

warmXtrophic Project: Seed Set Phenology Analyses

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Load in packages & data

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

# Load packages
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --

## v ggplot2 3.3.3      v purrr    0.3.4
## v tibble   3.0.6      v dplyr    1.0.4
## v tidyr    1.1.2      v stringr  1.4.0
## v readr    1.4.0      vforcats  0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()

library(ggplot2)
library(lme4)

## Loading required package: Matrix

##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyR':
## 
##     expand, pack, unpack

library(lmerTest)

##
## Attaching package: 'lmerTest'
```

```

## The following object is masked from 'package:lme4':
##
##     lmer

## The following object is masked from 'package:stats':
##
##     step

library(emmeans)
library(vegan)

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-7

library(car)

## Loading required package: carData

## Registered S3 methods overwritten by 'car':
##   method           from
##   influence.merMod      lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod      lme4
##   dfbetas.influence.merMod      lme4

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some

library(rstatix)

##
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':
##
##     filter

```

```

library(scales)

##
## Attaching package: 'scales'

## The following object is masked from 'package:purrr':
##
##     discard

## The following object is masked from 'package:readr':
##
##     col_factor

library(fitdistrplus)

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:rstatix':
##
##     select

## The following object is masked from 'package:dplyr':
##
##     select

## Loading required package: survival

library(moments) # for calculating skewness of data
library(ggpubr)
library(jtools) # summ() function
library(predictmeans)

## Loading required package: nlme

##
## Attaching package: 'nlme'

## The following object is masked from 'package:lme4':
##
##     lmList

## The following object is masked from 'package:dplyr':
##
##     collapse

## Loading required package: parallel

```

```

library(olsrr)

##
## Attaching package: 'olsrr'

## The following object is masked from 'package:MASS':
##
##     cement

## The following object is masked from 'package:datasets':
##
##     rivers

library(car)
library(fitdistrplus)
library(ggpubr)
library(interactions)
library(sjPlot)
library(effects)

## Use the command
##     lattice:::trellis.par.set(effectsTheme())
## to customize lattice options for effects plots.
## See ?effectsTheme for details.

library(glmmTMB)
library(GGally)  # ggpairs() function

## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2

##
## Attaching package: 'GGally'

## The following object is masked from 'package:emmeans':
##
##     pigs

library(bbmle)  # AICtab() function

## Loading required package: stats4

##
## Attaching package: 'bbmle'

## The following object is masked from 'package:dplyr':
##
##     slice

```

```

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

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

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
sd_species <- read.csv(file.path(L2_dir, "phenology/final_sd_species_L2.csv")) # species level data
sd_plot <- read.csv(file.path(L2_dir, "phenology/final_sd_plot_L2.csv")) # plot level data
sd_plot_origin <- read.csv(file.path(L2_dir, "phenology/final_sd_plot_origin_L2.csv")) # plot level data
sd_plot_growthhabit <- read.csv(file.path(L2_dir, "phenology/final_sd_plot_growthhabit_L2.csv")) # plot level data

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

sd_species$julian_min <- as.numeric(as.integer(sd_species$julian_min))
sd_plot$julian_min <- as.numeric(as.integer(sd_plot$julian_min))

# 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
sd_species$state <- as.factor(sd_species$state)
levels(sd_species$state)

## [1] "ambient" "warmed"

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

## [1] "warmed" "ambient"

# [1] 'warmed' 'ambient'

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

## [1] "ambient" "warmed"

```

```

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

## [1] "warmed"   "ambient"

# [1] 'warmed' 'ambient'

# make the year_factor a factor
sd_plot$year_factor <- as.factor(sd_plot$year_factor)
sd_species$year_factor <- as.factor(sd_species$year_factor)

umbs_sd_plot <- subset(sd_plot, site == "umbs") # pull out umbs only data at plot level
umbs_sd_plot <- subset(umbs_sd_plot, year != "2021") # delete 2021 data from umbs dataframe (doesn't matter)
umbs_sd_spp <- subset(sd_species, site == "umbs") # pull out umbs only data at species level
umbs_sd_spp <- subset(umbs_sd_spp, year != "2021") # delete 2021 data from umbs dataframe (doesn't matter)
kbs_sd_plot <- subset(sd_plot, site == "kbs") # pull out kbs only data at plot level
kbs_sd_spp <- subset(sd_species, site == "kbs") # pull out kbs only data at species level
kbs_sd_plot_origin <- subset(sd_plot_origin, site == "kbs")
kbs_sd_plot_growthhabit <- subset(sd_plot_growthhabit, site == "kbs")
umbs_sd_plot_origin <- subset(sd_plot_origin, site == "umbs")
umbs_sd_plot_origin <- subset(umbs_sd_plot_origin, year != "2021") # delete 2021 data
umbs_sd_plot_growthhabit <- subset(sd_plot_growthhabit, site == "umbs")
umbs_sd_plot_growthhabit <- subset(umbs_sd_plot_growthhabit, year != "2021") # delete 2021 data

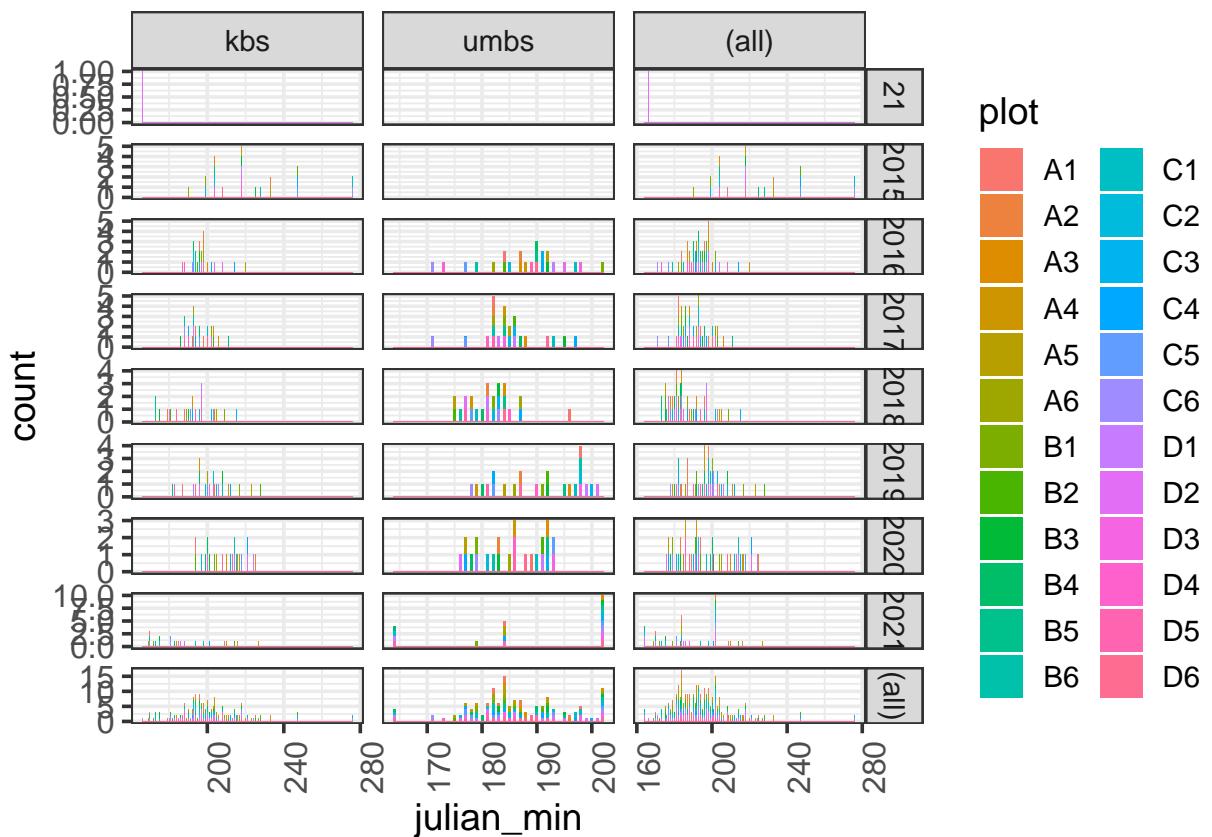
```

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

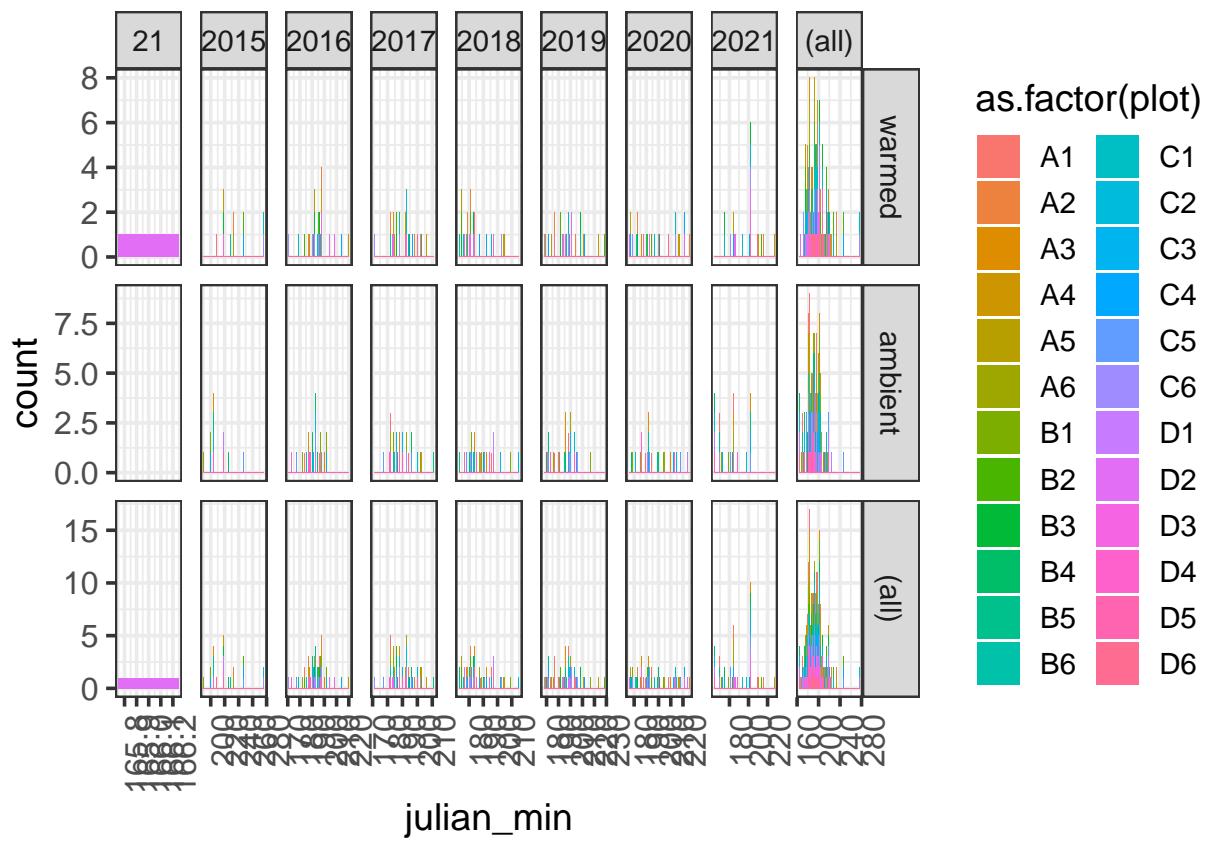
```

