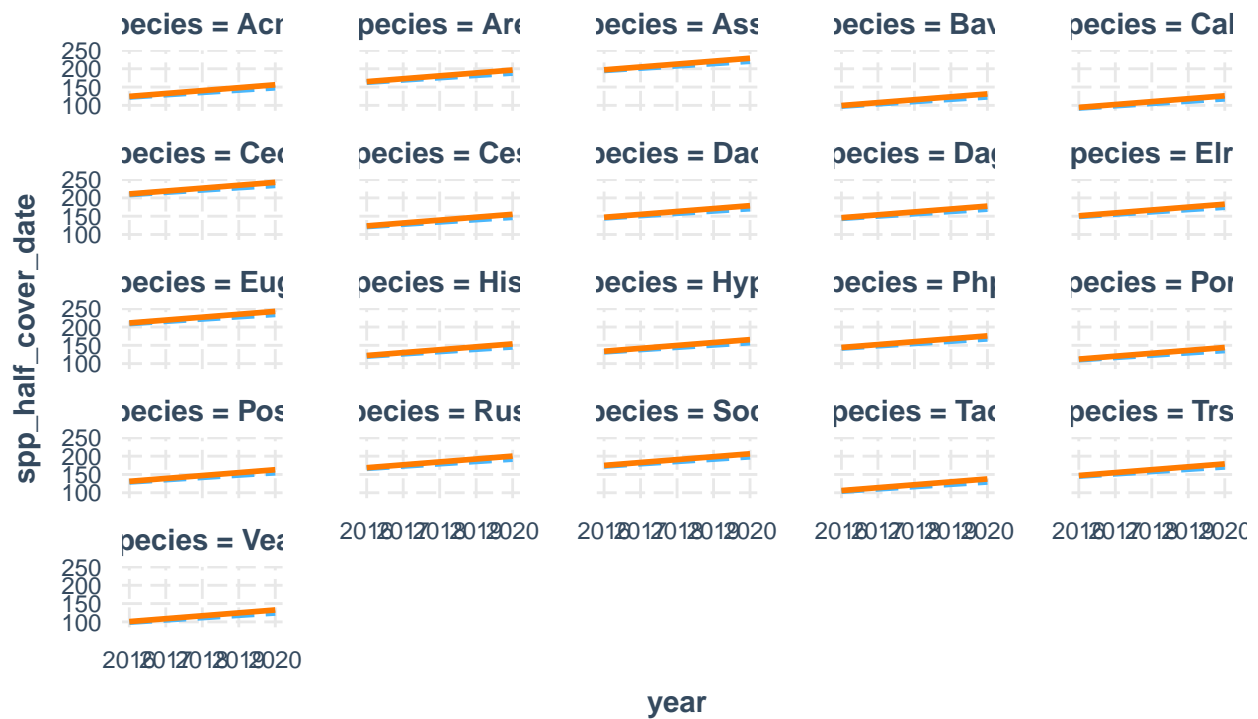
```
fit5 <- lm(spp_half_cover_date ~ state + year + species, data = green_kbs)
interact_plot(fit5, pred = year, modx = state)
```

```
## 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)
```

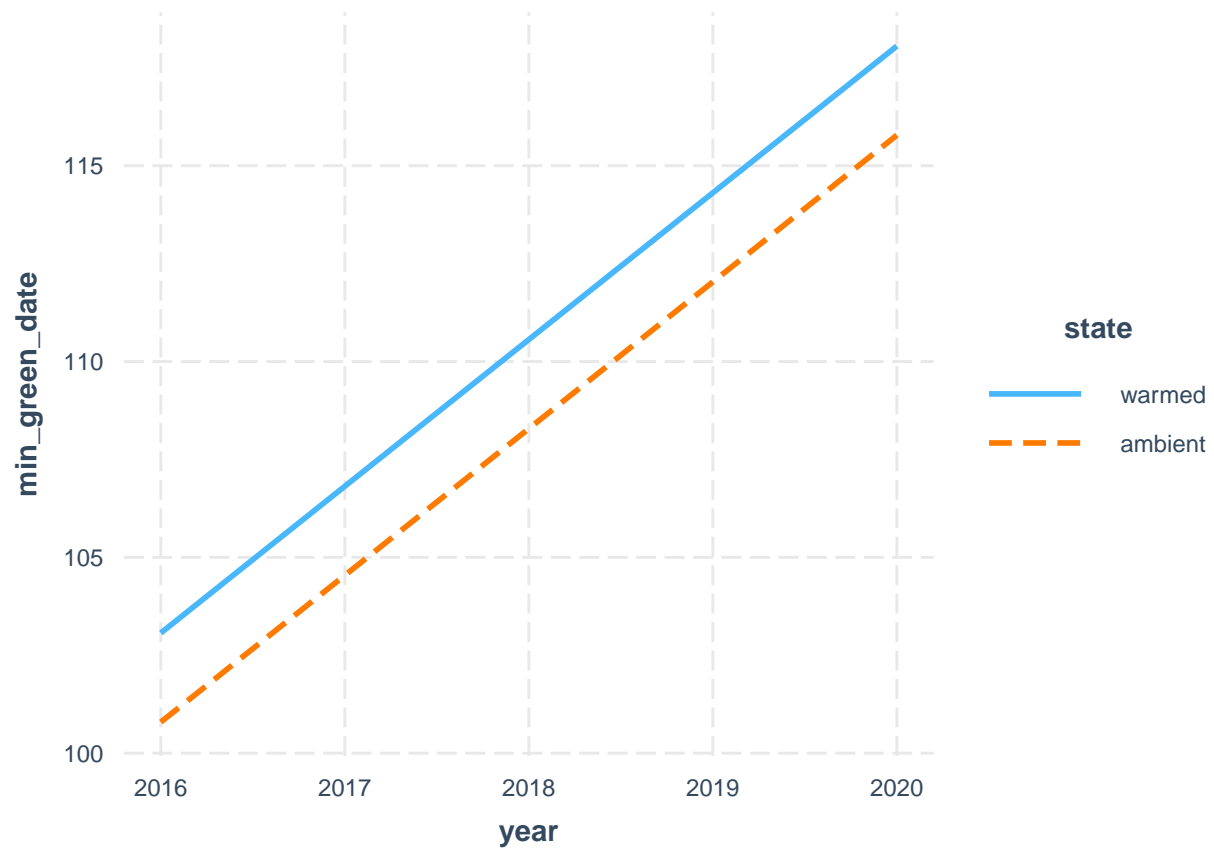
```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```



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.
```



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).
```

```
# Do we need to include plot as a random effect with the KBS
# models?
mod1 <- lmer(spp_half_cover_date ~ state * year + insecticide *
  year + (1 | species) + (1 | plot), green_kbs, REML = FALSE)
```

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

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

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

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

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

```
# 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           1272      1272     1 1235.9  0.5193    0.4713
## year          138894  138894     1 1241.4 56.6968 9.744e-14 ***
## insecticide     3587      3587     1 1233.9  1.4642    0.2265
## state:year       1276      1276     1 1235.9  0.5209    0.4706
## year:insecticide 3596      3596     1 1233.9  1.4681    0.2259
## ---
## 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           1312      1312     1 1247.2  0.5293    0.4670
## year          138522  138522     1 1252.3 55.8679 1.451e-13 ***
## insecticide     3950      3950     1 1247.7  1.5932    0.2071
## state:year       1316      1316     1 1247.2  0.5309    0.4664
## year:insecticide 3961      3961     1 1247.7  1.5977    0.2065
## ---
## 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) # They are different so plot as a random effect should stay in the model (we go with
```

```
## Data: green_kbs
## Models:
## mod2: spp_half_cover_date ~ state * year + insecticide * year + (1 |
## mod2:   species)
## mod1: spp_half_cover_date ~ state * year + insecticide * year + (1 |
## mod1:   species) + (1 | plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2    8 13587 13628 -6785.6    13571
## mod1    9 13586 13632 -6784.0    13568 3.374  1    0.06623 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * year + insecticide * year + (1 |
```

```

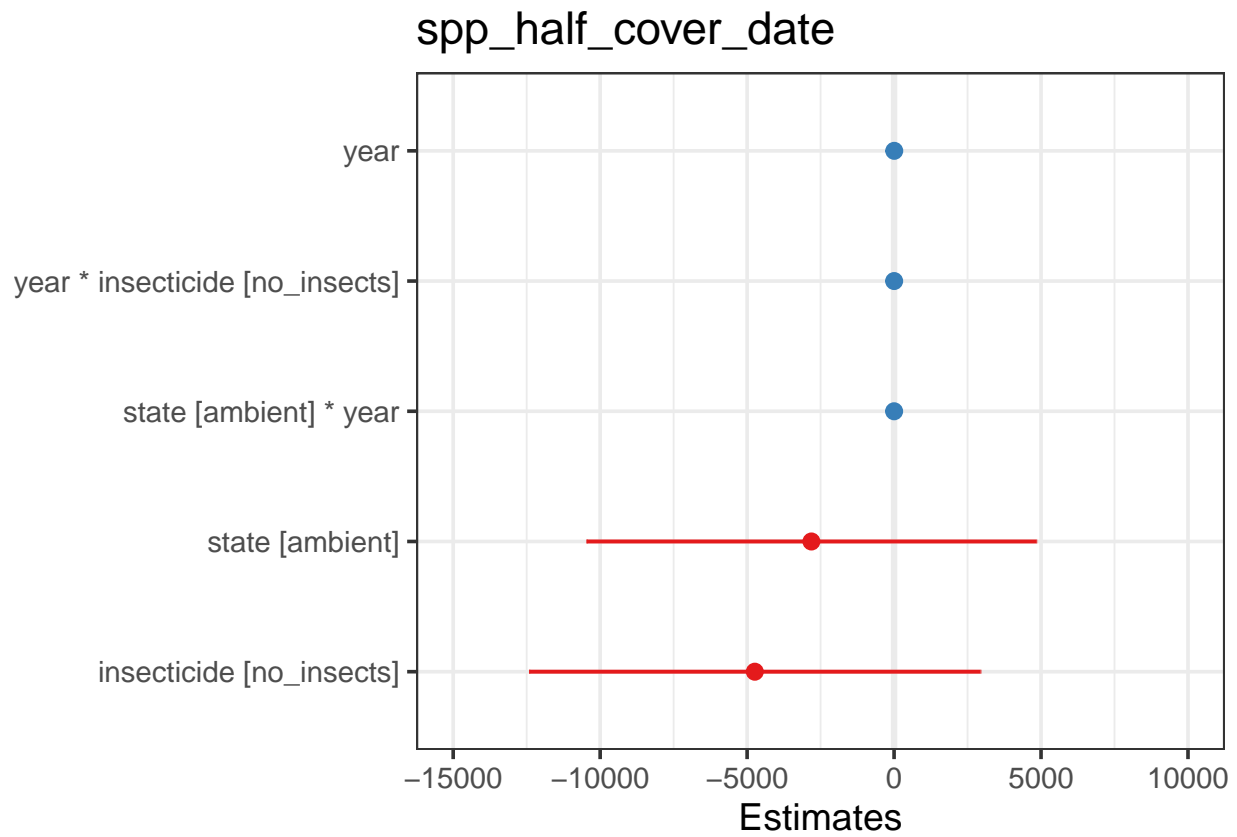
##      species) + (1 | plot)
##      Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 13585.9 13632.2 -6784.0 13567.9    1259
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1194 -0.7683 -0.2513  0.6857  3.2607
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
##      plot      (Intercept)    32.77    5.725
##      species  (Intercept)   930.34   30.502
##      Residual                2449.77  49.495
## Number of obs: 1268, groups: plot, 24; species, 21
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -11128.065    3367.723   1236.896   -3.304 0.000979
## stateambient     -2812.392    3902.785   1235.866   -0.721 0.471285
## year              5.589      1.669   1236.892    3.349 0.000836
## insecticideno_insects -4738.174   3915.775   1233.884   -1.210 0.226502
## stateambient:year      1.396      1.934   1235.875    0.722 0.470576
## year:insecticideno_insects 2.351      1.941   1233.896    1.212 0.225879
##
## (Intercept)          ***
## stateambient
## year                  ***
## insecticideno_insects
## stateambient:year
## year:insecticideno_insects
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year   insct_ sttmb:
## stateambint -0.583
## year        -1.000  0.583
## insctcdn_ns -0.519 -0.062  0.519
## statmbnt:yr  0.583 -1.000 -0.583  0.062
## yr:nsctcdn_  0.519  0.062 -0.519 -1.000 -0.062
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
summary(mod2)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * year + insecticide * year + (1 |
##      species)
##      Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 13587.3 13628.4 -6785.6 13571.3    1260

```

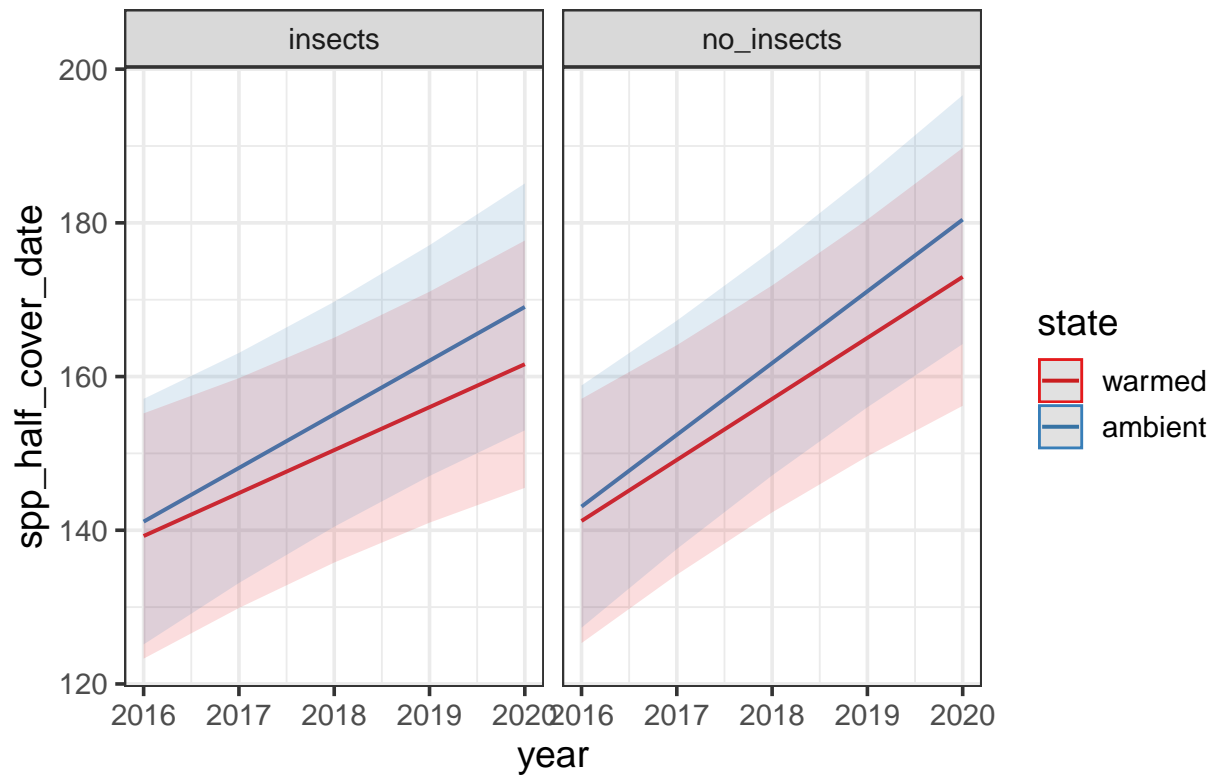
```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2600 -0.7665 -0.2441  0.6924  3.2567
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   species (Intercept) 951.2    30.84
##   Residual          2479.5    49.79
## Number of obs: 1268, groups: species, 21
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   -10945.494   3381.228  1247.990  -3.237  0.00124 **
## stateambient    -2850.741   3918.330  1247.175  -0.728  0.46703
## year              5.498     1.676   1247.982   3.282  0.00106 **
## insecticideno_insects -4965.169  3933.683  1247.647  -1.262  0.20711
## stateambient:year    1.415     1.942   1247.177   0.729  0.46635
## year:insecticideno_insects 2.464     1.949   1247.650   1.264  0.20647
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year   insct_ sttmb:
## stateambint -0.583
## year        -1.000  0.583
## insctcdn_ns -0.520 -0.061  0.520
## statmbnt:yr  0.583 -1.000 -0.583  0.061
## yr:nsctcdn_  0.520  0.061 -0.520 -1.000 -0.061
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling

# 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(mod1, sort.est = TRUE)
```

```
# these are the fixed predicted values:  
plot_model(mod1, type = "pred", terms = c("year", "state", "insecticide"))
```

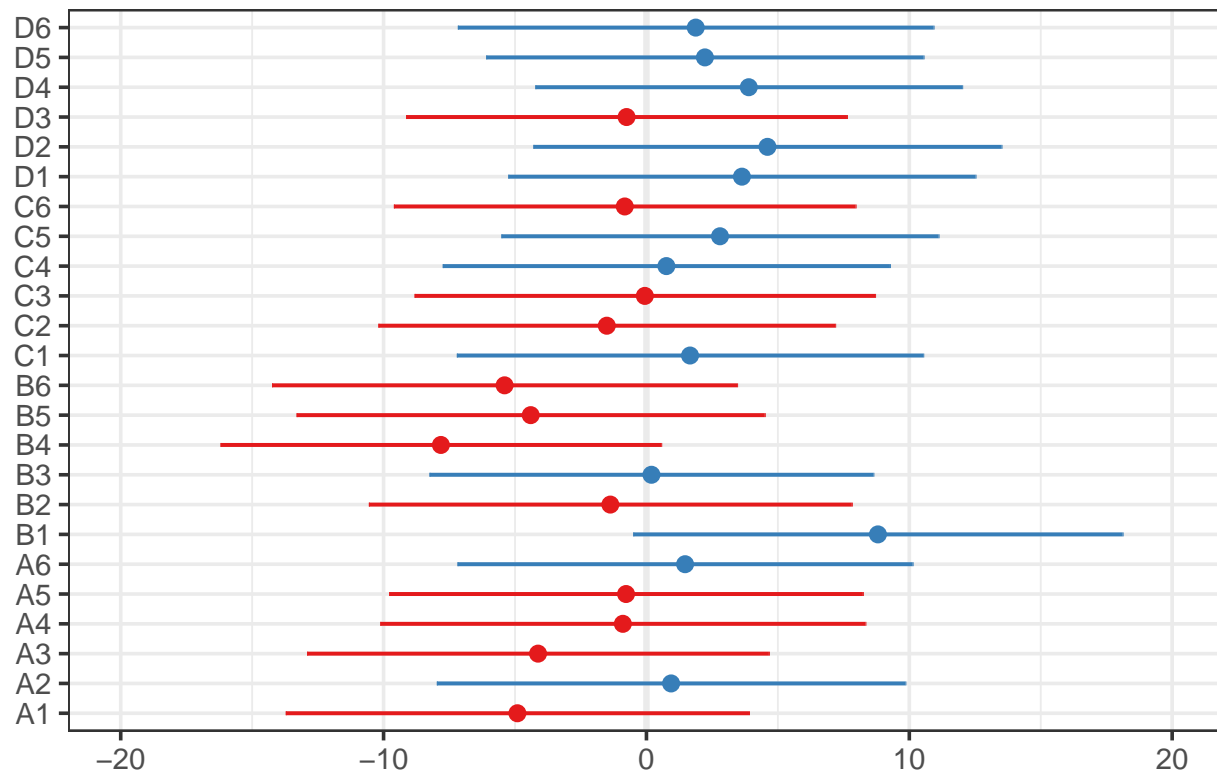
Predicted values of spp_half_cover_date



```
# these are the random effects estimates  
plot_model(mod1, type = "re", terms = c("species", "plot"))
```

```
## [[1]]
```

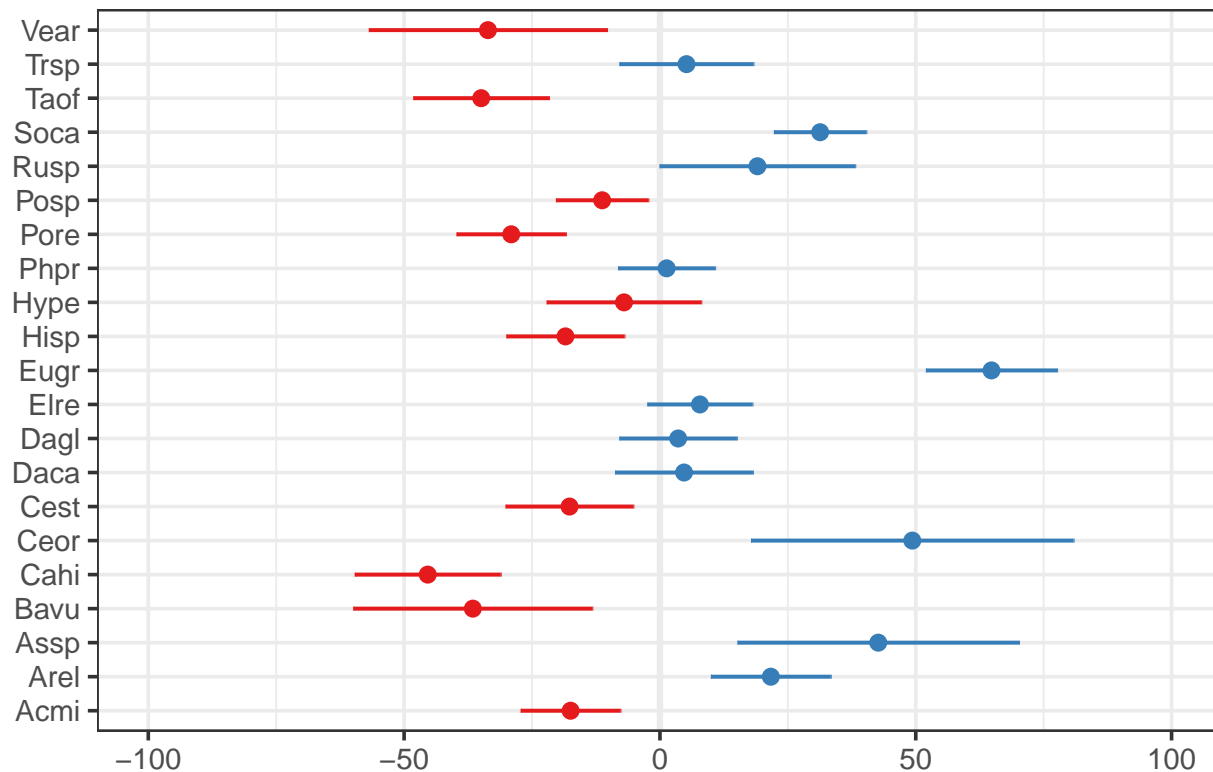
Random effects



##

[[2]]

Random effects



Do we need to include insecticide?

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

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

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

