warmXtrophic Project: Greenup Analyses

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Script Details:

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

script_tbl <- data.frame(Item = c("OVERVIEW", "COLLABORATORS",
    "REQUIRES", "DATA INPUT", "DATA OUTPUT", "NOTES"), Details = c("This script explores and analyses tl
    "Moriah Young, Mark Hammond, Pat Bills", "Prior to running this script, make sure plant_comp_clean_l
    "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 'gree

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 reacl
    "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)
```

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

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

# Get data
L1_dir <- Sys.getenv("L1DIR")
L2_dir <- Sys.getenv("L2DIR")
greenup <- read.csv(file.path(L2_dir, "greenup/final_greenup_species_L2.csv"))  # spp level greenup dat
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"))  # plot level greenup date
greenupp <- greenupp %>% select(-X)  # get rid of 'X' column that shows up

# 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" "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" ...
```

```r
# 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"
```

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

```
## [1] "warmed"  "ambient"
```

```r
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)
```

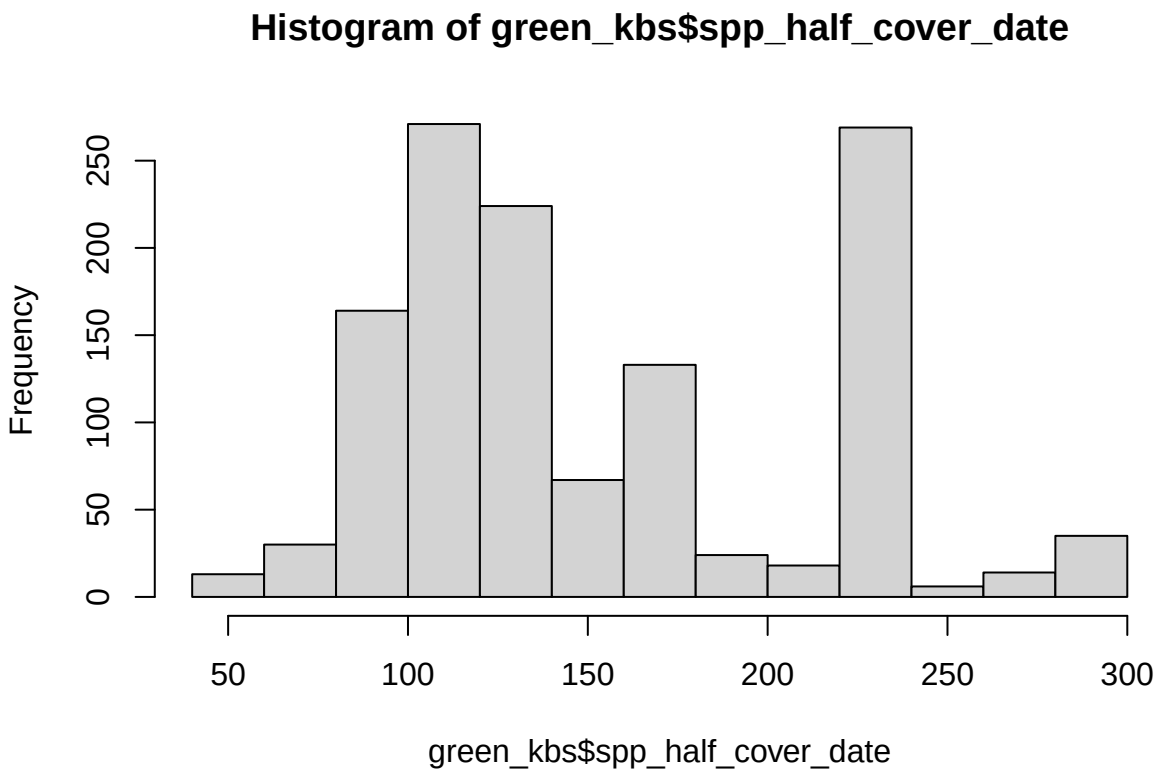
```
## [1] "warmed"  "ambient"
```

```
# 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")
```

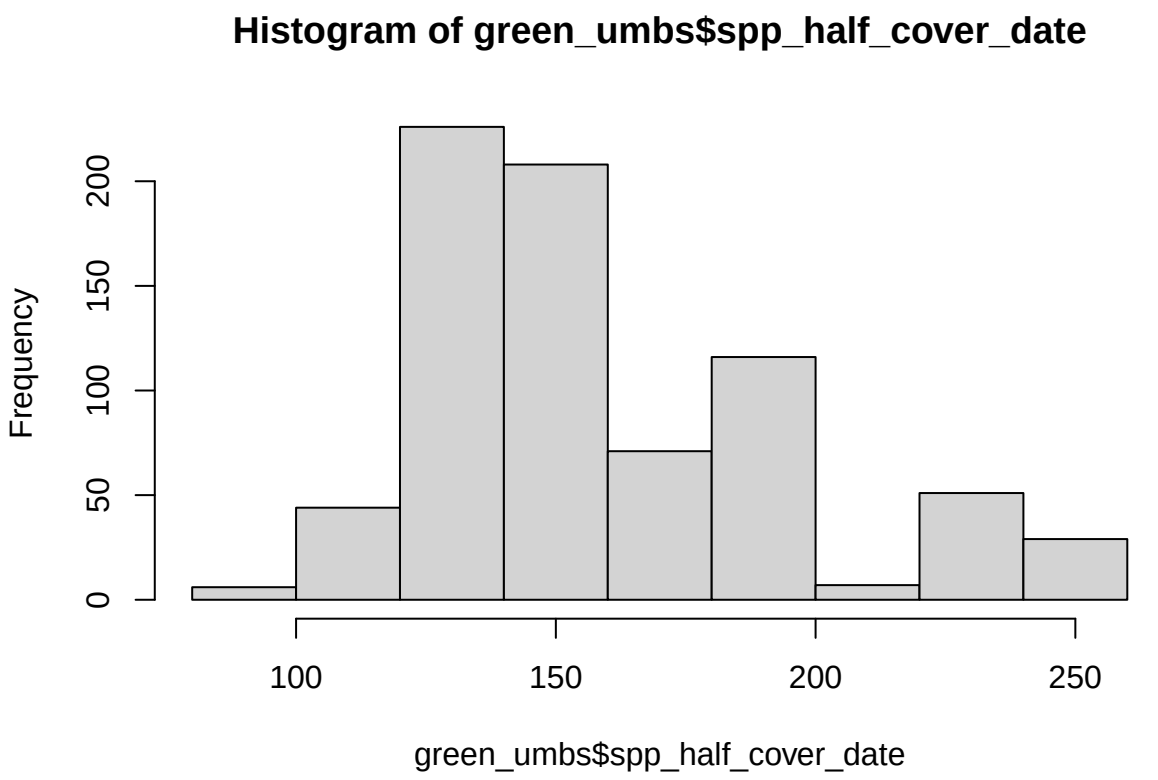
Data Exploration:

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

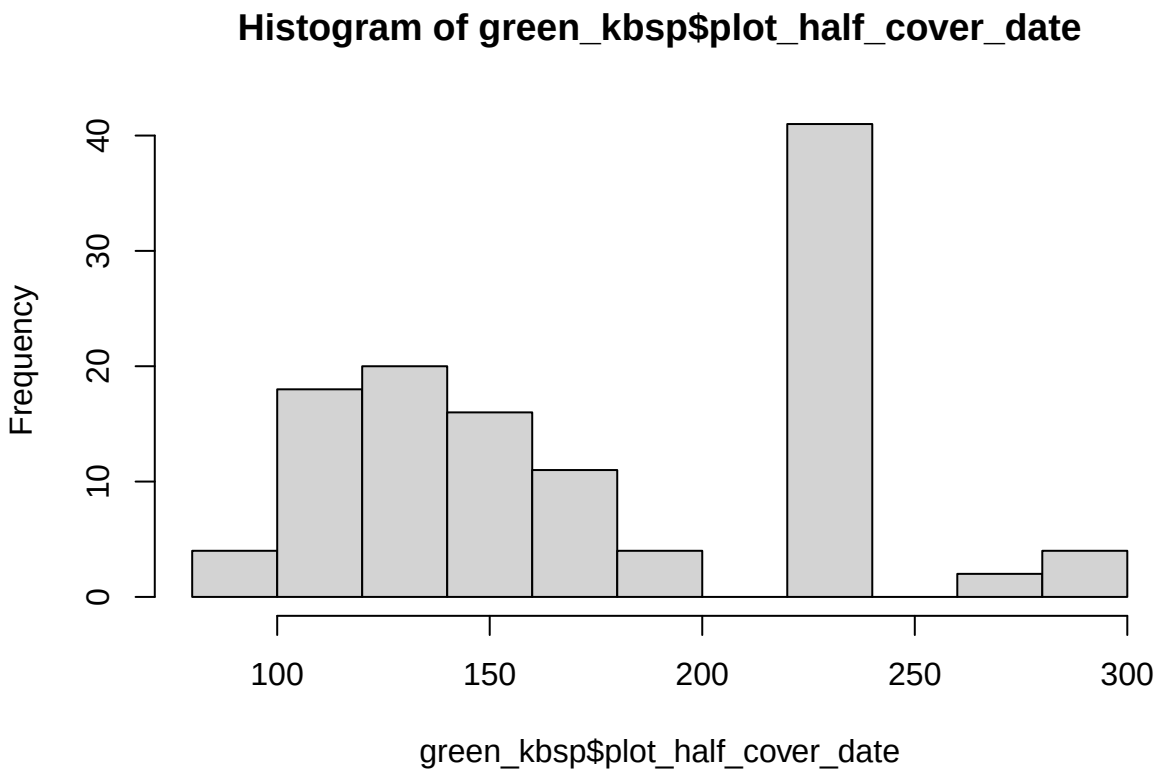
```
# species level
hist(green_kbs$spp_half_cover_date)
```



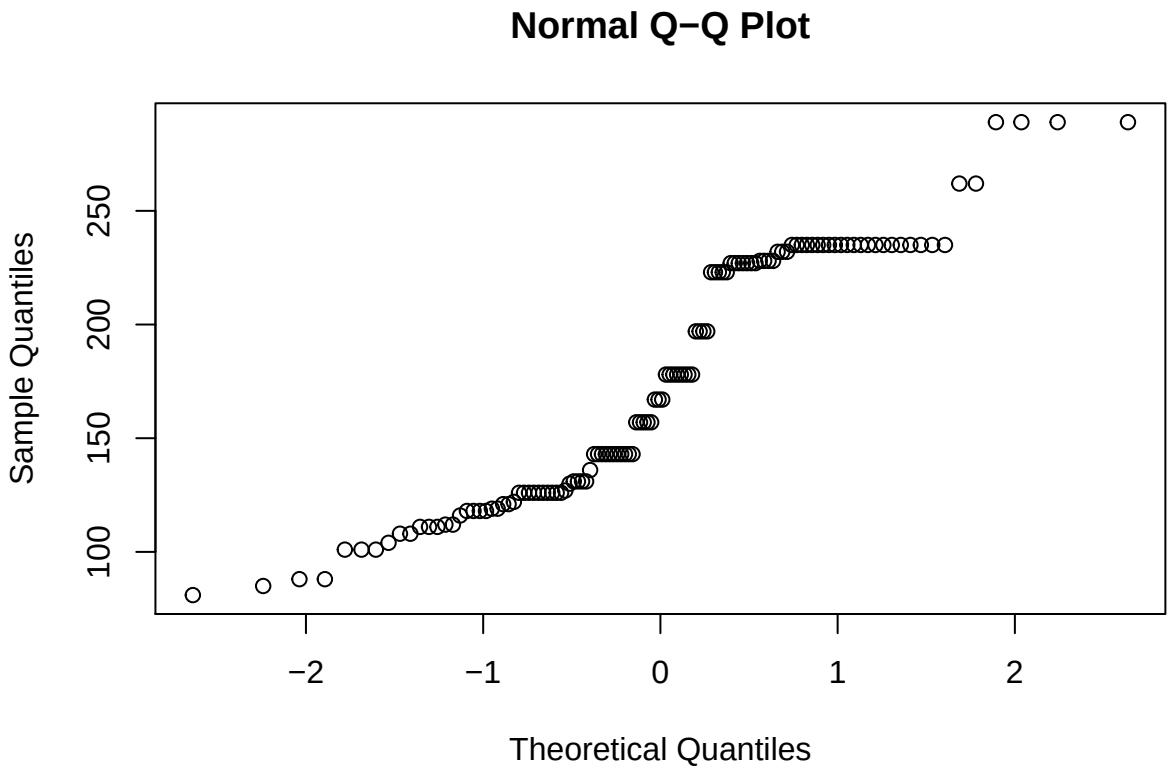

```
hist(green_umbs$spp_half_cover_date)
```




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




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

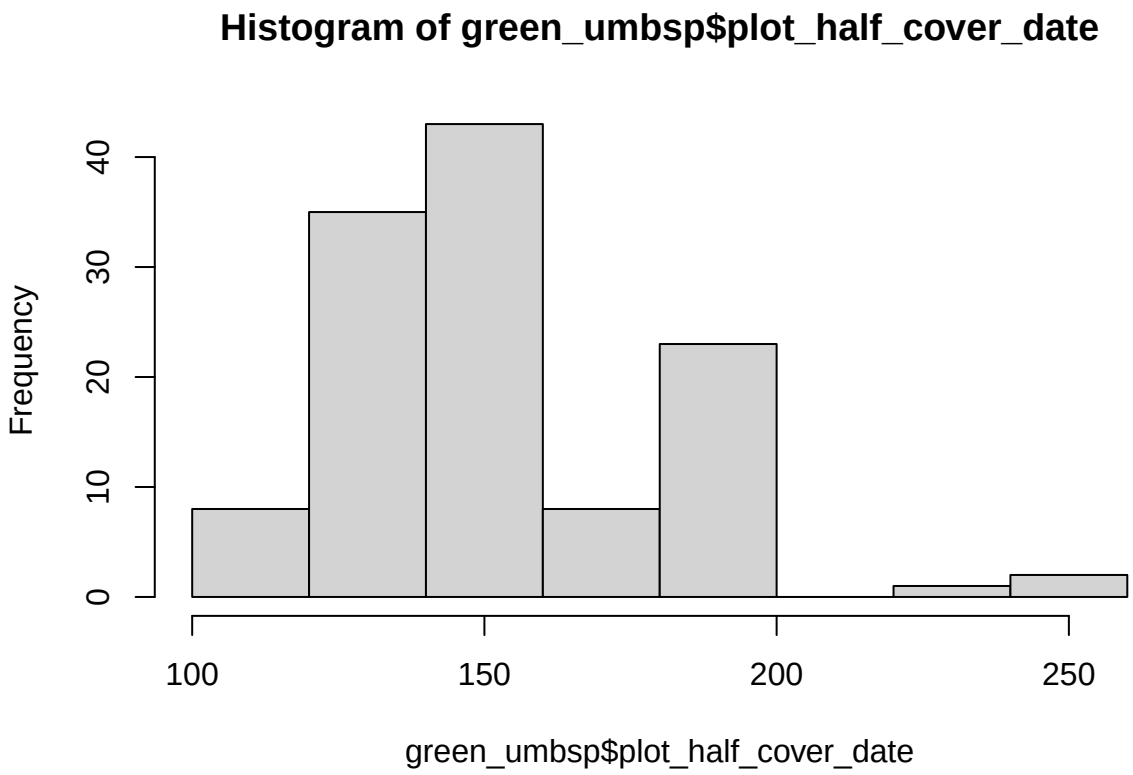



```
shapiro.test(green_kbsp$plot_half_cover_date)
```

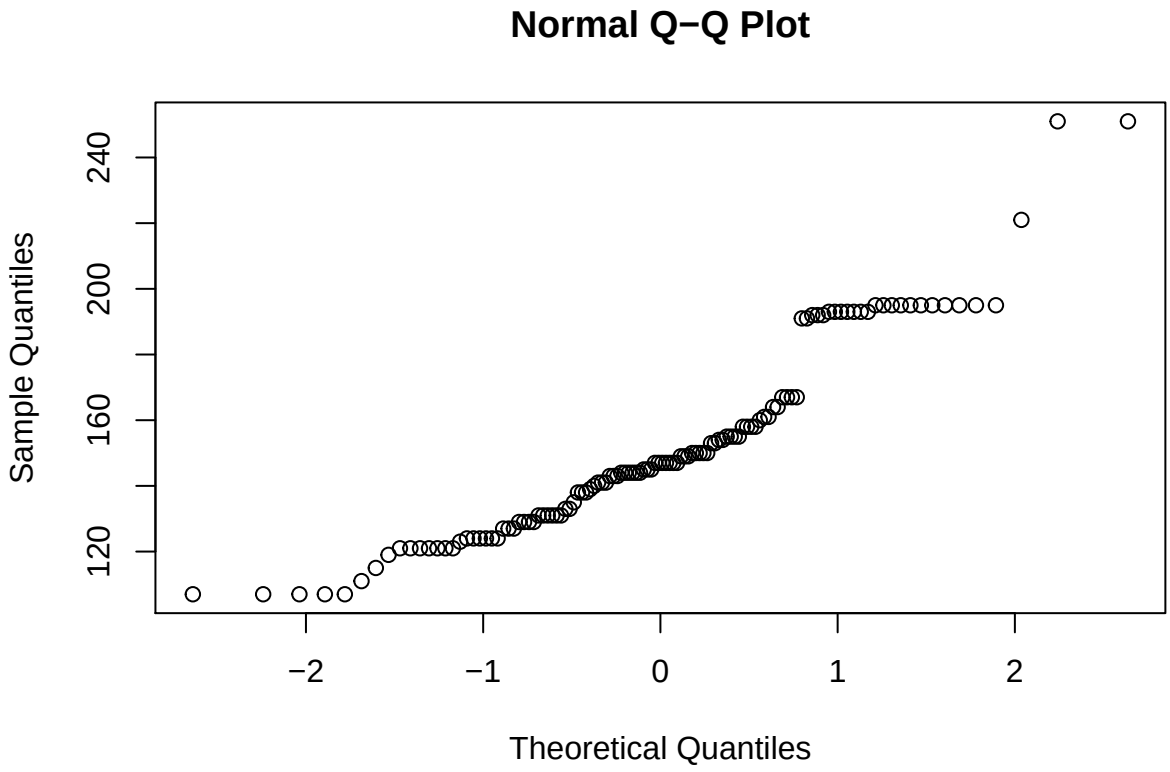
```
##
```

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

```
hist(green_umbsp$plot_half_cover_date)
```



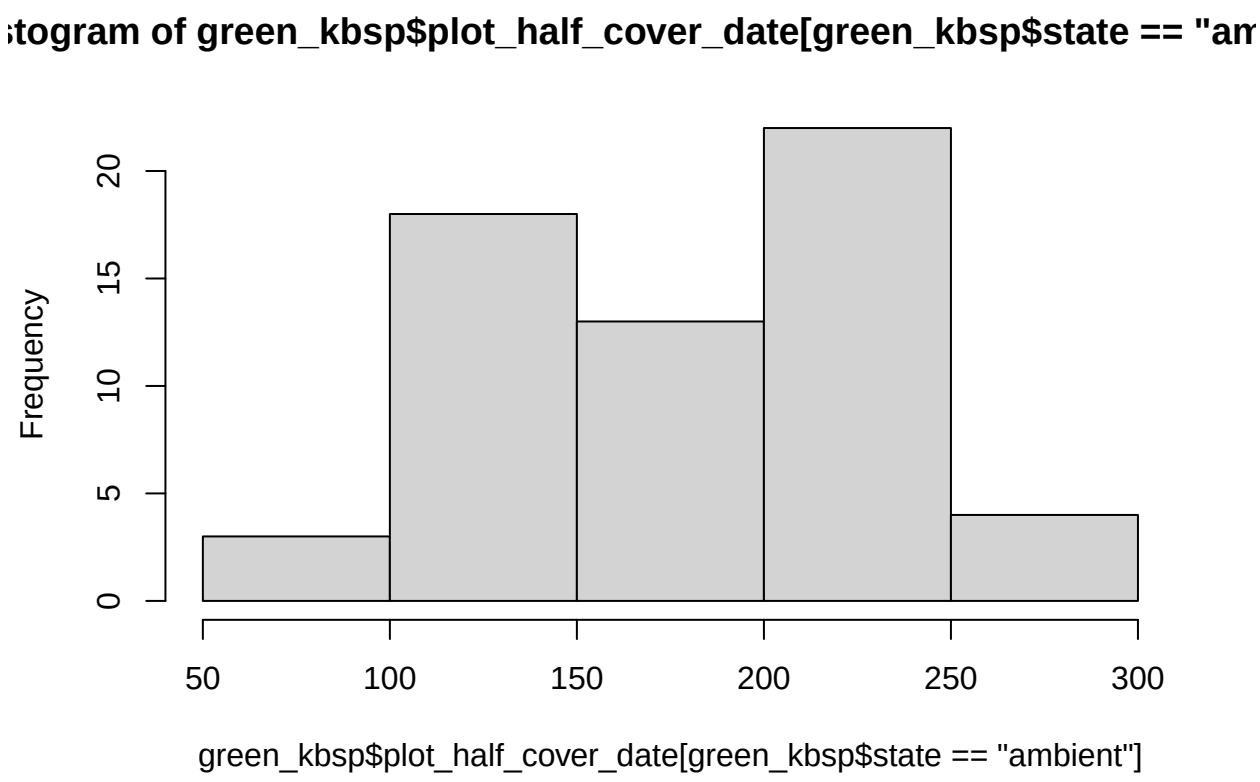

```
qqnorm(green_umbsp$plot_half_cover_date)
```



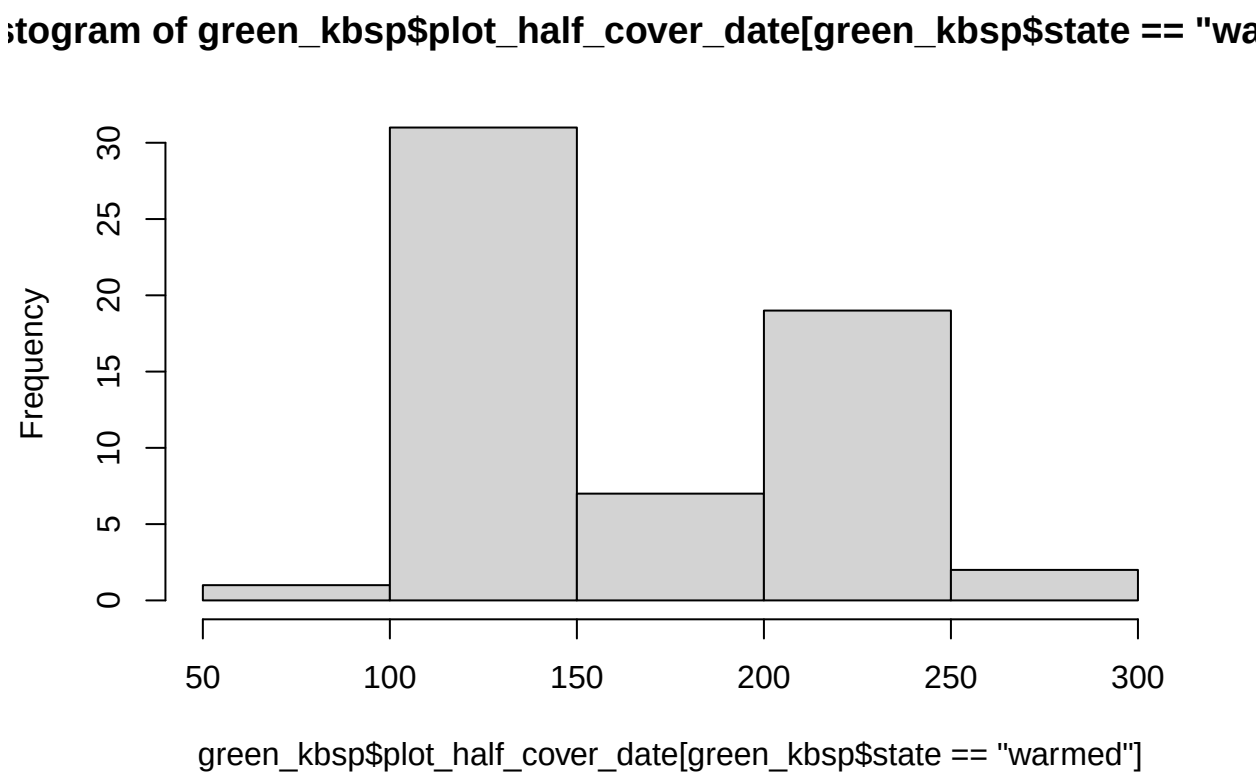

```
shapiro.test(green_umbsp$plot_half_cover_date)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbsp$plot_half_cover_date
## W = 0.91432, p-value = 1.143e-06
```

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

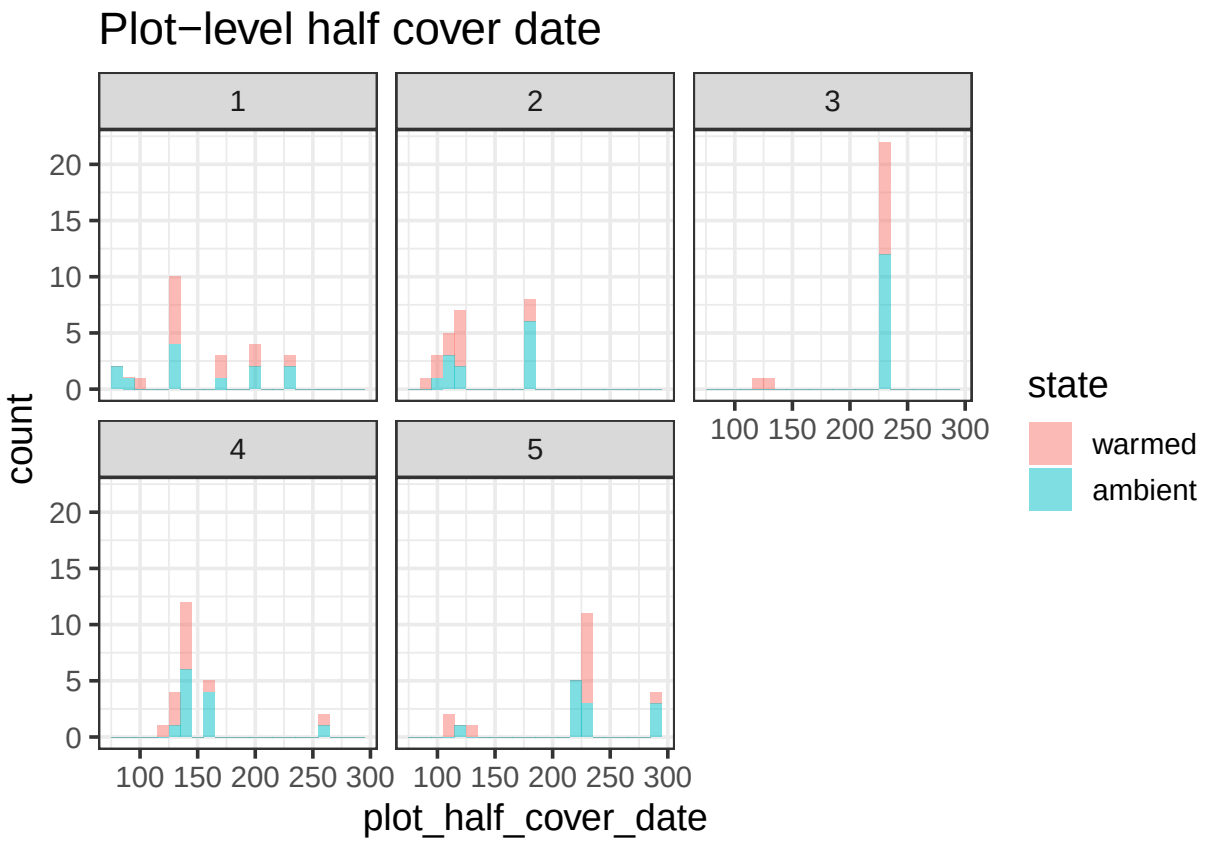



```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "warmed"])
```

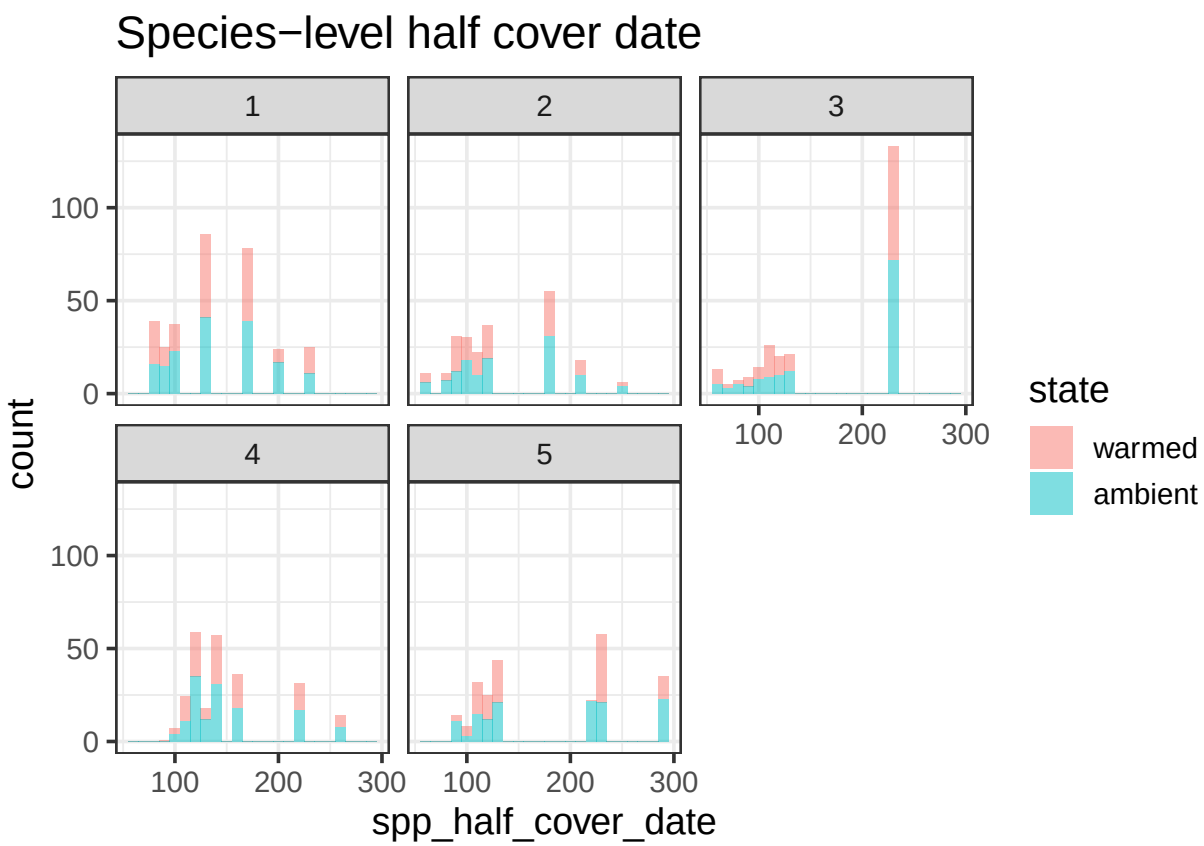



```
# histograms for each year - look at them together:
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
```

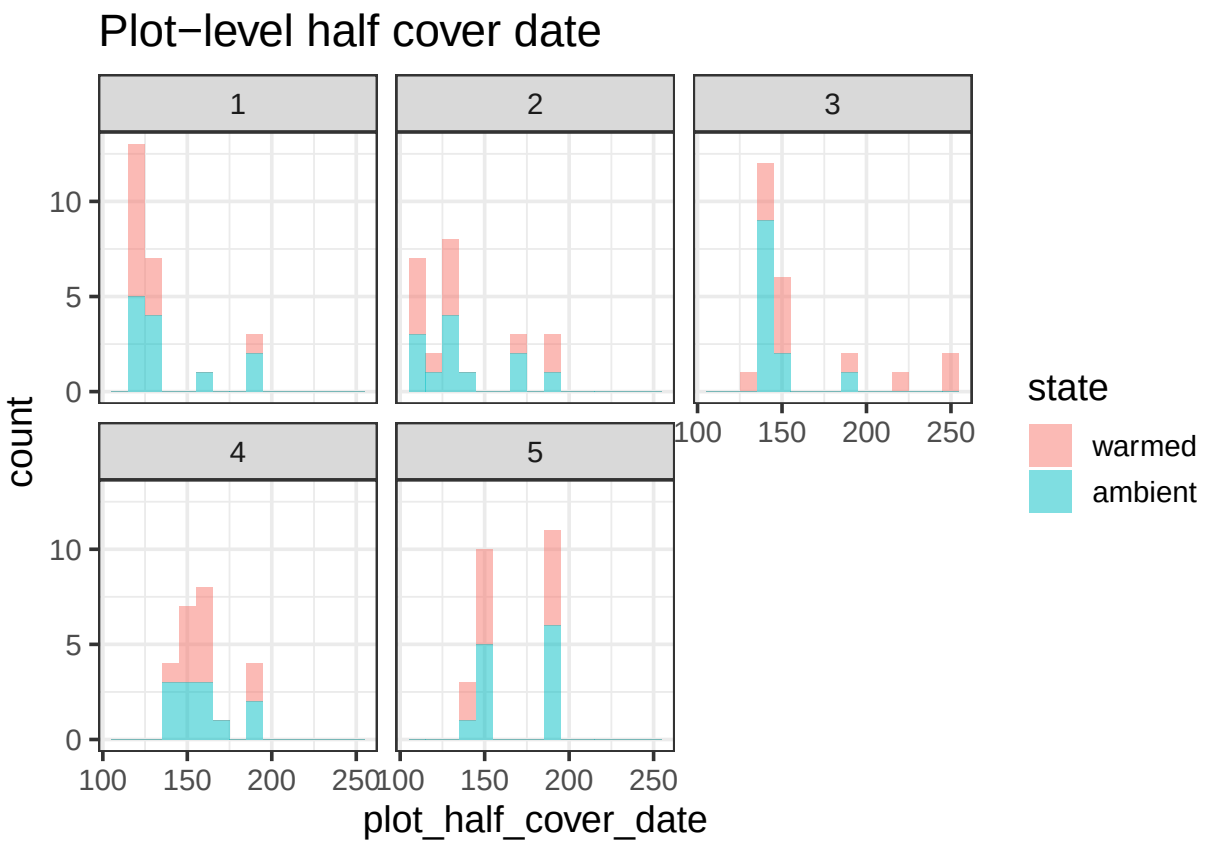
```
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



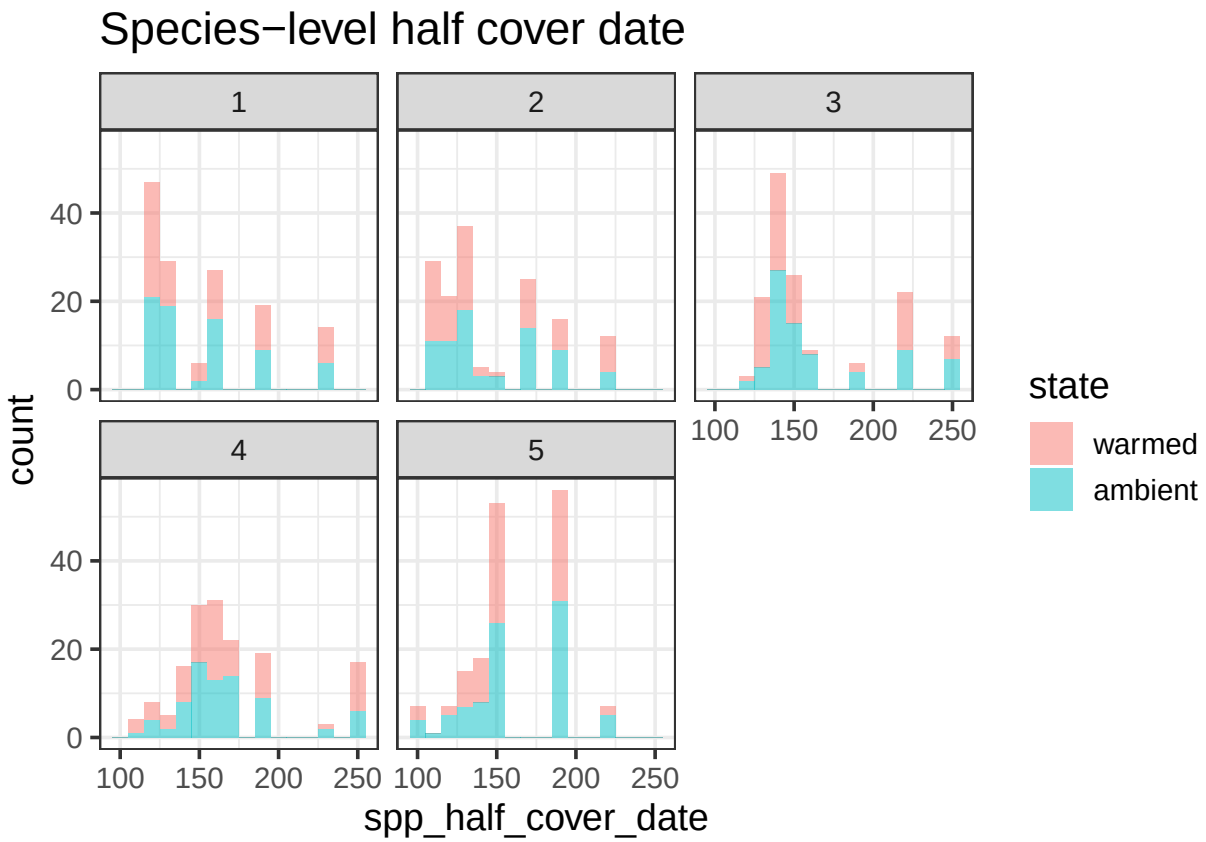

