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)
```

```
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 %>% dplyr::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 %>% dplyr::select(-X)  # get rid of 'X' column that shows up

# check variable types
str(greenup)
```

```
## 'data.frame':    2408 obs. of  18 variables:
##  $ site               : chr  "kbs" "kbs" "kbs" "kbs" ...
##  $ plot               : chr  "A1" "A1" "A1" "A1" ...
##  $ year               : int  2016 2017 2018 2019 2020 2021 2016 2017 2016 2017 ...
##  $ species            : chr  "Acmi" "Acmi" "Acmi" "Acmi" ...
##  $ spp_half_cover_date: int  104 101 122 120 223 257 88 108 101 99 ...
##  $ min_green_date     : int  81 80 122 120 107 92 81 108 85 80 ...
##  $ treatment_key      : chr  "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" ...
```

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

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

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

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

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

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

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

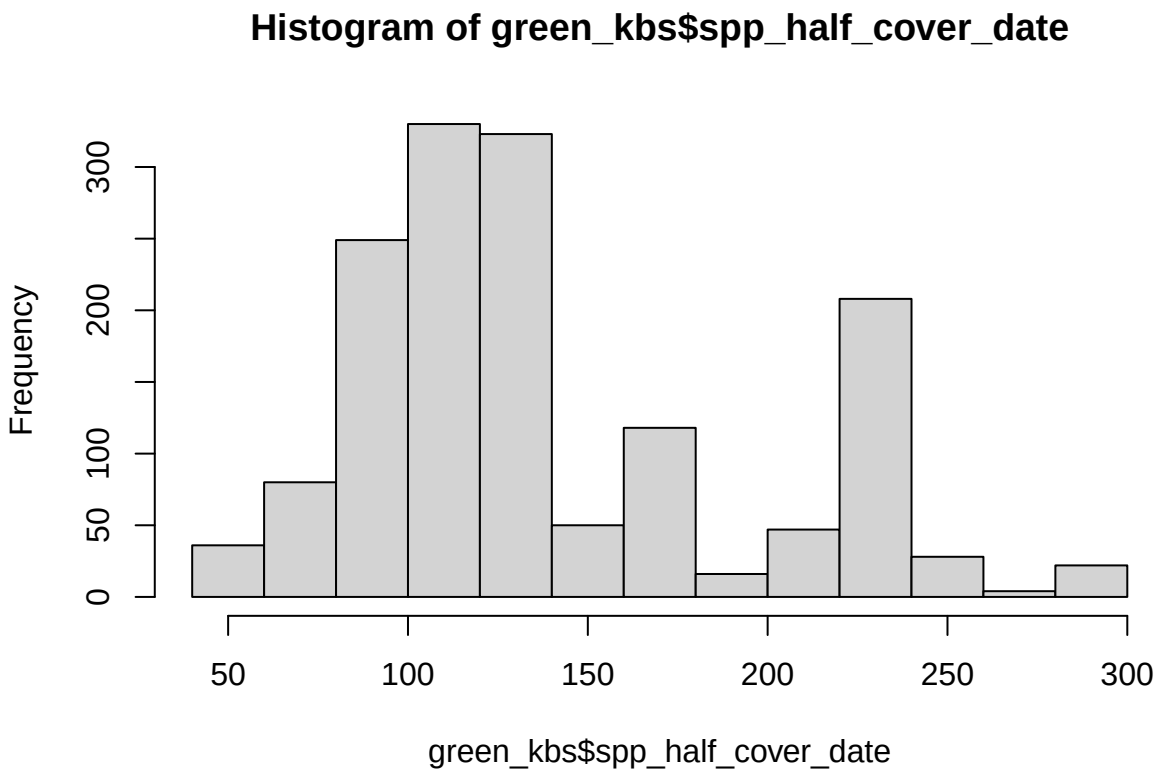
```
## [1] "warmed"  "ambient"
```

```
# adding sequential year variable starting at 1: this is
# because 2016... are large numbers compare with other values
# in the dataset. We can always label axes with these real
# years.
greenup$year_factor[greenup$year == 2016] <- 1
greenup$year_factor[greenup$year == 2017] <- 2
greenup$year_factor[greenup$year == 2018] <- 3
greenup$year_factor[greenup$year == 2019] <- 4
greenup$year_factor[greenup$year == 2020] <- 5
greenup$year_factor[greenup$year == 2021] <- 6

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
greenupp$year_factor[greenupp$year == 2021] <- 6

# 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")
```

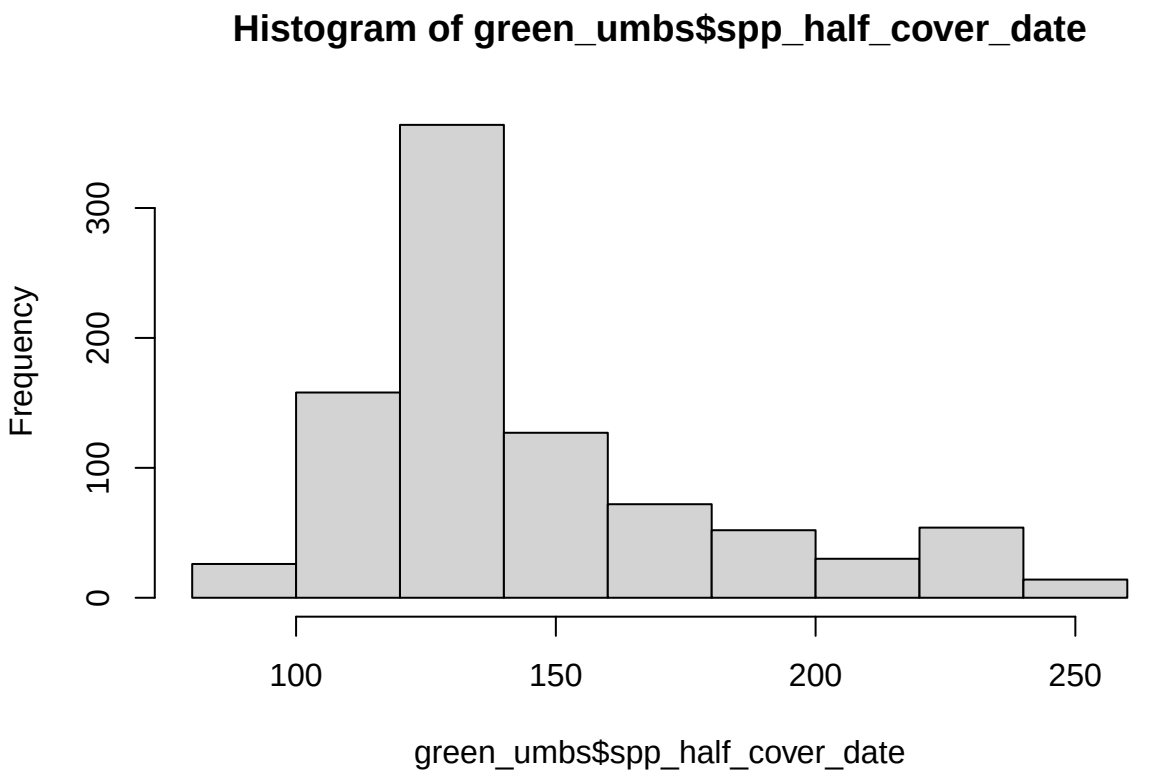
Data Exploration:

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.

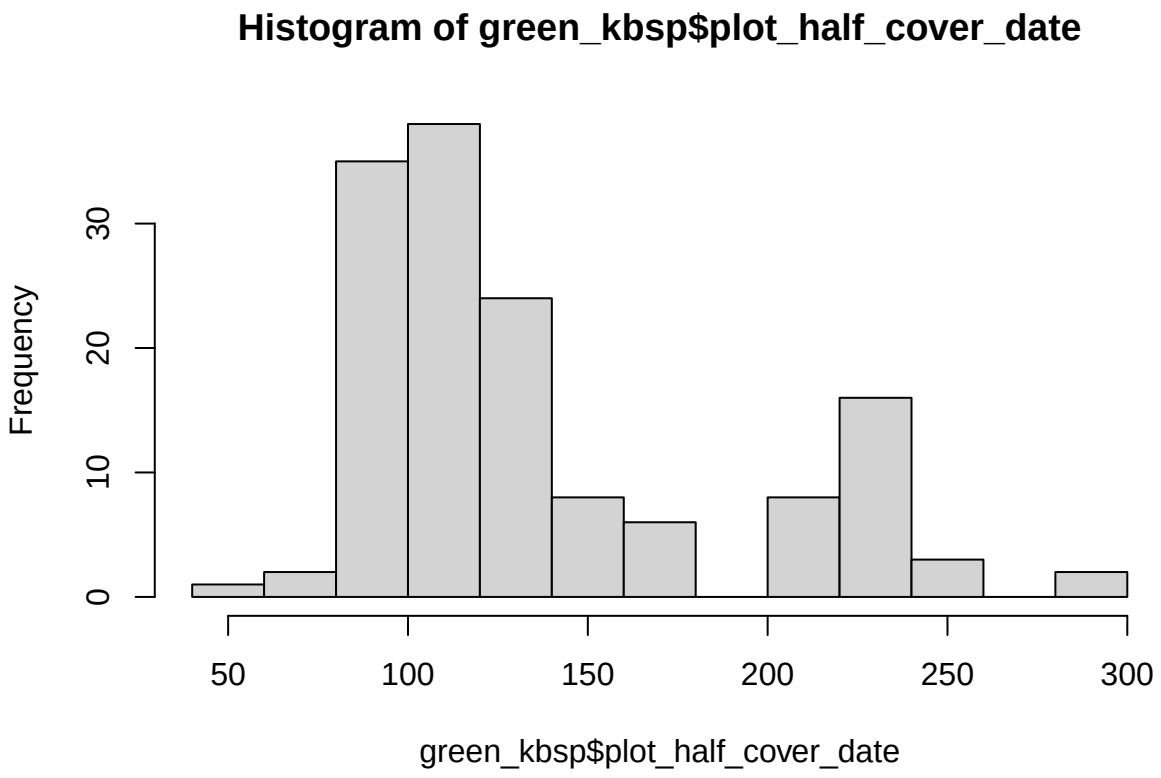
```
# species level
hist(green_kbs$spp_half_cover_date)
```



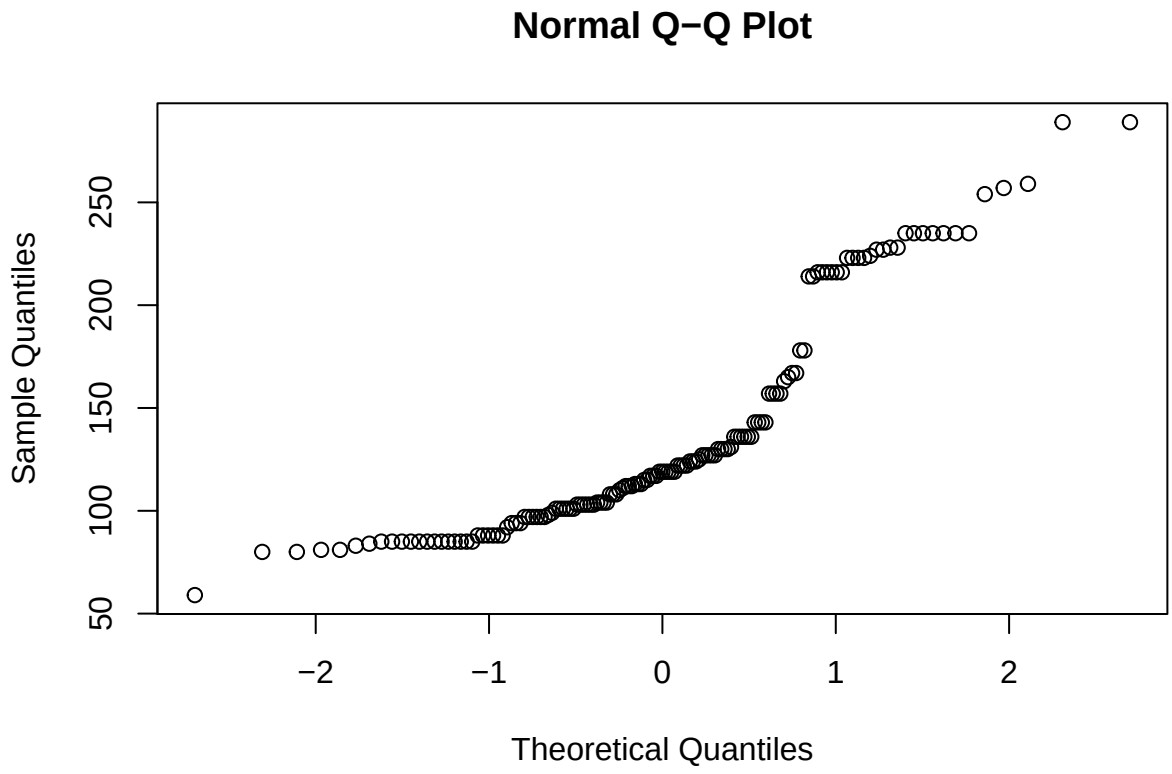

```
hist(green_umbs$spp_half_cover_date)
```




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




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

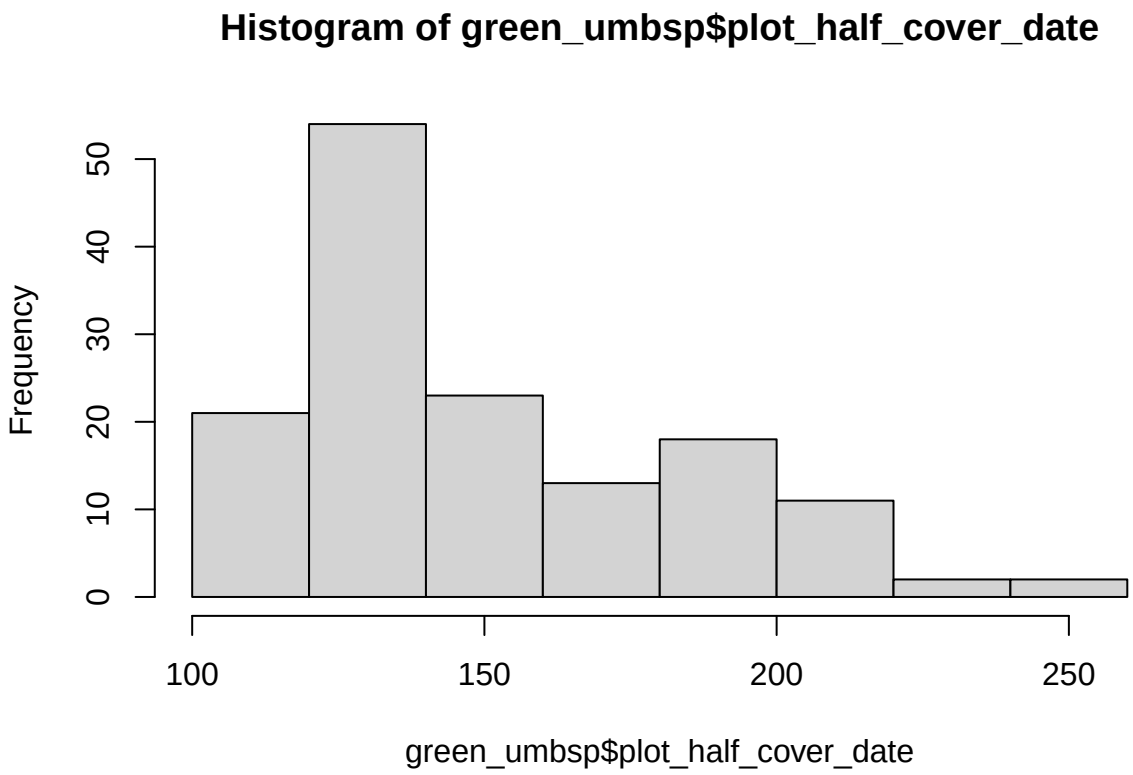



```
shapiro.test(green_kbsp$plot_half_cover_date)
```

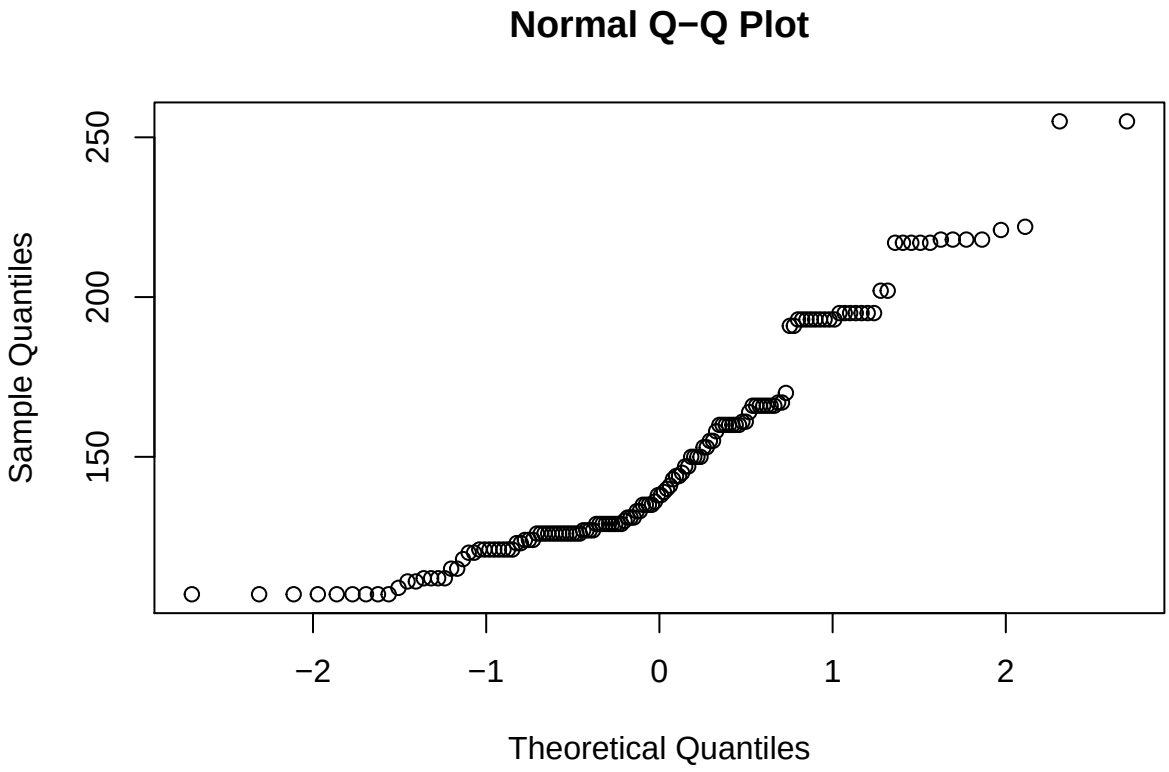
```
##
```

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

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



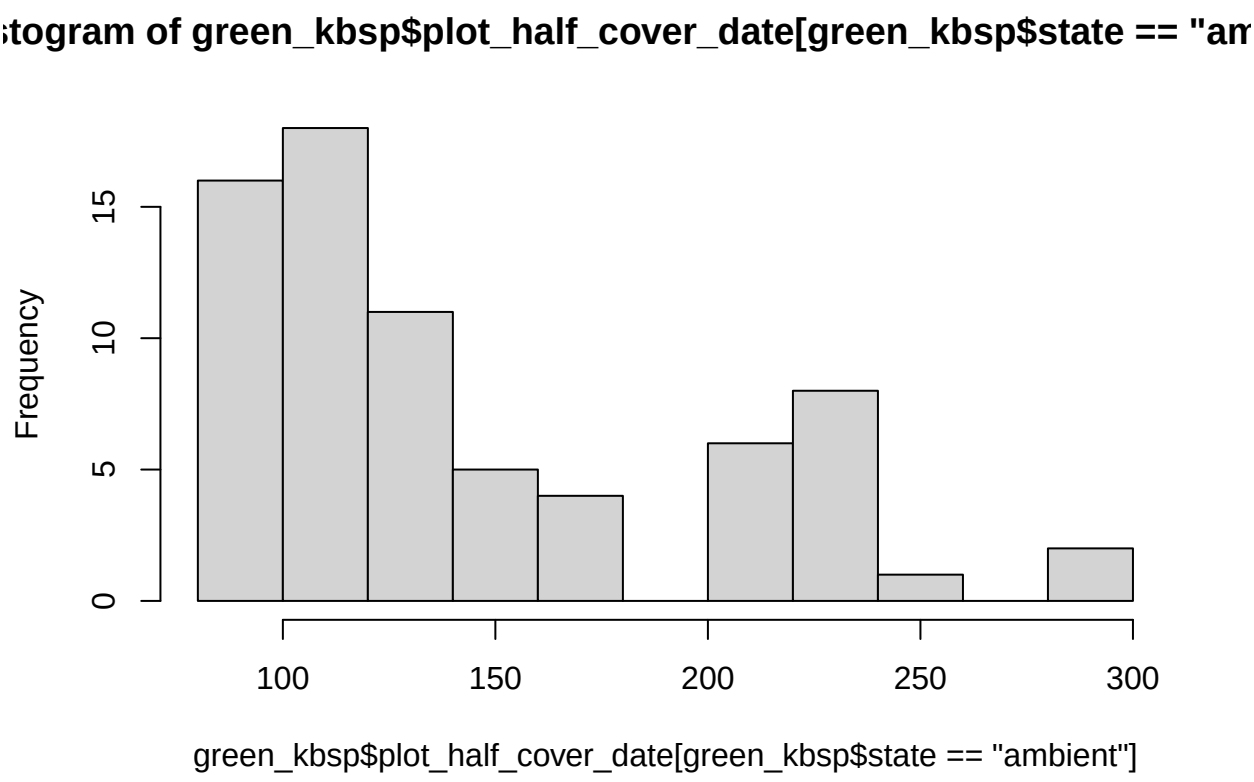

```
qqnorm(green_umbsp$plot_half_cover_date)
```



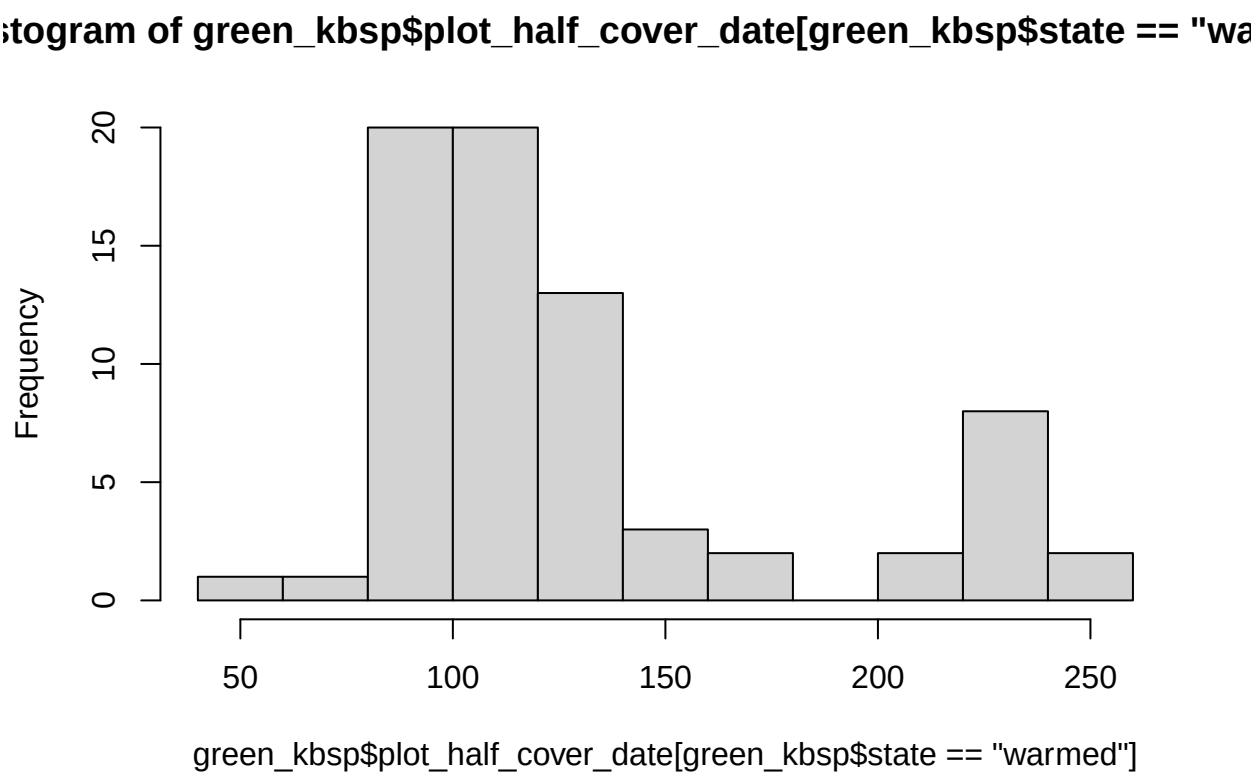

```
shapiro.test(green_umbsp$plot_half_cover_date)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbsp$plot_half_cover_date
## W = 0.89867, p-value = 1.874e-08
```

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

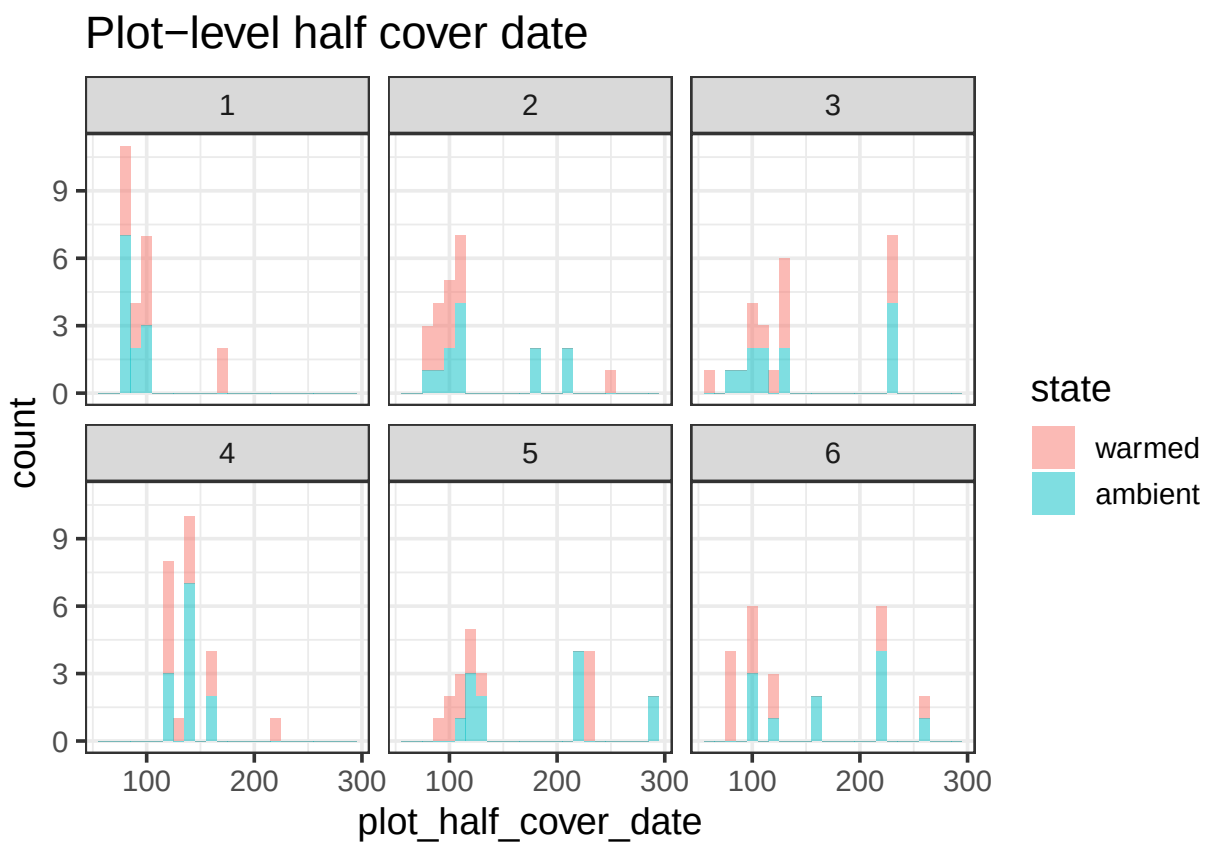



```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "warmed"])
```

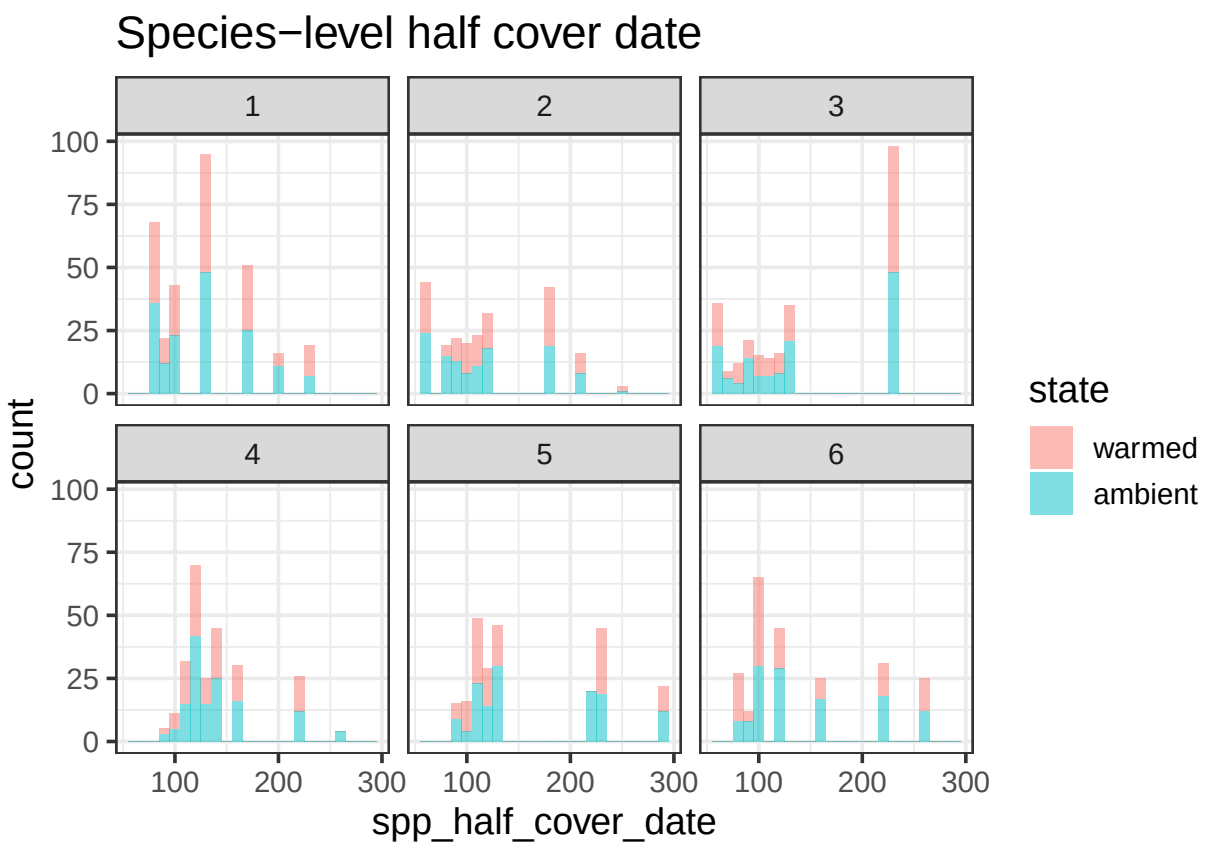



```
# histograms for each year - look at them together:
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
```

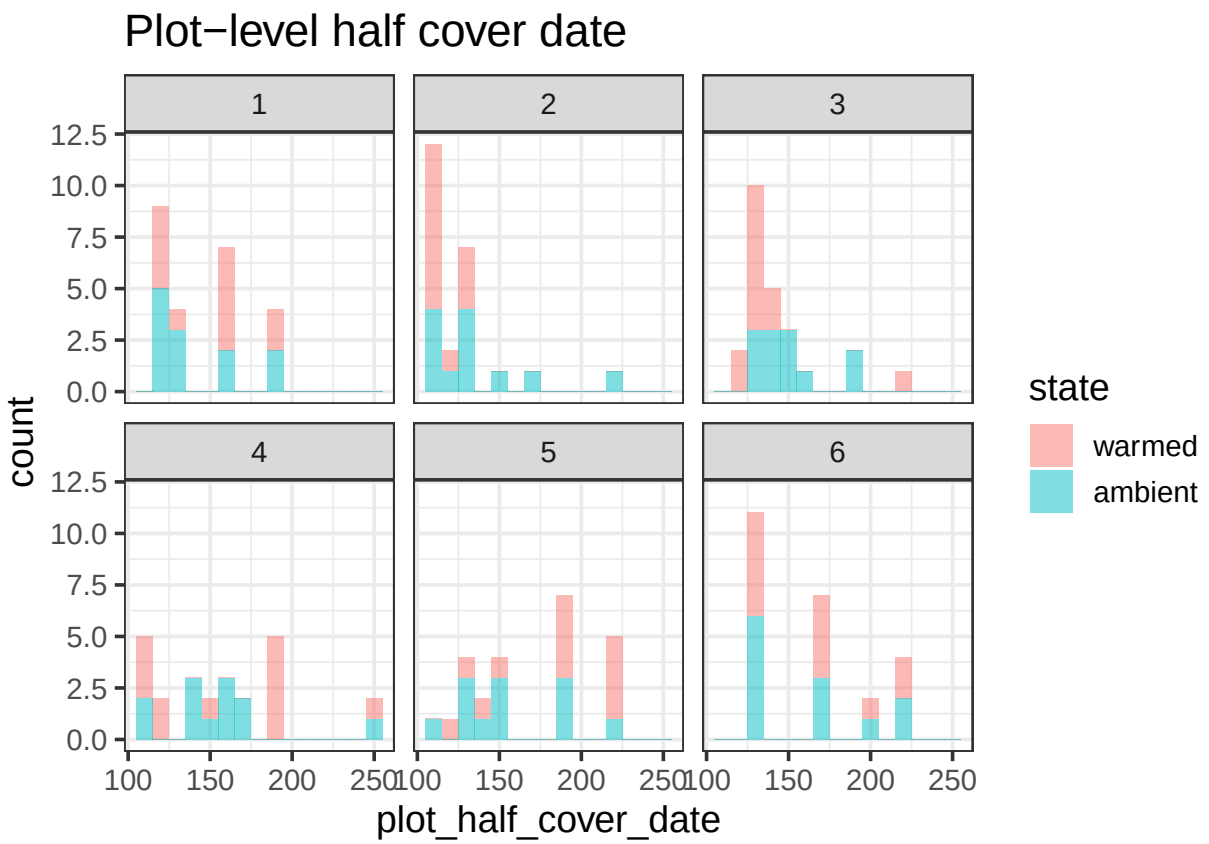
```
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



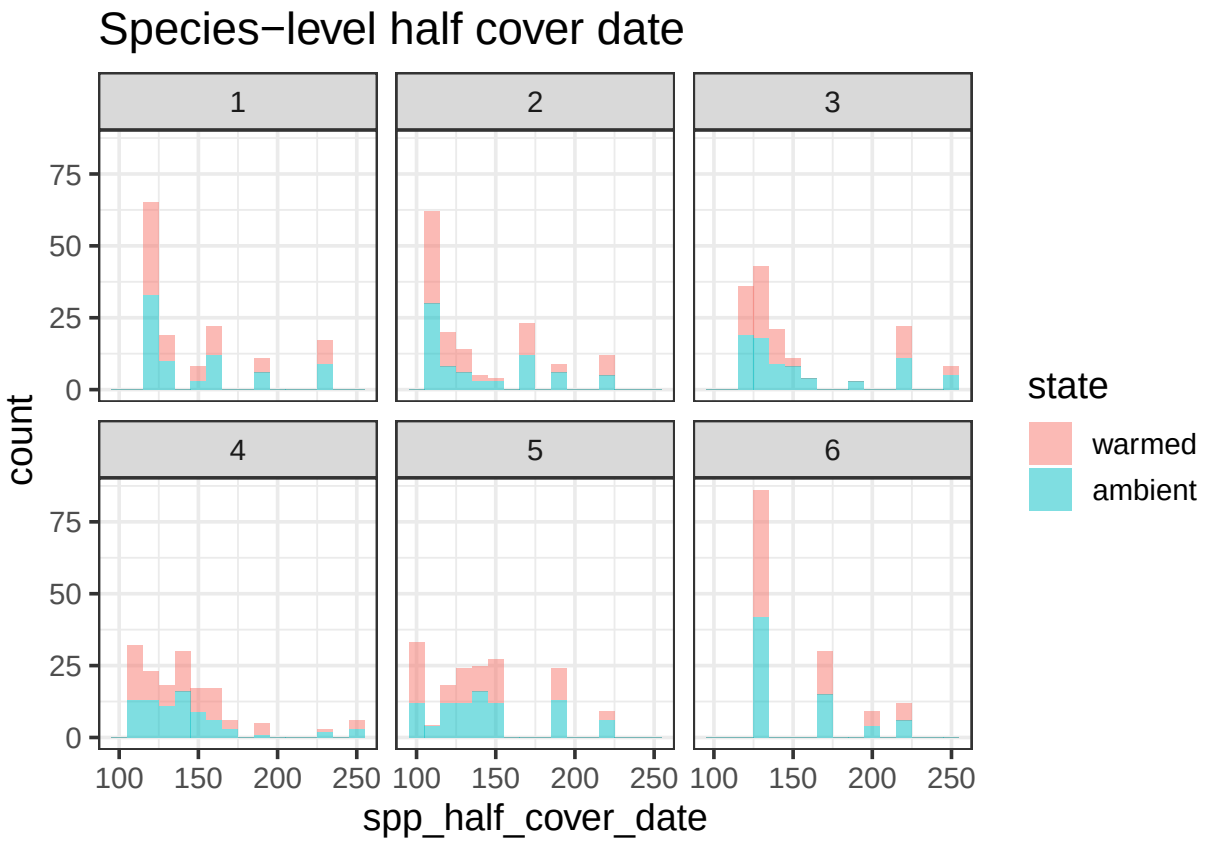

```
p1.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



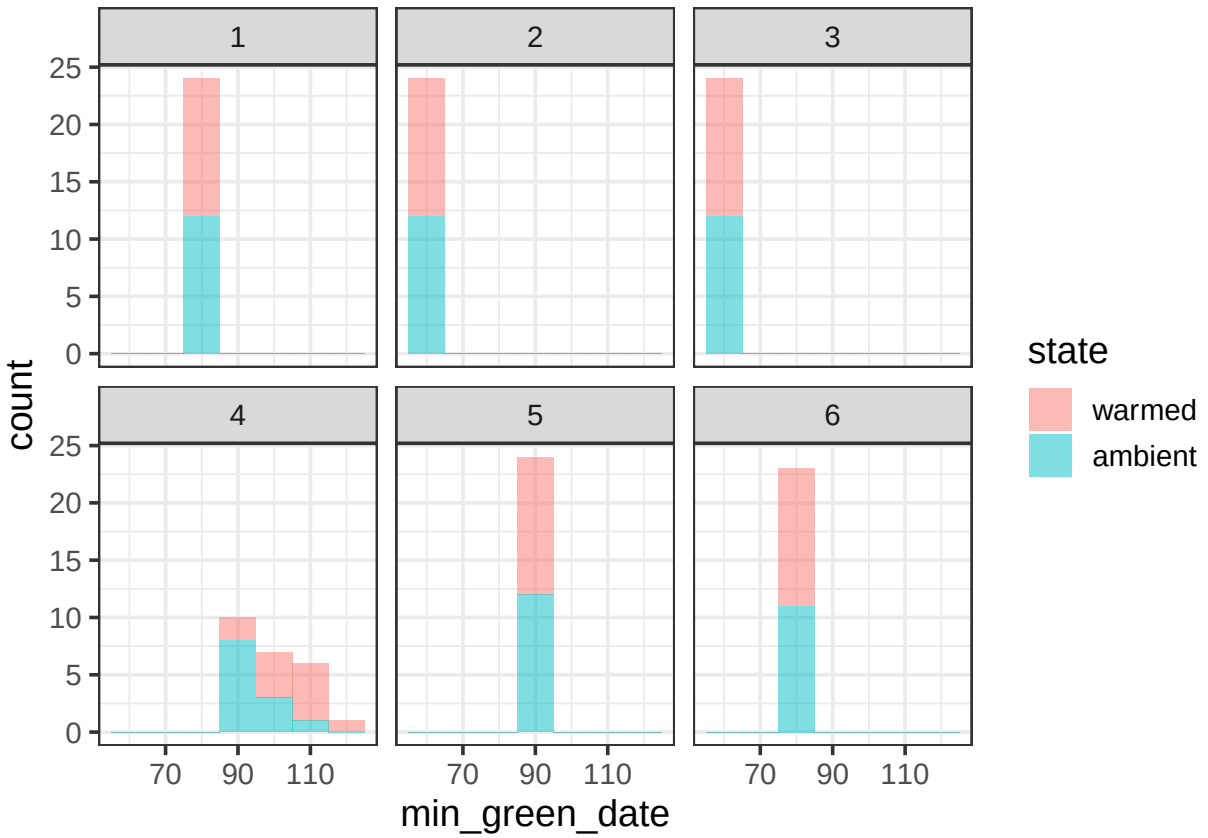

