warmXtrophic Project: Greenup Analyses

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Script Details:

```r
# 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  "A0" "A0" "A0" "A0" ...
##  $ 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" "Ac
##  $ 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
```

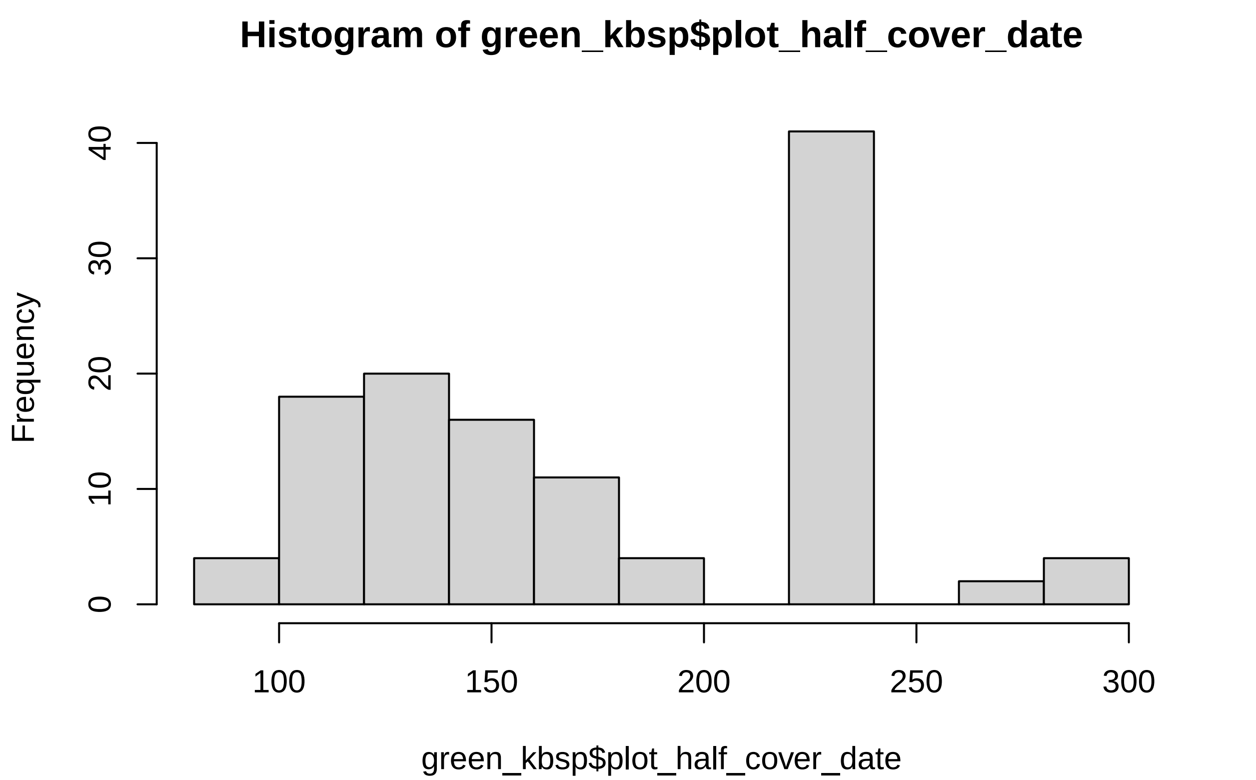
```r
# create dataframes for kbs and umbs - remember that these
# contain species within plots
green_kbs <- subset(greenup, site == "kbs")
green_umbs <- subset(greenup, site == "umbs")

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?

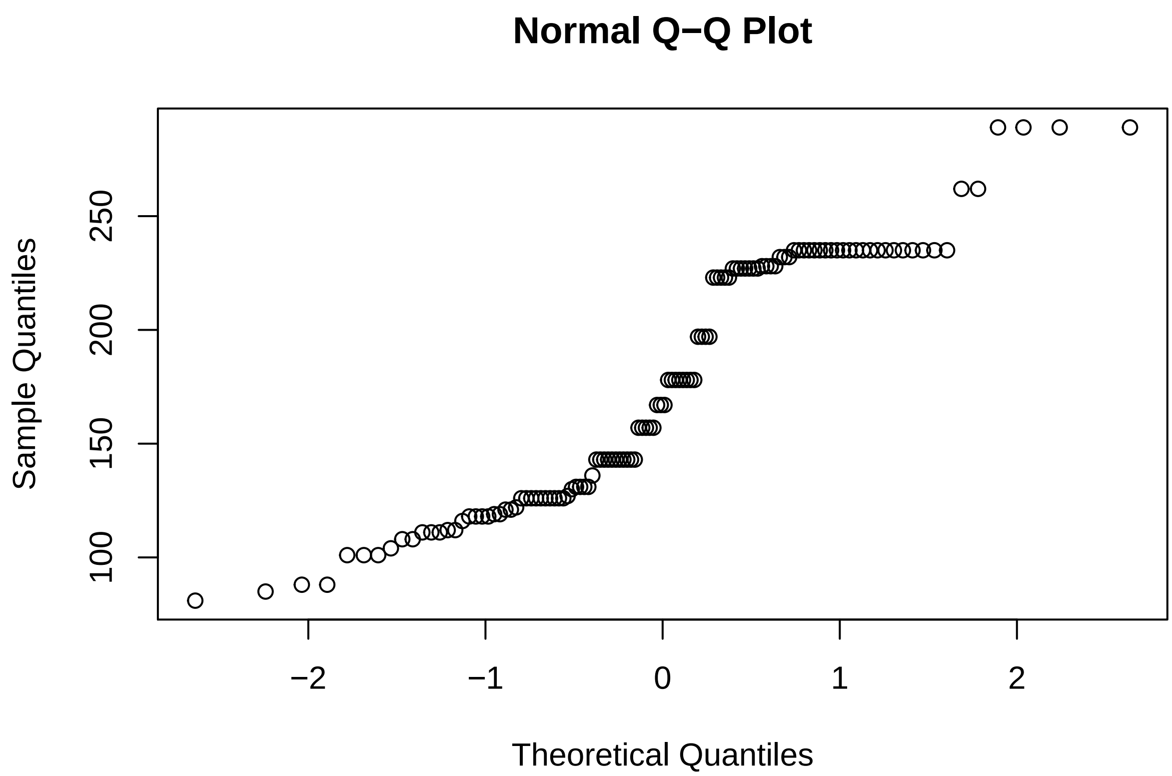
Starting with KBS

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.

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



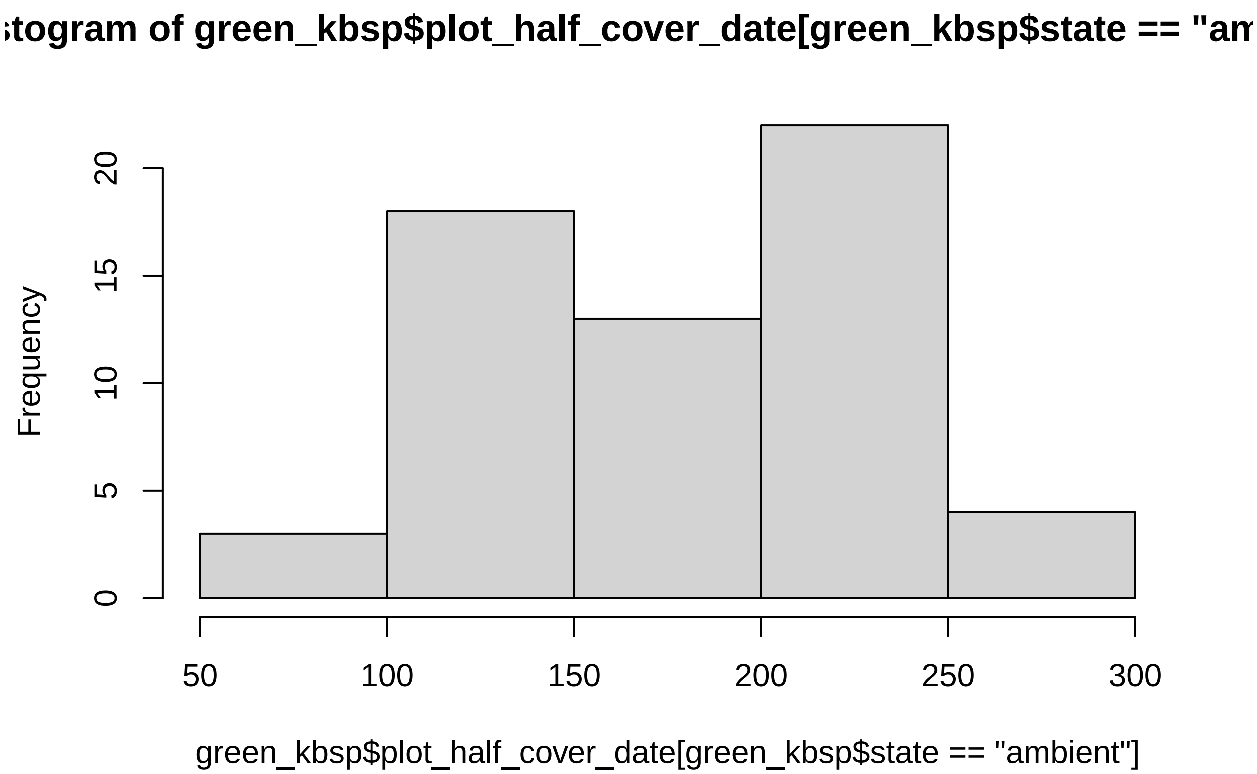

```r
qqnorm(green_kbsp$plot_half_cover_date)
```



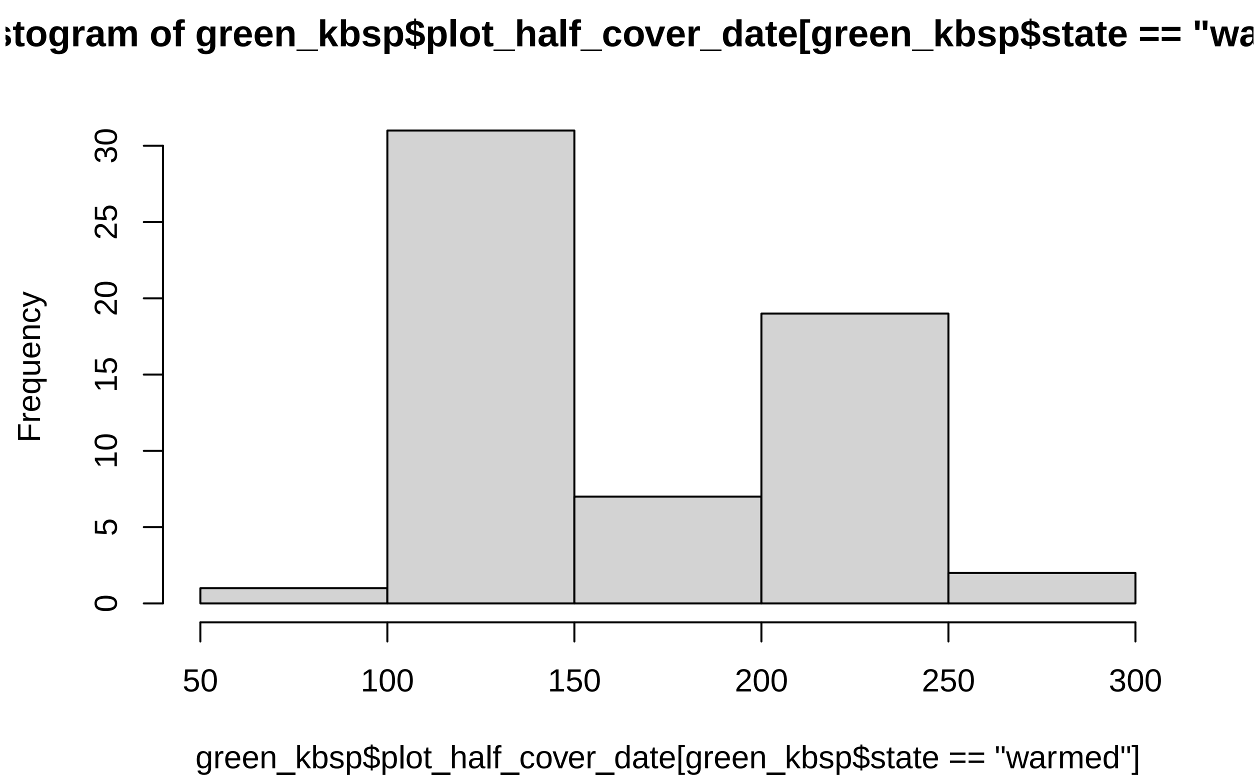

```
shapiro.test(green_kbsp$plot_half_cover_date)
```

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

```
# histograms for each treatment separately
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "ambient"])
```

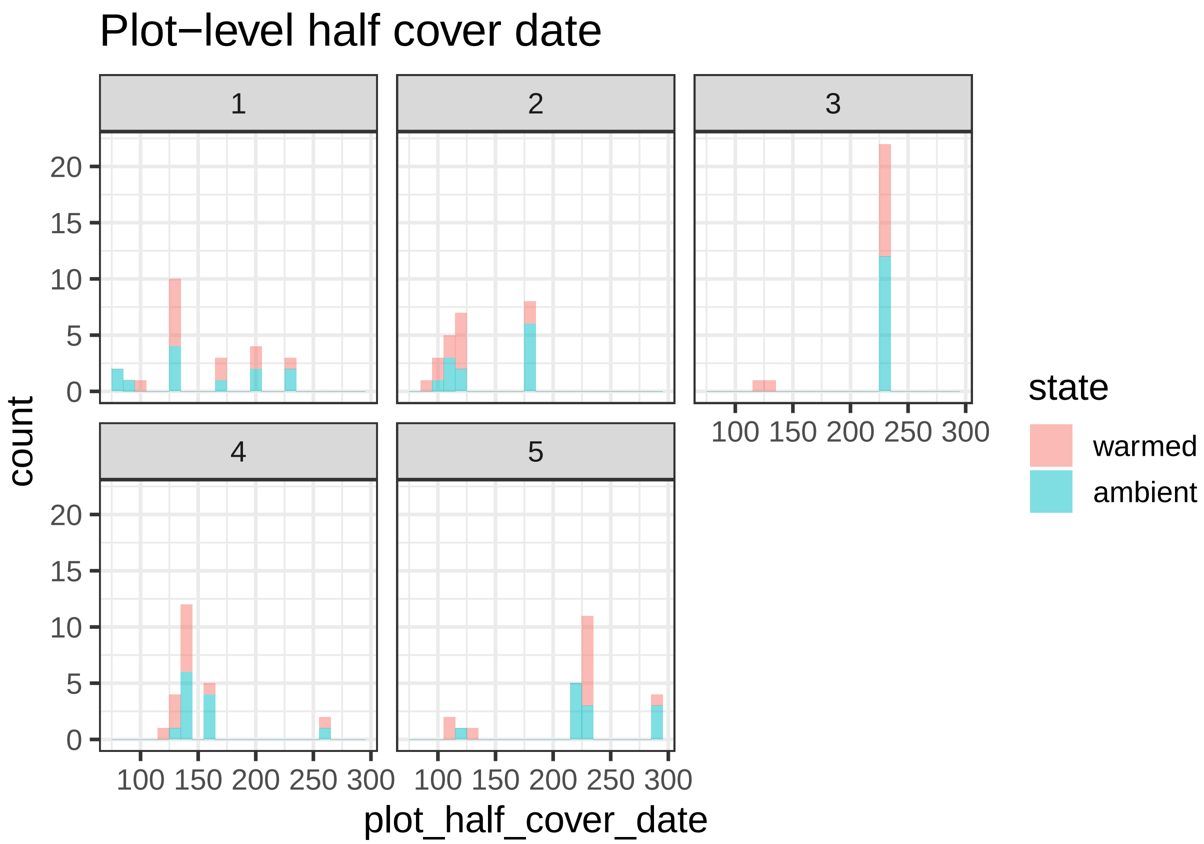



```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "warmed"])
```

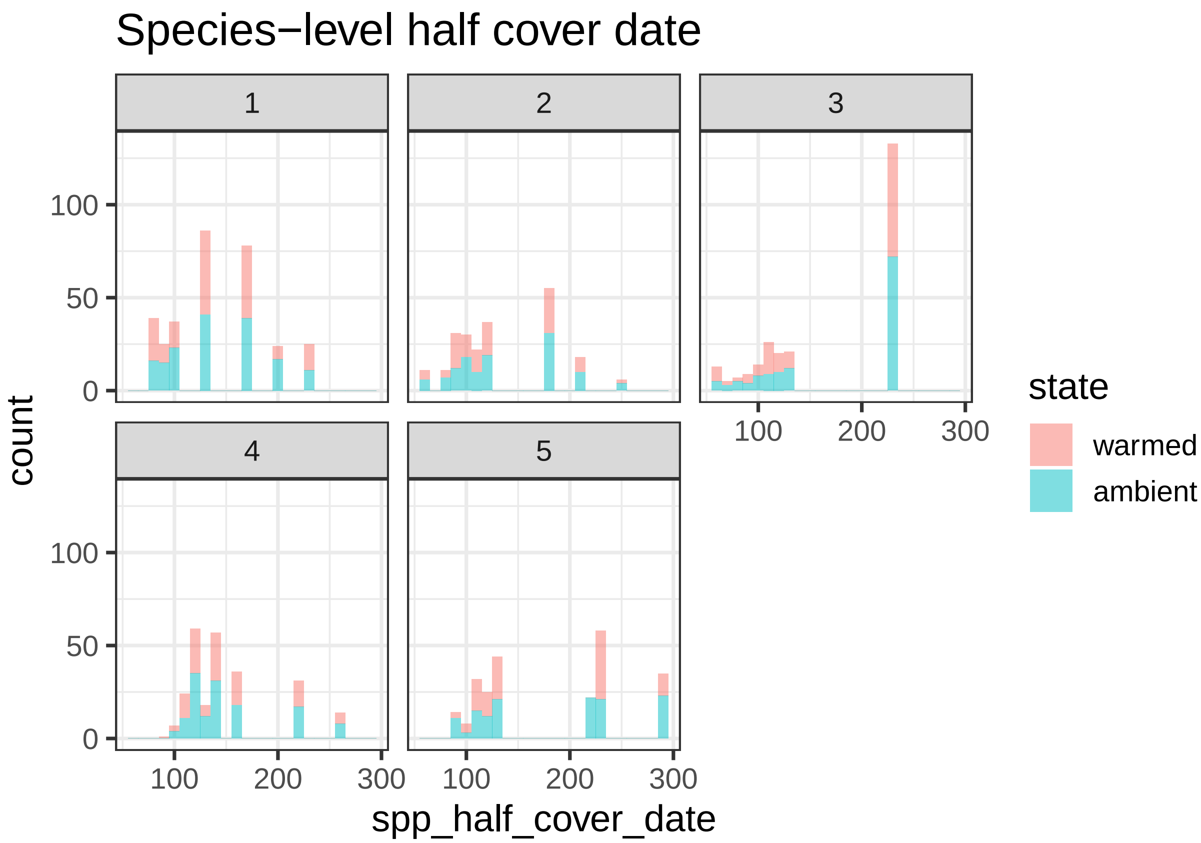



```
# histograms for each year - look at them together:
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
```

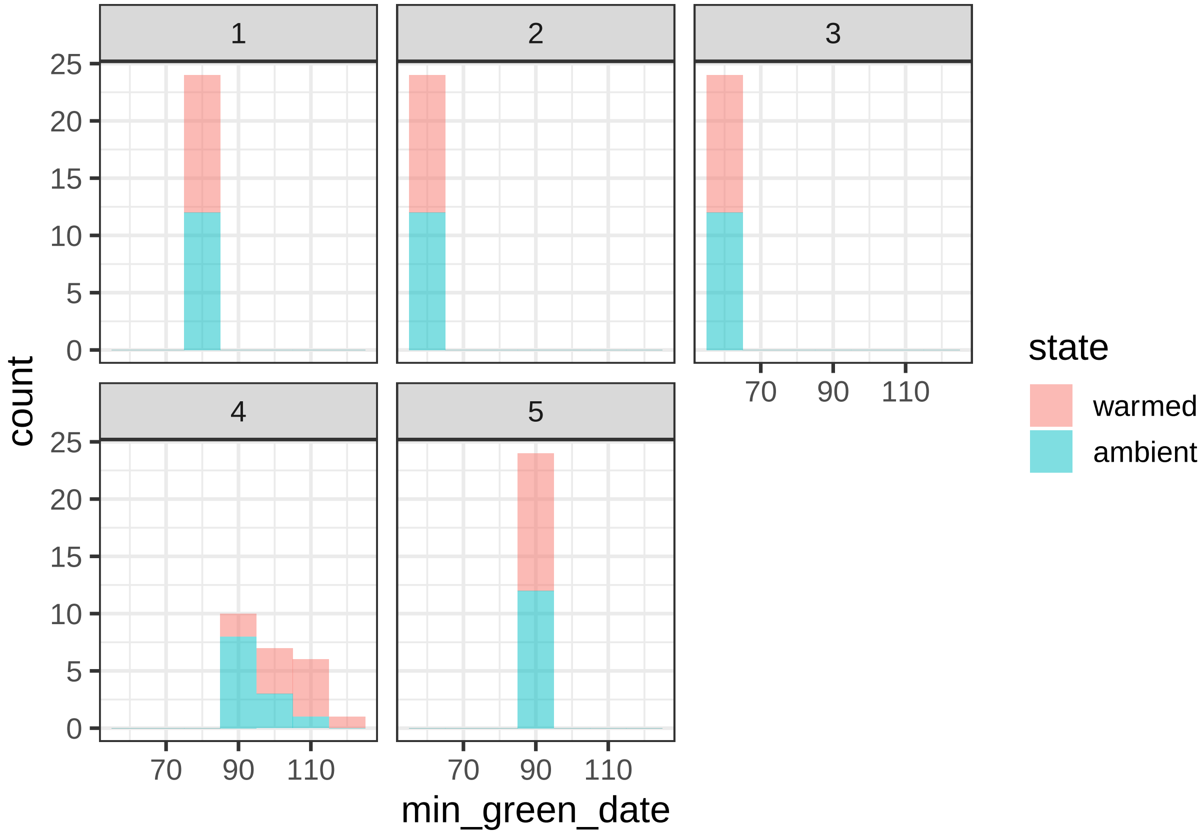
```r
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