```
p1.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



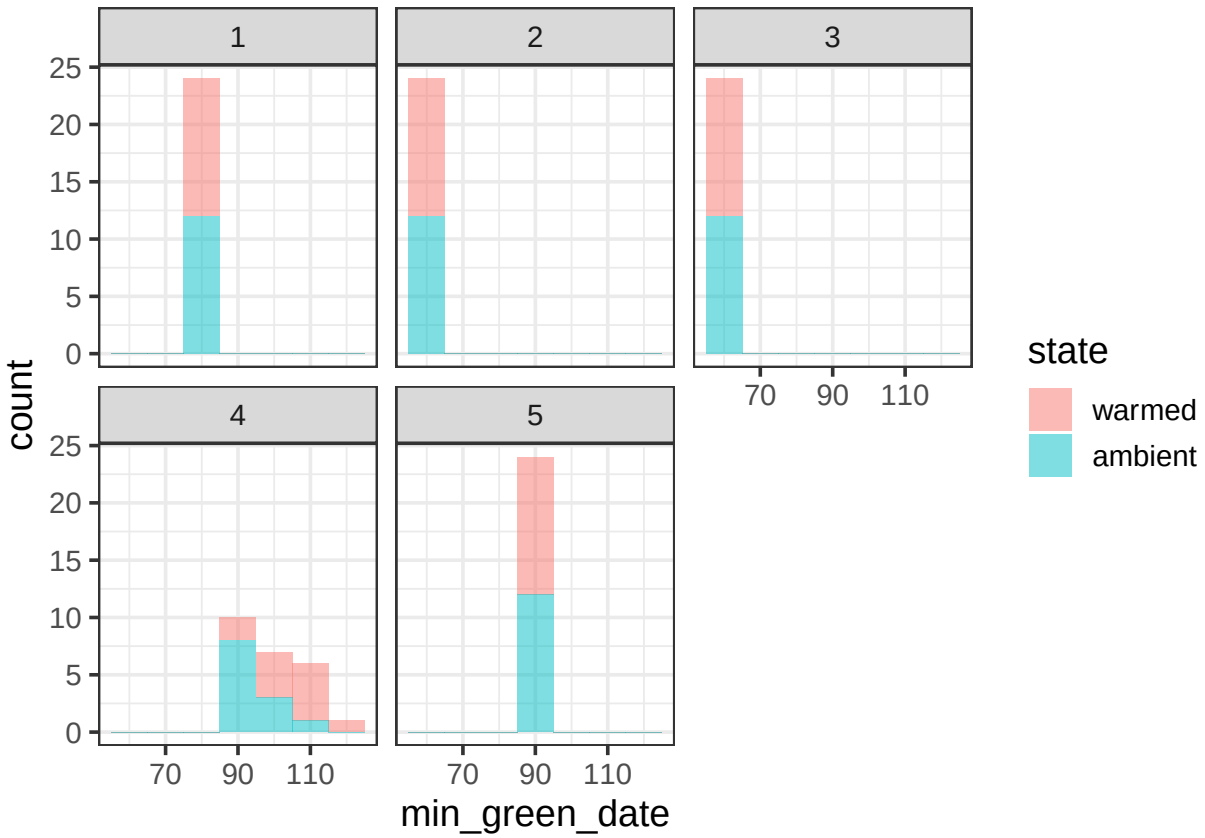

```
p1u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



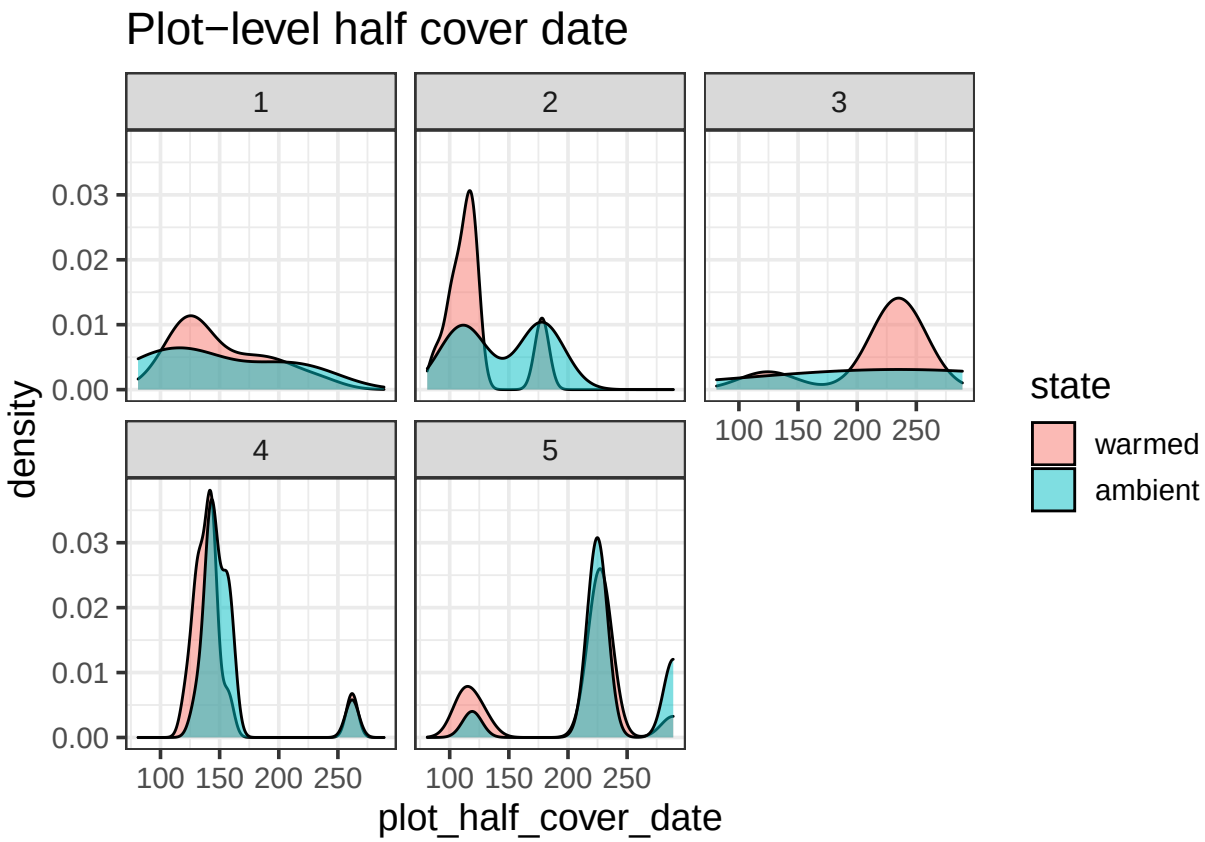

```
p1.2u <- ggplot(data = green_umbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2u + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



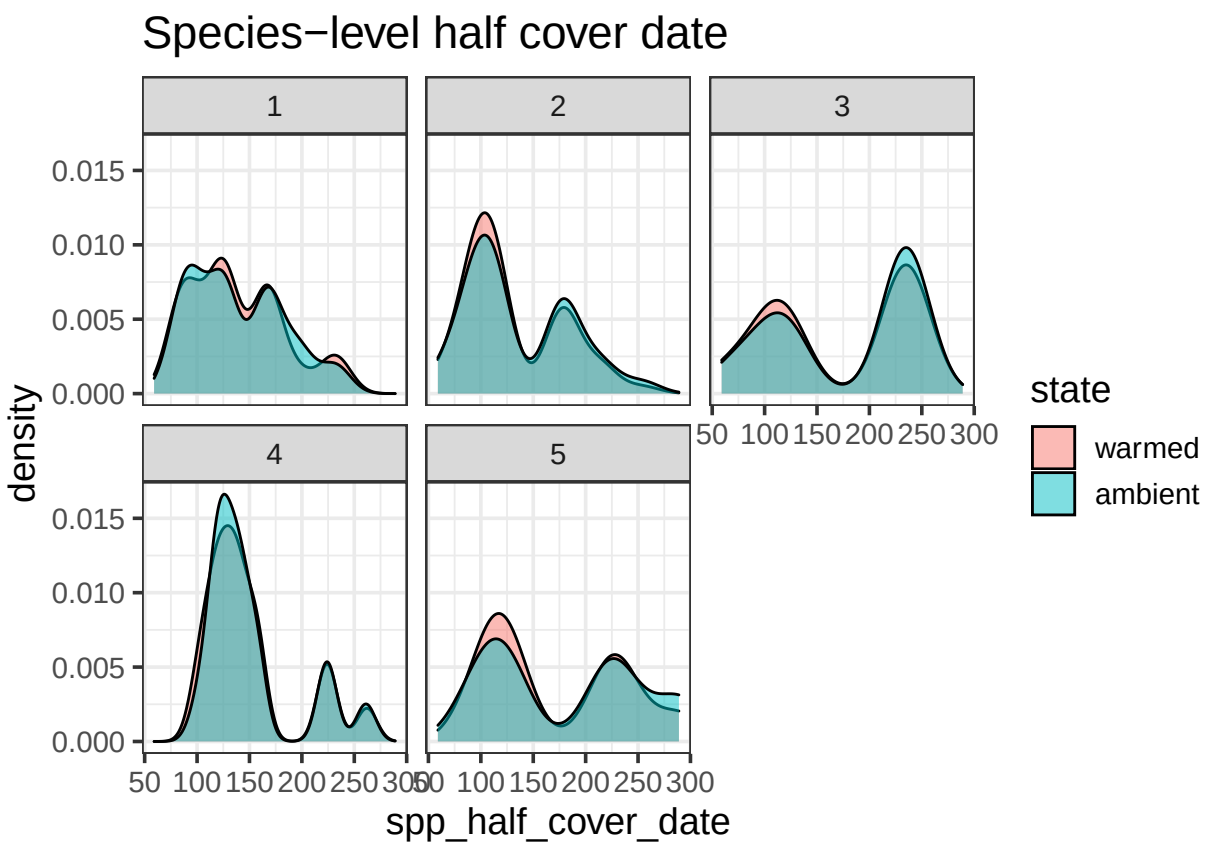

```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
    geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```



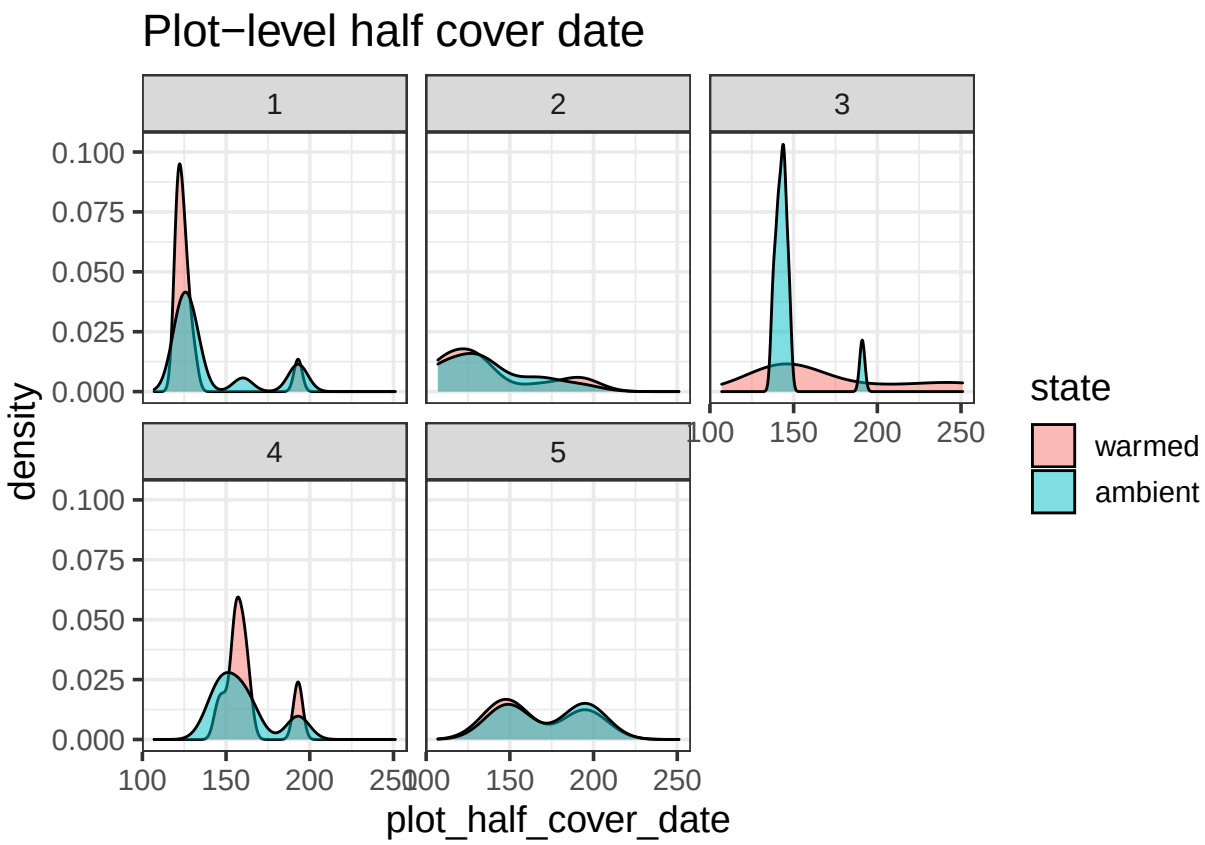

```
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



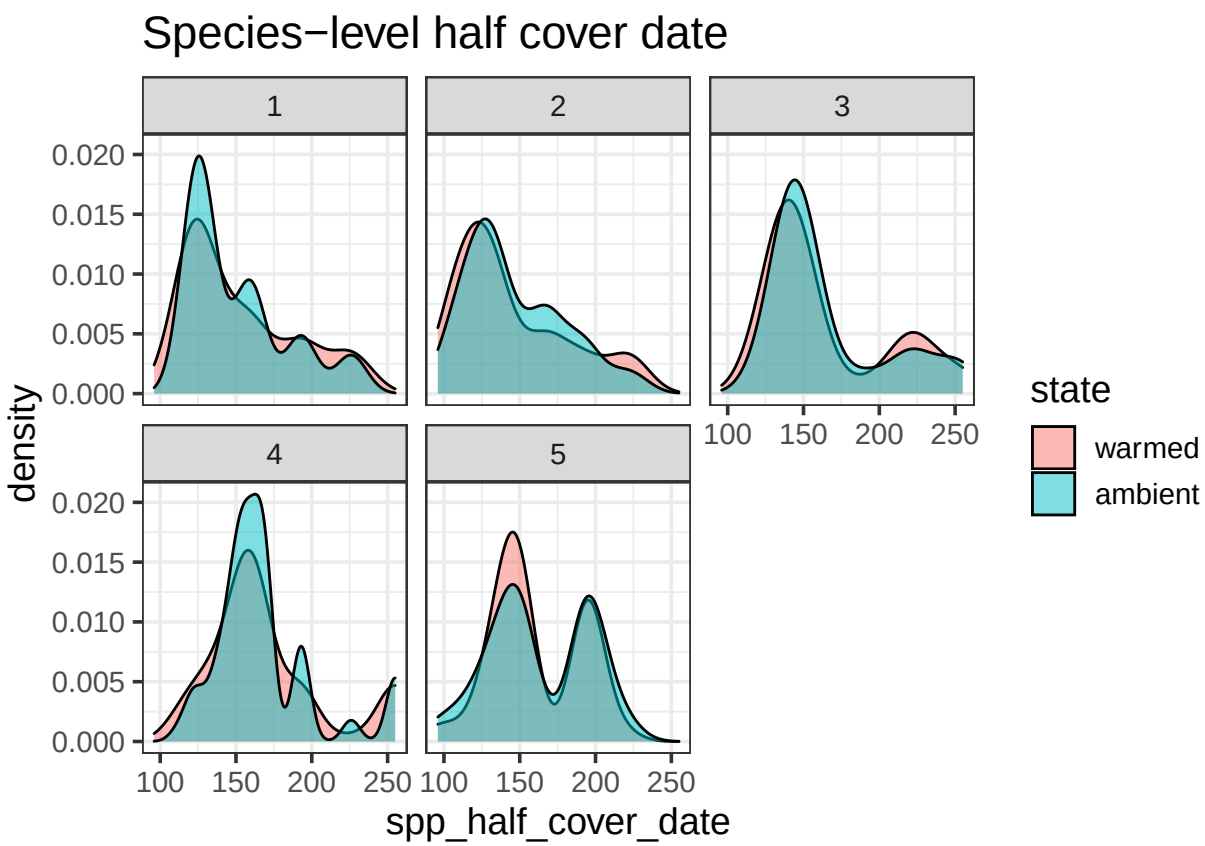

```
p3.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



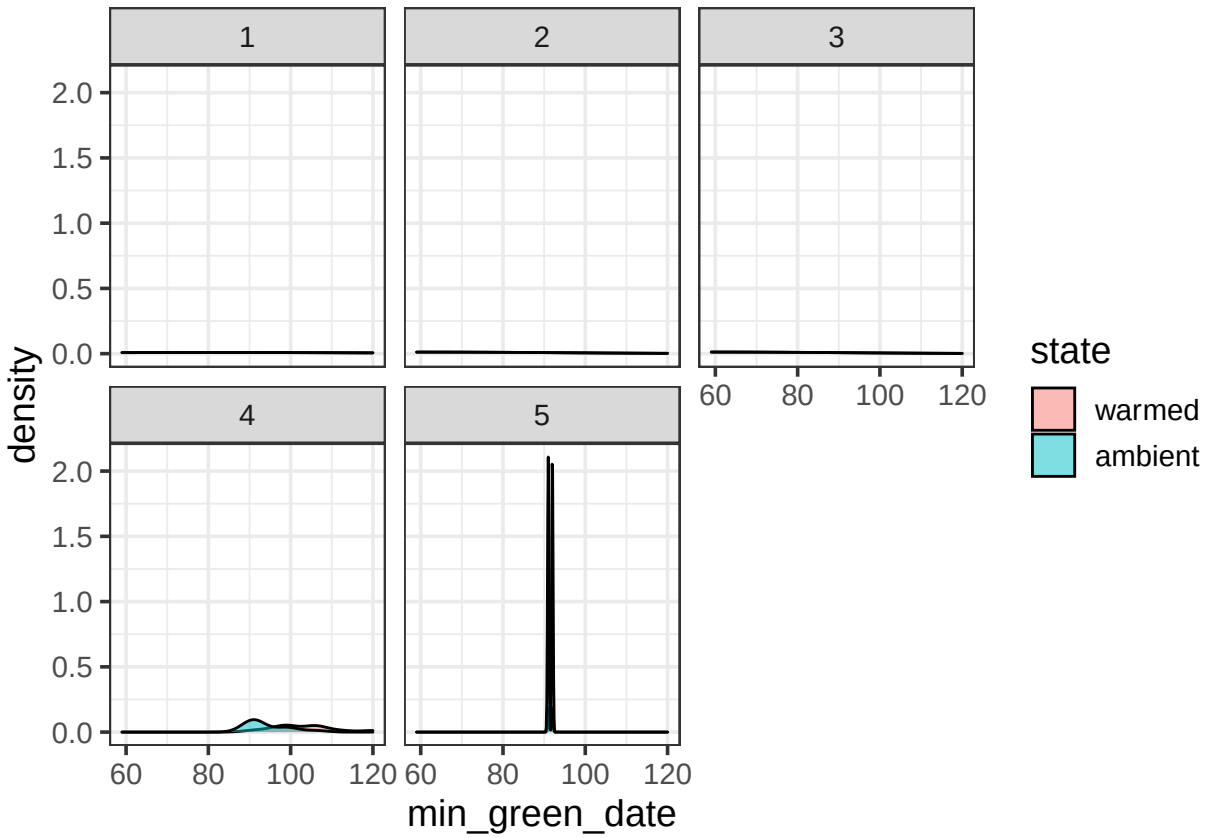

```
p3u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```




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




```
# 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)
```




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

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

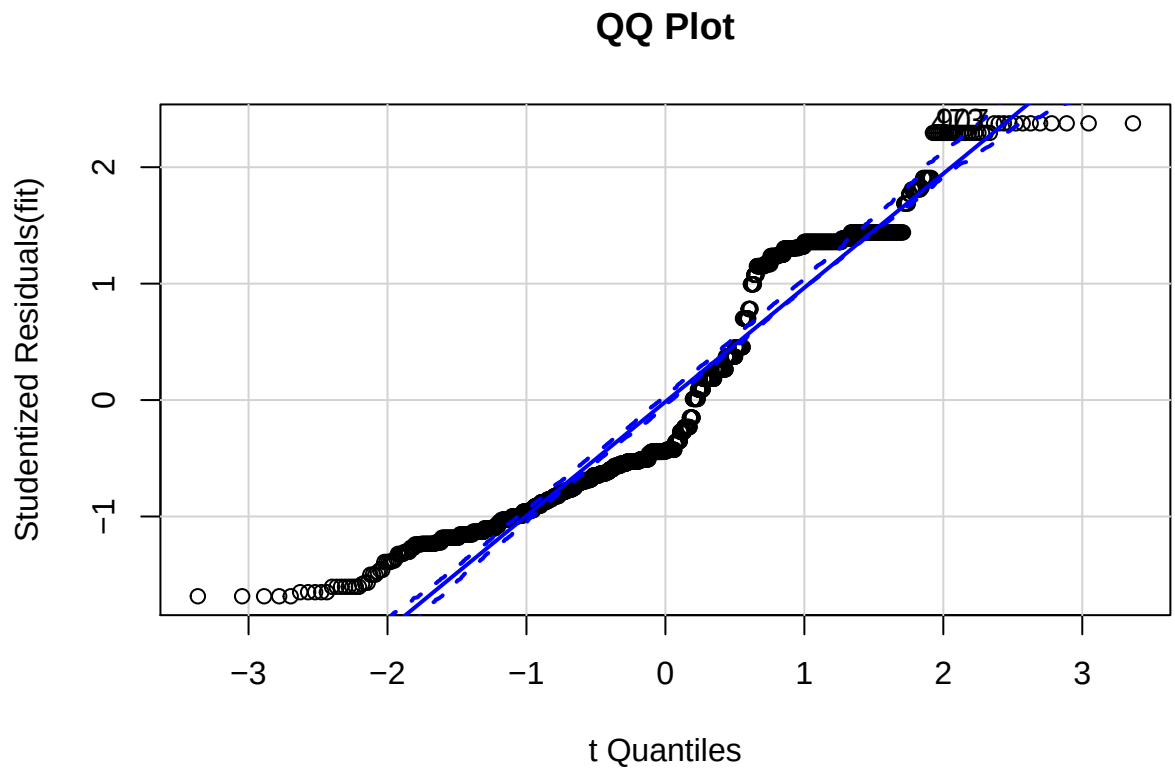
Leverage plots and detecting Outliers. https://www.statmethods.net/stats/rdiagnostics.html

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.

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

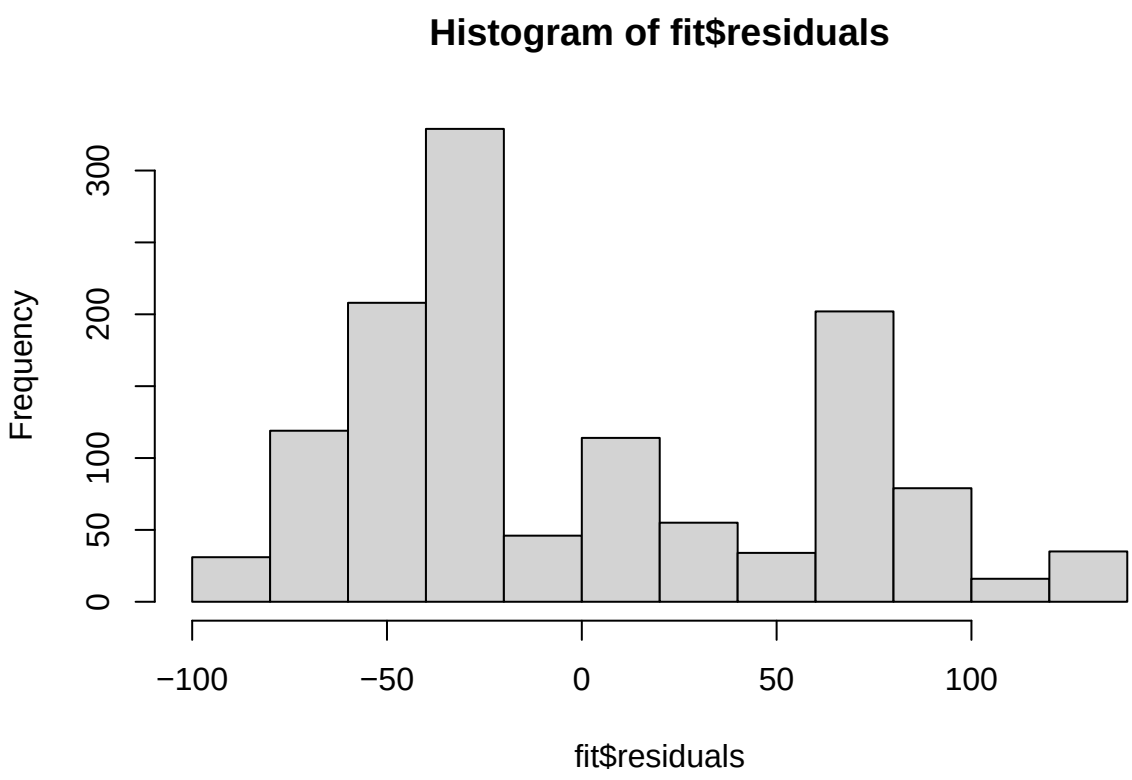
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 473 2.376821           0.017611           NA
```

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

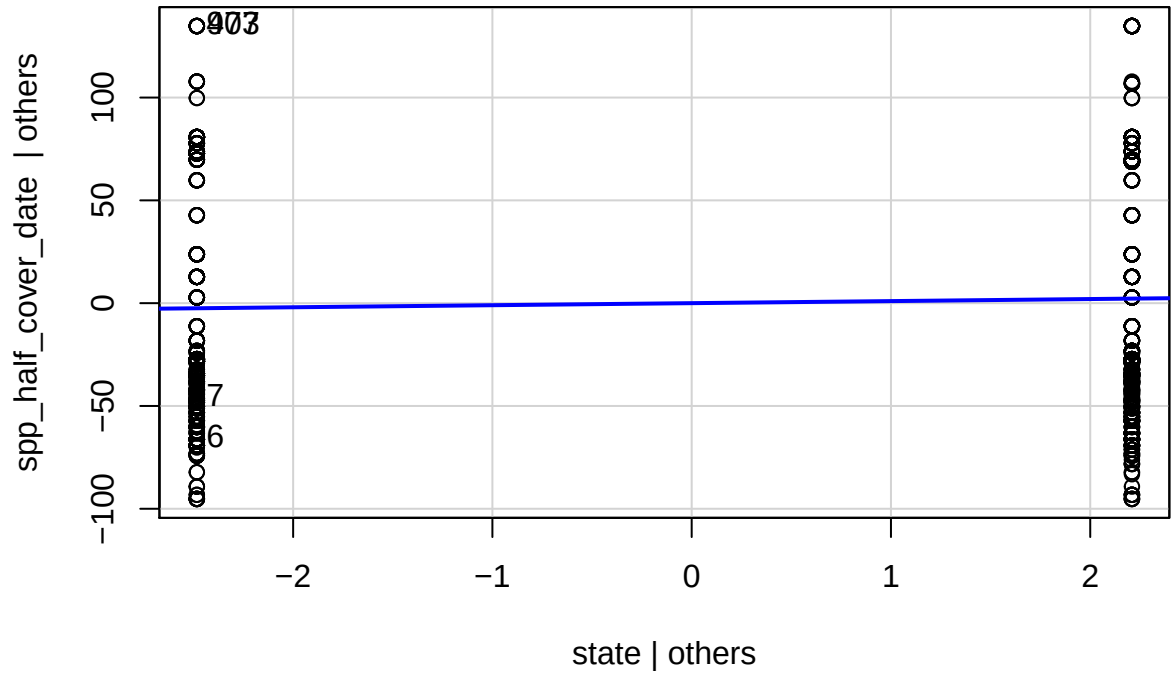



```
## 473 907
## 283 552
```

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



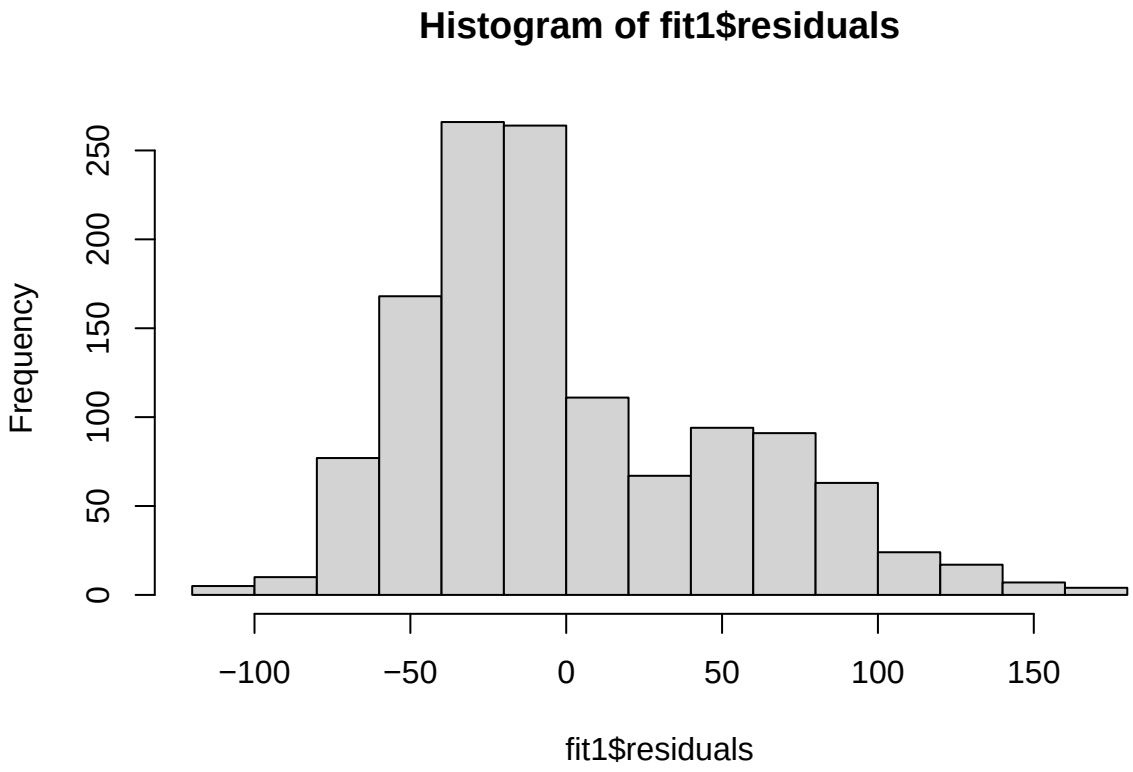
```r
leveragePlots(fit)
```




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

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

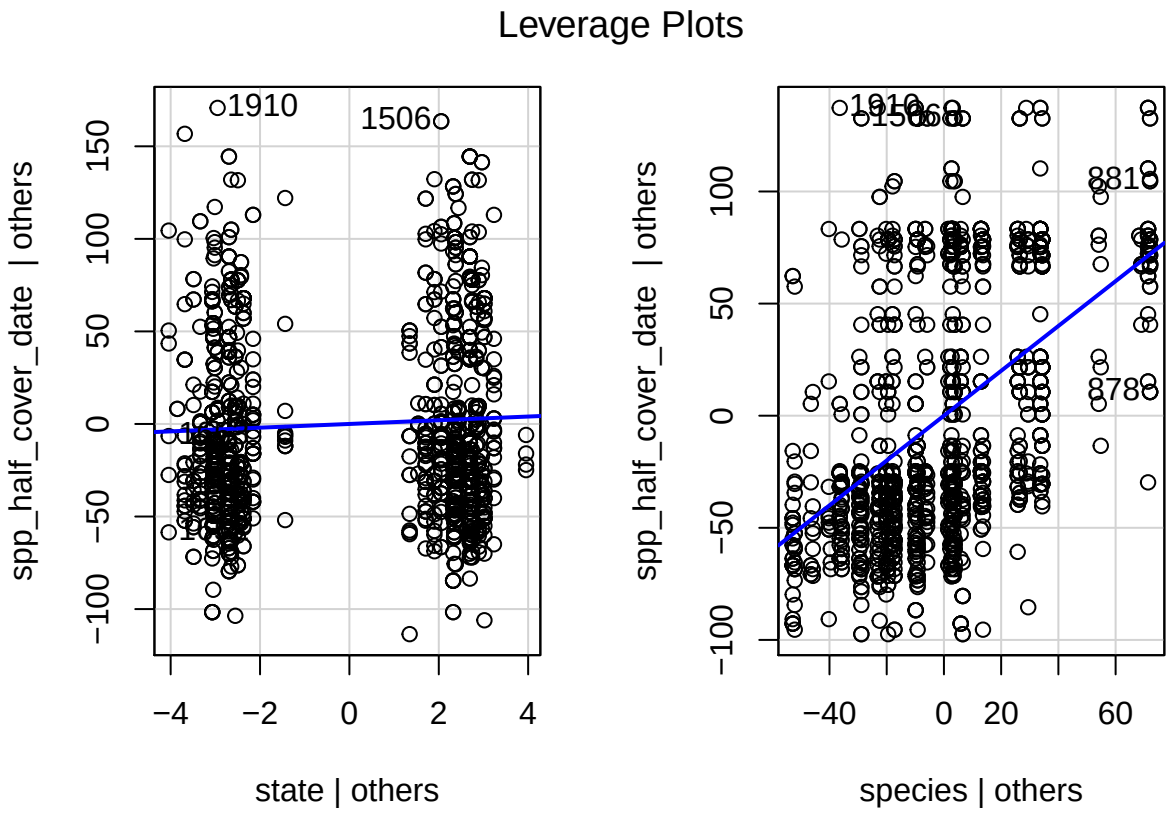
```r
hist(fit1$residuals)
```




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


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

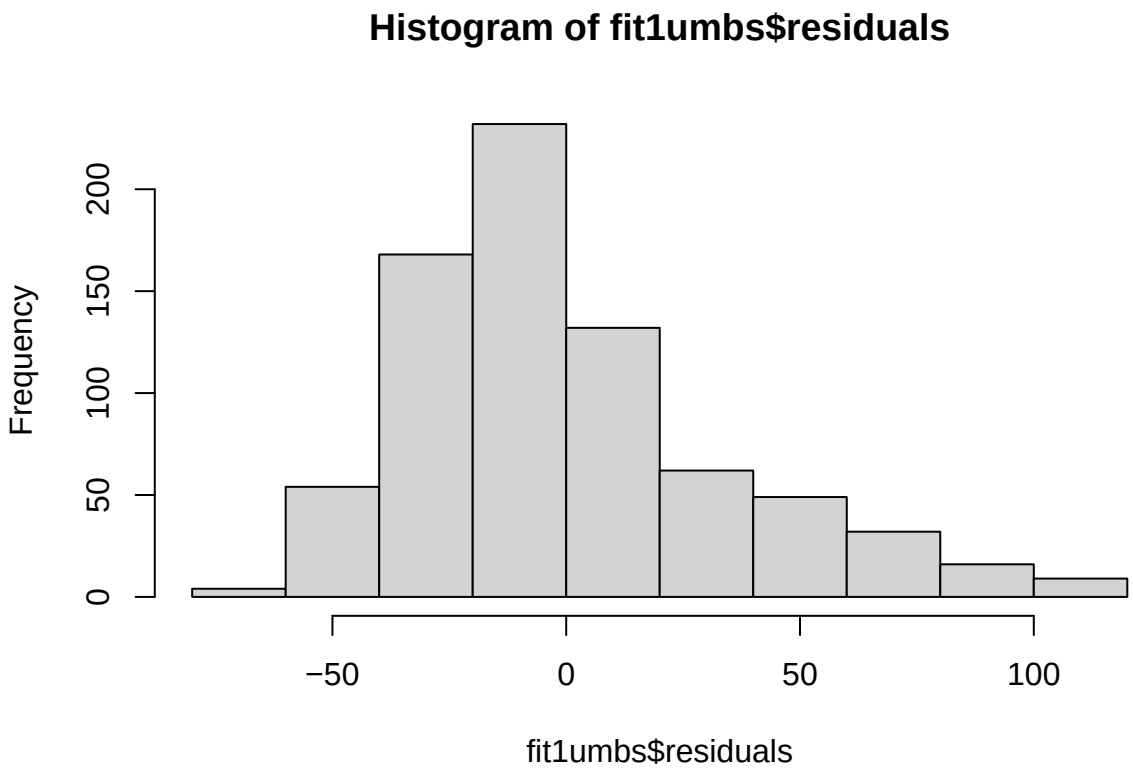
```r
leveragePlots(fit1)
```



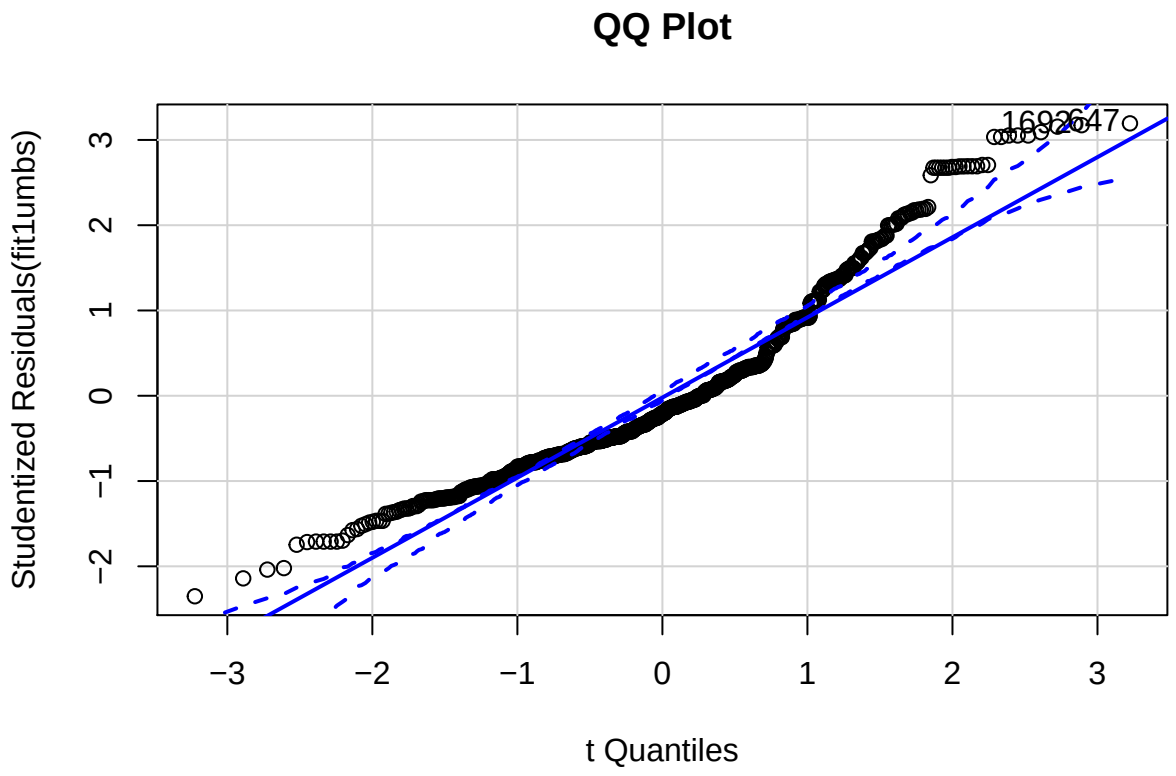