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

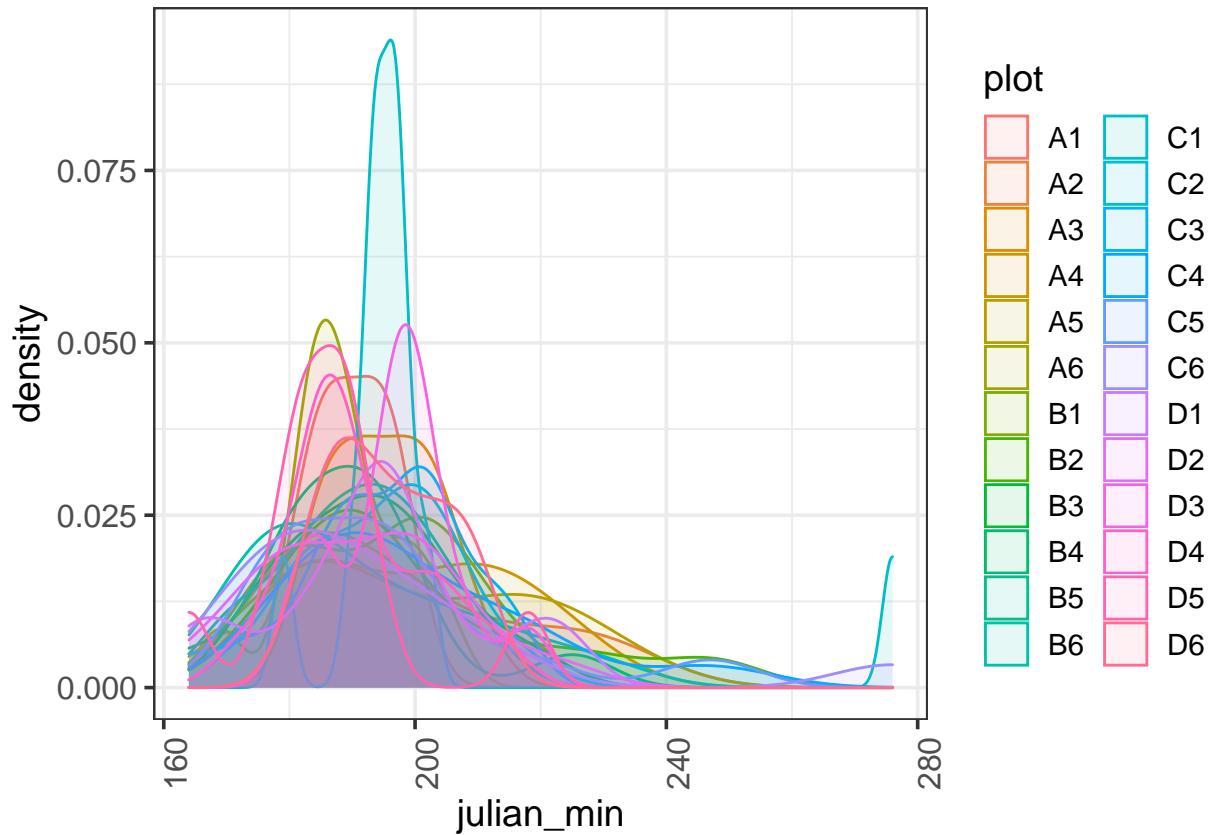
```



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



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



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



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

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## Inf

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

```

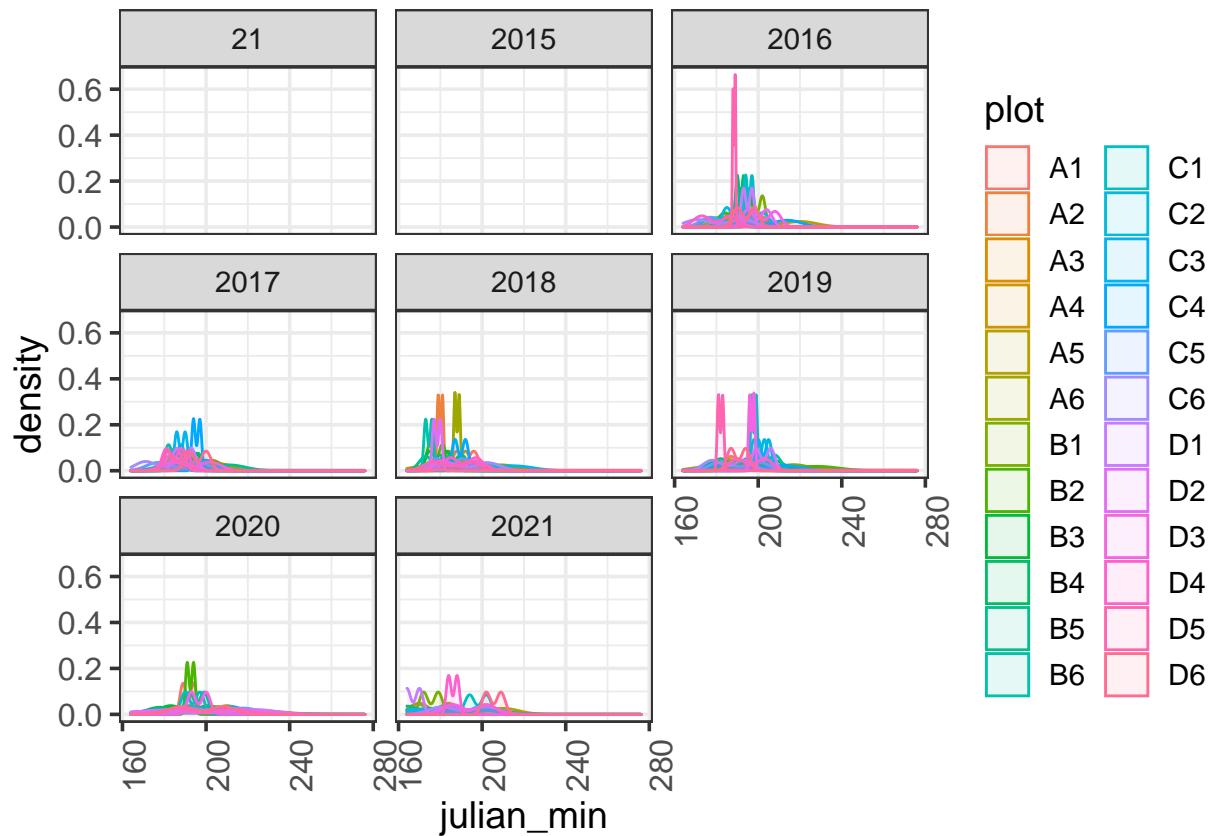
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

## 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

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

```



```

ggplot(sd_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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## Inf

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## Inf

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

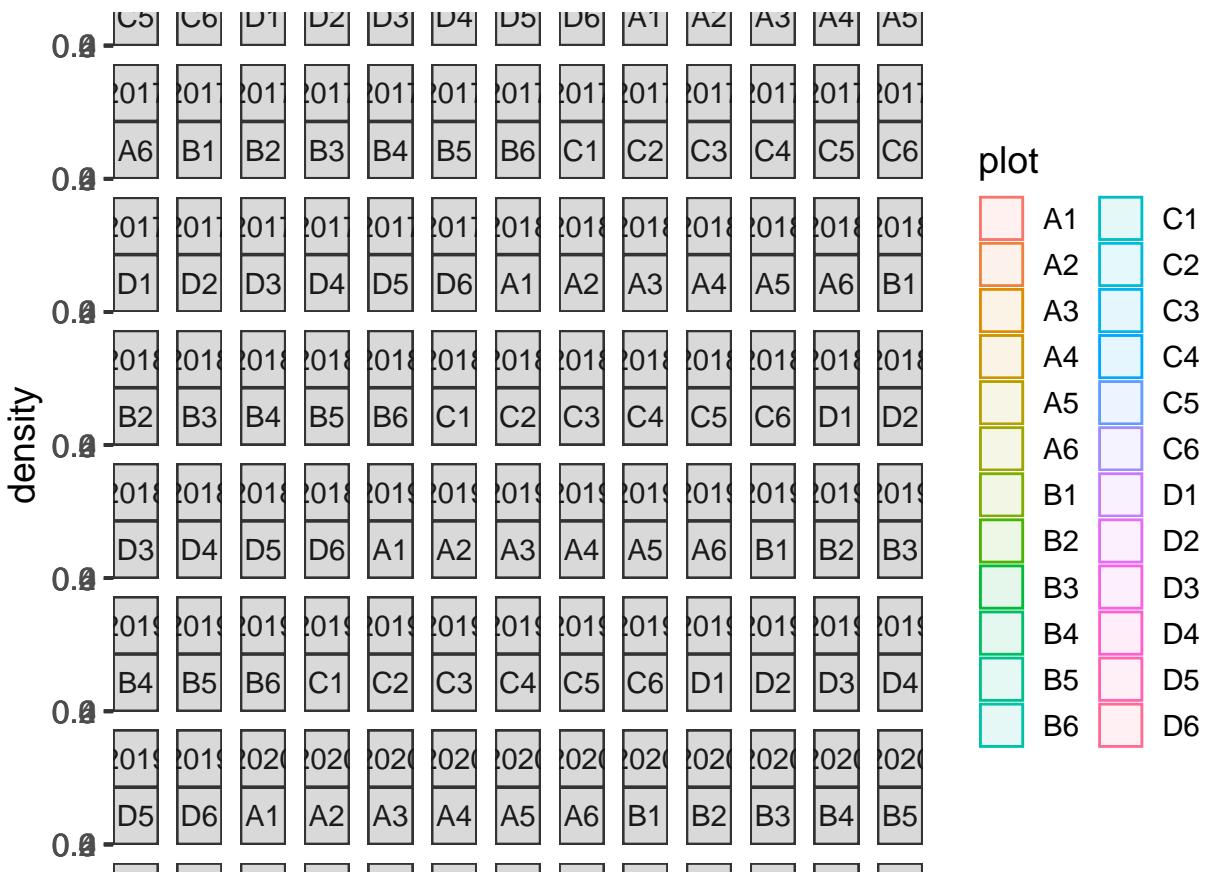
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