```
anova(mod1, mod3)
```

```
## Data: green_kbs
```

```
## Models:
```

```
## mod3: spp_half_cover_date ~ state * year + (1 | species)
```

```
## mod1: spp_half_cover_date ~ state * year + insecticide * year + (1 |
```

```
## mod1: species) + (1 | plot)
```

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

```
## mod3    6 13591 13622 -6789.5    13579
```

```
## mod1    9 13586 13632 -6784.0    13568 10.994  3    0.01176 *
```

```
## ---
```

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

```
AICctab(mod1, mod3, weights = T)
```

```
##      dAICc df weight
```

```
## mod1 0.0   9  0.921
```

```
## mod3 4.9   6  0.079
```

```

# Looks like yes  $P < 0.05$ , insecticide improves model fit so we
# will continue to include it and stick with mod1

# Does year need to be interactive with insecticide?
mod4 <- lmer(spp_half_cover_date ~ state * year + insecticide +
  (1 | species) + (1 | plot), green_kbs, REML = FALSE)

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

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

anova(mod1, mod4)

## Data: green_kbs
## Models:
## mod4: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## mod4: (1 | plot)
## mod1: spp_half_cover_date ~ state * year + insecticide * year + (1 |
## mod1: species) + (1 | plot)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod4     8 13585 13626 -6784.7    13569
## mod1     9 13586 13632 -6784.0    13568 1.4664  1      0.2259

# 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 + (1 | species)
## mod4: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## mod4: (1 | plot)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3     6 13591 13622 -6789.5    13579
## mod4     8 13585 13626 -6784.7    13569 9.5277  2    0.008533 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Yes,  $P < 0.05$  so insecticide still improves model fit so we
# will stay with mod4

# Does year need to be interactive with state?
mod5 <- lmer(spp_half_cover_date ~ state + year + insecticide +
  (1 | species) + (1 | plot), green_kbs, REML = FALSE)
anova(mod4, mod5)

## Data: green_kbs
## Models:
## mod5: spp_half_cover_date ~ state + year + insecticide + (1 | species) +
## mod5: (1 | plot)
## mod4: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## mod4: (1 | plot)
##      npar   AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5     7 13584 13620 -6785.0    13570

```

```
## mod4      8 13585 13626 -6784.7    13569 0.6369 1      0.4249
AICctab(mod4, mod5, weights = T)

##      dAICc df weight
## mod5 0.0   7  0.67
## mod4 1.4   8  0.33

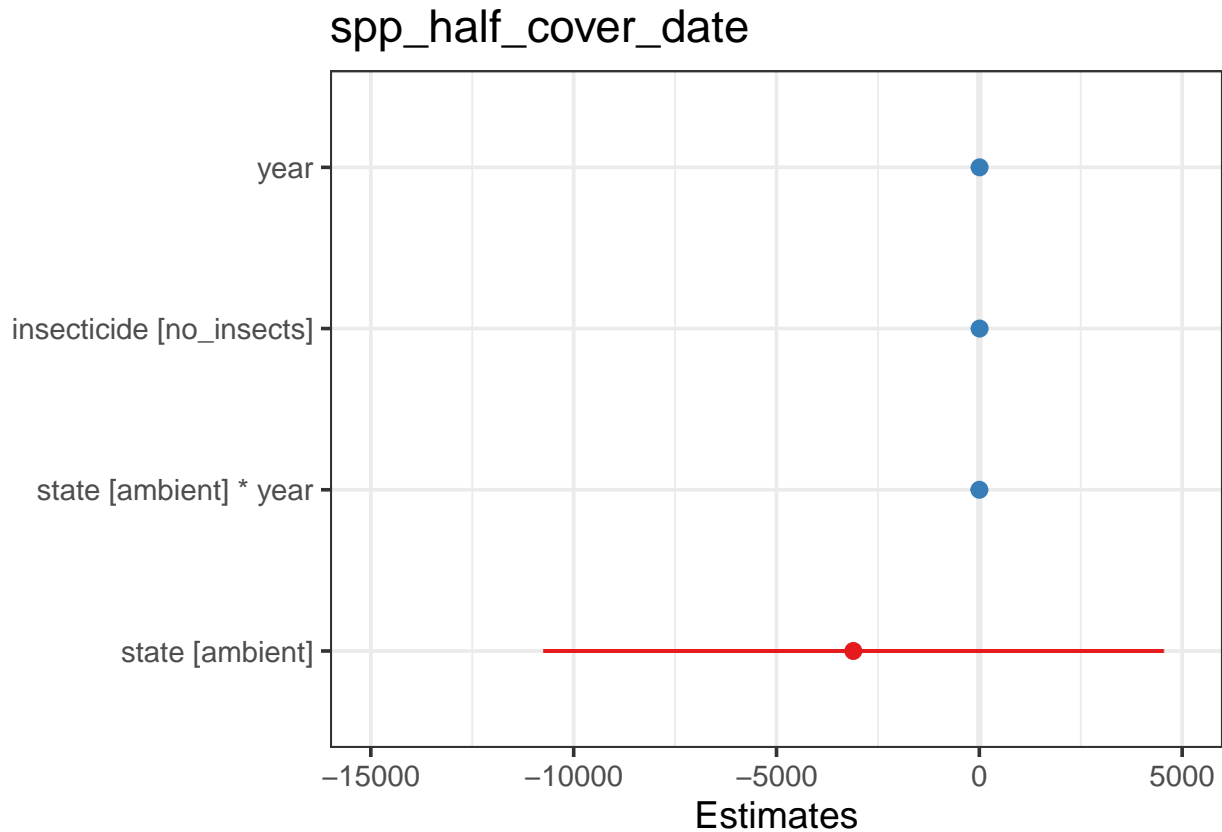
# No, P>0.05 so state*year doesn't improve model fit so we
# could drop it and go with mod5, but note that the AIC
# values are super close. mod4 makes sense, with increased
# divergence between warmed and ambient.
summary(mod5)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year + insecticide + (1 | species) +
## (1 | plot)
## Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
##    13584    13620    -6785    13570     1261
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1127 -0.7727 -0.2469  0.6665  3.1808
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 33.61 5.798
## species (Intercept) 931.11 30.514
## Residual 2453.43 49.532
## Number of obs: 1268, groups: plot, 24; species, 21
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -1.491e+04  1.995e+03  1.241e+03 -7.470 1.51e-13 ***
## stateambient  4.622e+00  3.701e+00  2.128e+01  1.249  0.2253
## year         7.461e+00  9.888e-01  1.241e+03  7.545 8.70e-14 ***
## insecticideno_insects 6.441e+00  3.692e+00  2.101e+01  1.745  0.0956 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year
## stateambint  0.025
## year        -1.000 -0.026
## insctcdn_ns -0.060 -0.038  0.059
anova(mod4)

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state         1558    1558      1 1235.90  0.6352  0.42561
## year        137200  137200      1 1241.48 55.9464 1.404e-13 ***
## insecticide   7282    7282      1   21.05  2.9693  0.09952 .
```

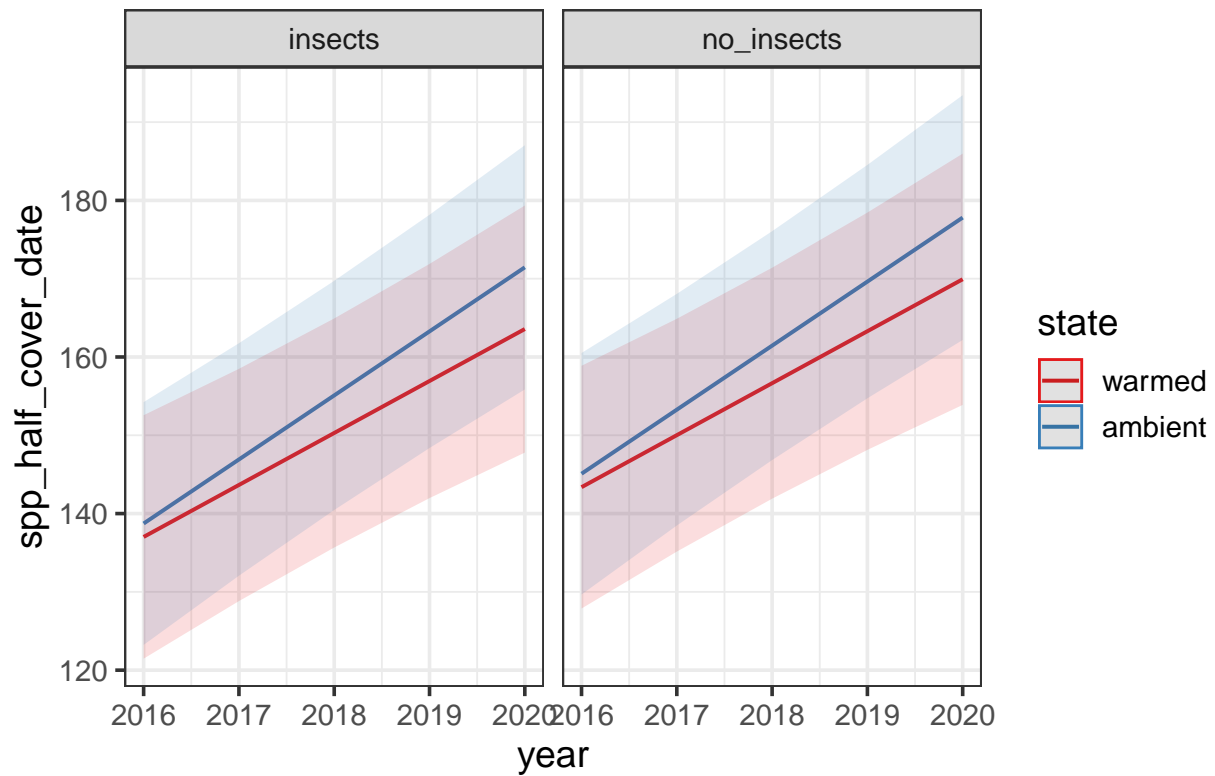
```
## state:year    1562    1562    1 1235.91  0.6371  0.42493
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# these are the fixed effects estimates from summary(mod4)
plot_model(mod4, sort.est = TRUE)
```



```
# these are the fixed predicted values:
plot_model(mod4, type = "pred", terms = c("year", "state", "insecticide"))
```

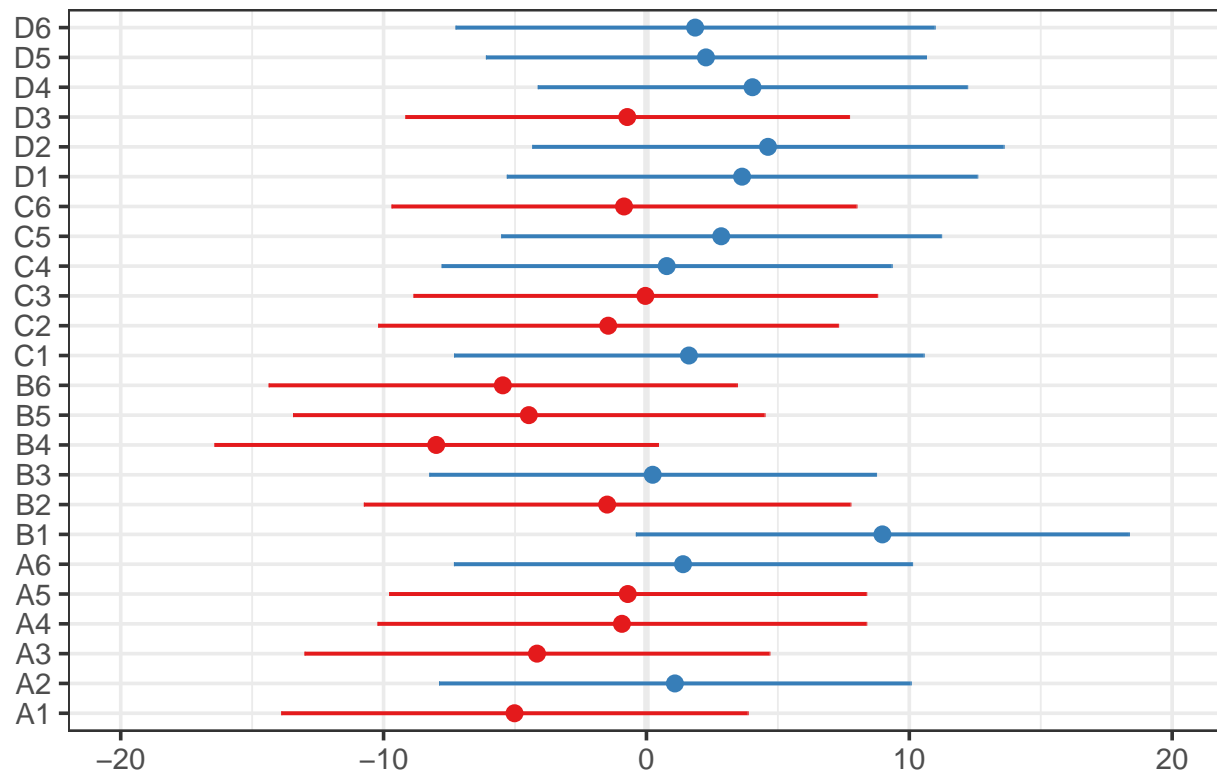
Predicted values of spp_half_cover_date



```
# these are the random effects estimates
plot_model(mod4, type = "re", terms = c("species", "plot"))
```

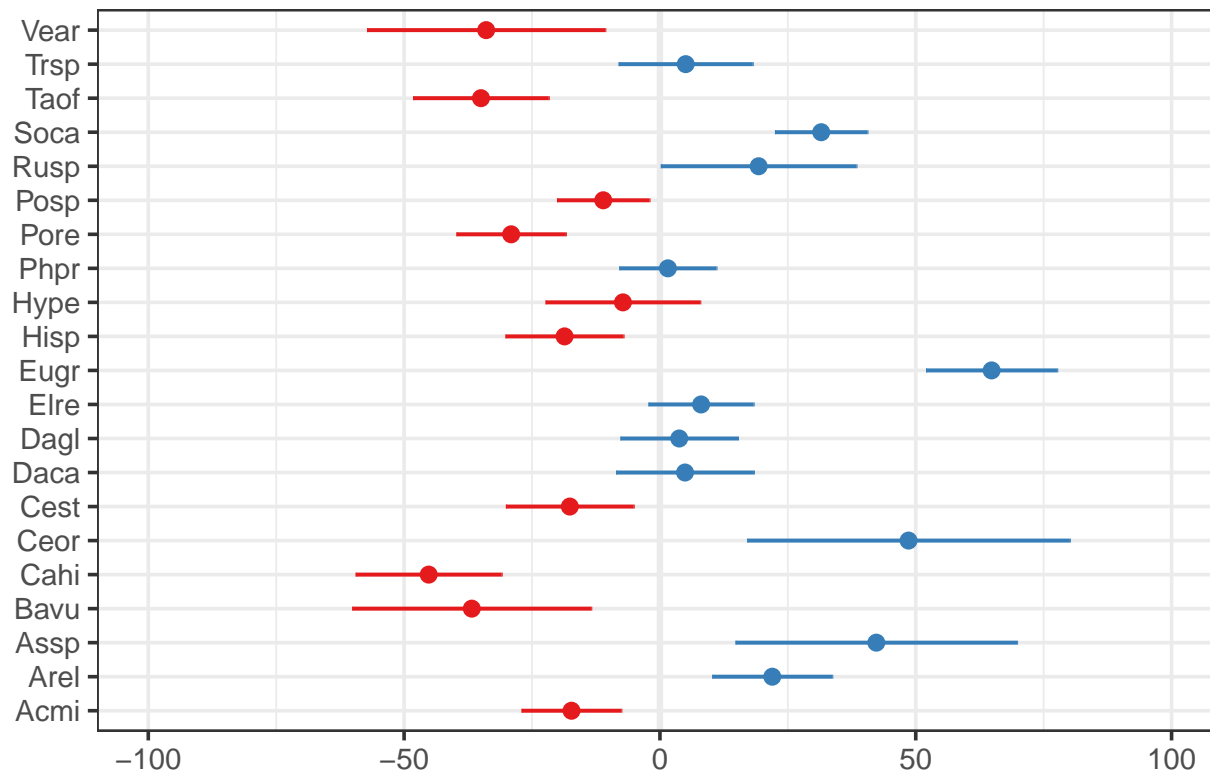
```
## [[1]]
```


Random effects



[[2]]

Random effects



```
# If we wanted to include plots nested within year it would
# look like this:
mod6 <- lmer(spp_half_cover_date ~ state * year + insecticide +
  (1 | species) + (1 + year | plot), green_kbs, REML = FALSE)
```

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

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

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -3.6e-01
```

```
anova(mod4, mod6)
```

```
## Data: green_kbs
```

```
## Models:
```

```
## mod4: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
```

```
## mod4: (1 | plot)
```

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

```
## mod6: (1 + year | plot)
```

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

```
## mod4      8 13585 13626 -6784.7   13569
```

```
## mod6     10 13596 13647 -6787.8   13576    0  2          1
```

```
anova(mod6)
```

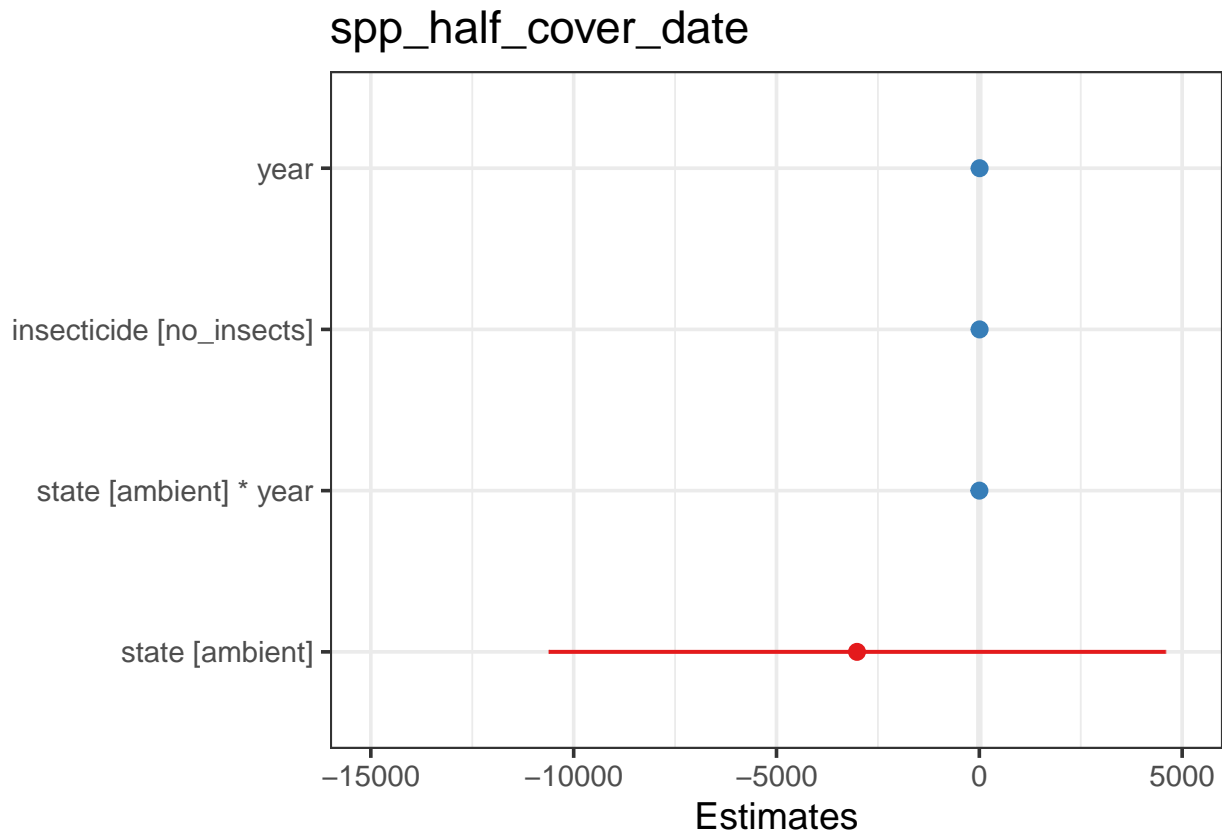
```
## Type III Analysis of Variance Table with Satterthwaite's method
```

```
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
```

```
## state      1467      1467      1 1232.41  0.6049   0.4369
## year       134924   134924      1 1238.24 55.6476 1.626e-13 ***
## insecticide 6552     6552      1   19.58  2.7021   0.1162
## state:year  1471     1471      1 1232.41  0.6068   0.4362
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Yup, seems to matter but it is making this more complex,
# though not overly so because it's on the random effects
# structure only.
```