```
p1u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



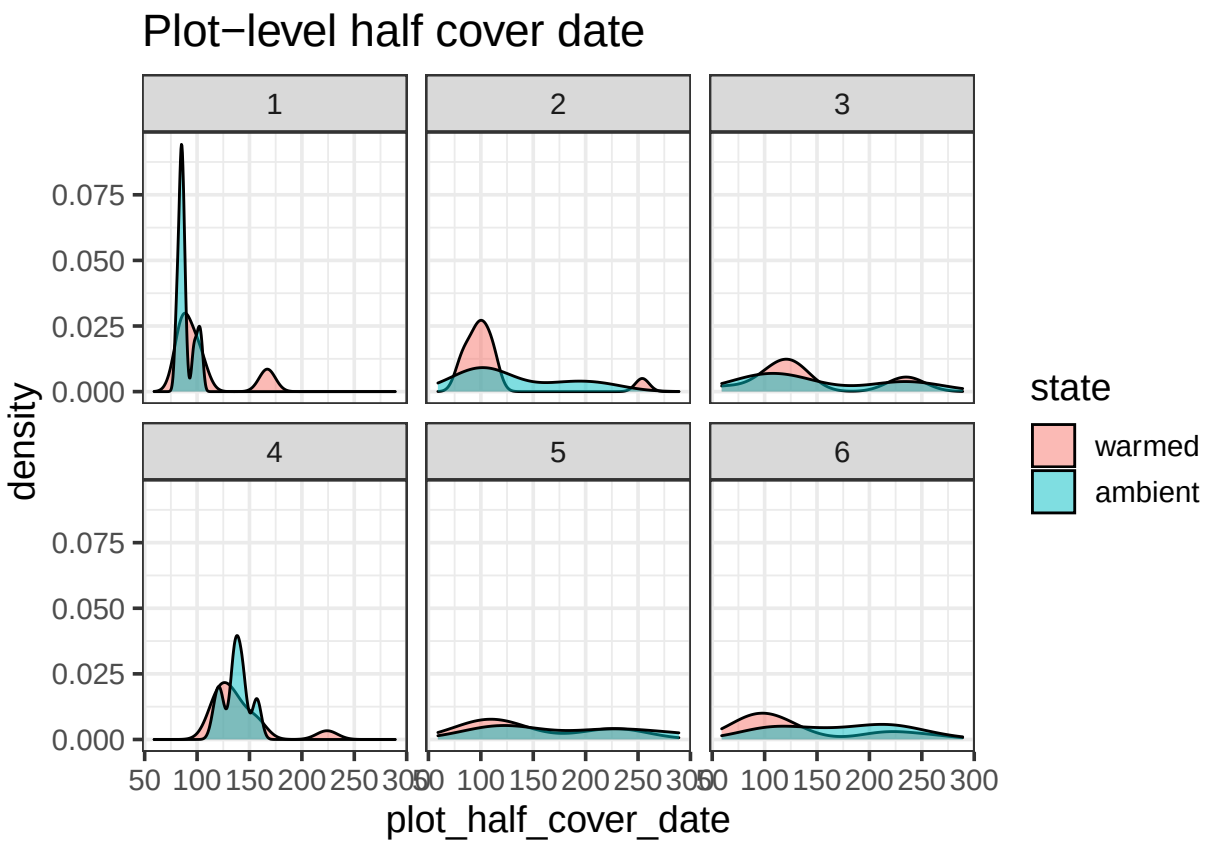

```
p1.2u <- ggplot(data = green_umbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2u + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



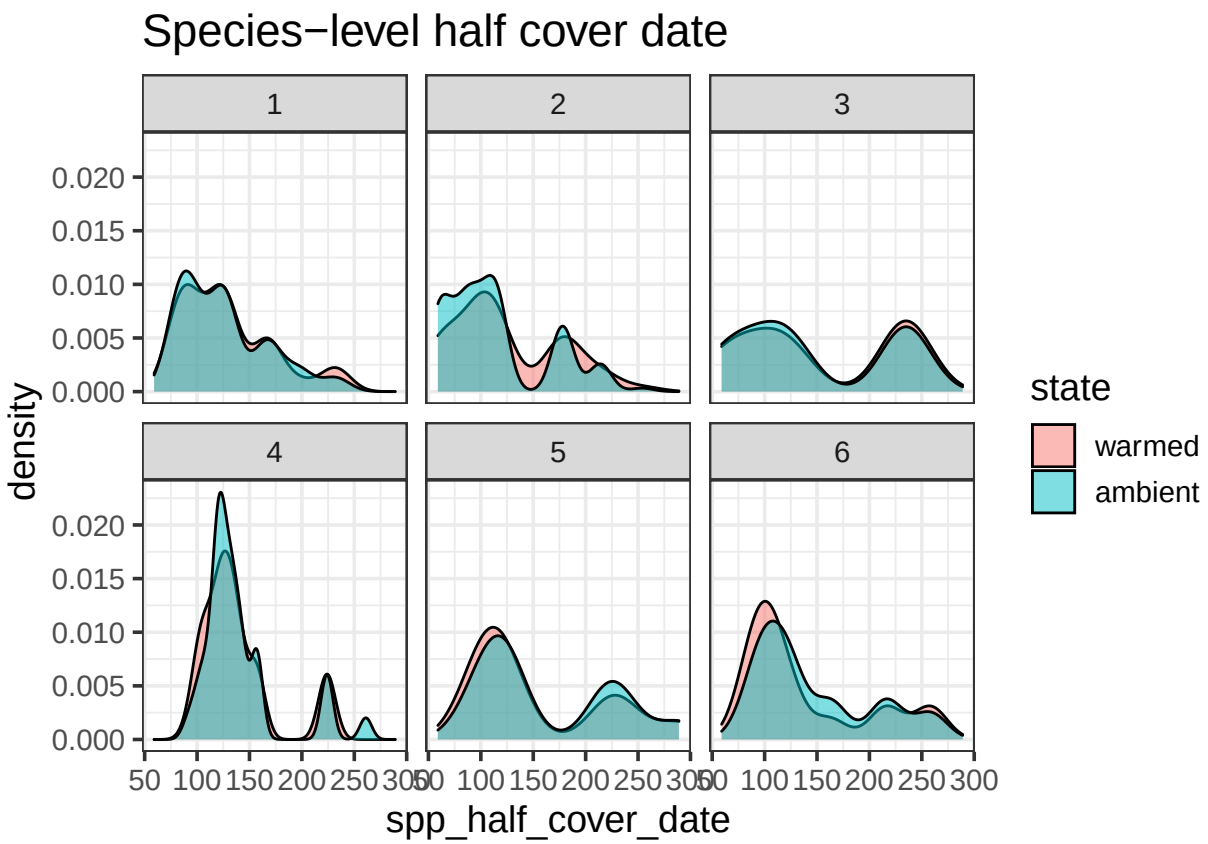

```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
    geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```



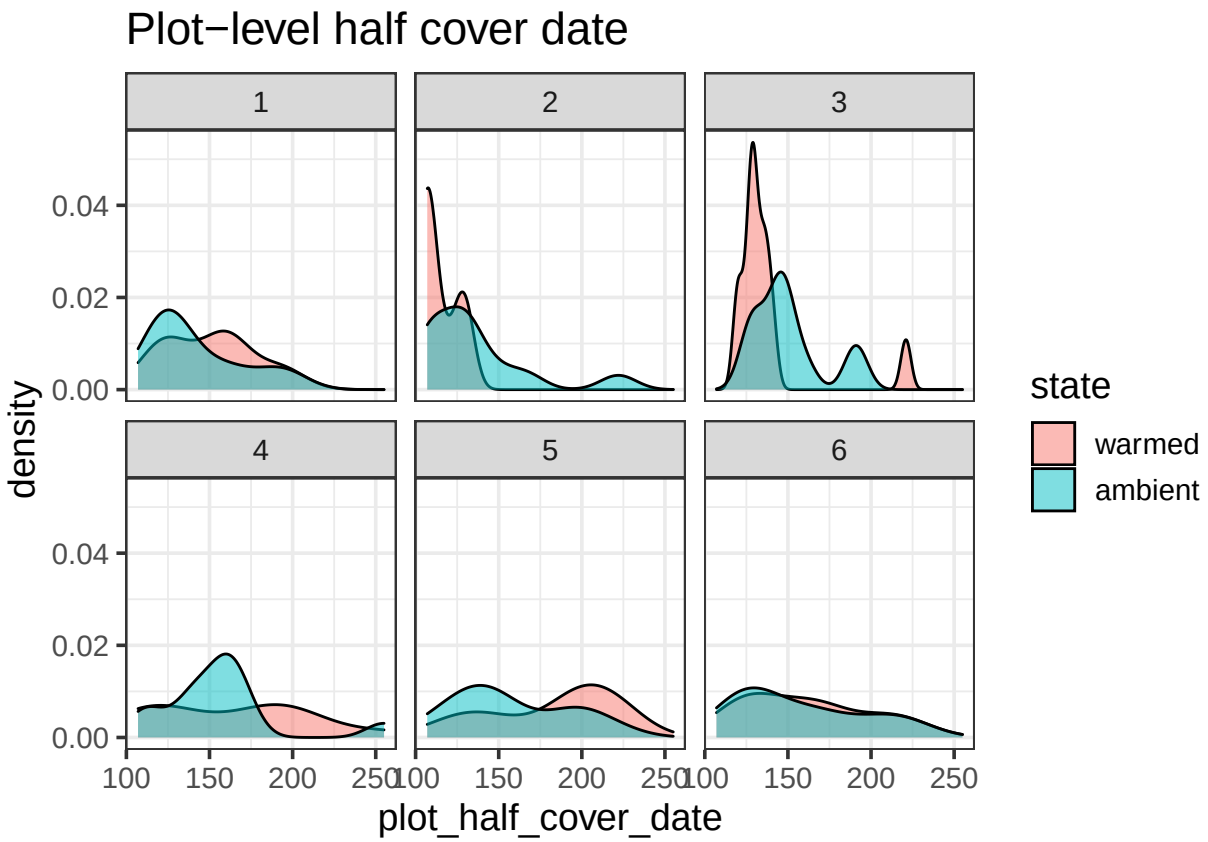

```
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



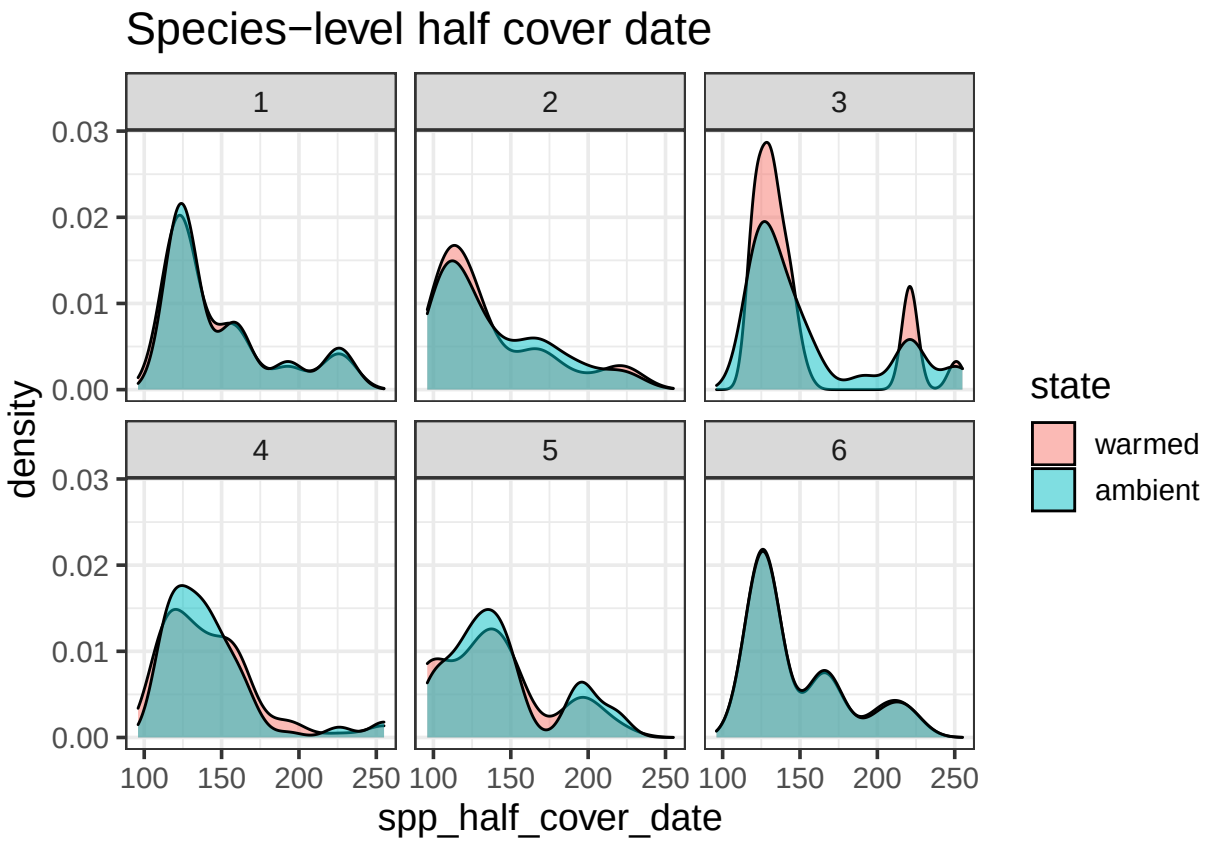

```
p3.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



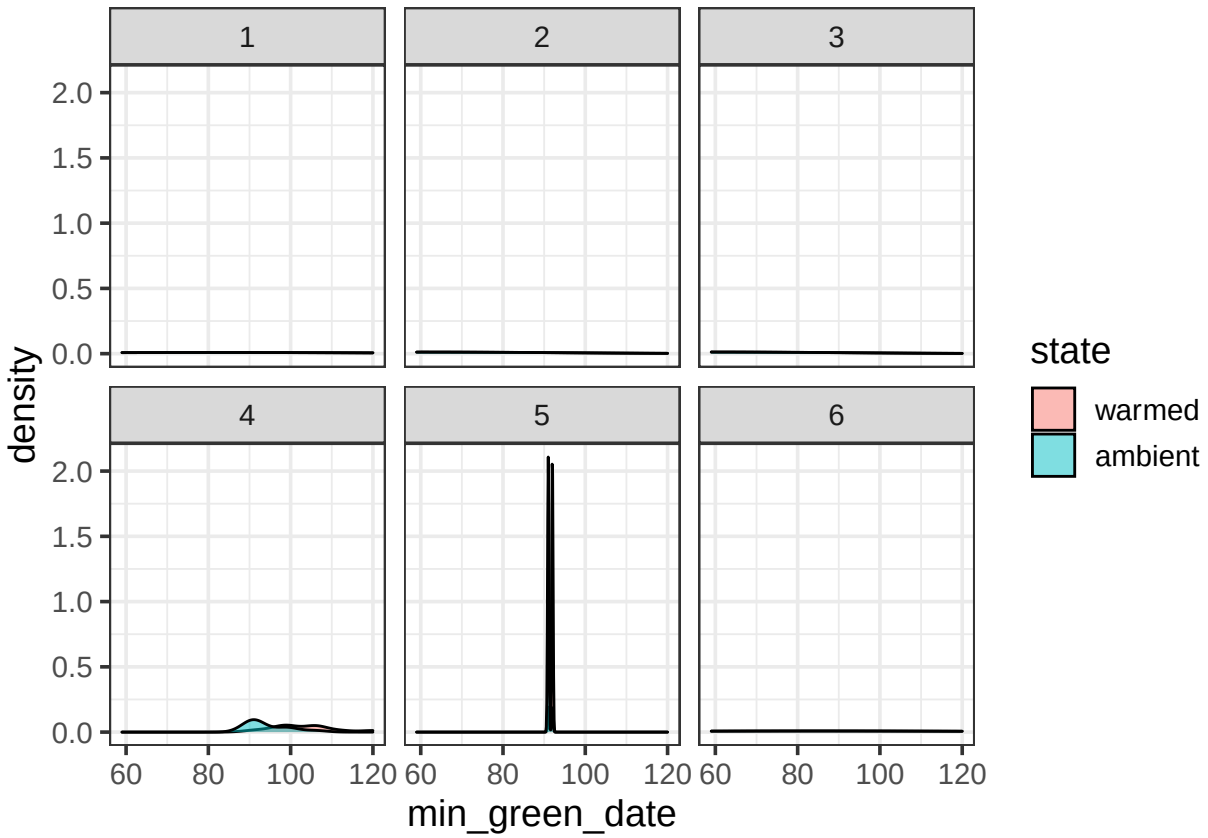

```
p3u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```




```
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
```

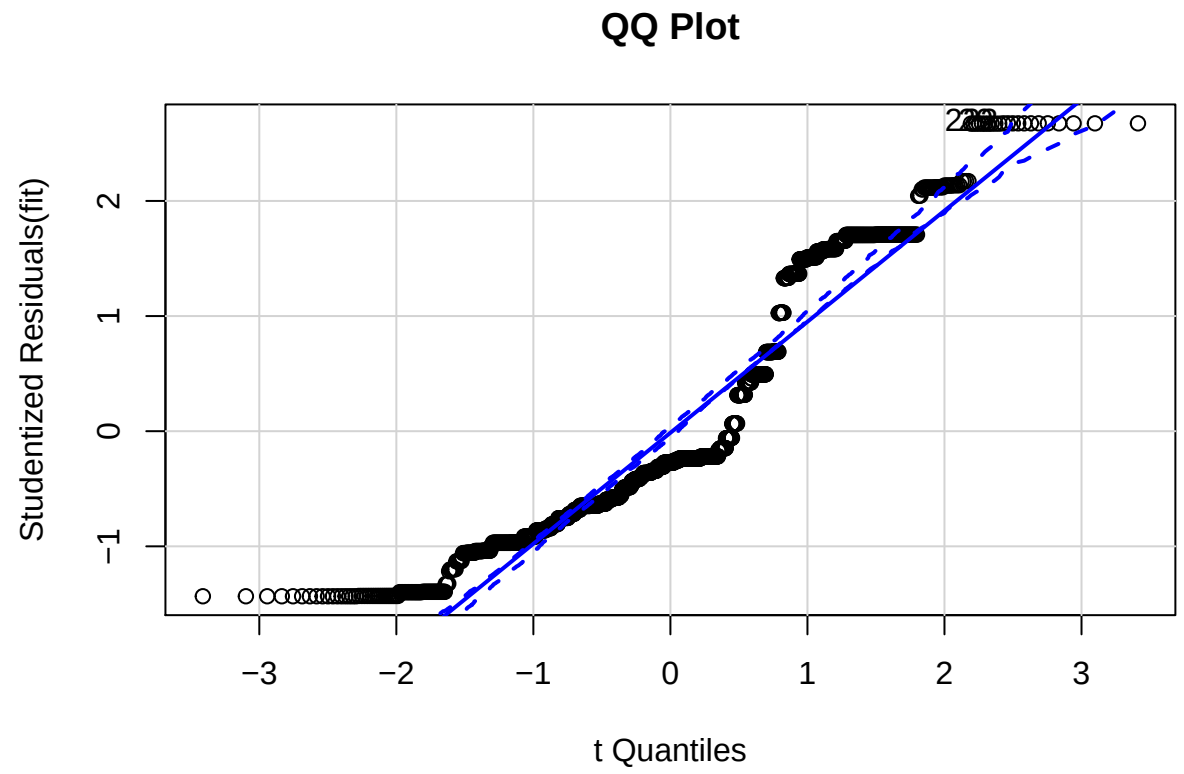
Leverage plots and detecting Outliers. https://www.statmethods.net/stats/rdiagnostics.html

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
```

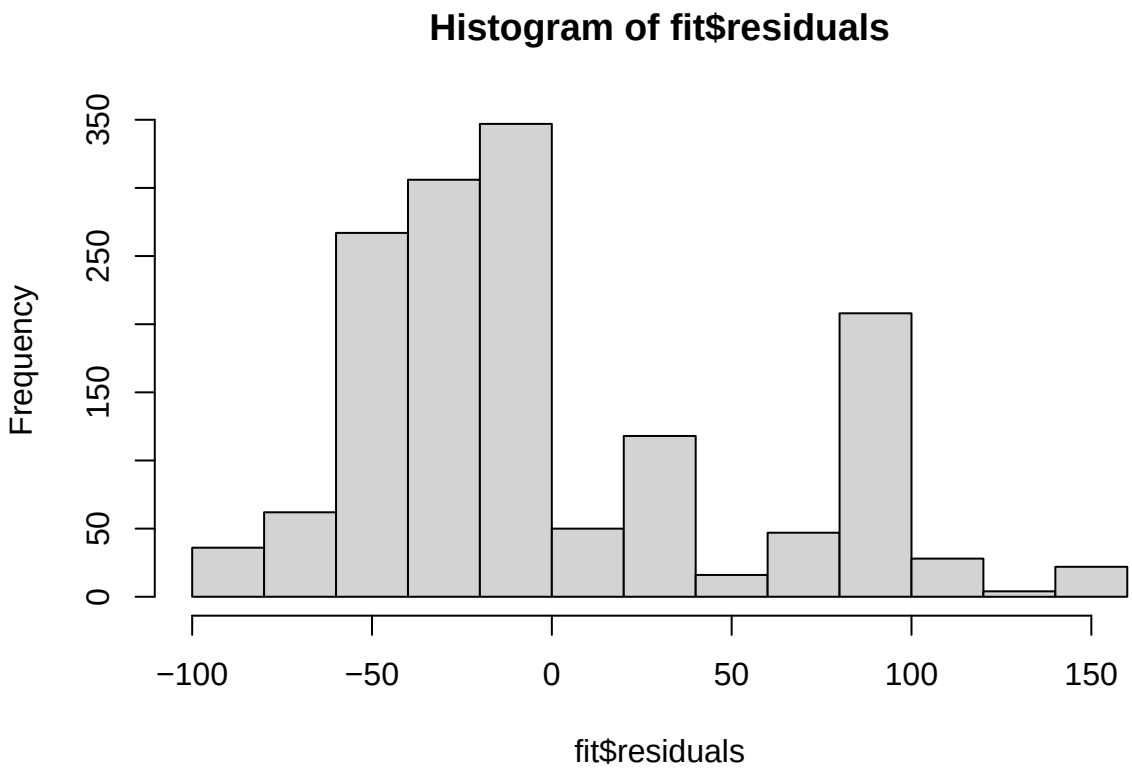
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 29 2.673942          0.0075775           NA
```

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

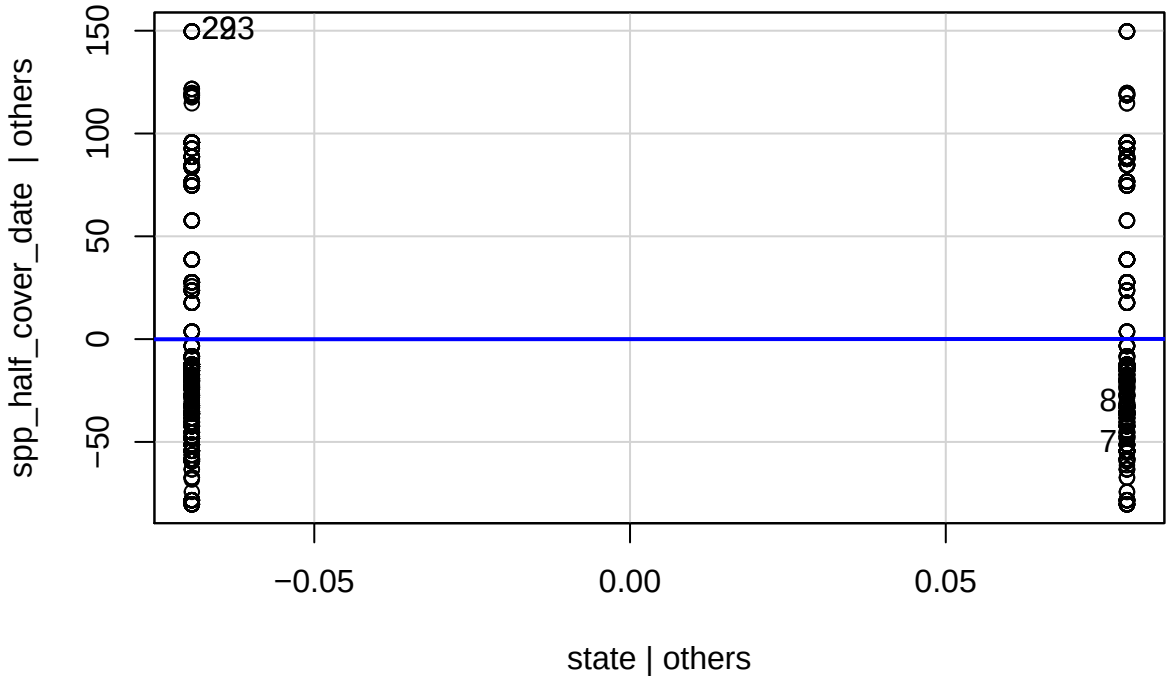



```
##  29 223
##  29 195
```

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



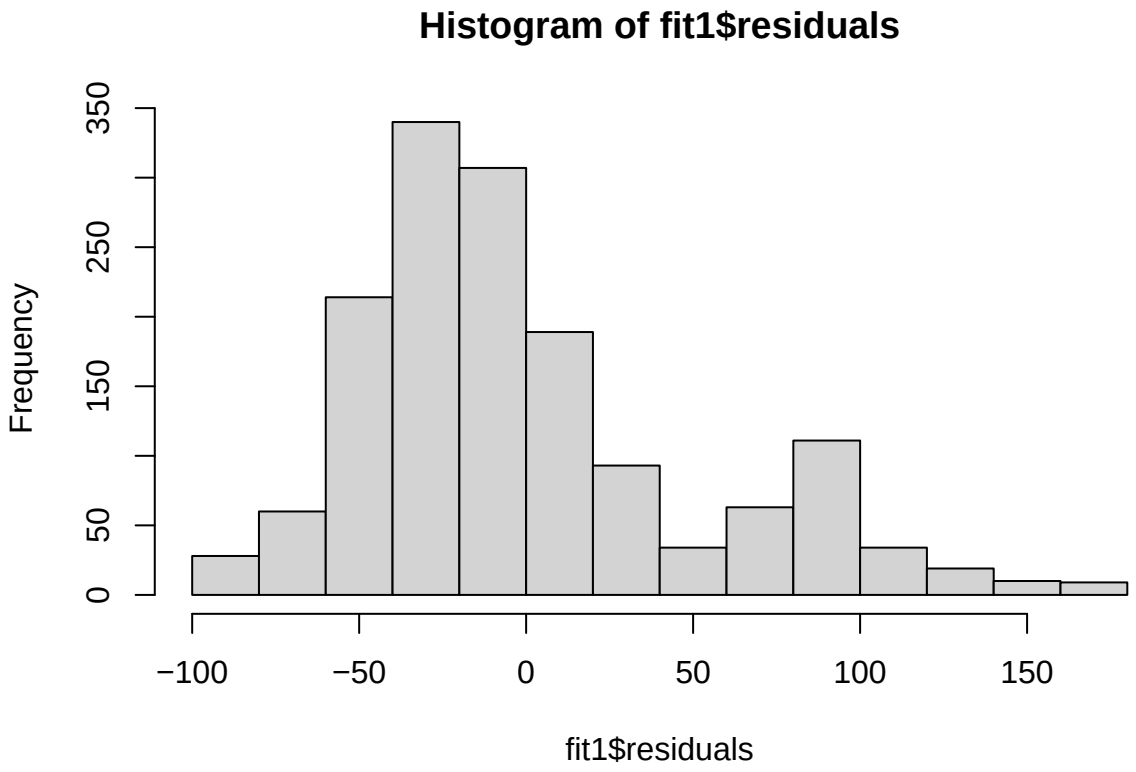
```
leveragePlots(fit)
```



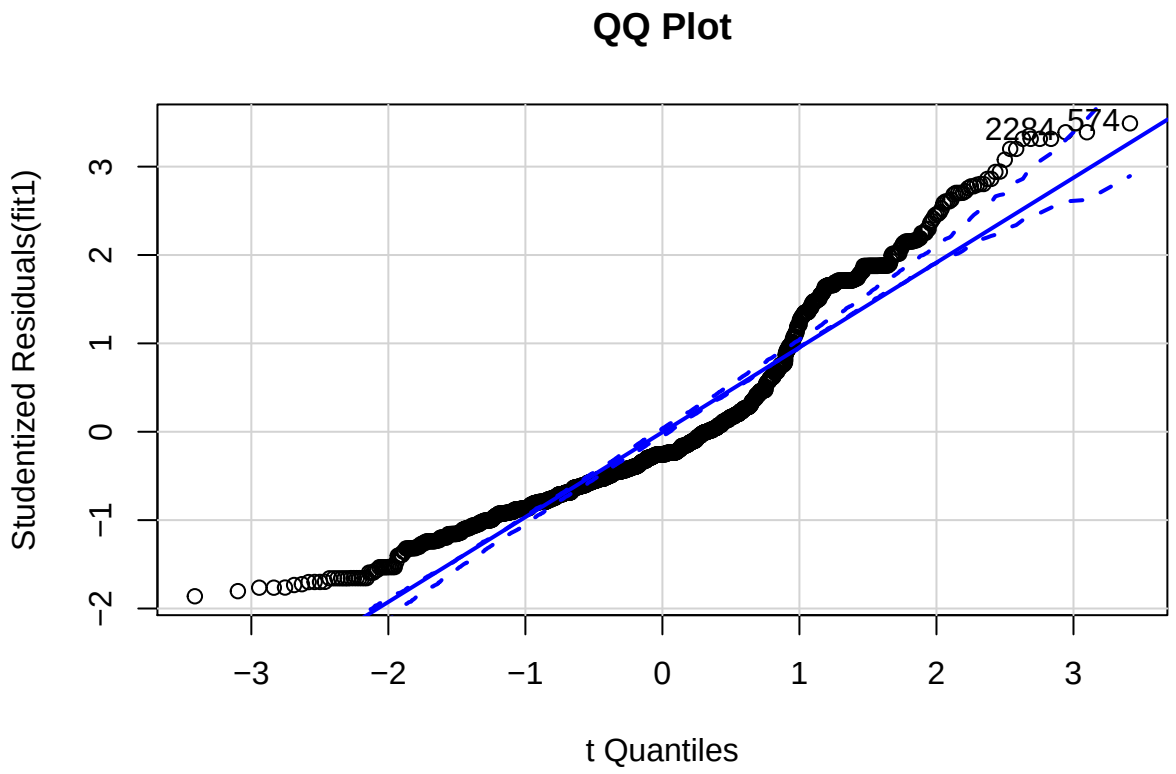

```
# KBS State and species model
fit1 <- lm(spp_half_cover_date ~ state + species, data = green_kbs)
outlierTest(fit1)  # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 574 3.489515         0.00049802      0.75251
```

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

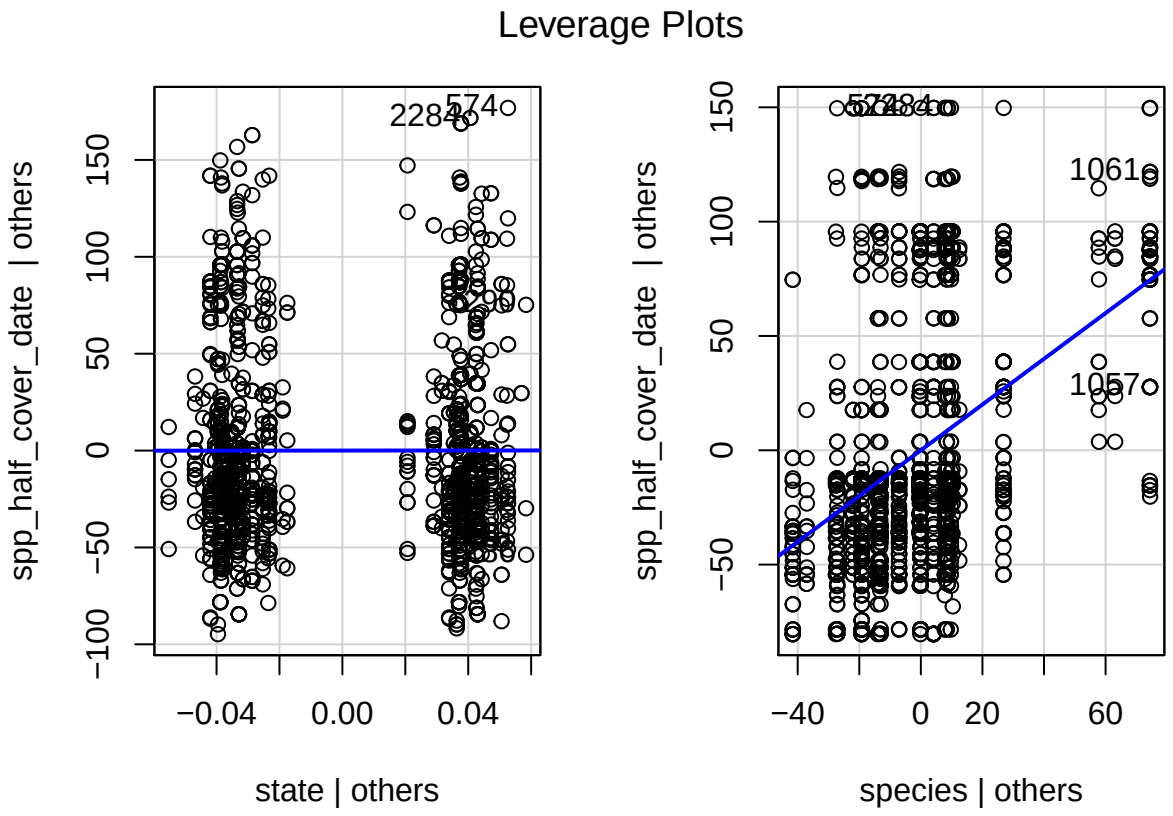



```
qqPlot(fit1, main = "QQ Plot")
```




```
##  574 2284
##  345 1387
```

```r
leveragePlots(fit1)
```




```r
ols_test_normality(fit1)  # p < 0.05 for all, so data is normal (I think)
```

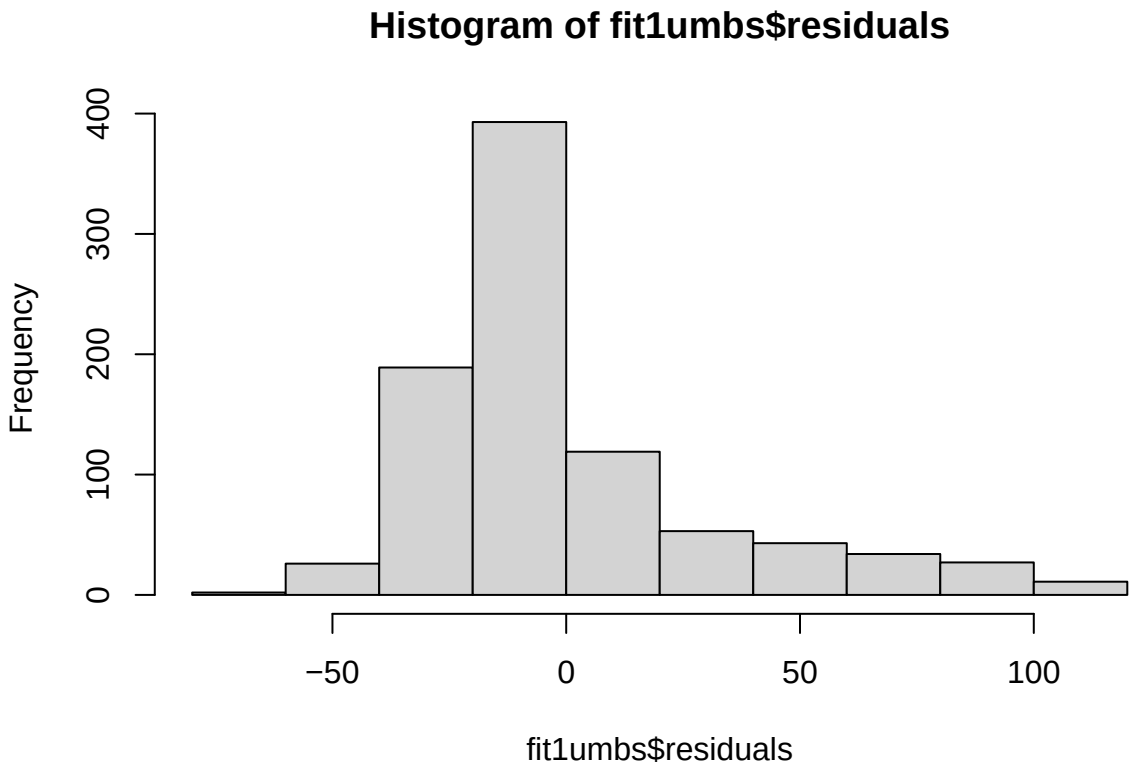
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

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

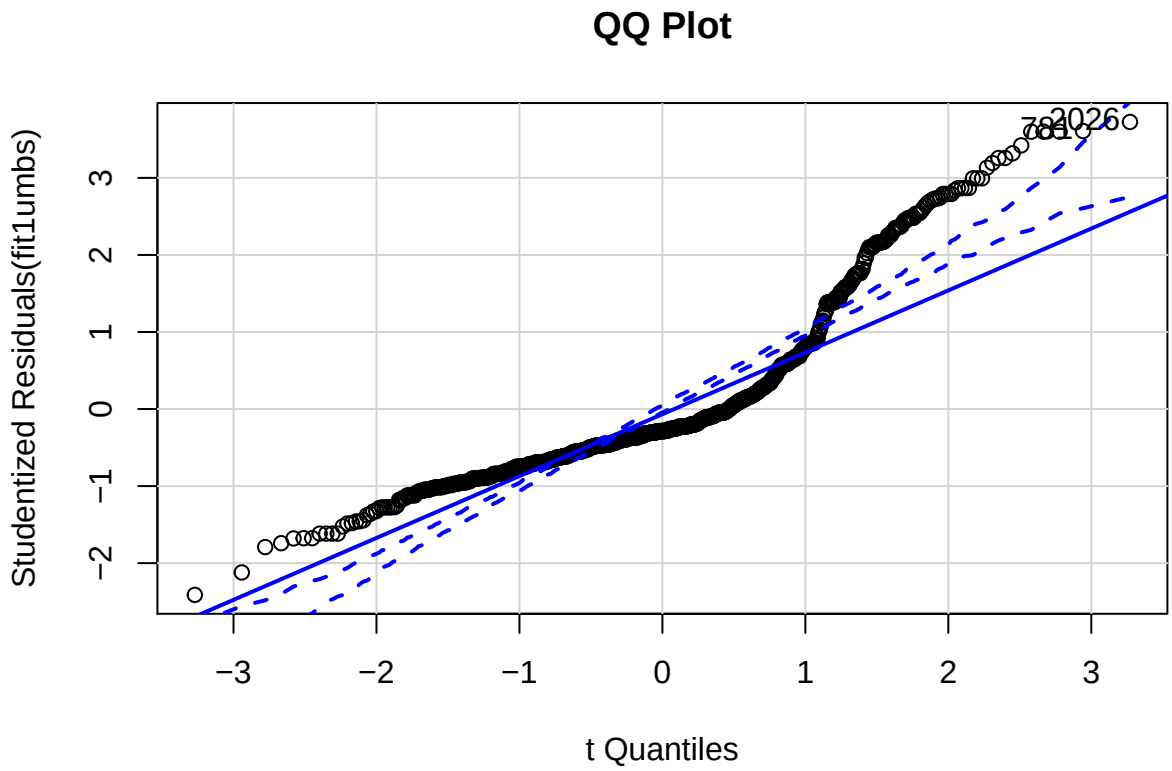
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 2026 3.725776         0.00020715      0.18581
```

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




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

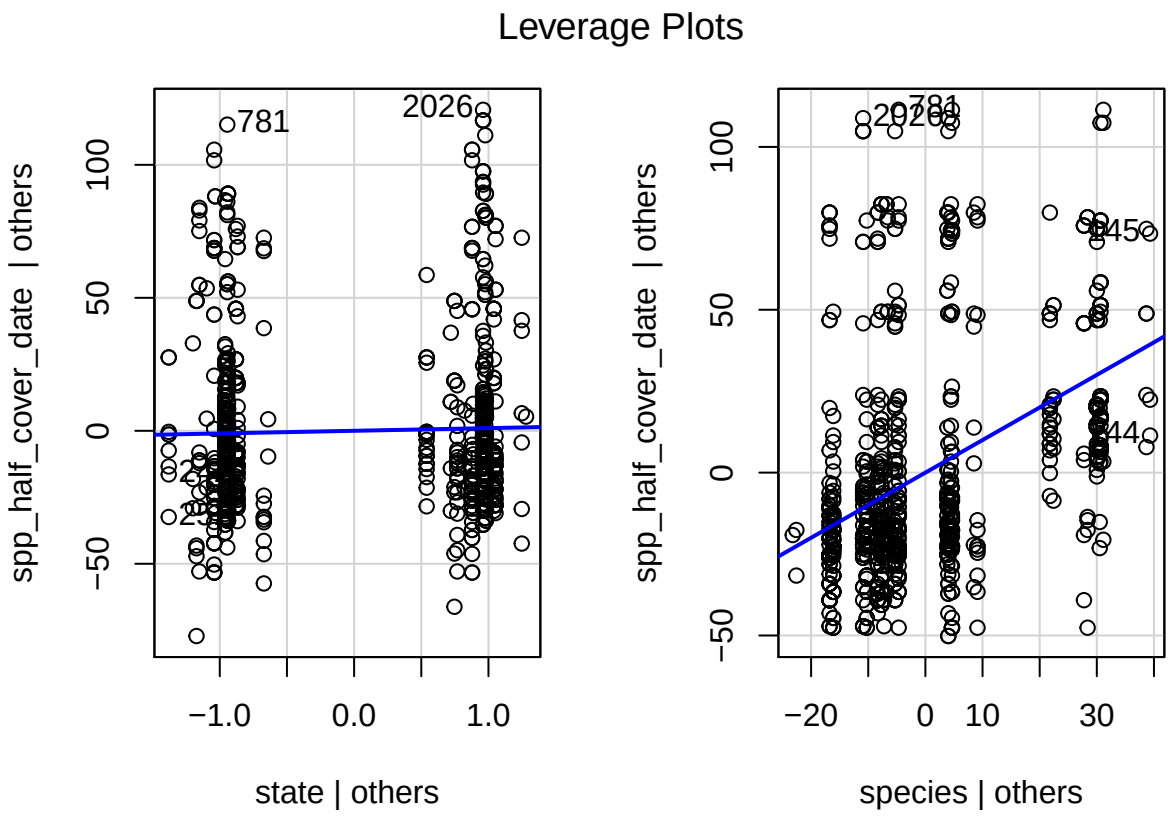
```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :
## 'rlm' failed to converge in 20 steps
```




```
##  781 2026
```

```
##  320  788
```

```
leveragePlots(fit1umbs)
```




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

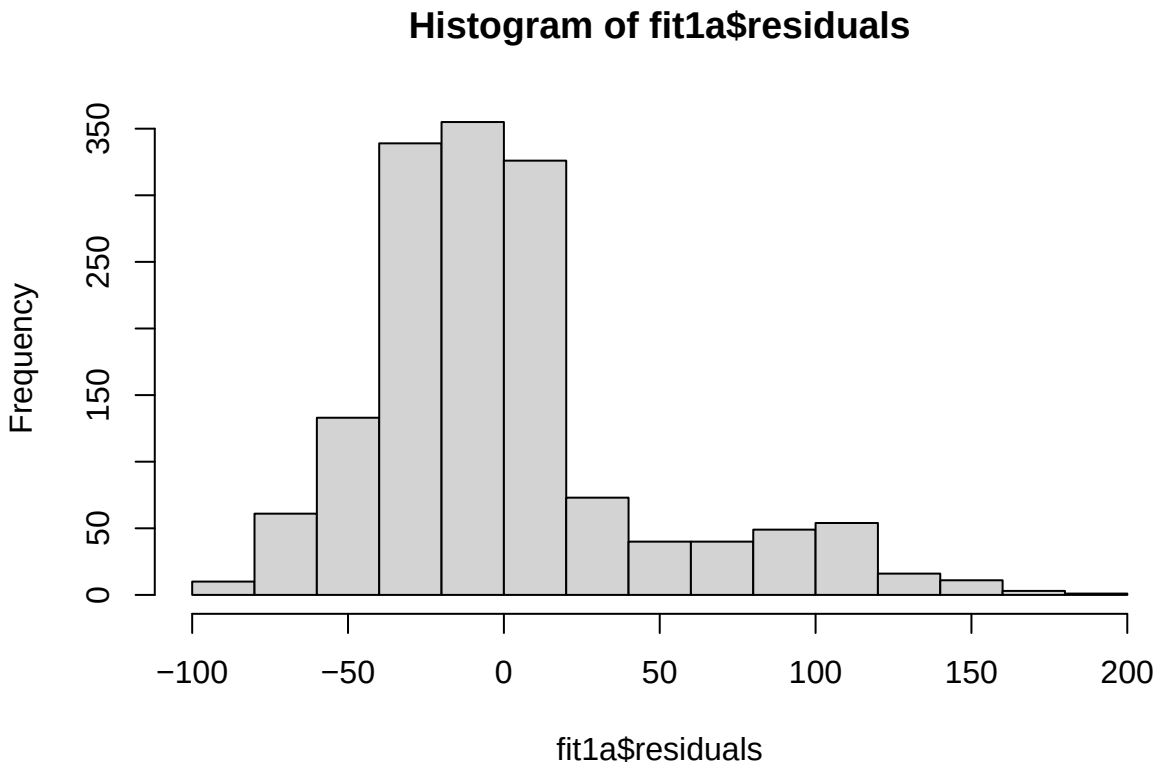
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.8553         0.0000
## Kolmogorov-Smirnov        0.1861         0.0000
## Cramer-von Mises        104.1103         0.0000
## Anderson-Darling         47.4699         0.0000
## -----------------------------------------------
```

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

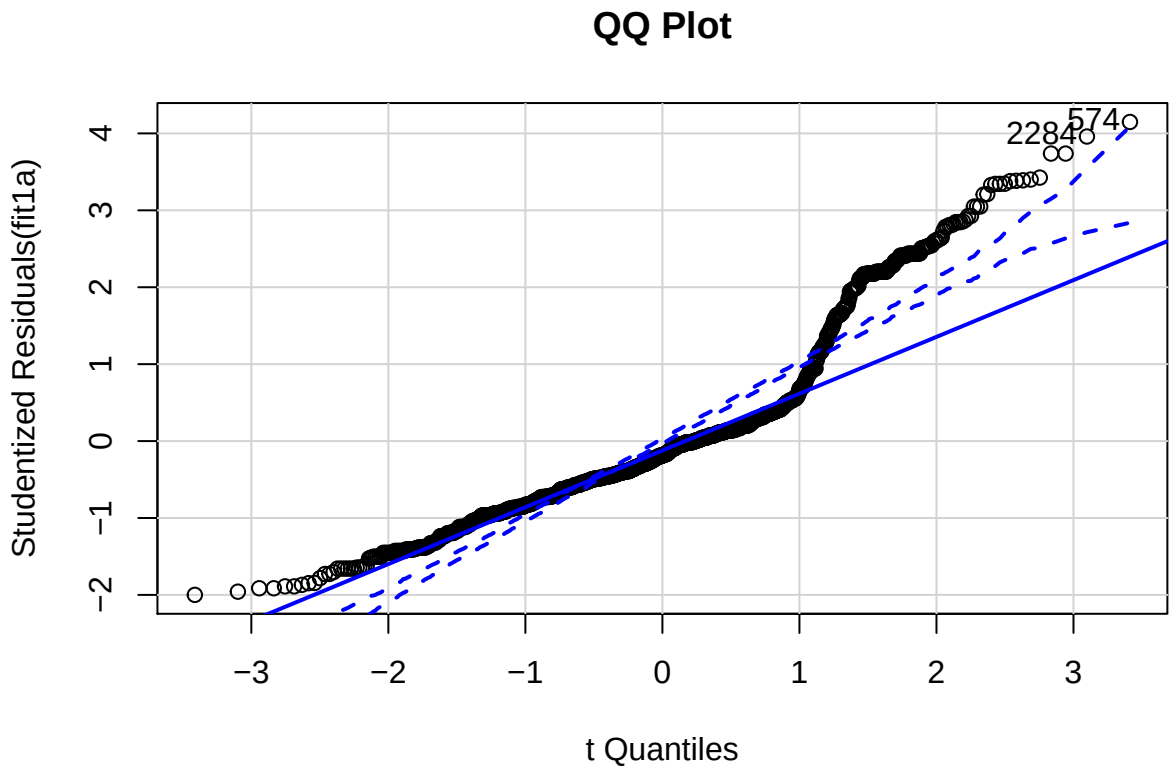
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 574 4.148749         3.5322e-05     0.053372
```

