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 (could fix this in clea
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':    2271 obs. of  18 variables:
##  $ site                : chr  "kbs" "kbs" "kbs" "kbs" ...
##  $ plot                : chr  "A1" "A1" "A1" "A1" ...
##  $ year                : int  2016 2017 2018 2019 2020 2021 2016 2017 2016 2017 ...
##  $ species             : chr  "Acmi" "Acmi" "Acmi" "Acmi" ...
##  $ spp_half_cover_date: int  104 101 122 120 223 257 88 108 101 99 ...
##  $ min_green_date      : int  81 80 122 120 107 92 81 108 85 80 ...
##  $ treatment_key       : chr  "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" ...
```

```
str(greenupp)
```

```
## 'data.frame':    263 obs. of  8 variables:
##  $ site                 : chr  "kbs" "kbs" "kbs" "kbs" ...
##  $ plot                 : chr  "A1" "A1" "A1" "A1" ...
##  $ year                 : int  2016 2017 2018 2019 2020 2021 2016 2017 2018 2019 ...
##  $ treatment_key        : chr  "A0" "A0" "A0" "A0" ...
##  $ state                : chr  "ambient" "ambient" "ambient" "ambient" ...
##  $ insecticide          : chr  "no_insects" "no_insects" "no_insects" "no_insects" ...
##  $ plot_half_cover_date: int  81 80 84 122 223 216 160 150 191 145 ...
##  $ min_green_date       : int  81 61 59 106 91 85 121 107 120 112 ...
```

```
# Order warm and ambient so that warm shows up first in
# plotting
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)
```

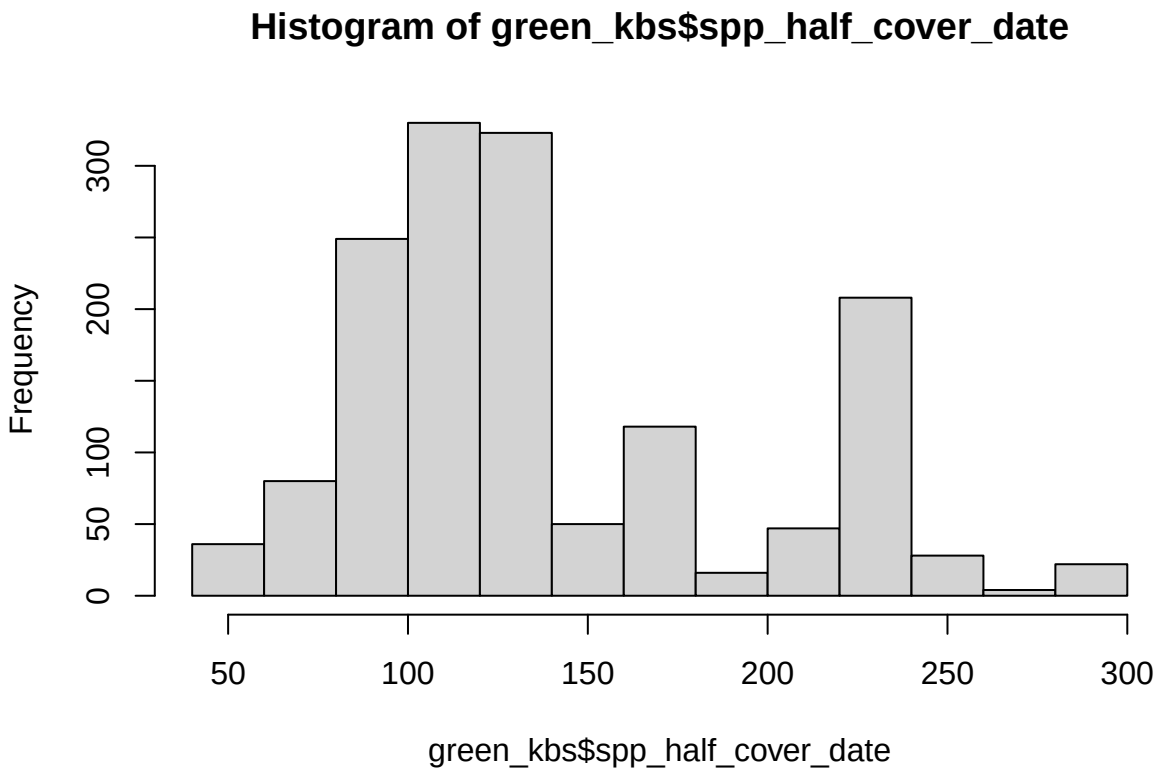
```
## [1] "warmed"  "ambient"
```

```
# 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
greenup$year_factor <- as.factor(greenup$year_factor)  # having year as numerical was messing with some

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
greenupp$year_factor <- as.factor(greenupp$year_factor)

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

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

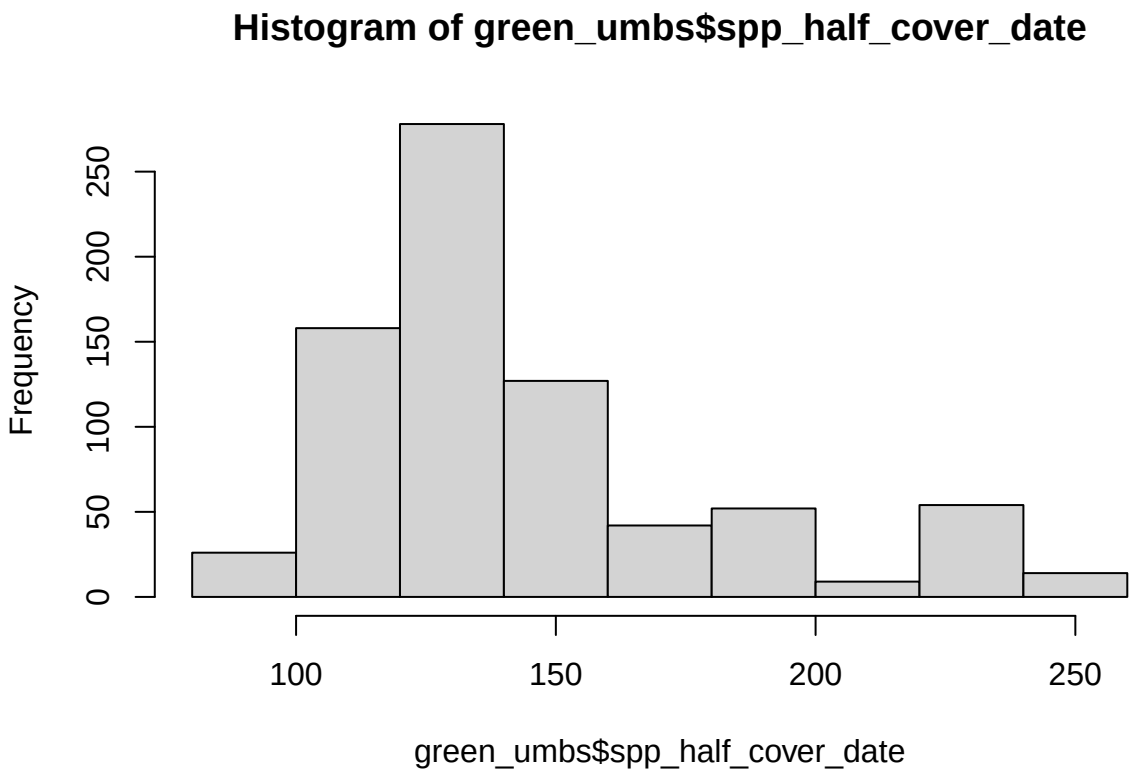
Data Exploration:

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.

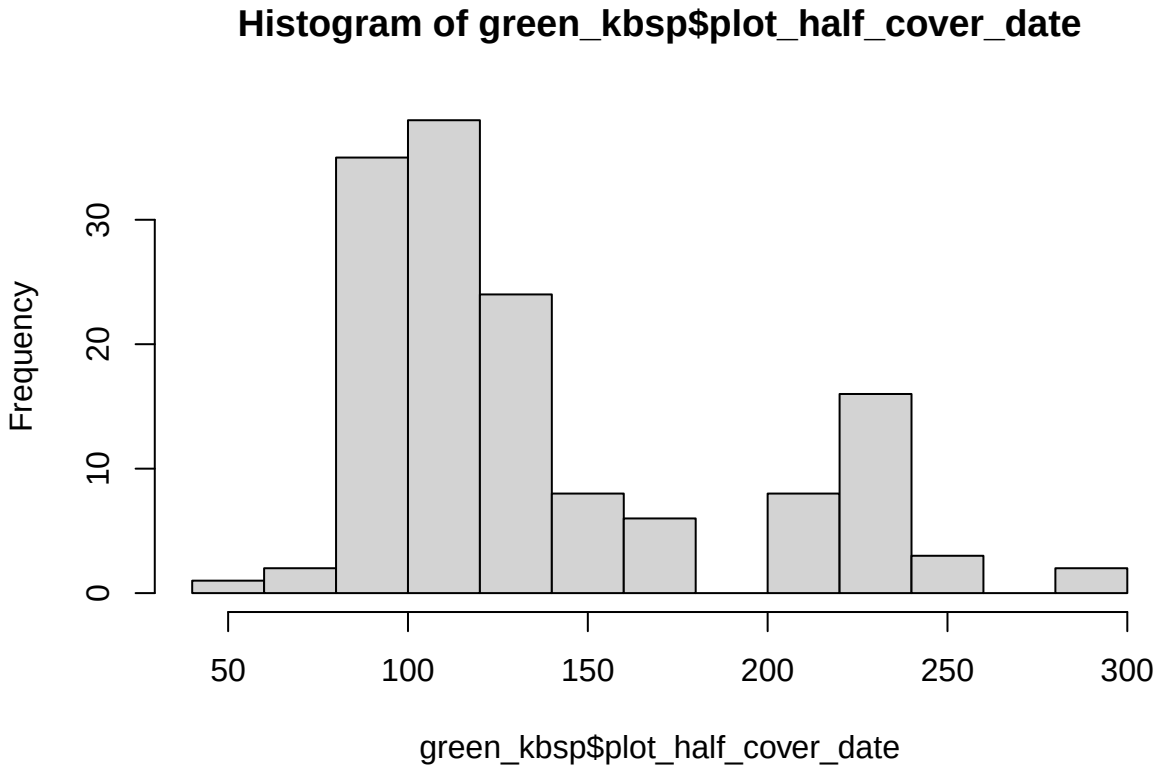
```
# species level
hist(green_kbs$spp_half_cover_date)
```



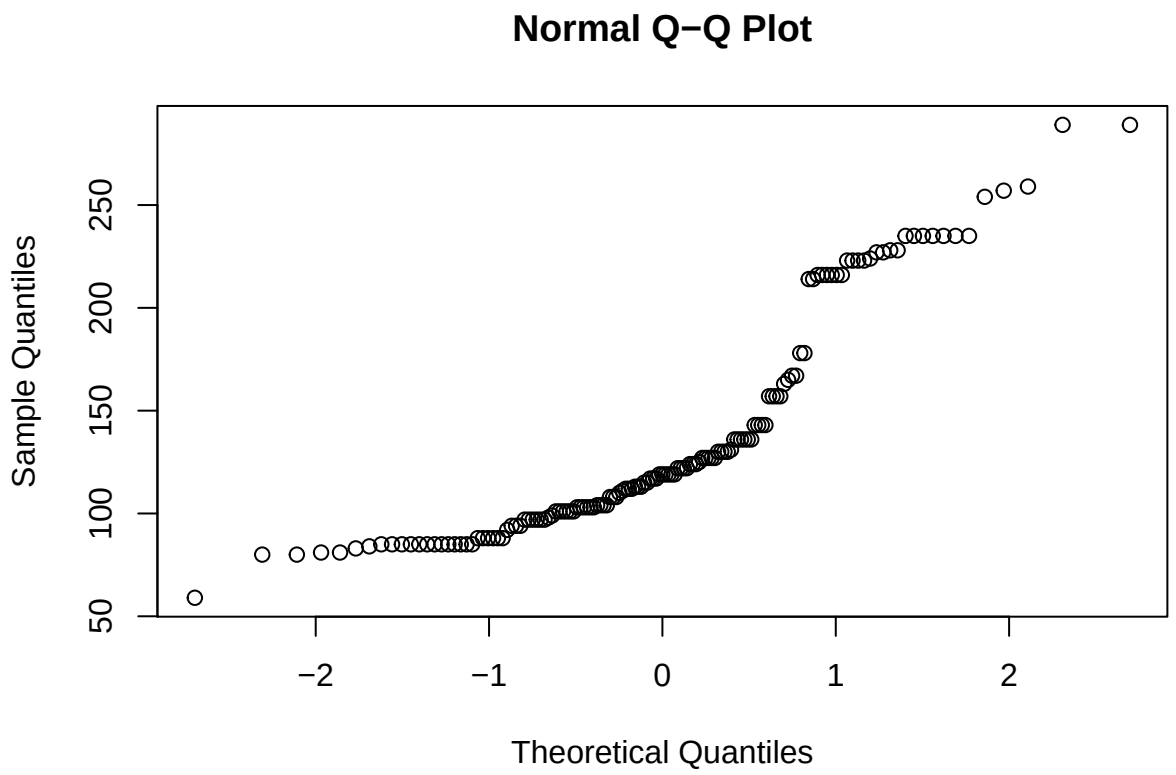

```
hist(green_umbs$spp_half_cover_date)
```




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



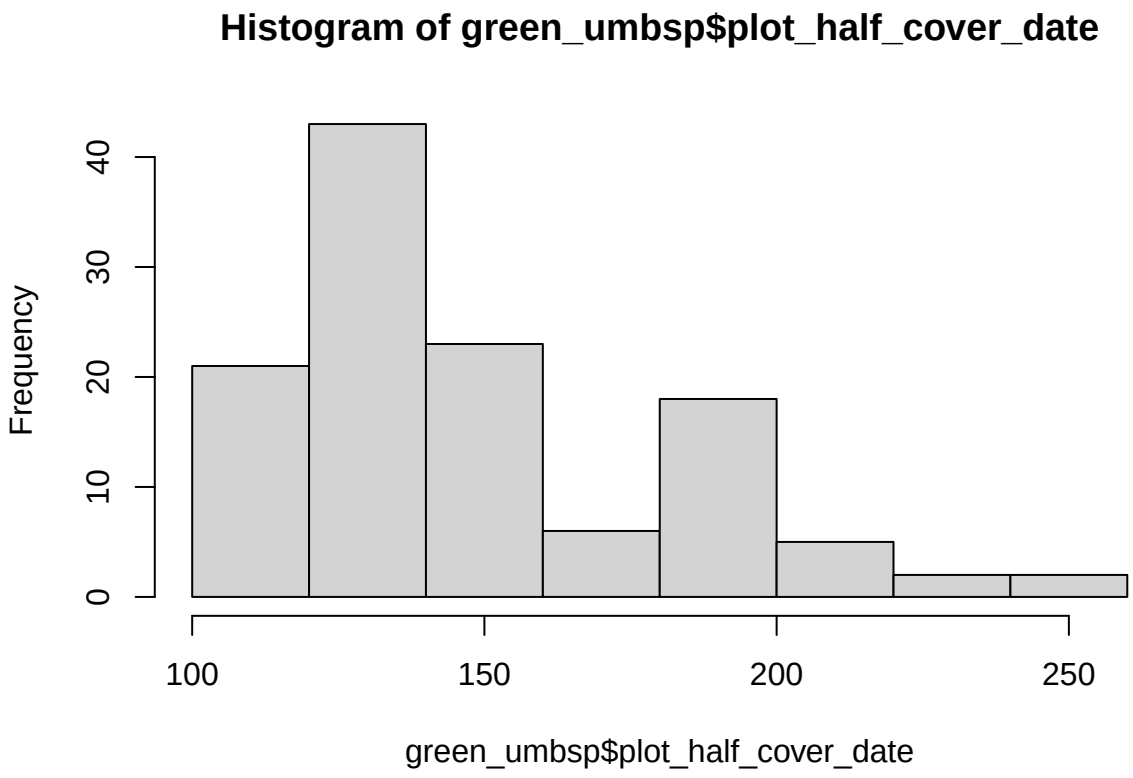
```
qqnorm(green_kbsp$plot_half_cover_date)
```



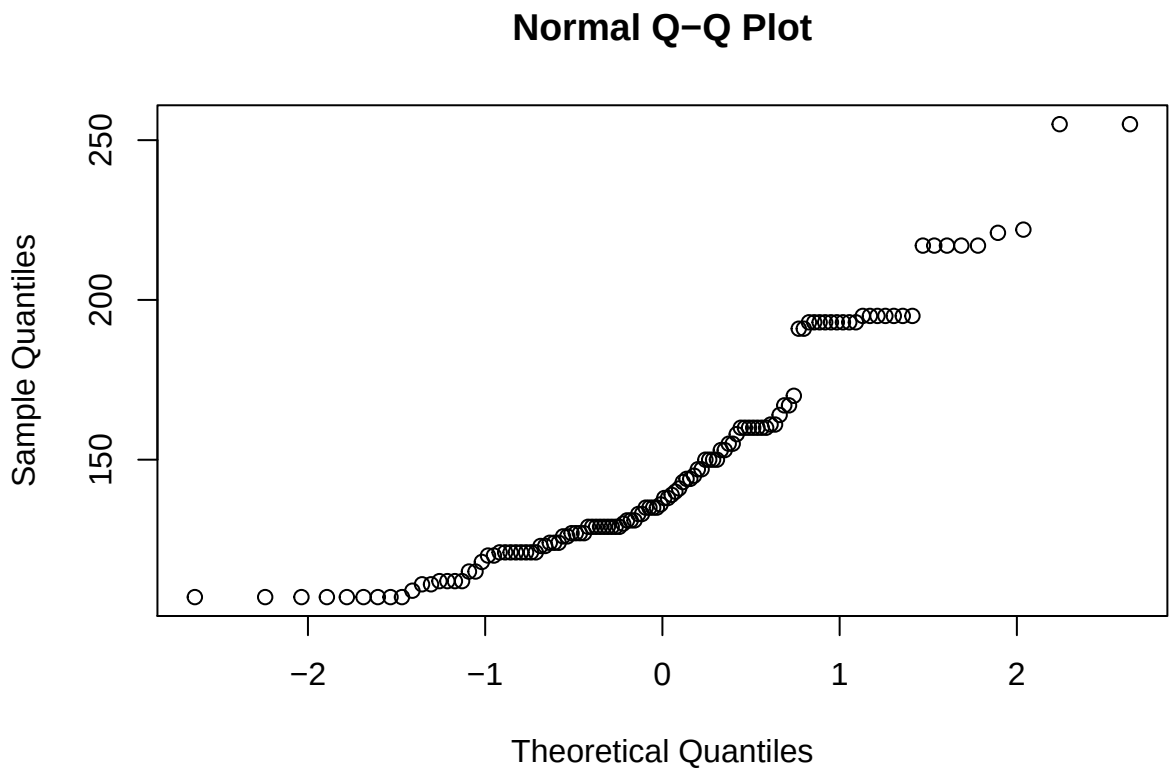

```
shapiro.test(green_kbsp$plot_half_cover_date)
```

```
##
##  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)
```

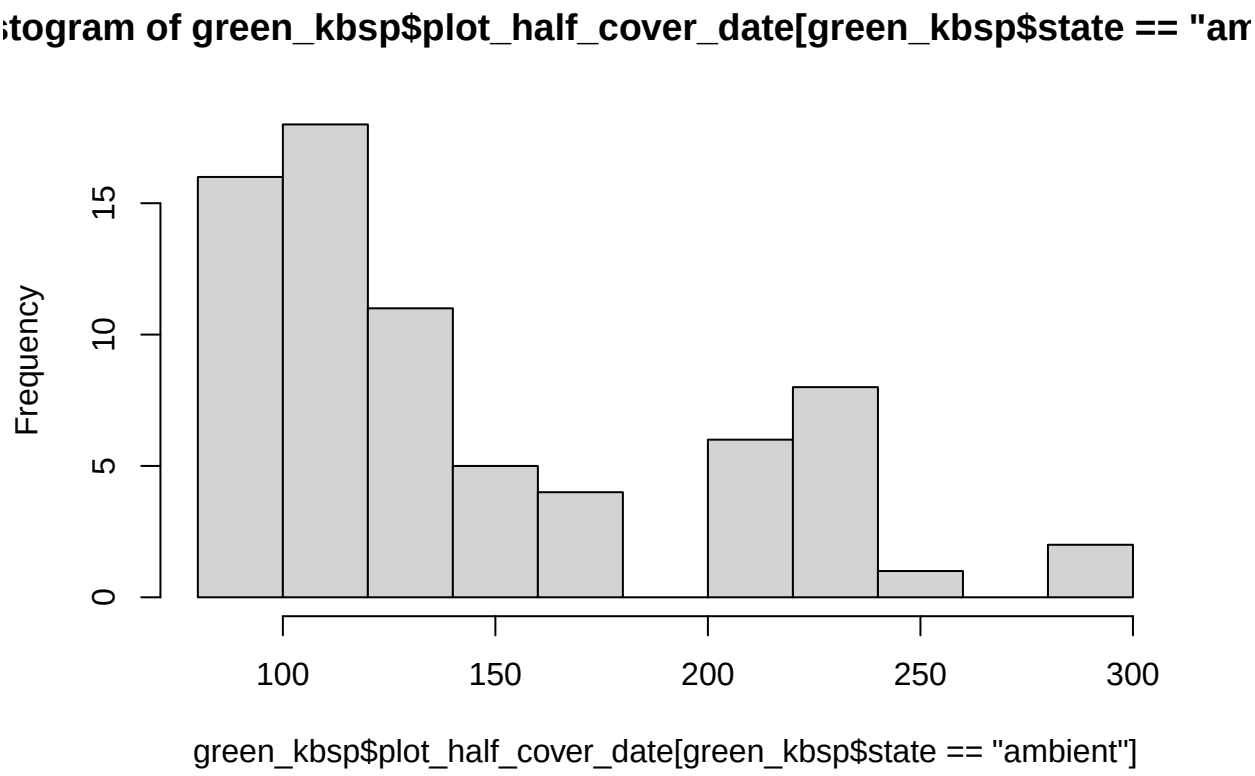



```
shapiro.test(green_umbsp$plot_half_cover_date)
```

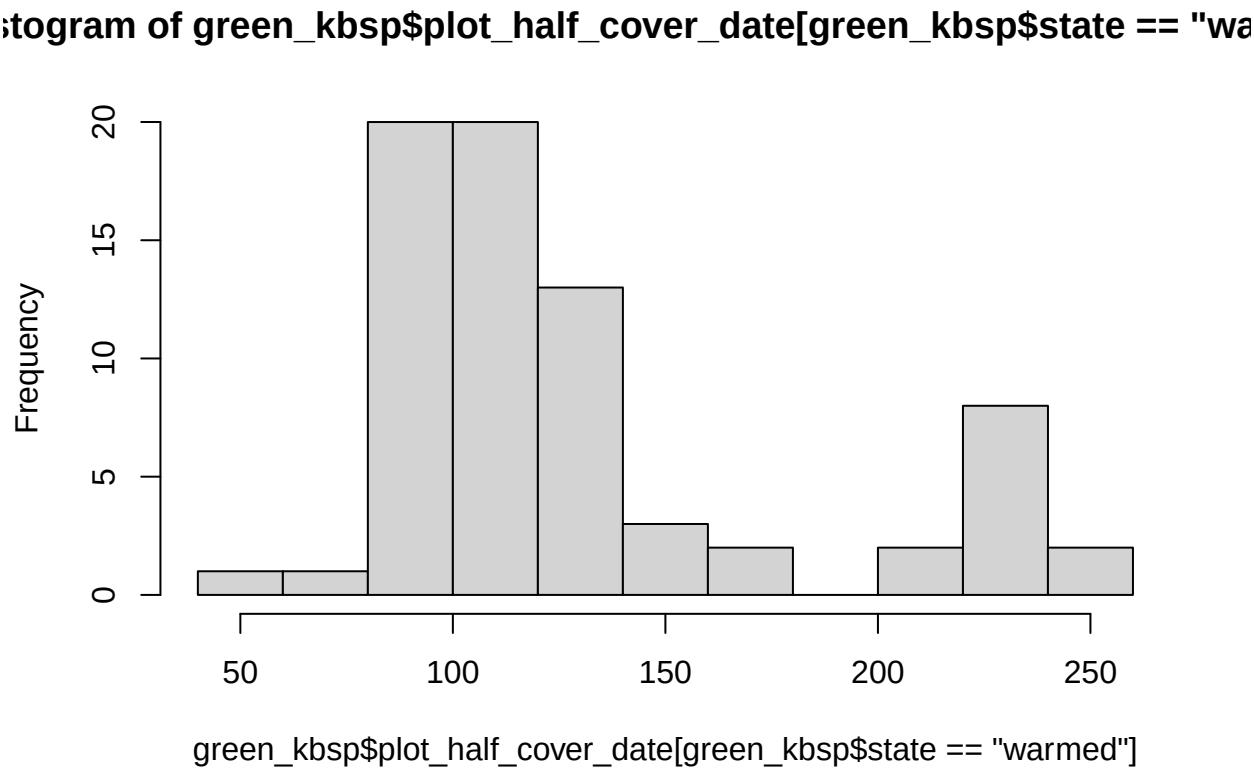
```
##
```

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

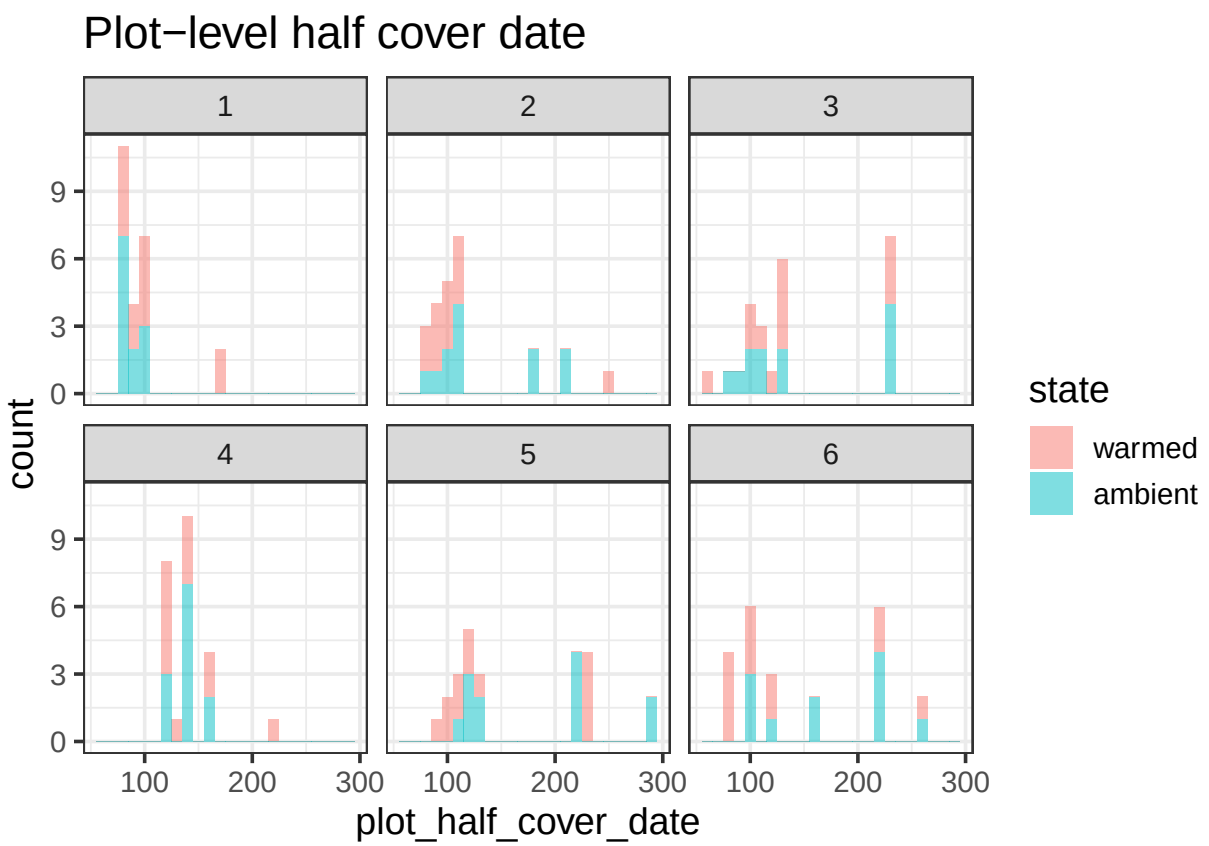
```
# histograms for each treatment separately - plot level
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "ambient"])
```



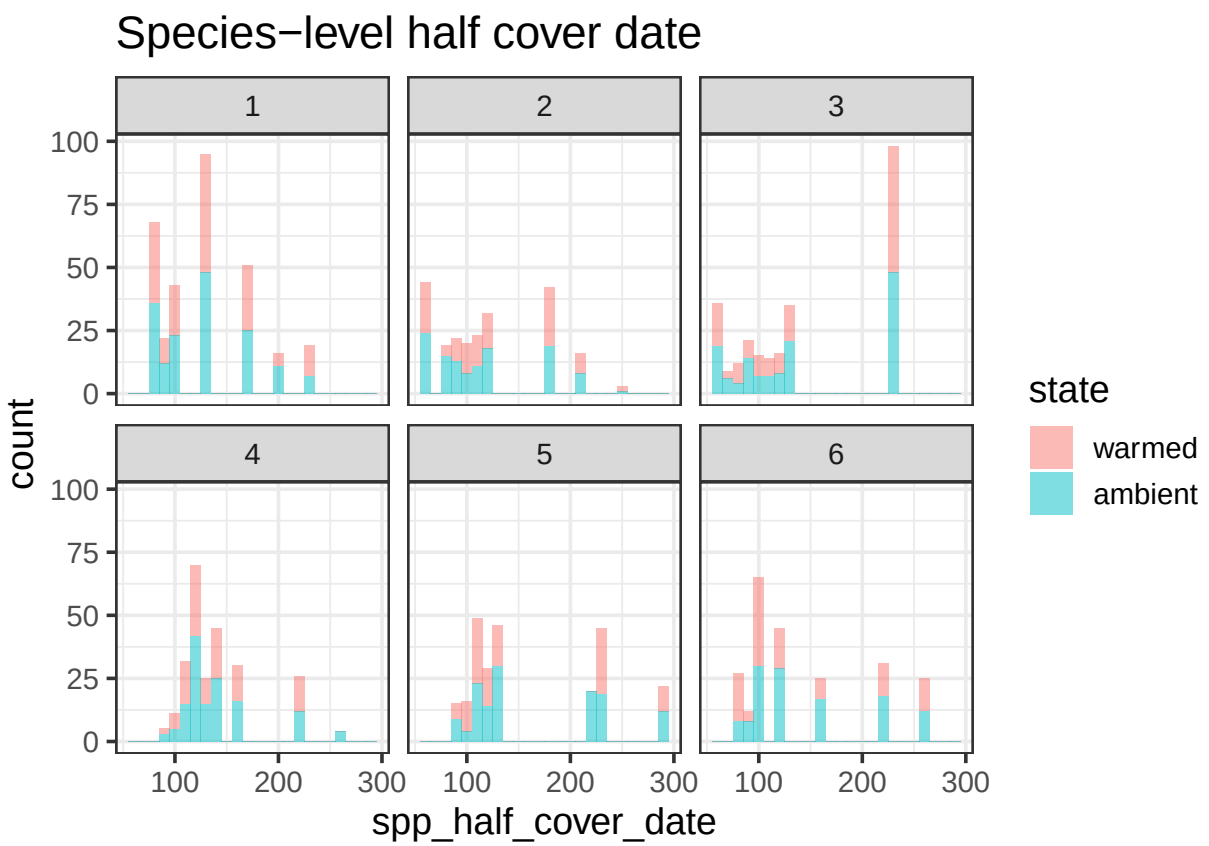

```
hist(green_kbsp$plot_half_cover_date[green_kbsp$state == "warmed"])
```



