

warmXtrophic Project: Flowering Phenology Analyses

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December 15, 2021

Load in packages & data

```
# clear all existing data
rm(list = ls())

# Load packages
library(tidyverse)
library(ggplot2)
library(lme4)
library(lmerTest)
library(emmeans)
library(vegan)
library(car)
library(rstatix)
library(scales)
library(fitdistrplus)
library(moments) # for calculating skewness of data
library(ggpubr)
library(jtools) # summ() function
library(predictmeans)
library(olsrr)
library(car)
library(fitdistrplus)
library(ggpubr)
library(interactions)
library(sjPlot)
library(effects)
library(glmmTMB)
library(GGally) # ggpairs() function
library(bbmle) # AICtab() function

# Set working directory
Sys.getenv("L1DIR")

## [1] "/Volumes/GoogleDrive/Shared drives/SpaCE_Lab_warmXtrophic/data/L1"

L0_dir <- Sys.getenv("LODIR")
L1_dir <- Sys.getenv("L1DIR")
L2_dir <- Sys.getenv("L2DIR")
```

```

# Set ggplot2 plotting This code for ggplot2 sets the theme to mostly black and
# white (Arial font, and large font, base size=24)
theme_set(theme_bw(14))
theme_update(axis.text.x = element_text(size = 12, angle = 90), axis.text.y = element_text(size = 12))

# Read in data
flwr_species <- read.csv(file.path(L2_dir, "phenology/final_flwr_species_L2.csv")) # species level data
flwr_plot <- read.csv(file.path(L2_dir, "phenology/final_flwr_plot_L2.csv")) # plot level data

# get rid of 'X' column that shows up
flwr_species$X <- NULL
flwr_plot$X <- NULL
# take a look at the data to see if looks good
View(flwr_species)
View(flwr_plot)

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

## [1] "ambient" "warmed"

# [1] 'ambient' 'warmed'
flwr_species$state <- factor(flwr_species$state, levels(flwr_species$state)[c(2,
  1)])
levels(flwr_species$state)

## [1] "warmed" "ambient"

# [1] 'warmed' 'ambient'

# again for plot level data
flwr_plot$state <- as.factor(flwr_plot$state)
levels(flwr_plot$state)

## [1] "ambient" "warmed"

# [1] 'ambient' 'warmed'
flwr_plot$state <- factor(flwr_plot$state, levels(flwr_plot$state)[c(2, 1)])
levels(flwr_plot$state)

## [1] "warmed" "ambient"

# [1] 'warmed' 'ambient'

umbs_flwr_plot <- subset(flwr_plot, site == "umbs") # pull out umbs only data at plot level
# delete 2021 data from umbs dataframe (doesn't make sense to have bc we can't
# get min flower/sd, median flower, or flower duration from 2021 UMBS)
umbs_flwr_plot <- subset(umbs_flwr_plot, year != "2021")

```

```

umbs_flwr_spp <- subset(flwr_species, site == "umbs") # pull out umbs only data at species level
umbs_flwr_spp <- subset(umbs_flwr_spp, year != "2021") # delete 2021 data
kbs_flwr_plot <- subset(flwr_plot, site == "kbs") # pull out kbs only data at plot level
kbs_flwr_spp <- subset(flwr_species, site == "kbs") # pull out kbs only data at species level

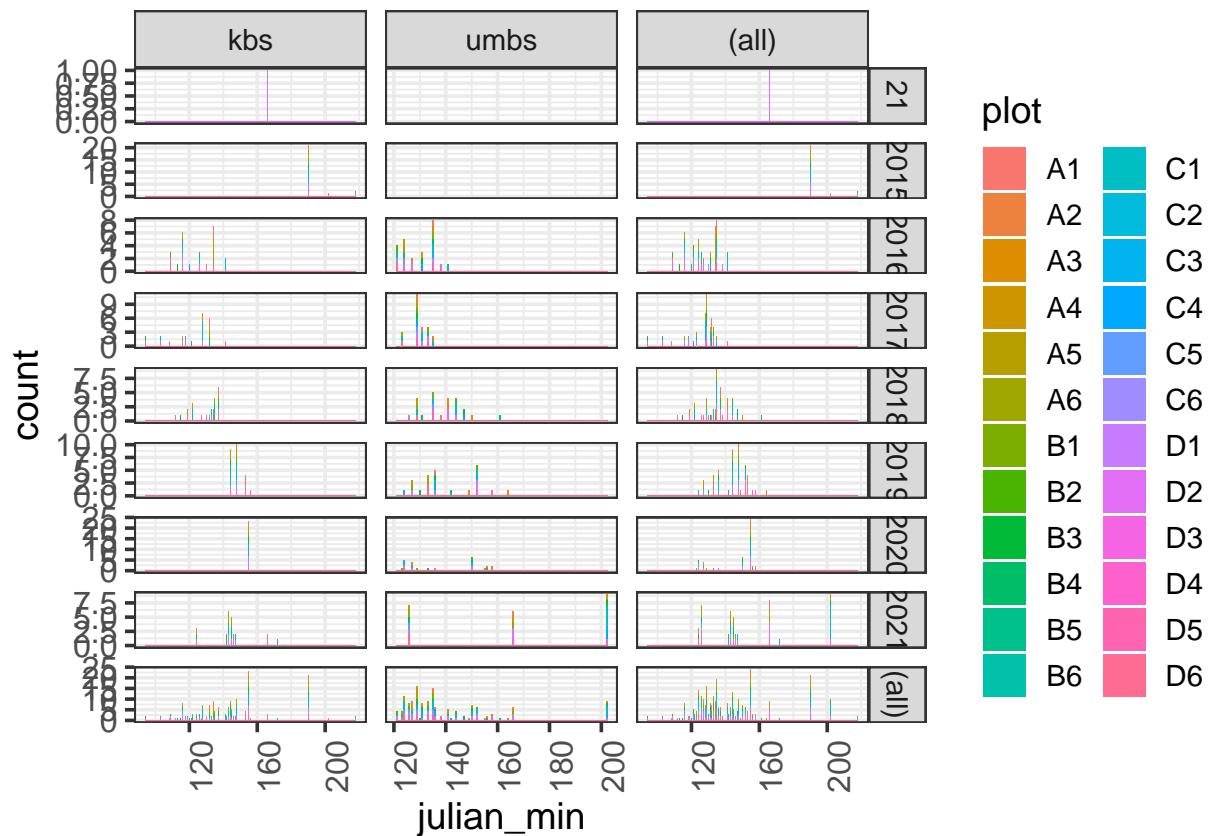
```

Data exploration for minimum (first) Julian date of flowering at the PLOT for both sites

```

# Visualizing avg minimum Julian date for both sites at the PLOT LEVEL
ggplot(fltr_plot, aes(julian_min, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

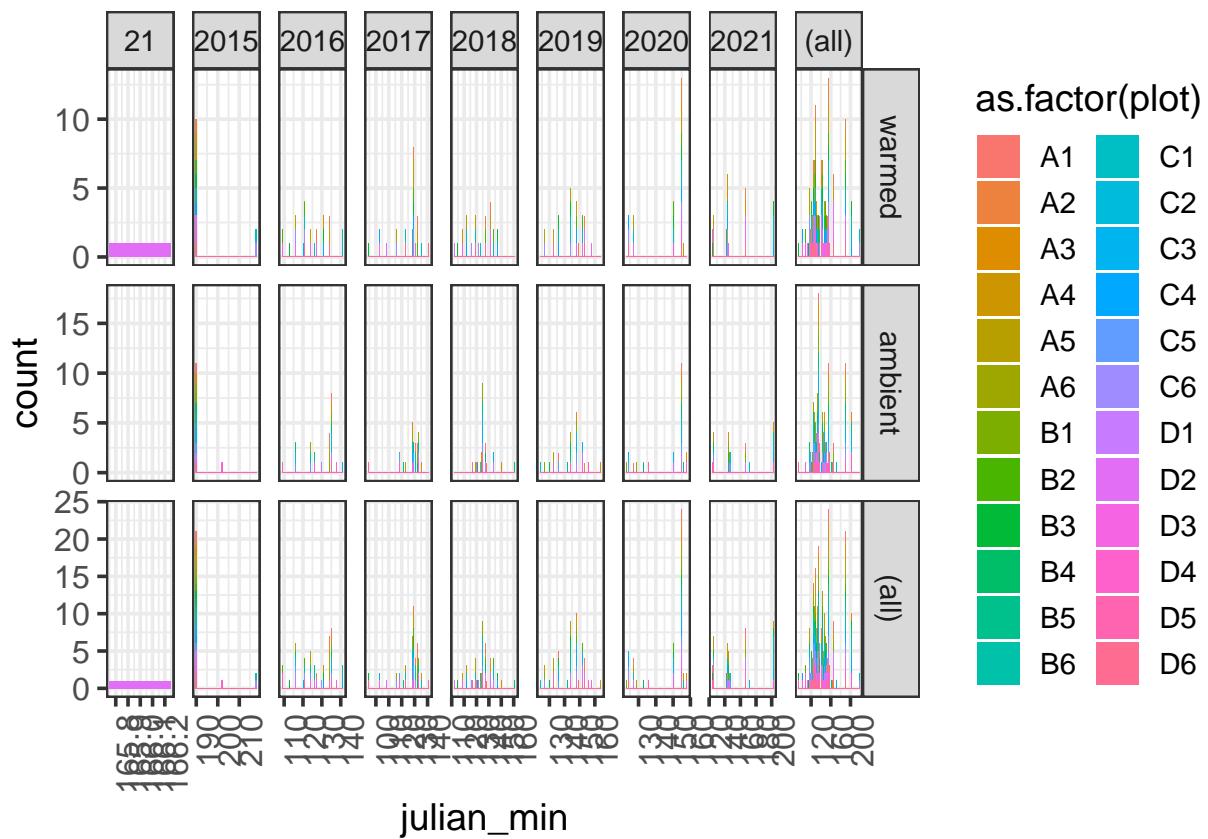
```



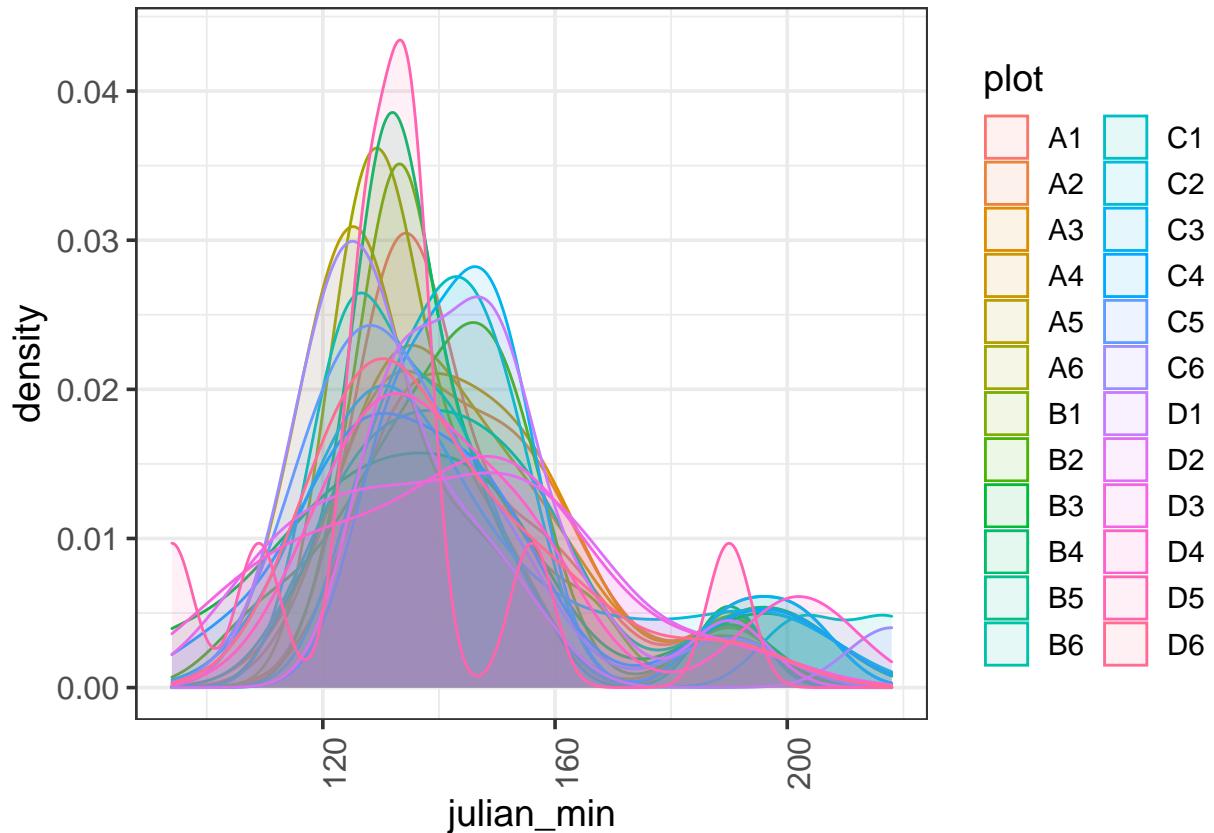
```

ggplot(fltr_plot, aes(julian_min, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

```



```
ggplot(fltrr_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(flrwr_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year)
```

```
## Warning: Groups with fewer than two data points have been dropped.
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```



```
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

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```

```

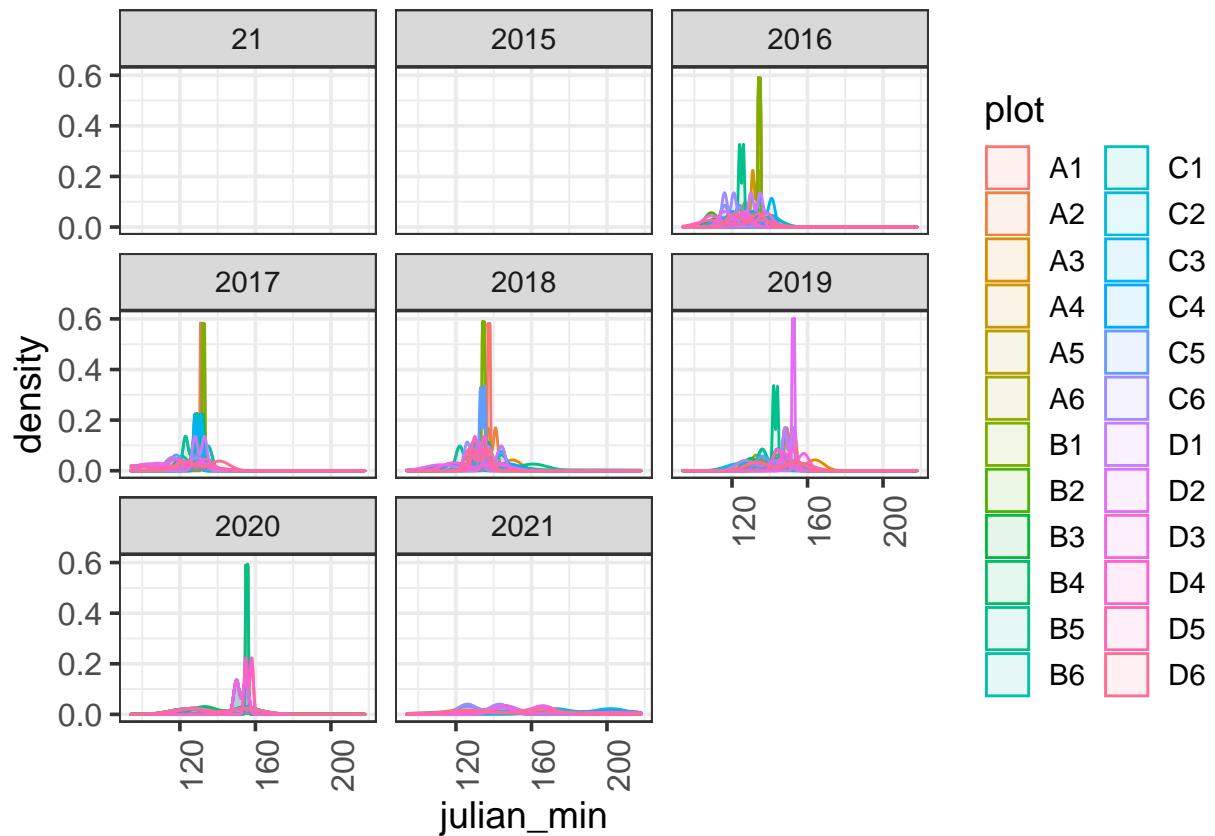
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## Inf

```



```

ggplot(fltrr_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)

```

```

## Warning: Groups with fewer than two data points have been dropped.

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```



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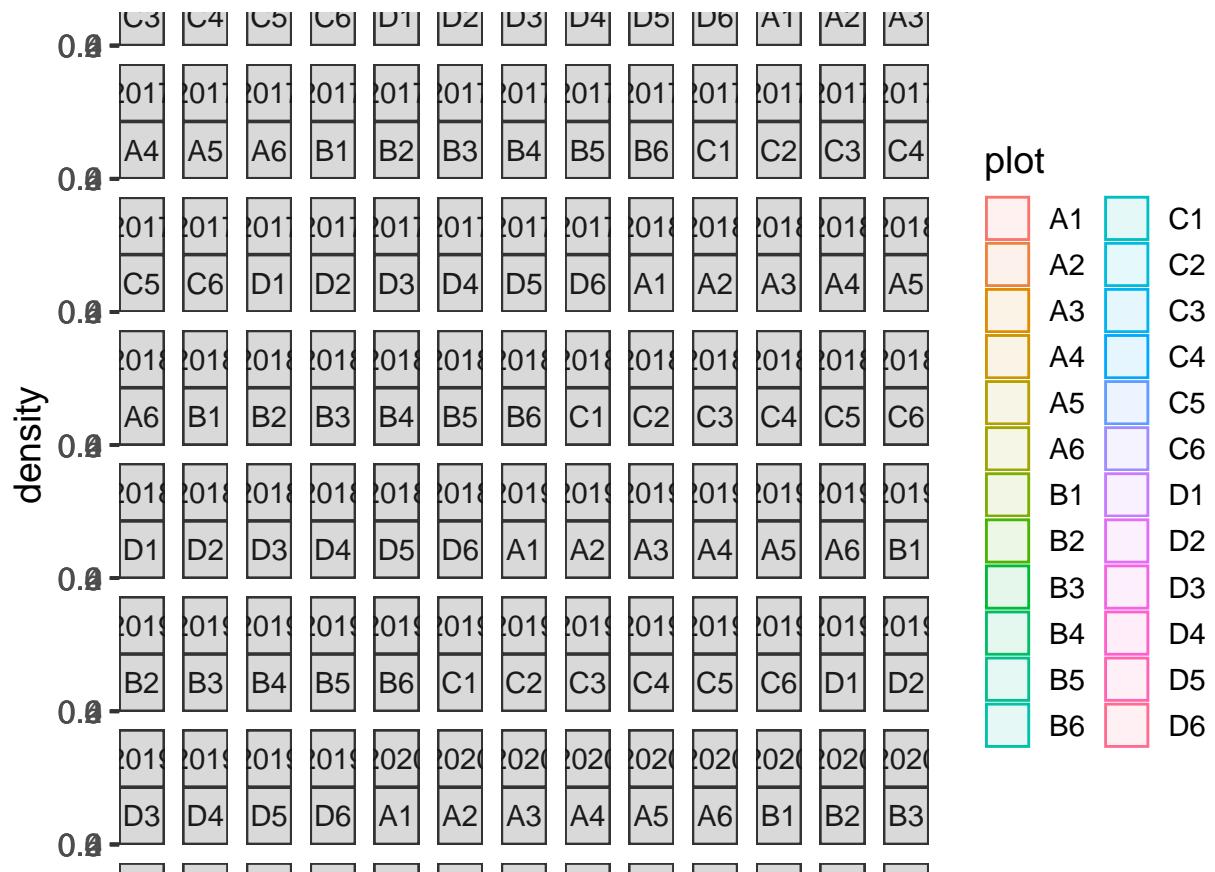
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## Inf

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## Inf

## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

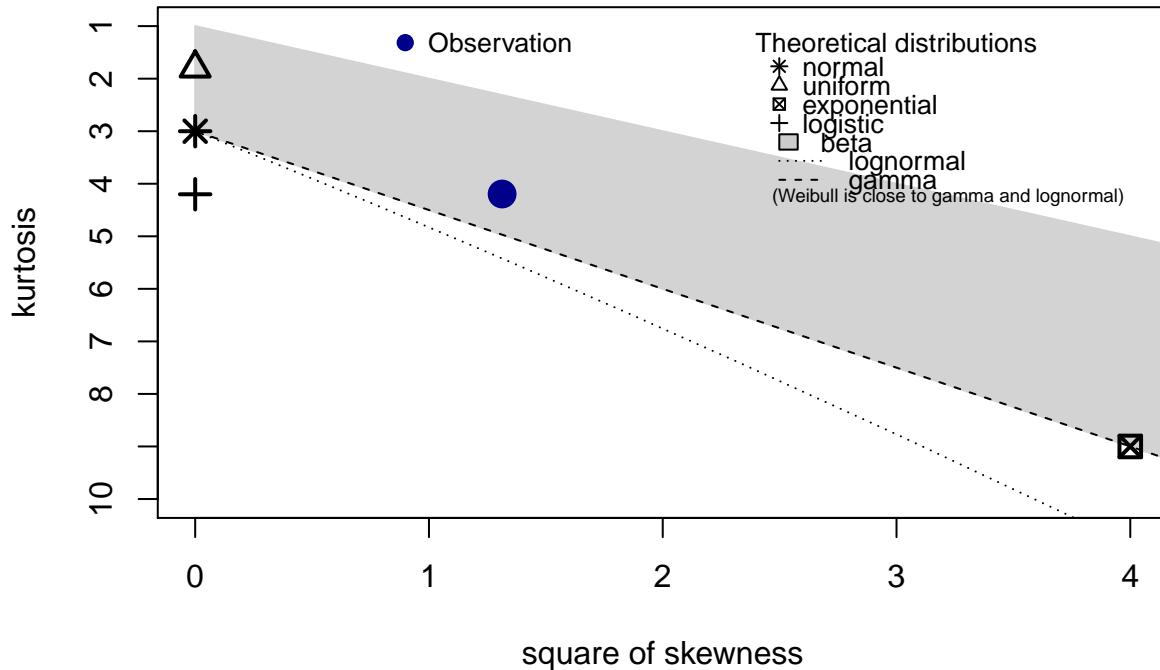
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

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## Inf
```



```
descdist(flwr_plot$julian_min, discrete = FALSE)
```

Cullen and Frey graph

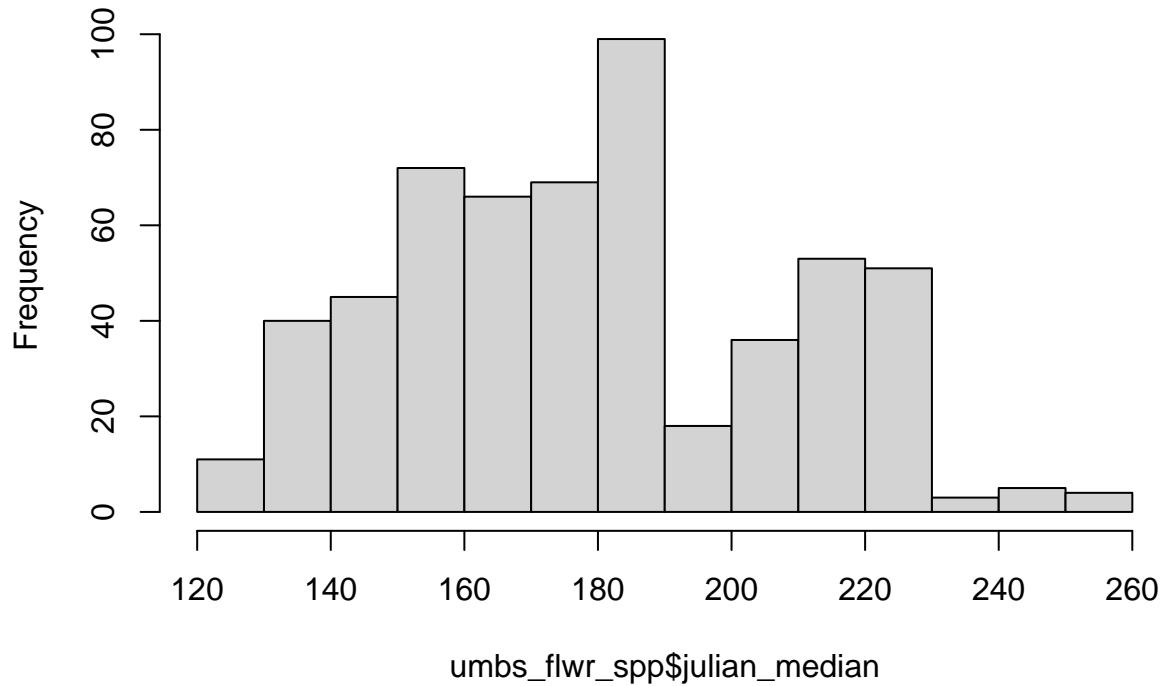


```
## summary statistics
## -----
## min: 94   max: 218
## median: 136
## mean: 143.0647
## estimated sd: 22.5183
## estimated skewness: 1.145825
## estimated kurtosis: 4.195345
```

UMBS SPECIES LEVEL - Looking at MEDIAN JULIAN DAY

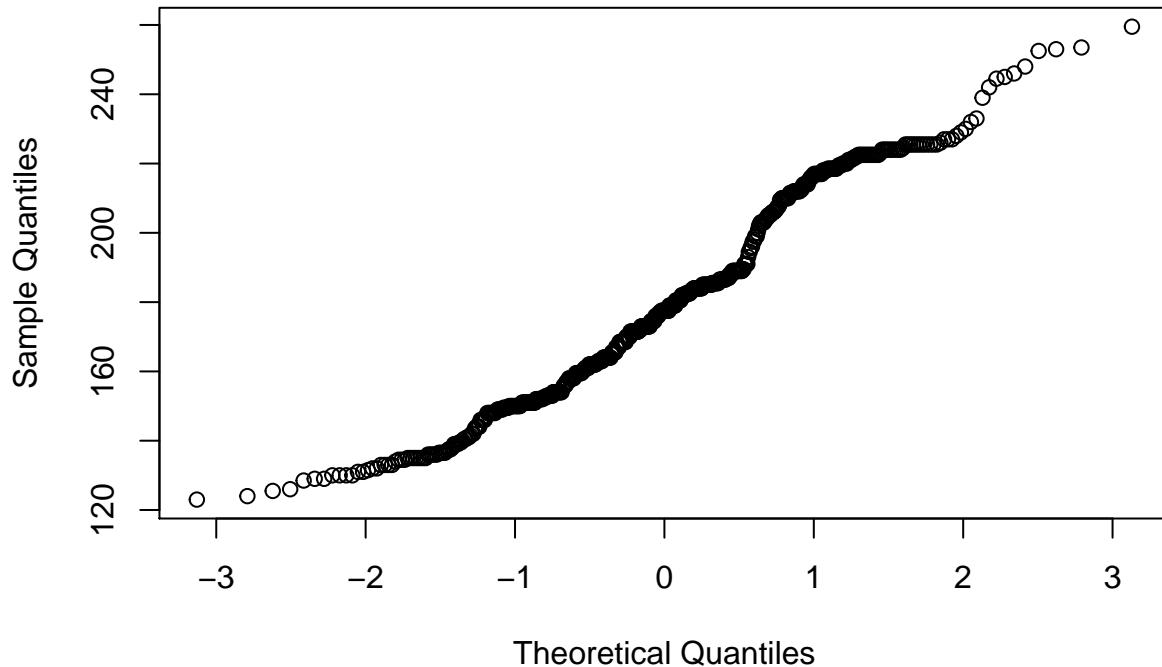
```
### UMBS ####
hist(umbs_flwr_spp$julian_median)
```

Histogram of umbs_flwr_spp\$julian_median



```
qqnorm(umbs_flwr_spp$julian_median) # this looks good
```

Normal Q-Q Plot



```

shapiro.test(umbs_flwr_spp$julian_median) # pvalue is < 0.05 so we reject the null hypothesis that the

##  

## Shapiro-Wilk normality test  

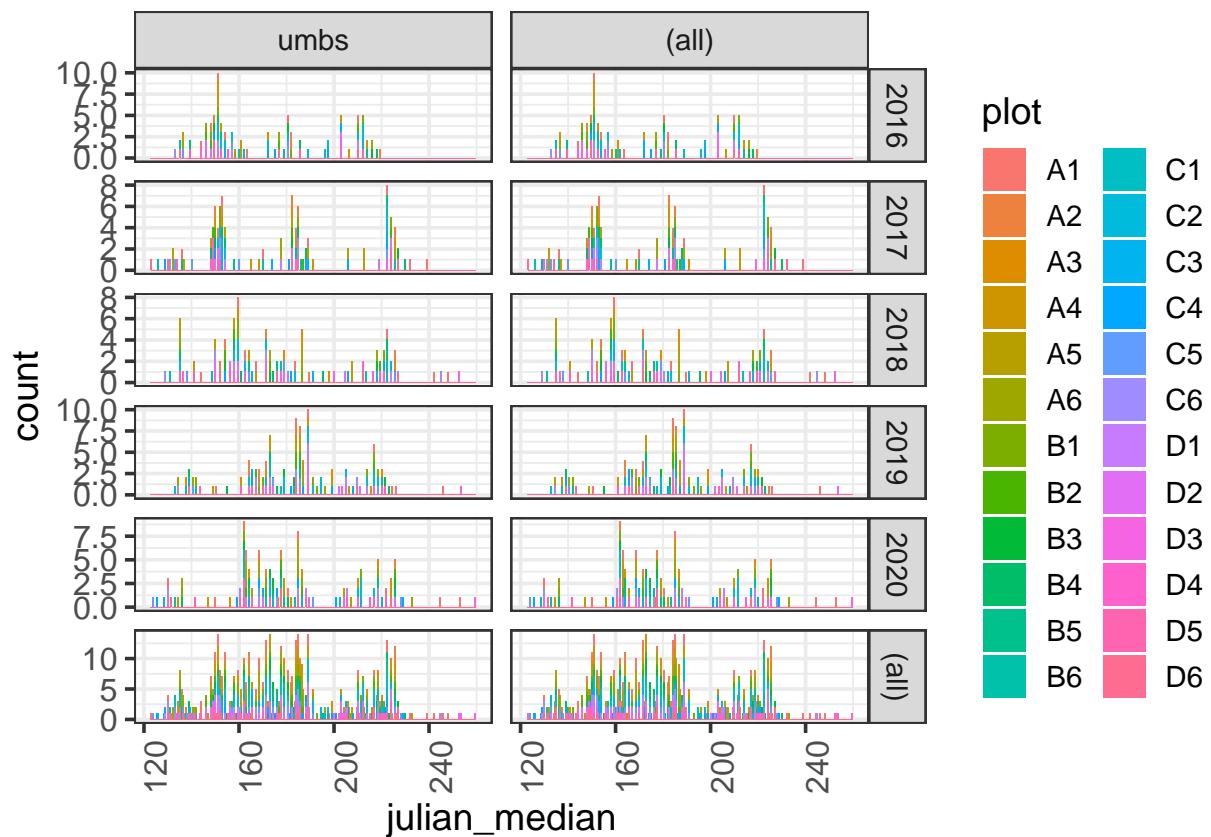
##  

## data: umbs_flwr_spp$julian_median  

## W = 0.9706, p-value = 2.693e-09

# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(umbs_flwr_spp, aes(julian_median, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

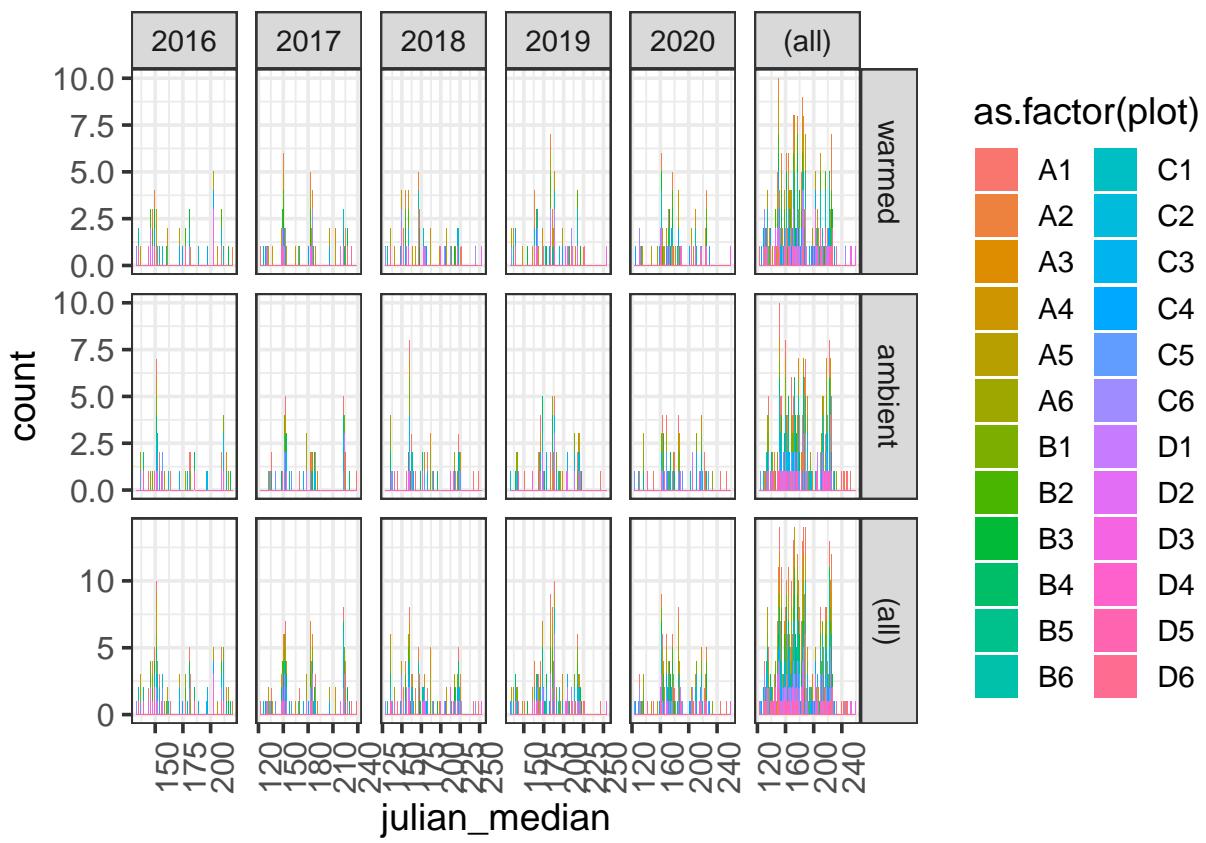
```



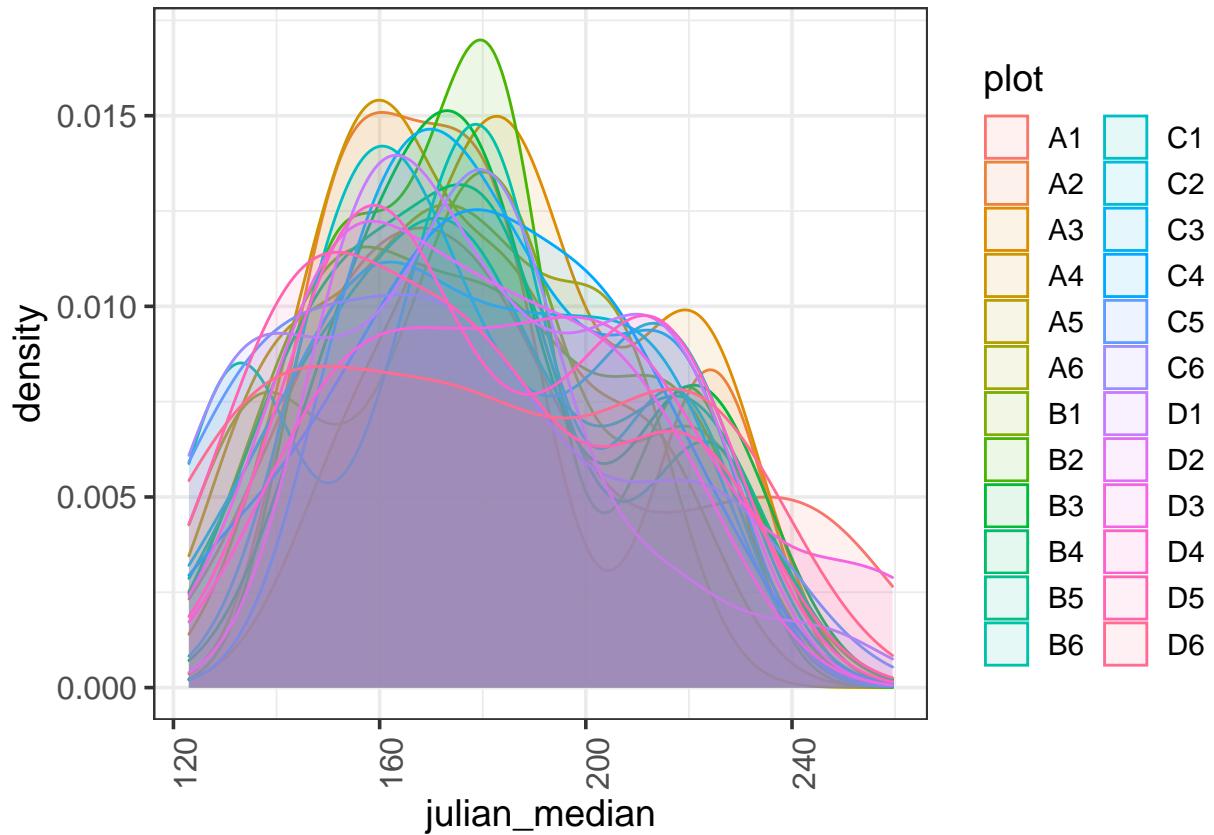
```

ggplot(umbs_flwr_spp, aes(julian_median, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

```



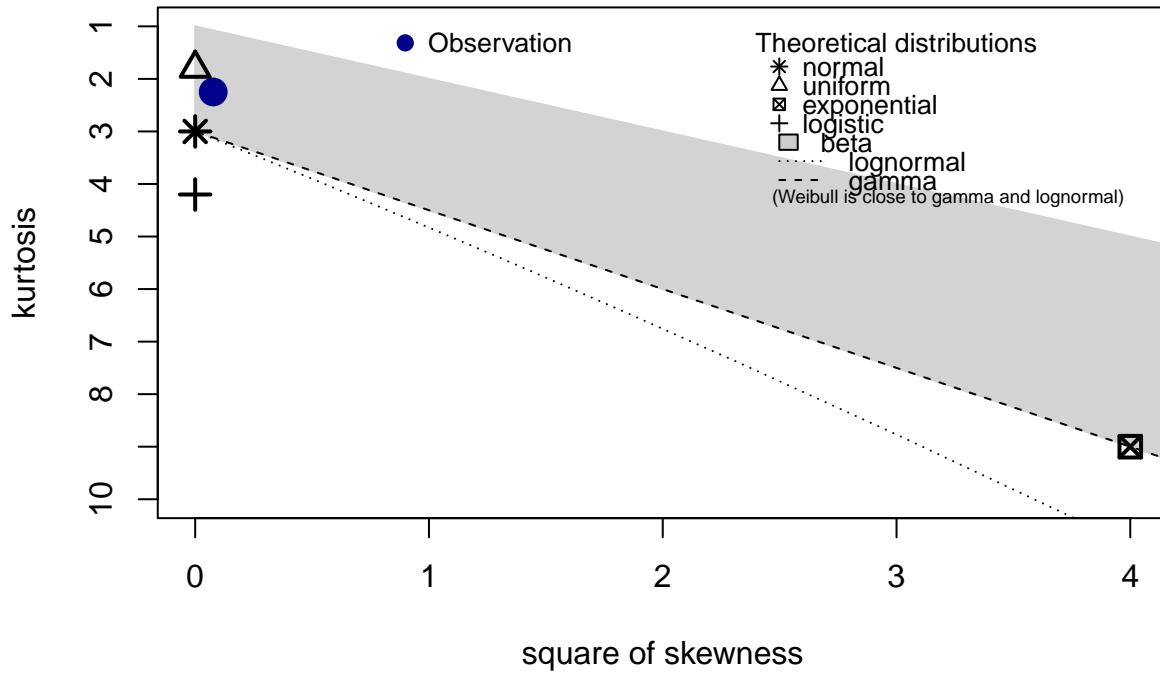
```
ggplot(umbs_flwr_spp, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

*# Exploring distributions for these right-skewed data:
descdist(umbs_flwr_spp\$julian_median, discrete = FALSE)*

Cullen and Frey graph

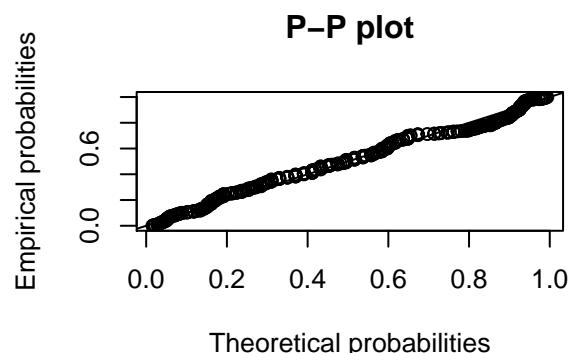
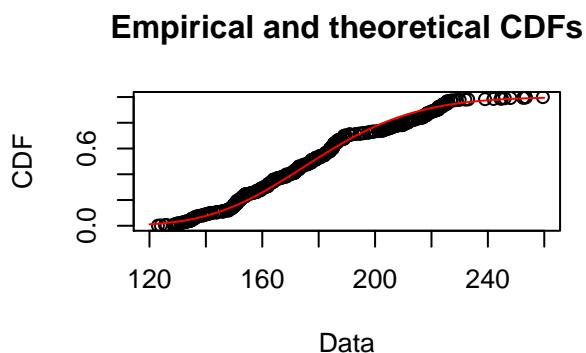
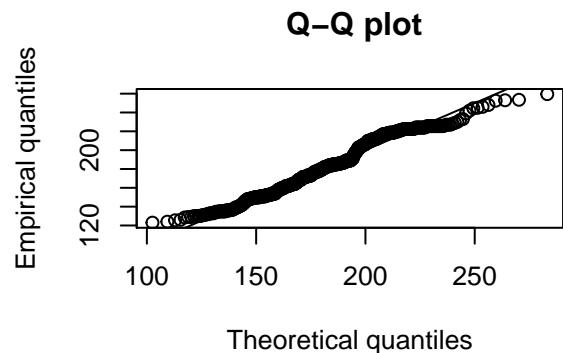
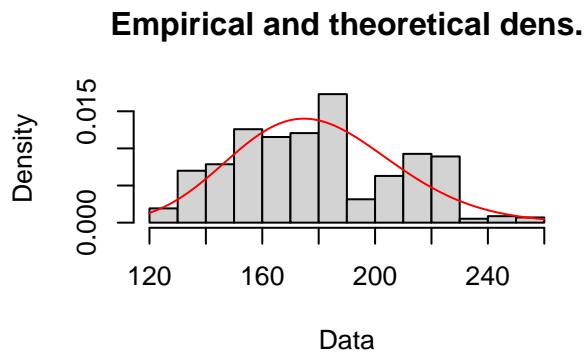


```

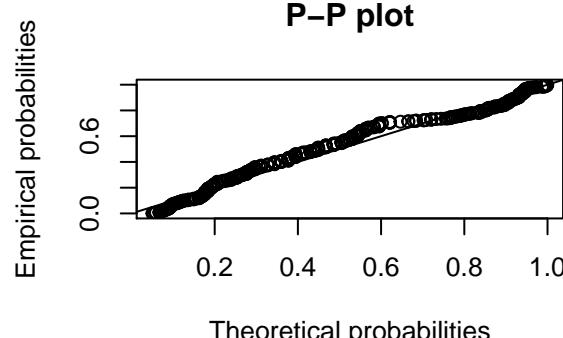
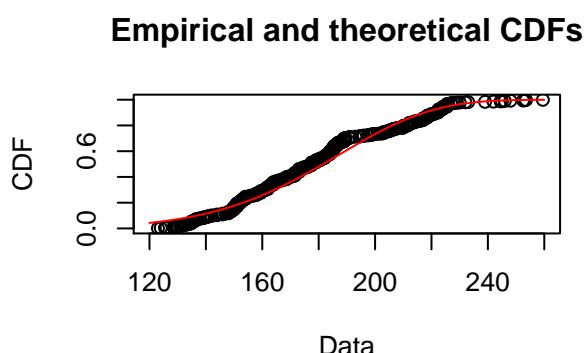
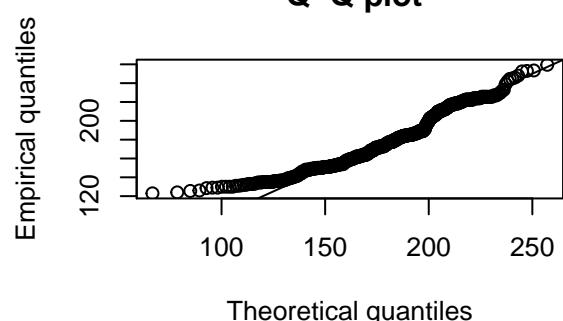
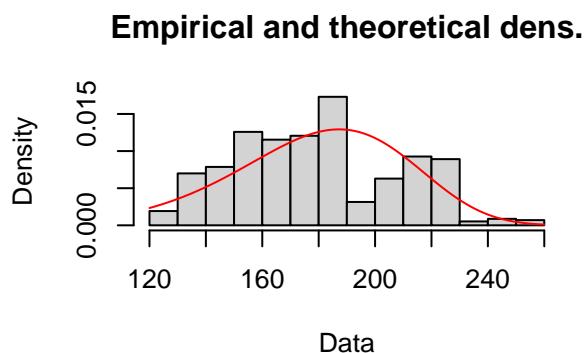
## summary statistics
## -----
## min: 123   max: 259.5
## median: 177.5
## mean: 179.3706
## estimated sd: 28.90832
## estimated skewness: 0.2778292
## estimated kurtosis: 2.249028

# Gamma distribution
fit.gamma <- fitdist(umbs_flwr_spp$julian_median, "gamma")
plot(fit.gamma)

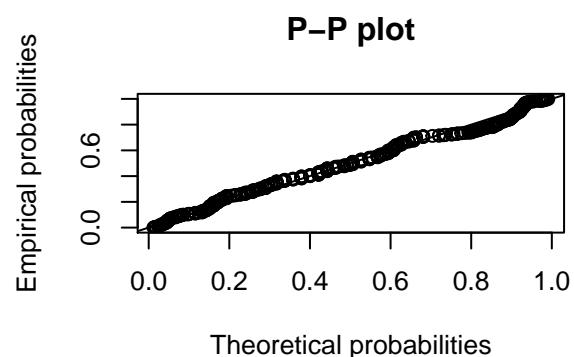
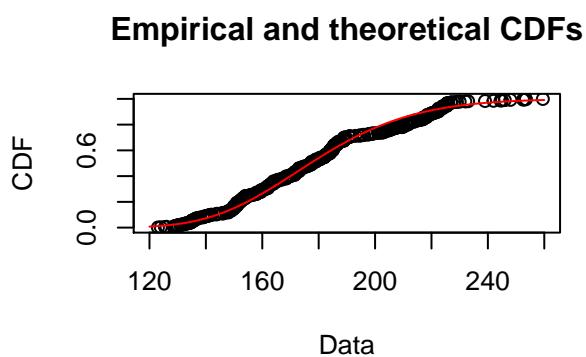
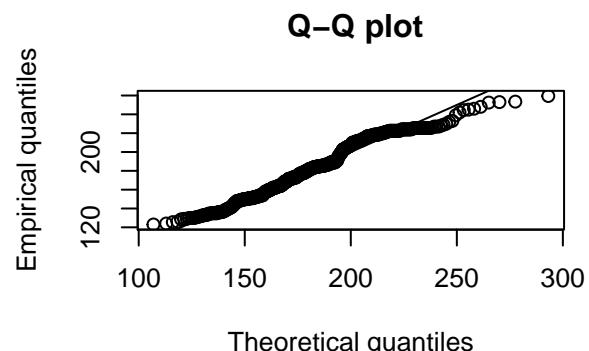
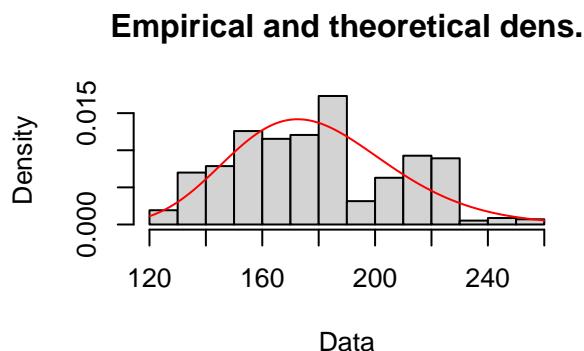
```



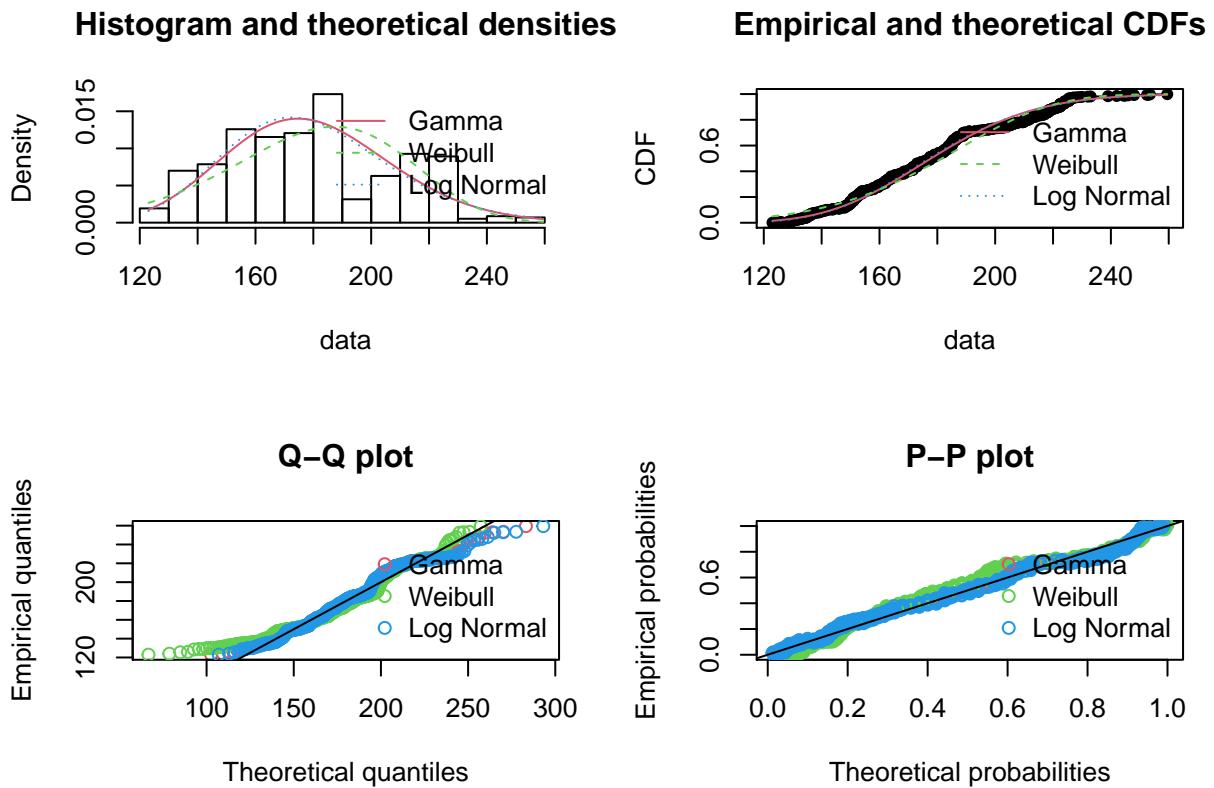
```
# Weibull distribution
fit.weibull <- fitdist(umbs_flwr_spp$julian_median, "weibull")
plot(fit.weibull)
```