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




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

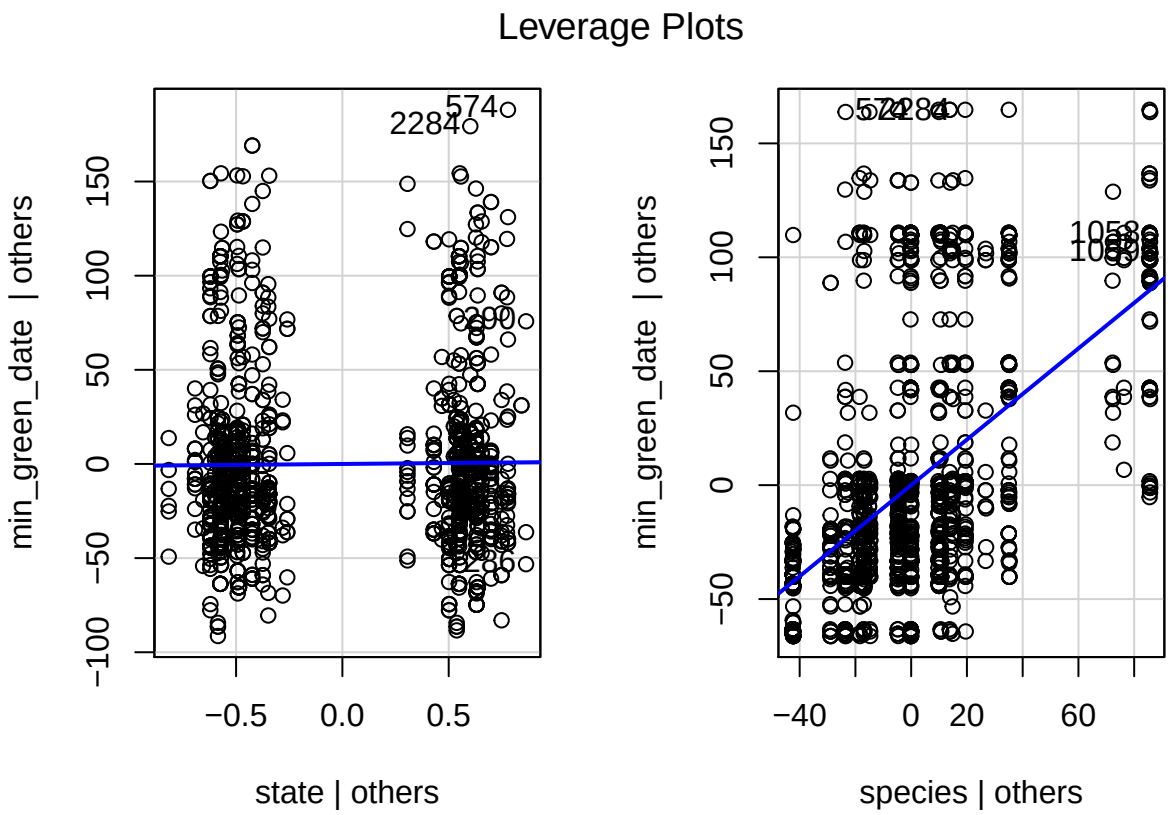
```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :
## 'rlm' failed to converge in 20 steps
```



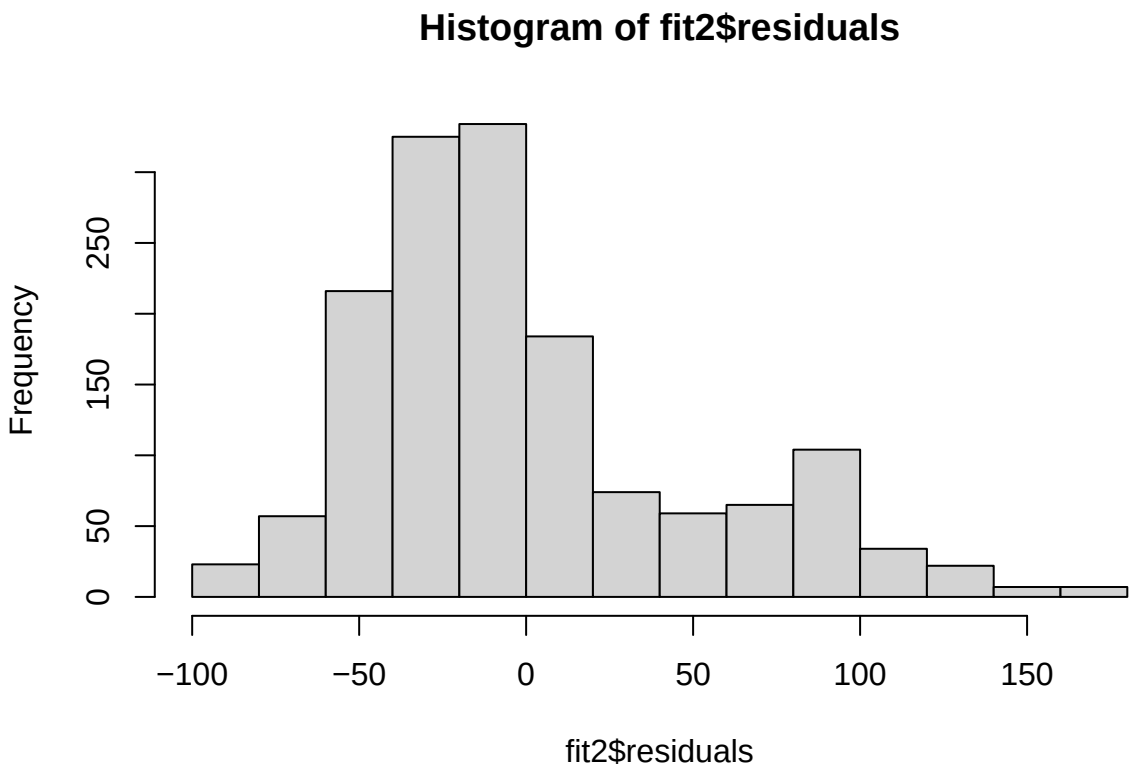

```
##  574 2284
```

```
##  345 1387
```

```
leveragePlots(fit1a)
```



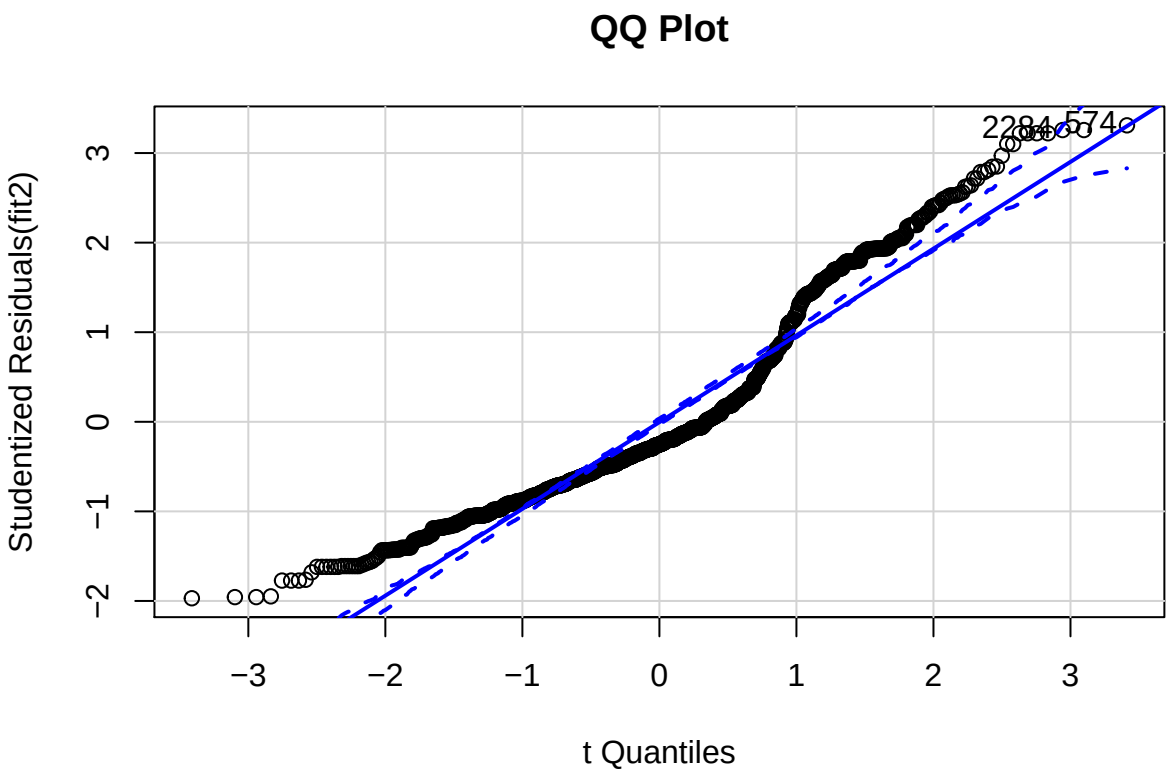

```
# checking fit for date as a function of state and year
fit2 <- lm(spp_half_cover_date ~ state + species + year_factor,
    data = green_kbs)
hist(fit2$residuals)
```




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

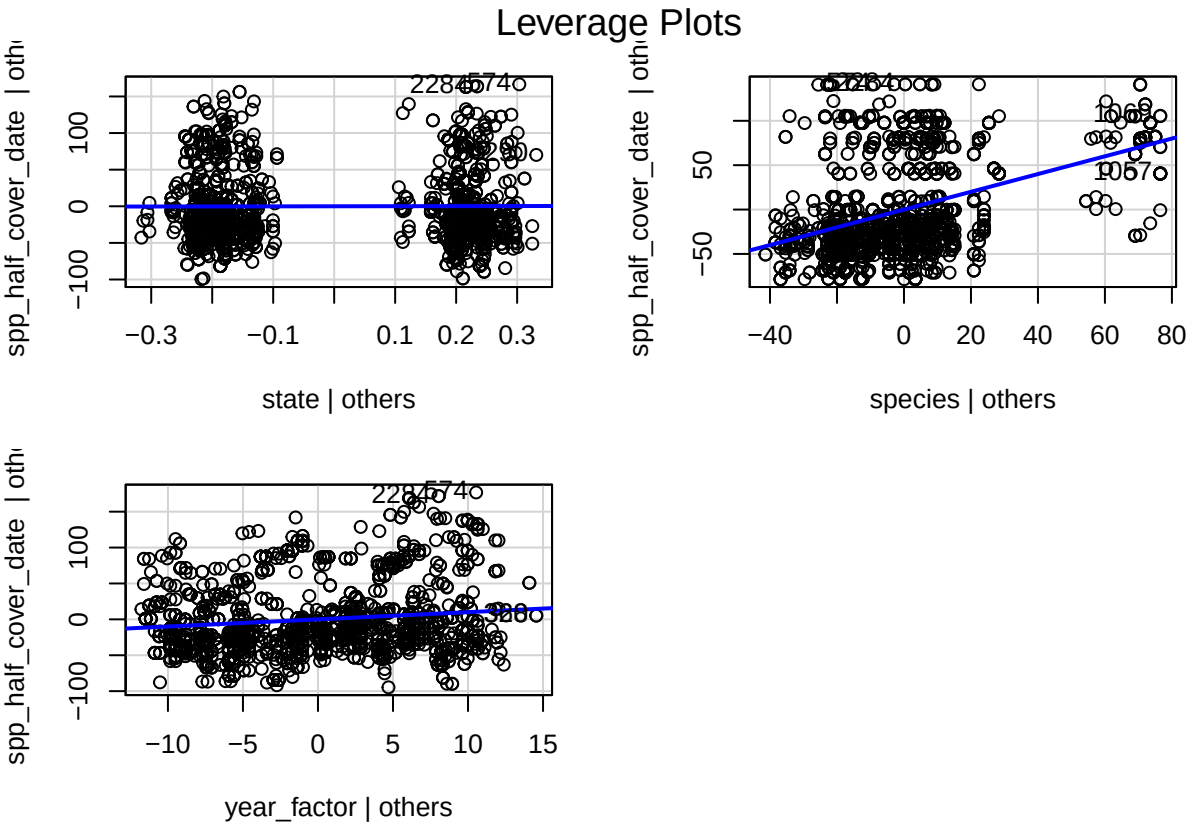
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 574 3.309272         0.00095778           NA
```

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




```
##  574 2284
##  345 1387
```

```
leveragePlots(fit2)
```




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

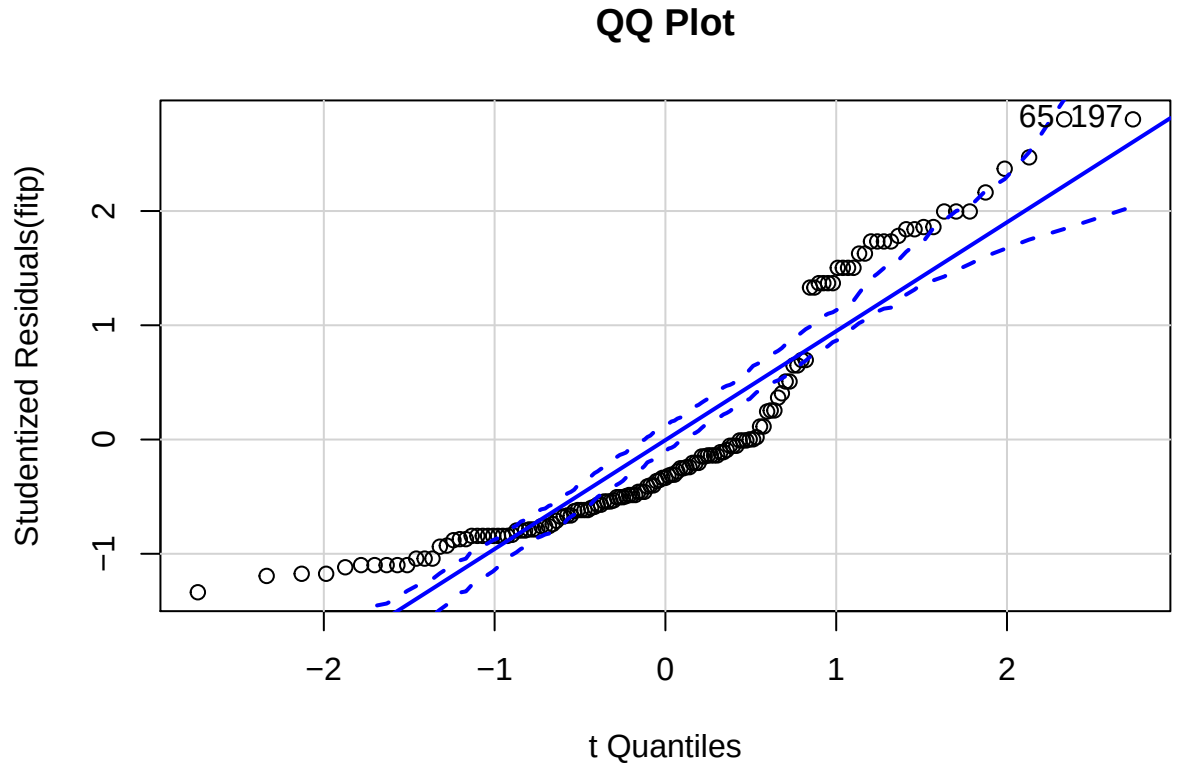
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.9203         0.0000
## Kolmogorov-Smirnov        0.145          0.0000
## Cramer-von Mises        151.9302         0.0000
## Anderson-Darling         45.7419         0.0000
## -----------------------------------------------
```

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

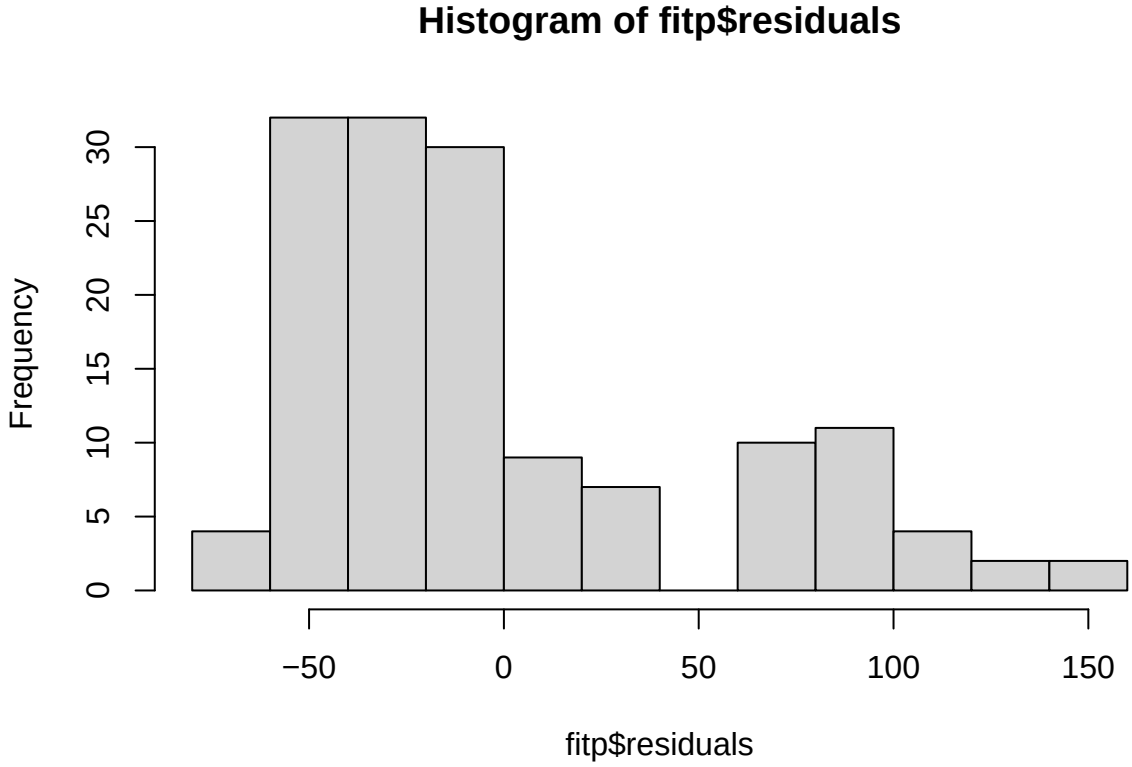
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 65 2.802256          0.0057943      0.82858
```

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

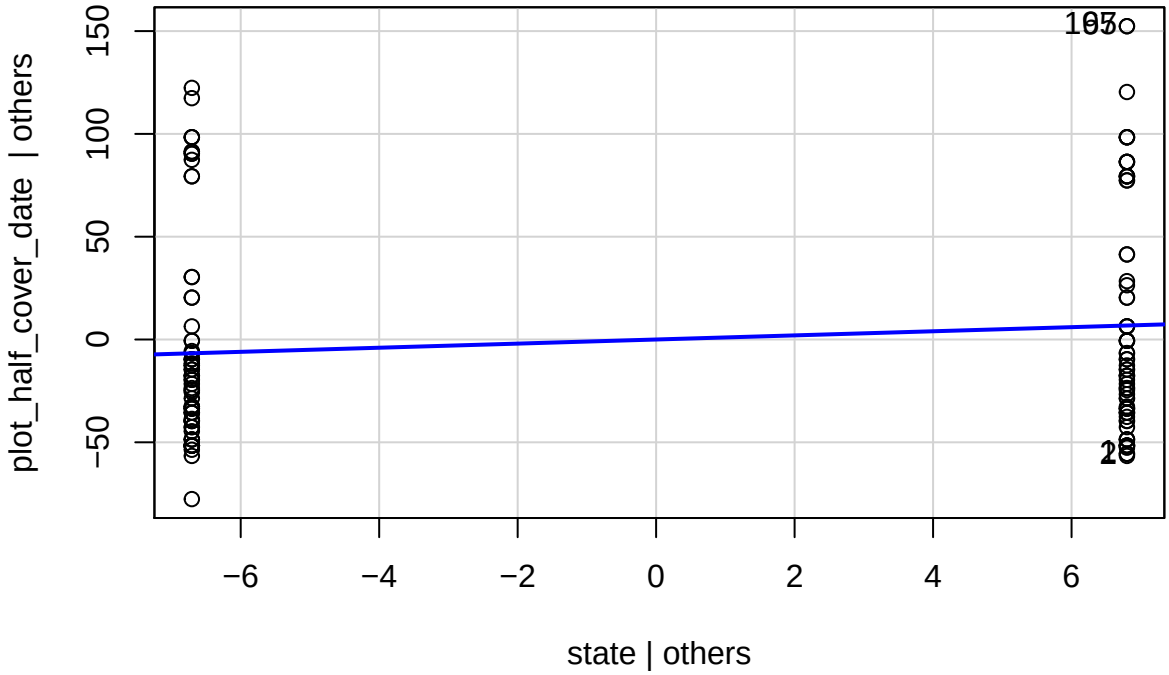



```
##  65 197
##  35 101
```

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



```
leveragePlots(fitp)
```




```
ols_test_normality(fitp)
```

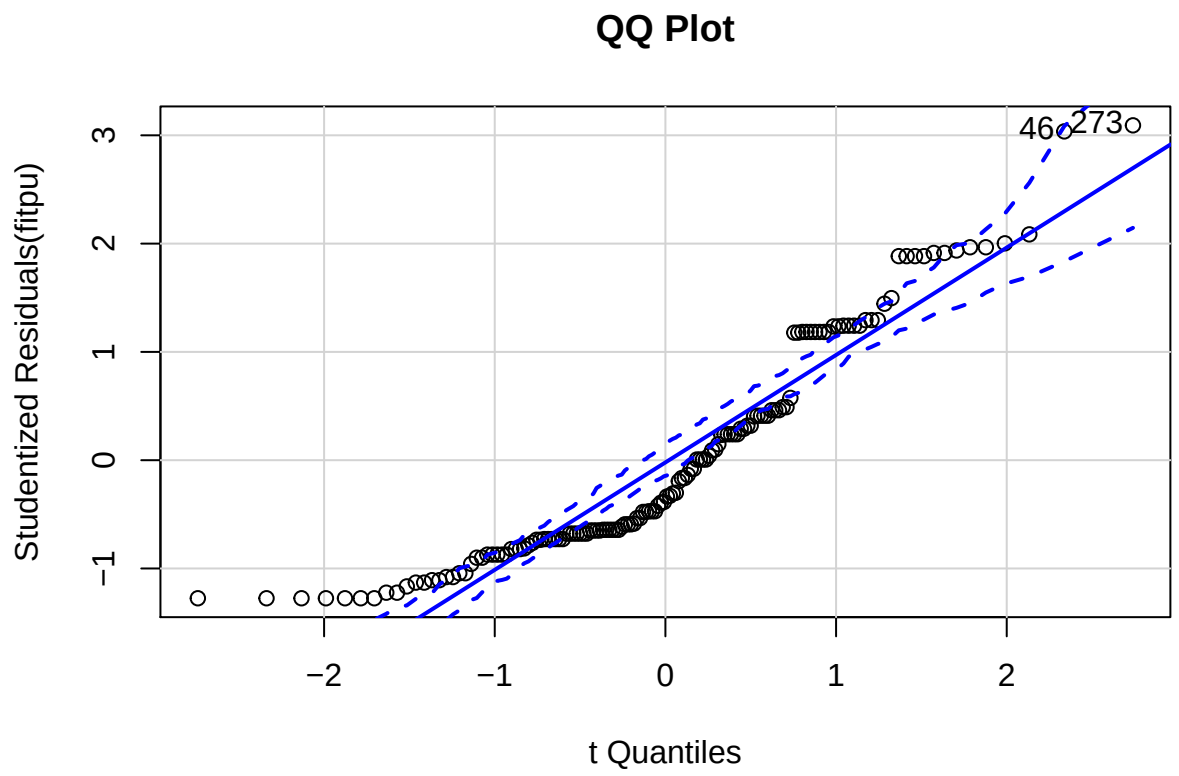
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

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

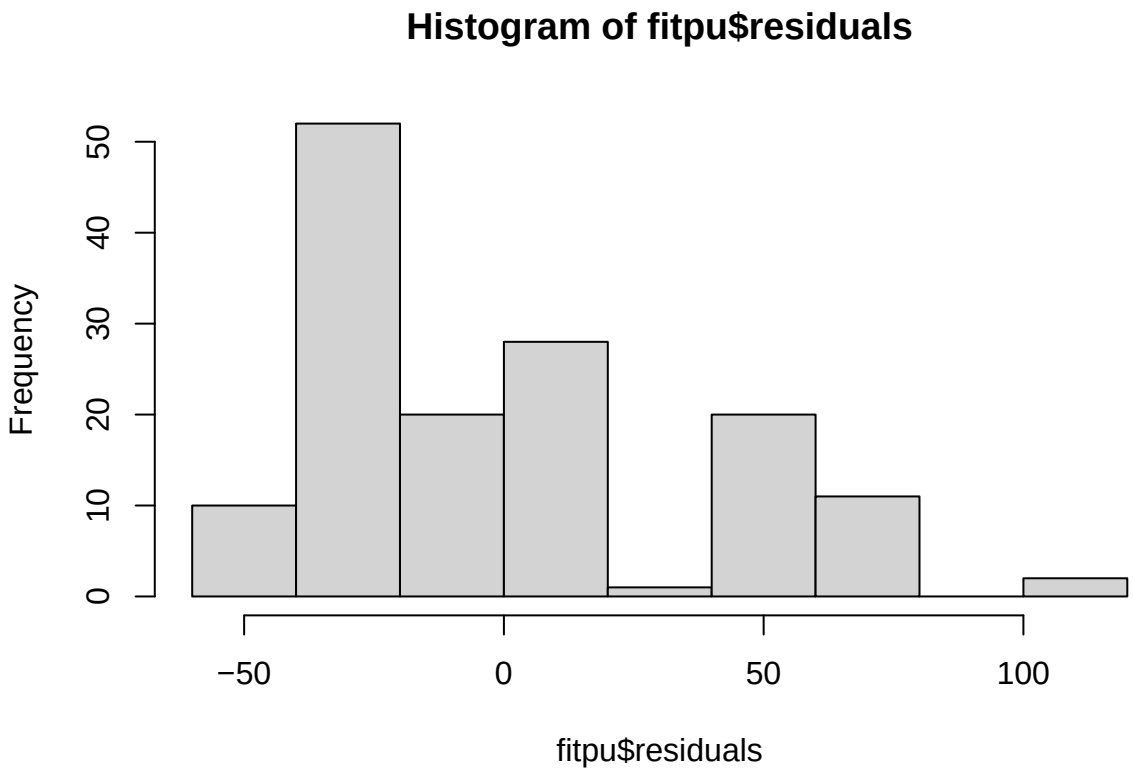
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 273 3.091959          0.0023971      0.34519
```

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

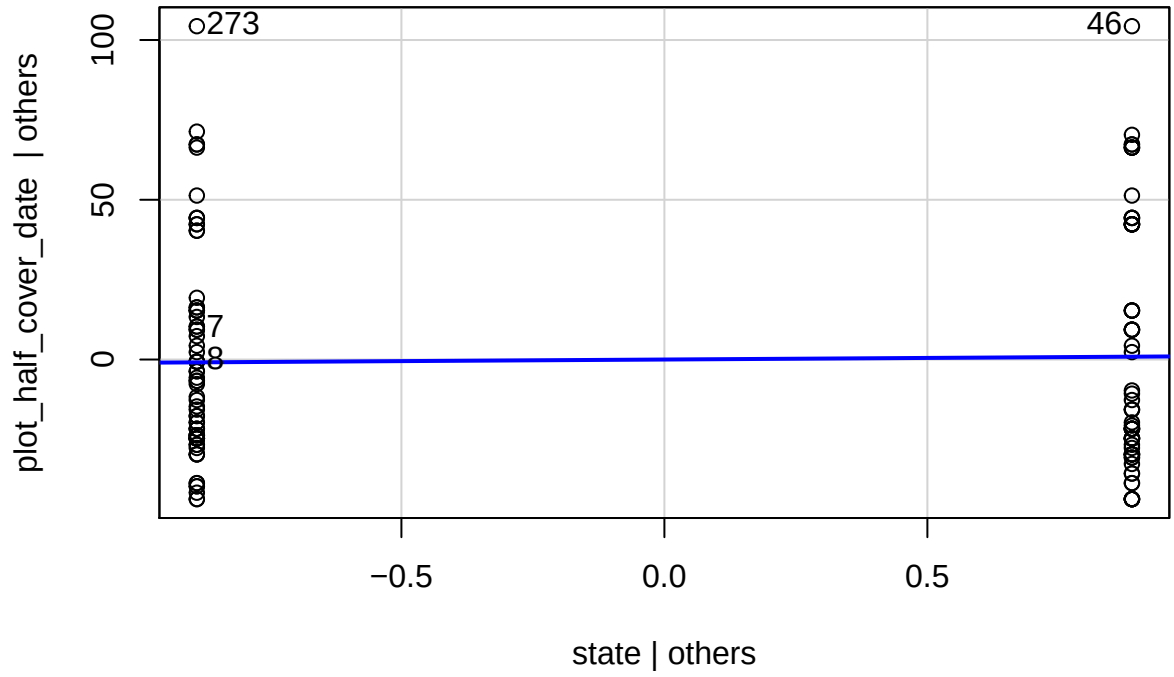



```
##  46 273
##  22 136
```

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



```
leveragePlots(fitpu)
```




```
ols_test_normality(fitpu)
```

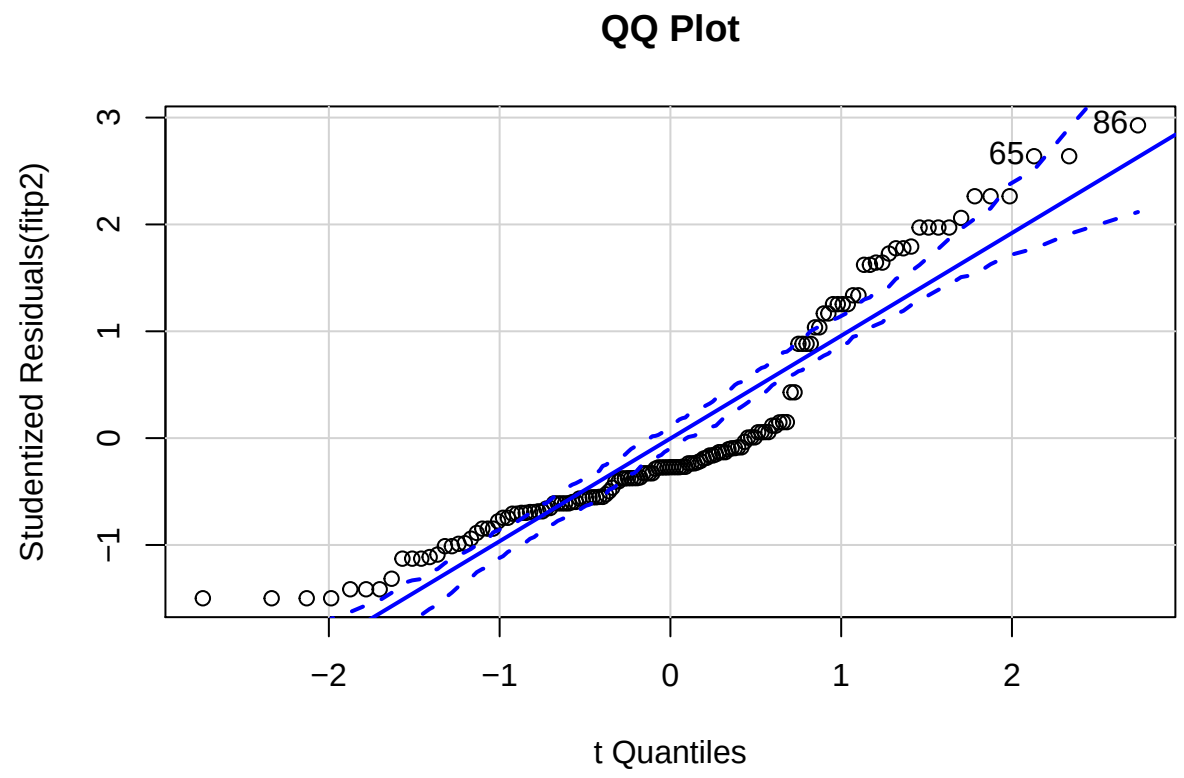
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.9034         0.0000
## Kolmogorov-Smirnov        0.1604         0.0012
## Cramer-von Mises         12.5625         0.0000
## Anderson-Darling          4.9616         0.0000
## -----------------------------------------------
```

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

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 86 2.927361          0.0039953      0.57133
```

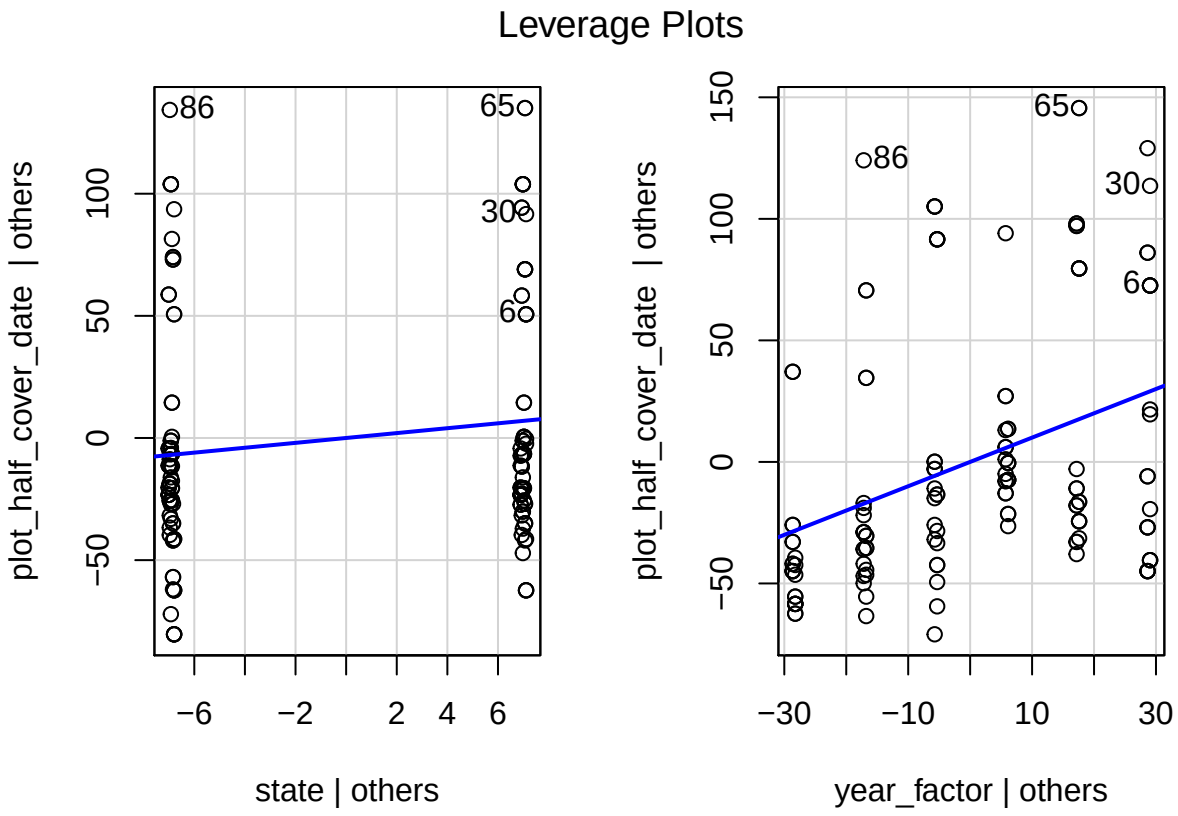
```
qqPlot(fitp2, main = "QQ Plot")
```




```
## 65 86
## 35 44
```

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

```r
leveragePlots(fitp2)
```




```r
ols_test_normality(fitp2)
```

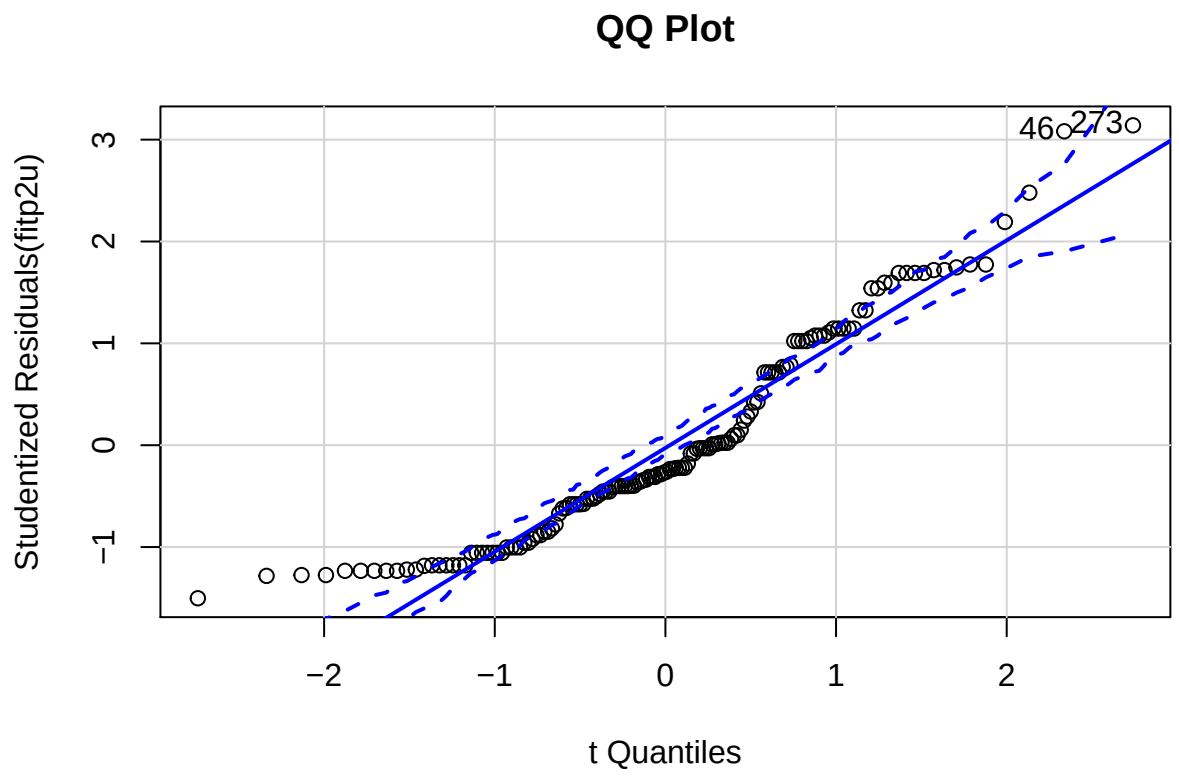
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.8875         0.0000
## Kolmogorov-Smirnov        0.1986         0.0000
## Cramer-von Mises         16.1941         0.0000
## Anderson-Darling          6.693          0.0000
## -----------------------------------------------
```

```r
# UMBS State and year model
fitp2u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
outlierTest(fitp2u)
```

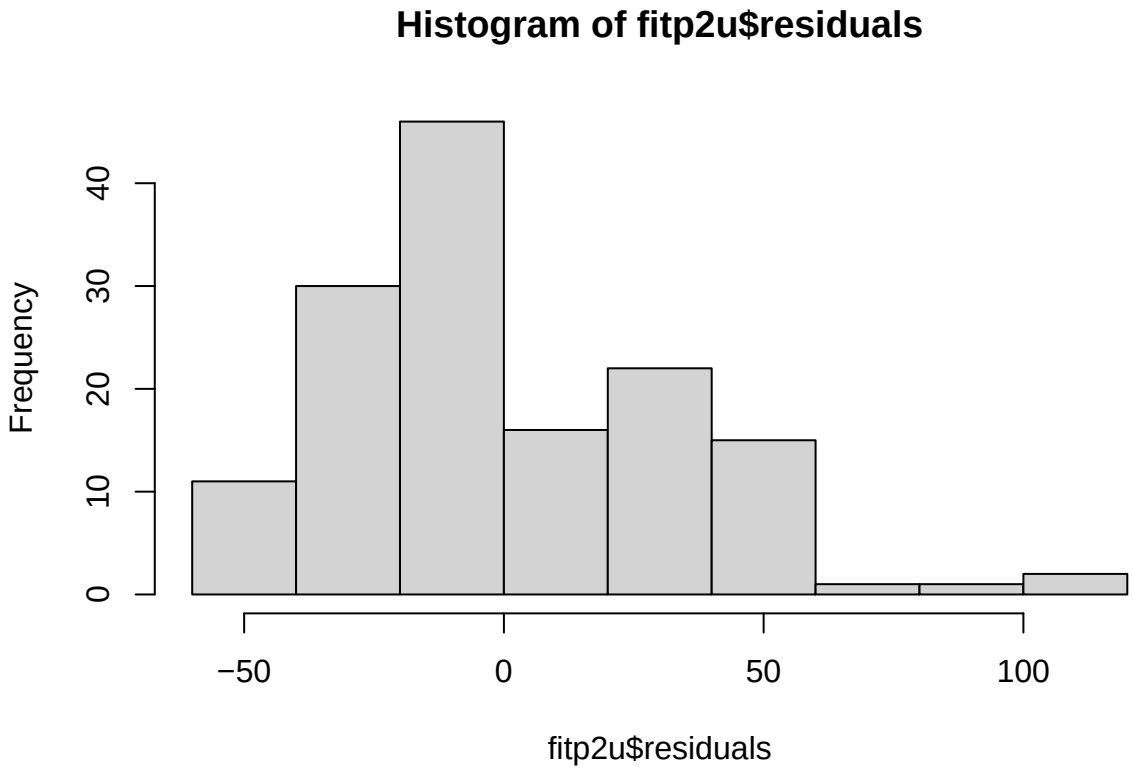
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 273 3.140252          0.0020596      0.29659
```