```r
# UMBS State and species model
fit1umbs <- lm(spp_half_cover_date ~ state + species, data = green_umbs)
outlierTest(fit1umbs)  # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 647 3.194361          0.0014607           NA
```

```r
hist(fit1umbs$residuals)
```

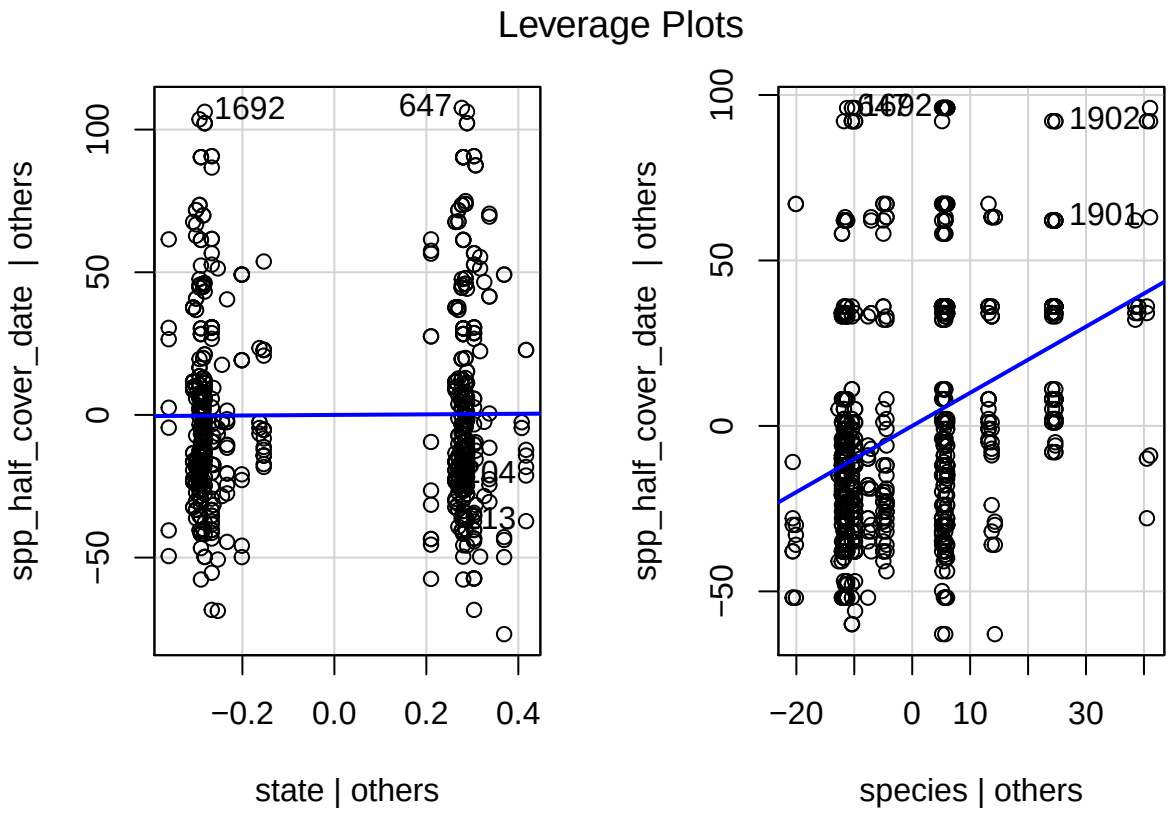



```
qqPlot(fit1umbs, main = "QQ Plot")
```




```
##  647 1692
##  267  666
```

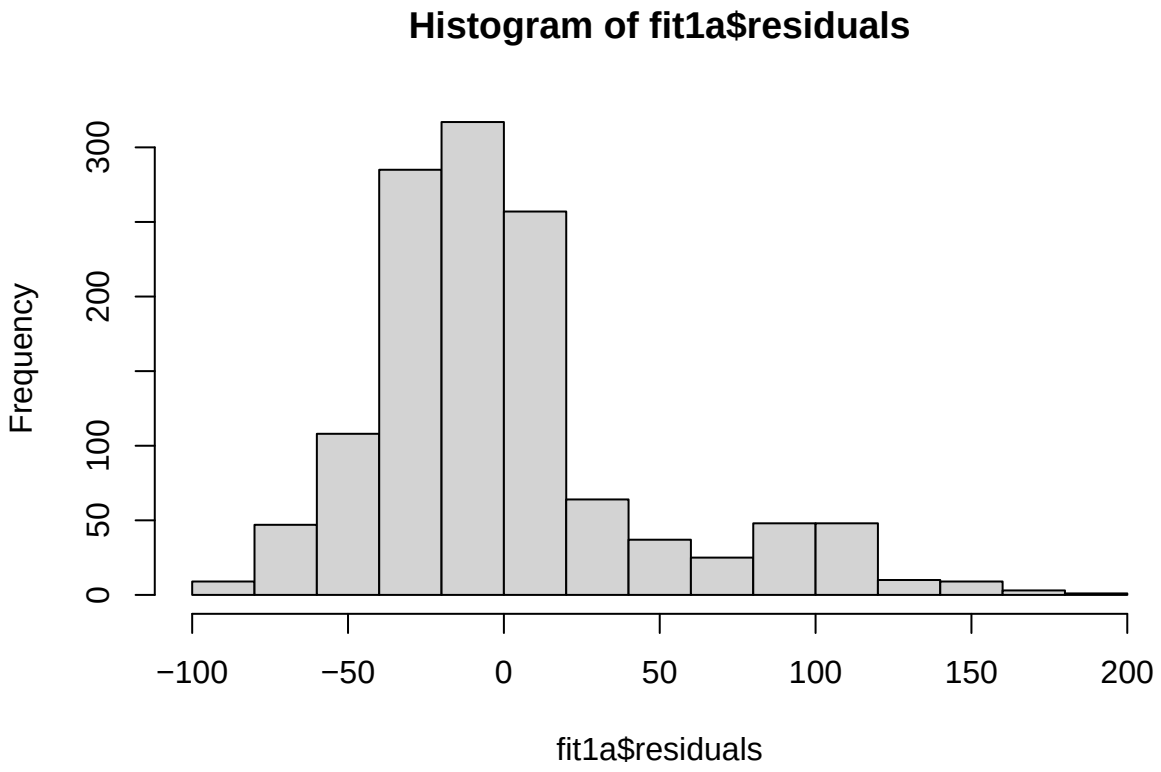
```
leveragePlots(fit1umbs)
```




```
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
```

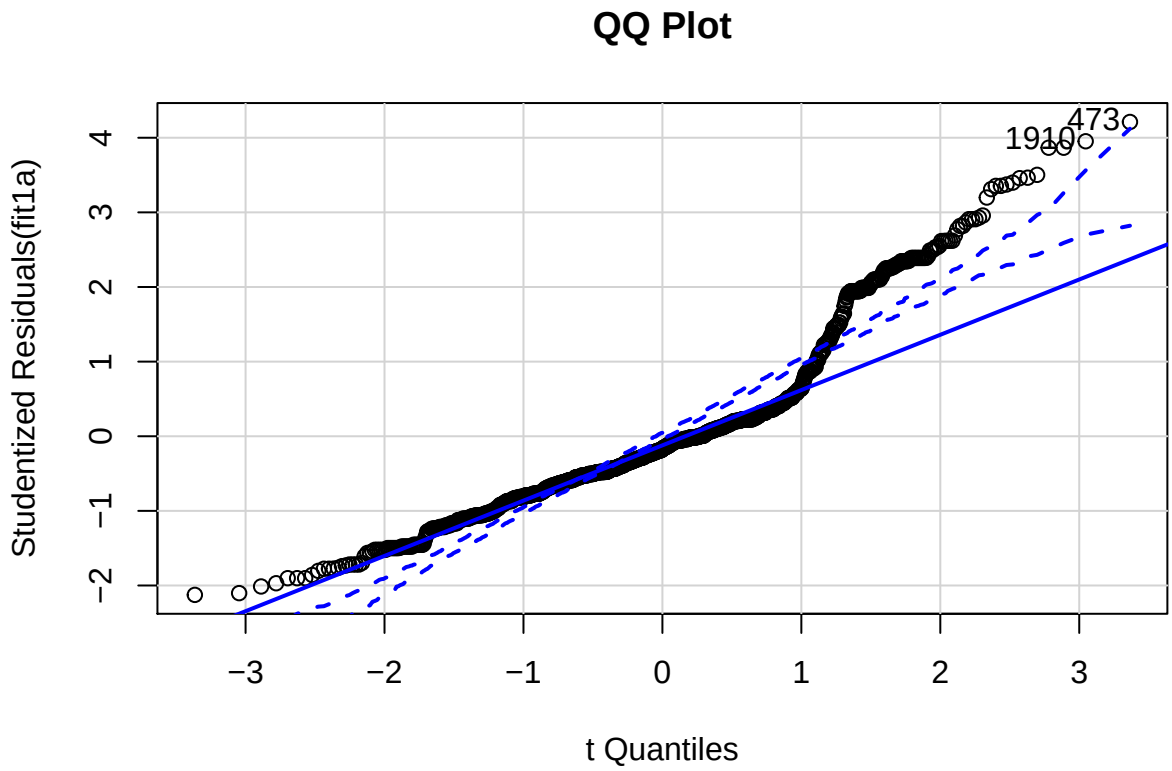
```
##     rstudent unadjusted p-value Bonferroni p
## 473 4.211351         2.7212e-05     0.034505
```

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




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

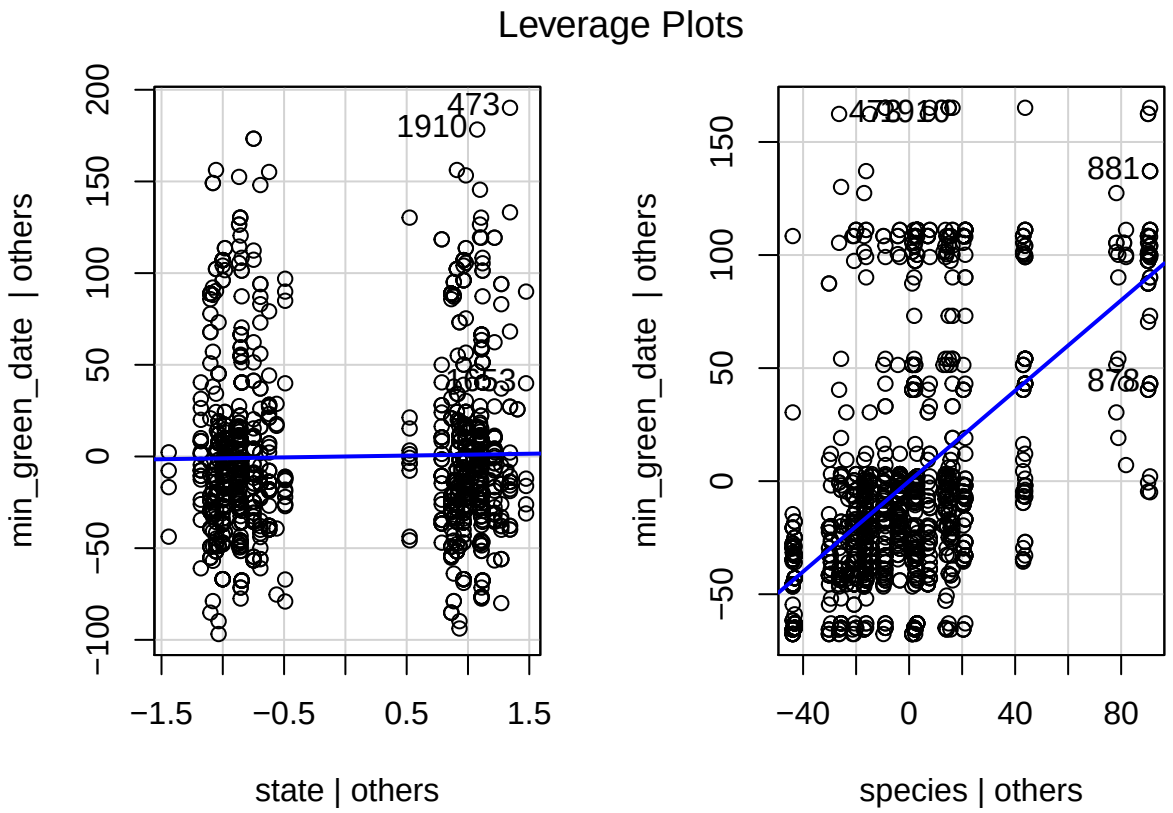
```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :
## 'rlm' failed to converge in 20 steps
```



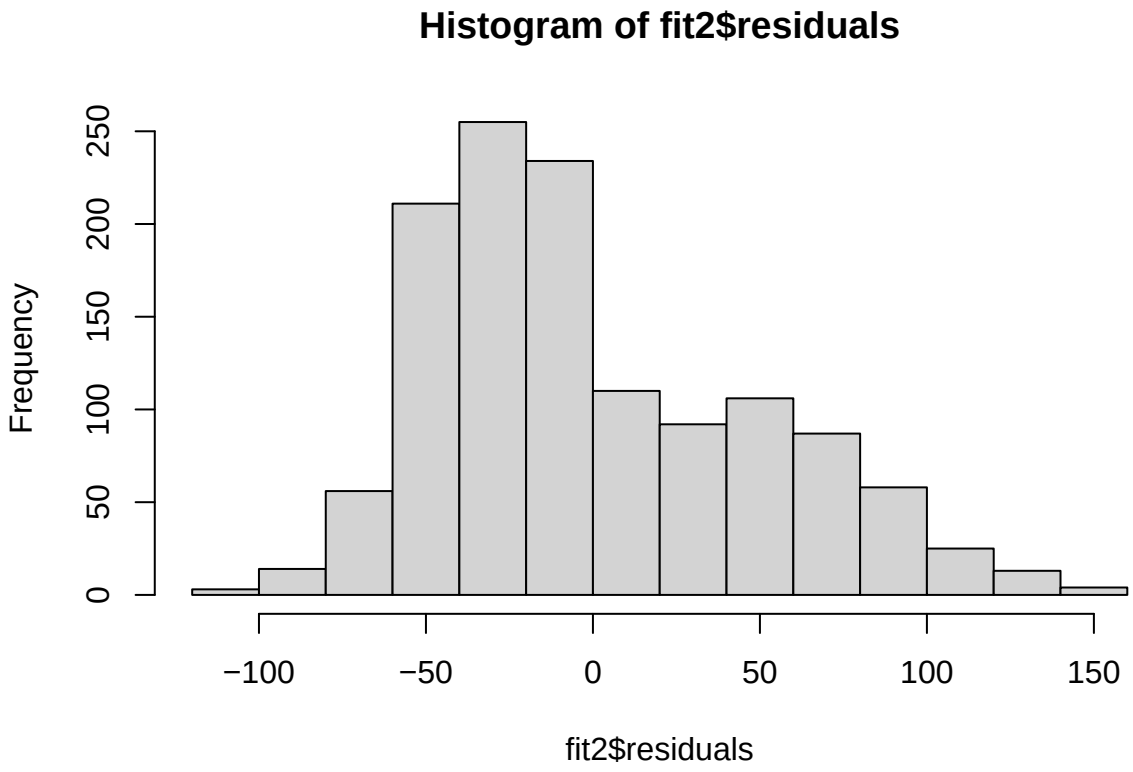

```
##  473 1910
```

```
##  283 1152
```

```
leveragePlots(fit1a)
```



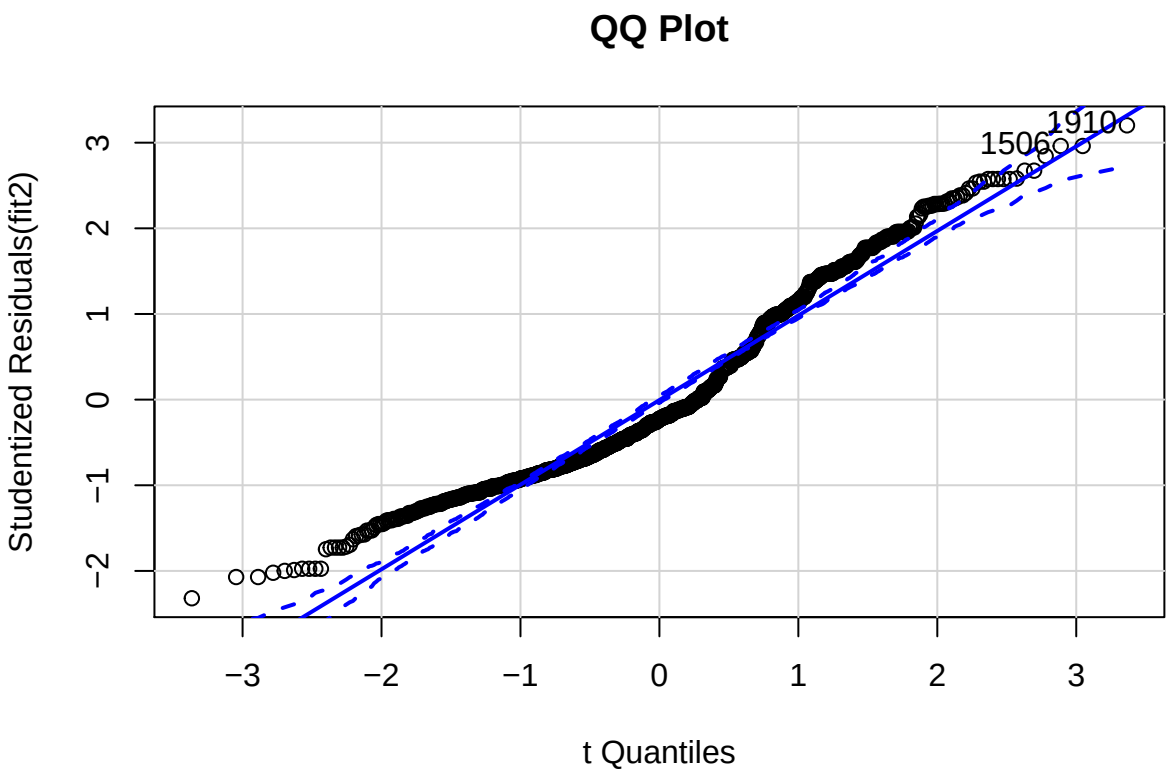

```
# checking fit for date as a function of state and year
fit2 <- lm(spp_half_cover_date ~ state + species + year, data = green_kbs)
hist(fit2$residuals)
```




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

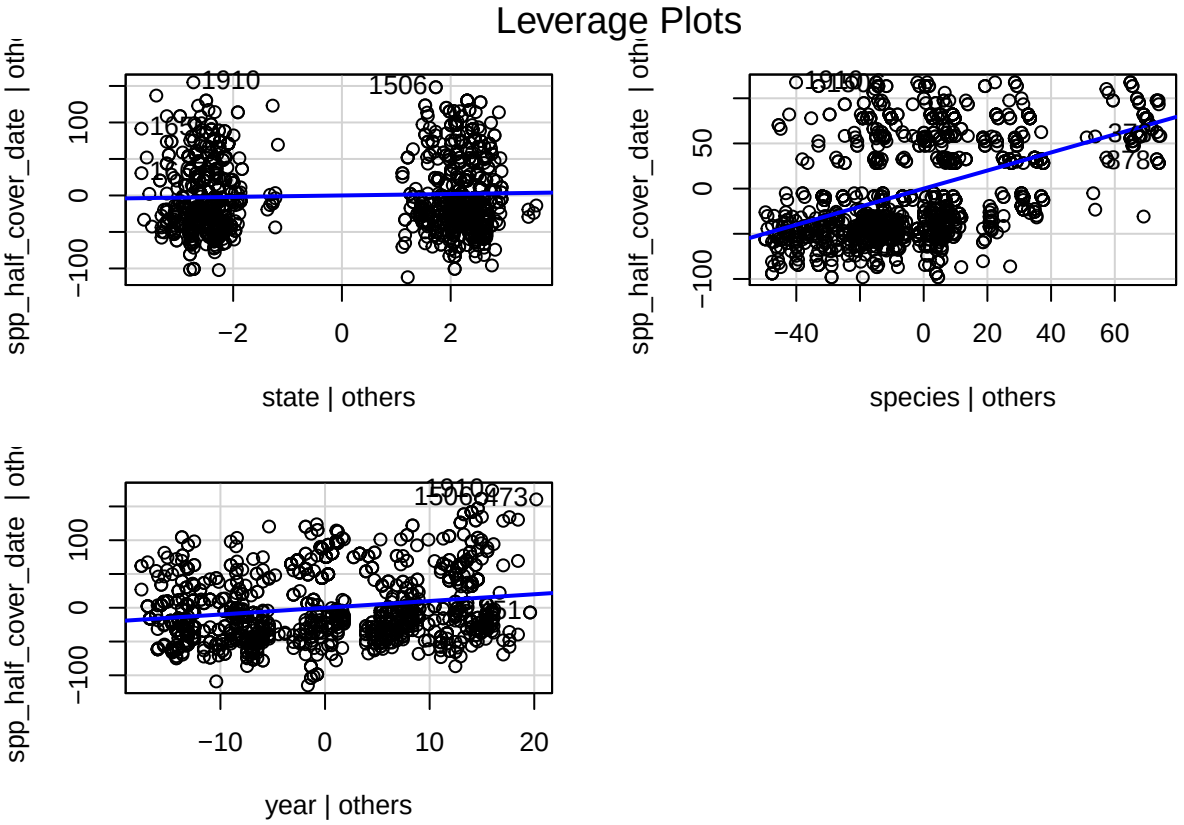
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1910 3.202366          0.0013976           NA
```

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




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

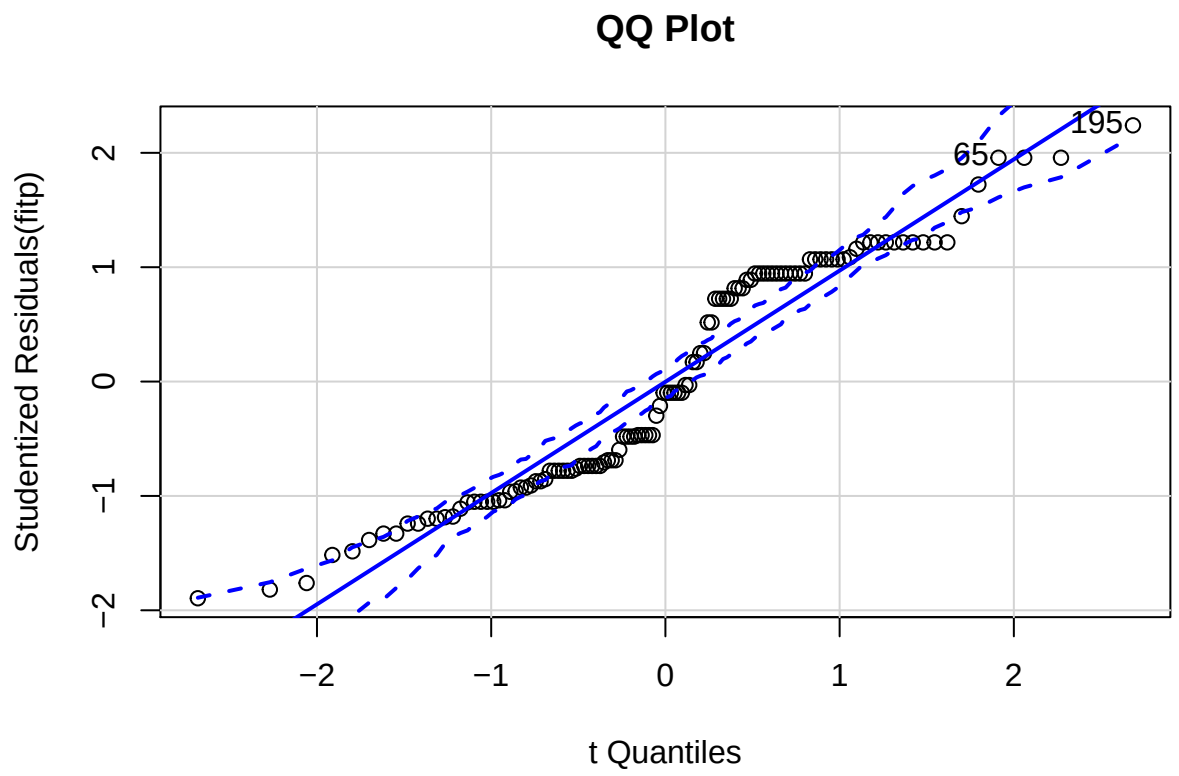
```
leveragePlots(fit2)
```




```
# plot level data KBS State-only model
fitp <- lm(plot_half_cover_date ~ state, data = green_kbsp)
outlierTest(fitp)  # no outliers
```

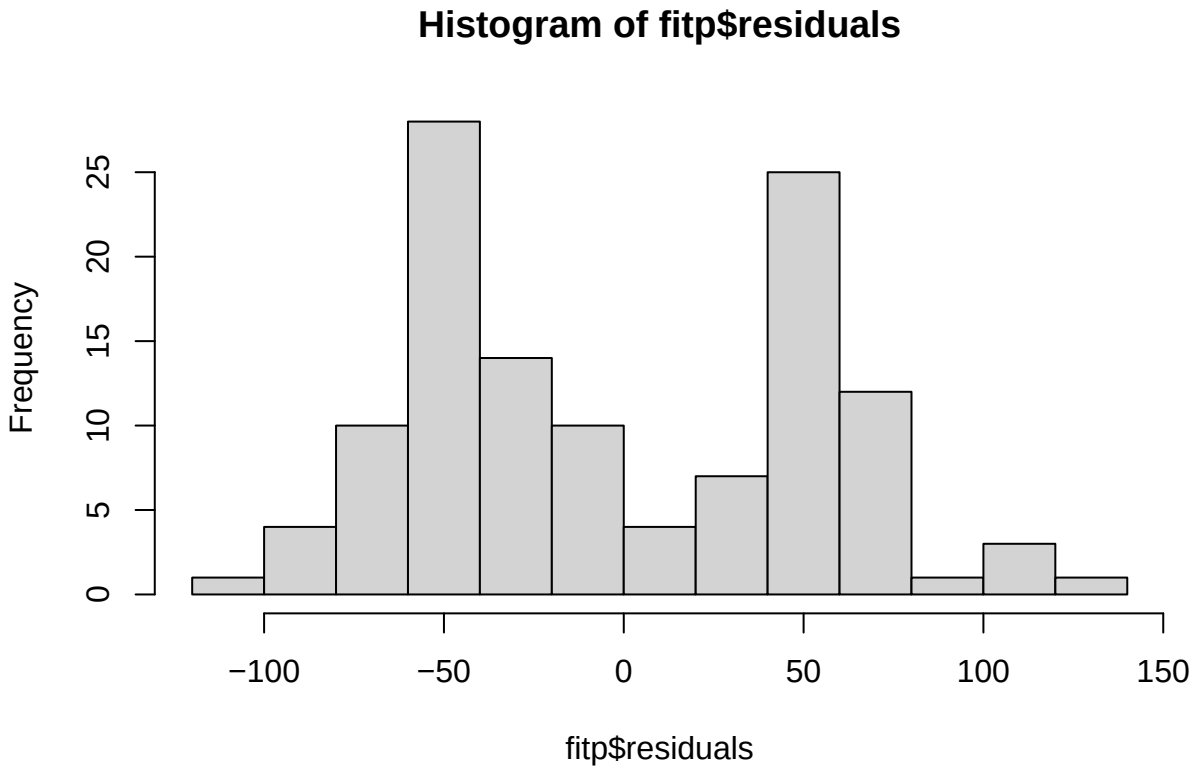
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 195 2.240402           0.026953           NA
```

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

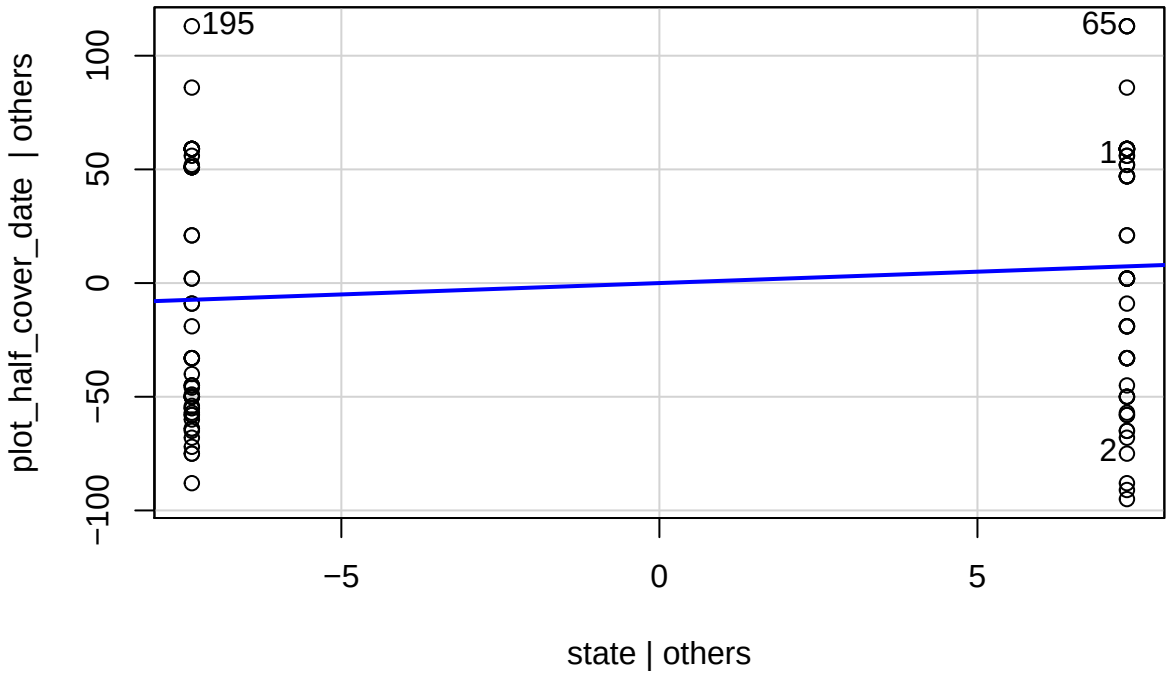



```
##  65 195
##  35 100
```

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



```r
leveragePlots(fitp)
```



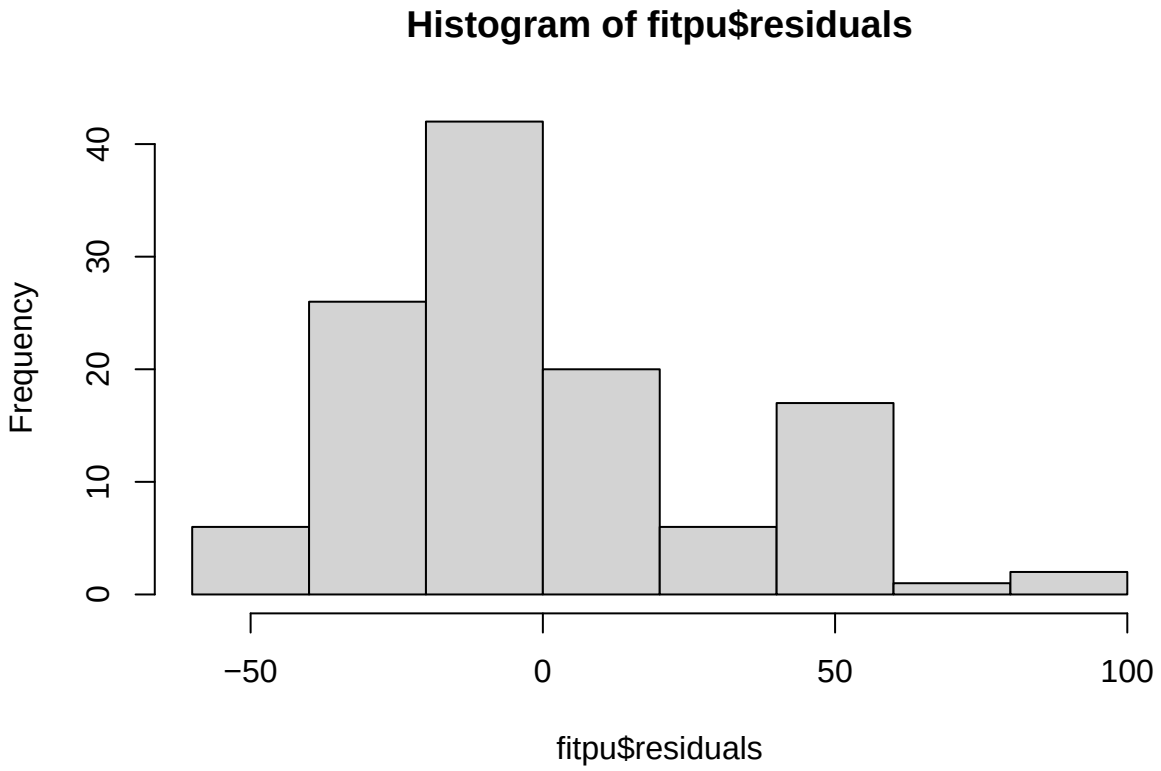

```r
# UMBS State-only model
fitpu <- lm(plot_half_cover_date ~ state, data = green_umbsp)
outlierTest(fitpu)  # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 118 3.490806         0.00068005     0.081605
```

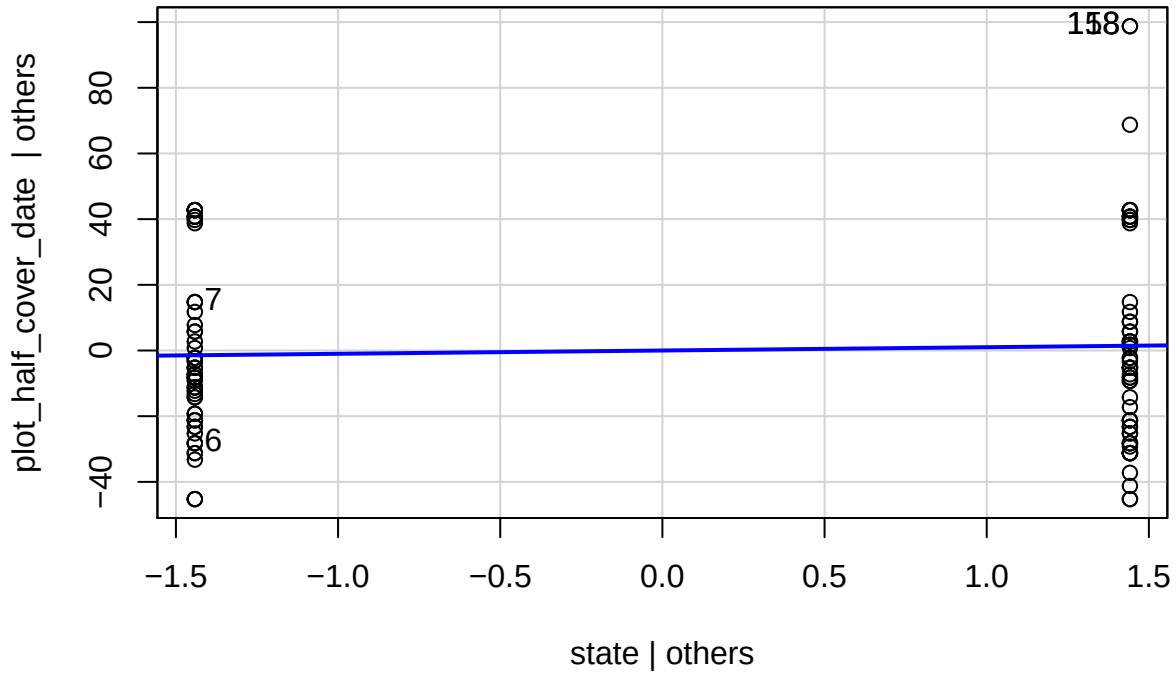
```r
qqPlot(fitpu, main = "QQ Plot")
```