```
# Lognormal distribution
fit.ln <- fitdist(umbs_flwr_spp$julian_median, "lnorm")
plot(fit.ln)
```



```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))

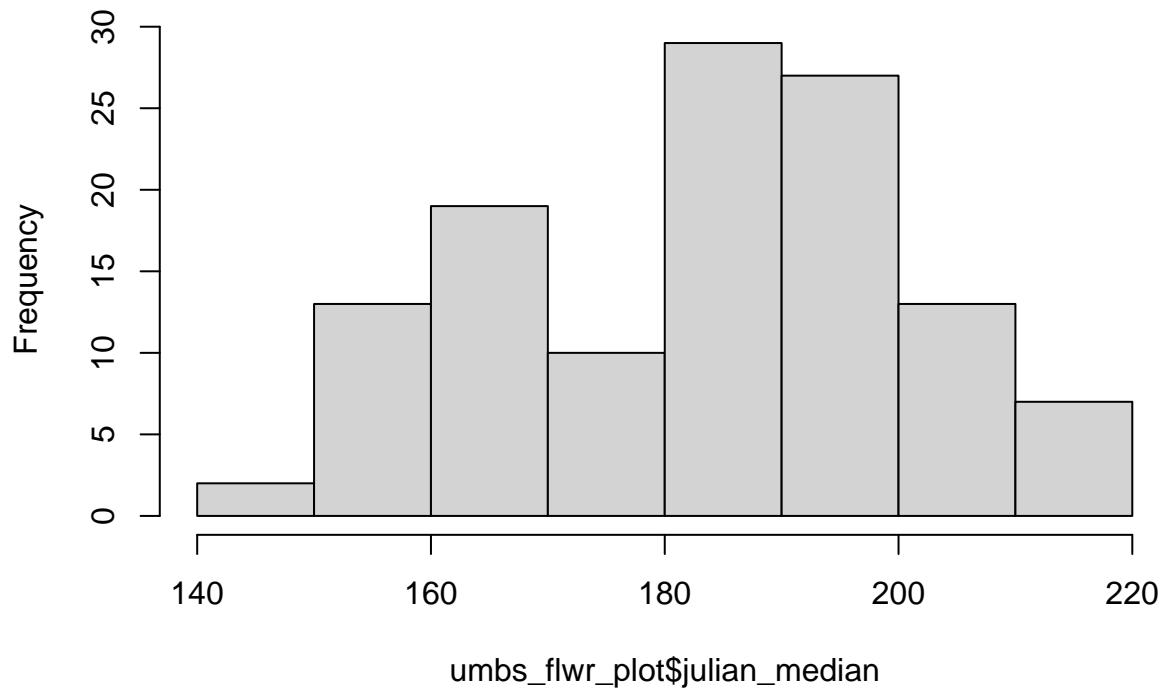
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.07251101 0.1040666 0.07215405
## Cramer-von Mises statistic   0.52738159 1.2693500 0.46115964
## Anderson-Darling statistic   3.91501557 7.8885552 3.58465528
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 5461.481 5512.411 5460.162
## Bayesian Information Criterion 5470.180 5521.109 5468.860

# Lognormal and gamma are very close, gamma slightly better, but going to go with
# log transforming
```

UMBS PLOT LEVEL - Looking at MEDIAN JULIAN DAY

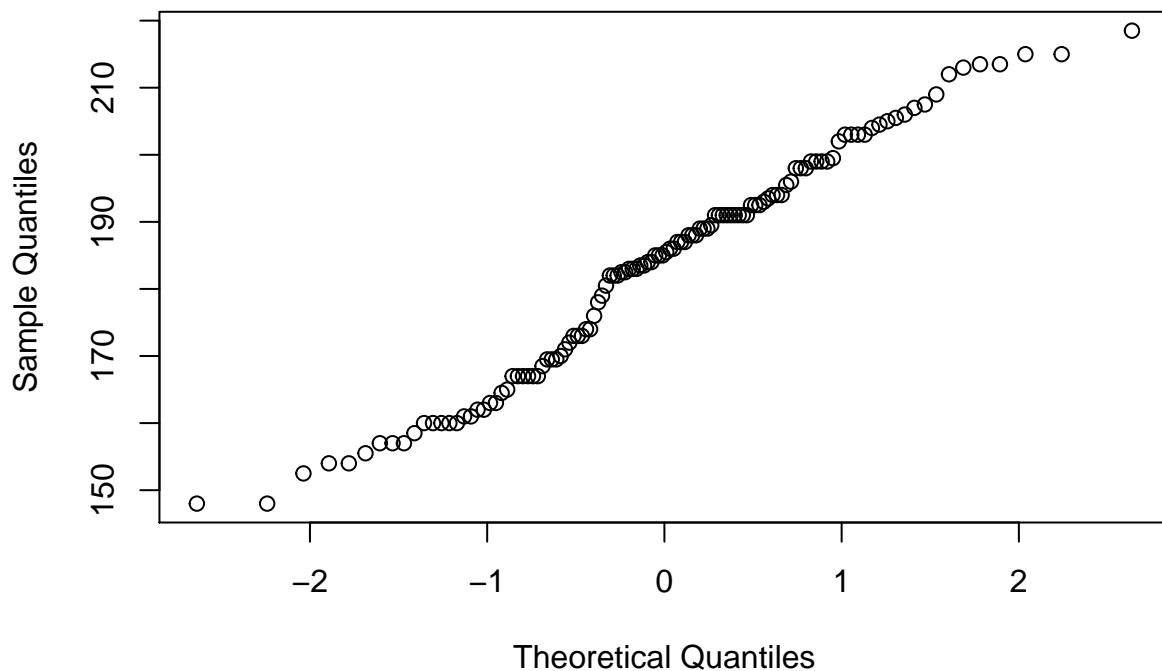
```
### UMBS ####
hist(umbs_flwr_plot$julian_median)
```

Histogram of umbs_flwr_plot\$julian_median



```
qqnorm(umbs_flwr_plot$julian_median)
```

Normal Q-Q Plot



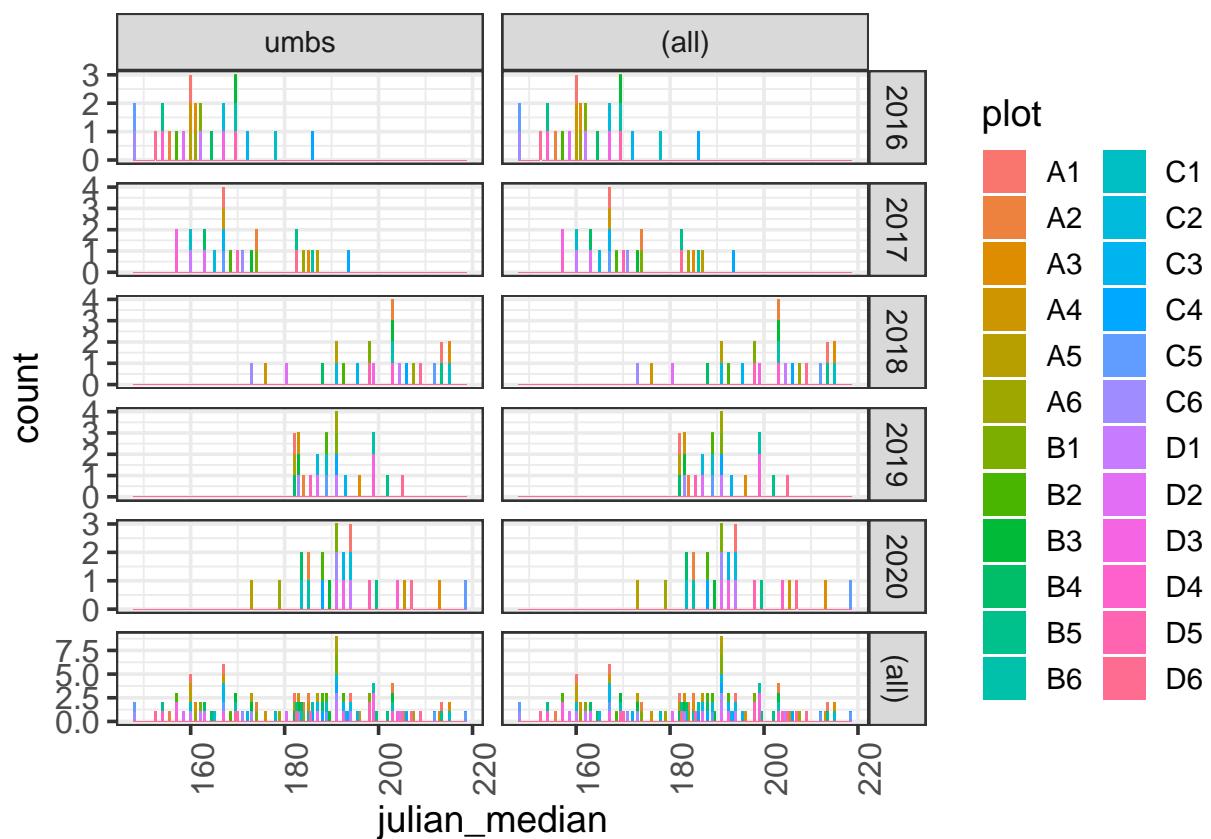
```

shapiro.test(umbs_flwr_plot$julian_median) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

## 
## Shapiro-Wilk normality test
## 
## data: umbs_flwr_plot$julian_median
## W = 0.97473, p-value = 0.02324

# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(umbs_flwr_plot, aes(julian_median, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

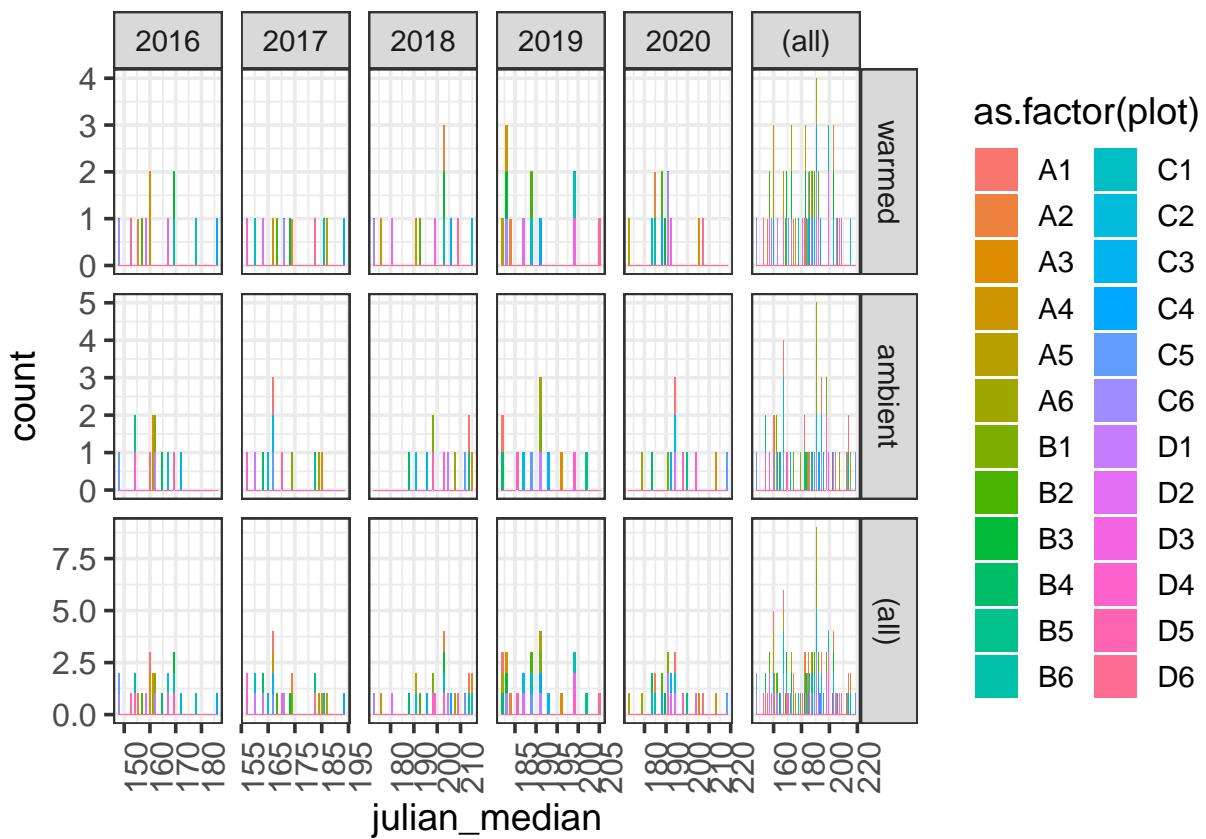
```



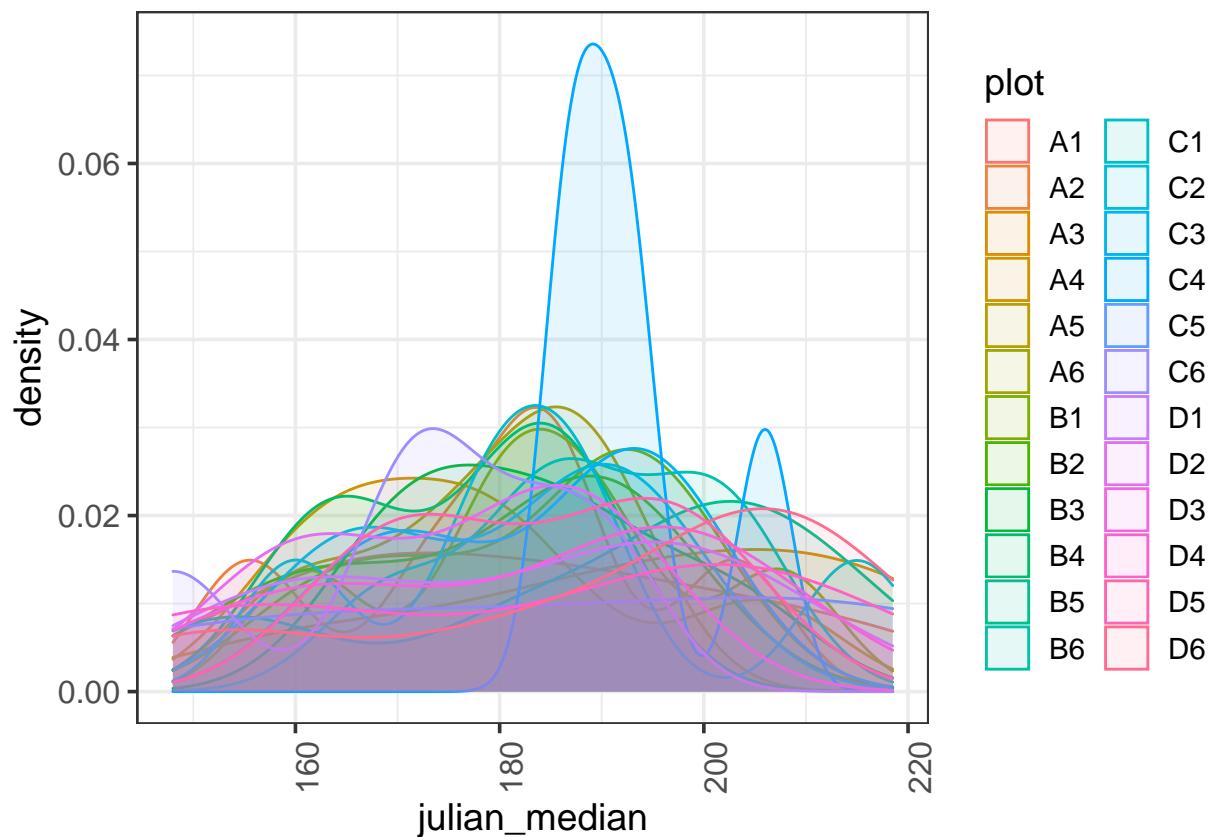
```

ggplot(umbs_flwr_plot, aes(julian_median, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

```



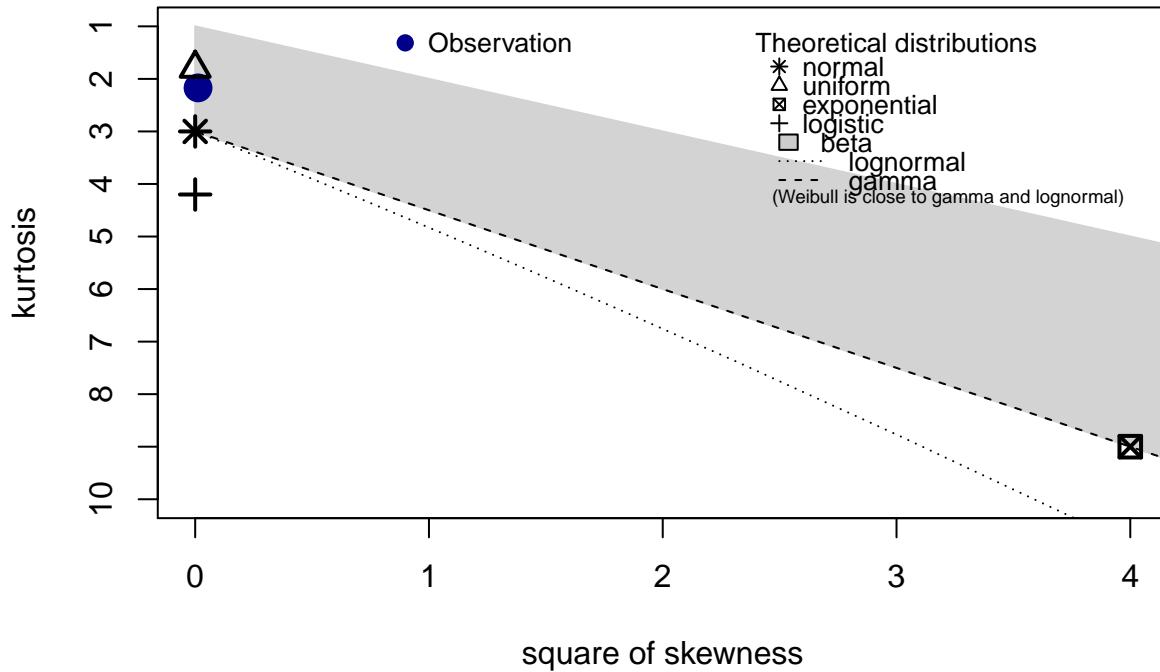
```
ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)

# Exploring distributions for these right-skewed data:
descdist(umbs_flwr_plot$julian_median, discrete = FALSE)
```

Cullen and Frey graph

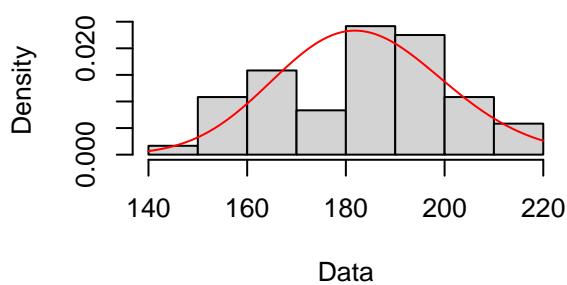
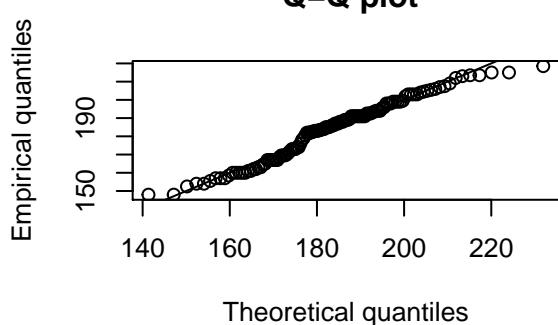
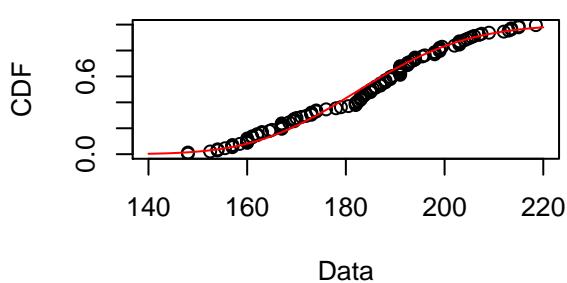
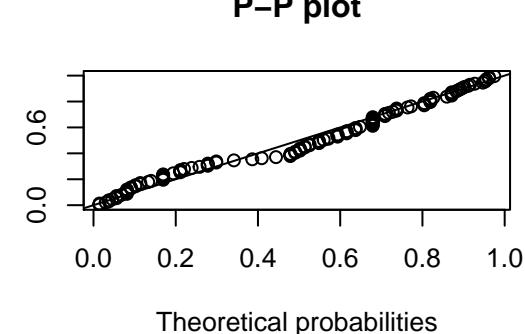


```

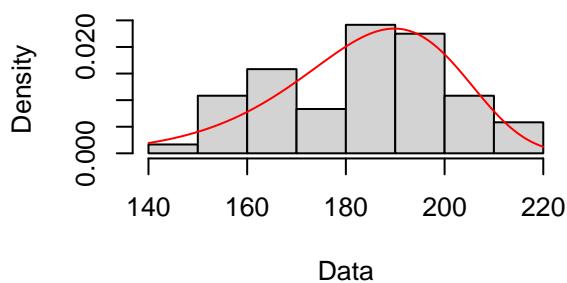
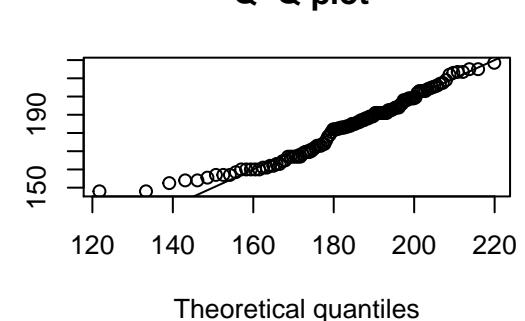
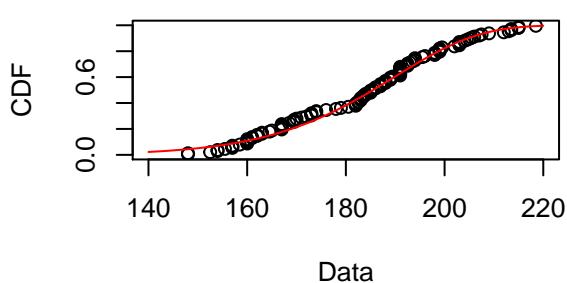
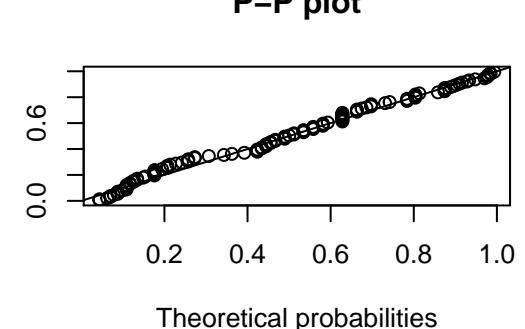
## summary statistics
## -----
## min: 148   max: 218.5
## median: 185.25
## mean: 183.4458
## estimated sd: 17.11231
## estimated skewness: -0.1108348
## estimated kurtosis: 2.171076

# Gamma distribution
fit.gamma <- fitdist(umbs_flwr_plot$julian_median, "gamma")
plot(fit.gamma)

```

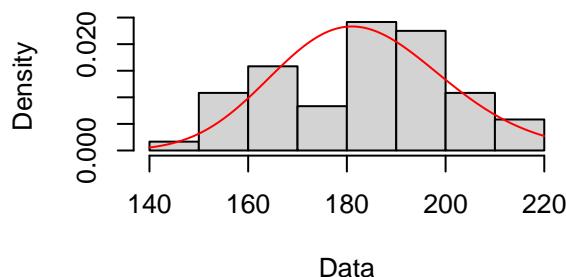
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(umbs_flwr_plot$julian_median, "weibull")
plot(fit.weibull)
```

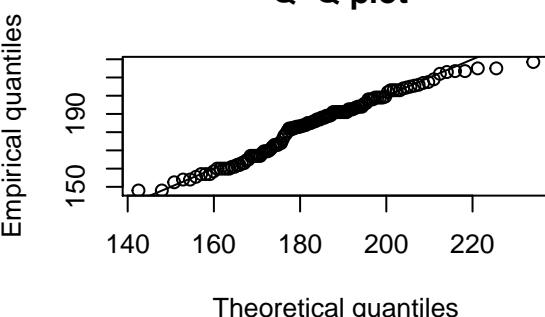
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(umbs_flwr_plot$julian_median, "lnorm")
plot(fit.ln)
```

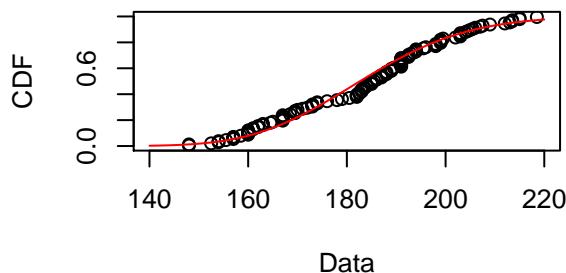
Empirical and theoretical dens.



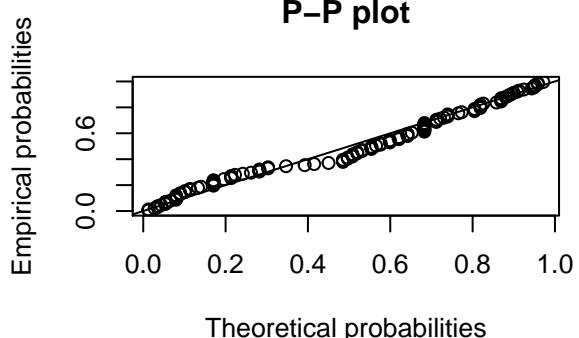
Q-Q plot



Empirical and theoretical CDFs

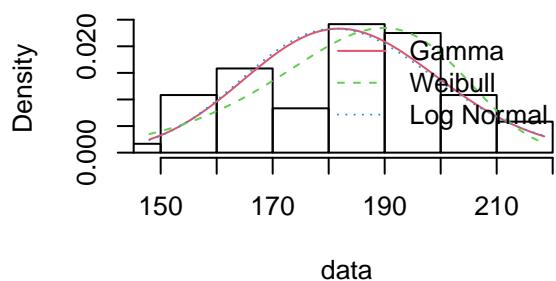


P-P plot

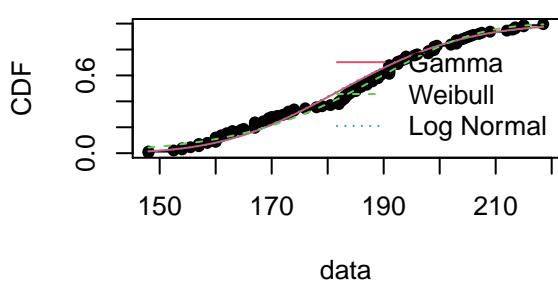


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

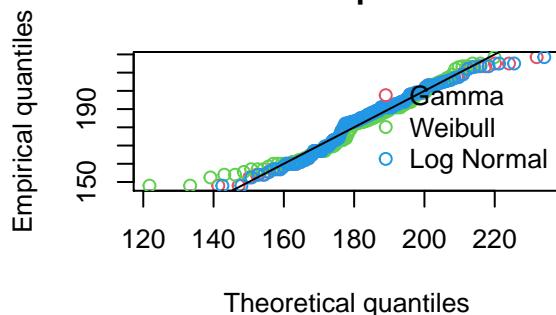
Histogram and theoretical densities



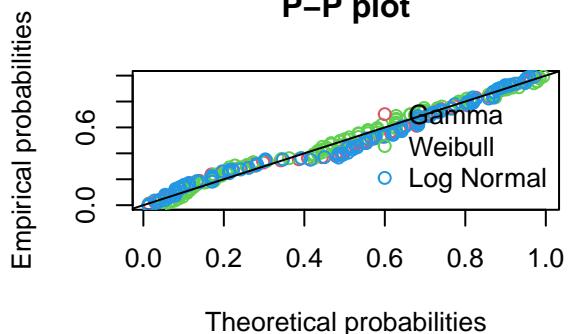
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

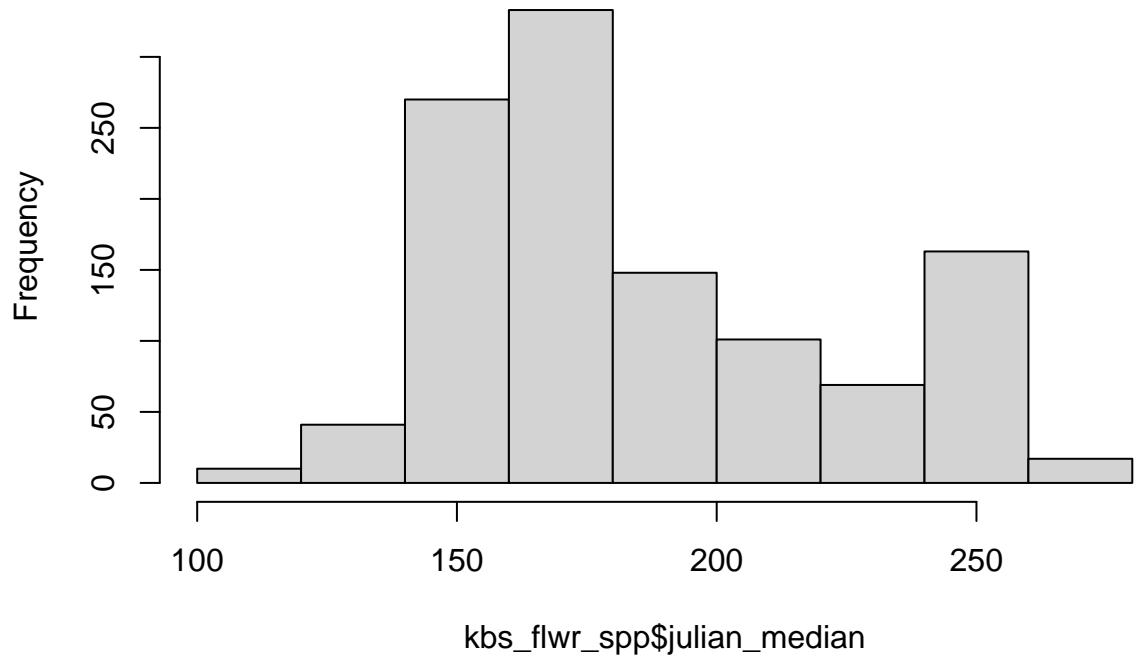
```
## Goodness-of-fit statistics
##                                     Gamma    Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1037869 0.06961748 0.1100430
## Cramer-von Mises statistic   0.2100089 0.10117834 0.2336692
## Anderson-Darling statistic   1.1562899 0.78167992 1.2698070
##
## Goodness-of-fit criteria
##                                     Gamma    Weibull Log Normal
## Akaike's Information Criterion 1026.159 1027.528 1027.067
## Bayesian Information Criterion 1031.734 1033.103 1032.641
```

```
# Weibull is the best...
```

KBS SPECIES LEVEL - Looking at MEDIAN JULIAN DAY

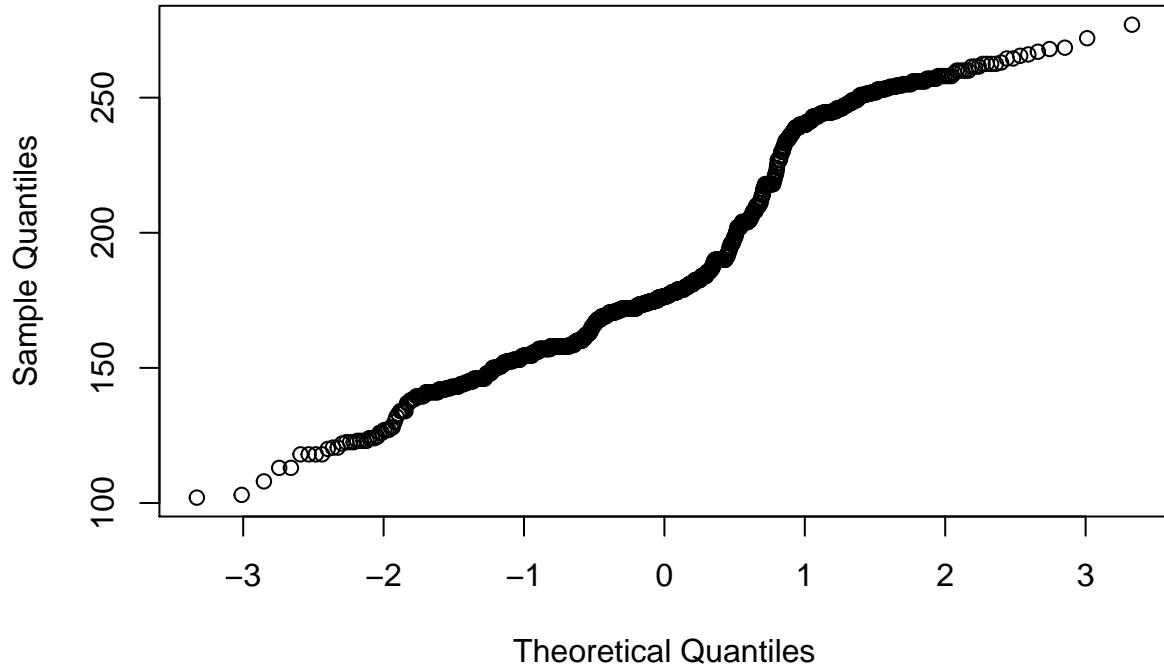
```
### KBS ####
hist(kbs_flwr_spp$julian_median)
```

Histogram of kbs_flwr_spp\$julian_median



```
qqnorm(kbs_flwr_spp$julian_median)
```

Normal Q-Q Plot



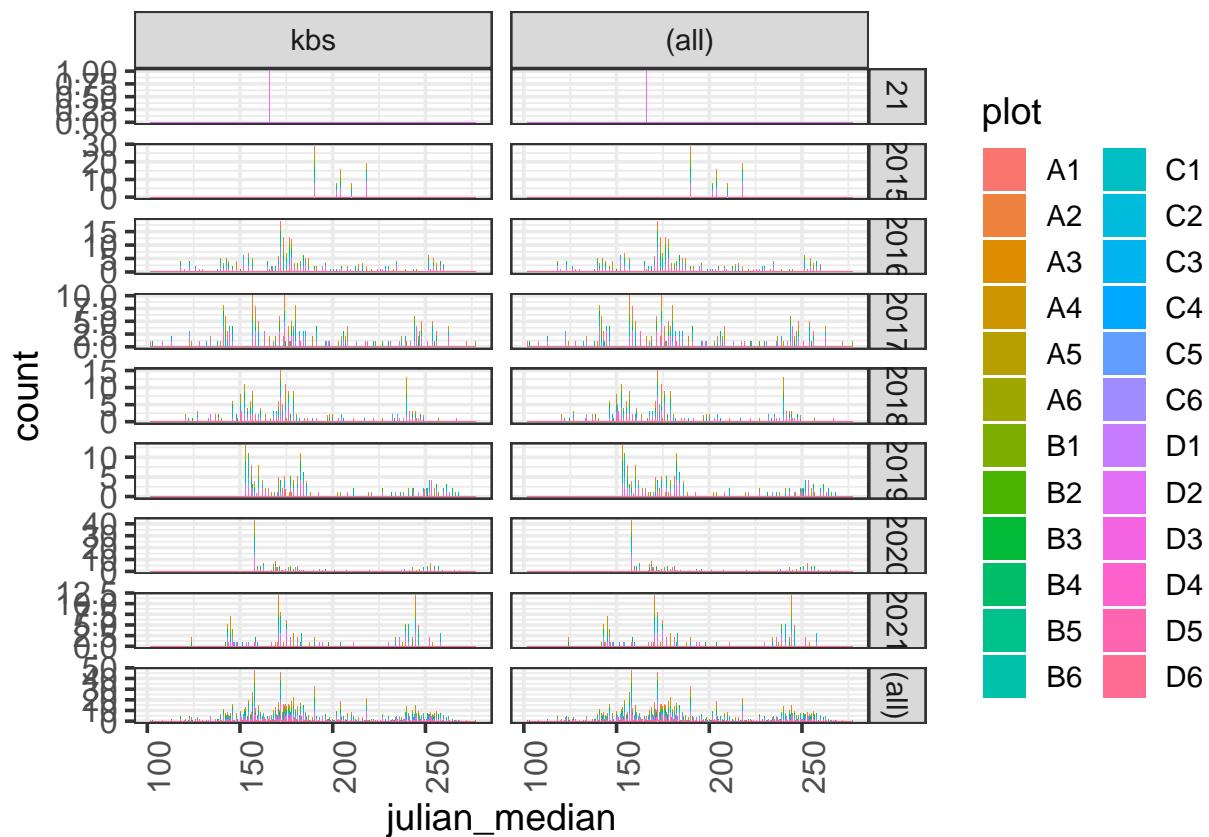
```

shapiro.test(kbs_flwr_spp$julian_median) # pvalue is < 0.05 so we reject the null hypothesis that the

##
## Shapiro-Wilk normality test
##
## data: kbs_flwr_spp$julian_median
## W = 0.92791, p-value < 2.2e-16

# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(kbs_flwr_spp, aes(julian_median, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

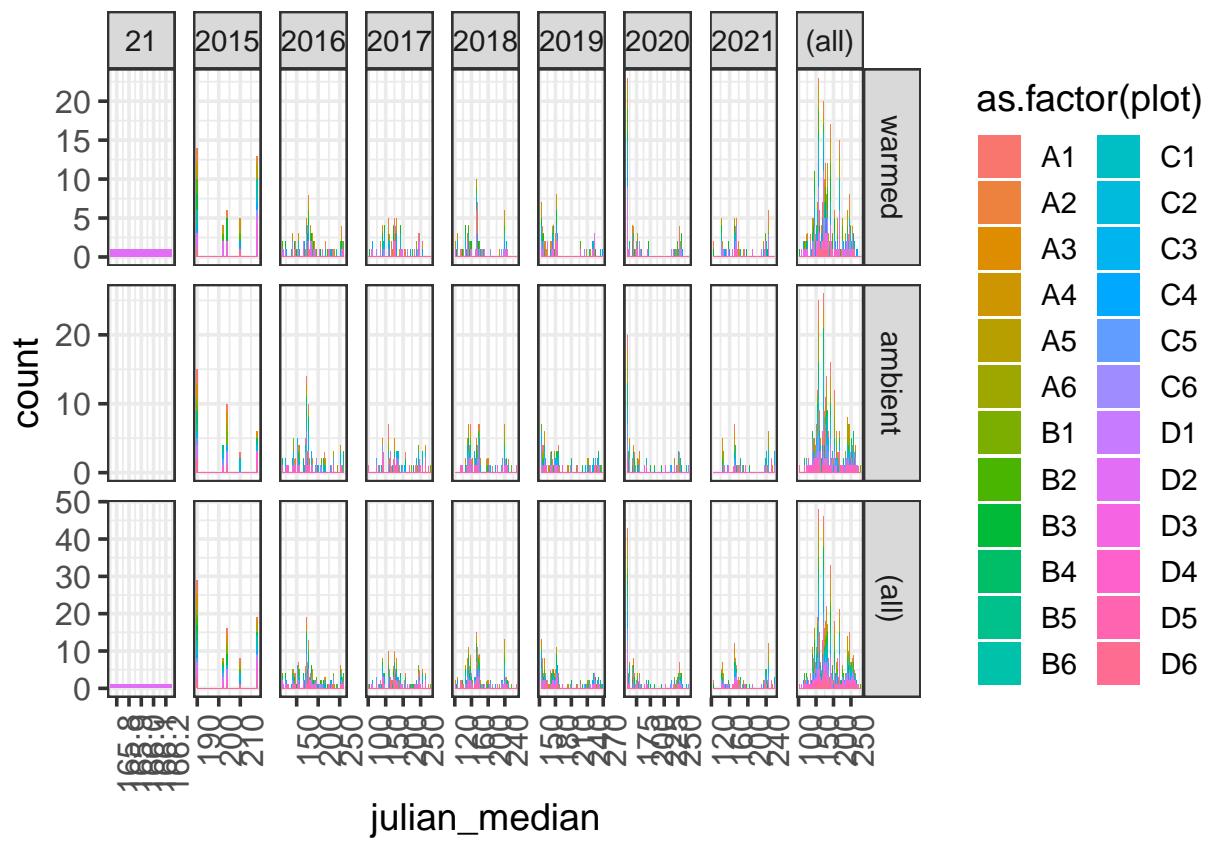
```



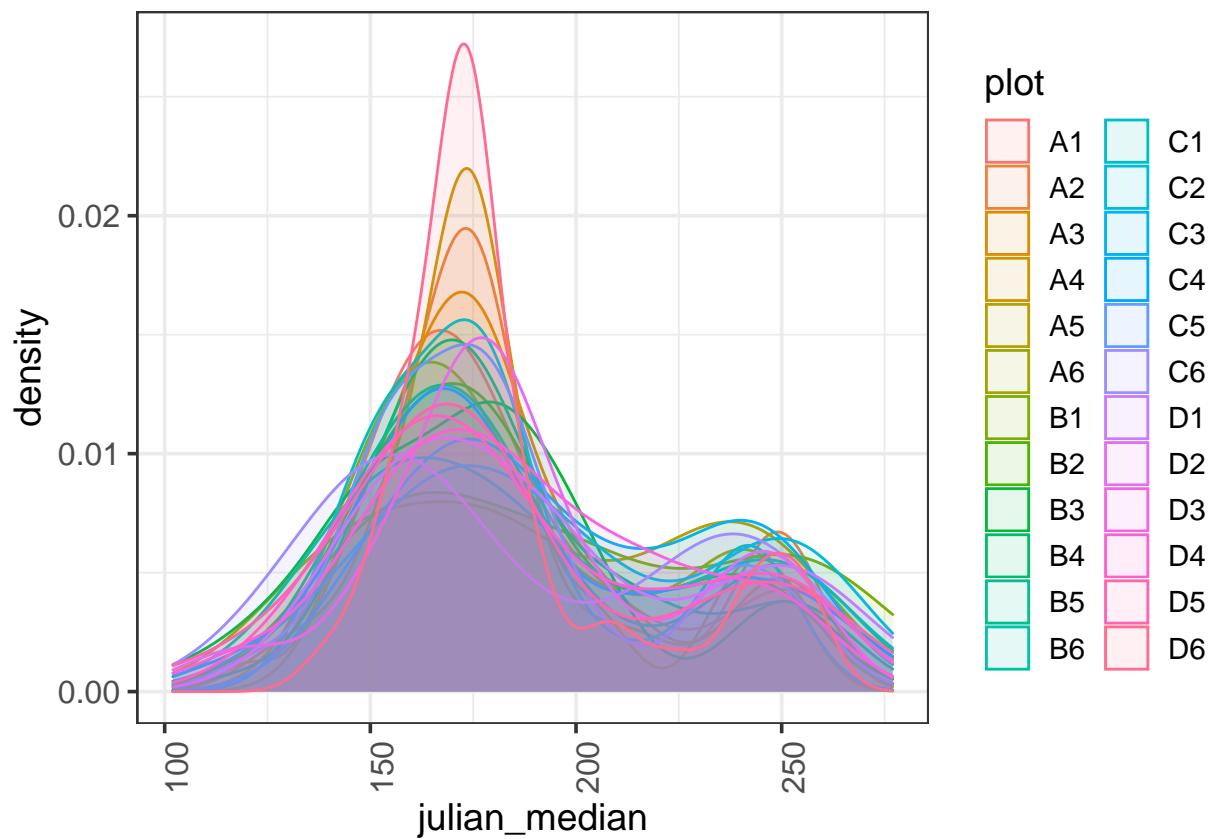
```

ggplot(kbs_flwr_spp, aes(julian_median, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