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

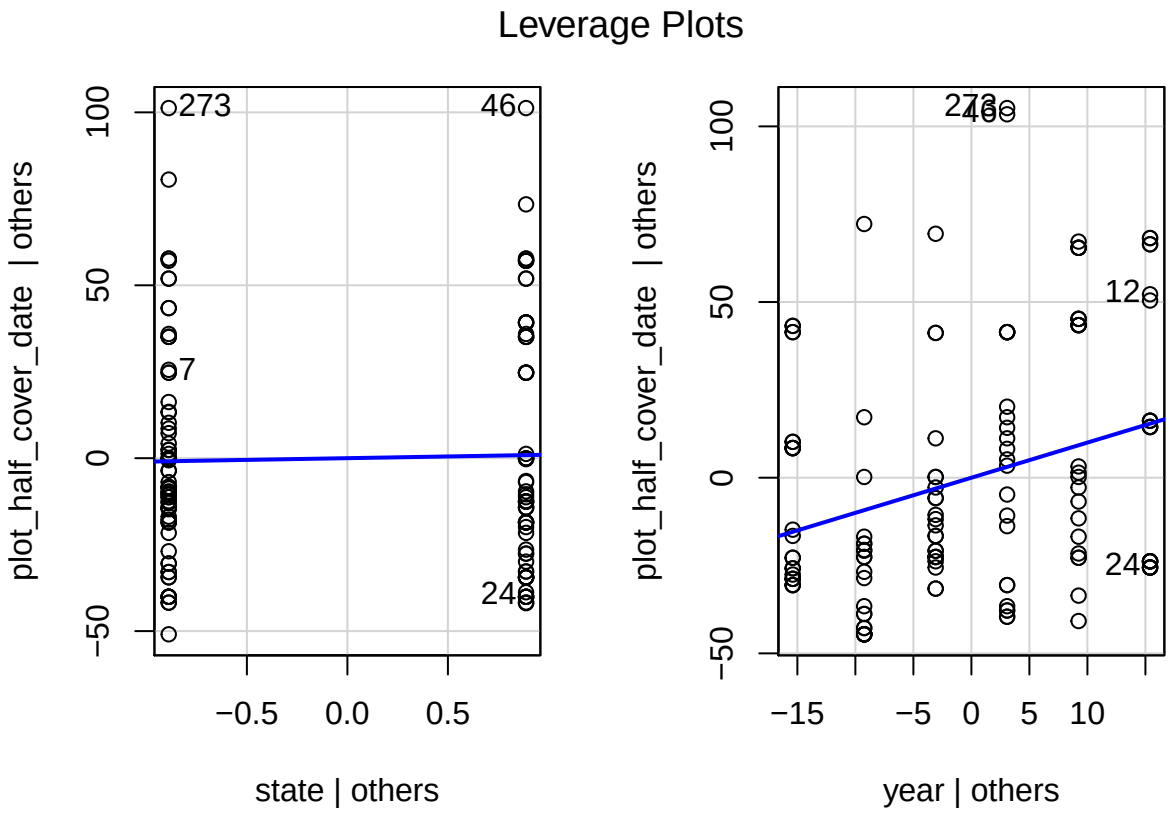



```
##  46 273
##  22 136
```

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



```
leveragePlots(fitp2u)
```




```
ols_test_normality(fitp2u)
```

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

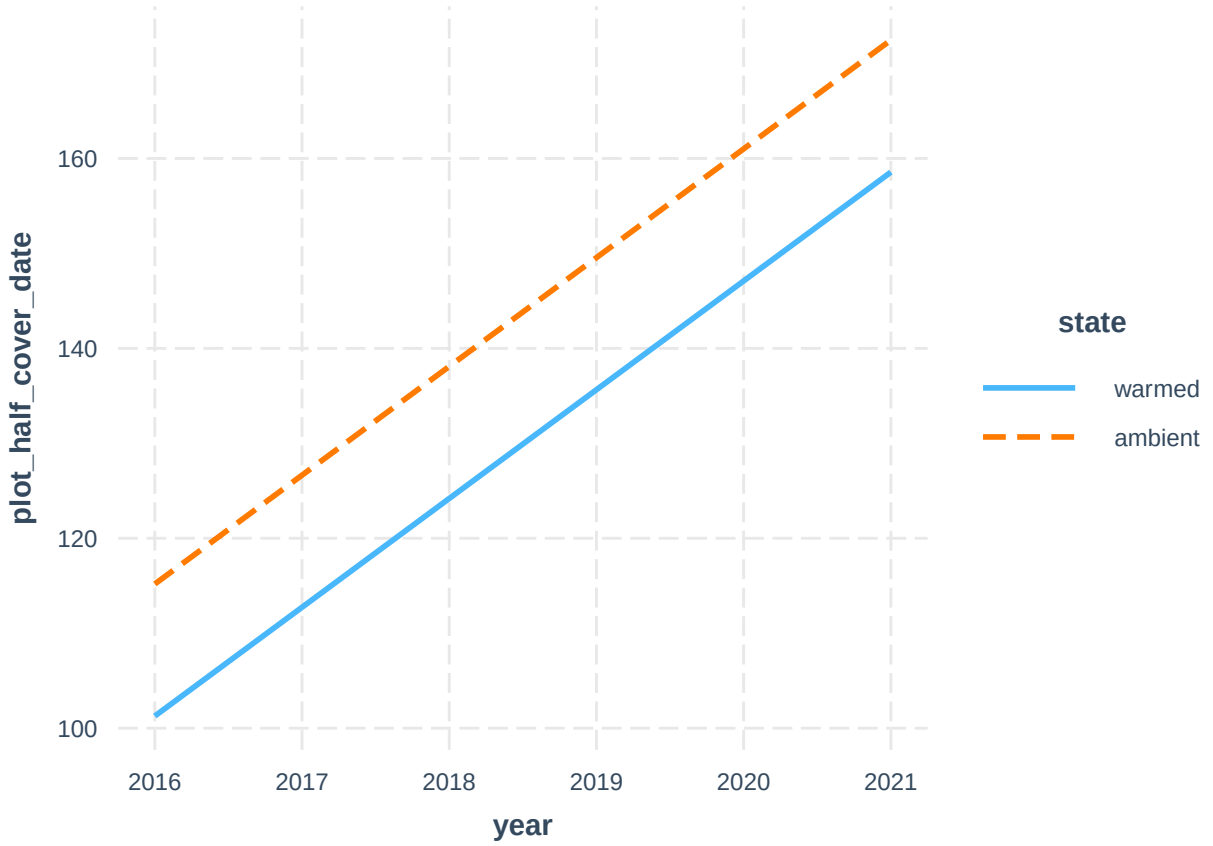
```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.9271         0.0000
## Kolmogorov-Smirnov        0.1362         0.0096
## Cramer-von Mises         12.9808         0.0000
## Anderson-Darling          3.3502         0.0000
## -----------------------------------------------
```

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

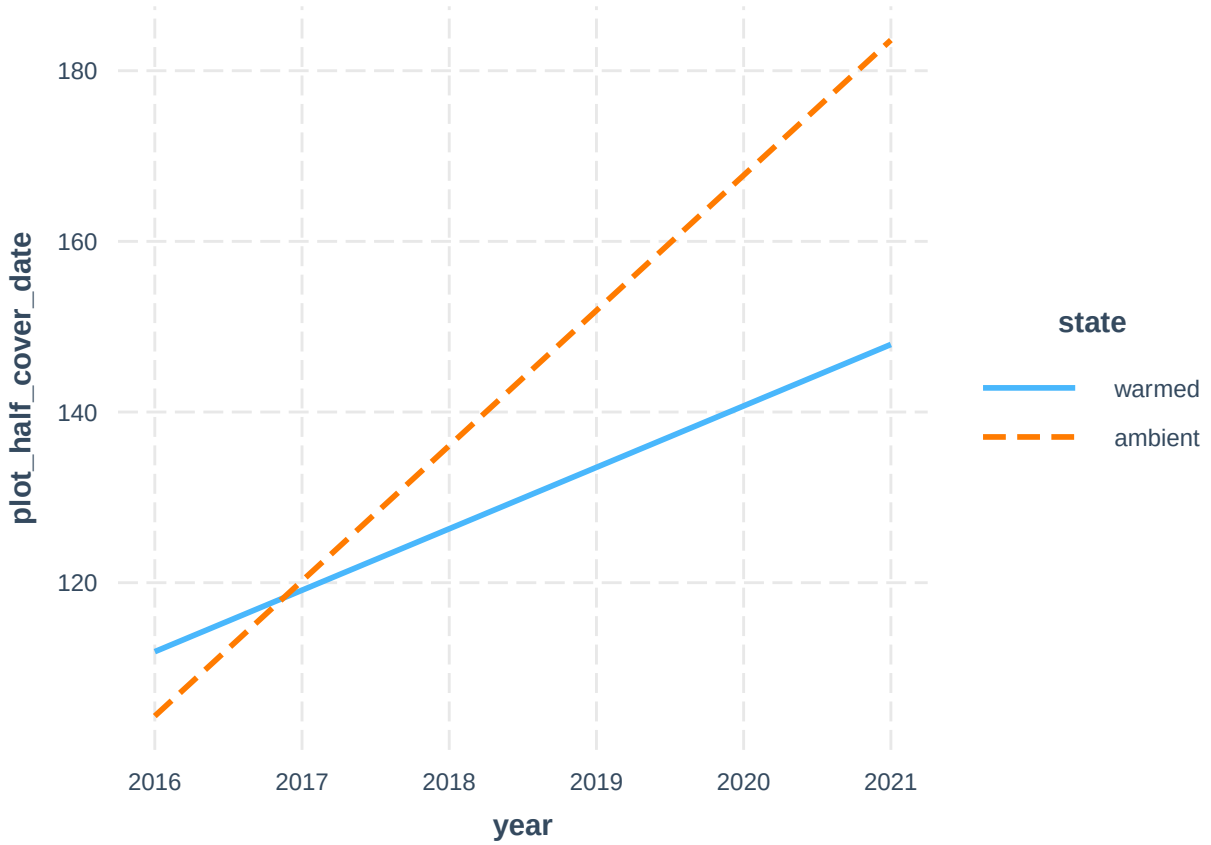
We should also think about how we're treating year. Some of the models have a state * year interaction as a fixed effect, which means that the warming or ambient treatment could affect the half_cover_date differently over time (there would be a different slope for each state in the relationship between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

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

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

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

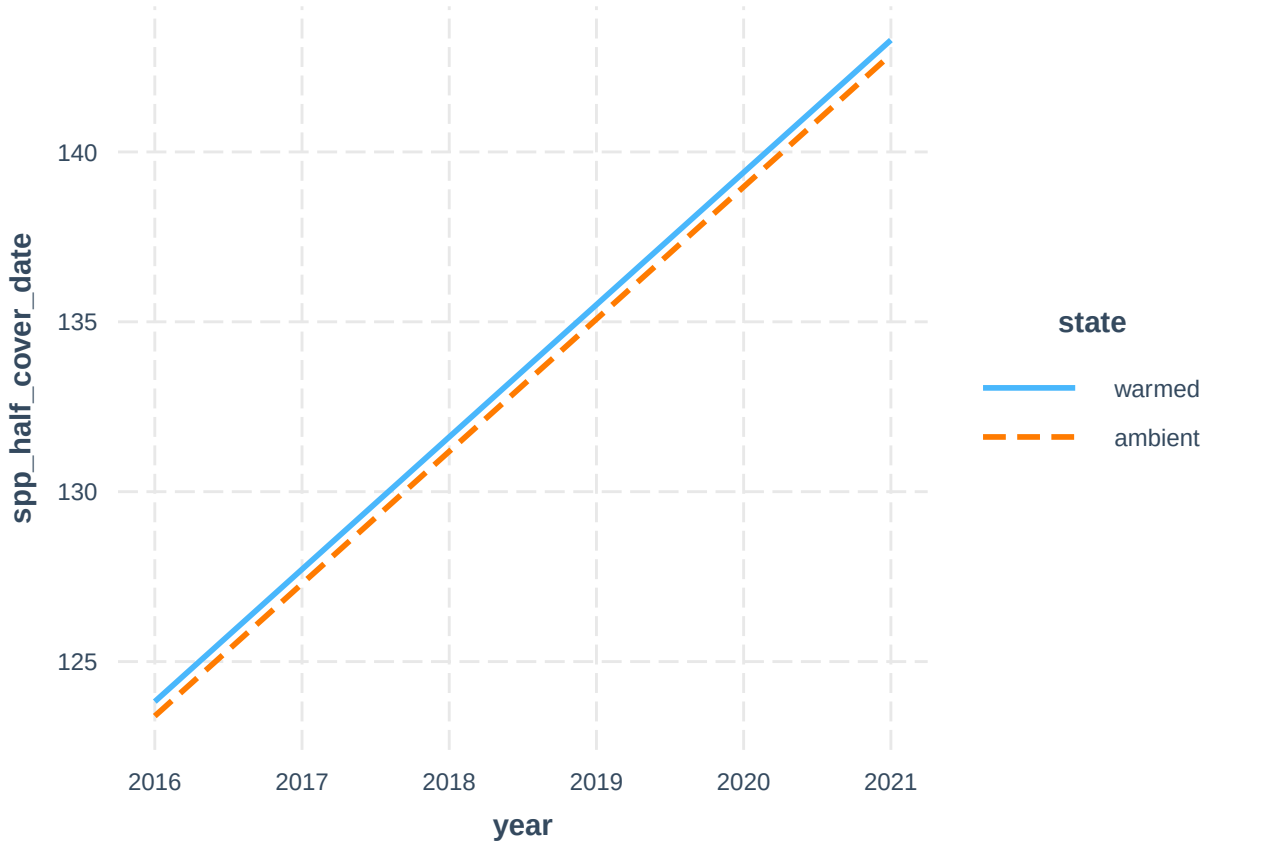



```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```



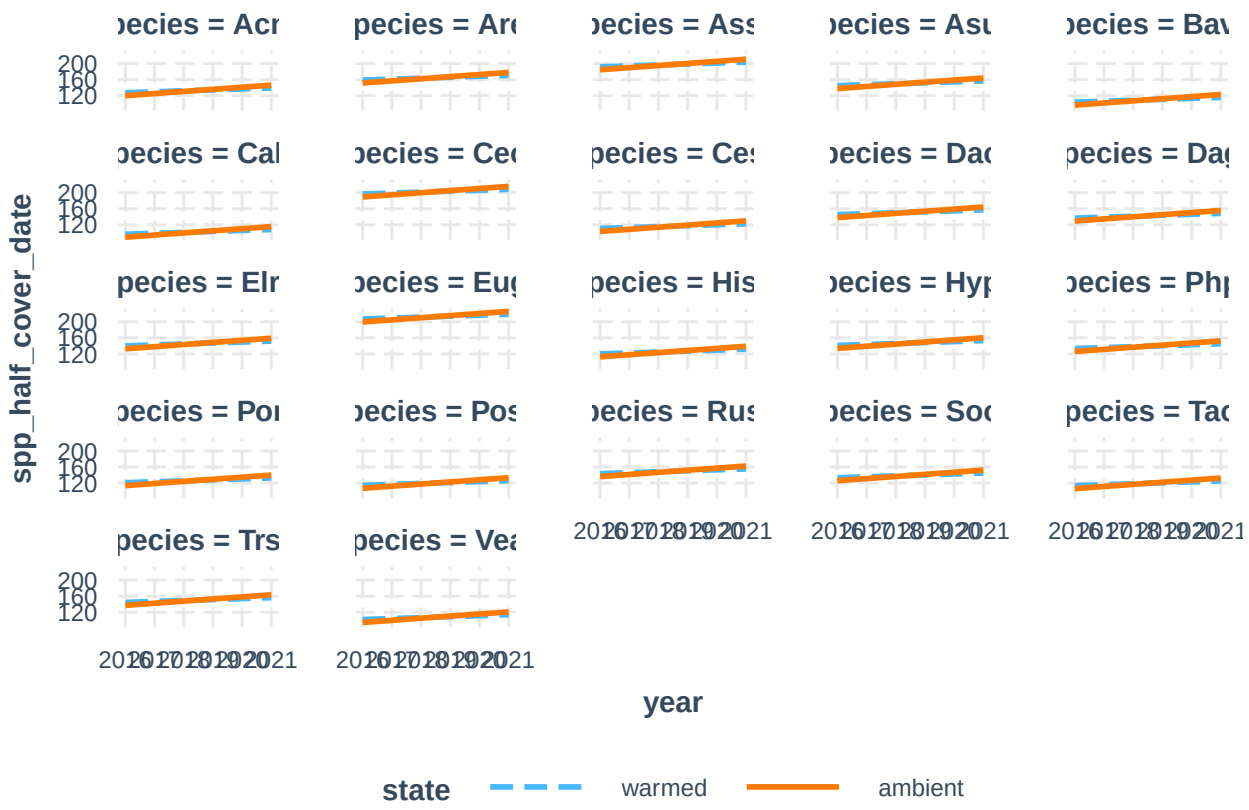

```
fit5 <- lm(spp_half_cover_date ~ state + year + species, data = green_kbs)
interact_plot(fit5, pred = year, modx = state)
```

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



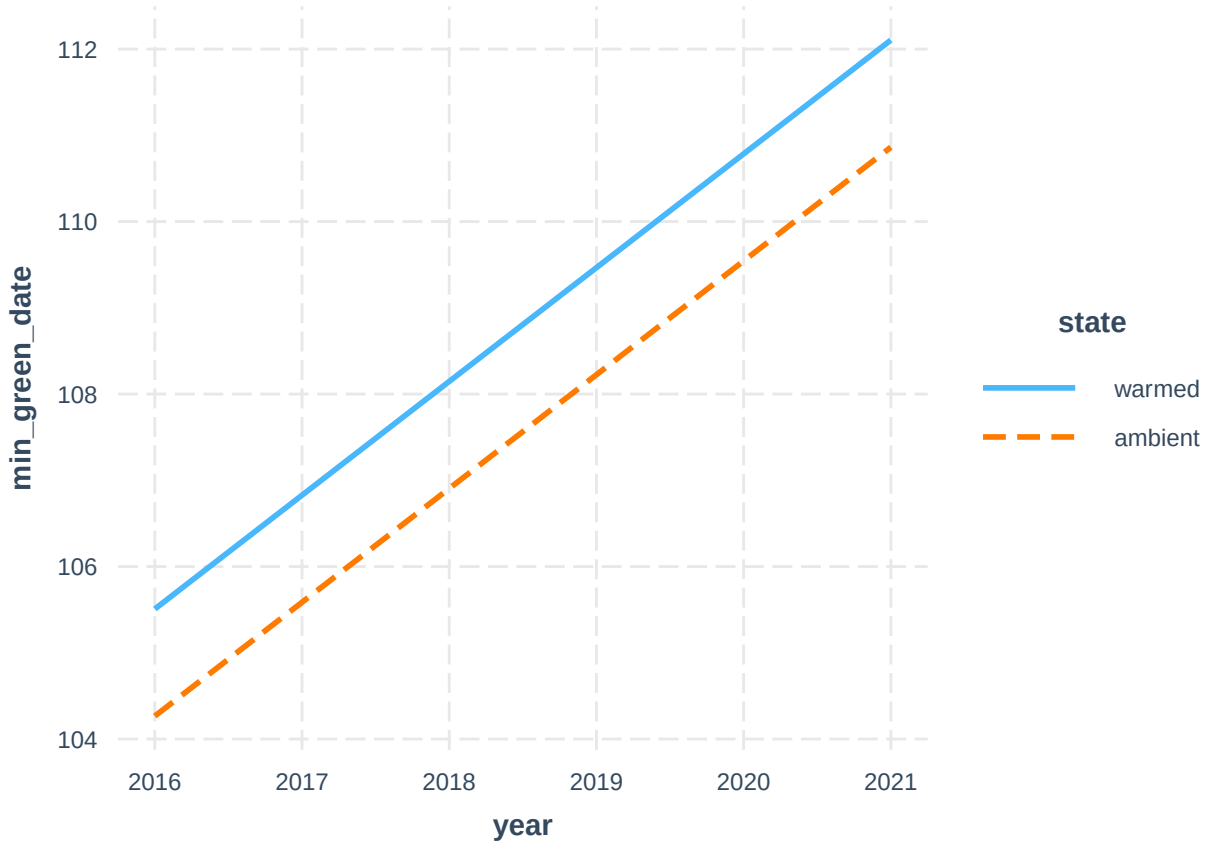

```
fit6 <- lm(spp_half_cover_date ~ state * year + species, data = green_kbs)
interact_plot(fit6, pred = year, modx = state, mod2 = species)
```

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



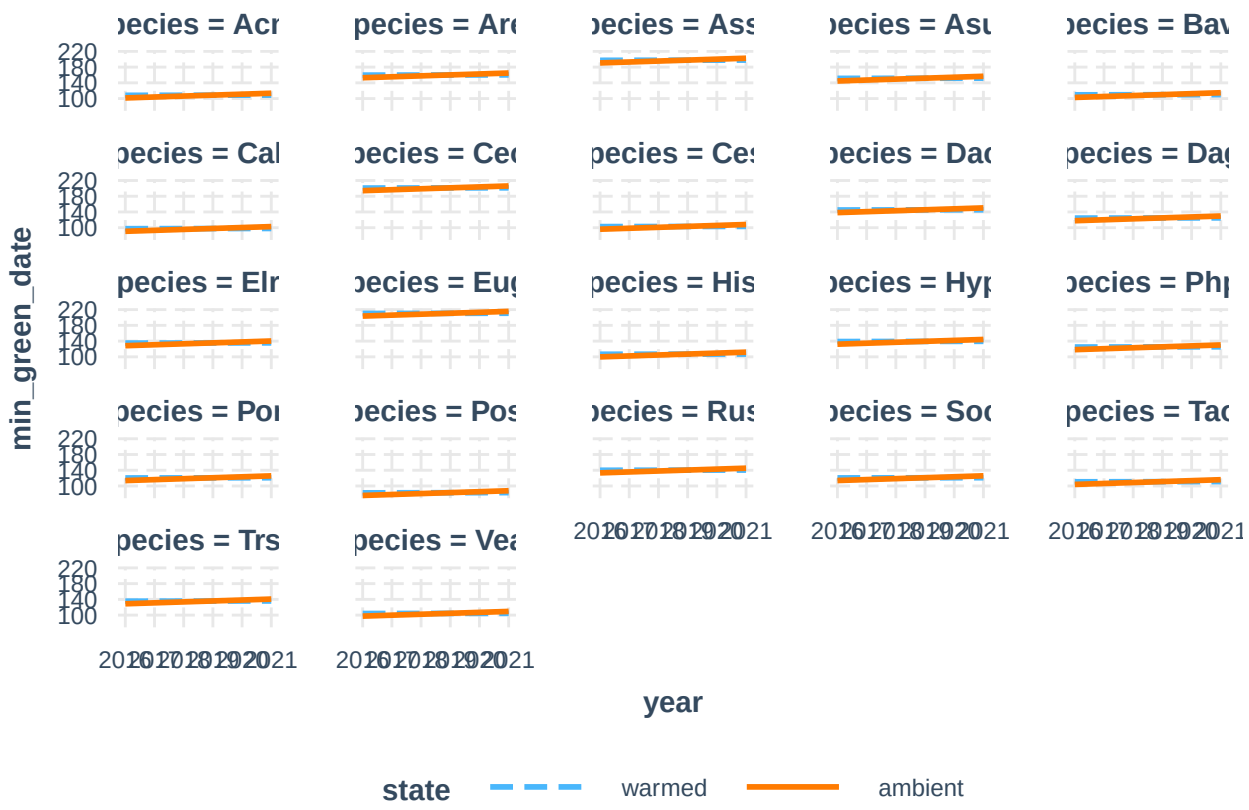

```
fit7 <- lm(min_green_date ~ state + year + species, data = green_kbs)
interact_plot(fit7, pred = year, modx = state)
```

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



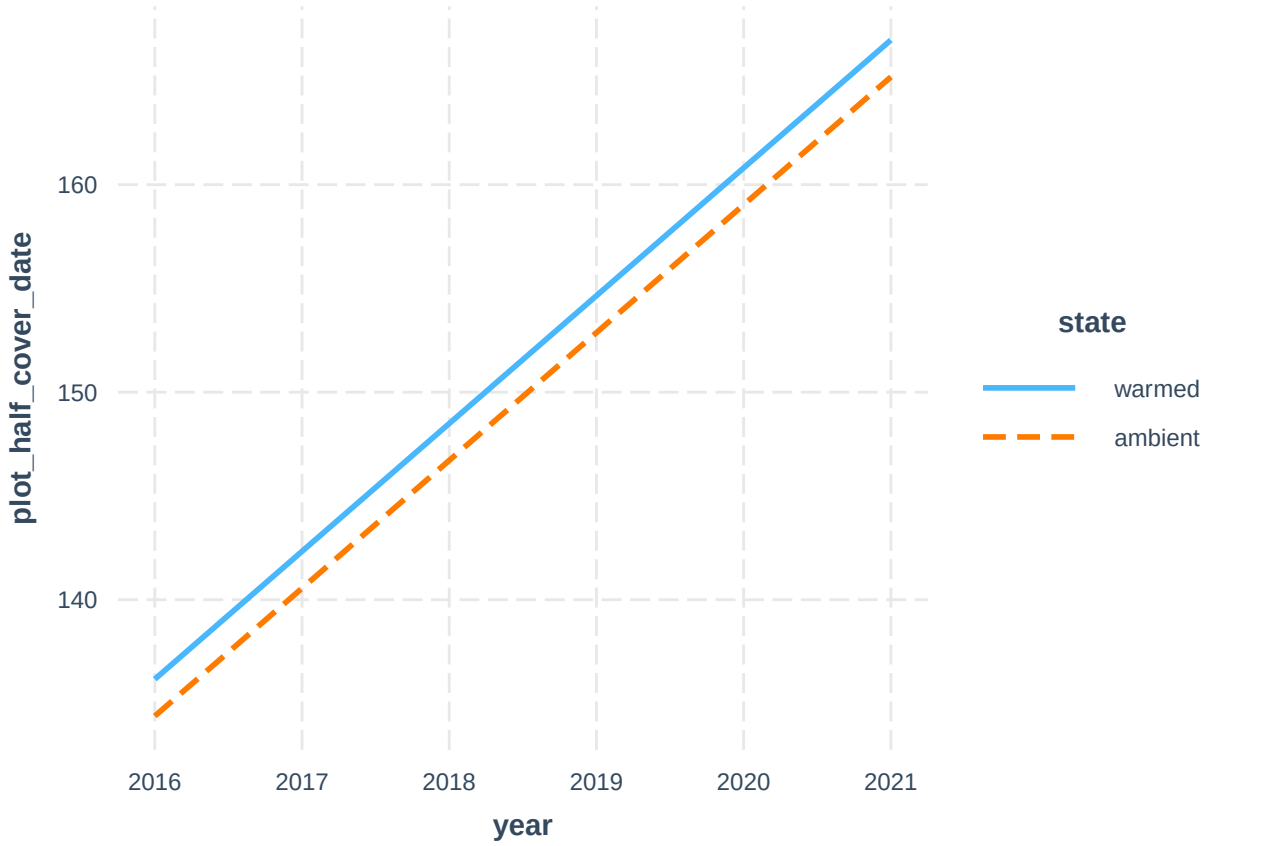

```
fit8 <- lm(min_green_date ~ state * year + species, data = green_kbs)
interact_plot(fit8, pred = year, modx = state, mod2 = species)
```

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

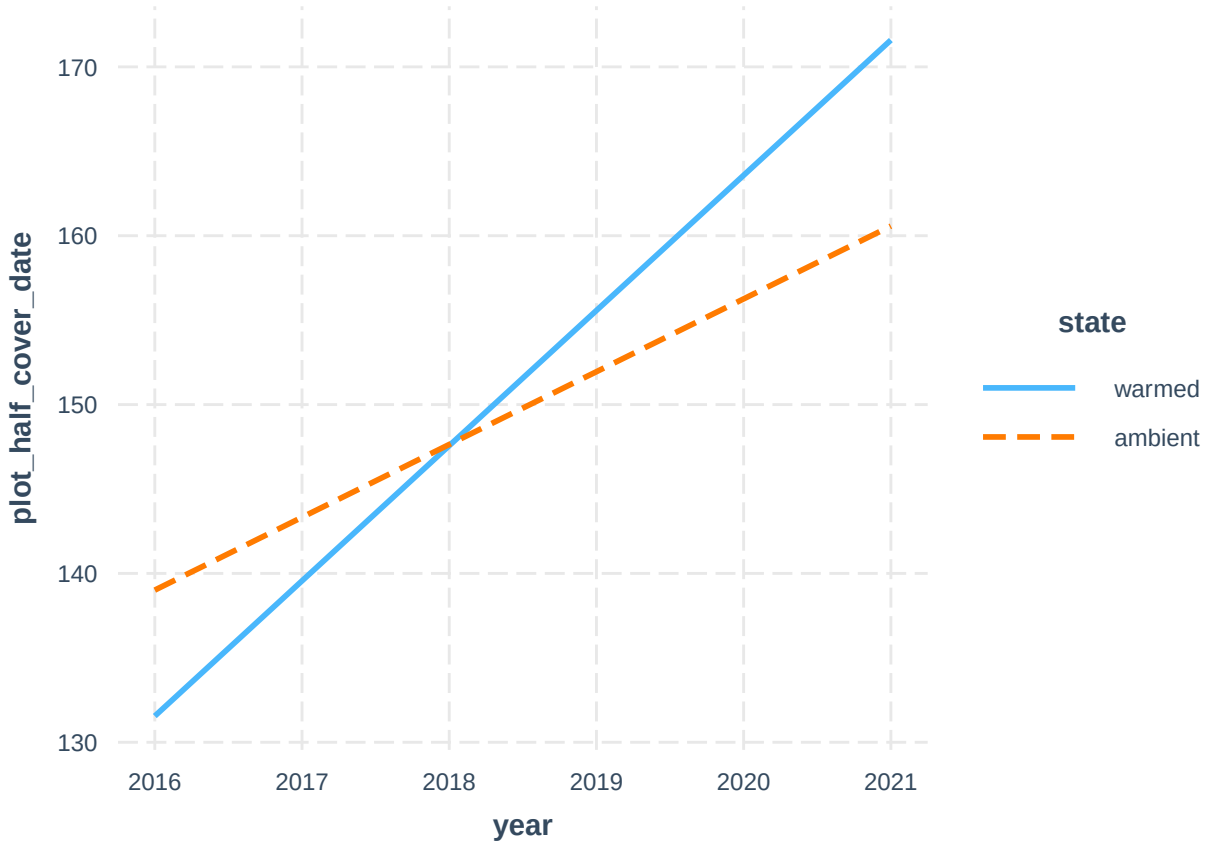



```
# UMBS
fit3u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
interact_plot(fit3u, pred = year, modx = state)
```

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

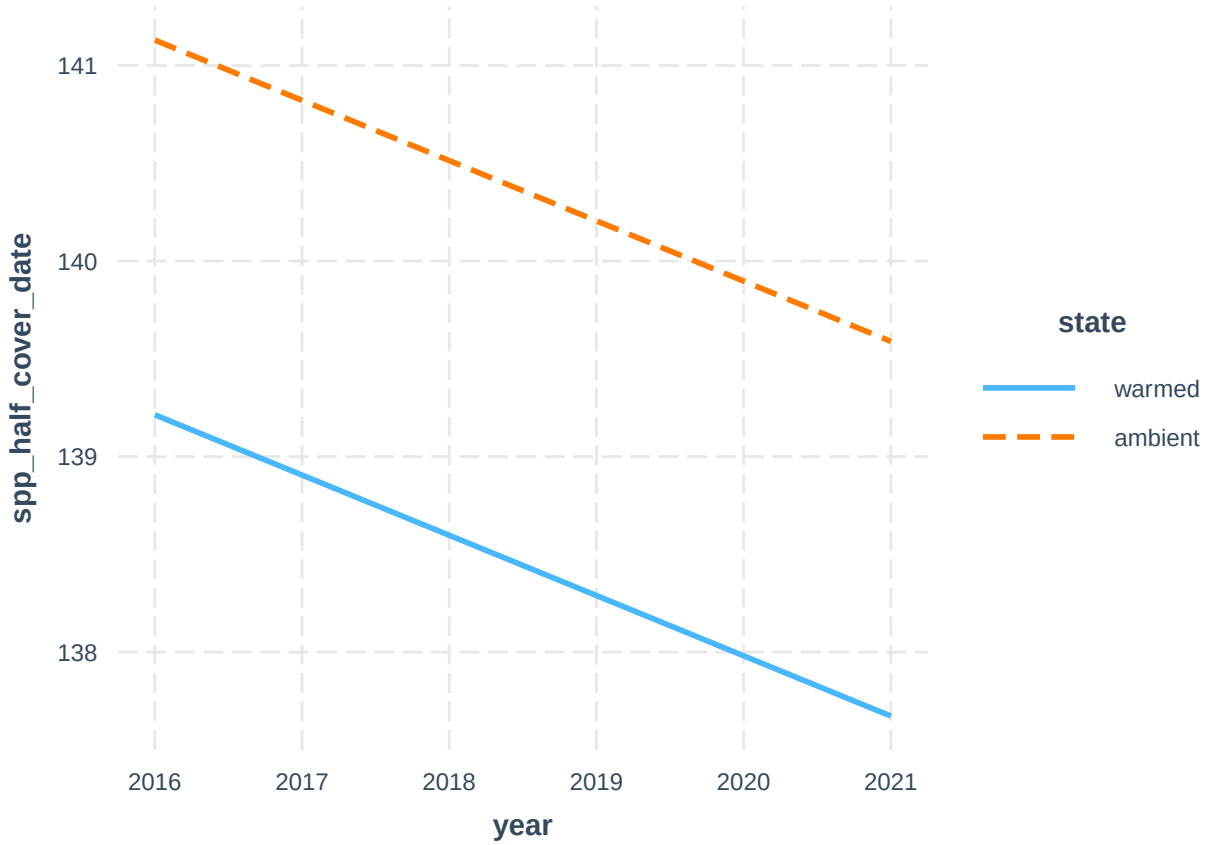



```
fit4u <- lm(plot_half_cover_date ~ state * year, data = green_umbsp)
interact_plot(fit4u, pred = year, modx = state)
```



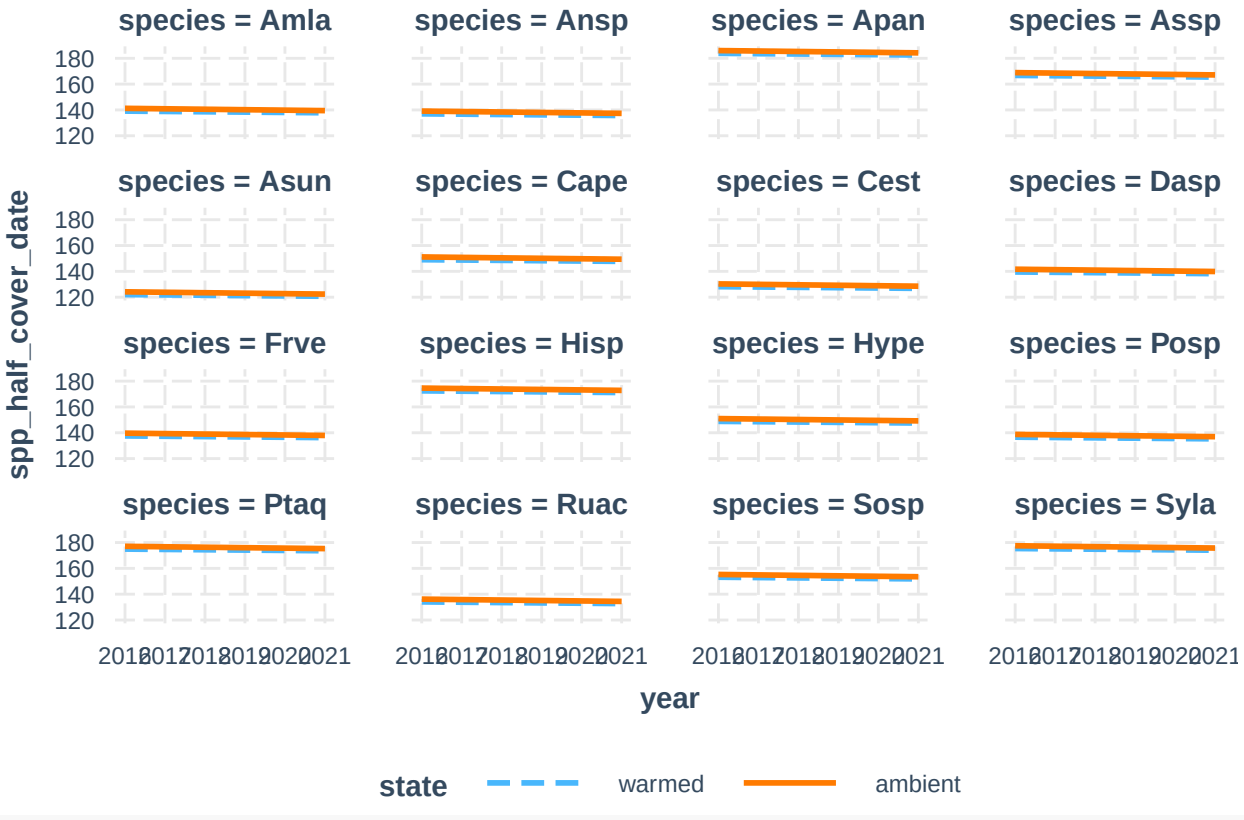

```
fit5u <- lm(spp_half_cover_date ~ state + year + species, data = green_umbs)
interact_plot(fit5u, pred = year, modx = state)
```

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



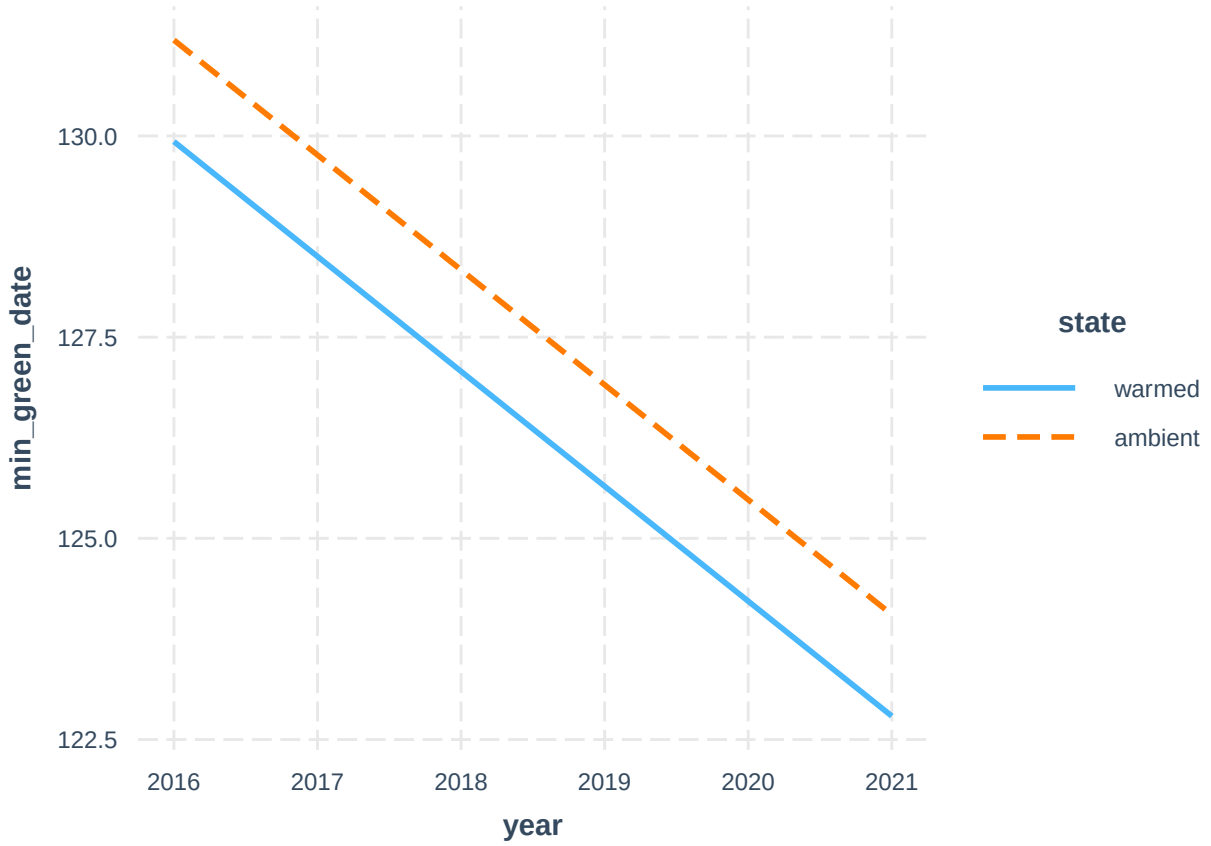

```
fit6u <- lm(spp_half_cover_date ~ state * year + species, data = green_umbs)
interact_plot(fit6u, pred = year, modx = state, mod2 = species)
```

```
## 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).