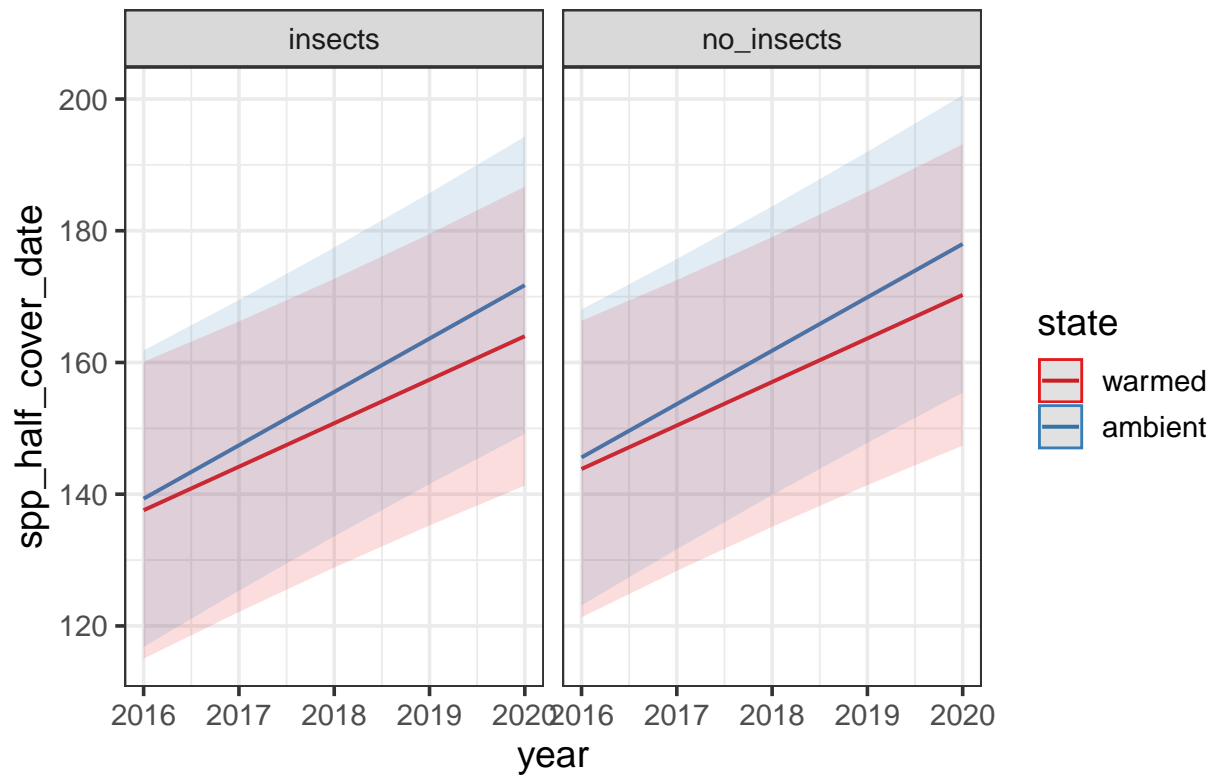
```
plot_model(mod6, sort.est = TRUE)
```



```
# these are the fixed predicted values:
```

```
plot_model(mod6, type = "pred", terms = c("year", "state", "insecticide"))
```

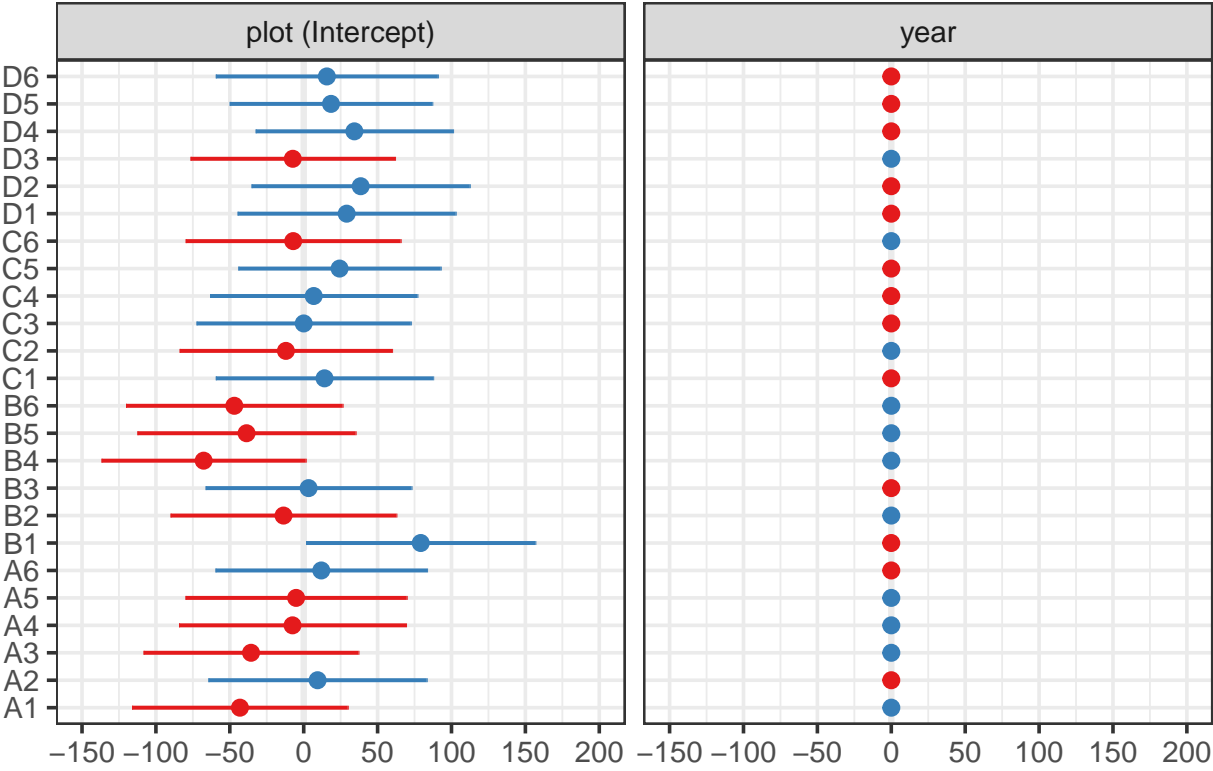
Predicted values of spp_half_cover_date



```
# these are the random effects estimates
plot_model(mod6, type = "re", terms = c("species", "plot"))
```

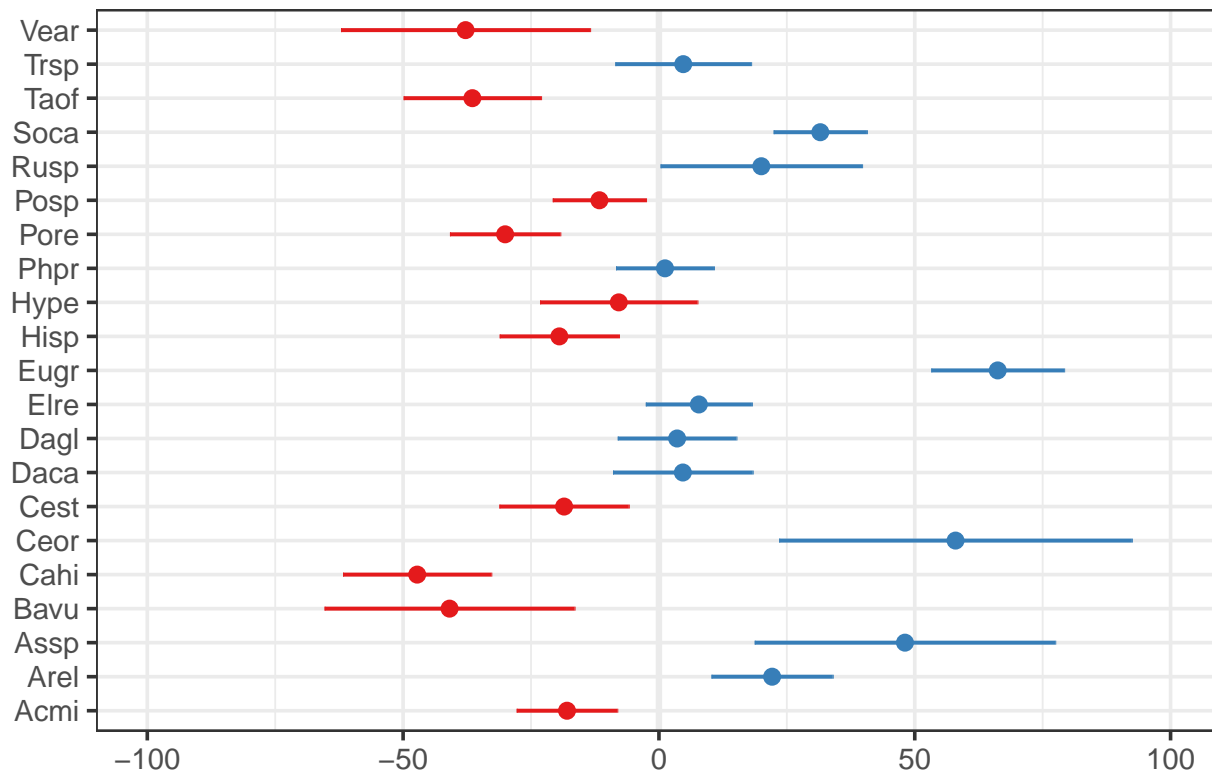
```
## [[1]]
```

Random effects



[[2]]

Random effects



mod4 (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. That would be something like this:

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

boundary (singular) fit: see ?isSingular

Warning: Model failed to converge with 1 negative eigenvalue: -3.2e-01

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

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

```
mod7c <- lmer(spp_half_cover_date ~ state + species + as.factor(year) + 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 + insecticide + (1 | species) + (1 + year | plot)

mod7: spp_half_cover_date ~ state + species + (1 + year | plot)

	np	AIC	BIC	logLik	deviance	Chisq	Df	Pr(>Chisq)
--	----	-----	-----	--------	----------	-------	----	------------

## mod6	10	13596	13647	-6787.8	13576			
---------	----	-------	-------	---------	-------	--	--	--

## mod7	26	13595	13729	-6771.6	13543	32.465	16	0.008694 **
---------	----	-------	-------	---------	-------	--------	----	-------------

```

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

anova(mod7, mod7a) #mod 7a

## Data: green_kbs
## Models:
## mod7: spp_half_cover_date ~ state + species + (1 + year | plot)
## mod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## mod7a:      plot)
##      npar   AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod7      26 13595 13729 -6771.6     13543
## mod7a     28 13455 13599 -6699.4     13399 144.32  2 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod7a, mod7b) #mod 7a

## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## mod7a:      plot)
## mod7b: spp_half_cover_date ~ state * as.factor(year) + species + (1 |
## mod7b:      plot)
##      npar   AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod7a     28 13455 13599 -6699.4     13399
## mod7b     32 13459 13623 -6697.3     13395 4.1458  4    0.3866

anova(mod7a, mod7c) #mod 7a slightly better

## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## mod7a:      plot)
## mod7c: spp_half_cover_date ~ state + species + as.factor(year) + insecticide +
## mod7c:      (1 | plot)
##      npar   AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod7a     28 13455 13599 -6699.4     13399
## mod7c     29 13454 13603 -6698.0     13396 2.8072  1    0.09384 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
##      plot)
##      Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 13454.8 13598.9 -6699.4 13398.8      1240
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6648 -0.7170 -0.1943  0.6198  3.2869
##

```

```

## Random effects:
##   Groups   Name      Variance Std.Dev.
##   plot     (Intercept)  35.3    5.941
##   Residual                2247.6  47.409
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    123.654     5.748  451.631  21.512 < 2e-16 ***
## stateambient      5.243     3.648   23.832   1.437 0.163721
## speciesArel     41.422     7.435  1258.614   5.571 3.10e-08 ***
## speciesAssp     80.596    15.859  1267.646   5.082 4.30e-07 ***
## speciesBavu    -27.568    13.237  1267.430  -2.083 0.037487 *
## speciesCahi    -30.744     8.540  1255.871  -3.600 0.000331 ***
## speciesCeor     84.134    18.748  1264.061   4.488 7.86e-06 ***
## speciesCest     -2.614     7.754  1252.277  -0.337 0.736086
## speciesDaca     24.683     8.163  1254.536   3.024 0.002548 **
## speciesDagl     20.035     7.330  1257.495   2.733 0.006359 **
## speciesElre     26.205     6.878  1251.167   3.810 0.000146 ***
## speciesEugr     84.966     7.895  1262.886  10.762 < 2e-16 ***
## speciesHisp     -6.264     7.377  1249.234  -0.849 0.395979
## speciesHype      8.179     8.903  1265.315   0.919 0.358396
## speciesPhpr     19.743     6.557  1248.336   3.011 0.002656 **
## speciesPore    -12.342     7.003  1254.702  -1.762 0.078254 .
## speciesPosp      6.442     6.393  1246.044   1.008 0.313763
## speciesRusp     39.348    10.895  1263.919   3.611 0.000316 ***
## speciesSoca     49.984     6.393  1246.044   7.819 1.13e-14 ***
## speciesTaof    -20.648     8.087  1264.115  -2.553 0.010793 *
## speciesTrsp     21.972     8.040  1252.783   2.733 0.006369 **
## speciesVear    -22.554    13.224  1263.495  -1.706 0.088335 .
## as.factor(year)2017  -9.787     4.260  1251.360  -2.298 0.021754 *
## as.factor(year)2018  33.419     4.089  1253.924   8.173 7.30e-16 ***
## as.factor(year)2019   5.276     4.092  1257.453   1.289 0.197478
## as.factor(year)2020  30.253     4.209  1257.038   7.188 1.12e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 26 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it
summary(mod7b)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * as.factor(year) + species + (1 |
##   plot)
##   Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 13458.6 13623.3 -6697.3 13394.6     1236
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max

```



```

## -2.6973 -0.7163 -0.1682  0.6292  3.3912
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 35.41 5.951
## Residual 2240.16 47.330
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 125.7975 6.1936 553.3646 20.311
## stateambient 0.9656 5.8888 155.2488 0.164
## as.factor(year)2017 -13.1741 6.1132 1251.5820 -2.155
## as.factor(year)2018 29.8897 5.8472 1255.6808 5.112
## as.factor(year)2019 6.9978 5.9825 1262.4862 1.170
## as.factor(year)2020 23.5298 6.0445 1258.9459 3.893
## speciesArel 41.7268 7.4289 1258.6223 5.617
## speciesAssp 81.0006 15.8432 1267.6530 5.113
## speciesBavu -27.9238 13.2306 1267.3688 -2.111
## speciesCahi -30.8026 8.5318 1255.7121 -3.610
## speciesCeor 84.0777 18.7363 1264.2642 4.487
## speciesCest -2.4431 7.7490 1252.3587 -0.315
## speciesDaca 24.8895 8.1517 1254.5198 3.053
## speciesDagl 20.2280 7.3186 1257.4827 2.764
## speciesElre 26.2674 6.8688 1251.3669 3.824
## speciesEugr 85.3064 7.8848 1262.8349 10.819
## speciesHisp -6.3397 7.3657 1249.1874 -0.861
## speciesHype 8.2829 8.8913 1265.1976 0.932
## speciesPhpr 19.8370 6.5478 1248.5353 3.030
## speciesPore -12.2319 6.9923 1254.6634 -1.749
## speciesPosp 6.5212 6.3834 1246.1660 1.022
## speciesRusp 39.4905 10.8787 1263.9851 3.630
## speciesSoca 50.0628 6.3834 1246.1660 7.843
## speciesTaof -20.8254 8.0766 1264.1496 -2.578
## speciesTrsp 22.0925 8.0287 1252.6912 2.752
## speciesVear -23.1384 13.2129 1263.2926 -1.751
## stateambient:as.factor(year)2017 6.4505 8.3525 1251.0547 0.772
## stateambient:as.factor(year)2018 6.8281 8.0846 1251.5621 0.845
## stateambient:as.factor(year)2019 -2.8863 8.1273 1256.3017 -0.355
## stateambient:as.factor(year)2020 12.6071 8.1763 1253.1143 1.542
## Pr(>|t|)
## (Intercept) < 2e-16 ***
## stateambient 0.869973
## as.factor(year)2017 0.031350 *
## as.factor(year)2018 3.69e-07 ***
## as.factor(year)2019 0.242342
## as.factor(year)2020 0.000104 ***
## speciesArel 2.39e-08 ***
## speciesAssp 3.66e-07 ***
## speciesBavu 0.035007 *
## speciesCahi 0.000318 ***
## speciesCeor 7.86e-06 ***
## speciesCest 0.752601
## speciesDaca 0.002311 **

```

```

## speciesDagl          0.005795 **
## speciesElre          0.000138 ***
## speciesEugr          < 2e-16 ***
## speciesHisp          0.389566
## speciesHype          0.351732
## speciesPhpr          0.002499 **
## speciesPore          0.080477 .
## speciesPosp          0.307178
## speciesRusp          0.000295 ***
## speciesSoca          9.42e-15 ***
## speciesTaof          0.010035 *
## speciesTrsp          0.006014 **
## speciesVear          0.080156 .
## stateambient:as.factor(year)2017 0.440090
## stateambient:as.factor(year)2018 0.398506
## stateambient:as.factor(year)2019 0.722547
## stateambient:as.factor(year)2020 0.123346
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 30 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)          if you need it
summary(mod7c)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state + species + as.factor(year) + insecticide +
## (1 | plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 13454.0 13603.2 -6698.0 13396.0      1239
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7189 -0.7068 -0.1873  0.6316  3.3152
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## plot     (Intercept)  23.66   4.864
## Residual                2249.49  47.429
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    120.676     5.908 318.033  20.425 < 2e-16 ***
## stateambient      4.996     3.372  22.048   1.481 0.152652
## speciesArel      41.339     7.434 1259.685   5.561 3.27e-08 ***
## speciesAssp      80.749    15.843 1267.904   5.097 3.98e-07 ***
## speciesBavu     -27.762    13.225 1267.994  -2.099 0.035993 *
## speciesCahi     -30.612     8.540 1256.369  -3.585 0.000351 ***

```

```
## speciesCeor      85.353      18.718 1259.154      4.560 5.62e-06 ***
## speciesCest      -2.354       7.756 1251.713     -0.304 0.761539
## speciesDaca      24.572       8.163 1255.105       3.010 0.002664 **
## speciesDagl      19.637       7.330 1257.847       2.679 0.007484 **
## speciesElre      26.119       6.880 1250.522       3.797 0.000154 ***
## speciesEugr      84.918       7.892 1264.055     10.760 < 2e-16 ***
## speciesHisp      -5.903       7.383 1245.948     -0.800 0.424116
## speciesHype       7.899       8.897 1266.760       0.888 0.374764
## speciesPhpr      19.531       6.560 1246.625       2.978 0.002962 **
## speciesPore     -12.176       7.003 1254.905     -1.739 0.082339 .
## speciesPosp       6.405       6.395 1244.445       1.002 0.316701
## speciesRusp      39.140      10.889 1260.889       3.594 0.000338 ***
## speciesSoca      49.947       6.395 1244.445       7.811 1.20e-14 ***
## speciesTaof     -20.361       8.083 1265.505     -2.519 0.011896 *
## speciesTrsp      22.288       8.043 1251.906       2.771 0.005666 **
## speciesVear     -22.166      13.221 1264.518     -1.677 0.093864 .
## as.factor(year)2017 -9.692       4.261 1250.679     -2.275 0.023099 *
## as.factor(year)2018 33.571       4.090 1253.570       8.208 5.52e-16 ***
## as.factor(year)2019  5.531       4.096 1253.927       1.350 0.177192
## as.factor(year)2020 30.582       4.214 1252.756       7.257 6.93e-13 ***
## insecticideno_insects 5.944       3.362  21.707       1.768 0.091101 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 27 > 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          4641     4641      1    23.83  2.0649 0.1637
## species       922795    46140     20 1259.50 20.5283 <2e-16 ***
## as.factor(year) 343250    85813      4 1252.77 38.1793 <2e-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 ~ as.factor(year)), adjust = "tukey")
```

```
## $`emmeans of year`
##   year emmean   SE  df lower.CL upper.CL
## 2016    145 3.28 228     138     151
## 2017    135 3.78 362     127     142
## 2018    178 3.61 305     171     185
## 2019    150 3.58 296     143     157
## 2020    175 3.72 338     168     182
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year`
```

```
## 1          estimate    SE    df t.ratio p.value
## 2016 - 2017      9.79 4.30 1276  2.275  0.1538
## 2016 - 2018     -33.42 4.13 1279 -8.090 <.0001
## 2016 - 2019      -5.28 4.13 1282 -1.276  0.7060
## 2016 - 2020     -30.25 4.25 1282 -7.114 <.0001
## 2017 - 2018     -43.21 4.48 1274 -9.652 <.0001
## 2017 - 2019     -15.06 4.49 1276 -3.356  0.0073
## 2017 - 2020     -40.04 4.55 1278 -8.794 <.0001
## 2018 - 2019      28.14 4.34 1276  6.489 <.0001
## 2018 - 2020       3.17 4.40 1279  0.719  0.9521
## 2019 - 2020     -24.98 4.38 1272 -5.697 <.0001
##
## 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(mod7a, list(pairwise ~ species), adjust = "tukey")
```