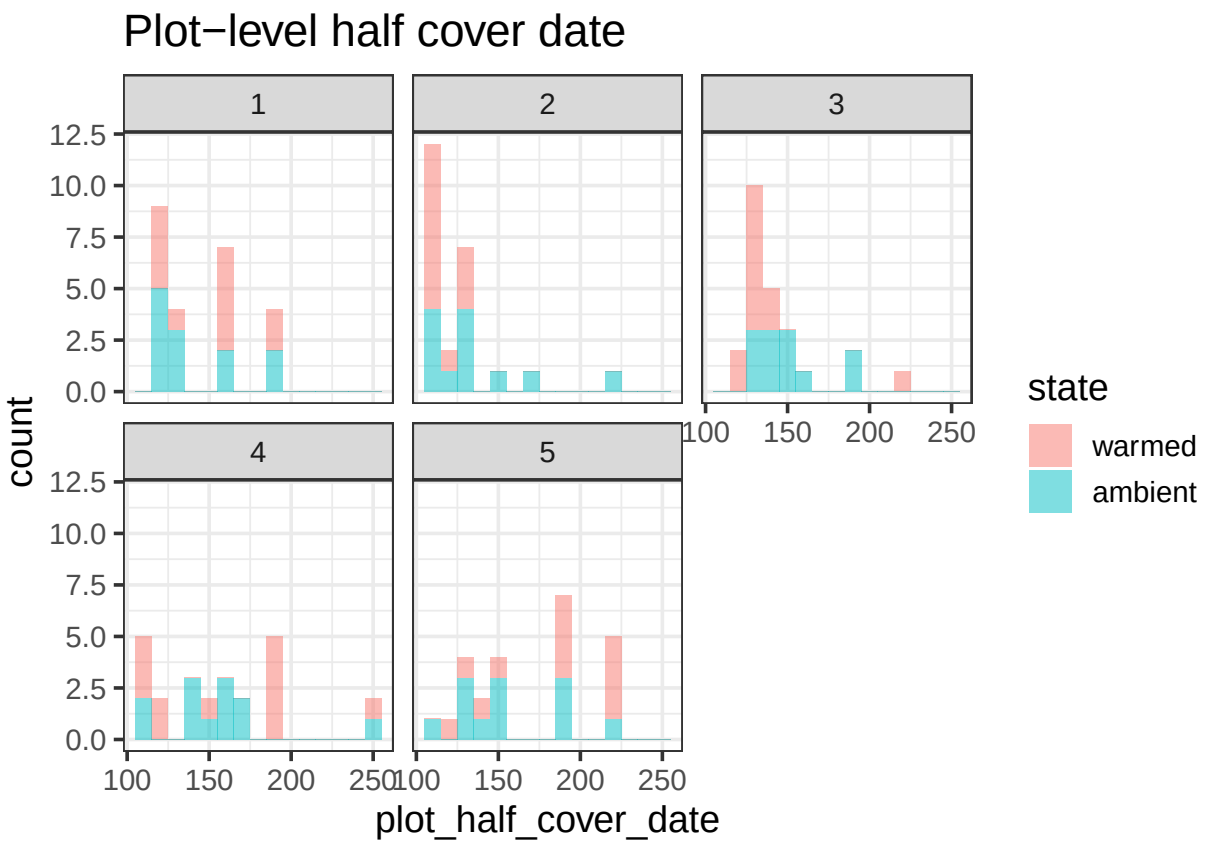

```
# histograms for each year - look at them together:
p1 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



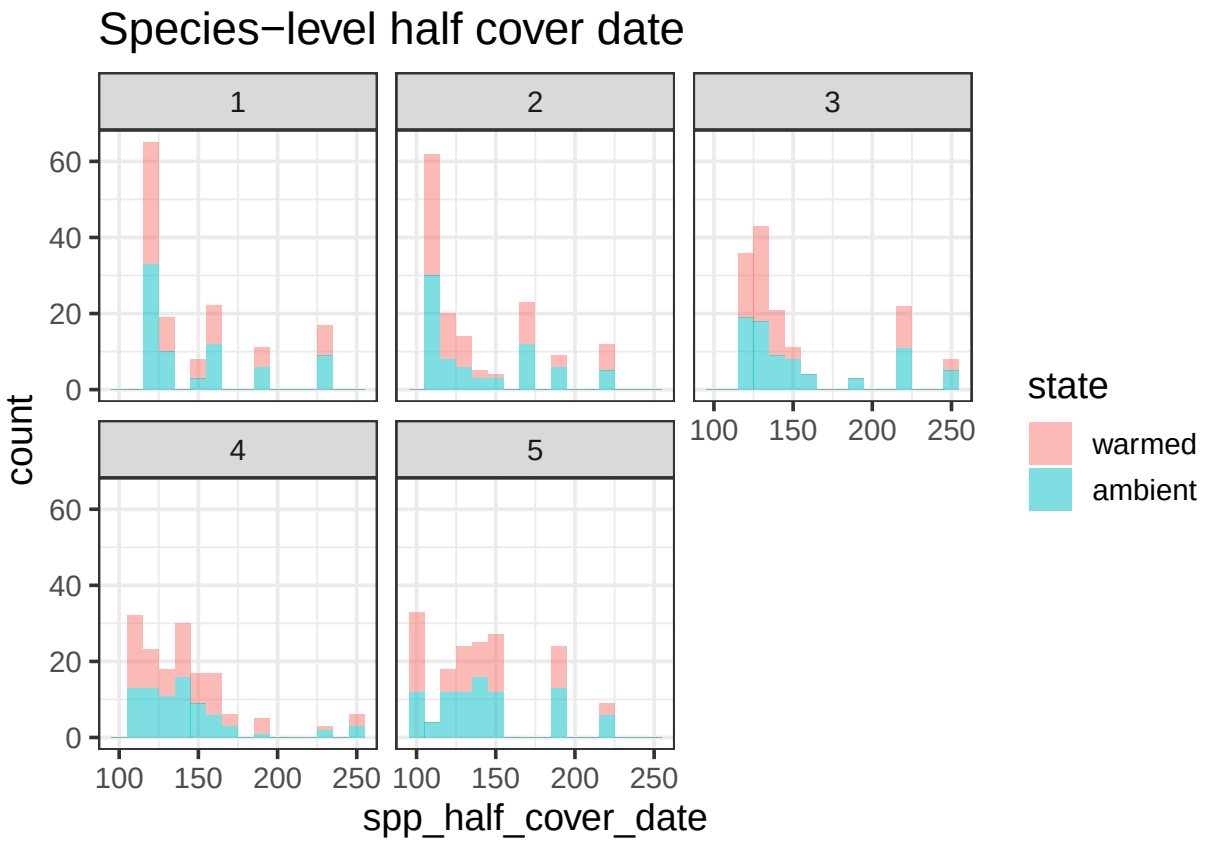

```
p1.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



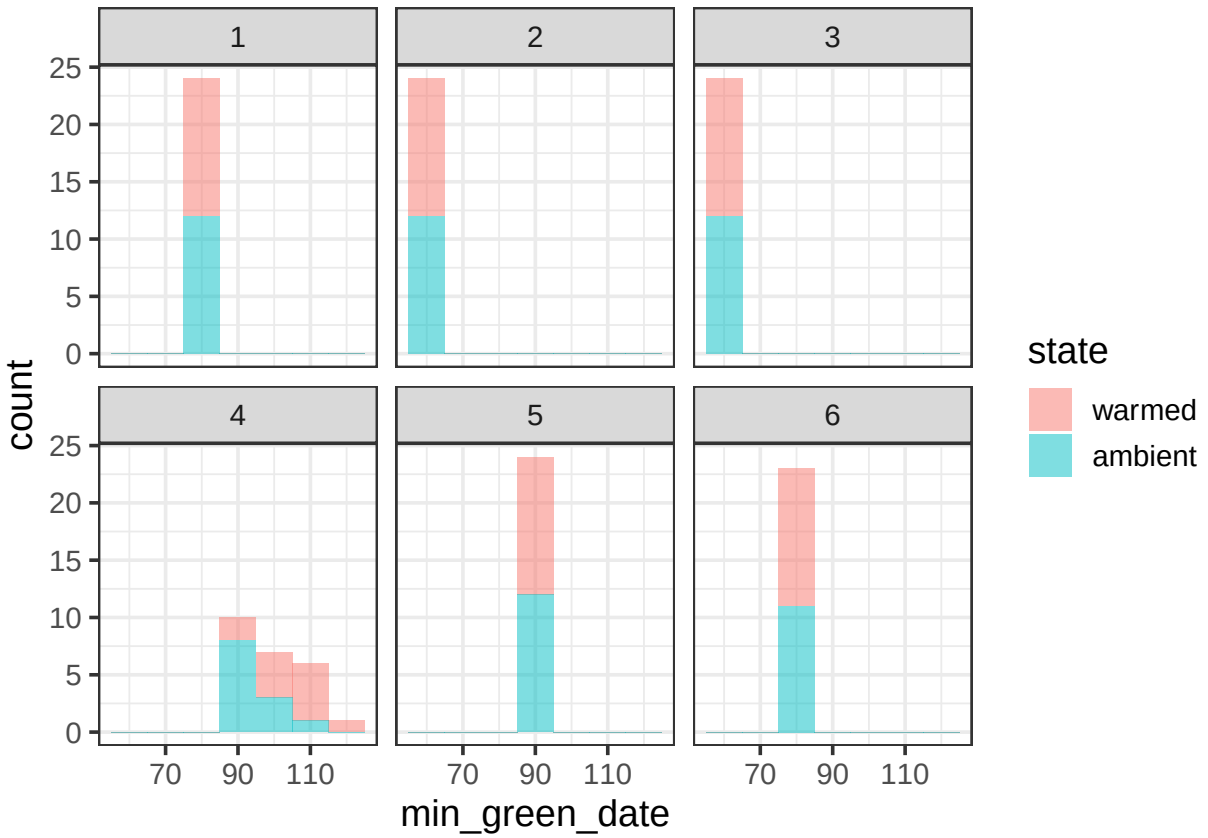

```
p1u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



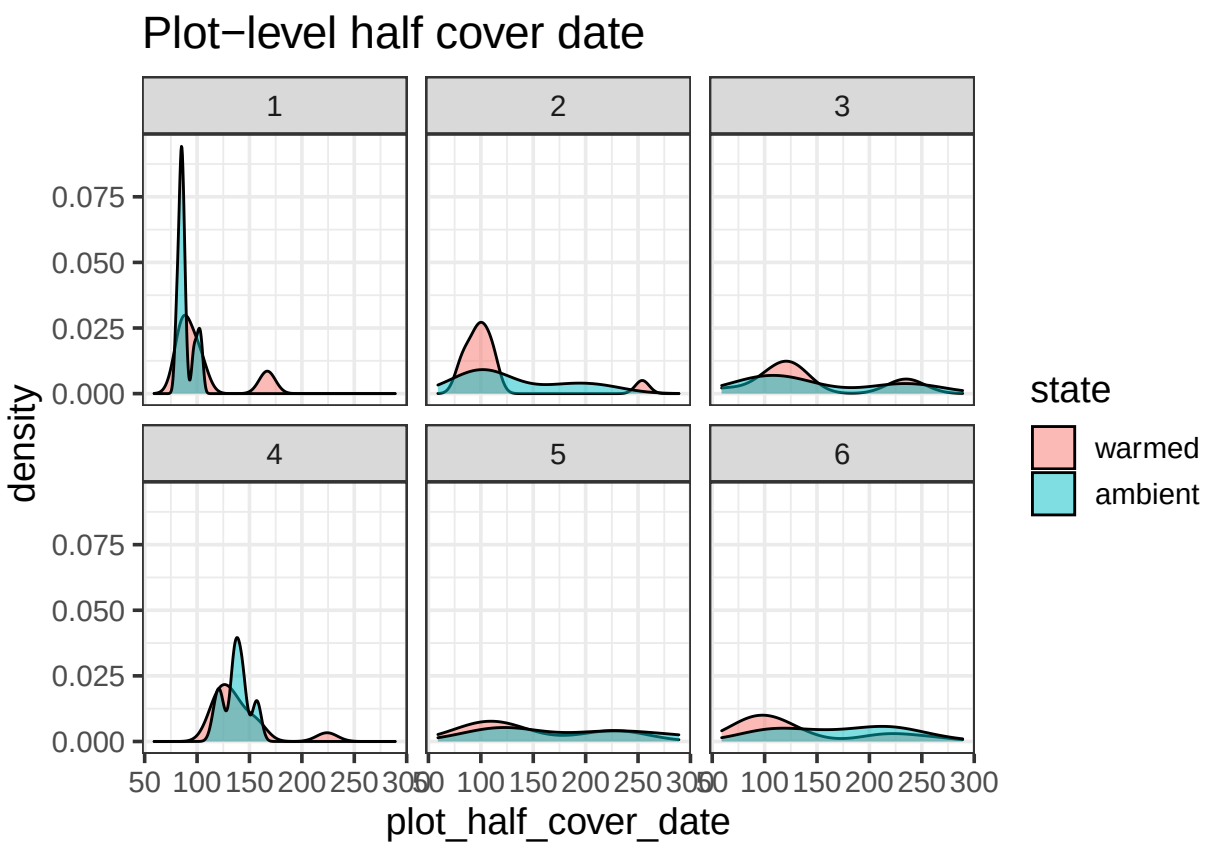

```
p1.2u <- ggplot(data = green_umbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_histogram(alpha = 0.5, binwidth = 10)
p1.2u + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



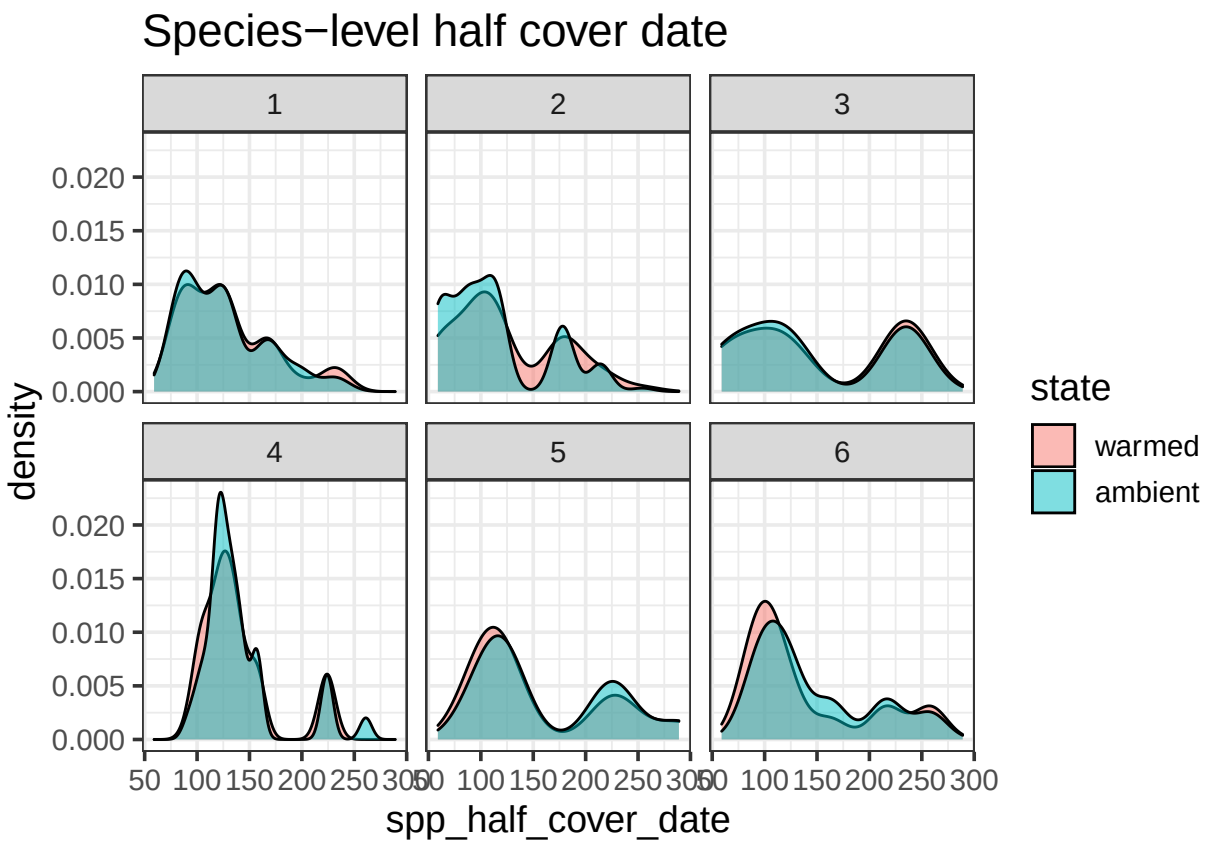

```
# this will just show sampling date artifact
p2 <- ggplot(data = green_kbsp, aes(x = min_green_date, fill = state)) +
    geom_histogram(alpha = 0.5, binwidth = 10)
p2 + facet_wrap(~year_factor)
```



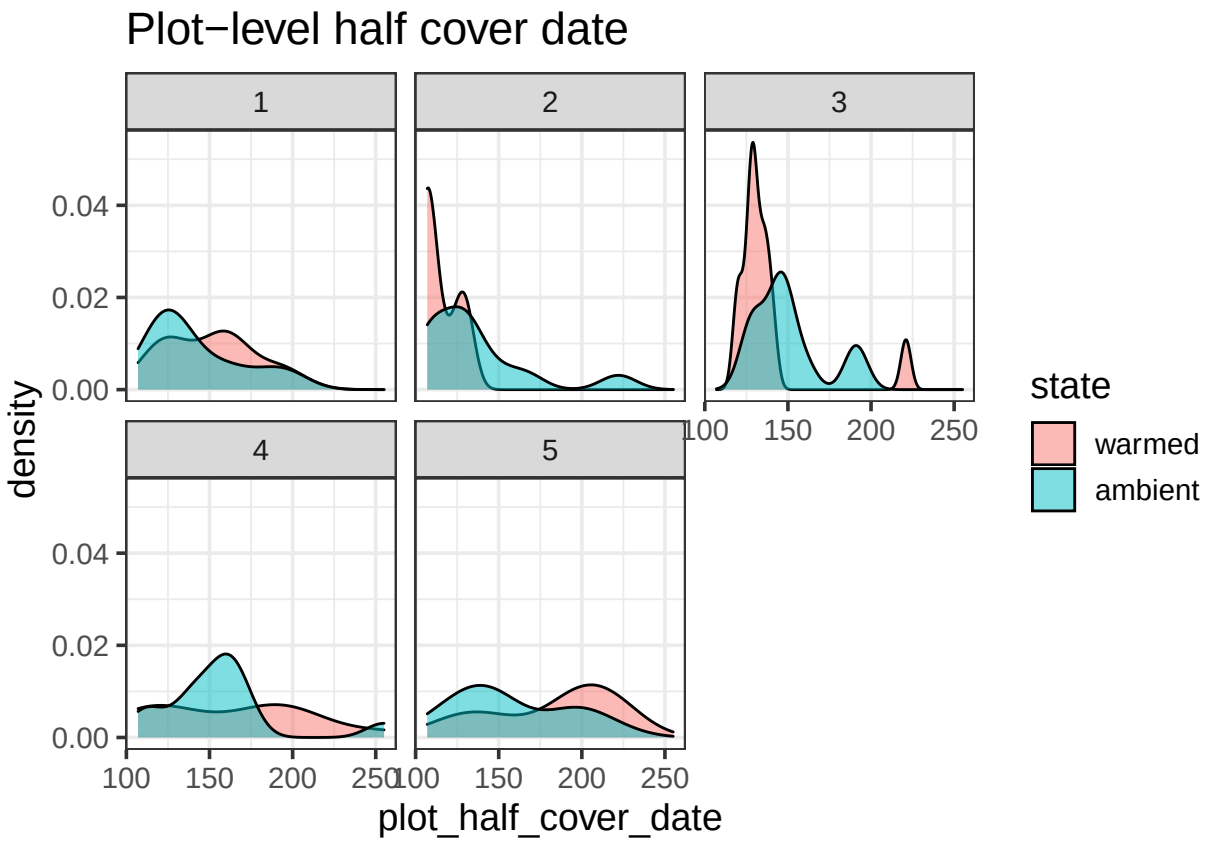

```
# Density plot
p3 <- ggplot(data = green_kbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3 + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```



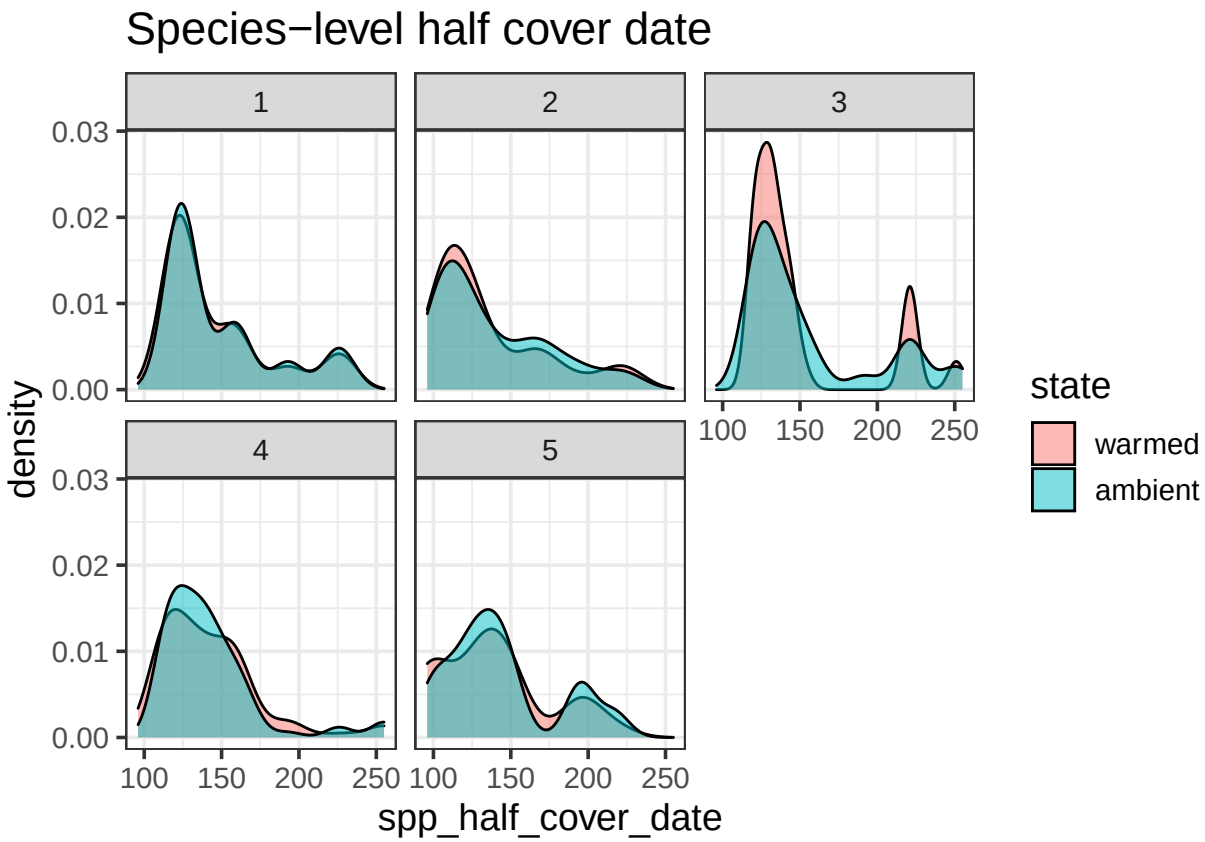

```
p3.2 <- ggplot(data = green_kbs, aes(x = spp_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3.2 + facet_wrap(~year_factor) + labs(title = "Species-level half cover date")
```



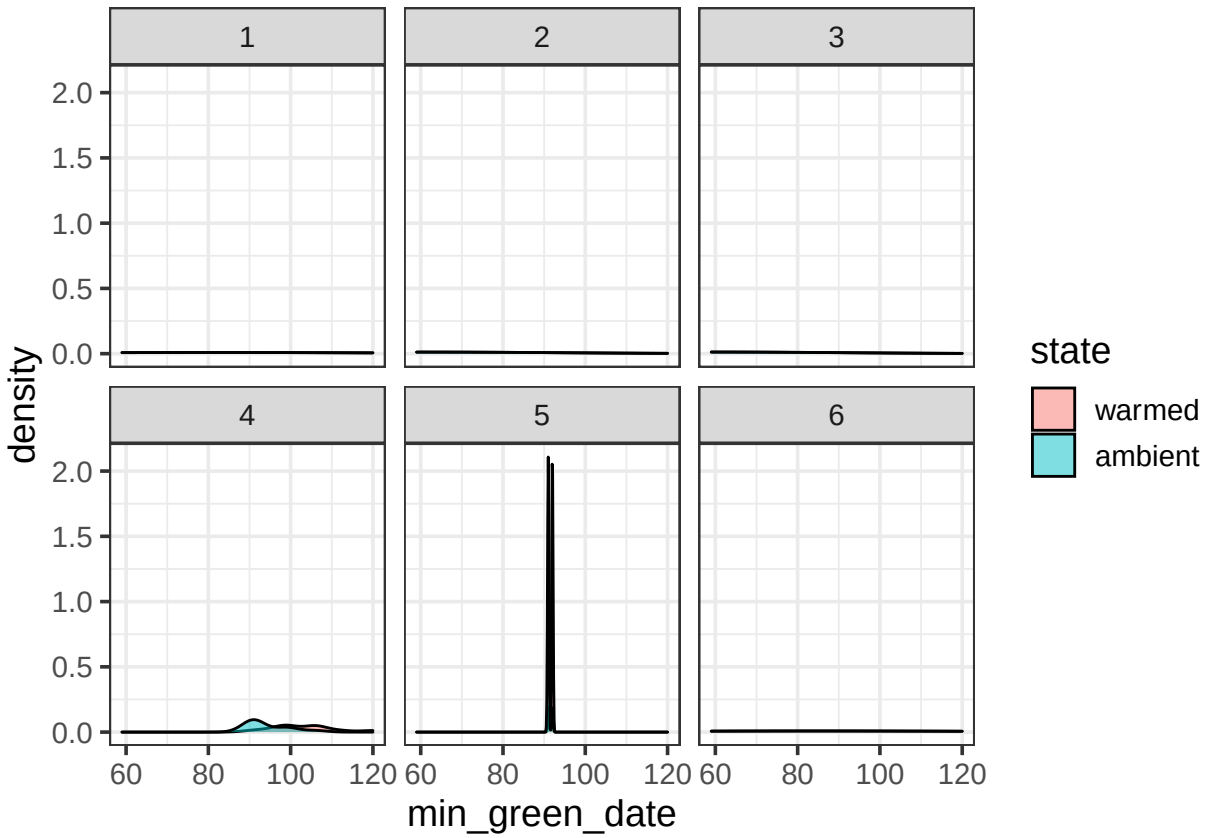

```
p3u <- ggplot(data = green_umbsp, aes(x = plot_half_cover_date,
    fill = state)) + geom_density(alpha = 0.5)
p3u + facet_wrap(~year_factor) + labs(title = "Plot-level half cover date")
```




```
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)
```




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

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

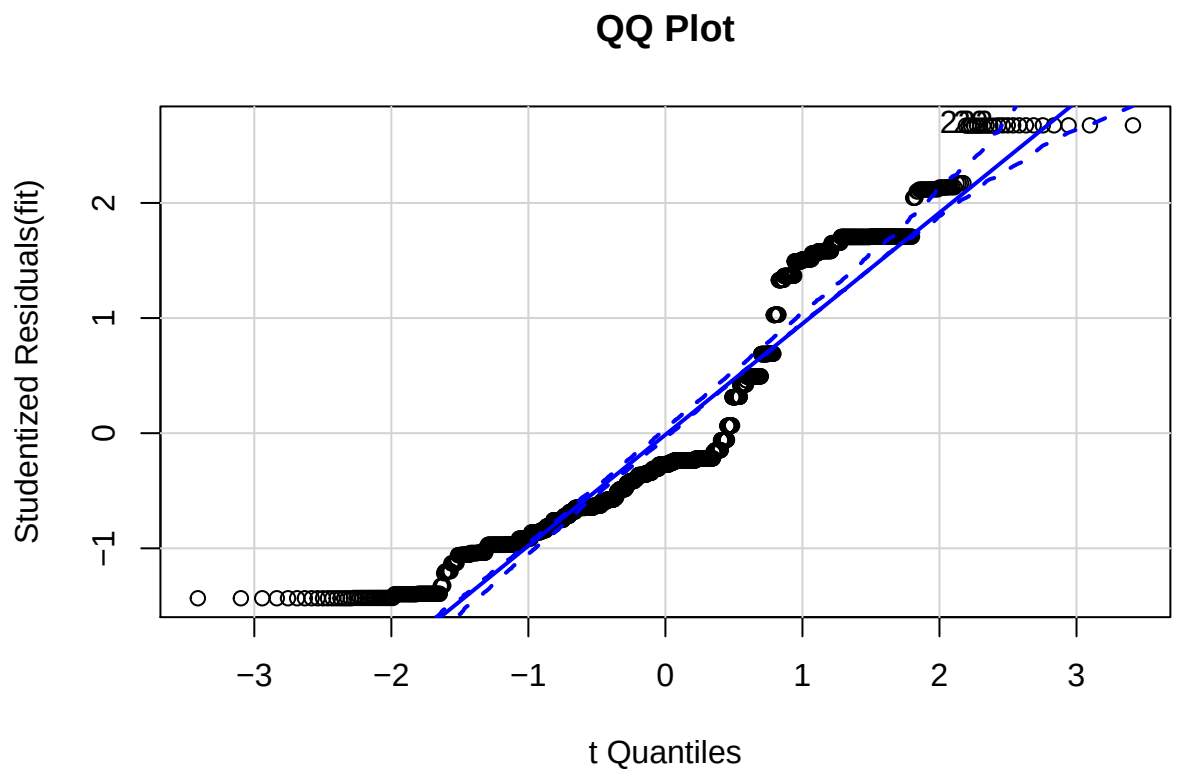
Leverage plots and detecting Outliers. https://www.statmethods.net/stats/rdiagnostics.html

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/species/year -
# 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
```

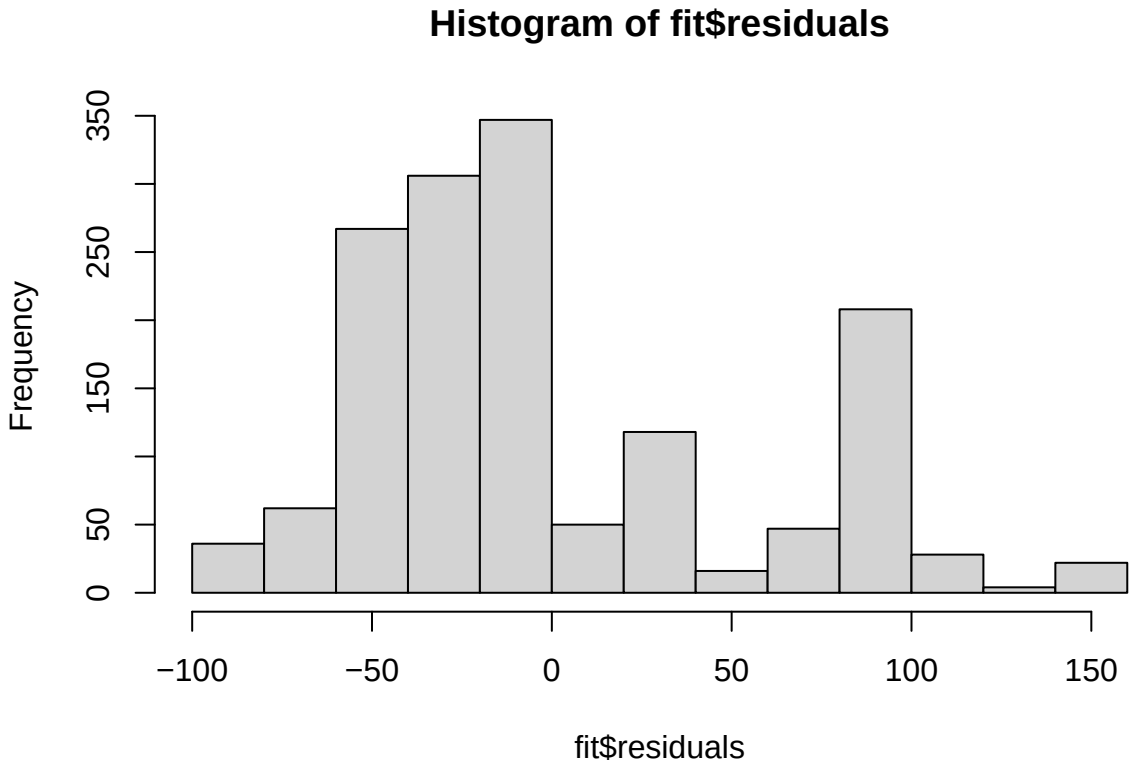
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 29 2.673942          0.0075775           NA
```

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

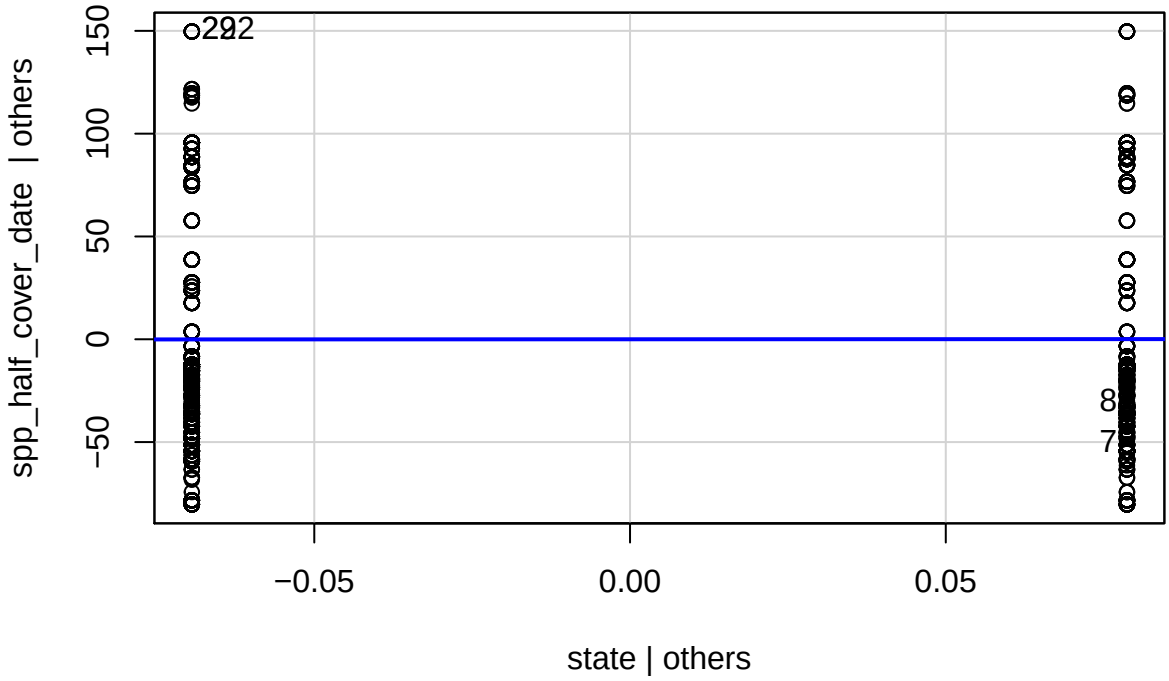