## Note: KD re-ran different models below, these are models by
## PLZ Do we need to include plot as a random effect with the
## KBS models?
mod1 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide *
    year_factor + (1 | species) + (1 | plot), green_kbs, REML = FALSE)
mod2 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide *
    year_factor + (1 | species), green_kbs, REML = FALSE)
# Run analysis of variance on each model (see this for more
# explanation on how anova on a linear mixed effects model is
# similar to an anove on a regular linear model:
# https://m-clark.github.io/docs/mixedModels/anovamixed.html)
anova(mod1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                        Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state                    8115    8115     1  244.32  3.1690   0.07629 .
## year_factor             64276   64276     1 1497.12 25.1011 6.086e-07 ***
## insecticide              2254    2254     1  242.91  0.8801   0.34911
```

```
## state:year_factor        11406   11406     1 1483.80  4.4542   0.03498 *
## year_factor:insecticide   3855    3855     1 1483.51  1.5053   0.22005
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(mod2)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                          Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state                      9079    9079     1 1489.3  3.5183   0.06089 .
## year_factor               64112   64112     1 1500.2 24.8449 6.935e-07 ***
## insecticide                2446    2446     1 1488.5  0.9480   0.33038
## state:year_factor         11187   11187     1 1489.3  4.3352   0.03750 *
## year_factor:insecticide    3567    3567     1 1490.0  1.3823   0.23990
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Data: green_kbs
## Models:
## mod2: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod2:     (1 | species)
## mod1: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod1:     (1 | species) + (1 | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod2    8 16234 16276 -8108.8    16218
## mod1    9 16233 16281 -8107.7    16215 2.2149  1     0.1367
```

```r
summary(mod1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
##     (1 | species) + (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16233.4  16281.3  -8107.7  16215.4     1502
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8990 -0.6766 -0.2621  0.4369  3.3088
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
```

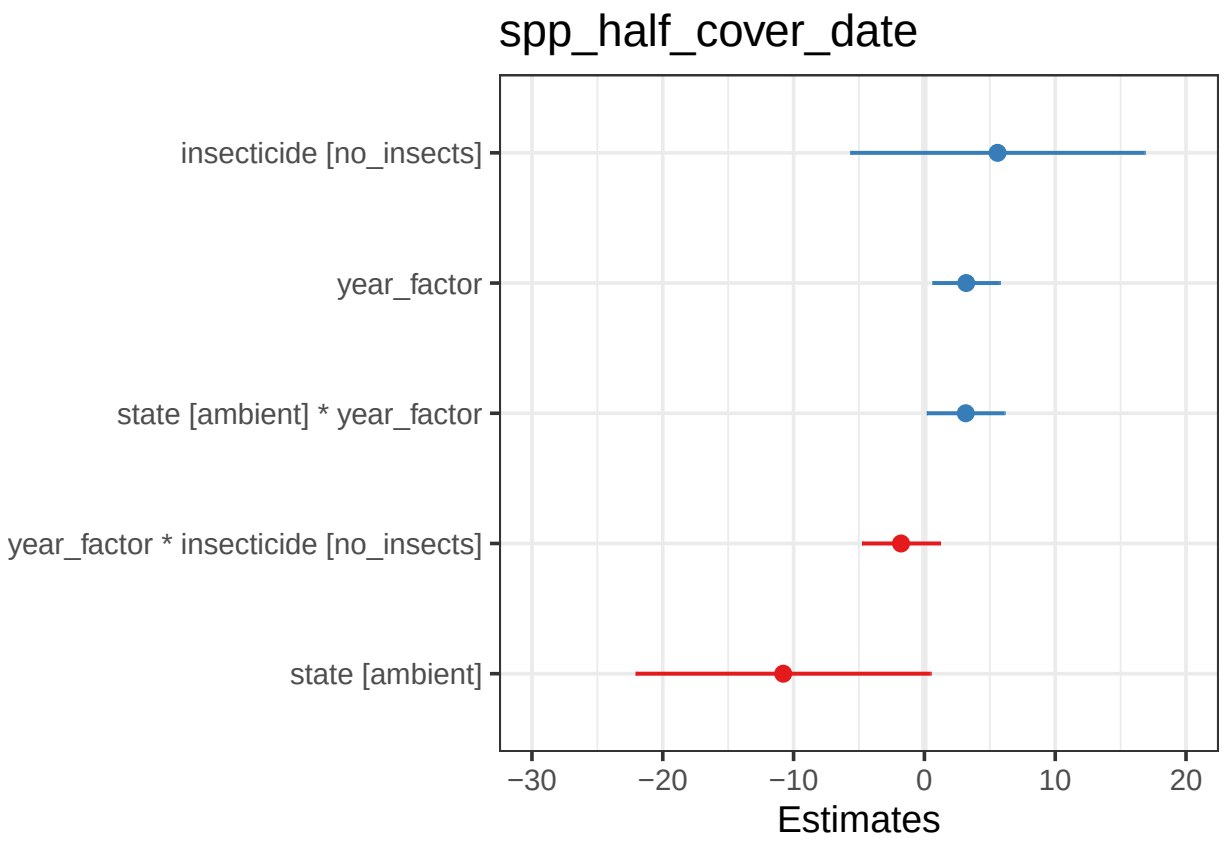
```
##  plot     (Intercept)   21.18   4.603
##  species  (Intercept)  668.39  25.853
##  Residual             2560.66  50.603
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                                  Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)                       131.339      7.723   60.639  17.006   <2e-16
## stateambient                      -10.754      6.041  244.319  -1.780   0.0763
## year_factor                         3.229      1.311 1488.120   2.463   0.0139
## insecticideno_insects               5.659      6.032  242.911   0.938   0.3491
## stateambient:year_factor            3.198      1.515 1483.797   2.110   0.0350
## year_factor:insecticideno_insects  -1.861      1.517 1483.513  -1.227   0.2201
##
## (Intercept)                      ***
## stateambient                     .
## year_factor                      *
## insecticideno_insects
## stateambient:year_factor         *
## year_factor:insecticideno_insects
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn yr_fct insct_ sttm:_
## stateambint -0.389
## year_factor -0.581  0.480
## insctcdn_ns -0.389 -0.038  0.471
## sttmbnt:yr_  0.324 -0.842 -0.568  0.045
## yr_fctr:ns_  0.321  0.048 -0.526 -0.843 -0.078
```

```
summary(mod2)
```

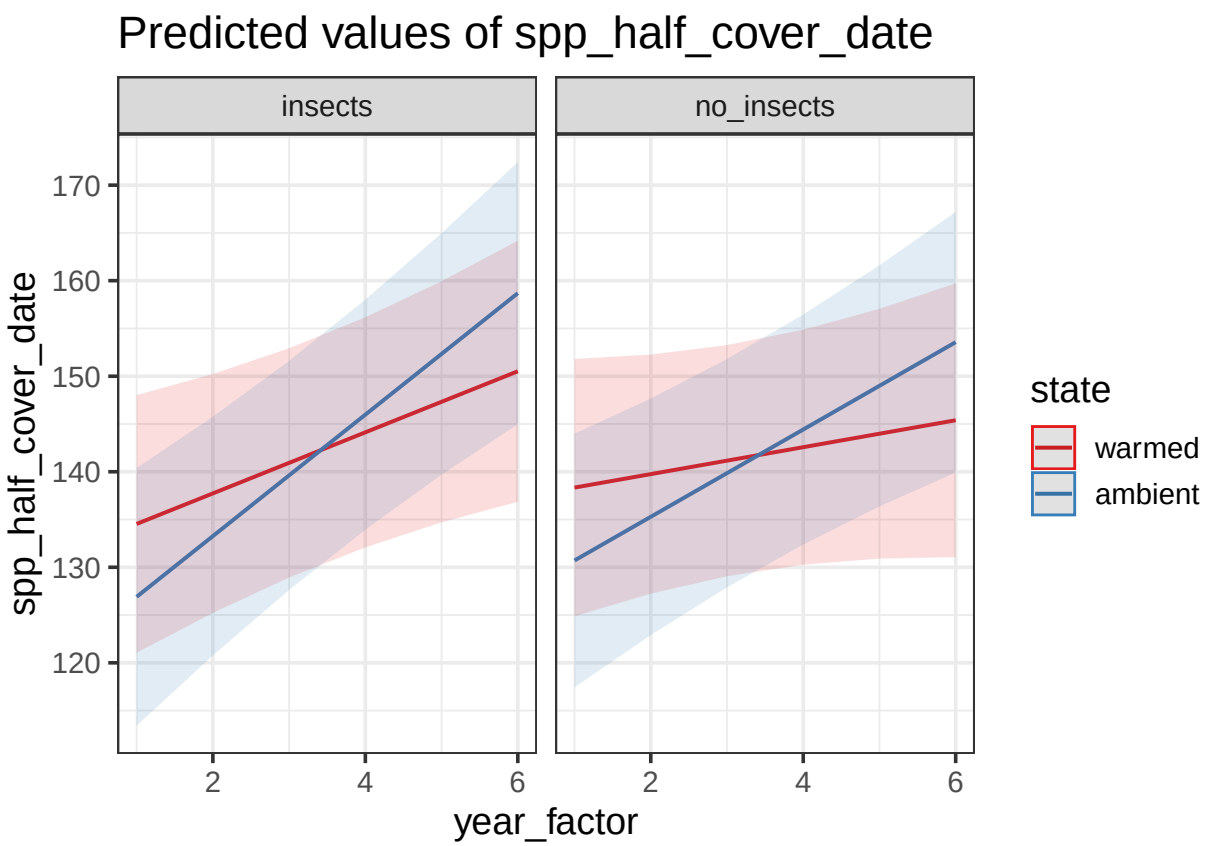
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
##     (1 | species)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16233.7  16276.2  -8108.8  16217.7     1503
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9057 -0.6717 -0.2580  0.4171  3.2782
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  species  (Intercept)  675.7   25.99
##  Residual             2580.5   50.80
## Number of obs: 1511, groups:  species, 22
##
## Fixed effects:
##                                  Estimate Std. Error       df t value Pr(>|t|)
```

```
## (Intercept)                          131.339      7.579   56.934  17.330   <2e-16
## stateambient                         -10.792      5.753 1489.307  -1.876   0.0609
## year_factor                            3.197      1.313 1492.649   2.434   0.0151
## insecticideno_insects                  5.593      5.744 1488.509   0.974   0.3304
## stateambient:year_factor               3.161      1.518 1489.288   2.082   0.0375
## year_factor:insecticideno_insects     -1.787      1.520 1489.948  -1.176   0.2399
##
## (Intercept)                         ***
## stateambient                        .
## year_factor                         *
## insecticideno_insects
## stateambient:year_factor            *
## year_factor:insecticideno_insects
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn yr_fct insct_ sttm:_
## stateambint -0.378
## year_factor -0.594  0.507
## insctcdn_ns -0.377 -0.041  0.495
## sttmbnt:yr_  0.332 -0.886 -0.569  0.047
## yr_fctr:ns_  0.327  0.049 -0.526 -0.888 -0.077
```

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

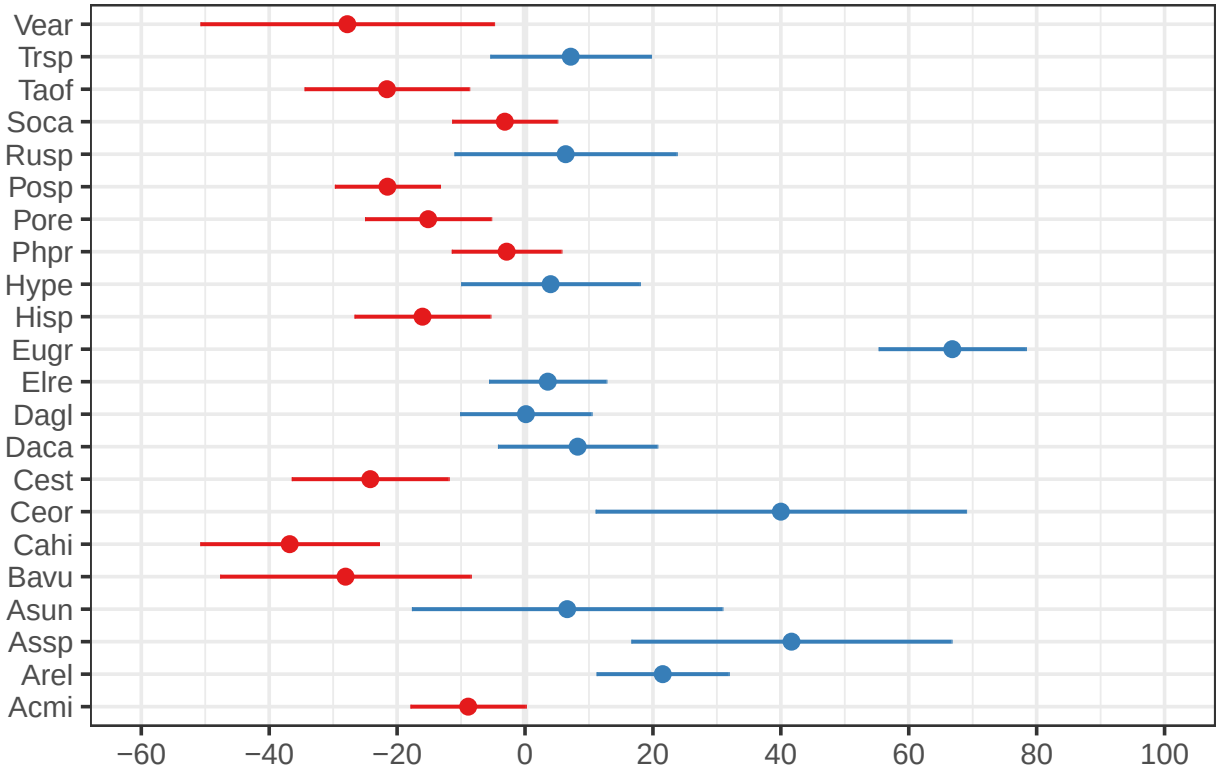



```
# these are the fixed predicted values:
plot_model(mod2, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```




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

Random effects




```
# Do we need to include insecticide?
mod3 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |
    species), green_kbs, REML = FALSE)
anova(mod2, mod3)
```

```
## Data: green_kbs
## Models:
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
## mod2: spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
## mod2:     (1 | species)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod3    6 16231 16263 -8109.5    16219
## mod2    8 16234 16276 -8108.8    16218 1.4045  2     0.4955
```

```
AICctab(mod2, mod3, weights = T)
```

```
##      dAICc df weight
## mod3 0.0   6  0.79
## mod2 2.6   8  0.21
```

```
# Dont' need insecticide, continue with mod3

# Does year need to be interactive with insecticide? -
# already removed insecticide mod4 <-
# lmer(spp_half_cover_date ~ state*year_factor + insecticide
# + (1|species) + (1|plot), green_kbs, #REML=FALSE)
# anova(mod1, mod4) No, P>0.05 so insecticide*year doesn't
# strongly improve model fit so we will shift to mod4
# anova(mod3, mod4) Yes, P<0.05 so insecticide still improves
```

```r
# 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 + (1 |
    species), green_kbs, REML = FALSE)
anova(mod3, mod5)
```

```
## Data: green_kbs
## Models:
## mod5: spp_half_cover_date ~ state + year_factor + (1 | species)
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod5    5 16233 16260 -8111.5    16223
## mod3    6 16231 16263 -8109.5    16219 3.9631  1    0.04651 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##      dAICc df weight
## mod3 0.0   6  0.73
## mod5 1.9   5  0.27
```

```r
# 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
summary(mod5)
```

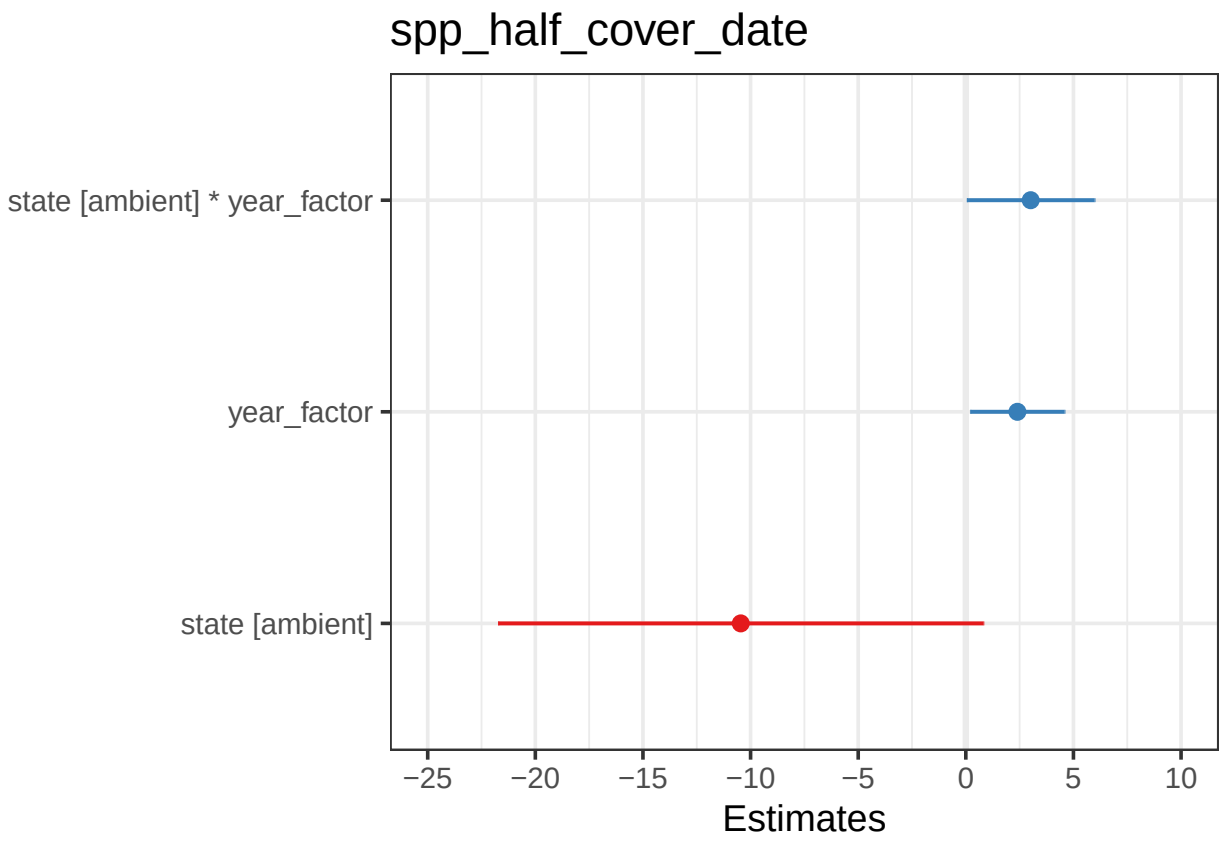
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + (1 | species)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16233.0  16259.6  -8111.5  16223.0     1506
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8874 -0.6635 -0.2604  0.4012  3.2349
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  species  (Intercept)  684.2   26.16
##  Residual             2589.3   50.89
## Number of obs: 1511, groups:  species, 22
##
## Fixed effects:
##               Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   128.7604     6.5313   30.6573  19.714  < 2e-16 ***
## stateambient   -0.2973     2.6585 1494.6051  -0.112    0.911
## year_factor     3.9892     0.7778 1499.6569   5.129  3.3e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
```

```
##             (Intr) sttmbn
## stateambint -0.209
## year_factor -0.388 -0.026
```

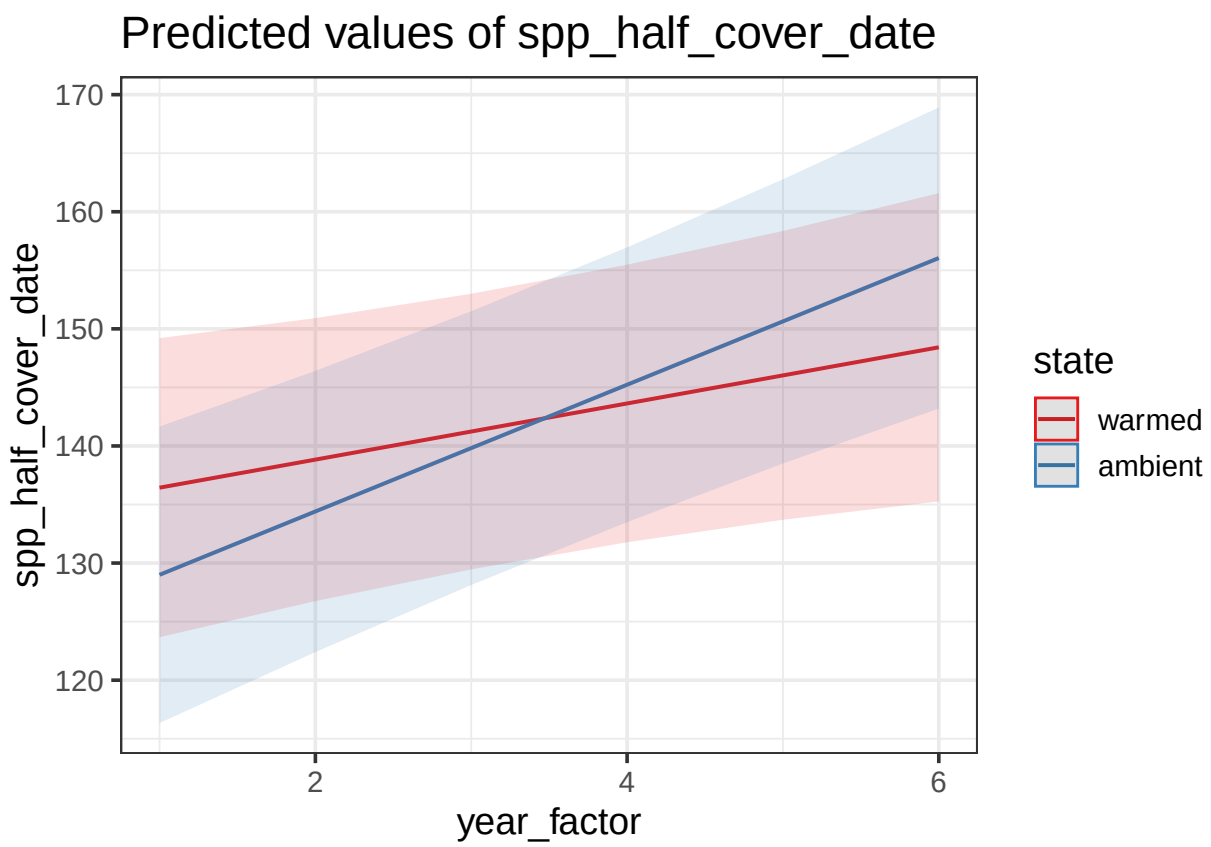
```
anova(mod3)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## state                8542    8542     1 1489.1  3.3073   0.06917 .
## year_factor         65017   65017     1 1499.8 25.1730 5.866e-07 ***
## state:year_factor   10251   10251     1 1488.8  3.9688   0.04653 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

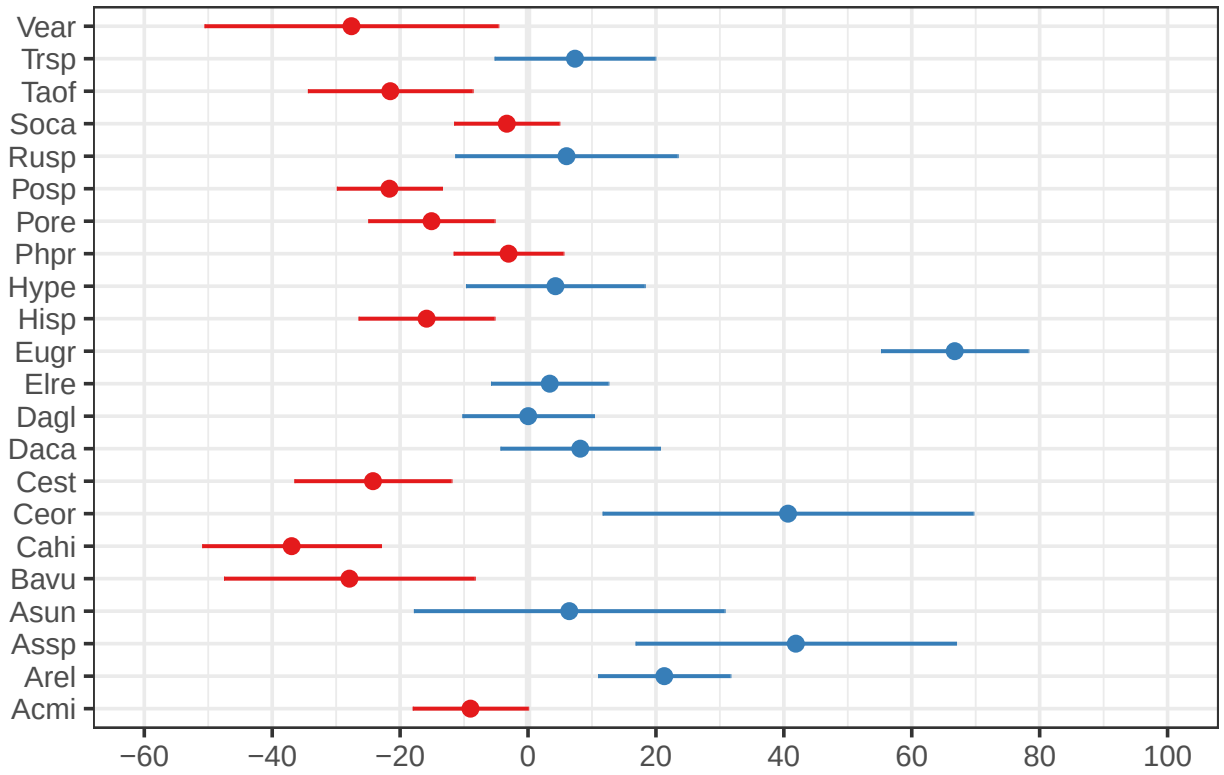
```
# these are the fixed effects estimates from summary(mod3)
plot_model(mod3, sort.est = TRUE)
```




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




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




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

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

```
## Warning: Model failed to converge with 2 negative eigenvalues: -2.8e+00 -5.7e+07
```

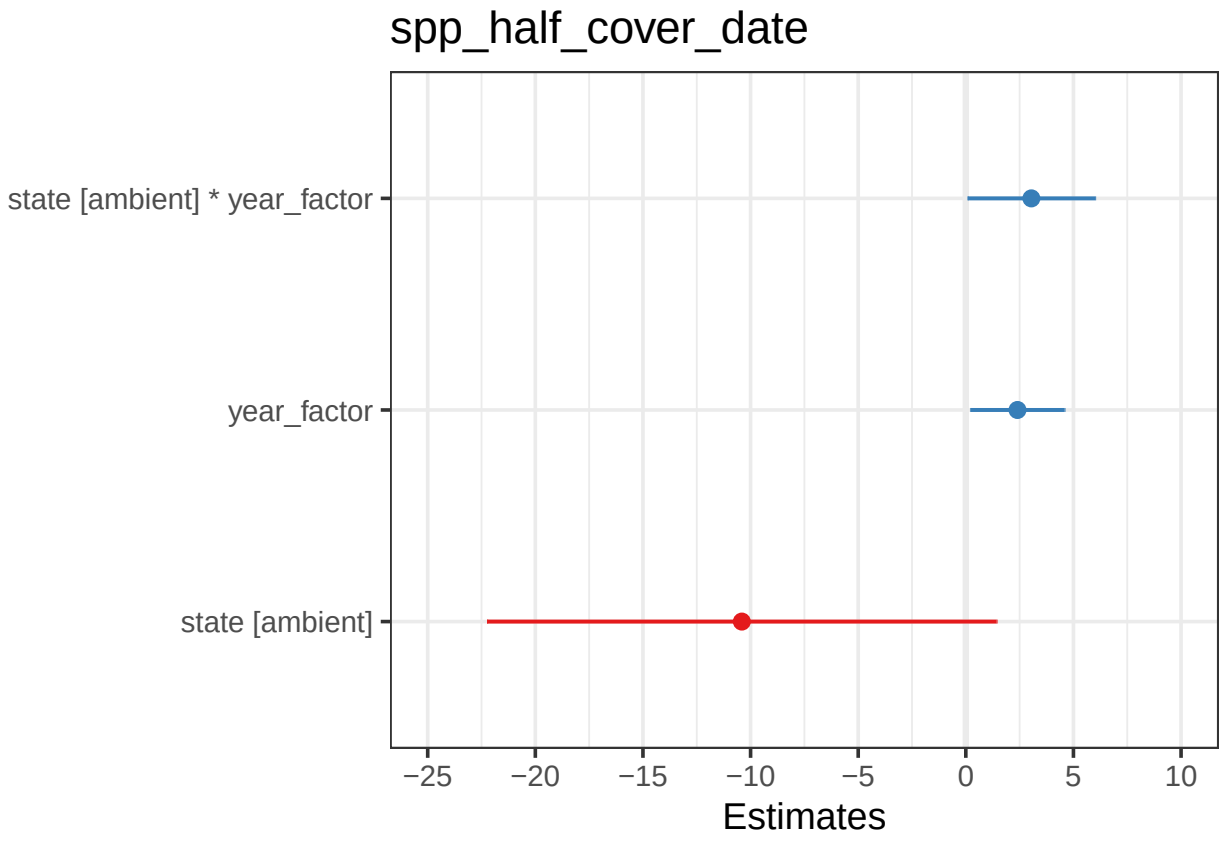
```
anova(mod3, mod6)
```

```
## Data: green_kbs
## Models:
## mod3: spp_half_cover_date ~ state * year_factor + (1 | species)
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +
## mod6:     year | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod3    6 16231 16263 -8109.5    16219
## mod6    9 16235 16283 -8108.6    16217 1.9644  3     0.5798
```

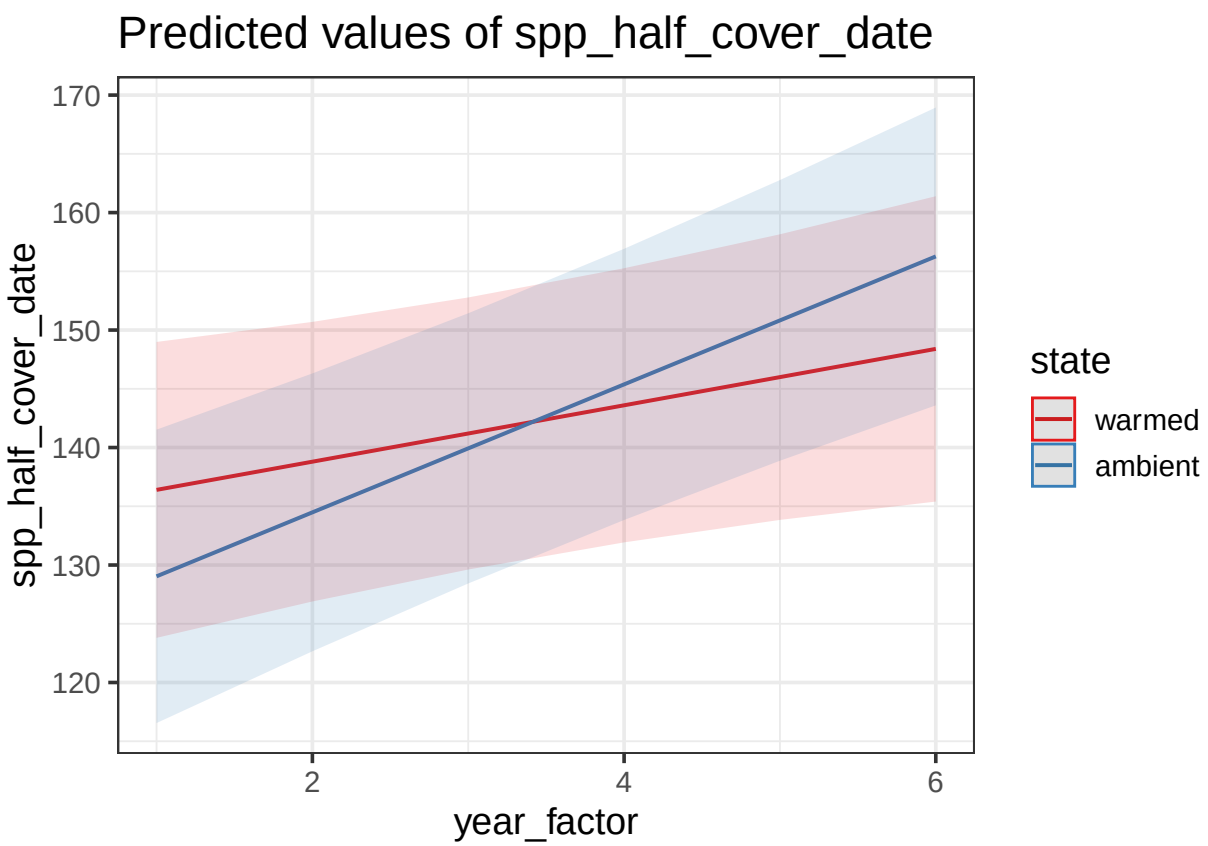
```
anova(mod6)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state               7625    7625     1  242.04  2.9705   0.08607 .
## year_factor        65330   65330     1 1498.65 25.4504 5.093e-07 ***
## state:year_factor  10432   10432     1 1483.77  4.0639   0.04399 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# mod 3 still better fit
plot_model(mod6, sort.est = TRUE)
```

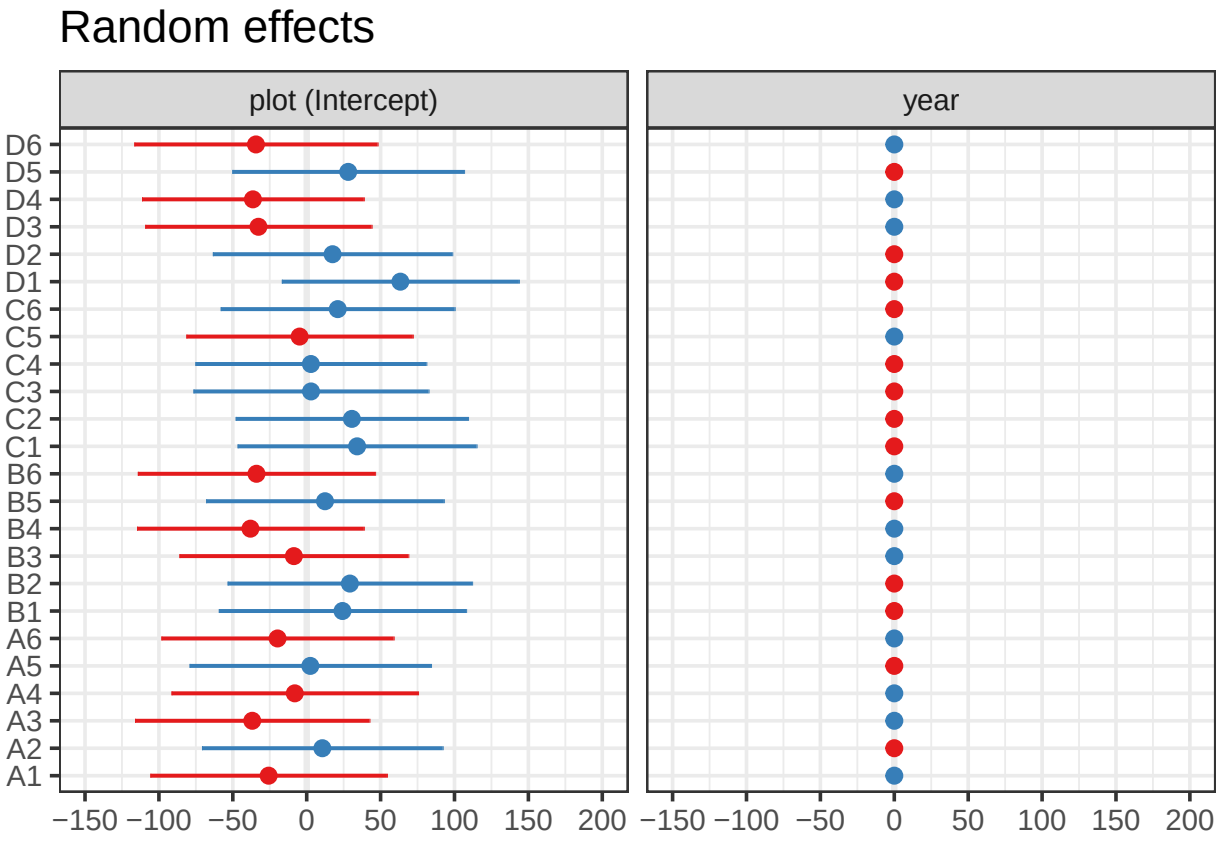



```r
# these are the fixed predicted values:
plot_model(mod6, type = "pred", terms = c("year_factor", "state"))
```

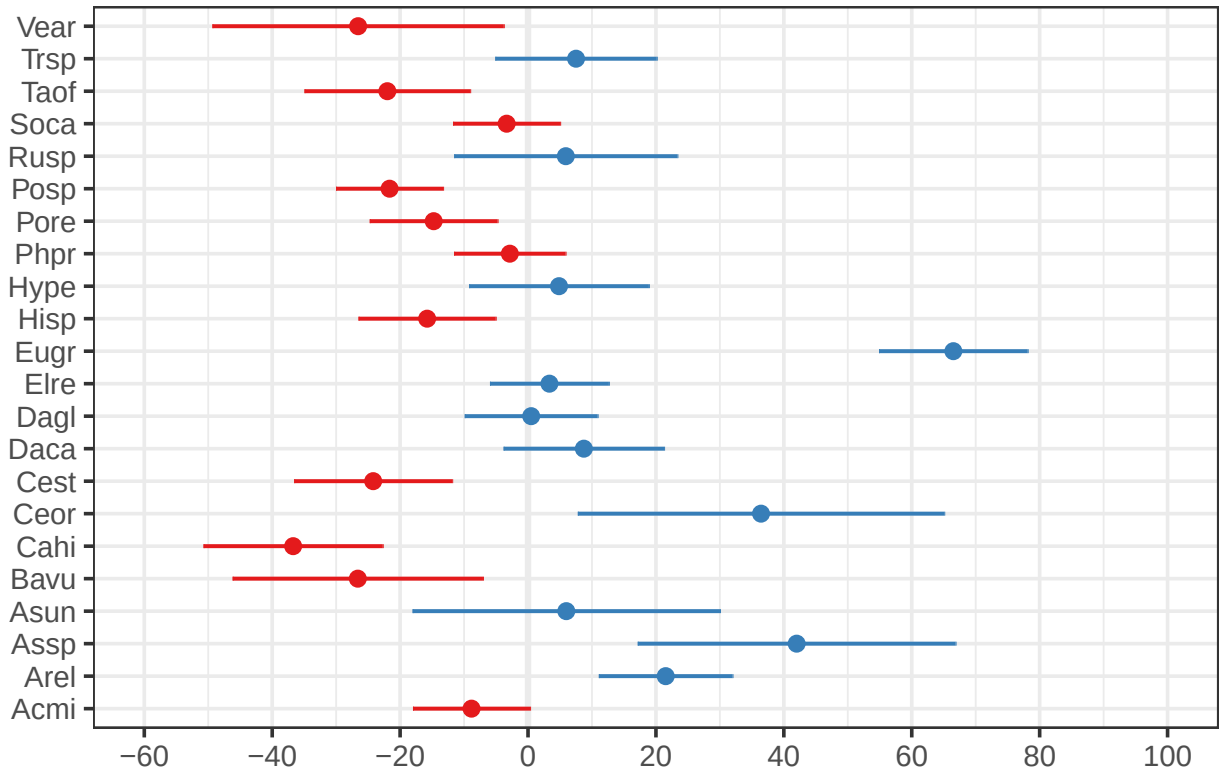



```
# these are the random effects estimates
plot_model(mod6, type = "re", terms = c("species", "plot"))
```

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


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

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




```
# mod3 (and mod6) are pretty complex in terms of
# interpretation (they actually don't have many parameters
# though). We could consider an alternative model that's
# simpler to understand and also one that provides more
# insight about the species.

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

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

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

```
## Data: green_kbs
## Models:
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +
## mod6:     year | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod6    9 16235 16283 -8108.6    16217
## mod7   27 16204 16348 -8075.0    16150 67.038 18  1.423e-07 ***
```

```
## ---
## 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   26 16190 16329 -8069.2    16138
## mod7    27 16204 16348 -8075.0    16150     0  1          1
```

```
anova(mod7a, mod7b)  #mod 7a
```

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   26 16190 16329 -8069.2    16138
## mod7b   27 16189 16332 -8067.3    16135 3.8685  1     0.0492 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod7a, mod7c)  #mod 7a
```

```
## Data: green_kbs
## Models:
## mod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## mod7c: spp_half_cover_date ~ state + species + year_factor + insecticide +
## mod7c:     (1 | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   26 16190 16329 -8069.2    16138
## mod7c   27 16192 16336 -8069.2    16138 0.0117  1     0.9138
```

```
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
##  16190.4  16328.8  -8069.2  16138.4     1485
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9692 -0.6752 -0.2534  0.4009  3.2536
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   15.67   3.958
##  Residual             2534.00  50.339
## Number of obs: 1511, groups:  plot, 24
##
## Fixed effects:
```

```
##                Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   119.9840     5.5678  662.5643  21.550  < 2e-16 ***
## stateambient   -0.3036     3.1002   23.4728  -0.098 0.922828
## speciesArel    31.4251     7.0955 1502.3501   4.429 1.02e-05 ***
## speciesAssp    66.0432    15.3341 1503.2467   4.307 1.76e-05 ***
## speciesAsun    17.2994    14.7379 1498.1244   1.174 0.240659
## speciesBavu   -22.9492    11.7723 1510.7468  -1.949 0.051430 .
## speciesCahi   -31.0568     8.7348 1502.5081  -3.556 0.000389 ***
## speciesCeor    66.8584    18.5274 1467.7484   3.609 0.000318 ***
## speciesCest   -16.9006     7.9415 1500.0954  -2.128 0.033489 *
## speciesDaca    18.4391     8.0012 1503.2548   2.305 0.021328 *
## speciesDagl     9.5679     7.0633 1501.7981   1.355 0.175753
## speciesElre    12.5795     6.6451 1497.1984   1.893 0.058545 .
## speciesEugr    79.4543     7.5924 1509.8471  10.465  < 2e-16 ***
## speciesHisp    -7.2615     7.1915 1495.7973  -1.010 0.312785
## speciesHype    14.0749     8.7202 1510.8310   1.614 0.106722
## speciesPhpr     5.9955     6.3979 1493.6550   0.937 0.348855
## speciesPore    -6.2895     6.8892 1500.1673  -0.913 0.361411
## speciesPosp   -13.2880     6.2681 1491.4524  -2.120 0.034175 *
## speciesRusp    15.5869    10.5160 1474.6799   1.482 0.138500
## speciesSoca     5.5511     6.2681 1491.4524   0.886 0.375965
## speciesTaof   -14.6163     8.1928 1510.6907  -1.784 0.074617 .
## speciesTrsp    17.3039     8.0414 1500.1042   2.152 0.031569 *
## speciesVear   -25.2734    13.8608 1509.9538  -1.823 0.068444 .
## year_factor     3.9056     0.7732 1510.0330   5.051 4.92e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 24 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
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           24      24     1   23.47  0.0096    0.9228
## species     770430   36687    21 1501.06 14.4780 < 2.2e-16 ***
## year_factor  64659   64659     1 1510.03 25.5167 4.919e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Yes, at least one of the species is different (they do not
# all have the same half cover dates).
emmeans(mod7a, list(pairwise ~ state + year_factor), adjust = "tukey")
```

```
## $`emmeans of state, year_factor`
##  state   year_factor emmean   SE   df lower.CL upper.CL
##  warmed         3.38    143 2.71 50.8      138      149
##  ambient        3.38    143 2.60 44.3      138      148
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
```

```
## $`pairwise differences of state, year_factor`
##  1                                                  estimate   SE   df t.ratio
##  warmed 3.37921906022502 - ambient 3.37921906022502    0.304 3.27 27.2 0.093
##  p.value
##  0.9267
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
```

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