```
## $`emmeans of species`
## species emmean    SE    df lower.CL upper.CL
## Acmi      138  4.93  754    128.4    148
## Arel      180  5.97  947    167.8    191
## Assp      219 15.39 1287    188.5    249
## Bavu      111 12.60 1267     85.8    135
## Cahi      107  7.35 1148     92.9    122
## Ceor      222 18.43 1278    186.1    258
## Cest      135  6.41 1053    122.9    148
## Daca      163  6.90 1113    149.2    176
## Dagl      158  5.83  940    146.7    170
## Elre      164  5.22  833    154.1    175
## Eugr      223  6.55 1017    210.2    236
## Hisp      132  5.90  981    120.3    143
## Hype      146  7.76 1134    131.1    162
## Phpr      158  4.80  714    148.4    167
## Pore      126  5.42  858    115.1    136
## Posp      145  4.57  647    135.6    154
## Rusp      177 10.04 1193    157.8    197
## Soca      188  4.57  647    179.1    197
## Taof      117  6.79 1062    104.1    131
## Trsp      160  6.73 1099    146.9    173
## Vear      116 12.58 1284     90.9    140
##
## Results are averaged over the levels of: state, year
## 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  -41.422  7.51 1284  -5.513 <.0001
## Acmi - Assp  -80.596 16.05 1294  -5.022  0.0001
## Acmi - Bavu   27.567 13.39 1293   2.059  0.8925
## Acmi - Cahi   30.744  8.63 1281   3.563  0.0523
## Acmi - Ceor  -84.134 18.99 1292  -4.431  0.0019
## Acmi - Cest    2.614  7.83 1277   0.334  1.0000
## Acmi - Daca  -24.683  8.25 1279  -2.993  0.2530
```

##	Acmi	-	Dagl	-20.035	7.41	1282	-2.705	0.4482
##	Acmi	-	Elre	-26.205	6.95	1276	-3.772	0.0258
##	Acmi	-	Eugr	-84.966	7.98	1288	-10.646	<.0001
##	Acmi	-	Hisp	6.264	7.45	1274	0.841	1.0000
##	Acmi	-	Hype	-8.179	9.00	1291	-0.909	1.0000
##	Acmi	-	Phpr	-19.743	6.62	1273	-2.981	0.2595
##	Acmi	-	Pore	12.342	7.08	1280	1.744	0.9781
##	Acmi	-	Posp	-6.442	6.46	1271	-0.998	1.0000
##	Acmi	-	Rusp	-39.348	11.04	1292	-3.565	0.0519
##	Acmi	-	Soca	-49.984	6.46	1271	-7.743	<.0001
##	Acmi	-	Taof	20.648	8.18	1289	2.525	0.5891
##	Acmi	-	Trsp	-21.972	8.12	1278	-2.705	0.4479
##	Acmi	-	Vear	22.554	13.37	1289	1.687	0.9849
##	Arel	-	Assp	-39.174	16.41	1294	-2.387	0.6952
##	Arel	-	Bavu	68.990	13.81	1293	4.996	0.0001
##	Arel	-	Cahi	72.166	9.31	1289	7.749	<.0001
##	Arel	-	Ceor	-42.711	19.27	1292	-2.216	0.8109
##	Arel	-	Cest	44.036	8.58	1290	5.133	0.0001
##	Arel	-	Daca	16.739	8.93	1283	1.875	0.9537
##	Arel	-	Dagl	21.387	8.11	1283	2.638	0.4998
##	Arel	-	Elre	15.217	7.69	1285	1.978	0.9238
##	Arel	-	Eugr	-43.544	8.64	1292	-5.041	0.0001
##	Arel	-	Hisp	47.686	8.17	1282	5.837	<.0001
##	Arel	-	Hype	33.243	9.60	1292	3.463	0.0716
##	Arel	-	Phpr	21.680	7.42	1285	2.920	0.2966
##	Arel	-	Pore	53.765	7.83	1287	6.866	<.0001
##	Arel	-	Posp	34.980	7.28	1285	4.807	0.0003
##	Arel	-	Rusp	2.074	11.50	1294	0.180	1.0000
##	Arel	-	Soca	-8.562	7.28	1285	-1.177	0.9999
##	Arel	-	Taof	62.070	8.82	1290	7.040	<.0001
##	Arel	-	Trsp	19.451	8.78	1283	2.216	0.8111
##	Arel	-	Vear	63.976	13.79	1289	4.639	0.0007
##	Assp	-	Bavu	108.164	19.80	1295	5.463	<.0001
##	Assp	-	Cahi	111.340	16.90	1291	6.589	<.0001
##	Assp	-	Ceor	-3.537	23.95	1294	-0.148	1.0000
##	Assp	-	Cest	83.211	16.57	1294	5.021	0.0001
##	Assp	-	Daca	55.913	16.70	1290	3.347	0.1012
##	Assp	-	Dagl	60.561	16.36	1293	3.702	0.0328
##	Assp	-	Elre	54.391	16.14	1294	3.370	0.0947
##	Assp	-	Eugr	-4.370	16.58	1290	-0.264	1.0000
##	Assp	-	Hisp	86.860	16.39	1293	5.299	<.0001
##	Assp	-	Hype	72.417	17.14	1294	4.224	0.0045
##	Assp	-	Phpr	60.854	16.00	1293	3.804	0.0230
##	Assp	-	Pore	92.939	16.18	1292	5.743	<.0001
##	Assp	-	Posp	74.154	15.94	1294	4.652	0.0007
##	Assp	-	Rusp	41.248	18.23	1292	2.263	0.7817
##	Assp	-	Soca	30.613	15.94	1294	1.921	0.9418
##	Assp	-	Taof	101.245	16.69	1292	6.065	<.0001
##	Assp	-	Trsp	58.625	16.66	1290	3.520	0.0600
##	Assp	-	Vear	103.150	19.67	1282	5.243	<.0001
##	Bavu	-	Cahi	3.176	14.42	1291	0.220	1.0000
##	Bavu	-	Ceor	-111.701	22.32	1291	-5.004	0.0001
##	Bavu	-	Cest	-24.953	14.04	1294	-1.777	0.9733
##	Bavu	-	Daca	-52.251	14.26	1294	-3.664	0.0374

##	Bavu	-	Dagl	-47.602	13.76	1294	-3.460	0.0723
##	Bavu	-	Elre	-53.773	13.50	1295	-3.984	0.0118
##	Bavu	-	Eugr	-112.534	14.04	1292	-8.017	<.0001
##	Bavu	-	Hisp	-21.303	13.81	1294	-1.543	0.9948
##	Bavu	-	Hype	-35.747	14.66	1295	-2.438	0.6572
##	Bavu	-	Phpr	-47.310	13.35	1294	-3.544	0.0555
##	Bavu	-	Pore	-15.225	13.62	1295	-1.118	0.9999
##	Bavu	-	Posp	-34.010	13.27	1294	-2.563	0.5590
##	Bavu	-	Rusp	-66.916	16.02	1294	-4.178	0.0055
##	Bavu	-	Soca	-77.551	13.27	1294	-5.845	<.0001
##	Bavu	-	Taof	-6.919	14.22	1295	-0.486	1.0000
##	Bavu	-	Trsp	-49.539	14.16	1292	-3.498	0.0642
##	Bavu	-	Vear	-5.014	17.72	1293	-0.283	1.0000
##	Cahi	-	Ceor	-114.877	19.71	1295	-5.828	<.0001
##	Cahi	-	Cest	-28.130	9.51	1284	-2.958	0.2735
##	Cahi	-	Daca	-55.427	9.85	1282	-5.626	<.0001
##	Cahi	-	Dagl	-50.779	9.22	1289	-5.505	<.0001
##	Cahi	-	Elre	-56.949	8.85	1285	-6.435	<.0001
##	Cahi	-	Eugr	-115.710	9.64	1282	-12.002	<.0001
##	Cahi	-	Hisp	-24.480	9.21	1284	-2.658	0.4840
##	Cahi	-	Hype	-38.923	10.50	1287	-3.707	0.0323
##	Cahi	-	Phpr	-50.486	8.57	1283	-5.891	<.0001
##	Cahi	-	Pore	-18.402	8.94	1288	-2.058	0.8928
##	Cahi	-	Posp	-37.186	8.45	1283	-4.403	0.0021
##	Cahi	-	Rusp	-70.092	12.31	1295	-5.695	<.0001
##	Cahi	-	Soca	-80.728	8.45	1283	-9.559	<.0001
##	Cahi	-	Taof	-10.096	9.81	1289	-1.030	1.0000
##	Cahi	-	Trsp	-52.715	9.71	1276	-5.427	<.0001
##	Cahi	-	Vear	-8.190	14.35	1283	-0.571	1.0000
##	Ceor	-	Cest	86.748	19.40	1292	4.471	0.0016
##	Ceor	-	Daca	59.450	19.58	1293	3.037	0.2287
##	Ceor	-	Dagl	64.099	19.26	1291	3.328	0.1071
##	Ceor	-	Elre	57.929	19.06	1294	3.039	0.2274
##	Ceor	-	Eugr	-0.833	19.47	1292	-0.043	1.0000
##	Ceor	-	Hisp	90.398	19.22	1293	4.704	0.0005
##	Ceor	-	Hype	75.954	19.96	1289	3.806	0.0228
##	Ceor	-	Phpr	64.391	18.97	1292	3.395	0.0881
##	Ceor	-	Pore	96.476	19.13	1290	5.042	0.0001
##	Ceor	-	Posp	77.691	18.89	1293	4.113	0.0071
##	Ceor	-	Rusp	44.785	20.84	1294	2.149	0.8490
##	Ceor	-	Soca	34.150	18.89	1293	1.808	0.9680
##	Ceor	-	Taof	104.782	19.50	1294	5.373	<.0001
##	Ceor	-	Trsp	62.162	19.47	1294	3.192	0.1554
##	Ceor	-	Vear	106.687	22.20	1294	4.805	0.0003
##	Cest	-	Daca	-27.297	9.15	1280	-2.983	0.2588
##	Cest	-	Dagl	-22.649	8.47	1288	-2.674	0.4716
##	Cest	-	Elre	-28.819	8.10	1281	-3.559	0.0529
##	Cest	-	Eugr	-87.580	8.99	1291	-9.746	<.0001
##	Cest	-	Hisp	3.650	8.45	1275	0.432	1.0000
##	Cest	-	Hype	-10.793	9.90	1291	-1.091	1.0000
##	Cest	-	Phpr	-22.357	7.78	1280	-2.872	0.3278
##	Cest	-	Pore	9.728	8.14	1278	1.195	0.9999
##	Cest	-	Posp	-9.056	7.64	1278	-1.185	0.9999
##	Cest	-	Rusp	-41.962	11.78	1291	-3.561	0.0526

##	Cest - Soca	-52.598	7.64	1278	-6.883	<.0001
##	Cest - Taof	18.034	9.11	1288	1.979	0.9235
##	Cest - Trsp	-24.586	9.06	1280	-2.714	0.4412
##	Cest - Vear	19.940	13.95	1290	1.429	0.9981
##	Daca - Dagl	4.648	8.83	1279	0.526	1.0000
##	Daca - Elre	-1.522	8.48	1281	-0.179	1.0000
##	Daca - Eugr	-60.283	9.33	1288	-6.462	<.0001
##	Daca - Hisp	30.947	8.86	1277	3.494	0.0650
##	Daca - Hype	16.504	10.22	1290	1.614	0.9909
##	Daca - Phpr	4.941	8.19	1279	0.603	1.0000
##	Daca - Pore	37.025	8.53	1278	4.339	0.0028
##	Daca - Posp	18.241	8.06	1280	2.263	0.7815
##	Daca - Rusp	-14.665	12.04	1294	-1.218	0.9998
##	Daca - Soca	-25.301	8.06	1280	-3.139	0.1782
##	Daca - Taof	45.331	9.48	1289	4.782	0.0004
##	Daca - Trsp	2.712	9.41	1276	0.288	1.0000
##	Daca - Vear	47.237	14.16	1285	3.335	0.1047
##	Dagl - Elre	-6.170	7.59	1278	-0.813	1.0000
##	Dagl - Eugr	-64.931	8.57	1293	-7.579	<.0001
##	Dagl - Hisp	26.299	8.08	1282	3.255	0.1314
##	Dagl - Hype	11.856	9.52	1292	1.245	0.9997
##	Dagl - Phpr	0.292	7.31	1277	0.040	1.0000
##	Dagl - Pore	32.377	7.72	1282	4.192	0.0052
##	Dagl - Posp	13.593	7.17	1281	1.897	0.9483
##	Dagl - Rusp	-19.313	11.44	1294	-1.688	0.9847
##	Dagl - Soca	-29.949	7.17	1281	-4.179	0.0055
##	Dagl - Taof	40.683	8.73	1288	4.659	0.0007
##	Dagl - Trsp	-1.937	8.71	1284	-0.222	1.0000
##	Dagl - Vear	42.589	13.75	1288	3.098	0.1972
##	Elre - Eugr	-58.761	8.15	1290	-7.209	<.0001
##	Elre - Hisp	32.469	7.67	1277	4.234	0.0044
##	Elre - Hype	18.026	9.16	1293	1.967	0.9276
##	Elre - Phpr	6.462	6.84	1272	0.945	1.0000
##	Elre - Pore	38.547	7.30	1279	5.281	<.0001
##	Elre - Posp	19.763	6.67	1271	2.962	0.2710
##	Elre - Rusp	-13.143	11.15	1295	-1.179	0.9999
##	Elre - Soca	-23.779	6.67	1271	-3.564	0.0521
##	Elre - Taof	46.853	8.36	1286	5.604	<.0001
##	Elre - Trsp	4.234	8.33	1279	0.508	1.0000
##	Elre - Vear	48.759	13.52	1290	3.605	0.0455
##	Eugr - Hisp	91.230	8.59	1290	10.615	<.0001
##	Eugr - Hype	76.787	9.97	1293	7.705	<.0001
##	Eugr - Phpr	65.224	7.89	1288	8.265	<.0001
##	Eugr - Pore	97.308	8.29	1292	11.737	<.0001
##	Eugr - Posp	78.524	7.76	1290	10.124	<.0001
##	Eugr - Rusp	45.618	11.79	1294	3.870	0.0181
##	Eugr - Soca	34.982	7.76	1290	4.510	0.0013
##	Eugr - Taof	105.614	9.19	1288	11.488	<.0001
##	Eugr - Trsp	62.995	9.16	1284	6.880	<.0001
##	Eugr - Vear	107.520	14.02	1288	7.668	<.0001
##	Hisp - Hype	-14.443	9.57	1291	-1.509	0.9960
##	Hisp - Phpr	-26.007	7.38	1278	-3.524	0.0593
##	Hisp - Pore	6.078	7.77	1276	0.783	1.0000
##	Hisp - Posp	-12.706	7.22	1275	-1.759	0.9760

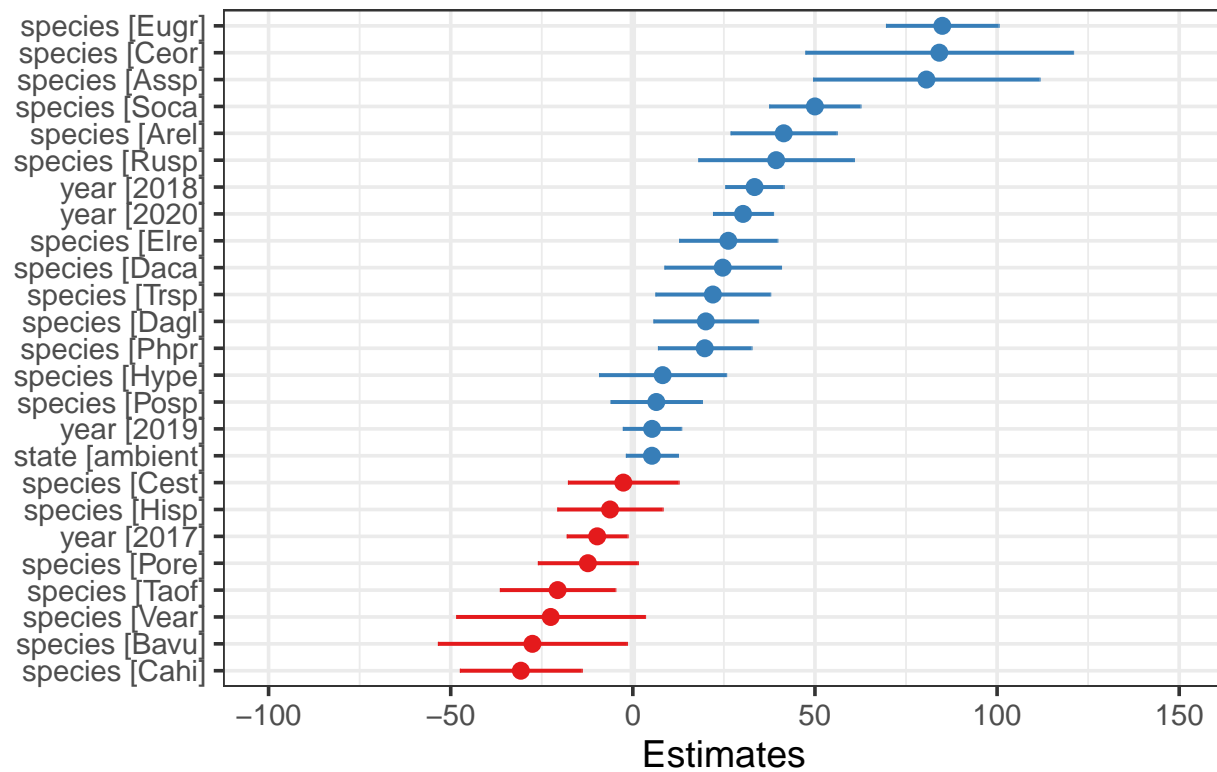
```
## Hisp - Rusp -45.612 11.50 1293 -3.965 0.0127
## Hisp - Soca -56.248 7.22 1275 -7.787 <.0001
## Hisp - Taof 14.384 8.74 1284 1.645 0.9887
## Hisp - Trsp -28.236 8.68 1276 -3.253 0.1320
## Hisp - Vear 16.290 13.71 1288 1.188 0.9999
## Hype - Phpr -11.563 8.93 1291 -1.295 0.9995
## Hype - Pore 20.521 9.29 1293 2.209 0.8150
## Hype - Posp 1.737 8.81 1292 0.197 1.0000
## Hype - Rusp -31.169 12.55 1294 -2.483 0.6223
## Hype - Soca -41.805 8.81 1292 -4.745 0.0004
## Hype - Taof 28.827 10.15 1294 2.841 0.3489
## Hype - Trsp -13.792 10.10 1290 -1.366 0.9990
## Hype - Vear 30.733 14.64 1287 2.099 0.8739
## Phpr - Pore 32.085 6.99 1277 4.592 0.0009
## Phpr - Posp 13.300 6.35 1270 2.093 0.8768
## Phpr - Rusp -19.606 10.96 1294 -1.788 0.9714
## Phpr - Soca -30.241 6.35 1270 -4.760 0.0004
## Phpr - Taof 40.391 8.09 1289 4.990 0.0001
## Phpr - Trsp -2.229 8.04 1279 -0.277 1.0000
## Phpr - Vear 42.297 13.33 1288 3.174 0.1629
## Pore - Posp -18.784 6.83 1278 -2.748 0.4154
## Pore - Rusp -51.690 11.24 1294 -4.601 0.0009
## Pore - Soca -62.326 6.83 1278 -9.119 <.0001
## Pore - Taof 8.306 8.46 1288 0.982 1.0000
## Pore - Trsp -34.314 8.41 1280 -4.078 0.0082
## Pore - Vear 10.212 13.54 1288 0.754 1.0000
## Posp - Rusp -32.906 10.87 1294 -3.027 0.2339
## Posp - Soca -43.542 6.18 1268 -7.046 <.0001
## Posp - Taof 27.090 7.96 1288 3.403 0.0859
## Posp - Trsp -15.529 7.91 1279 -1.963 0.9289
## Posp - Vear 28.996 13.25 1290 2.188 0.8274
## Rusp - Soca -10.636 10.87 1294 -0.978 1.0000
## Rusp - Taof 59.996 11.91 1294 5.037 0.0001
## Rusp - Trsp 17.377 11.93 1294 1.457 0.9975
## Rusp - Vear 61.902 15.97 1293 3.875 0.0177
## Soca - Taof 70.632 7.96 1288 8.873 <.0001
## Soca - Trsp 28.012 7.91 1279 3.540 0.0562
## Soca - Vear 72.538 13.25 1290 5.473 <.0001
## Taof - Trsp -42.620 9.31 1285 -4.579 0.0010
## Taof - Vear 1.906 14.12 1289 0.135 1.0000
## Trsp - Vear 44.525 14.04 1284 3.171 0.1641
##
```

```
## Results are averaged over the levels of: state, year
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 21 estimates
```