## 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

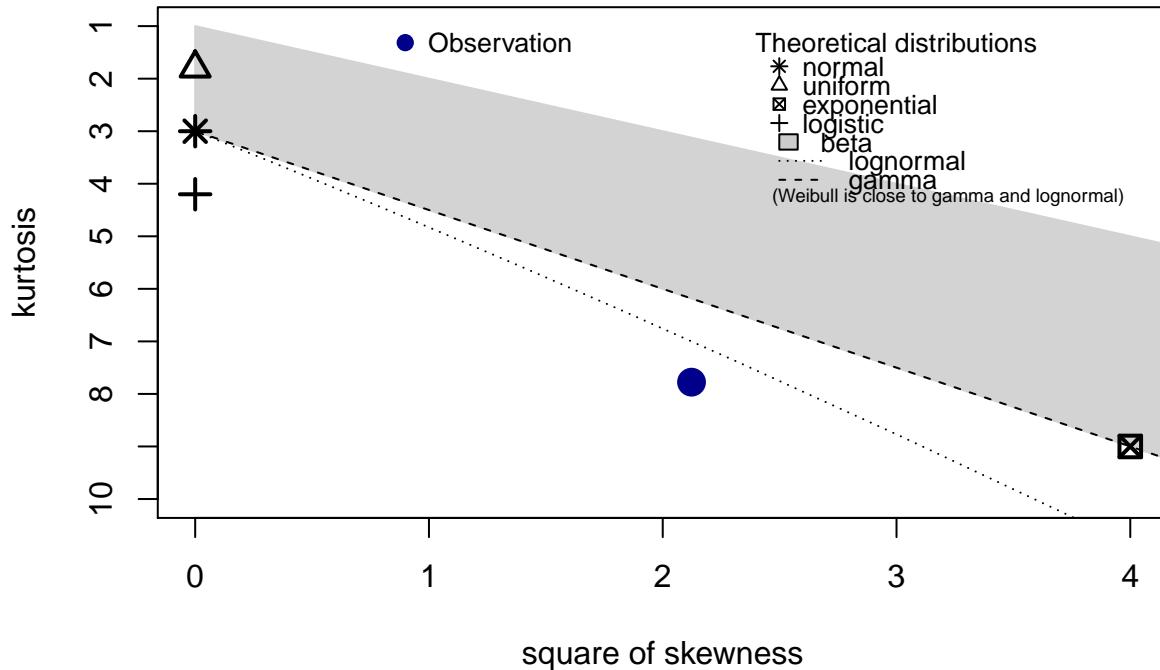
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning -
## Inf

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



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

Cullen and Frey graph

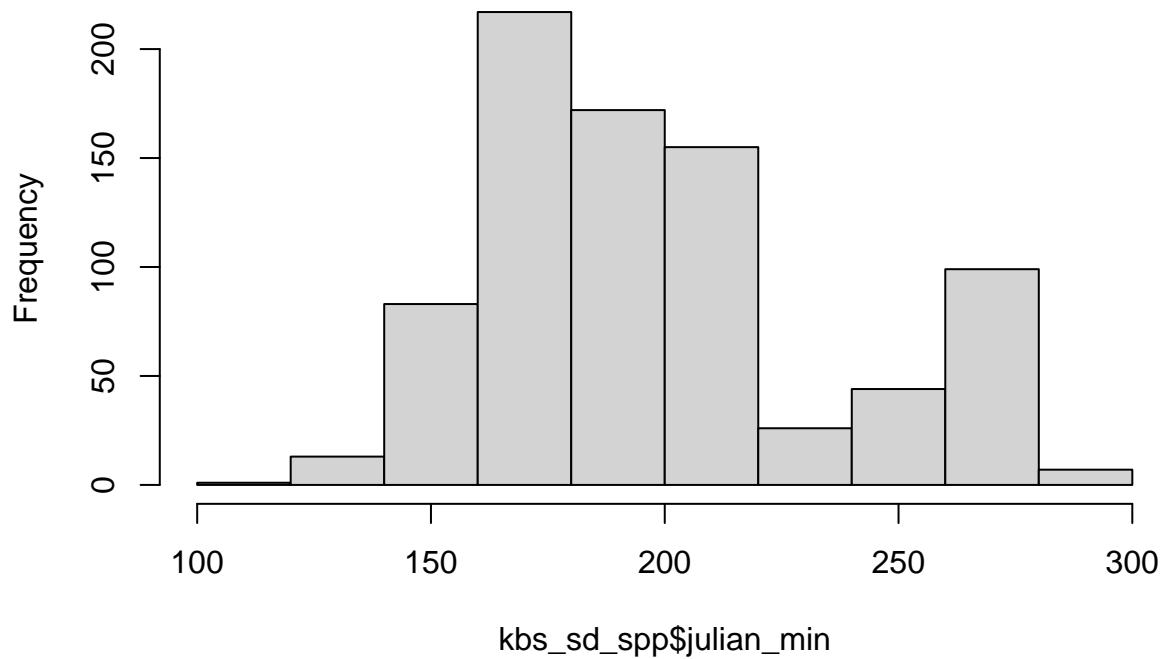


```
## summary statistics
## -----
## min: 164   max: 276
## median: 193
## mean: 194.2361
## estimated sd: 15.68764
## estimated skewness: 1.45713
## estimated kurtosis: 7.776184
```

**KBS SPECIES LEVEL - Looking at MINIMUM JULIAN DAY
(aka date of observed first seed set)**

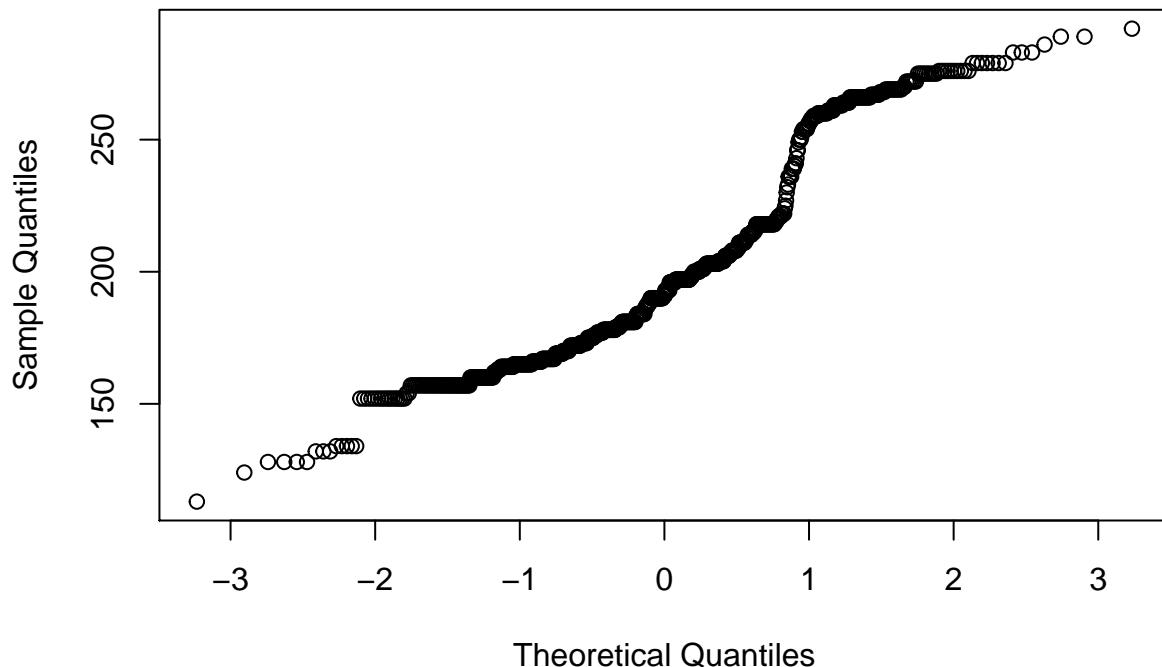
```
### KBS ####
hist(kbs_sd_spp$julian_min)
```