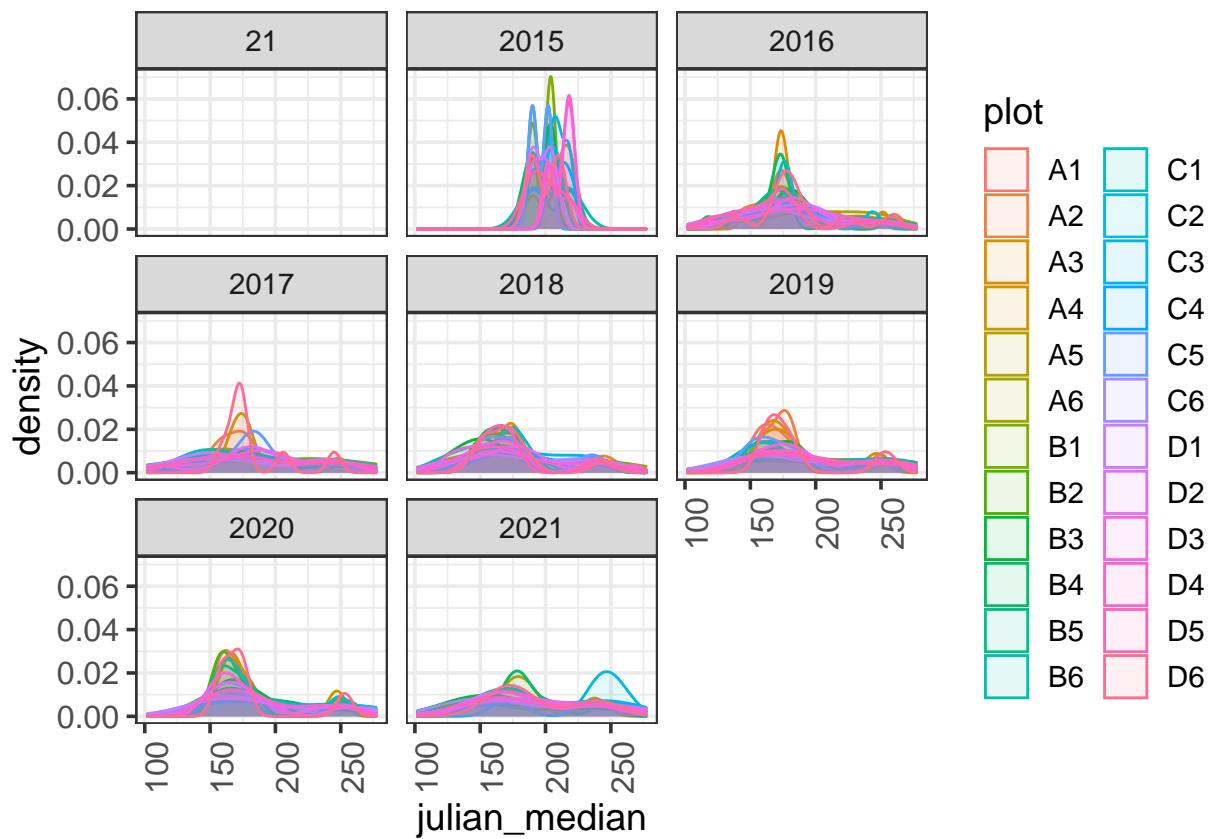
```



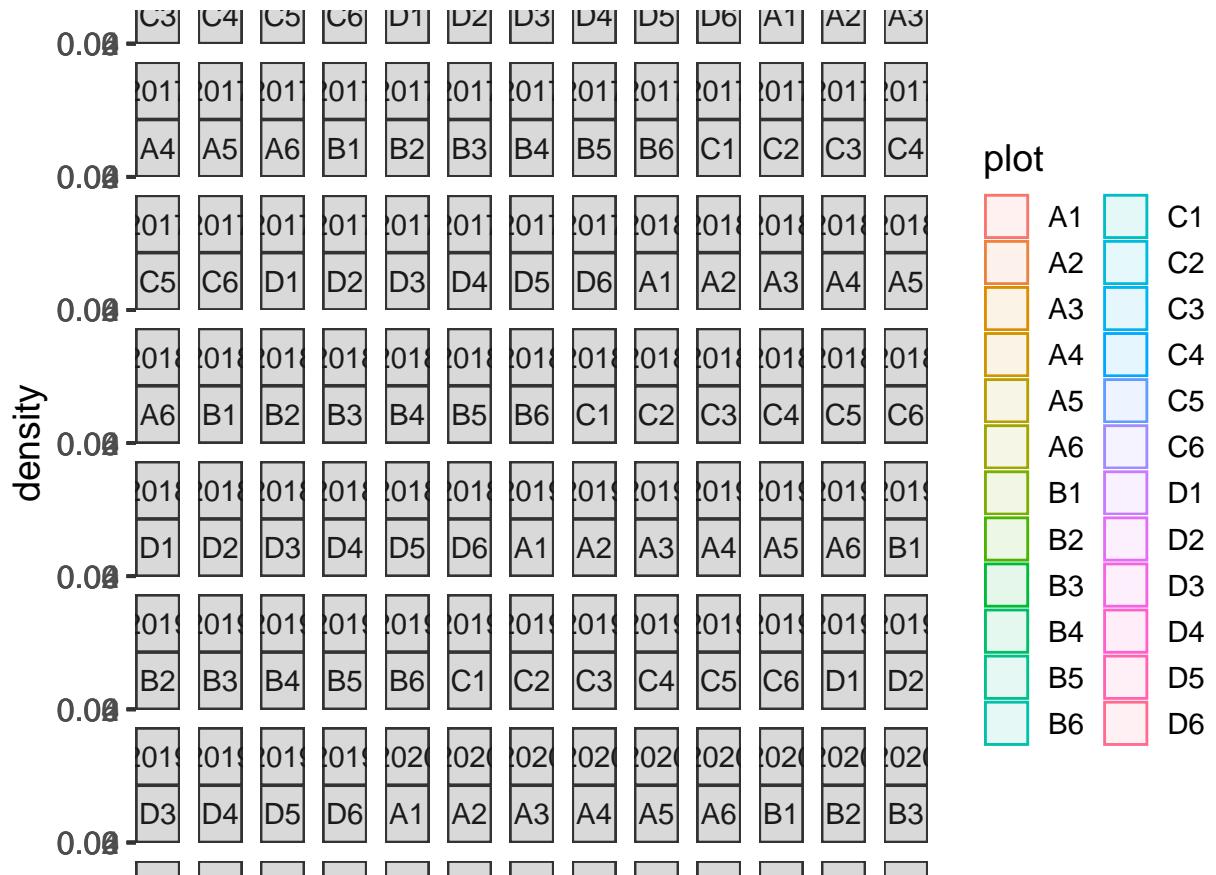
```
ggplot(kbs_flwr_spp, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(kbs_flwr_spp, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year)
```

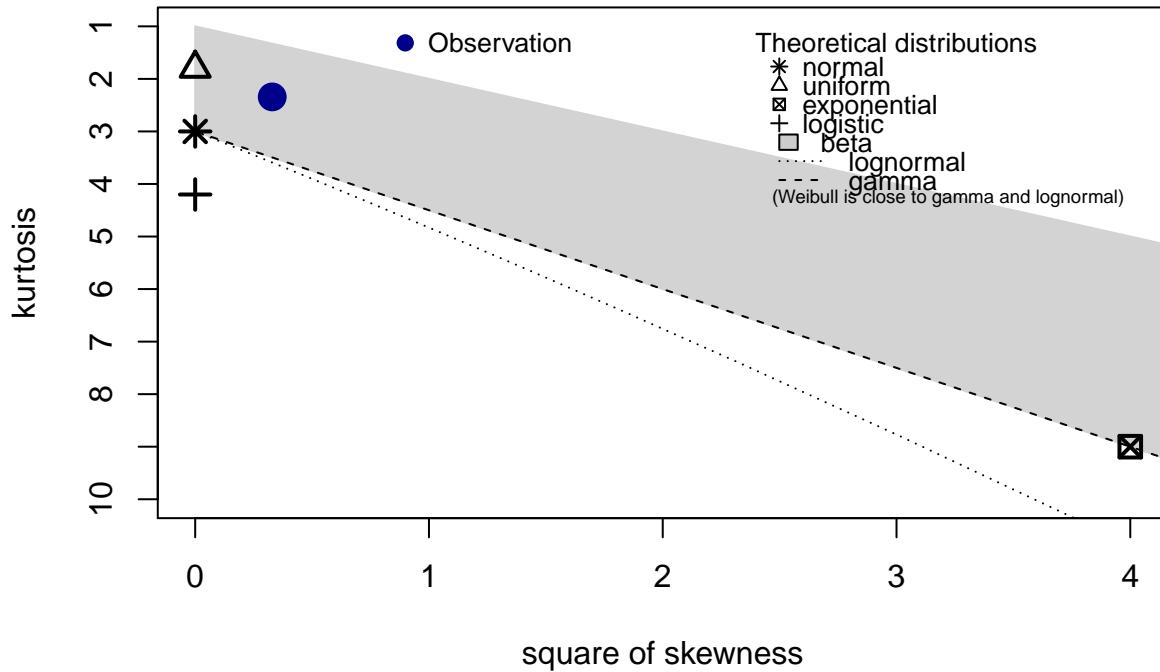


```
ggplot(kbs_flwr_spp, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(kbs_flwr_spp$julian_median, discrete = FALSE)
```

Cullen and Frey graph

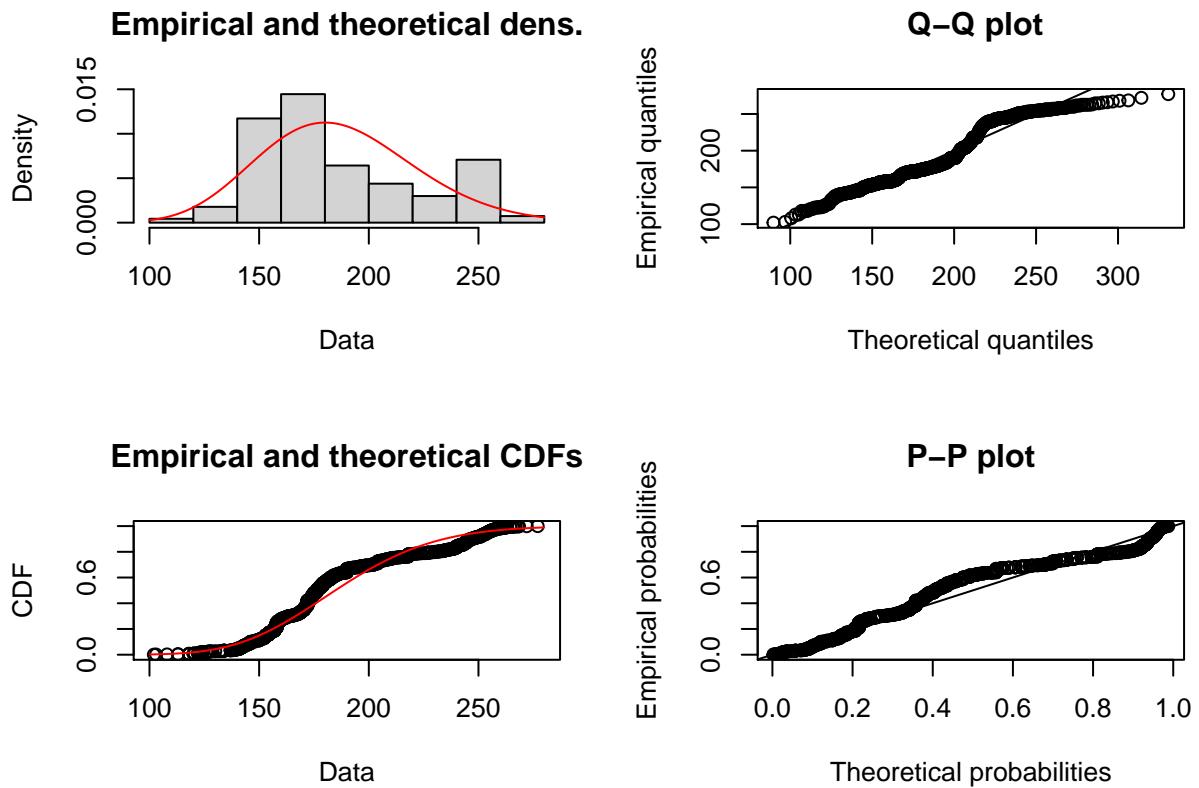


```

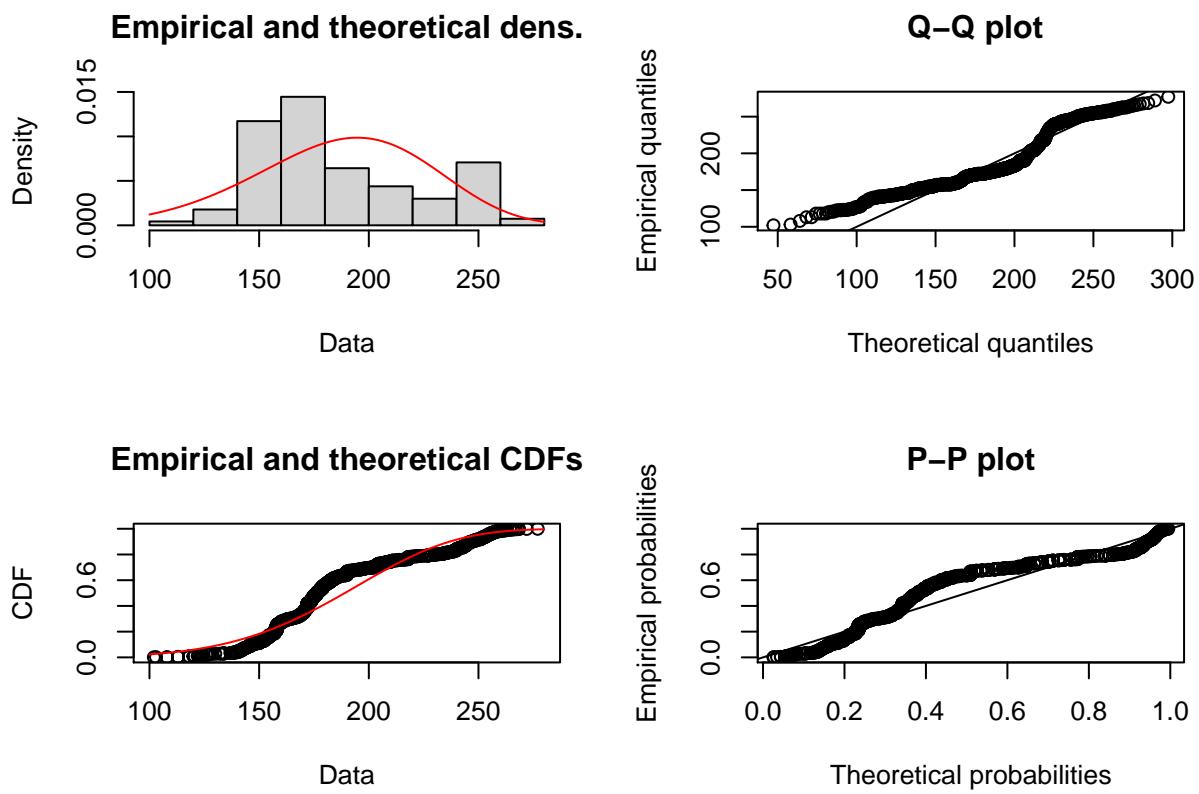
## summary statistics
## -----
## min: 102   max: 277
## median: 176.5
## mean: 187.0304
## estimated sd: 36.75702
## estimated skewness: 0.5740771
## estimated kurtosis: 2.342844

# Gamma distribution
fit.gamma <- fitdist(kbs_flwr_spp$julian_median, "gamma")
plot(fit.gamma)

```

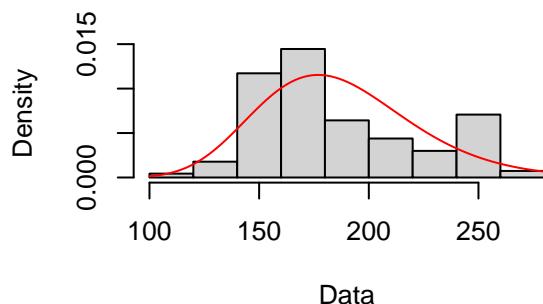


```
# Weibull distribution
fit.weibull <- fitdist(kbs_flwr_spp$julian_median, "weibull")
plot(fit.weibull)
```

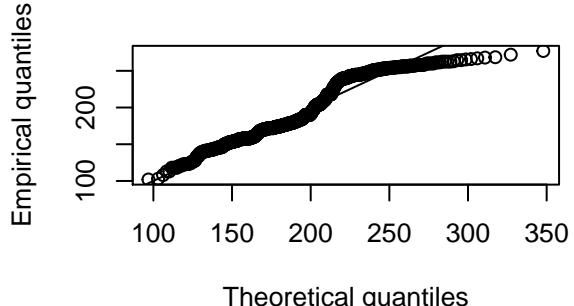


```
# Lognormal distribution
fit.ln <- fitdist(kbs_flwr_spp$julian_median, "lnorm")
plot(fit.ln)
```

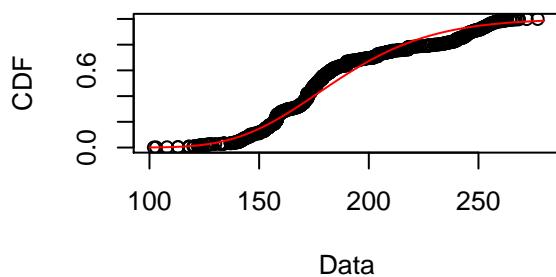
Empirical and theoretical dens.



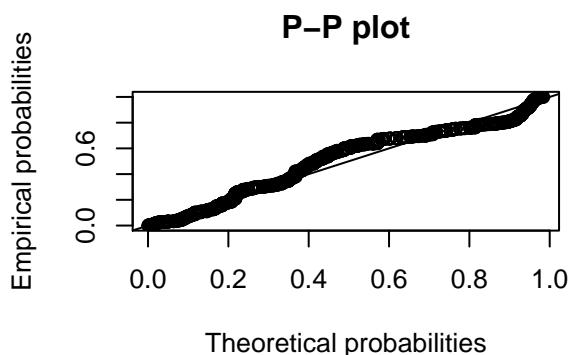
Q-Q plot



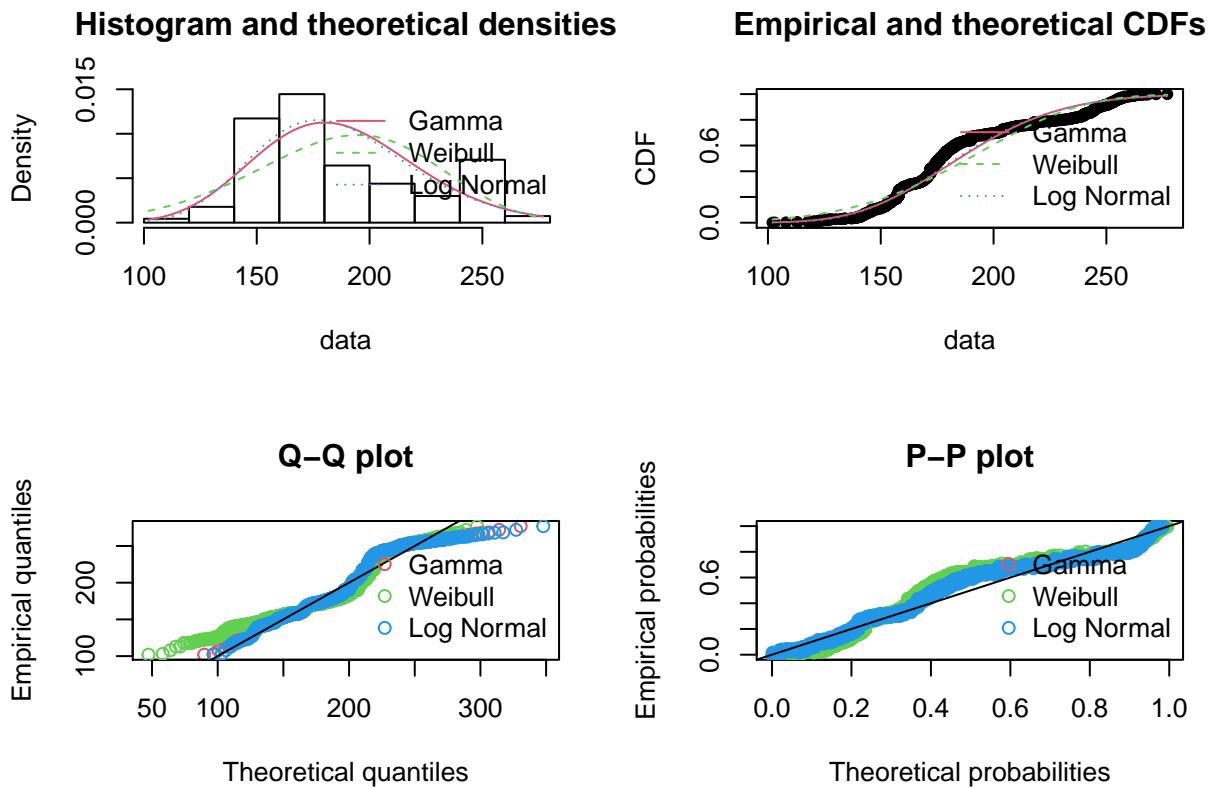
Empirical and theoretical CDFs



P-P plot



```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

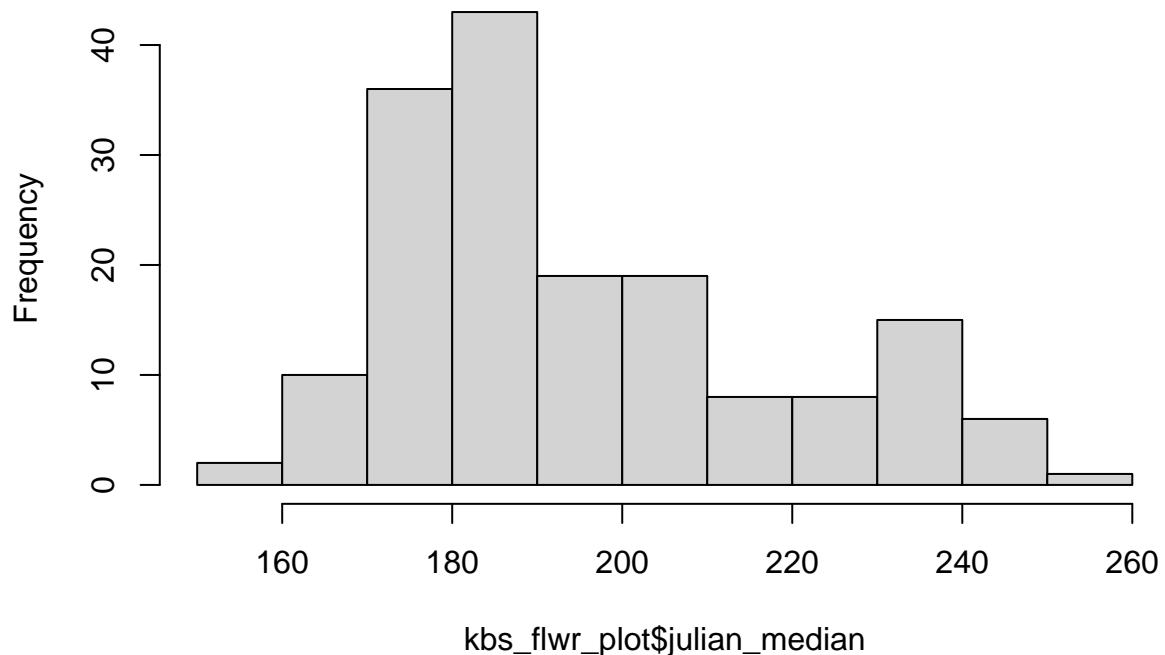
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1255364 0.1657855 0.112895
## Cramer-von Mises statistic  4.2217015 7.6018720 3.401248
## Anderson-Darling statistic 24.6691234 42.0641014 20.431315
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 11501.63 11668.78 11480.01
## Bayesian Information Criterion 11511.73 11678.88 11490.10
```

```
# Lognormal is the best so going to log transform response variable julian_median
```

KBS PLOT LEVEL - Looking at MEDIAN JULIAN DAY

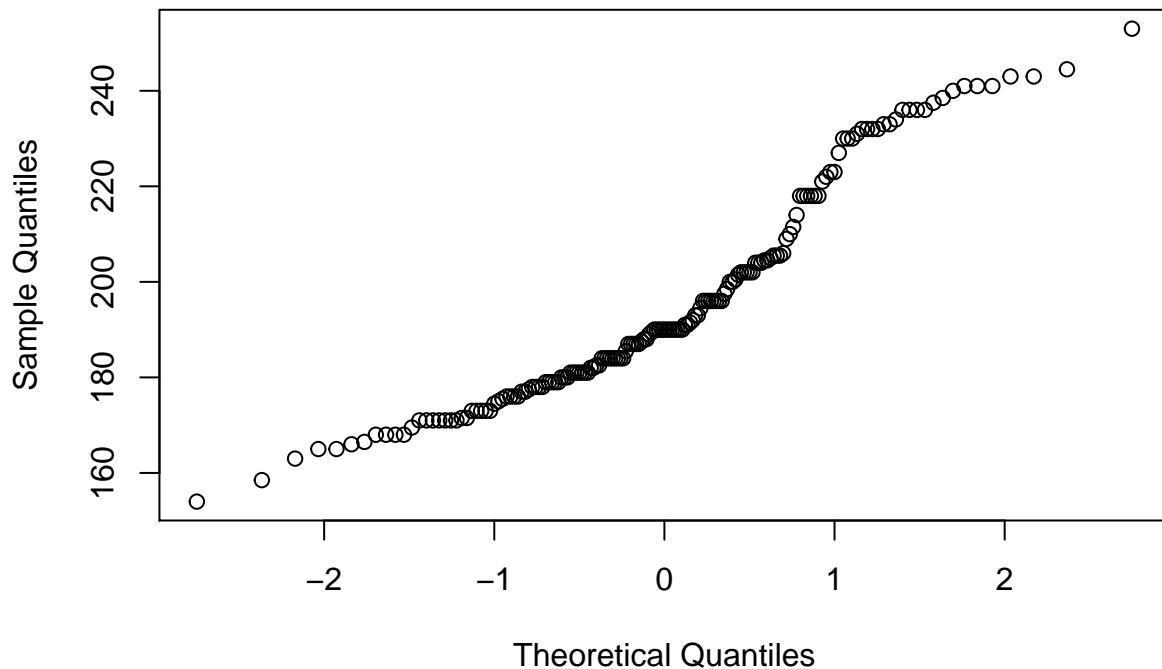
```
### UMBS ####
hist(kbs_flwr_plot$julian_median)
```

Histogram of kbs_flwr_plot\$julian_median



```
qqnorm(kbs_flwr_plot$julian_median)
```

Normal Q-Q Plot



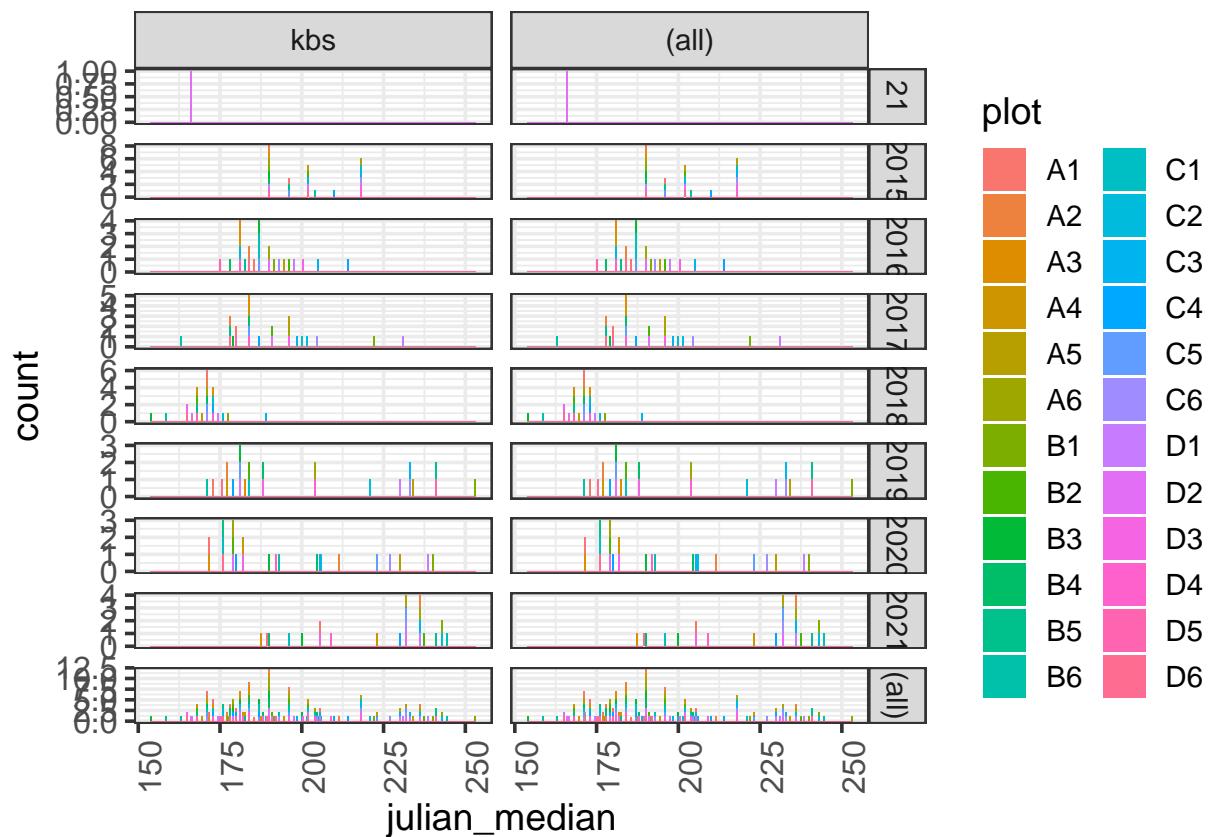
```

shapiro.test(kbs_flwr_plot$julian_median) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

## 
## Shapiro-Wilk normality test
## 
## data: kbs_flwr_plot$julian_median
## W = 0.92754, p-value = 1.982e-07

# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(kbs_flwr_plot, aes(julian_median, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

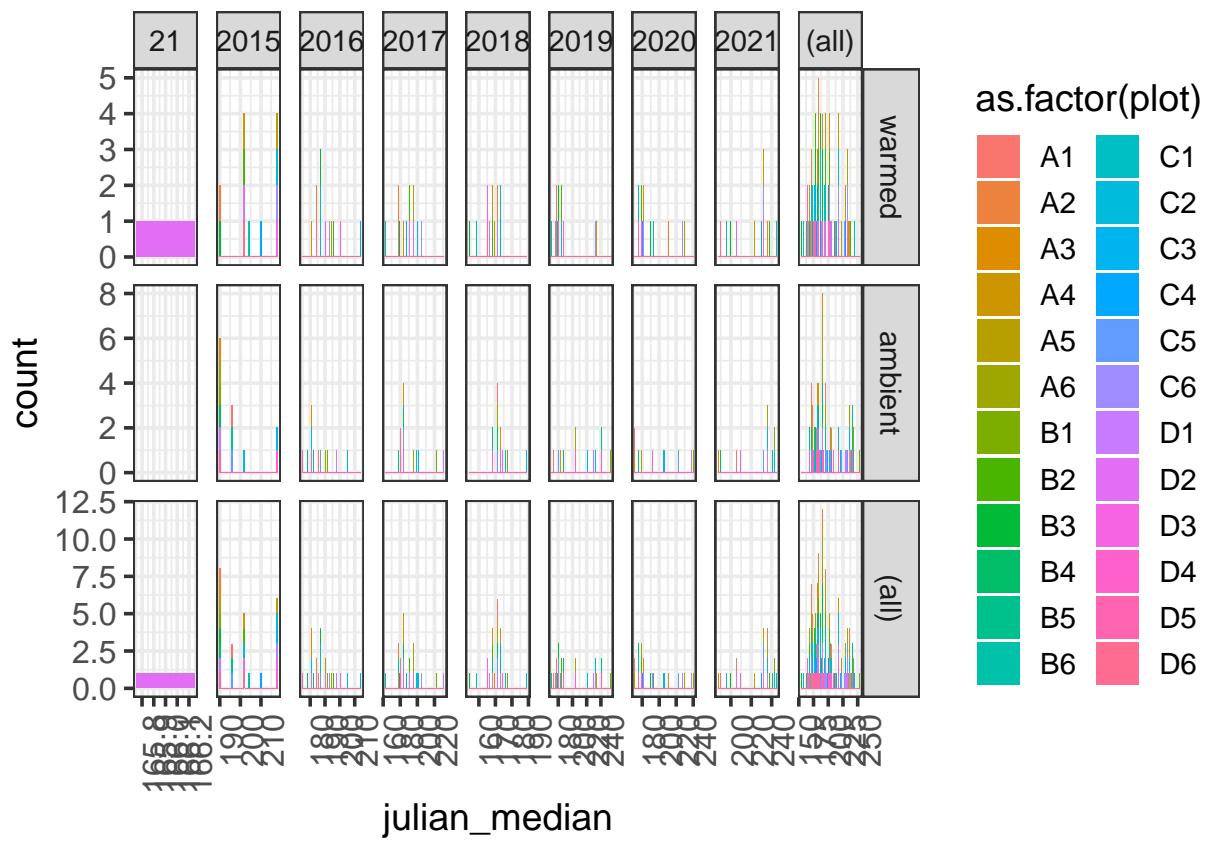
```



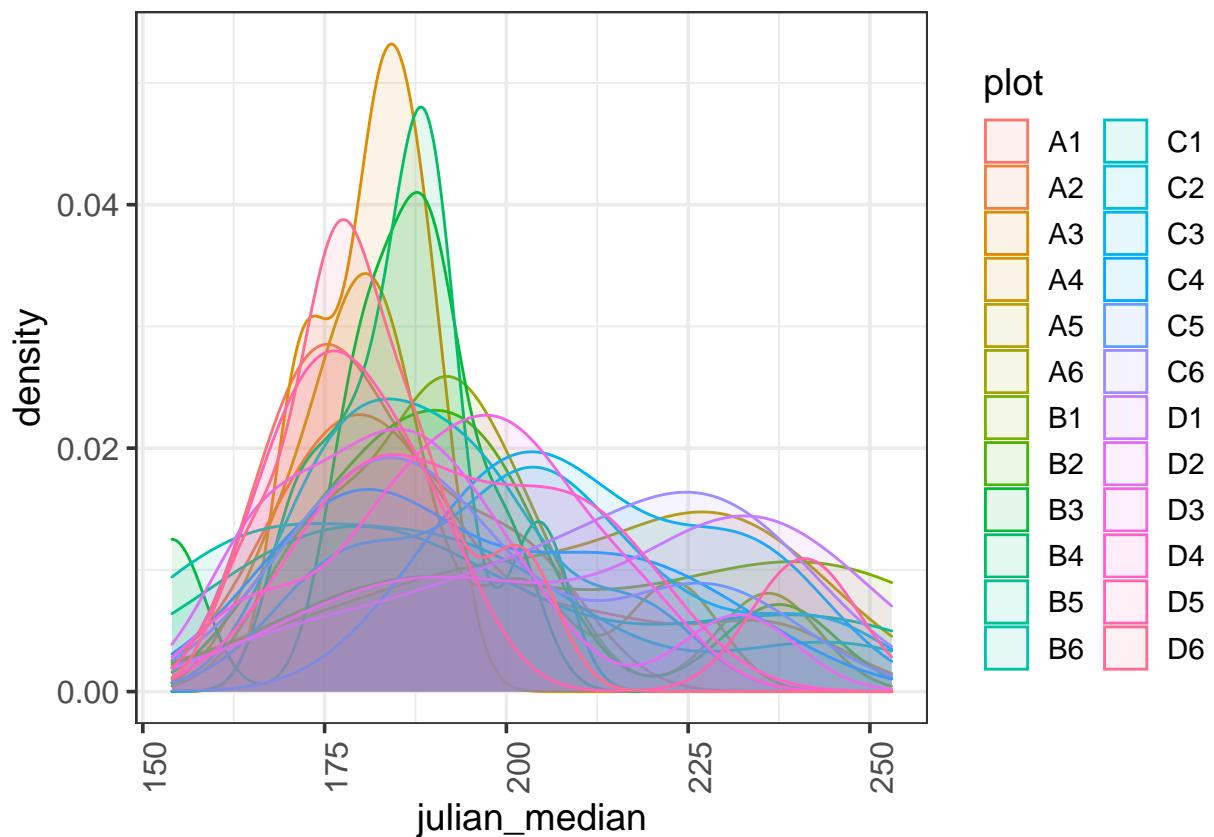
```

ggplot(kbs_flwr_plot, aes(julian_median, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

```



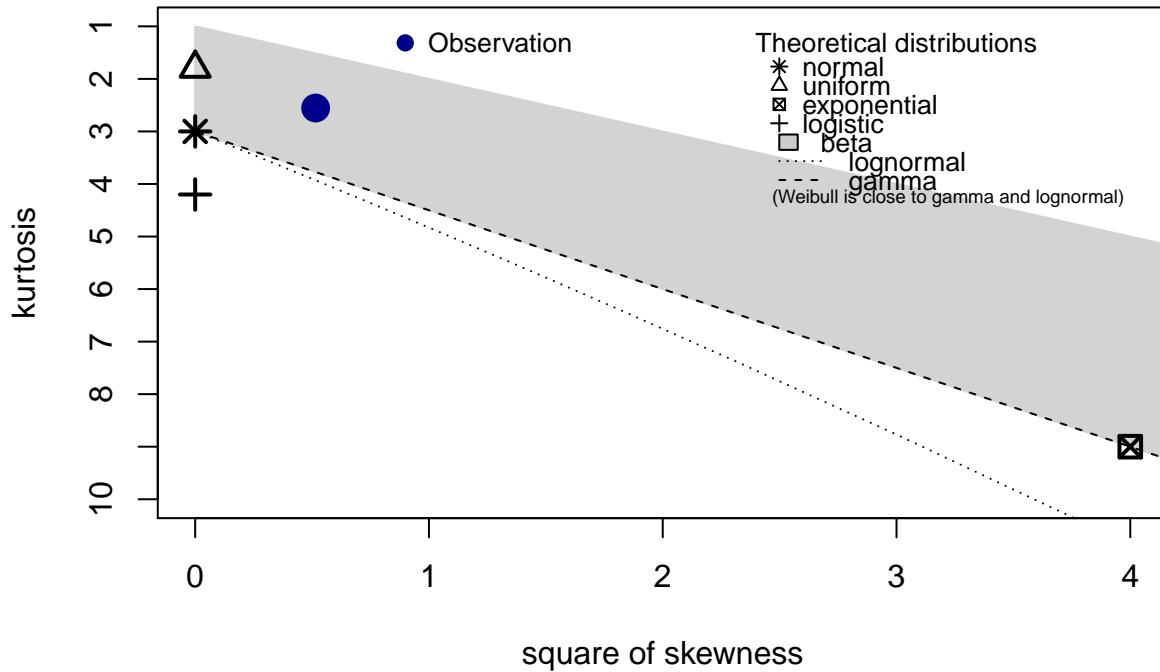
```
ggplot(kbs_flwr_plot, aes(julian_median, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

```
# Exploring distributions for these right-skewed data:
descdist(kbs_flwr_plot$julian_median, discrete = FALSE)
```

Cullen and Frey graph

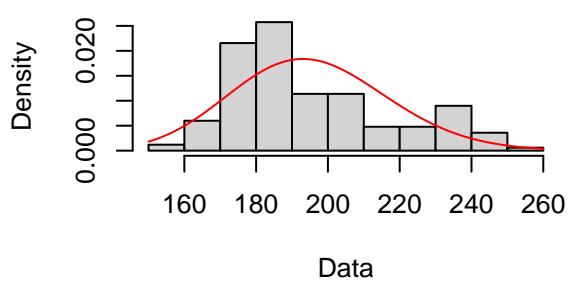
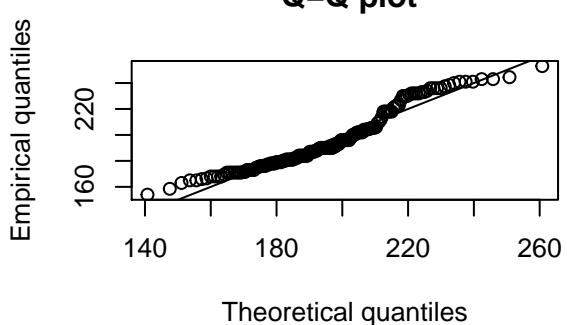
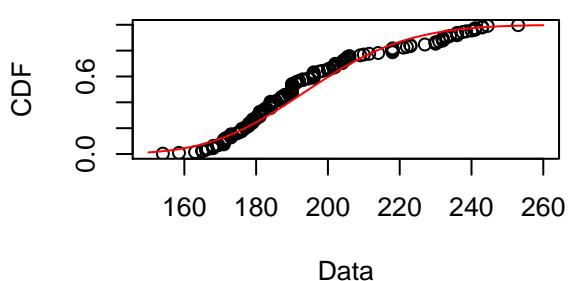
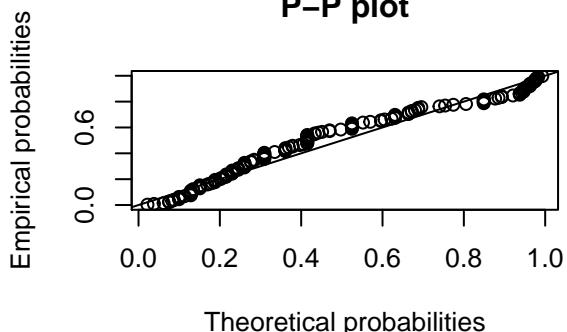


```

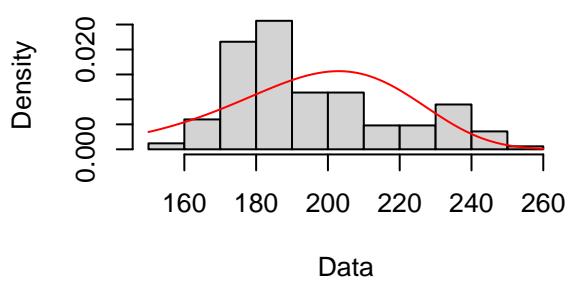
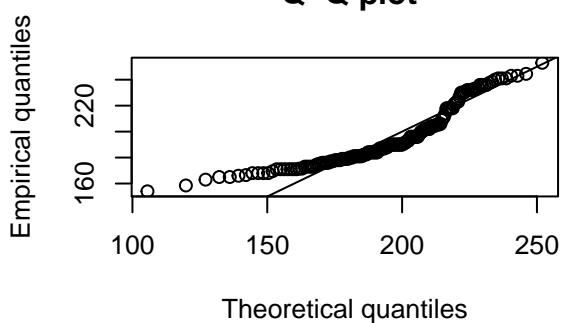
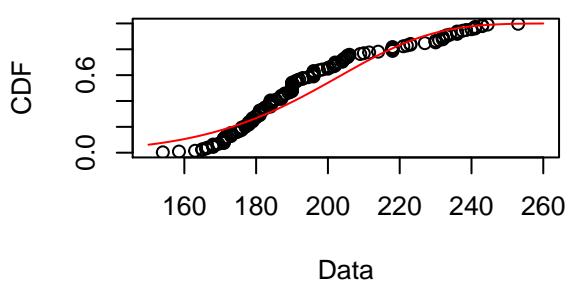
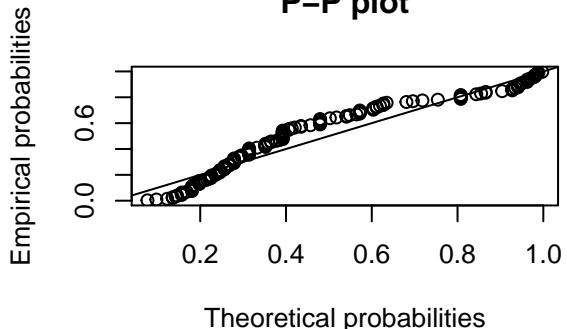
## summary statistics
## -----
## min: 154   max: 253
## median: 190
## mean: 195.4551
## estimated sd: 22.36882
## estimated skewness: 0.7177672
## estimated kurtosis: 2.554227

# Gamma distribution
fit.gamma <- fitdist(kbs_flwr_plot$julian_median, "gamma")
plot(fit.gamma)

```

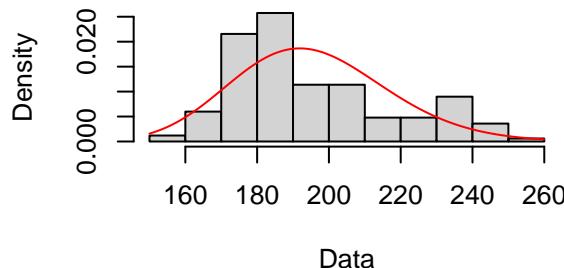
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(kbs_flwr_plot$julian_median, "weibull")
plot(fit.weibull)
```

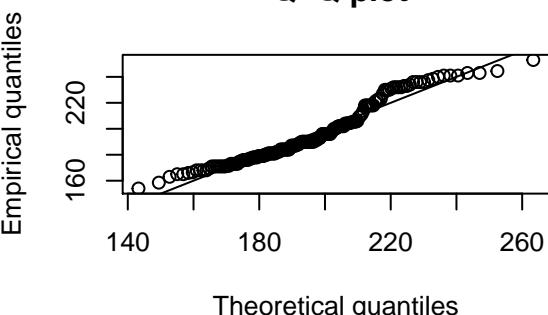
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(kbs_flwr_plot$julian_median, "lnorm")
plot(fit.ln)
```

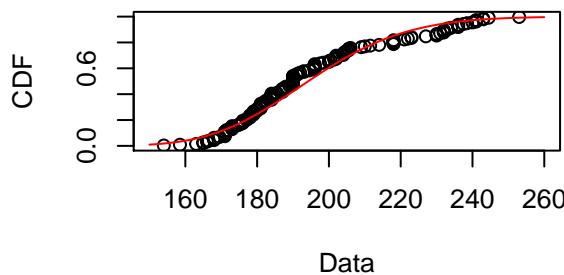
Empirical and theoretical dens.



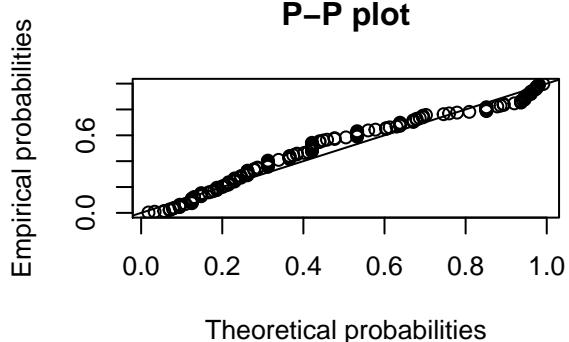
Q–Q plot



Empirical and theoretical CDFs

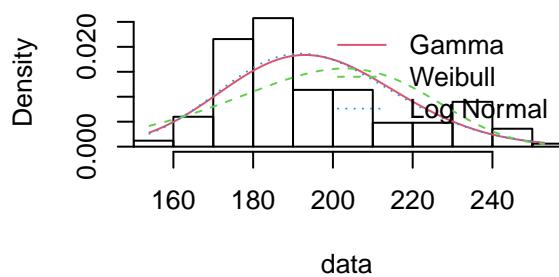


P–P plot

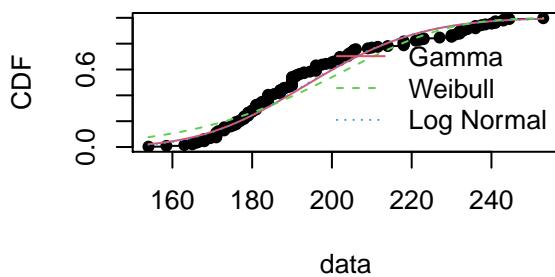


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

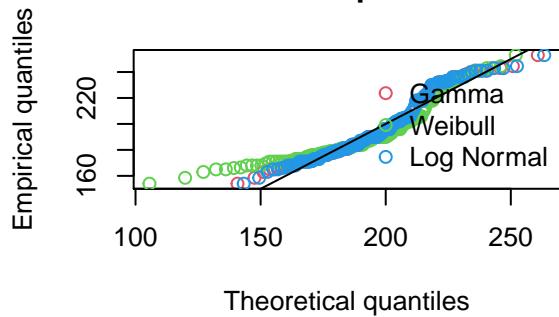
Histogram and theoretical densities



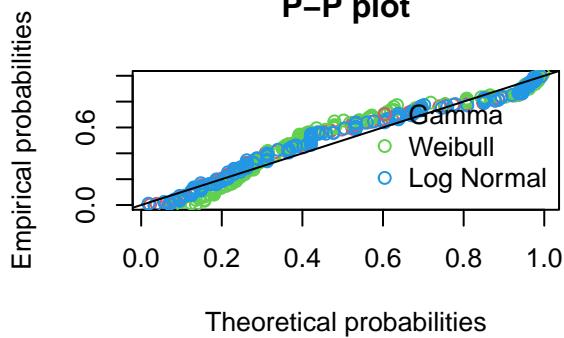
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1300085 0.1552035 0.1237967
## Cramer-von Mises statistic  0.5865903 1.1490303 0.5144716
## Anderson-Darling statistic  3.6124147 6.6542134 3.2100022
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 1506.460 1543.903 1502.958
## Bayesian Information Criterion 1512.696 1550.139 1509.194
```

```
# Log normal is the best first so going to log transform response variable
# julian_median
```

Centering and transforming data - Ignore right now!!