```
##  29 222
##  29 195
```

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



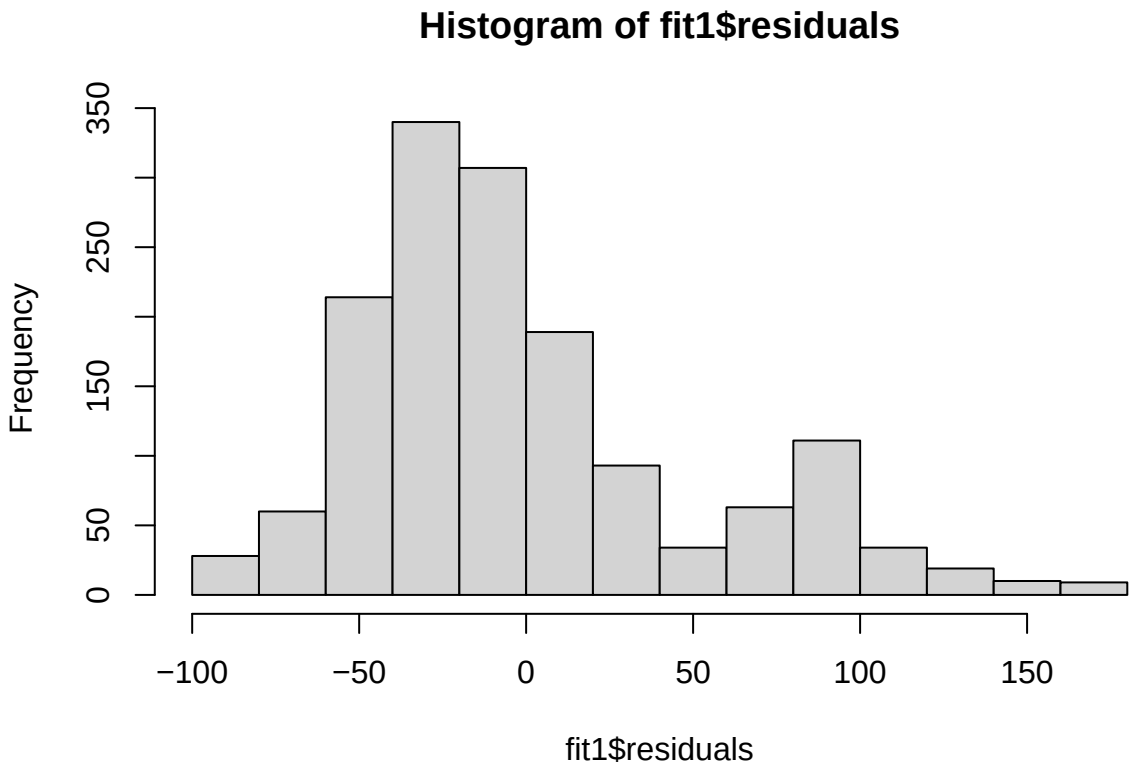
```
leveragePlots(fit)
```



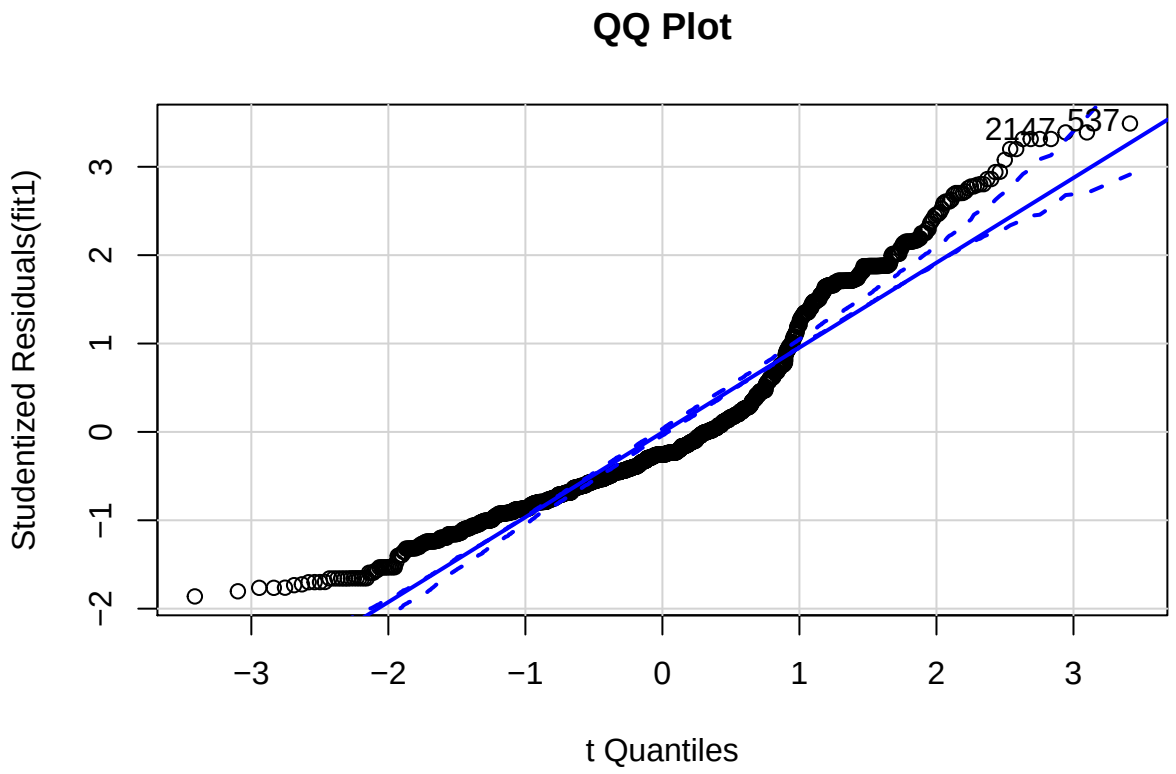

```
# KBS State and species model
fit1 <- lm(spp_half_cover_date ~ state + species, data = green_kbs)
outlierTest(fit1)  # no outliers
```

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

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

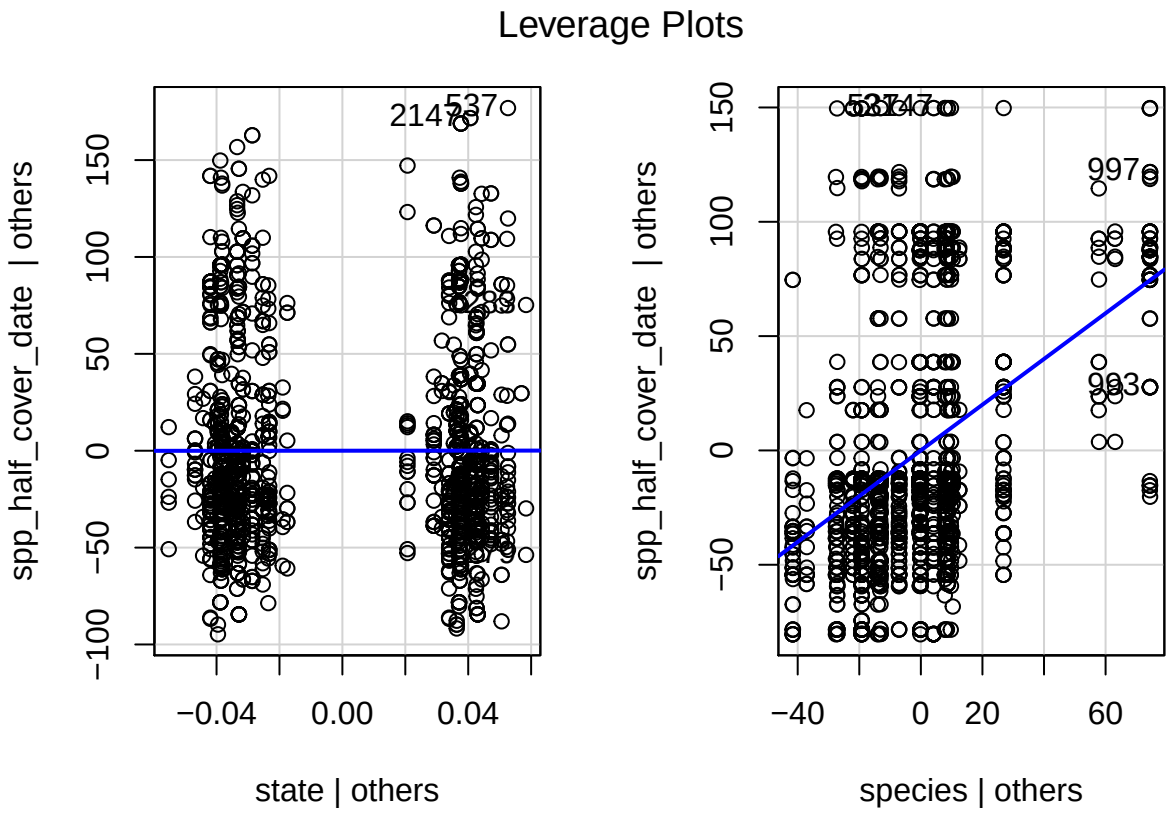



```
qqPlot(fit1, main = "QQ Plot")
```




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

```
leveragePlots(fit1)
```




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

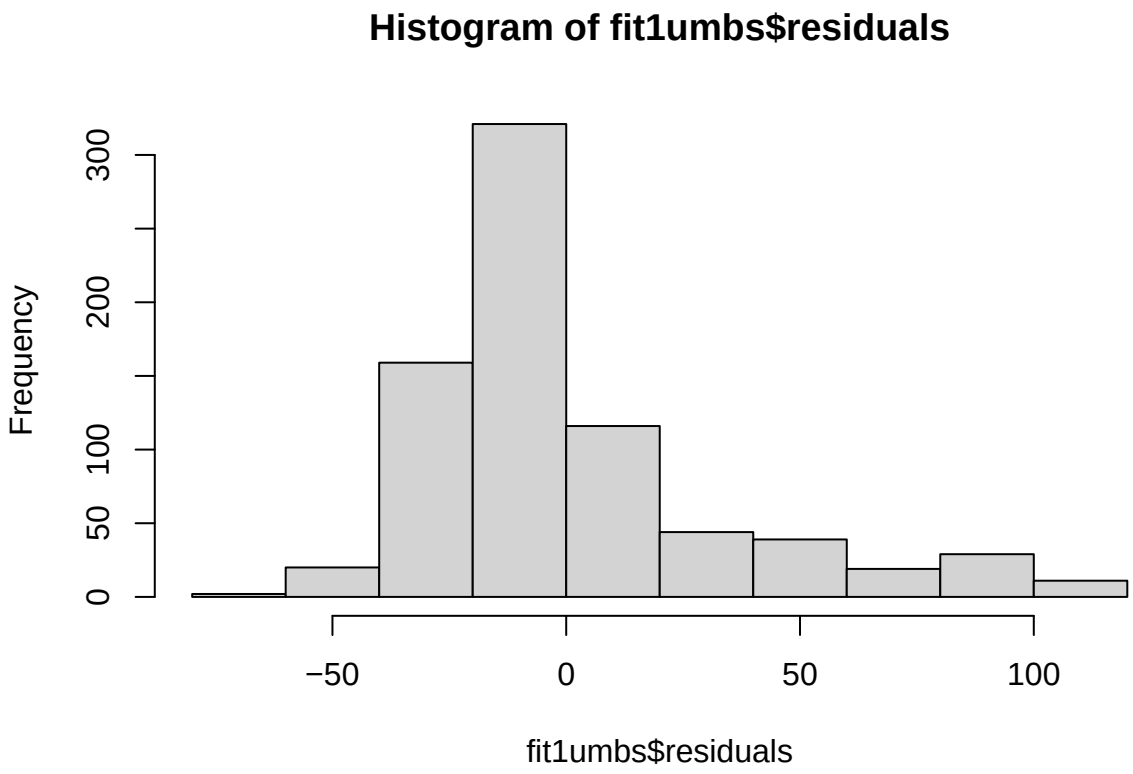
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

```
# UMBS State and species model
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
## 1906 3.595987         0.00034457      0.26187
```

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



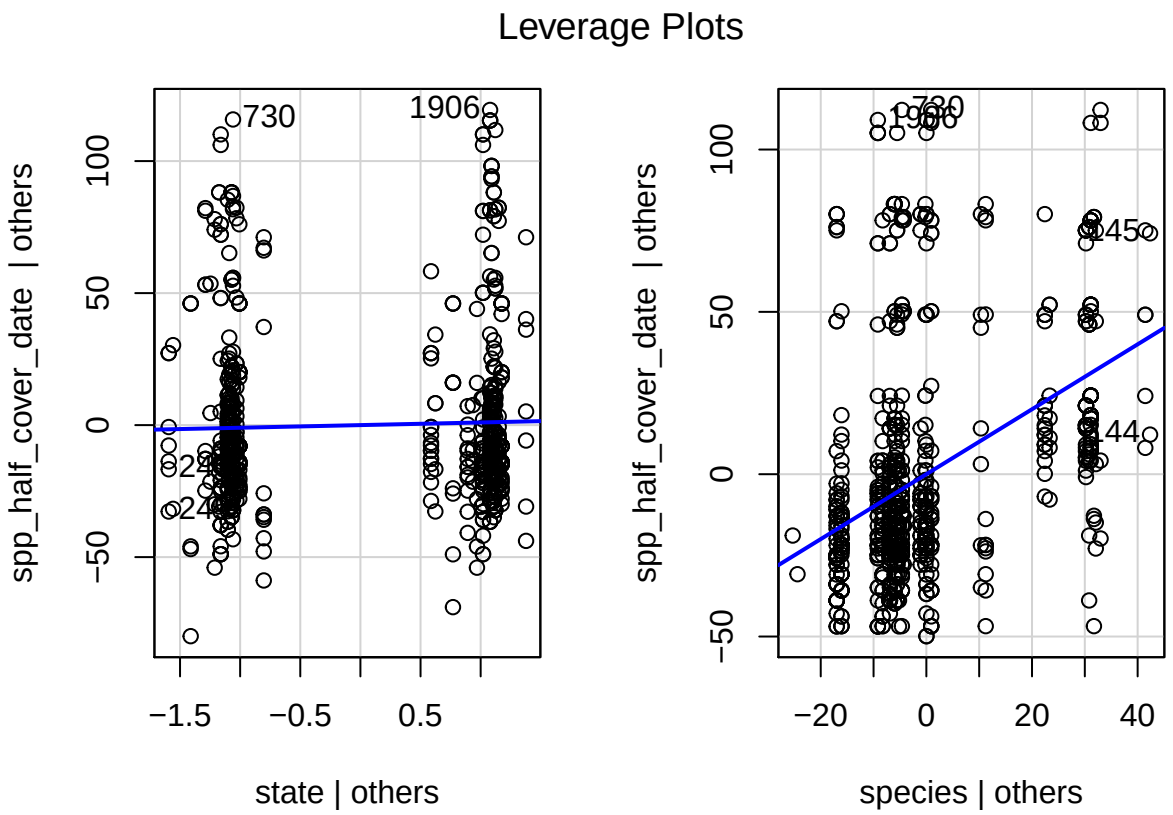

```
qqPlot(fit1umbs, main = "QQ Plot")
```

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


```
##  730 1906
```

```
##  269  668
```

```
leveragePlots(fit1umbs)
```




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

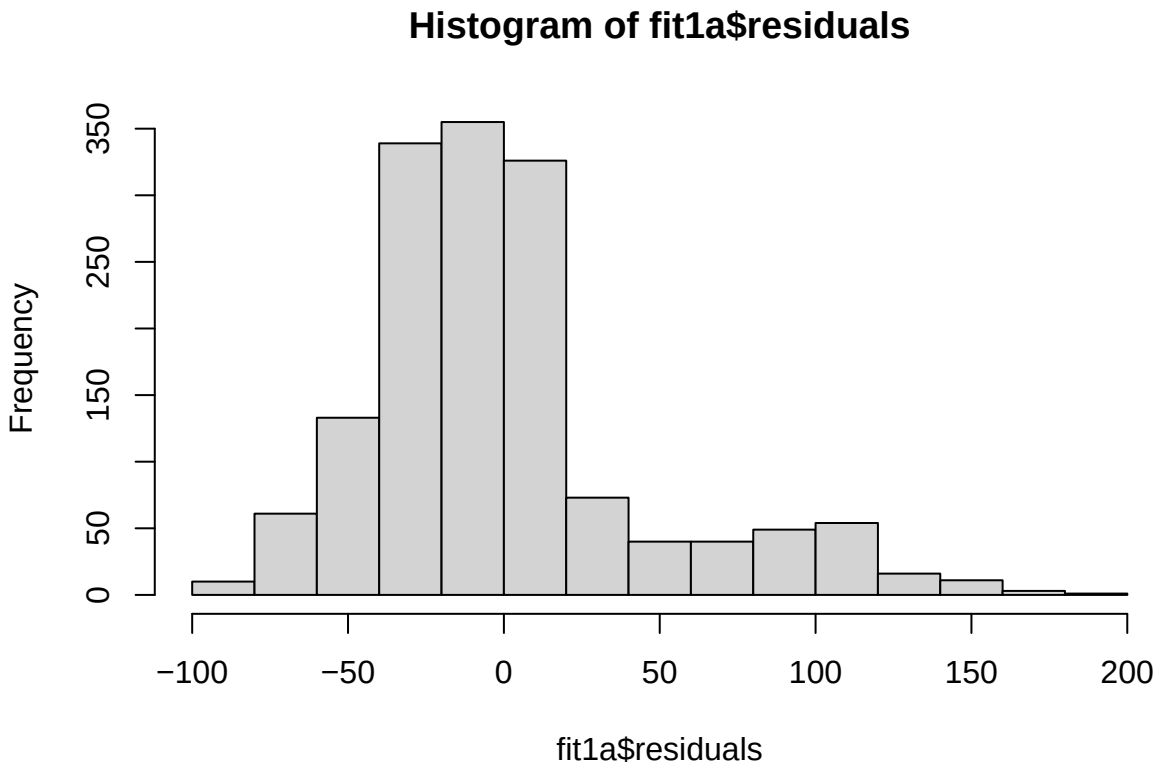
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

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

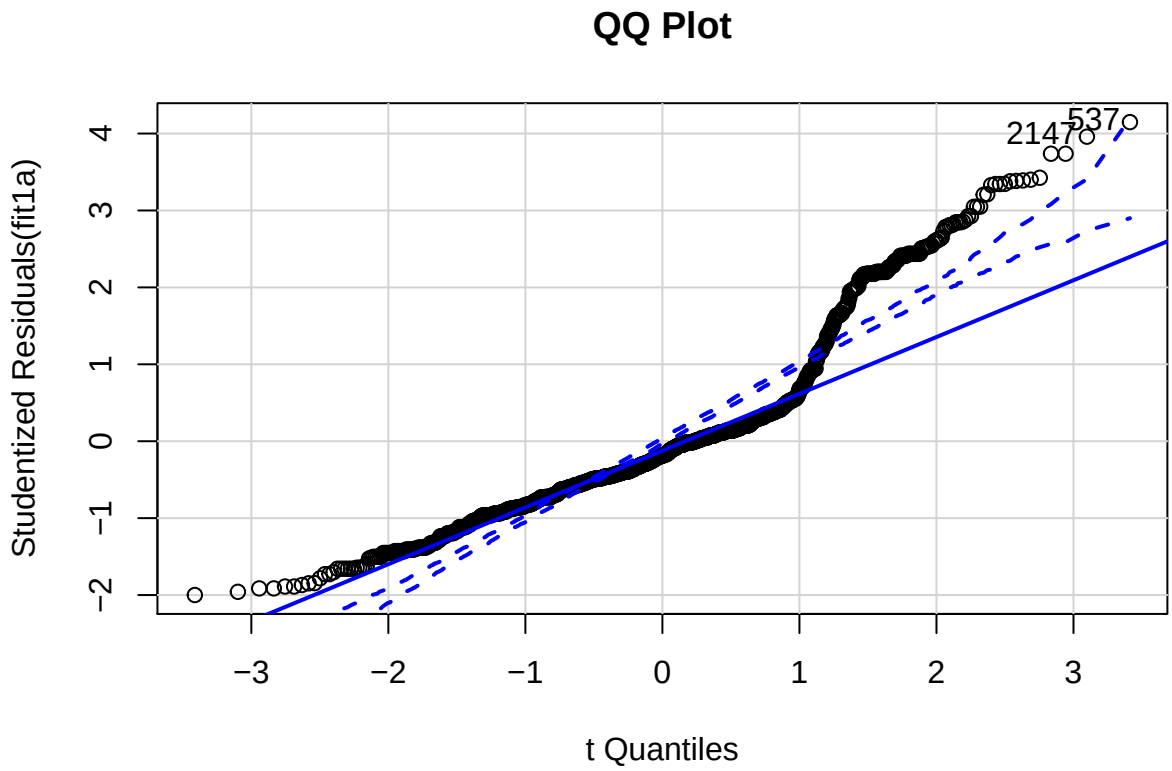
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 537 4.148749         3.5322e-05     0.053372
```

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




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

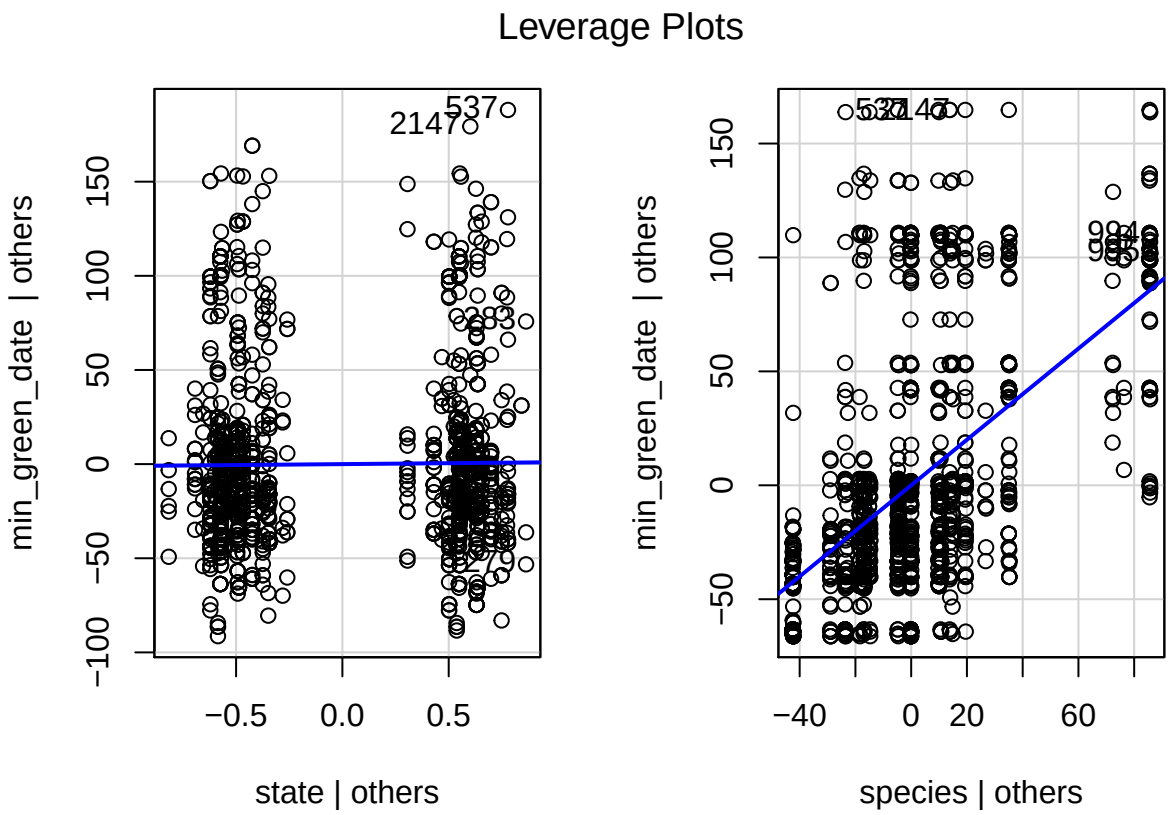
```
## Warning in rlm.default(x, y, weights, method = method, wt.method = wt.method, :
## 'rlm' failed to converge in 20 steps
```



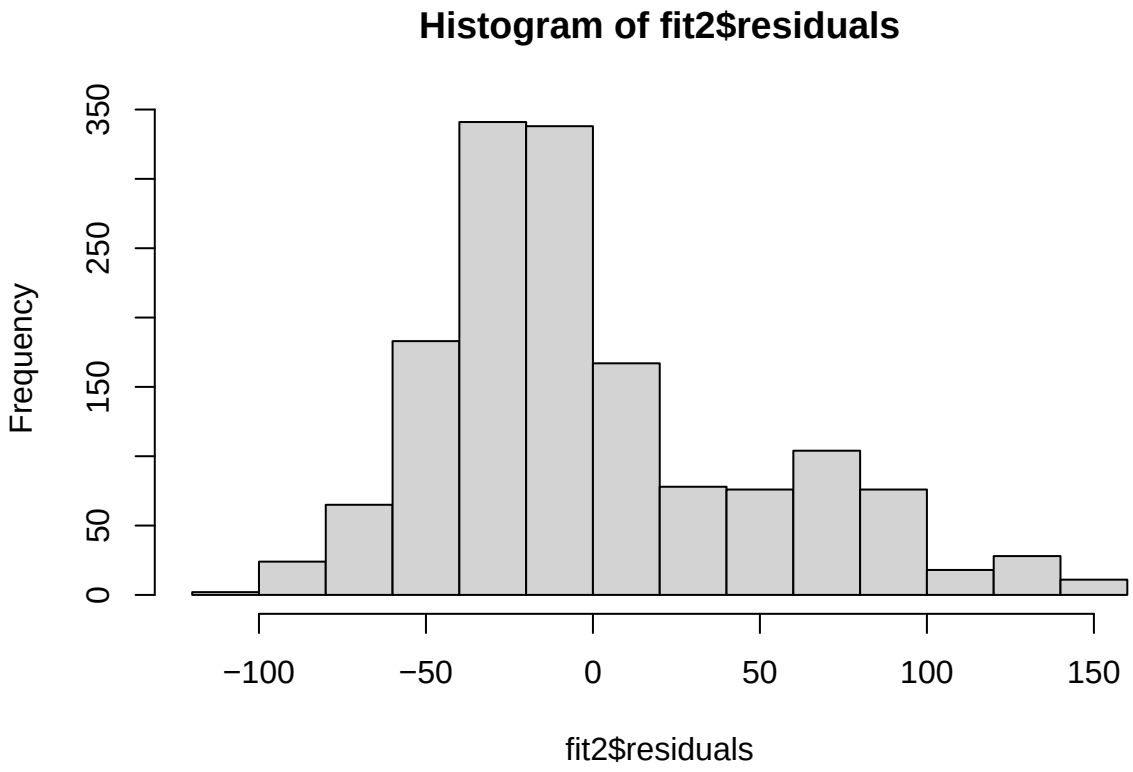

```
##  537 2147
```

```
##  345 1387
```

```
leveragePlots(fit1a)
```



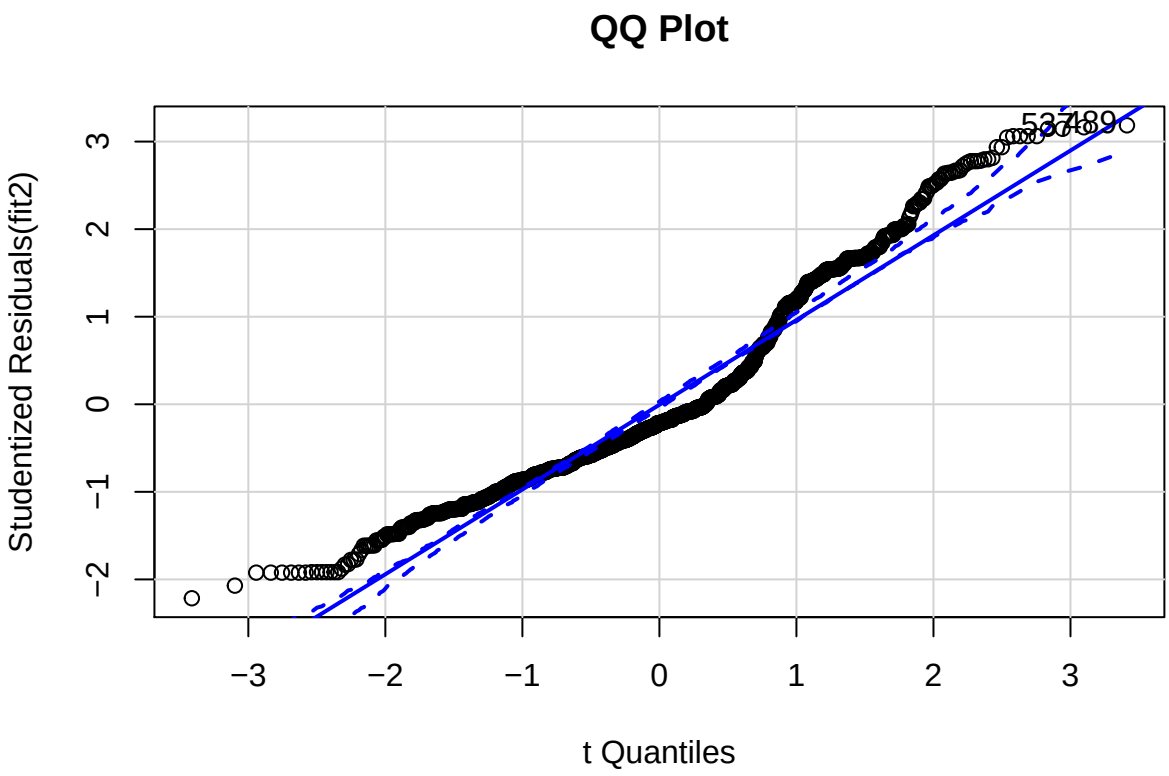

```
# KBS: checking fit for date as a function of state and year
fit2 <- lm(spp_half_cover_date ~ state + species + year_factor,
    data = green_kbs)
hist(fit2$residuals)
```




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

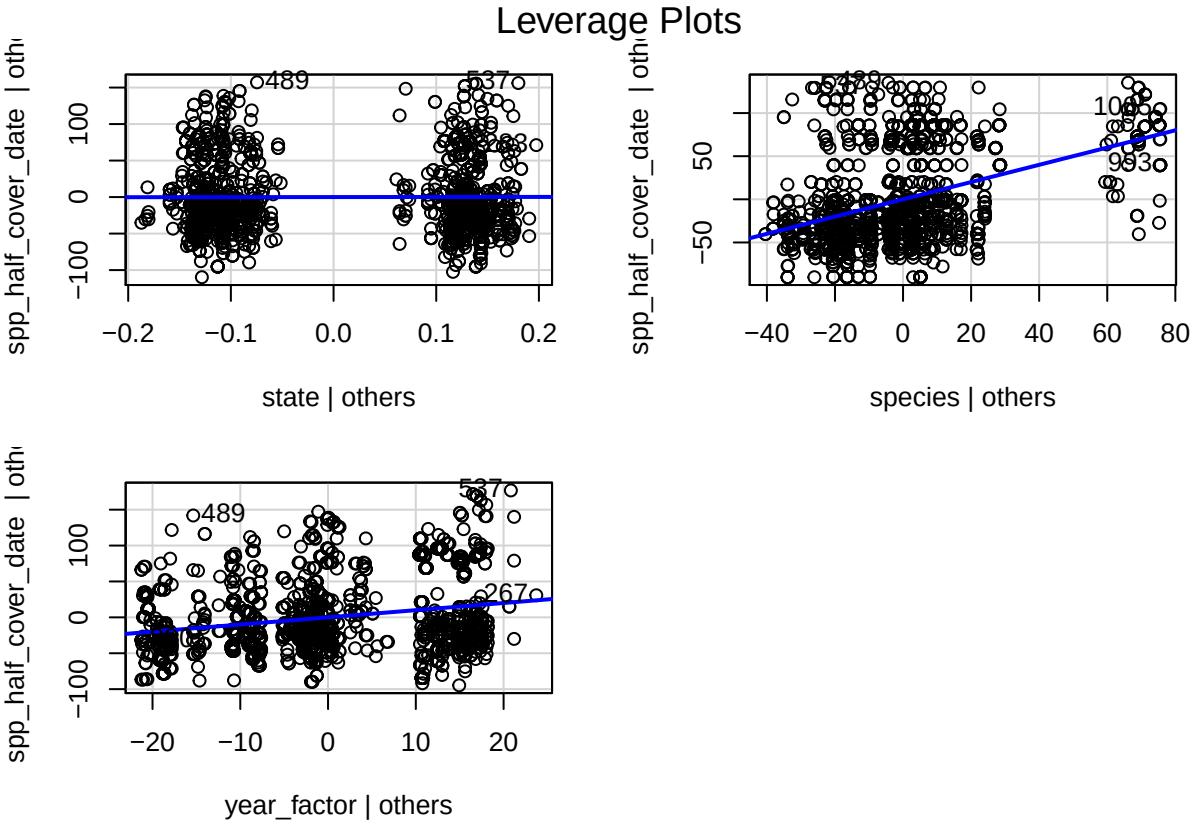
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 489 3.185508          0.0014751           NA
```

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