```
## $`emmeans of year_factor`
##  year_factor emmean   SE   df lower.CL upper.CL
##         3.38    143 2.09 72.2      139      147
##
## 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       133  4.77 1030    123.7      142
##  Arel       164  5.49 1167    153.7      175
##  Assp       199 14.81 1502    170.0      228
##  Asun       150 14.14 1536    122.6      178
##  Bavu       110 10.97 1474     88.6      132
##  Cahi       102  7.53 1435     87.2      117
##  Ceor       200 18.18 1472    164.2      236
##  Cest       116  6.60 1364    103.2      129
##  Daca       151  6.66 1356    138.4      165
##  Dagl       143  5.45 1182    131.9      153
##  Elre       146  4.87 1071    136.1      155
##  Eugr       212  6.14 1225    200.4      225
##  Hisp       126  5.63 1234    114.7      137
##  Hype       147  7.52 1340    132.4      162
##  Phpr       139  4.53  959    130.1      148
##  Pore       127  5.23 1129    116.5      137
##  Posp       120  4.34  895    111.2      128
##  Rusp       149  9.60 1364    129.8      167
##  Soca       139  4.34  895    130.1      147
##  Taof       118  6.89 1340    104.9      132
##  Trsp       150  6.70 1380    137.2      163
##  Vear       108 13.23 1526     81.8      134
##
## 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 -3.14e+01  7.15 1525  -4.393 0.0024
##  Acmi - Assp -6.60e+01 15.50 1532  -4.261 0.0042
##  Acmi - Asun -1.73e+01 14.86 1521  -1.165 0.9999
##  Acmi - Bavu  2.29e+01 11.89 1536   1.931 0.9483
##  Acmi - Cahi  3.11e+01  8.81 1525   3.527 0.0632
##  Acmi - Ceor -6.69e+01 18.75 1501  -3.566 0.0558
##  Acmi - Cest  1.69e+01  8.01 1523   2.111 0.8838
##  Acmi - Daca -1.84e+01  8.07 1526  -2.286 0.7874
##  Acmi - Dagl -9.57e+00  7.12 1525  -1.344 0.9994
##  Acmi - Elre -1.26e+01  6.70 1520  -1.878 0.9608
##  Acmi - Eugr -7.95e+01  7.66 1534 -10.372 <.0001
##  Acmi - Hisp  7.26e+00  7.25 1519   1.002 1.0000
##  Acmi - Hype -1.41e+01  8.80 1536  -1.599 0.9939
##  Acmi - Phpr -6.00e+00  6.45 1516  -0.930 1.0000
##  Acmi - Pore  6.29e+00  6.94 1523   0.906 1.0000
##  Acmi - Posp  1.33e+01  6.32 1514   2.104 0.8870
##  Acmi - Rusp -1.56e+01 10.64 1508  -1.465 0.9981
##  Acmi - Soca -5.55e+00  6.32 1514  -0.879 1.0000
##  Acmi - Taof  1.46e+01  8.27 1535   1.768 0.9796
##  Acmi - Trsp -1.73e+01  8.11 1523  -2.135 0.8727
##  Acmi - Vear  2.53e+01 13.99 1533   1.807 0.9740
##  Arel - Assp -3.46e+01 15.75 1529  -2.198 0.8396
##  Arel - Asun  1.41e+01 15.10 1524   0.936 1.0000
##  Arel - Bavu  5.44e+01 12.17 1535   4.466 0.0017
##  Arel - Cahi  6.25e+01  9.27 1533   6.737 <.0001
##  Arel - Ceor -3.54e+01 18.94 1506  -1.870 0.9625
##  Arel - Cest  4.83e+01  8.52 1533   5.674 <.0001
##  Arel - Daca  1.30e+01  8.54 1530   1.521 0.9968
##  Arel - Dagl  2.19e+01  7.60 1527   2.876 0.3438
##  Arel - Elre  1.88e+01  7.20 1527   2.619 0.5383
##  Arel - Eugr -4.80e+01  8.12 1536  -5.917 <.0001
##  Arel - Hisp  3.87e+01  7.75 1527   4.993 0.0001
##  Arel - Hype  1.74e+01  9.20 1536   1.885 0.9593
##  Arel - Phpr  2.54e+01  6.99 1527   3.636 0.0443
##  Arel - Pore  3.77e+01  7.46 1529   5.055 0.0001
##  Arel - Posp  4.47e+01  6.87 1527   6.506 <.0001
##  Arel - Rusp  1.58e+01 10.95 1523   1.446 0.9984
##  Arel - Soca  2.59e+01  6.87 1527   3.765 0.0285
##  Arel - Taof  4.60e+01  8.72 1534   5.282 <.0001
##  Arel - Trsp  1.41e+01  8.57 1527   1.647 0.9911
##  Arel - Vear  5.67e+01 14.28 1533   3.970 0.0134
##  Assp - Asun  4.87e+01 20.45 1536   2.384 0.7203
##  Assp - Bavu  8.90e+01 18.35 1533   4.849 0.0003
##  Assp - Cahi  9.71e+01 16.52 1536   5.879 <.0001
##  Assp - Ceor -8.15e-01 23.42 1510  -0.035 1.0000
##  Assp - Cest  8.29e+01 16.16 1532   5.133 0.0001
##  Assp - Daca  4.76e+01 16.15 1536   2.948 0.2959
##  Assp - Dagl  5.65e+01 15.72 1533   3.593 0.0511
##  Assp - Elre  5.35e+01 15.53 1531   3.443 0.0820
##  Assp - Eugr -1.34e+01 15.94 1535  -0.841 1.0000
```

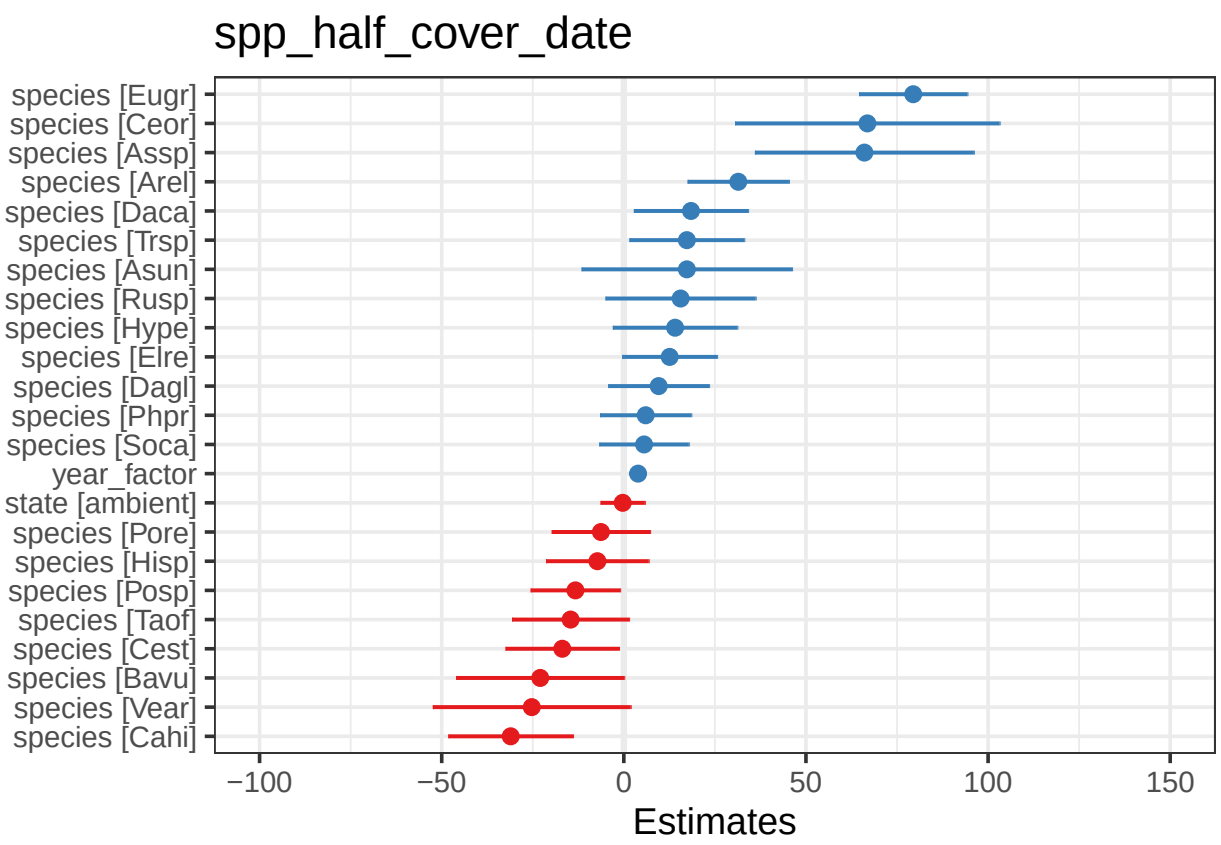
```
##  Assp - Hisp  7.33e+01 15.77 1534   4.647 0.0008
##  Assp - Hype  5.20e+01 16.55 1529   3.140 0.1895
##  Assp - Phpr  6.00e+01 15.42 1532   3.893 0.0180
##  Assp - Pore  7.23e+01 15.63 1535   4.628 0.0008
##  Assp - Posp  7.93e+01 15.37 1531   5.160 0.0001
##  Assp - Rusp  5.05e+01 17.55 1534   2.874 0.3449
##  Assp - Soca  6.05e+01 15.37 1531   3.935 0.0154
##  Assp - Taof  8.07e+01 16.26 1534   4.962 0.0002
##  Assp - Trsp  4.87e+01 16.17 1535   3.014 0.2560
##  Assp - Vear  9.13e+01 19.72 1529   4.630 0.0008
##  Asun - Bavu  4.02e+01 17.87 1534   2.252 0.8085
##  Asun - Cahi  4.84e+01 15.99 1525   3.024 0.2504
##  Asun - Ceor -4.96e+01 22.97 1531  -2.158 0.8612
##  Asun - Cest  3.42e+01 15.52 1519   2.203 0.8371
##  Asun - Daca -1.14e+00 15.56 1524  -0.073 1.0000
##  Asun - Dagl  7.73e+00 15.09 1527   0.512 1.0000
##  Asun - Elre  4.72e+00 14.90 1524   0.317 1.0000
##  Asun - Eugr -6.22e+01 15.35 1526  -4.049 0.0099
##  Asun - Hisp  2.46e+01 15.15 1521   1.622 0.9927
##  Asun - Hype  3.22e+00 15.97 1533   0.202 1.0000
##  Asun - Phpr  1.13e+01 14.79 1524   0.764 1.0000
##  Asun - Pore  2.36e+01 15.00 1523   1.572 0.9951
##  Asun - Posp  3.06e+01 14.73 1522   2.076 0.8991
##  Asun - Rusp  1.71e+00 17.04 1535   0.100 1.0000
##  Asun - Soca  1.17e+01 14.73 1522   0.797 1.0000
##  Asun - Taof  3.19e+01 15.67 1526   2.037 0.9147
##  Asun - Trsp -4.48e-03 15.60 1524   0.000 1.0000
##  Asun - Vear  4.26e+01 19.32 1528   2.203 0.8369
##  Bavu - Cahi  8.11e+00 13.24 1535   0.613 1.0000
##  Bavu - Ceor -8.98e+01 21.24 1497  -4.228 0.0048
##  Bavu - Cest -6.05e+00 12.79 1534  -0.473 1.0000
##  Bavu - Daca -4.14e+01 12.79 1535  -3.236 0.1478
##  Bavu - Dagl -3.25e+01 12.17 1534  -2.672 0.4960
##  Bavu - Elre -3.55e+01 11.90 1534  -2.985 0.2731
##  Bavu - Eugr -1.02e+02 12.45 1535  -8.223 <.0001
##  Bavu - Hisp -1.57e+01 12.27 1535  -1.279 0.9997
##  Bavu - Hype -3.70e+01 13.21 1532  -2.802 0.3966
##  Bavu - Phpr -2.89e+01 11.79 1534  -2.456 0.6664
##  Bavu - Pore -1.67e+01 12.10 1532  -1.376 0.9992
##  Bavu - Posp -9.66e+00 11.72 1534  -0.825 1.0000
##  Bavu - Rusp -3.85e+01 14.52 1523  -2.655 0.5096
##  Bavu - Soca -2.85e+01 11.72 1534  -2.432 0.6844
##  Bavu - Taof -8.33e+00 12.91 1531  -0.646 1.0000
##  Bavu - Trsp -4.03e+01 12.78 1536  -3.149 0.1852
##  Bavu - Vear  2.32e+00 17.14 1535   0.136 1.0000
##  Cahi - Ceor -9.79e+01 19.61 1523  -4.994 0.0001
##  Cahi - Cest -1.42e+01  9.87 1528  -1.435 0.9986
##  Cahi - Daca -4.95e+01  9.94 1525  -4.981 0.0002
##  Cahi - Dagl -4.06e+01  9.23 1531  -4.399 0.0023
##  Cahi - Elre -4.36e+01  8.91 1529  -4.899 0.0002
##  Cahi - Eugr -1.11e+02  9.63 1529 -11.474 <.0001
##  Cahi - Hisp -2.38e+01  9.31 1528  -2.556 0.5879
##  Cahi - Hype -4.51e+01 10.54 1532  -4.281 0.0039
##  Cahi - Phpr -3.71e+01  8.70 1528  -4.261 0.0042
```

```
##  Cahi - Pore -2.48e+01  9.08 1532  -2.727 0.4535
##  Cahi - Posp -1.78e+01  8.60 1527  -2.066 0.9034
##  Cahi - Rusp -4.66e+01 12.15 1530  -3.840 0.0218
##  Cahi - Soca -3.66e+01  8.60 1527  -4.256 0.0043
##  Cahi - Taof -1.64e+01 10.10 1534  -1.628 0.9923
##  Cahi - Trsp -4.84e+01  9.94 1520  -4.865 0.0003
##  Cahi - Vear -5.78e+00 15.08 1528  -0.384 1.0000
##  Ceor - Cest  8.38e+01 19.27 1506   4.346 0.0029
##  Ceor - Daca  4.84e+01 19.30 1508   2.509 0.6256
##  Ceor - Dagl  5.73e+01 18.94 1500   3.025 0.2499
##  Ceor - Elre  5.43e+01 18.77 1511   2.891 0.3335
##  Ceor - Eugr -1.26e+01 19.16 1498  -0.657 1.0000
##  Ceor - Hisp  7.41e+01 18.97 1511   3.907 0.0170
##  Ceor - Hype  5.28e+01 19.66 1488   2.684 0.4864
##  Ceor - Phpr  6.09e+01 18.70 1501   3.255 0.1405
##  Ceor - Pore  7.31e+01 18.88 1495   3.875 0.0192
##  Ceor - Posp  8.01e+01 18.64 1507   4.299 0.0036
##  Ceor - Rusp  5.13e+01 20.48 1510   2.504 0.6296
##  Ceor - Soca  6.13e+01 18.64 1507   3.289 0.1281
##  Ceor - Taof  8.15e+01 19.37 1515   4.206 0.0053
##  Ceor - Trsp  4.96e+01 19.30 1520   2.567 0.5794
##  Ceor - Vear  9.21e+01 22.44 1519   4.105 0.0080
##  Cest - Daca -3.53e+01  9.21 1525  -3.835 0.0222
##  Cest - Dagl -2.65e+01  8.47 1531  -3.124 0.1970
##  Cest - Elre -2.95e+01  8.14 1527  -3.620 0.0467
##  Cest - Eugr -9.64e+01  8.94 1535 -10.773 <.0001
##  Cest - Hisp -9.64e+00  8.54 1520  -1.129 1.0000
##  Cest - Hype -3.10e+01  9.93 1536  -3.121 0.1988
##  Cest - Phpr -2.29e+01  7.90 1526  -2.897 0.3295
##  Cest - Pore -1.06e+01  8.28 1522  -1.282 0.9997
##  Cest - Posp -3.61e+00  7.79 1524  -0.463 1.0000
##  Cest - Rusp -3.25e+01 11.60 1500  -2.802 0.3967
##  Cest - Soca -2.25e+01  7.79 1524  -2.881 0.3408
##  Cest - Taof -2.28e+00  9.41 1533  -0.243 1.0000
##  Cest - Trsp -3.42e+01  9.27 1526  -3.691 0.0368
##  Cest - Vear  8.37e+00 14.67 1534   0.571 1.0000
##  Daca - Dagl  8.87e+00  8.50 1527   1.044 1.0000
##  Daca - Elre  5.86e+00  8.17 1529   0.717 1.0000
##  Daca - Eugr -6.10e+01  8.97 1533  -6.805 <.0001
##  Daca - Hisp  2.57e+01  8.60 1523   2.990 0.2702
##  Daca - Hype  4.36e+00  9.96 1536   0.438 1.0000
##  Daca - Phpr  1.24e+01  7.95 1527   1.565 0.9953
##  Daca - Pore  2.47e+01  8.33 1524   2.967 0.2842
##  Daca - Posp  3.17e+01  7.85 1528   4.044 0.0101
##  Daca - Rusp  2.85e+00 11.61 1514   0.246 1.0000
##  Daca - Soca  1.29e+01  7.85 1528   1.643 0.9914
##  Daca - Taof  3.31e+01  9.47 1535   3.489 0.0712
##  Daca - Trsp  1.14e+00  9.32 1522   0.122 1.0000
##  Daca - Vear  4.37e+01 14.71 1531   2.972 0.2812
##  Dagl - Elre -3.01e+00  7.17 1520  -0.420 1.0000
##  Dagl - Eugr -6.99e+01  8.09 1535  -8.635 <.0001
##  Dagl - Hisp  1.68e+01  7.72 1526   2.181 0.8493
##  Dagl - Hype -4.51e+00  9.19 1536  -0.491 1.0000
##  Dagl - Phpr  3.57e+00  6.96 1519   0.514 1.0000
```

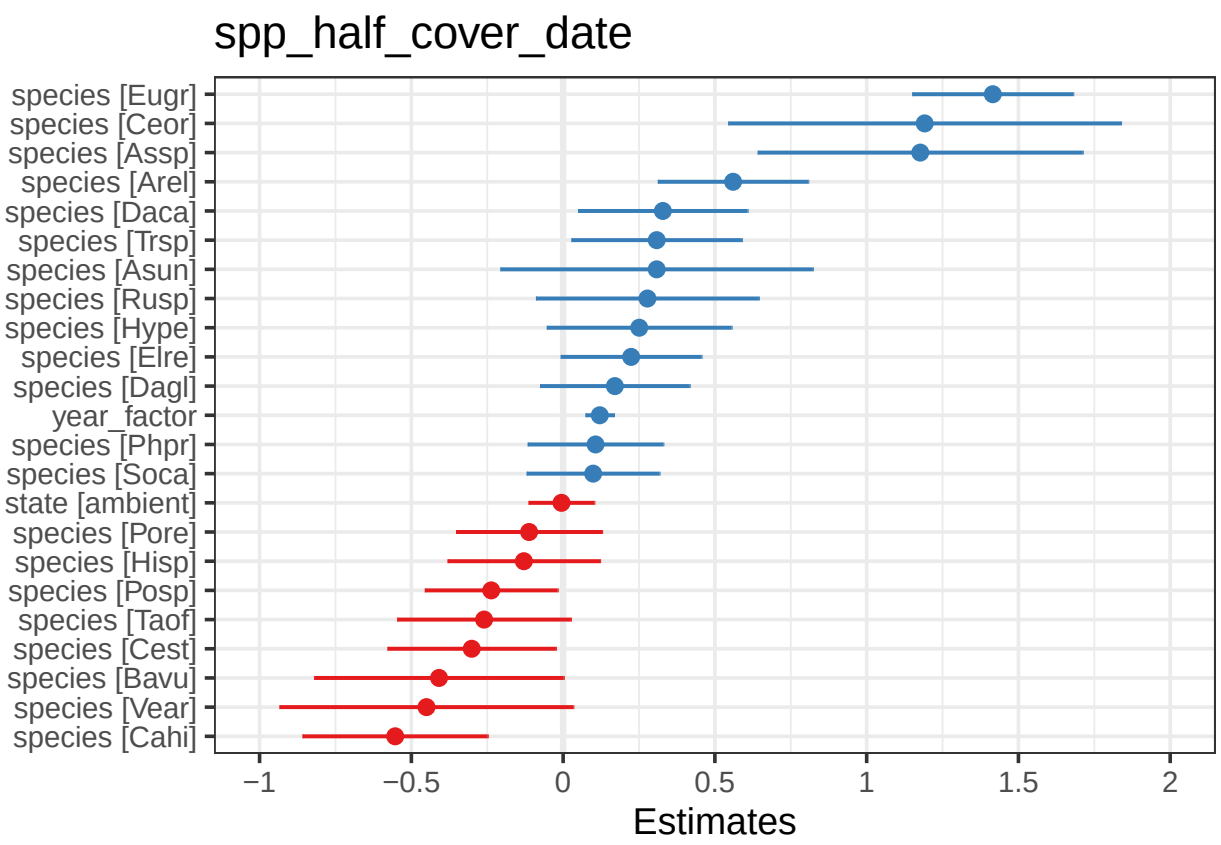
```
##  Dagl - Pore  1.59e+01  7.43 1525   2.135 0.8724
##  Dagl - Posp  2.29e+01  6.84 1523   3.342 0.1102
##  Dagl - Rusp -6.02e+00 10.94 1522  -0.550 1.0000
##  Dagl - Soca  4.02e+00  6.84 1523   0.587 1.0000
##  Dagl - Taof  2.42e+01  8.68 1533   2.785 0.4090
##  Dagl - Trsp -7.74e+00  8.54 1527  -0.906 1.0000
##  Dagl - Vear  3.48e+01 14.26 1533   2.444 0.6755
##  Elre - Eugr -6.69e+01  7.70 1535  -8.684 <.0001
##  Elre - Hisp  1.98e+01  7.33 1523   2.707 0.4689
##  Elre - Hype -1.50e+00  8.86 1534  -0.169 1.0000
##  Elre - Phpr  6.58e+00  6.51 1513   1.012 1.0000
##  Elre - Pore  1.89e+01  7.03 1523   2.684 0.4864
##  Elre - Posp  2.59e+01  6.38 1512   4.054 0.0097
##  Elre - Rusp -3.01e+00 10.66 1525  -0.282 1.0000
##  Elre - Soca  7.03e+00  6.38 1512   1.102 1.0000
##  Elre - Taof  2.72e+01  8.34 1532   3.261 0.1383
##  Elre - Trsp -4.72e+00  8.19 1525  -0.577 1.0000
##  Elre - Vear  3.79e+01 14.06 1535   2.692 0.4806
##  Eugr - Hisp  8.67e+01  8.22 1535  10.543 <.0001
##  Eugr - Hype  6.54e+01  9.60 1535   6.811 <.0001
##  Eugr - Phpr  7.35e+01  7.51 1534   9.787 <.0001
##  Eugr - Pore  8.57e+01  7.96 1535  10.774 <.0001
##  Eugr - Posp  9.27e+01  7.40 1534  12.538 <.0001
##  Eugr - Rusp  6.39e+01 11.27 1532   5.665 <.0001
##  Eugr - Soca  7.39e+01  7.40 1534   9.991 <.0001
##  Eugr - Taof  9.41e+01  9.12 1533  10.316 <.0001
##  Eugr - Trsp  6.22e+01  8.99 1533   6.911 <.0001
##  Eugr - Vear  1.05e+02 14.52 1533   7.211 <.0001
##  Hisp - Hype -2.13e+01  9.30 1536  -2.295 0.7815
##  Hisp - Phpr -1.33e+01  7.11 1523  -1.865 0.9635
##  Hisp - Pore -9.72e-01  7.55 1519  -0.129 1.0000
##  Hisp - Posp  6.03e+00  6.99 1520   0.863 1.0000
##  Hisp - Rusp -2.28e+01 11.05 1507  -2.067 0.9029
##  Hisp - Soca -1.28e+01  6.99 1520  -1.834 0.9695
##  Hisp - Taof  7.35e+00  8.78 1531   0.837 1.0000
##  Hisp - Trsp -2.46e+01  8.63 1519  -2.845 0.3655
##  Hisp - Vear  1.80e+01 14.30 1533   1.260 0.9998
##  Hype - Phpr  8.08e+00  8.67 1536   0.932 1.0000
##  Hype - Pore  2.04e+01  9.07 1535   2.246 0.8124
##  Hype - Posp  2.74e+01  8.58 1535   3.189 0.1673
##  Hype - Rusp -1.51e+00 12.12 1515  -0.125 1.0000
##  Hype - Soca  8.52e+00  8.58 1535   0.993 1.0000
##  Hype - Taof  2.87e+01 10.11 1534   2.837 0.3711
##  Hype - Trsp -3.23e+00  9.98 1535  -0.324 1.0000
##  Hype - Vear  3.93e+01 15.13 1532   2.600 0.5533
##  Phpr - Pore  1.23e+01  6.79 1521   1.809 0.9738
##  Phpr - Posp  1.93e+01  6.13 1511   3.144 0.1879
##  Phpr - Rusp -9.59e+00 10.52 1520  -0.911 1.0000
##  Phpr - Soca  4.44e-01  6.13 1511   0.072 1.0000
##  Phpr - Taof  2.06e+01  8.14 1534   2.532 0.6074
##  Phpr - Trsp -1.13e+01  7.98 1525  -1.417 0.9988
##  Phpr - Vear  3.13e+01 13.92 1534   2.246 0.8119
##  Pore - Posp  7.00e+00  6.67 1522   1.049 1.0000
##  Pore - Rusp -2.19e+01 10.84 1517  -2.019 0.9212
```

```
##  Pore - Soca -1.18e+01  6.67 1522  -1.775 0.9786
##  Pore - Taof  8.33e+00  8.53 1533   0.976 1.0000
##  Pore - Trsp -2.36e+01  8.39 1524  -2.814 0.3881
##  Pore - Vear  1.90e+01 14.15 1533   1.342 0.9995
##  Posp - Rusp -2.89e+01 10.45 1516  -2.763 0.4254
##  Posp - Soca -1.88e+01  6.00 1509  -3.141 0.1889
##  Posp - Taof  1.33e+00  8.04 1534   0.165 1.0000
##  Posp - Trsp -3.06e+01  7.88 1524  -3.884 0.0186
##  Posp - Vear  1.20e+01 13.86 1534   0.865 1.0000
##  Rusp - Soca  1.00e+01 10.45 1516   0.960 1.0000
##  Rusp - Taof  3.02e+01 11.70 1535   2.582 0.5672
##  Rusp - Trsp -1.72e+00 11.63 1528  -0.148 1.0000
##  Rusp - Vear  4.09e+01 16.29 1535   2.508 0.6262
##  Soca - Taof  2.02e+01  8.04 1534   2.510 0.6249
##  Soca - Trsp -1.18e+01  7.88 1524  -1.492 0.9975
##  Soca - Vear  3.08e+01 13.86 1534   2.223 0.8255
##  Taof - Trsp -3.19e+01  9.50 1533  -3.361 0.1043
##  Taof - Vear  1.07e+01 14.83 1534   0.719 1.0000
##  Trsp - Vear  4.26e+01 14.72 1530   2.893 0.3325
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 22 estimates
```

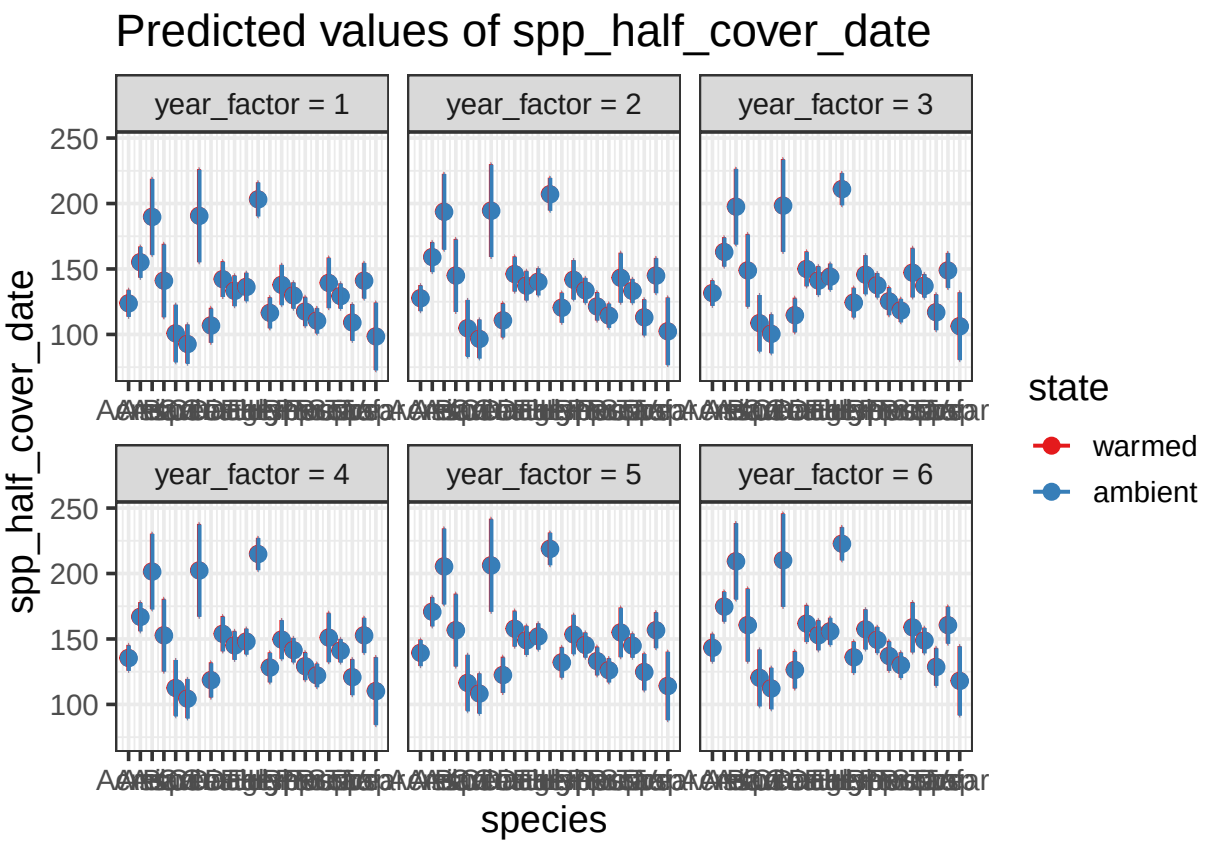
```
# using model 7a for overall greenup model #

# 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")
```

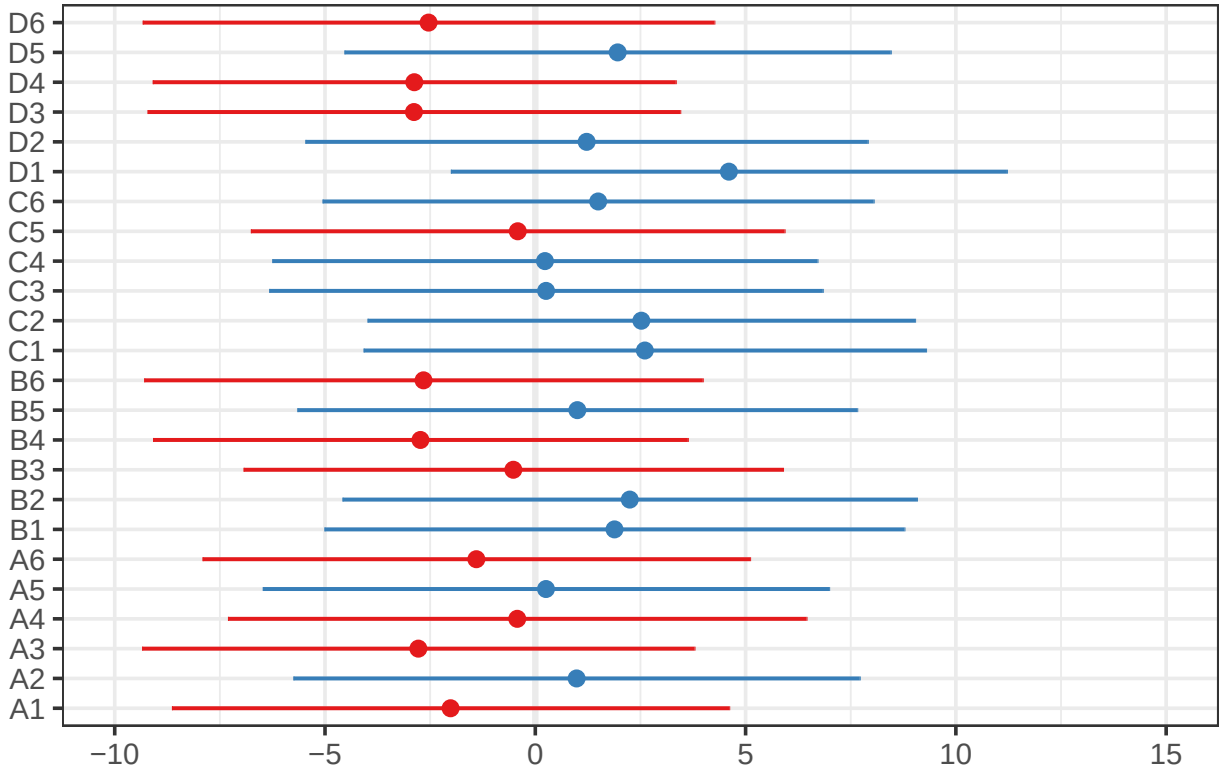



```
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7a, type = "pred", terms = c("species", "state",
    "year_factor"))
```




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

Random effects




```
# Start KD models - listed out possible models all at once,
# then compared:
mod_kd1 <- lmer(spp_half_cover_date ~ state + (1 | plot), green_kbs,
    REML = FALSE)
mod_kd2 <- lmer(spp_half_cover_date ~ state + (1 | year_factor),
    green_kbs, REML = FALSE)
mod_kd3 <- lmer(spp_half_cover_date ~ state + (1 + year_factor |
    plot), green_kbs, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00318752 (tol = 0.002, component 1)
```

```
mod_kd4 <- lmer(spp_half_cover_date ~ state + year_factor + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd4 <- lmer(spp_half_cover_date ~ state * year_factor + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd5 <- lmer(spp_half_cover_date ~ state + species + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd6 <- lmer(spp_half_cover_date ~ state * species + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd7 <- lmer(spp_half_cover_date ~ state + insecticide + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd8 <- lmer(spp_half_cover_date ~ state * insecticide + (1 |
    plot), green_kbs, REML = FALSE)
mod_kd9 <- lmer(spp_half_cover_date ~ state + insecticide + species +
    (1 | plot), green_kbs, REML = FALSE)
mod_kd10 <- lmer(spp_half_cover_date ~ state + insecticide +
    year_factor + (1 | plot), green_kbs, REML = FALSE)
```

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

```
##          dAICc df weight
## mod_kd11   0.0 26 0.74
## mod_kd12   2.1 27 0.26
## mod_kd5   23.2 25 <0.001
## mod_kd9   25.2 26 <0.001
## mod_kd6   46.3 46 <0.001
## mod_kd2  210.5 4  <0.001
## mod_kd4  232.3 6  <0.001
## mod_kd10 235.9 6  <0.001
## mod_kd3  256.7 6  <0.001
## mod_kd13 274.9 4  <0.001
## mod_kd1  274.9 4  <0.001
## mod_kd7  276.9 5  <0.001
## mod_kd8  278.9 6  <0.001
```

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

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + species + (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16190.4  16328.8  -8069.2  16138.4     1485
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9692 -0.6752 -0.2534  0.4009  3.2536
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   15.67   3.958
##  Residual             2534.00  50.339
## Number of obs: 1511, groups:  plot, 24
##
## Fixed effects:
##               Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   119.9840     5.5678  662.5643  21.550  < 2e-16 ***
## stateambient   -0.3036     3.1002   23.4728  -0.098 0.922828
## year_factor     3.9056     0.7732 1510.0330   5.051 4.92e-07 ***
## speciesArel    31.4251     7.0955 1502.3501   4.429 1.02e-05 ***
## speciesAssp    66.0432    15.3341 1503.2467   4.307 1.76e-05 ***
## speciesAsun    17.2994    14.7379 1498.1244   1.174 0.240659
## speciesBavu   -22.9492    11.7723 1510.7468  -1.949 0.051430 .
```

```
## speciesCahi   -31.0568     8.7348 1502.5081  -3.556 0.000389 ***
## speciesCeor    66.8584    18.5274 1467.7484   3.609 0.000318 ***
## speciesCest   -16.9006     7.9415 1500.0954  -2.128 0.033489 *
## speciesDaca    18.4391     8.0012 1503.2548   2.305 0.021328 *
## speciesDagl     9.5679     7.0633 1501.7981   1.355 0.175753
## speciesElre    12.5795     6.6451 1497.1984   1.893 0.058545 .
## speciesEugr    79.4543     7.5924 1509.8471  10.465  < 2e-16 ***
## speciesHisp    -7.2615     7.1915 1495.7973  -1.010 0.312785
## speciesHype    14.0749     8.7202 1510.8310   1.614 0.106722
## speciesPhpr     5.9955     6.3979 1493.6550   0.937 0.348855
## speciesPore    -6.2895     6.8892 1500.1673  -0.913 0.361411
## speciesPosp   -13.2880     6.2681 1491.4524  -2.120 0.034175 *
## speciesRusp    15.5869    10.5160 1474.6799   1.482 0.138500
## speciesSoca     5.5511     6.2681 1491.4524   0.886 0.375965
## speciesTaof   -14.6163     8.1928 1510.6907  -1.784 0.074617 .
## speciesTrsp    17.3039     8.0414 1500.1042   2.152 0.031569 *
## speciesVear   -25.2734    13.8608 1509.9538  -1.823 0.068444 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
# 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
```

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

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

```
mod9a <- lmer(spp_half_cover_date ~ state + origin + factor(year_factor) +
    (1 | plot), green_kbs, REML = FALSE)
mod9b <- lmer(spp_half_cover_date ~ state + origin + insecticide +
    factor(year_factor) + (1 | plot), green_kbs, REML = FALSE)
anova(mod8, mod9)  # model 9 is a better fit to data
```

```
## Data: green_kbs
## Models:
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## mod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod9    9 16418 16465 -8199.8    16400
## mod8   12 16421 16485 -8198.4    16397 2.6541  3     0.4481
```

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

```
## Data: green_kbs
## Models:
## mod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
```

```
## mod9a: spp_half_cover_date ~ state + origin + factor(year_factor) +
## mod9a:     (1 | plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod9     9 16418 16465 -8199.8    16400
## mod9a   12 16357 16421 -8166.4    16333 66.728  3  2.142e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod9a, mod9b)  # mod 9a
```

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

```
summary(mod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + origin + factor(year_factor) +
##     (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16356.8  16420.7  -8166.4  16332.8     1499
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.7493 -0.7254 -0.3268  0.8091  2.7626
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)   11.86   3.444
##  Residual             2886.39  53.725
## Number of obs: 1511, groups:  plot, 24
##
## Fixed effects:
##                       Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)           140.3973     4.4045  332.1637  31.876  < 2e-16 ***
## stateambient           -0.2628     3.1160   23.7557  -0.084 0.933483
## origin                -30.9606     5.2195 1493.6401  -5.932 3.72e-09 ***
## originBoth            -11.3637     4.9735 1509.7461  -2.285 0.022459 *
## originExotic          -15.2916     3.4880 1503.3942  -4.384 1.25e-05 ***
## factor(year_factor)2   -8.4820     4.7478 1497.7707  -1.786 0.074221 .
## factor(year_factor)3   22.4346     4.5361 1498.9553   4.946 8.44e-07 ***
## factor(year_factor)4   12.3891     4.5725 1502.6179   2.710 0.006815 **
## factor(year_factor)5   32.5549     4.6117 1500.3453   7.059 2.55e-12 ***
## factor(year_factor)6   15.8772     4.6777 1506.5918   3.394 0.000706 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn origin orgnBt orgnEx fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.352
## origin      -0.366 -0.002
## originBoth  -0.438 -0.023  0.334
## originExotc -0.577 -0.013  0.478  0.505
## fctr(yr_f)2 -0.461 -0.009 -0.009  0.097  0.016
## fctr(yr_f)3 -0.470 -0.006 -0.031  0.042  0.016  0.433
## fctr(yr_f)4 -0.463 -0.021 -0.009  0.031  0.021  0.428  0.447
## fctr(yr_f)5 -0.466 -0.015 -0.019  0.062  0.019  0.428  0.445  0.440
## fctr(yr_f)6 -0.462 -0.010 -0.005  0.057  0.019  0.421  0.437  0.433  0.432
```

```
anova(mod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state    1676    1676     1   89.34  0.5655     0.454
## origin 109657   36552     3 1489.38 12.3287 5.738e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## $`emmeans of state, origin`
##  state   origin emmean   SE    df lower.CL upper.CL
##  warmed  Native    153 3.50 142.6      146      160
##  ambient Native    153 3.47 143.4      146      159
##  warmed            122 4.71 421.6      113      131
##  ambient           122 4.67 426.4      112      131
##  warmed  Both      141 4.49 324.2      133      150
##  ambient Both      141 4.38 310.6      133      150
##  warmed  Exotic    138 2.68  47.8      132      143
##  ambient Exotic    137 2.57  41.7      132      143
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`
##  1                              estimate   SE     df t.ratio p.value
##  warmed Native - ambient Native    0.263 3.26   25.9  0.081  1.0000
##  warmed Native - warmed           30.961 5.23 1501.6  5.914  <.0001
##  warmed Native - ambient          31.223 6.17  325.2  5.065  <.0001
##  warmed Native - warmed Both      11.364 4.99 1519.0  2.275  0.3080
##  warmed Native - ambient Both     11.627 5.91  268.8  1.969  0.5052
##  warmed Native - warmed Exotic    15.292 3.50 1511.8  4.369  0.0004
##  warmed Native - ambient Exotic   15.554 4.76  121.8  3.270  0.0295
##  ambient Native - warmed          30.698 6.17  328.4  4.972  <.0001
##  ambient Native - ambient         30.961 5.23 1501.6  5.914  <.0001
##  ambient Native - warmed Both     11.101 6.03  287.7  1.842  0.5920
##  ambient Native - ambient Both    11.364 4.99 1519.0  2.275  0.3080
##  ambient Native - warmed Exotic   15.029 4.82  130.2  3.121  0.0447
##  ambient Native - ambient Exotic  15.292 3.50 1511.8  4.369  0.0004
##  warmed  - ambient                 0.263 3.26   25.9  0.081  1.0000
```

```
##  warmed  - warmed Both           -19.597 5.91 1517.6 -3.316  0.0209
##  warmed  - ambient Both          -19.334 6.70  409.8 -2.885  0.0783
##  warmed  - warmed Exotic         -15.669 4.71 1505.7 -3.329  0.0201
##  warmed  - ambient Exotic        -15.406 5.71  245.7 -2.699  0.1280
##  ambient  - warmed Both          -19.860 6.80  425.9 -2.920  0.0711
##  ambient  - ambient Both         -19.597 5.91 1517.6 -3.316  0.0209
##  ambient  - warmed Exotic        -15.932 5.75  254.7 -2.772  0.1069
##  ambient  - ambient Exotic       -15.669 4.71 1505.7 -3.329  0.0201
##  warmed Both - ambient Both        0.263 3.26   25.9  0.081  1.0000
##  warmed Both - warmed Exotic       3.928 4.42 1517.0  0.888  0.9871
##  warmed Both - ambient Exotic      4.191 5.54  213.5  0.757  0.9950
##  ambient Both - warmed Exotic      3.665 5.46  206.4  0.672  0.9976
##  ambient Both - ambient Exotic     3.928 4.42 1517.0  0.888  0.9871
##  warmed Exotic - ambient Exotic    0.263 3.26   25.9  0.081  1.0000
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

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

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

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

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

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

```
## Data: green_kbs
## Models:
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11:     plot)
## mod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## mod10:     plot)
##       npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod11    9 16445 16492 -8213.3    16427
## mod10   12 16449 16513 -8212.6    16425 1.4068  3      0.704
```

```
anova(mod11, mod11a)  # model 11a
```

```
## Data: green_kbs
## Models:
## mod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## mod11:     plot)
## mod11a: spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
## mod11a:     (1 | plot)
##        npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
```

```
## mod11     9 16445 16492 -8213.3    16427
## mod11a   12 16384 16448 -8180.1    16360 66.451  3  2.455e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod11a, mod11b)  # model 11a
```

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

```
summary(mod11a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + growth_habit + factor(year_factor) +
##     (1 | plot)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16384.1  16448.0  -8180.1  16360.1     1499
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.6850 -0.7388 -0.3369  0.7388  2.5016
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    3.749  1.936
##  Residual             2946.114 54.278
## Number of obs: 1511, groups:  plot, 24
##
## Fixed effects:
##                         Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)            127.2983     3.6569  215.2995  34.811  < 2e-16 ***
## stateambient            -0.5924     2.9167   23.4387  -0.203 0.840797
## growth_habit            -2.1183     4.4885 1505.1769  -0.472 0.637038
## growth_habitGraminoid    0.7180     3.0515 1510.8513   0.235 0.814020
## growth_habitVine        62.9345    19.3561 1421.6557   3.251 0.001175 **
## factor(year_factor)2    -8.6078     4.8090 1497.5236  -1.790 0.073668 .
## factor(year_factor)3    21.9800     4.5792 1500.4925   4.800 1.74e-06 ***
## factor(year_factor)4    12.1910     4.6253 1505.2357   2.636 0.008482 **
## factor(year_factor)5    32.2552     4.6818 1503.5078   6.889 8.21e-12 ***
## factor(year_factor)6    15.7438     4.7531 1509.5846   3.312 0.000947 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_V fc(_)2 fc(_)3 fc(_)4 fc(_)5
```

```
## stateambint -0.409
## growth_habt -0.255 -0.030
## grwth_hbtGr -0.291  0.029  0.284
## grwth_hbtVn -0.062 -0.030  0.051  0.064
## fctr(yr_f)2 -0.539 -0.015  0.099 -0.048  0.039
## fctr(yr_f)3 -0.546 -0.007 -0.005 -0.051  0.020  0.431
## fctr(yr_f)4 -0.532 -0.025  0.008 -0.065  0.003  0.429  0.447
## fctr(yr_f)5 -0.518 -0.021  0.013 -0.115  0.017  0.429  0.445  0.443
## fctr(yr_f)6 -0.515 -0.015  0.026 -0.113  0.016  0.424  0.438  0.437  0.438
```

```
anova(mod11a)
```

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

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

```
## $`emmeans of year_factor, growth_habit`
##  year_factor growth_habit emmean    SE   df lower.CL upper.CL
##            1 Forb            127  3.38  543      120      134
##            2 Forb            118  3.93  753      111      126
##            3 Forb            149  3.75  661      142      156
##            4 Forb            139  3.81  672      132      147
##            5 Forb            159  3.92  737      152      167
##            6 Forb            143  4.00  720      135      151
##            1                 125  4.78 1082      116      134
##            2                 116  5.58 1255      105      127
##            3                 147  5.03 1128      137      157
##            4                 137  5.13 1123      127      147
##            5                 157  5.23 1155      147      167
##            6                 141  5.34 1178      130      151
##            1 Graminoid       128  3.81  714      120      135
##            2 Graminoid       119  4.13  850      111      127
##            3 Graminoid       150  3.96  798      142      157
##            4 Graminoid       140  3.96  805      132      148
##            5 Graminoid       160  3.89  774      152      168
##            6 Graminoid       143  3.97  775      136      151
##            1 Vine            190 19.54 1420      152      228
##            2 Vine            181 19.81 1444      142      220
##            3 Vine            212 19.69 1435      173      251
##            4 Vine            202 19.63 1432      164      241
##            5 Vine            222 19.72 1422      184      261
##            6 Vine            206 19.72 1431      167      244
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor, growth_habit`
```