Histogram of kbs_sd_spp\$julian_min



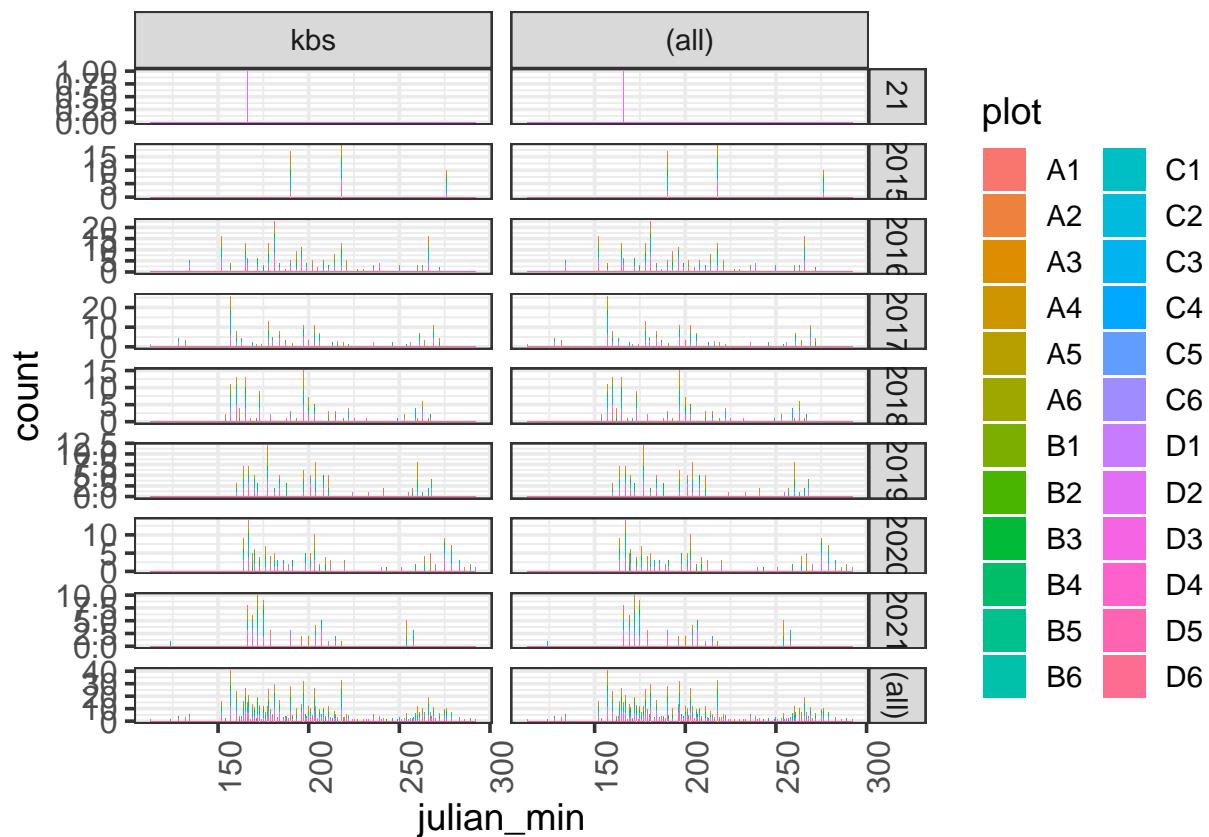
```
qqnorm(kbs_sd_spp$julian_min)
```

Normal Q-Q Plot

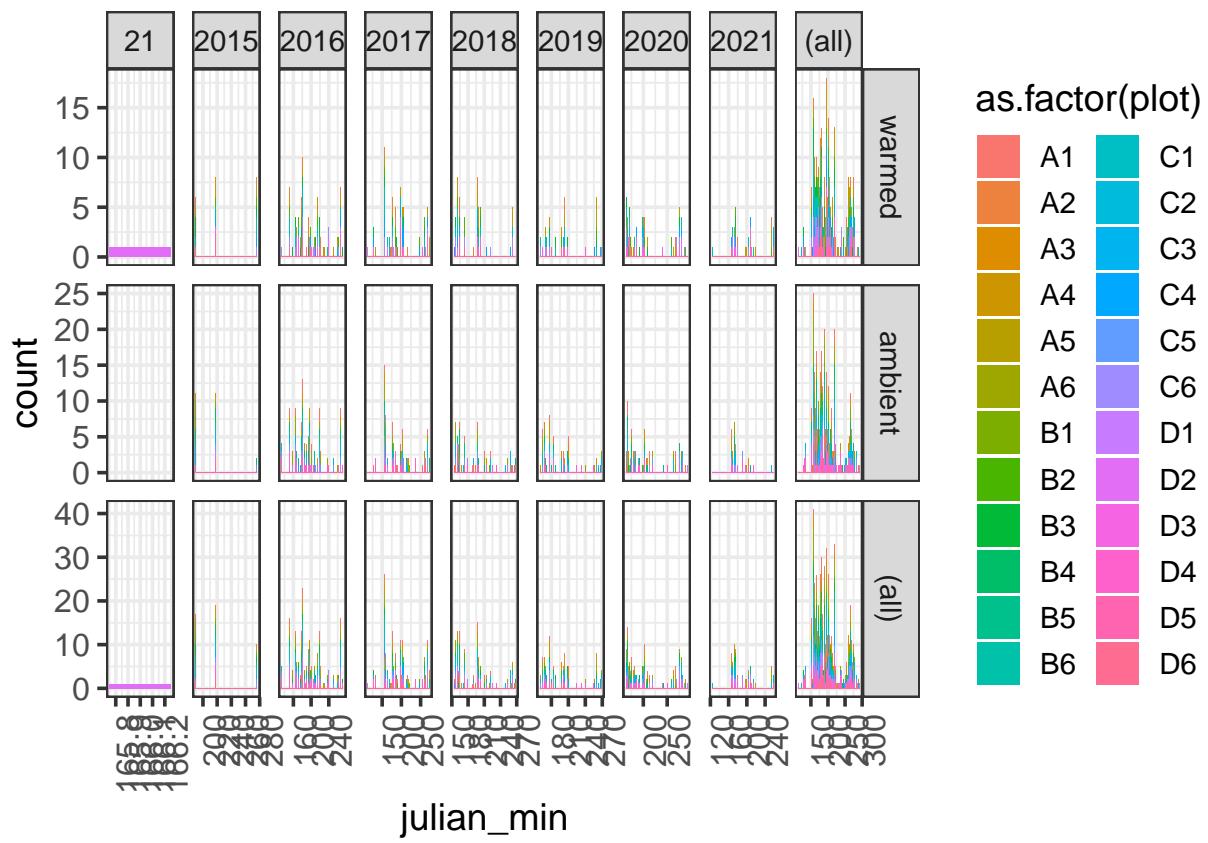


```
shapiro.test(kbs_sd_spp$julian_min) # pvalue is < 0.05 so we reject the null hypothesis that the data
```

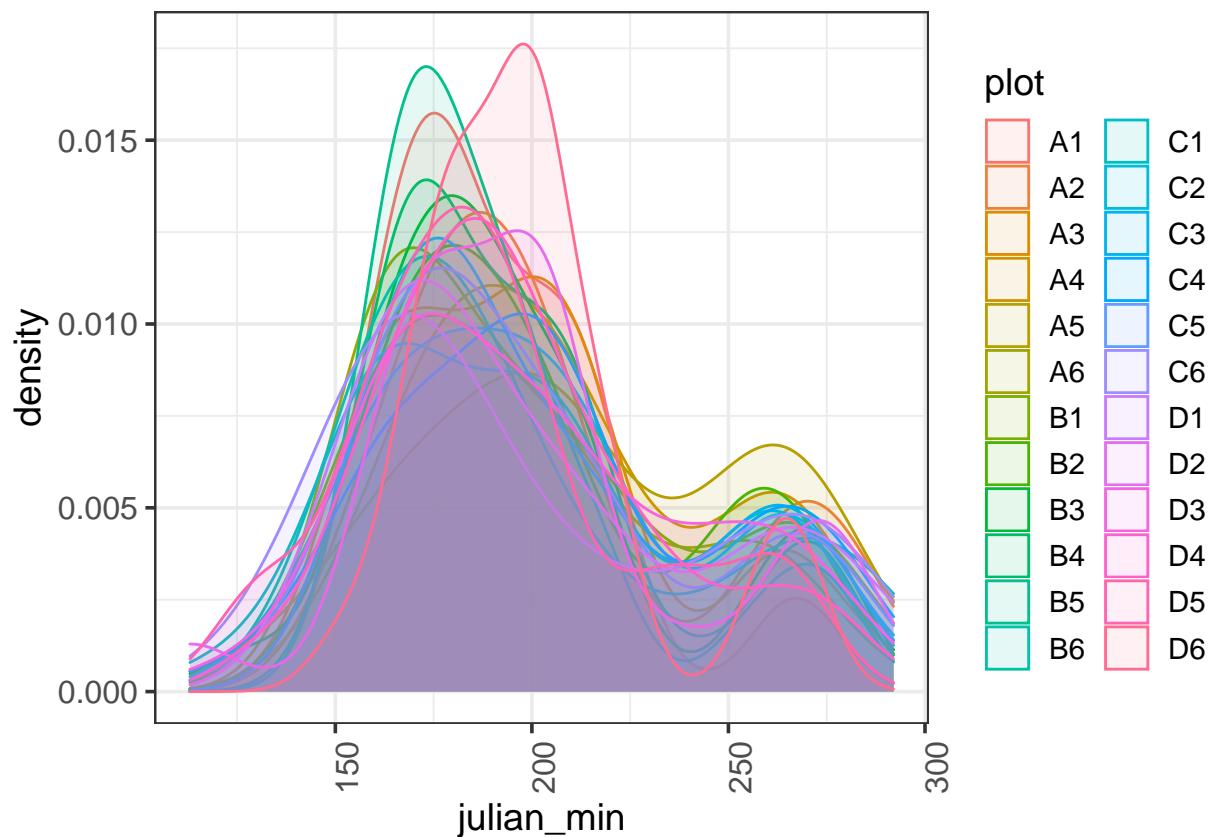
```
##  
## Shapiro-Wilk normality test  
##  
## data: kbs_sd_spp$julian_min  
## W = 0.91991, p-value < 2.2e-16  
  
# Visualizing first Julian date for kbs at the SPECIES LEVEL  
ggplot(kbs_sd_spp, aes(julian_min, fill = plot)) + geom_histogram(binwidth = 0.5) +  
  facet_grid(year ~ site, margins = TRUE, scales = "free")
```



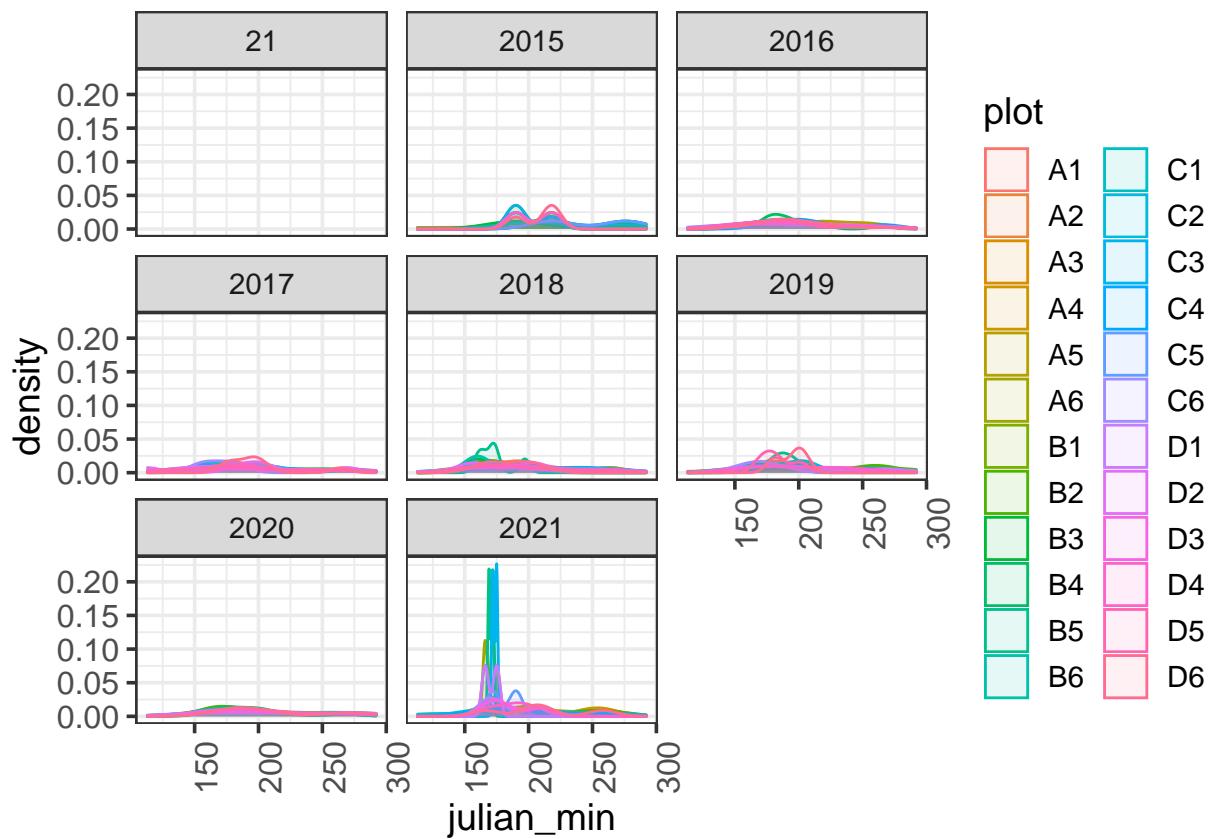
```
ggplot(kbs_sd_spp, aes(julian_min, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +  
  facet_grid(state ~ year, margins = TRUE, scales = "free")
```