```
## 489 537
## 327 345
```

```
leveragePlots(fit2)
```




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

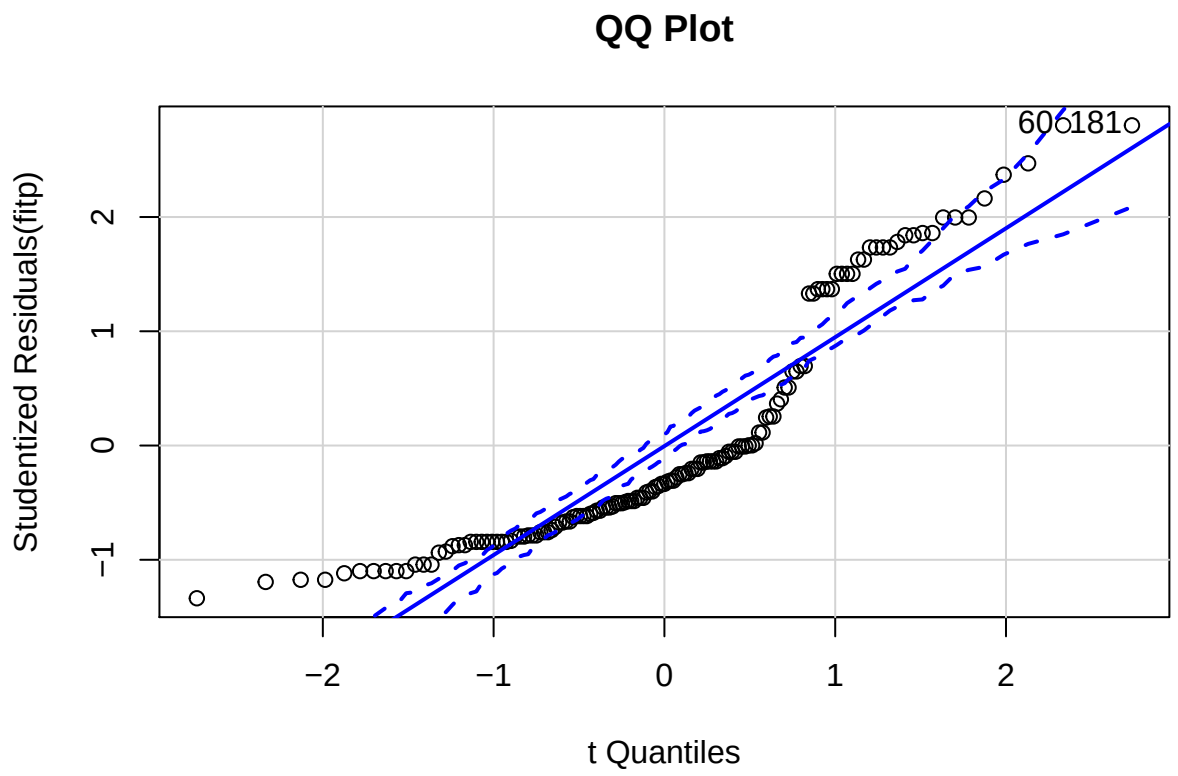
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

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

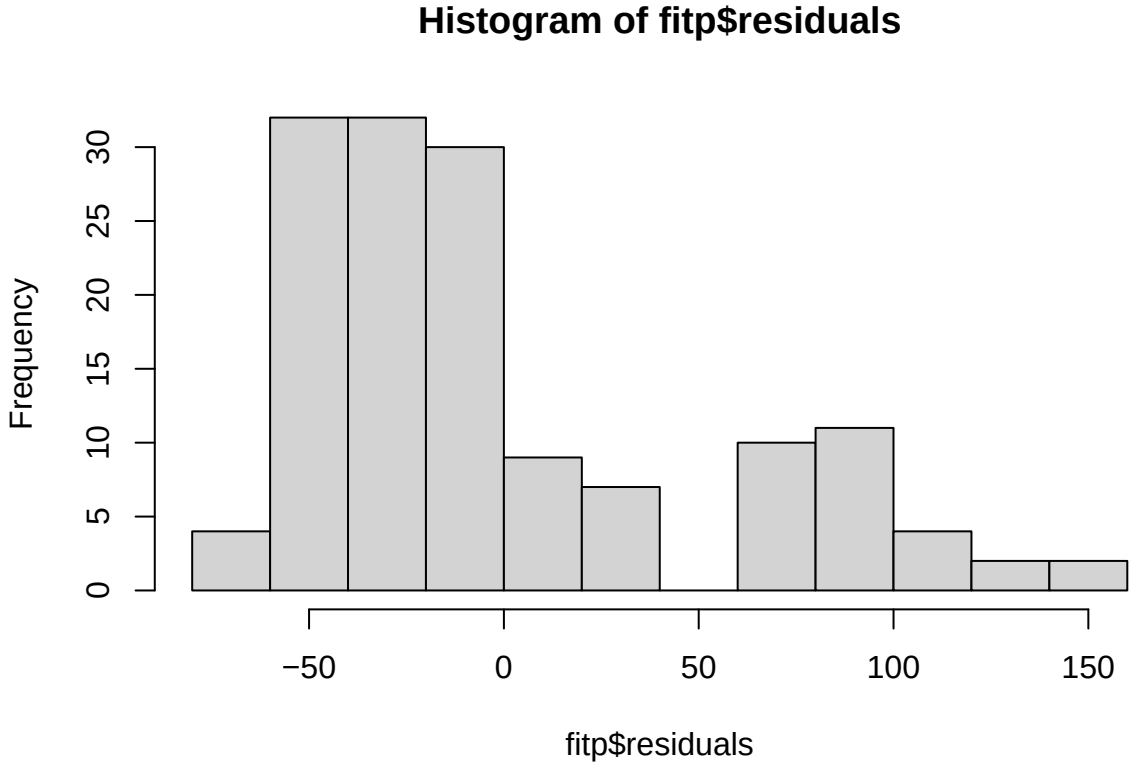
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 60 2.802256          0.0057943      0.82858
```

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

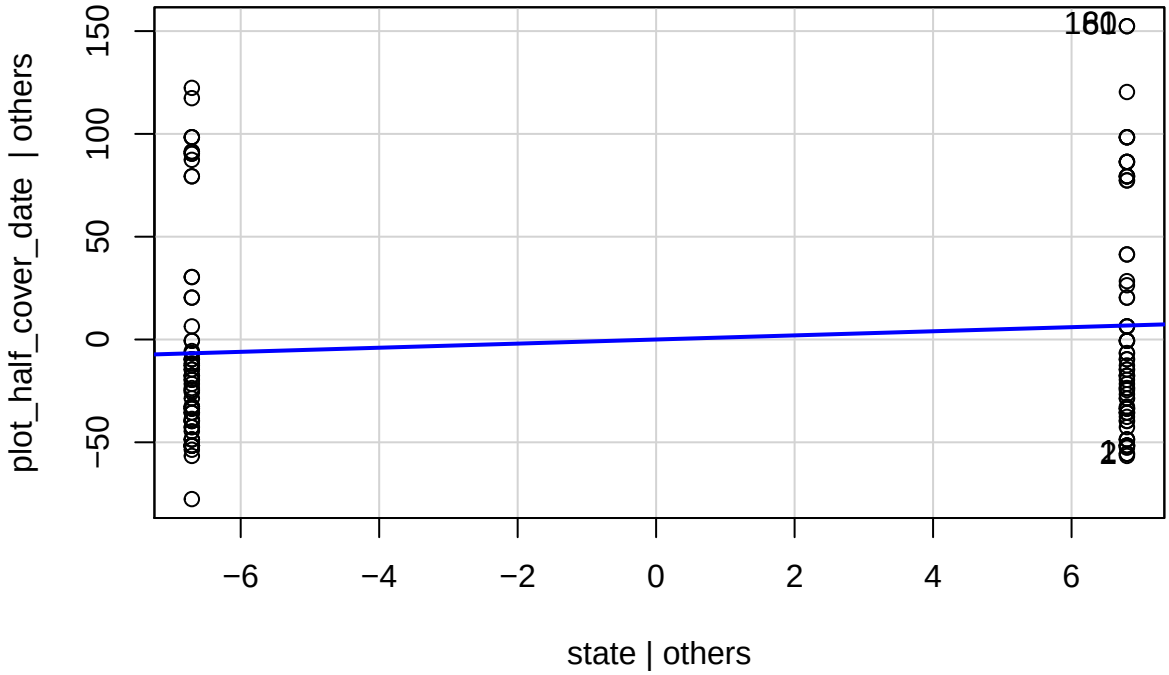



```
##  60 181
##  35 101
```

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



```
leveragePlots(fitp)
```




```
leveneTest(residuals(fitp) ~ green_kbsp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.4414 0.2319
##       141
```

```
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
## -----------------------------------------------
```

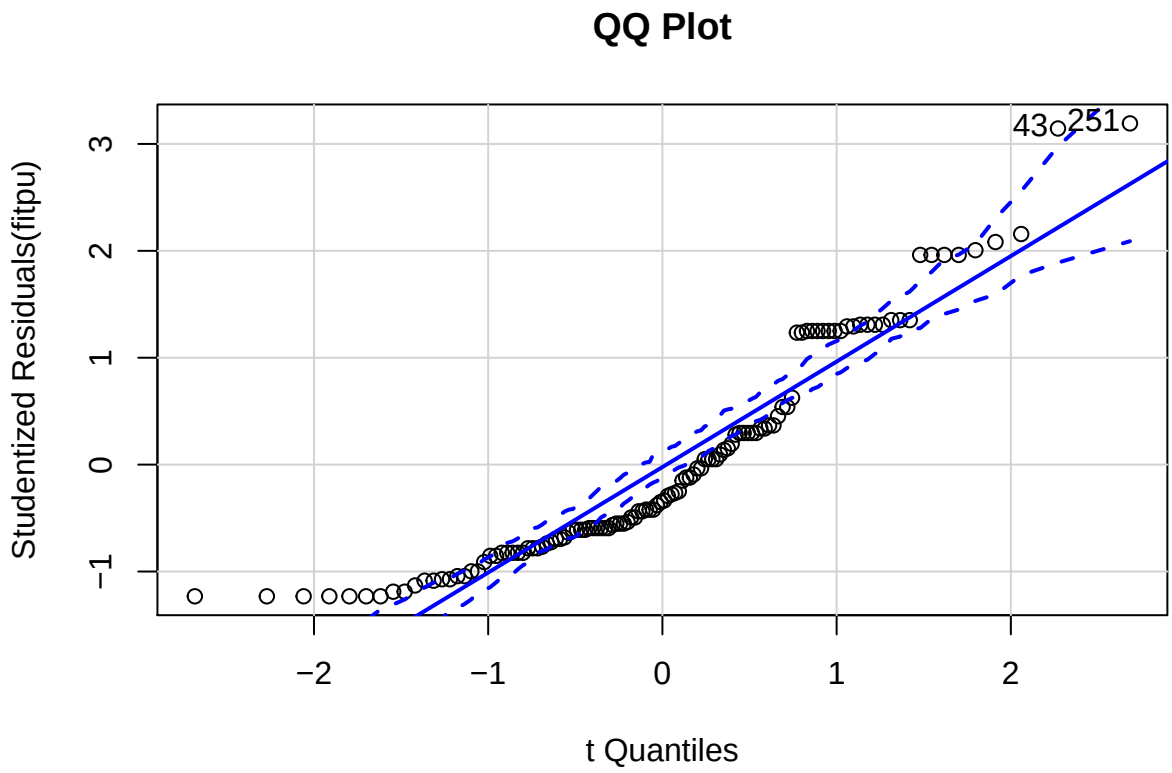
```
shapiro.test(resid(fitp))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(fitp)
## W = 0.85775, p-value = 2e-10
```

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

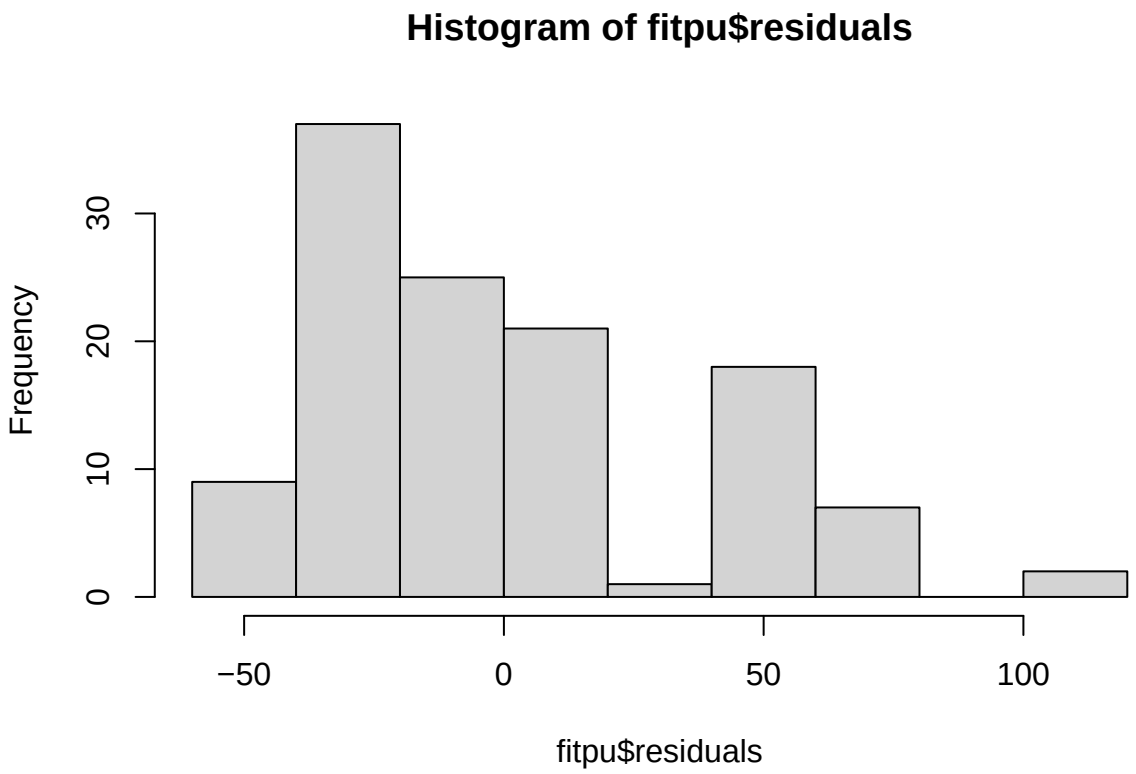
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 251 3.192341          0.0018128      0.21754
```

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

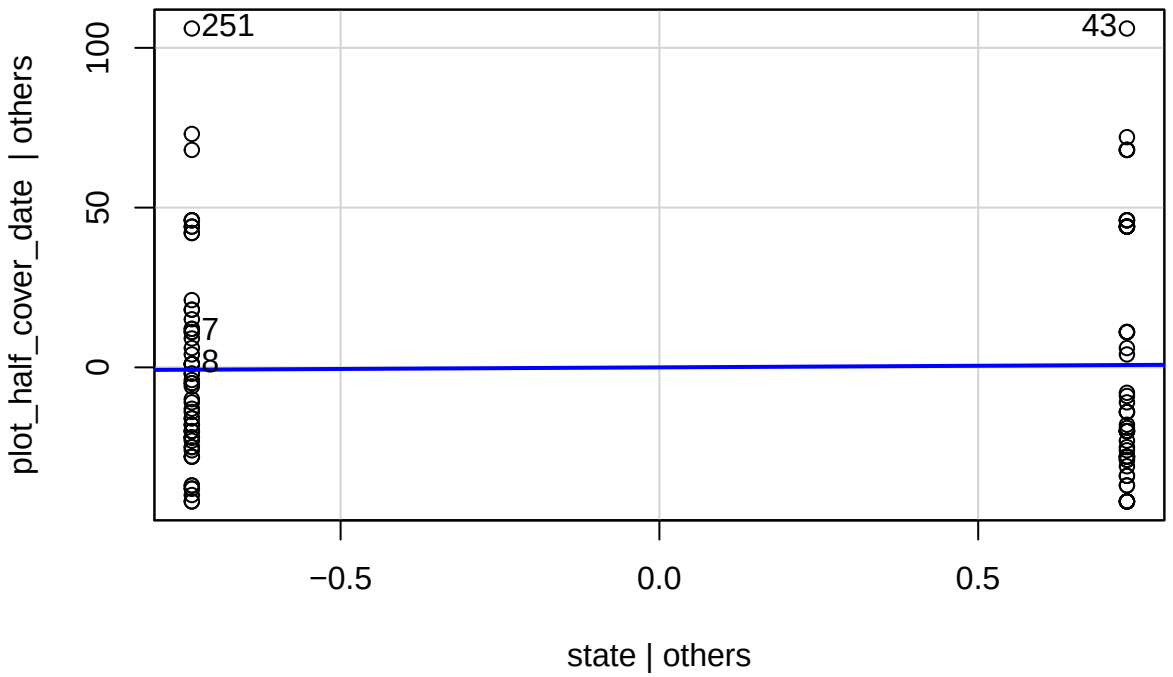



```
##  43 251
##  19 114
```

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




```
leveragePlots(fitpu)
```




```
leveneTest(residuals(fitpu) ~ green_umbsp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  2.4191 0.1225
##       118
```

```
ols_test_normality(fitpu)
```

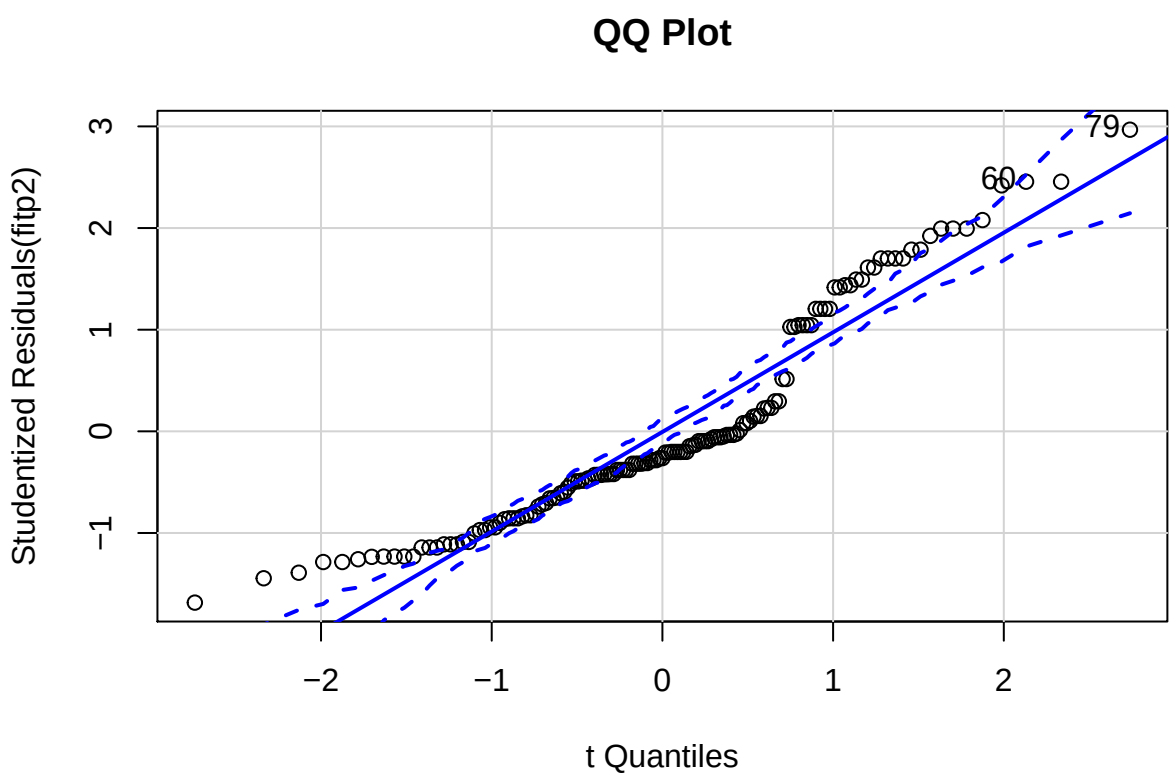
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

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

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

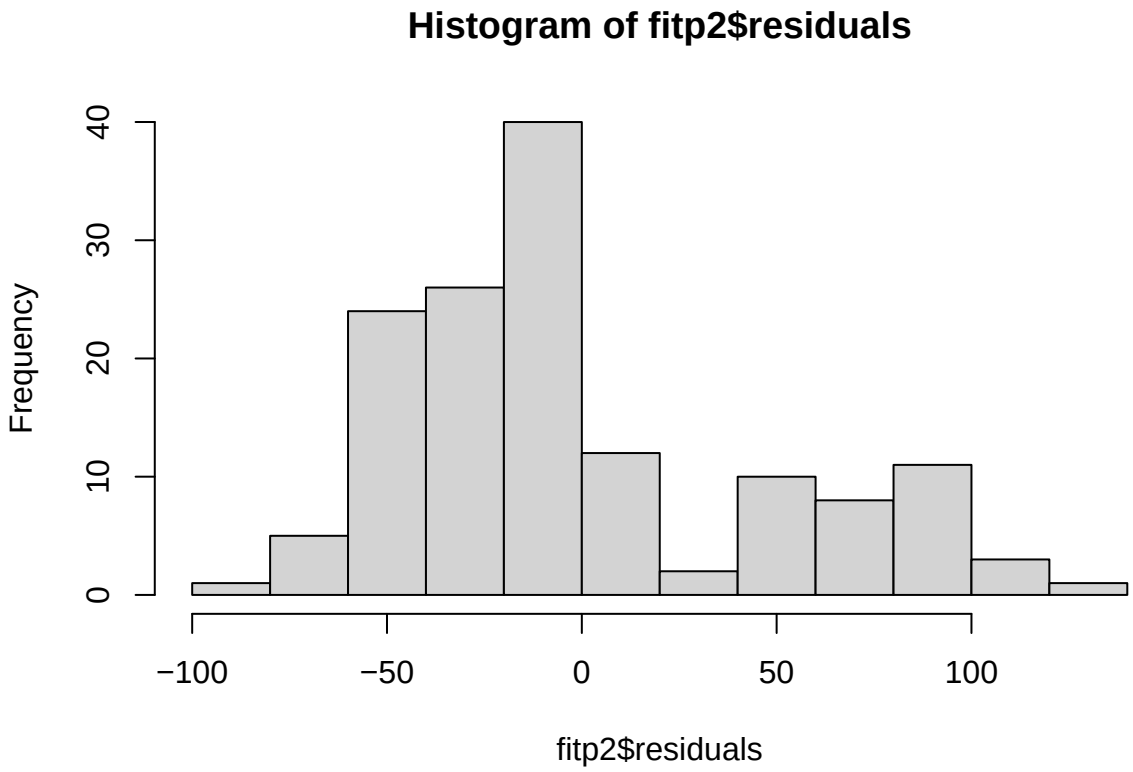
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 79 2.967344          0.0035544      0.50827
```

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

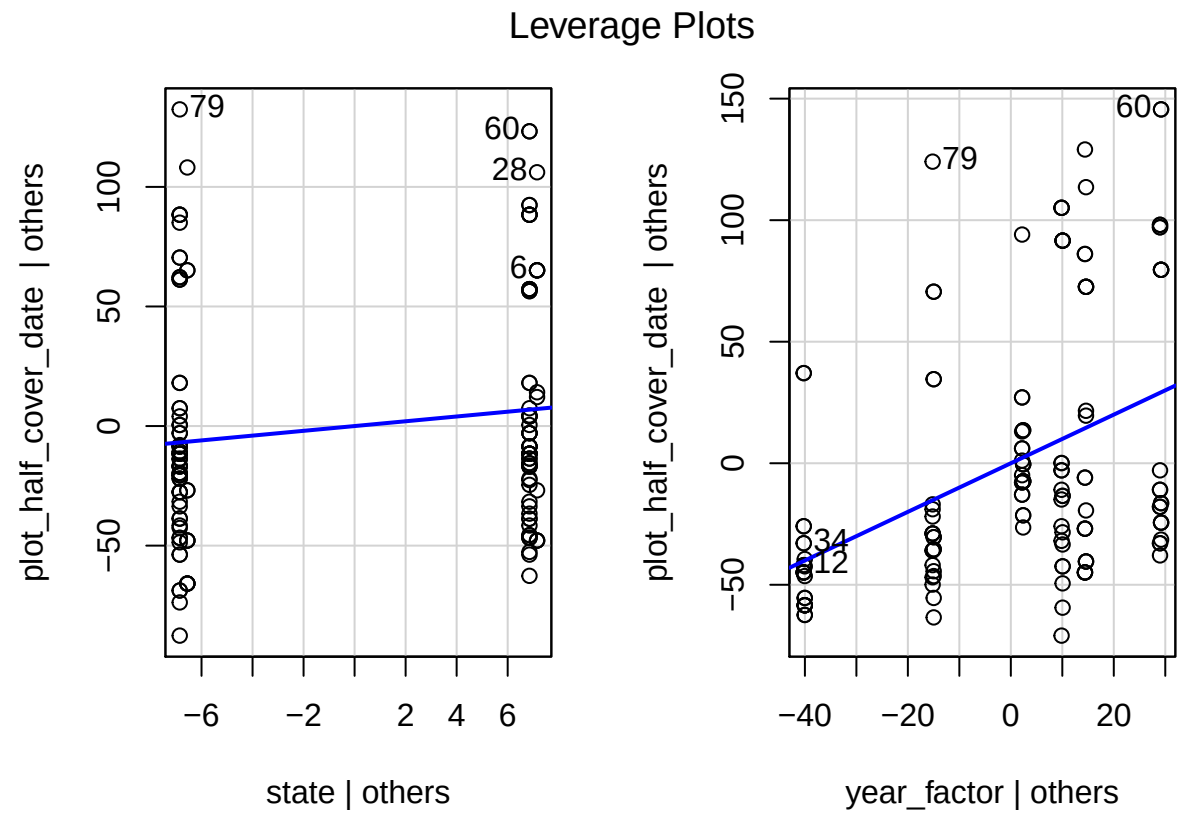



```
## 60 79
## 35 44
```

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




```
leveragePlots(fitp2)
```



```
leveneTest(residuals(fitp2) ~ green_kbsp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0979 0.7548
##       141
```

```
leveneTest(residuals(fitp2) ~ green_kbsp$year_factor)  # not met
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value    Pr(>F)
## group   5  5.0271 0.0002924 ***
##       137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ols_test_normality(fitp2)
```

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

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

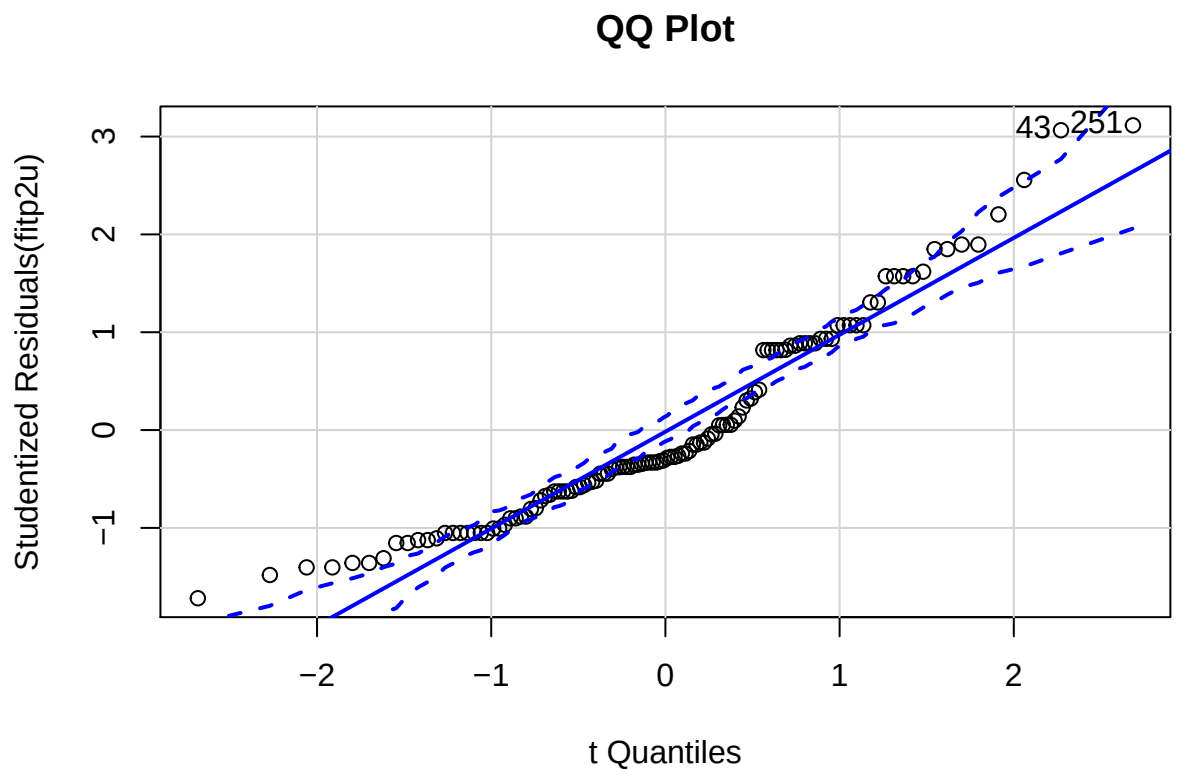
```
shapiro.test(resid(fitp2))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(fitp2)
## W = 0.90998, p-value = 8.975e-08
```

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

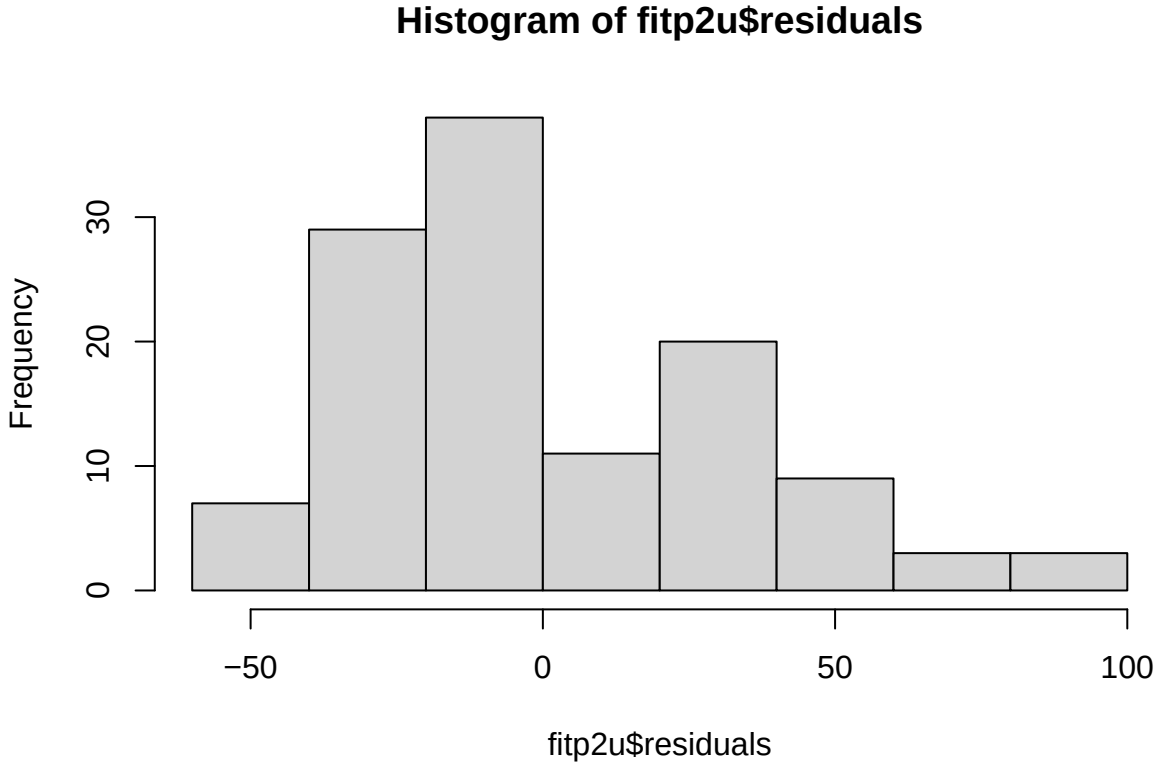
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##     rstudent unadjusted p-value Bonferroni p
## 251  3.11464          0.0023207      0.27849
```

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

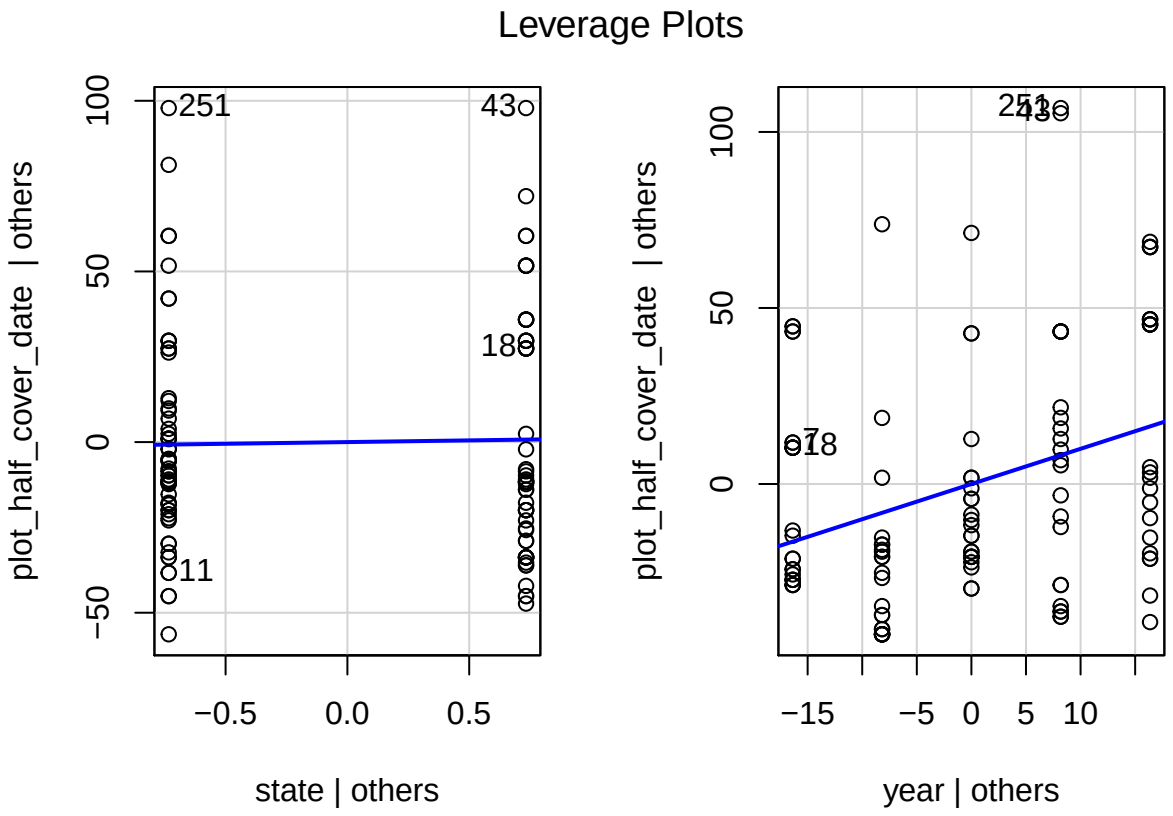