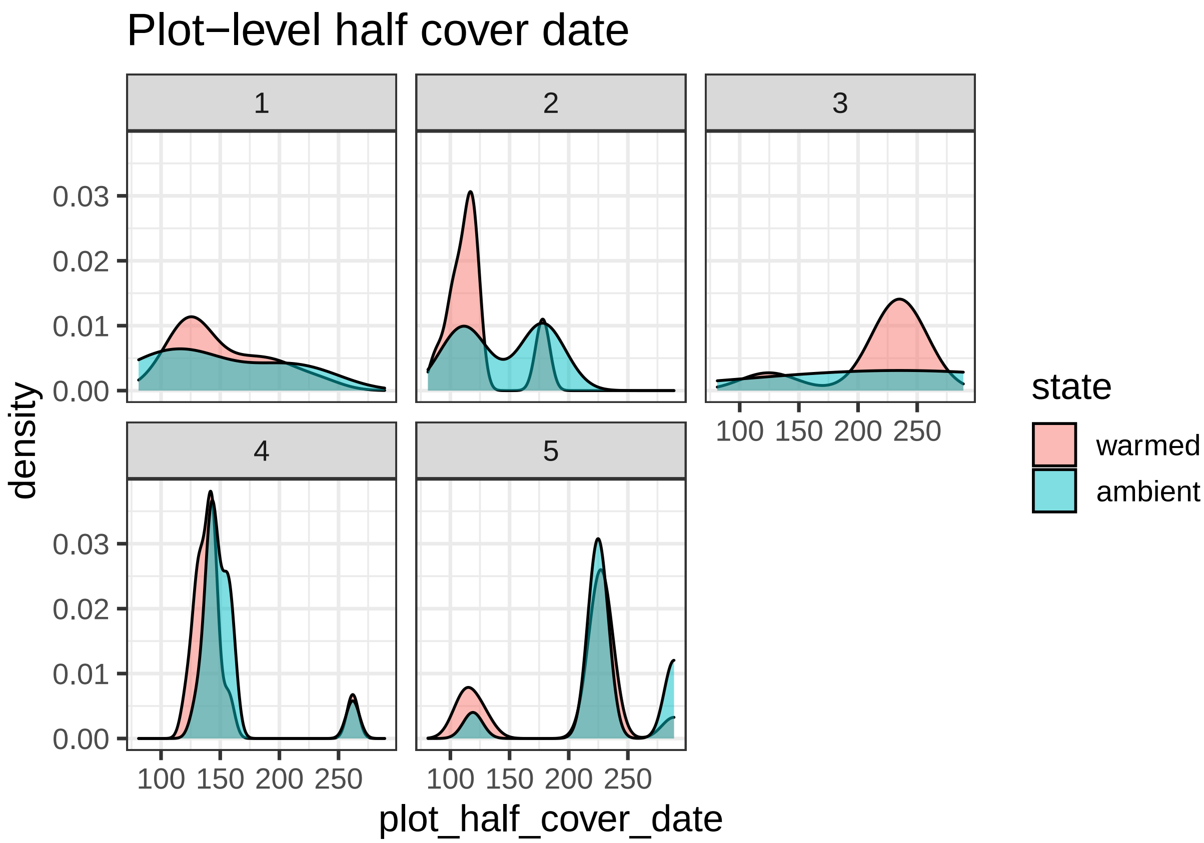

```r
p1 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date, fill = state)) +
    geom_histogram(alpha = 0.5, binwidth = 10)
p1 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



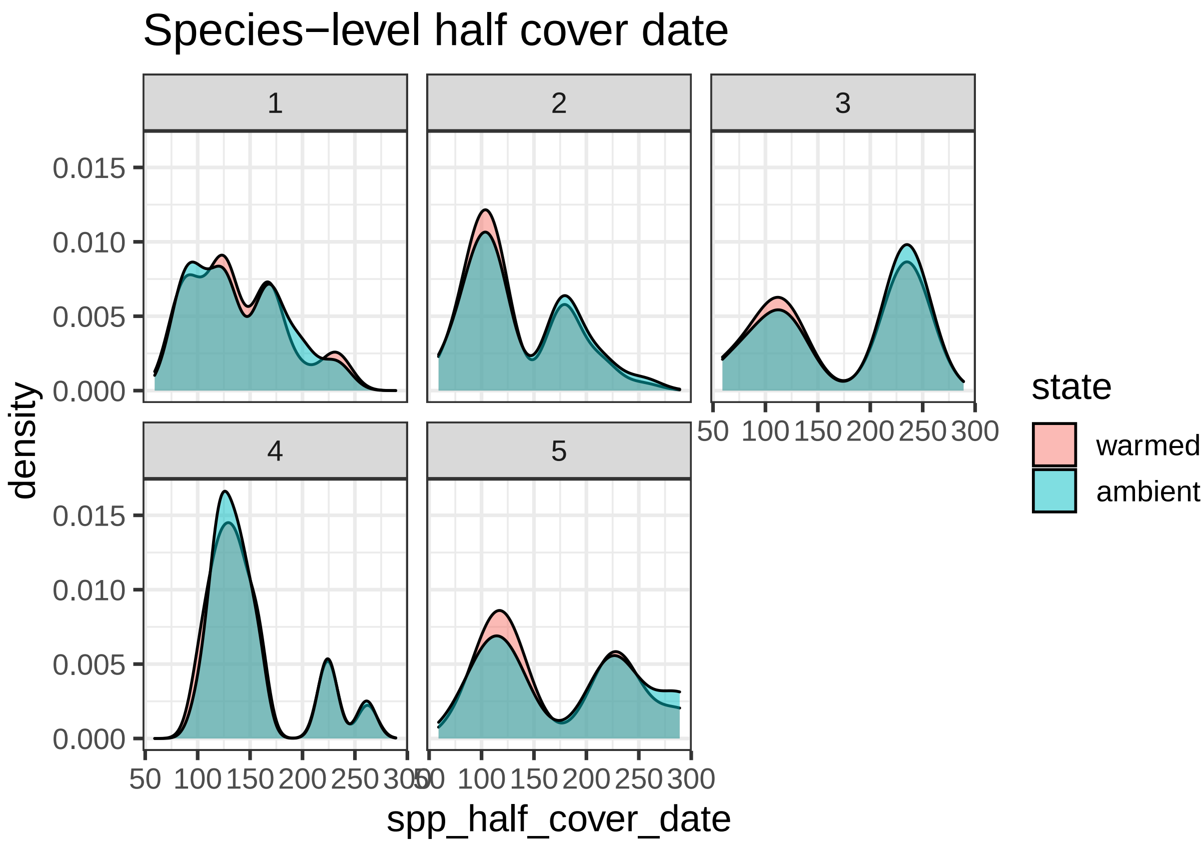

```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
    geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```



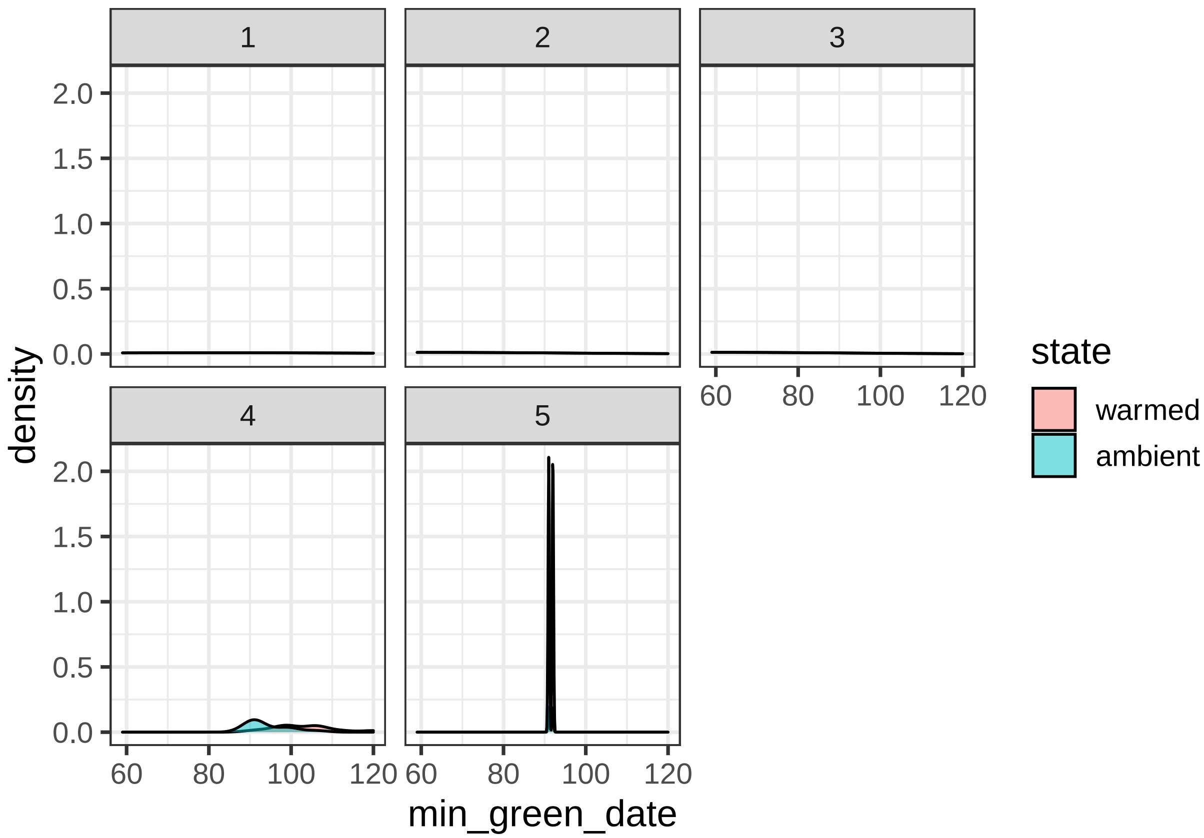

```r
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```




```
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")
```




```
# 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
```

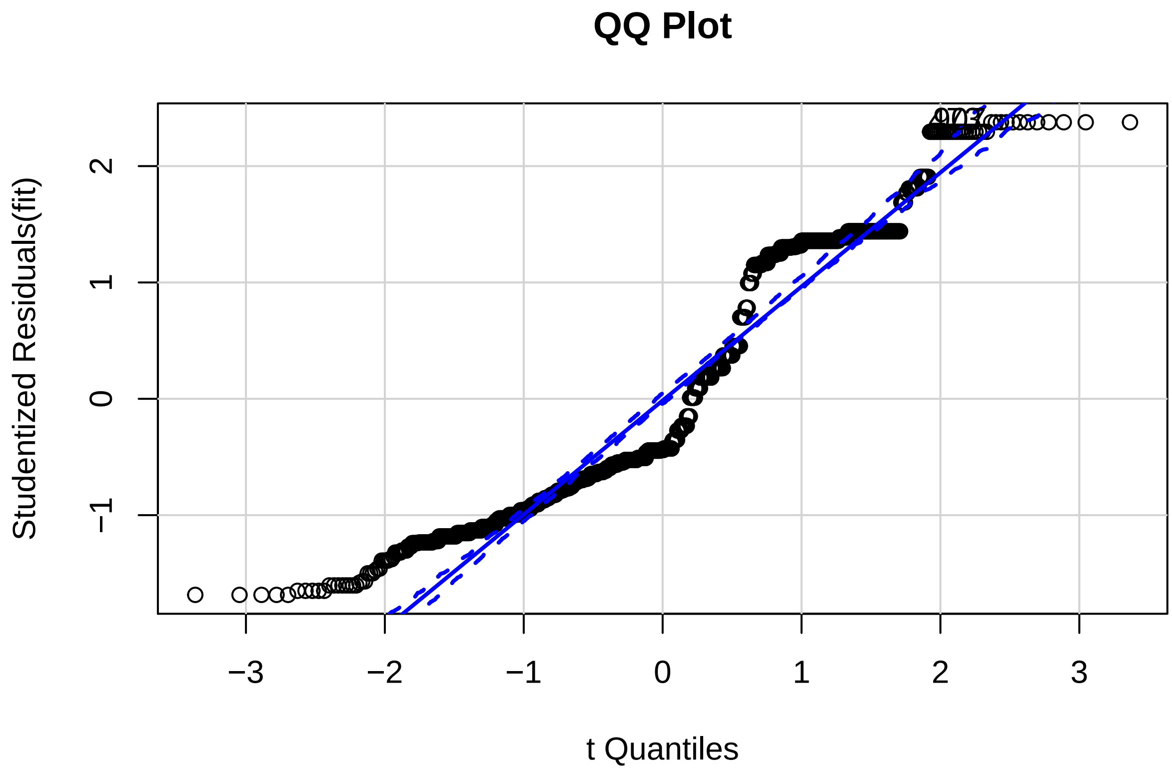
Leverage plots and detecting Outliers. https://www.statmethods.net/stats/rdiagnostics.html

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://daviddalpiaz.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
```

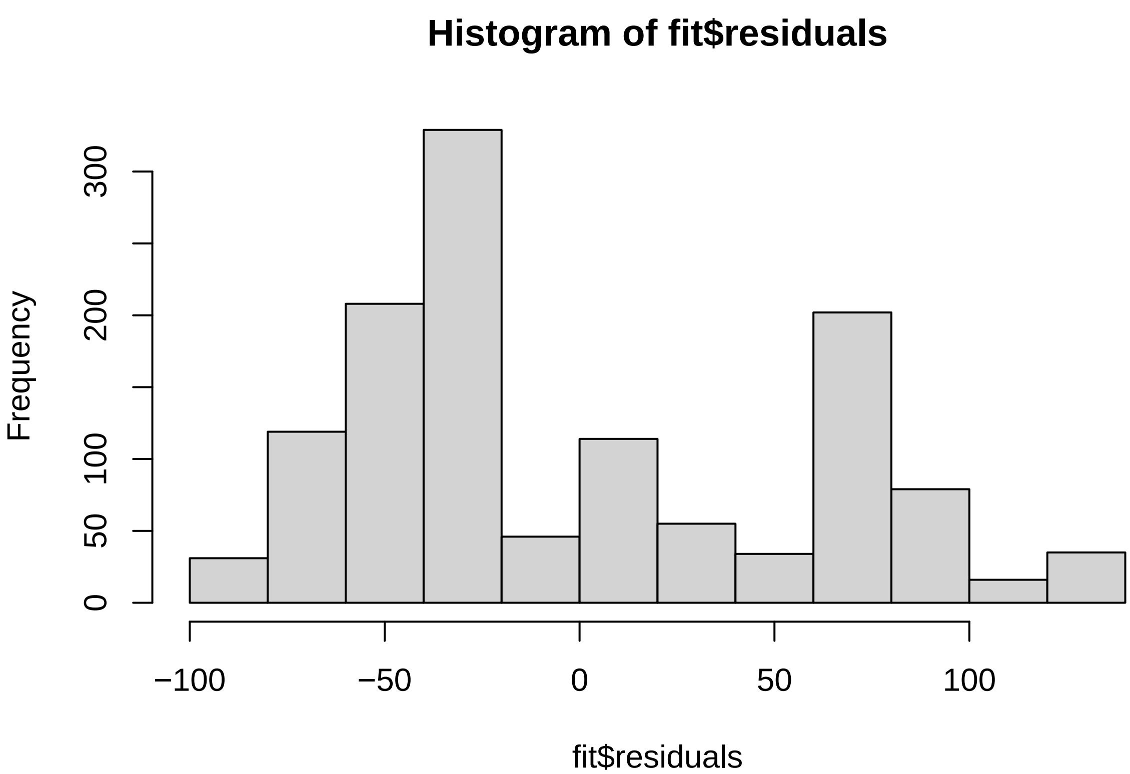
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 473 2.376821           0.017611           NA
```

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

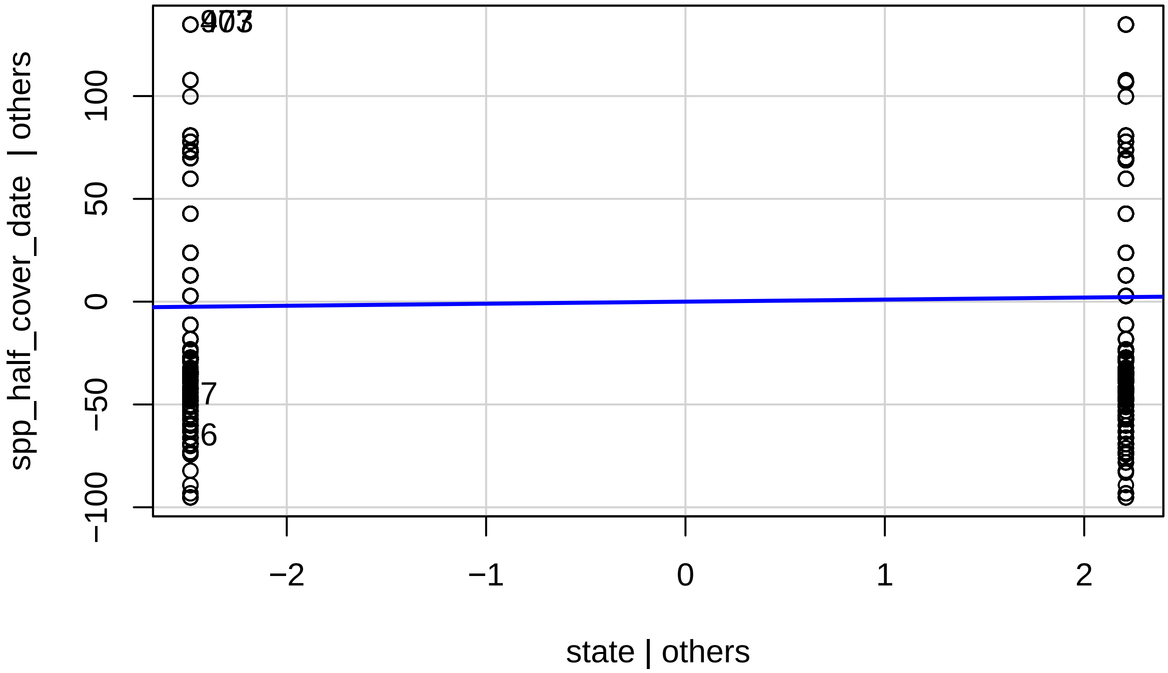



```
## 473 907
## 283 552
```

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



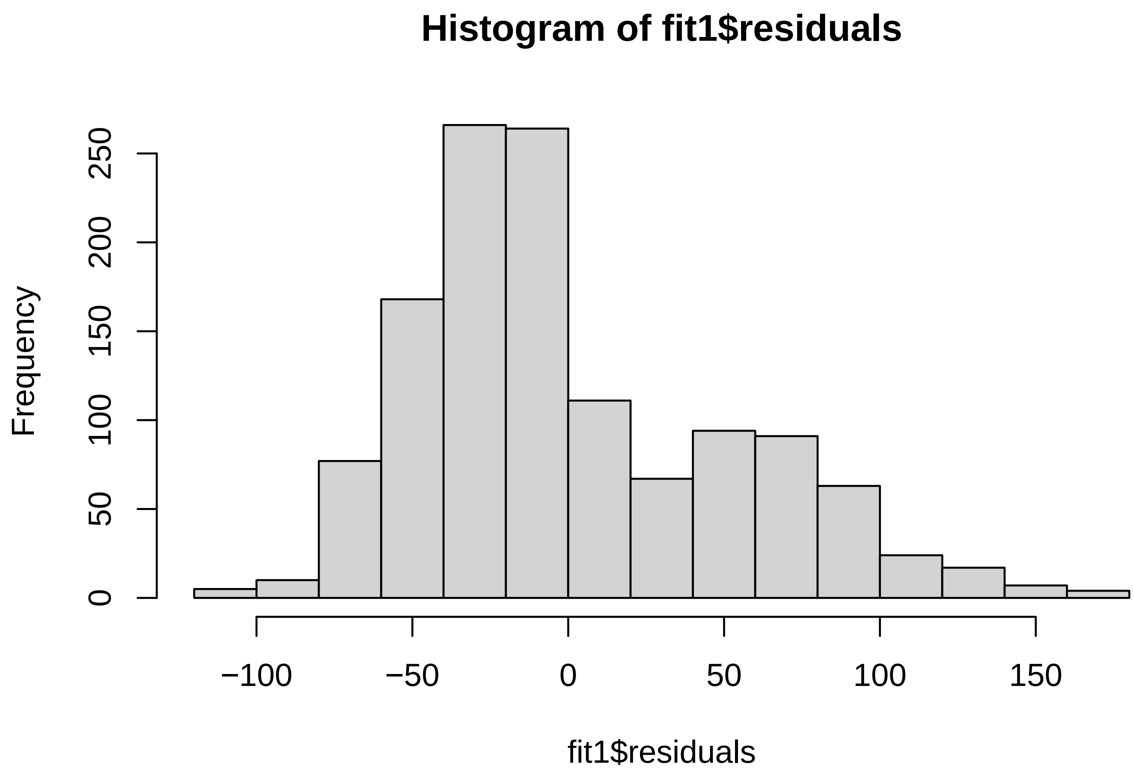
```r
leveragePlots(fit)
```



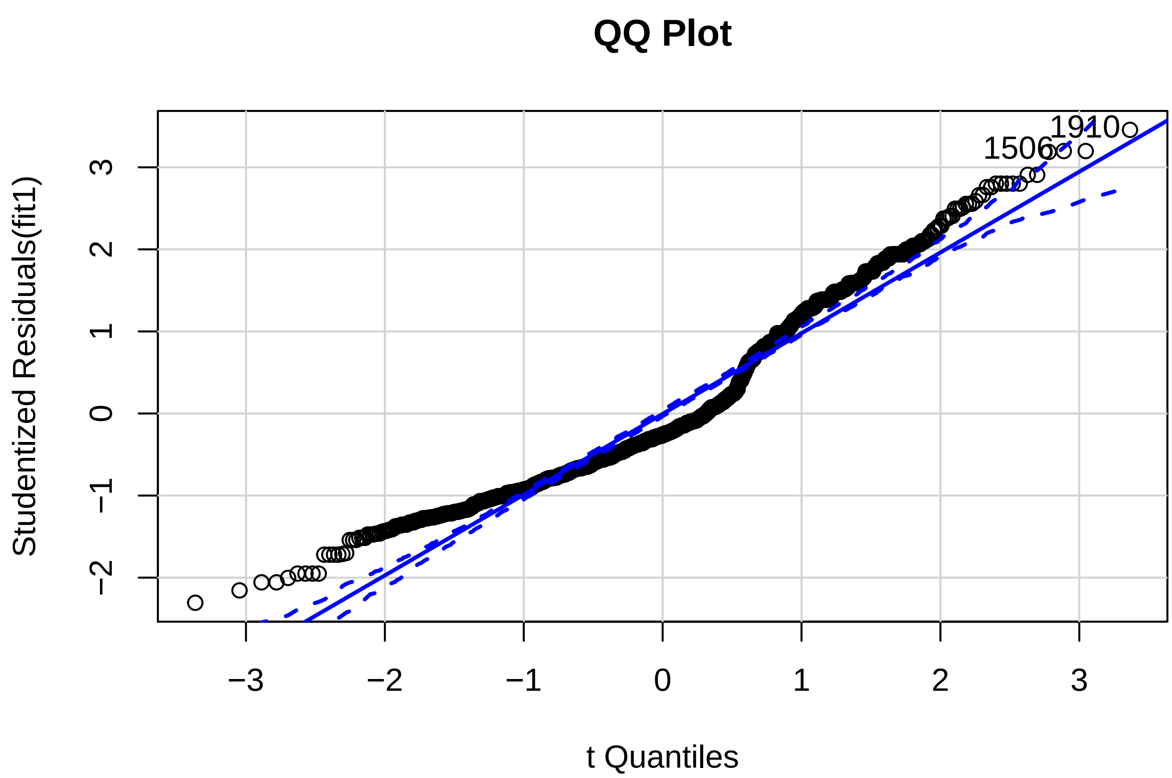