```
# 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).
```

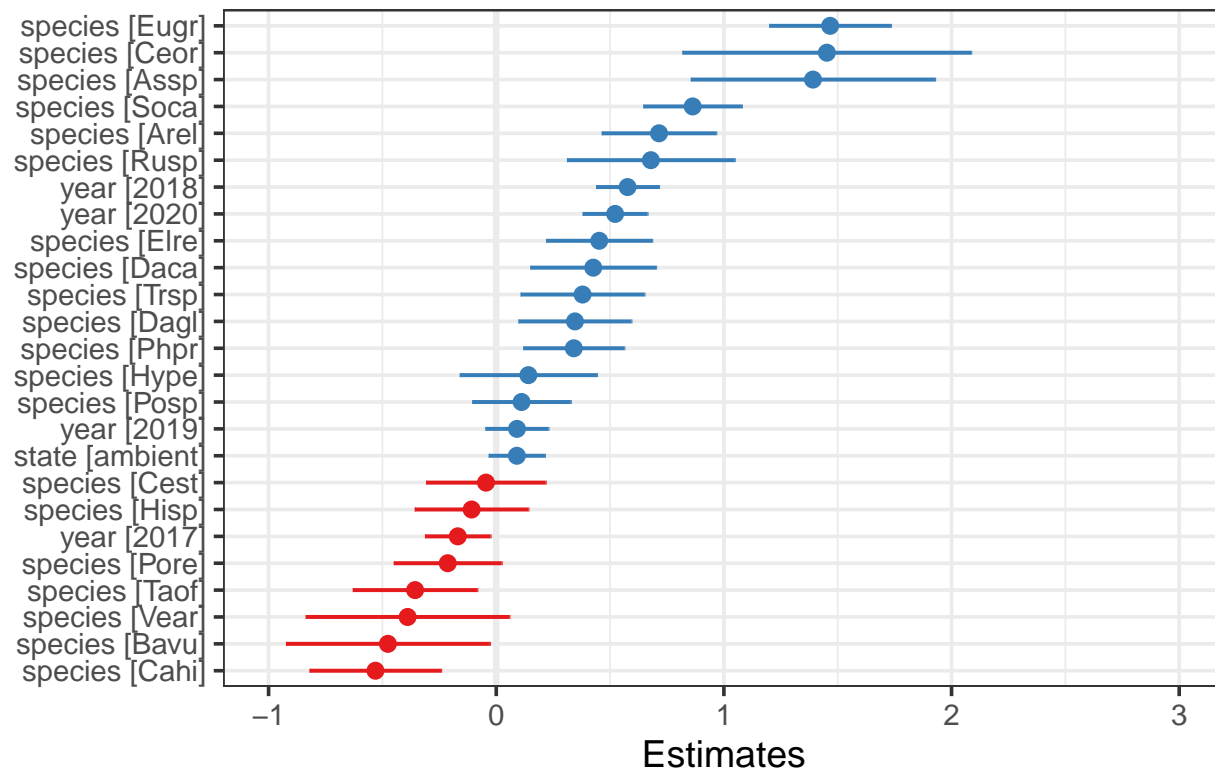
```
plot_model(mod7a, sort.est = TRUE)
```


spp_half_cover_date



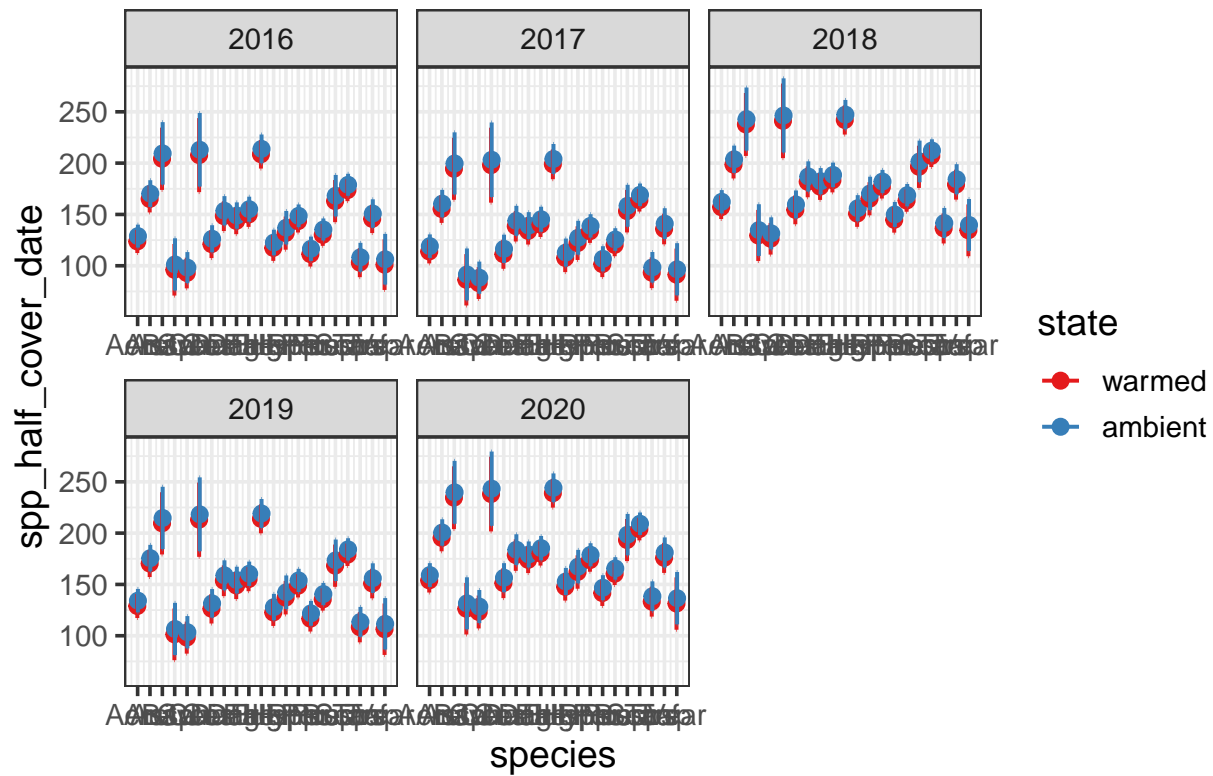
```
# if you want to standardize the estimates:
plot_model(mod7a, sort.est = TRUE, type = "std")
```

spp_half_cover_date



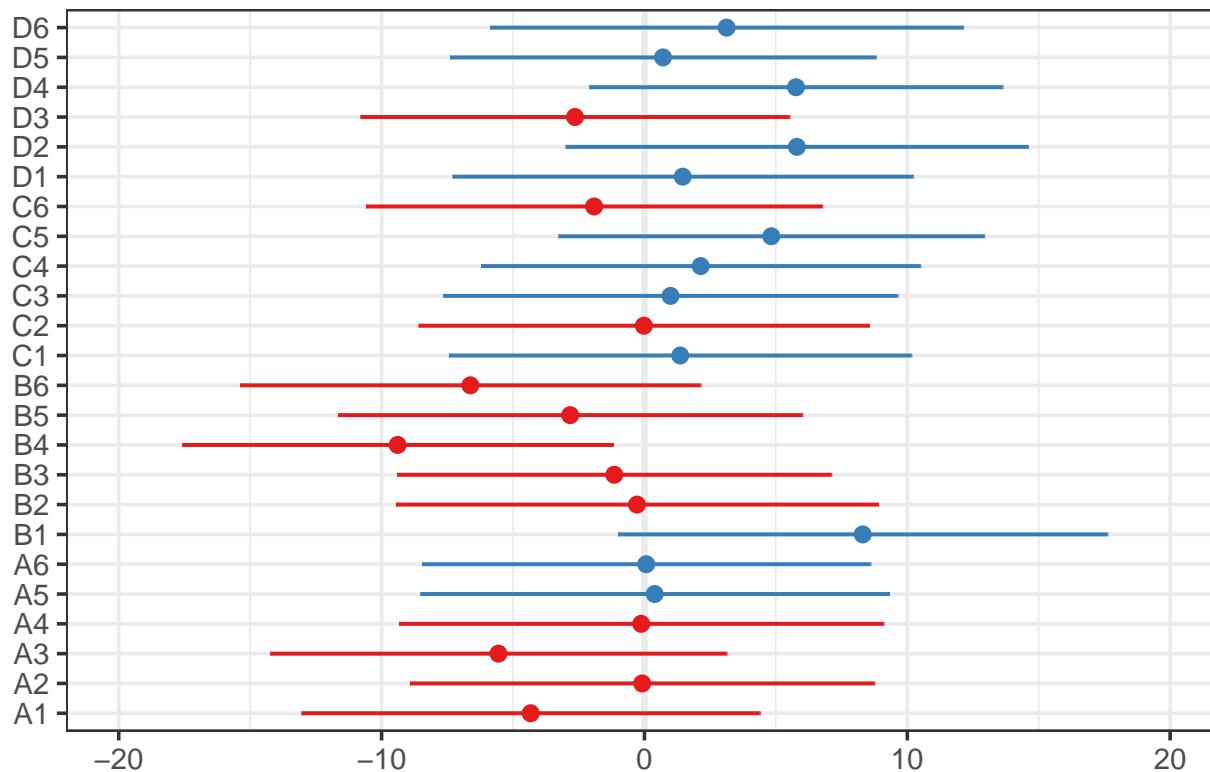
```
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7a, type = "pred", terms = c("species", "state",
      "year"))
```

Predicted values of spp_half_cover_date



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

Random effects



```
# including native vs. exotic - first with interaction term
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 |
  plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -3.0e+00
```

```
summary(mod8)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * origin + (1 + year | plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 13846.2 13908.0 -6911.1 13822.2    1256
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0748 -0.7603 -0.3229  0.8607  2.6743
##
## Random effects:
## Groups   Name                Variance Std.Dev. Corr
## plot     (Intercept)  3.166e+03  56.26769
##          year          9.676e-04  0.03111 -1.00
## Residual                3.143e+03  56.05923
```

```

## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      178.588      5.187   221.879   34.429 < 2e-16 ***
## stateambient       -3.424      7.232   212.864   -0.473 0.636370
## origin            -43.746      8.704  1250.532   -5.026 5.74e-07 ***
## originBoth        -27.722      8.206  1262.022   -3.378 0.000752 ***
## originExotic      -34.513      5.740  1258.877   -6.012 2.39e-09 ***
## stateambient:origin    22.708     12.248  1249.339    1.854 0.063967 .
## stateambient:originBoth  8.813     11.208  1261.312    0.786 0.431839
## stateambient:originExotic 8.712      7.947  1257.347    1.096 0.273127
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn origin orgnBt orgnEx sttmb: sttm:B
## stateambint -0.717
## origin      -0.518  0.371
## originBoth  -0.547  0.393  0.326
## originExotc -0.785  0.563  0.468  0.496
## sttmbnt:rgn  0.368 -0.511 -0.711 -0.232 -0.332
## sttmbnt:rgB  0.401 -0.557 -0.239 -0.732 -0.363  0.329
## sttmbnt:rgE  0.567 -0.787 -0.338 -0.359 -0.722  0.464  0.509
## convergence code: 0
## boundary (singular) fit: see ?isSingular

anova(mod8)

## Type III Analysis of Variance Table with Satterthwaite's method
##
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state          6109      6109      1    43.52  1.9438    0.1703
## origin        193547    64516      3 1256.73 20.5292 5.461e-13 ***
## state:origin   11046      3682      3 1256.73  1.1716    0.3193
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# including native vs. exotic - first with interaction term
mod9 <- lmer(spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
  plot), green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 1 negative eigenvalue: -5.4e+00
mod9a <- lmer(spp_half_cover_date ~ state + origin + as.factor(year) +
  (1 | plot), green_kbs, REML = FALSE)
anova(mod8, mod9) # model 9 is a better fit to data

## Data: green_kbs
## Models:
## mod8: spp_half_cover_date ~ state * origin + (1 + year | plot)
## mod9: spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
## mod9: plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod8   12 13846 13908 -6911.1   13822
## mod9   21 13765 13873 -6861.3   13723 99.539  9 < 2.2e-16 ***

```

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

anova(mod9, mod9a) # mod 9a?

## Data: green_kbs
## Models:
## mod9a: spp_half_cover_date ~ state + origin + as.factor(year) + (1 |
## mod9a:      plot)
## mod9: spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
## mod9:      plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9a  11 13712 13769 -6845.1   13690
## mod9   21 13765 13873 -6861.3   13723     0 10         1

summary(mod9a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + as.factor(year) + (1 |
##      plot)
## Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 13712.2 13768.8 -6845.1  13690.2     1257
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2420 -0.8016 -0.1692  0.8307  2.3952
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## plot    (Intercept)         47.45    6.888
## Residual                    2826.63   53.166
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    159.084     4.874  182.700  32.637 < 2e-16 ***
## stateambient      4.580     4.124   24.945   1.111   0.277
## origin        -32.473     5.808  1248.369  -5.591 2.77e-08 ***
## originBoth     -22.823     5.334  1259.899  -4.279 2.02e-05 ***
## originExotic   -29.419     3.767  1255.791  -7.810 1.20e-14 ***
## as.factor(year)2017  -6.407     4.707  1252.321  -1.361   0.174
## as.factor(year)2018   34.757     4.529  1252.946   7.674 3.33e-14 ***
## as.factor(year)2019   11.164     4.537  1256.268   2.461   0.014 *
## as.factor(year)2020   38.734     4.590  1254.150   8.439 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn origin orgnBt orgnEx a.()2017 a.()2018 a.()2019
## stateambint -0.423
## origin      -0.355  0.006
## originBoth -0.430 -0.013  0.326
```

```
## originExotc -0.563 -0.010 0.464 0.509
## as.fc()2017 -0.416 -0.007 -0.012 0.105 0.018
## as.fc()2018 -0.422 -0.002 -0.009 0.044 0.017 0.430
## as.fc()2019 -0.415 -0.018 -0.009 0.034 0.023 0.427 0.442
## as.fc()2020 -0.419 -0.012 -0.009 0.067 0.021 0.426 0.438 0.439
```

```
anova(mod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##      Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state      950      950      1 143.17 0.3414      0.56
## origin 188314  62771      3 1228.90 22.5519 3.243e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod9a, list(pairwise ~ state + origin), adjust = "tukey")
```

```
## $`emmeans of state, origin`
## state origin emmean SE df lower.CL upper.CL
## warmed Native 175 4.17 95.1 166 183
## ambient Native 179 4.13 93.7 171 188
## warmed 142 5.54 280.5 131 153
## ambient 147 5.54 284.9 136 158
## warmed Both 152 5.10 198.8 142 162
## ambient Both 156 5.02 189.7 147 166
## warmed Exotic 145 3.38 39.8 138 152
## ambient Exotic 150 3.28 35.8 143 157
##
## Results are averaged over the levels of: year
## 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 -4.58 4.31 25.9 -1.063 0.9589
## warmed Native - warmed 32.47 5.83 1254.6 5.574 <.0001
## warmed Native - ambient 27.89 7.27 214.0 3.839 0.0040
## warmed Native - warmed Both 22.82 5.35 1267.0 4.263 0.0006
## warmed Native - ambient Both 18.24 6.83 166.7 2.671 0.1391
## warmed Native - warmed Exotic 29.42 3.78 1262.6 7.783 <.0001
## warmed Native - ambient Exotic 24.84 5.70 83.1 4.355 0.0009
## ambient Native - warmed 37.05 7.22 210.1 5.130 <.0001
## ambient Native - ambient 32.47 5.83 1254.6 5.574 <.0001
## ambient Native - warmed Both 27.40 6.91 174.9 3.965 0.0027
## ambient Native - ambient Both 22.82 5.35 1267.0 4.263 0.0006
## ambient Native - warmed Exotic 34.00 5.76 87.2 5.905 <.0001
## ambient Native - ambient Exotic 29.42 3.78 1262.6 7.783 <.0001
## warmed - ambient -4.58 4.31 25.9 -1.063 0.9589
## warmed - warmed Both -9.65 6.50 1264.5 -1.484 0.8162
## warmed - ambient Both -14.23 7.74 263.0 -1.837 0.5951
## warmed - warmed Exotic -3.05 5.27 1256.5 -0.579 0.9991
## warmed - ambient Exotic -7.63 6.76 163.3 -1.129 0.9496
## ambient - warmed Both -5.07 7.86 276.5 -0.645 0.9982
## ambient - ambient Both -9.65 6.50 1264.5 -1.484 0.8162
## ambient - warmed Exotic 1.53 6.85 172.7 0.223 1.0000
```

```

## ambient - ambient Exotic          -3.05 5.27 1256.5 -0.579 0.9991
## warmed Both - ambient Both        -4.58 4.31   25.9 -1.063 0.9589
## warmed Both - warmed Exotic        6.60 4.73 1266.0  1.396 0.8594
## warmed Both - ambient Exotic       2.02 6.41  131.7  0.314 1.0000
## ambient Both - warmed Exotic      11.18 6.37  129.2  1.753 0.6524
## ambient Both - ambient Exotic      6.60 4.73 1266.0  1.396 0.8594
## warmed Exotic - ambient Exotic     -4.58 4.31   25.9 -1.063 0.9589
##
## Results are averaged over the levels of: year
## 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 +
  as.factor(year) | plot), green_kbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 1 negative eigenvalue: -6.7e+00
summary(mod10)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * growth_habit + (1 + as.factor(year) |
## plot)
## Data: green_kbs
##
##      AIC      BIC    logLik deviance df.resid
## 13818.8 13942.3 -6885.4 13770.8    1244
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4393 -0.7738 -0.2549  0.8535  2.7344
##
## Random effects:
## Groups   Name                Variance Std.Dev. Corr
## plot    (Intercept)            0.0    0.000
##          as.factor(year)2017    78.3    8.849    NaN
##          as.factor(year)2018 1053.3   32.455    NaN -0.67
##          as.factor(year)2019  110.5   10.512    NaN -0.34  0.93
##          as.factor(year)2020 1773.1   42.108    NaN -0.39  0.95  1.00
## Residual                2894.2   53.798
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)    139.714     3.521 206.660  39.684
## stateambient    -1.086     4.831 190.091  -0.225
## growth_habit    -6.601     7.352 1234.241  -0.898
## growth_habitGraminoid  2.947     4.795 1238.889   0.615
## growth_habitVine   92.286    38.203 1220.155   2.416
## stateambient:growth_habit  8.361     9.887 1233.686   0.846
## stateambient:growth_habitGraminoid  7.063     6.628 1236.516   1.066

```



```
## stateambient:growth_habitVine      -30.270      45.504 1222.794  -0.665
##                                     Pr(>|t|)
## (Intercept)                        <2e-16 ***
## stateambient                        0.8223
## growth_habit                       0.3694
## growth_habitGraminoid              0.5390
## growth_habitVine                   0.0159 *
## stateambient:growth_habit          0.3979
## stateambient:growth_habitGraminoid 0.2868
## stateambient:growth_habitVine      0.5060
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_V sttm:_ stt:_G
## stateambint -0.729
## growth_habt -0.366  0.267
## grwth_hbtGr -0.530  0.386  0.270
## grwth_hbtVn -0.092  0.067  0.034  0.049
## sttmbnt:gr_  0.272 -0.368 -0.744 -0.201 -0.025
## sttmbnt:g_G  0.383 -0.519 -0.195 -0.723 -0.035  0.272
## sttmbnt:g_V  0.077 -0.093 -0.028 -0.041 -0.840  0.044  0.058
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(mod10)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state           472    471.9      1 1121.0  0.1630 0.686450
## growth_habit    46117 15372.4      3 1231.7  5.3115 0.001224 **
## state:growth_habit 5861  1953.7      3 1231.7  0.6750 0.567381
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# including native vs. exotic - first with interaction term
```

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

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

```
mod11a <- lmer(spp_half_cover_date ~ state + growth_habit + as.factor(year) +
  (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 + as.factor(year) |
```

```
## mod11:      plot)
```

```
## mod10: spp_half_cover_date ~ state * growth_habit + (1 + as.factor(year) |
```

```
## mod10:      plot)
```

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

```
## mod11    21 13813 13921 -6885.4    13771
```

```
## mod10    24 13819 13942 -6885.4    13771 0.1111  3    0.9905
```

```
anova(mod11, mod11a)
```

```

## Data: green_kbs
## Models:
## mod11a: spp_half_cover_date ~ state + growth_habit + as.factor(year) +
## mod11a:      (1 | plot)
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + as.factor(year) |
## mod11:      plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11a   11 13761 13817 -6869.3    13739
## mod11    21 13813 13921 -6885.4    13771      0 10      1

summary(mod11a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + growth_habit + as.factor(year) +
##      (1 | plot)
##      Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
## 13760.7 13817.3 -6869.3 13738.7    1257
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2582 -0.8277 -0.2351  0.9132  2.3298
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 48.16 6.939
## Residual 2937.50 54.199
## Number of obs: 1268, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    134.400     4.225 102.262  31.814 < 2e-16 ***
## stateambient      4.357     4.183  25.156   1.042 0.307507
## growth_habit    -2.109     4.968 1256.244  -0.424 0.671310
## growth_habitGraminoid  6.586     3.343 1263.311   1.970 0.049037 *
## growth_habitVine   70.849    20.856 1263.622   3.397 0.000702 ***
## as.factor(year)2017  -6.491     4.817 1251.639  -1.348 0.178020
## as.factor(year)2018  34.812     4.623 1253.560   7.529 9.72e-14 ***
## as.factor(year)2019  10.968     4.637 1257.392   2.366 0.018152 *
## as.factor(year)2020  38.152     4.718 1255.646   8.087 1.42e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_V a.()2017 a.()2018 a.()2019
## stateambint -0.506
## growth_habt -0.248 -0.008
## grwth_hbtGr -0.275  0.026  0.269
## grwth_hbtVn -0.060 -0.020  0.053  0.064
## as.fc()2017 -0.467 -0.010  0.111 -0.054  0.038
## as.fc()2018 -0.471 -0.003  0.022 -0.059  0.020  0.431
## as.fc()2019 -0.455 -0.020  0.014 -0.075  0.001  0.429  0.444
## as.fc()2020 -0.443 -0.015  0.031 -0.128  0.017  0.430  0.441  0.443