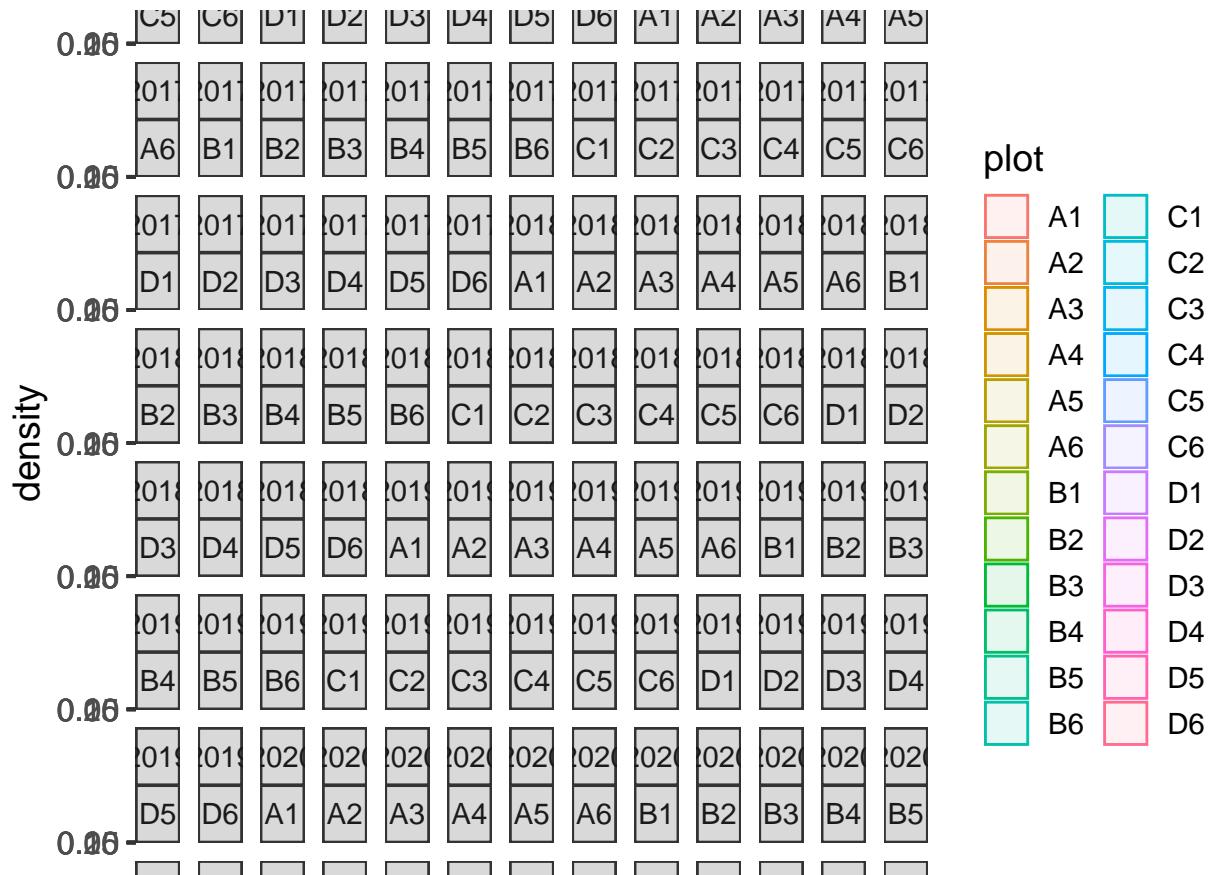
```
ggplot(kbs_sd_spp, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

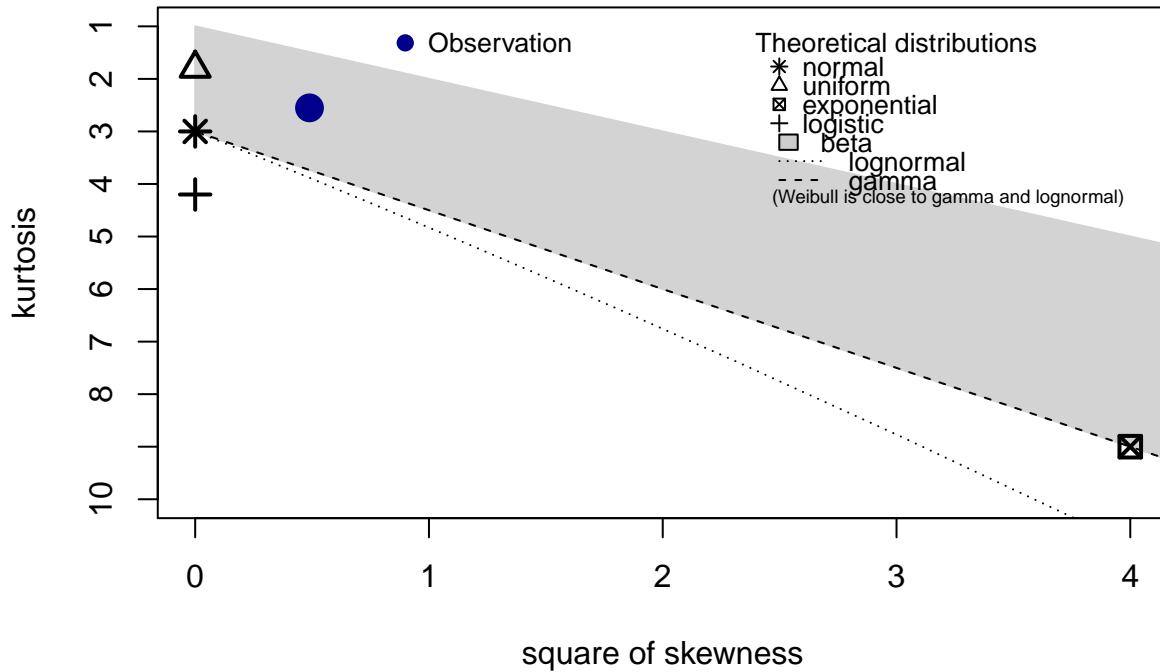


```
ggplot(kbs_sd_spp, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions
descdist(kbs_sd_spp$julian_min, discrete = FALSE)
```

Cullen and Frey graph

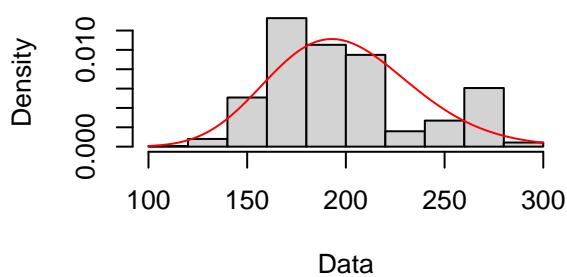
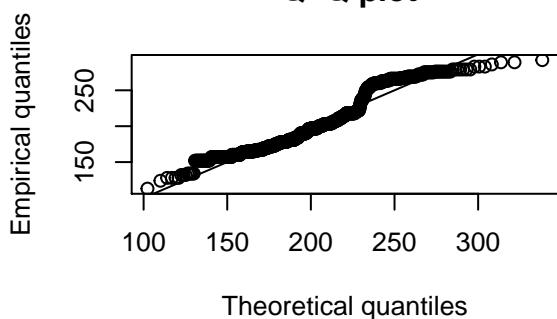
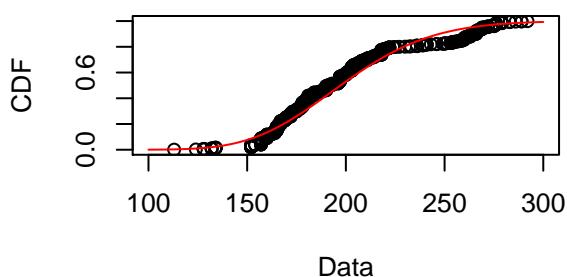
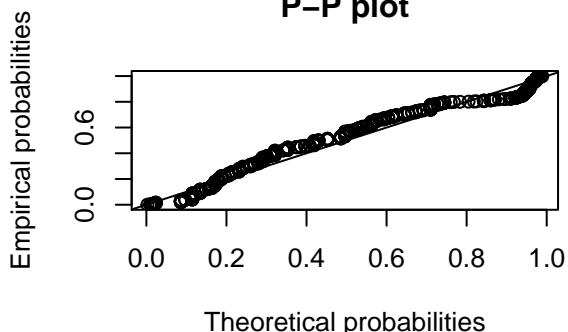


```

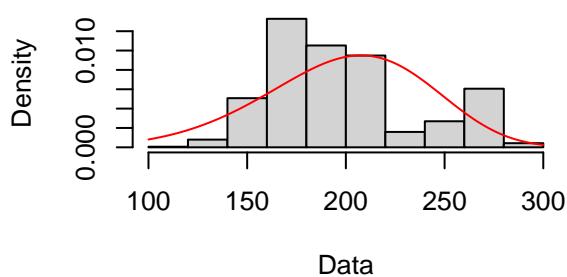
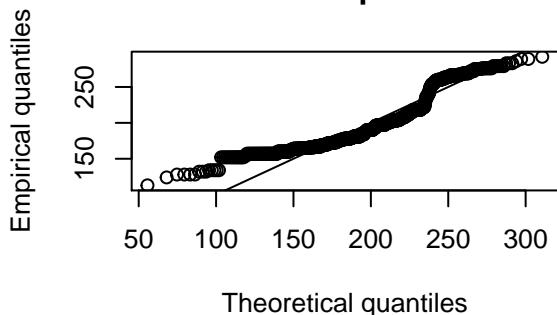
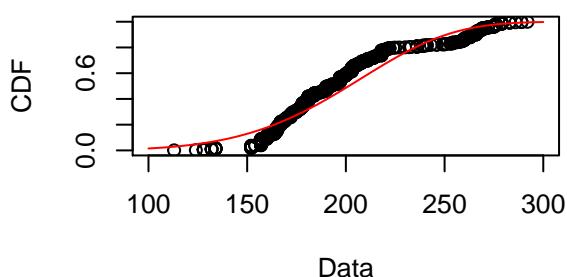
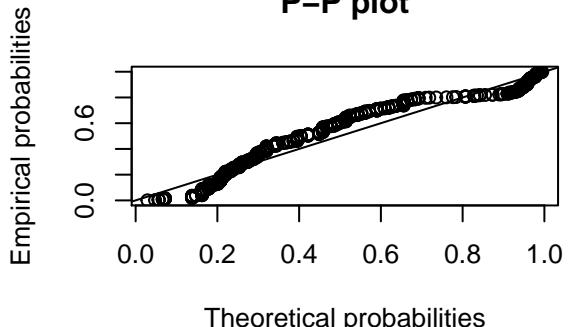
## summary statistics
## -----
## min: 113  max: 292
## median: 191
## mean: 199.5165
## estimated sd: 37.4115
## estimated skewness: 0.6993432
## estimated kurtosis: 2.551332