```r
# State and species model
fit1 <- lm(spp_half_cover_date ~ state + species, data = green_kbs)
outlierTest(fit1)  # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1910 3.455976         0.00056677      0.71866
```

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

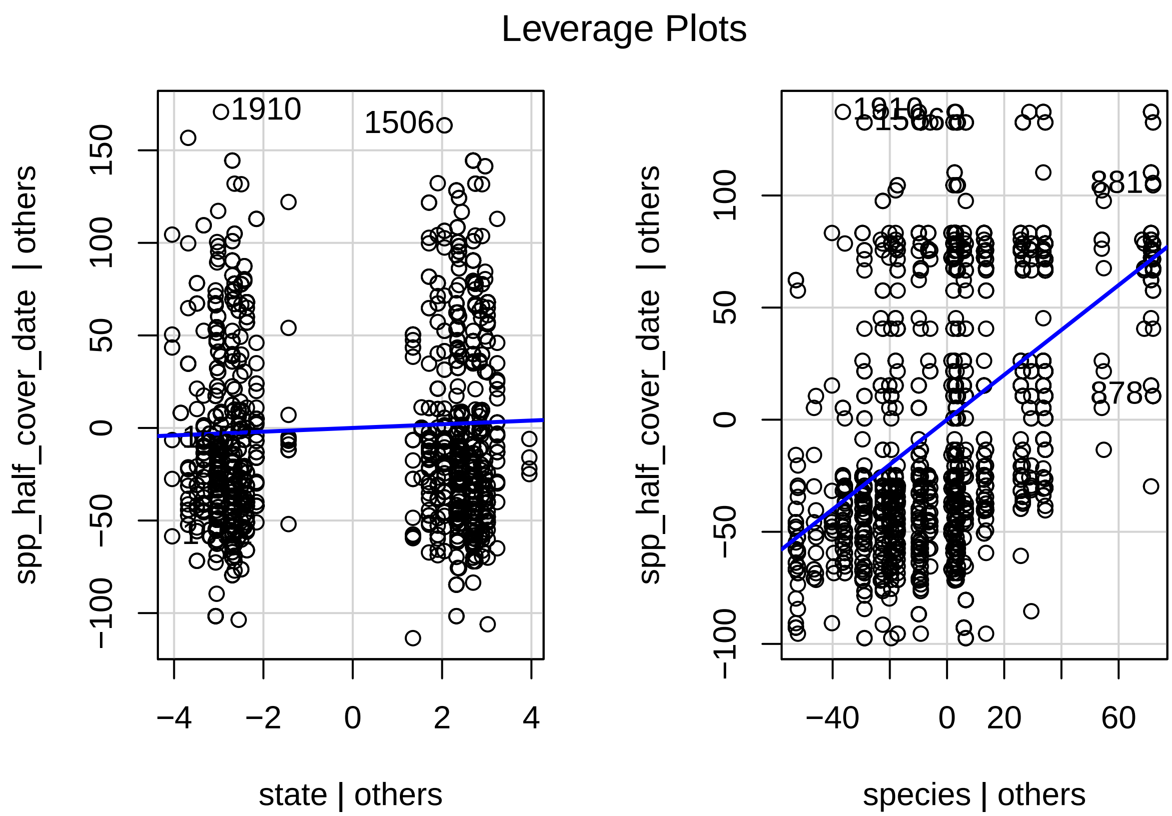



```r
qqPlot(fit1, main = "QQ Plot")
```




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

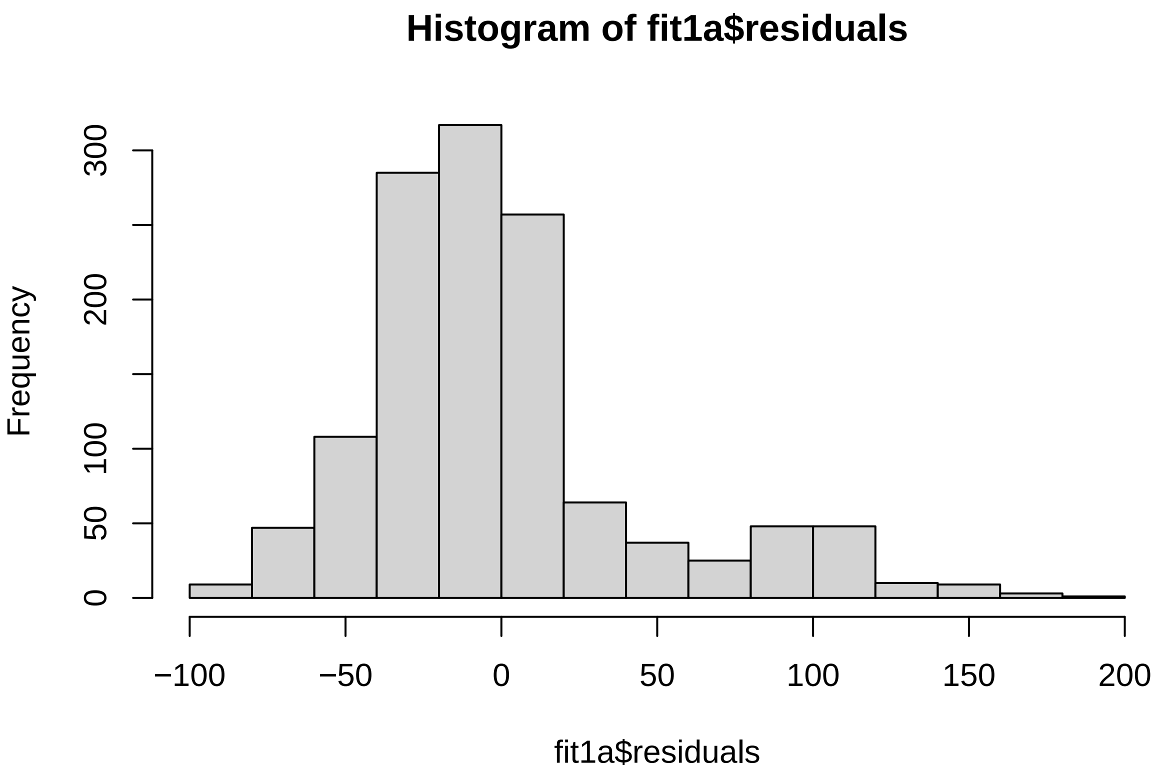
```r
leveragePlots(fit1)
```




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

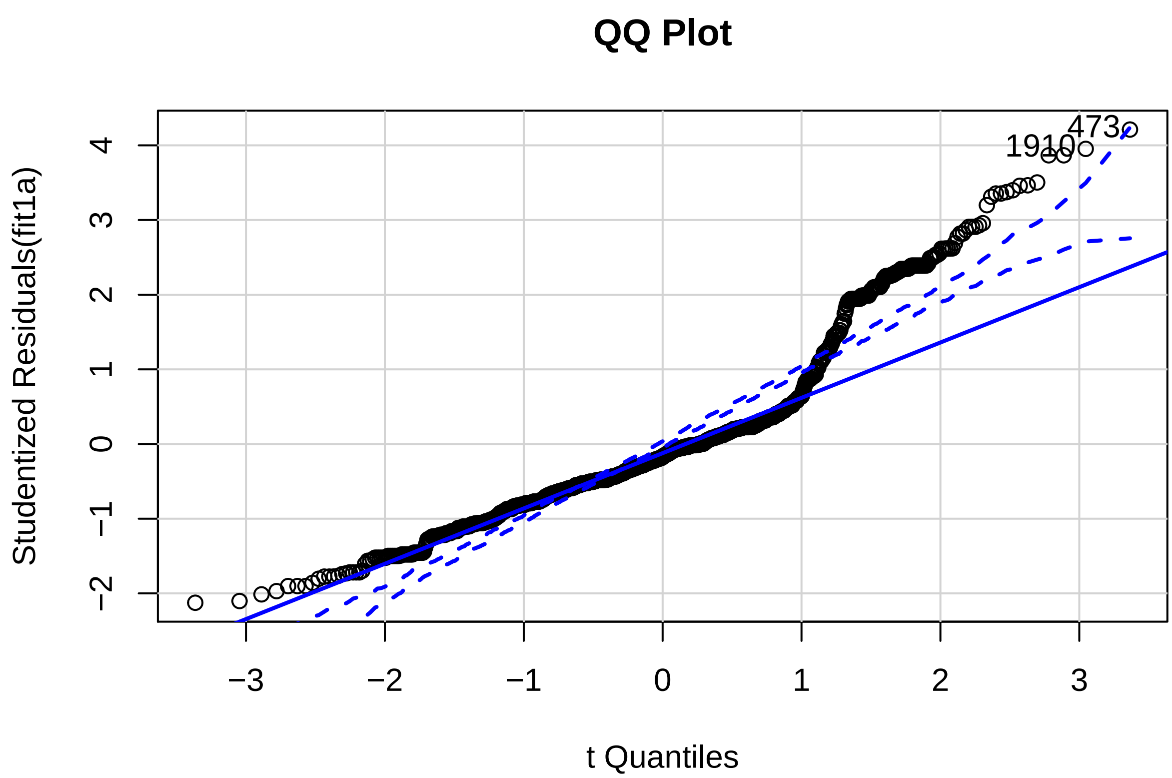
```
##     rstudent unadjusted p-value Bonferroni p
## 473 4.211351         2.7212e-05     0.034505
```

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




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

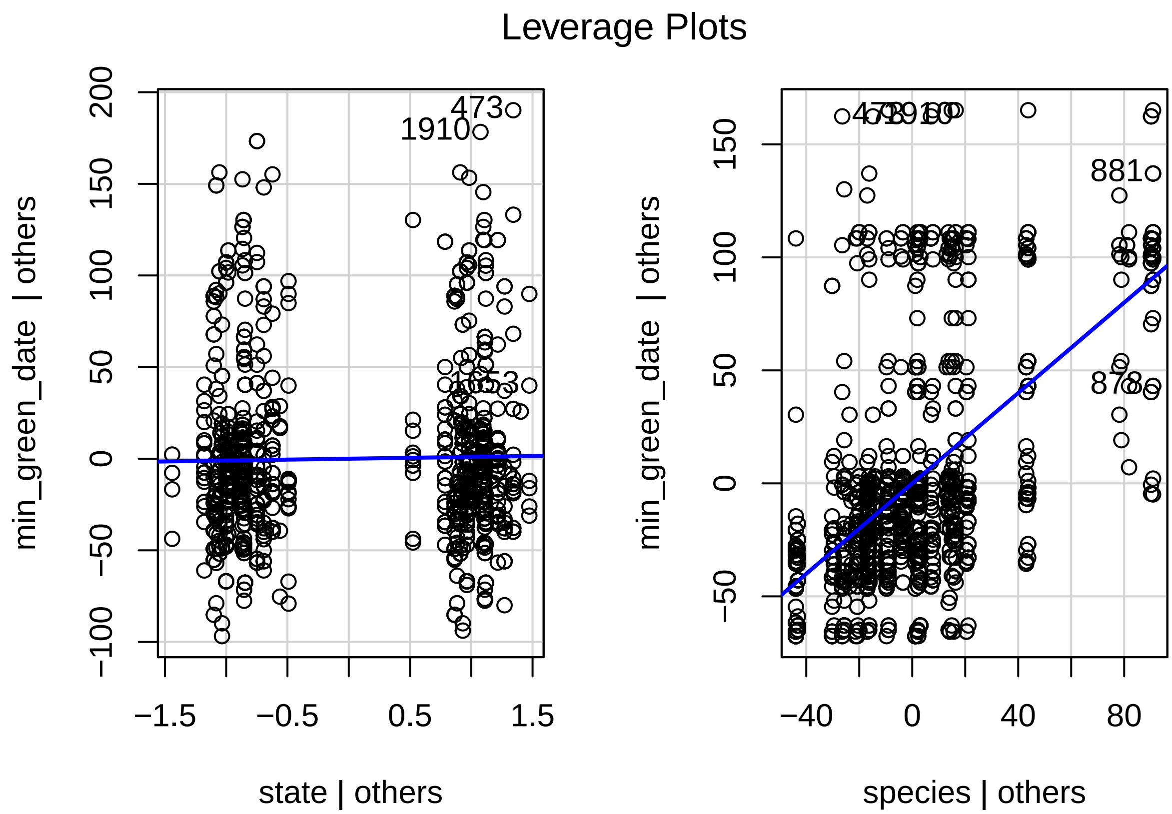
```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :
## 'rlm' failed to converge in 20 steps
```



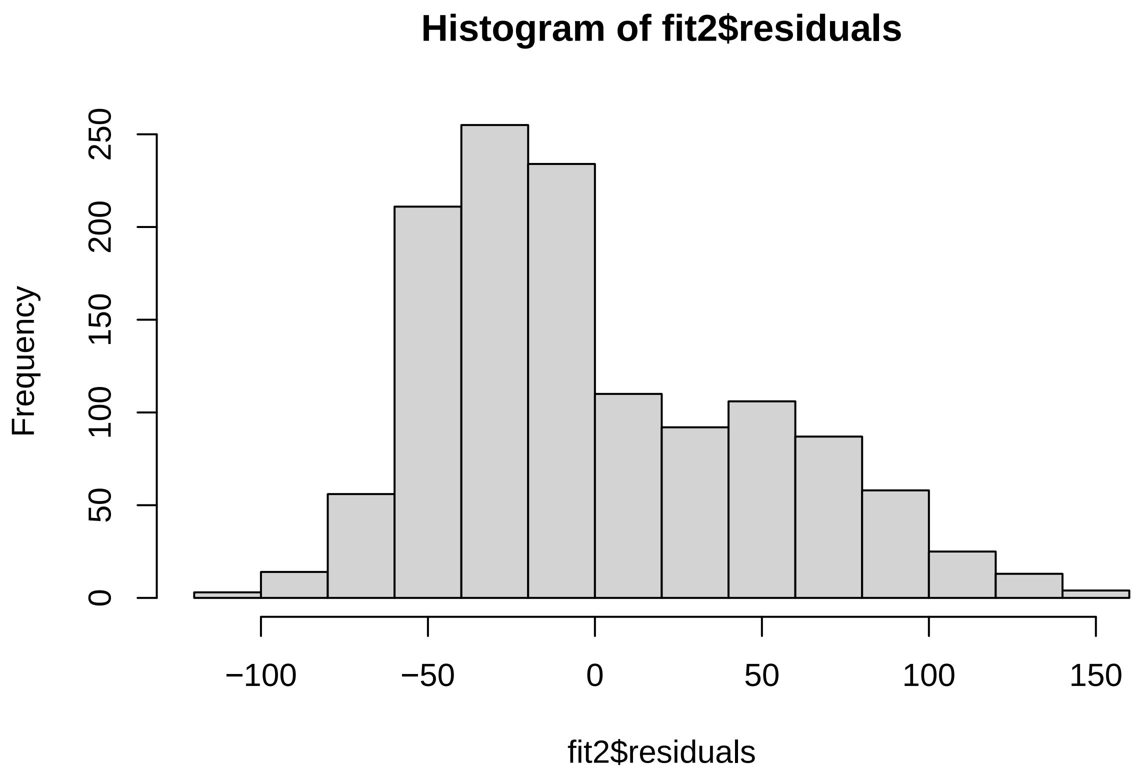

```
##  473 1910
```

```
##   283 1152
```

```r
leveragePlots(fit1a)
```



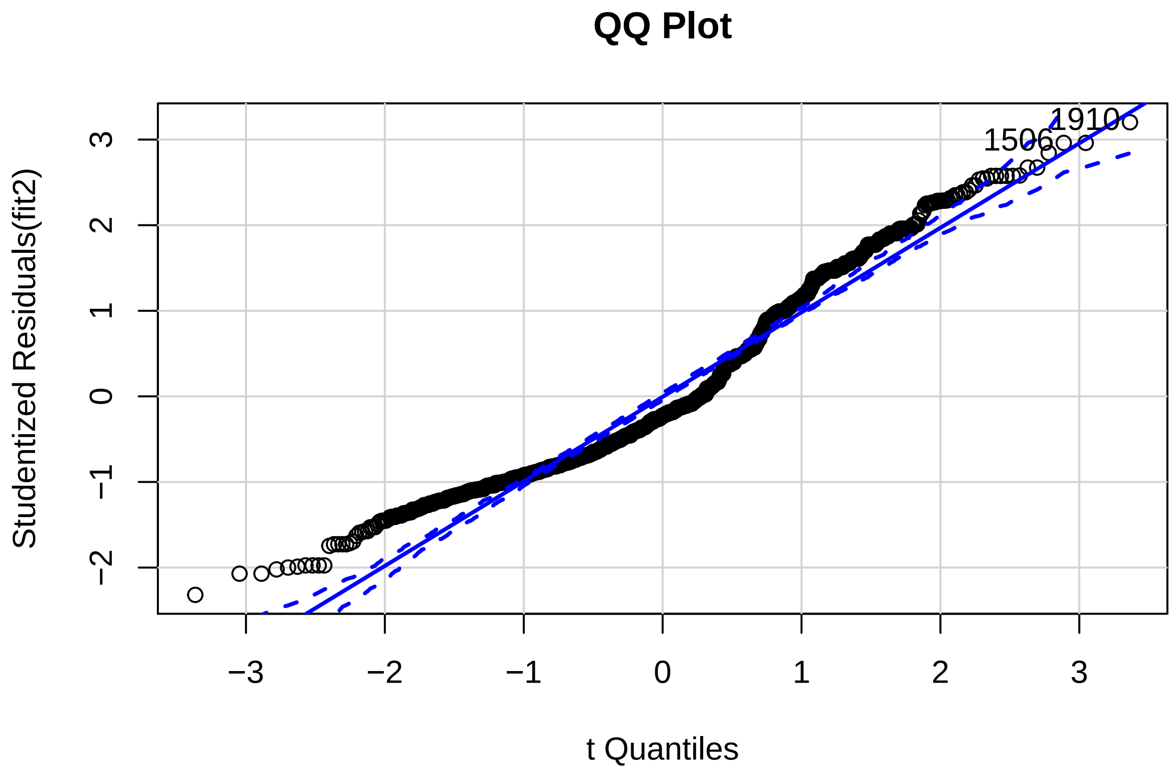

```r
# checking fit for date as a function of state and year
fit2 <- lm(spp_half_cover_date ~ state + species + year, data = green_kbs)
hist(fit2$residuals)
```




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

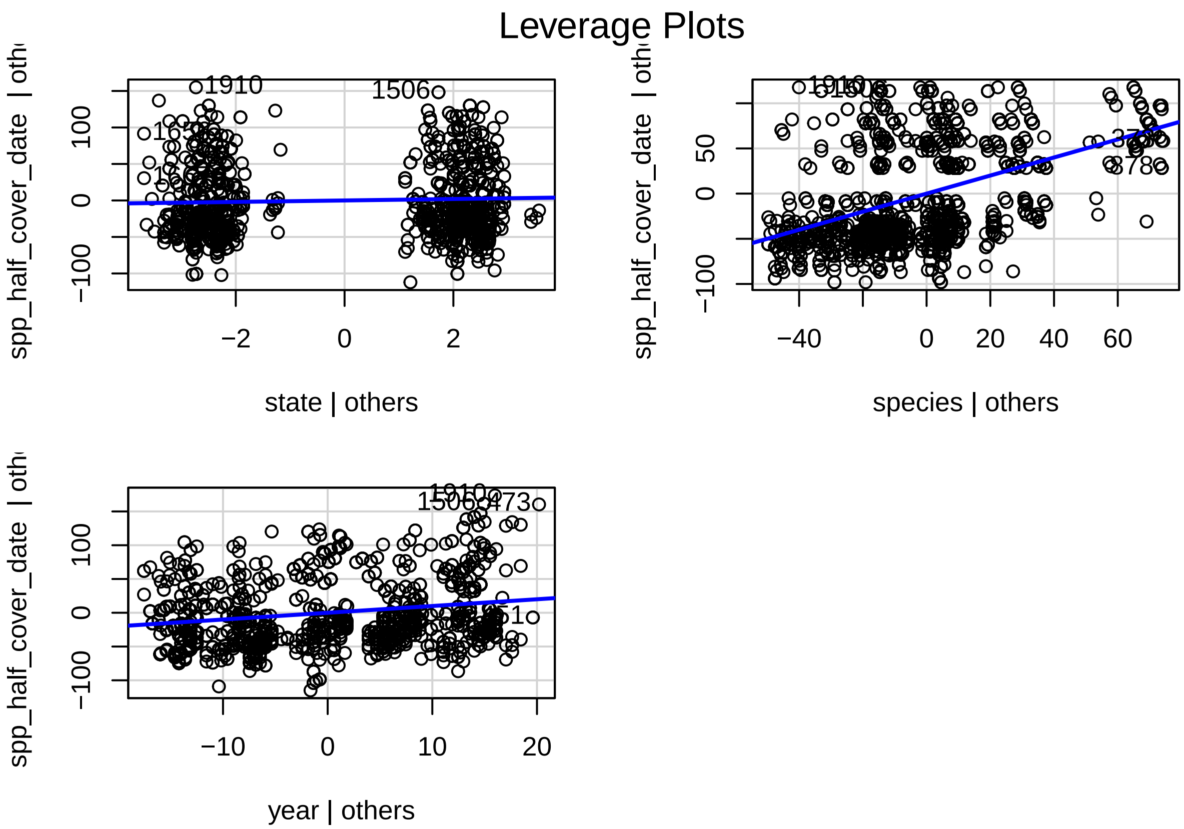
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1910 3.202366          0.0013976           NA
```