```
# umbs_flwr_plot$julianMin_centered = umbs_flwr_plot$julian_min -
# mean(umb_flwr_plot$log_julian_min) hist(umb_flwr_plot$julianMin_centered)
```

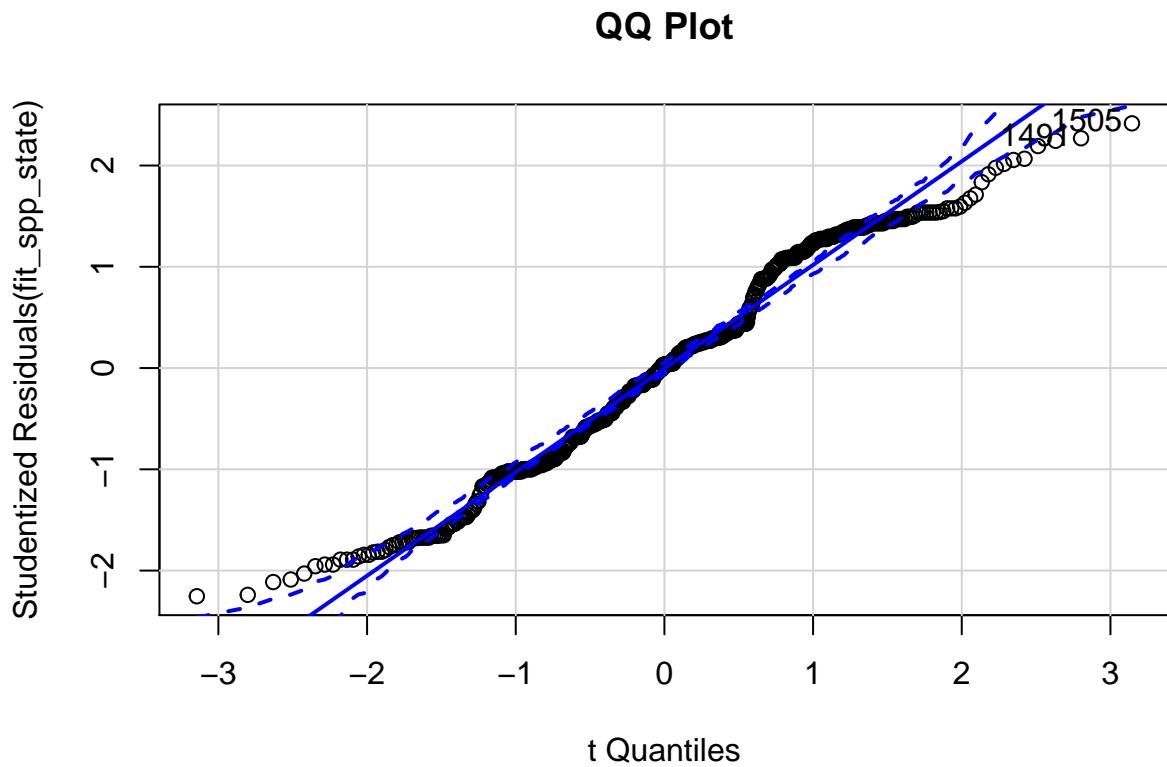
Leverage plots and detecting Outliers. <https://www.statmethods.net/stats/rdiagnostics.html>

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>

```
# species level data UMBS State-only model
fit_spp_state <- lm(log(julian_median) ~ state, data = umbs_flwr_spp)
outlierTest(fit_spp_state) # no outliers

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1505  2.416487          0.015985         NA

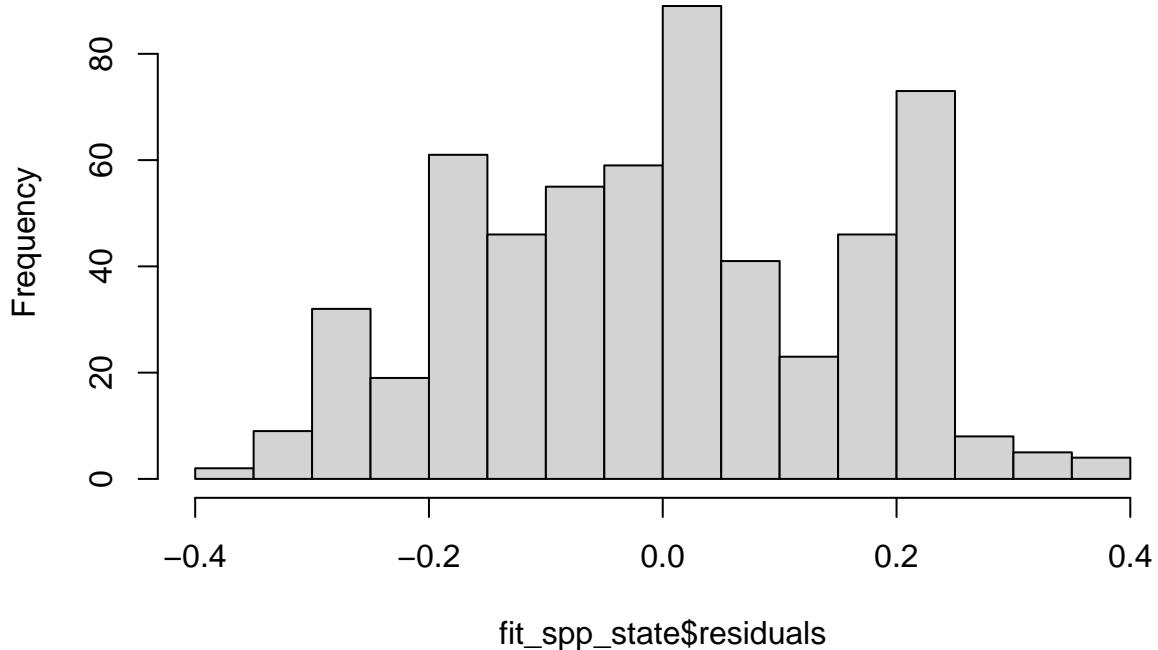
qqPlot(fit_spp_state, main = "QQ Plot")
```



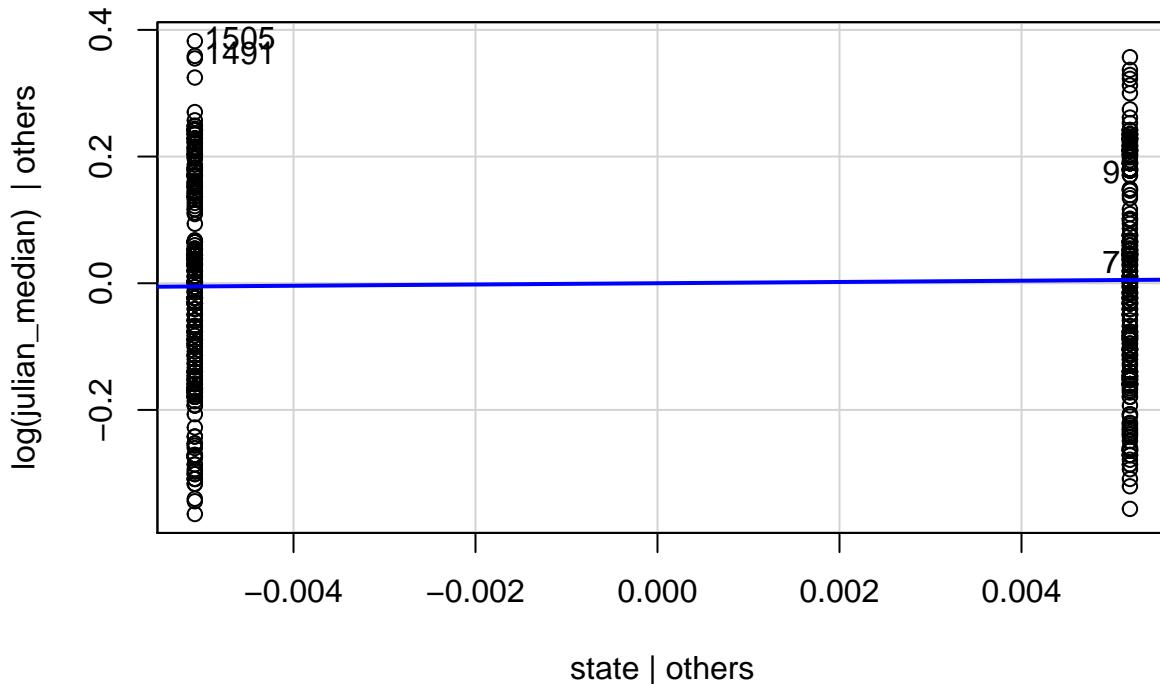
```
## 1491 1505
## 502 507
```

```
hist(fit_spp_state$residuals)
```

Histogram of fit_spp_state\$residuals



```
leveragePlots(fit_spp_state)
```



```
ols_test_normality(fit_spp_state)
```

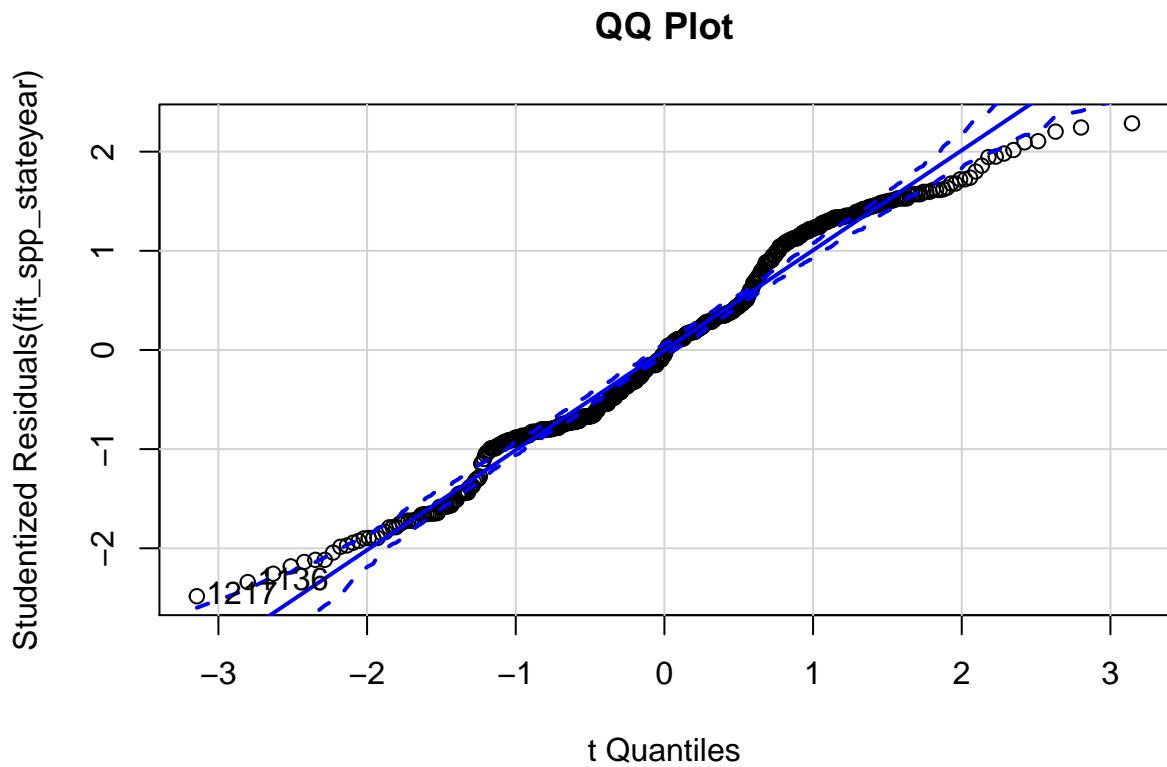
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9777       0.0000
## Kolmogorov-Smirnov 0.0747       0.0034
## Cramer-von Mises 133.5002      0.0000
## Anderson-Darling   3.6609       0.0000
## -----
```

```
# UMBS State and year model
fit_spp_stateyear <- lm(log(julian_median) ~ state + year_factor, data = umbs_flwr_spp)
outlierTest(fit_spp_stateyear) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##           rstudent unadjusted p-value Bonferroni p
## 1217    -2.483867          0.013284        NA
```

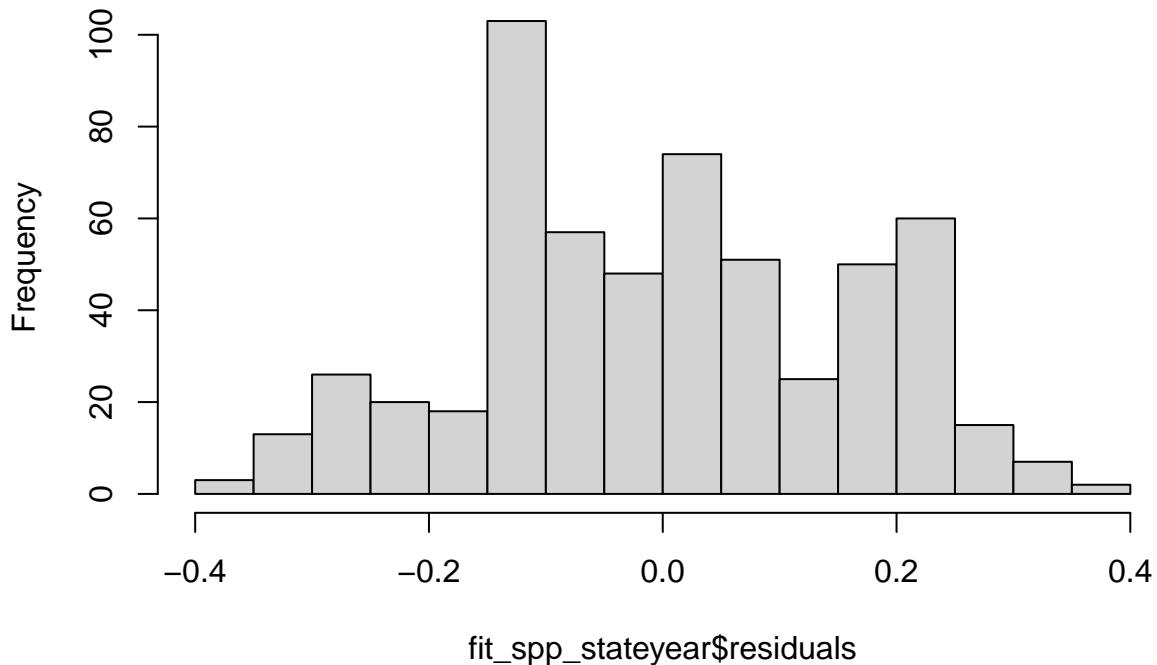
```
qqPlot(fit_spp_stateyear, main = "QQ Plot")
```



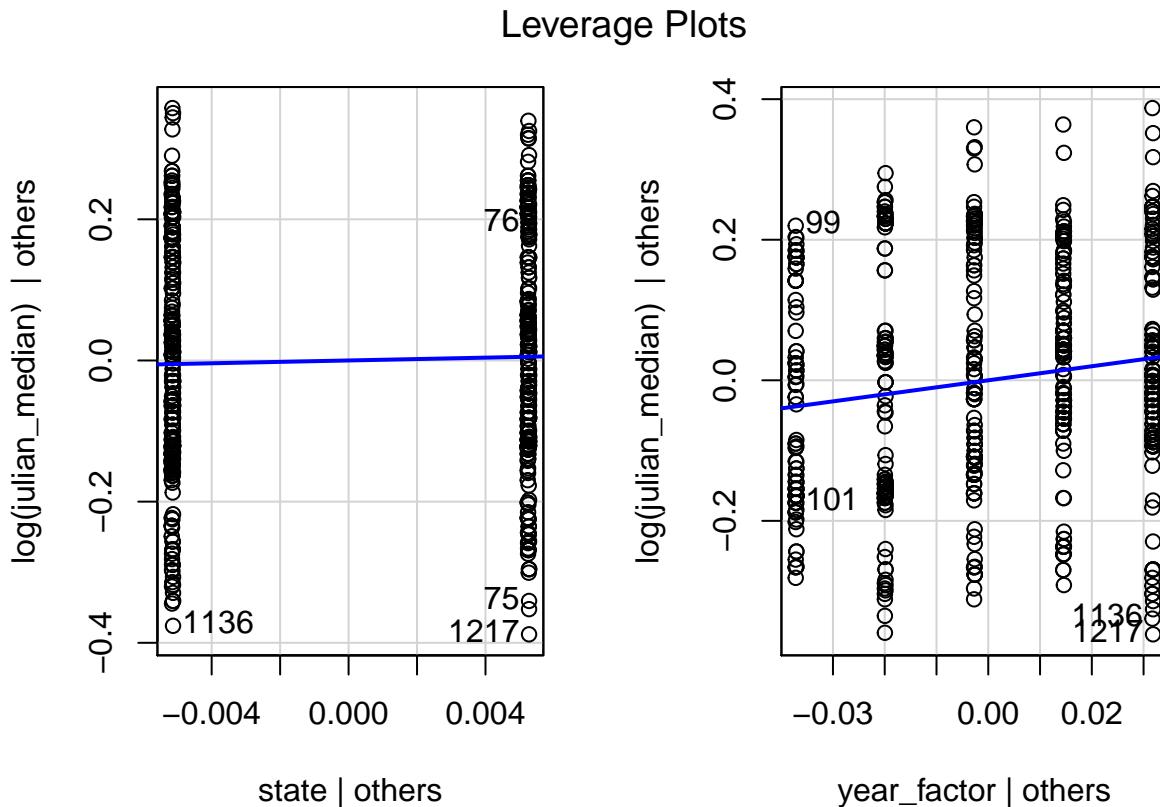
```
## 1136 1217
## 392 414
```

```
hist(fit_spp_stateyear$residuals)
```

Histogram of fit_spp_stateyear\$residuals



```
leveragePlots(fit_spp_stateyear)
```



```
ols_test_normality(fit_spp_stateyear)
```

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

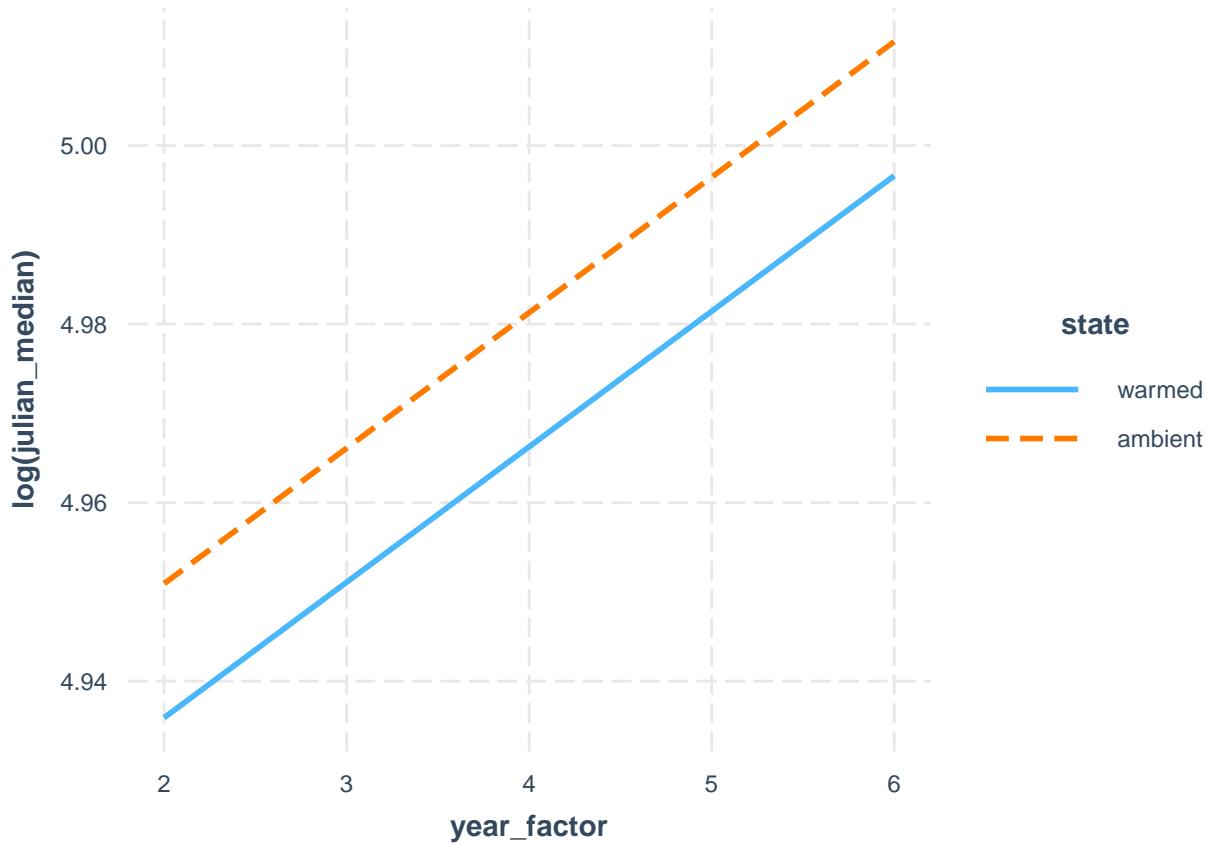
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9794      0.0000
## Kolmogorov-Smirnov 0.0715      0.0057
## Cramer-von Mises 133.7468      0.0000
## Anderson-Darling   3.8514      0.0000
## -----
```

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

```
fit3 <- lm(log(julian_median) ~ state + year_factor + species, data = umbs_flwr_spp)
interact_plot(fit3, pred = year_factor, modx = state)
```

```
## Using data umbs_flwr_spp from global environment. This could cause
## incorrect results if umbs_flwr_spp has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```

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



```
fit4 <- lm(log(julian_median) ~ state * year_factor + species, data = umbs_flwr_spp)
interact_plot(fit4, pred = year_factor, modx = state, mod2 = species)
```

```
## Using data umbs_flwr_spp from global environment. This could cause
## incorrect results if umbs_flwr_spp has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```

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

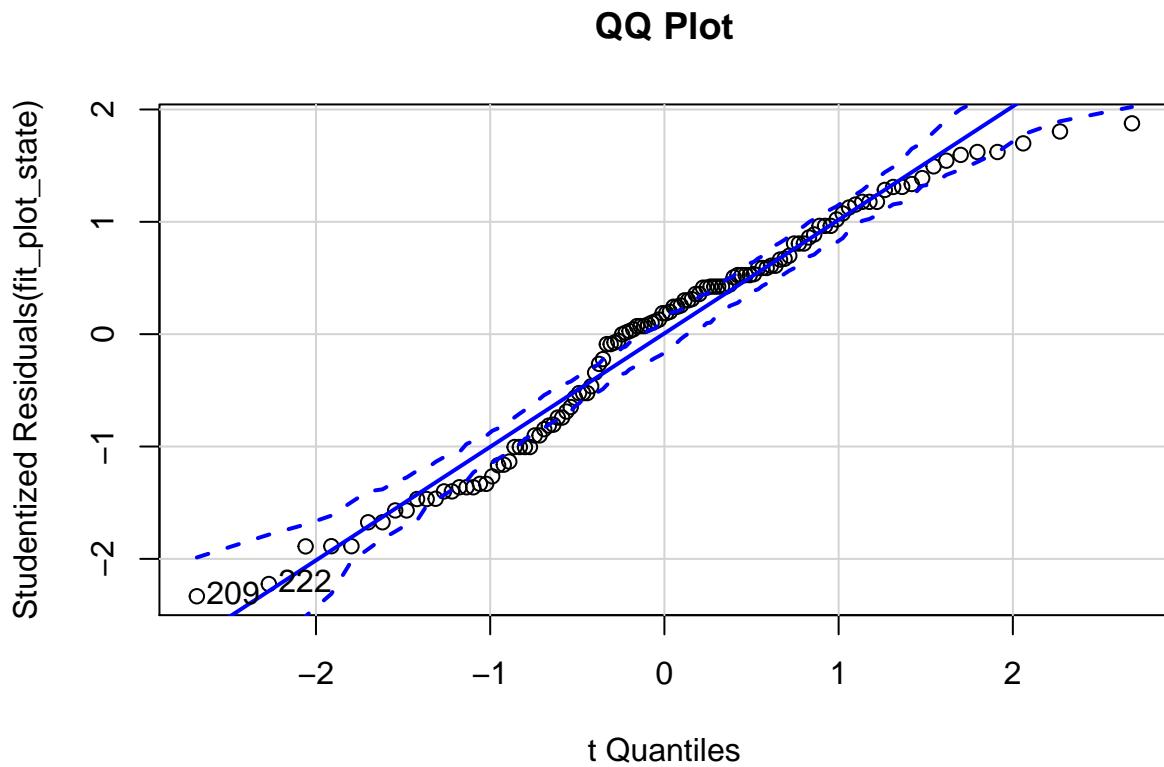


state —— dashed blue = warmed —— solid orange = ambient

```
# Plot level data UMBS State-only model
fit_plot_state <- lm(log(julian_median) ~ state, data = umbs_flwr_plot)
outlierTest(fit_plot_state) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 209 -2.332584          0.021379         NA
```

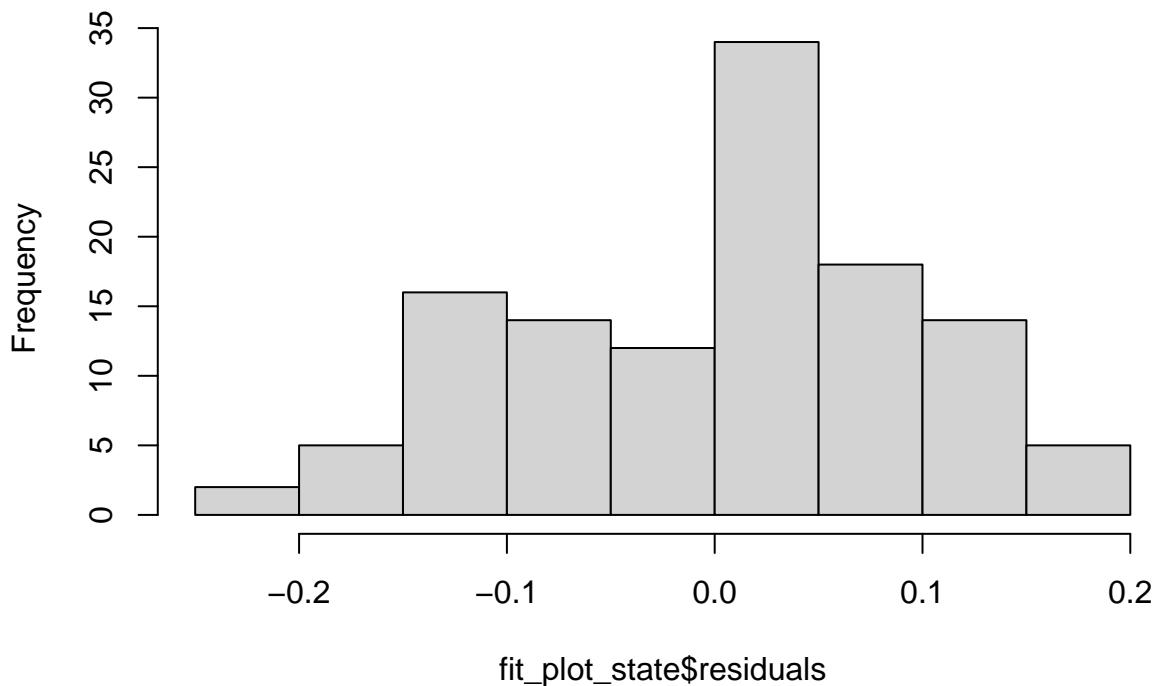
```
qqPlot(fit_plot_state, main = "QQ Plot")
```



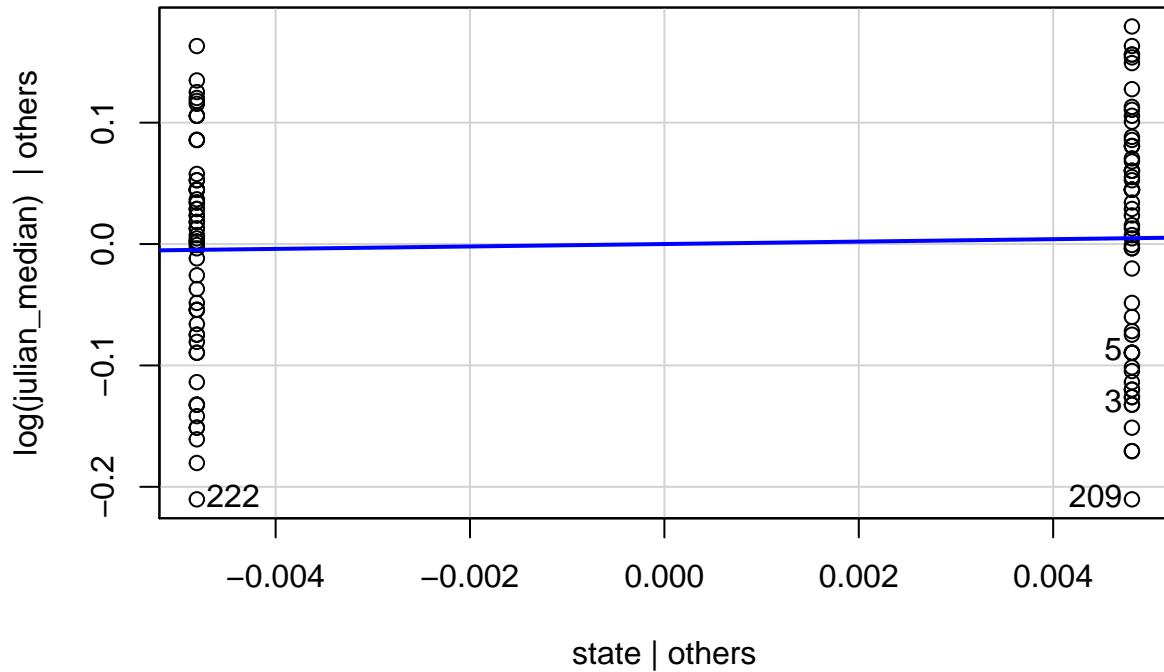
```
## 209 222
## 81 86
```

```
hist(fit_plot_state$residuals)
```

Histogram of fit_plot_state\$residuals



```
leveragePlots(fit_plot_state)
```



```
ols_test_normality(fit_plot_state) # looks ok besides Kolmogorov-Smirnov test
```

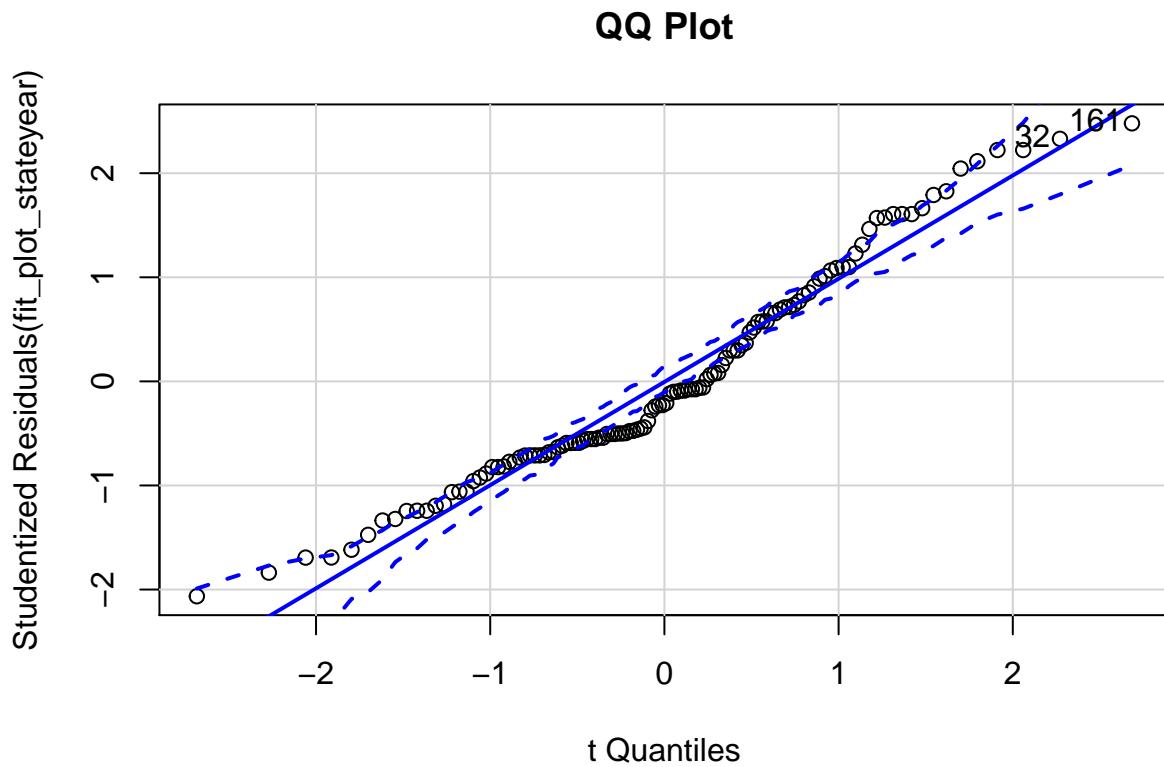
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9676      0.0055
## Kolmogorov-Smirnov 0.0994      0.1861
## Cramer-von Mises  32.7408      0.0000
## Anderson-Darling   1.3432      0.0017
## -----
```

```
# UMBS State and year model
fit_plot_stateyear <- lm(log(julian_median) ~ state + year_factor, data = umbs_flwr_plot)
outlierTest(fit_plot_stateyear) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 161  2.478948           0.014615        NA
```

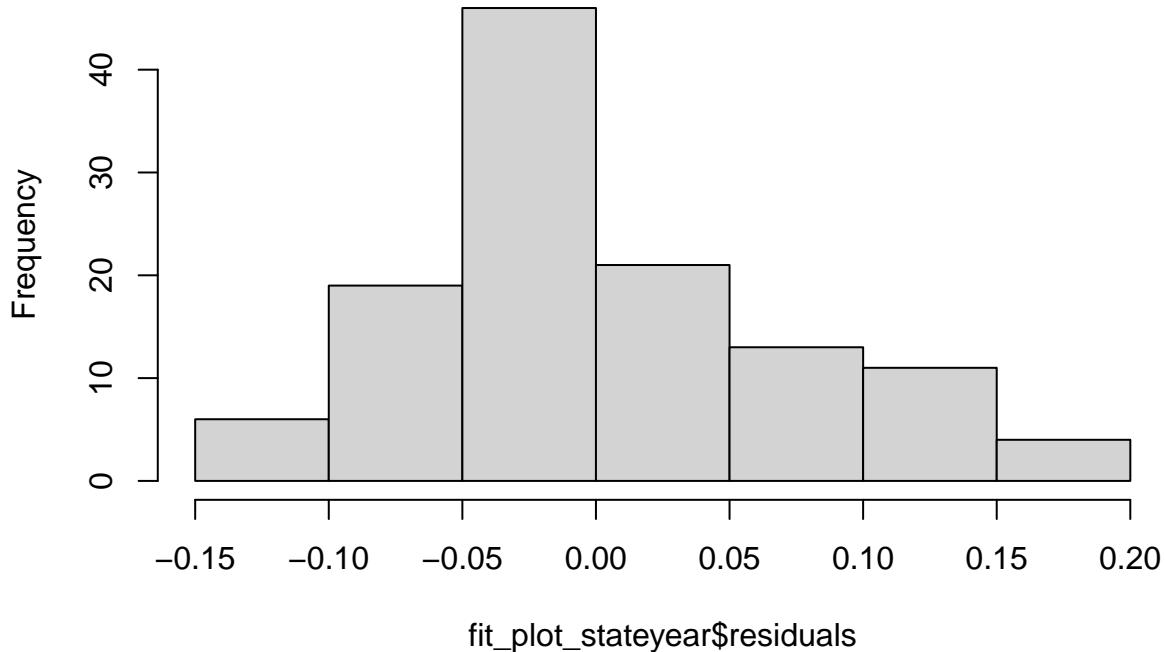
```
qqPlot(fit_plot_stateyear, main = "QQ Plot")
```



```
##  32 161
## 13 63
```

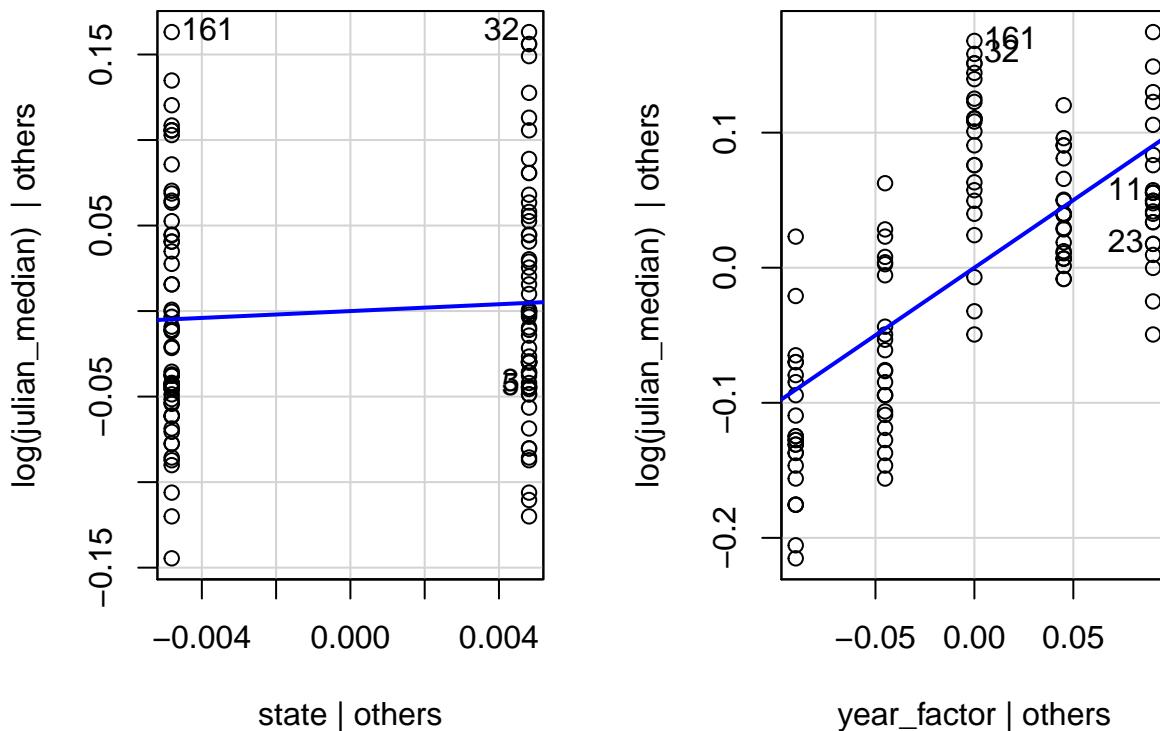
```
hist(fit_plot_stateyear$residuals)
```

Histogram of fit_plot_stateyear\$residuals



```
leveragePlots(fit_plot_stateyear)
```

Leverage Plots



```
ols_test_normality(fit_plot_stateyear) # all good
```

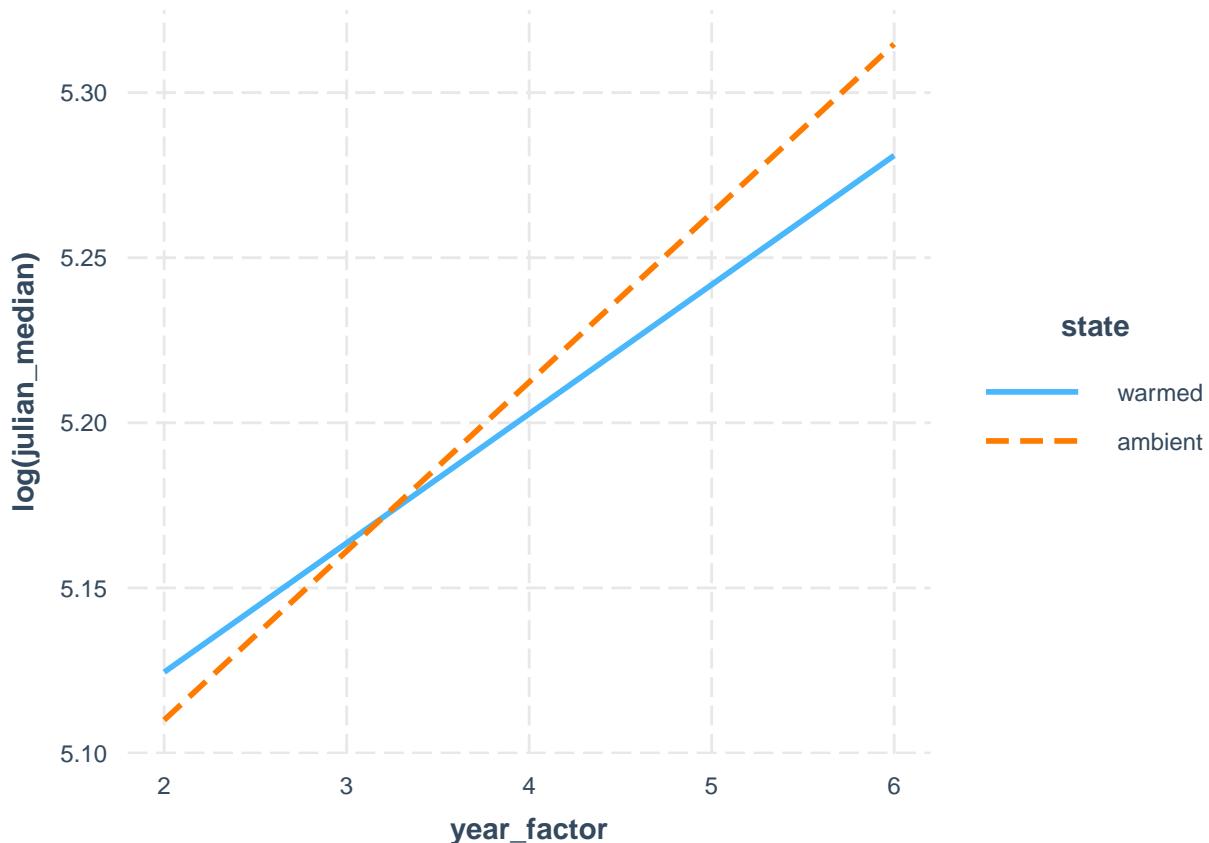
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test       Statistic     pvalue
## -----
## Shapiro-Wilk      0.9617    0.0017
## Kolmogorov-Smirnov   0.1293    0.0361
## Cramer-von Mises  34.4122    0.0000
## Anderson-Darling   1.7661    2e-04
## -----
```

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

```
fit3 <- lm(log(julian_median) ~ state * year_factor, data = umbs_flwr_plot)
interact_plot(fit3, pred = year_factor, modx = state)
```

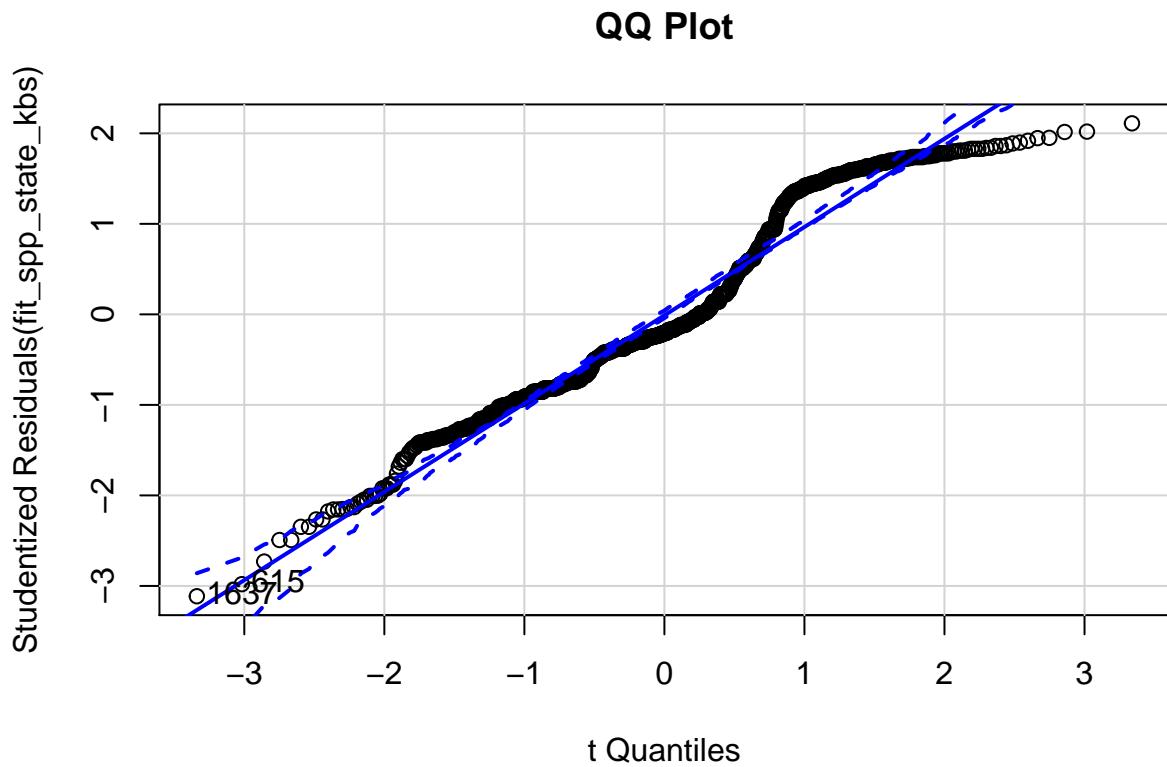
```
## Using data umbs_flwr_plot from global environment. This could cause
## incorrect results if umbs_flwr_plot has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```



```
# species level data KBS State-only model
fit_spp_state_kbs <- lm(log(julian_median) ~ state, data = kbs_flwr_spp)
outlierTest(fit_spp_state_kbs) # no outliers
```

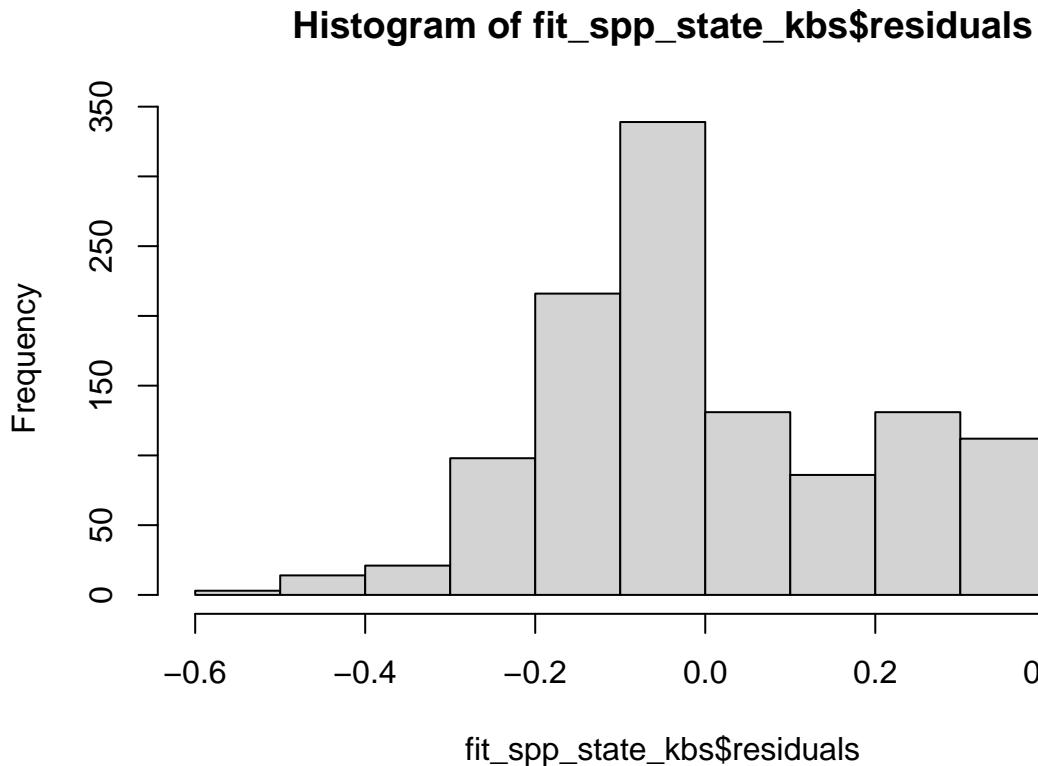
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1637 -3.11402          0.0018912        NA

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

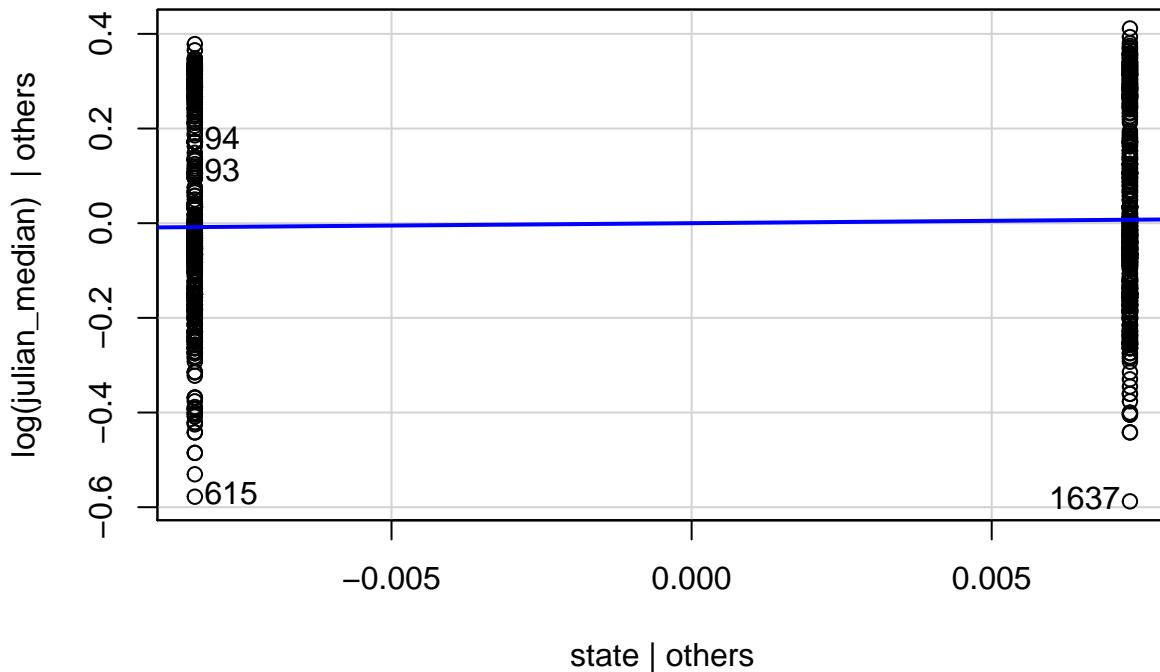


```
##   615 1637
##   383 1077
```

```
hist(fit_spp_state_kbs$residuals)
```



```
leveragePlots(fit_spp_state_kbs)
```



```
ols_test_normality(fit_spp_state_kbs)
```

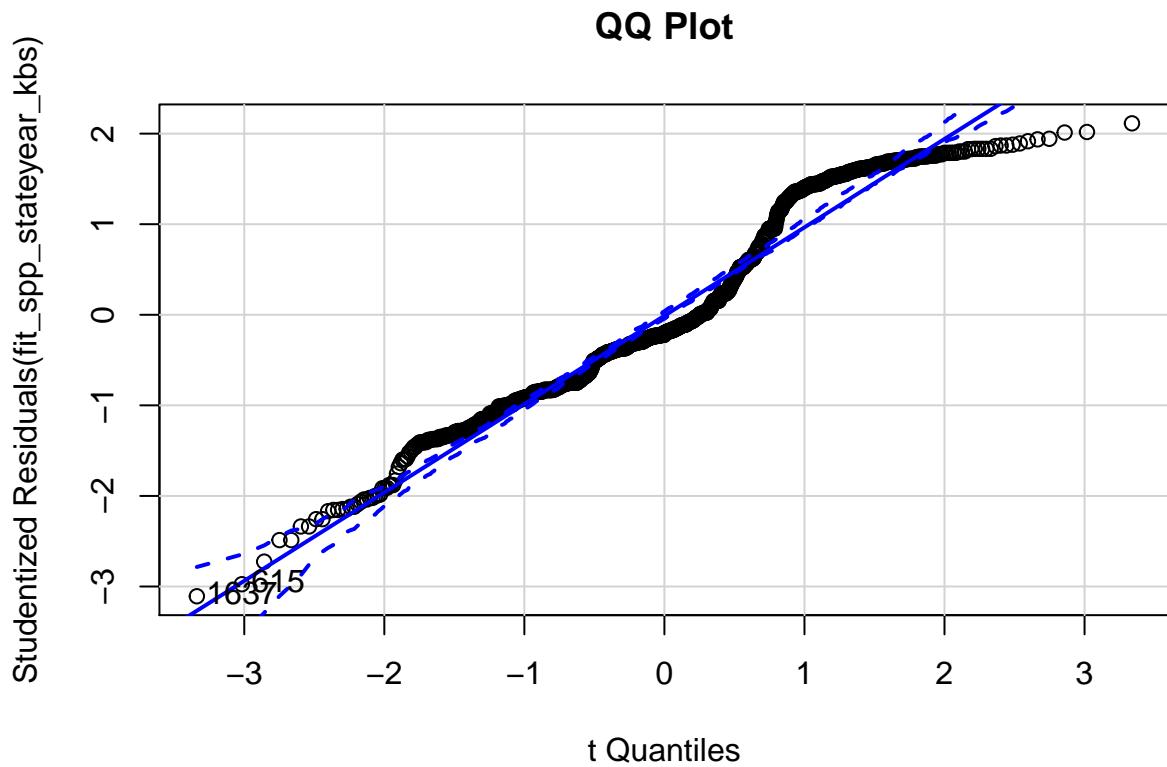
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##          Test      Statistic     pvalue
## -----
## Shapiro-Wilk      0.9563    0.0000
## Kolmogorov-Smirnov 0.1089    0.0000
## Cramer-von Mises 251.7392   0.0000
## Anderson-Darling 19.9905    0.0000
## -----
```