```
## 118 158
##  58  78
```

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



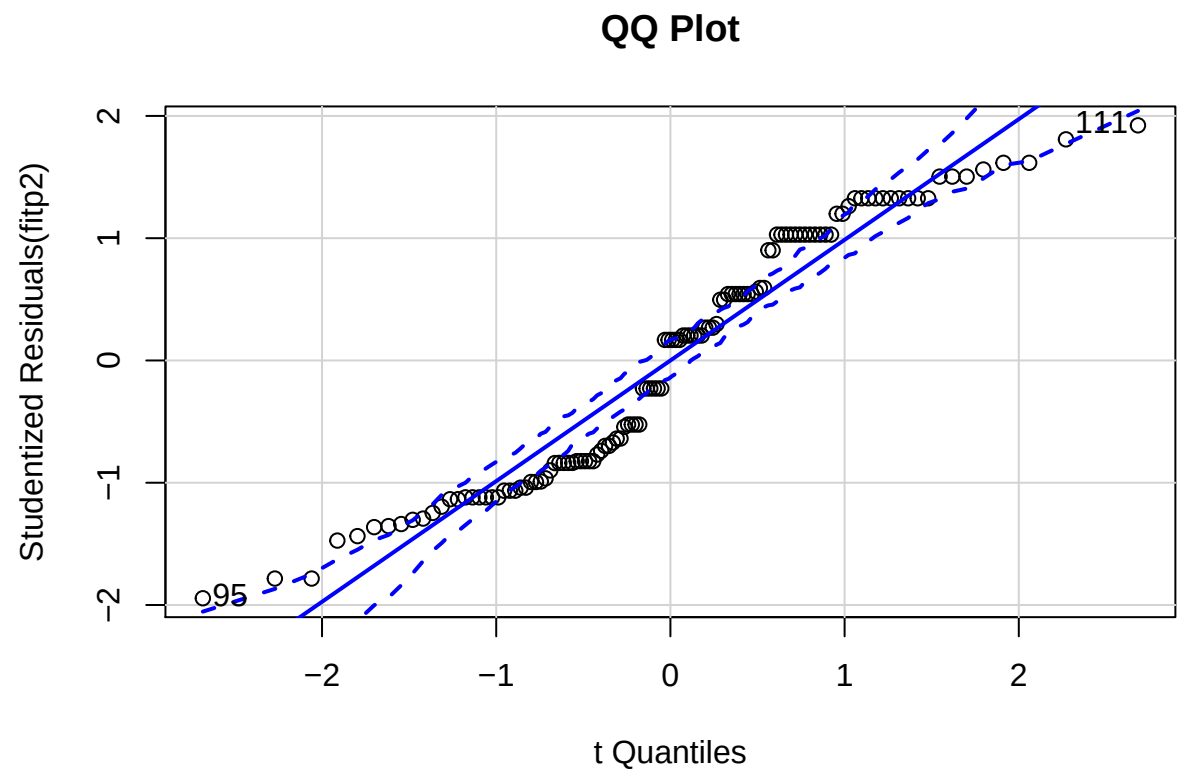
```
leveragePlots(fitpu)
```




```
# KBS State and year model
fitp2 <- lm(plot_half_cover_date ~ state + year, data = green_kbsp)
outlierTest(fitp2)  # no outliers
```

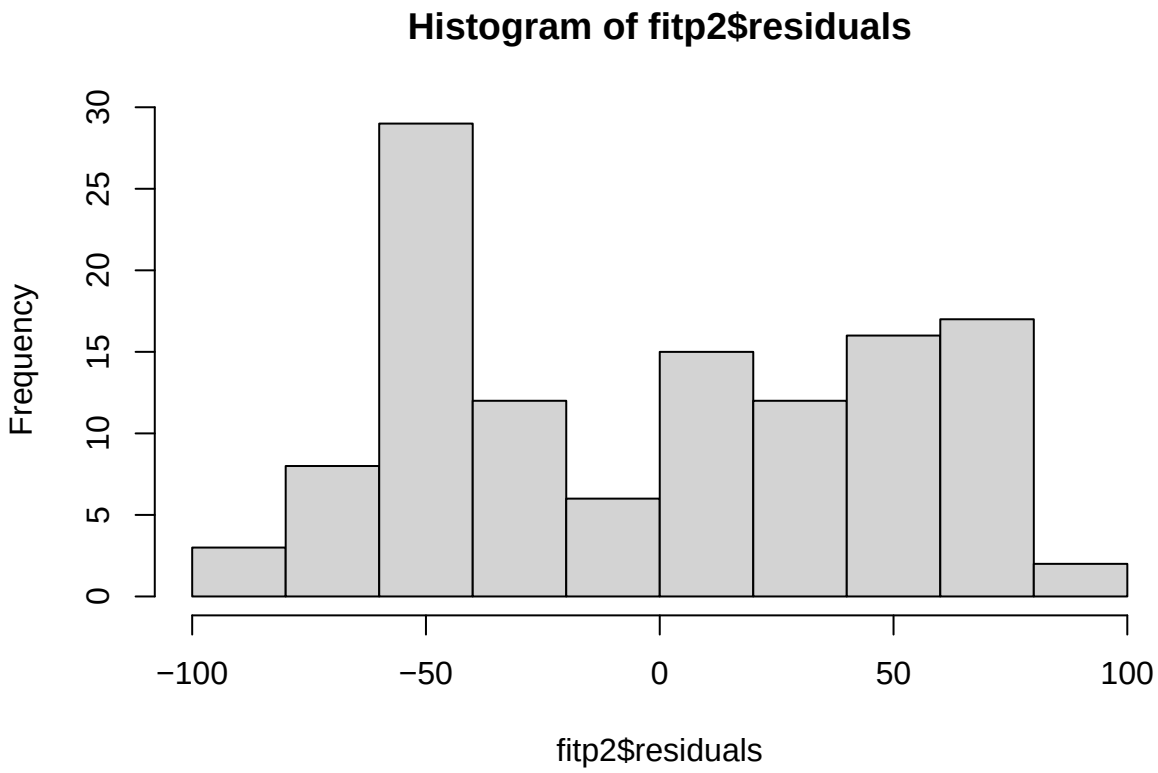
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 95 -1.944735           0.054227           NA
```

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

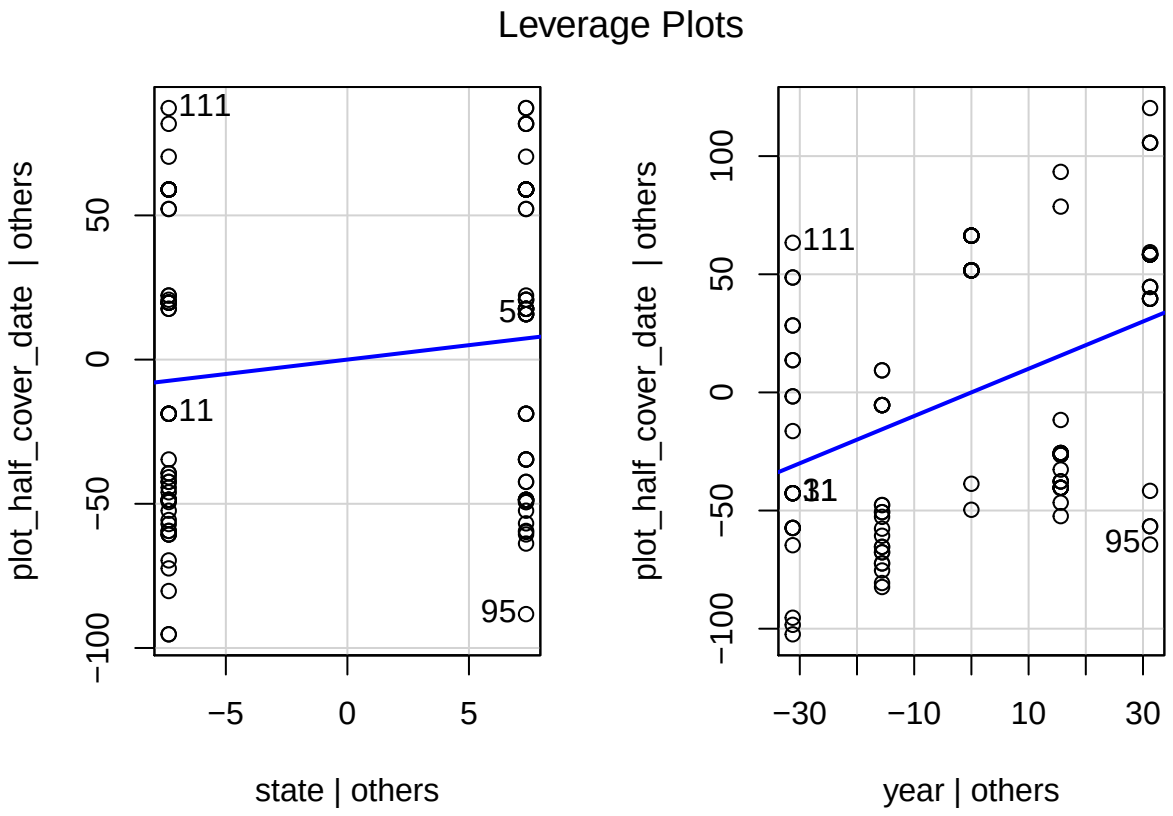



```
##  95 111
##  50  56
```

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



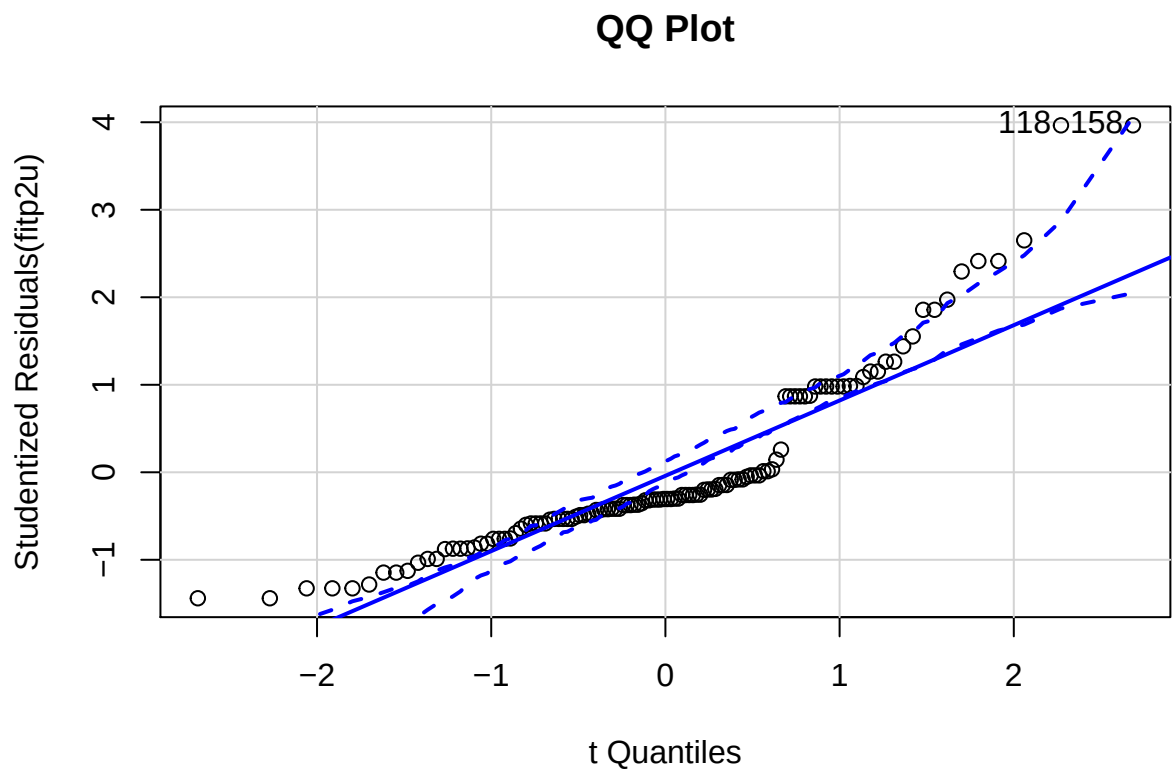
```
leveragePlots(fitp2)
```




```
# UMBS State and year model
fitp2u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
outlierTest(fitp2u)  # 118 and 158 are outliers - remove? look like the only plots with a half cover da
```

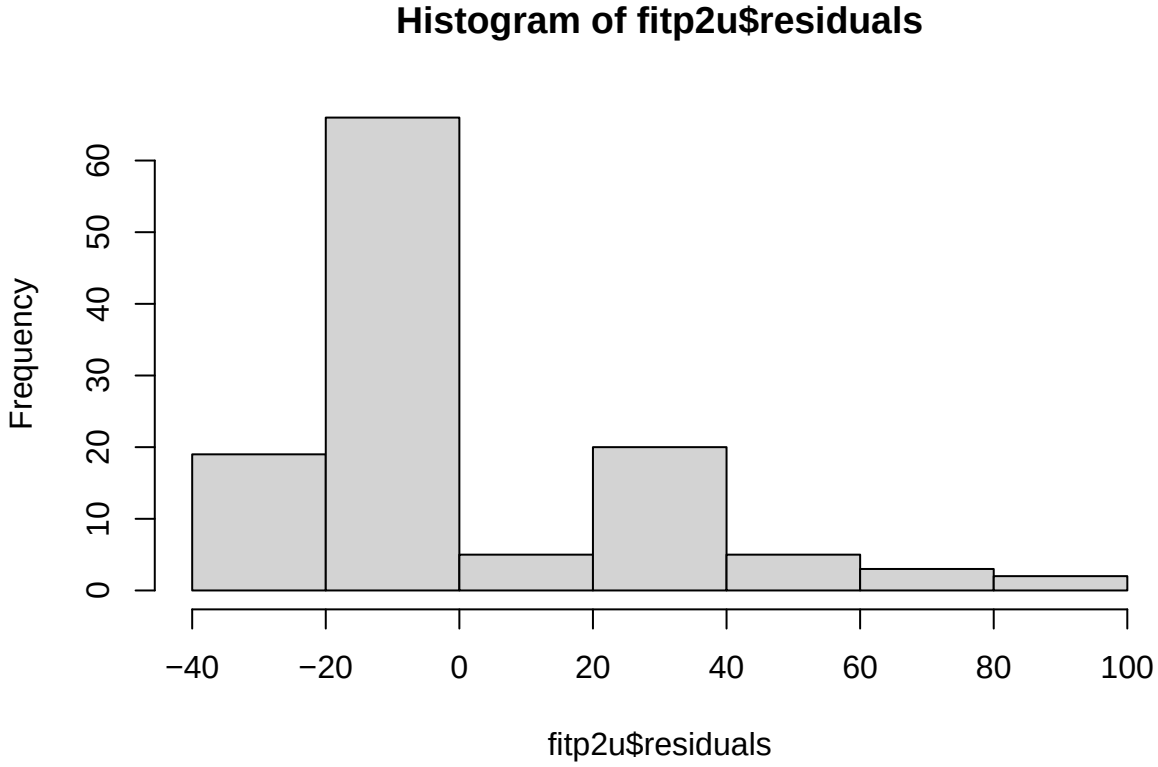
```
##     rstudent unadjusted p-value Bonferroni p
## 118 3.964625         0.00012753     0.015303
## 158 3.964625         0.00012753     0.015303
```

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

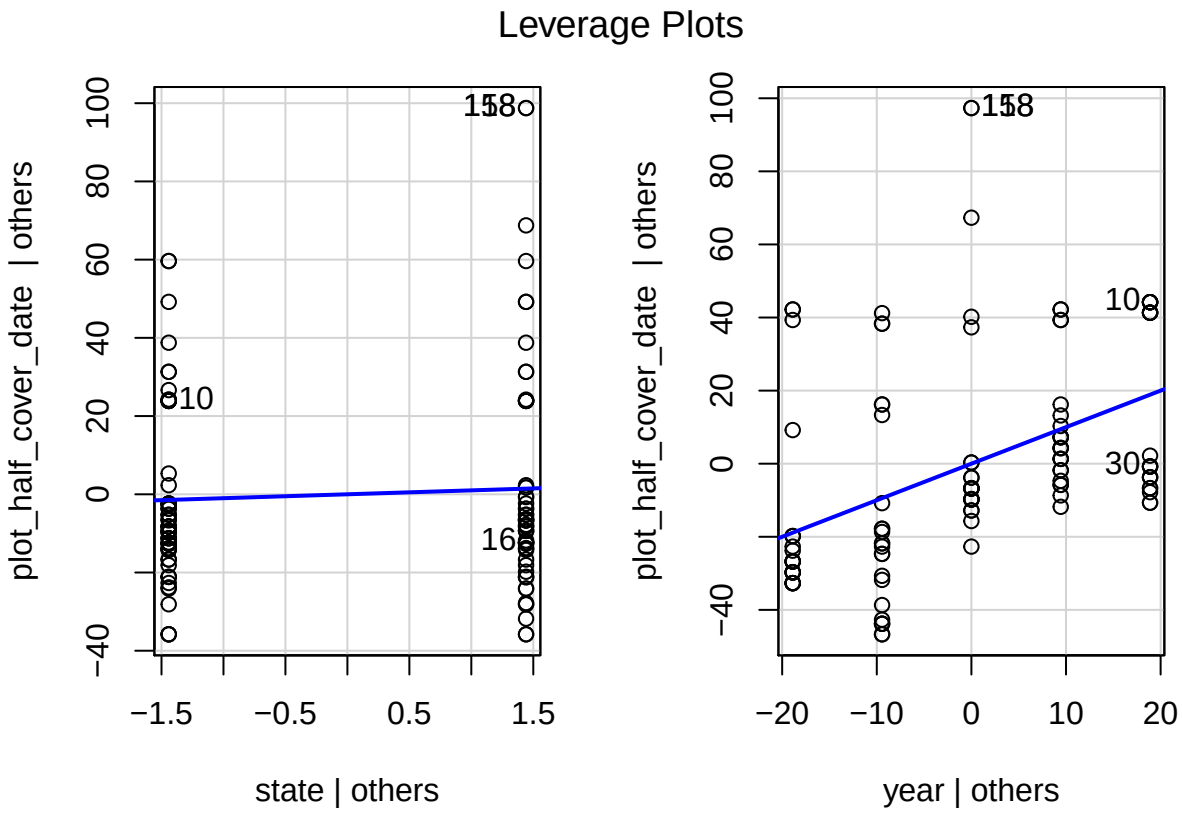



```
## 118 158
##  58  78
```

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



```
leveragePlots(fitp2u)
```

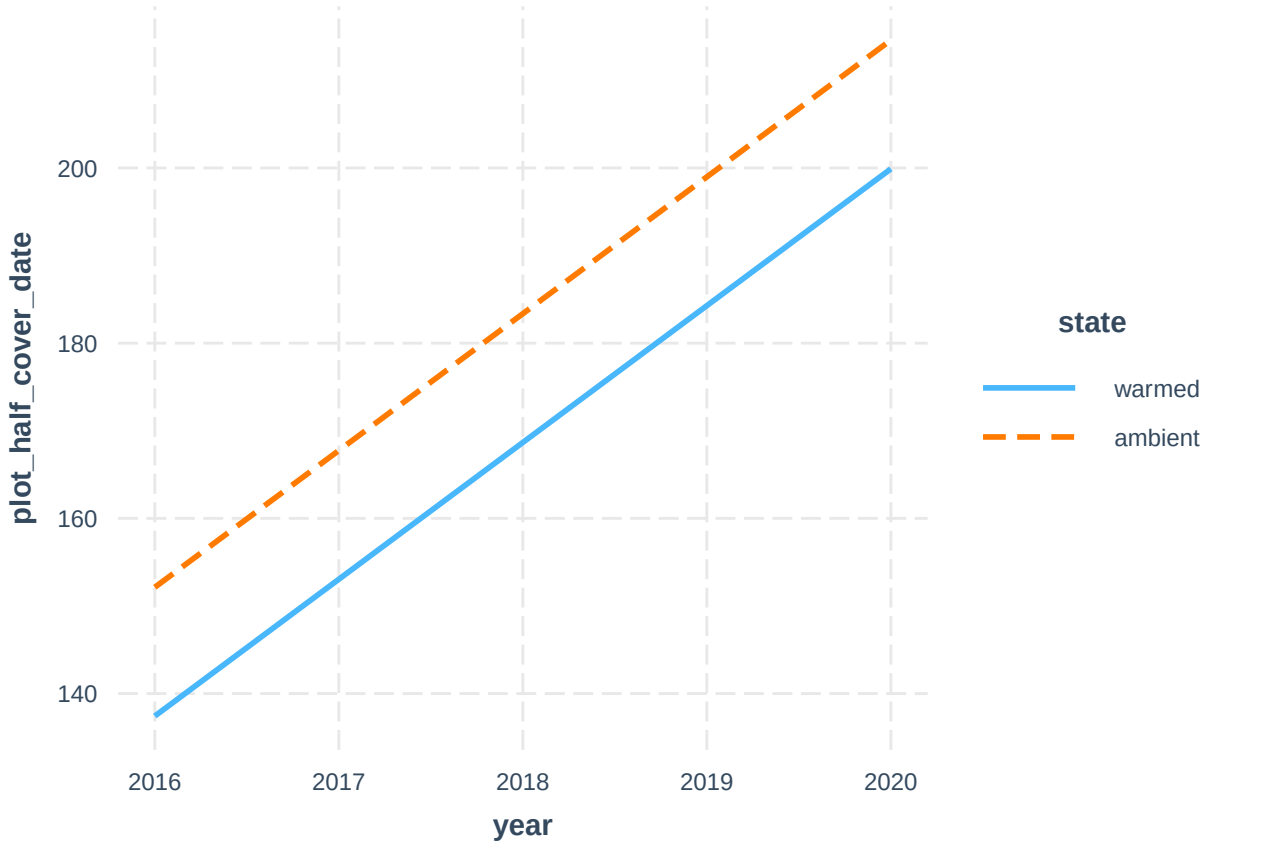


Normal distribution after accounting for species - we will be using species as a random effect to account for their variation. Set up some linear mixed effects models to evaluate. From Ben Bolker: "The traditional view of random effects is as a way to do correct statistical tests when some observations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

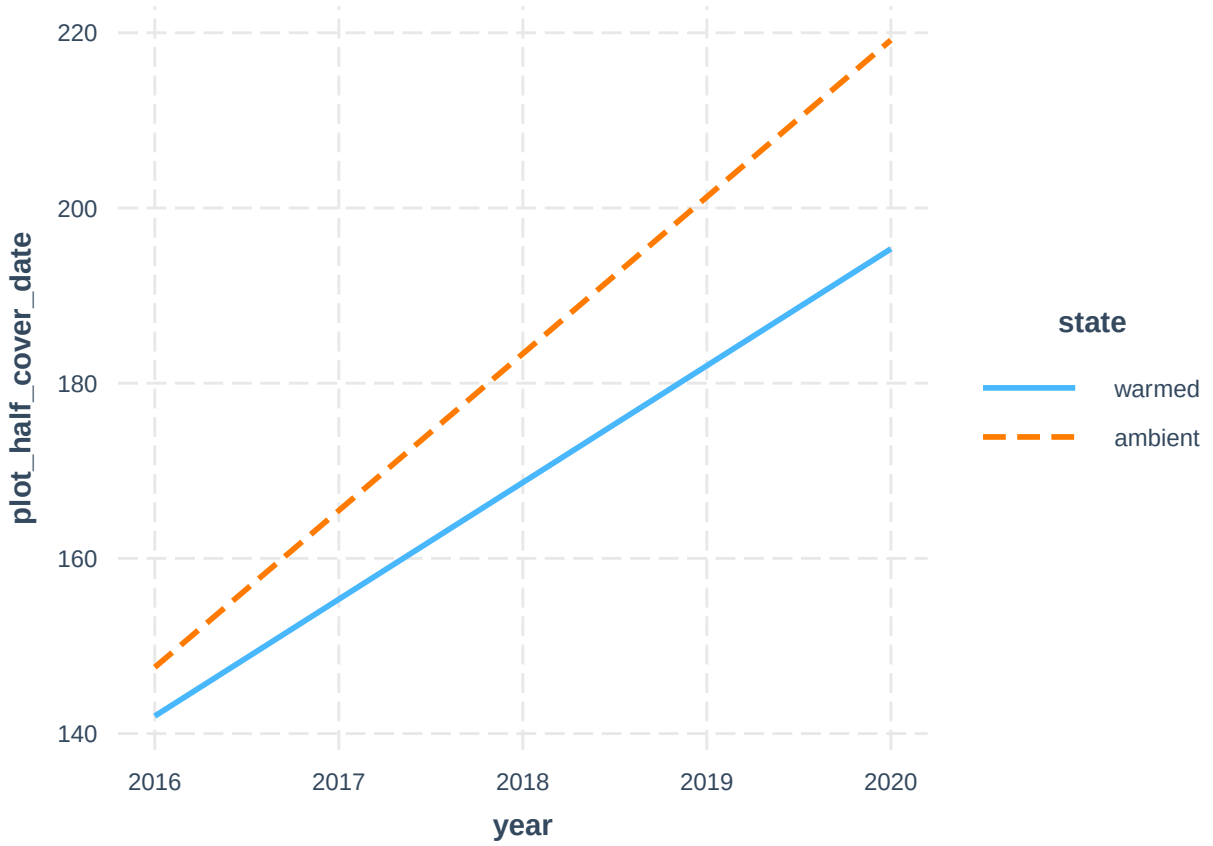
We should also think about how we're treating year. Some of the models have a state * year interaction as a fixed effect, which means that the warming or ambient treatment could affect the half_cover_date differently over time (there would be a different slope for each state in the relationship between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

# KBS
fit3 <- lm(plot_half_cover_date ~ state + year, data = green_kbsp)
interact_plot(fit3, pred = year, modx = state)
```

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

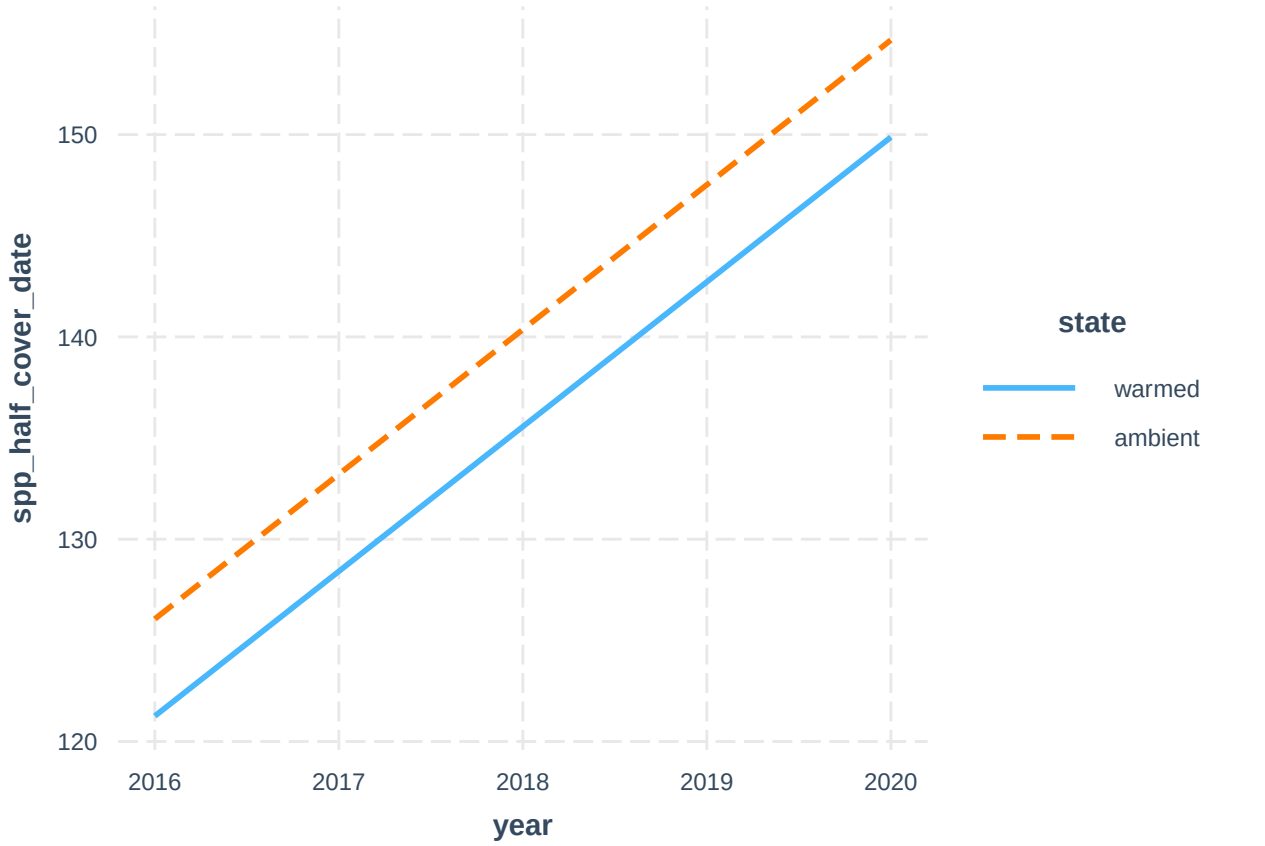



```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```




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

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

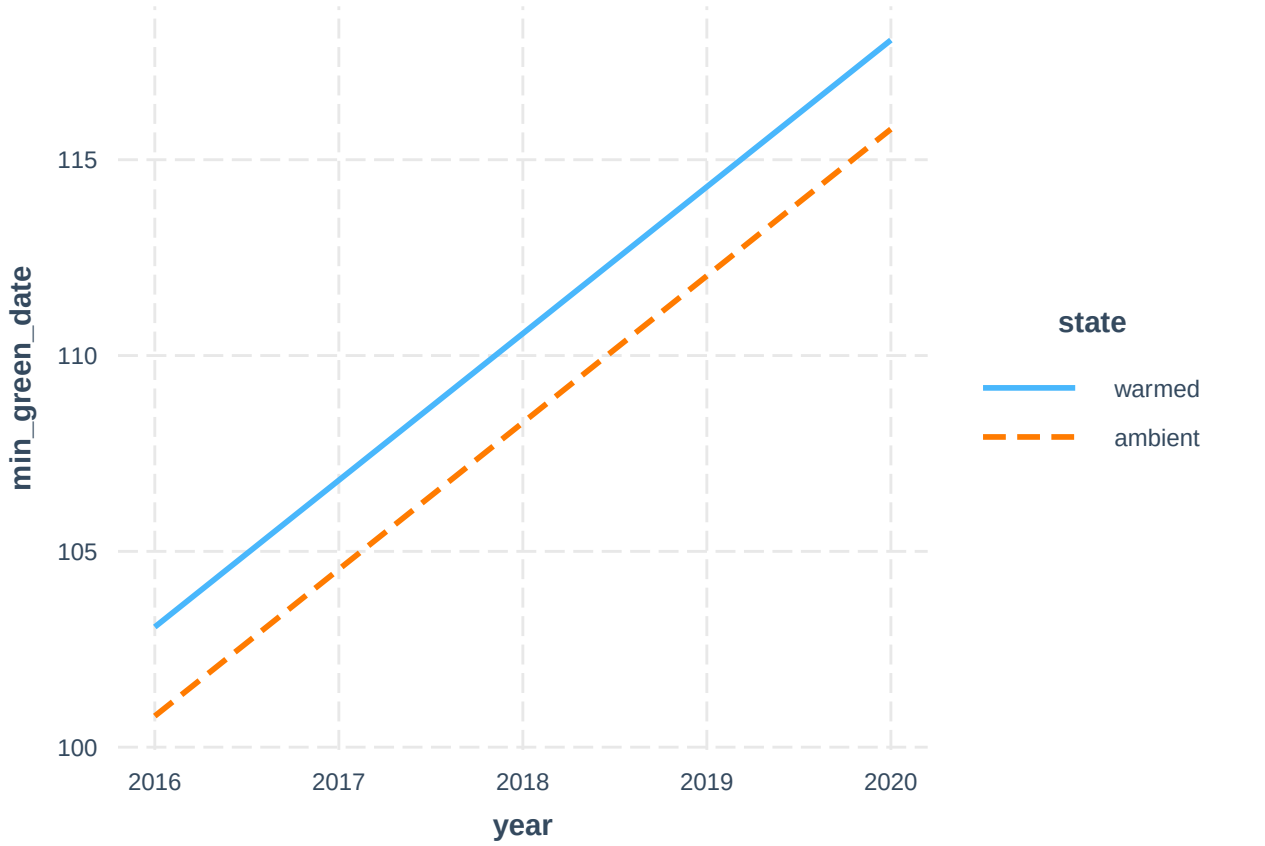



```
fit6 <- lm(spp_half_cover_date ~ state * year + species, data = green_kbs)
interact_plot(fit6, pred = year, modx = state, mod2 = species)
```

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


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

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

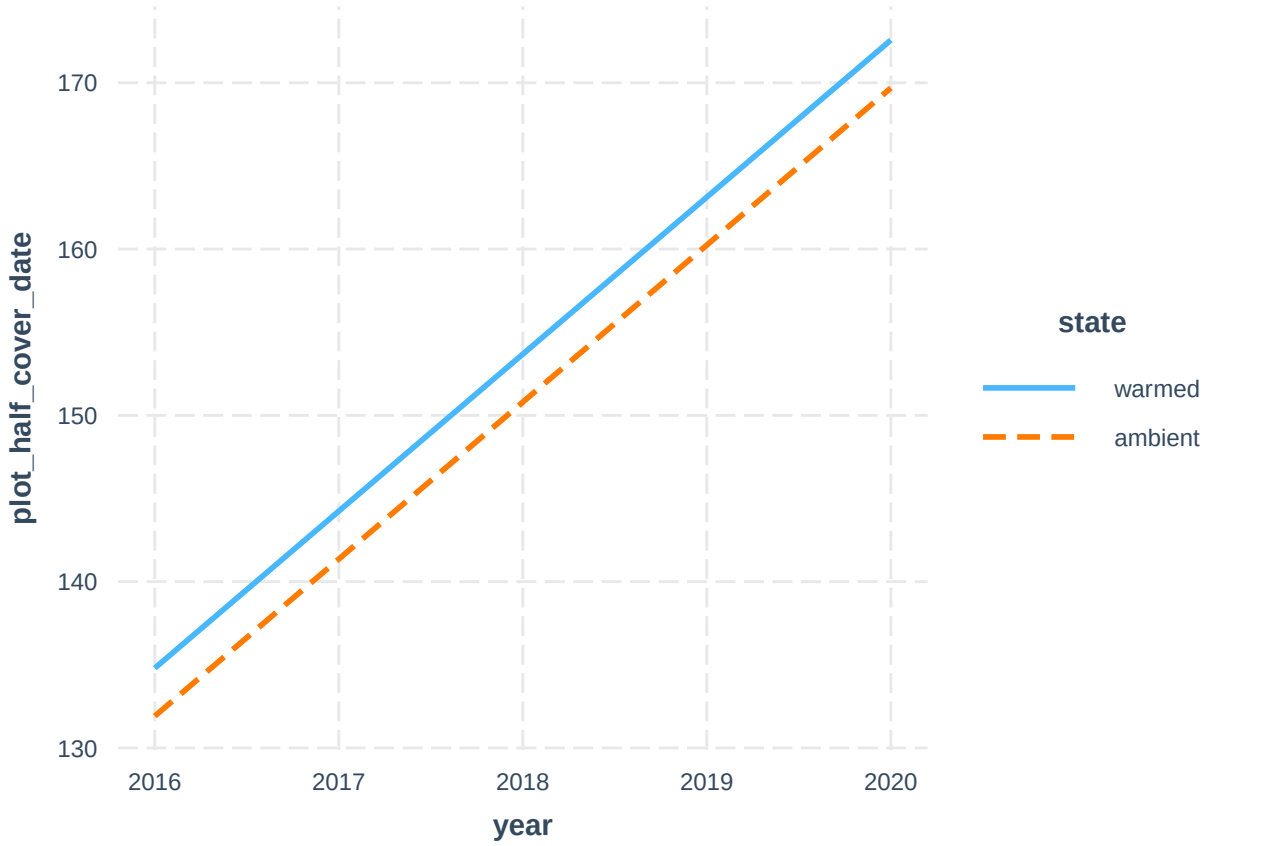



```
fit8 <- lm(min_green_date ~ state * year + species, data = green_kbs)
interact_plot(fit8, pred = year, modx = state, mod2 = species)
```