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




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

```
leveragePlots(fit2)
```

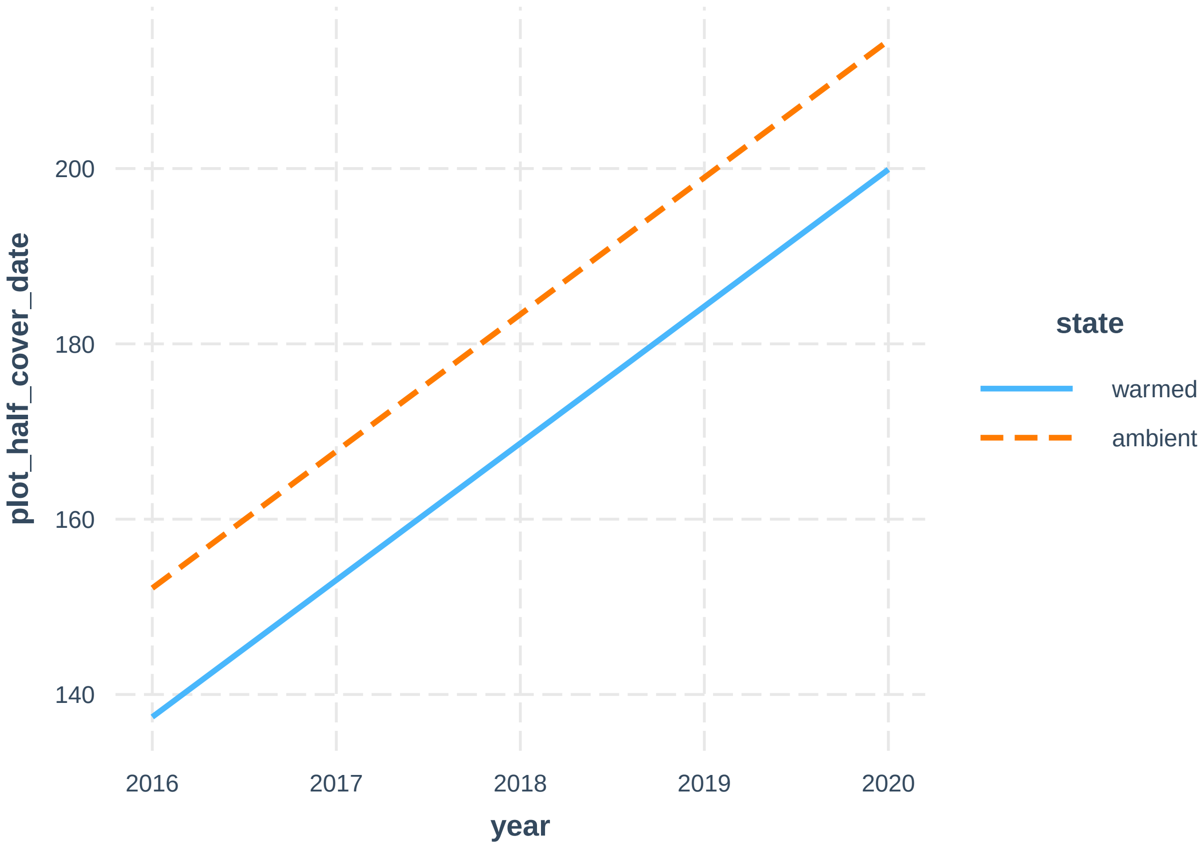

Leverage Plots
spp_half_cover_date | others
state | others
species | others
year | others
1910
1506

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.

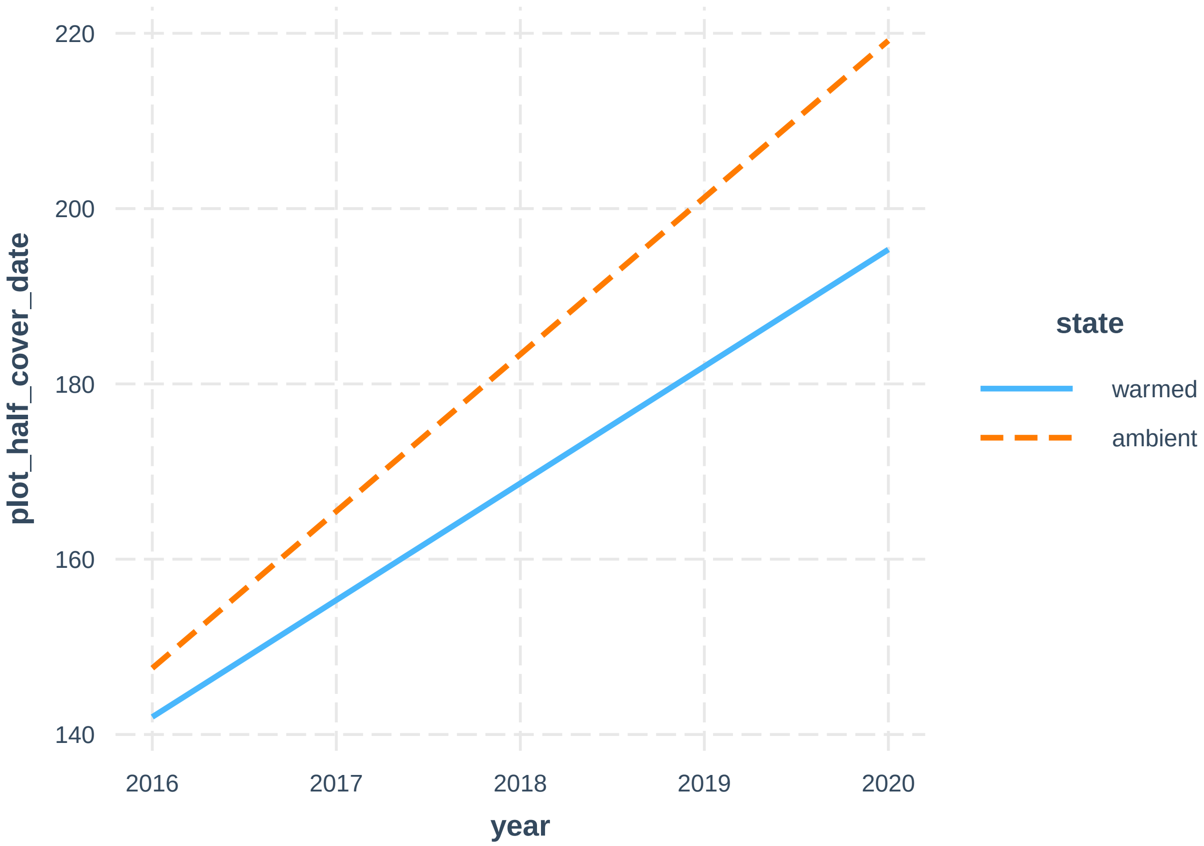
We should also think about how we're treating year. Some of the models have a state * year interaction as a fixed effect, which means that the warming or ambient treatment could affect the half_cover_date differently over time (there would be a different slope for each state in the relationship between 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.
```

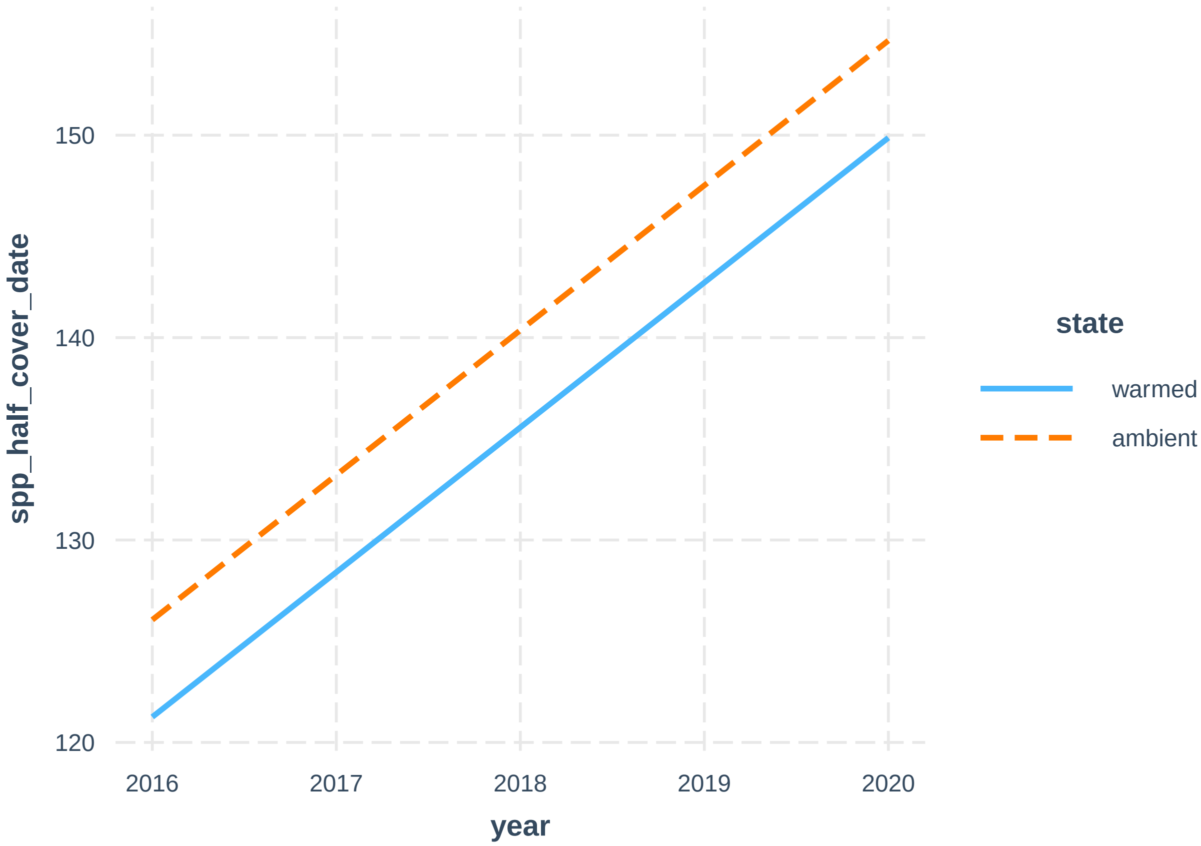



```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```




```
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.
```

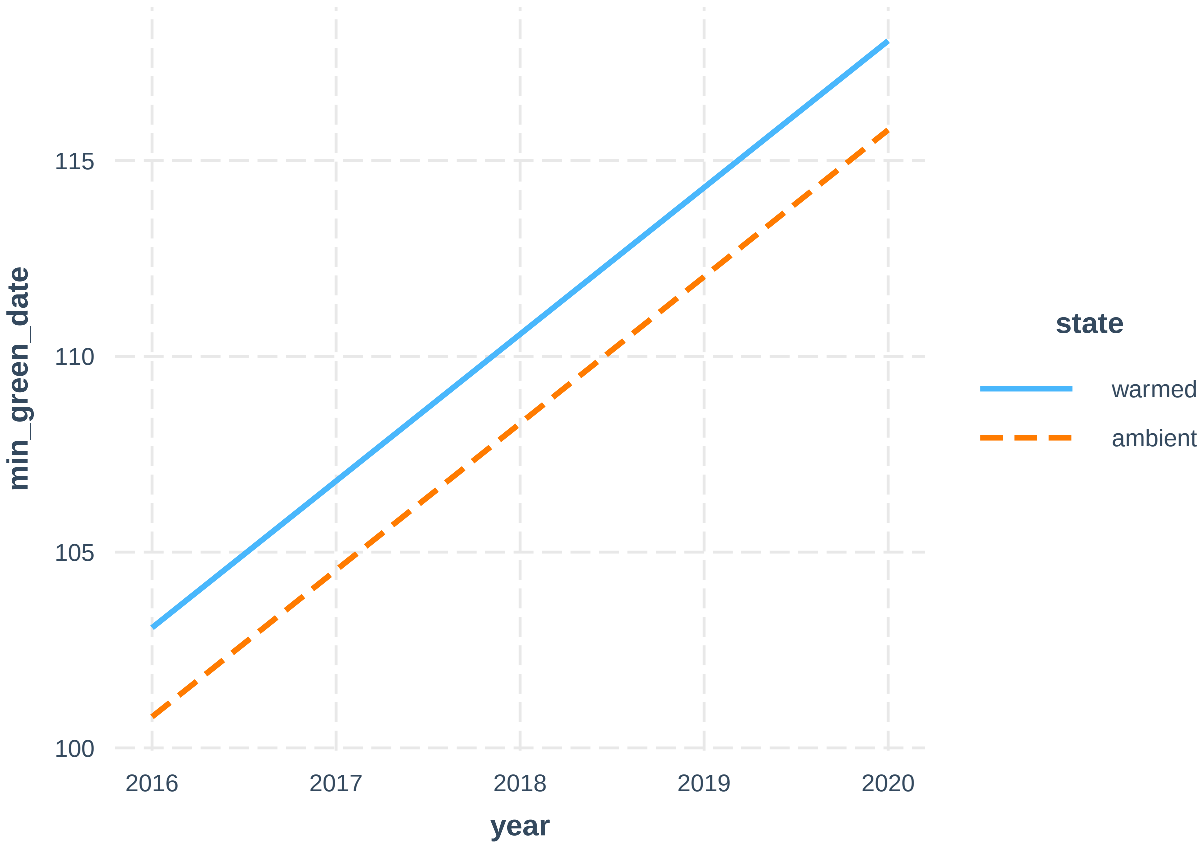



```r
fit6 <- lm(spp_half_cover_date ~ state * year + species, data = green_kbs)
interact_plot(fit6, pred = year, modx = state, mod2 = species)
```

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


```r
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 Oecologia
# 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
```

```r
# 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 anove 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
```

```r
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
```

```r
# 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
```

```r
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 |
```

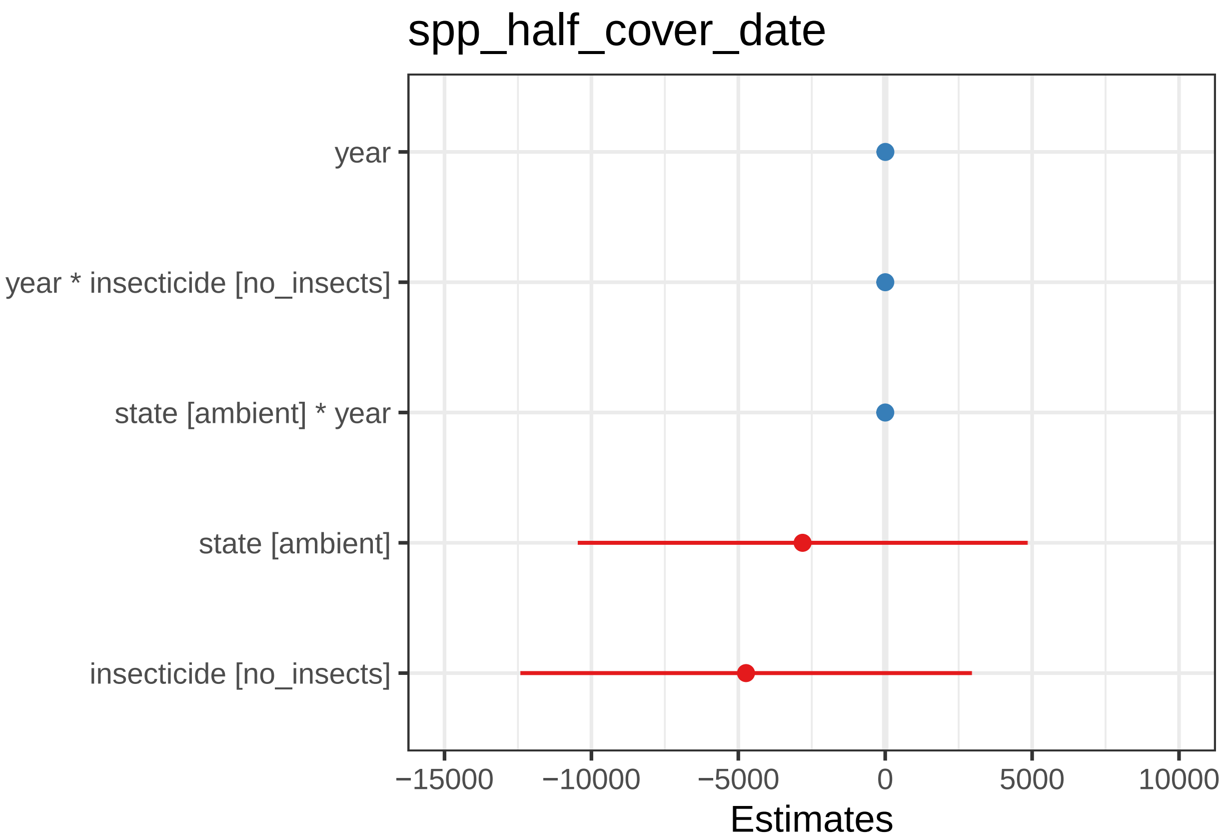
```
##     species) + (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13585.9  13632.2  -6784.0  13567.9     1259
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1194 -0.7683 -0.2513  0.6857  3.2607
##
## Random effects:
##  Groups   Name        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
```

```r
summary(mod2)
```

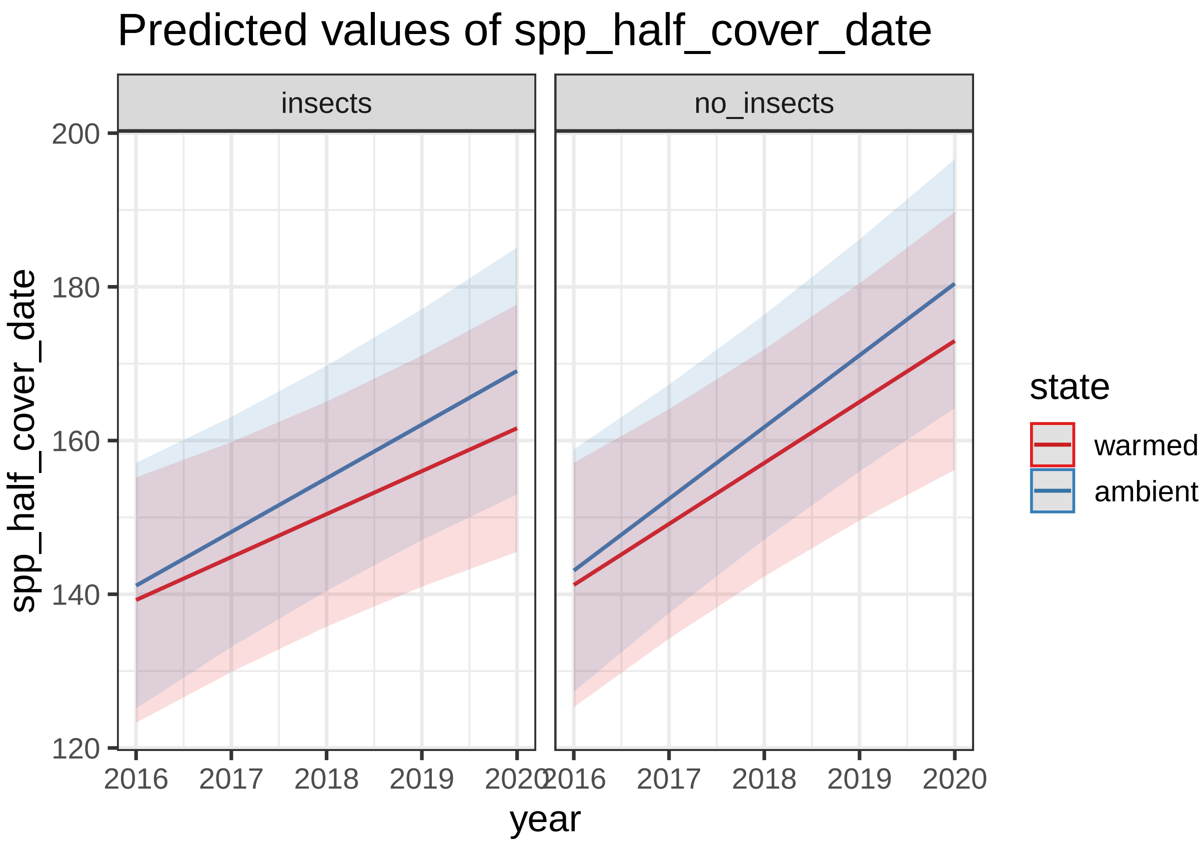
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state * year + insecticide * year + (1 |
##     species)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13587.3  13628.4  -6785.6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

```r
# Next, plot the model. There are multiple variables but
# here's one way to do it based on this package sjPlot:
# https://strengejacke.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)
```