```
##  1                          estimate    SE   df t.ratio p.value
##  1 Forb - 2 Forb               8.608  4.82 1506  1.784  0.9851
##  1 Forb - 3 Forb             -21.980  4.59 1509 -4.784  0.0005
##  1 Forb - 4 Forb             -12.191  4.64 1514 -2.626  0.5761
##  1 Forb - 5 Forb             -32.255  4.70 1512 -6.865  <.0001
##  1 Forb - 6 Forb             -15.744  4.77 1519 -3.298  0.1420
##  1 Forb - 1                    2.118  4.50 1514  0.470  1.0000
##  1 Forb - 2                   10.726  6.92 1509  1.550  0.9977
##  1 Forb - 3                  -19.862  6.42 1509 -3.095  0.2382
##  1 Forb - 4                  -10.073  6.49 1514 -1.551  0.9977
##  1 Forb - 5                  -30.137  6.55 1515 -4.600  0.0011
##  1 Forb - 6                  -13.626  6.65 1514 -2.050  0.9315
##  1 Forb - 1 Graminoid         -0.718  3.07 1521 -0.234  1.0000
##  1 Forb - 2 Graminoid          7.890  5.59 1508  1.411  0.9994
##  1 Forb - 3 Graminoid        -22.698  5.39 1504 -4.214  0.0060
##  1 Forb - 4 Graminoid        -12.909  5.39 1504 -2.396  0.7525
##  1 Forb - 5 Graminoid        -32.973  5.30 1506 -6.216  <.0001
##  1 Forb - 6 Graminoid        -16.462  5.37 1510 -3.066  0.2550
##  1 Forb - 1 Vine             -62.934 19.52 1444 -3.224  0.1732
##  1 Forb - 2 Vine             -54.327 20.28 1473 -2.679  0.5335
##  1 Forb - 3 Vine             -84.914 20.14 1466 -4.217  0.0060
##  1 Forb - 4 Vine             -75.126 20.07 1464 -3.743  0.0359
##  1 Forb - 5 Vine             -95.190 20.15 1455 -4.723  0.0006
##  1 Forb - 6 Vine             -78.678 20.16 1462 -3.902  0.0203
##  2 Forb - 3 Forb             -30.588  5.03 1505 -6.084  <.0001
##  2 Forb - 4 Forb             -20.799  5.06 1508 -4.110  0.0092
##  2 Forb - 5 Forb             -40.863  5.09 1508 -8.029  <.0001
##  2 Forb - 6 Forb             -24.352  5.15 1518 -4.725  0.0006
##  2 Forb - 1                   -6.490  6.27 1510 -1.036  1.0000
##  2 Forb - 2                    2.118  4.50 1514  0.470  1.0000
##  2 Forb - 3                  -28.470  6.41 1507 -4.444  0.0023
##  2 Forb - 4                  -18.681  6.48 1512 -2.884  0.3746
##  2 Forb - 5                  -38.745  6.52 1513 -5.946  <.0001
##  2 Forb - 6                  -22.233  6.61 1515 -3.365  0.1179
##  2 Forb - 1 Graminoid         -9.326  5.84 1517 -1.597  0.9965
##  2 Forb - 2 Graminoid         -0.718  3.07 1521 -0.234  1.0000
##  2 Forb - 3 Graminoid        -31.306  5.88 1507 -5.321  <.0001
##  2 Forb - 4 Graminoid        -21.517  5.88 1506 -3.662  0.0471
##  2 Forb - 5 Graminoid        -41.581  5.78 1509 -7.196  <.0001
##  2 Forb - 6 Graminoid        -25.070  5.83 1515 -4.297  0.0043
##  2 Forb - 1 Vine             -71.542 19.93 1435 -3.589  0.0599
##  2 Forb - 2 Vine             -62.934 19.52 1444 -3.224  0.1732
##  2 Forb - 3 Vine             -93.522 20.07 1450 -4.660  0.0009
##  2 Forb - 4 Vine             -83.733 20.00 1448 -4.186  0.0068
##  2 Forb - 5 Vine            -103.797 20.08 1437 -5.170  0.0001
##  2 Forb - 6 Vine             -87.286 20.08 1445 -4.346  0.0035
##  3 Forb - 4 Forb               9.789  4.85 1507  2.016  0.9419
##  3 Forb - 5 Forb             -10.275  4.90 1510 -2.098  0.9145
##  3 Forb - 6 Forb               6.236  4.97 1516  1.255  0.9999
##  3 Forb - 1                   24.098  6.45 1513  3.735  0.0368
##  3 Forb - 2                   32.706  7.08 1511  4.621  0.0010
##  3 Forb - 3                    2.118  4.50 1514  0.470  1.0000
##  3 Forb - 4                   11.907  6.67 1513  1.786  0.9849
##  3 Forb - 5                   -8.157  6.71 1515 -1.215  1.0000
```

```
##  3 Forb - 6                  8.354  6.80 1514  1.228  0.9999
##  3 Forb - 1 Graminoid       21.262  5.66 1520  3.759  0.0339
##  3 Forb - 2 Graminoid       29.870  5.89 1516  5.068  0.0001
##  3 Forb - 3 Graminoid       -0.718  3.07 1521 -0.234  1.0000
##  3 Forb - 4 Graminoid        9.071  5.70 1511  1.590  0.9967
##  3 Forb - 5 Graminoid      -10.993  5.62 1515 -1.958  0.9571
##  3 Forb - 6 Graminoid        5.518  5.68 1517  0.972  1.0000
##  3 Forb - 1 Vine           -40.955 19.97 1441 -2.051  0.9312
##  3 Forb - 2 Vine           -32.347 20.24 1463 -1.598  0.9965
##  3 Forb - 3 Vine           -62.934 19.52 1444 -3.224  0.1732
##  3 Forb - 4 Vine           -53.146 20.04 1454 -2.652  0.5551
##  3 Forb - 5 Vine           -73.210 20.12 1443 -3.639  0.0508
##  3 Forb - 6 Vine           -56.698 20.12 1451 -2.817  0.4245
##  4 Forb - 5 Forb           -20.064  4.93 1501 -4.073  0.0106
##  4 Forb - 6 Forb            -3.553  5.00 1512 -0.711  1.0000
##  4 Forb - 1                 14.309  6.44 1513  2.221  0.8594
##  4 Forb - 2                 22.917  7.06 1509  3.245  0.1638
##  4 Forb - 3                 -7.671  6.58 1507 -1.166  1.0000
##  4 Forb - 4                  2.118  4.50 1514  0.470  1.0000
##  4 Forb - 5                -17.946  6.69 1509 -2.682  0.5313
##  4 Forb - 6                 -1.435  6.78 1509 -0.211  1.0000
##  4 Forb - 1 Graminoid       11.473  5.73 1521  2.001  0.9461
##  4 Forb - 2 Graminoid       20.081  5.96 1519  3.370  0.1162
##  4 Forb - 3 Graminoid      -10.507  5.78 1516 -1.818  0.9813
##  4 Forb - 4 Graminoid       -0.718  3.07 1521 -0.234  1.0000
##  4 Forb - 5 Graminoid      -20.782  5.68 1513 -3.660  0.0474
##  4 Forb - 6 Graminoid       -4.271  5.74 1516 -0.744  1.0000
##  4 Forb - 1 Vine           -50.743 20.05 1443 -2.530  0.6524
##  4 Forb - 2 Vine           -42.136 20.33 1464 -2.073  0.9238
##  4 Forb - 3 Vine           -72.723 20.19 1457 -3.602  0.0574
##  4 Forb - 4 Vine           -62.934 19.52 1444 -3.224  0.1732
##  4 Forb - 5 Vine           -82.999 20.20 1447 -4.109  0.0092
##  4 Forb - 6 Vine           -66.487 20.21 1454 -3.290  0.1454
##  5 Forb - 6 Forb            16.511  5.02 1512  3.290  0.1453
##  5 Forb - 1                 34.373  6.47 1511  5.316  <.0001
##  5 Forb - 2                 42.981  7.07 1509  6.082  <.0001
##  5 Forb - 3                 12.393  6.59 1508  1.879  0.9726
##  5 Forb - 4                 22.182  6.66 1506  3.331  0.1299
##  5 Forb - 5                  2.118  4.50 1514  0.470  1.0000
##  5 Forb - 6                 18.630  6.78 1508  2.747  0.4796
##  5 Forb - 1 Graminoid       31.537  5.90 1521  5.345  <.0001
##  5 Forb - 2 Graminoid       40.145  6.10 1518  6.581  <.0001
##  5 Forb - 3 Graminoid        9.557  5.94 1515  1.610  0.9961
##  5 Forb - 4 Graminoid       19.346  5.92 1508  3.266  0.1552
##  5 Forb - 5 Graminoid       -0.718  3.07 1521 -0.234  1.0000
##  5 Forb - 6 Graminoid       15.793  5.88 1514  2.686  0.5278
##  5 Forb - 1 Vine           -30.679 20.00 1453 -1.534  0.9980
##  5 Forb - 2 Vine           -22.071 20.27 1473 -1.089  1.0000
##  5 Forb - 3 Vine           -52.659 20.13 1466 -2.616  0.5846
##  5 Forb - 4 Vine           -42.870 20.06 1466 -2.137  0.8991
##  5 Forb - 5 Vine           -62.934 19.52 1444 -3.224  0.1732
##  5 Forb - 6 Vine           -46.423 20.14 1464 -2.304  0.8122
##  6 Forb - 1                 17.862  6.48 1519  2.757  0.4716
##  6 Forb - 2                 26.470  7.08 1518  3.741  0.0361
```

```
##  6 Forb - 3                 -4.118  6.61 1516 -0.623  1.0000
##  6 Forb - 4                  5.671  6.67 1516  0.850  1.0000
##  6 Forb - 5                -14.393  6.70 1517 -2.147  0.8948
##  6 Forb - 6                  2.118  4.50 1514  0.470  1.0000
##  6 Forb - 1 Graminoid       15.026  5.96 1521  2.521  0.6600
##  6 Forb - 2 Graminoid       23.634  6.16 1521  3.840  0.0255
##  6 Forb - 3 Graminoid       -6.954  6.00 1520 -1.160  1.0000
##  6 Forb - 4 Graminoid        2.835  5.98 1516  0.474  1.0000
##  6 Forb - 5 Graminoid      -17.229  5.88 1518 -2.929  0.3428
##  6 Forb - 6 Graminoid       -0.718  3.07 1521 -0.234  1.0000
##  6 Forb - 1 Vine           -47.191 20.03 1444 -2.356  0.7791
##  6 Forb - 2 Vine           -38.583 20.29 1464 -1.902  0.9688
##  6 Forb - 3 Vine           -69.171 20.16 1458 -3.431  0.0974
##  6 Forb - 4 Vine           -59.382 20.09 1457 -2.956  0.3245
##  6 Forb - 5 Vine           -79.446 20.16 1447 -3.940  0.0177
##  6 Forb - 6 Vine           -62.934 19.52 1444 -3.224  0.1732
##  1  - 2                      8.608  4.82 1506  1.784  0.9851
##  1  - 3                    -21.980  4.59 1509 -4.784  0.0005
##  1  - 4                    -12.191  4.64 1514 -2.626  0.5761
##  1  - 5                    -32.255  4.70 1512 -6.865  <.0001
##  1  - 6                    -15.744  4.77 1519 -3.298  0.1420
##  1  - 1 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  1  - 2 Graminoid            5.772  6.28 1511  0.920  1.0000
##  1  - 3 Graminoid          -24.816  6.46 1509 -3.843  0.0251
##  1  - 4 Graminoid          -15.027  6.41 1506 -2.343  0.7880
##  1  - 5 Graminoid          -35.091  6.33 1506 -5.547  <.0001
##  1  - 6 Graminoid          -18.580  6.34 1515 -2.931  0.3415
##  1  - 1 Vine               -65.053 19.80 1467 -3.286  0.1472
##  1  - 2 Vine               -56.445 20.44 1488 -2.761  0.4681
##  1  - 3 Vine               -87.033 20.42 1484 -4.263  0.0049
##  1  - 4 Vine               -77.244 20.34 1483 -3.798  0.0295
##  1  - 5 Vine               -97.308 20.41 1475 -4.767  0.0005
##  1  - 6 Vine               -80.797 20.41 1480 -3.959  0.0164
##  2  - 3                    -30.588  5.03 1505 -6.084  <.0001
##  2  - 4                    -20.799  5.06 1508 -4.110  0.0092
##  2  - 5                    -40.863  5.09 1508 -8.029  <.0001
##  2  - 6                    -24.352  5.15 1518 -4.725  0.0006
##  2  - 1 Graminoid          -11.444  7.13 1515 -1.605  0.9963
##  2  - 2 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  2  - 3 Graminoid          -33.424  7.18 1510 -4.654  0.0009
##  2  - 4 Graminoid          -23.635  7.14 1507 -3.312  0.1369
##  2  - 5 Graminoid          -43.699  7.04 1508 -6.206  <.0001
##  2  - 6 Graminoid          -27.188  7.05 1516 -3.857  0.0239
##  2  - 1 Vine               -73.661 20.31 1461 -3.626  0.0531
##  2  - 2 Vine               -65.053 19.80 1467 -3.286  0.1472
##  2  - 3 Vine               -95.641 20.45 1472 -4.676  0.0008
##  2  - 4 Vine               -85.852 20.37 1471 -4.214  0.0060
##  2  - 5 Vine              -105.916 20.44 1462 -5.181  0.0001
##  2  - 6 Vine               -89.404 20.44 1467 -4.375  0.0031
##  3  - 4                      9.789  4.85 1507  2.016  0.9419
##  3  - 5                    -10.275  4.90 1510 -2.098  0.9145
##  3  - 6                      6.236  4.97 1516  1.255  0.9999
##  3  - 1 Graminoid           19.144  6.65 1518  2.879  0.3785
##  3  - 2 Graminoid           27.752  6.53 1515  4.249  0.0052
```

```
##  3  - 3 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  3  - 4 Graminoid            6.953  6.67 1509  1.043  1.0000
##  3  - 5 Graminoid          -13.111  6.57 1511 -1.995  0.9478
##  3  - 6 Graminoid            3.400  6.58 1517  0.516  1.0000
##  3  - 1 Vine               -43.073 20.24 1464 -2.129  0.9026
##  3  - 2 Vine               -34.465 20.40 1481 -1.689  0.9926
##  3  - 3 Vine               -65.053 19.80 1467 -3.286  0.1472
##  3  - 4 Vine               -55.264 20.30 1475 -2.723  0.4985
##  3  - 5 Vine               -75.328 20.37 1466 -3.698  0.0418
##  3  - 6 Vine               -58.817 20.36 1471 -2.888  0.3718
##  4  - 5                    -20.064  4.93 1501 -4.073  0.0106
##  4  - 6                     -3.553  5.00 1512 -0.711  1.0000
##  4  - 1 Graminoid            9.355  6.76 1521  1.385  0.9996
##  4  - 2 Graminoid           17.963  6.63 1519  2.709  0.5099
##  4  - 3 Graminoid          -12.625  6.81 1517 -1.853  0.9767
##  4  - 4 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  4  - 5 Graminoid          -22.900  6.67 1512 -3.434  0.0966
##  4  - 6 Graminoid           -6.389  6.68 1518 -0.956  1.0000
##  4  - 1 Vine               -52.862 20.34 1465 -2.599  0.5976
##  4  - 2 Vine               -44.254 20.50 1481 -2.159  0.8895
##  4  - 3 Vine               -74.842 20.48 1476 -3.655  0.0482
##  4  - 4 Vine               -65.053 19.80 1467 -3.286  0.1472
##  4  - 5 Vine               -85.117 20.47 1468 -4.159  0.0075
##  4  - 6 Vine               -68.606 20.46 1473 -3.353  0.1221
##  5  - 6                     16.511  5.02 1512  3.290  0.1453
##  5  - 1 Graminoid           29.419  6.91 1520  4.255  0.0051
##  5  - 2 Graminoid           38.027  6.78 1518  5.612  <.0001
##  5  - 3 Graminoid            7.439  6.96 1517  1.069  1.0000
##  5  - 4 Graminoid           17.228  6.91 1510  2.493  0.6812
##  5  - 5 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  5  - 6 Graminoid           13.675  6.82 1518  2.006  0.9449
##  5  - 1 Vine               -32.798 20.29 1474 -1.617  0.9959
##  5  - 2 Vine               -24.190 20.44 1488 -1.183  1.0000
##  5  - 3 Vine               -54.778 20.42 1484 -2.682  0.5311
##  5  - 4 Vine               -44.989 20.34 1484 -2.212  0.8642
##  5  - 5 Vine               -65.053 19.80 1467 -3.286  0.1472
##  5  - 6 Vine               -48.541 20.40 1481 -2.379  0.7640
##  6  - 1 Graminoid           12.908  7.00 1521  1.843  0.9782
##  6  - 2 Graminoid           21.515  6.86 1520  3.134  0.2169
##  6  - 3 Graminoid           -9.072  7.05 1518 -1.287  0.9999
##  6  - 4 Graminoid            0.717  7.00 1513  0.102  1.0000
##  6  - 5 Graminoid          -19.348  6.90 1513 -2.805  0.4339
##  6  - 6 Graminoid           -2.836  4.67 1519 -0.607  1.0000
##  6  - 1 Vine               -49.309 20.33 1467 -2.426  0.7311
##  6  - 2 Vine               -40.701 20.48 1482 -1.987  0.9499
##  6  - 3 Vine               -71.289 20.46 1478 -3.484  0.0832
##  6  - 4 Vine               -61.500 20.38 1478 -3.018  0.2843
##  6  - 5 Vine               -81.564 20.45 1470 -3.989  0.0147
##  6  - 6 Vine               -65.053 19.80 1467 -3.286  0.1472
##  1 Graminoid - 2 Graminoid   8.608  4.82 1506  1.784  0.9851
##  1 Graminoid - 3 Graminoid -21.980  4.59 1509 -4.784  0.0005
##  1 Graminoid - 4 Graminoid -12.191  4.64 1514 -2.626  0.5761
##  1 Graminoid - 5 Graminoid -32.255  4.70 1512 -6.865  <.0001
##  1 Graminoid - 6 Graminoid -15.744  4.77 1519 -3.298  0.1420
```

```
##  1 Graminoid - 1 Vine       -62.217 19.56 1451 -3.181  0.1935
##  1 Graminoid - 2 Vine       -53.609 20.35 1478 -2.634  0.5698
##  1 Graminoid - 3 Vine       -84.197 20.21 1470 -4.165  0.0074
##  1 Graminoid - 4 Vine       -74.408 20.16 1468 -3.691  0.0428
##  1 Graminoid - 5 Vine       -94.472 20.28 1460 -4.659  0.0009
##  1 Graminoid - 6 Vine       -77.960 20.29 1467 -3.843  0.0252
##  2 Graminoid - 3 Graminoid  -30.588  5.03 1505 -6.084  <.0001
##  2 Graminoid - 4 Graminoid  -20.799  5.06 1508 -4.110  0.0092
##  2 Graminoid - 5 Graminoid  -40.863  5.09 1508 -8.029  <.0001
##  2 Graminoid - 6 Graminoid  -24.352  5.15 1518 -4.725  0.0006
##  2 Graminoid - 1 Vine       -70.824 19.94 1442 -3.552  0.0673
##  2 Graminoid - 2 Vine       -62.217 19.56 1451 -3.181  0.1935
##  2 Graminoid - 3 Vine       -92.804 20.11 1455 -4.615  0.0011
##  2 Graminoid - 4 Vine       -83.015 20.05 1453 -4.140  0.0082
##  2 Graminoid - 5 Vine      -103.080 20.16 1444 -5.112  0.0001
##  2 Graminoid - 6 Vine       -86.568 20.17 1450 -4.291  0.0044
##  3 Graminoid - 4 Graminoid    9.789  4.85 1507  2.016  0.9419
##  3 Graminoid - 5 Graminoid  -10.275  4.90 1510 -2.098  0.9145
##  3 Graminoid - 6 Graminoid    6.236  4.97 1516  1.255  0.9999
##  3 Graminoid - 1 Vine       -40.237 19.97 1449 -2.015  0.9423
##  3 Graminoid - 2 Vine       -31.629 20.28 1470 -1.560  0.9975
##  3 Graminoid - 3 Vine       -62.217 19.56 1451 -3.181  0.1935
##  3 Graminoid - 4 Vine       -52.428 20.09 1460 -2.610  0.5892
##  3 Graminoid - 5 Vine       -72.492 20.20 1451 -3.588  0.0600
##  3 Graminoid - 6 Vine       -55.980 20.21 1458 -2.770  0.4613
##  4 Graminoid - 5 Graminoid  -20.064  4.93 1501 -4.073  0.0106
##  4 Graminoid - 6 Graminoid   -3.553  5.00 1512 -0.711  1.0000
##  4 Graminoid - 1 Vine       -50.026 20.05 1451 -2.495  0.6794
##  4 Graminoid - 2 Vine       -41.418 20.35 1471 -2.035  0.9363
##  4 Graminoid - 3 Vine       -72.005 20.22 1464 -3.561  0.0654
##  4 Graminoid - 4 Vine       -62.217 19.56 1451 -3.181  0.1935
##  4 Graminoid - 5 Vine       -82.281 20.27 1454 -4.058  0.0112
##  4 Graminoid - 6 Vine       -65.769 20.28 1461 -3.243  0.1651
##  5 Graminoid - 6 Graminoid   16.511  5.02 1512  3.290  0.1453
##  5 Graminoid - 1 Vine       -29.961 19.96 1460 -1.501  0.9986
##  5 Graminoid - 2 Vine       -21.354 20.26 1479 -1.054  1.0000
##  5 Graminoid - 3 Vine       -51.941 20.13 1471 -2.581  0.6125
##  5 Graminoid - 4 Vine       -42.152 20.07 1471 -2.101  0.9137
##  5 Graminoid - 5 Vine       -62.217 19.56 1451 -3.181  0.1935
##  5 Graminoid - 6 Vine       -45.705 20.18 1469 -2.264  0.8359
##  6 Graminoid - 1 Vine       -46.473 19.98 1452 -2.326  0.7990
##  6 Graminoid - 2 Vine       -37.865 20.28 1471 -1.867  0.9746
##  6 Graminoid - 3 Vine       -68.453 20.15 1464 -3.397  0.1078
##  6 Graminoid - 4 Vine       -58.664 20.09 1462 -2.920  0.3495
##  6 Graminoid - 5 Vine       -78.728 20.20 1454 -3.897  0.0207
##  6 Graminoid - 6 Vine       -62.217 19.56 1451 -3.181  0.1935
##  1 Vine - 2 Vine              8.608  4.82 1506  1.784  0.9851
##  1 Vine - 3 Vine            -21.980  4.59 1509 -4.784  0.0005
##  1 Vine - 4 Vine            -12.191  4.64 1514 -2.626  0.5761
##  1 Vine - 5 Vine            -32.255  4.70 1512 -6.865  <.0001
##  1 Vine - 6 Vine            -15.744  4.77 1519 -3.298  0.1420
##  2 Vine - 3 Vine            -30.588  5.03 1505 -6.084  <.0001
##  2 Vine - 4 Vine            -20.799  5.06 1508 -4.110  0.0092
##  2 Vine - 5 Vine            -40.863  5.09 1508 -8.029  <.0001
```

```
##  2 Vine - 6 Vine           -24.352  5.15 1518 -4.725  0.0006
##  3 Vine - 4 Vine             9.789  4.85 1507  2.016  0.9419
##  3 Vine - 5 Vine           -10.275  4.90 1510 -2.098  0.9145
##  3 Vine - 6 Vine             6.236  4.97 1516  1.255  0.9999
##  4 Vine - 5 Vine           -20.064  4.93 1501 -4.073  0.0106
##  4 Vine - 6 Vine            -3.553  5.00 1512 -0.711  1.0000
##  5 Vine - 6 Vine            16.511  5.02 1512  3.290  0.1453
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 24 estimates
```

```
# You could now run some post hoc tests on these (see:
# https://stats.stackexchange.com/questions/169543/output-of-fixed-effects-summary-in-lmertest-in-r-and

# Here are some other options for plotting these plots above:
# https://stackoverflow.com/questions/31075407/plot-mixed-effects-model-in-ggplot

# Here's another approach:
# https://stats.stackexchange.com/questions/98958/plots-to-illustrate-results-of-linear-mixed-effect-mo
# Not quite working yet: newdat <-
# expand.grid(state=unique(green_kbs$state),
# year=c(min(green_kbs$year), max(green_kbs$year)),
# insecticide=unique(green_kbs$insecticide)) p <-
# ggplot(green_kbs, aes(x=year, y=spp_half_cover_date,
# colour=state, shape=insecticide)) + geom_point(size=3) +
# geom_line(aes(y=predict(mod5), group=species,
# size='species')) + geom_line(data=newdat,
# aes(y=predict(mod5, level=0, newdata=newdat),
# size='Population')) + scale_size_manual(name='Predictions',
# values=c('species'=0.5, 'Population'=3)) +
# #facet_wrap(~insecticide) + theme_bw(base_size=22) print(p)

# 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
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge: degenerate Hessian with 1 negative eigenvalues
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.6e-02
```

```
# 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 ~ insecticide + (1 | plot),
    green_kbsp, REML = FALSE)
```

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

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

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

```
mod4p <- lmer(plot_half_cover_date ~ insecticide * state + (1 |
    plot), green_kbsp, REML = FALSE)
```

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

```
mod5p <- lmer(plot_half_cover_date ~ state + year_factor + (1 |
    plot), green_kbsp, REML = FALSE)
```

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

```
mod6p <- lmer(plot_half_cover_date ~ state + year_factor + insecticide +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

```
mod7p <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
    plot), green_kbsp, REML = FALSE)
```

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

```
mod8p <- lmer(plot_half_cover_date ~ state * year_factor + insecticide +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

```
mod9p <- lmer(plot_half_cover_date ~ state * insecticide + year_factor +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

```
mod10p <- lmer(plot_half_cover_date ~ state + insecticide * year_factor +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

```
mod11p <- lmer(plot_half_cover_date ~ state * year_factor * insecticide +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

```
AICctab(mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p, mod8p,
    mod9p, mod10p, mod11p, weights = T)  # model 11p and 10p the same
```

```
##        dAICc df weight
## mod11p  0.0  10 0.299
## mod10p  0.0  7  0.294
## mod8p   1.9  7  0.117
## mod7p   2.0  6  0.110
## mod6p   3.0  6  0.068
## mod5p   3.0  5  0.066
## mod9p   3.8  7  0.045
## mod1p  21.5  4  <0.001
## mod3p  21.8  5  <0.001
## mod2p  22.0  4  <0.001
## mod4p  22.9  6  <0.001
```

```
anova(mod10p, mod11p)  #11p just barely better, going with 10p because is simpler
```

```
## Data: green_kbsp
## Models:
## mod10p: plot_half_cover_date ~ state + insecticide * year_factor + (1 |
## mod10p:     plot)
## mod11p: plot_half_cover_date ~ state * year_factor * insecticide + (1 |
## mod11p:     plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod10p    7 1528.4 1549.2 -757.21   1514.4
## mod11p   10 1527.6 1557.2 -753.78   1507.6 6.8708  3    0.07613 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod10p)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + insecticide * year_factor + (1 |
##     plot)
##    Data: green_kbsp
##
##      AIC      BIC   logLik deviance df.resid
##   1528.4   1549.2   -757.2   1514.4      136
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9420 -0.5986 -0.2836  0.2347  2.9418
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
```

```
##  plot     (Intercept)    0      0.00
##  Residual             2327     48.24
## Number of obs: 143, groups:  plot, 24
##
## Fixed effects:
##                                  Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                        76.668     13.683 143.000   5.603 1.05e-07
## stateambient                       14.193      8.070 143.000   1.759   0.0808
## insecticideno_insects              25.452     18.387 143.000   1.384   0.1684
## year_factor                        17.003      3.381 143.000   5.029 1.45e-06
## insecticideno_insects:year_factor -10.851      4.745 143.000  -2.287   0.0237
##
## (Intercept)                       ***
## stateambient                      .
## insecticideno_insects
## year_factor                       ***
## insecticideno_insects:year_factor *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn insct_ yr_fct
## stateambint -0.303
## insctcdn_ns -0.678  0.006
## year_factor -0.860  0.015  0.637
## insctcdn_:_  0.613 -0.011 -0.899 -0.713
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
emmeans(mod10p, list(pairwise ~ state + insecticide * year_factor),
    adjust = "tukey")
```

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

```
## $`emmeans of state, insecticide, year_factor`
##  state   insecticide year_factor emmean   SE   df lower.CL upper.CL
##  warmed  insects            3.48    136 7.10 22.3      121      151
##  ambient insects            3.48    150 7.17 23.1      135      165
##  warmed  no_insects         3.48    124 7.10 22.3      109      138
##  ambient no_insects         3.48    138 7.10 22.3      123      152
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, insecticide, year_factor`
##  1
##  warmed insects 3.48251748251748 - ambient insects 3.48251748251748
##  warmed insects 3.48251748251748 - warmed no_insects 3.48251748251748
##  warmed insects 3.48251748251748 - ambient no_insects 3.48251748251748
##  ambient insects 3.48251748251748 - warmed no_insects 3.48251748251748
##  ambient insects 3.48251748251748 - ambient no_insects 3.48251748251748
##  warmed no_insects 3.48251748251748 - ambient no_insects 3.48251748251748
##  estimate    SE   df t.ratio p.value
##    -14.19  8.22 22.5 -1.728  0.3334
##     12.34  8.22 22.5  1.502  0.4531
```

```
##     -1.86 11.58 22.2 -0.160  0.9985
##     26.53 11.66 22.8  2.275  0.1337
##     12.34  8.22 22.5  1.502  0.4531
##    -14.19  8.22 22.5 -1.728  0.3334
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

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

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

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + factor(year_factor) + (1 | plot)
##    Data: species_kbs
##
##      AIC      BIC   logLik deviance df.resid
##    567.7    585.9   -274.8    549.7       47
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.3148 -0.5539 -0.1129  0.2388  4.0379
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept) 155.9    12.49
##  Residual             941.5    30.68
## Number of obs: 56, groups:  plot, 21
##
## Fixed effects:
##                      Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)           120.052      9.287  45.084  12.927   <2e-16 ***
## stateambient          -18.032     10.395  20.860  -1.735   0.0975 .
## factor(year_factor)2   -6.455     15.941  50.140  -0.405   0.6872
## factor(year_factor)3    1.826     13.289  49.205   0.137   0.8913
## factor(year_factor)4   14.201     12.850  51.489   1.105   0.2742
## factor(year_factor)5   29.594     11.545  47.823   2.563   0.0136 *
## factor(year_factor)6  -23.750     19.956  52.047  -1.190   0.2394
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4 fc(_)5
```

```
## stateambint -0.576
## fctr(yr_f)2 -0.317 -0.033
## fctr(yr_f)3 -0.372 -0.053  0.277
## fctr(yr_f)4 -0.460  0.054  0.282  0.330
## fctr(yr_f)5 -0.446 -0.038  0.295  0.347  0.358
## fctr(yr_f)6 -0.317  0.066  0.190  0.207  0.240  0.242
```

```
summary(mod_spp2)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: min_green_date ~ state + factor(year_factor) + (1 | plot)
##    Data: species_kbs
##
##      AIC      BIC   logLik deviance df.resid
##    544.5    562.7   -263.2    526.5       47
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9957 -0.4769 -0.1362  0.4147  5.9393
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)  49.15    7.011
##  Residual             663.65   25.762
## Number of obs: 56, groups:  plot, 21
##
## Fixed effects:
##                       Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)            114.371      7.359  48.916  15.542   <2e-16 ***
## stateambient           -13.709      7.846  22.356  -1.747   0.0943 .
## factor(year_factor)2    -8.624     13.188  52.518  -0.654   0.5160
## factor(year_factor)3     4.476     11.021  51.089   0.406   0.6864
## factor(year_factor)4     8.045     10.614  52.700   0.758   0.4518
## factor(year_factor)5    12.390      9.599  49.693   1.291   0.2028
## factor(year_factor)6   -16.684     16.441  54.211  -1.015   0.3147
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.555
## fctr(yr_f)2 -0.340 -0.037
## fctr(yr_f)3 -0.399 -0.058  0.264
## fctr(yr_f)4 -0.485  0.055  0.269  0.317
## fctr(yr_f)5 -0.475 -0.040  0.290  0.343  0.353
## fctr(yr_f)6 -0.336  0.075  0.178  0.201  0.227  0.233
```

UMBS Mixed Effects Models

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

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

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0162338 (tol = 0.002, component 1)
```

```
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   20 8815.5 8911.4 -4387.7   8775.5
## umod7    21 8816.4 8917.1 -4387.2   8774.4 1.1069  1     0.2928
```

```
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   20 8815.5 8911.4 -4387.7   8775.5
## umod7b   21 8817.5 8918.2 -4387.7   8775.5 0.0044  1     0.9473
```

```
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   20 8815.5 8911.4 -4387.7   8775.5
## umod7c   21 8817.2 8918.0 -4387.6   8775.2 0.2903  1       0.59
```

```
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
##   8815.5   8911.4  -4387.7   8775.5      877
##
## Scaled residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -2.3350 -0.6153 -0.2795  0.2495  3.7351
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    5.076  2.253
##  Residual             1033.551 32.149
## Number of obs: 897, groups:  plot, 24
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)  138.8631    12.5509 827.9179  11.064  < 2e-16 ***
## stateambient   2.0895     2.3582  20.9950   0.886  0.38563
## speciesAnsp   -1.8637    15.1927 879.6584  -0.123  0.90240
## speciesApan   45.7654    16.7072 888.7457   2.739  0.00628 **
## speciesAssp   28.4177    13.5009 843.8652   2.105  0.03560 *
## speciesAsun  -16.8864    22.2308 892.7542  -0.760  0.44770
## speciesCape   10.4695    12.6598 868.4170   0.827  0.40847
## speciesCest  -10.4007    12.5049 875.9204  -0.832  0.40579
## speciesDasp    0.9713    12.5671 875.8693   0.077  0.93841
## speciesFrve   -0.8105    13.8396 845.1448  -0.059  0.95331
## speciesHisp   33.9786    14.3837 892.5734   2.362  0.01838 *
## speciesHype   10.1703    12.8751 884.6622   0.790  0.42979
## speciesPosp   -1.9400    12.5182 877.2429  -0.155  0.87688
## speciesPtaq   36.6036    12.6442 883.2122   2.895  0.00389 **
## speciesRuac   -4.5221    12.5959 881.8956  -0.359  0.71967
## speciesSosp   15.1003    14.2041 886.6004   1.063  0.28803
## speciesSyla   37.0475    15.9064 890.6452   2.329  0.02008 *
## year_factor   -0.3056     0.6523 878.0655  -0.469  0.63954
## ---
## 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(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
##   8817.5   8918.2  -4387.7   8775.5      876
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3365 -0.6160 -0.2802  0.2489  3.7358
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    5.068  2.251
##  Residual             1033.552 32.149
```

```
## Number of obs: 897, groups:  plot, 24
##
## Fixed effects:
##                            Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)              138.70989   12.76514 830.16184  10.866  < 2e-16 ***
## stateambient               2.38724    5.08586 346.39280   0.469  0.63909
## year_factor               -0.26287    0.91841 878.78077  -0.286  0.77477
## speciesAnsp               -1.86766   15.19276 879.68546  -0.123  0.90219
## speciesApan               45.75721   16.70743 888.78687   2.739  0.00629 **
## speciesAssp               28.42692   13.50167 843.64394   2.105  0.03555 *
## speciesAsun              -16.91970   22.23643 892.86183  -0.761  0.44692
## speciesCape               10.47854   12.66063 868.16999   0.828  0.40810
## speciesCest              -10.39752   12.50501 875.83120  -0.831  0.40594
## speciesDasp                0.97602   12.56725 875.76109   0.078  0.93811
## speciesFrve               -0.80348   13.84005 844.99154  -0.058  0.95372
## speciesHisp               33.96487   14.38501 892.59540   2.361  0.01843 *
## speciesHype               10.17081   12.87505 884.63470   0.790  0.42976
## speciesPosp               -1.93605   12.51830 877.14464  -0.155  0.87713
## speciesPtaq               36.60336   12.64417 883.18778   2.895  0.00389 **
## speciesRuac               -4.52068   12.59585 881.85426  -0.359  0.71975
## speciesSosp               15.10496   14.20434 886.57425   1.063  0.28789
## speciesSyla               37.04484   15.90636 890.62221   2.329  0.02009 *
## stateambient:year_factor  -0.08482    1.28282 877.77767  -0.066  0.94730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 19 > 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
##   8817.2   8918.0  -4387.6   8775.2      876
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3269 -0.6059 -0.2827  0.2492  3.7143
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    4.136  2.034
##  Residual             1034.018 32.156
## Number of obs: 897, groups:  plot, 24
##
## Fixed effects:
##                       Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)           139.5123    12.5804 787.6869  11.090  < 2e-16 ***
```

```
## stateambient            2.0660     2.3240  19.9404   0.889  0.38461
## speciesAnsp            -1.7771    15.1870 876.7262  -0.117  0.90688
## speciesApan            46.2268    16.7390 892.7715   2.762  0.00587 **
## speciesAssp            28.1178    13.4948 834.8802   2.084  0.03750 *
## speciesAsun           -17.0242    22.2315 893.0167  -0.766  0.44402
## speciesCape            10.4664    12.6534 863.7423   0.827  0.40837
## speciesCest           -10.4166    12.4991 872.1750  -0.833  0.40486
## speciesDasp             0.9566    12.5612 872.1285   0.076  0.93931
## speciesFrve            -0.8005    13.8313 839.1076  -0.058  0.95386
## speciesHisp            34.1995    14.3903 893.4799   2.377  0.01768 *
## speciesHype            10.2103    12.8709 882.5629   0.793  0.42782
## speciesPosp            -1.9609    12.5124 873.6432  -0.157  0.87550
## speciesPtaq            36.5881    12.6399 880.8992   2.895  0.00389 **
## speciesRuac            -4.4951    12.5916 879.4633  -0.357  0.72119
## speciesSosp            15.2876    14.2131 887.8019   1.076  0.28240
## speciesSyla            37.1036    15.9039 889.4829   2.333  0.01987 *
## year_factor            -0.3005     0.6525 876.7175  -0.461  0.64526
## insecticideno_insects  -1.2791     2.3376  20.5312  -0.547  0.59014
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 19 > 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          811   811.4     1  20.99  0.7851 0.3856
## species     211433 14095.5    15 873.88 13.6379 <2e-16 ***
## year_factor    227   226.9     1 878.07  0.2195 0.6395
## ---
## 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
##         3.52    150 2.2 151      146      155
##
## 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       139 12.43 888    114.4      163
##  Ansp       137  9.12 914    119.1      155
##  Apan       185 11.64 885    161.8      207
##  Assp       167  5.87 775    155.7      179
##  Asun       122 18.90 915     84.9      159
##  Cape       149  3.42 637    142.6      156
##  Cest       128  2.77 495    123.0      134
##  Dasp       140  3.03 566    133.8      146
##  Frve       138  6.65 746    125.0      151
##  Hisp       173  7.73 903    157.6      188
##  Hype       149  4.20 744    140.8      157
##  Posp       137  2.84 519    131.3      142
##  Ptaq       175  3.39 606    168.8      182
##  Ruac       134  3.19 578    128.0      141
##  Sosp       154  7.43 792    139.4      169
##  Syla       176 10.47 829    155.3      196
##
## 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   1.8637 15.43 907   0.121 1.0000
##  Amla - Apan -45.7654 16.95 912  -2.699 0.3324
##  Amla - Assp -28.4178 13.75 881  -2.067 0.7854
##  Amla - Asun  16.8864 22.48 909   0.751 1.0000
##  Amla - Cape -10.4695 12.87 899  -0.814 1.0000
##  Amla - Cest  10.4007 12.71 904   0.819 1.0000
##  Amla - Dasp  -0.9713 12.77 904  -0.076 1.0000
##  Amla - Frve   0.8105 14.09 882   0.058 1.0000
##  Amla - Hisp -33.9786 14.59 915  -2.329 0.6021
##  Amla - Hype -10.1703 13.07 910  -0.778 1.0000
##  Amla - Posp   1.9400 12.72 905   0.153 1.0000
##  Amla - Ptaq -36.6037 12.84 909  -2.851 0.2424
##  Amla - Ruac   4.5221 12.79 908   0.354 1.0000
##  Amla - Sosp -15.1003 14.42 911  -1.047 0.9997
##  Amla - Syla -37.0475 16.14 914  -2.295 0.6275
##  Ansp - Apan -47.6291 14.77 916  -3.225 0.0939
##  Ansp - Assp -30.2814 10.81 915  -2.803 0.2693
##  Ansp - Asun  15.0227 21.03 915   0.714 1.0000
##  Ansp - Cape -12.3332  9.73 914  -1.268 0.9969
##  Ansp - Cest   8.5370  9.49 912   0.899 0.9999
##  Ansp - Dasp  -2.8350  9.55 911  -0.297 1.0000
##  Ansp - Frve  -1.0532 11.21 915  -0.094 1.0000
##  Ansp - Hisp -35.8422 11.88 913  -3.016 0.1640
##  Ansp - Hype -12.0340 10.01 911  -1.202 0.9983
##  Ansp - Posp   0.0763  9.52 913   0.008 1.0000
##  Ansp - Ptaq -38.4673  9.70 915  -3.964 0.0078
##  Ansp - Ruac   2.6584  9.62 909   0.276 1.0000
```

```
##  Ansp - Sosp -16.9640 11.70 906  -1.450 0.9874
##  Ansp - Syla -38.9111 13.88 892  -2.804 0.2686
##  Apan - Assp  17.3477 13.01 887   1.333 0.9946
##  Apan - Asun  62.6518 22.18 913   2.824 0.2570
##  Apan - Cape  35.2960 12.10 900   2.917 0.2084
##  Apan - Cest  56.1662 11.93 904   4.706 0.0003
##  Apan - Dasp  44.7941 12.00 906   3.732 0.0185
##  Apan - Frve  46.5760 13.42 869   3.471 0.0447
##  Apan - Hisp  11.7869 13.96 911   0.845 1.0000
##  Apan - Hype  35.5951 12.32 910   2.889 0.2225
##  Apan - Posp  47.7054 11.95 903   3.992 0.0070
##  Apan - Ptaq   9.1618 12.07 910   0.759 1.0000
##  Apan - Ruac  50.2876 12.02 909   4.182 0.0033
##  Apan - Sosp  30.6651 13.80 898   2.222 0.6813
##  Apan - Syla   8.7180 15.64 885   0.558 1.0000
##  Assp - Asun  45.3041 19.76 916   2.293 0.6295
##  Assp - Cape  17.9483  6.74 892   2.664 0.3556
##  Assp - Cest  38.8185  6.43 901   6.034 <.0001
##  Assp - Dasp  27.4464  6.55 908   4.193 0.0031
##  Assp - Frve  29.2283  8.79 881   3.324 0.0706
##  Assp - Hisp  -5.5608  9.65 914  -0.576 1.0000
##  Assp - Hype  18.2474  7.15 910   2.550 0.4353
##  Assp - Posp  30.3577  6.46 900   4.696 0.0003
##  Assp - Ptaq  -8.1859  6.71 909  -1.219 0.9980
##  Assp - Ruac  32.9399  6.62 906   4.977 0.0001
##  Assp - Sosp  13.3174  9.44 881   1.411 0.9903
##  Assp - Syla  -8.6297 11.92 894  -0.724 1.0000
##  Asun - Cape -27.3558 19.19 916  -1.425 0.9893
##  Asun - Cest  -6.4856 19.08 916  -0.340 1.0000
##  Asun - Dasp -17.8577 19.13 916  -0.933 0.9999
##  Asun - Frve -16.0758 19.99 916  -0.804 1.0000
##  Asun - Hisp -50.8649 20.39 915  -2.494 0.4768
##  Asun - Hype -27.0567 19.32 916  -1.400 0.9911
##  Asun - Posp -14.9464 19.09 916  -0.783 1.0000
##  Asun - Ptaq -53.4900 19.17 916  -2.791 0.2762
##  Asun - Ruac -12.3642 19.14 916  -0.646 1.0000
##  Asun - Sosp -31.9867 20.21 912  -1.583 0.9712
##  Asun - Syla -53.9338 21.40 895  -2.521 0.4573
##  Cape - Cest  20.8702  4.32 906   4.832 0.0002
##  Cape - Dasp   9.4981  4.50 912   2.109 0.7591
##  Cape - Frve  11.2800  7.42 881   1.520 0.9802
##  Cape - Hisp -23.5091  8.42 916  -2.792 0.2756
##  Cape - Hype   0.2992  5.35 915   0.056 1.0000
##  Cape - Posp  12.4095  4.36 906   2.846 0.2450
##  Cape - Ptaq -26.1342  4.74 915  -5.514 <.0001
##  Cape - Ruac  14.9916  4.61 915   3.250 0.0875
##  Cape - Sosp  -4.6308  8.15 881  -0.568 1.0000
##  Cape - Syla -26.5780 11.00 860  -2.417 0.5350
##  Cest - Dasp -11.3720  4.02 897  -2.831 0.2531
##  Cest - Frve  -9.5902  7.15 870  -1.342 0.9942
##  Cest - Hisp -44.3793  8.17 915  -5.433 <.0001
##  Cest - Hype -20.5710  4.96 914  -4.150 0.0038
##  Cest - Posp  -8.4607  3.87 889  -2.185 0.7075
##  Cest - Ptaq -47.0044  4.29 911 -10.954 <.0001
```