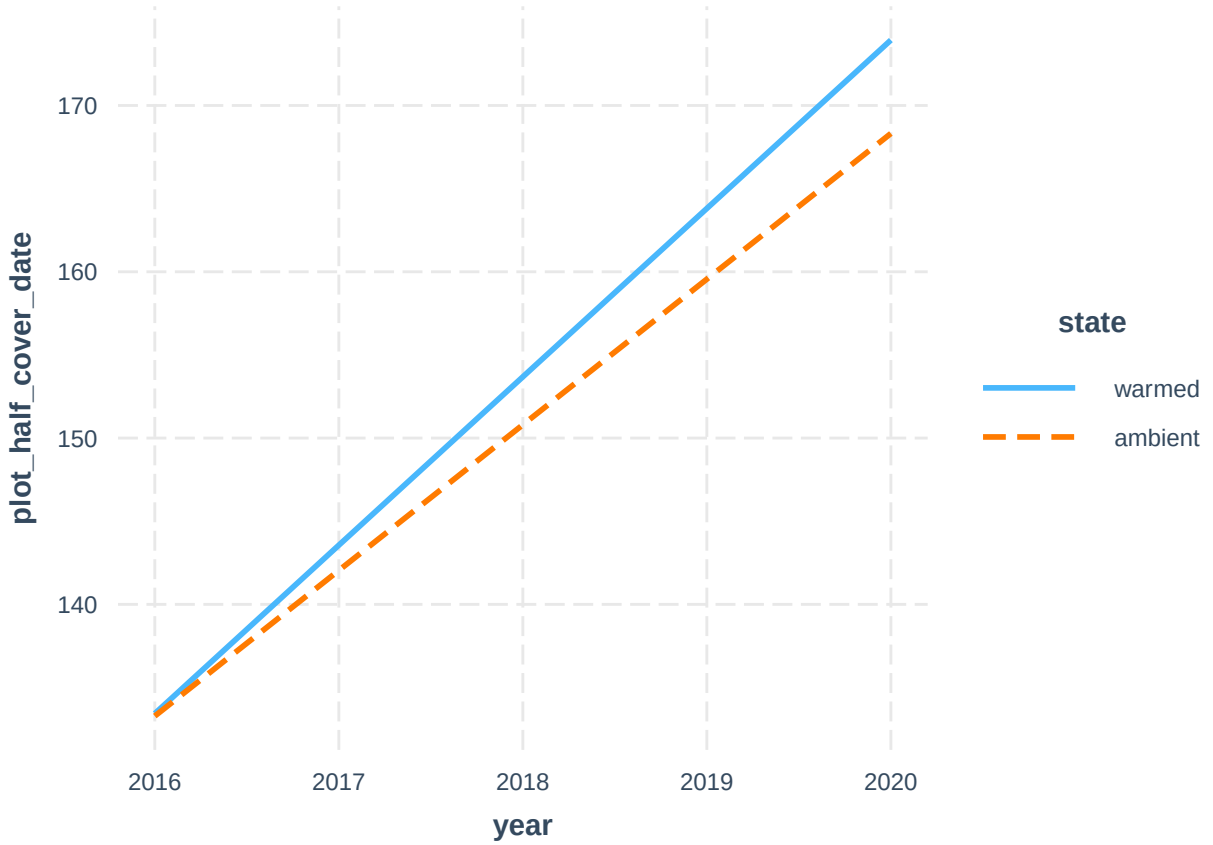
```
## Warning: year and state and species are not included in an interaction with one
## another in the model.
```


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

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

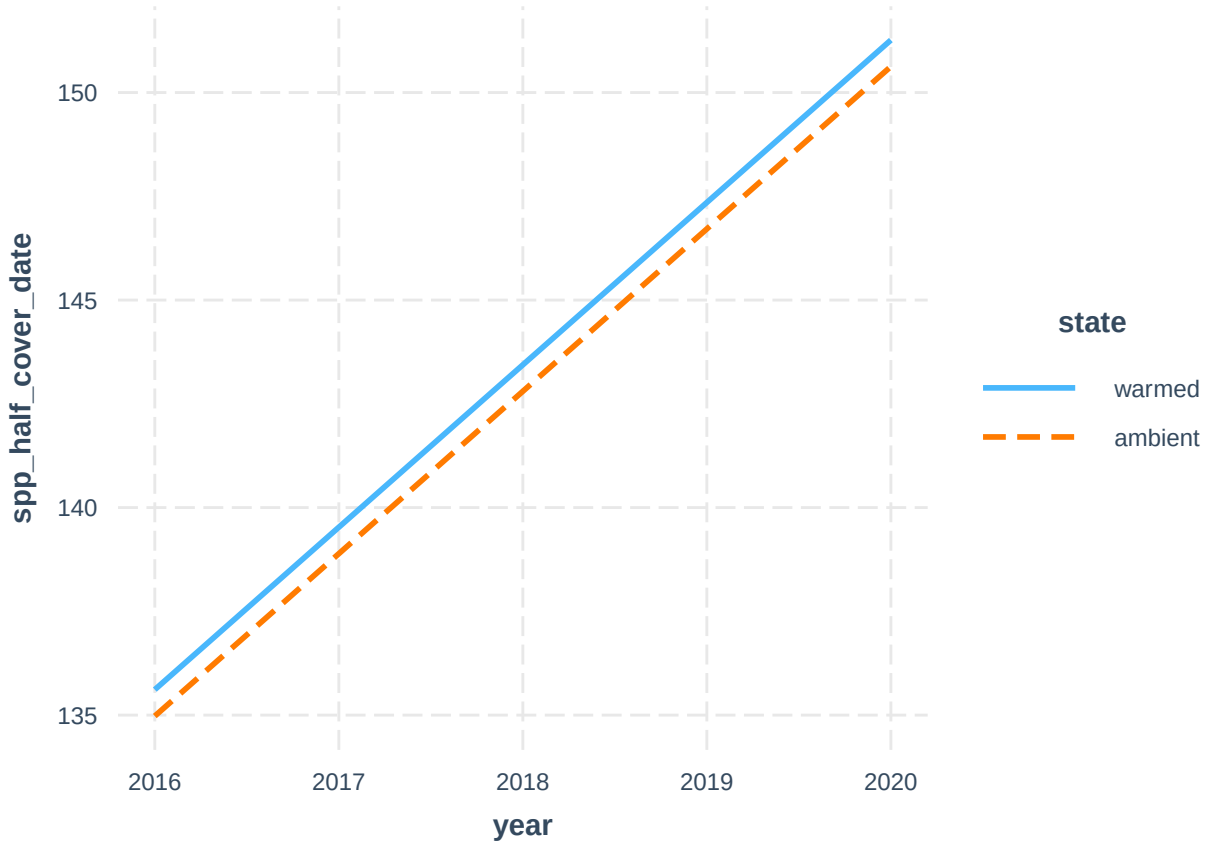



```
fit4u <- lm(plot_half_cover_date ~ state * year, data = green_umbsp)
interact_plot(fit4u, pred = year, modx = state)
```




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

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

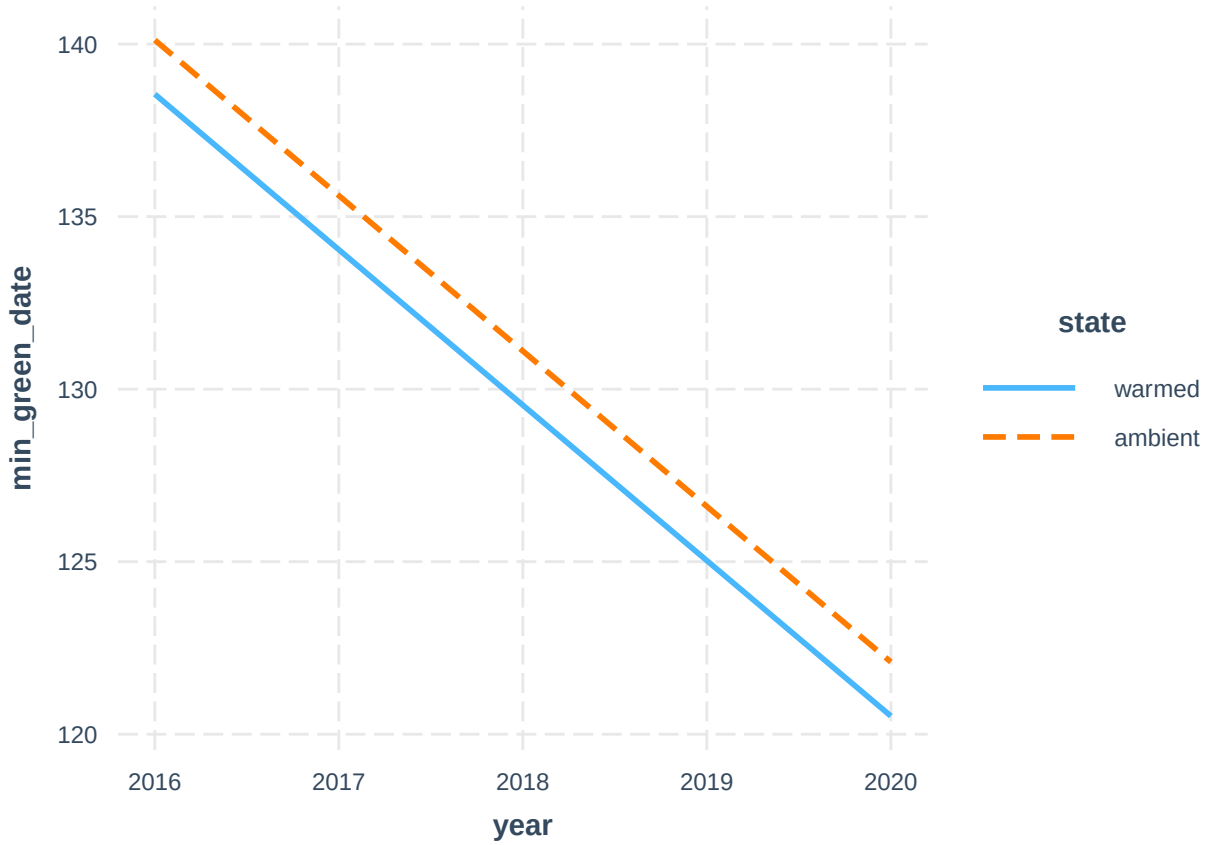



```
fit6u <- lm(spp_half_cover_date ~ state * year + species, data = green_umbs)
interact_plot(fit6u, pred = year, modx = state, mod2 = species)
```

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


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

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




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

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

KBS Species-level Mixed Effects Models:

```
# Start by replicating (almost) what we did in the 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_factor + (1 | species) + (1 | plot), green_kbs, REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
## 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_factor + (1 | species), green_kbs, REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
## 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 anove on a regular linear model:
# https://m-clark.github.io/docs/mixedModels/anovamixed.html)
# anova(mod1) anova(mod2)

# 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_factor +
## mod2:     (1 | species)
## mod1: spp_half_cover_date ~ state * year + insecticide * year_factor +
## mod1:     (1 | 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_factor +
##     (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:
```

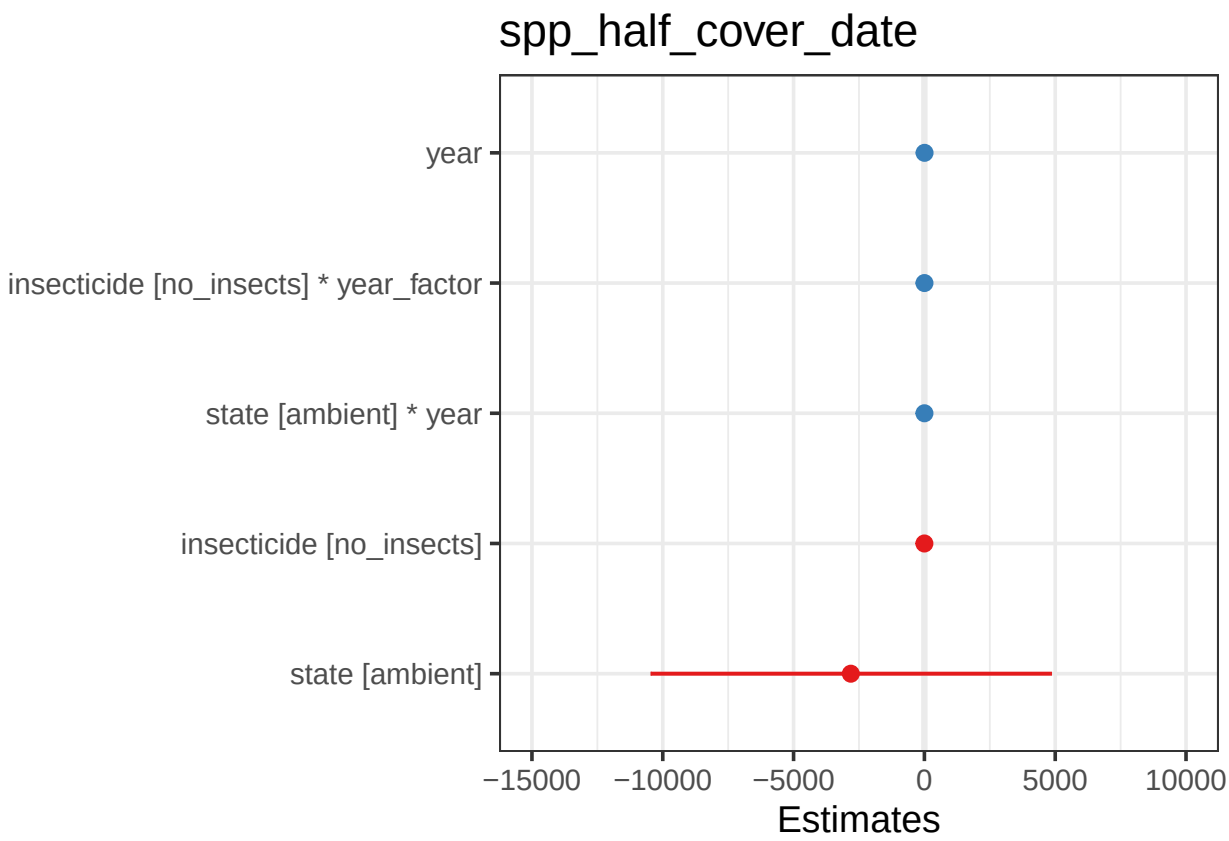
```
##                                   Estimate Std. Error         df t value
## (Intercept)                     -1.113e+04  3.368e+03  1.236e+03  -3.304
## stateambient                    -2.812e+03  3.903e+03  1.236e+03  -0.721
## year                             5.589e+00  1.669e+00  1.236e+03   3.349
## insecticideno_insects           -3.927e-01  6.678e+00  2.112e+02  -0.059
## stateambient:year                1.396e+00  1.934e+00  1.236e+03   0.722
## insecticideno_insects:year_factor  2.351e+00  1.940e+00  1.234e+03   1.212
##                                  Pr(>|t|)
## (Intercept)                      0.000979 ***
## stateambient                     0.471285
## year                             0.000836 ***
## insecticideno_insects            0.953167
## stateambient:year                0.470576
## insecticideno_insects:year_factor 0.225879
## ---
## 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 -0.463 -0.036  0.462
## statmbnt:yr  0.583 -1.000 -0.583  0.036
## insctcdn_:_  0.519  0.062 -0.519 -0.835 -0.062
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## 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_factor +
##     (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
## (Intercept)                     -1.095e+04  3.381e+03  1.247e+03  -3.237
## stateambient                    -2.851e+03  3.918e+03  1.247e+03  -0.728
## year                             5.498e+00  1.676e+00  1.247e+03   3.282
## insecticideno_insects           -1.336e-01  6.284e+00  1.246e+03  -0.021
```

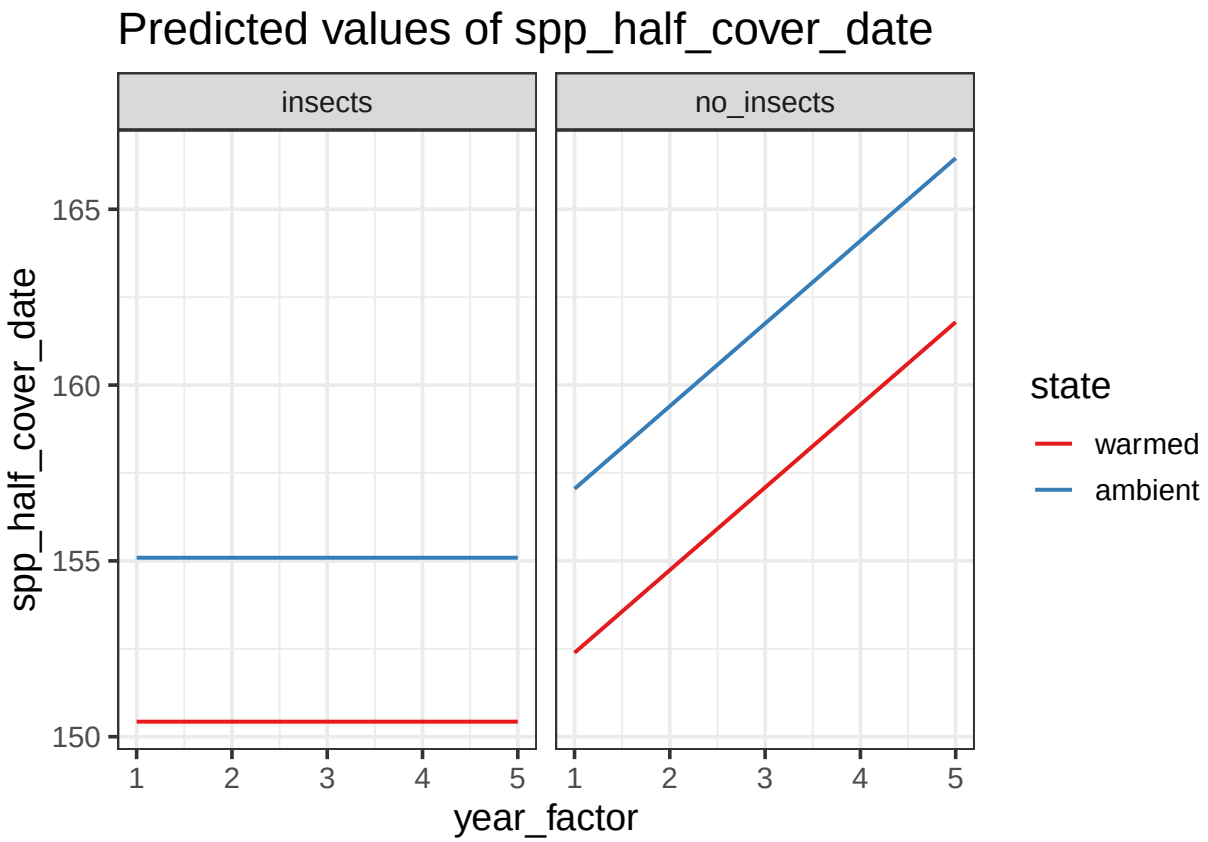
```
## stateambient:year                   1.415e+00  1.942e+00  1.247e+03   0.729
## insecticideno_insects:year_factor  2.464e+00  1.949e+00  1.248e+03   1.264
##                                   Pr(>|t|)
## (Intercept)                        0.00124 **
## stateambient                       0.46703
## year                               0.00106 **
## insecticideno_insects              0.98304
## stateambient:year                  0.46635
## insecticideno_insects:year_factor  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 -0.494 -0.039  0.494
## statmbnt:yr  0.583 -1.000 -0.583  0.039
## insctcdn_:_  0.520  0.061 -0.520 -0.893 -0.061
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## 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://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)
```



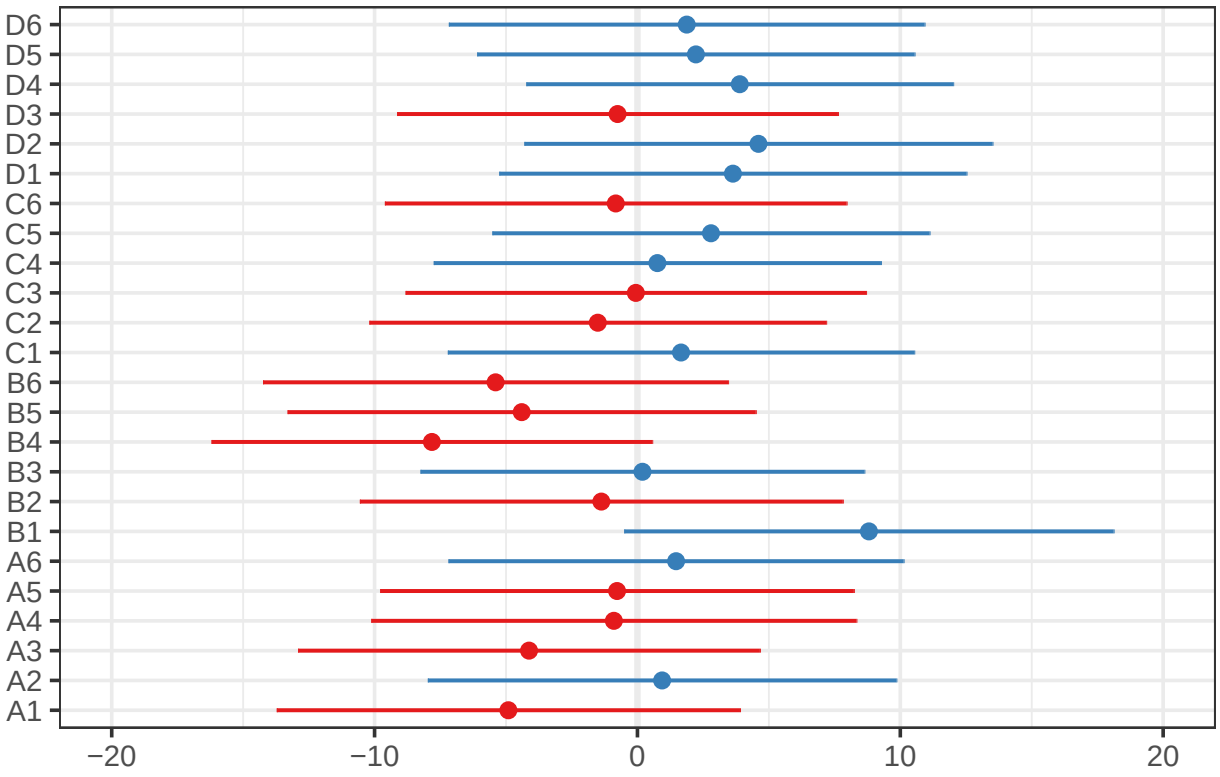

```
# these are the fixed predicted values:
plot_model(mod1, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```

```
## Error: Confidence intervals could not be computed.
## * Reason: "non-conformable arguments"
## * Source: mm %*% vcm
```

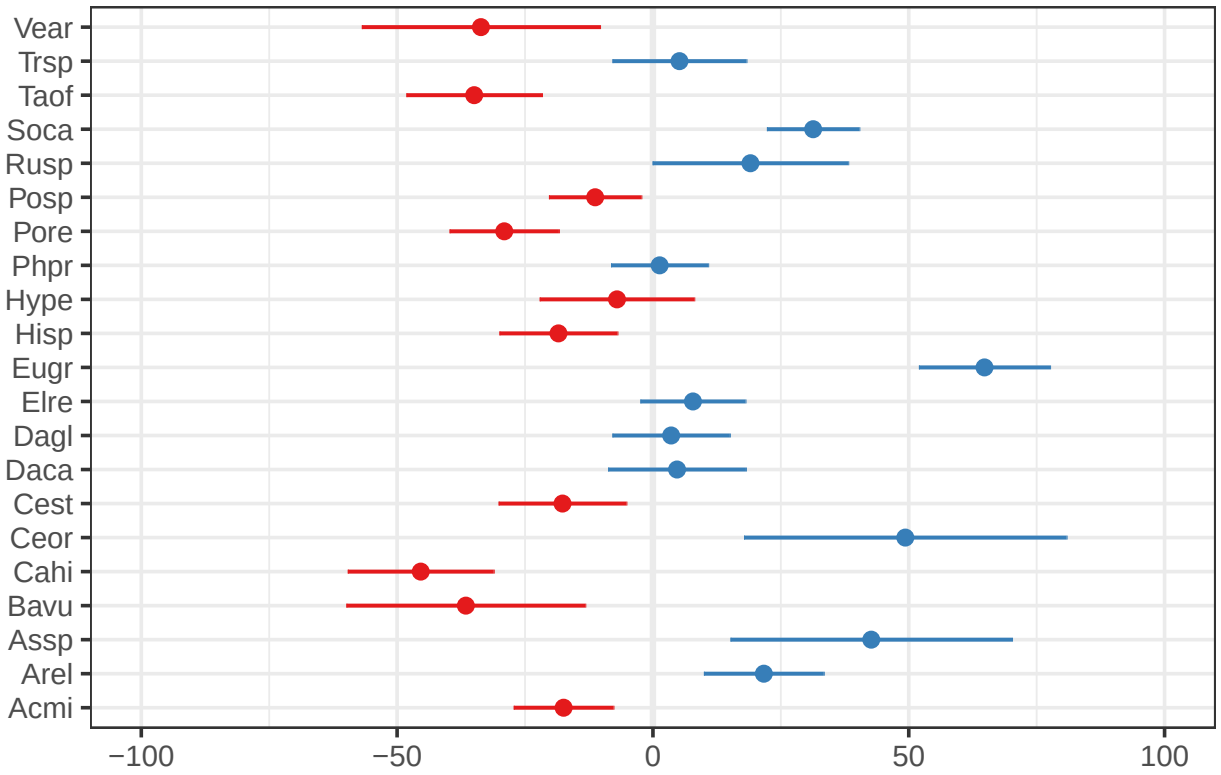



```
# these are the random effects estimates
plot_model(mod1, type = "re", terms = c("species", "plot"))
```

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




```
# Do we need to include insecticide?
mod3 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |
    species), green_kbs, REML = FALSE)
anova(mod1, mod3)
```

```
## Data: green_kbs
## Models:
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
## mod1: spp_half_cover_date ~ state * year + insecticide * year_factor +
## mod1:     (1 | 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_factor + insecticide +
    (1 | species) + (1 | plot), green_kbs, REML = FALSE)
anova(mod1, mod4)
```

```
## Data: green_kbs
## Models:
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:     species) + (1 | plot)
## mod1: spp_half_cover_date ~ state * year + insecticide * year_factor +
## mod1:     (1 | 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_factor + (1 | species)
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:     species) + (1 | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod3    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_factor + insecticide +
    (1 | species) + (1 | plot), green_kbs, REML = FALSE)
anova(mod4, mod5)
```

```
## Data: green_kbs
## Models:
## mod5: spp_half_cover_date ~ state + year_factor + insecticide + (1 |
## mod5:     species) + (1 | plot)
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:     species) + (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)
```

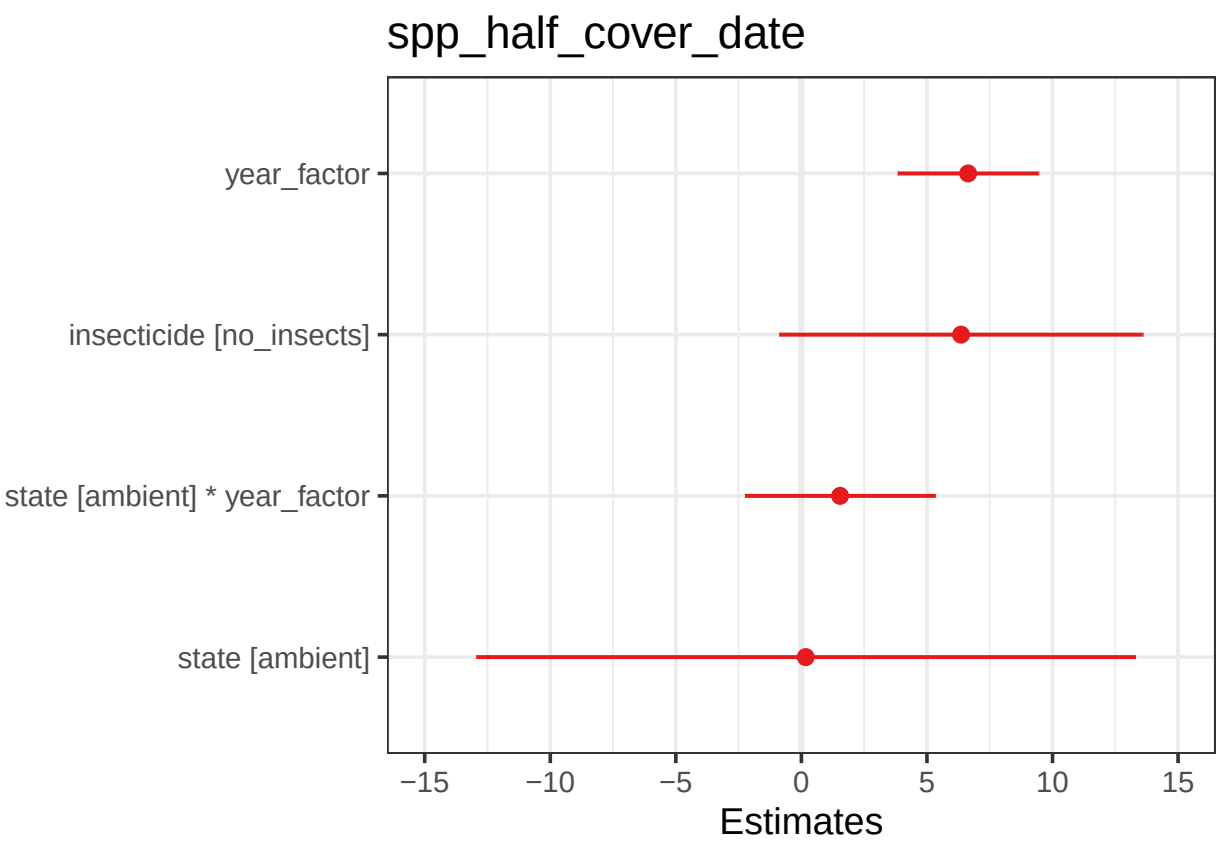
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
```

```
## Formula: spp_half_cover_date ~ state + year_factor + 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
## -2.1128 -0.7727 -0.2469  0.6665  3.1808
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   33.61   5.797
##  species  (Intercept)  931.15  30.515
##  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)           128.0160     8.0014   33.2411  15.999  < 2e-16 ***
## stateambient            4.6225     3.7014   21.2778   1.249   0.2253
## year_factor             7.4606     0.9888 1240.6406   7.545  8.7e-14 ***
## insecticideno_insects   6.4410     3.6917   21.0085   1.745   0.0956 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn yr_fct
## stateambint -0.221
## year_factor -0.358 -0.026
## insctcdn_ns -0.238 -0.038  0.059
```

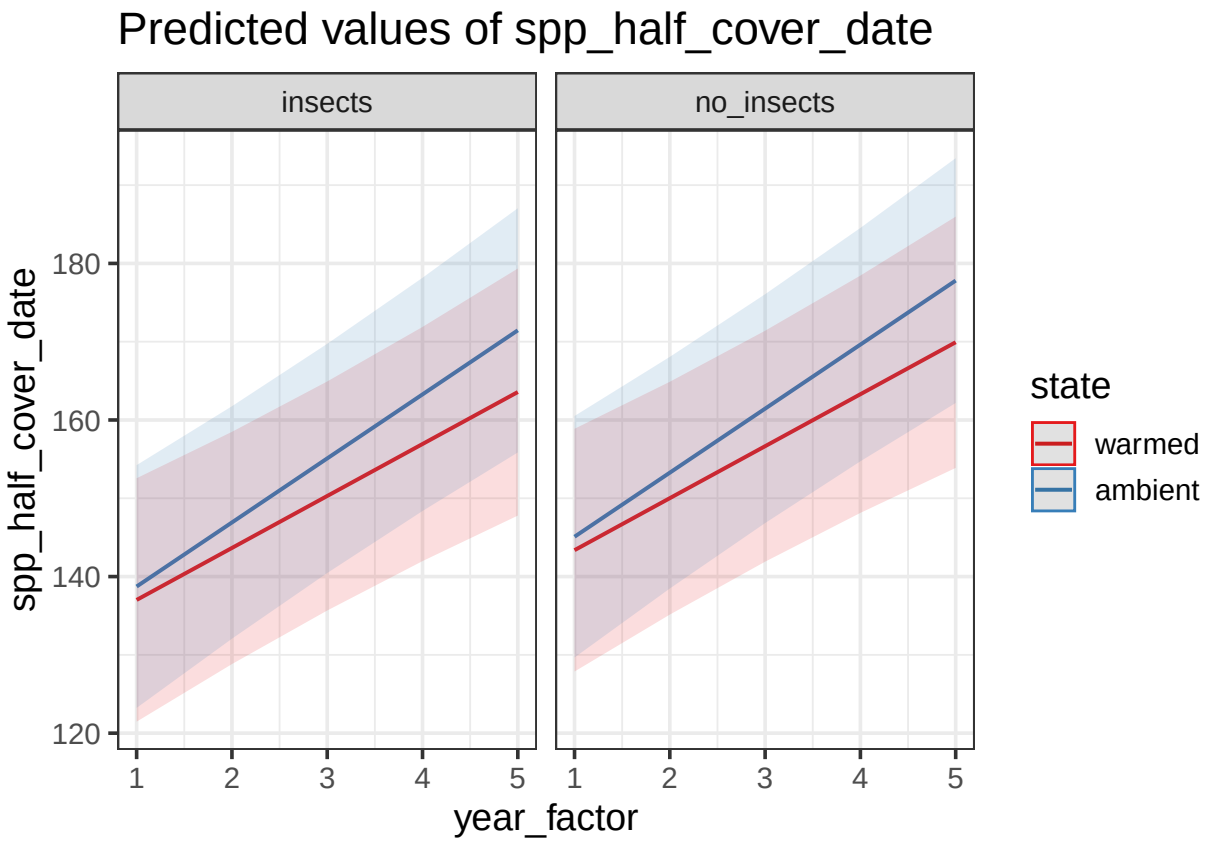
```
anova(mod4)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state                  2       2     1  208.20  0.0007   0.97938
## year_factor       137200  137200     1 1241.26 55.9464 1.404e-13 ***
## insecticide         7282    7282     1   21.05  2.9693   0.09952 .
## state:year_factor   1562    1562     1 1235.86  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)
```

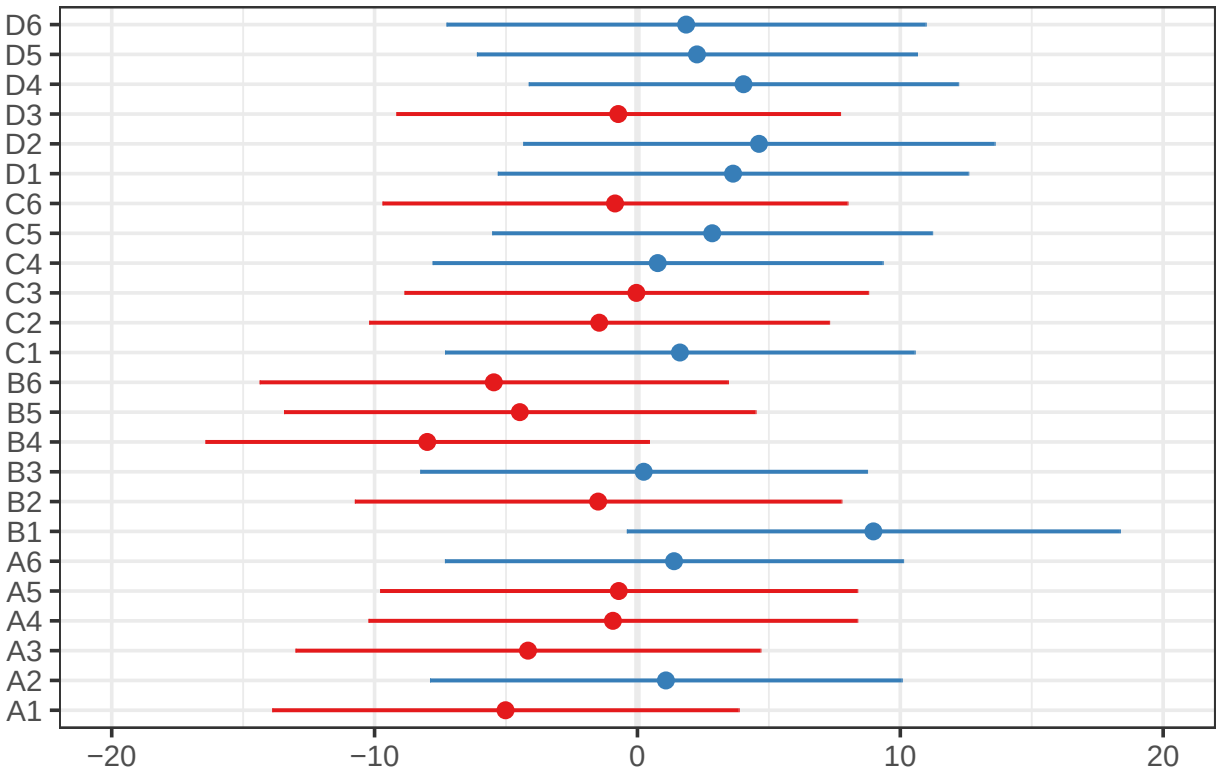



```
# these are the fixed predicted values:
plot_model(mod4, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```

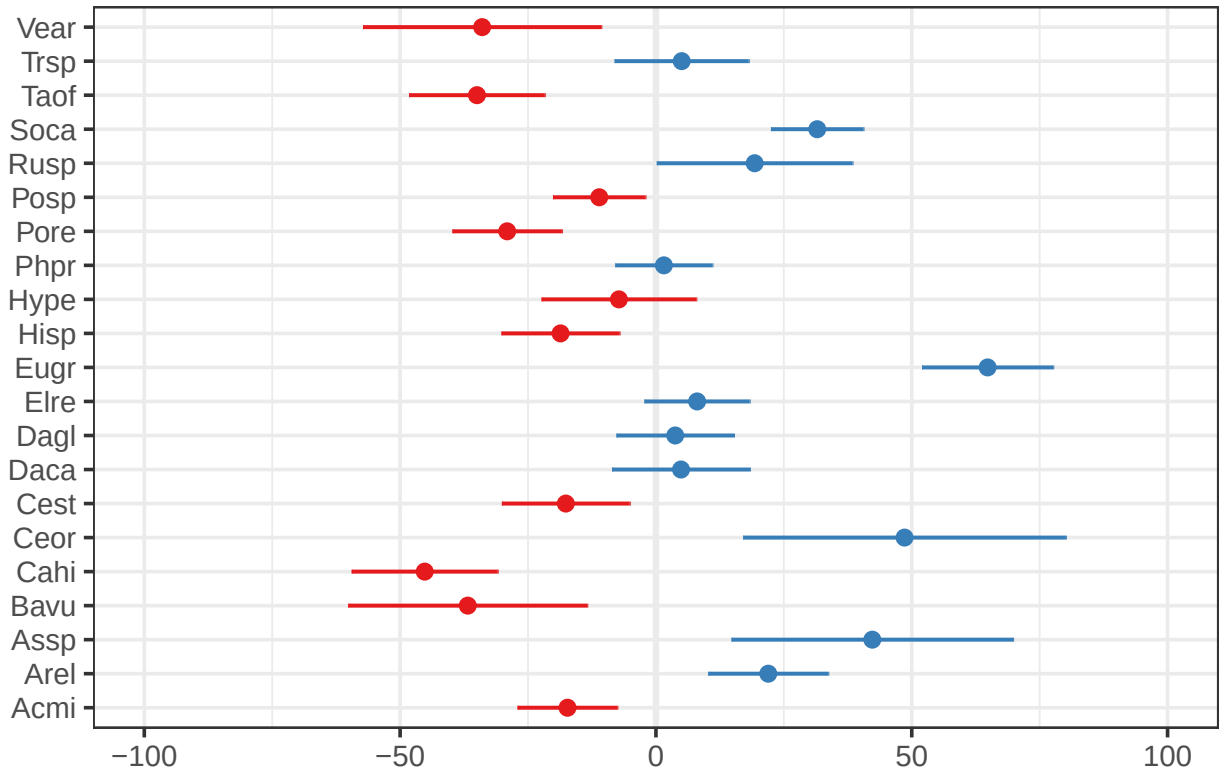