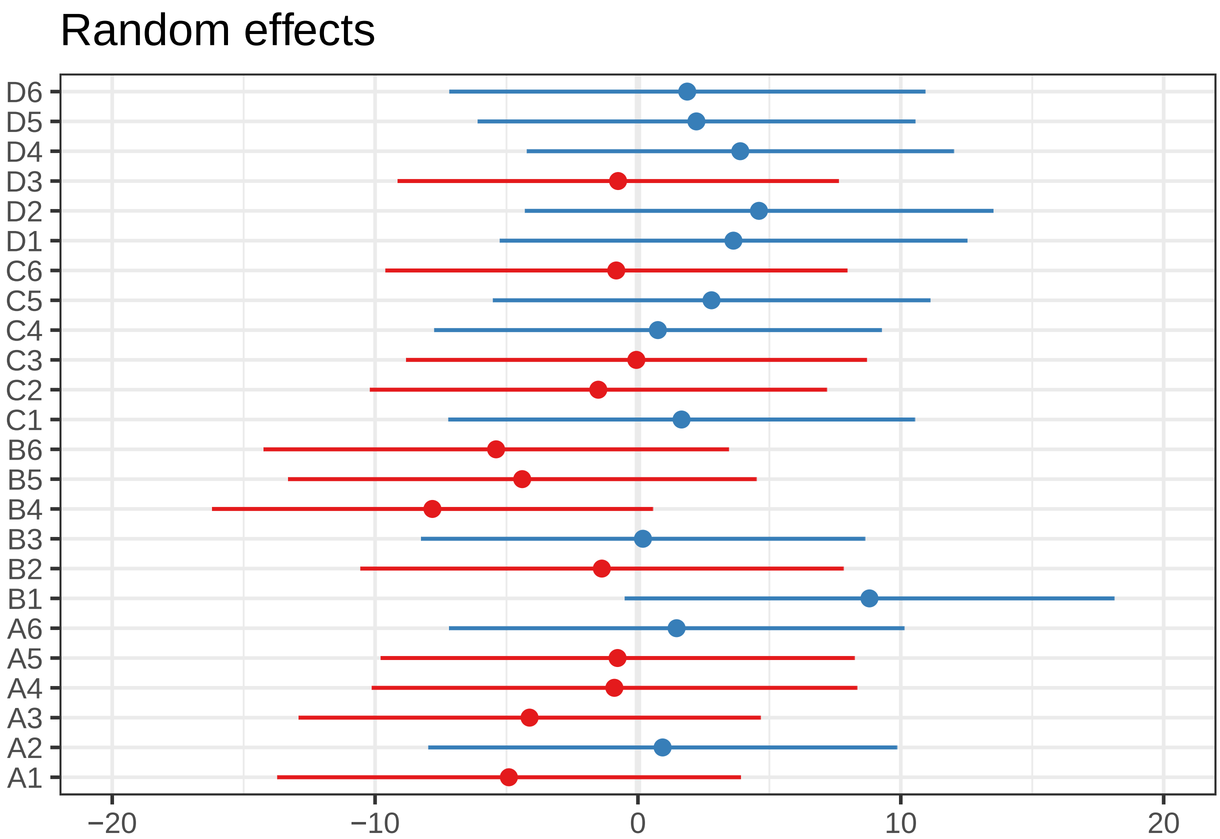



```r
# these are the fixed predicted values:
plot_model(mod1, type = "pred", terms = c("year", "state", "insecticide"))
```

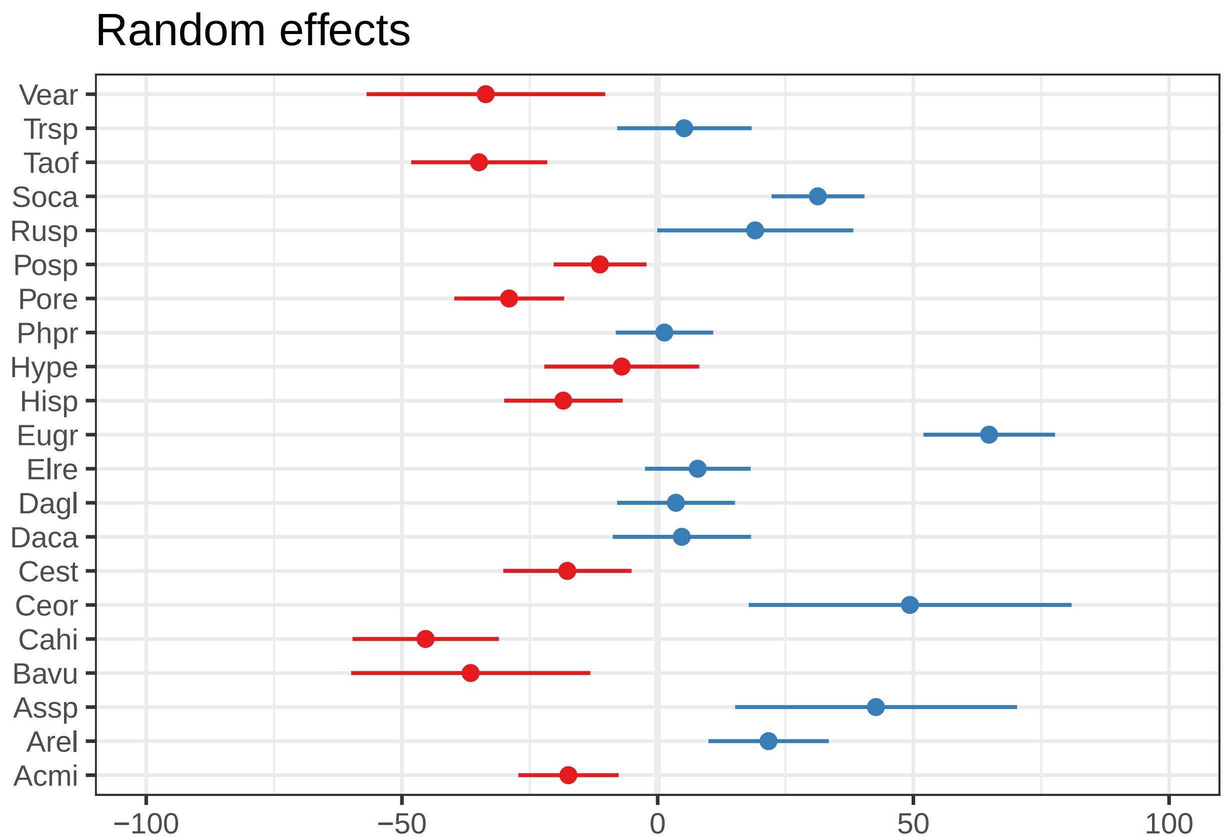



```r
# these are the random effects estimates
plot_model(mod1, type = "re", terms = c("species", "plot"))
```

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


Random effects
D6
D5
D4
D3
D2
D1
C6
C5
C4
C3
C2
C1
B6
B5
B4
B3
B2
B1
A6
A5
A4
A3
A2
A1
−20
−10
0
10
20

```
##
## [[2]]
```




```r
# 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
```

```r
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
```

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

```
##      dAICc df weight
## mod1 0.0   9  0.921
## mod3 4.9   6  0.079
```

```r
# 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
```

```r
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
```

```r
# 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
```

```r
# 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
```

```r
AICctab(mod4, mod5, weights = T)
```

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

```r
# 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)
```

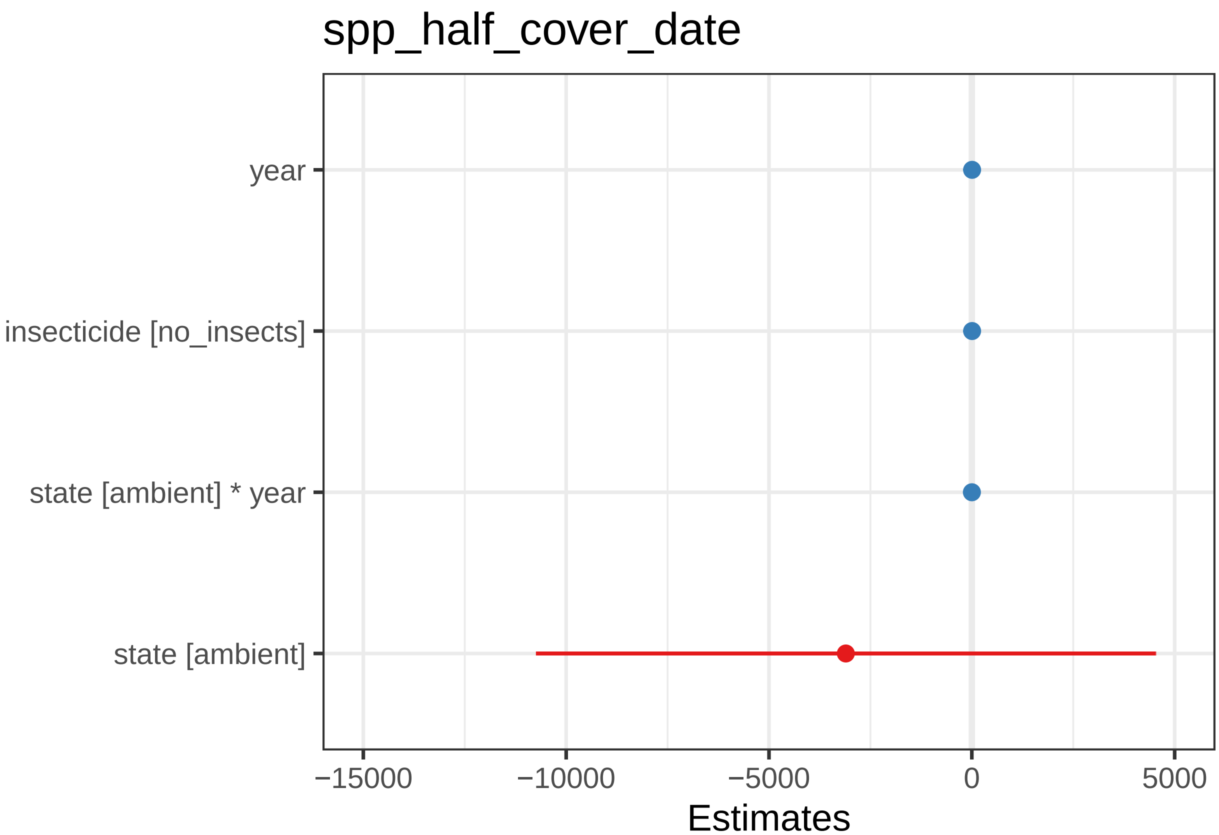
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year + insecticide + (1 | species) +
##     (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##    13584    13620    -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
```

```r
anova(mod4)
```

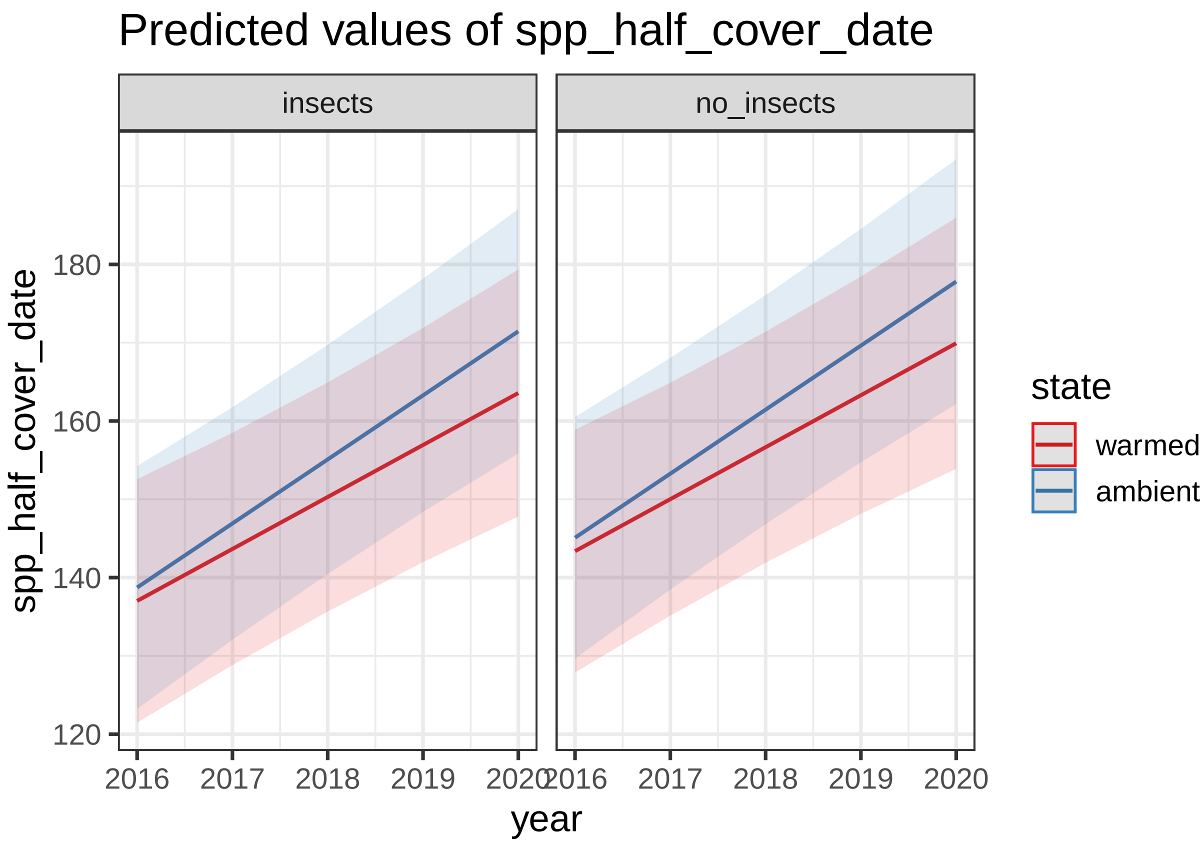
```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state         1558    1558     1 1235.90  0.6352   0.42561
## year        137200  137200     1 1241.48 55.9464 1.404e-13 ***
## insecticide   7282    7282     1   21.05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

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



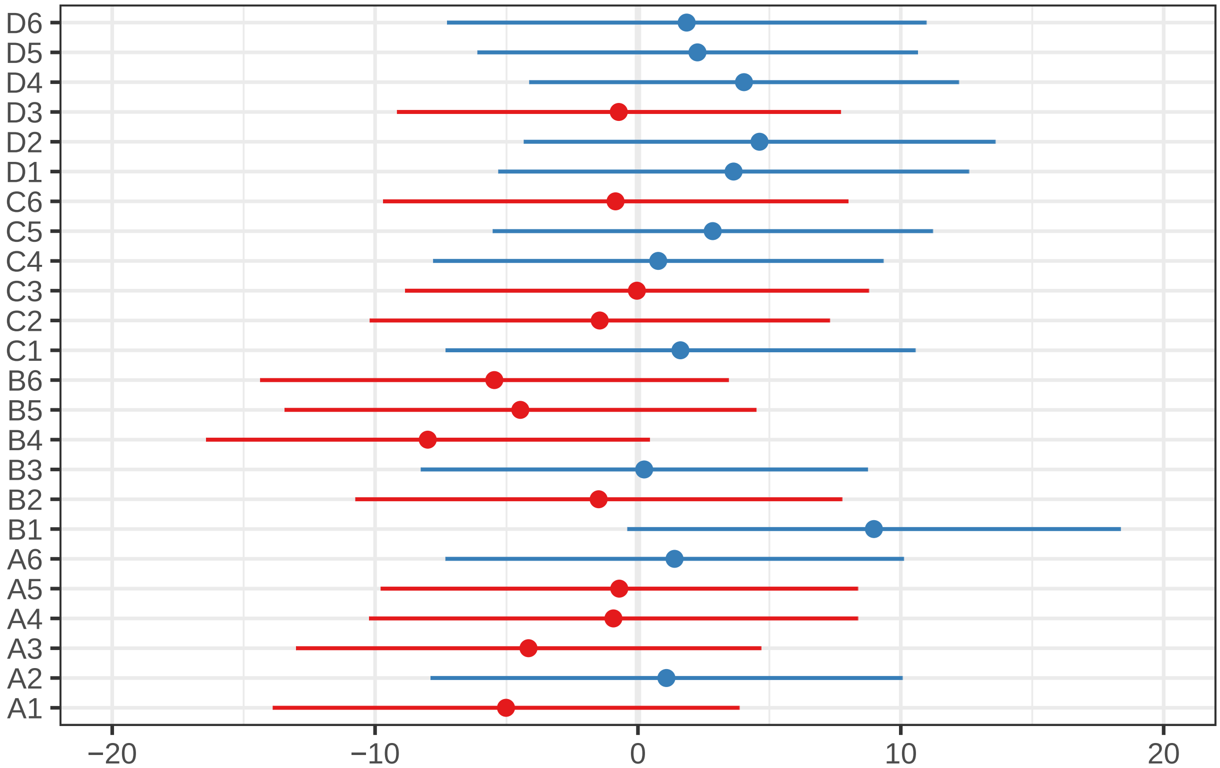

```r
# these are the fixed predicted values:
plot_model(mod4, type = "pred", terms = c("year", "state", "insecticide"))
```



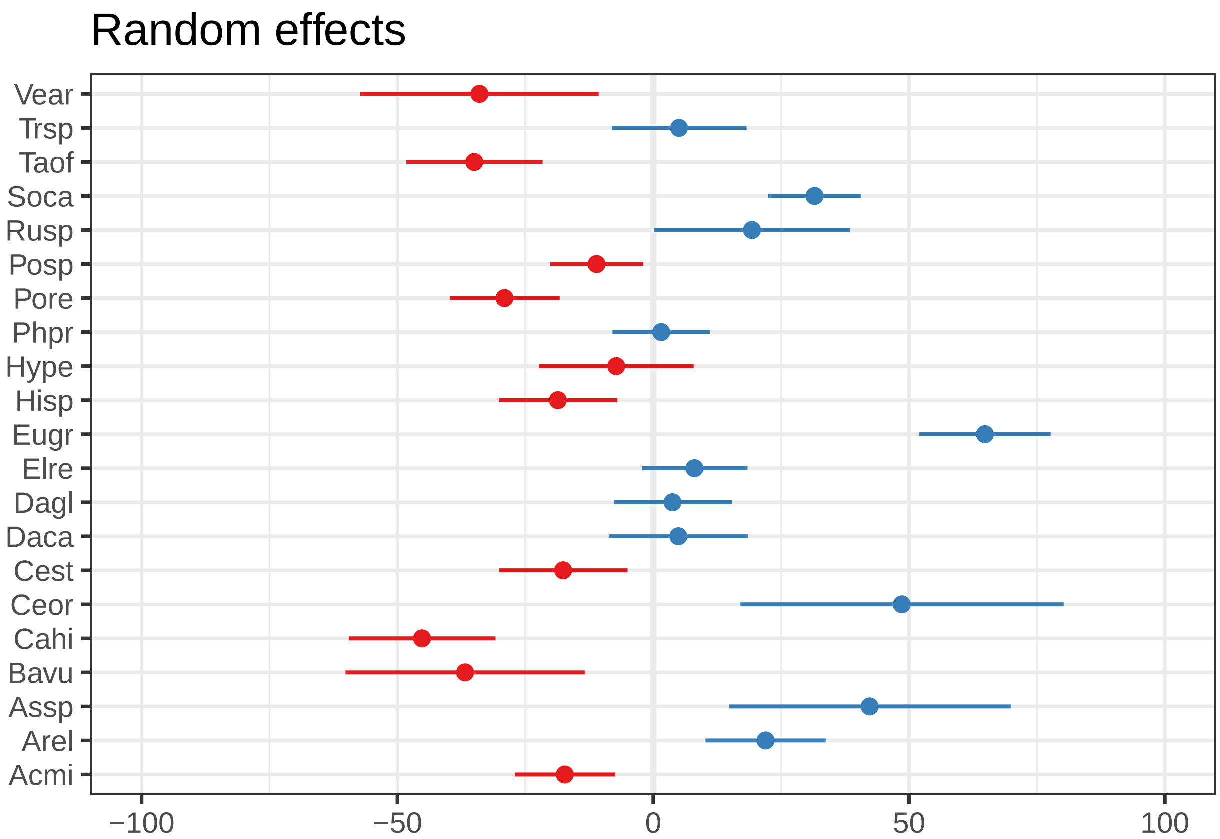

```
# these are the random effects estimates
plot_model(mod4, type = "re", terms = c("species", "plot"))
```

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

Random effects




```
##
## [[2]]
```




```r
# 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
```