# Gamma distribution
fit.gamma <- fitdist(kbs_sd_spp$julian_min, "gamma")
plot(fit.gamma)

```

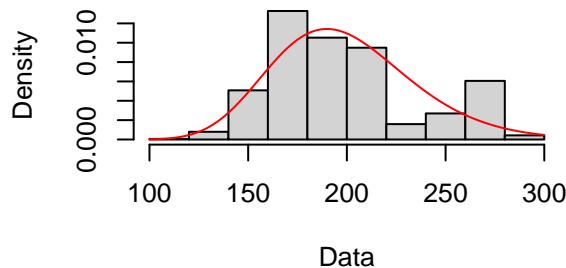
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

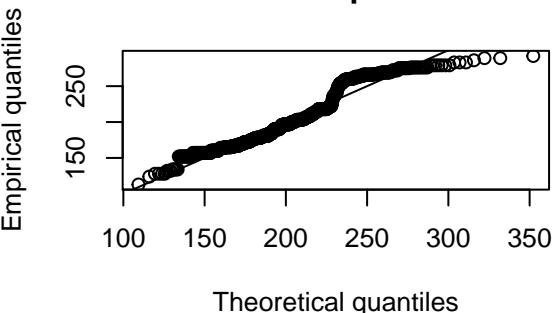
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

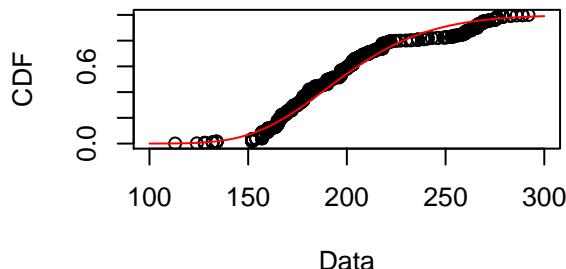
Empirical and theoretical dens.



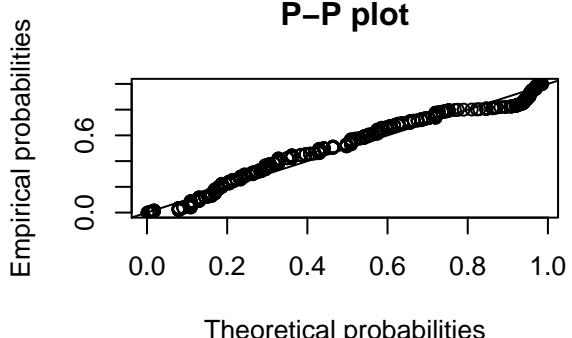
Q-Q plot



Empirical and theoretical CDFs

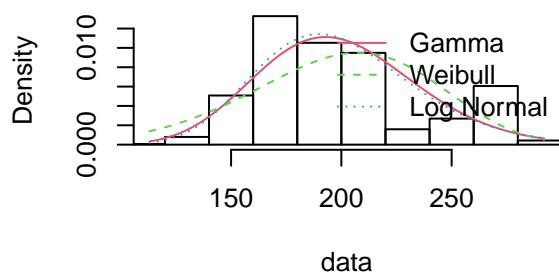


P-P plot

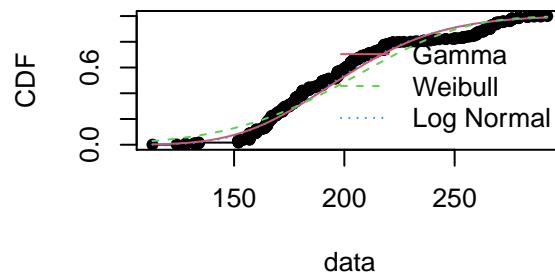


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

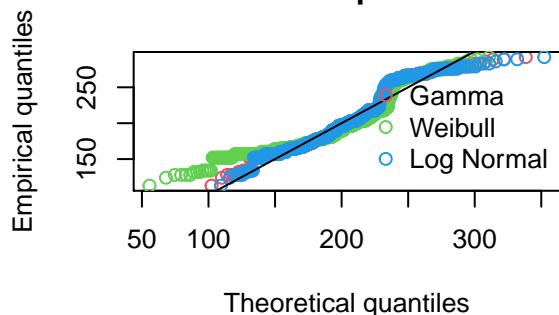
Histogram and theoretical densities



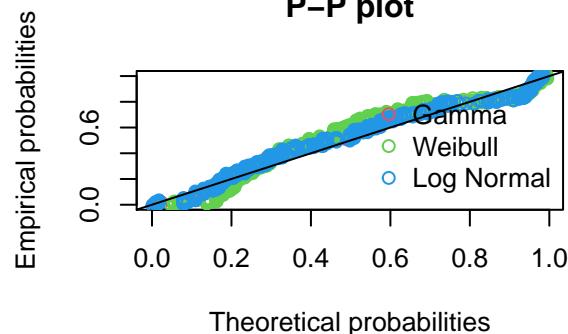
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

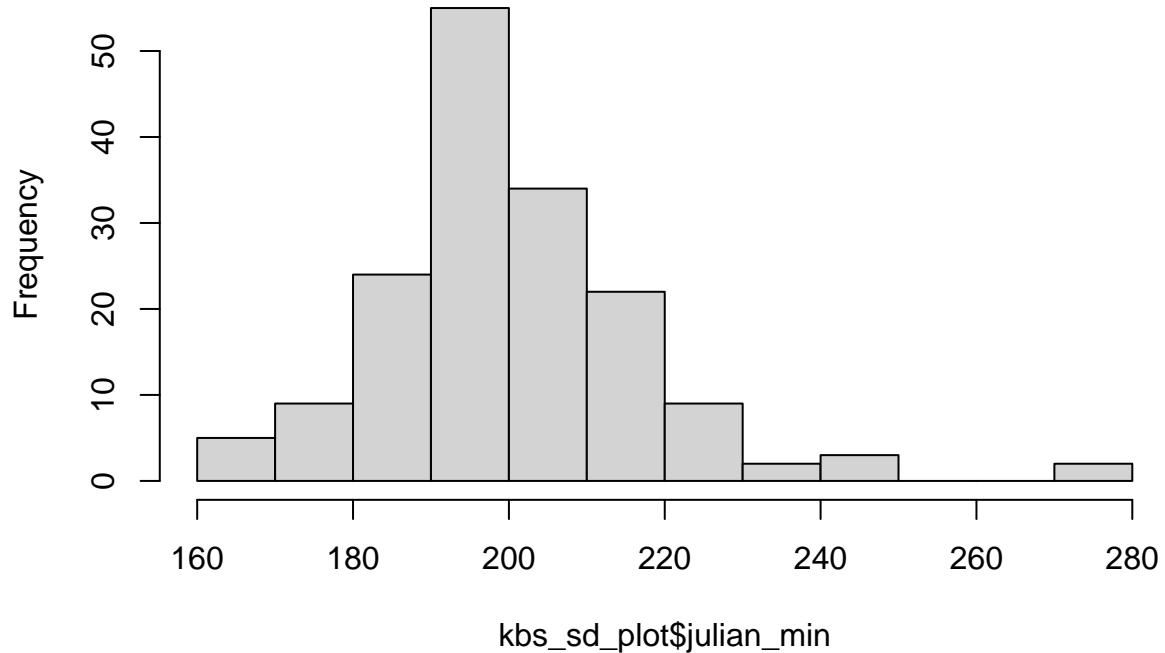
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull  Log Normal
## Kolmogorov-Smirnov statistic 0.09988396 0.1360783 0.09317306
## Cramer-von Mises statistic   2.41253973 5.0192692 1.88913912
## Anderson-Darling statistic  17.07536252 30.9119372 14.02047891
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull  Log Normal
## Akaike's Information Criterion 8177.095 8325.080 8155.683
## Bayesian Information Criterion 8186.506 8334.491 8165.094
```

```
# Lognormal is better - going with a lognormal transformation for kbs seed set at
# the species level
```

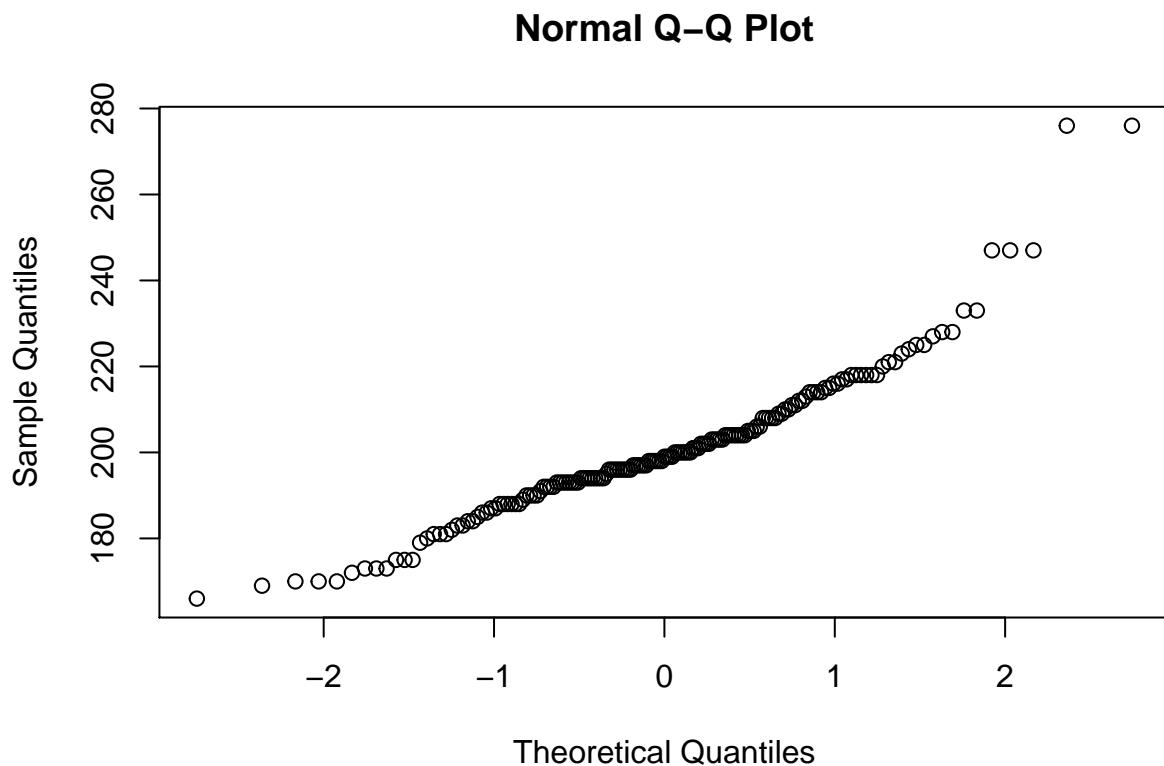
KBS PLOT LEVEL - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

```
### KBS ####
hist(kbs_sd_plot$julian_min)
```