```
# these are the random effects estimates
plot_model(mod4, type = "re", terms = c("species", "plot"))
```

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




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

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.6e+00
```

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

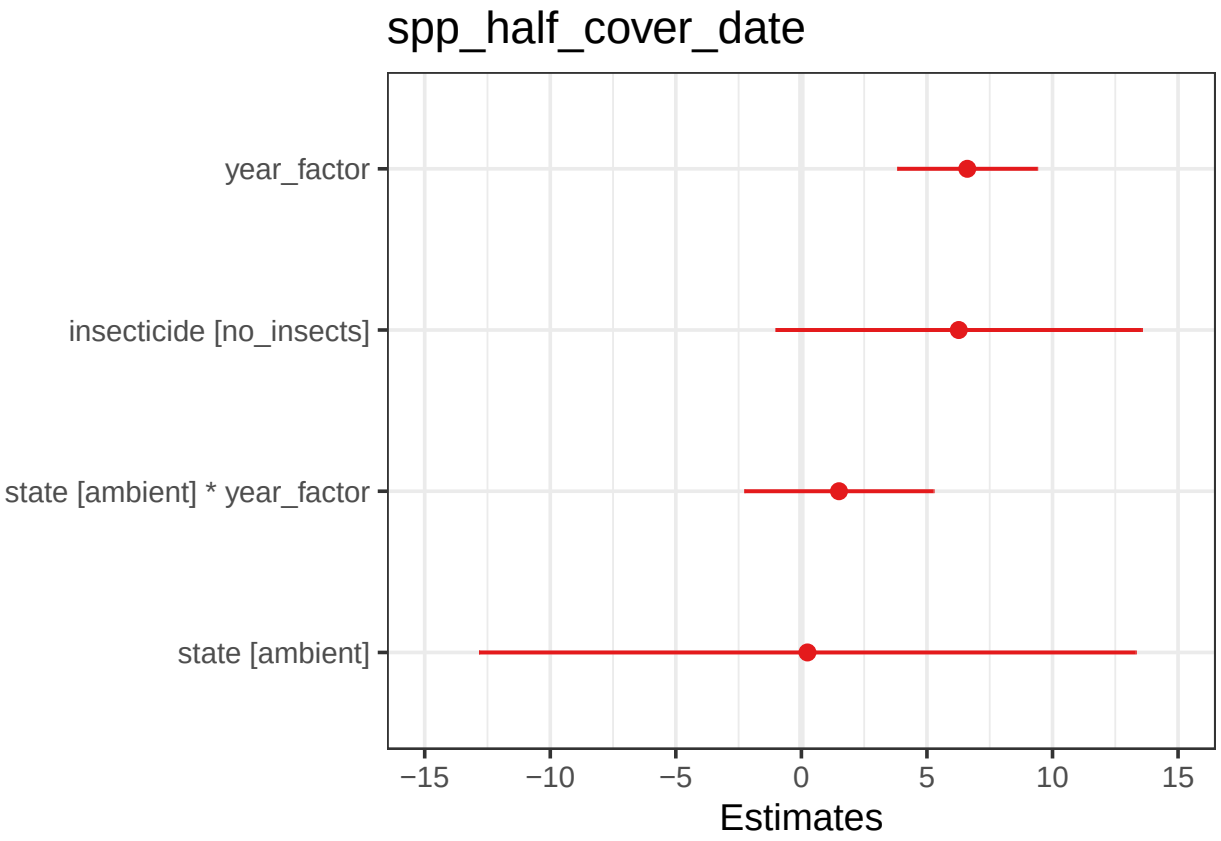
```
## Data: green_kbs
## Models:
## mod4: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod4:     species) + (1 | plot)
## mod6: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod6:     species) + (1 + year | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod4    8 13585 13626 -6784.7    13569
## mod6   10 13595 13647 -6787.6    13575     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                  3       3     1  200.93  0.0013   0.9712
## year_factor       134914  134914     1 1238.02 55.6051 1.66e-13 ***
## insecticide         6882    6882     1   20.59  2.8364   0.1072
## state:year_factor   1474    1474     1 1231.93  0.6074   0.4359
## ---
```

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

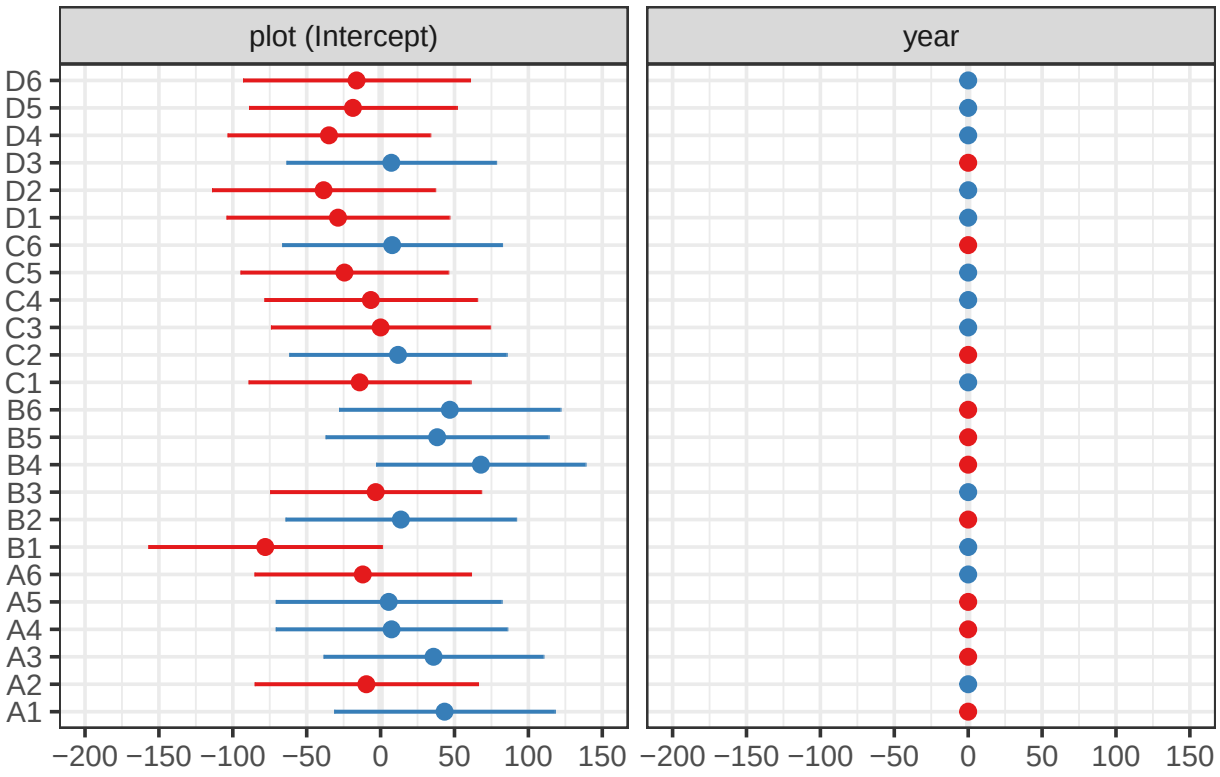
```
# Yup, seems to matter but it is making this more complex,
# though not overly so because it's on the random effects
# structure only.
plot_model(mod6, sort.est = TRUE)
```



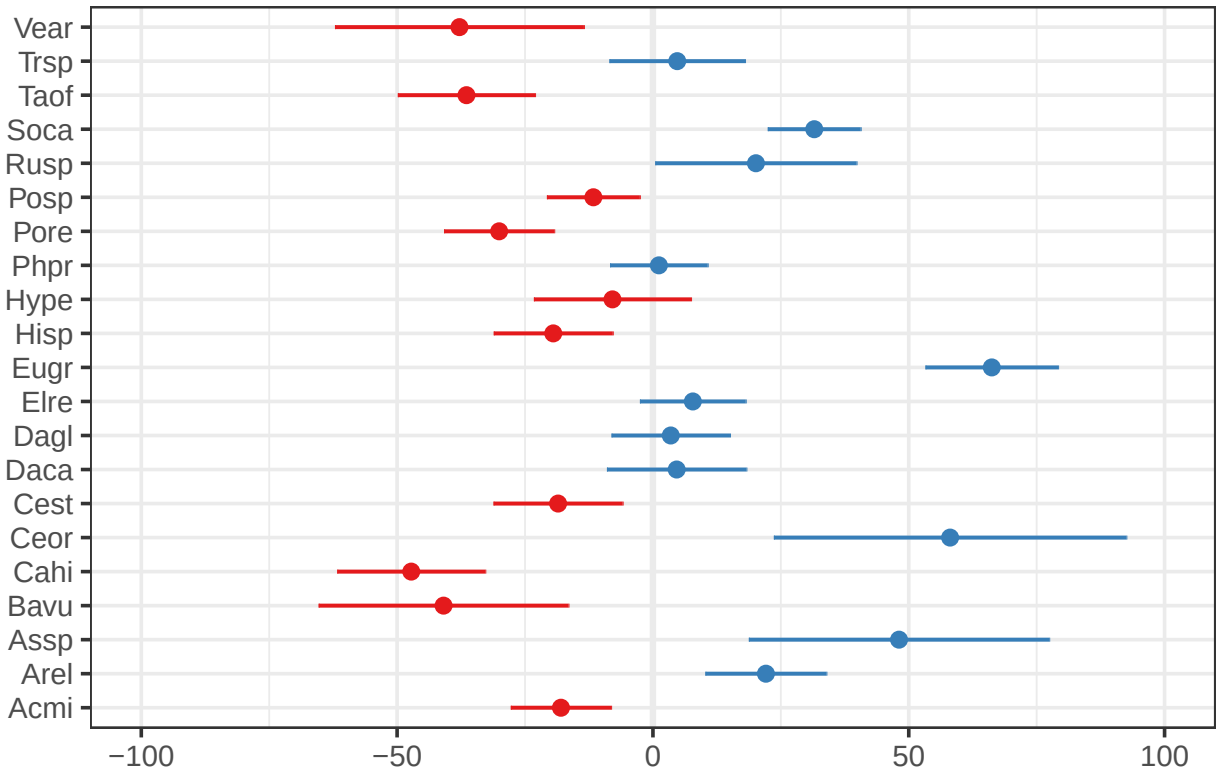

```
# these are the fixed predicted values:
plot_model(mod6, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```


```
# 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
−200 −150 −100 −50 0 50 100 150
−200 −150 −100 −50 0 50 100 150

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




```
# 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_factor |
    plot), green_kbs, REML = FALSE)
```

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

```
mod7a <- lmer(spp_half_cover_date ~ state + species + year_factor +
    (1 | plot), green_kbs, REML = FALSE)
mod7b <- lmer(spp_half_cover_date ~ state * year_factor + species +
    (1 | plot), green_kbs, REML = FALSE)
mod7c <- lmer(spp_half_cover_date ~ state + species + year_factor +
    insecticide + (1 | plot), green_kbs, REML = FALSE)
anova(mod6, mod7)  # model 7 is a better fit to data
```

```
## Data: green_kbs
## Models:
## mod6: spp_half_cover_date ~ state * year_factor + insecticide + (1 |
## mod6:     species) + (1 + year | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod6   10 13595 13647 -6787.6    13575
## mod7   26 13555 13688 -6751.3    13503 72.591 16  3.495e-09 ***
## ---
```

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

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

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7a   25 13539 13668 -6744.6    13489
## mod7    26 13555 13688 -6751.3    13503     0  1          1
```

```
anova(mod7a, mod7b)  #mod 7a.2 - interaction between state and year doesn't improve model
```

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   25 13539 13668 -6744.6    13489
## mod7b   26 13540 13674 -6744.2    13488 0.6487  1     0.4206
```

```
anova(mod7a, mod7c)  #mod 7a.2 slightly better
```

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7c: spp_half_cover_date ~ state + species + year_factor + insecticide +
## mod7c:     (1 | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   25 13539 13668 -6744.6    13489
## mod7c   26 13538 13672 -6743.1    13486 2.9664  1    0.08501 .
## ---
## 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 + year_factor + (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)   113.9583     6.0649  450.7559  18.790  < 2e-16 ***
## stateambient    4.7486     3.8464   23.6837   1.235 0.229105
## speciesArel    40.4606     7.6944 1258.0613   5.258 1.71e-07 ***
## speciesAssp    71.3590    16.4037 1267.3877   4.350 1.47e-05 ***
## speciesBavu   -25.3647    13.7051 1267.2627  -1.851 0.064438 .
## speciesCahi   -30.3892     8.8440 1255.5956  -3.436 0.000609 ***
## speciesCeor    84.6039    19.4064 1264.4777   4.360 1.41e-05 ***
## speciesCest    -0.9968     8.0302 1251.8628  -0.124 0.901234
## speciesDaca    22.8735     8.4537 1254.0641   2.706 0.006907 **
## speciesDagl    21.9625     7.5879 1257.1006   2.894 0.003864 **
## speciesElre    26.1058     7.1253 1250.8183   3.664 0.000259 ***
## speciesEugr    85.6023     8.1688 1262.0879  10.479  < 2e-16 ***
## speciesHisp    -1.9860     7.5978 1248.6621  -0.261 0.793833
## speciesHype    10.0686     9.2223 1264.8458   1.092 0.275143
## speciesPhpr    19.4282     6.7908 1248.0698   2.861 0.004294 **
## speciesPore   -12.4161     7.2532 1254.2066  -1.712 0.087177 .
## speciesPosp     6.3858     6.6222 1245.8443   0.964 0.335077
## speciesRusp    39.8126    11.2911 1264.8911   3.526 0.000437 ***
## speciesSoca    49.9275     6.6222 1245.8443   7.539 9.05e-14 ***
## speciesTaof   -19.2468     8.3548 1263.4009  -2.304 0.021402 *
## speciesTrsp    22.6301     8.2858 1252.1765   2.731 0.006399 **
## speciesVear   -22.9444    13.6644 1262.9713  -1.679 0.093372 .
## year_factor     7.2772     0.9805 1259.8102   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_factor 132866  132866     1 1259.81 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).
emmeans(mod7a, list(pairwise ~ year_factor), adjust = "tukey")
```

```
## $`emmeans of year_factor`
##  year_factor emmean   SE   df lower.CL upper.CL
##          2.9    156 2.42 55.1      151      161
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $` of year_factor`
##  1         estimate SE df z.ratio p.value
##  (nothing)   nonEst NA NA NA      NA
```

```
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
```

```
emmeans(mod7a, list(pairwise ~ species), adjust = "tukey")
```

```
## $`emmeans of species`
##  species emmean    SE   df lower.CL upper.CL
##  Acmi       137  5.12  730    127.4      147
##  Arel       178  6.19  931    165.8      190
##  Assp       209 15.89 1284    177.6      240
##  Bavu       112 13.03 1263     86.5      138
##  Cahi       107  7.60 1135     92.1      122
##  Ceor       222 19.05 1275    184.7      259
##  Cest       136  6.63 1036    123.4      149
##  Daca       160  7.14 1099    146.3      174
##  Dagl       159  6.05  920    147.5      171
##  Elre       164  5.42  812    152.9      174
##  Eugr       223  6.78 1005    209.7      236
##  Hisp       135  6.07  952    123.6      147
##  Hype       148  8.04 1126    131.7      163
##  Phpr       157  4.98  691    147.1      167
##  Pore       125  5.62  837    114.0      136
##  Posp       144  4.74  625    134.5      153
##  Rusp       177 10.40 1191    156.8      198
##  Soca       187  4.74  625    178.1      197
##  Taof       118  7.00 1047    104.4      132
##  Trsp       160  6.92 1079    146.5      174
##  Vear       114 12.98 1280     89.0      140
##
## Results are averaged over the levels of: state
## 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  -40.461  7.77 1280  -5.210 <.0001
##  Acmi - Assp  -71.359 16.58 1290  -4.305 0.0032
##  Acmi - Bavu   25.365 13.85 1290   1.832 0.9634
##  Acmi - Cahi   30.389  8.92 1277   3.405 0.0854
##  Acmi - Ceor  -84.604 19.63 1290  -4.309 0.0032
##  Acmi - Cest    0.997  8.10 1274   0.123 1.0000
##  Acmi - Daca  -22.874  8.53 1276  -2.682 0.4662
##  Acmi - Dagl  -21.962  7.66 1279  -2.868 0.3307
##  Acmi - Elre  -26.106  7.19 1272  -3.632 0.0417
##  Acmi - Eugr  -85.602  8.25 1284 -10.379 <.0001
##  Acmi - Hisp    1.986  7.66 1270   0.259 1.0000
##  Acmi - Hype  -10.069  9.31 1287  -1.081 1.0000
##  Acmi - Phpr  -19.428  6.85 1270  -2.836 0.3522
##  Acmi - Pore   12.416  7.32 1276   1.696 0.9839
##  Acmi - Posp   -6.386  6.68 1267  -0.956 1.0000
##  Acmi - Rusp  -39.813 11.42 1290  -3.485 0.0669
##  Acmi - Soca  -49.928  6.68 1267  -7.475 <.0001
##  Acmi - Taof   19.247  8.44 1286   2.281 0.7696
##  Acmi - Trsp  -22.630  8.36 1274  -2.707 0.4466
```

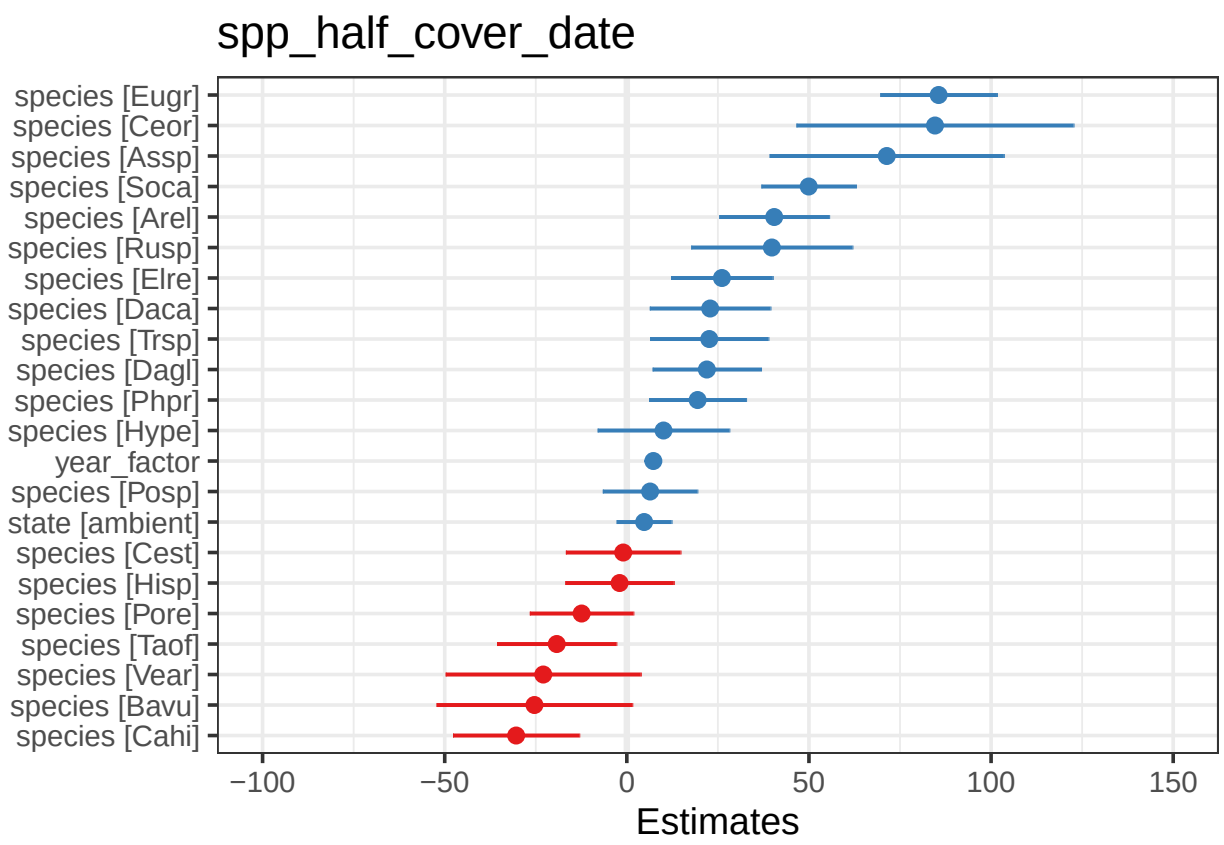
```
##  Acmi - Vear   22.944 13.80 1285   1.663 0.9872
##  Arel - Assp  -30.898 16.95 1291  -1.823 0.9652
##  Arel - Bavu   65.825 14.26 1290   4.616 0.0008
##  Arel - Cahi   70.850  9.63 1286   7.359 <.0001
##  Arel - Ceor  -44.143 19.94 1290  -2.214 0.8120
##  Arel - Cest   41.457  8.87 1286   4.675 0.0006
##  Arel - Daca   17.587  9.23 1280   1.905 0.9460
##  Arel - Dagl   18.498  8.38 1280   2.208 0.8156
##  Arel - Elre   14.355  7.95 1281   1.806 0.9683
##  Arel - Eugr  -45.142  8.94 1289  -5.051 0.0001
##  Arel - Hisp   42.447  8.42 1279   5.043 0.0001
##  Arel - Hype   30.392  9.92 1288   3.063 0.2147
##  Arel - Phpr   21.032  7.68 1281   2.740 0.4219
##  Arel - Pore   52.877  8.10 1283   6.528 <.0001
##  Arel - Posp   34.075  7.52 1281   4.530 0.0012
##  Arel - Rusp    0.648 11.90 1291   0.054 1.0000
##  Arel - Soca   -9.467  7.52 1281  -1.259 0.9997
##  Arel - Taof   59.707  9.12 1286   6.550 <.0001
##  Arel - Trsp   17.831  9.06 1280   1.967 0.9275
##  Arel - Vear   63.405 14.25 1285   4.450 0.0017
##  Assp - Bavu   96.724 20.45 1291   4.730 0.0005
##  Assp - Cahi  101.748 17.45 1287   5.830 <.0001
##  Assp - Ceor  -13.245 24.74 1291  -0.535 1.0000
##  Assp - Cest   72.356 17.11 1290   4.230 0.0044
##  Assp - Daca   48.485 17.26 1286   2.808 0.3717
##  Assp - Dagl   49.397 16.88 1290   2.926 0.2931
##  Assp - Elre   45.253 16.67 1290   2.714 0.4411
##  Assp - Eugr  -14.243 17.11 1287  -0.832 1.0000
##  Assp - Hisp   73.345 16.88 1289   4.345 0.0027
##  Assp - Hype   61.290 17.70 1291   3.463 0.0717
##  Assp - Phpr   51.931 16.53 1290   3.142 0.1767
##  Assp - Pore   83.775 16.72 1288   5.012 0.0001
##  Assp - Posp   64.973 16.46 1290   3.946 0.0136
##  Assp - Rusp   31.546 18.83 1289   1.675 0.9860
##  Assp - Soca   21.431 16.46 1290   1.302 0.9995
##  Assp - Taof   90.606 17.22 1288   5.261 <.0001
##  Assp - Trsp   48.729 17.18 1287   2.837 0.3516
##  Assp - Vear   94.303 20.30 1278   4.645 0.0007
##  Bavu - Cahi    5.024 14.91 1287   0.337 1.0000
##  Bavu - Ceor -109.969 23.06 1288  -4.769 0.0004
##  Bavu - Cest  -24.368 14.52 1291  -1.678 0.9857
##  Bavu - Daca  -48.238 14.74 1290  -3.273 0.1248
##  Bavu - Dagl  -47.327 14.23 1291  -3.327 0.1074
##  Bavu - Elre  -51.471 13.96 1291  -3.688 0.0345
##  Bavu - Eugr -110.967 14.50 1288  -7.655 <.0001
##  Bavu - Hisp  -23.379 14.24 1291  -1.642 0.9889
##  Bavu - Hype  -35.433 15.17 1291  -2.336 0.7322
##  Bavu - Phpr  -44.793 13.80 1291  -3.246 0.1344
##  Bavu - Pore  -12.949 14.08 1292  -0.920 1.0000
##  Bavu - Posp  -31.751 13.72 1291  -2.314 0.7472
##  Bavu - Rusp  -65.177 16.56 1291  -3.935 0.0142
##  Bavu - Soca  -75.292 13.72 1291  -5.488 <.0001
##  Bavu - Taof   -6.118 14.68 1292  -0.417 1.0000
##  Bavu - Trsp  -47.995 14.59 1289  -3.289 0.1193
```

```
##  Bavu - Vear   -2.420 18.27 1289  -0.132 1.0000
##  Cahi - Ceor -114.993 20.39 1292  -5.641 <.0001
##  Cahi - Cest  -29.392  9.84 1280  -2.987 0.2560
##  Cahi - Daca  -53.263 10.19 1278  -5.227 <.0001
##  Cahi - Dagl  -52.352  9.53 1286  -5.492 <.0001
##  Cahi - Elre  -56.495  9.15 1282  -6.172 <.0001
##  Cahi - Eugr -115.991  9.97 1278 -11.636 <.0001
##  Cahi - Hisp  -28.403  9.51 1280  -2.987 0.2560
##  Cahi - Hype  -40.458 10.86 1283  -3.726 0.0303
##  Cahi - Phpr  -49.817  8.86 1280  -5.623 <.0001
##  Cahi - Pore  -17.973  9.25 1285  -1.943 0.9351
##  Cahi - Posp  -36.775  8.74 1280  -4.210 0.0048
##  Cahi - Rusp  -70.202 12.73 1291  -5.513 <.0001
##  Cahi - Soca  -80.317  8.74 1280  -9.194 <.0001
##  Cahi - Taof  -11.142 10.13 1285  -1.100 1.0000
##  Cahi - Trsp  -53.019 10.02 1272  -5.289 <.0001
##  Cahi - Vear   -7.445 14.83 1279  -0.502 1.0000
##  Ceor - Cest   85.601 20.07 1290   4.266 0.0038
##  Ceor - Daca   61.730 20.25 1290   3.049 0.2221
##  Ceor - Dagl   62.641 19.91 1289   3.146 0.1750
##  Ceor - Elre   58.498 19.70 1291   2.969 0.2670
##  Ceor - Eugr   -0.998 20.14 1289  -0.050 1.0000
##  Ceor - Hisp   86.590 19.89 1291   4.354 0.0026
##  Ceor - Hype   74.535 20.64 1287   3.612 0.0445
##  Ceor - Phpr   65.176 19.61 1289   3.324 0.1083
##  Ceor - Pore   97.020 19.79 1288   4.903 0.0002
##  Ceor - Posp   78.218 19.53 1290   4.005 0.0109
##  Ceor - Rusp   44.791 21.55 1291   2.078 0.8839
##  Ceor - Soca   34.676 19.53 1290   1.775 0.9735
##  Ceor - Taof  103.851 20.17 1291   5.148 0.0001
##  Ceor - Trsp   61.974 20.15 1291   3.075 0.2087
##  Ceor - Vear  107.548 22.98 1291   4.680 0.0006
##  Cest - Daca  -23.870  9.46 1277  -2.523 0.5910
##  Cest - Dagl  -22.959  8.76 1284  -2.622 0.5128
##  Cest - Elre  -27.103  8.37 1277  -3.236 0.1380
##  Cest - Eugr  -86.599  9.29 1287  -9.320 <.0001
##  Cest - Hisp    0.989  8.73 1272   0.113 1.0000
##  Cest - Hype  -11.065 10.24 1287  -1.081 1.0000
##  Cest - Phpr  -20.425  8.05 1277  -2.538 0.5791
##  Cest - Pore   11.419  8.42 1274   1.357 0.9991
##  Cest - Posp   -7.383  7.90 1275  -0.934 1.0000
##  Cest - Rusp  -40.809 12.19 1289  -3.346 0.1014
##  Cest - Soca  -50.924  7.90 1275  -6.442 <.0001
##  Cest - Taof   18.250  9.41 1284   1.938 0.9366
##  Cest - Trsp  -23.627  9.34 1276  -2.529 0.5864
##  Cest - Vear   21.948 14.41 1286   1.523 0.9956
##  Daca - Dagl    0.911  9.12 1276   0.100 1.0000
##  Daca - Elre   -3.232  8.77 1277  -0.369 1.0000
##  Daca - Eugr  -62.729  9.64 1284  -6.505 <.0001
##  Daca - Hisp   24.860  9.12 1274   2.725 0.4333
##  Daca - Hype   12.805 10.57 1287   1.211 0.9998
##  Daca - Phpr    3.445  8.47 1276   0.407 1.0000
##  Daca - Pore   35.290  8.83 1275   3.998 0.0112
##  Daca - Posp   16.488  8.34 1277   1.978 0.9239
```

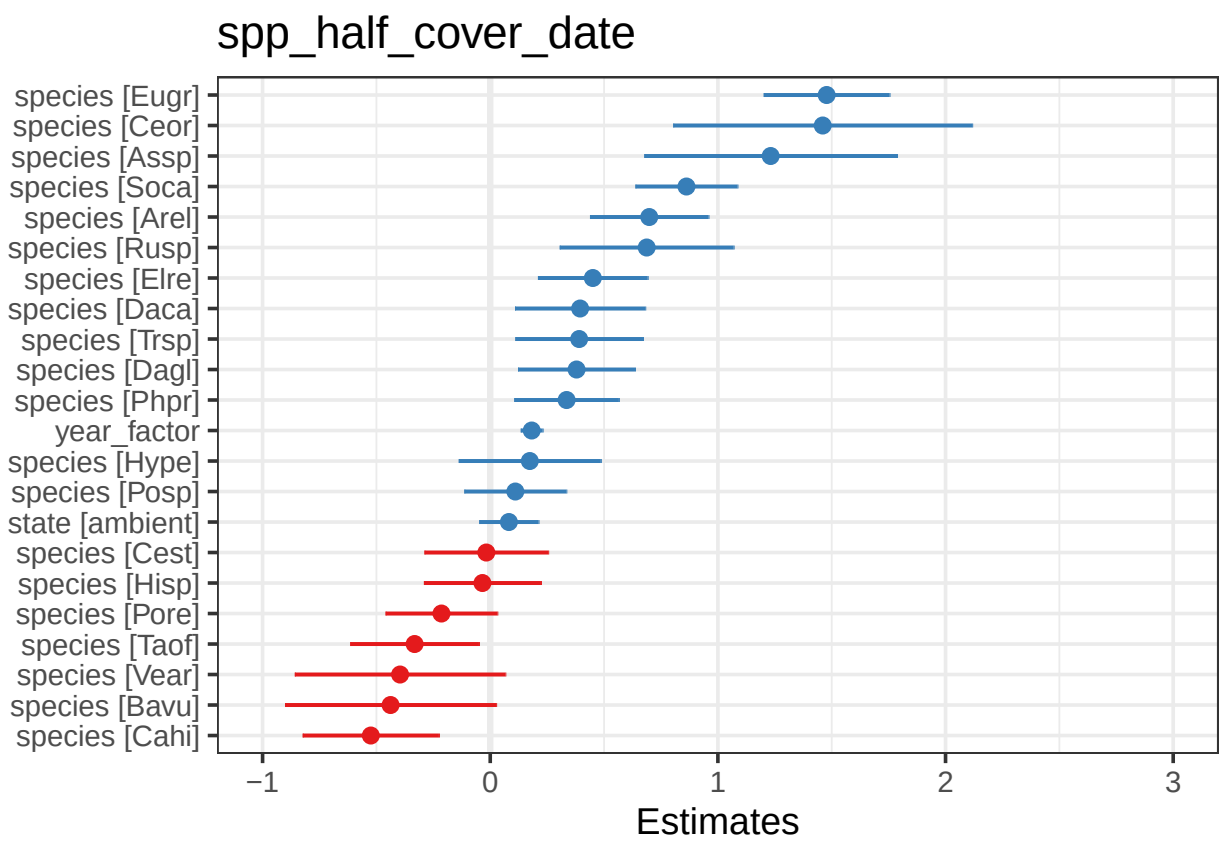
```
##  Daca - Rusp  -16.939 12.46 1291  -1.360 0.9990
##  Daca - Soca  -27.054  8.34 1277  -3.245 0.1348
##  Daca - Taof   42.120  9.79 1285   4.304 0.0033
##  Daca - Trsp    0.243  9.70 1273   0.025 1.0000
##  Daca - Vear   45.818 14.63 1282   3.132 0.1813
##  Dagl - Elre   -4.143  7.84 1275  -0.528 1.0000
##  Dagl - Eugr  -63.640  8.86 1289  -7.187 <.0001
##  Dagl - Hisp   23.948  8.32 1279   2.879 0.3233
##  Dagl - Hype   11.894  9.85 1289   1.208 0.9998
##  Dagl - Phpr    2.534  7.56 1274   0.335 1.0000
##  Dagl - Pore   34.379  7.99 1279   4.305 0.0032
##  Dagl - Posp   15.577  7.41 1277   2.102 0.8725
##  Dagl - Rusp  -17.850 11.84 1291  -1.508 0.9961
##  Dagl - Soca  -27.965  7.41 1277  -3.775 0.0255
##  Dagl - Taof   41.209  9.02 1284   4.570 0.0010
##  Dagl - Trsp   -0.668  8.97 1281  -0.074 1.0000
##  Dagl - Vear   44.907 14.18 1285   3.167 0.1659
##  Elre - Eugr  -59.496  8.42 1286  -7.066 <.0001
##  Elre - Hisp   28.092  7.89 1274   3.561 0.0526
##  Elre - Hype   16.037  9.48 1290   1.691 0.9844
##  Elre - Phpr    6.678  7.07 1269   0.945 1.0000
##  Elre - Pore   38.522  7.55 1275   5.103 0.0001
##  Elre - Posp   19.720  6.90 1268   2.857 0.3382
##  Elre - Rusp  -13.707 11.53 1292  -1.188 0.9999
##  Elre - Soca  -23.822  6.90 1268  -3.451 0.0743
##  Elre - Taof   45.353  8.62 1281   5.261 <.0001
##  Elre - Trsp    3.476  8.57 1276   0.406 1.0000
##  Elre - Vear   49.050 13.96 1287   3.515 0.0610
##  Eugr - Hisp   87.588  8.87 1286   9.871 <.0001
##  Eugr - Hype   75.534 10.30 1290   7.330 <.0001
##  Eugr - Phpr   66.174  8.16 1285   8.112 <.0001
##  Eugr - Pore   98.018  8.58 1288  11.430 <.0001
##  Eugr - Posp   79.216  8.02 1286   9.881 <.0001
##  Eugr - Rusp   45.790 12.19 1291   3.755 0.0273
##  Eugr - Soca   35.675  8.02 1286   4.450 0.0017
##  Eugr - Taof  104.849  9.51 1284  11.024 <.0001
##  Eugr - Trsp   62.972  9.46 1280   6.654 <.0001
##  Eugr - Vear  108.547 14.49 1284   7.489 <.0001
##  Hisp - Hype  -12.055  9.87 1288  -1.221 0.9998
##  Hisp - Phpr  -21.414  7.59 1274  -2.822 0.3619
##  Hisp - Pore   10.430  8.00 1273   1.304 0.9995
##  Hisp - Posp   -8.372  7.43 1271  -1.127 0.9999
##  Hisp - Rusp  -41.799 11.89 1290  -3.517 0.0606
##  Hisp - Soca  -51.913  7.43 1271  -6.987 <.0001
##  Hisp - Taof   17.261  9.03 1280   1.912 0.9442
##  Hisp - Trsp  -24.616  8.96 1272  -2.746 0.4173
##  Hisp - Vear   20.958 14.17 1284   1.479 0.9970
##  Hype - Phpr   -9.360  9.23 1287  -1.014 1.0000
##  Hype - Pore   22.485  9.61 1290   2.340 0.7295
##  Hype - Posp    3.683  9.11 1288   0.404 1.0000
##  Hype - Rusp  -29.744 12.99 1291  -2.289 0.7642
##  Hype - Soca  -39.859  9.11 1288  -4.373 0.0024
##  Hype - Taof   29.315 10.48 1291   2.797 0.3800
##  Hype - Trsp  -12.562 10.41 1286  -1.206 0.9998
```