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

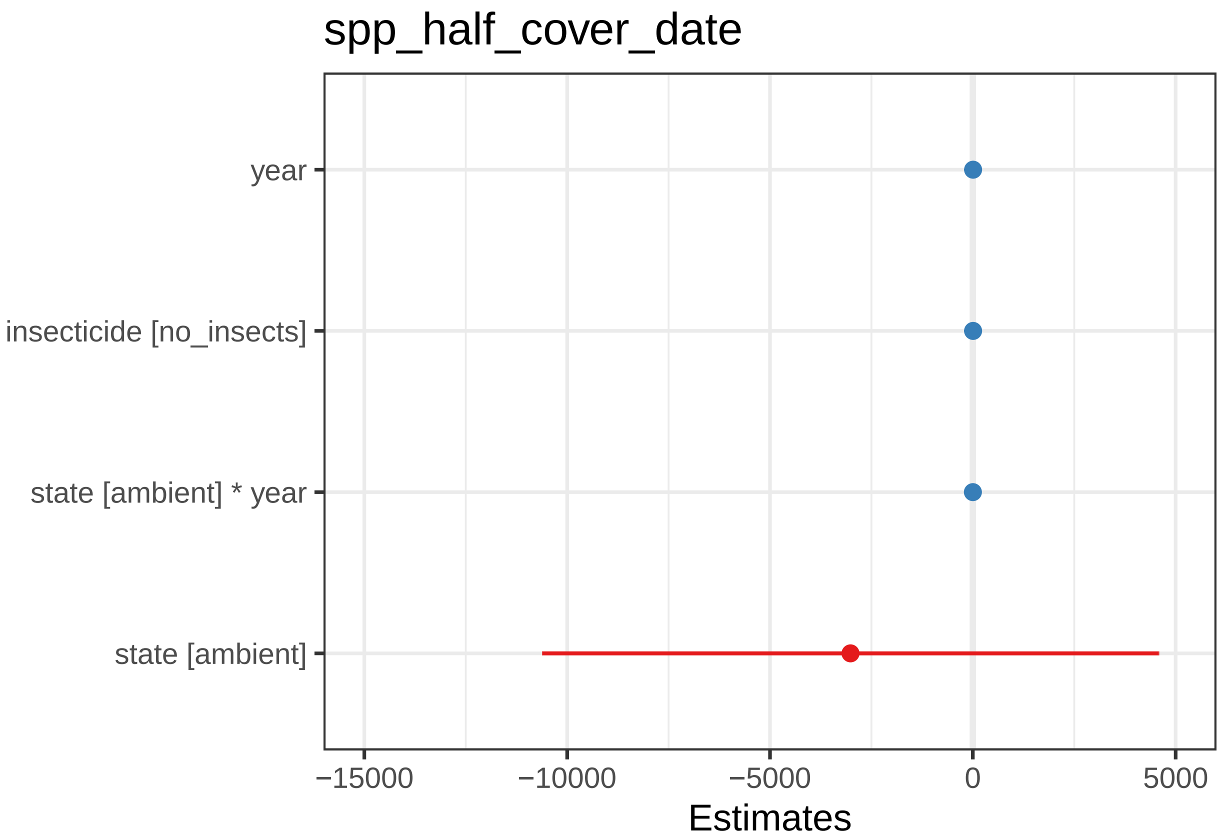
```
## Data: green_kbs
## Models:
## mod4: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## mod4:     (1 | plot)
## mod6: spp_half_cover_date ~ state * year + insecticide + (1 | species) +
## mod6:     (1 + year | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod4    8 13585 13626 -6784.7    13569
## mod6   10 13596 13647 -6787.8    13576     0  2          1
```

```r
anova(mod6)
```

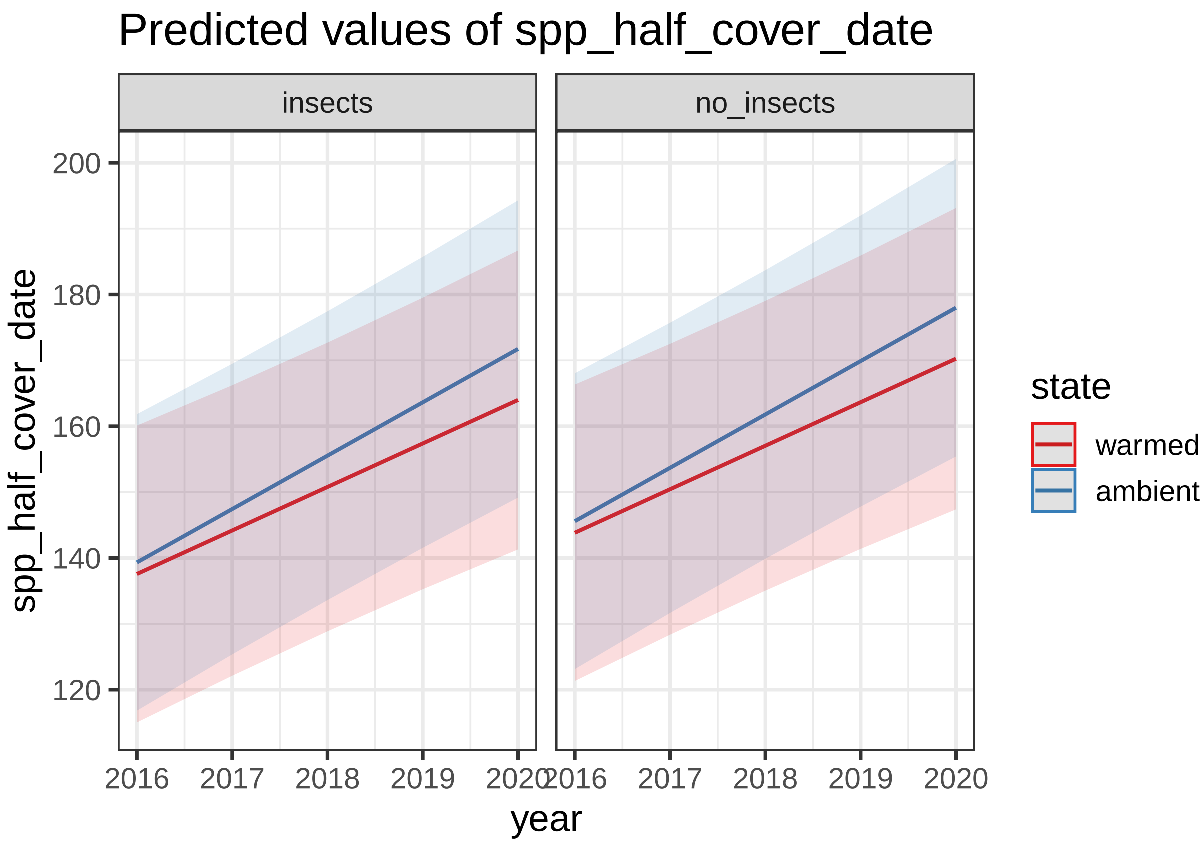
```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
```

```
## 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)
```

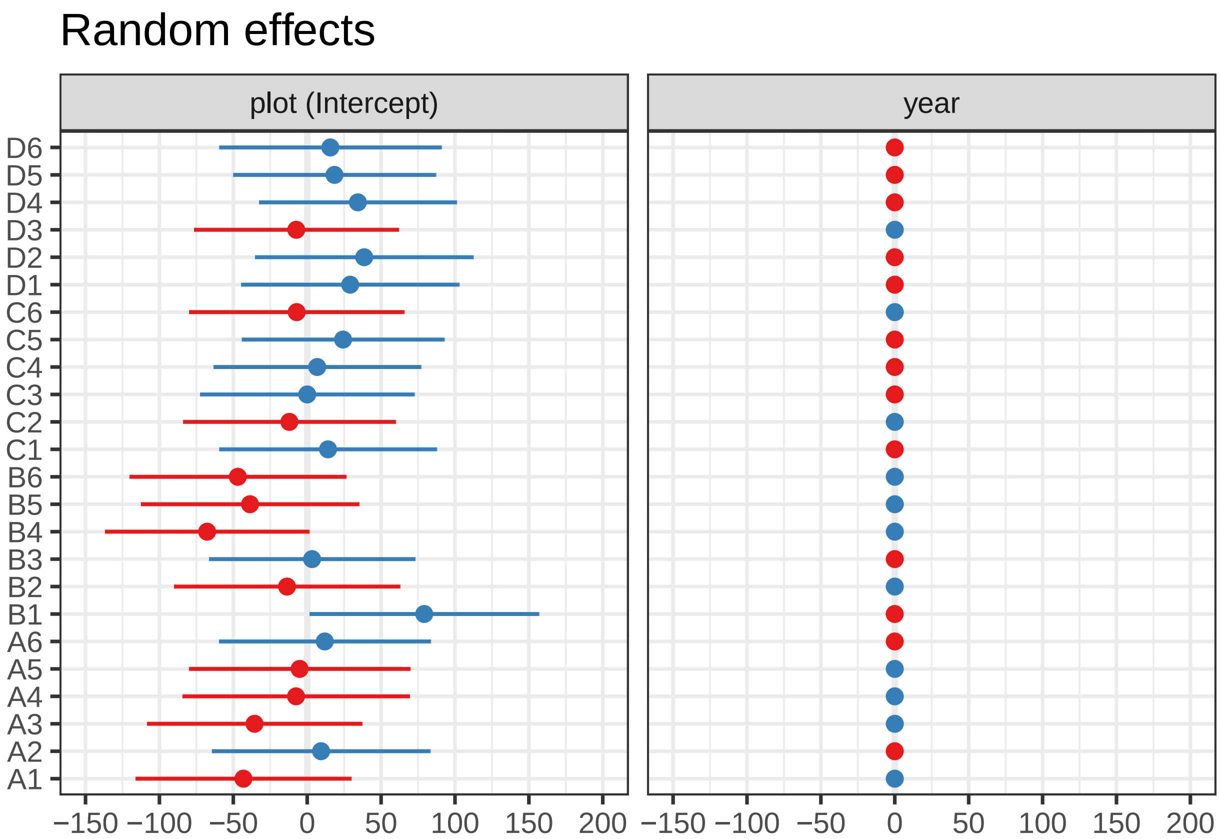



```
# these are the fixed predicted values:
plot_model(mod6, type = "pred", terms = c("year", "state", "insecticide"))
```

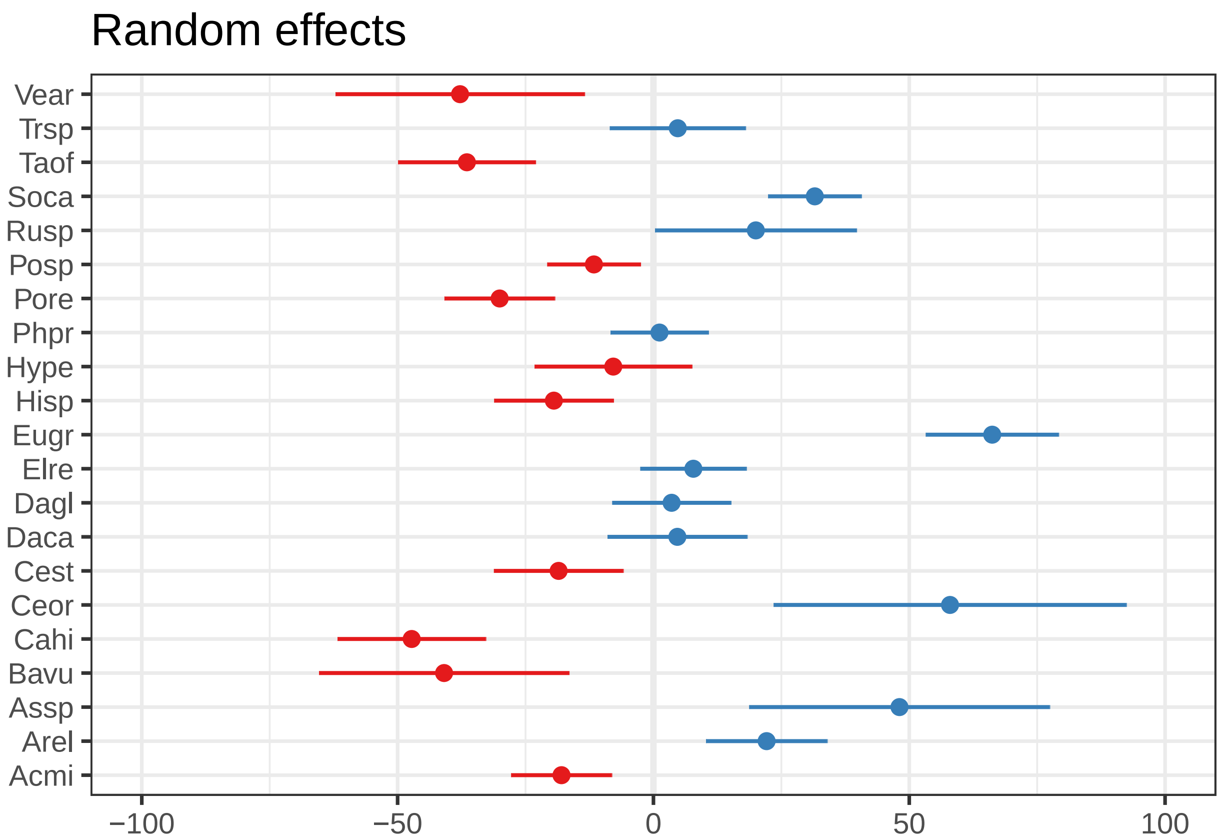



```r
# these are the random effects estimates
plot_model(mod6, type = "re", terms = c("species", "plot"))
```

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


Random effects
plot (Intercept)
year
D6
D5
D4
D3
D2
D1
C6
C5
C4
C3
C2
C1
B6
B5
B4
B3
B2
B1
A6
A5
A4
A3
A2
A1
−150 −100 −50 0 50 100 150 200
−150 −100 −50 0 50 100 150 200

```
##
## [[2]]
```




```r
# 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
```

```r
mod7a <- lmer(spp_half_cover_date ~ state + species + year +
    (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) +
## mod6:     (1 + year | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year | plot)
##      npar   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
```

```r
anova(mod7, mod7a)  #mod 7a?
```

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year + (1 | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7a   25 13539 13668 -6744.6    13489
## mod7    26 13595 13729 -6771.6    13543     0  1          1
```

```r
summary(mod7)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + (1 + year | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13595.1  13728.9  -6771.6  13543.1     1242
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1232 -0.7237 -0.2572  0.7334  3.4828
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  plot     (Intercept) 2.537e+03 50.36370
##           year        4.741e-04  0.02177 -1.00
##  Residual             2.518e+03 50.17603
## Number of obs: 1268, groups:  plot, 24
##
## Fixed effects:
##               Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)    133.901      5.546  302.106  24.143  < 2e-16 ***
## stateambient     5.412      3.897   21.438   1.389 0.179229
## speciesArel     44.169      7.844 1260.160   5.631 2.21e-08 ***
## speciesAssp     70.545     16.757 1267.942   4.210 2.73e-05 ***
## speciesBavu   -22.949     13.996 1267.915  -1.640 0.101318
## speciesCahi   -35.193      9.011 1257.335  -3.906 9.90e-05 ***
## speciesCeor    84.001     19.822 1261.449   4.238 2.42e-05 ***
## speciesCest    -5.209      8.183 1253.784  -0.637 0.524527
## speciesDaca    19.856      8.627 1256.246   2.302 0.021515 *
## speciesDagl    24.693      7.743 1258.750   3.189 0.001462 **
## speciesElre    30.733      7.252 1252.267   4.238 2.42e-05 ***
## speciesEugr    88.527      8.335 1264.020  10.621  < 2e-16 ***
## speciesHisp    -1.916      7.762 1250.982  -0.247 0.805081
## speciesHype    12.271      9.416 1266.314   1.303 0.192754
## speciesPhpr    20.661      6.936 1250.109   2.979 0.002948 **
## speciesPore   -11.775      7.410 1256.420  -1.589 0.112266
## speciesPosp     7.985      6.762 1247.878   1.181 0.237868
## speciesRusp    43.145     11.525 1262.439   3.744 0.000189 ***
## speciesSoca    51.527      6.762 1247.878   7.620 4.99e-14 ***
## speciesTaof   -19.080      8.535 1265.042  -2.236 0.025558 *
## speciesTrsp    20.983      8.462 1254.243   2.480 0.013279 *
```

```
## speciesVear   -27.931     13.943 1264.466  -2.003 0.045361 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
summary(mod7a)
```

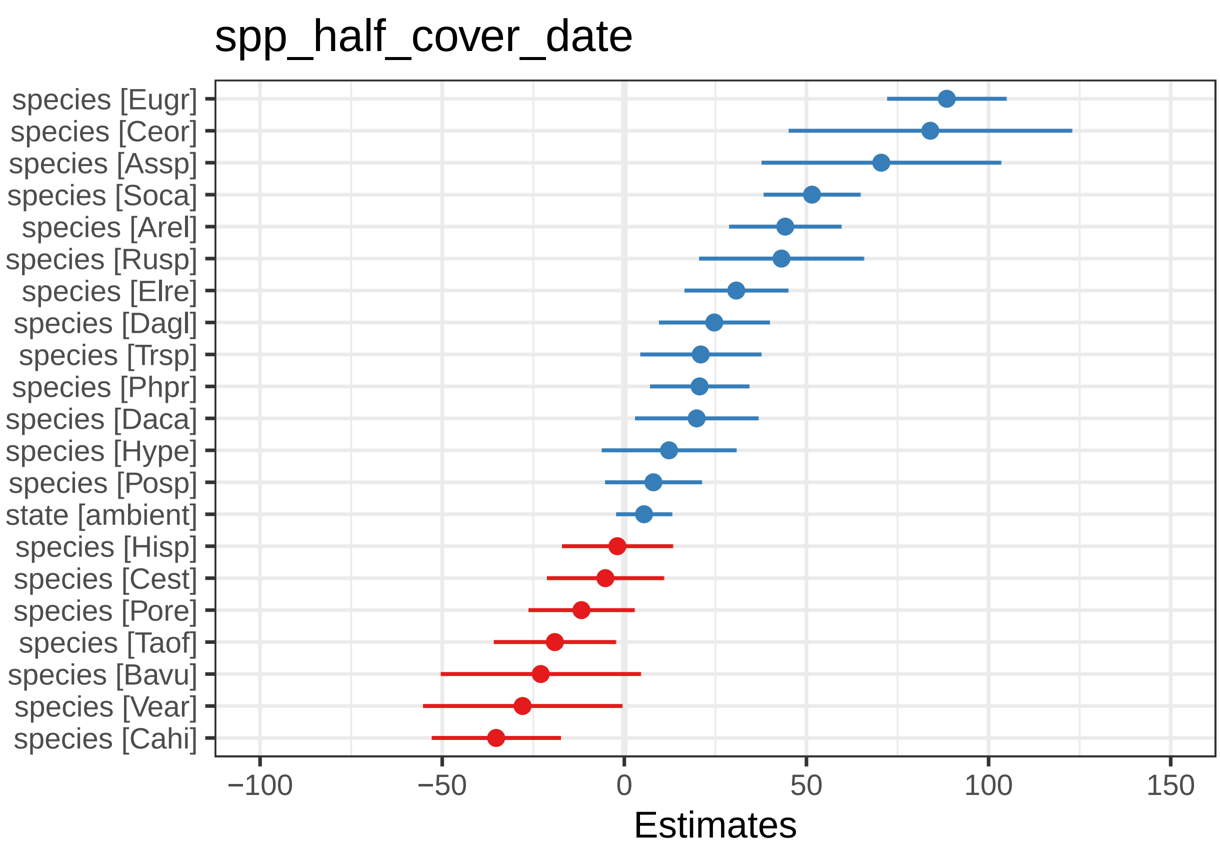
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year + (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13539.1  13667.8  -6744.6  13489.1     1243
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1388 -0.7706 -0.2263  0.6478  3.2151
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   40.94   6.398
##  Residual             2411.99  49.112
## Number of obs: 1268, groups:  plot, 24
##
## Fixed effects:
##                 Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)  -1.455e+04  1.978e+03  1.260e+03  -7.354 3.45e-13 ***
## stateambient  4.749e+00  3.846e+00  2.368e+01   1.235 0.229105
## speciesArel   4.046e+01  7.694e+00  1.258e+03   5.258 1.71e-07 ***
## speciesAssp   7.136e+01  1.640e+01  1.267e+03   4.350 1.47e-05 ***
## speciesBavu  -2.536e+01  1.371e+01  1.267e+03  -1.851 0.064438 .
## speciesCahi  -3.039e+01  8.844e+00  1.256e+03  -3.436 0.000609 ***
## speciesCeor   8.460e+01  1.941e+01  1.264e+03   4.360 1.41e-05 ***
## speciesCest  -9.968e-01  8.030e+00  1.252e+03  -0.124 0.901234
## speciesDaca   2.287e+01  8.454e+00  1.254e+03   2.706 0.006907 **
## speciesDagl   2.196e+01  7.588e+00  1.257e+03   2.894 0.003864 **
## speciesElre   2.611e+01  7.125e+00  1.251e+03   3.664 0.000259 ***
## speciesEugr   8.560e+01  8.169e+00  1.262e+03  10.479  < 2e-16 ***
## speciesHisp  -1.986e+00  7.598e+00  1.249e+03  -0.261 0.793833
## speciesHype   1.007e+01  9.222e+00  1.265e+03   1.092 0.275143
## speciesPhpr   1.943e+01  6.791e+00  1.248e+03   2.861 0.004294 **
## speciesPore  -1.242e+01  7.253e+00  1.254e+03  -1.712 0.087177 .
## speciesPosp   6.386e+00  6.622e+00  1.246e+03   0.964 0.335077
## speciesRusp   3.981e+01  1.129e+01  1.265e+03   3.526 0.000437 ***
## speciesSoca   4.993e+01  6.622e+00  1.246e+03   7.539 9.05e-14 ***
## speciesTaof  -1.925e+01  8.355e+00  1.263e+03  -2.304 0.021402 *
## speciesTrsp   2.263e+01  8.286e+00  1.252e+03   2.731 0.006399 **
## speciesVear  -2.294e+01  1.366e+01  1.263e+03  -1.679 0.093372 .
```

```
## year          7.277e+00  9.805e-01  1.260e+03   7.422 2.12e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 23 > 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
```