Histogram of kbs_sd_plot\$julian_min



```
qqnorm(kbs_sd_plot$julian_min)
```



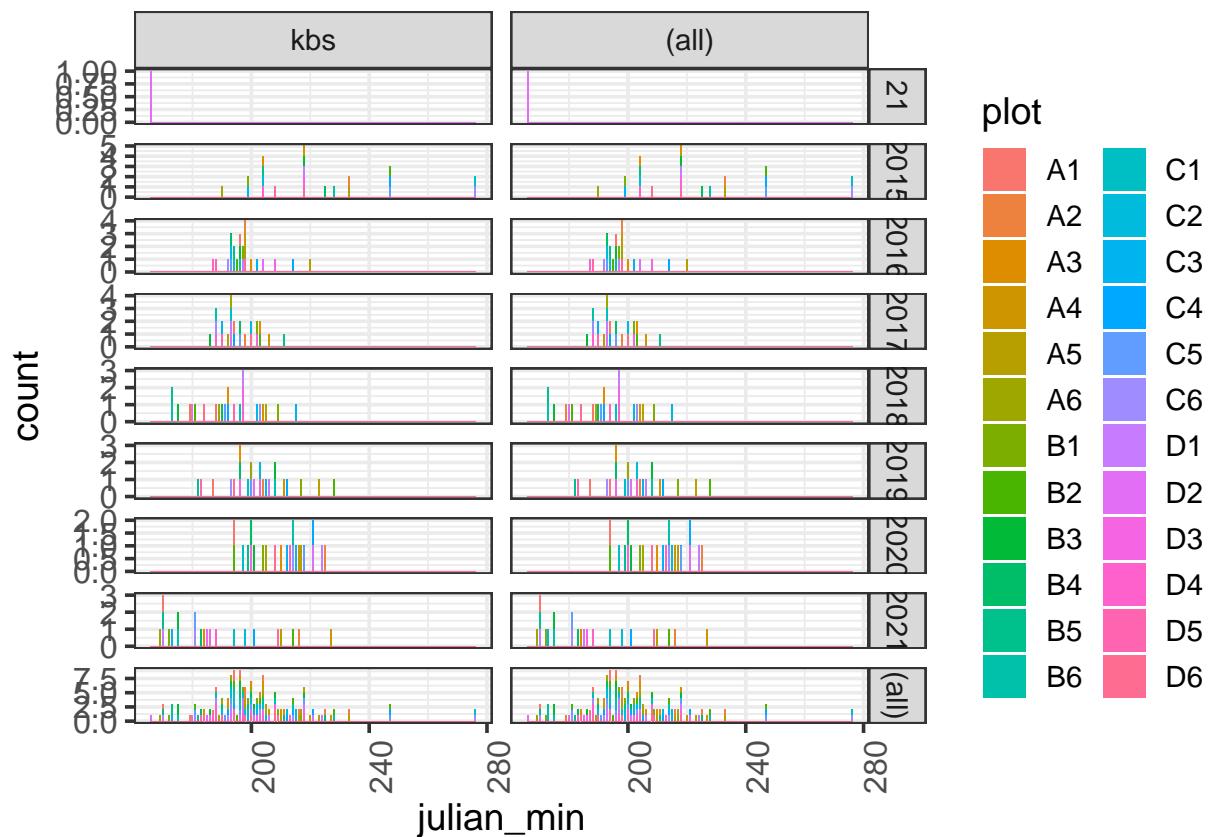
```

shapiro.test(kbs_sd_plot$julian_min) # pvalue is < 0.05 so we reject the null hypothesis that the data

## 
## Shapiro-Wilk normality test
## 
## data: kbs_sd_plot$julian_min
## W = 0.92701, p-value = 2.091e-07

# Visualizing first Julian date for kbs at the PLOT LEVEL
ggplot(kbs_sd_plot, aes(julian_min, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

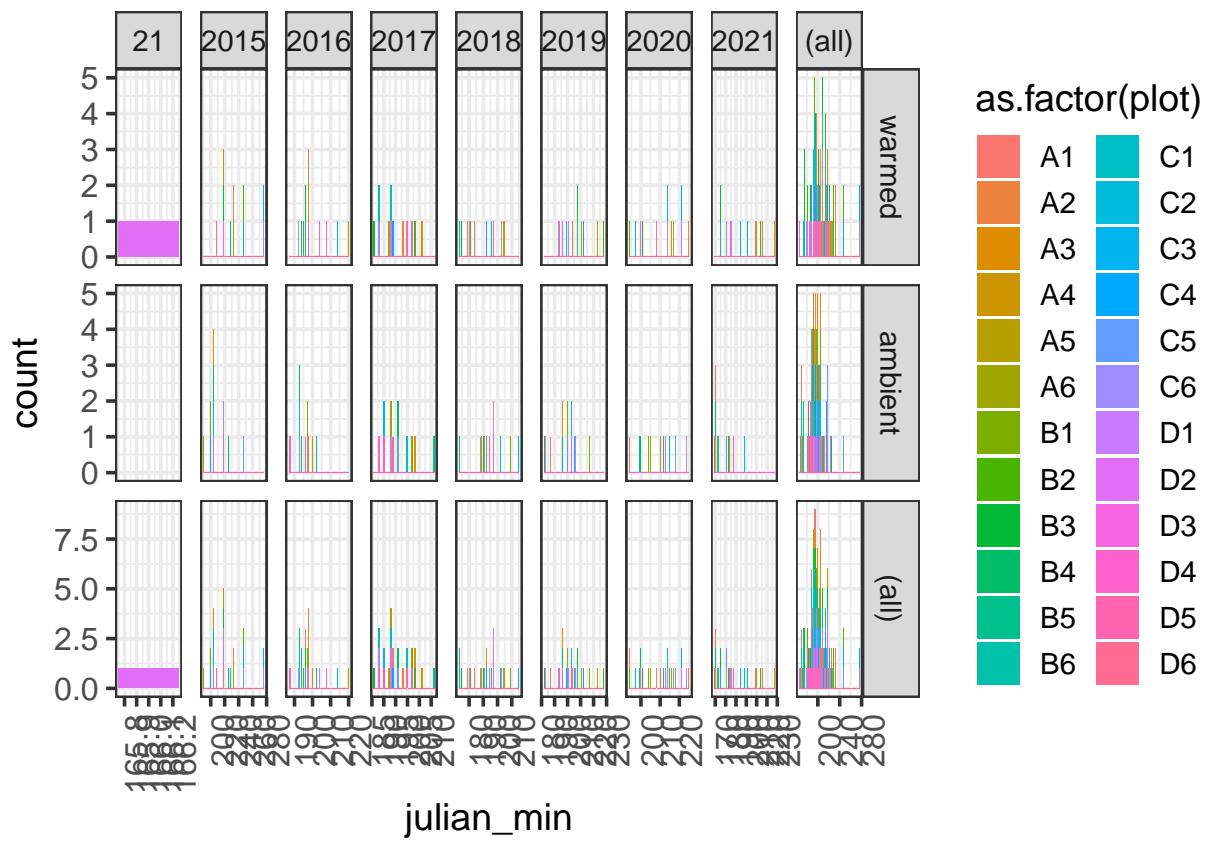
```



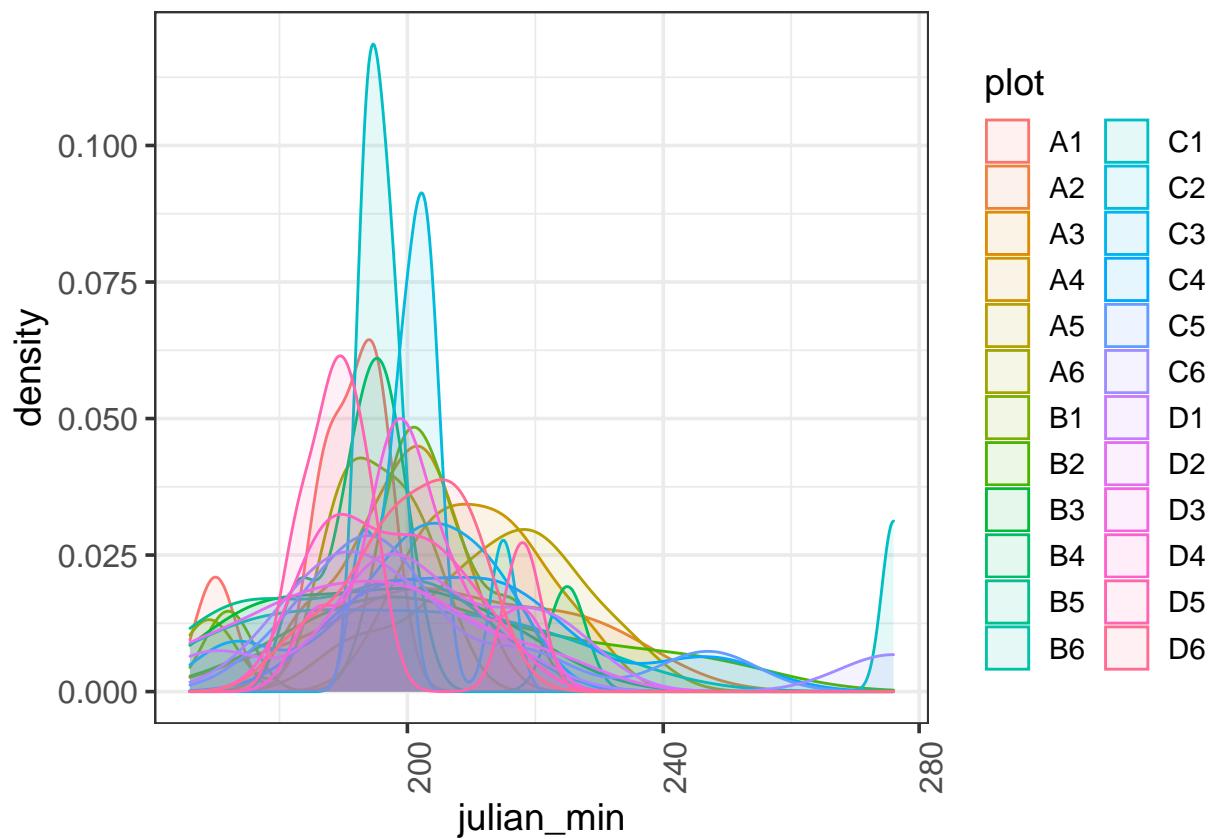
```

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

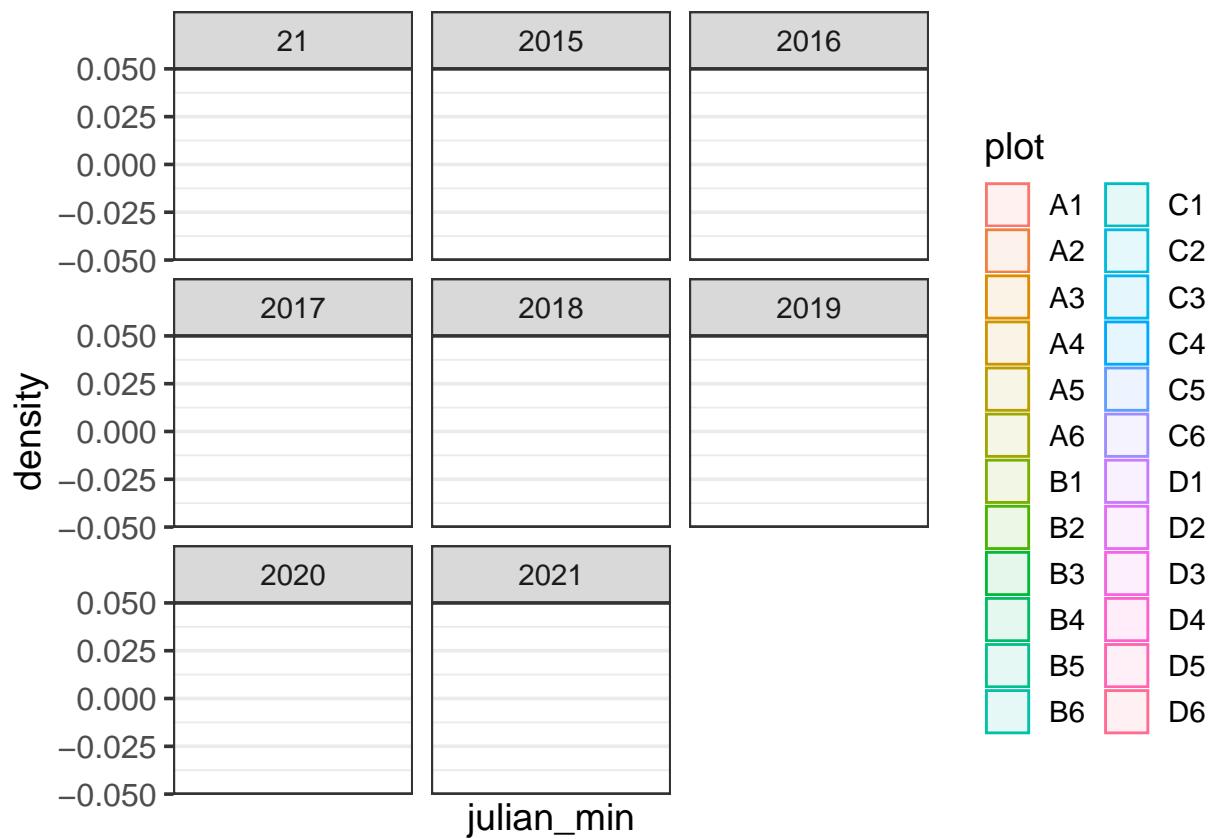
```