```
##  43 251
##  19 114
```

```
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
```

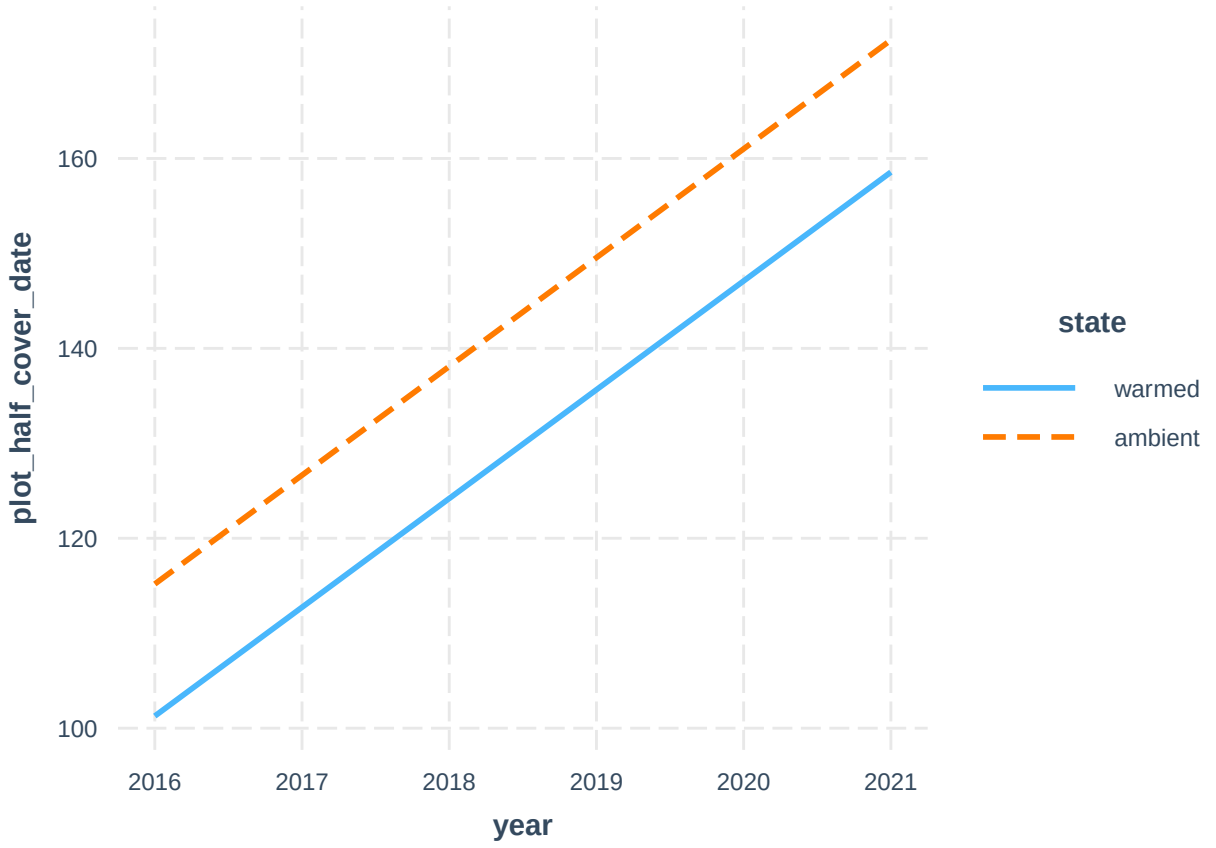
```
## -----------------------------------------------
##        Test             Statistic       pvalue
## -----------------------------------------------
## Shapiro-Wilk              0.9357         0.0000
## Kolmogorov-Smirnov        0.1443         0.0135
## Cramer-von Mises         11.6333       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

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

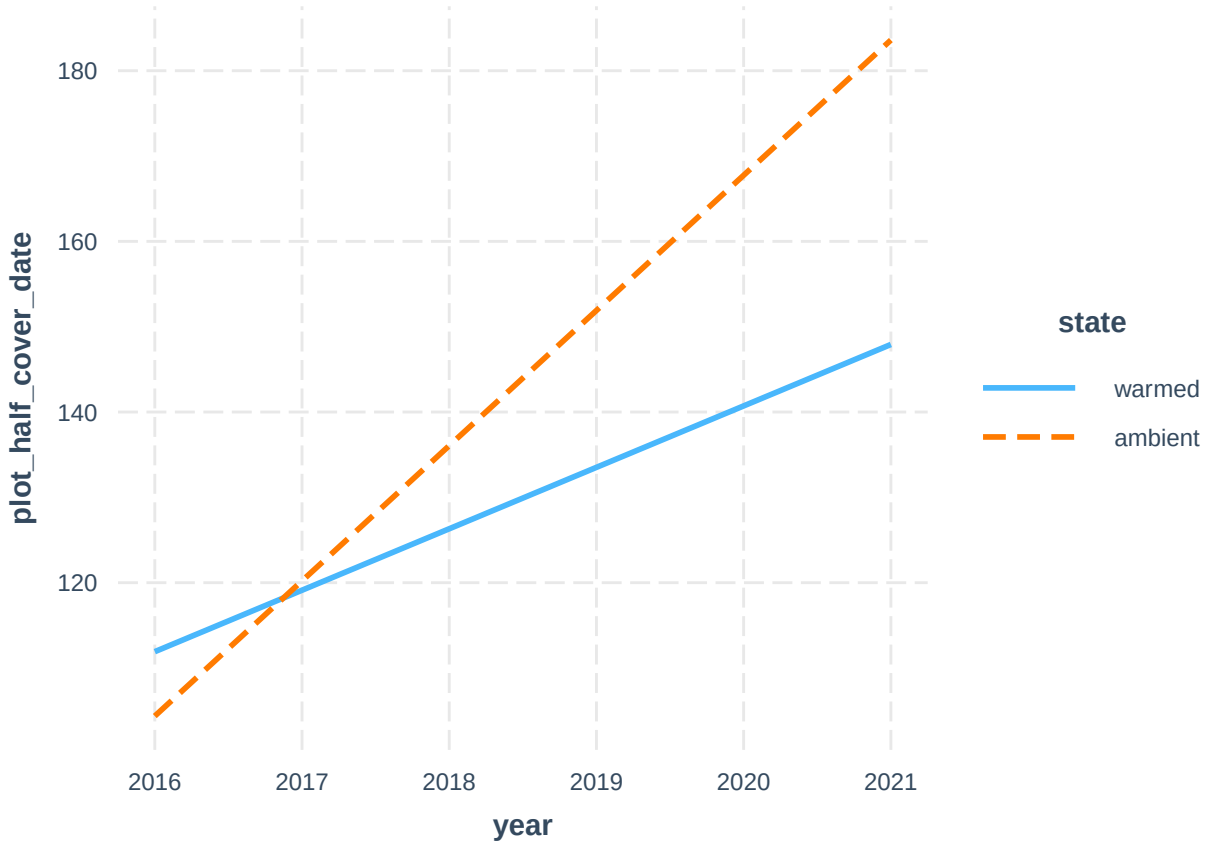
We should also think about how we're treating year. Some of the models have a state * year interaction as a fixed effect, which means that the warming or ambient treatment could affect the half_cover_date differently over time (there would be a different slope for each state in the relationship between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

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

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

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

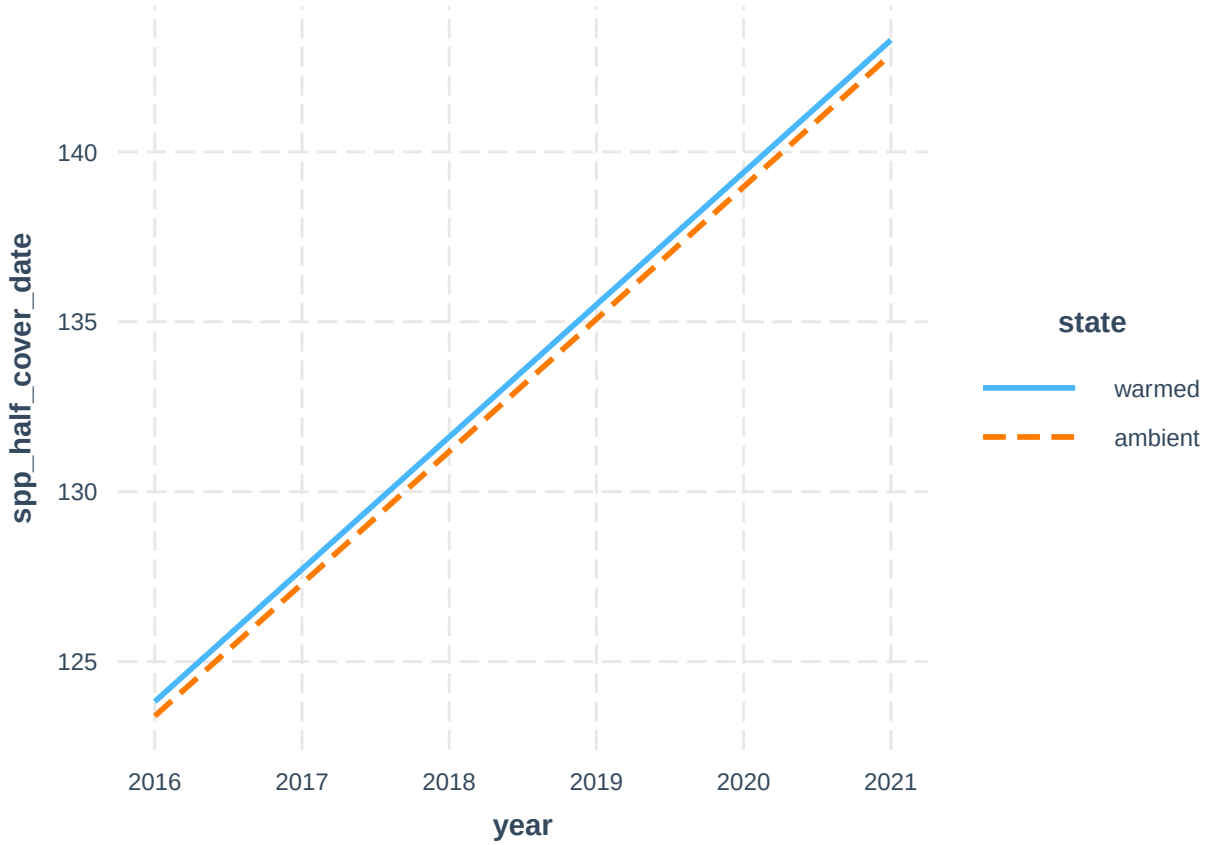



```
fit4 <- lm(plot_half_cover_date ~ state * year, data = green_kbsp)
interact_plot(fit4, pred = year, modx = state)
```



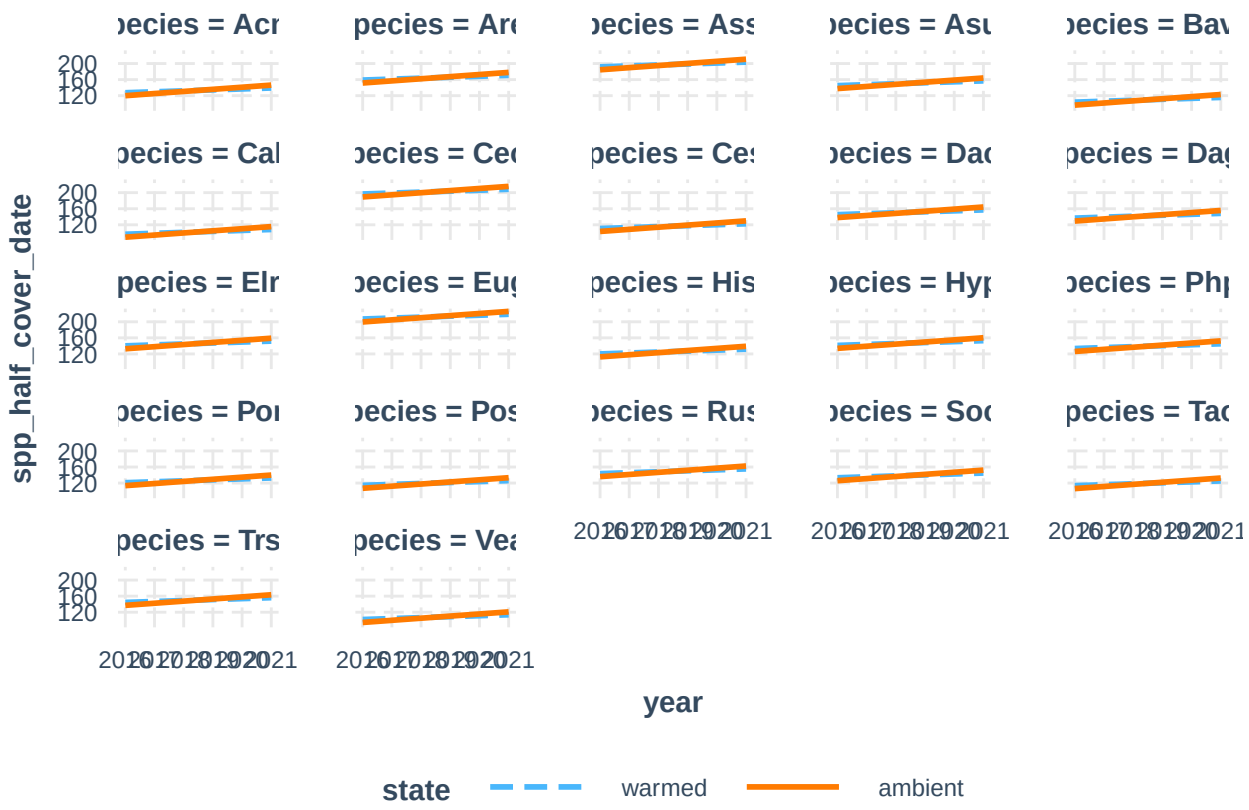

```
fit5 <- lm(spp_half_cover_date ~ state + year + species, data = green_kbs)
interact_plot(fit5, pred = year, modx = state)
```

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



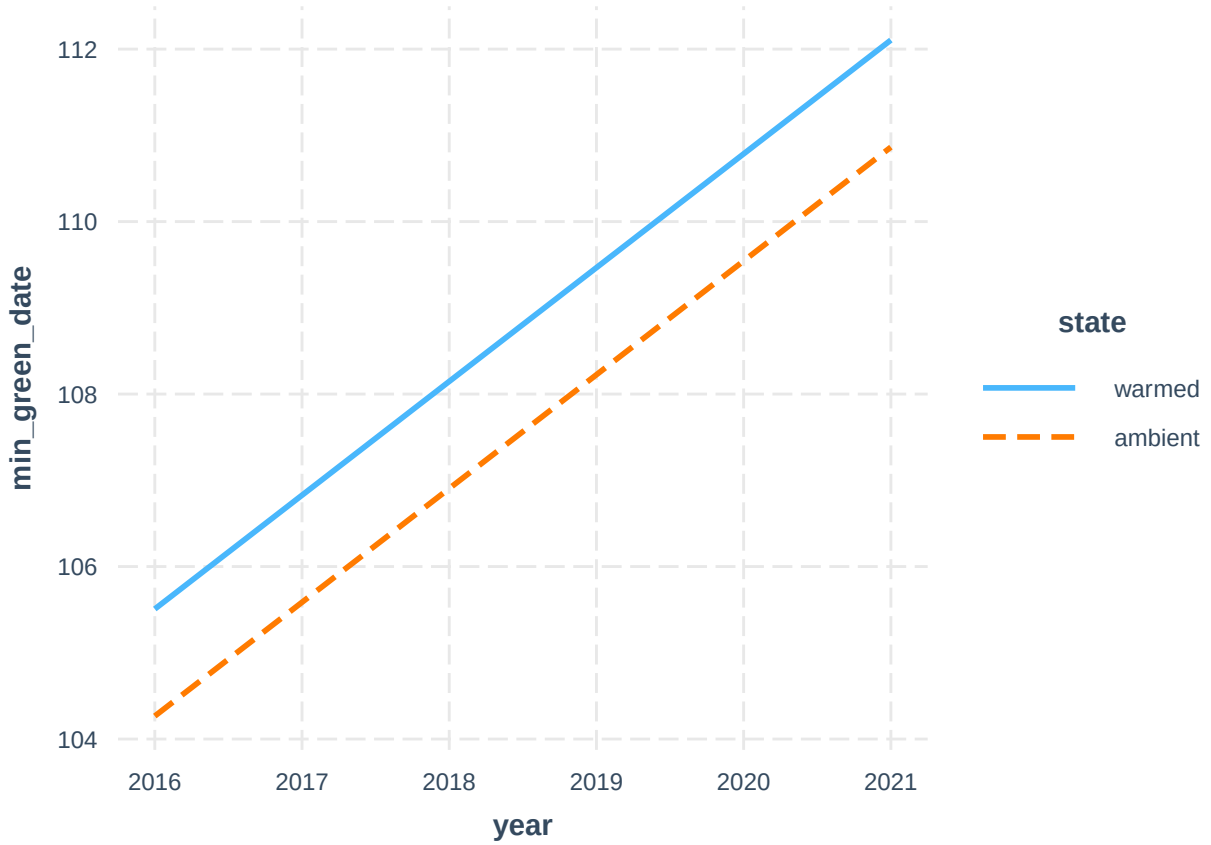

```
fit6 <- lm(spp_half_cover_date ~ state * year + species, data = green_kbs)
interact_plot(fit6, pred = year, modx = state, mod2 = species)
```

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



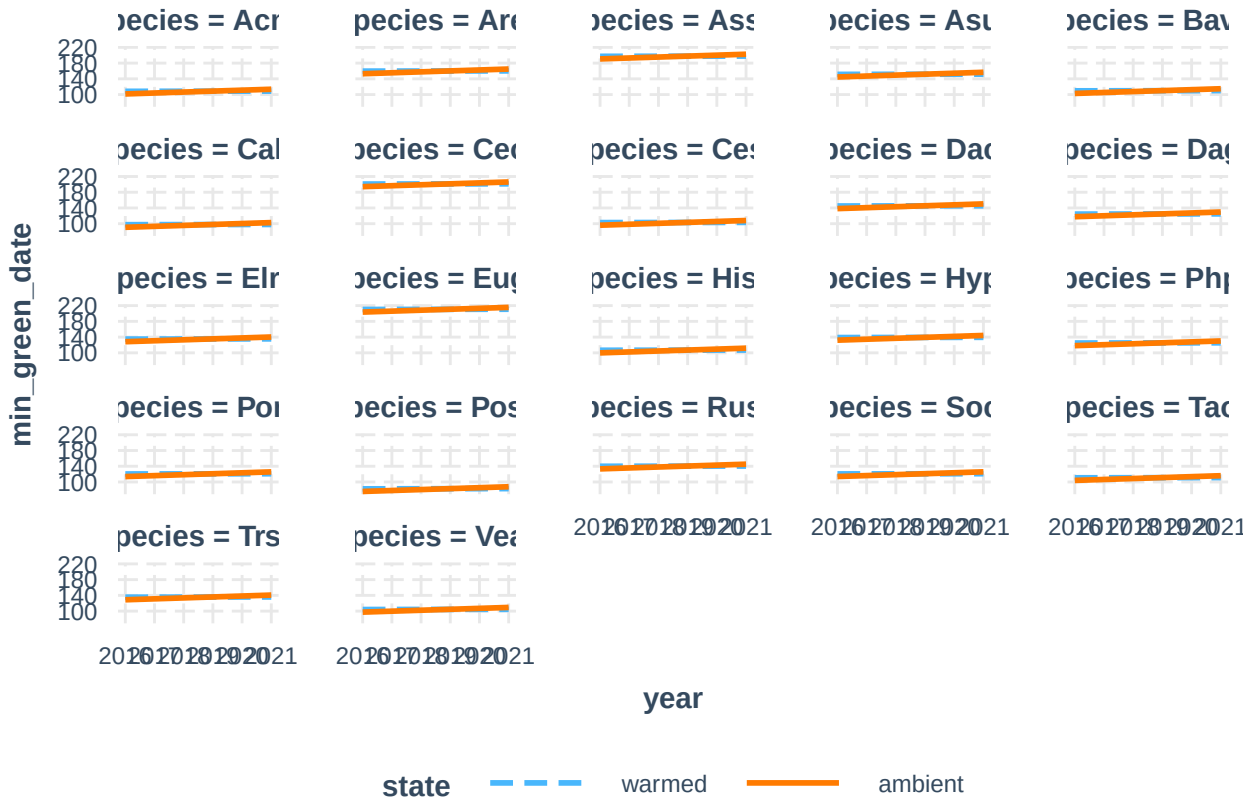

```
fit7 <- lm(min_green_date ~ state + year + species, data = green_kbs)
interact_plot(fit7, pred = year, modx = state)
```

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



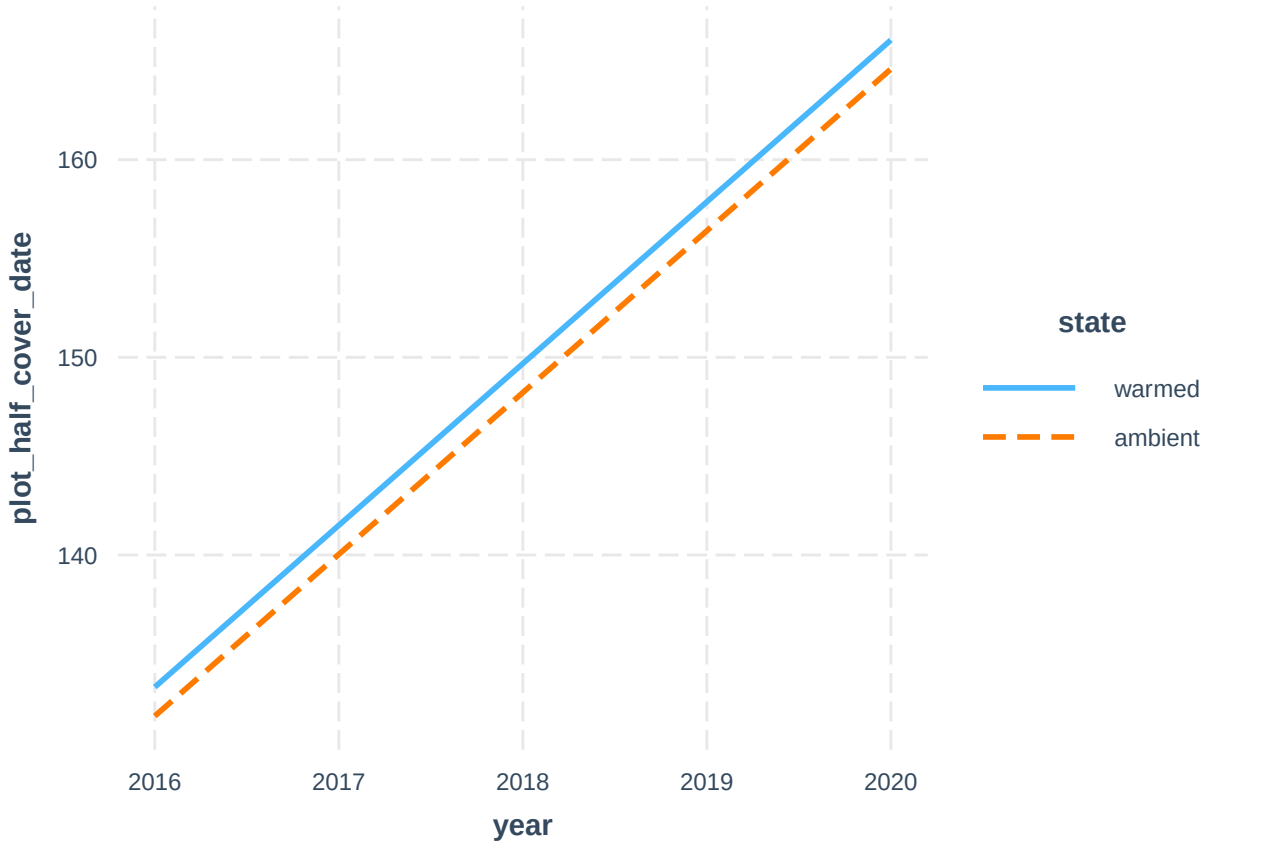

```
fit8 <- lm(min_green_date ~ state * year + species, data = green_kbs)
interact_plot(fit8, pred = year, modx = state, mod2 = species)
```

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

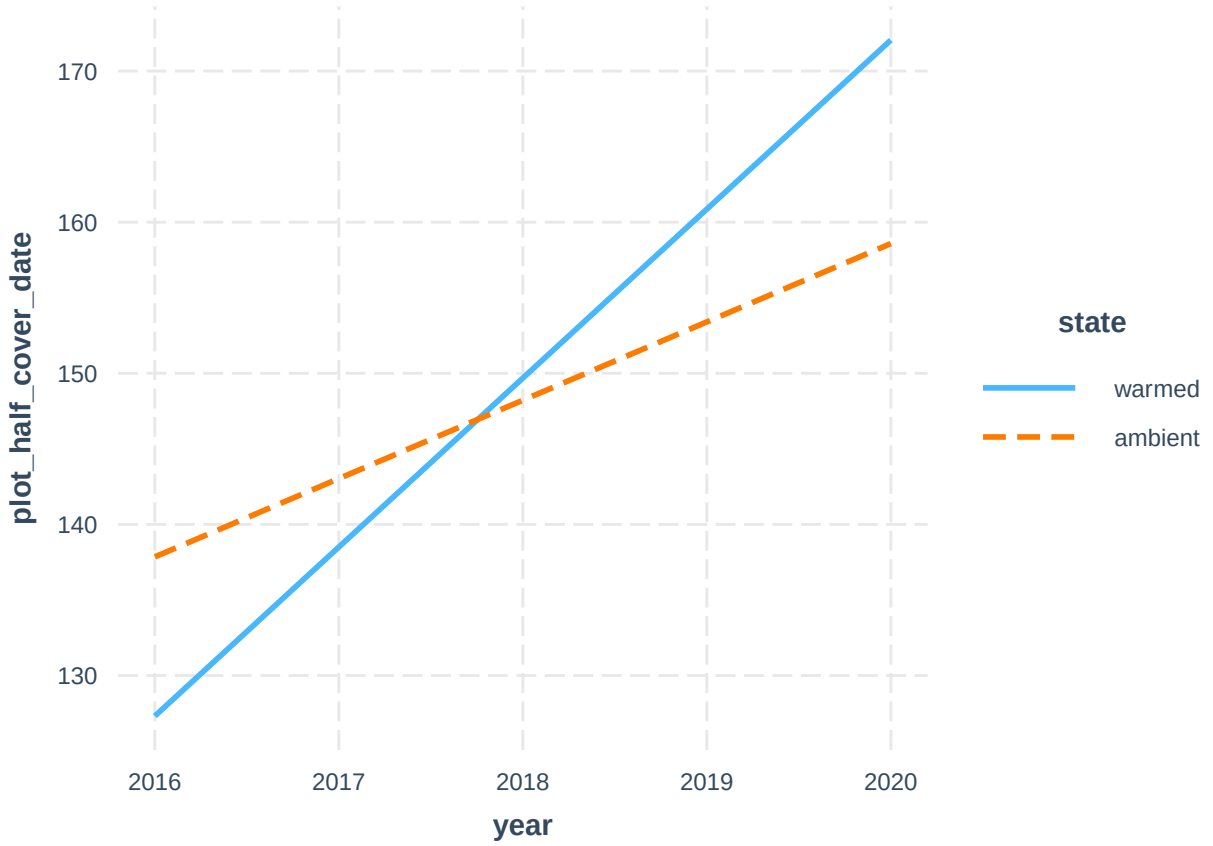



```
# UMBS
fit3u <- lm(plot_half_cover_date ~ state + year, data = green_umbsp)
interact_plot(fit3u, pred = year, modx = state)
```

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

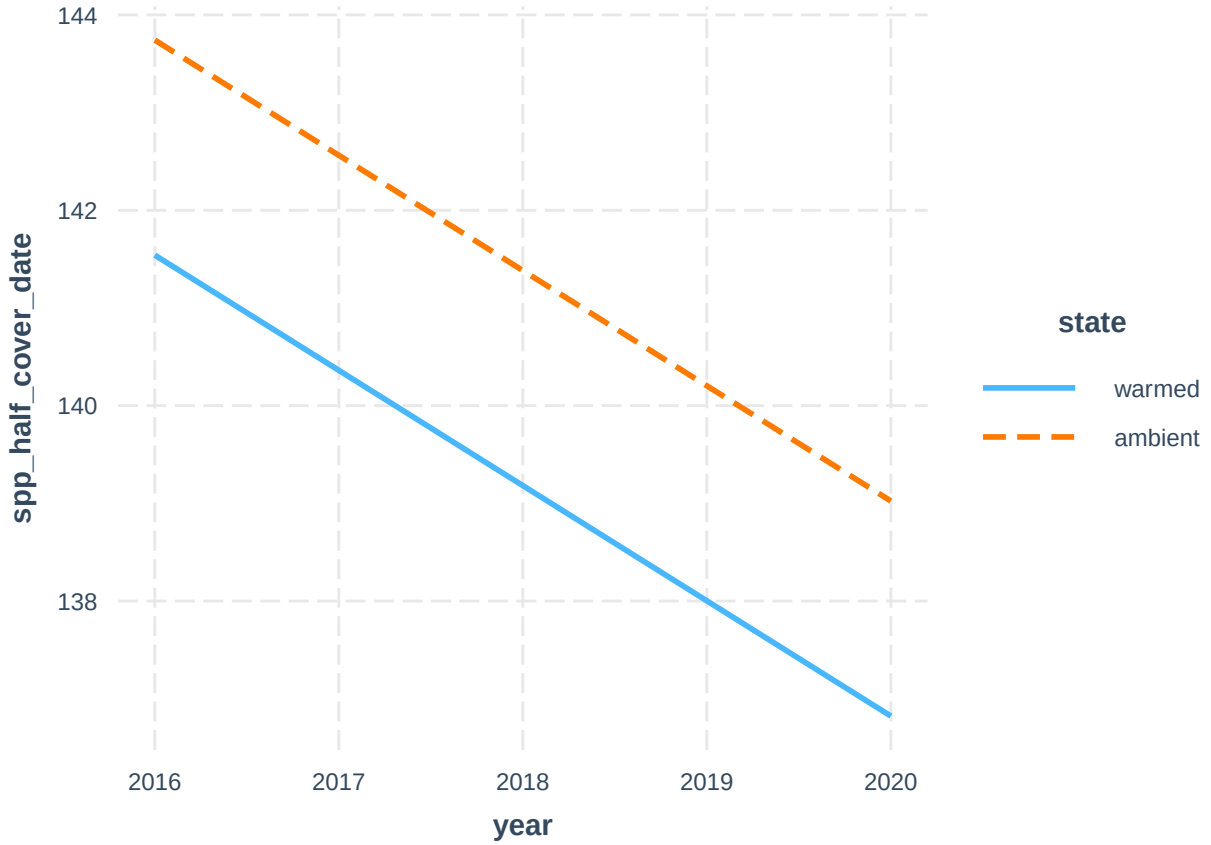



```
fit4u <- lm(plot_half_cover_date ~ state * year, data = green_umbsp)
interact_plot(fit4u, pred = year, modx = state)
```




```
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.
```

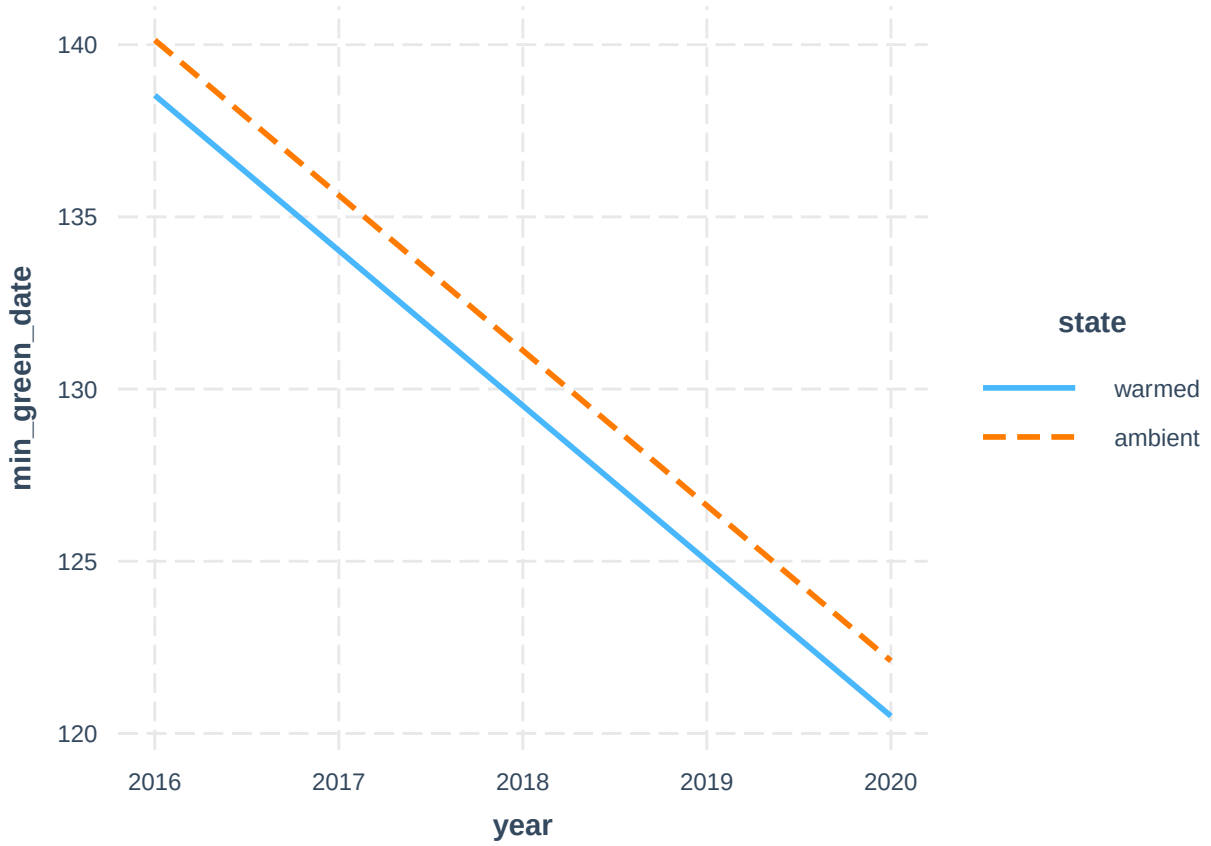



```
fit6u <- lm(spp_half_cover_date ~ state * year + species, data = green_umbs)
interact_plot(fit6u, pred = year, modx = state, mod2 = species)
```

```
## 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                       13      13     1   23.32  0.0051    0.9435
## year_factor             201178   40236     5 1481.69 16.3729 9.406e-16 ***
## insecticide                 64      64     1   22.92  0.0260    0.8734
```