```
# KBS State and year model
fit_spp_stateyear_kbs <- lm(log(julian_median) ~ state + year_factor, data = kbs_flwr_spp)
outlierTest(fit_spp_stateyear_kbs) # no outliers
```

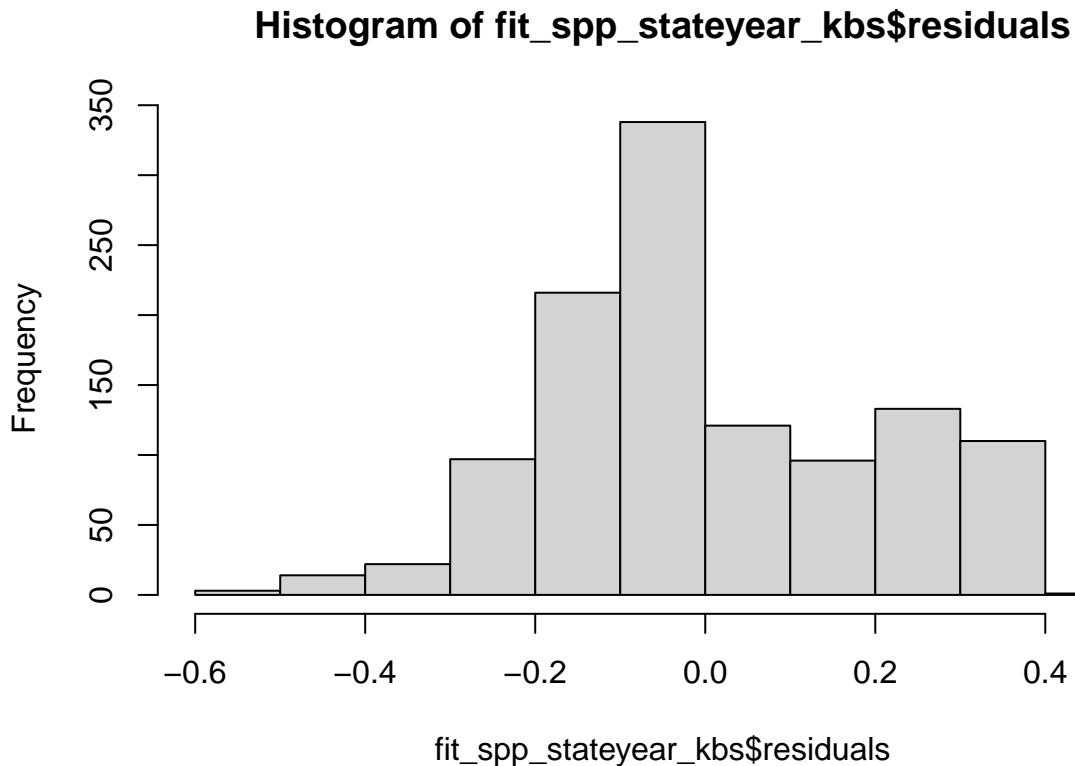
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1637 -3.10761        0.0019324       NA
```

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



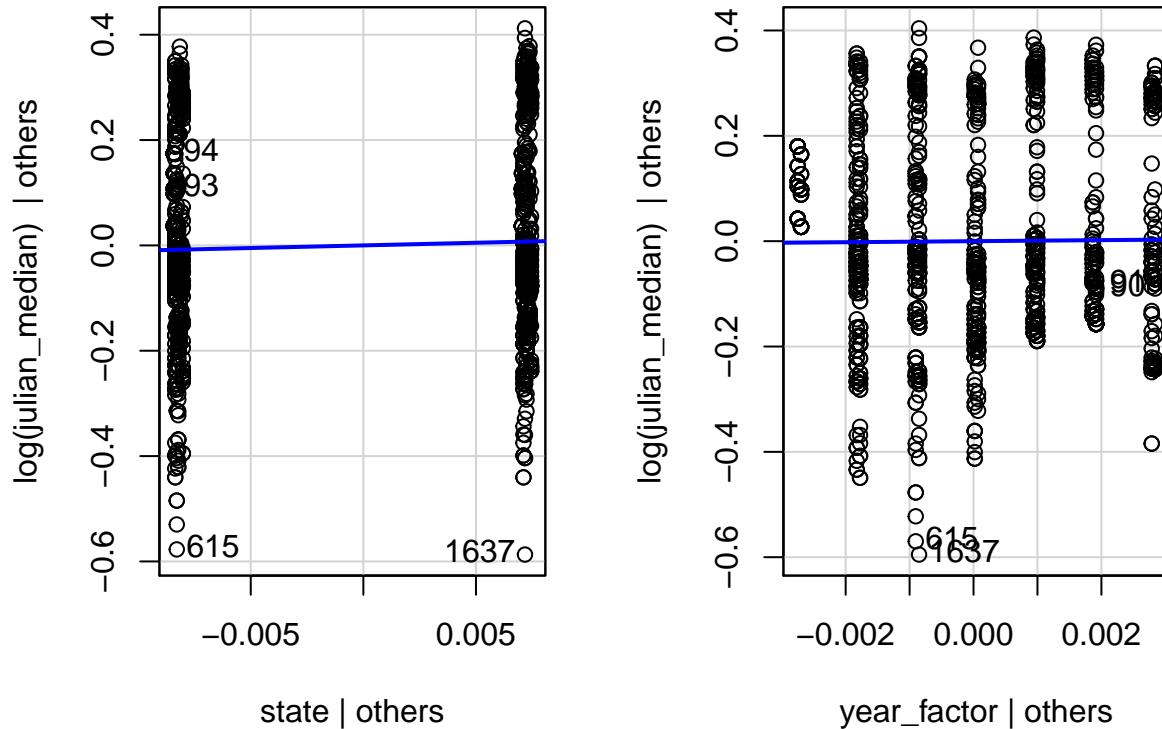
```
##   615 1637
##   383 1077
```

```
hist(fit_spp_stateyear_kbs$residuals)
```



```
leveragePlots(fit_spp_stateyear_kbs)
```

Leverage Plots



```
ols_test_normality(fit_spp_stateyear_kbs)
```

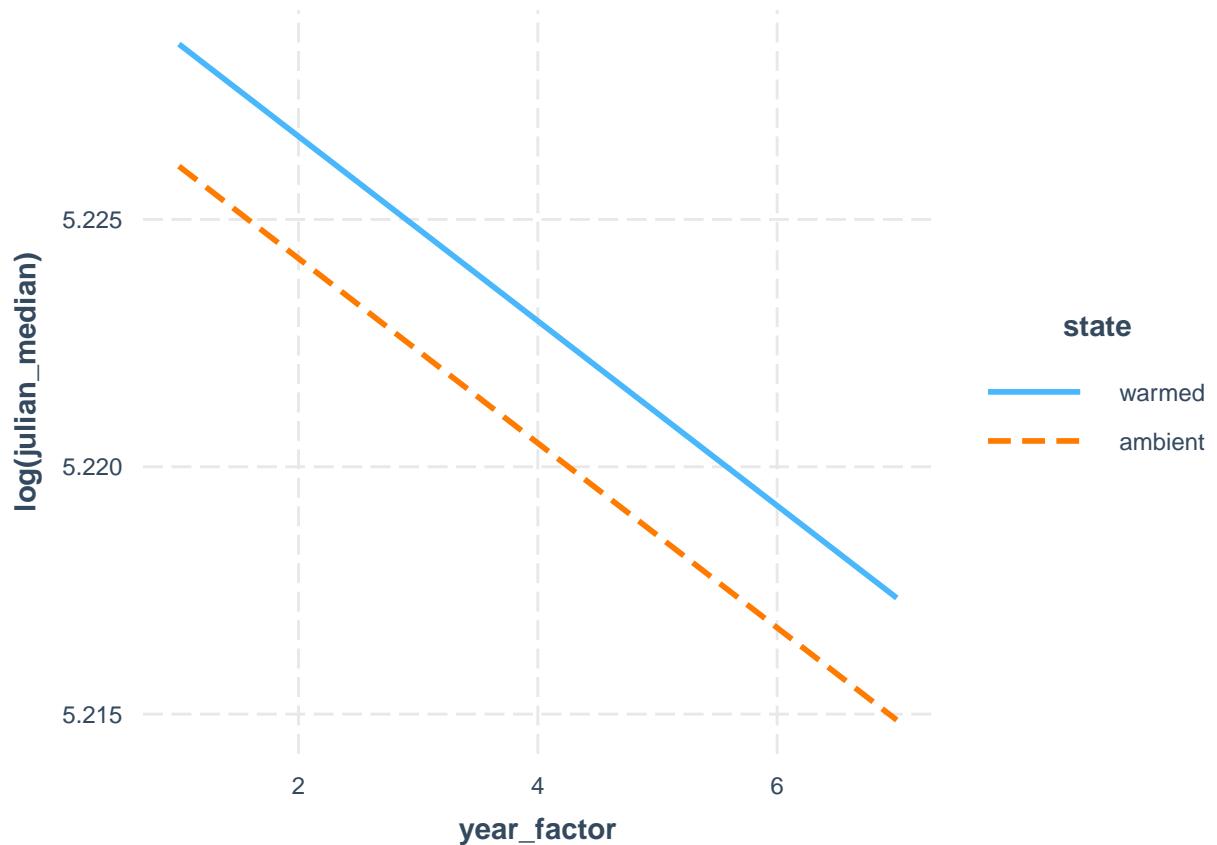
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##          Test      Statistic     pvalue
## -----
## Shapiro-Wilk      0.9565    0.0000
## Kolmogorov-Smirnov 0.1101    0.0000
## Cramer-von Mises   251.3042   0.0000
## Anderson-Darling    19.7878   0.0000
## -----
```

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

```
fit3_spp_kbs <- lm(log(julian_median) ~ state + year_factor + species, data = kbs_flwr_spp)
interact_plot(fit3_spp_kbs, pred = year_factor, modx = state, data = kbs_flwr_spp)
```

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

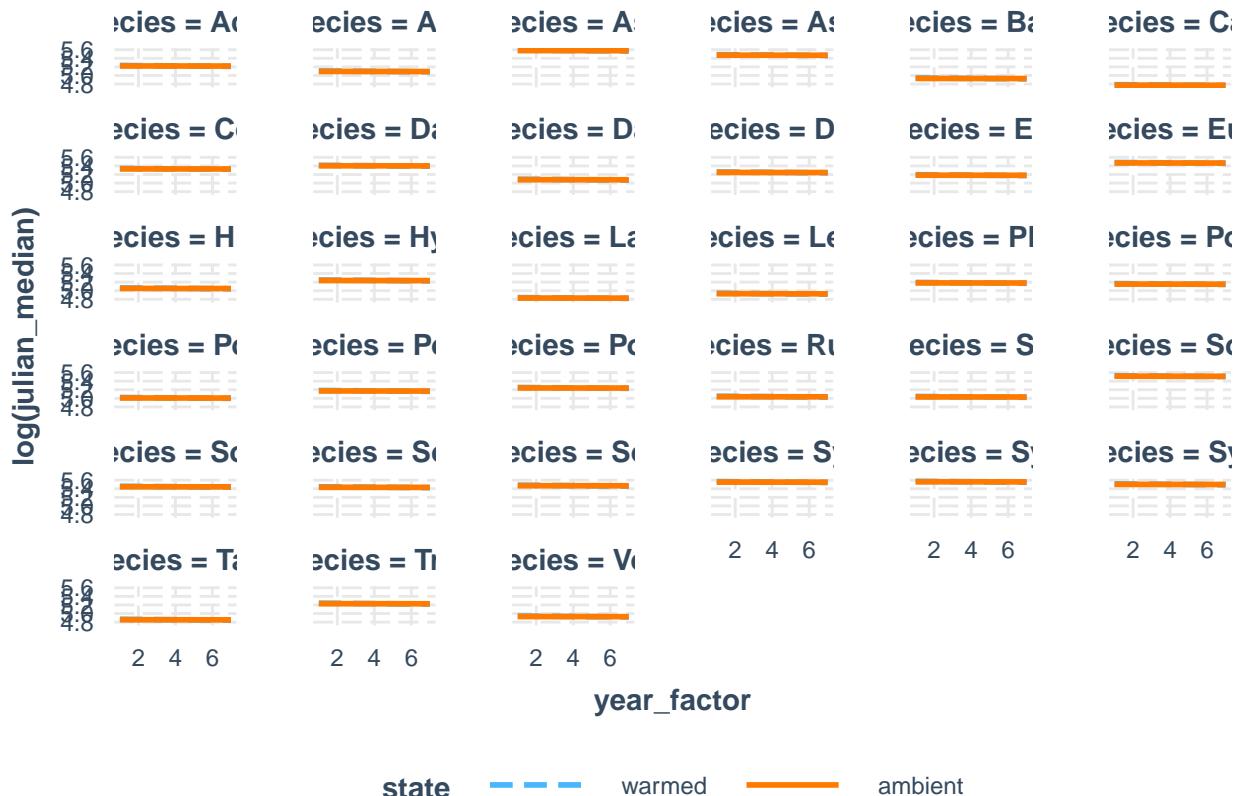


```

fit4_spp_kbs <- lm(log(julian_median) ~ state * year_factor + species, data = kbs_flwr_spp)
interact_plot(fit4_spp_kbs, pred = year_factor, modx = state, mod2 = species, data = kbs_flwr_spp)

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

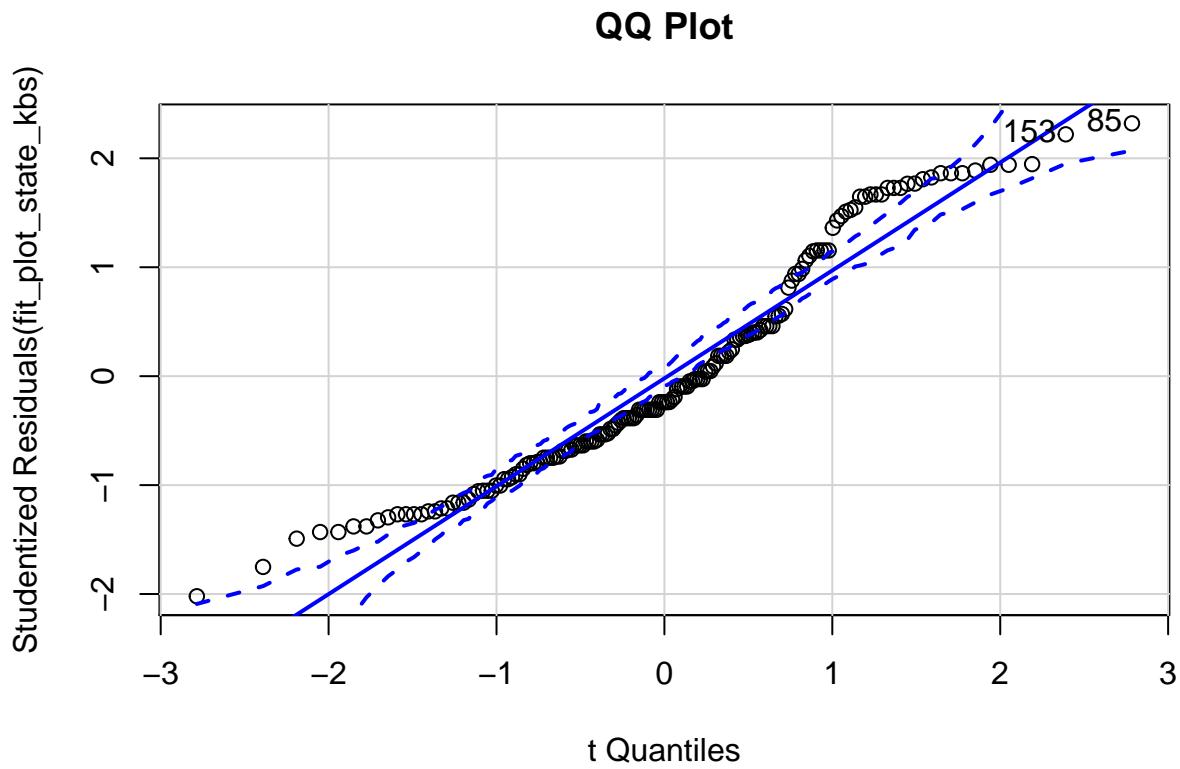
```



```
# Plot level data KBS State-only model
fit_plot_state_kbs <- lm(log(julian_median) ~ state, data = kbs_flwr_plot)
outlierTest(fit_plot_state_kbs) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstUDENT unadjusted p-value Bonferroni p
## 85 2.320858          0.021526           NA
```

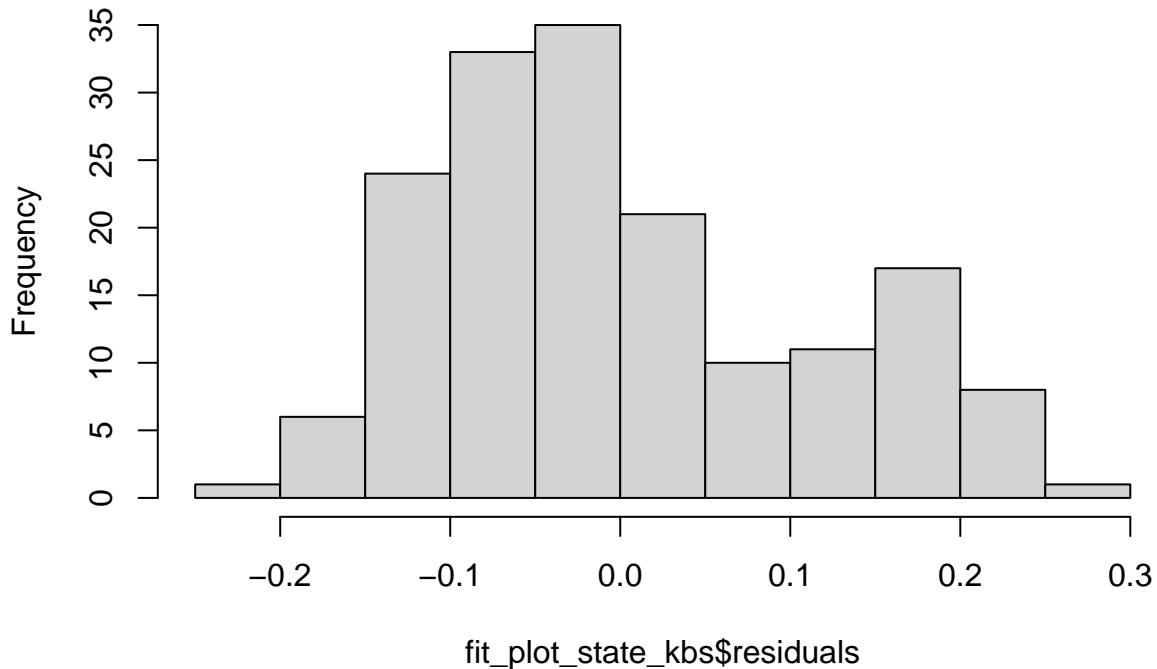
```
qqPlot(fit_plot_state_kbs, main = "QQ Plot")
```



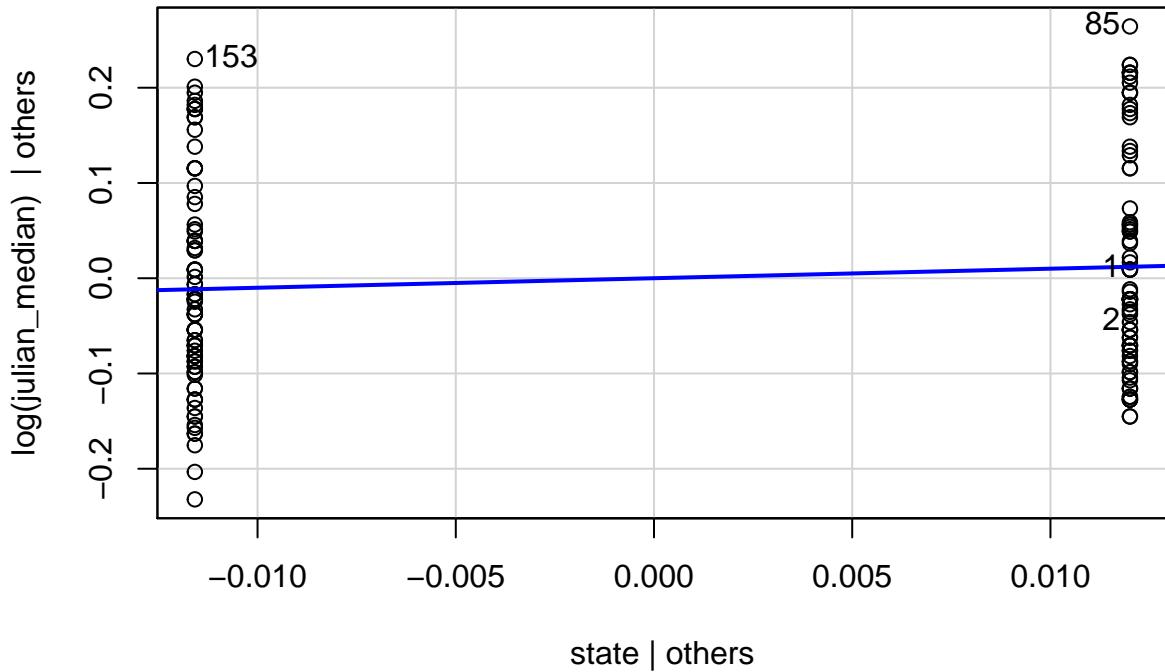
```
##   85 153
##   47 84
```

```
hist(fit_plot_state_kbs$residuals)
```

Histogram of fit_plot_state_kbs\$residuals



```
leveragePlots(fit_plot_state_kbs)
```



```
ols_test_normality(fit_plot_state_kbs)
```

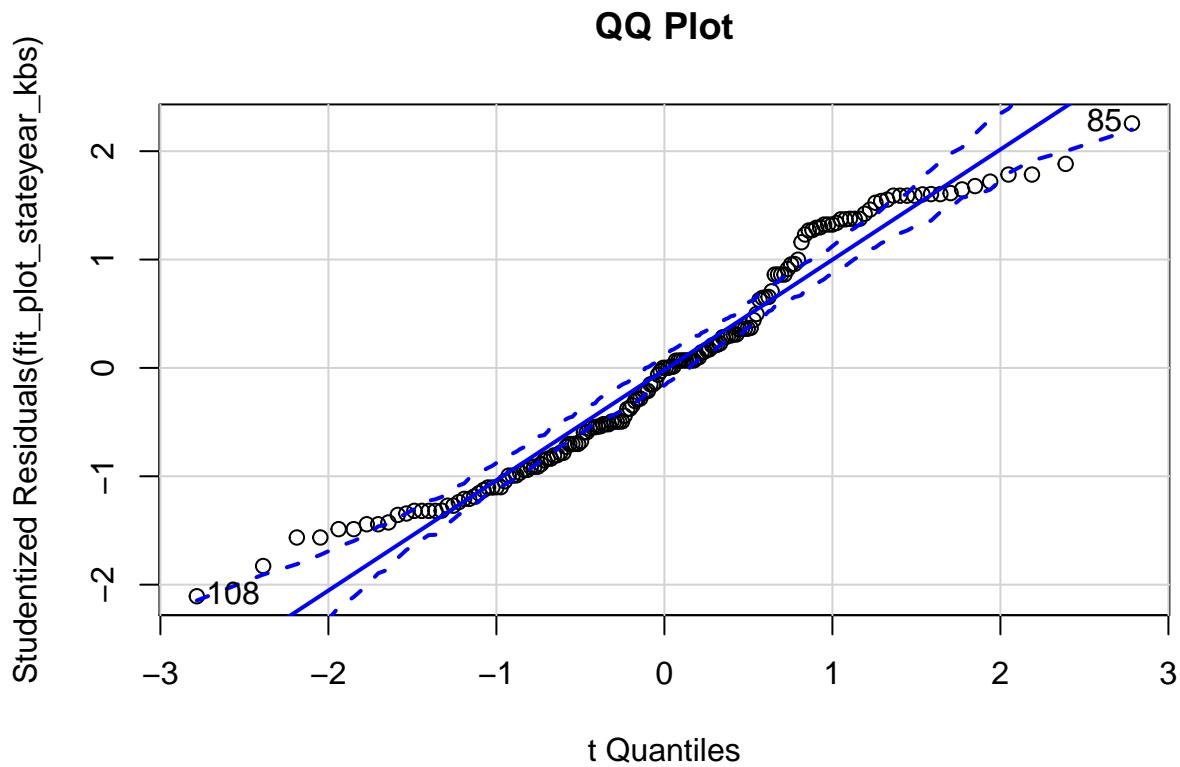
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----  
##          Test      Statistic    pvalue  
## -----  
## Shapiro-Wilk       0.9441    0.00000  
## Kolmogorov-Smirnov 0.1087    0.03871  
## Cramer-von Mises   43.6201   0.00000  
## Anderson-Darling   3.2161    0.00000  
## -----
```

```
# KBS State and year model
fit_plot_stateyear_kbs <- lm(log(julian_median) ~ state + year_factor, data = kbs_flwr_plot)
outlierTest(fit_plot_stateyear_kbs) # outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 85  2.256773        0.025359        NA
```

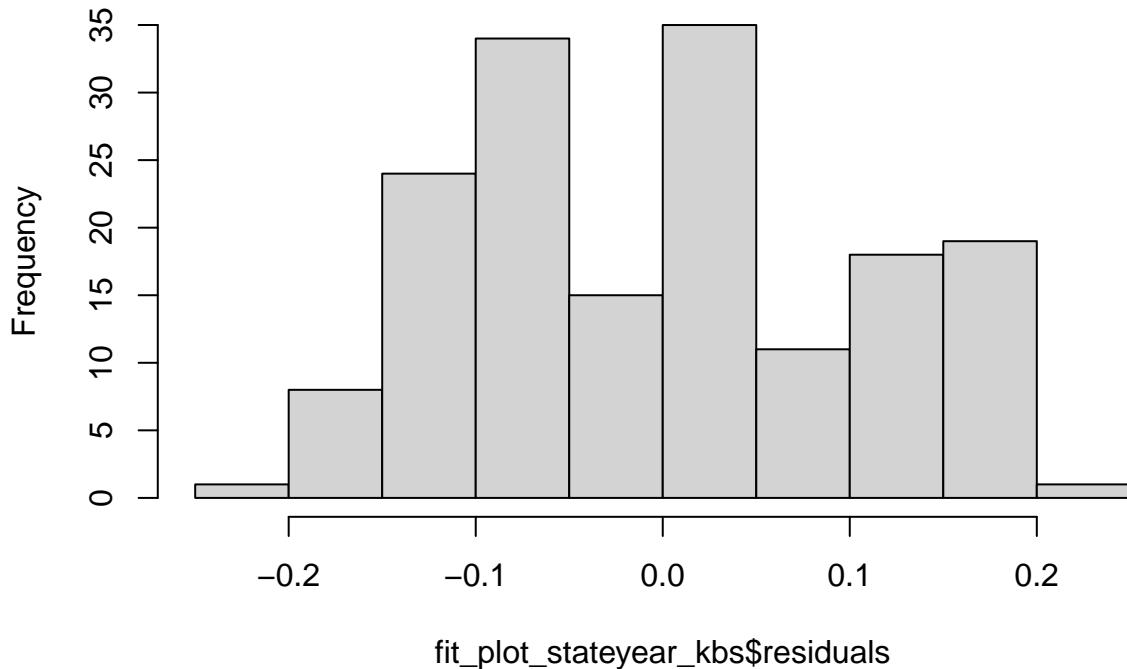
```
qqPlot(fit_plot_stateyear_kbs, main = "QQ Plot")
```



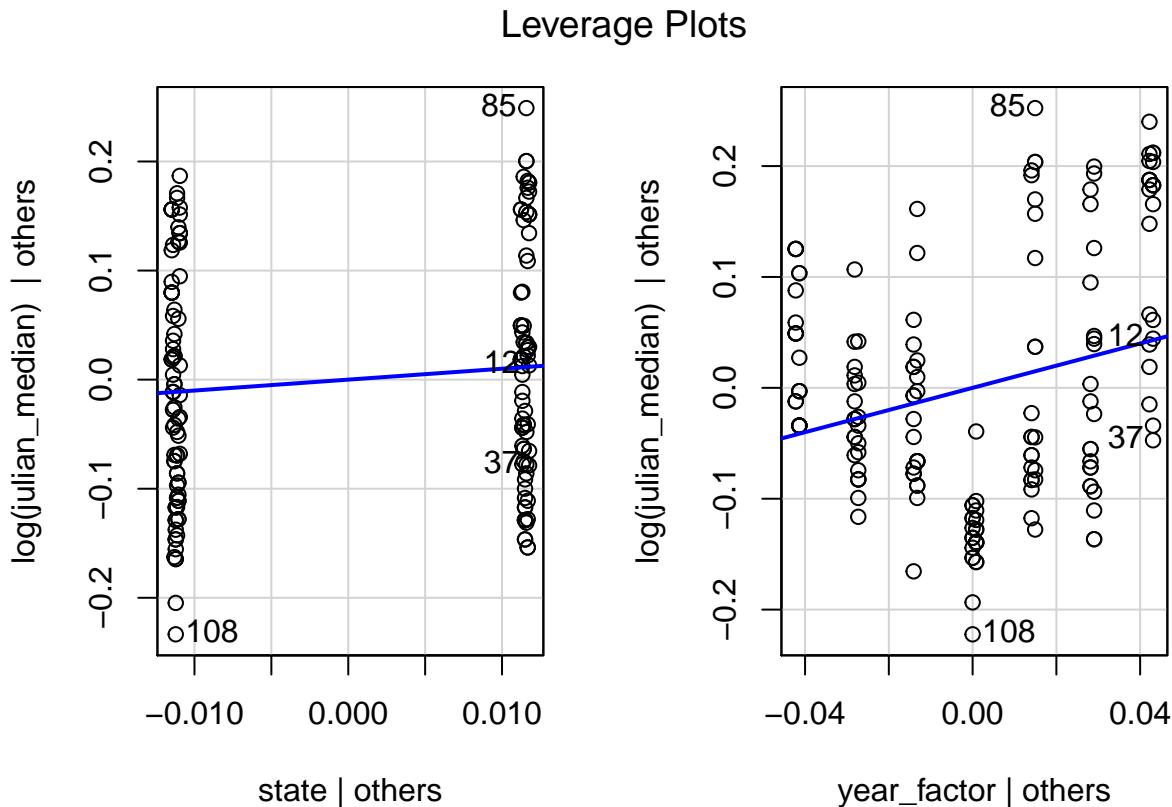
```
##   85 108
##   47 60
```

```
hist(fit_plot_stateyear_kbs$residuals)
```

Histogram of fit_plot_stateyear_kbs\$residuals



```
leveragePlots(fit_plot_stateyear_kbs)
```



```
ols_test_normality(fit_plot_stateyear_kbs)
```

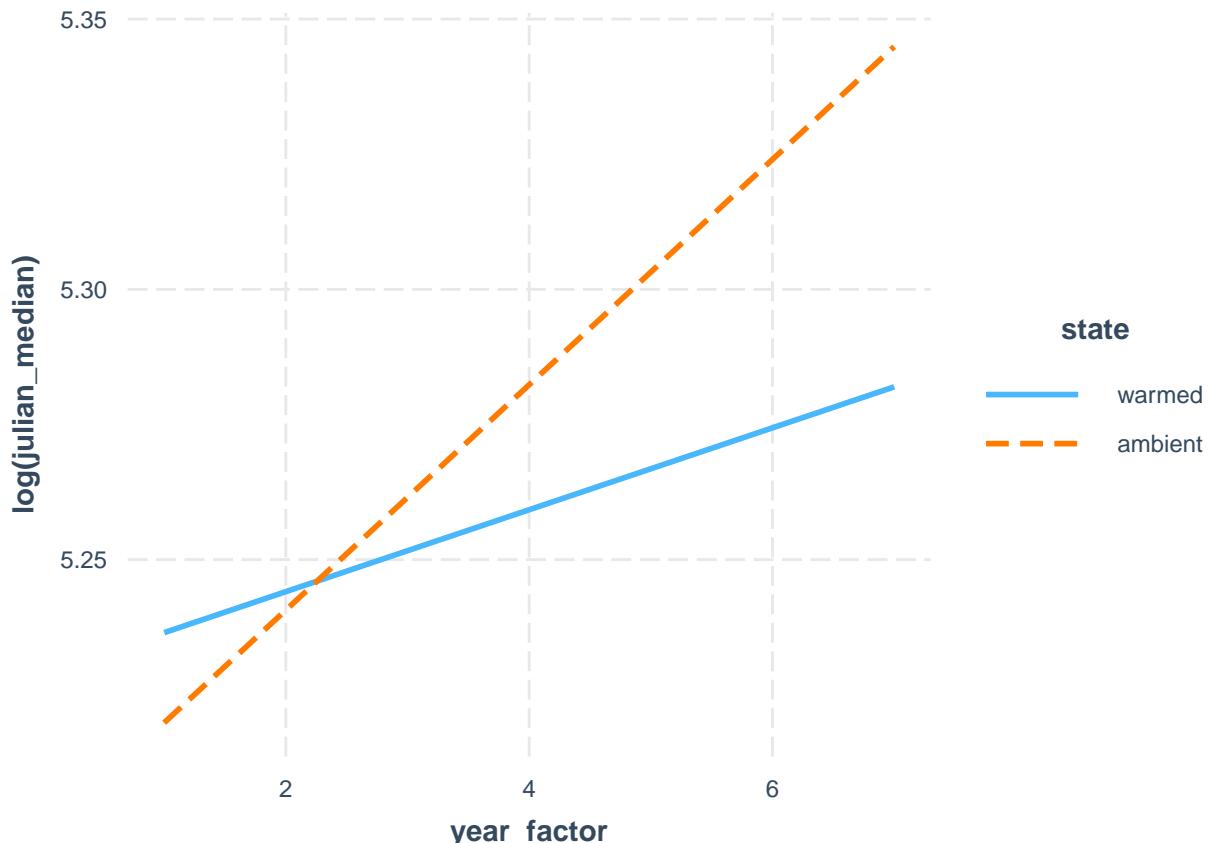
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9581      1e-04
## Kolmogorov-Smirnov 0.0958     0.0949
## Cramer-von Mises  43.6796     0.0000
## Anderson-Darling   2.1902     0.0000
## -----
```

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

```
fit3_plot_kbs <- lm(log(julian_median) ~ state * year_factor, data = kbs_flwr_plot)
interact_plot(fit3_plot_kbs, pred = year_factor, modx = state)
```

```
## Using data kbs_flwr_plot from global environment. This could cause
## incorrect results if kbs_flwr_plot has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```



MIXED EFFECT MODELS

UMBS Species-level Mixed Effects Models

```
# Including year as a fixed effect and as an interactive term. Our goal here is
# to find a model that is the best fit to the data. We also want to find a model
# that is the most parsimonious (one that has the fewest parameters).

# Do we need to include plot as a random effect with the UMBS models?
mod1 <- lmer(log(julian_median) ~ state * year_factor + insecticide * year_factor +
  (1 | species) + (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2 <- lmer(log(julian_median) ~ state * year_factor + insecticide * year_factor +
  (1 | species), umbs_flwr_spp, 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 anova on a regular
# linear model: https://m-clark.github.io/docs/mixedModels/anovamixed.html)
anova(mod1)

## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq  Mean Sq NumDF DenDF F value Pr(>F)
## state      0.002935 0.002935     1  558.00  1.0207 0.3128
## year_factor 0.240534 0.240534     1  558.43 83.6531 <2e-16 ***
## insecticide 0.002560 0.002560     1  558.09  0.8904 0.3458
```

```

## state:year_factor      0.000006 0.000006      1 557.98  0.0021 0.9635
## year_factor:insecticide 0.001030 0.001030      1 558.11  0.3581 0.5498
## ---
## 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          0.002935 0.002935      1 558.00  1.0207 0.3128
## year_factor    0.240534 0.240534      1 558.43 83.6531 <2e-16 ***
## insecticide    0.002560 0.002560      1 558.09  0.8904 0.3458
## state:year_factor 0.000006 0.000006      1 557.98  0.0021 0.9635
## year_factor:insecticide 0.001030 0.001030      1 558.11  0.3581 0.5498
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Run an ANOVA to test the 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(mod1, mod2) # Go with model 2 since pvalue >0.05, aka more complex model does not have something
```

```

## Data: umbs_flwr_spp
## Models:
## mod2: log(julian_median) ~ state * year_factor + insecticide * year_factor +
## mod2:      (1 | species)
## mod1: log(julian_median) ~ state * year_factor + insecticide * year_factor +
## mod1:      (1 | species) + (1 | plot)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2     8 -1631.8 -1597.0 823.91   -1647.8
## mod1     9 -1629.8 -1590.7 823.91   -1647.8      0  1       1

```

```
summ(mod1)
```

Observations	572
Dependent variable	log(julian_median)
Type	Mixed effects linear regression

AIC	-1629.82
BIC	-1590.68
Pseudo-R ² (fixed effects)	0.02
Pseudo-R ² (total)	0.92

```
summ(mod2)
```

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.12	0.05	105.12	15.97	0.00
stateambient	0.01	0.01	1.01	558.00	0.31
year_factor	0.01	0.00	4.84	558.06	0.00
insecticideno_insects	-0.01	0.01	-0.94	558.09	0.35
stateambient:year_factor	0.00	0.00	0.05	557.98	0.96
year_factor:insecticideno_insects	0.00	0.00	0.60	558.11	0.55

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
species	(Intercept)	0.18
	Residual	0.05

Grouping Variables		
Group	# groups	ICC
plot	24	0.00
species	14	0.91

Observations	572
Dependent variable	log(julian_median)
Type	Mixed effects linear regression

AIC	-1631.82
BIC	-1597.03
Pseudo-R ² (fixed effects)	0.02
Pseudo-R ² (total)	0.92

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.12	0.05	105.12	15.97	0.00
stateambient	0.01	0.01	1.01	558.00	0.31
year_factor	0.01	0.00	4.84	558.06	0.00
insecticideno_insects	-0.01	0.01	-0.94	558.09	0.35
stateambient:year_factor	0.00	0.00	0.05	557.98	0.96
year_factor:insecticideno_insects	0.00	0.00	0.60	558.11	0.55

p values calculated using Satterthwaite d.f.

```
AICctab(mod1, mod2, weights = T) # yup, model 2
```

```
##      dAICc df weight
## mod2  0.0   8  0.74
## mod1  2.1   9  0.26
```

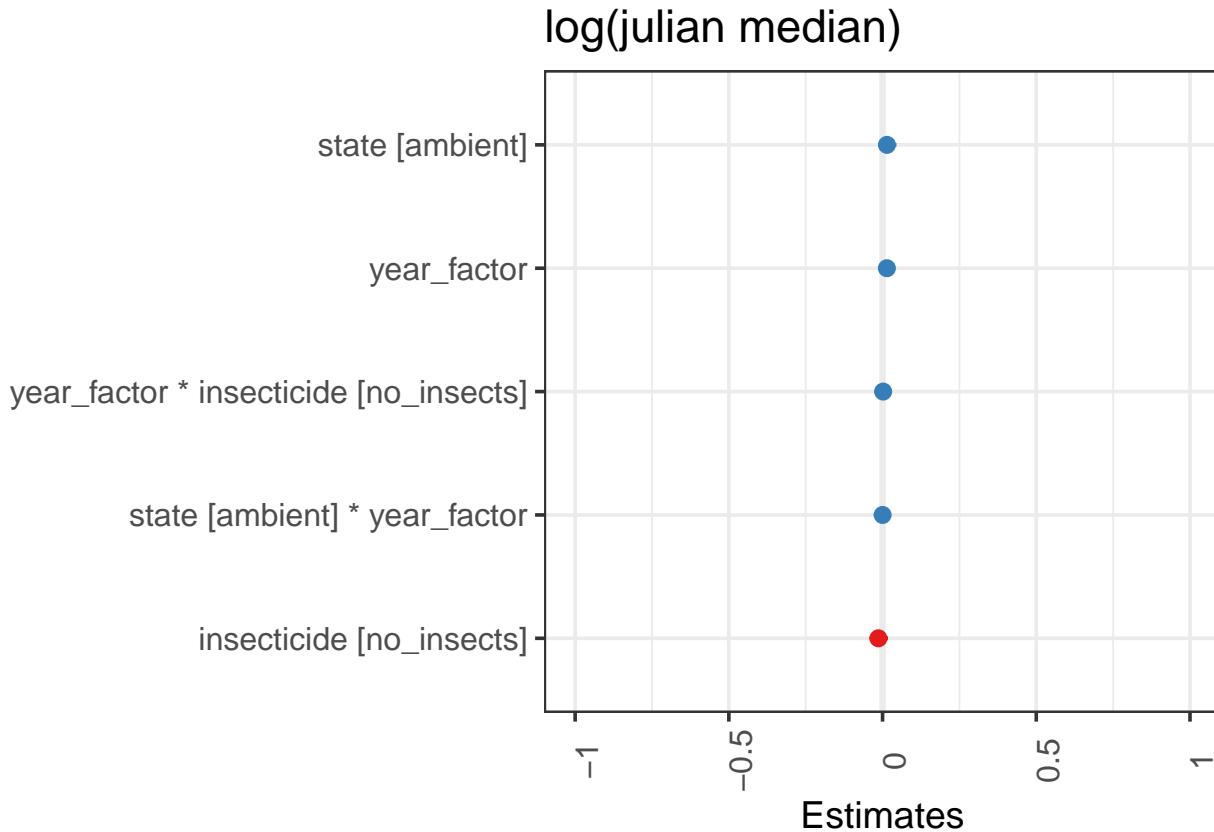
Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.18
Residual		0.05

Grouping Variables		
Group	# groups	ICC
species	14	0.91

```

# 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(mod1)
plot_model(mod2, sort.est = TRUE)

```



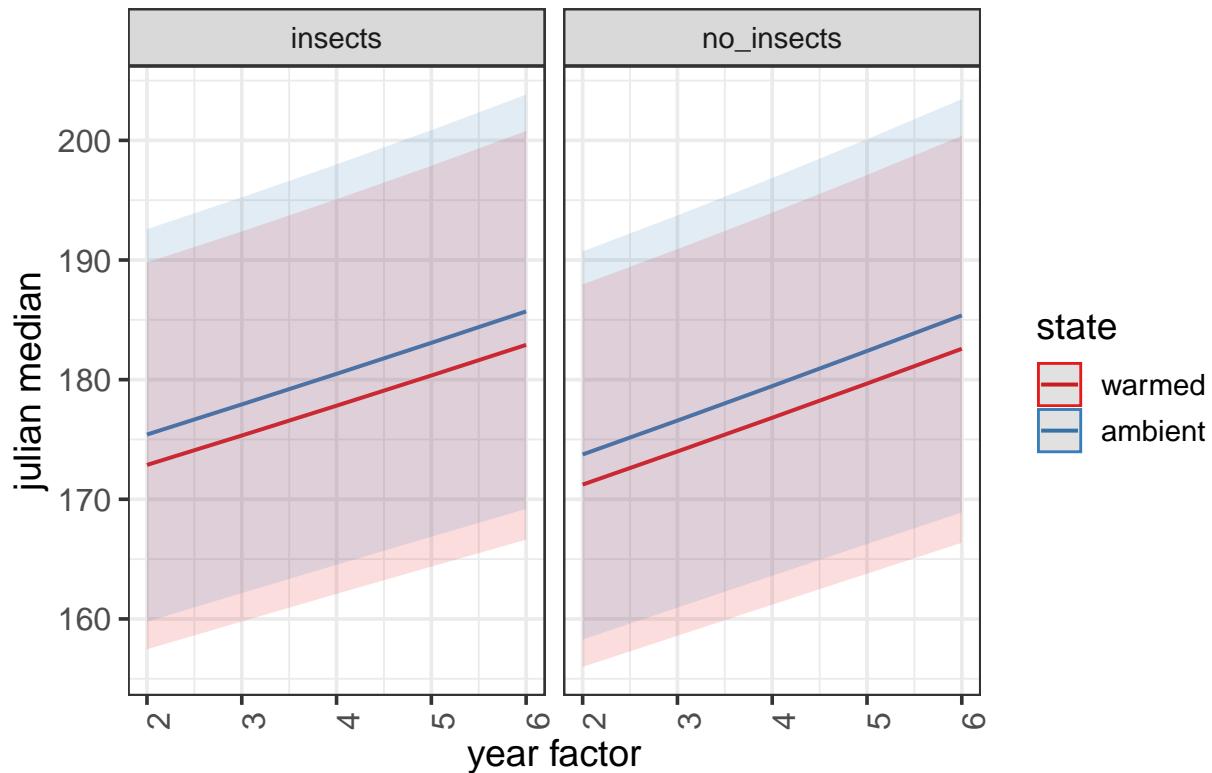
```

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

```

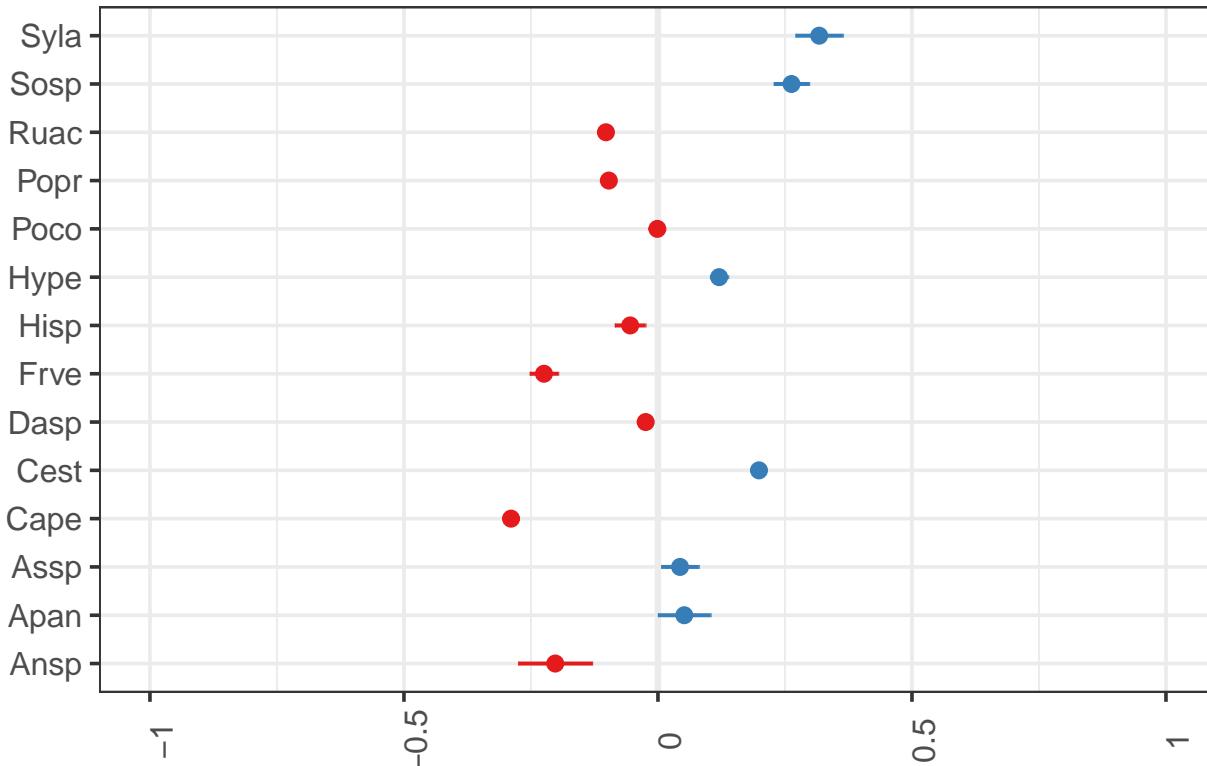
Model has log-transformed response. Back-transforming predictions to original response scale. Standardized residuals.