```
##  Cest - Ruac  -5.8786  4.14 906  -1.420 0.9897
##  Cest - Sosp -25.5010  7.88 881  -3.237 0.0910
##  Cest - Syla -47.4482 10.80 871  -4.395 0.0013
##  Dasp - Frve   1.7819  7.25 869   0.246 1.0000
##  Dasp - Hisp -33.0072  8.25 913  -4.002 0.0068
##  Dasp - Hype  -9.1990  5.11 913  -1.800 0.9163
##  Dasp - Posp   2.9113  4.07 898   0.716 1.0000
##  Dasp - Ptaq -35.6323  4.46 911  -7.983 <.0001
##  Dasp - Ruac   5.4935  4.32 903   1.273 0.9967
##  Dasp - Sosp -14.1290  7.97 876  -1.773 0.9252
##  Dasp - Syla -36.0761 10.86 873  -3.321 0.0712
##  Frve - Hisp -34.7891 10.08 915  -3.451 0.0477
##  Frve - Hype -10.9808  7.82 879  -1.404 0.9908
##  Frve - Posp   1.1295  7.18 874   0.157 1.0000
##  Frve - Ptaq -37.4142  7.42 861  -5.045 0.0001
##  Frve - Ruac   3.7116  7.32 872   0.507 1.0000
##  Frve - Sosp -15.9108  9.89 881  -1.609 0.9666
##  Frve - Syla -37.8580 12.29 902  -3.081 0.1390
##  Hisp - Hype  23.8083  8.74 910   2.723 0.3175
##  Hisp - Posp  35.9186  8.19 915   4.383 0.0014
##  Hisp - Ptaq  -2.6251  8.39 914  -0.313 1.0000
##  Hisp - Ruac  38.5007  8.31 912   4.633 0.0005
##  Hisp - Sosp  18.8783 10.65 913   1.772 0.9256
##  Hisp - Syla  -3.0689 12.93 913  -0.237 1.0000
##  Hype - Posp  12.1103  4.99 914   2.426 0.5285
##  Hype - Ptaq -26.4333  5.32 916  -4.968 0.0001
##  Hype - Ruac  14.6924  5.19 911   2.830 0.2539
##  Hype - Sosp  -4.9300  8.50 874  -0.580 1.0000
##  Hype - Syla -26.8772 11.24 885  -2.392 0.5543
##  Posp - Ptaq -38.5436  4.34 912  -8.891 <.0001
##  Posp - Ruac   2.5821  4.19 907   0.617 1.0000
##  Posp - Sosp -17.0403  7.90 883  -2.156 0.7279
##  Posp - Syla -38.9875 10.81 872  -3.606 0.0287
##  Ptaq - Ruac  41.1258  4.57 914   8.995 <.0001
##  Ptaq - Sosp  21.5034  8.11 884   2.652 0.3639
##  Ptaq - Syla  -0.4438 10.95 886  -0.041 1.0000
##  Ruac - Sosp -19.6224  8.04 881  -2.441 0.5170
##  Ruac - Syla -41.5696 10.90 881  -3.814 0.0138
##  Sosp - Syla -21.9472 12.67 916  -1.733 0.9377
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 16 estimates
```

```
# including native vs. exotic - first with interaction term
green_umbs <- within(green_umbs, origin <- relevel(factor(origin),
    ref = "Native"))  # releveling so native is the reference
umod8 <- lmer(spp_half_cover_date ~ state * origin + (1 + year_factor |
    plot), green_umbs, REML = FALSE)
```

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

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

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

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

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

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

```
## Data: green_umbs
## Models:
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## umod8: spp_half_cover_date ~ state * origin + (1 + year_factor | plot)
##       npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod9    9 8894.5 8937.7 -4438.3   8876.5
## umod8   12 8893.3 8950.9 -4434.7   8869.3 7.2034  3    0.06569 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Data: green_umbs
## Models:
## umod9: spp_half_cover_date ~ state + origin + (1 + year_factor | plot)
## umod9a: spp_half_cover_date ~ state + origin + factor(year_factor) +
## umod9a:     (1 | plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod9     9 8894.5 8937.7 -4438.3   8876.5
## umod9a   12 8875.2 8932.8 -4425.6   8851.2 25.332  3  1.316e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 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 + factor(year_factor) +
##     (1 | plot)
##    Data: green_umbs
##
##      AIC      BIC   logLik deviance df.resid
##   8875.2   8932.8  -4425.6   8851.2      885
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1090 -0.6546 -0.3354  0.2993  3.6228
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    0      0.00
##  Residual             1130     33.61
## Number of obs: 897, groups:  plot, 24
##
## Fixed effects:
##                     Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)          155.6057     3.2586 897.0000  47.753  < 2e-16 ***
## stateambient           1.1163     2.2545 897.0000   0.495 0.620629
```

```
## origin               -16.5176     3.3127 897.0000  -4.986 7.40e-07 ***
## originBoth            18.2229     5.0828 897.0000   3.585 0.000355 ***
## originExotic         -18.8232     2.5475 897.0000  -7.389 3.39e-13 ***
## factor(year_factor)2 -12.3586     3.9553 897.0000  -3.125 0.001838 **
## factor(year_factor)3   5.7297     3.9516 897.0000   1.450 0.147420
## factor(year_factor)4  -4.6638     3.8963 897.0000  -1.197 0.231621
## factor(year_factor)5  -6.9443     3.8563 897.0000  -1.801 0.072078 .
## factor(year_factor)6   0.4909     4.0309 897.0000   0.122 0.903095
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn origin orgnBt orgnEx fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.355
## origin      -0.235  0.011
## originBoth  -0.117 -0.080  0.171
## originExotc -0.327  0.012  0.342  0.219
## fctr(yr_f)2 -0.616  0.020 -0.032 -0.075  0.001
## fctr(yr_f)3 -0.604 -0.005 -0.035  0.001 -0.029  0.509
## fctr(yr_f)4 -0.618  0.013 -0.039 -0.013 -0.028  0.518  0.518
## fctr(yr_f)5 -0.617 -0.008 -0.027 -0.031 -0.030  0.524  0.523  0.531
## fctr(yr_f)6 -0.594  0.014 -0.047 -0.023 -0.033  0.501  0.501  0.509  0.514
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(umod9)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## state     437     437     1  74.68  0.3789 0.5401
## origin 100447   33482     3 886.05 29.0086 <2e-16 ***
## ---
## 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    153 2.10  64.0      148      157
##  ambient Native    154 2.10  61.1      150      158
##  warmed            136 3.09 280.8      130      142
##  ambient           137 3.12 289.1      131      143
##  warmed  Both      171 5.09 583.5      161      181
##  ambient Both      172 4.92 500.2      162      182
##  warmed  Exotic    134 2.26  85.8      129      138
##  ambient Exotic    135 2.28  90.2      130      139
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`
##  1                              estimate   SE    df t.ratio p.value
##  warmed Native - ambient Native    -1.12 2.36  24.8 -0.473  0.9997
##  warmed Native - warmed            16.52 3.33 897.7  4.956  <.0001
```

```
##  warmed Native - ambient           15.40 4.10 218.3  3.755  0.0054
##  warmed Native - warmed Both      -18.22 5.14 895.8 -3.548  0.0097
##  warmed Native - ambient Both     -19.34 5.49 367.4 -3.520  0.0113
##  warmed Native - warmed Exotic     18.82 2.57 907.1  7.331  <.0001
##  warmed Native - ambient Exotic    17.71 3.50 120.8  5.054  <.0001
##  ambient Native - warmed           17.63 4.06 203.7  4.340  0.0006
##  ambient Native - ambient          16.52 3.33 897.7  4.956  <.0001
##  ambient Native - warmed Both     -17.11 5.81 475.3 -2.947  0.0659
##  ambient Native - ambient Both    -18.22 5.14 895.8 -3.548  0.0097
##  ambient Native - warmed Exotic    19.94 3.47 111.4  5.749  <.0001
##  ambient Native - ambient Exotic   18.82 2.57 907.1  7.331  <.0001
##  warmed  - ambient                 -1.12 2.36  24.8 -0.473  0.9997
##  warmed  - warmed Both            -34.74 5.63 894.9 -6.168  <.0001
##  warmed  - ambient Both           -35.86 5.95 425.5 -6.030  <.0001
##  warmed  - warmed Exotic            2.31 3.44 894.0  0.671  0.9977
##  warmed  - ambient Exotic           1.19 4.16 227.9  0.286  1.0000
##  ambient  - warmed Both           -33.62 6.26 538.1 -5.371  <.0001
##  ambient  - ambient Both          -34.74 5.63 894.9 -6.168  <.0001
##  ambient  - warmed Exotic           3.42 4.17 229.4  0.820  0.9918
##  ambient  - ambient Exotic          2.31 3.44 894.0  0.671  0.9977
##  warmed Both - ambient Both        -1.12 2.36  24.8 -0.473  0.9997
##  warmed Both - warmed Exotic       37.05 5.22 894.9  7.099  <.0001
##  warmed Both - ambient Exotic      35.93 5.89 490.2  6.102  <.0001
##  ambient Both - warmed Exotic      38.16 5.56 370.8  6.865  <.0001
##  ambient Both - ambient Exotic     37.05 5.22 894.9  7.099  <.0001
##  warmed Exotic - ambient Exotic    -1.12 2.36  24.8 -0.473  0.9997
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

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

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

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

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

```
umod11a <- lmer(spp_half_cover_date ~ state + growth_habit +
    year_factor + (1 | plot), green_umbs, REML = FALSE)
```

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

```
anova(umod10, umod11)  # umodel 11 is a better fit to data
```

```
## Data: green_umbs
## Models:
## umod11: spp_half_cover_date ~ state + growth_habit + (1 + year_factor |
## umod11:     plot)
## umod10: spp_half_cover_date ~ state * growth_habit + (1 + year_factor |
## umod10:     plot)
```

```
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## umod11    9 8964.4 9007.6 -4473.2   8946.4
## umod10   12 8967.9 9025.5 -4471.9   8943.9 2.4634  3     0.4819
```

```
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 8962.5 9000.8 -4473.2   8946.5
## umod11     9 8964.4 9007.6 -4473.2   8946.4  0.09  1     0.7642
```

```
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
##   8962.5   9000.8  -4473.2   8946.5      889
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9282 -0.6333 -0.3806  0.4409  3.2455
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    0      0.00
##  Residual             1256     35.44
## Number of obs: 897, groups:  plot, 24
##
## Fixed effects:
##                         Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)           145.53951    3.15941 897.00000  46.065   <2e-16 ***
## stateambient            2.43853    2.36767 897.00000   1.030   0.3033
## growth_habit           19.00820    7.89435 897.00000   2.408   0.0162 *
## growth_habitGraminoid  -5.40645    2.45049 897.00000  -2.206   0.0276 *
## growth_habitTree       -7.34525   13.48977 897.00000  -0.545   0.5862
## year_factor            -0.04126    0.70596 897.00000  -0.058   0.9534
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_T
## stateambint -0.379
## growth_habt -0.112 -0.020
## grwth_hbtGr -0.304  0.000  0.125
## grwth_hbtTr -0.038 -0.012  0.022  0.074
## year_factor -0.784  0.001  0.028 -0.011 -0.018
```

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

```
anova(umod11)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value   Pr(>F)
## state          1343  1343.0     1 316.72  1.0716 0.301381
## growth_habit  15728  5242.6     3 887.31  4.1829 0.005941 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

```
## $`emmeans of state, growth_habit`
##  state   growth_habit emmean    SE    df lower.CL upper.CL
##  warmed  Forb            145  1.98  38.3      141      149
##  ambient Forb            148  1.97  34.0      144      152
##  warmed                  164  7.92 772.1      149      180
##  ambient                 167  7.87 769.5      151      182
##  warmed  Graminoid       140  2.25  66.9      135      144
##  ambient Graminoid       142  2.24  65.7      138      147
##  warmed  Tree            138 13.61 796.0      111      165
##  ambient Tree            140 13.57 805.9      114      167
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, growth_habit`
##  1                                  estimate    SE    df t.ratio p.value
##  warmed Forb - ambient Forb            -2.44  2.39  20.6 -1.021  0.9657
##  warmed Forb - warmed                 -19.01  7.95 902.3 -2.392  0.2464
##  warmed Forb - ambient                -21.45  8.25 687.9 -2.600  0.1577
##  warmed Forb - warmed Graminoid         5.41  2.47 900.0  2.192  0.3575
##  warmed Forb - ambient Graminoid        2.97  3.43  84.6  0.866  0.9883
##  warmed Forb - warmed Tree              7.35 13.62 855.5  0.539  0.9994
##  warmed Forb - ambient Tree             4.91 13.80 778.1  0.356  1.0000
##  ambient Forb - warmed                -16.57  8.35 678.4 -1.986  0.4924
##  ambient Forb - ambient               -19.01  7.95 902.3 -2.392  0.2464
##  ambient Forb - warmed Graminoid        7.84  3.44  77.1  2.281  0.3173
##  ambient Forb - ambient Graminoid       5.41  2.47 900.0  2.192  0.3575
##  ambient Forb - warmed Tree             9.78 13.87 752.1  0.706  0.9968
##  ambient Forb - ambient Tree            7.35 13.62 855.5  0.539  0.9994
##  warmed  - ambient                     -2.44  2.39  20.6 -1.021  0.9657
##  warmed  - warmed Graminoid            24.41  8.03 894.1  3.041  0.0497
##  warmed  - ambient Graminoid           21.98  8.42 654.1  2.609  0.1543
##  warmed  - warmed Tree                 26.35 15.60 893.0  1.689  0.6943
##  warmed  - ambient Tree                23.91 15.78 854.7  1.516  0.7989
##  ambient  - warmed Graminoid           26.85  8.33 646.7  3.223  0.0289
##  ambient  - ambient Graminoid          24.41  8.03 894.1  3.041  0.0497
##  ambient  - warmed Tree                28.79 15.79 842.2  1.824  0.6040
##  ambient  - ambient Tree               26.35 15.60 893.0  1.689  0.6943
##  warmed Graminoid - ambient Graminoid  -2.44  2.39  20.6 -1.021  0.9657
##  warmed Graminoid - warmed Tree         1.94 13.67 846.4  0.142  1.0000
```

```
##  warmed Graminoid - ambient Tree         -0.50 13.84 763.8 -0.036  1.0000
##  ambient Graminoid - warmed Tree          4.38 13.91 743.1  0.315  1.0000
##  ambient Graminoid - ambient Tree         1.94 13.67 846.4  0.142  1.0000
##  warmed Tree - ambient Tree              -2.44  2.39  20.6 -1.021  0.9657
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

UMBS Plot-level Mixed Effects Models:

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

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

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

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

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

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

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

```
## Data: green_umbsp
## Models:
## mod1pu: plot_half_cover_date ~ state + (1 | plot)
## mod3pu: plot_half_cover_date ~ state * year_factor + (1 | plot)
## mod2pu: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod1pu    4 1440.9 1452.8 -716.45   1432.9
## mod3pu    6 1430.0 1447.8 -709.00   1418.0 14.893  2  0.0005836 ***
## mod2pu    9 1424.0 1450.7 -702.99   1406.0 12.035  3  0.0072651 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod2pu)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
##    Data: green_umbsp
##
##      AIC      BIC   logLik deviance df.resid
##   1424.0   1450.7   -703.0   1406.0      135
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8838 -0.6975 -0.1632  0.4816  3.0703
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    0      0.00
```

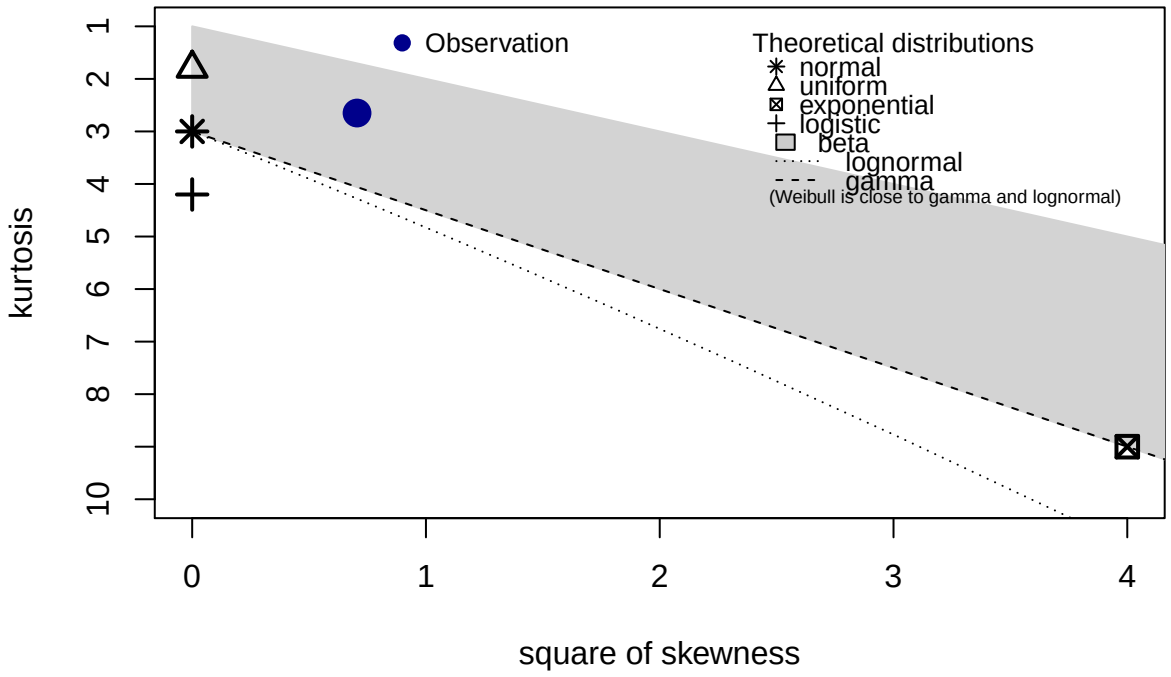
```
##  Residual             1018     31.91
## Number of obs: 144, groups:  plot, 24
##
## Fixed effects:
##                      Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)           147.306      7.035 144.000  20.938   <2e-16 ***
## stateambient           -1.778      5.318 144.000  -0.334   0.7387
## factor(year_factor)2  -21.500      9.212 144.000  -2.334   0.0210 *
## factor(year_factor)3   -2.583      9.212 144.000  -0.280   0.7795
## factor(year_factor)4   13.167      9.212 144.000   1.429   0.1551
## factor(year_factor)5   23.583      9.212 144.000   2.560   0.0115 *
## factor(year_factor)6   12.917      9.212 144.000   1.402   0.1630
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.378
## fctr(yr_f)2 -0.655  0.000
## fctr(yr_f)3 -0.655  0.000  0.500
## fctr(yr_f)4 -0.655  0.000  0.500  0.500
## fctr(yr_f)5 -0.655  0.000  0.500  0.500  0.500
## fctr(yr_f)6 -0.655  0.000  0.500  0.500  0.500  0.500
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

ORIGINAL CODE BELOW; not edited by Phoebe

can pretty much ignore everything below!

Seeing what other distribution could fit

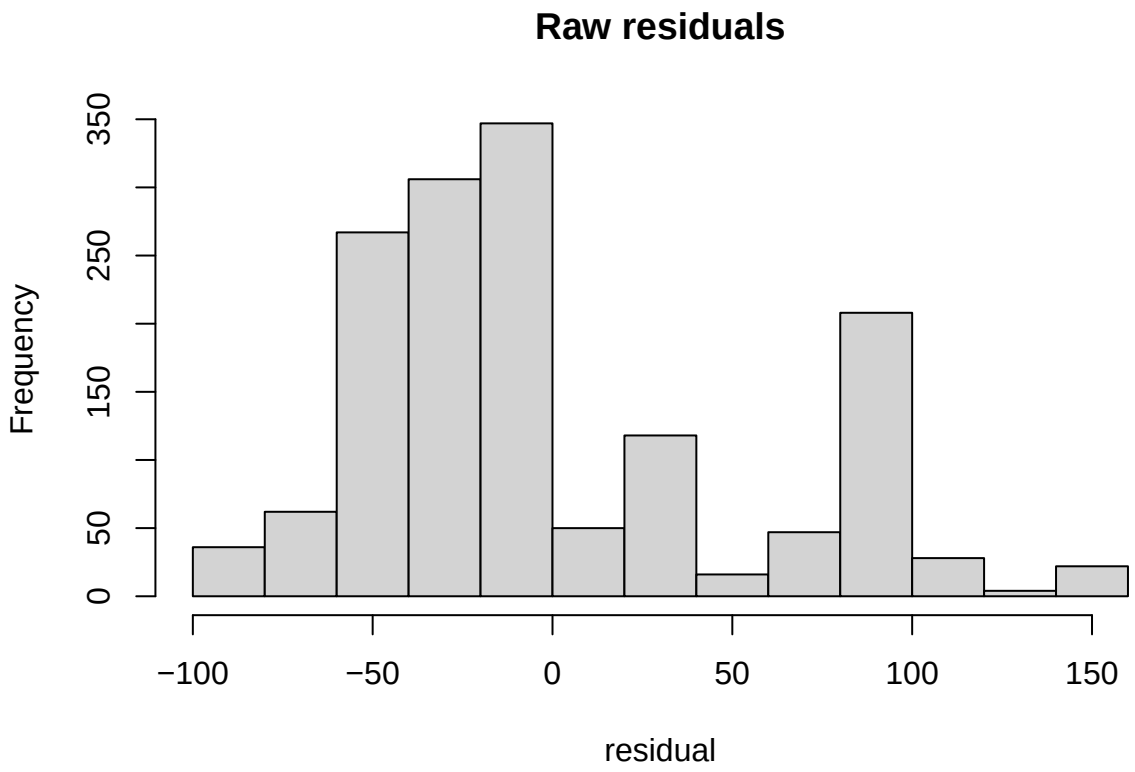
```
descdist(green_kbs$spp_half_cover_date, discrete = FALSE)
```



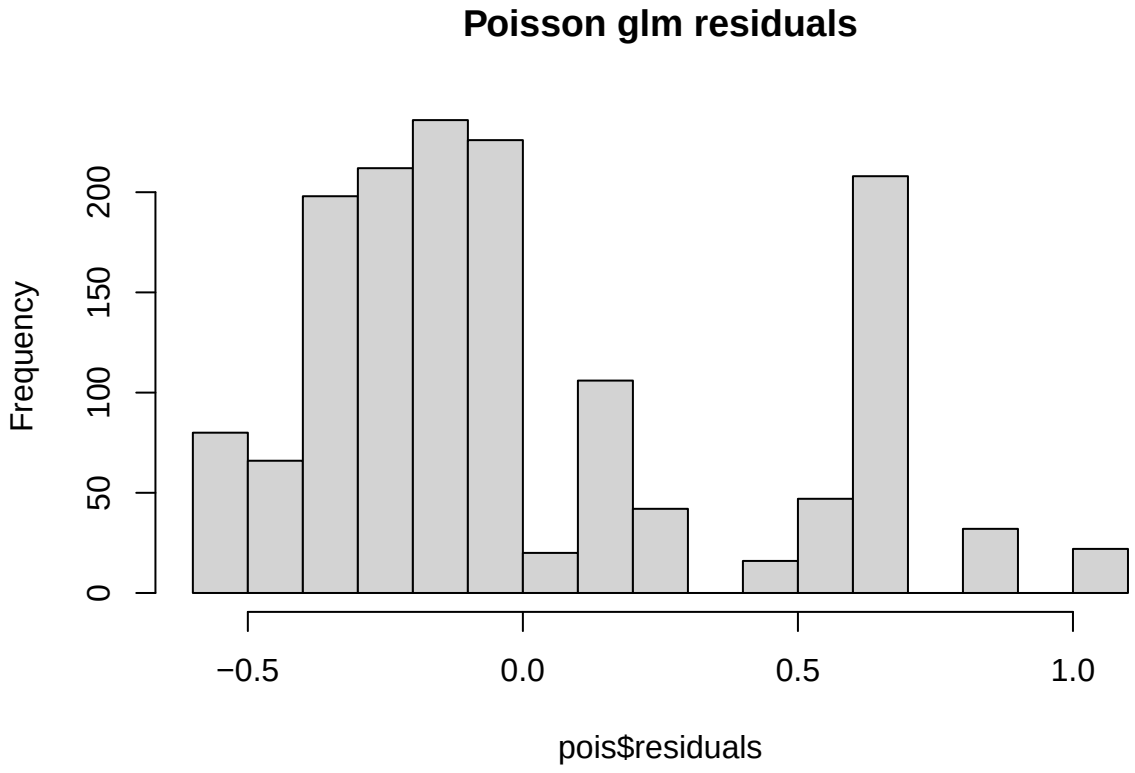

```
## summary statistics
## ------
## min:  59   max:  289
## median:  124
## mean:  139.3309
## estimated sd:  56.12957
## estimated skewness:  0.8397458
## estimated kurtosis:  2.650025
```

While uniform looks the closest, I'll try poisson

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




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



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

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

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

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

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0128739 (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
##  35773.3  35810.5 -17879.6  35759.3     1504
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -7.563 -2.897 -1.147  1.916 15.309
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plot    (Intercept) 0.003081 0.0555
##  species (Intercept) 0.035563 0.1886
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -28.182733   4.491500  -6.275 3.50e-10 ***
## stateambient          -43.588322   6.670109  -6.535 6.37e-11 ***
## year                    0.016413   0.002225   7.376 1.63e-13 ***
## insecticideno_insects  -0.006946   0.023100  -0.301    0.764
## stateambient:year       0.021594   0.003304   6.535 6.37e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn year   insct_
## stateambint -0.808
## year        -1.000  0.808
```

```
## insctcdn_ns -0.020  0.013  0.017
## statmbnt:yr  0.808 -1.000 -0.808 -0.013
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model failed to converge with max|grad| = 0.0128739 (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| = 0.00426111 (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
##  35843.8  35875.7 -17915.9  35831.8     1505
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -7.541 -2.891 -1.142  1.953 14.948
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plot    (Intercept) 0.003069 0.0554
##  species (Intercept) 0.035934 0.1896
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -5.122e+01  2.600e+00 -19.703   <2e-16 ***
## stateambient          -4.634e-04  2.306e-02  -0.020    0.984
## year                   2.783e-02  1.288e-03  21.608   <2e-16 ***
## insecticideno_insects -5.137e-03  2.306e-02  -0.223    0.824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn year
## stateambint  0.002
## year        -1.000 -0.007
## insctcdn_ns -0.016 -0.003  0.011
## convergence code: 0
## Model failed to converge with max|grad| = 0.00426111 (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?

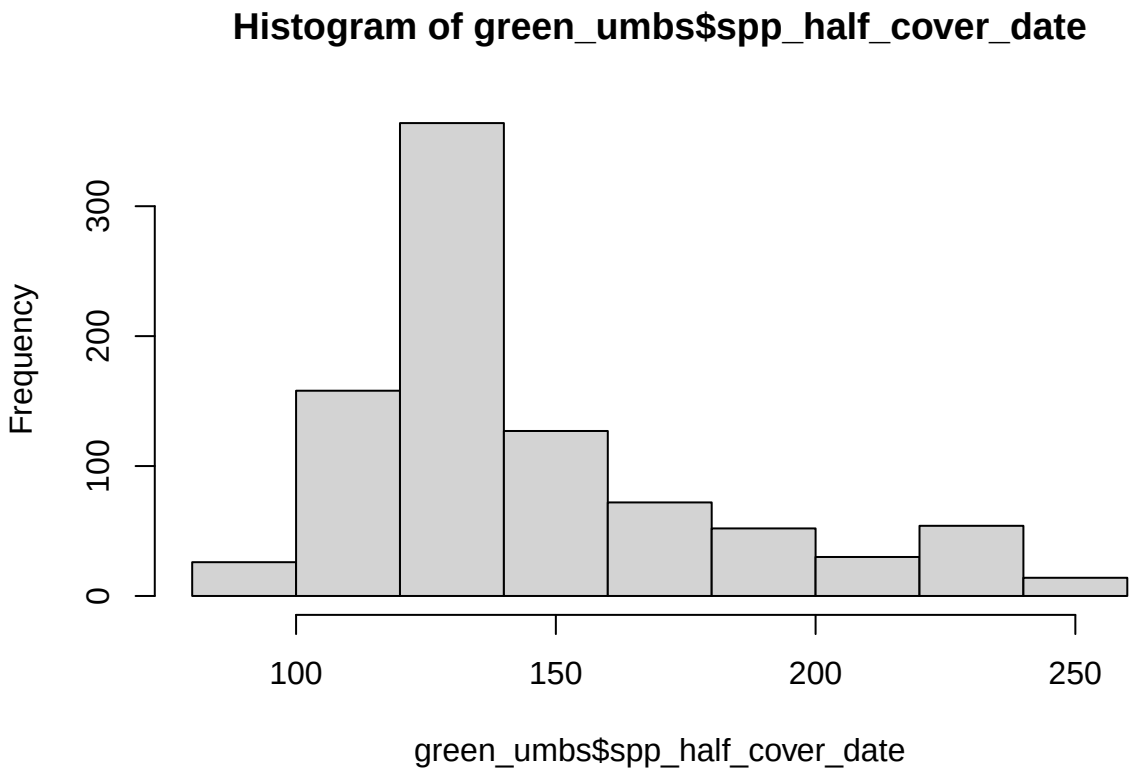
```
per1 <- adonis2(green_kbs$spp_half_cover_date ~ state * year +
    insecticide, data = green_kbs)
per1
per2 <- adonis(formula = green_kbs$spp_half_cover_date ~ state *
    year + insecticide, strata = green_kbs$plot, data = green_kbs)
per2
```

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

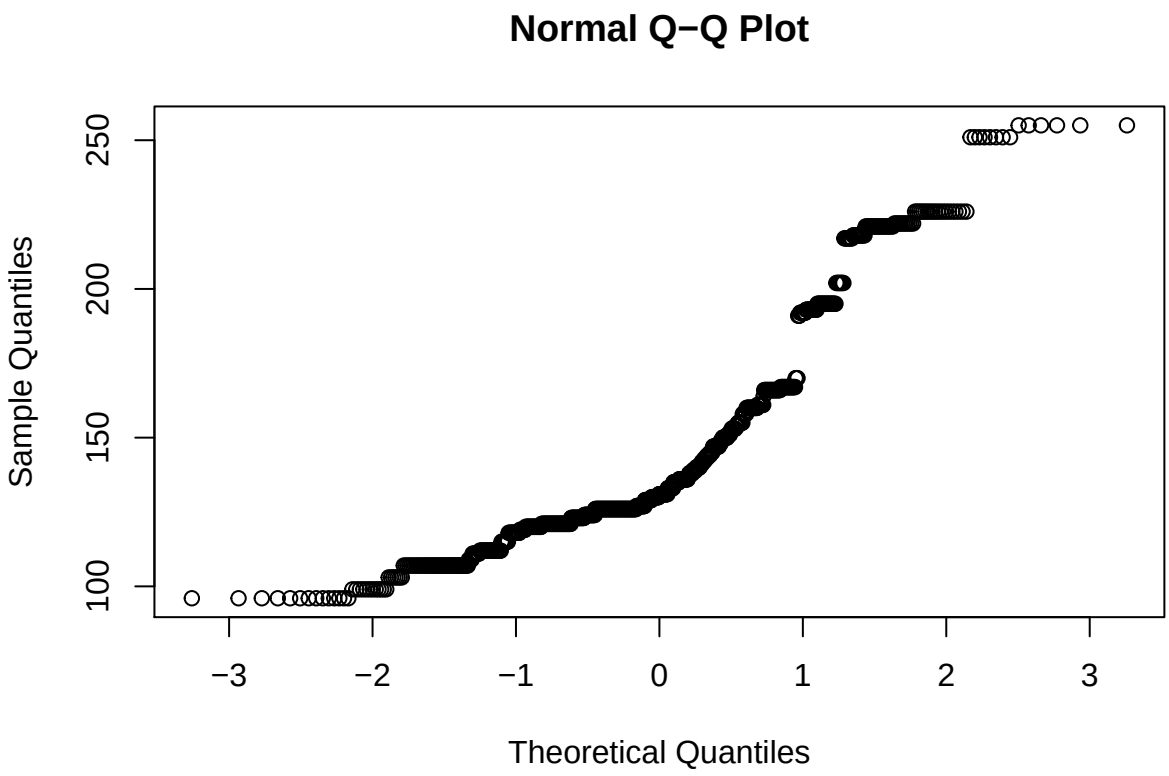
UMBS

Checking for normality

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



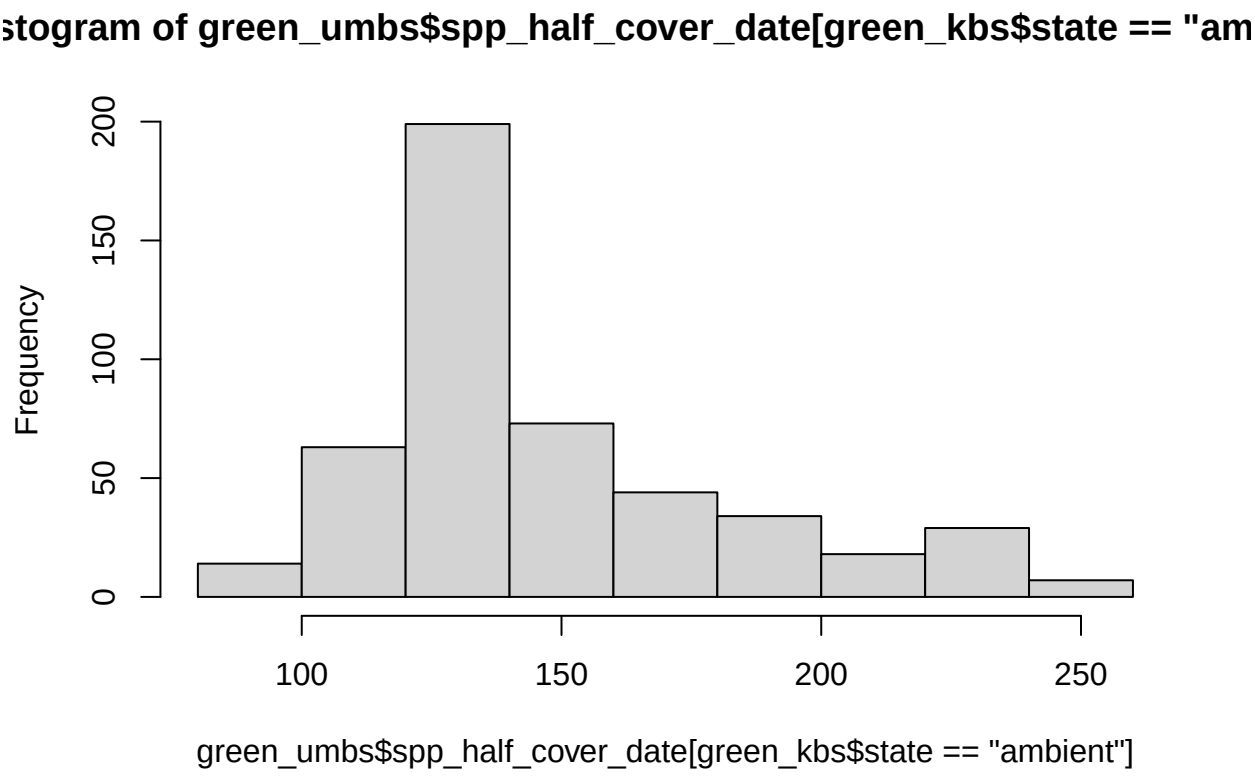

```
qqnorm(green_umbs$spp_half_cover_date)
```



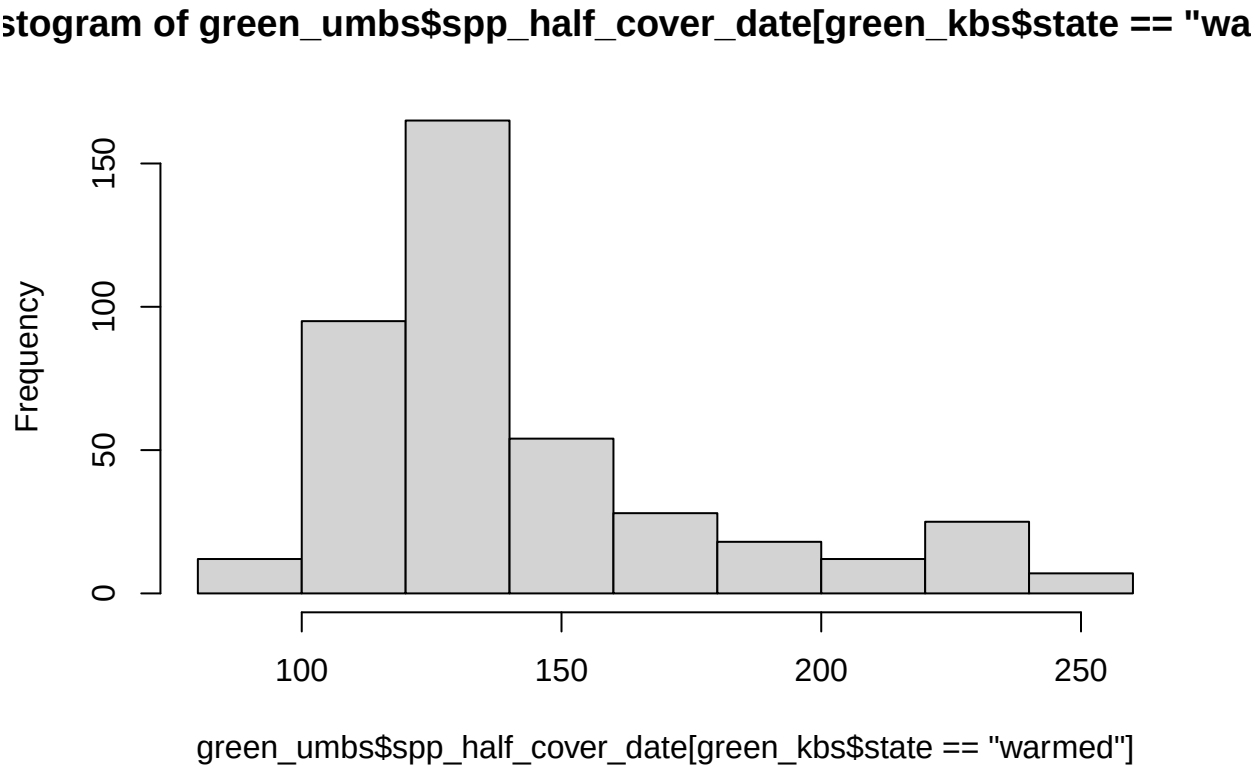

```
shapiro.test(green_umbs$spp_half_cover_date)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$spp_half_cover_date
## W = 0.86297, p-value < 2.2e-16
```

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



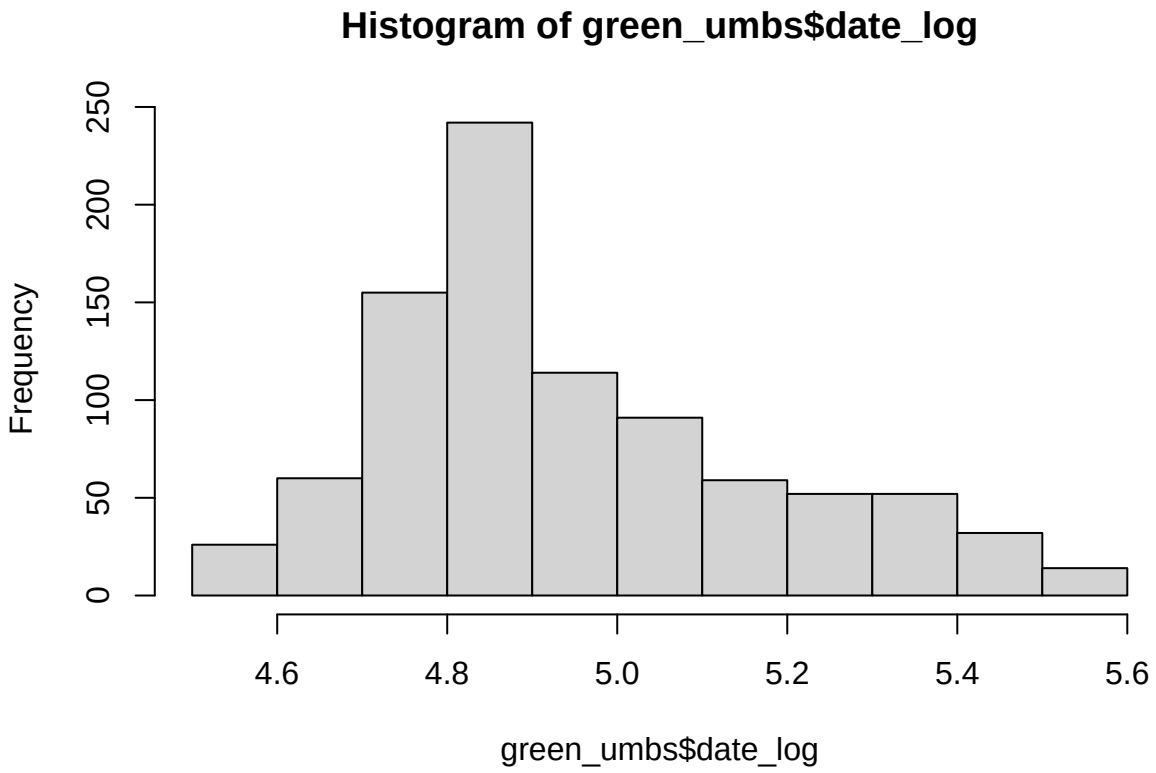

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "warmed"])
```



These look pretty good

Trying log transformation

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



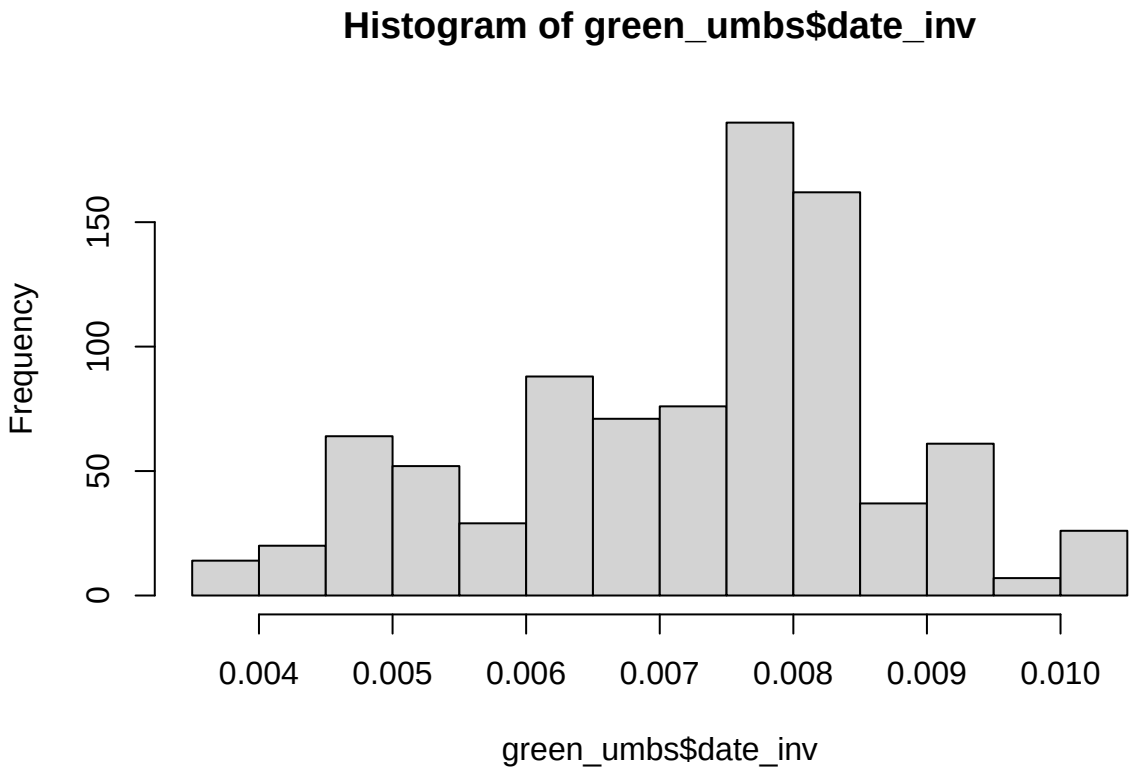

```
shapiro.test(green_umbs$date_log)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_log
## W = 0.9214, p-value < 2.2e-16
```

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

Trying inverse tranformation

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




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

```
##
##  Shapiro-Wilk normality test
##
## data:  green_umbs$date_inv
## W = 0.9592, p-value = 4.155e-15
```

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