```

```
anova(mod11)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state          1204  1203.8      1    51.82  0.4156 0.521978
## growth_habit  44960 14986.7      3 1227.57  5.1743 0.001482 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## $`emmeans of state, growth_habit`
## state growth_habit emmean SE df lower.CL upper.CL
## warmed Forb          150 3.50 43.1      143      157
## ambient Forb          154 3.39 38.6      147      161
## warmed              148 5.32 223.2      137      158
## ambient              152 5.22 210.6      142      162
## warmed Graminoid      156 3.70 55.4      149      164
## ambient Graminoid      161 3.69 55.3      153      168
## warmed Vine           221 21.09 1236.8      179      262
## ambient Vine           225 20.99 1236.8      184      266
##
## Results are averaged over the levels of: year
## 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 -4.36 4.37 25.9 -0.997 0.9708
## warmed Forb - warmed 2.11 4.99 1262.9 0.423 0.9999
## warmed Forb - ambient -2.25 6.60 139.7 -0.340 1.0000
## warmed Forb - warmed Graminoid -6.59 3.36 1270.9 -1.962 0.5082
## warmed Forb - ambient Graminoid -10.94 5.58 70.6 -1.962 0.5146
## warmed Forb - warmed Vine -70.85 20.98 1274.1 -3.376 0.0172
## warmed Forb - ambient Vine -75.21 21.35 1159.6 -3.522 0.0105
## ambient Forb - warmed 6.47 6.65 145.4 0.972 0.9777
## ambient Forb - ambient 2.11 4.99 1262.9 0.423 0.9999
## ambient Forb - warmed Graminoid -2.23 5.44 65.5 -0.410 0.9999
## ambient Forb - ambient Graminoid -6.59 3.36 1270.9 -1.962 0.5082
## ambient Forb - warmed Vine -66.49 21.51 1162.8 -3.091 0.0426
## ambient Forb - ambient Vine -70.85 20.98 1274.1 -3.376 0.0172
## warmed - ambient -4.36 4.37 25.9 -0.997 0.9708
## warmed - warmed Graminoid -8.69 5.21 1267.2 -1.669 0.7073
## warmed - ambient Graminoid -13.05 6.88 161.6 -1.897 0.5548
## warmed - warmed Vine -72.96 21.30 1276.2 -3.425 0.0147
## warmed - ambient Vine -77.31 21.68 1178.6 -3.567 0.0090
## ambient - warmed Graminoid -4.34 6.72 149.8 -0.646 0.9981
## ambient - ambient Graminoid -8.69 5.21 1267.2 -1.669 0.7073
## ambient - warmed Vine -68.60 21.82 1180.0 -3.144 0.0363
## ambient - ambient Vine -72.96 21.30 1276.2 -3.425 0.0147
## warmed Graminoid - ambient Graminoid -4.36 4.37 25.9 -0.997 0.9708
## warmed Graminoid - warmed Vine -64.26 21.04 1274.7 -3.055 0.0473
## warmed Graminoid - ambient Vine -68.62 21.39 1164.2 -3.209 0.0297
## ambient Graminoid - warmed Vine -59.91 21.58 1166.0 -2.776 0.1021
```

```
## ambient Graminoid - ambient Vine      -64.26 21.04 1274.7 -3.055 0.0473
## warmed Vine - ambient Vine            -4.36  4.37   25.9 -0.997 0.9708
##
```

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

```
# 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)
```

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

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

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

```
# 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)
```

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

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

UMBS

```
# 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 |
  plot), green_umbs, REML = FALSE)
```

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

```
umod7a <- lmer(spp_half_cover_date ~ state + species + as.factor(year) +
  (1 | plot), green_umbs, REML = FALSE)
umod7b <- lmer(spp_half_cover_date ~ state * as.factor(year) +
  species + (1 | plot), green_umbs, REML = FALSE)
umod7c <- lmer(spp_half_cover_date ~ state + species + as.factor(year) +
  insecticide + (1 | plot), green_umbs, REML = FALSE)
# anova(umod6, umod7) # umodel 7 is a better fit to data
anova(umod7, umod7a) #umod 7a
```

```
## Data: green_umbs
```

```
## Models:
```

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

```
## umod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## umod7a: plot)
```

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

```
## umod7      20 7518.3 7611.0 -3739.2 7478.3
```

```
## umod7a     22 7472.5 7574.4 -3714.3 7428.5 49.823 2 1.517e-11 ***
```

```
## ---
```

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

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

```
## Data: green_umbs
```

```
## Models:
```

```
## umod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## umod7a: plot)
```

```
## umod7b: spp_half_cover_date ~ state * as.factor(year) + species + (1 |
## umod7b: plot)
```

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

```
## umod7a     22 7472.5 7574.4 -3714.3 7428.5
```

```
## umod7b     26 7479.4 7599.8 -3713.7 7427.4 1.1255 4 0.8902
```

```
anova(umod7a, umod7c) #umod 7a
```

```
## Data: green_umbs
```

```
## Models:
```

```
## umod7a: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## umod7a: plot)
```

```
## umod7c: spp_half_cover_date ~ state + species + as.factor(year) + insecticide +
## umod7c: (1 | plot)
```

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

```
## umod7a     22 7472.5 7574.4 -3714.3 7428.5
```

```
## umod7c     23 7474.5 7581.0 -3714.3 7428.5 0.0112 1 0.9157
```

```
summary(umod7a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + as.factor(year) + (1 |
## plot)
## Data: green_umbs
##
##      AIC      BIC  logLik deviance df.resid
##  7472.5   7574.4  -3714.3   7428.5     736
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6745 -0.6530 -0.2394  0.4747  2.9700
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 10.74 3.276
## Residual 1046.74 32.353
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 133.1134    12.8538 704.3993 10.356 < 2e-16 ***
## stateambient -0.5515     2.7339 19.1712 -0.202 0.842264
## speciesAnsp  5.7713    15.4151 749.7399 0.374 0.708218
## speciesApan 53.1206    17.4131 757.0398 3.051 0.002363 **
## speciesAssp 32.8899    13.9671 726.5846 2.355 0.018797 *
## speciesCape 22.8314    12.9117 743.3551 1.768 0.077426 .
## speciesCest  7.8761    12.7323 746.8968 0.619 0.536375
## speciesDasp  8.8560    12.7915 747.2244 0.692 0.488942
## speciesFrve 14.0204    14.2505 731.2779 0.984 0.325514
## speciesHisp 41.5475    14.8013 757.8220 2.807 0.005129 **
## speciesHype 11.5257    13.1021 752.4986 0.880 0.379311
## speciesPosp 25.1399    12.7436 747.7821 1.973 0.048892 *
## speciesPtaq 44.6423    12.9197 751.8928 3.455 0.000580 ***
## speciesRuac  9.3281    12.8392 750.9381 0.727 0.467736
## speciesSosp 28.3815    14.4875 755.2403 1.959 0.050476 .
## speciesSyla 58.8876    16.4280 757.7411 3.585 0.000359 ***
## as.factor(year)2017 -7.1865     3.8666 738.1707 -1.859 0.063476 .
## as.factor(year)2018 13.6900     3.8376 735.2700 3.567 0.000384 ***
## as.factor(year)2019 16.9211     3.8038 738.8588 4.448 9.98e-06 ***
## as.factor(year)2020  8.3398     3.7580 735.9085 2.219 0.026777 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
```

```
summary(umod7b)
```

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

```

## Formula: spp_half_cover_date ~ state * as.factor(year) + species + (1 |
##   plot)
##   Data: green_umbs
##
##       AIC       BIC   logLik deviance df.resid
##  7479.4   7599.8 -3713.7   7427.4      732
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6202 -0.6651 -0.2375  0.4573  2.9845
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   plot     (Intercept)  10.69   3.27
##   Residual              1045.21  32.33
## Number of obs: 758, groups:  plot, 24
##
## Fixed effects:
##
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    134.6938    13.0808 708.2518  10.297 < 2e-16
## stateambient     -3.6383     5.6108 271.1711  -0.648 0.517239
## as.factor(year)2017 -9.7091     5.4205 740.1330  -1.791 0.073672
## as.factor(year)2018  11.5638     5.4916 735.4283   2.106 0.035568
## as.factor(year)2019  16.7821     5.3624 735.7349   3.130 0.001820
## as.factor(year)2020   5.2607     5.3966 735.1892   0.975 0.329972
## speciesAnsp        5.6244    15.4235 749.1458   0.365 0.715466
## speciesApan        52.8262    17.4050 757.0141   3.035 0.002487
## speciesAssp        32.7361    13.9621 725.9658   2.345 0.019314
## speciesCape        22.8775    12.9080 742.7820   1.772 0.076747
## speciesCest         7.8916    12.7279 746.4601   0.620 0.535428
## speciesDaspp        8.8200    12.7869 746.7437   0.690 0.490553
## speciesFrve        13.9343    14.2448 730.7106   0.978 0.328299
## speciesHispp       41.2249    14.8125 757.7409   2.783 0.005518
## speciesHype        11.6608    13.0972 752.3430   0.890 0.373571
## speciesPospp       25.1311    12.7390 747.3539   1.973 0.048891
## speciesPtaq        44.6797    12.9146 751.6467   3.460 0.000571
## speciesRuac         9.2860    12.8343 750.5913   0.724 0.469578
## speciesSosp        28.6224    14.4901 755.0126   1.975 0.048597
## speciesSyla        59.3797    16.4335 757.7035   3.613 0.000322
## stateambient:as.factor(year)2017  5.0564     7.6592 740.7728   0.660 0.509353
## stateambient:as.factor(year)2018  4.1236     7.6298 736.4377   0.540 0.589046
## stateambient:as.factor(year)2019  0.1245     7.5353 738.2554   0.017 0.986824
## stateambient:as.factor(year)2020  5.9042     7.4396 736.5687   0.794 0.427677
##
## (Intercept)          ***
## stateambient
## as.factor(year)2017      .
## as.factor(year)2018      *
## as.factor(year)2019     **
## as.factor(year)2020
## speciesAnsp
## speciesApan              **
## speciesAssp              *
## speciesCape              .

```

```

## speciesCest
## speciesDasp
## speciesFrve
## speciesHisp          **
## speciesHype
## speciesPosp          *
## speciesPtaq          ***
## speciesRuac
## speciesSosp          *
## speciesSyla          ***
## stateambient:as.factor(year)2017
## stateambient:as.factor(year)2018
## stateambient:as.factor(year)2019
## stateambient:as.factor(year)2020
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 24 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it
summary(umod7c)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state + species + as.factor(year) + insecticide +
## (1 | plot)
## Data: green_umbs
##
##      AIC      BIC  logLik deviance df.resid
## 7474.5   7581.0 -3714.3  7428.5      735
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6763 -0.6504 -0.2414  0.4738  2.9739
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## plot     (Intercept)  10.75   3.279
## Residual                1046.71  32.353
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   132.9841    12.9113  674.0975   10.300 < 2e-16 ***
## stateambient    -0.5516     2.7345   19.2096   -0.202 0.842263
## speciesAnsp      5.7484    15.4167  750.1819    0.373 0.709351
## speciesApan     53.0015    17.4502  757.9989    3.037 0.002469 **
## speciesAssp     32.9304    13.9719  727.1054    2.357 0.018693 *
## speciesCape     22.8169    12.9125  743.7702    1.767 0.077631 .
## speciesCest      7.8632    12.7329  747.2469    0.618 0.537062
## speciesDasp      8.8442    12.7920  747.5509    0.691 0.489536
## speciesFrve     14.0027    14.2516  732.3829    0.983 0.326160

```



```

## speciesHisp          41.4914      14.8109 757.9992      2.801 0.005218 **
## speciesHype          11.5040      13.1038 752.9656      0.878 0.380269
## speciesPosp          25.1292      12.7440 748.0597      1.972 0.048996 *
## speciesPtaq          44.6213      12.9212 752.3767      3.453 0.000585 ***
## speciesRuac           9.3071      12.8408 751.4619      0.725 0.468792
## speciesSosp          28.3158      14.5011 756.5082      1.953 0.051227 .
## speciesSyla          58.8631      16.4296 757.8121      3.583 0.000362 ***
## as.factor(year)2017   -7.1880       3.8665 738.2103     -1.859 0.063421 .
## as.factor(year)2018   13.6854       3.8378 735.1705      3.566 0.000386 ***
## as.factor(year)2019   16.9157       3.8041 738.6167      4.447 1.01e-05 ***
## as.factor(year)2020    8.3359       3.7581 735.7169      2.218 0.026853 *
## insecticideno_insects  0.2908       2.7469 19.6318      0.106 0.916761
## ---
## 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

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           43      42.6      1  19.17  0.0407    0.8423
## species       134557  9611.2     14 744.43  9.1820 < 2.2e-16 ***
## as.factor(year) 55399 13849.8      4 735.50 13.2313  2.05e-10 ***
## ---
## 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(umod7a, list(pairwise ~ as.factor(year)), adjust = "tukey")

## $`emmeans of year`
##   year emmean   SE  df lower.CL upper.CL
## 2016    157 3.32 409     151      164
## 2017    150 3.23 398     144      156
## 2018    171 3.21 379     165      177
## 2019    174 3.19 359     168      180
## 2020    165 3.11 352     159      172
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year`
##    1      estimate   SE  df t.ratio p.value
## 2016 - 2017      7.19 3.92 759   1.835 0.3539
## 2016 - 2018     -13.69 3.89 757  -3.524 0.0041
## 2016 - 2019     -16.92 3.85 760  -4.392 0.0001
## 2016 - 2020      -8.34 3.80 757  -2.192 0.1838
## 2017 - 2018     -20.88 3.90 756  -5.357 <.0001
## 2017 - 2019     -24.11 3.85 756  -6.255 <.0001
## 2017 - 2020     -15.53 3.81 758  -4.077 0.0005
## 2018 - 2019      -3.23 3.78 754  -0.856 0.9128

```

```

## 2018 - 2020      5.35 3.73 755  1.434  0.6055
## 2019 - 2020      8.58 3.67 755  2.336  0.1348
##
## 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")

## `$emmeans of species`
## species emmean SE df lower.CL upper.CL
## Amla      139 12.65 762      114      164
## Ansp      145  9.24 777      127      163
## Apan      192 12.63 768      168      217
## Assp      172  6.61 699      159      185
## Cape      162  3.85 566      154      170
## Cest      147  3.10 430      141      153
## Dasp      148  3.30 478      142      155
## Frve      153  7.18 687      139      167
## Hisp      181  8.21 774      165      197
## Hype      151  4.56 644      142      160
## Posp      164  3.18 452      158      171
## Ptaq      184  3.83 546      176      191
## Ruac      149  3.59 509      141      156
## Sosp      168  7.73 698      152      183
## Syla      198 11.19 737      176      220
##
## Results are averaged over the levels of: state, year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## `$pairwise differences of species`
## 1 estimate SE df t.ratio p.value
## Amla - Ansp -5.771 15.70 776 -0.368 1.0000
## Amla - Apan -53.121 17.71 779 -2.999 0.1561
## Amla - Assp -32.890 14.26 763 -2.306 0.5862
## Amla - Cape -22.831 13.16 773 -1.734 0.9220
## Amla - Cest -7.876 12.98 775 -0.607 1.0000
## Amla - Dasp -8.856 13.04 775 -0.679 1.0000
## Amla - Frve -14.020 14.54 765 -0.964 0.9998
## Amla - Hisp -41.547 15.05 779 -2.761 0.2708
## Amla - Hype -11.526 13.34 777 -0.864 0.9999
## Amla - Posp -25.140 12.99 775 -1.936 0.8343
## Amla - Ptaq -44.642 13.16 777 -3.393 0.0515
## Amla - Ruac -9.328 13.08 777 -0.713 1.0000
## Amla - Sosp -28.381 14.74 778 -1.925 0.8401
## Amla - Syla -58.888 16.71 779 -3.525 0.0338
## Ansp - Apan -47.349 15.63 778 -3.029 0.1448
## Ansp - Assp -27.119 11.30 777 -2.400 0.5157
## Ansp - Cape -17.060  9.98 776 -1.709 0.9301
## Ansp - Cest -2.105  9.68 773 -0.217 1.0000
## Ansp - Dasp -3.085  9.73 773 -0.317 1.0000
## Ansp - Frve -8.249 11.61 778 -0.711 1.0000
## Ansp - Hisp -35.776 12.22 773 -2.928 0.1856
## Ansp - Hype -5.754 10.28 772 -0.560 1.0000

```

##	Ansp - Posp	-19.369	9.71	774	-1.995	0.8013
##	Ansp - Ptaq	-38.871	9.95	777	-3.905	0.0088
##	Ansp - Ruac	-3.557	9.83	769	-0.362	1.0000
##	Ansp - Sosp	-22.610	11.98	776	-1.887	0.8590
##	Ansp - Syla	-53.116	14.51	772	-3.661	0.0213
##	Apan - Assp	20.231	14.22	769	1.423	0.9852
##	Apan - Cape	30.289	13.14	776	2.306	0.5864
##	Apan - Cest	45.245	12.95	777	3.493	0.0375
##	Apan - Dasp	44.265	13.01	778	3.402	0.0501
##	Apan - Frve	39.100	14.54	765	2.689	0.3136
##	Apan - Hisp	11.573	15.04	779	0.769	1.0000
##	Apan - Hype	41.595	13.32	779	3.123	0.1128
##	Apan - Posp	27.981	12.97	777	2.157	0.6956
##	Apan - Ptaq	8.478	13.13	779	0.646	1.0000
##	Apan - Ruac	43.793	13.06	779	3.354	0.0580
##	Apan - Sosp	24.739	14.79	776	1.672	0.9409
##	Apan - Syla	-5.767	16.82	772	-0.343	1.0000
##	Assp - Cape	10.058	7.57	771	1.329	0.9923
##	Assp - Cest	25.014	7.21	776	3.470	0.0403
##	Assp - Dasp	24.034	7.29	778	3.296	0.0691
##	Assp - Frve	18.870	9.65	772	1.956	0.8233
##	Assp - Hisp	-8.658	10.48	778	-0.826	1.0000
##	Assp - Hype	21.364	7.92	778	2.696	0.3090
##	Assp - Posp	7.750	7.25	776	1.070	0.9992
##	Assp - Ptaq	-11.752	7.54	778	-1.559	0.9666
##	Assp - Ruac	23.562	7.42	777	3.176	0.0977
##	Assp - Sosp	4.508	10.11	768	0.446	1.0000
##	Assp - Syla	-25.998	12.88	773	-2.018	0.7873
##	Cape - Cest	14.955	4.81	766	3.111	0.1168
##	Cape - Dasp	13.975	4.96	771	2.819	0.2386
##	Cape - Frve	8.811	8.07	770	1.091	0.9990
##	Cape - Hisp	-18.716	9.02	776	-2.075	0.7516
##	Cape - Hype	11.306	5.84	778	1.937	0.8337
##	Cape - Posp	-2.309	4.85	765	-0.476	1.0000
##	Cape - Ptaq	-21.811	5.31	776	-4.104	0.0040
##	Cape - Ruac	13.503	5.15	779	2.621	0.3574
##	Cape - Sosp	-5.550	8.59	766	-0.646	1.0000
##	Cape - Syla	-36.056	11.79	758	-3.058	0.1342
##	Cest - Dasp	-0.980	4.38	756	-0.224	1.0000
##	Cest - Frve	-6.144	7.74	768	-0.794	1.0000
##	Cest - Hisp	-33.671	8.70	774	-3.870	0.0100
##	Cest - Hype	-3.650	5.39	774	-0.677	1.0000
##	Cest - Posp	-17.264	4.28	752	-4.029	0.0054
##	Cest - Ptaq	-36.766	4.79	771	-7.677	<.0001
##	Cest - Ruac	-1.452	4.60	767	-0.316	1.0000
##	Cest - Sosp	-20.505	8.25	767	-2.486	0.4520
##	Cest - Syla	-51.012	11.55	764	-4.416	0.0011
##	Dasp - Frve	-5.164	7.82	767	-0.660	1.0000
##	Dasp - Hisp	-32.692	8.76	771	-3.731	0.0167
##	Dasp - Hype	-2.670	5.52	772	-0.484	1.0000
##	Dasp - Posp	-16.284	4.44	757	-3.668	0.0208
##	Dasp - Ptaq	-35.786	4.92	770	-7.274	<.0001
##	Dasp - Ruac	-0.472	4.74	765	-0.100	1.0000
##	Dasp - Sosp	-19.525	8.32	766	-2.346	0.5565

```
## Dasp - Syla -50.032 11.61 765 -4.311 0.0017
## Frve - Hisp -27.527 10.79 776 -2.551 0.4050
## Frve - Hype 2.495 8.43 771 0.296 1.0000
## Frve - Posp -11.120 7.77 770 -1.430 0.9844
## Frve - Ptaq -30.622 8.06 763 -3.799 0.0130
## Frve - Ruac 4.692 7.94 769 0.591 1.0000
## Frve - Sosp -14.361 10.44 770 -1.375 0.9892
## Frve - Syla -44.867 13.16 776 -3.410 0.0487
## Hisp - Hype 30.022 9.34 766 3.213 0.0879
## Hisp - Posp 16.408 8.72 773 1.882 0.8619
## Hisp - Ptaq -3.095 8.98 773 -0.345 1.0000
## Hisp - Ruac 32.219 8.87 769 3.631 0.0237
## Hisp - Sosp 13.166 11.14 778 1.181 0.9977
## Hisp - Syla -17.340 13.78 779 -1.258 0.9955
## Hype - Posp -13.614 5.43 774 -2.507 0.4368
## Hype - Ptaq -33.117 5.83 776 -5.677 <.0001
## Hype - Ruac 2.198 5.66 770 0.388 1.0000
## Hype - Sosp -16.856 8.94 764 -1.886 0.8596
## Hype - Syla -47.362 12.00 770 -3.947 0.0075
## Posp - Ptaq -19.502 4.84 772 -4.026 0.0055
## Posp - Ruac 15.812 4.65 768 3.400 0.0504
## Posp - Sosp -3.242 8.28 768 -0.392 1.0000
## Posp - Syla -33.748 11.57 765 -2.916 0.1910
## Ptaq - Ruac 35.314 5.12 775 6.903 <.0001
## Ptaq - Sosp 16.261 8.54 769 1.905 0.8504
## Ptaq - Syla -14.245 11.74 771 -1.214 0.9969
## Ruac - Sosp -19.053 8.44 769 -2.257 0.6231
## Ruac - Syla -49.559 11.67 769 -4.246 0.0023
## Sosp - Syla -30.506 13.37 775 -2.282 0.6043
##
```

```
## Results are averaged over the levels of: state, year
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 15 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 |
  plot), green_umbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.7e+07
```

```
summary(umod8)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * origin + (1 + year | plot)
## Data: green_umbs
##
##      AIC      BIC    logLik deviance df.resid
## 7576.9 7632.5 -3776.5 7552.9      746
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -1.9570 -0.7223 -0.2045 0.6954 3.0315
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## plot (Intercept) 1.237e+03 35.172
## year 2.561e-04 0.016 -1.00
## Residual 1.237e+03 35.169
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 164.178 2.847 74.307 57.666 < 2e-16 ***
## stateambient -2.796 4.023 72.983 -0.695 0.4892
## origin 4.618 5.361 743.894 0.861 0.3893
## originBoth -4.721 10.150 756.283 -0.465 0.6420
## originExotic -16.445 4.091 755.205 -4.020 6.41e-05 ***
## stateambient:origin -5.563 7.630 745.072 -0.729 0.4662
## stateambient:originBoth 21.693 12.329 757.924 1.759 0.0789 .
## stateambient:originExotic 5.652 5.794 755.076 0.975 0.3297
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) sttmbn origin orgnBt orgnEx sttmb: sttm:B
## stateambint -0.708
## origin -0.486 0.344
## originBoth -0.256 0.181 0.136
## originExotc -0.636 0.450 0.338 0.179
## sttmbnt:rgn 0.341 -0.482 -0.703 -0.095 -0.237
## sttmbnt:rgB 0.210 -0.296 -0.112 -0.823 -0.148 0.156
## sttmbnt:rgE 0.449 -0.634 -0.238 -0.127 -0.706 0.334 0.207
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(umod8)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state 586 585.6 1 61.49 0.4734 0.4940
## origin 37258 12419.4 3 752.78 10.0409 1.712e-06 ***
## state:origin 6322 2107.2 3 752.78 1.7037 0.1648
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# including native vs. exotic - first with interaction term
```

```
umod9 <- lmer(spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
  plot), green_umbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.3e-01
```

```
umod9a <- lmer(spp_half_cover_date ~ state + origin + as.factor(year) +
  (1 | plot), green_umbs, REML = FALSE)
```

```
anova(umod8, umod9) # umodel 9 is a better fit to data
```

```
## Data: green_umbs
```

```

## Models:
## umod8: spp_half_cover_date ~ state * origin + (1 + year | plot)
## umod9: spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
## umod9:      plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod8      12 7576.9 7632.5 -3776.5   7552.9
## umod9      21 7573.1 7670.3 -3765.5   7531.1 21.819   9    0.00947 **
## ---
## 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 + as.factor(year) + (1 |
## umod9a:      plot)
## umod9: spp_half_cover_date ~ state + origin + (1 + as.factor(year) |
## umod9:      plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## umod9a      11 7527.7 7578.6 -3752.9   7505.7
## umod9       21 7573.1 7670.3 -3765.5   7531.1    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 + as.factor(year) + (1 |
##      plot)
## Data: green_umbs
##
##      AIC      BIC logLik deviance df.resid
## 7527.7 7578.6 -3752.9   7505.7      747
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.4160 -0.7093 -0.3134  0.5747  2.8516
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 7.374 2.715
## Residual 1162.529 34.096
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
##      Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 156.4535 3.4715 176.0230 45.068 < 2e-16 ***
## stateambient -0.8766 2.7346 19.2906 -0.321 0.751989
## origin 1.4685 3.7018 745.1570 0.397 0.691710
## originBoth 12.5359 5.5910 756.4928 2.242 0.025241 *
## originExotic -14.6098 2.8121 755.3493 -5.195 2.63e-07 ***
## as.factor(year)2017 -7.2180 4.0177 740.5875 -1.797 0.072814 .
## as.factor(year)2018 13.4844 4.0112 737.3246 3.362 0.000815 ***
## as.factor(year)2019 18.0350 3.9666 739.0262 4.547 6.37e-06 ***
## as.factor(year)2020 9.8293 3.9142 736.3709 2.511 0.012246 *
## ---