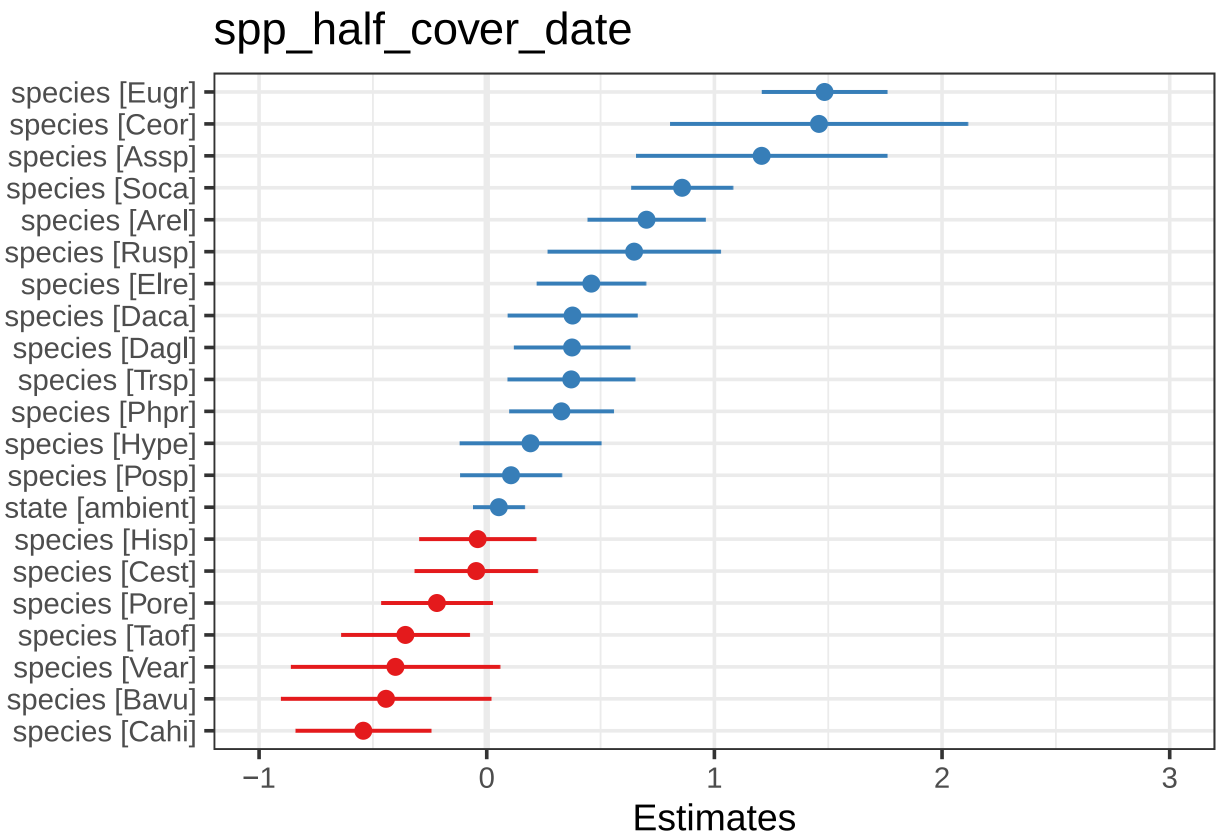
```
## Type III Analysis of Variance Table with Satterthwaite's method
##         Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state     3676    3676     1   23.68  1.5241    0.2291
## species 890400   44520    20 1259.23 18.4578 < 2.2e-16 ***
## year    132866  132866     1 1259.80 55.0857 2.116e-13 ***
## ---
## 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).

# Take a look at the estimates for each fixed effect. These
# are the estimates from summary(mod8). 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(mod7, sort.est = TRUE)
```

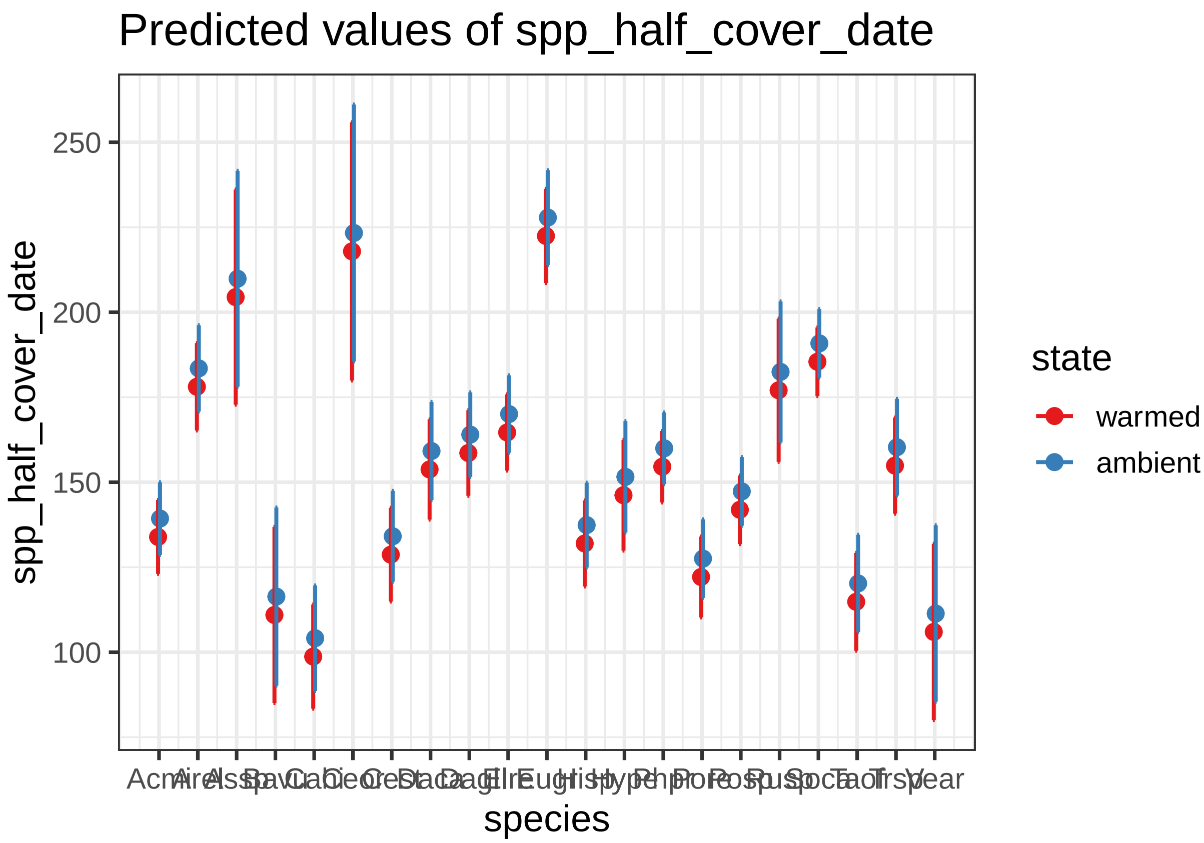


```r
# if you want to standardize the estimates:
plot_model(mod7, sort.est = TRUE, type = "std")
```

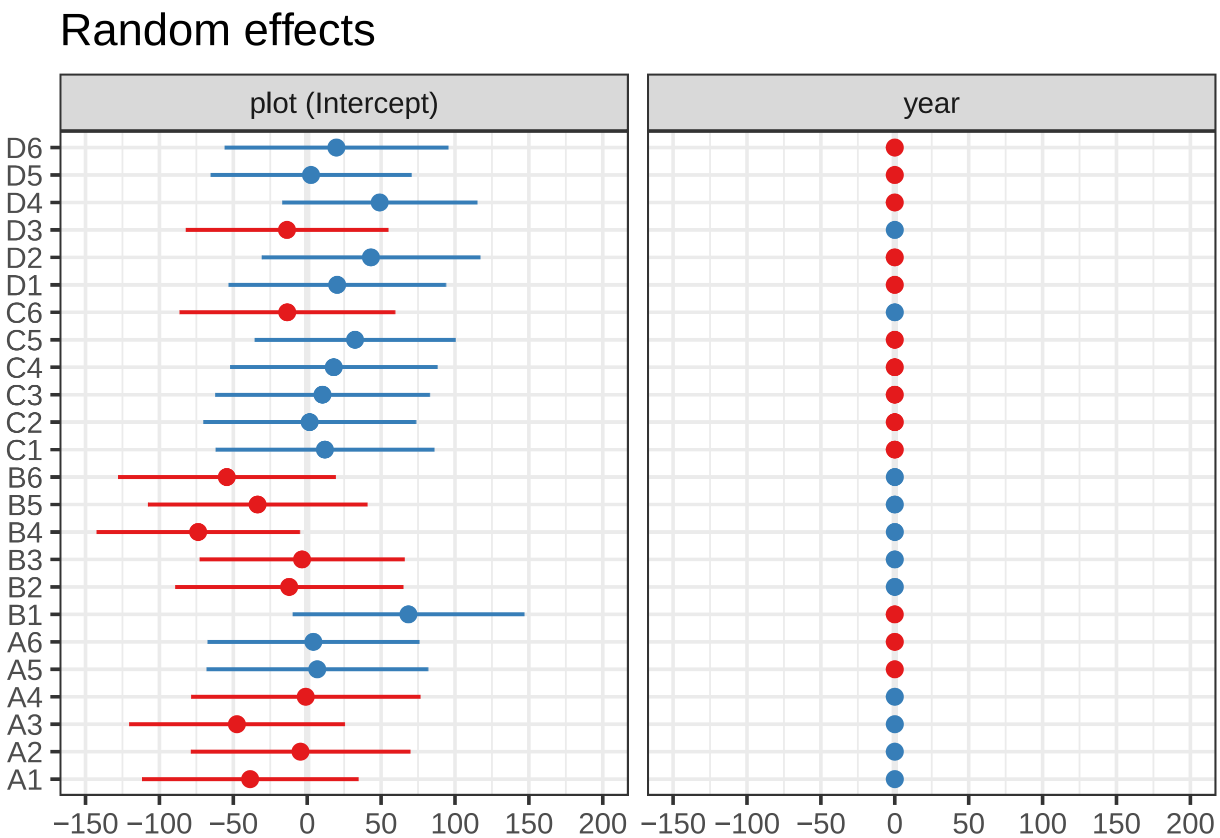
```
## boundary (singular) fit: see ?isSingular
```




```r
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7, type = "pred", terms = c("species", "state"))
```




```
# these are the random effects estimates
plot_model(mod7, type = "re")
```




```
# 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
```

```r
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
```

```r
# including native vs. exotic - first with interaction term
mod9 <- 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 2 negative eigenvalues: -3.7e+00 -3.1e+07
```

```r
mod9a <- lmer(spp_half_cover_date ~ state + origin + year + (1 |
    plot), green_kbs, REML = FALSE)
anova(mod8, mod9)  # model 9 is a better fit to data
```

```
## Data: green_kbs
## Models:
## mod9: spp_half_cover_date ~ state + origin + (1 + year | plot)
## mod8: spp_half_cover_date ~ state * origin + (1 + year | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod9    9 13844 13890 -6912.9    13826                     
## mod8   12 13846 13908 -6911.1    13822 3.5035  3     0.3203
```

```r
anova(mod9, mod9a)  # mod 9a?
```

```
## Data: green_kbs
## Models:
## mod9a: spp_half_cover_date ~ state + origin + year + (1 | plot)
## mod9: spp_half_cover_date ~ state + origin + (1 + year | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod9a    8 13768 13810 -6876.2    13752
## mod9     9 13844 13890 -6912.9    13826     0  1          1
```

```r
summary(mod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + year + (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13768.3  13809.5  -6876.2  13752.3     1260
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0457 -0.7656 -0.3324  0.8431  2.4332
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   51.94   7.207
##  Residual             2967.56  54.475
## Number of obs: 1268, groups:  plot, 24
##
## Fixed effects:
##                Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)  -18454.477   2137.756   1256.943  -8.633  < 2e-16 ***
## stateambient      4.139      4.267     24.778   0.970    0.341
## origin          -32.633      5.951   1248.129  -5.484 5.03e-08 ***
## originBoth      -21.481      5.436   1259.517  -3.952 8.20e-05 ***
## originExotic    -29.216      3.859   1255.517  -7.570 7.19e-14 ***
## year              9.232      1.059   1256.954   8.714  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn origin orgnBt orgnEx
## stateambint  0.014
## origin       0.007  0.006
## originBoth  -0.037 -0.013  0.329
## originExotc -0.023 -0.010  0.464  0.511
## year        -1.000 -0.015 -0.008  0.037  0.022
```

```r
anova(mod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state    4238    4238     1   25.56  1.3439    0.2571
## origin 192106   64035     3 1256.32 20.3066 7.471e-13 ***
```

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

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

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -6.0e+00
```

```r
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 + year | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  13889.9  13951.6  -6932.9  13865.9     1256
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8681 -0.7547 -0.3932  1.0247  2.6078
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  plot     (Intercept) 3.983e+03 63.11457
##           year        1.192e-03  0.03453 -1.00
##  Residual             3.253e+03 57.03605
## Number of obs: 1268, groups:  plot, 24
##
## Fixed effects:
##                                     Estimate Std. Error       df t value
## (Intercept)                          149.324      3.813   65.819  39.166
## stateambient                           1.475      5.245   59.894   0.281
## growth_habit                          -4.164      7.763 1256.291  -0.536
## growth_habitGraminoid                  6.806      5.034 1266.650   1.352
## growth_habitVine                      79.828     40.617 1264.869   1.965
## stateambient:growth_habit              7.807     10.439 1257.052   0.748
## stateambient:growth_habitGraminoid     6.101      6.979 1263.506   0.874
## stateambient:growth_habitVine        -11.817     48.233 1267.988  -0.245
##                                     Pr(>|t|)
## (Intercept)                           <2e-16 ***
## stateambient                          0.7796
## growth_habit                          0.5919
## growth_habitGraminoid                 0.1767
## growth_habitVine                      0.0496 *
## stateambient:growth_habit             0.4547
## stateambient:growth_habitGraminoid    0.3822
## stateambient:growth_habitVine         0.8065
## ---
## 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 -0.727
## growth_habt -0.365  0.265
## grwth_hbtGr -0.571  0.415  0.276
## grwth_hbtVn -0.074  0.054  0.037  0.055
## sttmbnt:gr_  0.271 -0.367 -0.744 -0.205 -0.027
## sttmbnt:g_G  0.412 -0.554 -0.199 -0.721 -0.040  0.276
## sttmbnt:g_V  0.063 -0.084 -0.031 -0.047 -0.842  0.043  0.062
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```r
anova(mod10)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state                  81    81.2     1  801.41  0.0250 0.8744865
## growth_habit        56135 18711.6     3 1262.77  5.7519 0.0006596 ***
## state:growth_habit   3710  1236.6     3 1262.77  0.3801 0.7673416
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# including native vs. exotic - first with interaction term
mod11 <- lmer(spp_half_cover_date ~ state + growth_habit + (1 +
    year | plot), green_kbs, REML = FALSE)
```

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

## Warning: Model failed to converge with 1 negative eigenvalue: -3.9e-01
```

```r
mod11a <- lmer(spp_half_cover_date ~ state + growth_habit + 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 + year | plot)
## mod10: spp_half_cover_date ~ state * growth_habit + (1 + year | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod11    9 13885 13932 -6933.6    13867
## mod10   12 13890 13952 -6932.9    13866 1.4284  3     0.6989
```

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

```
## Data: green_kbs
## Models:
## mod11a: spp_half_cover_date ~ state + growth_habit + year + (1 | plot)
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year | plot)
##        npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11a    8 13815 13856 -6899.4    13799
## mod11     9 13885 13932 -6933.6    13867     0  1          1
```

```r
summary(mod11a)
```

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

```
##
##      AIC      BIC   logLik deviance df.resid
##  13814.9  13856.0  -6899.4  13798.9     1260
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8570 -0.8206 -0.3565  0.9522  2.3273
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   52.34   7.235
##  Residual             3079.28  55.491
## Number of obs: 1268, groups:  plot, 24
##
## Fixed effects:
##                        Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)          -1.824e+04  2.193e+03  1.259e+03  -8.318 2.31e-16 ***
## stateambient          3.904e+00  4.319e+00  2.498e+01   0.904 0.374654
## growth_habit         -1.793e-01  5.051e+00  1.256e+03  -0.035 0.971689
## growth_habitGraminoid  6.475e+00  3.420e+00  1.263e+03   1.893 0.058551 .
## growth_habitVine      7.104e+01  2.134e+01  1.264e+03   3.329 0.000896 ***
## year                  9.114e+00  1.087e+00  1.259e+03   8.385  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_V
## stateambint  0.017
## growth_habt  0.005 -0.008
## grwth_hbtGr  0.123  0.026  0.275
## grwth_hbtVn -0.003 -0.019  0.049  0.066
## year        -1.000 -0.018 -0.006 -0.124  0.003
```

```r
anova(mod11)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state          3586  3585.8     1   23.02  1.1027 0.3045818
## growth_habit  59585 19861.7     3 1260.56  6.1077 0.0004003 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# 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) +
```

```r
# 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)
```

```r
# 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
```

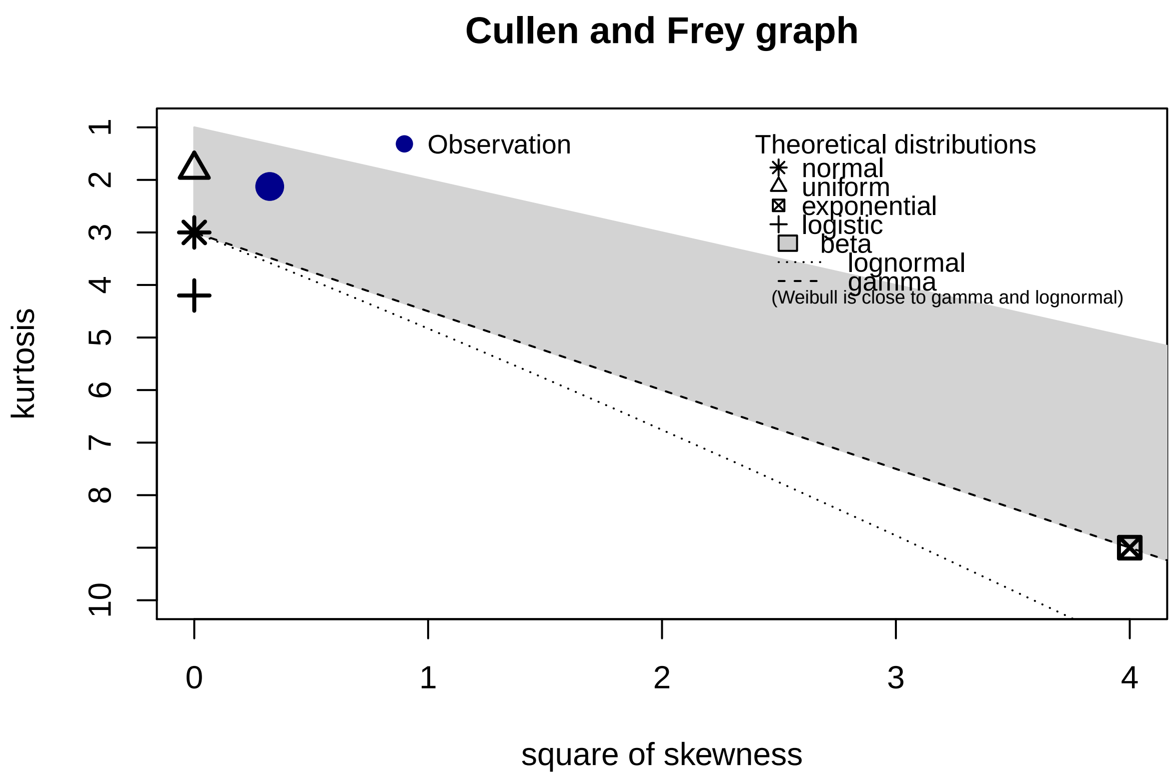
```r
# So another version of this model would include the
# interaction but not include the nesting (and thus would
# assume that species aren't observed ea yr) updated mod5
mod13 <- lmer(spp_half_cover_date ~ state * year + (1 | species),
    green_kbs)
```

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

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

ORIGINAL CODE BELOW; not edited by Phoebe

Seeing what other distribution could fit

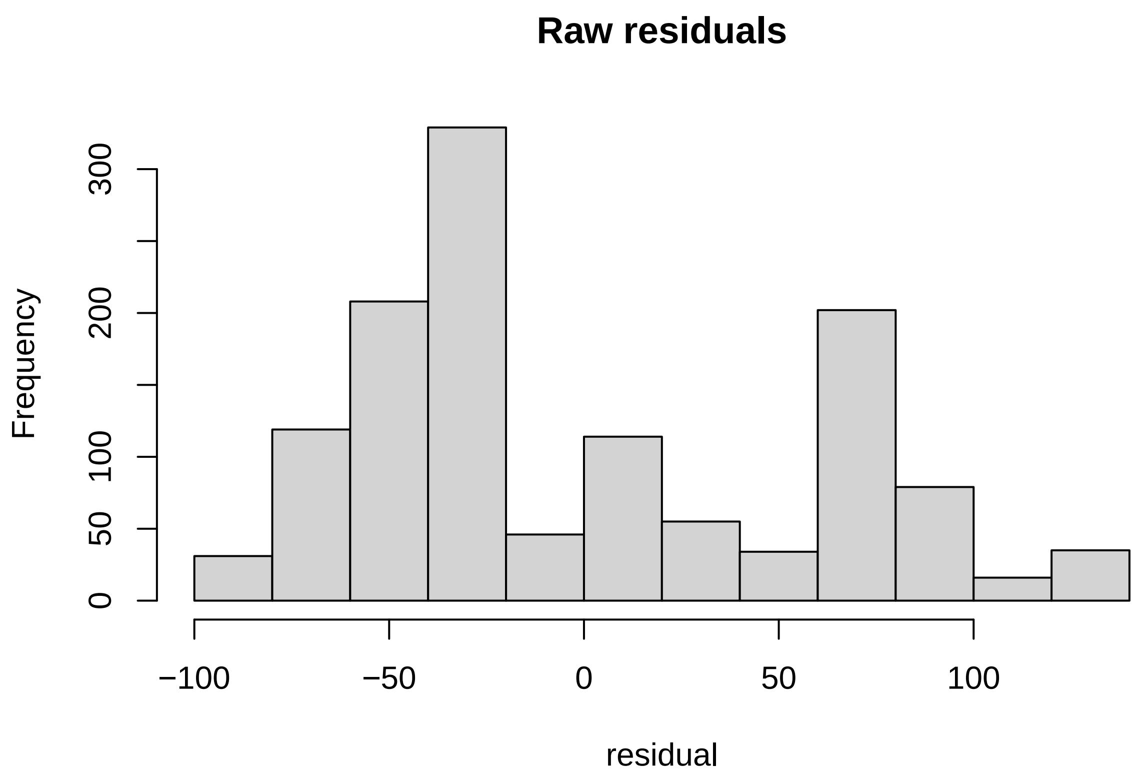
```r
descdist(green_kbs$spp_half_cover_date, discrete = FALSE)
```