Predicted values of julian median



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

Random effects



```
# Do we need to include insecticide? (dropping insecticide from the model)
mod3 <- lmer(log(julian_median) ~ state * year_factor + (1 | species), umbs_flwr_spp,
    REML = FALSE)
anova(mod2, mod3) # Looks like no pvalue > 0.05, so insecticide does not improve model fit so we will ...
```

```
## Data: umbs_flwr_spp
## Models:
## mod3: log(julian_median) ~ state * year_factor + (1 | species)
## mod2: log(julian_median) ~ state * year_factor + insecticide * year_factor +
## mod2: (1 | species)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3     6 -1634.1 -1608  823.05   -1646.1
## mod2     8 -1631.8 -1597  823.91   -1647.8 1.7163  2      0.4239
```

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

```
##      dAICc df weight
## mod3 0.0   6  0.77
## mod2 2.4   8  0.23
```

```
# Does year need to be interactive with insecticide? - already removed
# insecticide mod4 <- lmer(log(julian_median) ~ state*year_factor + insecticide +
# (1/species) + (1/plot), umbs_flwr_spp, REML=FALSE)
```

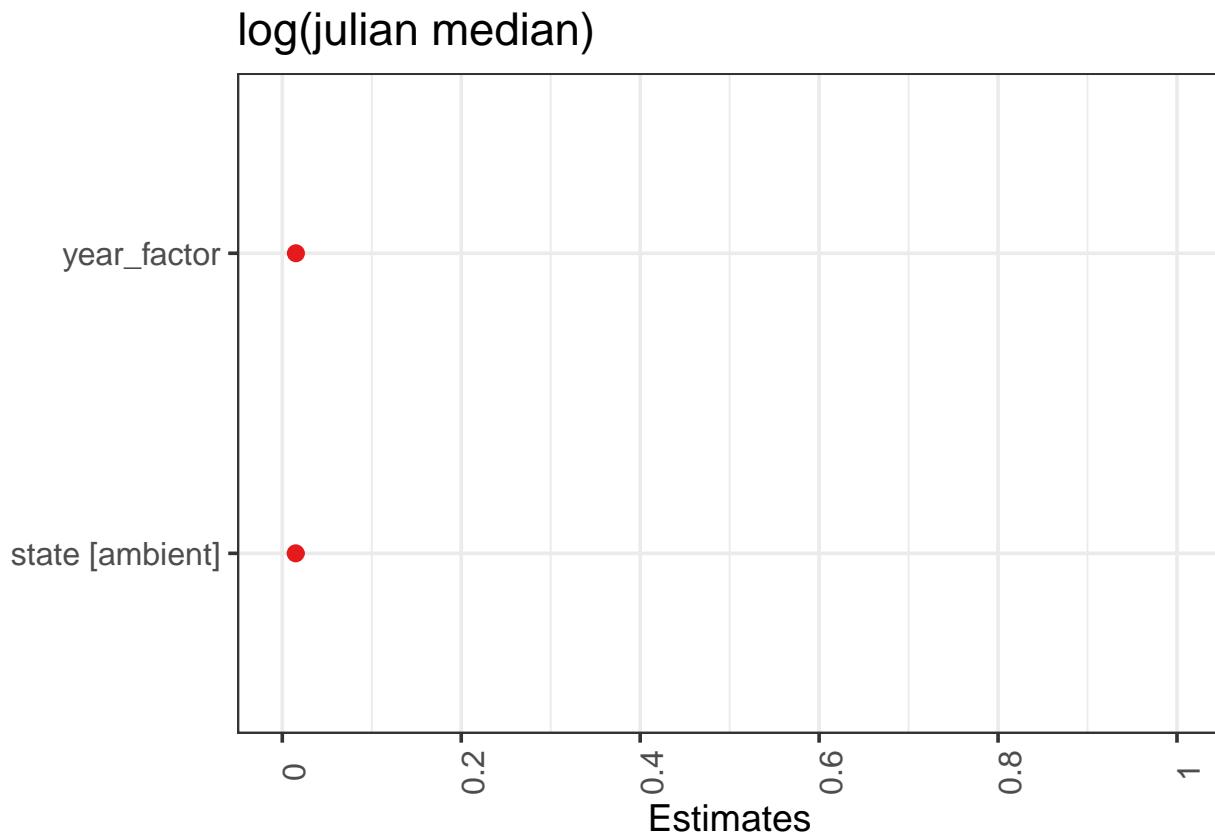
```
# Does year need to be interactive with state?
```

```
mod5 <- lmer(log(julian_median) ~ state + year_factor + (1 | species), umbs_flwr_spp,
  REML = FALSE)
anova(mod3, mod5)
```

```
## Data: umbs_flwr_spp
## Models:
## mod5: log(julian_median) ~ state + year_factor + (1 | species)
## mod3: log(julian_median) ~ state * year_factor + (1 | species)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5     5 -1636.1 -1614.3 823.05   -1646.1
## mod3     6 -1634.1 -1608.0 823.05   -1646.1 0.0045  1      0.9463
```

*# No, P>0.05 so state*year_factor doesn't strongly improve model fit so we will
shift to mod5, but AIC values are super close!!*

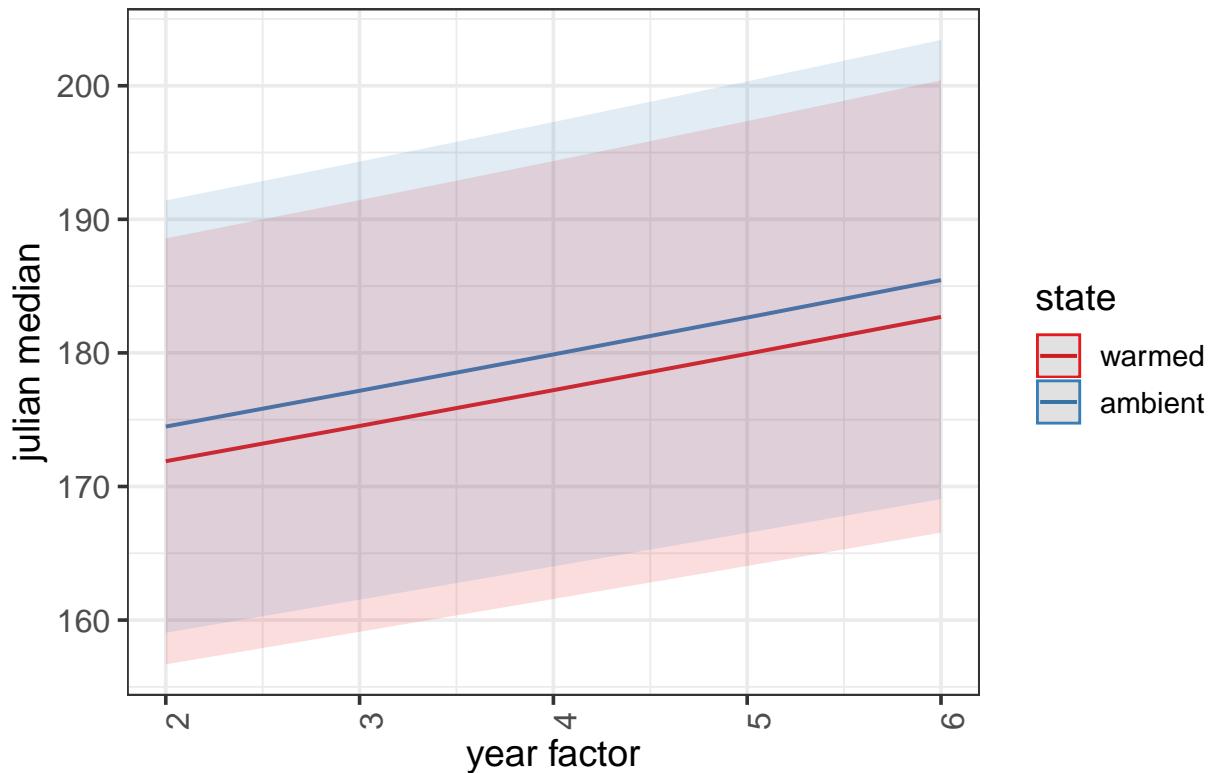
*# Plot the fixed effects estimates for different models these are the fixed
effects estimates from summary(mod5)*
plot_model(mod5, sort.est = TRUE)



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

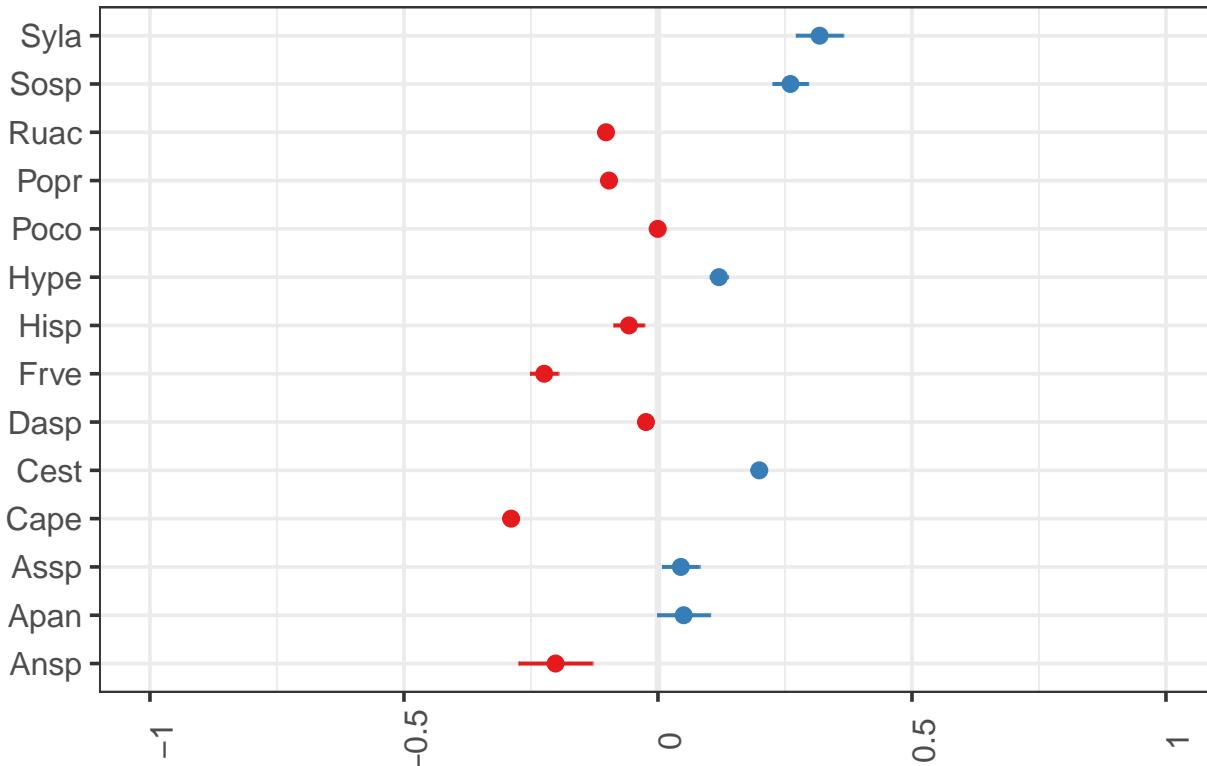
Model has log-transformed response. Back-transforming predictions to original response scale. Standard

Predicted values of julian median



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

Random effects



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

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

## Warning: Model failed to converge with 1 negative eigenvalue: -9.0e-02

# model failed to converge...
anova(mod5, mod6)
```

```
## Data: umbs_flwr_spp
## Models:
## mod5: log(julian_median) ~ state + year_factor + (1 | species)
## mod6: log(julian_median) ~ state + year_factor + (1 | species) + (1 +
##       year | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5     5 -1636.1 -1614.3  823.05   -1646.1
## mod6     8 -1620.1 -1585.3  818.04   -1636.1      0  3          1
```

```
anova(mod5)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq  Mean Sq NumDF DenDF F value    Pr(>F)
## state      0.031325 0.031325     1  558.16 10.860  0.001045 **
```

```

## year_factor 0.244442 0.244442      1 558.46  84.747 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# mod4 (and mod5) are pretty complex in terms of interpretation (they actually
# don't have many parameters though). We could consider an alternative model
# that's simpler to understand and also one that provides more insight about the
# species. That would be something like this:
mod7 <- lmer(log(julian_median) ~ state + species + (1 + factor(year_factor) | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7a <- lmer(log(julian_median) ~ state + species + factor(year_factor) + (1 | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7b <- lmer(log(julian_median) ~ state * factor(year_factor) + species + (1 | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7c <- lmer(log(julian_median) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod5, mod7)  # model 7 is a better fit to data

## Data: umbs_flwr_spp
## Models:
## mod5: log(julian_median) ~ state + year_factor + (1 | species)
## mod7: log(julian_median) ~ state + species + (1 + factor(year_factor) |
## mod7:   plot)
##     npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod5    5 -1636.1 -1614.3 823.05   -1646.1
## mod7   31 -1661.8 -1527.0 861.91   -1723.8 77.714 26  4.696e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod7, mod7a)  #mod 7a

## Data: umbs_flwr_spp
## Models:
## mod7a: log(julian_median) ~ state + species + factor(year_factor) +
## mod7a:   (1 | plot)
## mod7: log(julian_median) ~ state + species + (1 + factor(year_factor) |
## mod7:   plot)
##     npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a   21 -1724.2 -1632.9 883.11   -1766.2
## mod7   31 -1661.8 -1527.0 861.91   -1723.8      0 10          1

```

```

anova(mod7a, mod7b) #mod 7a - interaction between state and year does not improve model, but pvalue = 0.9131

## Data: umbs_flwr_spp
## Models:
## mod7a: log(julian_median) ~ state + species + factor(year_factor) +
## mod7a:      (1 | plot)
## mod7b: log(julian_median) ~ state * factor(year_factor) + species +
## mod7b:      (1 | plot)
##      npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   21 -1724.2 -1632.9 883.11  -1766.2
## mod7b   25 -1717.2 -1608.5 883.60  -1767.2 0.9783  4      0.9131

```

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

```

## Data: umbs_flwr_spp
## Models:
## mod7a: log(julian_median) ~ state + species + factor(year_factor) +
## mod7a:      (1 | plot)
## mod7c: log(julian_median) ~ state + species + factor(year_factor) +
## mod7c:      insecticide + (1 | plot)
##      npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod7a   21 -1724.2 -1632.9 883.11  -1766.2
## mod7c   22 -1723.8 -1628.1 883.89  -1767.8 1.5511  1      0.213

```

```
summ(mod7a)
```

Observations	572
Dependent variable	log(julian_median)
Type	Mixed effects linear regression

AIC	-1724.23
BIC	-1632.90
Pseudo-R ² (fixed effects)	0.90
Pseudo-R ² (total)	0.90

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

```

## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state       0.0316 0.03162     1    572 11.844 0.0006208 ***
## species     12.8865 0.99127    13    572 371.266 < 2.2e-16 ***
## factor(year_factor) 0.3246 0.08114     4    572 30.391 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
# Yes, at least one of the species is different (they do not all have the median
# first flwr dates).
```

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

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	4.92	0.04	131.84	572.00	0.00
stateambient	0.02	0.00	3.44	572.00	0.00
speciesApan	0.27	0.05	5.97	572.00	0.00
speciesAssp	0.26	0.04	6.25	572.00	0.00
speciesCape	-0.08	0.04	-2.00	572.00	0.05
speciesCest	0.41	0.04	11.16	572.00	0.00
speciesDasp	0.19	0.04	5.14	572.00	0.00
speciesFrve	-0.01	0.04	-0.26	572.00	0.80
speciesHisp	0.16	0.04	4.08	572.00	0.00
speciesHype	0.34	0.04	8.84	572.00	0.00
speciesPoco	0.21	0.04	5.69	572.00	0.00
speciesPopr	0.12	0.04	3.19	572.00	0.00
speciesRuac	0.11	0.04	3.00	572.00	0.00
speciesSosp	0.48	0.04	11.76	572.00	0.00
speciesSyla	0.54	0.04	12.42	572.00	0.00
factor(year_factor)3	0.03	0.01	3.68	572.00	0.00
factor(year_factor)4	0.04	0.01	4.87	572.00	0.00
factor(year_factor)5	0.07	0.01	10.22	572.00	0.00
factor(year_factor)6	0.06	0.01	7.67	572.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.05

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```

## boundary (singular) fit: see ?isSingular

## $`emmeans of state, year_factor`
##   state  year_factor emmean      SE    df lower.CL upper.CL
##   warmed          2  5.139 0.007277 313.4    5.124   5.153
##   ambient          2  5.154 0.007218 273.1    5.139   5.168
##   warmed          3  5.166 0.006848 254.7    5.152   5.179
##   ambient          3  5.181 0.006755 219.1    5.168   5.194
##   warmed          4  5.175 0.006843 246.3    5.161   5.188
##   ambient          4  5.190 0.006766 209.8    5.176   5.203
##   warmed          5  5.212 0.006645 240.3    5.199   5.225
##   ambient          5  5.227 0.006577 212.6    5.214   5.240
##   warmed          6  5.194 0.006561 226.6    5.181   5.207
##   ambient          6  5.209 0.006488 192.4    5.196   5.222
##
## Results are averaged over the levels of: species

```

```

## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, year_factor`
##   1           estimate      SE    df t.ratio p.value
## warmed 2 - ambient 2 -0.01505 0.00447 21.2 -3.366 0.0683
## warmed 2 - warmed 3 -0.02732 0.00755 574.5 -3.617 0.0119
## warmed 2 - ambient 3 -0.04237 0.00875 242.1 -4.840 0.0001
## warmed 2 - warmed 4 -0.03608 0.00754 579.1 -4.785 0.0001
## warmed 2 - ambient 4 -0.05112 0.00875 235.1 -5.840 <.0001
## warmed 2 - warmed 5 -0.07361 0.00733 577.9 -10.037 <.0001
## warmed 2 - ambient 5 -0.08866 0.00859 229.9 -10.325 <.0001
## warmed 2 - warmed 6 -0.05535 0.00734 578.9 -7.538 <.0001
## warmed 2 - ambient 6 -0.07040 0.00859 224.6 -8.194 <.0001
## ambient 2 - warmed 3 -0.01227 0.00880 239.6 -1.394 0.9280
## ambient 2 - ambient 3 -0.02732 0.00755 574.5 -3.617 0.0119
## ambient 2 - warmed 4 -0.02103 0.00878 235.5 -2.396 0.3329
## ambient 2 - ambient 4 -0.03608 0.00754 579.1 -4.785 0.0001
## ambient 2 - warmed 5 -0.05857 0.00859 217.9 -6.816 <.0001
## ambient 2 - ambient 5 -0.07361 0.00733 577.9 -10.037 <.0001
## ambient 2 - warmed 6 -0.04031 0.00860 222.3 -4.685 0.0002
## ambient 2 - ambient 6 -0.05535 0.00734 578.9 -7.538 <.0001
## warmed 3 - ambient 3 -0.01505 0.00447 21.2 -3.366 0.0683
## warmed 3 - warmed 4 -0.00876 0.00715 572.8 -1.226 0.9681
## warmed 3 - ambient 4 -0.02381 0.00844 215.0 -2.820 0.1364
## warmed 3 - warmed 5 -0.04630 0.00694 572.0 -6.667 <.0001
## warmed 3 - ambient 5 -0.06134 0.00828 209.2 -7.407 <.0001
## warmed 3 - warmed 6 -0.02804 0.00692 572.5 -4.051 0.0023
## warmed 3 - ambient 6 -0.04308 0.00826 202.7 -5.216 <.0001
## ambient 3 - warmed 4 0.00629 0.00842 217.7 0.747 0.9991
## ambient 3 - ambient 4 -0.00876 0.00715 572.8 -1.226 0.9681
## ambient 3 - warmed 5 -0.03125 0.00824 199.6 -3.794 0.0074
## ambient 3 - ambient 5 -0.04630 0.00694 572.0 -6.667 <.0001
## ambient 3 - warmed 6 -0.01299 0.00822 202.5 -1.580 0.8564
## ambient 3 - ambient 6 -0.02804 0.00692 572.5 -4.051 0.0023
## warmed 4 - ambient 4 -0.01505 0.00447 21.2 -3.366 0.0683
## warmed 4 - warmed 5 -0.03754 0.00686 573.7 -5.476 <.0001
## warmed 4 - ambient 5 -0.05258 0.00819 203.7 -6.418 <.0001
## warmed 4 - warmed 6 -0.01928 0.00681 575.5 -2.830 0.1290
## warmed 4 - ambient 6 -0.03432 0.00815 195.2 -4.209 0.0016
## ambient 4 - warmed 5 -0.02249 0.00818 191.8 -2.751 0.1614
## ambient 4 - ambient 5 -0.03754 0.00686 573.7 -5.476 <.0001
## ambient 4 - warmed 6 -0.00423 0.00814 192.5 -0.519 1.0000
## ambient 4 - ambient 6 -0.01928 0.00681 575.5 -2.830 0.1290
## warmed 5 - ambient 5 -0.01505 0.00447 21.2 -3.366 0.0683
## warmed 5 - warmed 6 0.01826 0.00658 572.3 2.777 0.1467
## warmed 5 - ambient 6 0.00321 0.00795 177.5 0.404 1.0000
## ambient 5 - warmed 6 0.03331 0.00795 186.4 4.187 0.0017
## ambient 5 - ambient 6 0.01826 0.00658 572.3 2.777 0.1467
## warmed 6 - ambient 6 -0.01505 0.00447 21.2 -3.366 0.0683
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger

```

```

## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 10 estimates

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

## boundary (singular) fit: see ?isSingular

## $`emmeans of year_factor`
##   year_factor emmean      SE    df lower.CL upper.CL
##       2     5.146 0.006894 445.6    5.133    5.160
##       3     5.173 0.006424 380.4    5.161    5.186
##       4     5.182 0.006427 364.5    5.170    5.195
##       5     5.220 0.006221 373.0    5.208    5.232
##       6     5.202 0.006130 346.2    5.189    5.214
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
##   1     estimate      SE  df t.ratio p.value
##   2 - 3 -0.02732 0.00755 575 -3.617 0.0030
##   2 - 4 -0.03608 0.00754 579 -4.785 <.0001
##   2 - 5 -0.07361 0.00733 578 -10.037 <.0001
##   2 - 6 -0.05535 0.00734 579 -7.538 <.0001
##   3 - 4 -0.00876 0.00715 573 -1.226 0.7363
##   3 - 5 -0.04630 0.00694 572 -6.667 <.0001
##   3 - 6 -0.02804 0.00692 573 -4.051 0.0006
##   4 - 5 -0.03754 0.00686 574 -5.476 <.0001
##   4 - 6 -0.01928 0.00681 575 -2.830 0.0386
##   5 - 6  0.01826 0.00658 572  2.777 0.0447
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 5 estimates

```

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

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

```
## $`emmeans of species`
##   species emmean      SE    df lower.CL upper.CL
##   Ansp    4.970 0.037582 591.4    4.896    5.044
##   Apan    5.239 0.026624 530.3    5.187    5.291
##   Assp    5.228 0.018847 573.3    5.191    5.265
##   Cape    4.895 0.007577 399.5    4.880    4.910
##   Cest    5.384 0.004904 336.4    5.375    5.394
##   Dasp    5.161 0.005742 397.7    5.150    5.173
##   Frve    4.960 0.014315 398.6    4.932    4.988
##   Hisp    5.132 0.015477 527.3    5.101    5.162
```

```

##   Hype      5.305 0.009155 485.1      5.287      5.323
##   Poco      5.182 0.006874 450.5      5.169      5.196
##   Popr      5.088 0.005144 360.2      5.078      5.098
##   Ruac      5.082 0.006370 363.0      5.069      5.094
##   Sosp      5.447 0.017854 357.1      5.412      5.483
##   Syla      5.511 0.023853 520.0      5.465      5.558
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of species'
##   1           estimate      SE  df t.ratio p.value
## Ansp - Apan -0.26930 0.04618 583  -5.831 <.0001
## Ansp - Assp -0.25816 0.04220 590  -6.118 <.0001
## Ansp - Cape  0.07511 0.03836 592   1.958 0.7932
## Ansp - Cest -0.41446 0.03790 592 -10.936 <.0001
## Ansp - Dasp -0.19148 0.03801 592  -5.038 0.0001
## Ansp - Frve  0.01007 0.04029 585   0.250 1.0000
## Ansp - Hisp -0.16210 0.04058 591  -3.995 0.0056
## Ansp - Hype -0.33557 0.03879 591  -8.651 <.0001
## Ansp - Poco -0.21266 0.03816 592  -5.572 <.0001
## Ansp - Popr -0.11837 0.03792 592  -3.121 0.1025
## Ansp - Ruac -0.11220 0.03811 592  -2.944 0.1623
## Ansp - Sosp -0.47768 0.04162 576 -11.476 <.0001
## Ansp - Syla -0.54167 0.04465 583 -12.131 <.0001
## Apan - Assp  0.01114 0.03263 537   0.341 1.0000
## Apan - Cape  0.34441 0.02764 548  12.461 <.0001
## Apan - Cest -0.14516 0.02706 547  -5.364 <.0001
## Apan - Dasp  0.07782 0.02728 545   2.853 0.2019
## Apan - Frve  0.27937 0.03022 495   9.246 <.0001
## Apan - Hisp  0.10721 0.03092 556   3.467 0.0366
## Apan - Hype -0.06627 0.02807 551  -2.361 0.5102
## Apan - Poco  0.05664 0.02748 528   2.062 0.7273
## Apan - Popr  0.15094 0.02710 545   5.570 <.0001
## Apan - Ruac  0.15711 0.02734 558   5.747 <.0001
## Apan - Sosp -0.20837 0.03208 479  -6.495 <.0001
## Apan - Syla -0.27236 0.03568 526  -7.633 <.0001
## Assp - Cape  0.33327 0.02032 583  16.405 <.0001
## Assp - Cest -0.15629 0.01948 588  -8.024 <.0001
## Assp - Dasp  0.06668 0.01966 590   3.391 0.0465
## Assp - Frve  0.26823 0.02349 577  11.418 <.0001
## Assp - Hisp  0.09607 0.02435 590   3.945 0.0068
## Assp - Hype -0.07741 0.02095 583  -3.695 0.0170
## Assp - Poco  0.04550 0.02017 580   2.256 0.5881
## Assp - Popr  0.13980 0.01956 586   7.147 <.0001
## Assp - Ruac  0.14597 0.01988 590   7.343 <.0001
## Assp - Sosp -0.21951 0.02592 552  -8.468 <.0001
## Assp - Syla -0.28350 0.03039 577  -9.328 <.0001
## Cape - Cest -0.48957 0.00902 580  -54.265 <.0001
## Cape - Dasp -0.26659 0.00952 588  -28.003 <.0001
## Cape - Frve -0.06504 0.01620 463  -4.015 0.0053
## Cape - Hisp -0.23720 0.01728 562  -13.730 <.0001

```

```

##  Cape - Hype -0.41068 0.01184 552 -34.675 <.0001
##  Cape - Poco -0.28777 0.01017 588 -28.285 <.0001
##  Cape - Popr -0.19347 0.00915 580 -21.153 <.0001
##  Cape - Ruac -0.18730 0.00992 498 -18.887 <.0001
##  Cape - Sosp -0.55278 0.01937 446 -28.540 <.0001
##  Cape - Syla -0.61677 0.02503 515 -24.642 <.0001
##  Cest - Dasp  0.22298 0.00756 583  29.482 <.0001
##  Cest - Frve  0.42453 0.01513 481  28.062 <.0001
##  Cest - Hisp  0.25236 0.01625 570  15.527 <.0001
##  Cest - Hype  0.07889 0.01037 588   7.605 <.0001
##  Cest - Poco  0.20180 0.00842 590  23.963 <.0001
##  Cest - Popr  0.29609 0.00710 575  41.703 <.0001
##  Cest - Ruac  0.30226 0.00803 592  37.637 <.0001
##  Cest - Sosp -0.06322 0.01851 407  -3.414 0.0441
##  Cest - Syla -0.12721 0.02434 543  -5.226 <.0001
##  Dasp - Frve 0.20155 0.01542 485  13.070 <.0001
##  Dasp - Hisp  0.02939 0.01643 579   1.789 0.8805
##  Dasp - Hype -0.14409 0.01083 590  -13.301 <.0001
##  Dasp - Poco -0.02118 0.00902 592  -2.348 0.5202
##  Dasp - Popr  0.07311 0.00774 587   9.451 <.0001
##  Dasp - Ruac  0.07929 0.00858 591   9.236 <.0001
##  Dasp - Sosp -0.28620 0.01876 422  -15.255 <.0001
##  Dasp - Syla -0.35019 0.02456 548  -14.256 <.0001
##  Frve - Hisp -0.17216 0.02097 588  -8.209 <.0001
##  Frve - Hype -0.34564 0.01699 479  -20.341 <.0001
##  Frve - Poco -0.22273 0.01589 518  -14.017 <.0001
##  Frve - Popr -0.12843 0.01521 491  -8.446 <.0001
##  Frve - Ruac -0.12226 0.01567 463  -7.802 <.0001
##  Frve - Sosp -0.48774 0.02276 514  -21.429 <.0001
##  Frve - Syla -0.55173 0.02772 563  -19.903 <.0001
##  Hisp - Hype -0.17348 0.01806 577  -9.605 <.0001
##  Hisp - Poco -0.05057 0.01706 565  -2.964 0.1545
##  Hisp - Popr  0.04373 0.01635 570   2.675 0.2962
##  Hisp - Ruac  0.04990 0.01675 577   2.979 0.1489
##  Hisp - Sosp -0.31558 0.02357 524  -13.389 <.0001
##  Hisp - Syla -0.37957 0.02846 566  -13.336 <.0001
##  Hype - Poco  0.12291 0.01140 559   10.783 <.0001
##  Hype - Popr  0.21720 0.01048 588   20.731 <.0001
##  Hype - Ruac  0.22338 0.01111 590   20.105 <.0001
##  Hype - Sosp -0.14210 0.02010 384  -7.069 <.0001
##  Hype - Syla -0.20610 0.02546 557  -8.095 <.0001
##  Poco - Popr  0.09429 0.00853 589   11.055 <.0001
##  Poco - Ruac  0.10047 0.00936 556   10.739 <.0001
##  Poco - Sosp -0.26502 0.01907 444  -13.896 <.0001
##  Poco - Syla -0.32901 0.02477 534  -13.285 <.0001
##  Popr - Ruac  0.00617 0.00818 591   0.755 1.0000
##  Popr - Sosp -0.35931 0.01856 421  -19.357 <.0001
##  Popr - Syla -0.42330 0.02438 542  -17.362 <.0001
##  Ruac - Sosp -0.36548 0.01895 399  -19.286 <.0001
##  Ruac - Syla -0.42947 0.02464 557  -17.429 <.0001
##  Sosp - Syla -0.06399 0.02962 550  -2.160 0.6586
## 

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

```

```
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 14 estimates
```

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

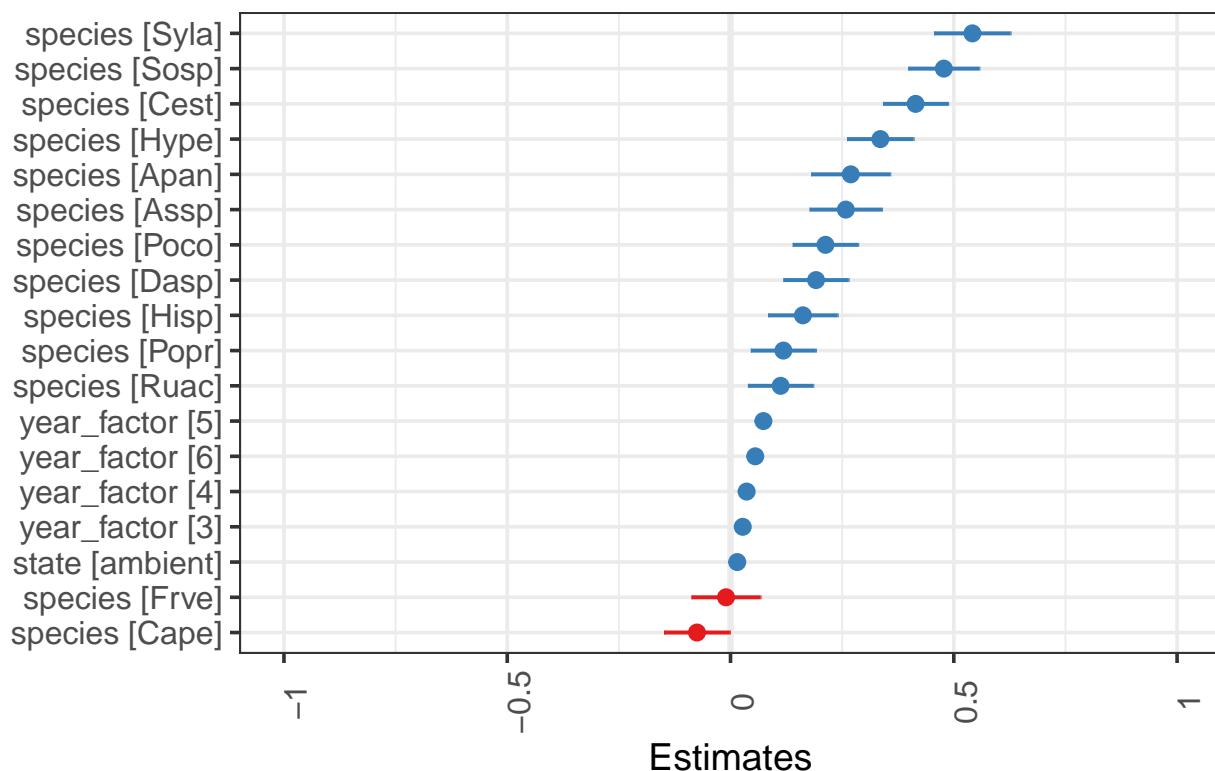
```
## boundary (singular) fit: see ?isSingular
```

```
## Error in emmeans(object = object, specs = specs[[i]], name = contr.name, : No variable named insectici
```

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)
```

log(julian median)

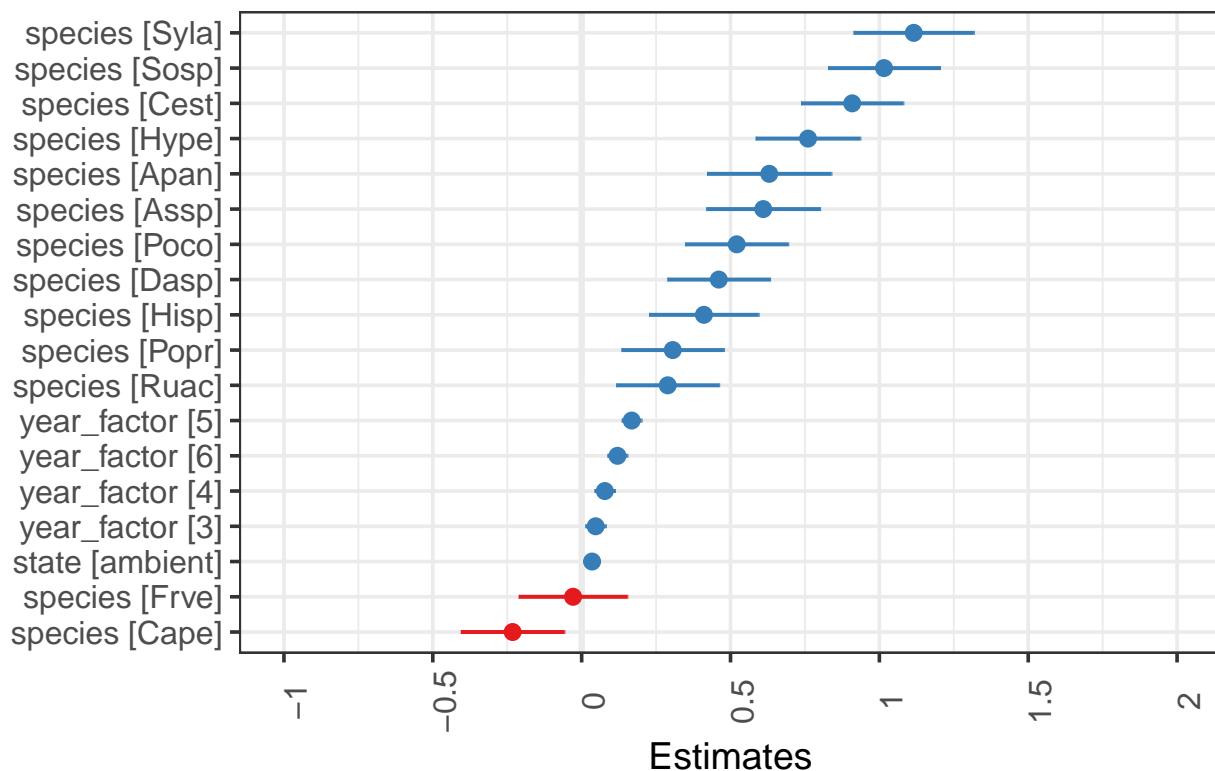


if you want to standardize the estimates:

```
plot_model(mod7a, sort.est = TRUE, type = "std")
```

```
## Formula contains log- or sqrt-terms. See help("standardize") for how such terms are standardized.
## boundary (singular) fit: see ?isSingular
```

log(julian median)

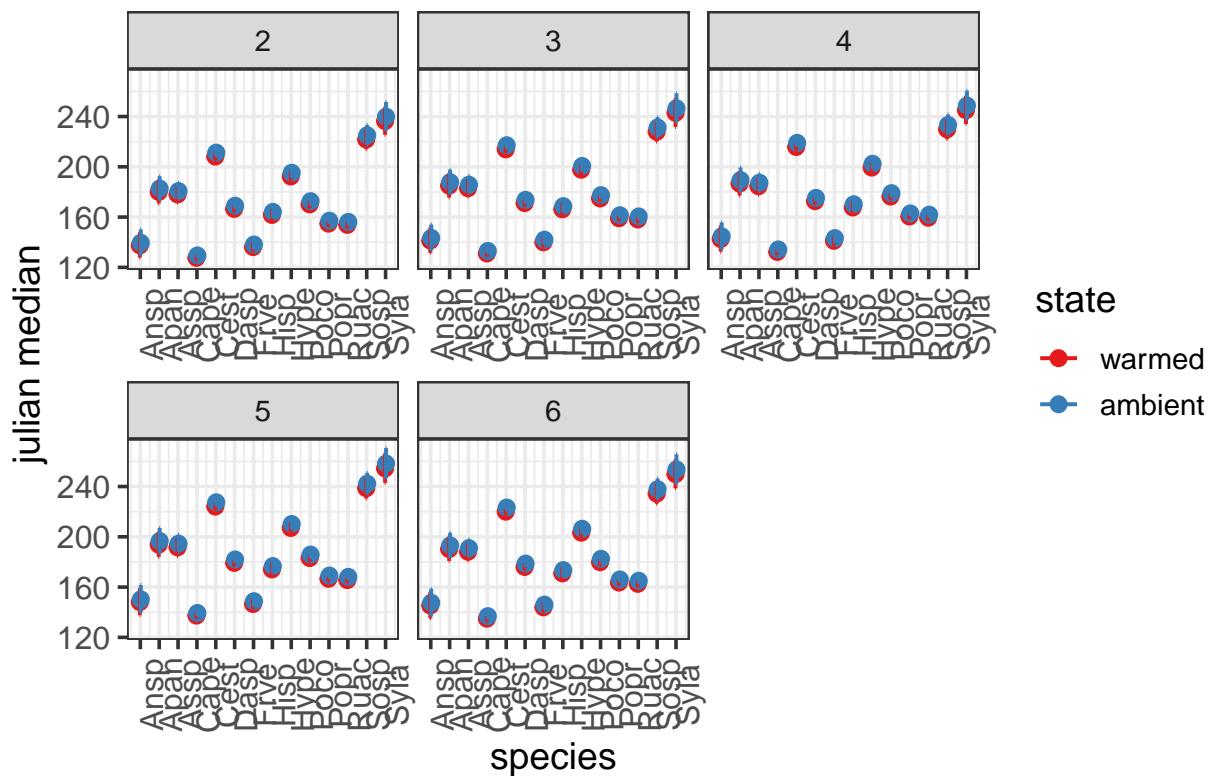


these are the fixed predicted values: - note this is a new plot

```
plot_model(mod7a, type = "pred", terms = c("species", "state", "year_factor"))
```

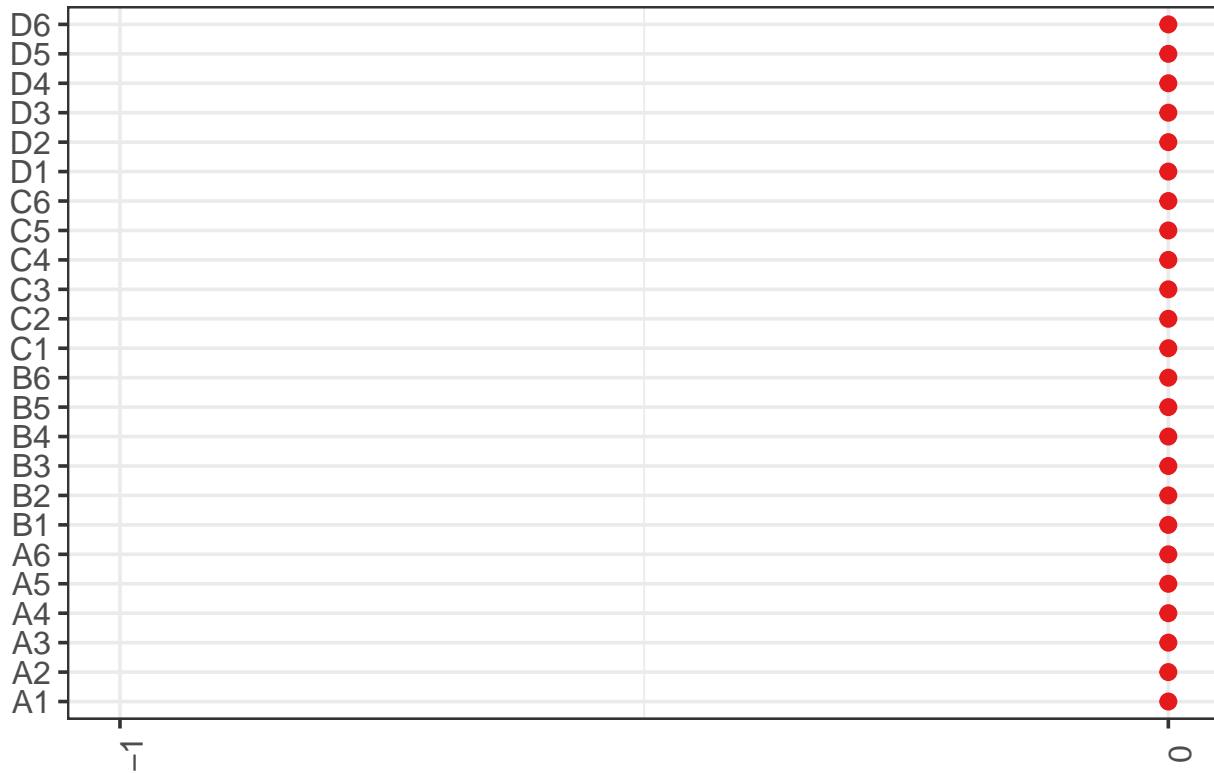
Model has log-transformed response. Back-transforming predictions to original response scale. Standardized residuals are back-transformed using the mean residual.

Predicted values of julian median



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

Random effects



```
# including native vs. exotic
umbss_flwr_spp <- within(umbss_flwr_spp, origin <- relevel(factor(origin), ref = "Native")) # releveling
mod8 <- lmer(log(julian_median) ~ state * origin + (1 + factor(year_factor) | plot),
umbss_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9 <- lmer(log(julian_median) ~ state + origin + (1 + factor(year_factor) | plot),
umbss_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9a <- lmer(log(julian_median) ~ state + origin + factor(year_factor) + (1 | plot),
umbss_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9b <- lmer(log(julian_median) ~ state + origin + insecticide + factor(year_factor) +
(1 | plot), umbss_flwr_spp, REML = FALSE)

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

```
anova(mod8, mod9) # model 9 is a better fit to data
```

```
## Data: umbs_flwr_spp
## Models:
## mod9: log(julian_median) ~ state + origin + (1 + factor(year_factor) |
## mod9:     plot)
## mod8: log(julian_median) ~ state * origin + (1 + factor(year_factor) |
## mod8:     plot)
##      npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod9   20 -497.84 -410.85 268.92   -537.84
## mod8   22 -494.95 -399.26 269.47   -538.95 1.1094  2     0.5742
```

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

```
## Data: umbs_flwr_spp
## Models:
## mod9a: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
## mod9a:     plot)
## mod9: log(julian_median) ~ state + origin + (1 + factor(year_factor) |
## mod9:     plot)
##      npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod9a   10 -530.70 -487.21 275.35   -550.70
## mod9    20 -497.84 -410.85 268.92   -537.84      0 10          1
```

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

```
## Data: umbs_flwr_spp
## Models:
## mod9a: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
## mod9a:     plot)
## mod9b: log(julian_median) ~ state + origin + insecticide + factor(year_factor) +
## mod9b:     (1 | plot)
##      npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mod9a   10 -530.70 -487.21 275.35   -550.70
## mod9b   11 -528.83 -480.99 275.41   -550.83 0.1286  1     0.7199
```

```
summary(mod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
##     plot)
## Data: umbs_flwr_spp
##
##      AIC      BIC      logLik deviance df.resid
##    -530.7   -487.2    275.3   -550.7      562
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max
## -1.9687 -0.9202 -0.1915  0.8779  3.0575
##
```

```

## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.00000  0.0000
## Residual          0.02236  0.1495
## Number of obs: 572, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                5.05556  0.01892 572.00000 267.204 < 2e-16 ***
## stateambient               0.01304  0.01251 572.00000  1.042  0.29770
## originBoth                 0.07581  0.03562 572.00000  2.128  0.03375 *
## originExotic               0.11855  0.01390 572.00000  8.527 < 2e-16 ***
## factor(year_factor)3       0.01108  0.02118 572.00000  0.523  0.60099
## factor(year_factor)4       0.02887  0.02116 572.00000  1.364  0.17308
## factor(year_factor)5       0.06335  0.02056 572.00000  3.082  0.00216 **
## factor(year_factor)6       0.04603  0.02051 572.00000  2.244  0.02520 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) sttmbn orgnBt orgnEx fc(_)3 fc(_)4 fc(_)5
## stateambint -0.338
## originBoth  -0.276 -0.013
## originExotc -0.445  0.025  0.257
## fctr(yr_f)3 -0.583  0.001  0.090 -0.069
## fctr(yr_f)4 -0.577 -0.002  0.087 -0.082  0.549
## fctr(yr_f)5 -0.598 -0.002  0.097 -0.077  0.565  0.567
## fctr(yr_f)6 -0.598  0.000  0.108 -0.088  0.568  0.570  0.587
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod9a)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state            0.02429 0.02429     1    572  1.0864  0.2977
## origin           1.62573 0.81287     2    572 36.3592 1.366e-15 ***
## factor(year_factor) 0.29150 0.07288     4    572  3.2597  0.0117 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

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

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

```

## $`emmeans of state, origin`
##   state   origin emmean      SE      df lower.CL upper.CL
##   warmed  Native  5.085 0.013383  82.27    5.059    5.112
##   ambient Native  5.098 0.013272  75.69    5.072    5.125
##   warmed  Both    5.161 0.034968 438.54    5.093    5.230
##   ambient Both   5.174 0.034798 409.14    5.106    5.243
##   warmed  Exotic  5.204 0.009929  32.60    5.184    5.224

```

```

## ambient Exotic 5.217 0.010184 35.42    5.196    5.238
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of state, origin'
## 1
##   estimate      SE   df t.ratio p.value
## warmed Native - ambient Native -0.0130 0.0127 21.0 -1.029 0.9028
## warmed Native - warmed Both -0.0758 0.0361 571.6 -2.100 0.2889
## warmed Native - ambient Both -0.0888 0.0381 377.8 -2.329 0.1850
## warmed Native - warmed Exotic -0.1186 0.0141 561.4 -8.409 <.0001
## warmed Native - ambient Exotic -0.1316 0.0192 90.4 -6.865 <.0001
## ambient Native - warmed Both -0.0628 0.0384 418.7 -1.635 0.5755
## ambient Native - ambient Both -0.0758 0.0361 571.6 -2.100 0.2889
## ambient Native - warmed Exotic -0.1055 0.0187 80.0 -5.630 <.0001
## ambient Native - ambient Exotic -0.1186 0.0141 561.4 -8.409 <.0001
## warmed Both - ambient Both -0.0130 0.0127 21.0 -1.029 0.9028
## warmed Both - warmed Exotic -0.0427 0.0353 550.8 -1.210 0.8319
## warmed Both - ambient Exotic -0.0558 0.0377 379.4 -1.478 0.6787
## ambient Both - warmed Exotic -0.0297 0.0373 330.5 -0.796 0.9680
## ambient Both - ambient Exotic -0.0427 0.0353 550.8 -1.210 0.8319
## warmed Exotic - ambient Exotic -0.0130 0.0127 21.0 -1.029 0.9028
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 6 estimates

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

## boundary (singular) fit: see ?isSingular

mod11 <- lmer(log(julian_median) ~ state + growth_habit + (1 + factor(year_factor) |
  plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11a <- lmer(log(julian_median) ~ state + growth_habit + factor(year_factor) +
  (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11b <- lmer(log(julian_median) ~ state + growth_habit + factor(year_factor) +
  insecticide + (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

anova(mod10, mod11) # model 11 is a better fit to data

## Data: umbs_flwr_spp
## Models:
## mod11: log(julian_median) ~ state + growth_habit + (1 + factor(year_factor) | 
## mod11:     plot)
## mod10: log(julian_median) ~ state * growth_habit + (1 + factor(year_factor) | 
## mod10:     plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11   20 -610.61 -523.62 325.30  -650.61
## mod10   22 -607.47 -511.79 325.74  -651.47 0.8678  2      0.648

```

```

anova(mod11, mod11a) # model 11a is still a better fit to data

```

```

## Data: umbs_flwr_spp
## Models:
## mod11a: log(julian_median) ~ state + growth_habit + factor(year_factor) + 
## mod11a:     (1 | plot)
## mod11: log(julian_median) ~ state + growth_habit + (1 + factor(year_factor) | 
## mod11:     plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11a   10 -648.44 -604.95 334.22  -668.44
## mod11    20 -610.61 -523.62 325.30  -650.61      0 10          1

```