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

```
anova(mod2)
```

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

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

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

```
summary(mod1)
```

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

```
##  plot     (Intercept)   21.19   4.604
##  species  (Intercept)  701.14  26.479
##  Residual             2457.46  49.573
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                                    Estimate Std. Error        df t value
## (Intercept)                        132.5912     7.7803   57.5190  17.042
## stateambient                        -3.5259     5.9191  241.3907  -0.596
## year_factor2                        -7.0774     7.7297 1472.4624  -0.916
## year_factor3                        26.2075     7.3481 1474.5216   3.567
## year_factor4                         6.7615     7.2793 1478.4970   0.929
## year_factor5                        21.8553     7.3785 1478.4944   2.962
## year_factor6                         9.2088     7.4941 1484.7880   1.229
## insecticideno_insects                3.7585     5.9185  241.1836   0.635
## stateambient:year_factor2           -4.5737     8.7486 1473.8850  -0.523
## stateambient:year_factor3           -1.1482     8.3975 1477.4538  -0.137
## stateambient:year_factor4            2.0347     8.5280 1480.6286   0.239
## stateambient:year_factor5           15.3518     8.5364 1475.4692   1.798
## stateambient:year_factor6           10.8806     8.7035 1481.9963   1.250
## year_factor2:insecticideno_insects  -0.7372     8.7408 1474.0530  -0.084
## year_factor3:insecticideno_insects  -7.7324     8.3948 1477.9488  -0.921
## year_factor4:insecticideno_insects   1.7398     8.5364 1478.9656   0.204
## year_factor5:insecticideno_insects  -8.1151     8.5551 1473.6907  -0.949
## year_factor6:insecticideno_insects -10.8238     8.6939 1481.9730  -1.245
##                                   Pr(>|t|)
## (Intercept)                        < 2e-16 ***
## stateambient                      0.551948
## year_factor2                      0.360025
## year_factor3                      0.000373 ***
## year_factor4                      0.353109
## year_factor5                      0.003105 **
## year_factor6                      0.219339
## insecticideno_insects             0.525995
## stateambient:year_factor2         0.601201
## stateambient:year_factor3         0.891264
## stateambient:year_factor4         0.811455
## stateambient:year_factor5         0.072319 .
## stateambient:year_factor6         0.211445
## year_factor2:insecticideno_insects 0.932801
## year_factor3:insecticideno_insects 0.357152
## year_factor4:insecticideno_insects 0.838529
## year_factor5:insecticideno_insects 0.342992
## year_factor6:insecticideno_insects 0.213330
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

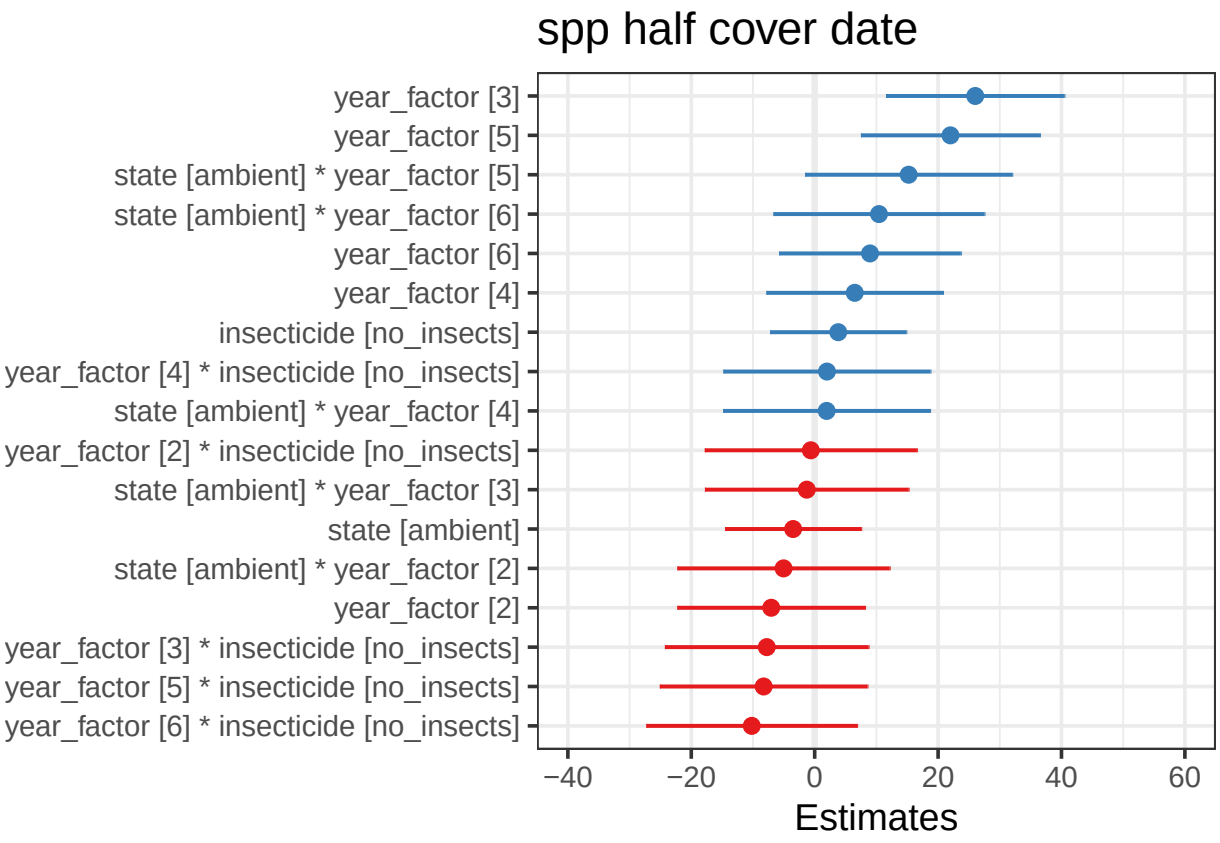
```
summary(mod2)
```

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

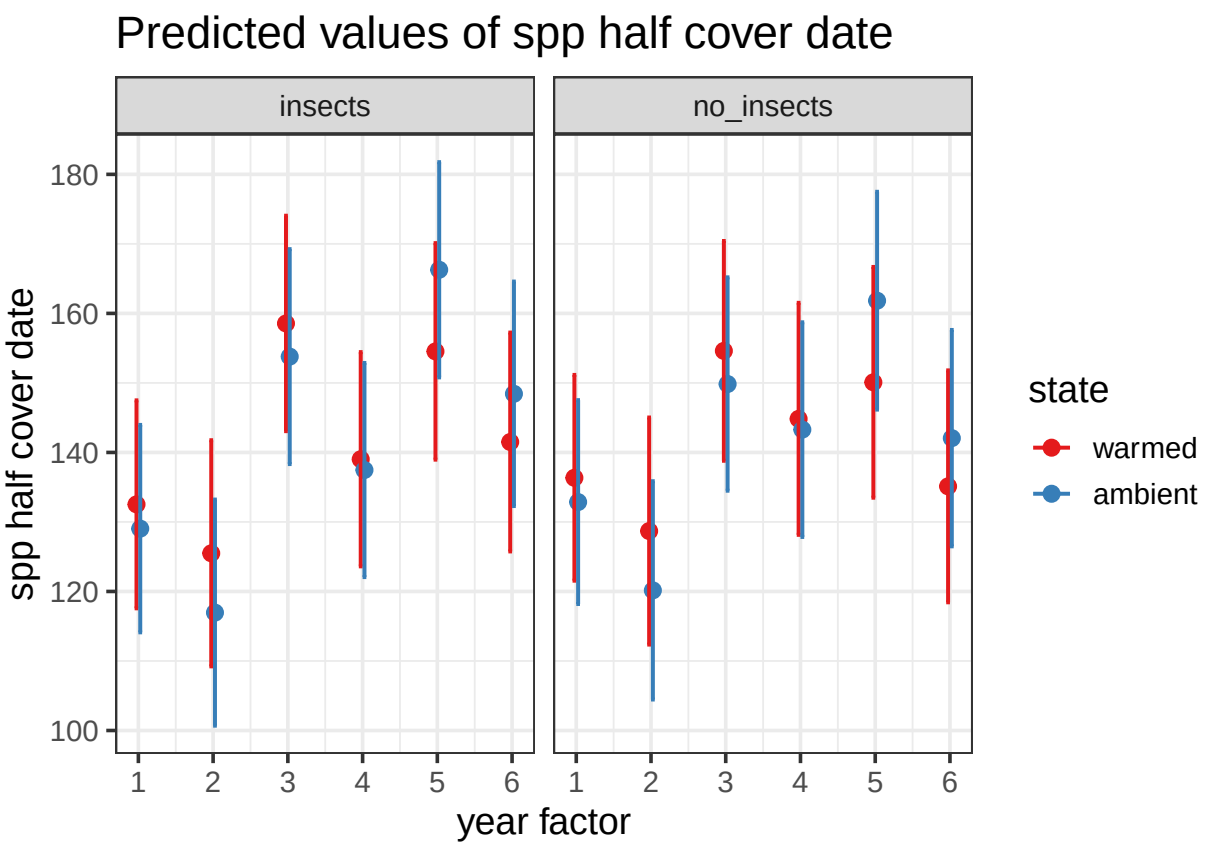
```
##   method [lmerModLmerTest]
## Formula:
## spp_half_cover_date ~ state * year_factor + insecticide * year_factor +
##     (1 | species)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16197.7  16304.2  -8078.9  16157.7     1491
##
## Scaled residuals:
##     Min   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

```
## year_factor3:insecticideno_insects 0.356417
## year_factor4:insecticideno_insects 0.816236
## year_factor5:insecticideno_insects 0.335420
## year_factor6:insecticideno_insects 0.241864
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

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

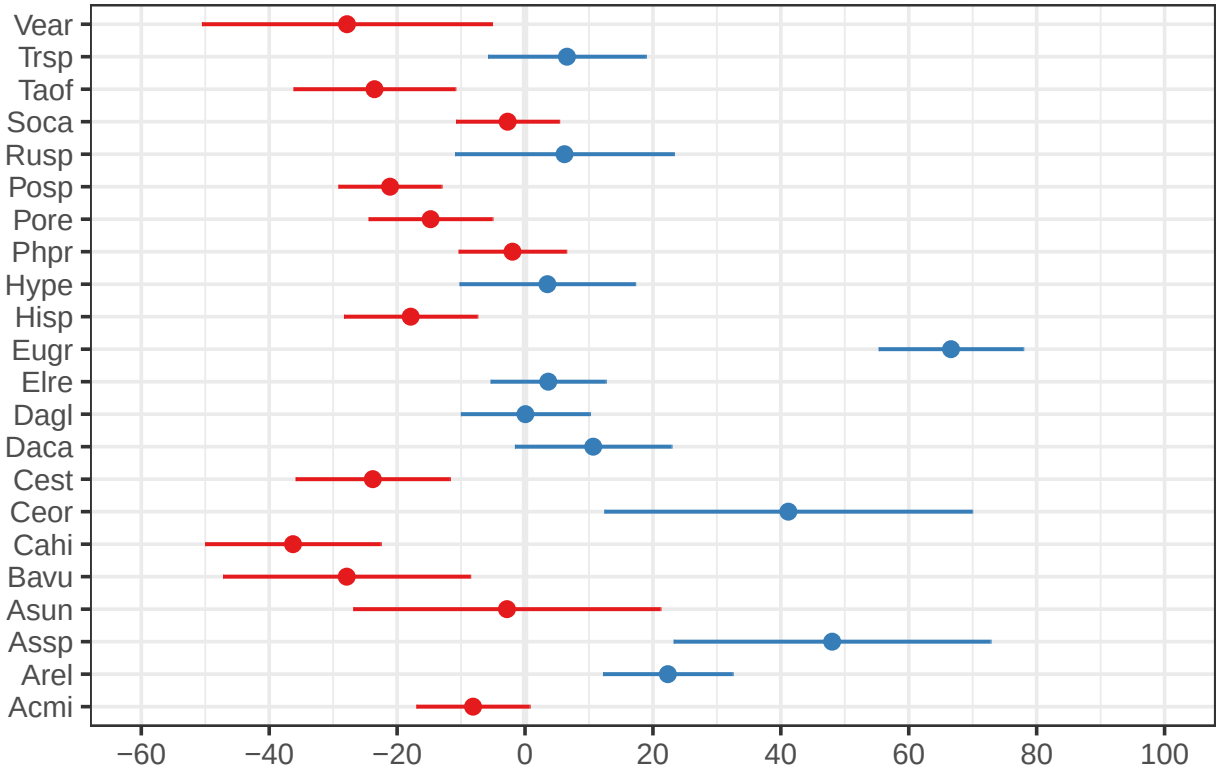



```
# these are the fixed predicted values:
plot_model(mod2, type = "pred", terms = c("year_factor", "state",
    "insecticide"))
```




```
# 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   14 16189 16264 -8080.5    16161
## mod2   20 16198 16304 -8078.9    16158 3.2951  6      0.771
```

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

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

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

# Does year need to be interactive with insecticide? -
# already removed insecticide
mod4 <- lmer(spp_half_cover_date ~ state * year_factor + insecticide +
    (1 | species) + (1 | plot), green_kbs, REML = FALSE)
anova(mod2, mod4)
```

```
## Data: green_kbs
```

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

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

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

```
# Still continue with no insecticide model 3

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

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

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

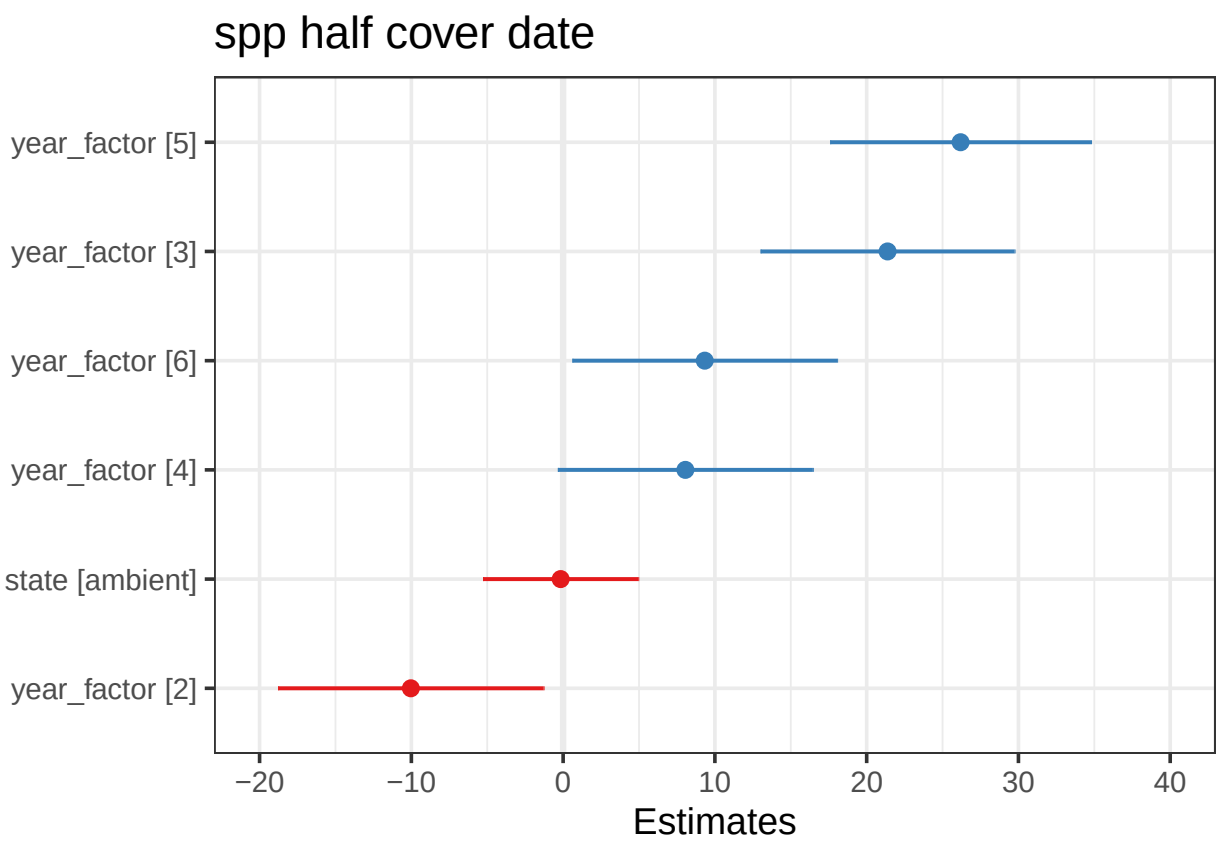
```
##      dAICc df weight
## mod5  0.0  9  0.86
## mod3  3.7  14 0.14
```

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

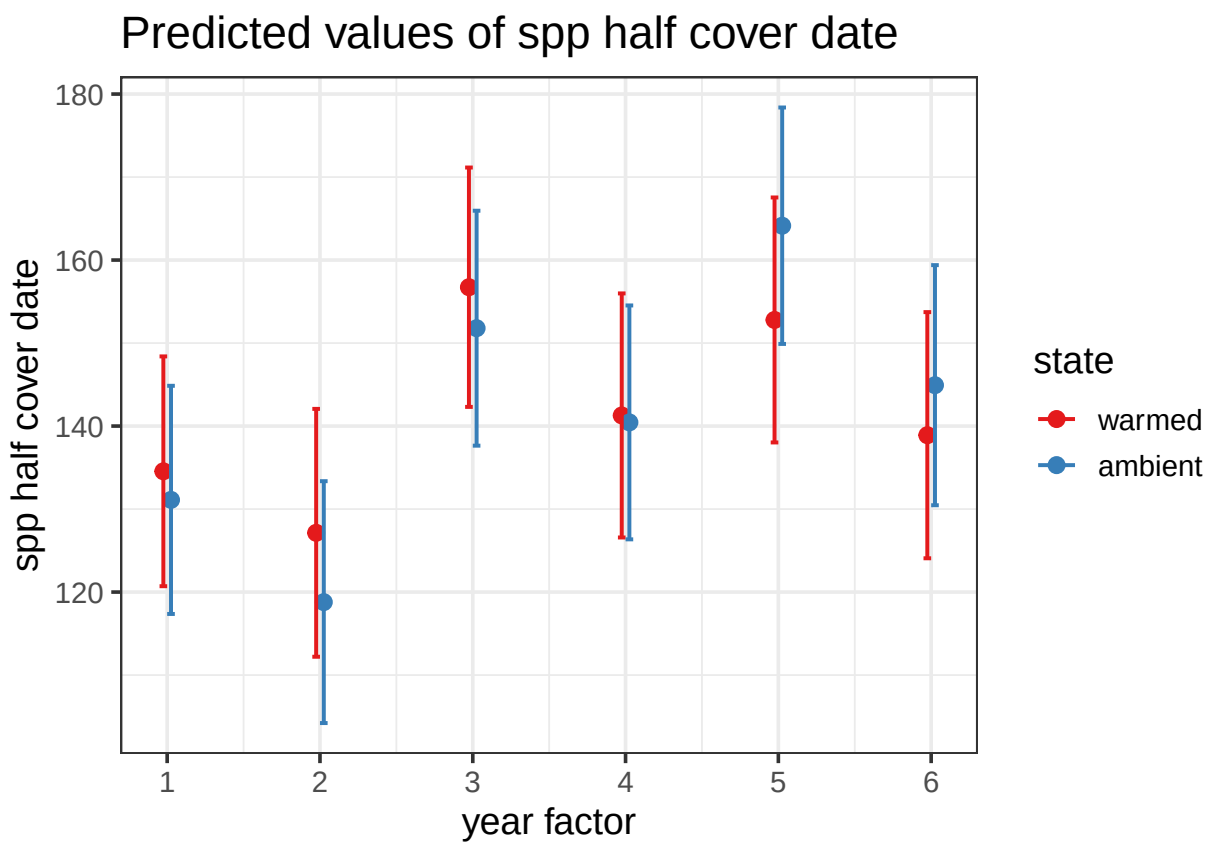
```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: spp_half_cover_date ~ state + year_factor + (1 | species)
##    Data: green_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  16185.5  16233.4  -8083.8  16167.5     1502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

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

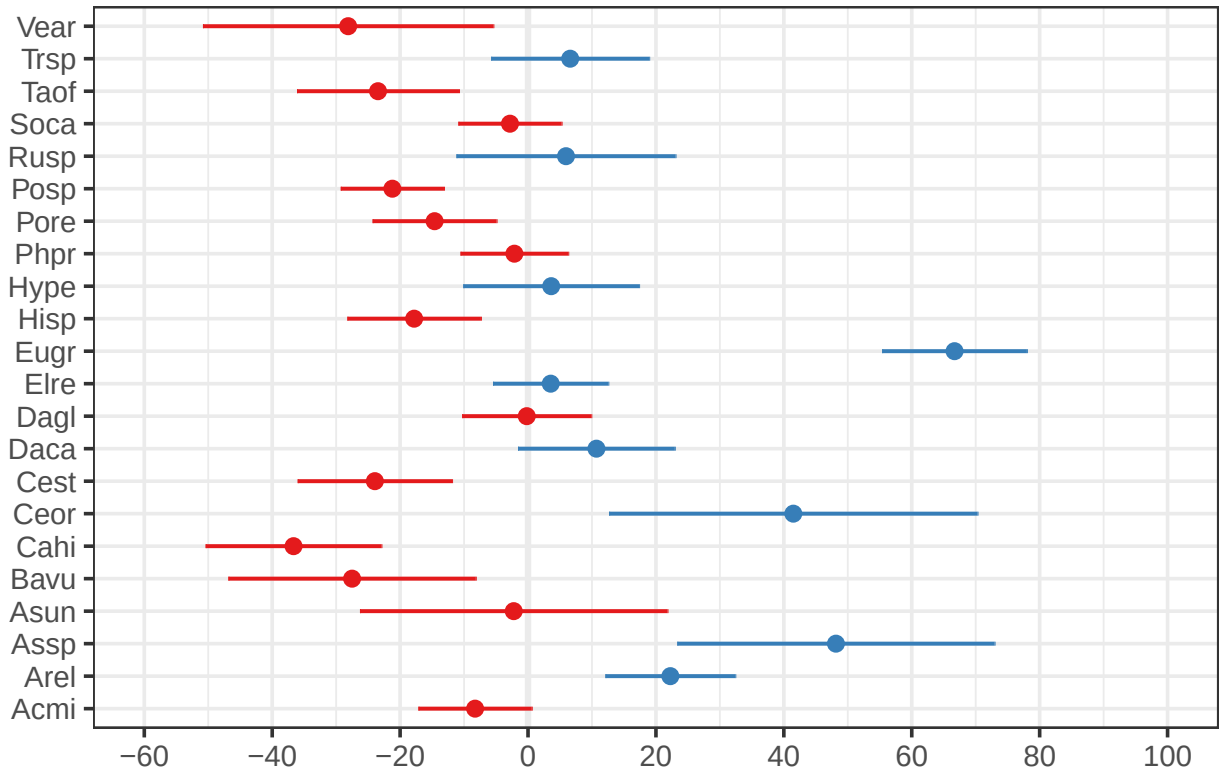
```
# these are the fixed effects estimates from summary(mod3)
plot_model(mod5, sort.est = TRUE)
```




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




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




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

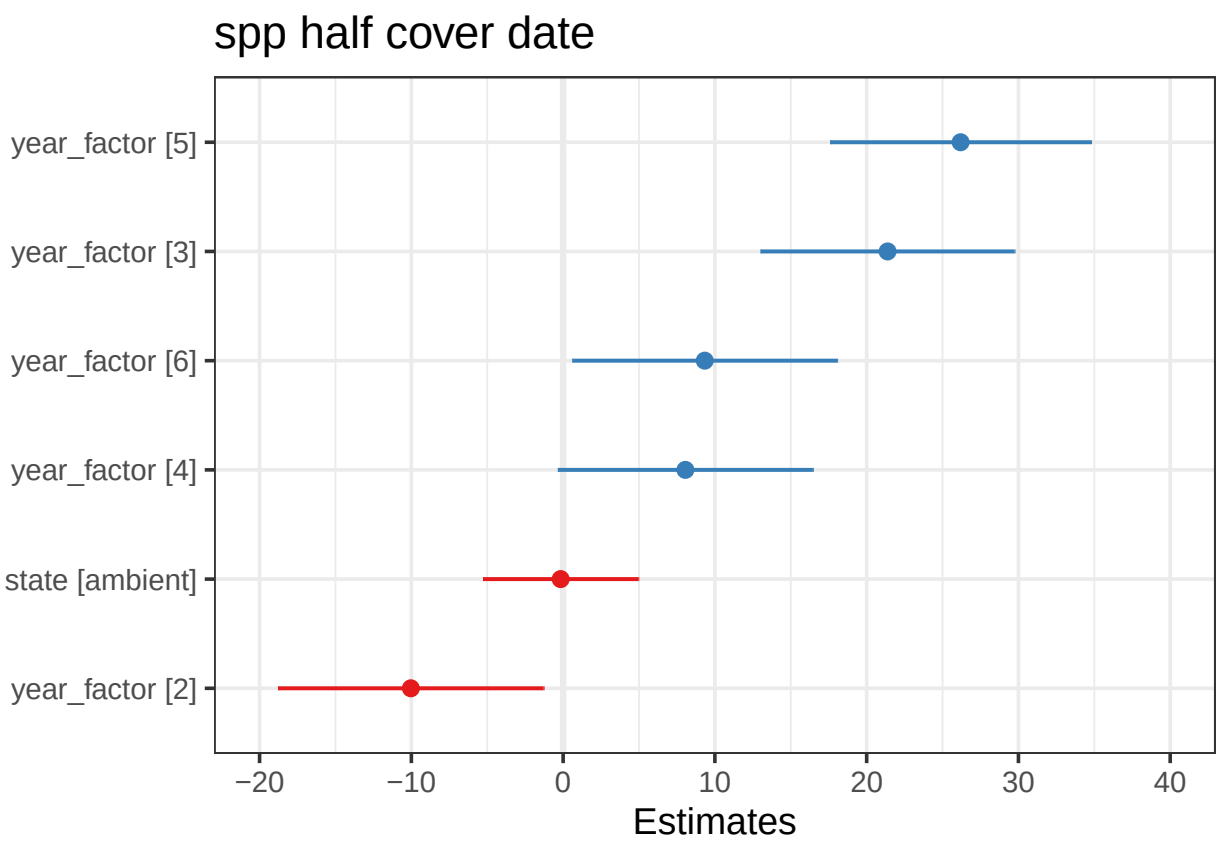
```
## boundary (singular) fit: see ?isSingular
```

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

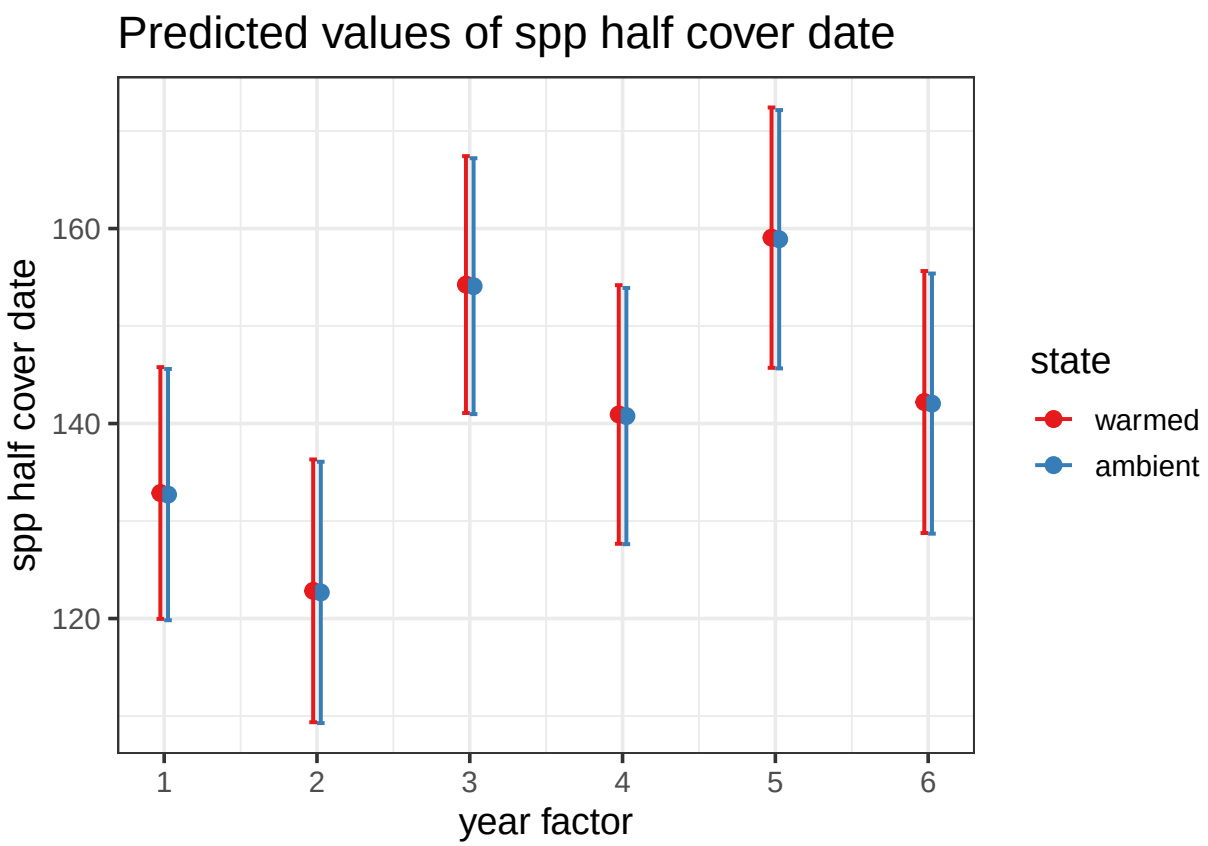
```
anova(mod5, mod6)
```

```
## Data: green_kbs
## Models:
## mod5: spp_half_cover_date ~ state + year_factor + (1 | species)
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +
## mod6:     year | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod5    9 16186 16233 -8083.8    16168
## mod6   17 16193 16283 -8079.4    16159 8.6671  8     0.3712
```

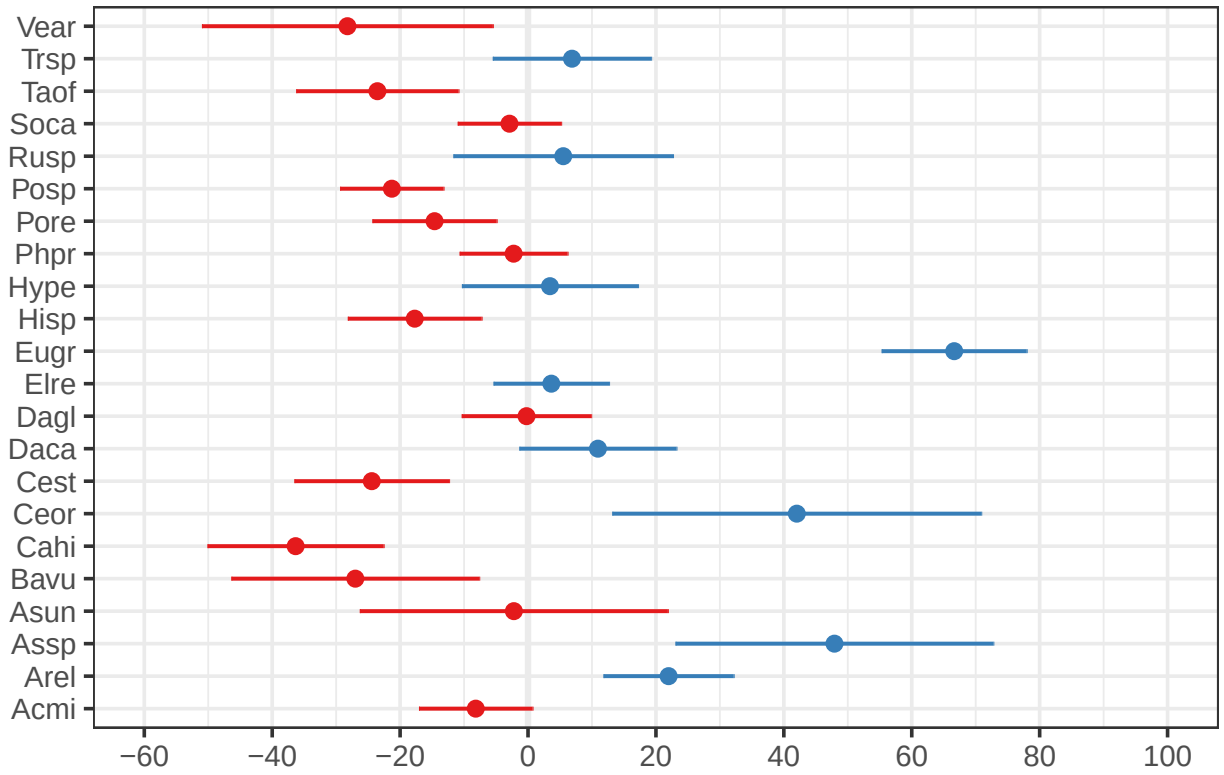
```
# mod 5 still better fit
plot_model(mod5, sort.est = TRUE)
```