```
##  Hype - Vear   33.013 15.11 1283   2.185 0.8292
##  Phpr - Pore   31.844  7.23 1273   4.406 0.0021
##  Phpr - Posp   13.042  6.57 1267   1.984 0.9215
##  Phpr - Rusp  -20.384 11.35 1291  -1.796 0.9700
##  Phpr - Soca  -30.499  6.57 1267  -4.640 0.0007
##  Phpr - Taof   38.675  8.36 1285   4.629 0.0008
##  Phpr - Trsp   -3.202  8.28 1275  -0.387 1.0000
##  Phpr - Vear   42.373 13.75 1285   3.081 0.2058
##  Pore - Posp  -18.802  7.07 1275  -2.659 0.4835
##  Pore - Rusp  -52.229 11.63 1291  -4.491 0.0014
##  Pore - Soca  -62.344  7.07 1275  -8.817 <.0001
##  Pore - Taof    6.831  8.74 1284   0.782 1.0000
##  Pore - Trsp  -35.046  8.68 1276  -4.038 0.0096
##  Pore - Vear   10.528 13.99 1284   0.753 1.0000
##  Posp - Rusp  -33.427 11.25 1291  -2.971 0.2656
##  Posp - Soca  -43.542  6.39 1265  -6.810 <.0001
##  Posp - Taof   25.633  8.21 1284   3.120 0.1867
##  Posp - Trsp  -16.244  8.15 1275  -1.994 0.9181
##  Posp - Vear   29.330 13.68 1286   2.144 0.8516
##  Rusp - Soca  -10.115 11.25 1291  -0.899 1.0000
##  Rusp - Taof   59.059 12.32 1290   4.795 0.0004
##  Rusp - Trsp   17.183 12.32 1291   1.395 0.9986
##  Rusp - Vear   62.757 16.50 1290   3.802 0.0231
##  Soca - Taof   69.174  8.21 1284   8.421 <.0001
##  Soca - Trsp   27.297  8.15 1275   3.351 0.1002
##  Soca - Vear   72.872 13.68 1286   5.327 <.0001
##  Taof - Trsp  -41.877  9.63 1282  -4.351 0.0027
##  Taof - Vear    3.698 14.60 1286   0.253 1.0000
##  Trsp - Vear   45.575 14.53 1281   3.138 0.1787
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 21 estimates
```

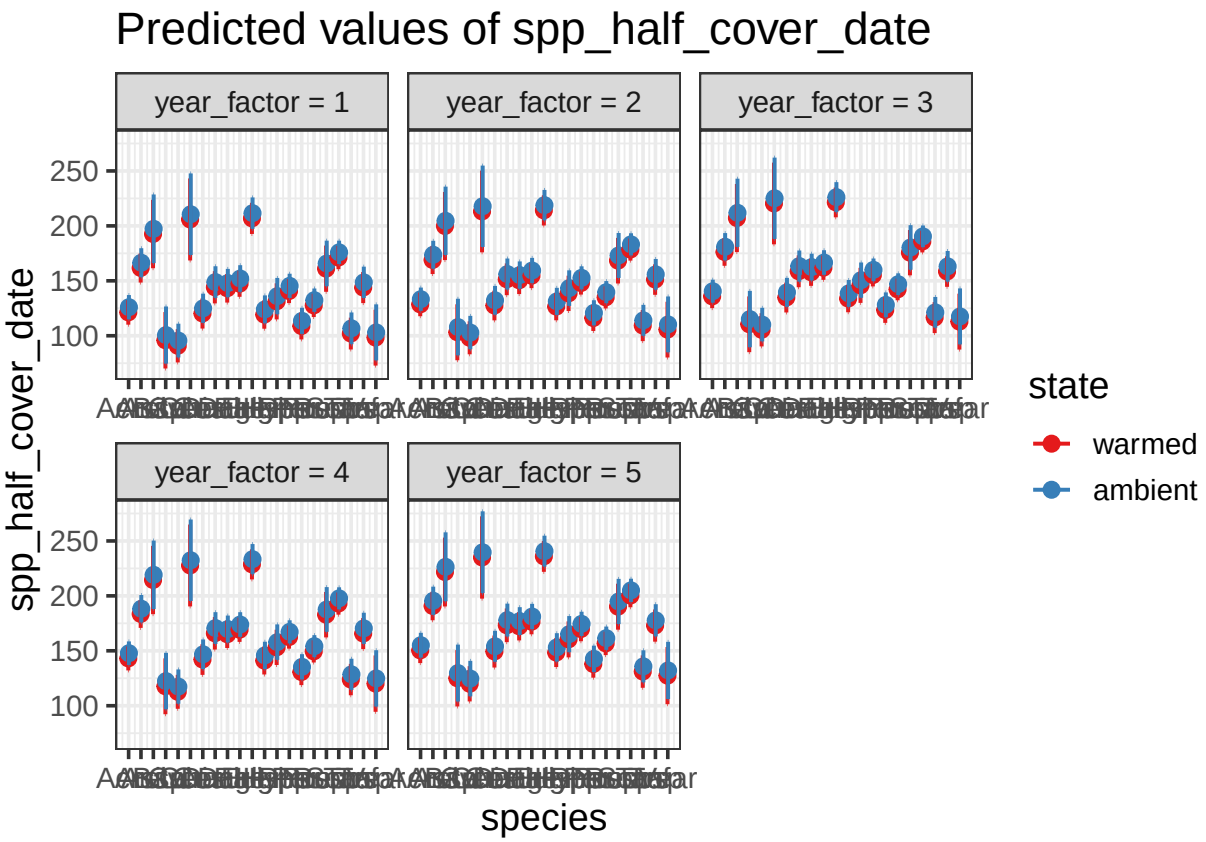
```
# using model 7a for overall greenup model #

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




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

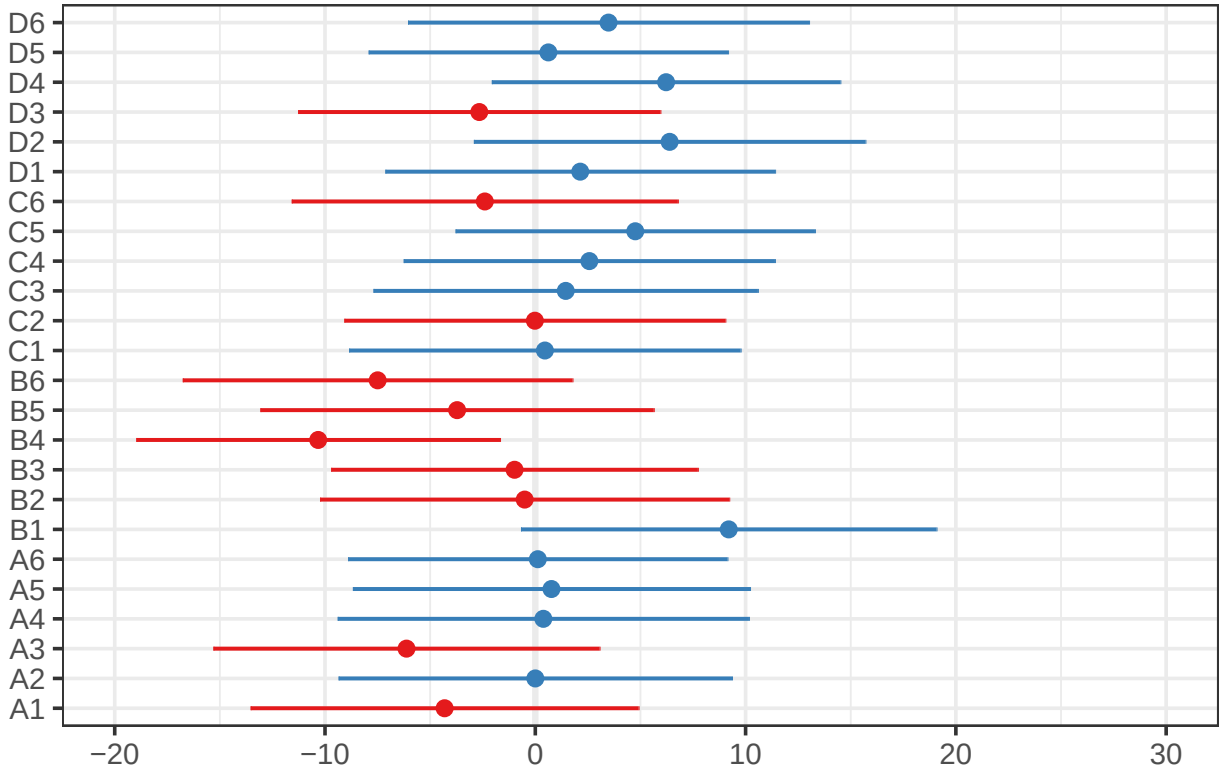



```
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7a, type = "pred", terms = c("species", "state",
    "year_factor"))
```




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

Random effects




```
# including native vs. exotic
green_kbs <- within(green_kbs, origin <- relevel(factor(origin),
    ref = "Native"))  # releveling so native is the reference
mod8 <- lmer(spp_half_cover_date ~ state * origin + (1 + year_factor |
    plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -4.3e+02
```

```
mod9 <- lmer(spp_half_cover_date ~ state + origin + (1 + year_factor |
    plot), green_kbs, REML = FALSE)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -4.4e+02
```

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

```
## Data: green_kbs
## Models:
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## mod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod9    9 13805 13851 -6893.3    13787
## mod8   12 13806 13868 -6891.1    13782 4.4194  3     0.2196
```

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

```
## Data: green_kbs
## Models:
## mod9a: spp_half_cover_date ~ state + origin + year_factor + (1 | plot)
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod9a    8 13768 13810 -6876.2    13752
## mod9     9 13805 13851 -6893.3    13787     0  1          1
```

```
summary(mod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + year_factor + (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)   147.418      5.212  203.427  28.284  < 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_factor     9.232      1.059 1256.864   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 -0.407
## origin      -0.342  0.006
## originBoth  -0.392 -0.013  0.329
## originExotc -0.539 -0.010  0.464  0.511
## year_factor -0.595 -0.015 -0.008  0.037  0.022
```

```
anova(mod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF   DenDF F value   Pr(>F)
## state     231     231     1  169.36  0.0783     0.78
## origin 186320   62107     3 1231.80 21.0643 2.61e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## $`emmeans of state, origin`
##  state   origin emmean   SE    df lower.CL upper.CL
##  warmed  Native    174 4.29  93.4      166      183
##  ambient Native    178 4.25  92.2      170      187
##  warmed            142 5.69 274.0      130      153
##  ambient           146 5.69 278.5      135      157
##  warmed  Both      153 5.20 189.3      142      163
##  ambient Both      157 5.11 180.9      147      167
##  warmed  Exotic    145 3.48  39.3      138      152
##  ambient Exotic    149 3.39  35.5      142      156
##
## 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    -4.139 4.46   25.9 -0.929  0.9802
##  warmed Native - warmed             32.633 5.96 1251.5  5.474  <.0001
##  warmed Native - ambient            28.494 7.47  209.2  3.817  0.0043
##  warmed Native - warmed Both        21.481 5.45 1263.6  3.941  0.0022
##  warmed Native - ambient Both       17.341 7.00  161.4  2.478  0.2126
##  warmed Native - warmed Exotic      29.216 3.87 1259.3  7.553  <.0001
##  warmed Native - ambient Exotic     25.077 5.87   81.8  4.269  0.0013
##  ambient Native - warmed            36.772 7.42  205.4  4.955  <.0001
##  ambient Native - ambient           32.633 5.96 1251.5  5.474  <.0001
##  ambient Native - warmed Both       25.620 7.08  169.2  3.618  0.0092
##  ambient Native - ambient Both      21.481 5.45 1263.6  3.941  0.0022
##  ambient Native - warmed Exotic     33.355 5.93   85.8  5.627  <.0001
##  ambient Native - ambient Exotic    29.216 3.87 1259.3  7.553  <.0001
##  warmed  - ambient                  -4.139 4.46   25.9 -0.929  0.9802
##  warmed  - warmed Both             -11.152 6.63 1261.0 -1.683  0.6985
##  warmed  - ambient Both            -15.291 7.93  254.8 -1.929  0.5326
##  warmed  - warmed Exotic            -3.417 5.39 1253.2 -0.633  0.9984
##  warmed  - ambient Exotic           -7.556 6.95  159.8 -1.087  0.9587
##  ambient  - warmed Both             -7.013 8.04  267.6 -0.872  0.9883
##  ambient  - ambient Both           -11.152 6.63 1261.0 -1.683  0.6985
##  ambient  - warmed Exotic            0.722 7.04  168.9  0.103  1.0000
##  ambient  - ambient Exotic          -3.417 5.39 1253.2 -0.633  0.9984
##  warmed Both - ambient Both         -4.139 4.46   25.9 -0.929  0.9802
##  warmed Both - warmed Exotic         7.735 4.81 1262.8  1.609  0.7451
##  warmed Both - ambient Exotic        3.596 6.58  127.5  0.547  0.9994
##  ambient Both - warmed Exotic       11.874 6.54  125.3  1.817  0.6100
##  ambient Both - ambient Exotic       7.735 4.81 1262.8  1.609  0.7451
##  warmed Exotic - ambient Exotic     -4.139 4.46   25.9 -0.929  0.9802
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

```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_factor | plot), green_kbs, REML = FALSE)
```

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

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

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -4.8e+02
```

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

```
## Data: green_kbs
## Models:
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11:     plot)
## mod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## mod10:     plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod11    9 13851 13898 -6916.6    13833
## mod10   12 13840 13902 -6908.3    13816 16.764  3  0.0007904 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Data: green_kbs
## Models:
## mod11a: spp_half_cover_date ~ state + growth_habit + year_factor + (1 |
## mod11a:     plot)
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11:     plot)
##        npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11a    8 13815 13856 -6899.4    13799
## mod11     9 13851 13898 -6916.6    13833     0  1          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 + year_factor + (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)            123.0075     4.5507  118.9402  27.031  < 2e-16 ***
## stateambient             3.9039     4.3187   24.9788   0.904 0.374654
## growth_habit            -0.1793     5.0509 1255.9654  -0.035 0.971689
## growth_habitGraminoid    6.4752     3.4201 1263.2381   1.893 0.058551 .
## growth_habitVine        71.0413    21.3388 1263.6544   3.329 0.000896 ***
## year_factor              9.1144     1.0870 1258.6830   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 -0.481
## growth_habt -0.198 -0.008
## grwth_hbtGr -0.239  0.026  0.275
## grwth_hbtVn -0.044 -0.019  0.049  0.066
## year_factor -0.648 -0.018 -0.006 -0.124  0.003
```

```
anova(mod11a)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state          2516    2516     1   24.98  0.8171  0.374654
## growth_habit  44231   14744     3 1260.85  4.7881  0.002538 **
## year_factor  216501  216501     1 1258.68 70.3090 < 2.2e-16 ***
## ---
## 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            149  3.60   42.4      142      157
##  ambient Forb            153  3.49   38.1      146      160
##  warmed                  149  5.41  211.8      139      160
##  ambient                 153  5.30  200.3      143      164
##  warmed  Graminoid       156  3.81   55.1      148      164
##  ambient Graminoid       160  3.81   55.1      152      167
##  warmed  Vine            220 21.55 1233.0      178      263
##  ambient Vine            224 21.45 1233.0      182      266
##
## 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           -3.904  4.51   25.9 -0.865  0.9868
##  warmed Forb - warmed                  0.179  5.06 1259.7  0.035  1.0000
##  warmed Forb - ambient                -3.725  6.76  135.5 -0.551  0.9993
##  warmed Forb - warmed Graminoid       -6.475  3.43 1267.8 -1.888  0.5596
##  warmed Forb - ambient Graminoid     -10.379  5.74   69.7 -1.809  0.6162
```

```
##  warmed Forb - warmed Vine             -71.041 21.44 1271.2 -3.313  0.0213
##  warmed Forb - ambient Vine            -74.945 21.83 1154.7 -3.433  0.0143
##  ambient Forb - warmed                   4.083  6.80  140.6  0.600  0.9988
##  ambient Forb - ambient                  0.179  5.06 1259.7  0.035  1.0000
##  ambient Forb - warmed Graminoid        -2.571  5.60   64.7 -0.459  0.9998
##  ambient Forb - ambient Graminoid       -6.475  3.43 1267.8 -1.888  0.5596
##  ambient Forb - warmed Vine            -67.137 22.00 1157.7 -3.052  0.0477
##  ambient Forb - ambient Vine           -71.041 21.44 1271.2 -3.313  0.0213
##  warmed  - ambient                      -3.904  4.51   25.9 -0.865  0.9868
##  warmed  - warmed Graminoid             -6.654  5.28 1264.2 -1.261  0.9130
##  warmed  - ambient Graminoid           -10.558  7.02  155.4 -1.503  0.8047
##  warmed  - warmed Vine                 -71.221 21.79 1273.3 -3.269  0.0245
##  warmed  - ambient Vine                -75.125 22.17 1174.9 -3.388  0.0166
##  ambient  - warmed Graminoid            -2.751  6.86  144.4 -0.401  0.9999
##  ambient  - ambient Graminoid           -6.654  5.28 1264.2 -1.261  0.9130
##  ambient  - warmed Vine                -67.317 22.32 1176.3 -3.016  0.0531
##  ambient  - ambient Vine               -71.221 21.79 1273.3 -3.269  0.0245
##  warmed Graminoid - ambient Graminoid   -3.904  4.51   25.9 -0.865  0.9868
##  warmed Graminoid - warmed Vine        -64.566 21.49 1271.7 -3.004  0.0548
##  warmed Graminoid - ambient Vine       -68.470 21.86 1159.0 -3.132  0.0376
##  ambient Graminoid - warmed Vine       -60.662 22.06 1160.7 -2.750  0.1091
##  ambient Graminoid - ambient Vine      -64.566 21.49 1271.7 -3.004  0.0548
##  warmed Vine - ambient Vine             -3.904  4.51   25.9 -0.865  0.9868
##
## 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
```

KBS Plot-level Mixed Effects Models:

```
mod1p <- lmer(plot_half_cover_date ~ state + (1 | plot), green_kbsp,
    REML = FALSE)
```

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

```
mod2p <- lmer(plot_half_cover_date ~ state + year_factor + (1 |
    plot), green_kbsp, REML = FALSE)
```

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

```
mod3p <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
    plot), green_kbsp, REML = FALSE)
```

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

```
anova(mod1p, mod2p, mod3p)  #mod2p
```

```
## Data: green_kbsp
## Models:
## mod1p: plot_half_cover_date ~ state + (1 | plot)
## mod2p: plot_half_cover_date ~ state + year_factor + (1 | plot)
## mod3p: plot_half_cover_date ~ state * year_factor + (1 | plot)
##       npar    AIC    BIC  logLik deviance   Chisq Df Pr(>Chisq)
## mod1p    4 1308.6 1319.8 -650.32   1300.6
## mod2p    5 1289.2 1303.1 -639.60   1279.2 21.4246  1   3.68e-06 ***
## mod3p    6 1290.7 1307.4 -639.35   1278.7  0.5025  1     0.4784
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod2p)
```

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

```
##   method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + year_factor + (1 | plot)
##    Data: green_kbsp
##
##      AIC      BIC   logLik deviance df.resid
##   1289.2   1303.1   -639.6   1279.2      115
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9138 -0.8568  0.1682  1.0336  1.8931
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    0      0.00
##  Residual             2495     49.95
## Number of obs: 120, groups:  plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   121.817     11.626 120.000  10.478  < 2e-16 ***
## stateambient   14.700      9.120 120.000   1.612     0.11
## year_factor    15.617      3.224 120.000   4.843 3.85e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn
## stateambint -0.392
## year_factor -0.832  0.000
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
mod2p.2 <- lmer(plot_half_cover_date ~ state + year_factor +
    insecticide + (1 | plot), green_kbsp, REML = FALSE)
```

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

```
anova(mod2p, mod2p.2)  #mod2p
```

```
## Data: green_kbsp
## Models:
## mod2p: plot_half_cover_date ~ state + year_factor + (1 | plot)
## mod2p.2: plot_half_cover_date ~ state + year_factor + insecticide + (1 |
## mod2p.2:     plot)
##         npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod2p      5 1289.2 1303.1 -639.60   1279.2
## mod2p.2    6 1291.0 1307.8 -639.52   1279.0 0.1647  1     0.6849
```

UMBS Mixed Effects Models

```
# umod4 (and umod6) are pretty complex in terms of
# interpretation (they actually don't have many parameters
# though). We could consider an alternative umodel that's
# simpler to understand and also one that provides more
```

```
# insight about the species. That would be something like
# this:
umod7 <- lmer(spp_half_cover_date ~ state + species + (1 + year_factor |
    plot), green_umbs, REML = FALSE)
```

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

```
umod7a <- lmer(spp_half_cover_date ~ state + species + year_factor +
    (1 | plot), green_umbs, REML = FALSE)
umod7b <- lmer(spp_half_cover_date ~ state * year_factor + species +
    (1 | plot), green_umbs, REML = FALSE)
umod7c <- lmer(spp_half_cover_date ~ state + species + year_factor +
    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:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##        npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## umod7a   19 7497.7 7585.7 -3729.8   7459.7
## umod7    20 7509.8 7602.4 -3734.9   7469.8     0  1          1
```

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

```
## Data: green_umbs
## Models:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod7a   19 7497.7 7585.7 -3729.8   7459.7
## umod7b   20 7499.6 7592.2 -3729.8   7459.6 0.0588  1     0.8085
```

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

```
## Data: green_umbs
## Models:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7c: spp_half_cover_date ~ state + species + year_factor + insecticide +
## umod7c:     (1 | plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod7a   19 7497.7 7585.7 -3729.8   7459.7
## umod7c   20 7499.7 7592.3 -3729.8   7459.7 0.0208  1     0.8854
```

```
summary(umod7a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   7497.7   7585.7  -3729.8   7459.7      739
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -2.5835 -0.6079 -0.2494  0.4752  3.1253
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    9.4    3.066
##  Residual             1092.1   33.046
## Number of obs: 758, groups:  plot, 24
##
## Fixed effects:
##               Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)  131.17082   13.13233 698.99506   9.988  < 2e-16 ***
## stateambient  -0.51847    2.73549  18.95368  -0.190 0.851689
## speciesAnsp    0.08818   15.69454 746.26222   0.006 0.995519
## speciesApan   51.11999   17.76623 756.25039   2.877 0.004123 **
## speciesAssp   29.71719   14.22495 719.48551   2.089 0.037050 *
## speciesCape   20.04356   13.15689 739.06765   1.523 0.128080
## speciesCest    4.47430   12.96925 743.11707   0.345 0.730197
## speciesDasp    5.23558   13.02731 743.48921   0.402 0.687878
## speciesFrve   10.38974   14.50633 724.31057   0.716 0.474086
## speciesHisp   31.07700   14.95040 757.06388   2.079 0.037984 *
## speciesHype    9.44938   13.35464 750.28371   0.708 0.479430
## speciesPosp   21.66218   12.98183 744.17278   1.669 0.095607 .
## speciesPtaq   40.75255   13.15100 749.25912   3.099 0.002016 **
## speciesRuac    5.98322   13.08141 748.10341   0.457 0.647528
## speciesSosp   23.83121   14.75435 753.60933   1.615 0.106686
## speciesSyla   56.42041   16.75388 757.29228   3.368 0.000797 ***
## year_factor    3.89359    0.86526 737.50628   4.500  7.9e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 17 > 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 * year_factor + species + (1 | plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   7499.6   7592.2  -3729.8   7459.6      738
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.5719 -0.6104 -0.2469  0.4666  3.1257
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    9.434  3.072
##  Residual             1091.945 33.045
## Number of obs: 758, groups:  plot, 24
##
```

```
## Fixed effects:
##                           Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)              131.8256    13.4082 703.4460   9.832  < 2e-16 ***
## stateambient              -1.7775     5.8711 307.8369  -0.303 0.762288
## year_factor                3.6822     1.2283 735.0831   2.998 0.002811 **
## speciesAnsp                0.1050    15.6942 746.3583   0.007 0.994665
## speciesApan               51.0666    17.7671 756.2431   2.874 0.004164 **
## speciesAssp               29.6707    14.2261 719.5153   2.086 0.037361 *
## speciesCape               20.0150    13.1571 739.0296   1.521 0.128628
## speciesCest                4.4662    12.9689 743.1594   0.344 0.730661
## speciesDasp                5.2264    13.0270 743.5325   0.401 0.688392
## speciesFrve               10.3662    14.5064 724.3909   0.715 0.475088
## speciesHisp               31.0973    14.9501 757.0795   2.080 0.037854 *
## speciesHype                9.4365    13.3543 750.3046   0.707 0.480019
## speciesPosp               21.6472    12.9816 744.1937   1.668 0.095831 .
## speciesPtaq               40.7584    13.1506 749.3119   3.099 0.002012 **
## speciesRuac                5.9792    13.0810 748.1476   0.457 0.647738
## speciesSosp               23.8092    14.7542 753.6366   1.614 0.107005
## speciesSyla               56.4880    16.7555 757.2835   3.371 0.000786 ***
## stateambient:year_factor   0.4114     1.6970 737.1355   0.242 0.808507
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
summary(umod7c)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + species + year_factor + insecticide +
##     (1 | plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   7499.7   7592.3  -3729.8   7459.7      738
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.5860 -0.6093 -0.2500  0.4756  3.1306
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    9.418  3.069
##  Residual             1092.013 33.046
## Number of obs: 758, groups:  plot, 24
##
## Fixed effects:
##                          Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)             130.99606   13.18765 668.26073   9.933  < 2e-16 ***
## stateambient             -0.51887    2.73602  19.01321  -0.190 0.851599
## speciesAnsp               0.05593   15.69604 746.83227   0.004 0.997158
## speciesApan              50.95022   17.80572 757.89874   2.861 0.004333 **
```

```
## speciesAssp            29.77413   14.23004 720.04210   2.092 0.036757 *
## speciesCape            20.02311   13.15757 739.59718   1.522 0.128488
## speciesCest             4.45599   12.96981 743.56984   0.344 0.731270
## speciesDasp             5.21894   13.02774 743.91429   0.401 0.688828
## speciesFrve            10.36379   14.50747 725.71680   0.714 0.475224
## speciesHisp            30.99767   14.96048 757.70548   2.072 0.038606 *
## speciesHype             9.41831   13.35633 750.89419   0.705 0.480931
## speciesPosp            21.64688   12.98219 744.53702   1.667 0.095850 .
## speciesPtaq            40.72289   13.15258 749.89255   3.096 0.002033 **
## speciesRuac             5.95334   13.08303 748.78234   0.455 0.649210
## speciesSosp            23.73807   14.76866 755.35081   1.607 0.108401
## speciesSyla            56.38543   16.75547 757.42449   3.365 0.000803 ***
## year_factor             3.89196    0.86531 737.13965   4.498 7.98e-06 ***
## insecticideno_insects   0.39630    2.75007  19.48138   0.144 0.886897
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
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           39    39.2     1  18.95  0.0359    0.8517
## species     129594  9256.7    14 743.23  8.4764 < 2.2e-16 ***
## year_factor  22113 22113.4     1 737.51 20.2493 7.896e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## $`emmeans of year_factor`
##  year_factor emmean   SE   df lower.CL upper.CL
##         3.07    164 2.14 95.8      159      168
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $` of year_factor`
##  1         estimate SE df z.ratio p.value
##  (nothing)   nonEst NA NA NA      NA
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
```

```
emmeans(umod7a, list(pairwise ~ species), adjust = "tukey")
```

```
## $`emmeans of species`
##  species emmean    SE  df lower.CL upper.CL
##  Amla       143 12.86 756      118      168
##  Ansp       143  9.40 774      124      161
```

```
##  Apan       194 12.86 764      169      219
##  Assp       173  6.72 696      159      186
##  Cape       163  3.91 574      155      171
##  Cest       147  3.15 446      141      154
##  Dasp       148  3.36 493      141      155
##  Frve       153  7.31 680      139      168
##  Hisp       174  8.20 771      158      190
##  Hype       152  4.62 647      143      161
##  Posp       165  3.22 466      158      171
##  Ptaq       184  3.89 554      176      191
##  Ruac       149  3.64 521      142      156
##  Sosp       167  7.87 694      151      182
##  Syla       199 11.39 730      177      222
##
## Results are averaged over the levels of: state
## 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  -0.0882 15.96 772 -0.006  1.0000
##  Amla - Apan -51.1200 18.04 776 -2.834  0.2311
##  Amla - Assp -29.7172 14.50 756 -2.049  0.7680
##  Amla - Cape -20.0436 13.39 768 -1.497  0.9766
##  Amla - Cest  -4.4743 13.20 770 -0.339  1.0000
##  Amla - Dasp  -5.2356 13.26 770 -0.395  1.0000
##  Amla - Frve -10.3897 14.78 759 -0.703  1.0000
##  Amla - Hisp -31.0770 15.18 776 -2.048  0.7690
##  Amla - Hype  -9.4494 13.58 774 -0.696  1.0000
##  Amla - Posp -21.6622 13.21 771 -1.640  0.9493
##  Amla - Ptaq -40.7525 13.37 773 -3.048  0.1379
##  Amla - Ruac  -5.9832 13.30 773 -0.450  1.0000
##  Amla - Sosp -23.8312 14.99 775 -1.590  0.9607
##  Amla - Syla -56.4204 17.01 776 -3.317  0.0649
##  Ansp - Apan -51.0318 15.91 775 -3.208  0.0893
##  Ansp - Assp -29.6290 11.49 775 -2.579  0.3855
##  Ansp - Cape -19.9554 10.15 773 -1.966  0.8177
##  Ansp - Cest  -4.3861  9.84 771 -0.446  1.0000
##  Ansp - Dasp  -5.1474  9.90 770 -0.520  1.0000
##  Ansp - Frve -10.3016 11.80 775 -0.873  0.9999
##  Ansp - Hisp -30.9888 12.39 770 -2.501  0.4407
##  Ansp - Hype  -9.3612 10.44 770 -0.896  0.9999
##  Ansp - Posp -21.5740  9.88 771 -2.183  0.6769
##  Ansp - Ptaq -40.6644 10.12 774 -4.019  0.0057
##  Ansp - Ruac  -5.8950 10.00 767 -0.589  1.0000
##  Ansp - Sosp -23.7430 12.20 772 -1.947  0.8283
##  Ansp - Syla -56.3322 14.76 766 -3.817  0.0122
##  Apan - Assp  21.4028 14.48 764  1.478  0.9790
##  Apan - Cape  31.0764 13.38 772  2.323  0.5736
##  Apan - Cest  46.6457 13.19 774  3.536  0.0326
##  Apan - Dasp  45.8844 13.25 774  3.463  0.0413
##  Apan - Frve  40.7303 14.80 759  2.752  0.2761
##  Apan - Hisp  20.0430 15.20 776  1.319  0.9928
##  Apan - Hype  41.6706 13.56 775  3.072  0.1294
```

```
##  Apan - Posp  29.4578 13.21 773  2.230  0.6429
##  Apan - Ptaq  10.3674 13.36 776  0.776  1.0000
##  Apan - Ruac  45.1368 13.30 775  3.394  0.0513
##  Apan - Sosp  27.2888 15.06 772  1.812  0.8929
##  Apan - Syla  -5.3004 17.13 768 -0.309  1.0000
##  Assp - Cape   9.6736  7.70 767  1.256  0.9956
##  Assp - Cest  25.2429  7.34 773  3.440  0.0444
##  Assp - Dasp  24.4816  7.42 775  3.298  0.0687
##  Assp - Frve  19.3274  9.82 768  1.967  0.8170
##  Assp - Hisp  -1.3598 10.51 776 -0.129  1.0000
##  Assp - Hype  20.2678  8.07 775  2.512  0.4328
##  Assp - Posp   8.0550  7.37 772  1.093  0.9990
##  Assp - Ptaq -11.0354  7.68 775 -1.438  0.9837
##  Assp - Ruac  23.7340  7.55 773  3.142  0.1074
##  Assp - Sosp   5.8860 10.29 763  0.572  1.0000
##  Assp - Syla -26.7032 13.12 768 -2.035  0.7769
##  Cape - Cest  15.5693  4.90 763  3.179  0.0970
##  Cape - Dasp  14.8080  5.05 768  2.933  0.1837
##  Cape - Frve   9.6538  8.22 765  1.175  0.9978
##  Cape - Hisp -11.0334  9.03 774 -1.222  0.9967
##  Cape - Hype  10.5942  5.94 775  1.782  0.9048
##  Cape - Posp  -1.6186  4.94 762 -0.327  1.0000
##  Cape - Ptaq -20.7090  5.41 773 -3.830  0.0116
##  Cape - Ruac  14.0603  5.25 776  2.679  0.3196
##  Cape - Sosp  -3.7876  8.74 761 -0.433  1.0000
##  Cape - Syla -36.3768 12.01 751 -3.030  0.1445
##  Cest - Dasp  -0.7613  4.46 753 -0.171  1.0000
##  Cest - Frve  -5.9154  7.88 762 -0.751  1.0000
##  Cest - Hisp -26.6027  8.71 771 -3.054  0.1356
##  Cest - Hype  -4.9751  5.49 771 -0.907  0.9999
##  Cest - Posp -17.1879  4.37 749 -3.937  0.0078
##  Cest - Ptaq -36.2782  4.88 768 -7.441  <.0001
##  Cest - Ruac  -1.5089  4.68 764 -0.322  1.0000
##  Cest - Sosp -19.3569  8.40 762 -2.305  0.5872
##  Cest - Syla -51.9461 11.76 758 -4.416  0.0011
##  Dasp - Frve  -5.1541  7.96 761 -0.647  1.0000
##  Dasp - Hisp -25.8414  8.78 769 -2.944  0.1789
##  Dasp - Hype  -4.2138  5.61 769 -0.751  1.0000
##  Dasp - Posp -16.4266  4.52 753 -3.632  0.0236
##  Dasp - Ptaq -35.5170  5.01 767 -7.088  <.0001
##  Dasp - Ruac  -0.7476  4.82 762 -0.155  1.0000
##  Dasp - Sosp -18.5956  8.47 761 -2.194  0.6690
##  Dasp - Syla -51.1848 11.82 759 -4.330  0.0016
##  Frve - Hisp -20.6873 10.85 774 -1.907  0.8495
##  Frve - Hype   0.9404  8.58 766  0.110  1.0000
##  Frve - Posp -11.2724  7.91 764 -1.425  0.9849
##  Frve - Ptaq -30.3628  8.21 757 -3.699  0.0186
##  Frve - Ruac   4.4065  8.08 764  0.545  1.0000
##  Frve - Sosp -13.4415 10.63 765 -1.265  0.9953
##  Frve - Syla -46.0307 13.40 772 -3.435  0.0451
##  Hisp - Hype  21.6276  9.33 763  2.319  0.5768
##  Hisp - Posp   9.4148  8.74 771  1.077  0.9991
##  Hisp - Ptaq  -9.6755  9.00 770 -1.075  0.9992
##  Hisp - Ruac  25.0938  8.88 766  2.825  0.2354
```

```
##  Hisp - Sosp   7.2458 11.27 776  0.643  1.0000
##  Hisp - Syla -25.3434 13.91 776 -1.821  0.8891
##  Hype - Posp -12.2128  5.52 772 -2.211  0.6571
##  Hype - Ptaq -31.3032  5.93 773 -5.275  <.0001
##  Hype - Ruac   3.4662  5.76 768  0.601  1.0000
##  Hype - Sosp -14.3818  9.09 759 -1.583  0.9621
##  Hype - Syla -46.9710 12.22 765 -3.843  0.0111
##  Posp - Ptaq -19.0904  4.93 769 -3.874  0.0099
##  Posp - Ruac  15.6790  4.74 766  3.310  0.0664
##  Posp - Sosp  -2.1690  8.43 763 -0.257  1.0000
##  Posp - Syla -34.7582 11.78 758 -2.950  0.1762
##  Ptaq - Ruac  34.7693  5.21 772  6.677  <.0001
##  Ptaq - Sosp  16.9213  8.69 764  1.947  0.8281
##  Ptaq - Syla -15.6679 11.95 766 -1.311  0.9933
##  Ruac - Sosp -17.8480  8.59 764 -2.077  0.7500
##  Ruac - Syla -50.4372 11.89 763 -4.243  0.0023
##  Sosp - Syla -32.5892 13.61 773 -2.394  0.5200
##
## Results are averaged over the levels of: state
## 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_factor |
    plot), green_umbs, REML = FALSE)
```