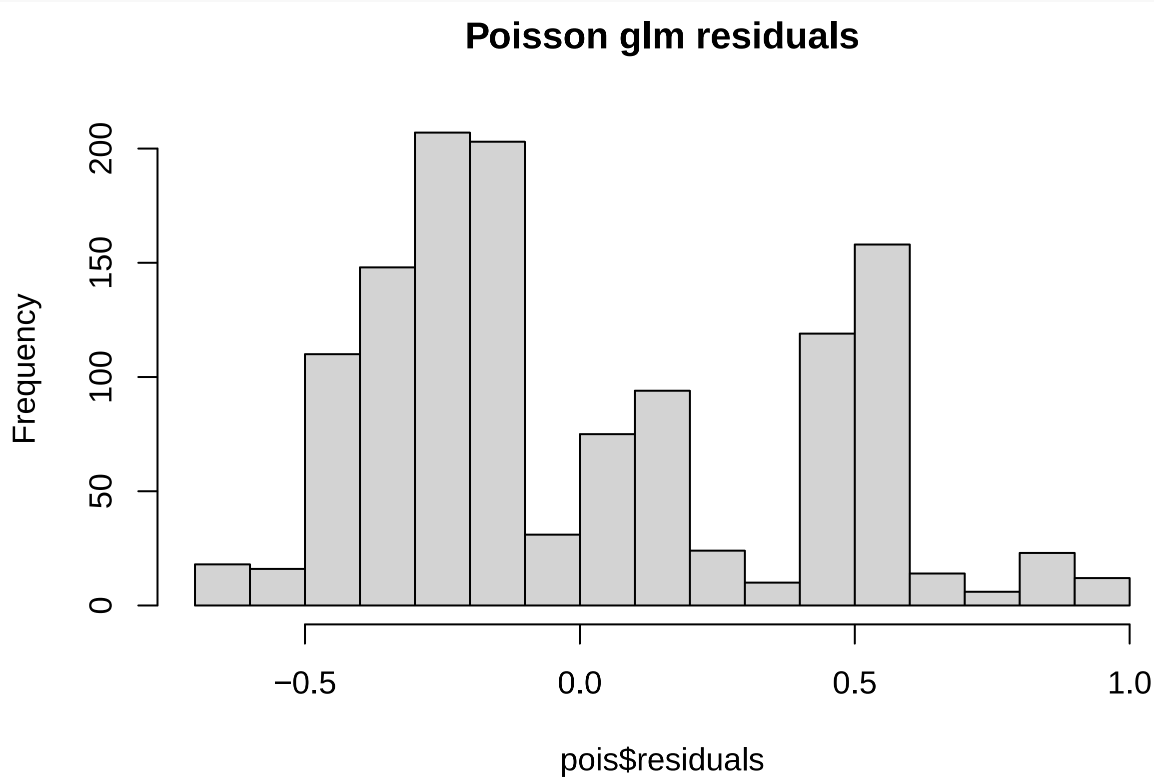

```
## summary statistics
## ------
## min:   59   max:  289
## median:  127
## mean:  154.2169
## estimated sd:  57.9311
## estimated skewness:  0.5680173
## estimated kurtosis:  2.125259
```

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")
```



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 unider
##  - 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 unider
##  - 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?

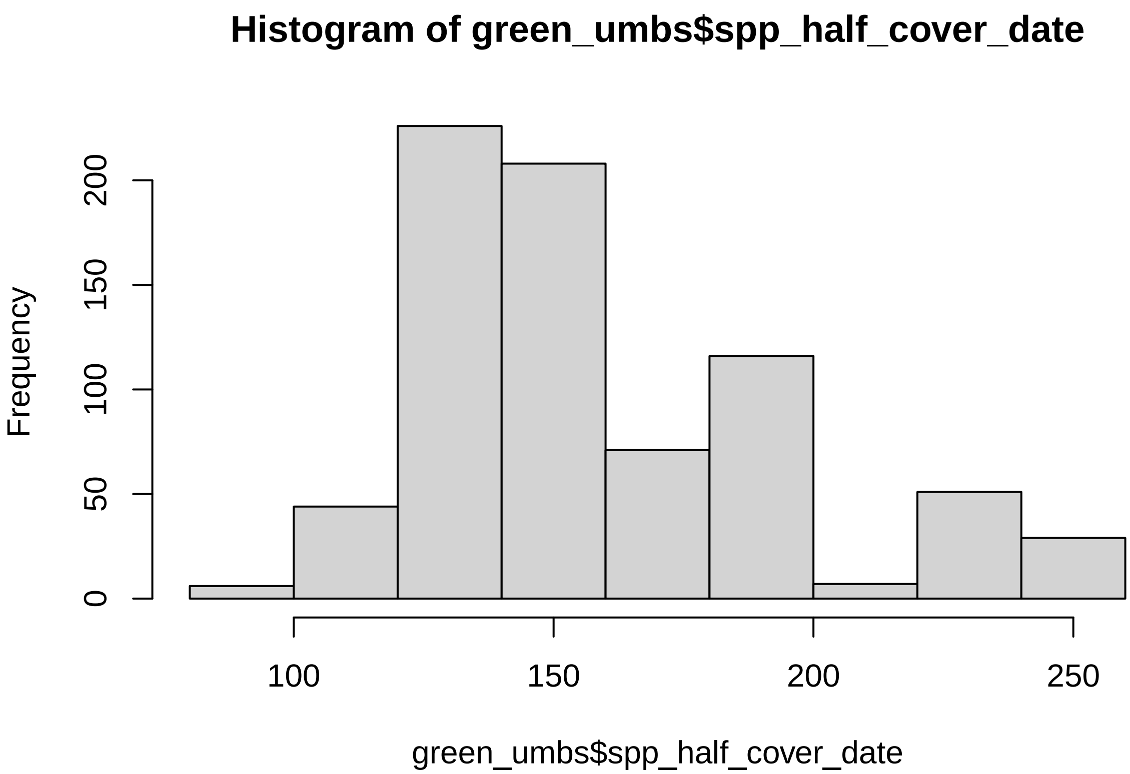
```
per1 <- adonis2(green_kbs$spp_half_cover_date ~ state * year +
    insecticide, data = green_kbs)
per1
per2 <- adonis(formula = green_kbs$spp_half_cover_date ~ state *
    year + insecticide, strata = green_kbs$plot, data = green_kbs)
per2
```

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

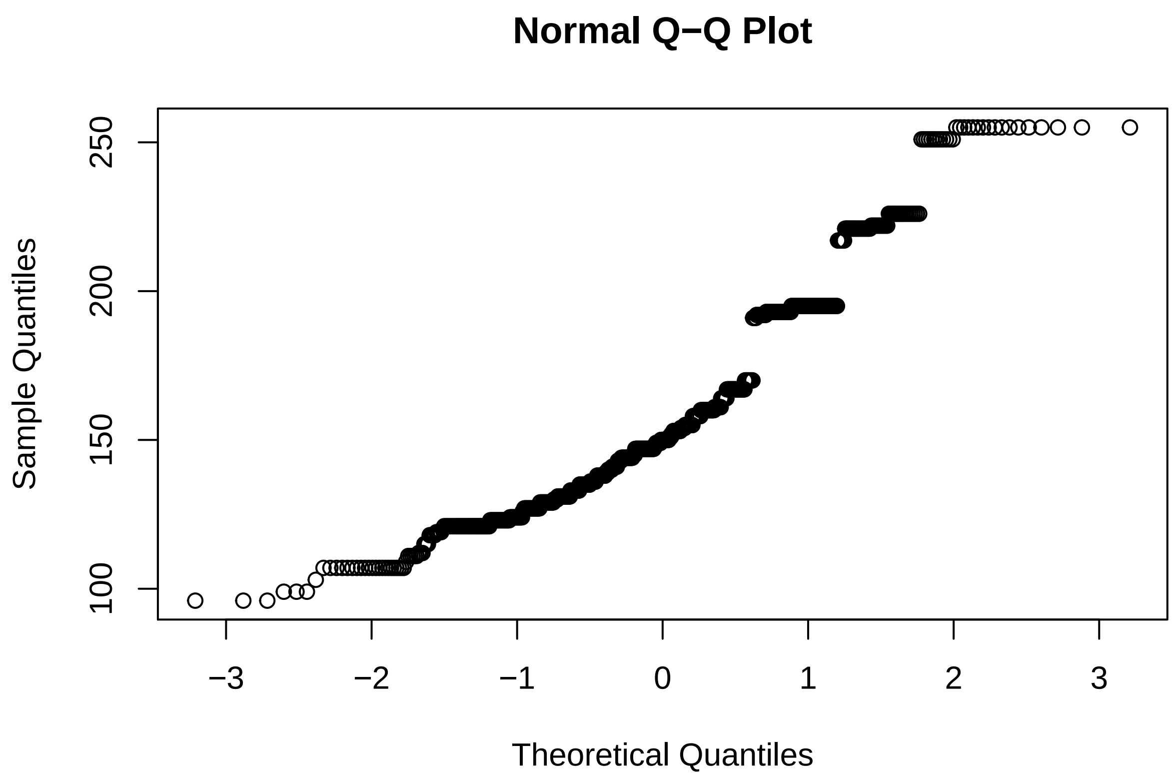
UMBS

Checking for normality

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



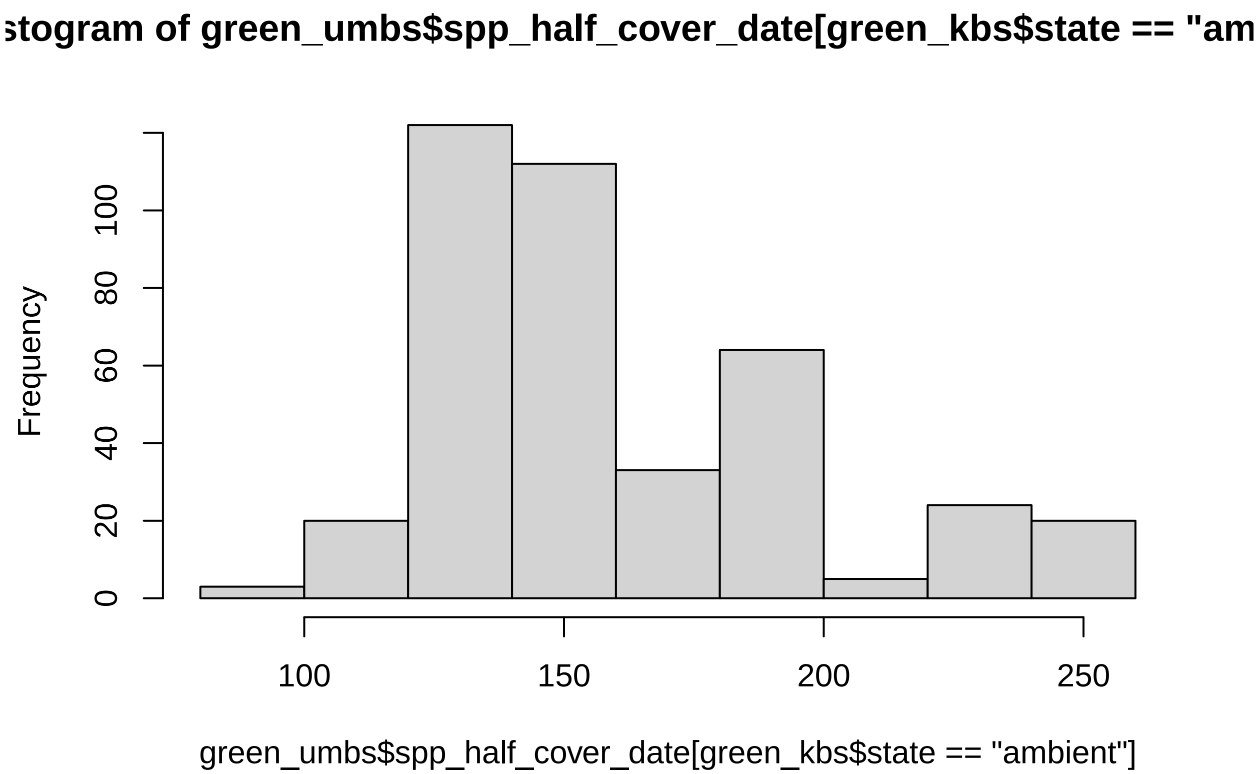

```
qqnorm(green_umbs$spp_half_cover_date)
```



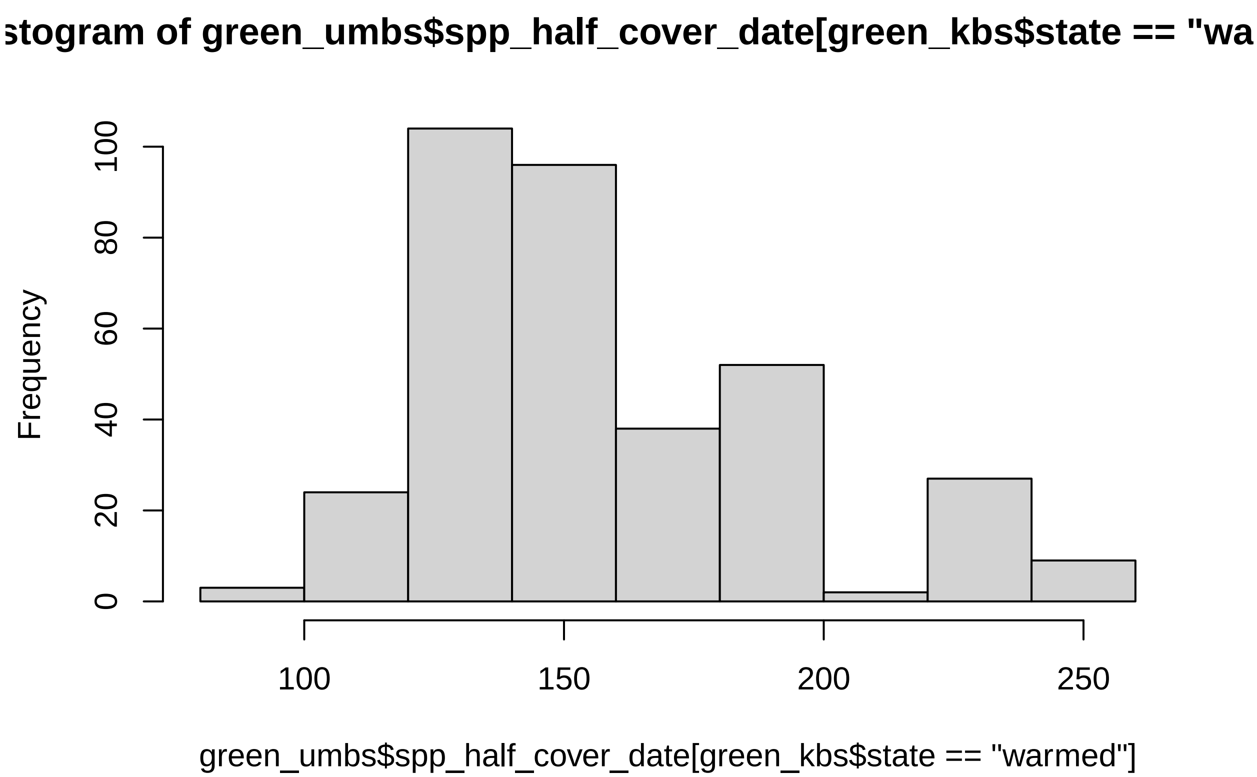

```
shapiro.test(green_umbs$spp_half_cover_date)
```

```
##
##  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"])
```



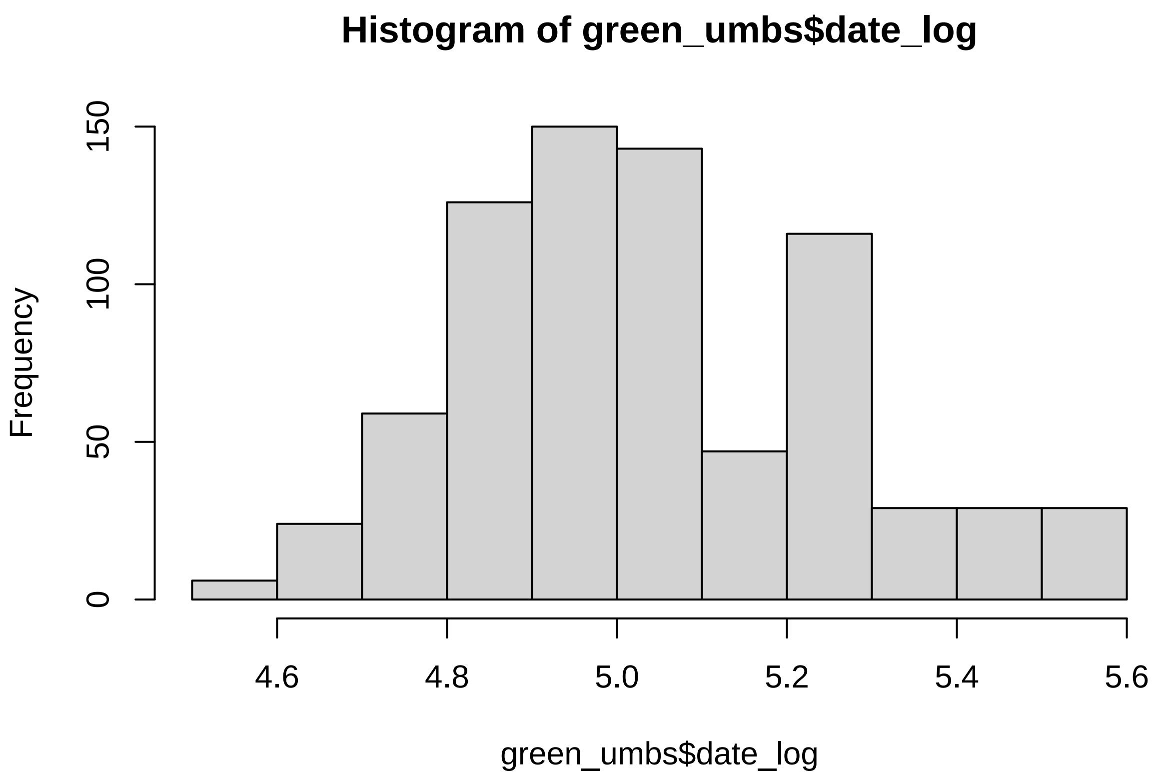

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "warmed"])
```



These look pretty good

Trying log transformation

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



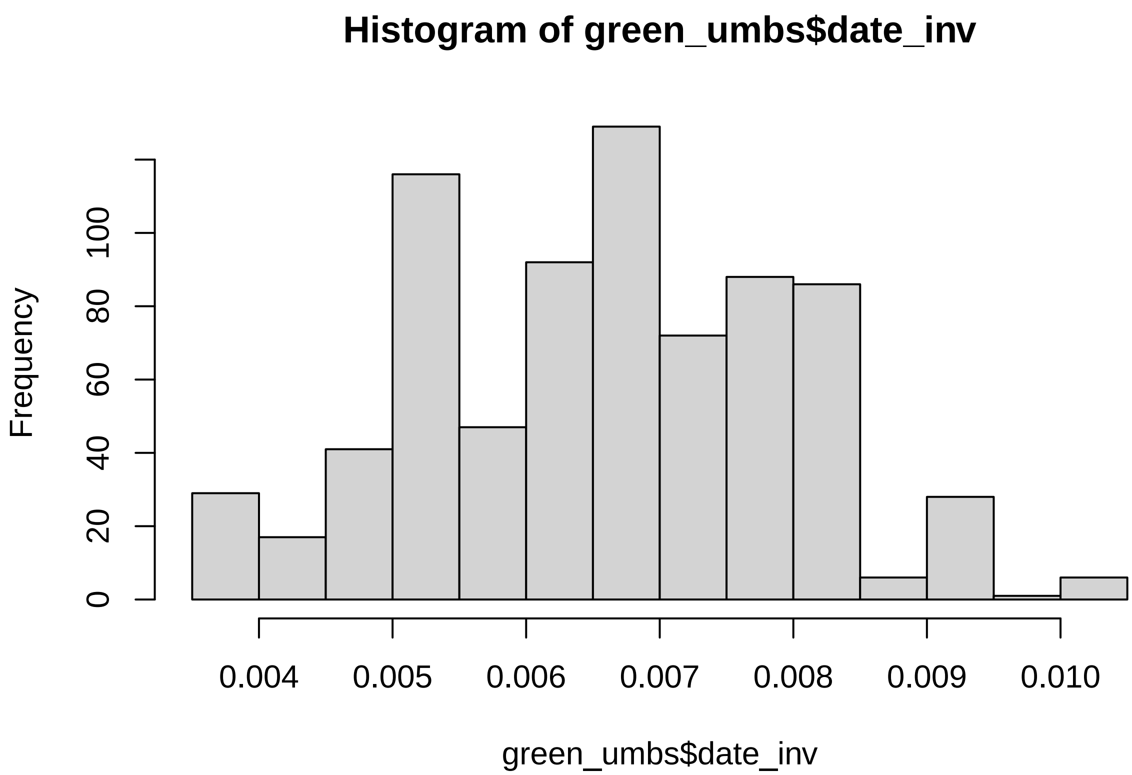

```
shapiro.test(green_umbs$date_log)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_log
## W = 0.96356, 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