```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn origin orgnBt orgnEx a.(.)2017 a.(.)2018 a.(.)2019
## stateambint -0.399
## origin      -0.241  0.005
## originBoth  -0.117 -0.079  0.167
## originExotc -0.336  0.004  0.335  0.218
## as.fc()2017 -0.586  0.020 -0.035 -0.081  0.002
## as.fc()2018 -0.573 -0.005 -0.039  0.001 -0.032  0.509
## as.fc()2019 -0.587  0.014 -0.034 -0.014 -0.031  0.516    0.517
## as.fc()2020 -0.585 -0.007 -0.030 -0.033 -0.032  0.524    0.523    0.529
```

```
anova(umod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state         42    41.7      1  43.25  0.0365    0.8494
## origin    47144 15714.6      3 716.23 13.7429 1.008e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(umod9a, list(pairwise ~ state + origin), adjust = "tukey")
```

```
## $`emmeans of state, origin`
## state origin emmean SE df lower.CL upper.CL
## warmed Native 163 2.48 59.1 158 168
## ambient Native 162 2.48 58.5 157 167
## warmed 165 3.59 246.5 158 172
## ambient 164 3.60 252.2 157 171
## warmed Both 176 5.68 532.4 165 187
## ambient Both 175 5.47 473.3 164 186
## warmed Exotic 149 2.66 79.6 143 154
## ambient Exotic 148 2.67 81.9 142 153
##
## Results are averaged over the levels of: year
## 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 0.877 2.90 26.8 0.303 1.0000
## warmed Native - warmed -1.468 3.72 753.9 -0.394 0.9999
## warmed Native - ambient -0.592 4.73 189.1 -0.125 1.0000
## warmed Native - warmed Both -12.536 5.64 767.2 -2.221 0.3403
## warmed Native - ambient Both -11.659 6.16 331.3 -1.894 0.5562
## warmed Native - warmed Exotic 14.610 2.83 763.5 5.157 <.0001
## warmed Native - ambient Exotic 15.486 4.06 106.3 3.816 0.0054
## ambient Native - warmed -2.345 4.71 182.8 -0.498 0.9997
## ambient Native - ambient -1.468 3.72 753.9 -0.394 0.9999
## ambient Native - warmed Both -13.412 6.53 415.4 -2.055 0.4462
## ambient Native - ambient Both -12.536 5.64 767.2 -2.221 0.3403
## ambient Native - warmed Exotic 13.733 4.04 102.9 3.395 0.0211
## ambient Native - ambient Exotic 14.610 2.83 763.5 5.157 <.0001
## warmed - ambient 0.877 2.90 26.8 0.303 1.0000
```

```

## warmed - warmed Both -11.067 6.23 767.3 -1.777 0.6359
## warmed - ambient Both -10.191 6.69 393.3 -1.524 0.7943
## warmed - warmed Exotic 16.078 3.85 751.3 4.178 0.0009
## warmed - ambient Exotic 16.955 4.81 200.1 3.523 0.0121
## ambient - warmed Both -11.944 7.04 474.9 -1.696 0.6902
## ambient - ambient Both -11.067 6.23 767.3 -1.777 0.6359
## ambient - warmed Exotic 15.202 4.82 201.7 3.153 0.0386
## ambient - ambient Exotic 16.078 3.85 751.3 4.178 0.0009
## warmed Both - ambient Both 0.877 2.90 26.8 0.303 1.0000
## warmed Both - warmed Exotic 27.146 5.74 767.4 4.729 0.0001
## warmed Both - ambient Exotic 28.022 6.61 428.9 4.237 0.0007
## ambient Both - warmed Exotic 26.269 6.24 341.0 4.210 0.0009
## ambient Both - ambient Exotic 27.146 5.74 767.4 4.729 0.0001
## warmed Exotic - ambient Exotic 0.877 2.90 26.8 0.303 1.0000
##
## Results are averaged over the levels of: year
## 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 | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 1 negative eigenvalue: -1.7e-03
summary(umod10)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * growth_habit + (1 + year | plot)
## Data: green_umbs
##
## AIC BIC logLik deviance df.resid
## 7608.3 7663.8 -3792.1 7584.3 746
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -1.7964 -0.7531 -0.2309 0.8667 2.7747
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## plot (Intercept) 1.290e+03 35.91108
## year 3.799e-04 0.01949 -1.00
## Residual 1.287e+03 35.86919
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 158.5344 2.6503 48.1638 59.817
## stateambient 0.6004 3.7276 45.0895 0.161
## growth_habit -5.4268 14.9069 757.4390 -0.364
## growth_habitGraminoid 1.0787 3.8445 756.6928 0.281

```



```

## growth_habitTree          -9.3525    21.0267 743.4674 -0.445
## stateambient:growth_habit  29.3839    18.5815 754.6353  1.581
## stateambient:growth_habitGraminoid -3.1829     5.4205 757.8068 -0.587
## stateambient:growth_habitTree -7.4359    27.8277 746.1621 -0.267
##                               Pr(>|t|)
## (Intercept)                <2e-16 ***
## stateambient                0.873
## growth_habit                0.716
## growth_habitGraminoid       0.779
## growth_habitTree            0.657
## stateambient:growth_habit    0.114
## stateambient:growth_habitGraminoid 0.557
## stateambient:growth_habitTree 0.789
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_T sttm:_ stt:_G
## stateambint -0.711
## growth_habt -0.147  0.105
## grwth_hbtGr -0.594  0.423  0.103
## grwth_hbtTr -0.101  0.072  0.020  0.069
## sttmbnt:gr_  0.118 -0.166 -0.802 -0.083 -0.016
## sttmbnt:g_G  0.422 -0.592 -0.073 -0.709 -0.049  0.115
## sttmbnt:g_T  0.076 -0.110 -0.015 -0.052 -0.756  0.024  0.076
## convergence code: 0
## boundary (singular) fit: see ?isSingular

anova(umod10)

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## state           495.6   495.56     1  409.77  0.3852 0.5352
## growth_habit    2546.0   848.66     3  752.74  0.6596 0.5771
## state:growth_habit 4067.9 1355.98     3  752.74  1.0539 0.3680

# including native vs. exotic - first with interaction term
umod11 <- lmer(spp_half_cover_date ~ state + growth_habit + (1 +
  as.factor(year) | plot), green_umbs, REML = FALSE)

## boundary (singular) fit: see ?isSingular

umod11a <- lmer(spp_half_cover_date ~ state + growth_habit +
  as.factor(year) + (1 | plot), green_umbs, REML = FALSE)
anova(umod10, umod11) # umodel 11 is a better fit to data

## Data: green_umbs
## Models:
## umod10: spp_half_cover_date ~ state * growth_habit + (1 + year | plot)
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + as.factor(year) |
## umod11: plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## umod10    12 7608.3 7663.8 -3792.1  7584.3
## umod11    21 7604.5 7701.7 -3781.2  7562.5 21.754  9  0.009693 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
anova(umod11, umod11a)
```

```
## Data: green_umbs
## Models:
## umod11a: spp_half_cover_date ~ state + growth_habit + as.factor(year) +
## umod11a:      (1 | plot)
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + as.factor(year) |
## umod11:      plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## umod11a   11 7560.3 7611.2 -3769.1   7538.3
## umod11    21 7604.5 7701.7 -3781.2   7562.5      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 + as.factor(year) +
##      (1 | plot)
##      Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##  7560.3   7611.2 -3769.1   7538.3      747
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5061 -0.7165 -0.3517  0.6928  2.5177
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
##      plot      (Intercept)    9.441   3.073
##      Residual              1212.170 34.816
## Number of obs: 758, groups: plot, 24
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    152.1958     3.4660 155.5695  43.911 < 2e-16 ***
## stateambient     -0.3559     2.8391  19.5766  -0.125  0.9015
## growth_habit     22.2608     8.8125  751.3993   2.526  0.0117 *
## growth_habitGraminoid -0.6466     2.6316  757.9117  -0.246  0.8060
## growth_habitTree  -20.0360    13.3996  745.1234  -1.495  0.1353
## as.factor(year)2017  -7.5796     4.1500  740.2524  -1.826  0.0682 .
## as.factor(year)2018   13.3452     4.1034  737.3614   3.252  0.0012 **
## as.factor(year)2019   17.6497     4.0547  739.4156   4.353 1.53e-05 ***
## as.factor(year)2020    9.5077     4.0004  736.8924   2.377  0.0177 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) sttmbn grwth_ grwt_G grwt_T a.()2017 a.()2018 a.()2019
## stateambint -0.420
## growth_habt -0.015 -0.040
## grwth_hbtGr -0.283  0.005  0.121
## grwth_hbtTr -0.016 -0.011  0.018  0.078
## as.fc()2017 -0.593  0.020 -0.173 -0.035 -0.005
```

```
## as.fc()2018 -0.590 -0.003 -0.004 -0.035 -0.068 0.503
## as.fc()2019 -0.606 0.015 -0.032 -0.029 -0.045 0.514 0.518
## as.fc()2020 -0.608 -0.006 -0.042 -0.020 -0.043 0.522 0.524 0.530
```

```
anova(umod11)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state           0.2      0.2      1  52.35  0.0002 0.98854
## growth_habit 10033.8  3344.6      3 720.65  2.8013 0.03911 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## $`emmeans of state, growth_habit`
## state growth_habit emmean SE df lower.CL upper.CL
## warmed Forb          159 2.40 43.8      154      164
## ambient Forb          158 2.39 41.3      154      163
## warmed          181 8.94 735.6      163      199
## ambient          181 8.83 732.1      163      198
## warmed Graminoid      158 2.65 68.0      153      163
## ambient Graminoid      158 2.65 69.2      152      163
## warmed Tree          139 13.59 730.2      112      165
## ambient Tree          138 13.55 733.1      112      165
##
## Results are averaged over the levels of: year
## 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          0.356 3.01 26.4 0.118 1.0000
## warmed Forb - warmed          -22.261 8.87 759.2 -2.509 0.1931
## warmed Forb - ambient          -21.905 9.26 654.6 -2.366 0.2599
## warmed Forb - warmed Graminoid      0.647 2.65 766.7 0.244 1.0000
## warmed Forb - ambient Graminoid      1.002 4.02 87.6 0.250 1.0000
## warmed Forb - warmed Tree      20.036 13.56 761.9 1.478 0.8193
## warmed Forb - ambient Tree      20.392 13.85 704.6 1.472 0.8221
## ambient Forb - warmed          -22.617 9.48 664.5 -2.386 0.2497
## ambient Forb - ambient          -22.261 8.87 759.2 -2.509 0.1931
## ambient Forb - warmed Graminoid      0.291 4.00 82.1 0.073 1.0000
## ambient Forb - ambient Graminoid      0.647 2.65 766.7 0.244 1.0000
## ambient Forb - warmed Tree      19.680 13.93 696.2 1.413 0.8512
## ambient Forb - ambient Tree      20.036 13.56 761.9 1.478 0.8193
## warmed - ambient          0.356 3.01 26.4 0.118 1.0000
## warmed - warmed Graminoid      22.907 8.95 763.9 2.558 0.1731
## warmed - ambient Graminoid      23.263 9.56 656.3 2.434 0.2266
## warmed - warmed Tree      42.297 16.06 767.5 2.634 0.1454
## warmed - ambient Tree      42.653 16.37 750.3 2.606 0.1553
## ambient - warmed Graminoid      22.552 9.33 639.4 2.416 0.2352
## ambient - ambient Graminoid      22.907 8.95 763.9 2.558 0.1731
## ambient - warmed Tree      41.941 16.31 745.7 2.572 0.1679
## ambient - ambient Tree      42.297 16.06 767.5 2.634 0.1454
## warmed Graminoid - ambient Graminoid      0.356 3.01 26.4 0.118 1.0000
```

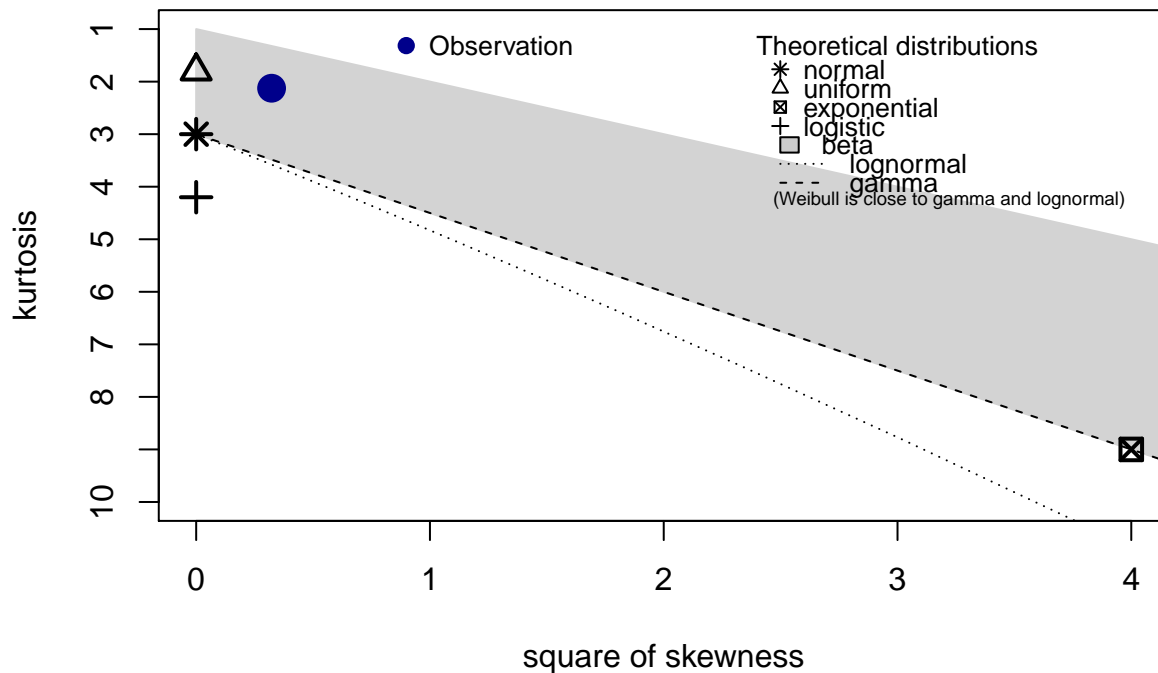
```
## warmed Graminoid - warmed Tree      19.389 13.62 759.4  1.424  0.8461
## warmed Graminoid - ambient Tree     19.745 13.91 697.3  1.420  0.8480
## ambient Graminoid - warmed Tree     19.034 13.98 691.3  1.361  0.8745
## ambient Graminoid - ambient Tree    19.389 13.62 759.4  1.424  0.8461
## warmed Tree - ambient Tree           0.356  3.01  26.4  0.118  1.0000
##
## Results are averaged over the levels of: year
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

ORIGINAL CODE BELOW; not edited by Phoebe

Seeing what other distribution could fit

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

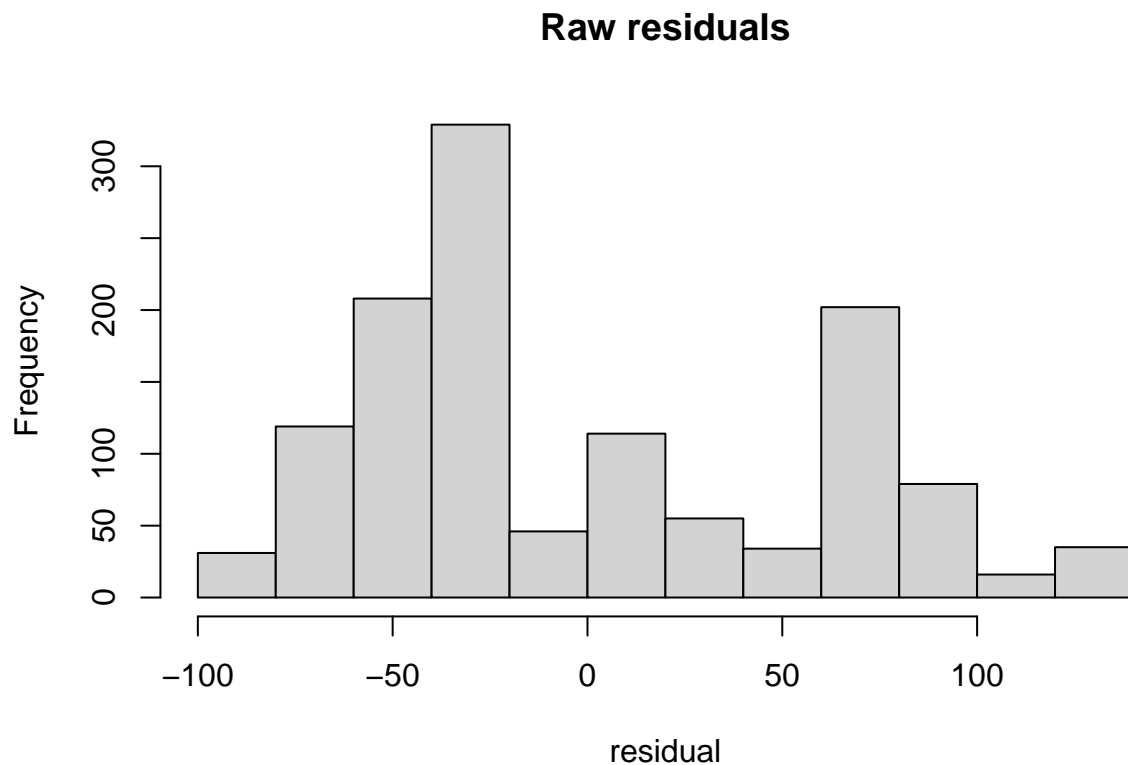
Cullen and Frey graph



```
## summary statistics
## -----
## min: 59  max: 289
## median: 127
## mean: 154.2169
## estimated sd: 57.9311
## estimated skewness: 0.5680173
## estimated kurtosis: 2.125259
```