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




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




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

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

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

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

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

```
## Data: green_kbs
## Models:
## mod6: spp_half_cover_date ~ state * year_factor + (1 | species) + (1 +
## mod6:     year | plot)
## mod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod6   17 16193 16283 -8079.4    16159
```

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

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

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

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

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

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

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

```
summary(mod7a)
```

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

```
## (Intercept)   124.6679     5.5355  658.1208  22.522  < 2e-16 ***
## stateambient   -0.1218     3.0925   23.4606  -0.039 0.968910
## speciesArel    31.5237     6.9674 1502.0715   4.524 6.53e-06 ***
## speciesAssp    71.8944    15.0713 1504.7956   4.770 2.02e-06 ***
## speciesAsun     4.9822    14.5648 1497.4397   0.342 0.732343
## speciesBavu   -21.9349    11.5623 1510.9007  -1.897 0.058004 .
## speciesCahi   -30.8244     8.5743 1502.0958  -3.595 0.000335 ***
## speciesCeor    65.0746    18.2061 1473.6005   3.574 0.000362 ***
## speciesCest   -17.7608     7.7939 1499.7908  -2.279 0.022819 *
## speciesDaca    20.4666     7.8568 1502.9399   2.605 0.009279 **
## speciesDagl     8.5034     6.9340 1501.4392   1.226 0.220267
## speciesElre    12.0669     6.5205 1496.9446   1.851 0.064424 .
## speciesEugr    78.4509     7.4574 1509.7734  10.520  < 2e-16 ***
## speciesHisp   -10.1581     7.0897 1495.7777  -1.433 0.152123
## speciesHype    12.5225     8.5592 1510.9369   1.463 0.143660
## speciesPhpr     6.1822     6.2777 1493.4067   0.985 0.324886
## speciesPore    -6.5550     6.7603 1499.9341  -0.970 0.332387
## speciesPosp   -13.5300     6.1492 1491.2662  -2.200 0.027940 *
## speciesRusp    14.6457    10.3229 1478.7658   1.419 0.156182
## speciesSoca     5.3091     6.1492 1491.2662   0.863 0.388067
## speciesTaof   -17.2928     8.0633 1510.5669  -2.145 0.032142 *
## speciesTrsp    15.8169     7.9265 1499.7857   1.995 0.046174 *
## speciesVear   -25.8562    13.6356 1509.6798  -1.896 0.058121 .
## year_factor2  -10.0690     4.4226 1495.7614  -2.277 0.022943 *
## year_factor3   21.6909     4.2345 1498.3063   5.122 3.41e-07 ***
## year_factor4    7.9005     4.2476 1503.0642   1.860 0.063082 .
## year_factor5   25.8202     4.3513 1503.1515   5.934 3.67e-09 ***
## year_factor6    9.0605     4.4186 1507.1045   2.051 0.040484 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 28 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

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

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## state            4       4     1   23.46  0.0016    0.9689
## species     779402   37114    21 1501.43 15.2207 < 2.2e-16 ***
## year_factor 207080   41416     5 1499.58 16.9847 2.297e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

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

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

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

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

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

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

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

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

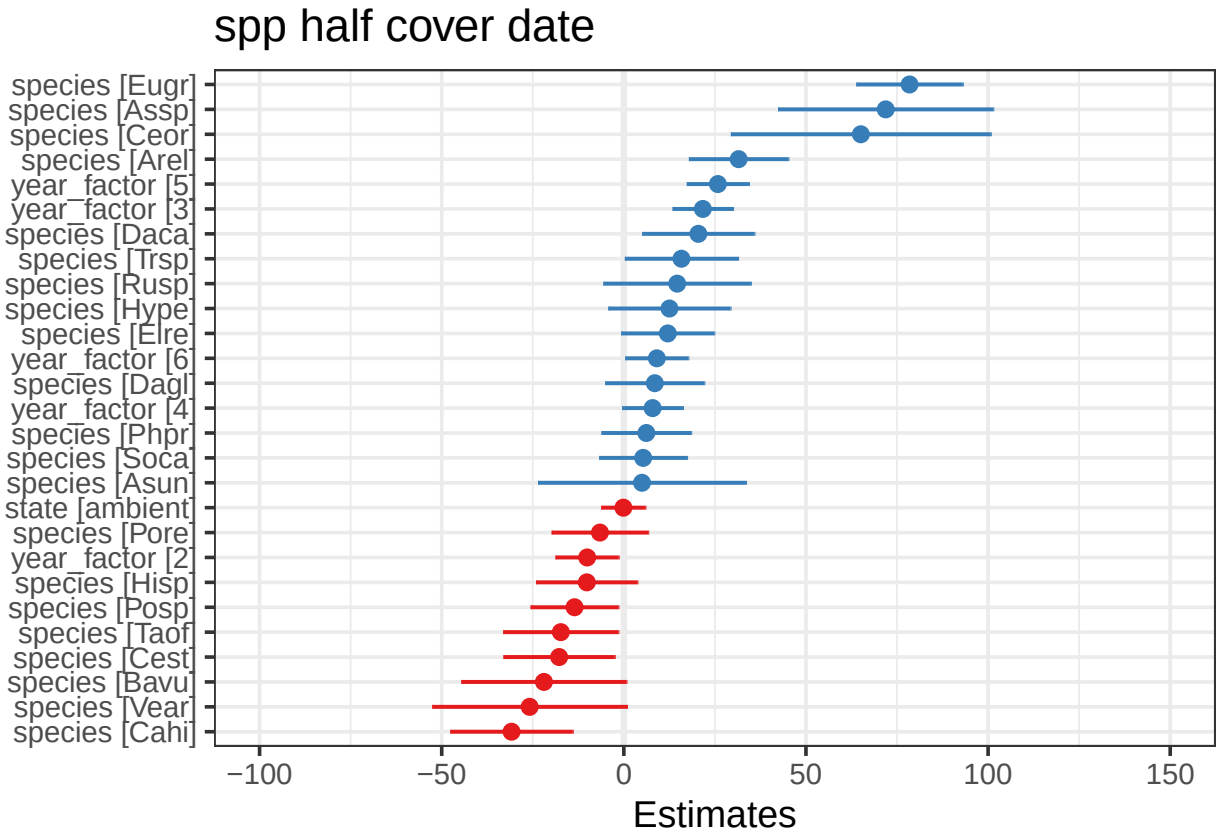
```
##  Asun - Ceor  -60.092 22.66 1536  -2.652 0.5117
##  Asun - Cest   22.743 15.34 1523   1.482 0.9977
##  Asun - Daca  -15.484 15.42 1527  -1.004 1.0000
##  Asun - Dagl   -3.521 14.92 1530  -0.236 1.0000
##  Asun - Elre   -7.085 14.73 1527  -0.481 1.0000
##  Asun - Eugr  -73.469 15.19 1530  -4.837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

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

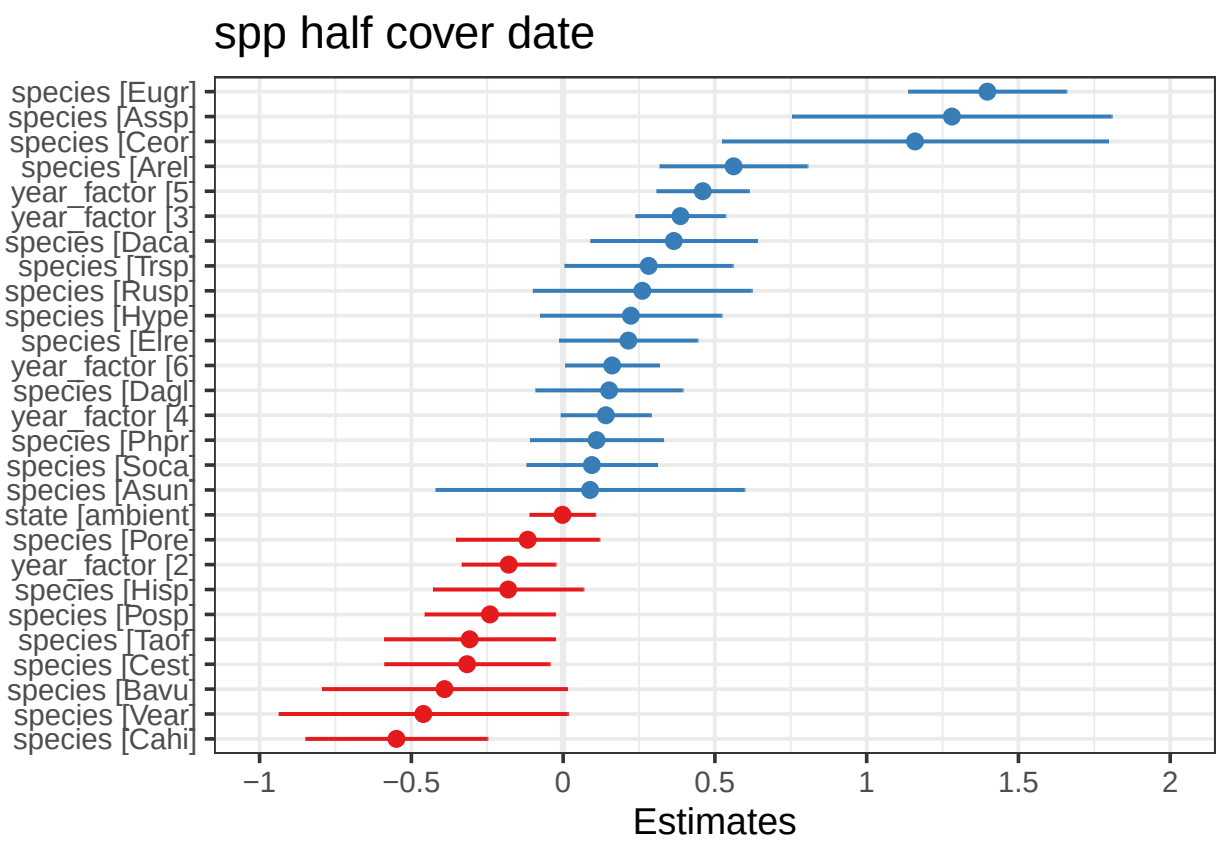
```
##  Elre - Posp   25.597  6.27 1516   4.084 0.0087
##  Elre - Rusp   -2.579 10.48 1531  -0.246 1.0000
##  Elre - Soca    6.758  6.27 1516   1.078 1.0000
##  Elre - Taof   29.360  8.22 1536   3.572 0.0547
##  Elre - Trsp   -3.750  8.09 1529  -0.464 1.0000
##  Elre - Vear   37.923 13.86 1539   2.737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

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

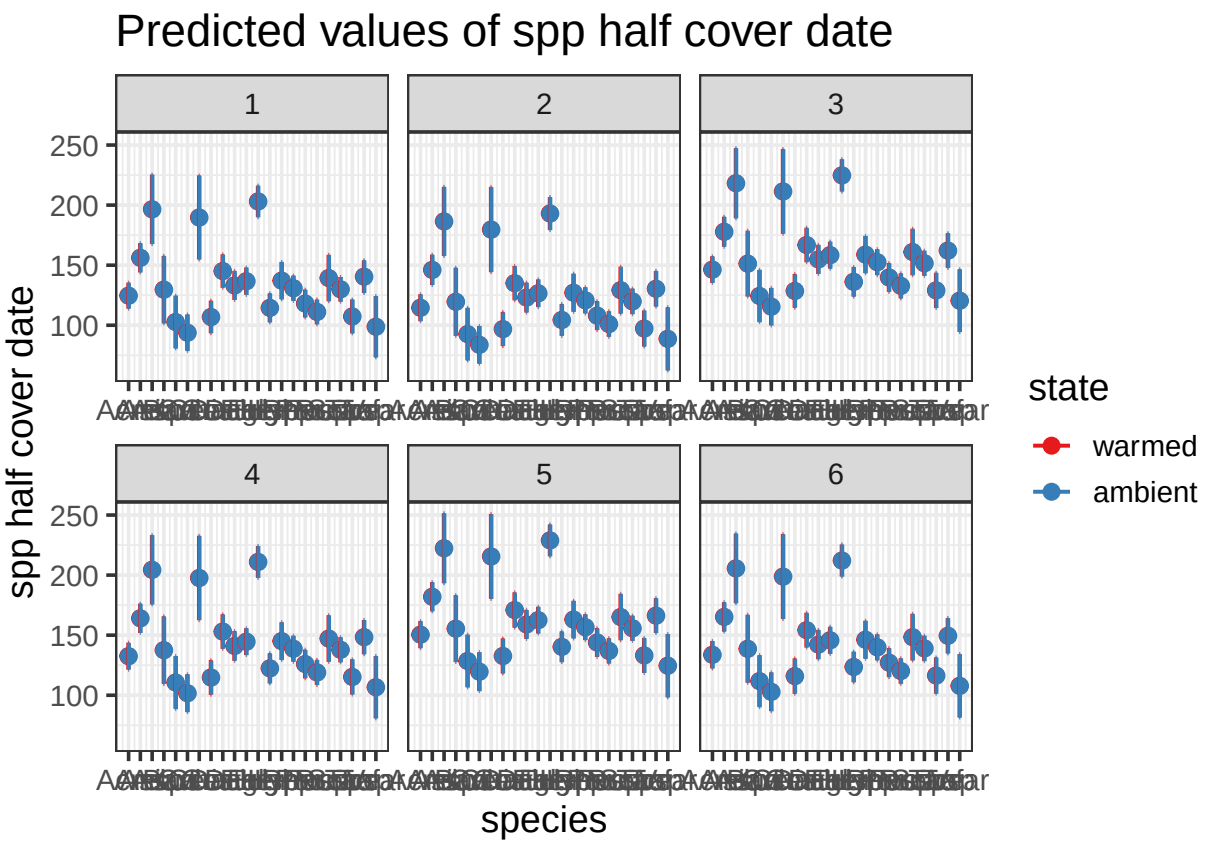
```
# using model 7a for overall species - level greenup model #

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




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

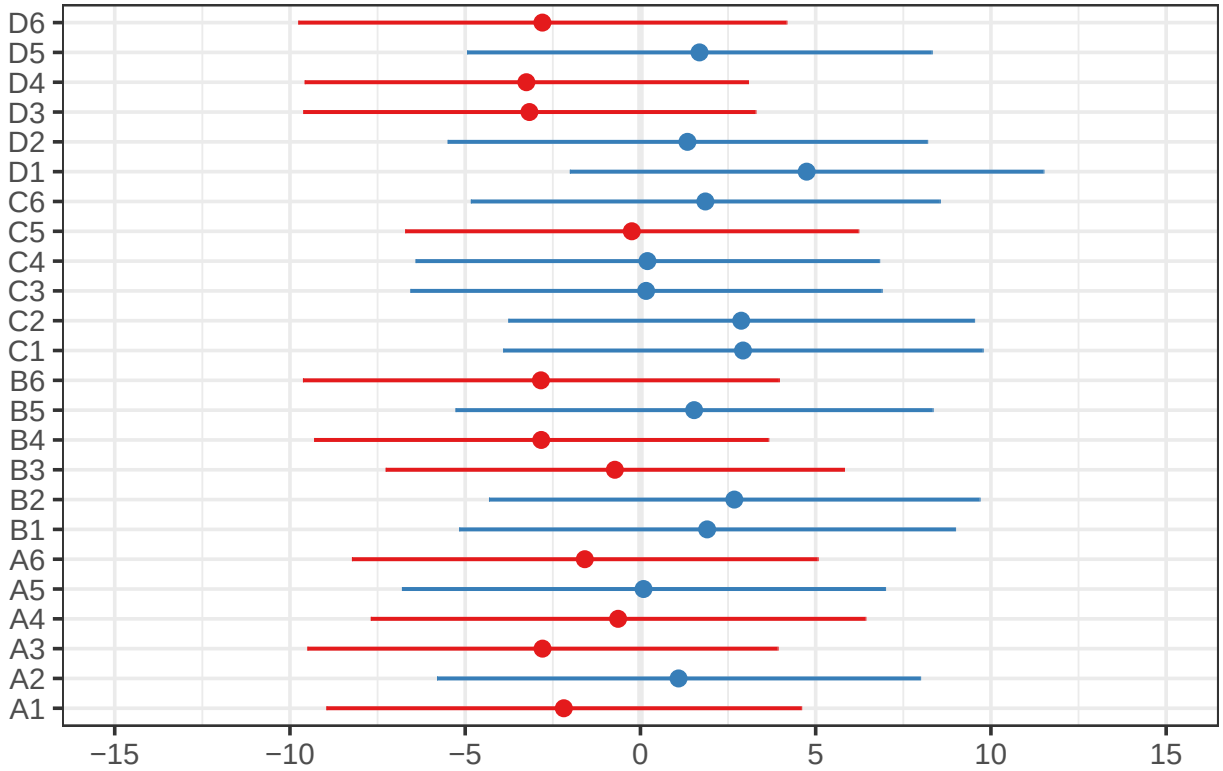



```
# these are the fixed predicted values: - note this is a new
# plot
plot_model(mod7a, type = "pred", terms = c("species", "state",
    "year_factor"))
```




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

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

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

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

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

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

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

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

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

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

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

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

```
## Warning: Model failed to converge with 2 negative eigenvalues: -1.7e-02 -1.0e+00
```

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

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

```
## Warning: Model failed to converge with 2 negative eigenvalues: -3.7e-02 -3.1e+00
```

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

```
## Data: green_kbs
```

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

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

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

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

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

```
summary(mod9a)
```

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

```
## originBoth            -11.3637     4.9735 1509.7461  -2.285 0.022459 *
## originExotic          -15.2916     3.4880 1503.3942  -4.384 1.25e-05 ***
## factor(year_factor)2   -8.4820     4.7478 1497.7707  -1.786 0.074221 .
## factor(year_factor)3   22.4346     4.5361 1498.9553   4.946 8.44e-07 ***
## factor(year_factor)4   12.3891     4.5725 1502.6179   2.710 0.006815 **
## factor(year_factor)5   32.5549     4.6117 1500.3453   7.059 2.55e-12 ***
## factor(year_factor)6   15.8772     4.6777 1506.5918   3.394 0.000706 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn origin orgnBt orgnEx fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.352
## origin      -0.366 -0.002
## originBoth  -0.438 -0.023  0.334
## originExotc -0.577 -0.013  0.478  0.505
## 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    3019    3019     1   42.21   1.056     0.31
## origin 110931   36977     3 1470.01  12.934 2.43e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

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

```
##  warmed Native - warmed Both       11.364 4.99 1519.0  2.275  0.3080
##  warmed Native - ambient Both      11.627 5.91  268.8  1.969  0.5052
##  warmed Native - warmed Exotic     15.292 3.50 1511.8  4.369  0.0004
##  warmed Native - ambient Exotic    15.554 4.76  121.8  3.270  0.0295
##  ambient Native - warmed           30.698 6.17  328.4  4.972  <.0001
##  ambient Native - ambient          30.961 5.23 1501.6  5.914  <.0001
##  ambient Native - warmed Both      11.101 6.03  287.7  1.842  0.5920
##  ambient Native - ambient Both     11.364 4.99 1519.0  2.275  0.3080
##  ambient Native - warmed Exotic    15.029 4.82  130.2  3.121  0.0447
##  ambient Native - ambient Exotic   15.292 3.50 1511.8  4.369  0.0004
##  warmed  - ambient                  0.263 3.26   25.9  0.081  1.0000
##  warmed  - warmed Both            -19.597 5.91 1517.6 -3.316  0.0209
##  warmed  - ambient Both           -19.334 6.70  409.8 -2.885  0.0783
##  warmed  - warmed Exotic          -15.669 4.71 1505.7 -3.329  0.0201
##  warmed  - ambient Exotic         -15.406 5.71  245.7 -2.699  0.1280
##  ambient  - warmed Both           -19.860 6.80  425.9 -2.920  0.0711
##  ambient  - ambient Both          -19.597 5.91 1517.6 -3.316  0.0209
##  ambient  - warmed Exotic         -15.932 5.75  254.7 -2.772  0.1069
##  ambient  - ambient Exotic        -15.669 4.71 1505.7 -3.329  0.0201
##  warmed Both - ambient Both         0.263 3.26   25.9  0.081  1.0000
##  warmed Both - warmed Exotic        3.928 4.42 1517.0  0.888  0.9871
##  warmed Both - ambient Exotic       4.191 5.54  213.5  0.757  0.9950
##  ambient Both - warmed Exotic       3.665 5.46  206.4  0.672  0.9976
##  ambient Both - ambient Exotic      3.928 4.42 1517.0  0.888  0.9871
##  warmed Exotic - ambient Exotic     0.263 3.26   25.9  0.081  1.0000
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

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

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

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

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

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

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

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

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

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

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

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

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

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

```
summary(mod11a)
```

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

```
## growth_habitGraminoid    0.7180     3.0515 1510.8513   0.235 0.814020
## growth_habitVine        62.9345    19.3561 1421.6557   3.251 0.001175 **
## factor(year_factor)2    -8.6078     4.8090 1497.5236  -1.790 0.073668 .
## factor(year_factor)3    21.9800     4.5792 1500.4925   4.800 1.74e-06 ***
## factor(year_factor)4    12.1910     4.6253 1505.2357   2.636 0.008482 **
## factor(year_factor)5    32.2552     4.6818 1503.5078   6.889 8.21e-12 ***
## factor(year_factor)6    15.7438     4.7531 1509.5846   3.312 0.000947 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_V fc(_)2 fc(_)3 fc(_)4 fc(_)5
## stateambint -0.409
## growth_habt -0.255 -0.030
## grwth_hbtGr -0.291  0.029  0.284
## grwth_hbtVn -0.062 -0.030  0.051  0.064
## 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")
```

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

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

```
##  5           Graminoid       160  3.89  774      152      168
##  6           Graminoid       143  3.97  775      136      151
##  1           Vine            190 19.54 1420      152      228
##  2           Vine            181 19.81 1444      142      220
##  3           Vine            212 19.69 1435      173      251
##  4           Vine            202 19.63 1432      164      241
##  5           Vine            222 19.72 1422      184      261
##  6           Vine            206 19.72 1431      167      244
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor, growth_habit`
##  1                         estimate    SE   df t.ratio p.value
##  1 Forb - 2 Forb              8.608  4.82 1506  1.784  0.9851
##  1 Forb - 3 Forb            -21.980  4.59 1509 -4.784  0.0005
##  1 Forb - 4 Forb            -12.191  4.64 1514 -2.626  0.5761
##  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)

# KD note: these models are included below in plot-level
# section New version of our model incorporating interaction
# term and species within year so that there is a separate
# intercept and slope for each species. The issue here is
# that there are some species that are not found each year.
# Easiest to remove those from another version of this
# dataframe before running below. Otherwise, it's not a
```

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

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

KBS Plot-level Mixed Effects Models:

```
# plot-level models using the species summarized data frame
# with specific random effects note: we decided this was not
# the best approach - better to use the summarized dataframes
# mod1ps <- lmer(spp_half_cover_date ~ state +
# (1|plot/species), green_kbs, REML=FALSE) mod2ps <-
# lmer(spp_half_cover_date ~ state + insecticide +
# (1|plot/species), green_kbs, REML=FALSE) mod3ps <-
# lmer(spp_half_cover_date ~ state + insecticide +
# year_factor + (1|plot/species), green_kbs, #REML=FALSE)
# mod4ps <- lmer(spp_half_cover_date ~ state + year_factor +
# (1|plot/species), green_kbs, REML=FALSE) mod5ps <-
# lmer(spp_half_cover_date ~ state + year_factor +
# (1|species) + (1|plot), green_kbs, REML=FALSE) mod6ps <-
# lmer(spp_half_cover_date ~ state + year_factor +
# insecticide + (1|species) + (1|plot), #green_kbs,
# REML=FALSE) mod7ps <- lmer(spp_half_cover_date ~ state +
# year_factor + insecticide + (1|species), green_kbs,
# #REML=FALSE) anova(mod1ps,mod2ps) #1 anova(mod1ps,mod3ps)
# #3 anova(mod4ps,mod3ps) #4 anova(mod4ps,mod5ps) #5
# anova(mod6ps,mod5ps) #5 anova(mod5ps,mod7ps) # the same...?
# AICctab(mod1ps, mod2ps, mod3ps, mod4ps, mod5ps, mod6ps,
# mod7ps,weights=T) summary(mod5ps) anova(mod4ps)

# plot-level models using the re-summarized data frame
modfull <- lmer(plot_half_cover_date ~ state * year_factor +
    insecticide * year_factor + (1 | plot), green_kbsp, REML = F)
```

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

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

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

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

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

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

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

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

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

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

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

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

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

```
mod7p <- lmer(plot_half_cover_date ~ state * year_factor + (1 |
    plot), green_kbsp, REML = FALSE)
mod8p <- lmer(plot_half_cover_date ~ state * year_factor + insecticide +
    (1 | plot), green_kbsp, REML = FALSE)
```

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

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

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

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

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

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

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

```
AICtab(modfull, mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p,
    mod8p, mod9p, mod10p, mod11p, weights = T)  # 5p, 6p, or 9p
```

```
##         dAIC df weight
## mod6p    0.0 10 0.3286
## mod5p    0.3 9  0.2862
## mod9p    0.6 11 0.2443
## mod8p    3.9 15 0.0472
## mod10p   3.9 15 0.0470
## mod7p    4.3 14 0.0381
## modfull  7.4 20 0.0082
## mod11p  14.1 26 <0.001
## mod1p   18.2 4  <0.001
## mod3p   18.4 5  <0.001
## mod2p   18.7 4  <0.001
## mod4p   19.3 6  <0.001
```

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

```
## Data: green_kbsp
## Models:
## mod5p: plot_half_cover_date ~ state + year_factor + (1 | plot)
```

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

```
anova(mod9p, mod5p)  # should I go with 9p? includes insecticide as well
```

```
## Data: green_kbsp
## Models:
## mod5p: plot_half_cover_date ~ state + year_factor + (1 | plot)
## mod9p: plot_half_cover_date ~ state * insecticide + year_factor + (1 |
## mod9p:     plot)
##       npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5p    9 1532.5 1559.2 -757.25   1514.5
## mod9p   11 1532.8 1565.4 -755.41   1510.8 3.684  2     0.1585
```

```
summary(mod9p)
```

```
## 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
##   1532.8   1565.4   -755.4   1510.8      132
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.6653 -0.7315 -0.2379  0.3021  2.9538
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)    0      0.00
##  Residual             2269     47.64
## Number of obs: 143, groups:  plot, 24
##
## Fixed effects:
##                                    Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                          90.969     11.914 143.000   7.635 2.93e-12
## stateambient                         23.345     11.311 143.000   2.064 0.040837
## insecticideno_insects                -2.722     11.228 143.000  -0.242 0.808784
## year_factor2                         25.042     13.752 143.000   1.821 0.070701
## year_factor3                         50.083     13.752 143.000   3.642 0.000378
## year_factor4                         42.417     13.752 143.000   3.084 0.002448
## year_factor5                         69.208     13.752 143.000   5.033 1.43e-06
## year_factor6                         55.101     13.904 143.000   3.963 0.000116
## stateambient:insecticideno_insects  -18.956     15.938 143.000  -1.189 0.236268
##
## (Intercept)                         ***
## stateambient                        *
## insecticideno_insects
## year_factor2                        .
## year_factor3                        ***
```

```
## year_factor4                       **
## year_factor5                       ***
## year_factor6                       ***
## stateambient:insecticideno_insects
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn insct_ yr_fc2 yr_fc3 yr_fc4 yr_fc5 yr_fc6
## stateambint -0.471
## insctcdn_ns -0.471  0.496
## year_factr2 -0.577  0.000  0.000
## year_factr3 -0.577  0.000  0.000  0.500
## year_factr4 -0.577  0.000  0.000  0.500  0.500
## year_factr5 -0.577  0.000  0.000  0.500  0.500  0.500
## year_factr6 -0.575  0.018  0.000  0.495  0.495  0.495  0.495
## sttmbnt:ns_  0.334 -0.710 -0.705  0.000  0.000  0.000  0.000 -0.013
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(mod9p)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## state               6872  6871.5     1   143  3.0280  0.08399 .
## insecticide         5319  5319.0     1   143  2.3439  0.12799
## year_factor        72059 14411.9     5   143  6.3507 2.35e-05 ***
## state:insecticide   3210  3210.2     1   143  1.4146  0.23627
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod9p, list(pairwise ~ state * insecticide), adjust = "tukey")
```

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

```
## $`emmeans of state, insecticide`
##  state   insecticide emmean   SE   df lower.CL upper.CL
##  warmed  insects        131 8.20 22.5      114      148
##  ambient insects        155 8.33 23.6      137      172
##  warmed  no_insects     129 8.20 22.5      112      146
##  ambient no_insects     133 8.20 22.5      116      150
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, insecticide`
##  1                                    estimate   SE   df t.ratio p.value
##  warmed insects - ambient insects        -23.34 11.7 23.0 -1.997  0.2180
##  warmed insects - warmed no_insects        2.72 11.6 22.5  0.235  0.9953
##  warmed insects - ambient no_insects      -1.67 11.6 22.5 -0.144  0.9989
##  ambient insects - warmed no_insects      26.07 11.7 23.0  2.230  0.1448
##  ambient insects - ambient no_insects     21.68 11.7 23.0  1.855  0.2746
##  warmed no_insects - ambient no_insects   -4.39 11.6 22.5 -0.378  0.9811
##
## 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 4 estimates
```

```
mod9p.emm <- emmeans(mod9p, ~state * insecticide)  # why are the comparisons the same for each year?
```

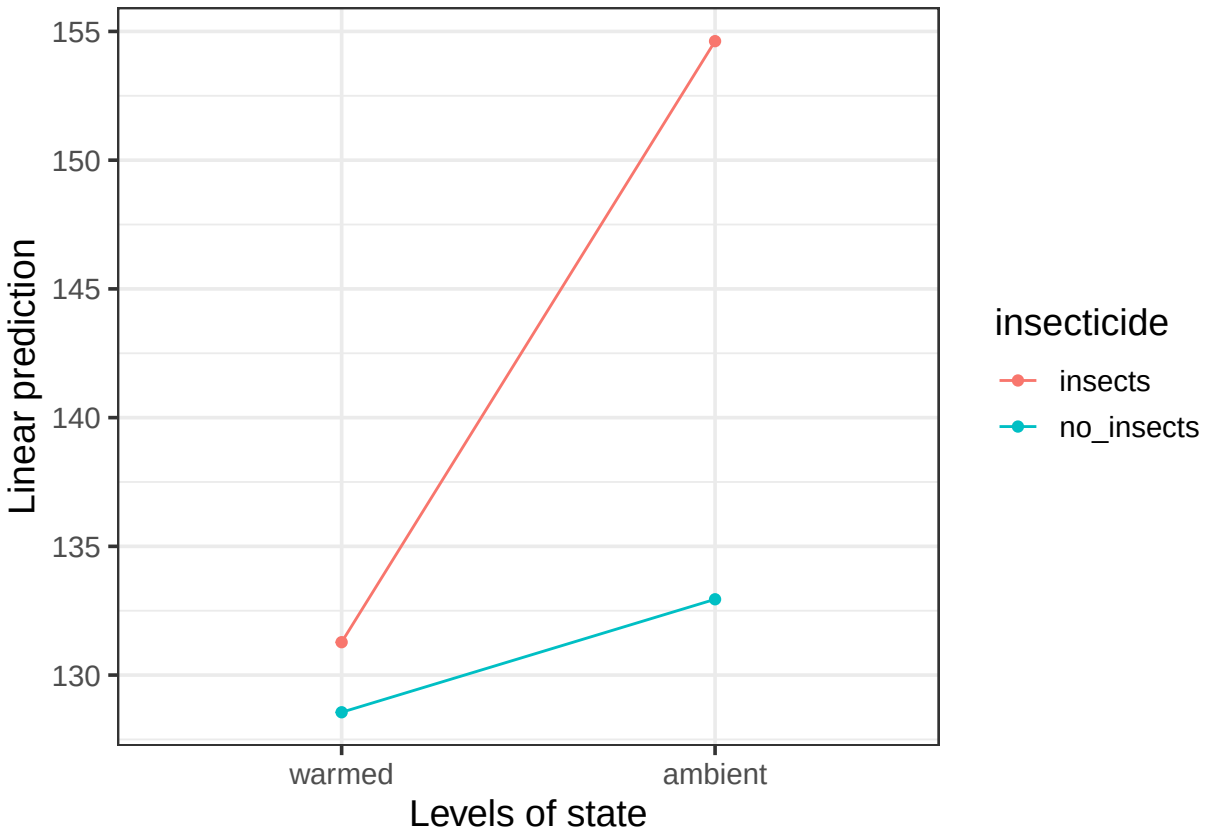
```
## boundary (singular) fit: see ?isSingular
```

```
contrast(mod9p.emm, "consec", simple = "each", combine = F, adjust = "mvt")
```

```
## $`simple contrasts for state`
## insecticide = insects:
##  contrast         estimate   SE   df t.ratio p.value
##  ambient - warmed    23.34 11.7 23.0 1.997   0.0577
##
## insecticide = no_insects:
##  contrast         estimate   SE   df t.ratio p.value
##  ambient - warmed     4.39 11.6 22.5 0.378   0.7087
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
##
## $`simple contrasts for insecticide`
## state = warmed:
##  contrast             estimate   SE   df t.ratio p.value
##  no_insects - insects    -2.72 11.6 22.5 -0.235  0.8166
##
## state = ambient:
##  contrast             estimate   SE   df t.ratio p.value
##  no_insects - insects   -21.68 11.7 23.0 -1.855  0.0765
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
```

```
emmip(mod9p, insecticide ~ state)
```