```

anova(mod11a, mod11b) # model 11a still a better fit to data

```

```

## Data: umbs_flwr_spp
## Models:
## mod11a: log(julian_median) ~ state + growth_habit + factor(year_factor) + 
## mod11a:     (1 | plot)
## mod11b: log(julian_median) ~ state + growth_habit + factor(year_factor) + 
## mod11b:     insecticide + (1 | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11a   10 -648.44 -604.95 334.22  -668.44
## mod11b   11 -647.84 -600.00 334.92  -669.84 1.4004  1      0.2367

```

```

summary(mod11a)

```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + growth_habit + factor(year_factor) + 
##           (1 | plot)
## Data: umbs_flwr_spp
##
##      AIC      BIC      logLik deviance df.resid
##    -648.4   -605.0    334.2    -668.4      562
## 
## Scaled residuals:
##       Min     1Q Median     3Q    Max
## -2.6685 -0.5723  0.1949  0.8177  2.0564
## 

```

```

## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0000   0.0000
## Residual          0.0182   0.1349
## Number of obs: 572, groups: plot, 24
##
## Fixed effects:
##                         Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)            5.222936  0.016510 572.000000 316.344 < 2e-16 ***
## stateambient          0.002125  0.011307 572.000000  0.188 0.850983
## growth_habit          -0.135338  0.040330 572.000000 -3.356 0.000844 ***
## growth_habitGraminoid -0.169526  0.011457 572.000000 -14.796 < 2e-16 ***
## factor(year_factor)3   0.032751  0.019018 572.000000  1.722 0.085589 .
## factor(year_factor)4   0.041751  0.018997 572.000000  2.198 0.028361 *
## factor(year_factor)5   0.074759  0.018530 572.000000  4.035 6.21e-05 ***
## factor(year_factor)6   0.058423  0.018401 572.000000  3.175 0.001579 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttmbn grwth_G fc(_)3 fc(_)4 fc(_)5
## stateambint -0.366
## growth_habt -0.227  0.055
## grwth_hbtGr -0.379  0.046  0.155
## fctr(yr_f)3 -0.617  0.007  0.070 -0.038
## fctr(yr_f)4 -0.635  0.007  0.095  0.001  0.543
## fctr(yr_f)5 -0.656  0.009  0.135 -0.002  0.560  0.563
## fctr(yr_f)6 -0.661  0.011  0.121  0.003  0.562  0.566  0.584
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod11a)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state       0.0006 0.00064     1    572  0.0353  0.850983
## growth_habit 4.0049 2.00243     2    572 110.0400 < 2.2e-16 ***
## factor(year_factor) 0.3363 0.08408     4    572  4.6207  0.001117 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

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

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

```

## $`emmeans of year_factor, growth_habit`
##   year_factor growth_habit emmean      SE      df lower.CL upper.CL
##   2 Forb        5.224 0.01551 421.9    5.194    5.254
##   3 Forb        5.257 0.01470 389.6    5.228    5.286
##   4 Forb        5.266 0.01431 355.3    5.238    5.294
##   5 Forb        5.299 0.01354 331.4    5.272    5.325
##   6 Forb        5.282 0.01338 320.9    5.256    5.309

```

```

##          2      5.089 0.04043 535.4      5.009      5.168
##          3      5.121 0.04150 531.3      5.040      5.203
##          4      5.130 0.04184 531.7      5.048      5.213
##          5      5.163 0.04225 537.5      5.080      5.246
##          6      5.147 0.04194 531.0      5.065      5.229
## 2 Graminoid  5.054 0.01528 437.0      5.024      5.085
## 3 Graminoid  5.087 0.01386 371.1      5.060      5.114
## 4 Graminoid  5.096 0.01406 381.8      5.069      5.124
## 5 Graminoid  5.129 0.01325 351.4      5.103      5.155
## 6 Graminoid  5.113 0.01317 335.3      5.087      5.139
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## ## $'pairwise differences of year_factor, growth_habit'
##   1           estimate      SE  df t.ratio p.value
## 2 Forb - 3 Forb -0.03275 0.0192 564 -1.709  0.9298
## 2 Forb - 4 Forb -0.04175 0.0191 567 -2.181  0.6787
## 2 Forb - 5 Forb -0.07476 0.0187 564 -4.004  0.0062
## 2 Forb - 6 Forb -0.05842 0.0185 564 -3.151  0.1055
## 2 Forb - 2      0.13534 0.0409 570  3.308  0.0675
## 2 Forb - 3      0.10259 0.0464 575  2.211  0.6570
## 2 Forb - 4      0.09359 0.0468 575  1.999  0.7984
## 2 Forb - 5      0.06058 0.0472 576  1.283  0.9945
## 2 Forb - 6      0.07692 0.0469 575  1.639  0.9495
## 2 Forb - 2 Graminoid 0.16953 0.0116 564 14.605 <.0001
## 2 Forb - 3 Graminoid 0.13678 0.0220 577  6.209 <.0001
## 2 Forb - 4 Graminoid 0.12778 0.0224 576  5.707 <.0001
## 2 Forb - 5 Graminoid 0.09477 0.0220 576  4.314  0.0018
## 2 Forb - 6 Graminoid 0.11110 0.0219 577  5.072  0.0001
## 3 Forb - 4 Forb -0.00900 0.0183 563 -0.492  1.0000
## 3 Forb - 5 Forb -0.04201 0.0177 563 -2.367  0.5408
## 3 Forb - 6 Forb -0.02567 0.0176 563 -1.455  0.9817
## 3 Forb - 2      0.16809 0.0439 578  3.827  0.0120
## 3 Forb - 3      0.13534 0.0409 570  3.308  0.0675
## 3 Forb - 4      0.12634 0.0453 577  2.792  0.2543
## 3 Forb - 5      0.09333 0.0457 577  2.044  0.7709
## 3 Forb - 6      0.10967 0.0454 576  2.417  0.5032
## 3 Forb - 2 Graminoid 0.20228 0.0228 575  8.882 <.0001
## 3 Forb - 3 Graminoid 0.16953 0.0116 564 14.605 <.0001
## 3 Forb - 4 Graminoid 0.16053 0.0221 574  7.278 <.0001
## 3 Forb - 5 Graminoid 0.12752 0.0216 575  5.910 <.0001
## 3 Forb - 6 Graminoid 0.14385 0.0215 576  6.678 <.0001
## 4 Forb - 5 Forb -0.03301 0.0177 564 -1.867  0.8684
## 4 Forb - 6 Forb -0.01667 0.0176 565 -0.949  0.9998
## 4 Forb - 2      0.17709 0.0435 577  4.074  0.0047
## 4 Forb - 3      0.14434 0.0444 576  3.252  0.0794
## 4 Forb - 4      0.13534 0.0409 570  3.308  0.0675
## 4 Forb - 5      0.10233 0.0452 577  2.264  0.6179
## 4 Forb - 6      0.11867 0.0449 575  2.642  0.3441
## 4 Forb - 2 Graminoid 0.21128 0.0224 578  9.436 <.0001
## 4 Forb - 3 Graminoid 0.17853 0.0213 579  8.387 <.0001

```

## 4 Forb - 4 Graminoid	0.16953	0.0116	564	14.605	<.0001
## 4 Forb - 5 Graminoid	0.13652	0.0211	578	6.462	<.0001
## 4 Forb - 6 Graminoid	0.15285	0.0211	579	7.247	<.0001
## 5 Forb - 6 Forb	0.01634	0.0170	561	0.963	0.9998
## 5 Forb - 2	0.21010	0.0426	576	4.932	0.0001
## 5 Forb - 3	0.17735	0.0435	574	4.076	0.0047
## 5 Forb - 4	0.16835	0.0439	574	3.832	0.0118
## 5 Forb - 5	0.13534	0.0409	570	3.308	0.0675
## 5 Forb - 6	0.15167	0.0440	574	3.444	0.0444
## 5 Forb - 2 Graminoid	0.24429	0.0220	578	11.102	<.0001
## 5 Forb - 3 Graminoid	0.21153	0.0208	579	10.154	<.0001
## 5 Forb - 4 Graminoid	0.20253	0.0212	577	9.568	<.0001
## 5 Forb - 5 Graminoid	0.16953	0.0116	564	14.605	<.0001
## 5 Forb - 6 Graminoid	0.18586	0.0206	578	9.021	<.0001
## 6 Forb - 2	0.19376	0.0428	578	4.527	0.0007
## 6 Forb - 3	0.16101	0.0437	576	3.682	0.0201
## 6 Forb - 4	0.15201	0.0441	576	3.444	0.0444
## 6 Forb - 5	0.11900	0.0445	577	2.672	0.3249
## 6 Forb - 6	0.13534	0.0409	570	3.308	0.0675
## 6 Forb - 2 Graminoid	0.22795	0.0218	577	10.436	<.0001
## 6 Forb - 3 Graminoid	0.19520	0.0207	578	9.436	<.0001
## 6 Forb - 4 Graminoid	0.18620	0.0210	576	8.855	<.0001
## 6 Forb - 5 Graminoid	0.15319	0.0205	576	7.475	<.0001
## 6 Forb - 6 Graminoid	0.16953	0.0116	564	14.605	<.0001
## 2 - 3	-0.03275	0.0192	564	-1.709	0.9298
## 2 - 4	-0.04175	0.0191	567	-2.181	0.6787
## 2 - 5	-0.07476	0.0187	564	-4.004	0.0062
## 2 - 6	-0.05842	0.0185	564	-3.151	0.1055
## 2 - 2 Graminoid	0.03419	0.0408	557	0.838	1.0000
## 2 - 3 Graminoid	0.00144	0.0436	572	0.033	1.0000
## 2 - 4 Graminoid	-0.00756	0.0434	571	-0.174	1.0000
## 2 - 5 Graminoid	-0.04057	0.0425	569	-0.955	0.9998
## 2 - 6 Graminoid	-0.02423	0.0427	571	-0.567	1.0000
## 3 - 4	-0.00900	0.0183	563	-0.492	1.0000
## 3 - 5	-0.04201	0.0177	563	-2.367	0.5408
## 3 - 6	-0.02567	0.0176	563	-1.455	0.9817
## 3 - 2 Graminoid	0.06694	0.0465	568	1.440	0.9834
## 3 - 3 Graminoid	0.03419	0.0408	557	0.838	1.0000
## 3 - 4 Graminoid	0.02519	0.0445	570	0.566	1.0000
## 3 - 5 Graminoid	-0.00782	0.0436	566	-0.179	1.0000
## 3 - 6 Graminoid	0.00852	0.0438	569	0.194	1.0000
## 4 - 5	-0.03301	0.0177	564	-1.867	0.8684
## 4 - 6	-0.01667	0.0176	565	-0.949	0.9998
## 4 - 2 Graminoid	0.07594	0.0467	568	1.625	0.9527
## 4 - 3 Graminoid	0.04319	0.0450	569	0.960	0.9998
## 4 - 4 Graminoid	0.03419	0.0408	557	0.838	1.0000
## 4 - 5 Graminoid	0.00118	0.0438	566	0.027	1.0000
## 4 - 6 Graminoid	0.01752	0.0441	568	0.398	1.0000
## 5 - 6	0.01634	0.0170	561	0.963	0.9998
## 5 - 2 Graminoid	0.10895	0.0471	570	2.311	0.5829
## 5 - 3 Graminoid	0.07620	0.0454	571	1.679	0.9389
## 5 - 4 Graminoid	0.06720	0.0451	571	1.489	0.9774
## 5 - 5 Graminoid	0.03419	0.0408	557	0.838	1.0000
## 5 - 6 Graminoid	0.05052	0.0445	571	1.136	0.9985

```

##   6 - 2 Graminoid      0.09261 0.0468 568  1.977  0.8111
##   6 - 3 Graminoid      0.05986 0.0451 569  1.328  0.9923
##   6 - 4 Graminoid      0.05086 0.0448 569  1.135  0.9985
##   6 - 5 Graminoid      0.01785 0.0439 566  0.406  1.0000
##   6 - 6 Graminoid      0.03419 0.0408 557  0.838  1.0000
## 2 Graminoid - 3 Graminoid -0.03275 0.0192 564 -1.709  0.9298
## 2 Graminoid - 4 Graminoid -0.04175 0.0191 567 -2.181  0.6787
## 2 Graminoid - 5 Graminoid -0.07476 0.0187 564 -4.004  0.0062
## 2 Graminoid - 6 Graminoid -0.05842 0.0185 564 -3.151  0.1055
## 3 Graminoid - 4 Graminoid -0.00900 0.0183 563 -0.492  1.0000
## 3 Graminoid - 5 Graminoid -0.04201 0.0177 563 -2.367  0.5408
## 3 Graminoid - 6 Graminoid -0.02567 0.0176 563 -1.455  0.9817
## 4 Graminoid - 5 Graminoid -0.03301 0.0177 564 -1.867  0.8684
## 4 Graminoid - 6 Graminoid -0.01667 0.0176 565 -0.949  0.9998
## 5 Graminoid - 6 Graminoid  0.01634 0.0170 561  0.963  0.9998
##
## Results are averaged over the levels of: state
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 15 estimates

```

```

# 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(log(julian_median) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), umbs_flwr_spp)

```

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

```

# 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(log(julian_median) ~ state * factor(year_factor) + (1 | species), umbs_flwr_spp)

# All the models ran:
mod1 <- lmer(log(julian_median) ~ state * year_factor + insecticide * year_factor +
  (1 | species) + (1 | plot), umbs_flwr_spp, REML = FALSE)

```

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

```

mod2 <- lmer(log(julian_median) ~ state * year_factor + insecticide * year_factor +
  (1 | species), umbs_flwr_spp, REML = FALSE)
mod3 <- lmer(log(julian_median) ~ state * year_factor + (1 | species), umbs_flwr_spp,
  REML = FALSE)
mod4 <- lmer(log(julian_median) ~ state * year_factor + insecticide + (1 | species) +
  (1 | plot), umbs_flwr_spp, REML = FALSE)

```

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

```

mod5 <- lmer(log(julian_median) ~ state + year_factor + (1 | species), umbs_flwr_spp,
  REML = FALSE)
mod6 <- lmer(log(julian_median) ~ state + year_factor + (1 | species) + (1 + year |
  plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -9.0e-02

mod7 <- lmer(log(julian_median) ~ state + species + (1 + factor(year_factor) | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7a <- lmer(log(julian_median) ~ state + species + factor(year_factor) + (1 | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7b <- lmer(log(julian_median) ~ state * factor(year_factor) + species + (1 | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7c <- lmer(log(julian_median) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod8 <- lmer(log(julian_median) ~ state * origin + (1 + factor(year_factor) | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9 <- lmer(log(julian_median) ~ state + origin + (1 + factor(year_factor) | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9a <- lmer(log(julian_median) ~ state + origin + factor(year_factor) + (1 | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod10 <- lmer(log(julian_median) ~ state * growth_habit + (1 + factor(year_factor) | plot),
  umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

mod11 <- lmer(log(julian_median) ~ state + growth_habit + (1 + factor(year_factor) | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11a <- lmer(log(julian_median) ~ state + growth_habit + factor(year_factor) + (1 | plot), umbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod12 <- lmer(log(julian_median) ~ state * factor(year_factor) + (1 + factor(year_factor) | species), umbs_flwr_spp)

## boundary (singular) fit: see ?isSingular

mod13 <- lmer(log(julian_median) ~ state * factor(year_factor) + (1 | species), umbs_flwr_spp)
AICctab(mod1, mod2, mod3, mod5, mod6, mod7, mod7a, mod7b, mod7c, mod8, mod9, mod9a, mod10, mod11, mod11a, mod13, weights = T) #mod7a is the best fitting model (took out mod12 bc it w

##          dAICc   df weight
## mod7a      0.0  21  0.569
## mod7c      0.6  22  0.419
## mod7b     7.7  25  0.012
## mod7     64.4  31 <0.001
## mod5     86.6  5  <0.001
## mod3     88.6  6  <0.001
## mod2     91.0  8  <0.001
## mod1     93.0  9  <0.001
## mod6    102.7  8  <0.001
## mod13   145.5 12 <0.001
## mod11a  1074.5 10 <0.001
## mod11   1113.5 20 <0.001
## mod10   1116.9 22 <0.001
## mod9a   1192.2 10 <0.001
## mod9    1226.2 20 <0.001
## mod8    1229.4 22 <0.001

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + species + factor(year_factor) +
##           (1 | plot)
## Data: umbs_flwr_spp
##
##          AIC      BIC      logLik deviance df.resid
## -1724.2 -1632.9    883.1   -1766.2      551
##
## Scaled residuals:
##       Min      1Q  Median      3Q      Max

```

```

## -6.3936 -0.5403 -0.0484  0.6020  3.2104
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.00000  0.00000
## Residual           0.00267  0.05167
## Number of obs: 572, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                4.923754  0.037345 572.00000 131.844 < 2e-16 ***
## stateambient               0.015047  0.004372 572.00000  3.441 0.000621 ***
## speciesApan                0.269304  0.045135 572.00000  5.967 4.25e-09 ***
## speciesAssp                0.258165  0.041286 572.00000  6.253 7.88e-10 ***
## speciesCape                -0.075106 0.037567 572.00000 -1.999 0.046051 *
## speciesCest                0.414459  0.037123 572.00000 11.165 < 2e-16 ***
## speciesDasp                0.191482  0.037233 572.00000  5.143 3.72e-07 ***
## speciesFrve                -0.010067 0.039373 572.00000 -0.256 0.798296
## speciesHisp                0.162096  0.039753 572.00000  4.078 5.20e-05 ***
## speciesHype                0.335573  0.037967 572.00000  8.838 < 2e-16 ***
## speciesPoco                0.212661  0.037383 572.00000  5.689 2.04e-08 ***
## speciesPopr                0.118368  0.037146 572.00000  3.187 0.001518 **
## speciesRuac                0.112195  0.037338 572.00000  3.005 0.002774 **
## speciesSosp                0.477677  0.040627 572.00000 11.757 < 2e-16 ***
## speciesSyla                0.541668  0.043618 572.00000 12.418 < 2e-16 ***
## factor(year_factor)3       0.027319  0.007423 572.00000  3.680 0.000255 ***
## factor(year_factor)4       0.036078  0.007406 572.00000  4.871 1.44e-06 ***
## factor(year_factor)5       0.073615  0.007206 572.00000 10.216 < 2e-16 ***
## factor(year_factor)6       0.055354  0.007214 572.00000  7.673 7.27e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ',' 1

##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

anova(mod7a)

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.0316 0.03162     1    572 11.844 0.0006208 ***
## species                     12.8865 0.99127    13    572 371.266 < 2.2e-16 ***
## factor(year_factor)        0.3246 0.08114     4    572 30.391 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ',' 1

```

UMBS Plot-level Mixed Effects Models:

```
mod1p <- lmer(log(julian_median) ~ state + (1 | plot), umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2p <- lmer(log(julian_median) ~ insecticide + (1 | plot), umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod3p <- lmer(log(julian_median) ~ insecticide + state + (1 | plot), umbs_flwr_plot,
    REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod4p <- lmer(log(julian_median) ~ insecticide * state + (1 | plot), umbs_flwr_plot,
    REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod5p <- lmer(log(julian_median) ~ state + year_factor + (1 | plot), umbs_flwr_plot,
    REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod6p <- lmer(log(julian_median) ~ state + year_factor + insecticide + (1 | plot),
    umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7p <- lmer(log(julian_median) ~ state * year_factor + (1 | plot), umbs_flwr_plot,
    REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod8p <- lmer(log(julian_median) ~ state * year_factor + insecticide + (1 | plot),
    umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9p <- lmer(log(julian_median) ~ state * insecticide + year_factor + (1 | plot),
    umbs_flwr_plot, REML = FALSE)

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

```

mod10p <- lmer(log(julian_median) ~ state + insecticide * year_factor + (1 | plot),
  umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11p <- lmer(log(julian_median) ~ state * year_factor * insecticide + (1 | plot),
  umbs_flwr_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

AICctab(mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p, mod8p, mod9p, mod10p, mod11p,
  weights = T) # model 5p and 7p are the top models

```

```

##      dAICc df weight
## mod5p    0.0  5  0.3597
## mod7p    0.4  6  0.2997
## mod6p    2.2  6  0.1202
## mod8p    2.6  7  0.0982
## mod10p   3.1  7  0.0754
## mod9p    4.4  7  0.0389
## mod11p   7.6  10 0.0079
## mod1p   72.2  4 <0.001
## mod2p   72.5  4 <0.001
## mod3p   74.4  5 <0.001
## mod4p   76.6  6 <0.001

```

```

anova(mod5p, mod7p) # go with simpler model 5p

```

```

## Data: umbs_flwr_plot
## Models:
## mod5p: log(julian_median) ~ state + year_factor + (1 | plot)
## mod7p: log(julian_median) ~ state * year_factor + (1 | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5p     5 -291.43 -277.49 150.71  -301.43
## mod7p     6 -291.28 -274.55 151.64  -303.28 1.8521  1      0.1735

```

```

AICctab(mod5p, mod7p, weights = T)

```

```

##      dAICc df weight
## mod5p 0.0  5  0.55
## mod7p 0.4  6  0.45

```

```

summ(mod5p)

```

Observations	120
Dependent variable	log(julian_median)
Type	Mixed effects linear regression

AIC	-291.42
BIC	-277.49
Pseudo-R ² (fixed effects)	0.47
Pseudo-R ² (total)	0.47

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.02	0.02	252.44	120.00	0.00
stateambient	0.01	0.01	0.76	120.00	0.45
year_factor	0.05	0.00	10.15	120.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.07

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
summary(mod5p)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + year_factor + (1 | plot)
##   Data: umbs_flwr_plot
##
##      AIC      BIC    logLik deviance df.resid
## -291.4   -277.5   150.7    -301.4      115
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.0276 -0.6865 -0.2186  0.6979  2.4365
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0000000 0.00000
## Residual           0.004749  0.06892
## Number of obs: 120, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error       df t value Pr(>|t|)    
## (Intercept) 5.022e+00 1.989e-02 1.200e+02 252.442 <2e-16 ***
## stateambient 9.621e-03 1.258e-02 1.200e+02   0.765   0.446    
## year_factor  4.515e-02 4.448e-03 1.200e+02  10.150 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

## 
## Correlation of Fixed Effects:
##           (Intr) sttmbn
## stateambint -0.316
## year_factor -0.894  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

emmeans(mod5p, list(pairwise ~ state + year_factor), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## $`emmeans of state, year_factor`
##   state   year_factor emmean      SE    df lower.CL upper.CL
##   warmed            4  5.203 0.00901 23.14    5.184    5.221
##   ambient            4  5.212 0.00901 23.14    5.194    5.231
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, year_factor`
##   1             estimate      SE    df t.ratio p.value
##   warmed 4 - ambient 4 -0.00962 0.0127 23.1 -0.755  0.4578
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

```

KBS Species-level Mixed Effects Models

```

kmod7 <- lmer(log(julian_median) ~ state + species + (1 + factor(year_factor) | plot),
  kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

kmod7a <- lmer(log(julian_median) ~ state + species + factor(year_factor) + (1 |
  plot), kbs_flwr_spp, REML = FALSE)
kmod7b <- lmer(log(julian_median) ~ state * factor(year_factor) + species + (1 |
  plot), kbs_flwr_spp, REML = FALSE)
kmod7c <- lmer(log(julian_median) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), kbs_flwr_spp, REML = FALSE)
anova(kmod7, kmod7a) #kmod 7a

## Data: kbs_flwr_spp
## Models:
## kmod7a: log(julian_median) ~ state + species + factor(year_factor) +
## kmod7a:     (1 | plot)
## kmod7: log(julian_median) ~ state + species + (1 + factor(year_factor) |
## kmod7:     plot)

```

```

##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod7a    42 -3917.8 -3705.8 2000.9   -4001.8
## kmod7     63 -3839.7 -3521.6 1982.8   -3965.7      0 21           1

anova(kmod7a, kmod7b)  #kmod 7a but only slightly so (pvalue = 0.058), im going to go with 7b

## Data: kbs_flwr_spp
## Models:
## kmod7a: log(julian_median) ~ state + species + factor(year_factor) +
## kmod7a:      (1 | plot)
## kmod7b: log(julian_median) ~ state * factor(year_factor) + species +
## kmod7b:      (1 | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod7a    42 -3917.8 -3705.8 2000.9   -4001.8
## kmod7b    48 -3917.9 -3675.6 2007.0   -4013.9 12.154  6   0.05862 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(kmod7b, kmod7c) #kmod 7b

## Data: kbs_flwr_spp
## Models:
## kmod7c: log(julian_median) ~ state + species + factor(year_factor) +
## kmod7c:      insecticide + (1 | plot)
## kmod7b: log(julian_median) ~ state * factor(year_factor) + species +
## kmod7b:      (1 | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod7c    43 -3918.0 -3700.9 2002   -4004.0
## kmod7b    48 -3917.9 -3675.6 2007   -4013.9 9.9748  5   0.07595 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(kmod7b)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state * factor(year_factor) + species +
##          (1 | plot)
## Data: kbs_flwr_spp
##
##          AIC      BIC  logLik deviance df.resid
## -3917.9 -3675.6  2007.0   -4013.9      1103
##
## Scaled residuals:
##       Min     1Q Median     3Q    Max
## -6.7122 -0.5795 -0.0169  0.5254  4.3401
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 1.536e-05 0.003919
## Residual            1.778e-03 0.042163
## Number of obs: 1151, groups: plot, 24

```

```

## 
## Fixed effects:
## 
## (Intercept) 5.270e+00 8.731e-03 1.016e+03 603.659
## stateambient 7.217e-03 9.612e-03 8.368e+02 0.751
## factor(year_factor)2 -3.835e-02 8.010e-03 1.143e+03 -4.788
## factor(year_factor)3 -6.781e-02 8.405e-03 1.144e+03 -8.067
## factor(year_factor)4 -6.048e-02 8.441e-03 1.146e+03 -7.165
## factor(year_factor)5 -3.705e-02 8.645e-03 1.141e+03 -4.286
## factor(year_factor)6 -4.202e-02 8.609e-03 1.138e+03 -4.881
## factor(year_factor)7 -6.077e-02 8.920e-03 1.140e+03 -6.813
## speciesArel -1.294e-01 7.621e-03 1.149e+03 -16.978
## speciesAspi 3.660e-01 1.845e-02 1.140e+03 19.842
## speciesAssp 2.584e-01 1.538e-02 1.136e+03 16.801
## speciesBavu -2.873e-01 1.361e-02 1.145e+03 -21.110
## speciesCahi -4.374e-01 1.117e-02 1.146e+03 -39.158
## speciesCest 9.878e-02 7.615e-03 1.144e+03 12.972
## speciesDaca 1.810e-01 1.050e-02 1.147e+03 17.231
## speciesDagl -1.400e-01 8.124e-03 1.150e+03 -17.229
## speciesDlre 5.169e-02 4.286e-02 1.147e+03 1.206
## speciesElre -3.811e-02 7.550e-03 1.150e+03 -5.048
## speciesEugr 2.391e-01 8.475e-03 1.150e+03 28.208
## speciesHisp -1.642e-01 7.646e-03 1.146e+03 -21.479
## speciesHype 6.975e-03 9.472e-03 1.147e+03 0.736
## speciesLapu -3.928e-01 4.305e-02 1.148e+03 -9.124
## speciesLesp -2.781e-01 4.292e-02 1.148e+03 -6.479
## speciesPhpr -4.361e-02 7.047e-03 1.145e+03 -6.188
## speciesPoco -6.827e-02 8.441e-03 1.150e+03 -8.088
## speciesPopr -2.110e-01 6.911e-03 1.146e+03 -30.528
## speciesPore -4.861e-02 8.228e-03 1.148e+03 -5.908
## speciesPosp -2.635e-02 2.240e-02 1.149e+03 -1.176
## speciesRusp -1.831e-01 1.157e-02 1.143e+03 -15.825
## speciesSila -1.898e-01 4.284e-02 1.147e+03 -4.432
## speciesSoca 2.949e-01 6.813e-03 1.145e+03 43.281
## speciesSoga 2.427e-01 3.059e-02 1.148e+03 7.934
## speciesSogr 2.293e-01 1.468e-02 1.149e+03 15.616
## speciesSora 2.686e-01 1.715e-02 1.143e+03 15.664
## speciesSyla 3.314e-01 4.307e-02 1.149e+03 7.695
## speciesSypi 3.381e-01 1.177e-02 1.150e+03 28.730
## speciesSyur 2.777e-01 4.307e-02 1.149e+03 6.447
## speciesTaof -3.547e-01 1.270e-02 1.151e+03 -27.920
## speciesTrsp -1.095e-02 9.492e-03 1.137e+03 -1.154
## speciesVear -2.797e-01 3.056e-02 1.146e+03 -9.150
## stateambient:factor(year_factor)2 -2.250e-02 1.103e-02 1.140e+03 -2.040
## stateambient:factor(year_factor)3 5.148e-04 1.133e-02 1.140e+03 0.045
## stateambient:factor(year_factor)4 -1.229e-02 1.126e-02 1.144e+03 -1.091
## stateambient:factor(year_factor)5 -1.040e-02 1.156e-02 1.137e+03 -0.900
## stateambient:factor(year_factor)6 -3.856e-03 1.172e-02 1.140e+03 -0.329
## stateambient:factor(year_factor)7 3.003e-03 1.226e-02 1.142e+03 0.245
## 
## (Intercept) < 2e-16 ***
## stateambient 0.4529
## factor(year_factor)2 1.91e-06 ***
## factor(year_factor)3 1.80e-15 ***

```

```

## factor(year_factor)4      1.39e-12 ***
## factor(year_factor)5      1.97e-05 ***
## factor(year_factor)6      1.21e-06 ***
## factor(year_factor)7      1.54e-11 ***
## speciesArel               < 2e-16 ***
## speciesAspi               < 2e-16 ***
## speciesAssp               < 2e-16 ***
## speciesBavu               < 2e-16 ***
## speciesCahi               < 2e-16 ***
## speciesCest               < 2e-16 ***
## speciesDaca               < 2e-16 ***
## speciesDagl               < 2e-16 ***
## speciesDlre               0.2281
## speciesElre               5.20e-07 ***
## speciesEugr               < 2e-16 ***
## speciesHisp               < 2e-16 ***
## speciesHype               0.4617
## speciesLapu               < 2e-16 ***
## speciesLesp               1.36e-10 ***
## speciesPhpr               8.45e-10 ***
## speciesPoco               1.53e-15 ***
## speciesPopr               < 2e-16 ***
## speciesPore               4.57e-09 ***
## speciesPosp               0.2398
## speciesRusp               < 2e-16 ***
## speciesSila               1.02e-05 ***
## speciesSoca               < 2e-16 ***
## speciesSoga               5.00e-15 ***
## speciesSogr               < 2e-16 ***
## speciesSora               < 2e-16 ***
## speciesSyla               3.03e-14 ***
## speciesSypi               < 2e-16 ***
## speciesSyur               1.67e-10 ***
## speciesTaof               < 2e-16 ***
## speciesTrsp               0.2488
## speciesVear               < 2e-16 ***
## stateambient:factor(year_factor)2  0.0416 *
## stateambient:factor(year_factor)3  0.9638
## stateambient:factor(year_factor)4  0.2753
## stateambient:factor(year_factor)5  0.3685
## stateambient:factor(year_factor)6  0.7422
## stateambient:factor(year_factor)7  0.8065
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 46 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

anova(kmod7b)  # 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                               0.000 0.00009     1   25.76  0.0506 0.82383
## factor(year_factor)                0.276 0.04598     6 1140.47 25.8644 < 2e-16 ***
## species                            38.469 1.20216    32 1143.53 676.2364 < 2e-16 ***
## state:factor(year_factor)         0.022 0.00362     6 1139.02  2.0364 0.05818 .
## ---
## 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(kmod7b, list(pairwise ~ year_factor), adjust = "tukey")

```

NOTE: Results may be misleading due to involvement in interactions

```

## $`emmeans of year_factor`
##   year_factor emmean      SE   df lower.CL upper.CL
##   1      5.271 0.006567 1085.1   5.258   5.284
##   2      5.221 0.004810  862.3   5.212   5.231
##   3      5.203 0.004822  837.8   5.194   5.213
##   4      5.204 0.004820  839.0   5.195   5.214
##   5      5.229 0.005199  894.5   5.218   5.239
##   6      5.227 0.005338  947.2   5.216   5.237
##   7      5.212 0.005393  927.2   5.201   5.222
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
##   1 estimate      SE   df t.ratio p.value
##   1 - 2  0.049605 0.00603 1190  8.223 <.0001
##   1 - 3  0.067551 0.00640 1190 10.554 <.0001
##   1 - 4  0.066624 0.00641 1193 10.390 <.0001
##   1 - 5  0.042252 0.00655 1192  6.446 <.0001
##   1 - 6  0.043949 0.00666 1193  6.594 <.0001
##   1 - 7  0.059271 0.00694 1194  8.538 <.0001
##   2 - 3  0.017946 0.00442 1183  4.061 0.0010
##   2 - 4  0.017019 0.00435 1182  3.915 0.0018
##   2 - 5 -0.007353 0.00459 1190 -1.602 0.6809
##   2 - 6 -0.005656 0.00470 1190 -1.205 0.8926
##   2 - 7  0.009666 0.00511 1195  1.890 0.4873
##   3 - 4 -0.000927 0.00452 1179 -0.205 1.0000
##   3 - 5 -0.025299 0.00480 1189 -5.269 <.0001
##   3 - 6 -0.023602 0.00493 1194 -4.787 <.0001
##   3 - 7 -0.008280 0.00532 1197 -1.557 0.7098
##   4 - 5 -0.024372 0.00464 1183 -5.258 <.0001
##   4 - 6 -0.022675 0.00476 1188 -4.764 <.0001
##   4 - 7 -0.007353 0.00516 1193 -1.425 0.7884
##   5 - 6  0.001697 0.00488 1181  0.348 0.9999
##   5 - 7  0.017019 0.00523 1183  3.254 0.0200
##   6 - 7  0.015322 0.00533 1179  2.877 0.0620
##

```

```

## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 7 estimates

emmeans(kmod7b, list(pairwise ~ species), adjust = "tukey")

## $`emmeans of species`
##   species emmean      SE    df lower.CL upper.CL
##   Acmi     5.227 0.005950 1049.2    5.215    5.239
##   Arel     5.097 0.005122  931.6    5.087    5.108
##   Aspi     5.593 0.018016 1197.3    5.558    5.628
##   Assp     5.485 0.014708 1198.6    5.456    5.514
##   Bavu     4.940 0.012716 1124.3    4.915    4.965
##   Cahi     4.789 0.009946 1178.3    4.770    4.809
##   Cest     5.326 0.005376  965.2    5.315    5.336
##   Daca     5.408 0.009143 1172.9    5.390    5.426
##   Dagl     5.087 0.006004 1019.3    5.075    5.099
##   Dlre     5.279 0.043446 1194.9    5.193    5.364
##   Elre     5.189 0.004999  926.3    5.179    5.199
##   Eugr     5.466 0.006349 1029.8    5.453    5.478
##   Hisp     5.063 0.005351  970.9    5.052    5.073
##   Hype     5.234 0.007787 1051.4    5.219    5.249
##   Lapu     4.834 0.043529 1195.3    4.749    4.919
##   Lesp     4.949 0.043456 1196.6    4.863    5.034
##   Phpr     5.183 0.004320  754.9    5.175    5.192
##   Poco     5.159 0.006261 1039.1    5.146    5.171
##   Popr     5.016 0.004015  708.9    5.008    5.024
##   Pore     5.178 0.006209 1061.5    5.166    5.190
##   Posp     5.200 0.022162 1198.1    5.157    5.244
##   Rusp     5.044 0.010379 1130.8    5.023    5.064
##   Sila     5.037 0.043413 1195.4    4.952    5.122
##   Soca     5.522 0.003815  645.0    5.514    5.529
##   Soga     5.470 0.030700 1196.3    5.409    5.530
##   Sogr     5.456 0.013880 1198.6    5.429    5.483
##   Sora     5.495 0.016653 1198.6    5.463    5.528
##   Syla     5.558 0.043581 1197.1    5.473    5.644
##   Sypi     5.565 0.010484 1189.1    5.544    5.586
##   Syur     5.505 0.043581 1197.1    5.419    5.590
##   Taof     4.872 0.011748 1182.1    4.849    4.895
##   Trsp     5.216 0.007917 1181.0    5.200    5.231
##   Vear     4.947 0.030713 1196.3    4.887    5.007
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of species`
##   1           estimate      SE    df t.ratio p.value
##   Acmi - Arel  0.12940 0.00779 1196  16.619 <.0001
##   Acmi - Aspi -0.36603 0.01883 1187 -19.438 <.0001
##   Acmi - Assp -0.25841 0.01570 1183 -16.464 <.0001
##   Acmi - Bavu  0.28729 0.01393 1196  20.624 <.0001

```

```

## Acmi - Cahи 0.43744 0.01141 1193 38.341 <.0001
## Acmi - Cest -0.09878 0.00777 1190 -12.705 <.0001
## Acmi - Daca -0.18096 0.01073 1193 -16.871 <.0001
## Acmi - Dagл 0.13997 0.00830 1197 16.859 <.0001
## Acmi - Dlre -0.05169 0.04378 1193 -1.181 1.0000
## Acmi - Elre 0.03811 0.00771 1197 4.940 0.0004
## Acmi - Eugr -0.23906 0.00866 1197 -27.604 <.0001
## Acmi - Hisp 0.16423 0.00781 1193 21.032 <.0001
## Acmi - Hype -0.00697 0.00970 1197 -0.719 1.0000
## Acmi - Lapu 0.39279 0.04398 1195 8.931 <.0001
## Acmi - Lesp 0.27810 0.04385 1195 6.343 <.0001
## Acmi - Phpr 0.04361 0.00720 1192 6.060 <.0001
## Acmi - Poco 0.06827 0.00863 1197 7.915 <.0001
## Acmi - Popr 0.21099 0.00706 1193 29.893 <.0001
## Acmi - Pore 0.04861 0.00841 1195 5.783 <.0001
## Acmi - Posp 0.02635 0.02289 1196 1.151 1.0000
## Acmi - Rusp 0.18313 0.01185 1195 15.454 <.0001
## Acmi - Sila 0.18985 0.04376 1194 4.338 0.0066
## Acmi - Soca -0.29487 0.00696 1191 -42.385 <.0001
## Acmi - Soga -0.24268 0.03124 1194 -7.767 <.0001
## Acmi - Sogr -0.22926 0.01500 1196 -15.284 <.0001
## Acmi - Sora -0.26858 0.01751 1189 -15.342 <.0001
## Acmi - Syla -0.33141 0.04400 1196 -7.532 <.0001
## Acmi - Sypi -0.33810 0.01203 1197 -28.116 <.0001
## Acmi - Syur -0.27767 0.04400 1196 -6.311 <.0001
## Acmi - Taof 0.35470 0.01299 1199 27.301 <.0001
## Acmi - Trsp 0.01095 0.00969 1184 1.131 1.0000
## Acmi - Vear 0.27965 0.03122 1193 8.958 <.0001
## Arel - Aspi -0.49542 0.01873 1192 -26.445 <.0001
## Arel - Assp -0.38781 0.01554 1188 -24.948 <.0001
## Arel - Bavу 0.15790 0.01364 1168 11.575 <.0001
## Arel - Cahи 0.30804 0.01109 1198 27.785 <.0001
## Arel - Cest -0.22817 0.00742 1199 -30.747 <.0001
## Arel - Daca -0.31035 0.01038 1197 -29.891 <.0001
## Arel - Dagл 0.01058 0.00769 1197 1.376 1.0000
## Arel - Dlre -0.18108 0.04376 1194 -4.138 0.0148
## Arel - Elre -0.09129 0.00697 1196 -13.098 <.0001
## Arel - Eugr -0.36845 0.00800 1199 -46.039 <.0001
## Arel - Hisp 0.03483 0.00722 1196 4.826 0.0007
## Arel - Hype -0.13637 0.00927 1197 -14.706 <.0001
## Arel - Lapu 0.26339 0.04380 1194 6.013 <.0001
## Arel - Lesp 0.14870 0.04371 1195 3.402 0.1712
## Arel - Phpr -0.08578 0.00654 1198 -13.114 <.0001
## Arel - Poco -0.06112 0.00786 1198 -7.776 <.0001
## Arel - Popr 0.08159 0.00627 1191 13.007 <.0001
## Arel - Pore -0.08079 0.00791 1197 -10.210 <.0001
## Arel - Posp -0.10305 0.02287 1193 -4.506 0.0032
## Arel - Rusp 0.05374 0.01144 1188 4.697 0.0014
## Arel - Sila 0.06045 0.04368 1195 1.384 1.0000
## Arel - Soca -0.42426 0.00614 1190 -69.050 <.0001
## Arel - Soga -0.37207 0.03106 1193 -11.980 <.0001
## Arel - Sogr -0.35866 0.01472 1195 -24.368 <.0001
## Arel - Sora -0.39797 0.01745 1194 -22.803 <.0001
## Arel - Syla -0.46081 0.04385 1196 -10.508 <.0001

```

```

## Arel - Sypi -0.46749 0.01146 1195 -40.801 <.0001
## Arel - Syur -0.40706 0.04385 1196 -9.283 <.0001
## Arel - Taof 0.22530 0.01273 1199 17.701 <.0001
## Arel - Trsp -0.11844 0.00946 1186 -12.521 <.0001
## Arel - Vear 0.15026 0.03111 1194 4.829 0.0007
## Aspi - Assp 0.10761 0.02275 1182 4.731 0.0012
## Aspi - Bavu 0.65332 0.02194 1197 29.776 <.0001
## Aspi - Cahí 0.80346 0.02052 1191 39.149 <.0001
## Aspi - Cest 0.26725 0.01875 1192 14.255 <.0001
## Aspi - Daca 0.18507 0.02005 1189 9.229 <.0001
## Aspi - Dagl 0.50600 0.01893 1192 26.724 <.0001
## Aspi - Dlre 0.31434 0.04701 1192 6.686 <.0001
## Aspi - Elre 0.40413 0.01869 1192 21.627 <.0001
## Aspi - Eogr 0.12697 0.01912 1194 6.642 <.0001
## Aspi - Hisp 0.53025 0.01864 1191 28.443 <.0001
## Aspi - Hype 0.35905 0.01959 1198 18.324 <.0001
## Aspi - Lapu 0.75881 0.04714 1194 16.098 <.0001
## Aspi - Lesp 0.64412 0.04705 1195 13.692 <.0001
## Aspi - Phpr 0.40964 0.01848 1191 22.167 <.0001
## Aspi - Poco 0.43430 0.01904 1191 22.808 <.0001
## Aspi - Popr 0.57701 0.01837 1190 31.406 <.0001
## Aspi - Pore 0.41463 0.01891 1193 21.923 <.0001
## Aspi - Posp 0.39237 0.02869 1196 13.676 <.0001
## Aspi - Rusp 0.54916 0.02066 1193 26.587 <.0001
## Aspi - Sila 0.55587 0.04699 1193 11.828 <.0001
## Aspi - Soca 0.07116 0.01834 1190 3.881 0.0385
## Aspi - Soga 0.12335 0.03562 1195 3.463 0.1449
## Aspi - Sogr 0.13676 0.02268 1194 6.030 <.0001
## Aspi - Sora 0.09745 0.02422 1189 4.024 0.0229
## Aspi - Syla 0.03461 0.04702 1193 0.736 1.0000
## Aspi - Sypi 0.02793 0.02079 1186 1.343 1.0000
## Aspi - Syur 0.08836 0.04702 1193 1.879 0.9948
## Aspi - Taof 0.72072 0.02131 1190 33.827 <.0001
## Aspi - Trsp 0.37698 0.01973 1188 19.106 <.0001
## Aspi - Vear 0.64568 0.03536 1191 18.263 <.0001
## Assp - Bavu 0.54571 0.01933 1199 28.227 <.0001
## Assp - Cahí 0.69585 0.01765 1185 39.428 <.0001
## Assp - Cest 0.15964 0.01559 1189 10.239 <.0001
## Assp - Daca 0.07746 0.01711 1184 4.527 0.0029
## Assp - Dagl 0.39839 0.01579 1187 25.237 <.0001
## Assp - Dlre 0.20673 0.04576 1190 4.517 0.0031
## Assp - Elre 0.29652 0.01549 1191 19.147 <.0001
## Assp - Eogr 0.01936 0.01603 1192 1.207 1.0000
## Assp - Hisp 0.42264 0.01548 1190 27.307 <.0001
## Assp - Hype 0.25144 0.01660 1197 15.150 <.0001
## Assp - Lapu 0.65120 0.04598 1194 14.162 <.0001
## Assp - Lesp 0.53651 0.04588 1195 11.693 <.0001
## Assp - Phpr 0.30203 0.01524 1187 19.812 <.0001
## Assp - Poco 0.32669 0.01594 1190 20.493 <.0001
## Assp - Popr 0.46940 0.01514 1189 31.007 <.0001
## Assp - Pore 0.30702 0.01579 1187 19.447 <.0001
## Assp - Posp 0.28476 0.02671 1194 10.661 <.0001
## Assp - Rusp 0.44155 0.01788 1197 24.700 <.0001
## Assp - Sila 0.44826 0.04579 1190 9.789 <.0001

```

```

## Assp - Soca -0.03645 0.01510 1189 -2.415 0.8686
## Assp - Soga  0.01574 0.03406 1195  0.462 1.0000
## Assp - Sogr  0.02915 0.02014 1194  1.448 1.0000
## Assp - Sora -0.01016 0.02187 1188 -0.465 1.0000
## Assp - Syla -0.07300 0.04600 1194 -1.587 0.9997
## Assp - Sypi -0.07969 0.01799 1189 -4.429 0.0045
## Assp - Syur -0.01926 0.04600 1194 -0.419 1.0000
## Assp - Taof  0.61311 0.01863 1194 32.906 <.0001
## Assp - Trsp  0.26937 0.01675 1185 16.077 <.0001
## Assp - Vear  0.53807 0.03382 1189 15.910 <.0001
## Bavu - Cahи  0.15014 0.01600 1194  9.385 <.0001
## Bavu - Cest -0.38607 0.01382 1173 -27.944 <.0001
## Bavu - Daca -0.46825 0.01559 1191 -30.032 <.0001
## Bavu - Dagl -0.14732 0.01398 1173 -10.539 <.0001
## Bavu - Dlre -0.33898 0.04521 1197 -7.497 <.0001
## Bavu - Elre -0.24919 0.01354 1181 -18.405 <.0001
## Bavu - Eugr -0.52635 0.01412 1185 -37.266 <.0001
## Bavu - Hisp -0.12307 0.01372 1172 -8.970 <.0001
## Bavu - Hype -0.29427 0.01485 1183 -19.813 <.0001
## Bavu - Lapu  0.10549 0.04528 1198  2.330 0.9083
## Bavu - Lesp -0.00919 0.04520 1195 -0.203 1.0000
## Bavu - Phpr -0.24368 0.01337 1173 -18.231 <.0001
## Bavu - Poco -0.21902 0.01408 1173 -15.559 <.0001
## Bavu - Popr -0.07630 0.01322 1176 -5.771 <.0001
## Bavu - Pore -0.23869 0.01412 1173 -16.906 <.0001
## Bavu - Posp -0.26094 0.02571 1199 -10.150 <.0001
## Bavu - Rusp -0.10416 0.01630 1191 -6.391 <.0001
## Bavu - Sila -0.09745 0.04520 1198 -2.156 0.9626
## Bavu - Soca -0.58216 0.01316 1177 -44.254 <.0001
## Bavu - Soga -0.52997 0.03321 1199 -15.958 <.0001
## Bavu - Sogr -0.51655 0.01872 1198 -27.591 <.0001
## Bavu - Sora -0.55587 0.02078 1197 -26.755 <.0001
## Bavu - Syla -0.61871 0.04538 1198 -13.635 <.0001
## Bavu - Sypi -0.62539 0.01645 1190 -38.014 <.0001
## Bavu - Syur -0.56496 0.04538 1198 -12.451 <.0001
## Bavu - Taof  0.06741 0.01724 1187  3.911 0.0346
## Bavu - Trsp -0.27634 0.01506 1180 -18.350 <.0001
## Bavu - Vear -0.00764 0.03322 1199 -0.230 1.0000
## Cahи - Cest -0.53621 0.01123 1199 -47.759 <.0001
## Cahи - Daca -0.61840 0.01340 1197 -46.150 <.0001
## Cahи - Dagl -0.29746 0.01142 1197 -26.037 <.0001
## Cahи - Dlre -0.48913 0.04442 1191 -11.010 <.0001
## Cahи - Elre -0.39933 0.01097 1197 -36.404 <.0001
## Cahи - Eugr -0.67649 0.01177 1197 -57.479 <.0001
## Cahи - Hisp -0.27321 0.01114 1198 -24.523 <.0001
## Cahи - Hype -0.44441 0.01256 1198 -35.388 <.0001
## Cahи - Lapu 0.04465 0.04470 1196 -0.999 1.0000
## Cahи - Lesp -0.15934 0.04436 1193 -3.592 0.0994
## Cahи - Phpr -0.39383 0.01071 1196 -36.766 <.0001
## Cahи - Poco -0.36917 0.01168 1197 -31.616 <.0001
## Cahи - Popr -0.22645 0.01059 1198 -21.392 <.0001
## Cahи - Pore -0.38883 0.01160 1198 -33.530 <.0001
## Cahи - Posp -0.41109 0.02440 1196 -16.848 <.0001
## Cahи - Rusp -0.25430 0.01424 1198 -17.855 <.0001