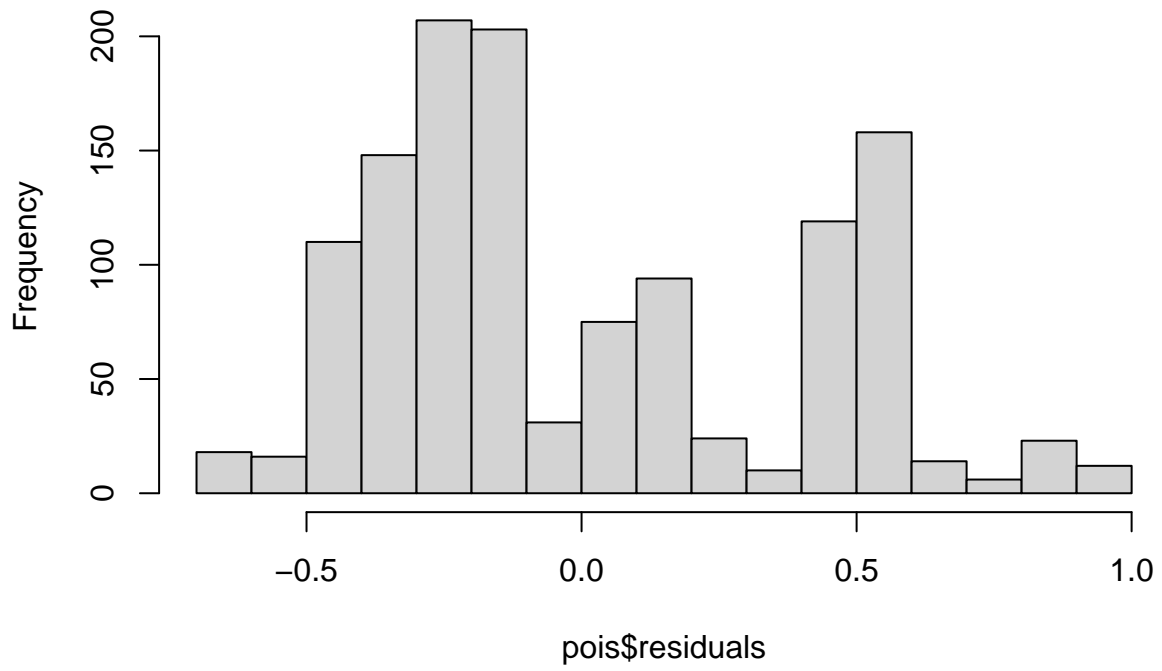
While uniform looks the closest, I'll try poisson

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



```
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| = 0.0232094 (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
## 27686.8 27722.8 -13836.4 27672.8      1261
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -8.3234 -3.0092 -0.9901  2.4141 14.4417
```

```
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 0.003601 0.06001
## species (Intercept) 0.043398 0.20832
## Number of obs: 1268, groups: plot, 24; species, 21
```

```
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -82.699485   4.741076 -17.443  <2e-16 ***
## stateambient    -15.581997   6.330178  -2.462   0.0138 *
## year              0.043454   0.002349  18.497  <2e-16 ***
## insecticideno_insects 0.036029   0.024939   1.445   0.1485
## stateambient:year  0.007736   0.003137   2.466   0.0137 *
```

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

```
## Correlation of Fixed Effects:
##              (Intr) sttmbn year  insct_
## stateambint -0.727
## year        -1.000  0.727
```

```
## insctcdn_ns -0.017  0.007  0.015
## statmbnt:yr  0.727 -1.000 -0.727 -0.007
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model failed to converge with max|grad| = 0.0232094 (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| = 0.00310689 (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
## 27690.8 27721.7 -13839.4 27678.8      1262
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -8.3309 -3.0222 -0.9997  2.3954 14.2765
##
## Random effects:
## Groups Name Variance Std.Dev.
## plot (Intercept) 0.003606 0.06005
## species (Intercept) 0.043488 0.20854
## Number of obs: 1268, groups: plot, 24; species, 21
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -91.116751   3.172907 -28.717 <2e-16 ***
## stateambient      0.030236   0.024956  1.212  0.226
## year              0.047625   0.001572 30.293 <2e-16 ***
## insecticideno_insects 0.036450   0.024954  1.461  0.144
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) sttmbn year
## stateambint  0.002
## year        -1.000 -0.006
## insctcdn_ns -0.018 -0.002  0.014
## convergence code: 0
## Model failed to converge with max|grad| = 0.00310689 (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?

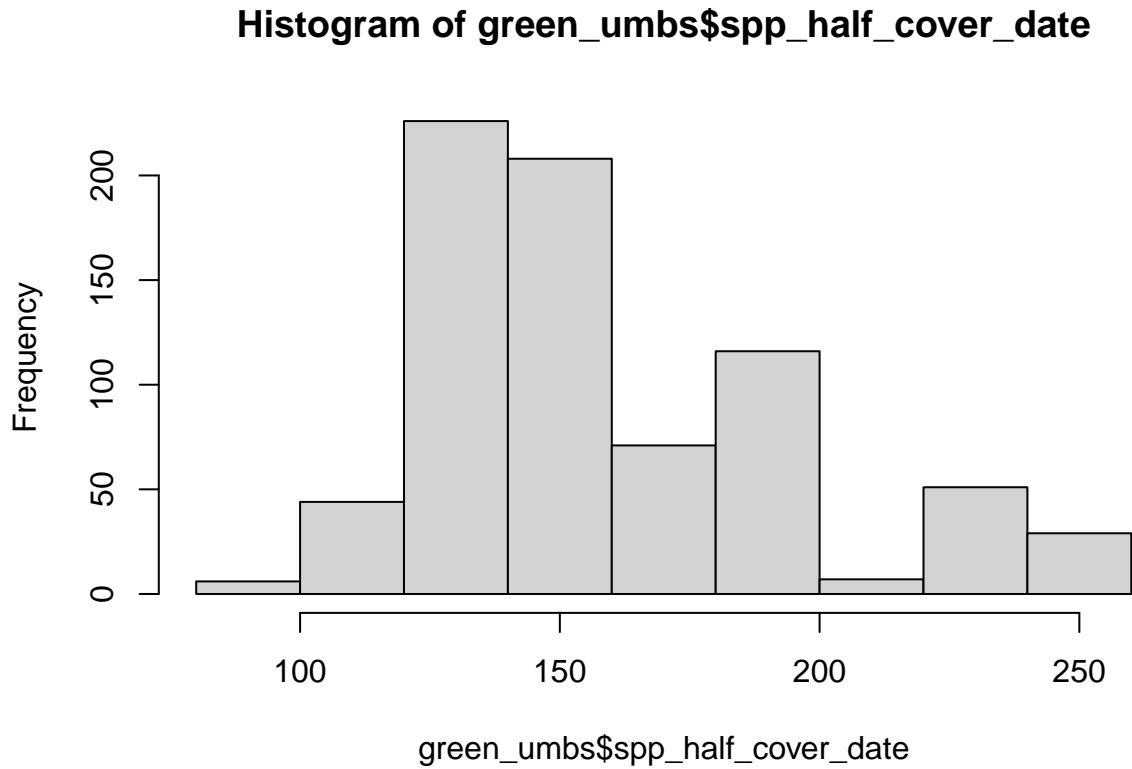
```
per1 <- adonis2(green_kbs$spp_half_cover_date ~ state * year +  
  insecticide, data = green_kbs)  
per1  
per2 <- adonis(formula = green_kbs$spp_half_cover_date ~ state *  
  year + insecticide, strata = green_kbs$plot, data = green_kbs)  
per2
```

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

UMBS

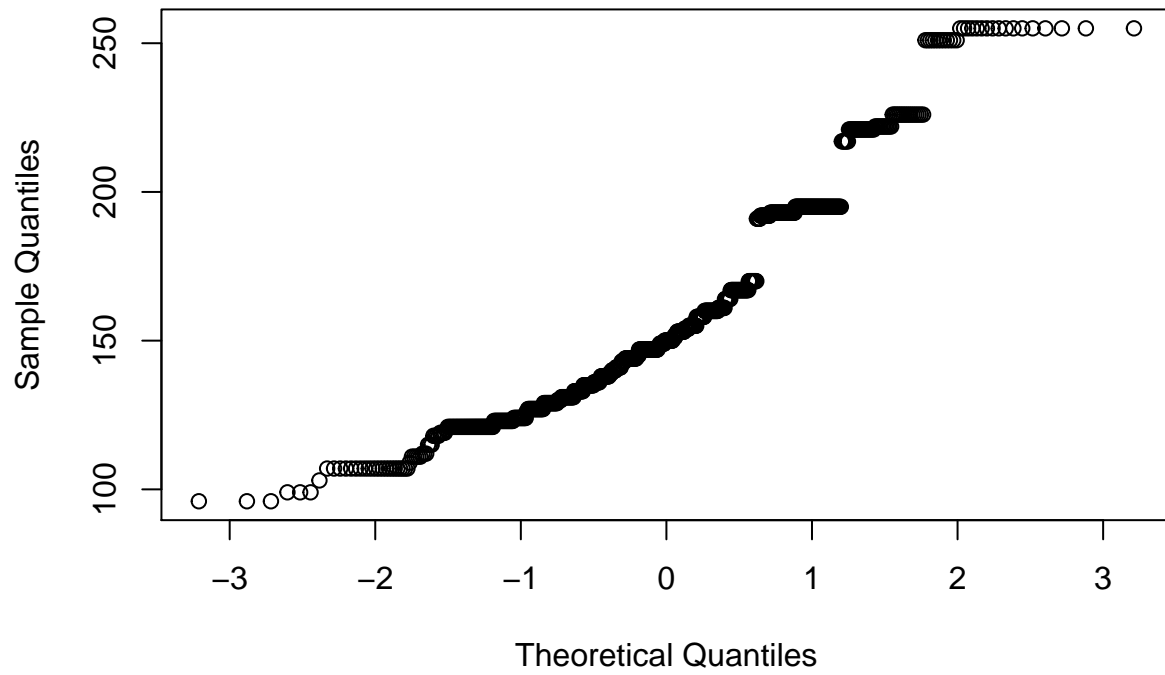
Checking for normality

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



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

Normal Q-Q Plot

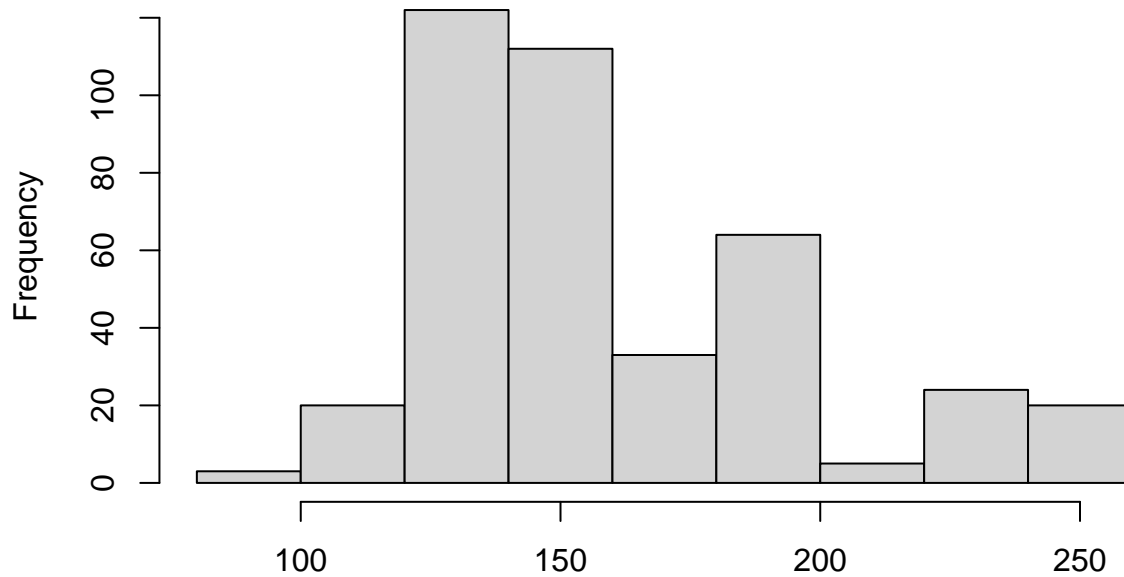


```
shapiro.test(green_umbs$spp_half_cover_date)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  green_umbs$spp_half_cover_date  
## W = 0.92247, p-value < 2.2e-16
```

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

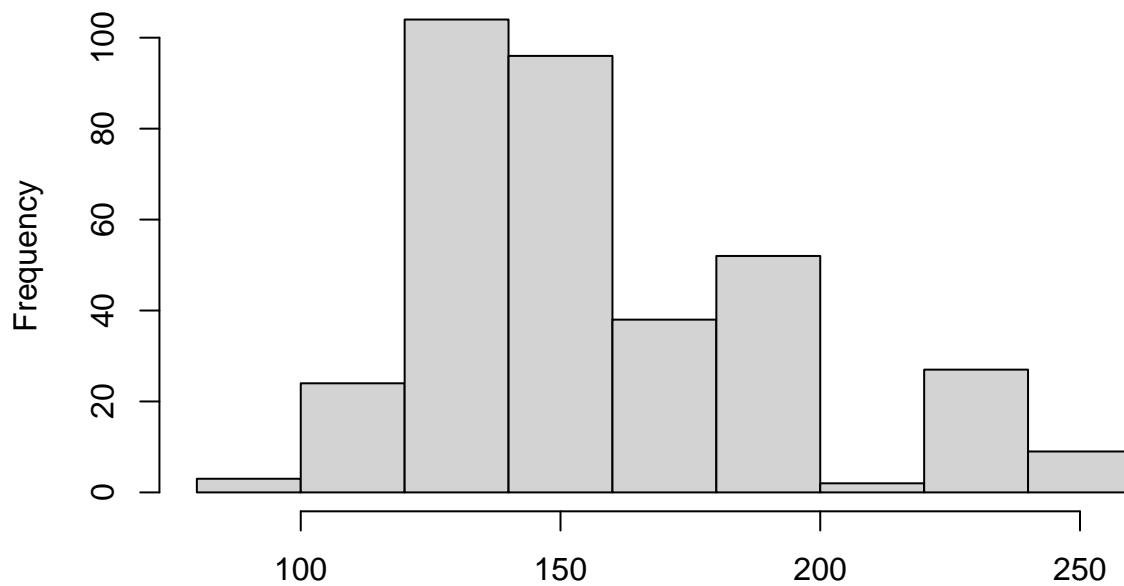
istogram of green_umbs\$spp_half_cover_date[green_kbs\$state == "am



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



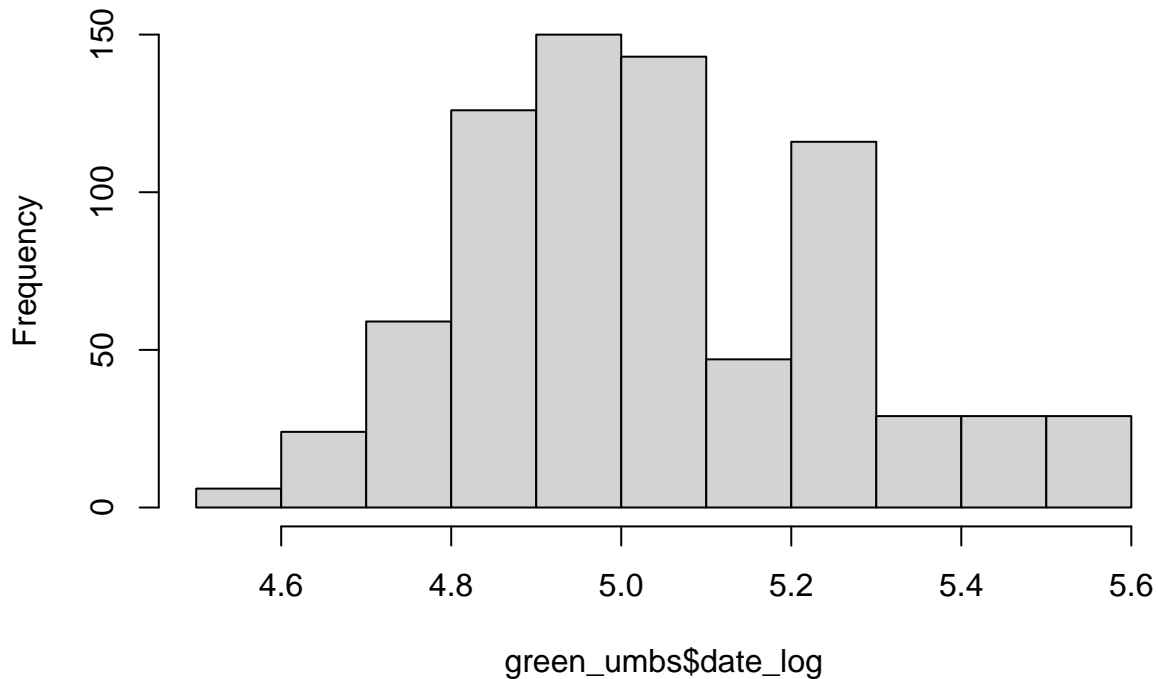
green_umbs\$spp_half_cover_date[green_kbs\$state == "warmed"]

These look pretty good

Trying log transformation

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

Histogram of green_umbs\$date_log



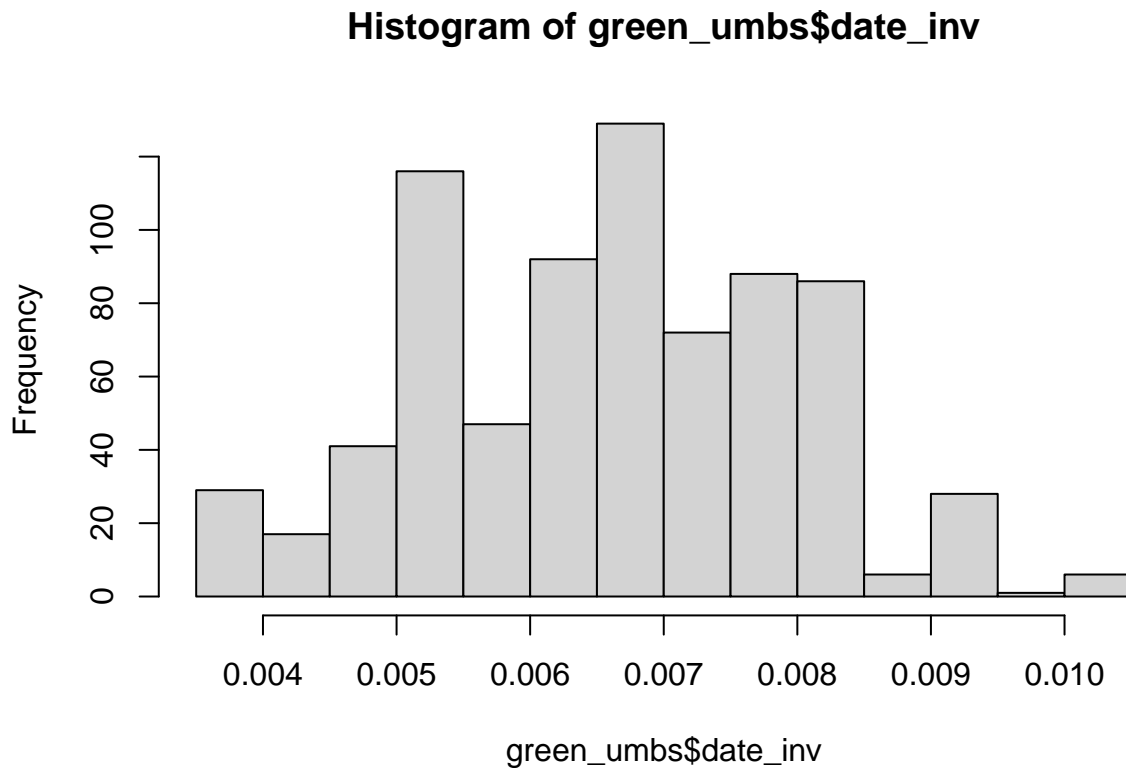
```
shapiro.test(green_umbs$date_log)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_log
## W = 0.96356, p-value = 8.516e-13
```

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)
```



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

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_inv
## W = 0.97928, p-value = 6.952e-09
```

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