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



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)
```

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

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

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

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

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

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

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

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

```
## Data: green_umbs
## Models:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7: spp_half_cover_date ~ state + species + (1 + year_factor | plot)
##        npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## umod7a   23 7488.0 7594.6 -3721.0   7442.0
## umod7    33 7520.8 7673.7 -3727.4   7454.8     0 10          1
```

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

```
## Data: green_umbs
## Models:
## umod7a: spp_half_cover_date ~ state + species + year_factor + (1 | plot)
## umod7b: spp_half_cover_date ~ state * year_factor + species + (1 | plot)
```

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

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

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

```
summary(umod7a)
```

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

```
## year_factor3    5.802      3.837 760.000   1.512 0.130919
## year_factor4   -5.806      3.802 760.000  -1.527 0.127098
## year_factor5   -8.756      3.757 760.000  -2.330 0.020042 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
summary(umod7b)
```

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

```
## speciesSyla                39.5456    16.3453 760.0000   2.419  0.01578 *
## stateambient:year_factor2   0.7435     7.6547 760.0000   0.097  0.92265
## stateambient:year_factor3   3.4439     7.6289 760.0000   0.451  0.65181
## stateambient:year_factor4  -1.5988     7.5098 760.0000  -0.213  0.83147
## stateambient:year_factor5   4.0002     7.4386 760.0000   0.538  0.59089
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 25 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
## convergence code: 0
## boundary (singular) fit: see ?isSingular
summary(umod7c)

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

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

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

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

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

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

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

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

```
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 5 estimates
```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```
summary(umod9a)
```

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

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

```
anova(umod9)
```

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

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

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

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

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

```
##  1                               estimate   SE    df t.ratio p.value
##  warmed Native - ambient Native    -1.51 2.53  21.4 -0.598  0.9985
##  warmed Native - warmed             13.92 3.72 760.5  3.739  0.0049
##  warmed Native - ambient            12.40 4.51 188.2  2.749  0.1147
##  warmed Native - warmed Both       -21.38 5.66 760.6 -3.777  0.0042
##  warmed Native - ambient Both      -22.89 6.00 304.4 -3.816  0.0040
##  warmed Native - warmed Exotic      18.14 2.85 769.0  6.374  <.0001
##  warmed Native - ambient Exotic     16.63 3.82 102.5  4.358  0.0008
##  ambient Native - warmed            15.43 4.49 179.8  3.438  0.0163
##  ambient Native - ambient           13.92 3.72 760.5  3.739  0.0049
##  ambient Native - warmed Both      -19.86 6.39 414.0 -3.107  0.0420
##  ambient Native - ambient Both     -21.38 5.66 760.6 -3.777  0.0042
##  ambient Native - warmed Exotic     19.65 3.80  96.9  5.173  <.0001
##  ambient Native - ambient Exotic    18.14 2.85 769.0  6.374  <.0001
##  warmed  - ambient                  -1.51 2.53  21.4 -0.598  0.9985
##  warmed  - warmed Both             -35.29 6.23 762.0 -5.664  <.0001
##  warmed  - ambient Both            -36.80 6.53 363.0 -5.635  <.0001
##  warmed  - warmed Exotic             4.22 3.85 759.0  1.097  0.9573
##  warmed  - ambient Exotic            2.71 4.60 199.4  0.589  0.9990
##  ambient  - warmed Both            -33.78 6.91 472.3 -4.887  <.0001
##  ambient  - ambient Both           -35.29 6.23 762.0 -5.664  <.0001
##  ambient  - warmed Exotic            5.74 4.61 199.4  1.244  0.9175
##  ambient  - ambient Exotic           4.22 3.85 759.0  1.097  0.9573
##  warmed Both - ambient Both         -1.51 2.53  21.4 -0.598  0.9985
##  warmed Both - warmed Exotic        39.51 5.76 760.2  6.863  <.0001
##  warmed Both - ambient Exotic       38.00 6.49 426.9  5.860  <.0001
##  ambient Both - warmed Exotic       41.03 6.09 309.6  6.742  <.0001
##  ambient Both - ambient Exotic      39.51 5.76 760.2  6.863  <.0001
##  warmed Exotic - ambient Exotic     -1.51 2.53  21.4 -0.598  0.9985
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

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

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -4.1e+00
```

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

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

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

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

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

```
## Data: green_umbs
```

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

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

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

```
summary(umod11a)
```

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

```
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_ grwt_G grwt_T yr_fc2 yr_fc3 yr_fc4
## stateambint -0.392
## growth_habt -0.021 -0.043
## grwth_hbtGr -0.290  0.008  0.131
## grwth_hbtTr -0.019 -0.011  0.019  0.081
## year_factr2 -0.615  0.022 -0.164 -0.036 -0.004
## year_factr3 -0.611 -0.003 -0.005 -0.035 -0.068  0.504
## year_factr4 -0.630  0.017 -0.056 -0.029 -0.045  0.520  0.518
## year_factr5 -0.630 -0.008 -0.040 -0.020 -0.042  0.522  0.524  0.532
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(umod11)
```

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

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

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

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

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

UMBS Plot-level Mixed Effects Models:

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

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

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

```
## Data: green_umbsp
## Models:
## mod1pu: plot_half_cover_date ~ state + (1 | plot)
## mod2pu: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
## mod3pu: plot_half_cover_date ~ state * year_factor + (1 | plot)
##        npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod1pu    4 1200.0 1211.1 -595.98   1192.0
## mod2pu    8 1181.9 1204.2 -582.97   1165.9 26.024  4   3.13e-05 ***
## mod3pu   12 1181.3 1214.7 -578.65   1157.3  8.642  4     0.0707 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod2pu)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: plot_half_cover_date ~ state + factor(year_factor) + (1 | plot)
##    Data: green_umbsp
##
##      AIC      BIC   logLik deviance df.resid
##   1181.9   1204.2   -583.0   1165.9      112
```

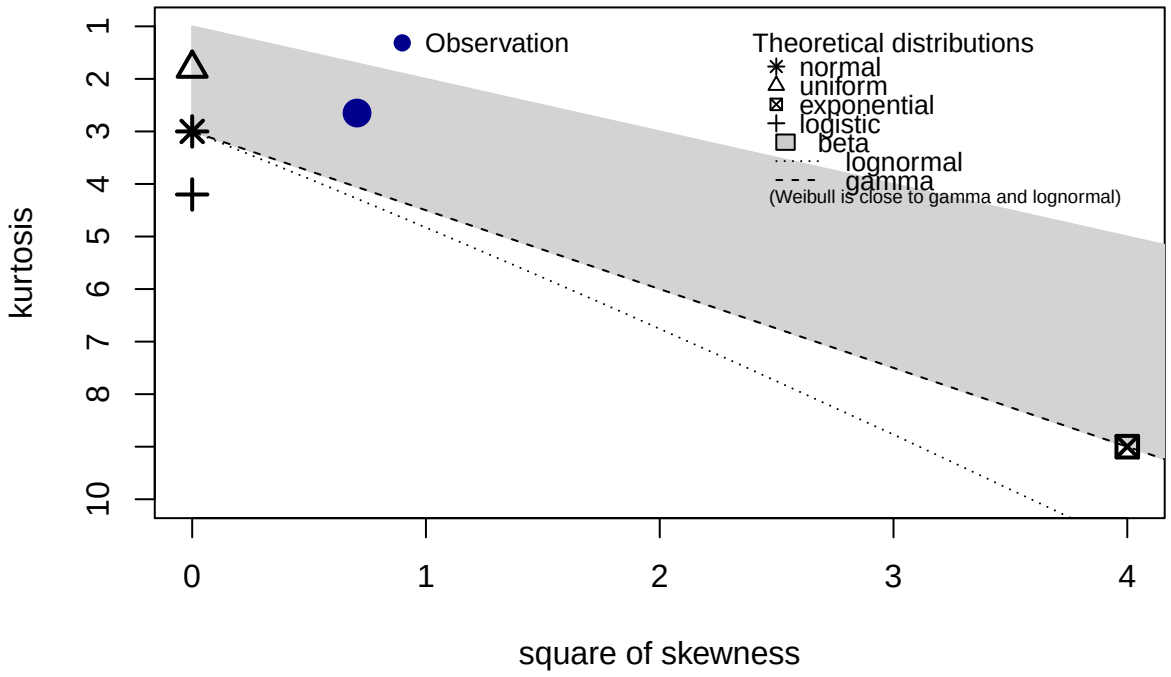
```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8579 -0.6259 -0.2222  0.5474  3.0755
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept)  30.97    5.565
##  Residual             941.80   30.689
## Number of obs: 120, groups:  plot, 24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

ORIGINAL CODE BELOW; not edited by Phoebe

can pretty much ignore everything below!

Seeing what other distribution could fit

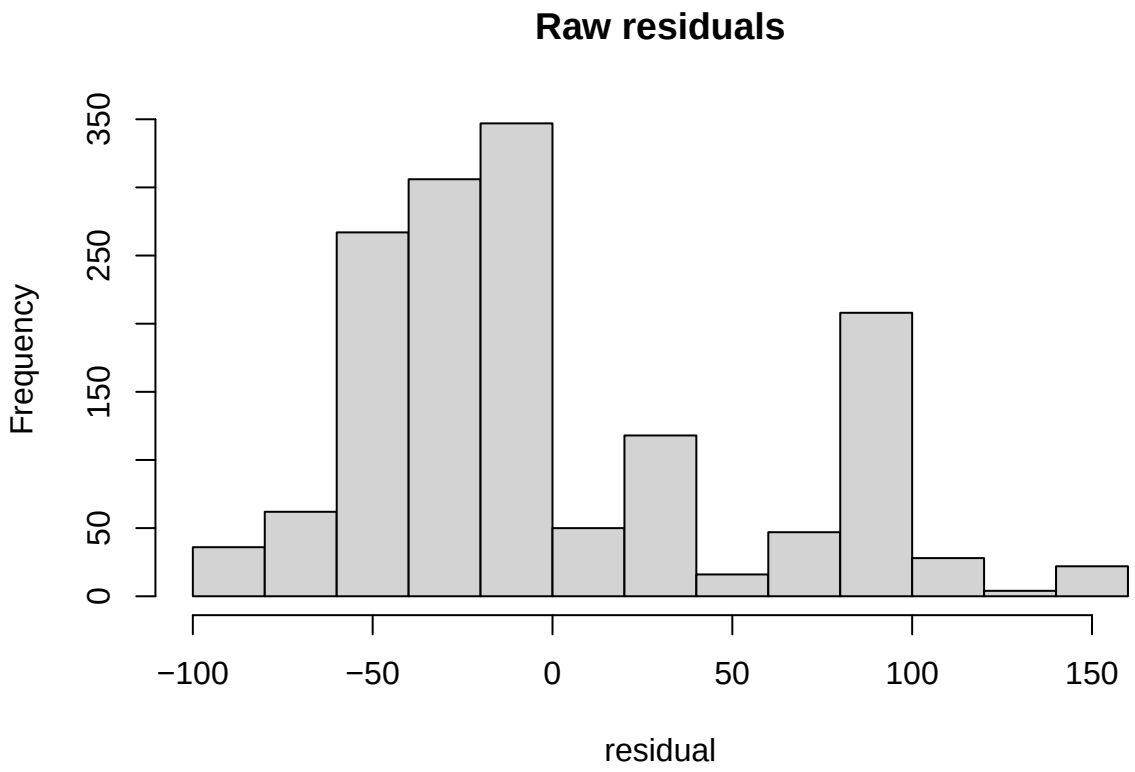
```
descdist(green_kbs$spp_half_cover_date, discrete = FALSE)
```



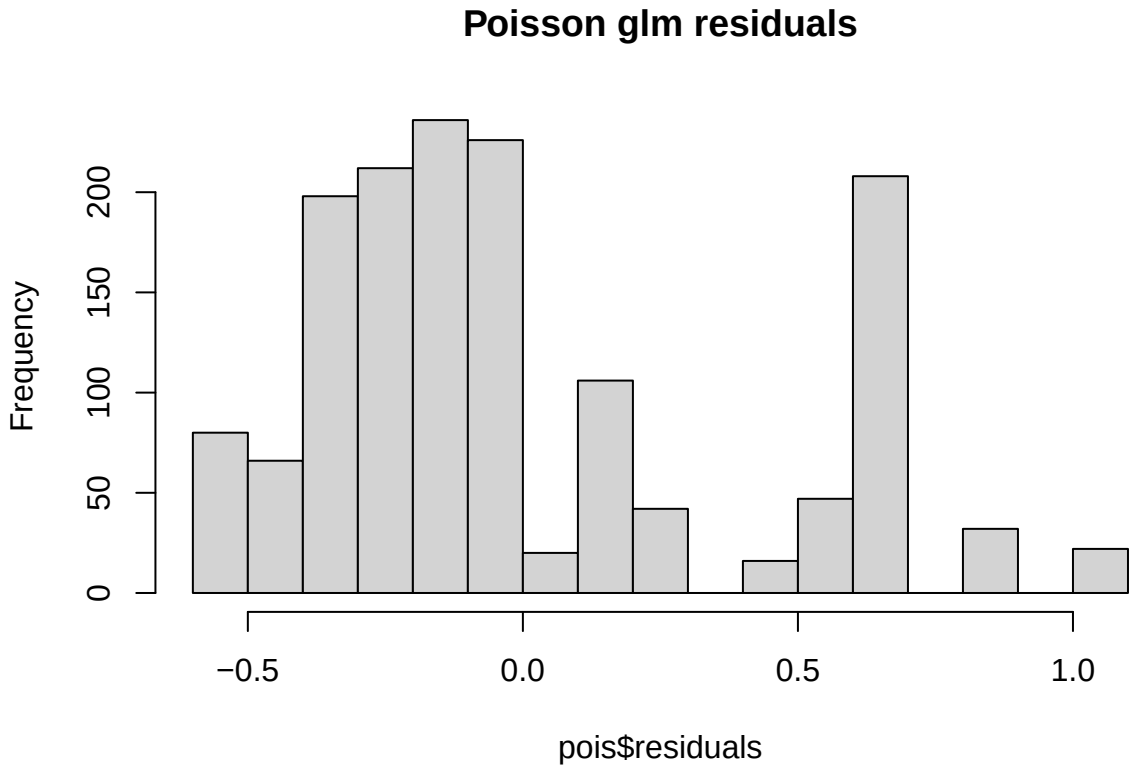

```
## summary statistics
## ------
## min:  59   max:  289
## median:  124
## mean:  139.3309
## estimated sd:  56.12957
## estimated skewness:  0.8397458
## estimated kurtosis:  2.650025
```

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| = 0.0107867 (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) 0.035562 0.1886
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -28.182598   3.682645  -7.653 1.97e-14 ***
## stateambient          -43.588658   4.908873  -8.880  < 2e-16 ***
## year                    0.016413   0.001824   8.996  < 2e-16 ***
## insecticideno_insects  -0.006946   0.023099  -0.301    0.764
## stateambient:year       0.021595   0.002432   8.880  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn year   insct_
## stateambint -0.701
## year        -1.000  0.701
```

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

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

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

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

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly 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) 0.035936 0.1896
## Number of obs: 1511, groups:  plot, 24; species, 22
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -5.122e+01  2.628e+00 -19.493   <2e-16 ***
## stateambient          -4.661e-04  2.306e-02  -0.020    0.984
## year                   2.783e-02  1.302e-03  21.378   <2e-16 ***
## insecticideno_insects -5.141e-03  2.306e-02  -0.223    0.824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation of Fixed Effects:
##             (Intr) sttmbn year
## stateambint  0.003
## year        -1.000 -0.007
## insctcdn_ns -0.016 -0.003  0.011
## convergence code: 0
## Model failed to converge with max|grad| = 0.00446952 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
##  - Rescale variables?
```

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

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

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

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

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

Can't figure out what this means

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

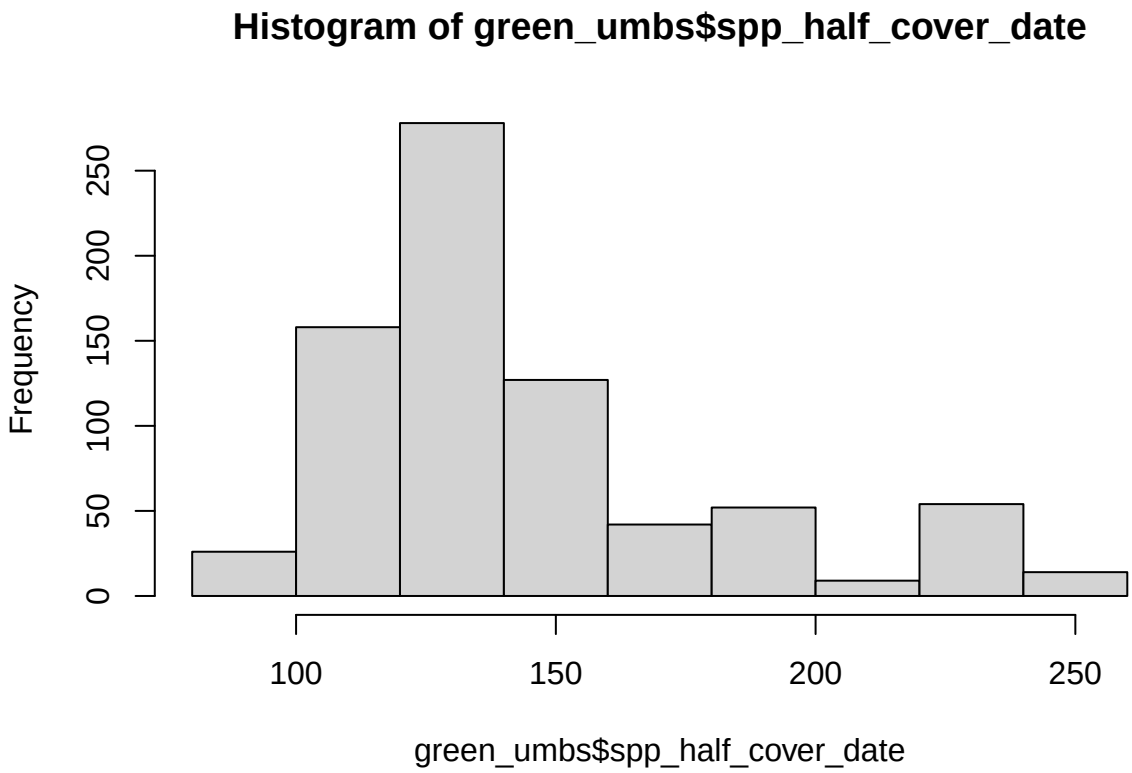
```
# friedman_kbs <- green_kbs %>%
# friedman_test(spp_half_cover_date ~ state | plot)
```

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

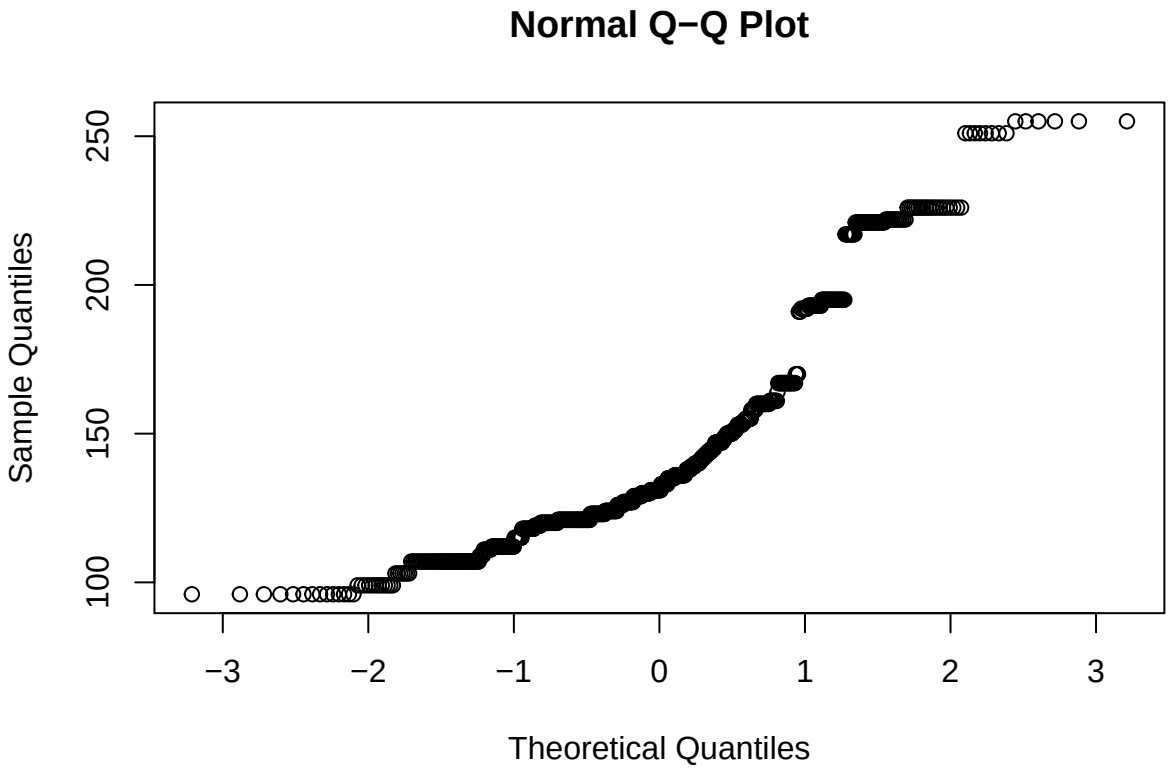
UMBS

Checking for normality

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



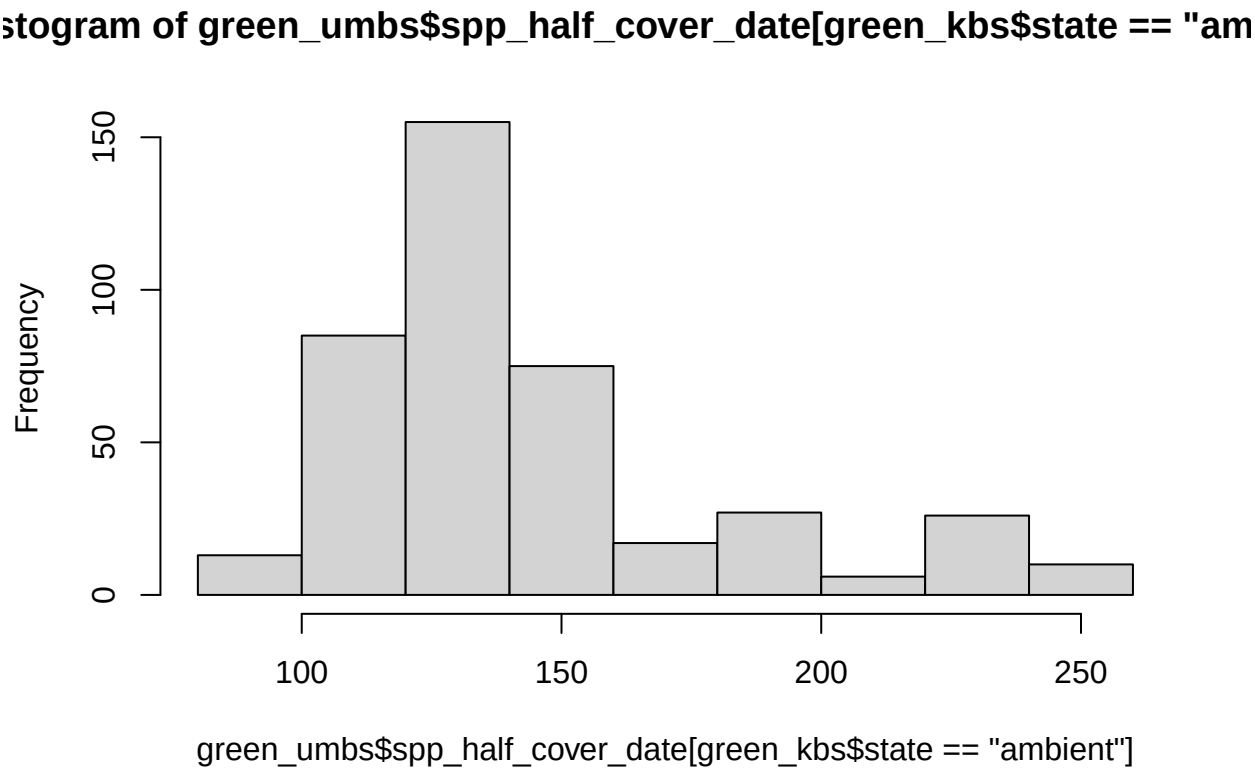

```
qqnorm(green_umbs$spp_half_cover_date)
```



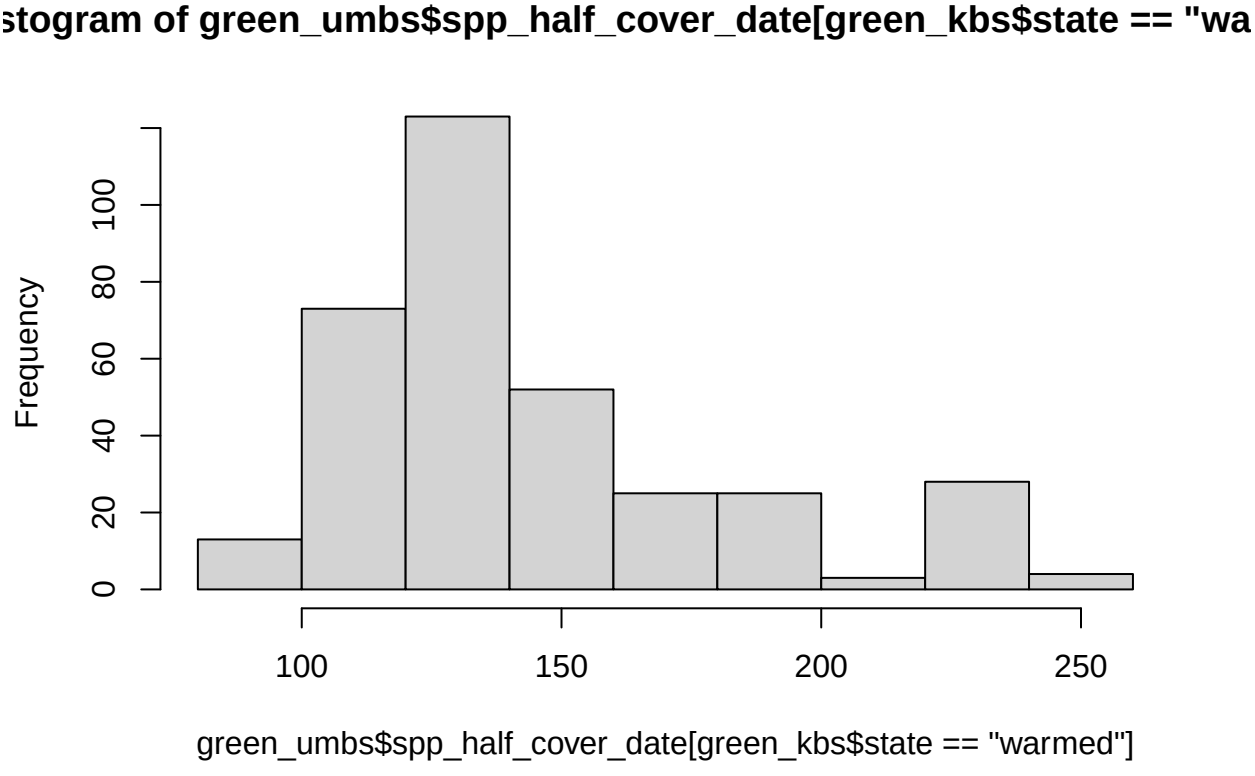

```
shapiro.test(green_umbs$spp_half_cover_date)
```

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

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



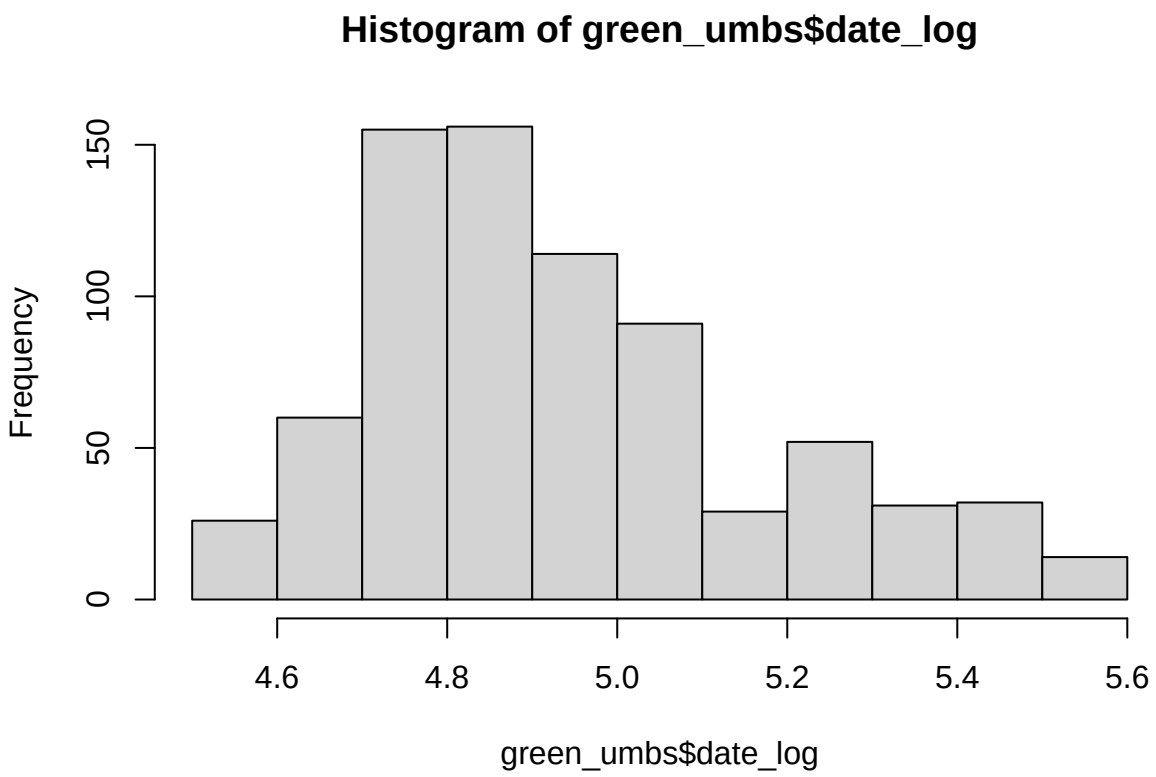

```
hist(green_umbs$spp_half_cover_date[green_kbs$state == "warmed"])
```



These look pretty good

Trying log transformation

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



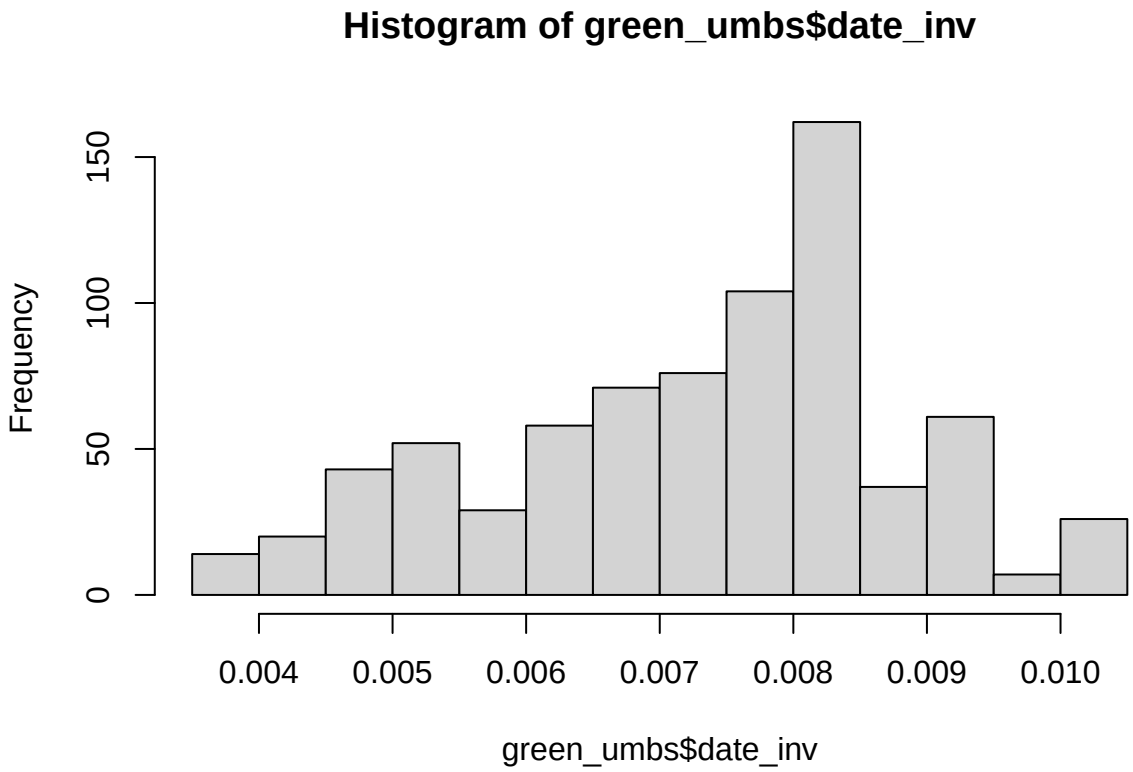

```
shapiro.test(green_umbs$date_log)
```

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

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

Trying inverse tranformation

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




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

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

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