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## Cahi - Sila -0.24759 0.04439 1191 -5.578 <.0001
## Cahi - Soca -0.73231 0.01051 1198 -69.650 <.0001
## Cahi - Soga -0.68012 0.03217 1197 -21.140 <.0001
## Cahi - Sogr -0.66670 0.01687 1196 -39.517 <.0001
## Cahi - Sora -0.70602 0.01920 1188 -36.766 <.0001
## Cahi - Syla -0.76885 0.04474 1197 -17.187 <.0001
## Cahi - Sypi -0.77554 0.01446 1197 -53.628 <.0001
## Cahi - Syur -0.71511 0.04474 1197 -15.985 <.0001
## Cahi - Taof -0.08274 0.01519 1199 -5.445 <.0001
## Cahi - Trsp -0.42648 0.01264 1194 -33.736 <.0001
## Cahi - Vear -0.15778 0.03212 1192 -4.913 0.0005
## Cest - Daca -0.08218 0.01047 1193 -7.853 <.0001
## Cest - Dagl 0.23875 0.00799 1198 29.888 <.0001
## Cest - Dlre 0.04709 0.04377 1193 1.076 1.0000
## Cest - Elre 0.13689 0.00735 1197 18.633 <.0001
## Cest - Eugr -0.14028 0.00828 1199 -16.947 <.0001
## Cest - Hisp 0.26300 0.00748 1191 35.141 <.0001
## Cest - Hype 0.09180 0.00933 1193 9.839 <.0001
## Cest - Lapu 0.49157 0.04389 1194 11.200 <.0001
## Cest - Lesp 0.37688 0.04380 1196 8.605 <.0001
## Cest - Phpr 0.14239 0.00675 1191 21.082 <.0001
## Cest - Poco 0.16705 0.00831 1199 20.112 <.0001
## Cest - Popr 0.30977 0.00668 1191 46.347 <.0001
## Cest - Pore 0.14738 0.00805 1193 18.313 <.0001
## Cest - Posp 0.12513 0.02254 1194 5.550 <.0001
## Cest - Rusp 0.28191 0.01167 1178 24.156 <.0001
## Cest - Sila 0.28862 0.04369 1194 6.606 <.0001
## Cest - Soca -0.19609 0.00658 1192 -29.812 <.0001
## Cest - Soga -0.14390 0.03115 1195 -4.619 0.0020
## Cest - Sogr -0.13048 0.01485 1197 -8.784 <.0001
## Cest - Sora -0.16980 0.01747 1194 -9.721 <.0001
## Cest - Syla -0.23264 0.04394 1196 -5.294 0.0001
## Cest - Sypi -0.23932 0.01178 1198 -20.311 <.0001
## Cest - Syur -0.17889 0.04394 1196 -4.071 0.0192
## Cest - Taof 0.45348 0.01283 1198 35.335 <.0001
## Cest - Trsp 0.10973 0.00918 1182 11.955 <.0001
## Cest - Vear 0.37843 0.03115 1193 12.150 <.0001
## Daca - Dagl 0.32093 0.01079 1194 29.735 <.0001
## Daca - Dlre 0.12927 0.04431 1192 2.918 0.4955
## Daca - Elre 0.21907 0.01036 1198 21.138 <.0001
## Daca - Eugr -0.05810 0.01110 1199 -5.235 0.0001
## Daca - Hisp 0.34519 0.01043 1198 33.080 <.0001
## Daca - Hype 0.17398 0.01193 1199 14.583 <.0001
## Daca - Lapu 0.57375 0.04452 1195 12.889 <.0001
## Daca - Lesp 0.45906 0.04443 1196 10.333 <.0001
## Daca - Phpr 0.22457 0.00998 1195 22.493 <.0001
## Daca - Poco 0.24923 0.01102 1197 22.619 <.0001
## Daca - Popr 0.39195 0.00987 1197 39.705 <.0001
## Daca - Pore 0.22957 0.01088 1196 21.098 <.0001
## Daca - Posp 0.20731 0.02396 1192 8.652 <.0001
## Daca - Rusp 0.36409 0.01369 1198 26.597 <.0001
## Daca - Sila 0.37080 0.04430 1192 8.370 <.0001
## Daca - Soca -0.11391 0.00980 1197 -11.624 <.0001
## Daca - Soga -0.06172 0.03203 1195 -1.927 0.9922

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## Daca - Sogr -0.04830 0.01656 1198 -2.918 0.4954
## Daca - Sora -0.08762 0.01883 1191 -4.654 0.0017
## Daca - Syla -0.15046 0.04457 1197 -3.376 0.1837
## Daca - Sypi -0.15714 0.01378 1198 -11.405 <.0001
## Daca - Syur -0.09671 0.04457 1197 -2.170 0.9594
## Daca - Taof 0.53566 0.01476 1199 36.292 <.0001
## Daca - Trsp 0.19191 0.01201 1191 15.981 <.0001
## Daca - Vear 0.46061 0.03199 1194 14.398 <.0001
## Dagl - Dlre -0.19166 0.04380 1193 -4.376 0.0056
## Dagl - Elre -0.10187 0.00763 1197 -13.359 <.0001
## Dagl - Eogr -0.37903 0.00865 1199 -43.827 <.0001
## Dagl - Hisp 0.02425 0.00783 1199 3.098 0.3535
## Dagl - Hype -0.14695 0.00978 1195 -15.032 <.0001
## Dagl - Lapu 0.25281 0.04389 1192 5.760 <.0001
## Dagl - Lesp 0.13812 0.04383 1196 3.151 0.3157
## Dagl - Phpr -0.09636 0.00720 1189 -13.384 <.0001
## Dagl - Poco -0.07170 0.00849 1190 -8.446 <.0001
## Dagl - Popr 0.07101 0.00701 1198 10.126 <.0001
## Dagl - Pore -0.09137 0.00845 1190 -10.816 <.0001
## Dagl - Posp -0.11363 0.02307 1194 -4.925 0.0005
## Dagl - Rusp 0.04316 0.01184 1195 3.646 0.0841
## Dagl - Sila 0.04987 0.04376 1193 1.140 1.0000
## Dagl - Soca -0.43484 0.00690 1197 -63.019 <.0001
## Dagl - Soga -0.38265 0.03123 1196 -12.253 <.0001
## Dagl - Sogr -0.36923 0.01498 1195 -24.646 <.0001
## Dagl - Sora -0.40855 0.01761 1194 -23.201 <.0001
## Dagl - Syla -0.47139 0.04404 1197 -10.705 <.0001
## Dagl - Sypi -0.47807 0.01199 1199 -39.858 <.0001
## Dagl - Syur -0.41764 0.04404 1197 -9.484 <.0001
## Dagl - Taof 0.21472 0.01304 1199 16.467 <.0001
## Dagl - Trsp -0.12902 0.00992 1190 -13.007 <.0001
## Dagl - Vear 0.13968 0.03121 1192 4.475 0.0037
## Dlre - Elre 0.08980 0.04369 1194 2.055 0.9801
## Dlre - Eogr -0.18737 0.04392 1193 -4.266 0.0089
## Dlre - Hisp 0.21592 0.04373 1193 4.938 0.0004
## Dlre - Hype 0.04471 0.04408 1192 1.014 1.0000
## Dlre - Lapu 0.44448 0.06157 1196 7.219 <.0001
## Dlre - Lesp 0.32979 0.06146 1195 5.366 <.0001
## Dlre - Phpr 0.09530 0.04363 1193 2.184 0.9559
## Dlre - Poco 0.11996 0.04391 1195 2.732 0.6498
## Dlre - Popr 0.26268 0.04359 1194 6.026 <.0001
## Dlre - Pore 0.10029 0.04384 1192 2.288 0.9246
## Dlre - Posp 0.07804 0.04885 1195 1.598 0.9997
## Dlre - Rusp 0.23482 0.04465 1195 5.260 0.0001
## Dlre - Sila 0.24153 0.06114 1172 3.951 0.0300
## Dlre - Soca -0.24318 0.04358 1194 -5.580 <.0001
## Dlre - Soga -0.19099 0.05321 1194 -3.590 0.1000
## Dlre - Sogr -0.17757 0.04548 1192 -3.905 0.0354
## Dlre - Sora -0.21689 0.04620 1190 -4.695 0.0014
## Dlre - Syla -0.27973 0.06156 1195 -4.544 0.0027
## Dlre - Sypi -0.28641 0.04471 1194 -6.407 <.0001
## Dlre - Syur -0.22598 0.06156 1195 -3.671 0.0777
## Dlre - Taof 0.40639 0.04494 1195 9.044 <.0001
## Dlre - Trsp 0.06264 0.04418 1192 1.418 1.0000

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## Dlre - Vear  0.33134 0.05303 1181   6.248 <.0001
## Elre - Eugr -0.27716 0.00796 1199 -34.835 <.0001
## Elre - Hisp  0.12612 0.00717 1196  17.583 <.0001
## Elre - Hype -0.04508 0.00921 1192 -4.897 0.0005
## Elre - Lapu  0.35468 0.04376 1194  8.104 <.0001
## Elre - Lesp  0.23999 0.04368 1196  5.495 <.0001
## Elre - Phpr  0.00550 0.00645 1191  0.853 1.0000
## Elre - Poco  0.03016 0.00780 1195  3.869 0.0401
## Elre - Popr  0.17288 0.00619 1186 27.935 <.0001
## Elre - Pore  0.01050 0.00787 1192  1.334 1.0000
## Elre - Posp -0.01176 0.02282 1195 -0.515 1.0000
## Elre - Rusp  0.14503 0.01142 1197 12.700 <.0001
## Elre - Sila  0.15174 0.04368 1194  3.474 0.1404
## Elre - Soca -0.33298 0.00606 1185 -54.950 <.0001
## Elre - Soga -0.28079 0.03104 1194 -9.045 <.0001
## Elre - Sogr -0.26737 0.01464 1194 -18.269 <.0001
## Elre - Sora -0.30669 0.01732 1191 -17.712 <.0001
## Elre - Syla -0.36952 0.04387 1197 -8.422 <.0001
## Elre - Sypi -0.37621 0.01154 1195 -32.591 <.0001
## Elre - Syur -0.31578 0.04387 1197 -7.197 <.0001
## Elre - Taof  0.31659 0.01268 1199 24.967 <.0001
## Elre - Trsp -0.02715 0.00942 1189 -2.881 0.5256
## Elre - Vear  0.24155 0.03107 1195  7.774 <.0001
## Eugr - Hisp  0.40328 0.00823 1199 48.972 <.0001
## Eugr - Hype  0.23208 0.00997 1191 23.287 <.0001
## Eugr - Lapu  0.63184 0.04391 1194 14.389 <.0001
## Eugr - Lesp  0.51715 0.04396 1197 11.765 <.0001
## Eugr - Phpr  0.28267 0.00759 1199 37.247 <.0001
## Eugr - Poco  0.30733 0.00879 1198 34.951 <.0001
## Eugr - Popr  0.45004 0.00740 1199 60.826 <.0001
## Eugr - Pore  0.28766 0.00885 1199 32.501 <.0001
## Eugr - Posp  0.26540 0.02305 1196 11.513 <.0001
## Eugr - Rusp  0.42219 0.01205 1199 35.037 <.0001
## Eugr - Sila  0.42890 0.04382 1194  9.787 <.0001
## Eugr - Soca -0.05581 0.00727 1199 -7.673 <.0001
## Eugr - Soga -0.00362 0.03135 1193 -0.116 1.0000
## Eugr - Sogr  0.00980 0.01527 1188  0.641 1.0000
## Eugr - Sora -0.02952 0.01783 1184 -1.656 0.9994
## Eugr - Syla -0.09236 0.04399 1197 -2.099 0.9734
## Eugr - Sypi -0.09904 0.01220 1199 -8.121 <.0001
## Eugr - Syur -0.03861 0.04399 1197 -0.878 1.0000
## Eugr - Taof  0.59376 0.01333 1198 44.557 <.0001
## Eugr - Trsp  0.25001 0.01006 1192 24.857 <.0001
## Eugr - Vear  0.51871 0.03139 1195 16.525 <.0001
## Hisp - Hype -0.17120 0.00940 1193 -18.222 <.0001
## Hisp - Lapu  0.22856 0.04386 1194  5.211 0.0001
## Hisp - Lesp  0.11387 0.04375 1195  2.603 0.7500
## Hisp - Phpr -0.12062 0.00671 1197 -17.986 <.0001
## Hisp - Poco -0.09595 0.00811 1198 -11.827 <.0001
## Hisp - Popr  0.04676 0.00645 1189  7.244 <.0001
## Hisp - Pore -0.11562 0.00797 1192 -14.504 <.0001
## Hisp - Posp -0.13788 0.02292 1195 -6.015 <.0001
## Hisp - Rusp  0.01891 0.01153 1186  1.639 0.9995
## Hisp - Sila  0.02562 0.04370 1194  0.586 1.0000

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##  Hisp - Soca -0.45910 0.00634 1191 -72.362 <.0001
##  Hisp - Soga -0.40691 0.03110 1193 -13.085 <.0001
##  Hisp - Sogr -0.39349 0.01474 1194 -26.693 <.0001
##  Hisp - Sora -0.43281 0.01735 1192 -24.949 <.0001
##  Hisp - Syla -0.49564 0.04392 1197 -11.284 <.0001
##  Hisp - Sypi -0.50233 0.01166 1198 -43.095 <.0001
##  Hisp - Syur -0.44190 0.04392 1197 -10.061 <.0001
##  Hisp - Taof  0.19047 0.01272 1199  14.975 <.0001
##  Hisp - Trsp -0.15327 0.00954 1182 -16.066 <.0001
##  Hisp - Vear  0.11543 0.03110 1194   3.712 0.0681
##  Hype - Lapu  0.39976 0.04422 1195   9.040 <.0001
##  Hype - Lesp  0.28507 0.04409 1192   6.466 <.0001
##  Hype - Phpr  0.05059 0.00881 1194   5.740 <.0001
##  Hype - Poco  0.07525 0.00996 1190   7.554 <.0001
##  Hype - Popr  0.21796 0.00871 1192  25.026 <.0001
##  Hype - Pore  0.05558 0.00990 1193   5.615 <.0001
##  Hype - Posp  0.03332 0.02334 1195   1.428 1.0000
##  Hype - Rusp  0.19011 0.01290 1195  14.741 <.0001
##  Hype - Sila  0.19682 0.04404 1193   4.469 0.0038
##  Hype - Soca -0.28789 0.00861 1192 -33.424 <.0001
##  Hype - Soga -0.23570 0.03166 1194  -7.446 <.0001
##  Hype - Sogr -0.22229 0.01588 1197 -13.995 <.0001
##  Hype - Sora -0.26160 0.01831 1196 -14.285 <.0001
##  Hype - Syla -0.32444 0.04426 1198  -7.330 <.0001
##  Hype - Sypi -0.33113 0.01305 1197 -25.365 <.0001
##  Hype - Syur -0.27069 0.04426 1198  -6.116 <.0001
##  Hype - Taof  0.36167 0.01407 1196  25.712 <.0001
##  Hype - Trsp  0.01793 0.01097 1199   1.635 0.9996
##  Hype - Vear  0.28663 0.03166 1195   9.054 <.0001
##  Lapu - Lesp -0.11469 0.06155 1196  -1.863 0.9954
##  Lapu - Phpr -0.34918 0.04374 1194  -7.984 <.0001
##  Lapu - Poco -0.32452 0.04389 1193  -7.393 <.0001
##  Lapu - Popr -0.18180 0.04369 1194  -4.161 0.0135
##  Lapu - Pore -0.34418 0.04398 1193  -7.826 <.0001
##  Lapu - Posp -0.36644 0.04894 1195  -7.487 <.0001
##  Lapu - Rusp -0.20965 0.04474 1196  -4.686 0.0014
##  Lapu - Sila -0.20294 0.06153 1196  -3.298 0.2239
##  Lapu - Soca -0.68766 0.04366 1194 -15.752 <.0001
##  Lapu - Soga -0.63547 0.05330 1195 -11.923 <.0001
##  Lapu - Sogr -0.62205 0.04569 1193 -13.615 <.0001
##  Lapu - Sora -0.66137 0.04666 1196 -14.174 <.0001
##  Lapu - Syla -0.72420 0.06162 1195 -11.754 <.0001
##  Lapu - Sypi -0.73089 0.04479 1194 -16.318 <.0001
##  Lapu - Syur -0.67046 0.06162 1195 -10.881 <.0001
##  Lapu - Taof -0.03809 0.04506 1192  -0.845 1.0000
##  Lapu - Trsp -0.38183 0.04430 1194  -8.619 <.0001
##  Lapu - Vear -0.11313 0.05332 1195  -2.122 0.9694
##  Lesp - Phpr -0.23449 0.04365 1196  -5.372 <.0001
##  Lesp - Poco -0.20983 0.04386 1196  -4.784 0.0009
##  Lesp - Popr -0.06711 0.04360 1196  -1.539 0.9999
##  Lesp - Pore -0.22949 0.04386 1196  -5.232 0.0001
##  Lesp - Posp -0.25175 0.04887 1197  -5.151 0.0002
##  Lesp - Rusp -0.09496 0.04469 1197  -2.125 0.9688
##  Lesp - Sila -0.08825 0.06145 1196  -1.436 1.0000

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##  Lesp - Soca -0.57297 0.04358 1195 -13.146 <.0001
##  Lesp - Soga -0.52078 0.05301 1196 -9.824 <.0001
##  Lesp - Sogr -0.50736 0.04548 1196 -11.154 <.0001
##  Lesp - Sora -0.54668 0.04655 1196 -11.744 <.0001
##  Lesp - Syla -0.60951 0.06156 1196 -9.900 <.0001
##  Lesp - Sypi -0.61620 0.04471 1196 -13.782 <.0001
##  Lesp - Syur -0.55577 0.06156 1196 -9.027 <.0001
##  Lesp - Taof  0.07660 0.04496 1197  1.704 0.9990
##  Lesp - Trsp -0.26714 0.04421 1196 -6.042 <.0001
##  Lesp - Vear  0.00156 0.05301 1195  0.029 1.0000
##  Phpr - Poco  0.02466 0.00746 1190  3.307 0.2193
##  Phpr - Popr  0.16738 0.00572 1191 29.268 <.0001
##  Phpr - Pore  0.00500 0.00739 1188  0.676 1.0000
##  Phpr - Posp -0.01726 0.02259 1195 -0.764 1.0000
##  Phpr - Rusp  0.13952 0.01113 1194 12.535 <.0001
##  Phpr - Sila  0.14624 0.04358 1194  3.355 0.1936
##  Phpr - Soca -0.33848 0.00558 1188 -60.640 <.0001
##  Phpr - Soga -0.28629 0.03097 1196 -9.243 <.0001
##  Phpr - Sogr -0.27287 0.01445 1196 -18.885 <.0001
##  Phpr - Sora -0.31219 0.01714 1192 -18.218 <.0001
##  Phpr - Syla -0.37502 0.04381 1196 -8.561 <.0001
##  Phpr - Sypi -0.38171 0.01125 1198 -33.943 <.0001
##  Phpr - Syur -0.32128 0.04381 1196 -7.334 <.0001
##  Phpr - Taof  0.31109 0.01243 1199 25.036 <.0001
##  Phpr - Trsp -0.03266 0.00893 1183 -3.658 0.0810
##  Phpr - Vear  0.23604 0.03097 1193  7.622 <.0001
##  Poco - Popr  0.14272 0.00723 1199 19.745 <.0001
##  Poco - Pore -0.01967 0.00870 1194 -2.261 0.9338
##  Poco - Posp -0.04192 0.02318 1195 -1.809 0.9972
##  Poco - Rusp  0.11486 0.01196 1199  9.601 <.0001
##  Poco - Sila  0.12157 0.04389 1196  2.770 0.6188
##  Poco - Soca -0.36314 0.00711 1198 -51.064 <.0001
##  Poco - Soga -0.31095 0.03126 1195 -9.947 <.0001
##  Poco - Sogr -0.29753 0.01512 1198 -19.681 <.0001
##  Poco - Sora -0.33685 0.01779 1196 -18.932 <.0001
##  Poco - Syla -0.39969 0.04396 1196 -9.092 <.0001
##  Poco - Sypi -0.40637 0.01201 1199 -33.830 <.0001
##  Poco - Syur -0.34594 0.04396 1196 -7.869 <.0001
##  Poco - Taof  0.28643 0.01326 1199 21.608 <.0001
##  Poco - Trsp -0.05732 0.01025 1192 -5.591 <.0001
##  Poco - Vear  0.21138 0.03132 1195  6.750 <.0001
##  Popr - Pore -0.16238 0.00723 1195 -22.463 <.0001
##  Popr - Posp -0.18464 0.02265 1194 -8.150 <.0001
##  Popr - Rusp -0.02786 0.01100 1188 -2.531 0.7997
##  Popr - Sila -0.02114 0.04357 1194 -0.485 1.0000
##  Popr - Soca -0.50586 0.00525 1173 -96.275 <.0001
##  Popr - Soga -0.45367 0.03090 1194 -14.681 <.0001
##  Popr - Sogr -0.44025 0.01433 1195 -30.718 <.0001
##  Popr - Sora -0.47957 0.01704 1192 -28.149 <.0001
##  Popr - Syla -0.54240 0.04374 1196 -12.401 <.0001
##  Popr - Sypi -0.54909 0.01109 1195 -49.533 <.0001
##  Popr - Syur -0.48866 0.04374 1196 -11.172 <.0001
##  Popr - Taof  0.14371 0.01229 1199 11.690 <.0001
##  Popr - Trsp -0.20004 0.00894 1181 -22.380 <.0001

```

```

## Popr - Vear  0.06866 0.03092 1194   2.221 0.9462
## Pore - Posp -0.02226 0.02304 1196  -0.966 1.0000
## Pore - Rusp  0.13453 0.01197 1191  11.242 <.0001
## Pore - Sila  0.14124 0.04382 1193   3.223 0.2682
## Pore - Soca -0.34348 0.00713 1194  -48.145 <.0001
## Pore - Soga -0.29129 0.03126 1195  -9.317 <.0001
## Pore - Sogr -0.27787 0.01507 1195 -18.443 <.0001
## Pore - Sora -0.31719 0.01767 1195 -17.955 <.0001
## Pore - Syla -0.38002 0.04403 1197  -8.631 <.0001
## Pore - Sypi -0.38671 0.01206 1199 -32.063 <.0001
## Pore - Syur -0.32628 0.04403 1197  -7.410 <.0001
## Pore - Taof  0.30609 0.01312 1199  23.336 <.0001
## Pore - Trsp -0.03765 0.00998 1188  -3.772 0.0558
## Pore - Vear  0.23105 0.03124 1192   7.397 <.0001
## Posp - Rusp  0.15679 0.02458 1198   6.379 <.0001
## Posp - Sila  0.16350 0.04879 1195   3.351 0.1958
## Posp - Soca -0.32122 0.02263 1194 -14.197 <.0001
## Posp - Soga -0.26903 0.03790 1190  -7.099 <.0001
## Posp - Sogr -0.25561 0.02628 1196  -9.727 <.0001
## Posp - Sora -0.29493 0.02785 1197 -10.590 <.0001
## Posp - Syla -0.35776 0.04900 1197  -7.301 <.0001
## Posp - Sypi -0.36445 0.02468 1198 -14.765 <.0001
## Posp - Syur -0.30402 0.04900 1197  -6.204 <.0001
## Posp - Taof  0.32835 0.02518 1197  13.040 <.0001
## Posp - Trsp -0.01540 0.02313 1195  -0.666 1.0000
## Posp - Vear  0.25331 0.03798 1196   6.670 <.0001
## Rusp - Sila  0.00671 0.04460 1196   0.151 1.0000
## Rusp - Soca -0.47800 0.01093 1190 -43.742 <.0001
## Rusp - Soga -0.42581 0.03234 1194 -13.166 <.0001
## Rusp - Sogr -0.41239 0.01724 1198 -23.923 <.0001
## Rusp - Sora -0.45171 0.01950 1193 -23.168 <.0001
## Rusp - Syla -0.51455 0.04480 1198 -11.485 <.0001
## Rusp - Sypi -0.52123 0.01459 1197 -35.719 <.0001
## Rusp - Syur -0.46080 0.04480 1198 -10.286 <.0001
## Rusp - Taof  0.17157 0.01549 1198  11.077 <.0001
## Rusp - Trsp -0.17218 0.01305 1198 -13.195 <.0001
## Rusp - Vear  0.09652 0.03241 1198   2.978 0.4460
## Sila - Soca -0.48472 0.04355 1194 -11.130 <.0001
## Sila - Soga -0.43252 0.05318 1195  -8.133 <.0001
## Sila - Sogr -0.41911 0.04555 1192  -9.202 <.0001
## Sila - Sora -0.45843 0.04645 1190  -9.870 <.0001
## Sila - Syla -0.52126 0.06154 1195  -8.471 <.0001
## Sila - Sypi -0.52795 0.04467 1194 -11.819 <.0001
## Sila - Syur -0.46752 0.06154 1195  -7.597 <.0001
## Sila - Taof  0.16485 0.04494 1195   3.668 0.0784
## Sila - Trsp -0.17889 0.04404 1193  -4.062 0.0198
## Sila - Vear  0.08981 0.05301 1181   1.694 0.9991
## Soca - Soga  0.05219 0.03089 1194   1.690 0.9992
## Soca - Sogr  0.06561 0.01429 1195   4.591 0.0022
## Soca - Sora  0.02629 0.01700 1192   1.547 0.9998
## Soca - Syla -0.03655 0.04371 1196  -0.836 1.0000
## Soca - Sypi -0.04323 0.01102 1194  -3.924 0.0329
## Soca - Syur  0.01720 0.04371 1196   0.393 1.0000
## Soca - Taof  0.64957 0.01224 1199  53.072 <.0001

```

```

## Soca - Trsp  0.30582 0.00885 1181  34.543 <.0001
## Soca - Vear  0.57452 0.03090 1194  18.594 <.0001
## Soga - Sogr  0.01342 0.03343 1187   0.401 1.0000
## Soga - Sora -0.02590 0.03490 1192  -0.742 1.0000
## Soga - Syla -0.08874 0.05334 1196  -1.664 0.9994
## Soga - Sypi -0.09542 0.03239 1196  -2.946 0.4720
## Soga - Syur -0.03499 0.05334 1196  -0.656 1.0000
## Soga - Taof  0.59738 0.03271 1187  18.264 <.0001
## Soga - Trsp  0.25363 0.03174 1193   7.992 <.0001
## Soga - Vear  0.52233 0.04331 1195  12.059 <.0001
## Sogr - Sora -0.03932 0.02146 1182  -1.832 0.9965
## Sogr - Syla -0.10215 0.04578 1197  -2.232 0.9431
## Sogr - Sypi -0.10884 0.01729 1197  -6.293 <.0001
## Sogr - Syur -0.04841 0.04578 1197  -1.058 1.0000
## Sogr - Taof  0.58396 0.01794 1185  32.551 <.0001
## Sogr - Trsp  0.24021 0.01605 1191  14.969 <.0001
## Sogr - Vear  0.50891 0.03357 1194  15.162 <.0001
## Sora - Syla -0.06284 0.04670 1197  -1.346 1.0000
## Sora - Sypi -0.06952 0.01969 1193  -3.531 0.1190
## Sora - Syur -0.00909 0.04670 1197  -0.195 1.0000
## Sora - Taof  0.62328 0.02016 1191  30.924 <.0001
## Sora - Trsp  0.27953 0.01849 1189  15.115 <.0001
## Sora - Vear  0.54823 0.03479 1192  15.759 <.0001
## Syla - Sypi -0.00669 0.04471 1193  -0.150 1.0000
## Syla - Syur  0.05374 0.06080 1171   0.884 1.0000
## Syla - Taof  0.68611 0.04512 1194  15.207 <.0001
## Syla - Trsp  0.34237 0.04434 1195   7.721 <.0001
## Syla - Vear  0.61107 0.05335 1196  11.454 <.0001
## Sypi - Syur  0.06043 0.04471 1193   1.351 1.0000
## Sypi - Taof  0.69280 0.01570 1198  44.135 <.0001
## Sypi - Trsp  0.34905 0.01324 1192  26.355 <.0001
## Sypi - Vear  0.61775 0.03246 1195  19.029 <.0001
## Syur - Taof  0.63237 0.04512 1194  14.016 <.0001
## Syur - Trsp  0.28862 0.04434 1195   6.509 <.0001
## Syur - Vear  0.55732 0.05335 1196  10.447 <.0001
## Taof - Trsp -0.34375 0.01409 1197  -24.397 <.0001
## Taof - Vear -0.07505 0.03279 1197  -2.289 0.9242
## Trsp - Vear  0.26870 0.03174 1192   8.466 <.0001
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 33 estimates

# including native vs. exotic - first with interaction term
kbs_flwr_spp <- within(kbs_flwr_spp, origin <- relevel(factor(origin), ref = "Native")) # releveling s
km0d8 <- lmer(log(julian_median) ~ state * origin + (1 + factor(year_factor) | plot),
  kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -4.7e+00

```

```

kmod9 <- lmer(log(julian_median) ~ state + origin + (1 + factor(year_factor) | plot),
  kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

kmod9a <- lmer(log(julian_median) ~ state + origin + factor(year_factor) + (1 | plot),
  kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

kmod9b <- lmer(log(julian_median) ~ state + origin + factor(year_factor) + insecticide +
  (1 | plot), kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(kmod8, kmod9) # kmod 9 is a better fit to data

## Data: kbs_flwr_spp
## Models:
## kmod9: log(julian_median) ~ state + origin + (1 + factor(year_factor) |
## kmod9:   plot)
## kmod8: log(julian_median) ~ state * origin + (1 + factor(year_factor) |
## kmod8:   plot)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod9    34 -1329.8 -1159.0 698.92   -1397.8
## kmod8    37 -1326.7 -1140.7 700.33   -1400.7 2.8067  3      0.4224

anova(kmod9, kmod9a) # kmod 9a

## Data: kbs_flwr_spp
## Models:
## kmod9a: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
## kmod9a:   plot)
## kmod9: log(julian_median) ~ state + origin + (1 + factor(year_factor) |
## kmod9:   plot)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod9a   13 -1415.2 -1349.9 720.61   -1441.2
## kmod9    34 -1329.8 -1159.0 698.92   -1397.8      0 21          1

anova(kmod9a, kmod9b) # kmod 9a

## Data: kbs_flwr_spp
## Models:
## kmod9a: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
## kmod9a:   plot)
## kmod9b: log(julian_median) ~ state + origin + factor(year_factor) + insecticide +
## kmod9b:   (1 | plot)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod9a   13 -1415.2 -1349.9 720.61   -1441.2
## kmod9b   14 -1414.0 -1343.6 720.99   -1442.0 0.7434  1      0.3886

```

```
summary(kmod9a)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + origin + factor(year_factor) + (1 |
##   plot)
## Data: kbs_flwr_spp
##
##          AIC      BIC  logLik deviance df.resid
## -1415.2 -1349.9    720.6   -1441.2     1112
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.8470 -0.5993  0.1929  0.5541  3.5658
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.00000  0.0000
## Residual           0.01626  0.1275
## Number of obs: 1125, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) 5.566e+00 1.678e-02 1.125e+03 331.792 < 2e-16 ***
## stateambient 1.438e-02 7.657e-03 1.125e+03  1.877   0.0607 .
## origin       -3.262e-01 6.583e-02 1.125e+03 -4.955 8.33e-07 ***
## originBoth    -3.291e-01 1.377e-02 1.125e+03 -23.903 < 2e-16 ***
## originExotic  -3.149e-01 9.173e-03 1.125e+03 -34.328 < 2e-16 ***
## factor(year_factor)2 -1.382e-01 1.689e-02 1.125e+03 -8.182 7.49e-16 ***
## factor(year_factor)3 -1.500e-01 1.745e-02 1.125e+03 -8.597 < 2e-16 ***
## factor(year_factor)4 -1.608e-01 1.732e-02 1.125e+03 -9.282 < 2e-16 ***
## factor(year_factor)5 -1.013e-01 1.768e-02 1.125e+03 -5.732 1.27e-08 ***
## factor(year_factor)6 -1.163e-01 1.797e-02 1.125e+03 -6.469 1.47e-10 ***
## factor(year_factor)7 -1.328e-01 1.877e-02 1.125e+03 -7.078 2.57e-12 ***
## ---
## 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 -0.216
## origin      -0.242 -0.003
## originBoth   -0.308 -0.054  0.082
## originExotc  -0.424  0.023  0.107  0.488
## fctr(yr_f)2 -0.758 -0.031  0.195  0.018  0.021
## fctr(yr_f)3 -0.734 -0.033  0.189  0.028  0.017  0.728
## fctr(yr_f)4 -0.733 -0.040  0.189  0.061 -0.013  0.733  0.711
## fctr(yr_f)5 -0.733 -0.045  0.189  0.076  0.028  0.719  0.697  0.705
## fctr(yr_f)6 -0.722 -0.014  0.185  0.063  0.018  0.706  0.684  0.692  0.679
## fctr(yr_f)7 -0.714 -0.007  0.182  0.104  0.058  0.677  0.657  0.664  0.653
##           fc(_)6
## stateambint
## origin
## originBoth
```

```

## originExotc
## fctr(yr_f)2
## fctr(yr_f)3
## fctr(yr_f)4
## fctr(yr_f)5
## fctr(yr_f)6
## fctr(yr_f)7  0.641
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

anova(kmod9)

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state     0.028  0.0280     1   63.20  1.7308 0.1931
## origin   20.534  6.8448     3 676.87 422.9865 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(kmod9a, list(pairwise ~ state + origin), adjust = "tukey")

## $`emmeans of state, origin`
##   state origin emmean      SE    df lower.CL upper.CL
##   warmed Native  5.452 0.009086 166.61   5.434   5.470
##   ambient Native  5.466 0.008893 161.26   5.449   5.484
##   warmed        5.126 0.065648 1135.99   4.997   5.254
##   ambient        5.140 0.065619 1135.23   5.011   5.269
##   warmed Both    5.123 0.012471 442.37   5.098   5.147
##   ambient Both   5.137 0.011867 382.29   5.114   5.160
##   warmed Exotic 5.137 0.006473  44.06   5.124   5.150
##   ambient Exotic 5.151 0.006475  43.57   5.138   5.164
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`
##   1             estimate      SE    df t.ratio p.value
##   warmed Native - ambient Native -0.014375 0.00800  25.4 -1.796  0.6279
##   warmed Native - warmed          0.326208 0.06627 1135.9  4.923 <.0001
##   warmed Native - ambient         0.311833 0.06675 1127.5  4.672  0.0001
##   warmed Native - warmed Both   0.329121 0.01385 1133.5 23.762 <.0001
##   warmed Native - ambient Both  0.314746 0.01564  311.7 20.124 <.0001
##   warmed Native - warmed Exotic 0.314901 0.00923 1136.0 34.106 <.0001
##   warmed Native - ambient Exotic 0.300526 0.01236 138.9 24.314 <.0001
##   ambient Native - warmed       0.340582 0.06675 1132.7  5.102 <.0001
##   ambient Native - ambient      0.326208 0.06627 1135.9  4.923 <.0001
##   ambient Native - warmed Both  0.343496 0.01634  372.9 21.017 <.0001
##   ambient Native - ambient Both 0.329121 0.01385 1133.5 23.762 <.0001
##   ambient Native - warmed Exotic 0.329275 0.01207 134.3 27.271 <.0001
##   ambient Native - ambient Exotic 0.314901 0.00923 1136.0 34.106 <.0001
##   warmed - ambient            -0.014375 0.00800  25.4 -1.796  0.6279

```

```

##  warmed - warmed Both          0.002913 0.06659 1136.0  0.044  1.0000
##  warmed - ambient Both        -0.011461 0.06698 1132.5 -0.171  1.0000
##  warmed - warmed Exotic      -0.011307 0.06591 1135.5 -0.172  1.0000
##  warmed - ambient Exotic     -0.025681 0.06643 1133.5 -0.387  0.9999
##  ambient - warmed Both        0.017288 0.06715 1127.9  0.257  1.0000
##  ambient - ambient Both       0.002913 0.06659 1136.0  0.044  1.0000
##  ambient - warmed Exotic     0.003068 0.06637 1129.2  0.046  1.0000
##  ambient - ambient Exotic    -0.011307 0.06591 1135.5 -0.172  1.0000
##  warmed Both - ambient Both   -0.014375 0.00800 25.4   -1.796  0.6279
##  warmed Both - warmed Exotic  -0.014220 0.01235 1135.9 -1.152  0.9450
##  warmed Both - ambient Exotic -0.028595 0.01521 289.1   -1.880  0.5655
##  ambient Both - warmed Exotic  0.000154 0.01420 229.2   0.011  1.0000
##  ambient Both - ambient Exotic -0.014220 0.01235 1135.9 -1.152  0.9450
##  warmed Exotic - ambient Exotic -0.014375 0.00800 25.4   -1.796  0.6279
##
## Results are averaged over the levels of: year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates

# including growth form - first with interaction term
kbs_flwr_spp <- within(kbs_flwr_spp, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
kmod10 <- lmer(log(julian_median) ~ state * growth_habit + (1 + year_factor | plot),
  kbs_flwr_spp, REML = FALSE)

## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## boundary (singular) fit: see ?isSingular

kmod11 <- lmer(log(julian_median) ~ state + growth_habit + (1 + year_factor | plot),
  kbs_flwr_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

kmod11a <- lmer(log(julian_median) ~ state + growth_habit + year_factor + (1 | plot),
  kbs_flwr_spp, REML = FALSE)
kmod11b <- lmer(log(julian_median) ~ state + growth_habit + year_factor + insecticide +
  (1 | plot), kbs_flwr_spp, REML = FALSE)
anova(kmod10, kmod11) # kmodel 11 is a better fit to data

## Data: kbs_flwr_spp
## Models:
## kmod11: log(julian_median) ~ state + growth_habit + (1 + year_factor |
## kmod11:      plot)
## kmod10: log(julian_median) ~ state * growth_habit + (1 + year_factor |
## kmod10:      plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod11     9 -1004.6 -959.41 511.32  -1022.6
## kmod10    11 -1003.9 -948.62 512.95  -1025.9 3.2552  2      0.1964

```

```

anova(kmod11, kmod11a) # kmod 11a

## Data: kbs_flwr_spp
## Models:
## kmod11a: log(julian_median) ~ state + growth_habit + year_factor + (1 |
## kmod11a:     plot)
## kmod11: log(julian_median) ~ state + growth_habit + (1 + year_factor | 
## kmod11:     plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod11a     8 -1017.8 -977.57 516.89   -1033.8
## kmod11     9 -1004.6 -959.41 511.32   -1022.6      0   1           1

```

```

anova(kmod11a, kmod11b) # kmod 11a

```

```

## Data: kbs_flwr_spp
## Models:
## kmod11a: log(julian_median) ~ state + growth_habit + year_factor + (1 |
## kmod11a:     plot)
## kmod11b: log(julian_median) ~ state + growth_habit + year_factor + insecticide +
## kmod11b:     (1 | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## kmod11a     8 -1017.8 -977.57 516.89   -1033.8
## kmod11b     9 -1016.6 -971.34 517.29   -1034.6 0.7967  1       0.3721

```

```

summary(kmod11a)

```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + growth_habit + year_factor + (1 |
##     plot)
## Data: kbs_flwr_spp
##
##      AIC      BIC      logLik deviance df.resid
## -1017.8 -977.6     516.9    -1033.8      1117
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.5492 -0.4798  0.0751  0.6355  2.0532
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0001551 0.01246
## Residual            0.0232239 0.15239
## Number of obs: 1125, groups: plot, 24
##
## Fixed effects:
##                   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      5.297e+00  1.334e-02  2.087e+02 397.218 < 2e-16 ***
## stateambient    2.757e-03  1.051e-02  2.272e+01   0.262 0.795385
## growth_habit    -2.276e-01  1.547e-02  1.121e+03 -14.717 < 2e-16 ***
## growth_habitForb/herb -5.426e-01  1.532e-01  1.123e+03 -3.541 0.000415 ***
## growth_habitGraminoid -2.262e-01  9.804e-03  1.125e+03 -23.072 < 2e-16 ***

```

```

## year_factor           8.679e-03  2.575e-03  1.124e+03   3.371 0.000774 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn grwth_ grwt_G
## stateambient -0.426
## growth_habit -0.263 -0.034
## grwth_hbtF/  0.004  0.029  0.014
## grwth_hbtGr -0.270  0.063  0.292  0.043
## year_factor   -0.720 -0.003  0.073 -0.055 -0.158

anova(kmod11a)

## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state        0.0016  0.0016     1     1 22.72  0.0688 0.7953853
## growth_habit 14.1323  4.7108     3 1122.82 202.8404 < 2.2e-16 ***
## year_factor   0.2639  0.2639     1 1123.59 11.3638 0.0007744 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(kmod11a, list(pairwise ~ state + growth_habit), adjust = "tukey")

## $`emmeans of state, growth_habit`
##   state   growth_habit emmean      SE      df lower.CL upper.CL
##   warmed   Forb      5.332 0.009593  61.86    5.312  5.351
##   ambient   Forb      5.334 0.009088  50.04    5.316  5.353
##   warmed   ambient    5.104 0.015704 365.88    5.073  5.135
##   ambient   ambient    5.107 0.015044 322.78    5.077  5.136
##   warmed   Forb/herb  4.789 0.153568 1129.32    4.488  5.090
##   ambient   Forb/herb 4.792 0.153838 1129.19    4.490  5.094
##   warmed   Graminoid  5.105 0.009267  54.31    5.087  5.124
##   ambient   Graminoid 5.108 0.009462  59.11    5.089  5.127
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, growth_habit`
##   1                           estimate      SE      df t.ratio
##   warmed Forb - ambient Forb -0.00276 0.01104  26.4 -0.250
##   warmed Forb - warmed          0.22761 0.01552 1126.3 14.668
##   warmed Forb - ambient          0.22485 0.01876 214.2 11.989
##   warmed Forb - (warmed Forb/herb) 0.54257 0.15378 1127.6 3.528
##   warmed Forb - (ambient Forb/herb) 0.53982 0.15447 1130.4 3.495
##   warmed Forb - warmed Graminoid  0.22620 0.00985 1130.8 22.974
##   warmed Forb - ambient Graminoid 0.22344 0.01523  97.9 14.674
##   ambient Forb - warmed          0.23037 0.01933 239.4 11.920
##   ambient Forb - ambient          0.22761 0.01552 1126.3 14.668
##   ambient Forb - (warmed Forb/herb) 0.54533 0.15387 1130.5 3.544
##   ambient Forb - (ambient Forb/herb) 0.54257 0.15378 1127.6 3.528
##   ambient Forb - warmed Graminoid  0.22895 0.01434  78.1 15.963

```

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## ambient Forb - ambient Graminoid          0.22620 0.00985 1130.8 22.974
## warmed - ambient                         -0.00276 0.01104   26.4 -0.250
## warmed - (warmed Forb/herb)              0.31496 0.15434 1127.7 2.041
## warmed - (ambient Forb/herb)             0.31220 0.15507 1130.4 2.013
## warmed - warmed Graminoid                -0.00142 0.01577 1130.1 -0.090
## warmed - ambient Graminoid               -0.00417 0.01987  255.9 -0.210
## ambient - (warmed Forb/herb)              0.31772 0.15440 1130.6 2.058
## ambient - (ambient Forb/herb)             0.31496 0.15434 1127.7 2.041
## ambient - warmed Graminoid                0.00134 0.01862  205.4 0.072
## ambient - ambient Graminoid               -0.00142 0.01577 1130.1 -0.090
## (warmed Forb/herb) - (ambient Forb/herb) -0.00276 0.01104   26.4 -0.250
## (warmed Forb/herb) - warmed Graminoid     -0.31638 0.15366 1127.2 -2.059
## (warmed Forb/herb) - ambient Graminoid    -0.31913 0.15380 1130.4 -2.075
## (ambient Forb/herb) - warmed Graminoid    -0.31362 0.15431 1130.2 -2.032
## (ambient Forb/herb) - ambient Graminoid    -0.31638 0.15366 1127.2 -2.059
## warmed Graminoid - ambient Graminoid      -0.00276 0.01104   26.4 -0.250
## p.value
## 1.0000
## <.0001
## <.0001
## 0.0103
## 0.0116
## <.0001
## <.0001
## <.0001
## <.0001
## <.0001
## 0.0097
## 0.0103
## <.0001
## <.0001
## 1.0000
## 0.4547
## 0.4732
## 1.0000
## 1.0000
## 0.4433
## 0.4547
## 1.0000
## 1.0000
## 1.0000
## 0.4425
## 0.4318
## 0.4603
## 0.4425
## 1.0000
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates

```

KBS Plot-level Mixed Effects Models:

```

mod1pk <- lmer(log(julian_median) ~ state + (1 | plot), kbs_flwr_plot, REML = FALSE)
mod2pk <- lmer(log(julian_median) ~ state + factor(year_factor) + (1 | plot), kbs_flwr_plot,
REML = FALSE)
mod3pk <- lmer(log(julian_median) ~ state * factor(year_factor) + (1 | plot), kbs_flwr_plot,
REML = FALSE)
anova(mod1pk, mod2pk) # this wont work for some reason

## Error in anova.merMod(mod1pk, mod2pk): models were not all fitted to the same size of dataset

anova(mod2pk, mod3pk) #mod2pk

## Data: kbs_flwr_plot
## Models:
## mod2pk: log(julian_median) ~ state + factor(year_factor) + (1 | plot)
## mod3pk: log(julian_median) ~ state * factor(year_factor) + (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2pk   10 -363.38 -332.27 191.69   -383.38
## mod3pk   16 -373.94 -324.15 202.97   -405.94 22.556   6  0.0009597 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(mod2pk)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + factor(year_factor) + (1 | plot)
## Data: kbs_flwr_plot
##
##      AIC      BIC logLik deviance df.resid
## -363.4   -332.3   191.7   -383.4      156
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max
## -1.90904 -0.66579 -0.04988  0.53054  2.70703
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.001780 0.04219
## Residual           0.004843 0.06959
## Number of obs: 166, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)  5.29354   0.01948  271.756 < 2e-16 ***
## stateambient 0.02327   0.02034  24.16832   1.144  0.26395  
## factor(year_factor)2 -0.06515   0.02009 142.17889  -3.243  0.00147 ** 
## factor(year_factor)3 -0.05860   0.02009 142.17889  -2.917  0.00411 ** 
## factor(year_factor)4 -0.16873   0.02009 142.17889  -8.399 4.18e-14 ***
## factor(year_factor)5 -0.01183   0.02009 142.17889  -0.589  0.55688 

```

```

## factor(year_factor)6 -0.03181    0.02034 142.54598 -1.564  0.12002
## factor(year_factor)7   0.09595    0.02034 142.54598  4.718 5.62e-06 ***
## ---
## 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 fc(_)_6
## stateambint -0.522
## fctr(yr_f)_2 -0.516  0.000
## fctr(yr_f)_3 -0.516  0.000  0.500
## fctr(yr_f)_4 -0.516  0.000  0.500  0.500
## fctr(yr_f)_5 -0.516  0.000  0.500  0.500  0.500
## fctr(yr_f)_6 -0.513  0.008  0.494  0.494  0.494  0.494
## fctr(yr_f)_7 -0.513  0.008  0.494  0.494  0.494  0.494  0.491

emmeans(mod2p, list(pairwise ~ state + factor(year_factor)), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## Error in emmeans(object = object, specs = specs[[i]], name = contr.name, : No variable named state in

mod2pk.2 <- lmer(log(julian_median) ~ state + factor(year_factor) + insecticide +
  (1 | plot), kbs_flwr_plot, REML = FALSE)
anova(mod2pk, mod2pk.2)  #mod2p

## Data: kbs_flwr_plot
## Models:
## mod2pk: log(julian_median) ~ state + factor(year_factor) + (1 | plot)
## mod2pk.2: log(julian_median) ~ state + factor(year_factor) + insecticide +
## mod2pk.2:      (1 | plot)
##       npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2pk     10 -363.38 -332.27 191.69  -383.38
## mod2pk.2   11 -361.39 -327.16 191.69  -383.39 0.0029  1     0.9567

summary(mod2pk)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_median) ~ state + factor(year_factor) + (1 | plot)
## Data: kbs_flwr_plot
##
##       AIC      BIC      logLik deviance df.resid
## -363.4   -332.3    191.7    -383.4      156
##
## Scaled residuals:
##       Min     1Q   Median     3Q     Max
## -1.90904 -0.66579 -0.04988  0.53054  2.70703
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.001780 0.04219

```

```

## Residual           0.004843 0.06959
## Number of obs: 166, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 5.29354   0.01948 72.57830 271.756 < 2e-16 ***
## stateambient 0.02327   0.02034 24.16832   1.144  0.26395
## factor(year_factor)2 -0.06515   0.02009 142.17889  -3.243  0.00147 **
## factor(year_factor)3 -0.05860   0.02009 142.17889  -2.917  0.00411 **
## factor(year_factor)4 -0.16873   0.02009 142.17889  -8.399 4.18e-14 ***
## factor(year_factor)5 -0.01183   0.02009 142.17889  -0.589  0.55688
## factor(year_factor)6 -0.03181   0.02034 142.54598  -1.564  0.12002
## factor(year_factor)7  0.09595   0.02034 142.54598   4.718 5.62e-06 ***
## ---
## 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 fc(_)6
## stateambint -0.522
## fctr(yr_f)2 -0.516  0.000
## fctr(yr_f)3 -0.516  0.000  0.500
## fctr(yr_f)4 -0.516  0.000  0.500  0.500
## fctr(yr_f)5 -0.516  0.000  0.500  0.500  0.500
## fctr(yr_f)6 -0.513  0.008  0.494  0.494  0.494  0.494
## fctr(yr_f)7 -0.513  0.008  0.494  0.494  0.494  0.494  0.491

```