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

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

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

```
umod9a <- lmer(spp_half_cover_date ~ state + origin + year_factor +
    (1 | plot), green_umbs, REML = FALSE)
anova(umod8, umod9)  # umodel 9 is a better fit to data
```

```
## Data: green_umbs
## Models:
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## umod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##       npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod9    9 7566.6 7608.3 -3774.3   7548.6
## umod8   12 7567.1 7622.7 -3771.5   7543.1 5.4874  3     0.1394
```

```
anova(umod9, umod9a)  # umod 9a?
```

```
## Data: green_umbs
## Models:
## umod9a: spp_half_cover_date ~ state + origin + year_factor + (1 | plot)
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
##        npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## umod9a    8 7549.8 7586.9 -3766.9   7533.8
## umod9     9 7566.6 7608.3 -3774.3   7548.6     0  1          1
```

```
summary(umod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + year_factor + (1 | plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   7549.8   7586.9  -3766.9   7533.8      750
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4628 -0.6648 -0.2797  0.6304  2.9794
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    6.849  2.617
##  Residual             1207.175 34.744
## Number of obs: 758, groups:  plot, 24
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)  149.9167     3.5890 192.7399  41.771  < 2e-16 ***
## stateambient  -0.7694     2.7599  19.4947  -0.279   0.7834
## origin         1.4282     3.7694 745.6043   0.379   0.7049
## originBoth     9.9785     5.6683 756.3062   1.760   0.0787 .
## originExotic -14.2582     2.8640 755.5438  -4.978 7.95e-07 ***
## year_factor    4.4146     0.8912 738.1225   4.954 9.04e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn origin orgnBt orgnEx
## stateambint -0.378
## origin      -0.250  0.006
## originBoth  -0.147 -0.078  0.167
## originExotc -0.320  0.004  0.335  0.221
## year_factor -0.741 -0.010 -0.025  0.002 -0.043
```

```
anova(umod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state     126   126.1     1  51.70  0.1051    0.7471
## origin  43190 14396.8     3 737.23 11.9967 1.125e-07 ***
## ---
## 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 2.51  59.6      158      168
##  ambient Native    163 2.51  58.9      158      168
##  warmed            165 3.64 250.2      158      172
```

```
##  ambient           164 3.65 256.2      157      171
##  warmed  Both      173 5.74 531.3      162      185
##  ambient Both      173 5.53 472.5      162      184
##  warmed  Exotic    149 2.69  80.4      144      155
##  ambient Exotic    148 2.70  82.4      143      154
##
## 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    0.769 2.92  26.7  0.263  1.0000
##  warmed Native - warmed            -1.428 3.78 751.1 -0.377  0.9999
##  warmed Native - ambient           -0.659 4.79 192.2 -0.137  1.0000
##  warmed Native - warmed Both       -9.978 5.71 764.1 -1.747  0.6562
##  warmed Native - ambient Both      -9.209 6.23 332.3 -1.478  0.8185
##  warmed Native - warmed Exotic     14.258 2.88 760.6  4.952  <.0001
##  warmed Native - ambient Exotic    15.028 4.11 107.6  3.657  0.0091
##  ambient Native - warmed           -2.198 4.77 185.1 -0.461  0.9998
##  ambient Native - ambient          -1.428 3.78 751.1 -0.377  0.9999
##  ambient Native - warmed Both     -10.748 6.60 415.7 -1.629  0.7325
##  ambient Native - ambient Both     -9.978 5.71 764.1 -1.747  0.6562
##  ambient Native - warmed Exotic    13.489 4.10 104.2  3.293  0.0285
##  ambient Native - ambient Exotic   14.258 2.88 760.6  4.952  <.0001
##  warmed  - ambient                  0.769 2.92  26.7  0.263  1.0000
##  warmed  - warmed Both             -8.550 6.31 764.2 -1.355  0.8771
##  warmed  - ambient Both            -7.781 6.77 394.9 -1.149  0.9454
##  warmed  - warmed Exotic           15.686 3.91 748.3  4.012  0.0017
##  warmed  - ambient Exotic          16.456 4.88 202.8  3.375  0.0196
##  ambient  - warmed Both            -9.320 7.13 476.3 -1.307  0.8961
##  ambient  - ambient Both           -8.550 6.31 764.2 -1.355  0.8771
##  ambient  - warmed Exotic          14.917 4.89 205.1  3.052  0.0515
##  ambient  - ambient Exotic         15.686 3.91 748.3  4.012  0.0017
##  warmed Both - ambient Both         0.769 2.92  26.7  0.263  1.0000
##  warmed Both - warmed Exotic       24.237 5.80 764.3  4.177  0.0009
##  warmed Both - ambient Exotic      25.006 6.68 429.2  3.743  0.0050
##  ambient Both - warmed Exotic      23.467 6.31 341.7  3.720  0.0056
##  ambient Both - ambient Exotic     24.237 5.80 764.3  4.177  0.0009
##  warmed Exotic - ambient Exotic     0.769 2.92  26.7  0.263  1.0000
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

```
# including growth form - first with interaction term
green_umbs <- within(green_umbs, growth_habit <- relevel(factor(growth_habit),
    ref = "Forb"))  # releveling so forb is the reference
umod10 <- lmer(spp_half_cover_date ~ state * growth_habit + (1 +
    year_factor | plot), green_umbs, REML = FALSE)
```

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

```
umod11 <- lmer(spp_half_cover_date ~ state + growth_habit + (1 +
    year_factor | plot), green_umbs, REML = FALSE)
```

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

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

```
## Data: green_umbs
## Models:
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## umod11:     plot)
## umod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## umod10:     plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod11    9 7596.5 7638.2 -3789.3   7578.5
## umod10   12 7599.7 7655.3 -3787.9   7575.7 2.7863  3     0.4258
```

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

```
## Data: green_umbs
## Models:
## umod11a: spp_half_cover_date ~ state + growth_habit + year_factor + (1 |
## umod11a:     plot)
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## umod11:     plot)
##         npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## umod11a    8 7581.2 7618.3 -3782.6   7565.2
## umod11     9 7596.5 7638.2 -3789.3   7578.5     0  1          1
```

```
summary(umod11a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + growth_habit + year_factor + (1 |
##     plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   7581.2   7618.3  -3782.6   7565.2      750
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4212 -0.7012 -0.3584  0.7439  2.6628
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    9.641  3.105
##  Residual             1256.137 35.442
## Number of obs: 758, groups:  plot, 24
##
## Fixed effects:
##                       Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)           145.8170     3.6139 172.1373  40.349  < 2e-16 ***
## stateambient           -0.2661     2.8843  19.8044  -0.092   0.9274
## growth_habit           15.0043     8.7901 751.3840   1.707   0.0882 .
## growth_habitGraminoid  -0.6708     2.6768 757.9303  -0.251   0.8022
## growth_habitTree      -16.9489    13.6146 744.4640  -1.245   0.2136
## year_factor             4.3214     0.9101 738.3063   4.748 2.46e-06 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_T
## stateambint -0.397
## growth_habt -0.097 -0.037
## grwth_hbtGr -0.293  0.006  0.119
## grwth_hbtTr -0.010 -0.012  0.024  0.078
## year_factor -0.764 -0.009  0.030 -0.013 -0.055
```

```
anova(umod11)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## state          36.6   36.62     1  46.04  0.0293 0.8648
## growth_habit 6429.6 2143.21     3 738.29  1.7166 0.1621
```

```
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  2.44  43.7      154      164
##  ambient Forb            159  2.43  41.0      154      164
##  warmed                  174  8.91 730.0      157      192
##  ambient                 174  8.80 726.5      157      191
##  warmed  Graminoid       158  2.69  67.9      153      164
##  ambient Graminoid       158  2.69  69.1      153      163
##  warmed  Tree            142 13.78 726.4      115      169
##  ambient Tree            142 13.74 729.3      115      169
##
## 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            0.266  3.05  26.3  0.087  1.0000
##  warmed Forb - warmed                -15.004  8.83 756.0 -1.699  0.6880
##  warmed Forb - ambient               -14.738  9.24 644.9 -1.595  0.7536
##  warmed Forb - warmed Graminoid        0.671  2.69 763.7  0.249  1.0000
##  warmed Forb - ambient Graminoid       0.937  4.08  87.6  0.230  1.0000
##  warmed Forb - warmed Tree            16.949 13.75 758.5  1.233  0.9221
##  warmed Forb - ambient Tree           17.215 14.04 700.8  1.226  0.9242
##  ambient Forb - warmed               -15.270  9.44 654.0 -1.617  0.7401
##  ambient Forb - ambient              -15.004  8.83 756.0 -1.699  0.6880
##  ambient Forb - warmed Graminoid       0.405  4.06  81.8  0.100  1.0000
##  ambient Forb - ambient Graminoid      0.671  2.69 763.7  0.249  1.0000
##  ambient Forb - warmed Tree           16.683 14.13 692.4  1.181  0.9372
##  ambient Forb - ambient Tree          16.949 13.75 758.5  1.233  0.9221
##  warmed  - ambient                     0.266  3.05  26.3  0.087  1.0000
##  warmed  - warmed Graminoid           15.675  8.93 760.8  1.756  0.6503
##  warmed  - ambient Graminoid          15.941  9.54 646.7  1.671  0.7059
##  warmed  - warmed Tree                31.953 16.15 764.4  1.979  0.4972
##  warmed  - ambient Tree               32.219 16.46 745.2  1.958  0.5116
##  ambient  - warmed Graminoid          15.409  9.33 630.3  1.651  0.7187
```

```
##  ambient  - ambient Graminoid           15.675  8.93 760.8  1.756  0.6503
##  ambient  - warmed Tree                 31.687 16.41 740.5  1.931  0.5302
##  ambient  - ambient Tree                31.953 16.15 764.4  1.979  0.4972
##  warmed Graminoid - ambient Graminoid    0.266  3.05  26.3  0.087  1.0000
##  warmed Graminoid - warmed Tree         16.278 13.81 756.0  1.179  0.9379
##  warmed Graminoid - ambient Tree        16.544 14.10 693.4  1.173  0.9394
##  ambient Graminoid - warmed Tree        16.012 14.19 687.5  1.129  0.9505
##  ambient Graminoid - ambient Tree       16.278 13.81 756.0  1.179  0.9379
##  warmed Tree - ambient Tree              0.266  3.05  26.3  0.087  1.0000
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

UMBS Plot-level Mixed Effects Models:

```
mod1pu <- lmer(plot_half_cover_date ~ state + (1 | plot), green_umbsp,
    REML = FALSE)
mod2pu <- lmer(plot_half_cover_date ~ state + year_factor + (1 |
    plot), green_umbsp, REML = FALSE)
mod3pu <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
    plot), green_umbsp, REML = FALSE)
anova(mod1pu, mod2pu, mod3pu)  #mod2pu
```

```
## Data: green_umbsp
## Models:
## mod1pu: plot_half_cover_date ~ state + (1 | plot)
## mod2pu: plot_half_cover_date ~ state + year_factor + (1 | plot)
## mod3pu: plot_half_cover_date ~ state * year_factor + (1 | plot)
##        npar    AIC    BIC  logLik deviance   Chisq Df Pr(>Chisq)
## mod1pu    4 1157.9 1169.0 -574.93   1149.9
## mod2pu    5 1129.5 1143.5 -559.78   1119.5 30.3054  1  3.691e-08 ***
## mod3pu    6 1131.4 1148.1 -559.68   1119.4  0.1868  1     0.6656
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod2pu)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + year_factor + (1 | plot)
##    Data: green_umbsp
##
##      AIC      BIC   logLik deviance df.resid
##   1129.6   1143.5   -559.8   1119.6      115
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4880 -0.5653 -0.2716  0.3457  3.8657
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)  72.17    8.495
##  Residual             600.40   24.503
## Number of obs: 120, groups:  plot, 24
```

```
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   125.358      6.208  92.959  20.194  < 2e-16 ***
## stateambient   -2.883      5.661  24.000  -0.509    0.615
## year_factor     9.442      1.582  96.000   5.969 3.99e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn
## stateambint -0.456
## year_factor -0.764  0.000
```

```
outlierTest(mod2pu)  # remove these outliers?
```

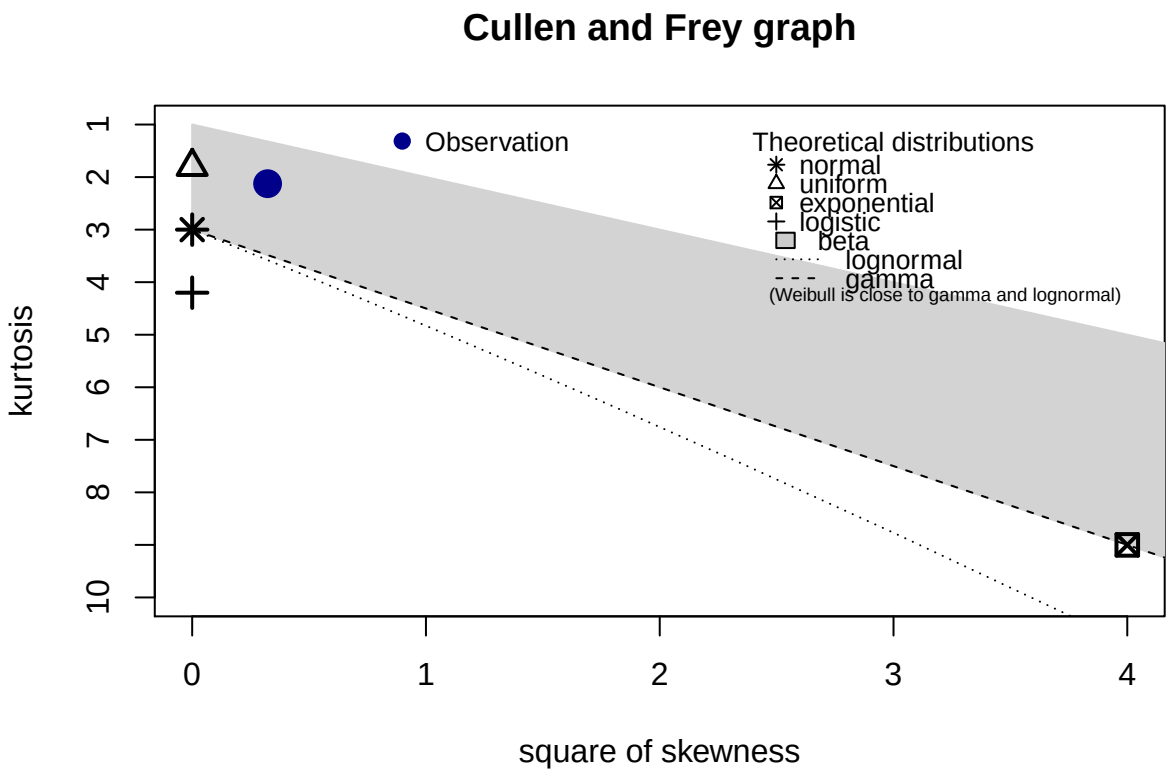
```
##     rstudent unadjusted p-value Bonferroni p
## 118 4.042307         9.6488e-05     0.011579
## 158 3.757143         2.7250e-04     0.032700
```

ORIGINAL CODE BELOW; not edited by Phoebe

can pretty much ignore everything below!

Seeing what other distribution could fit

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

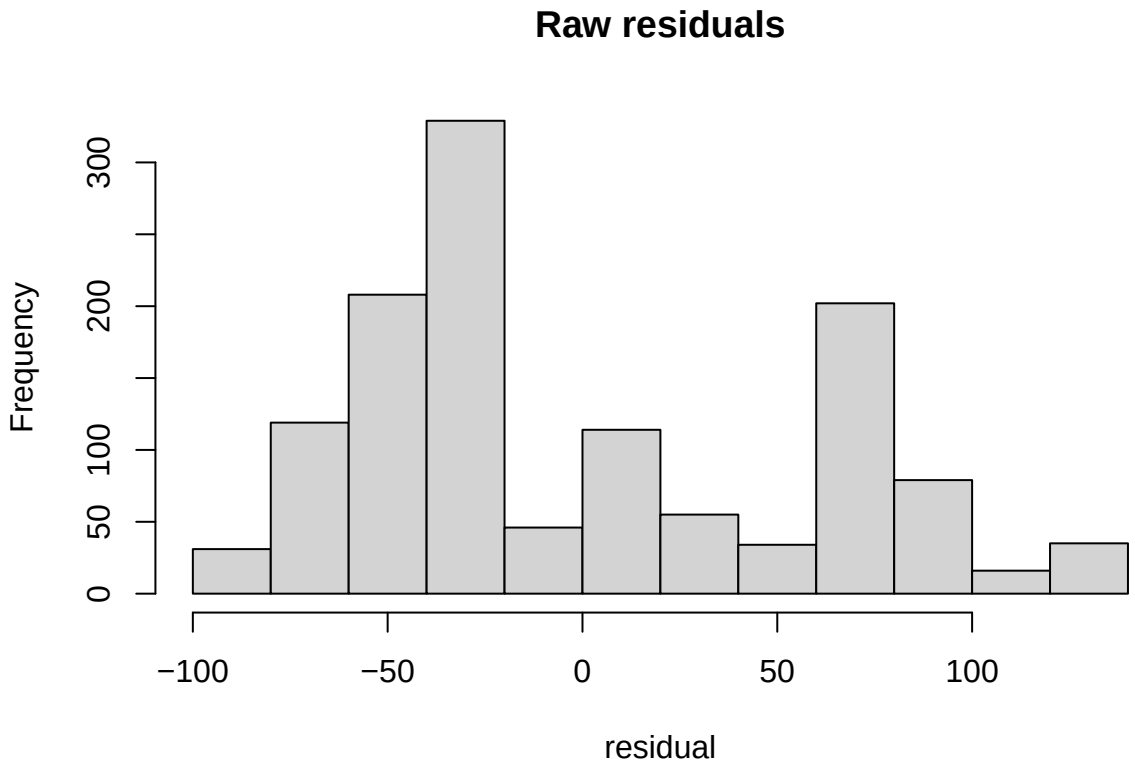



```
## summary statistics
```

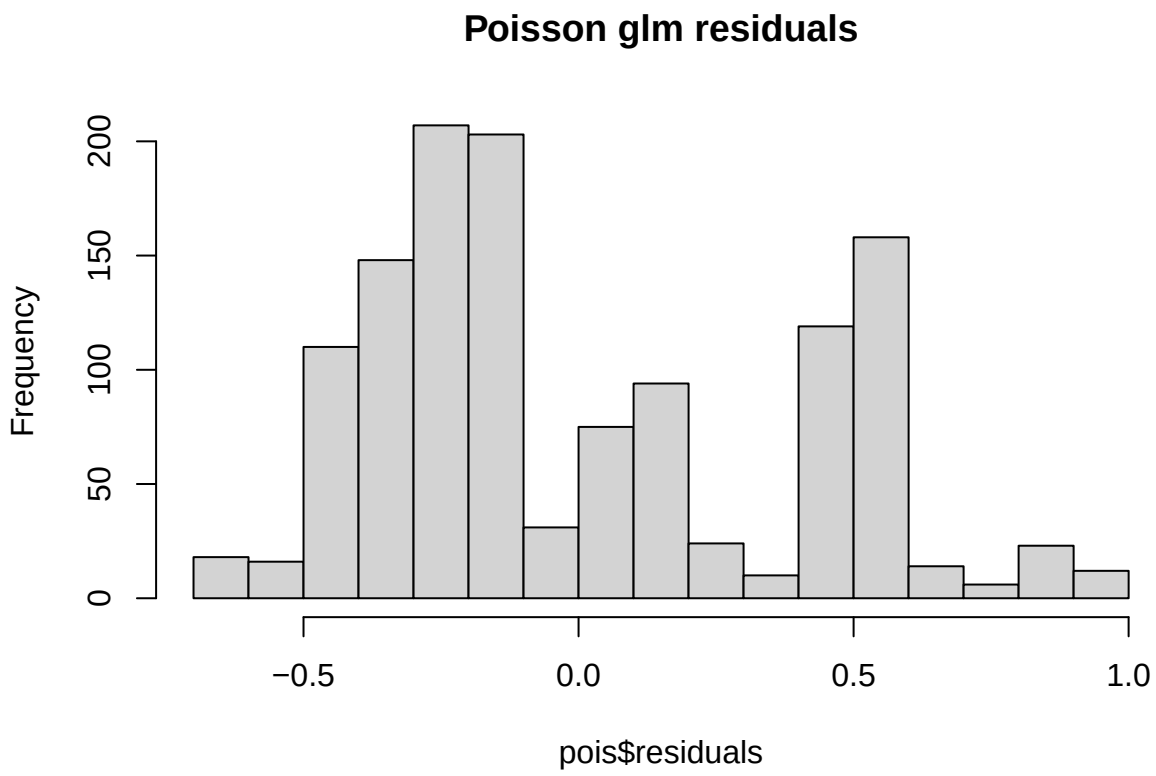
```
## ------
## min:  59   max:  289
## median:  127
## mean:  154.2169
## estimated sd:  57.9311
## estimated skewness:  0.5680173
## estimated kurtosis:  2.125259
```

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
Frequency
0
50
100
150
200
−0.5
0.0
0.5
1.0
pois$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 unide
##  - 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 unide
##  - 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?

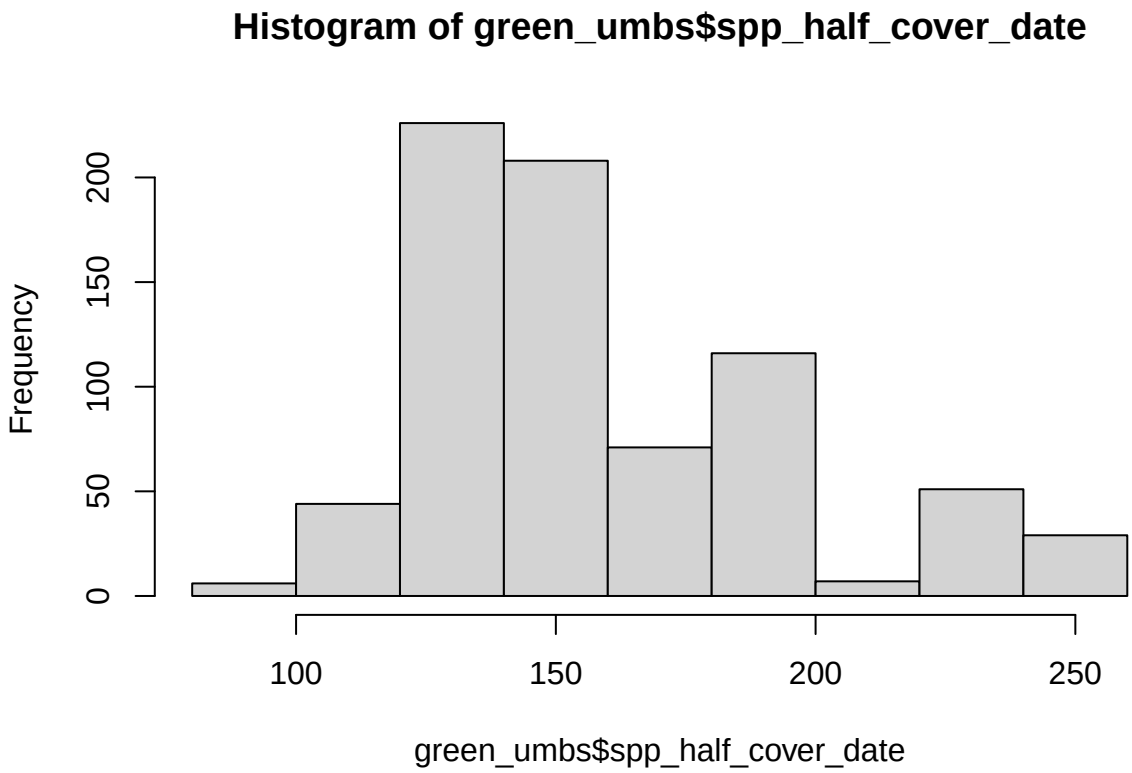
```
per1 <- adonis2(green_kbs$spp_half_cover_date ~ state * year +
    insecticide, data = green_kbs)
per1
per2 <- adonis(formula = green_kbs$spp_half_cover_date ~ state *
    year + insecticide, strata = green_kbs$plot, data = green_kbs)
per2
```

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

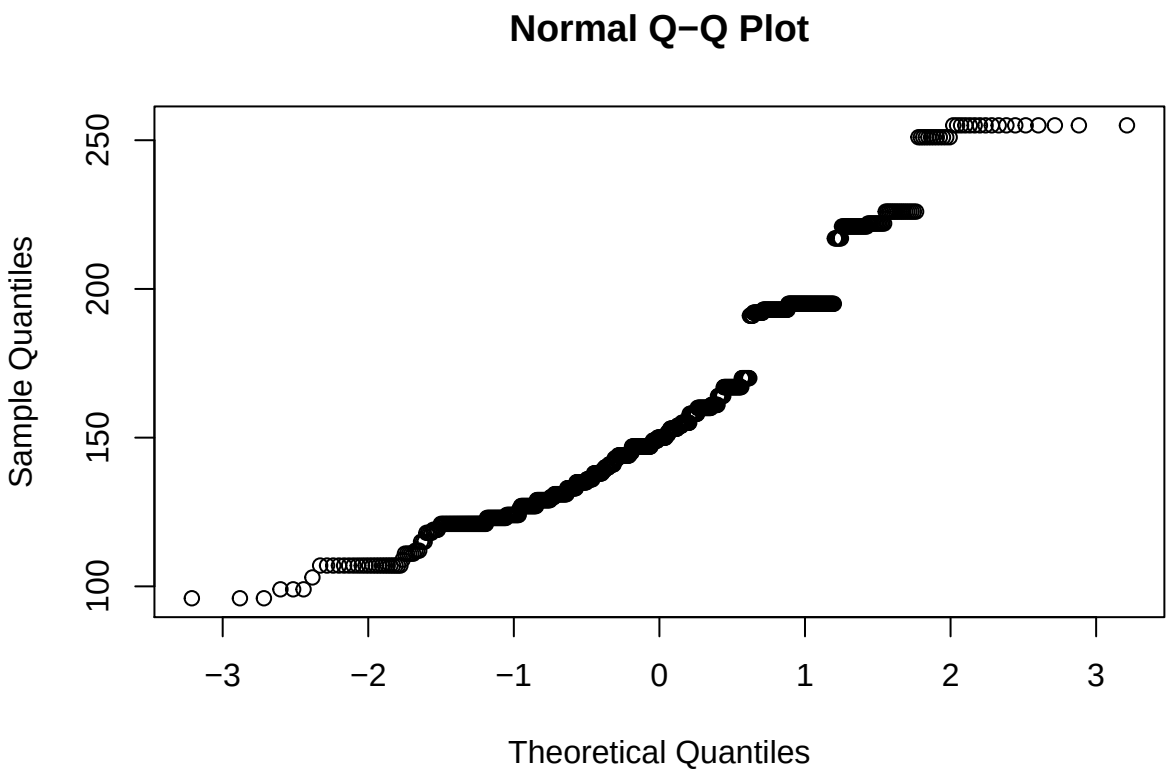
UMBS

Checking for normality

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



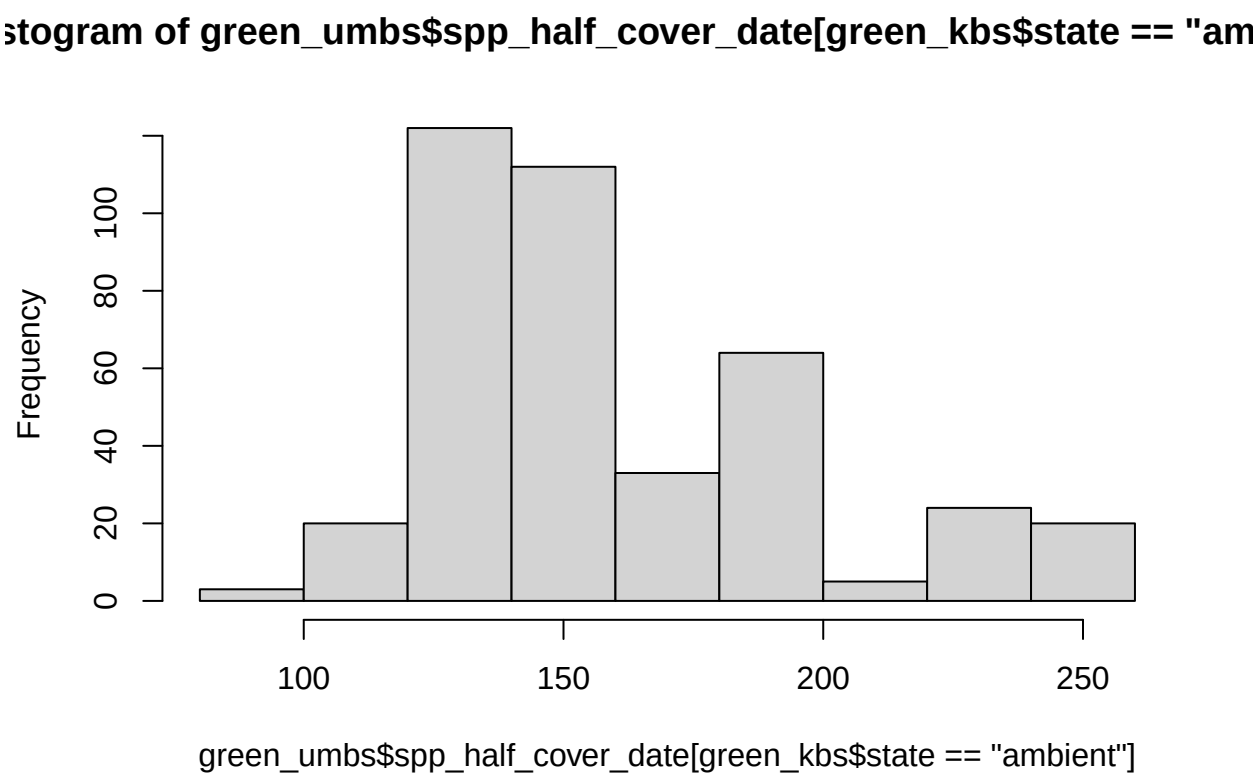

```
qqnorm(green_umbs$spp_half_cover_date)
```



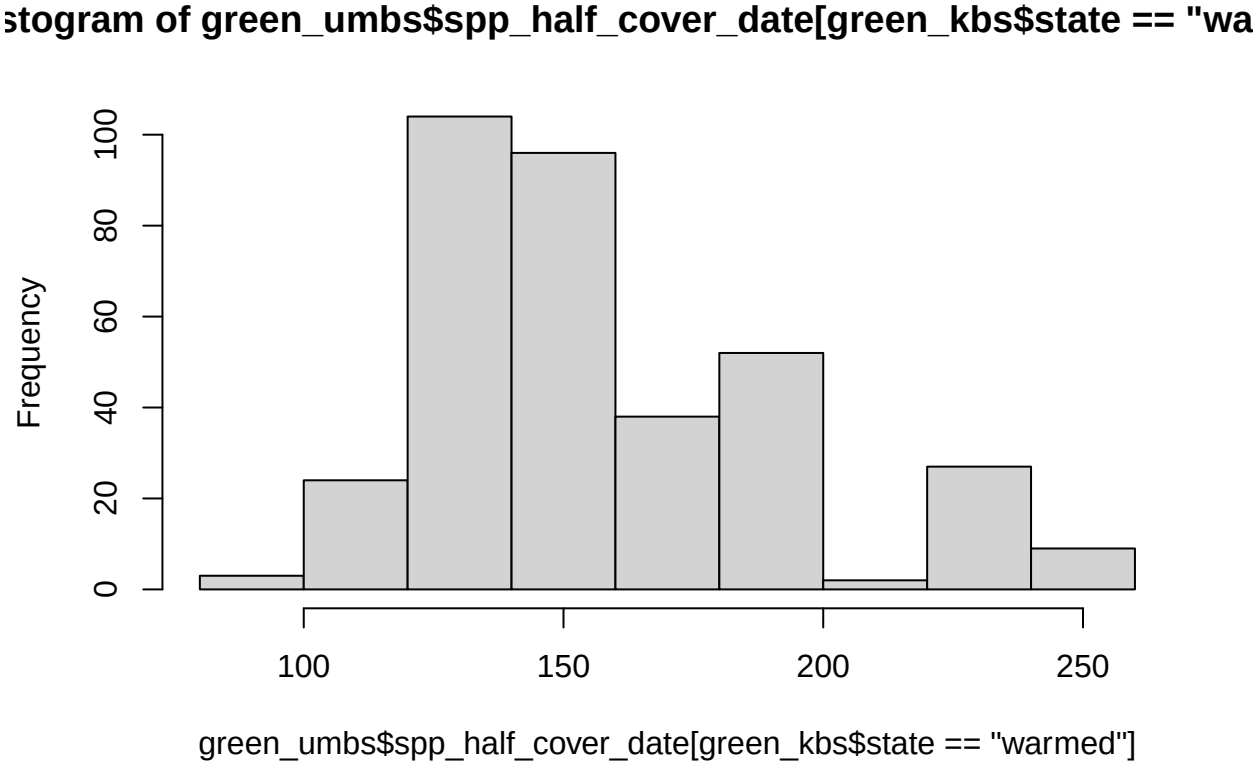

```
shapiro.test(green_umbs$spp_half_cover_date)
```

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



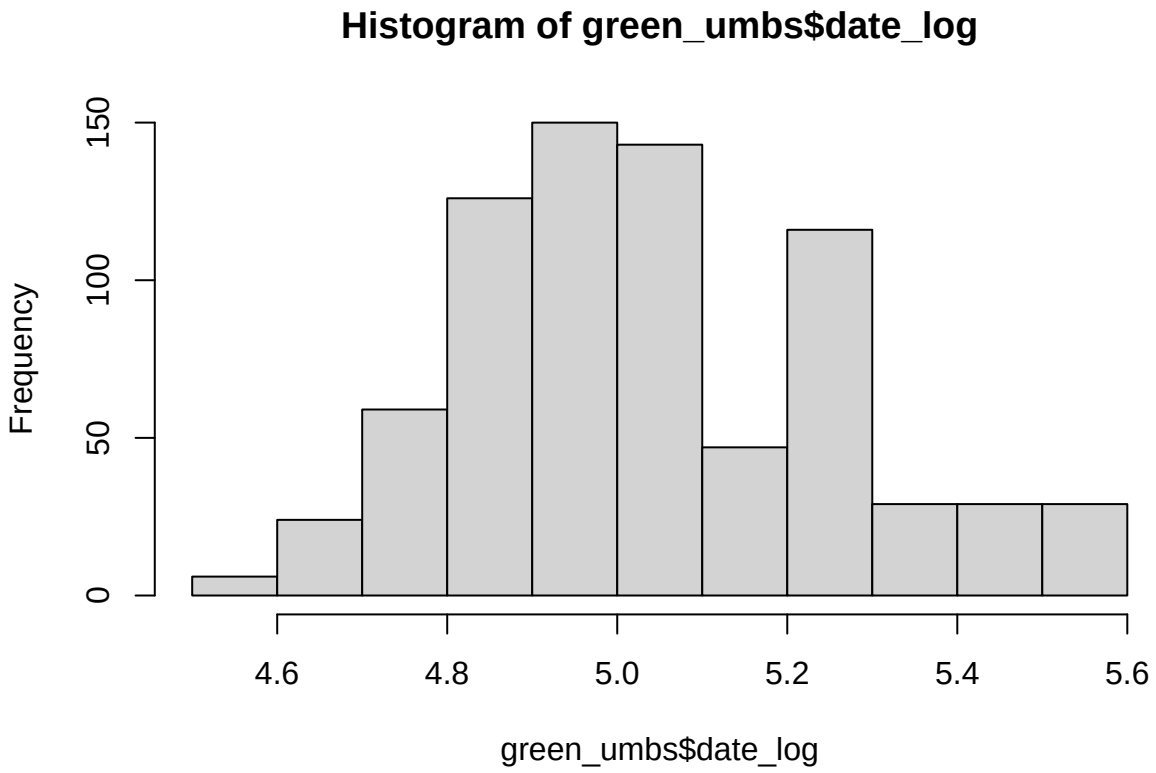

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "warmed"])
```



These look pretty good

Trying log transformation

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



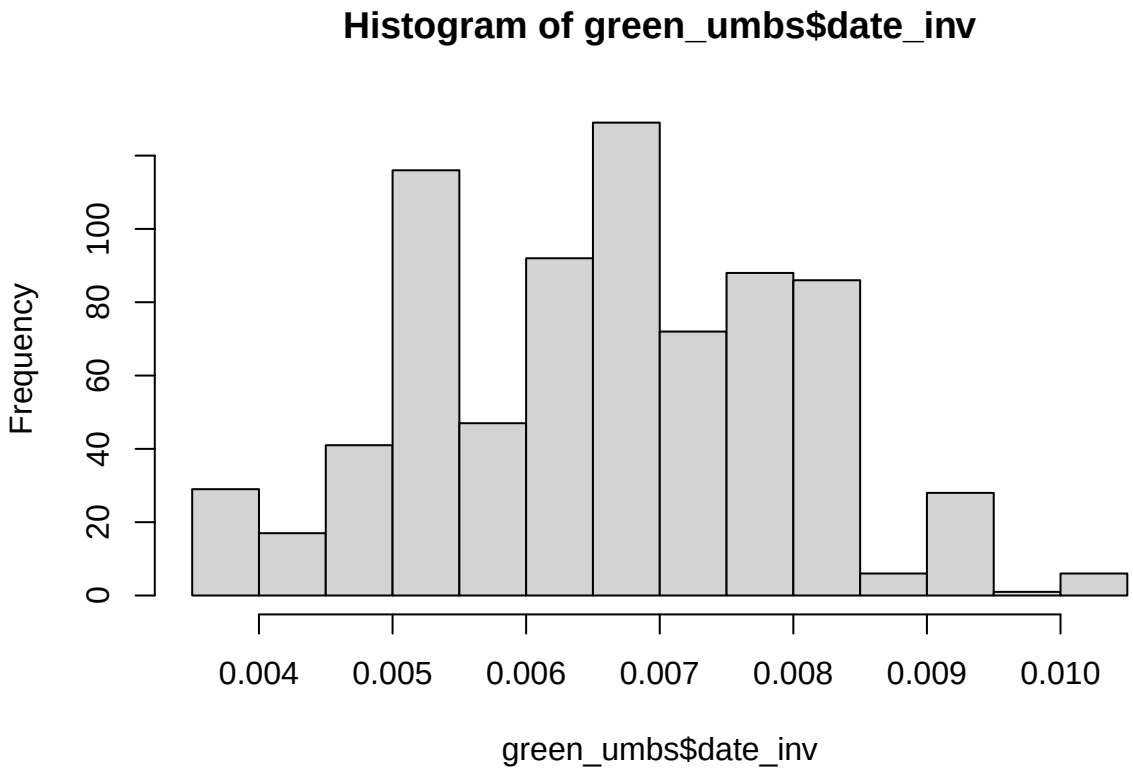

```
shapiro.test(green_umbs$date_log)
```

```
##
##  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