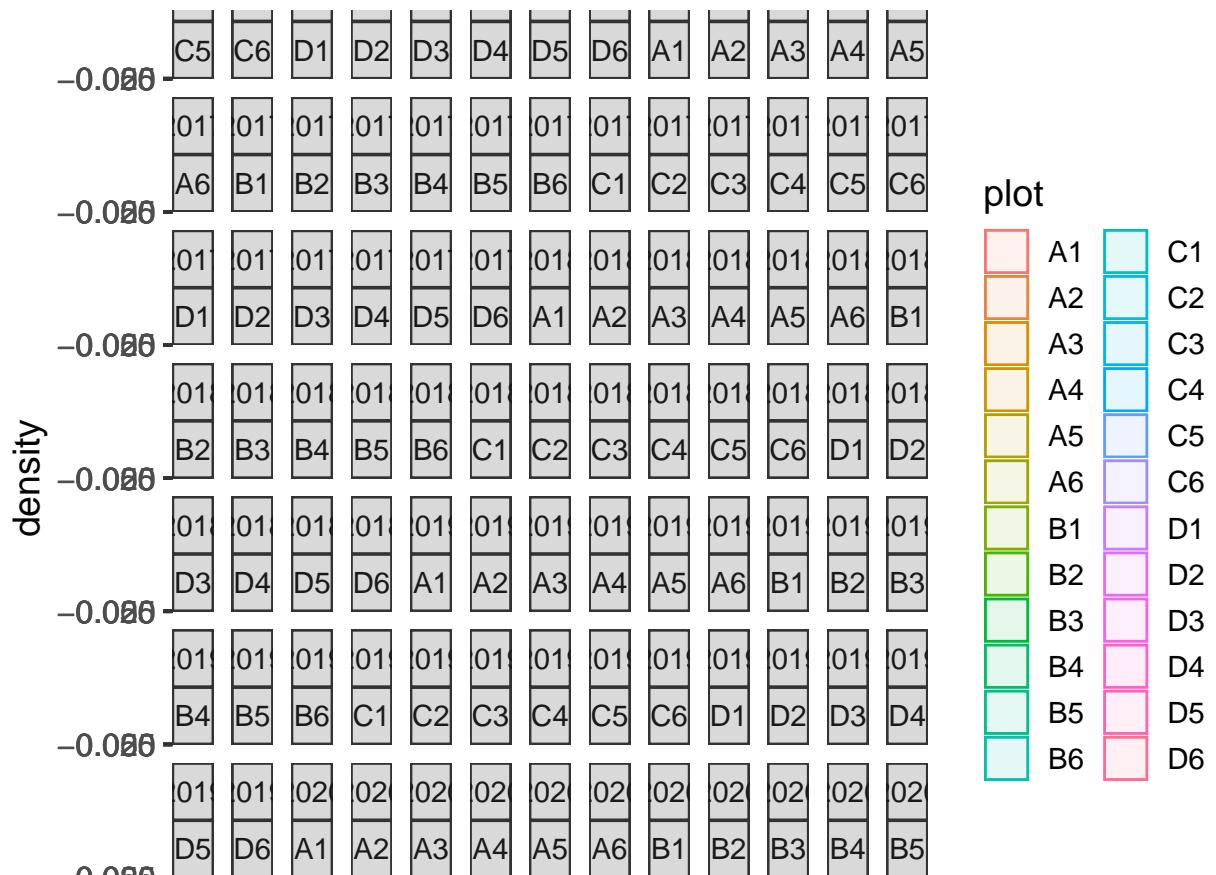
```
ggplot(kbs_sd_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

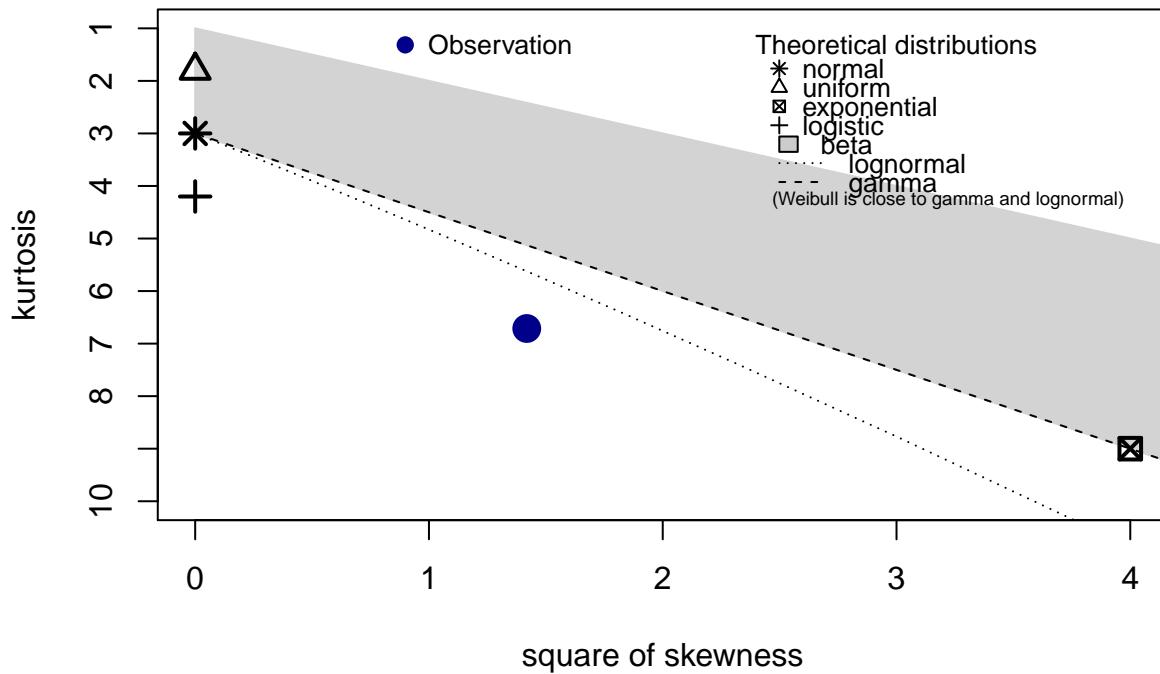


```
ggplot(kbs_sd_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



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

Cullen and Frey graph

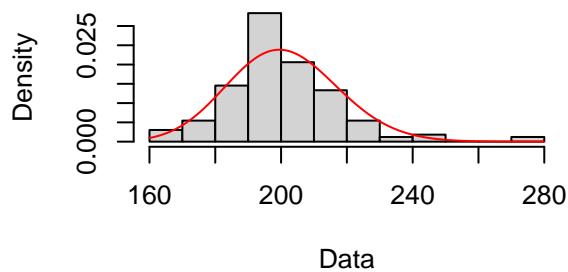
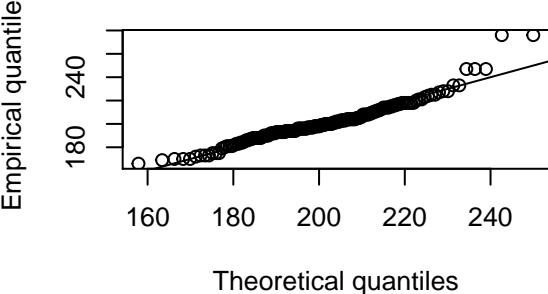
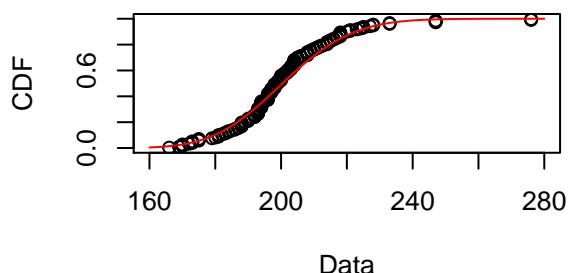
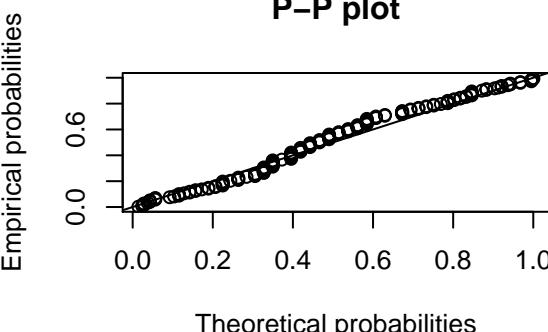


```

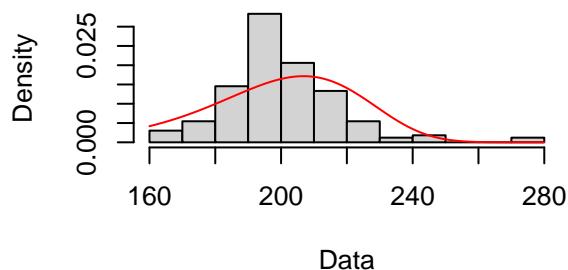
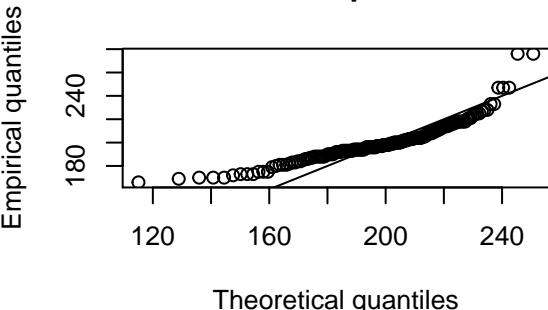
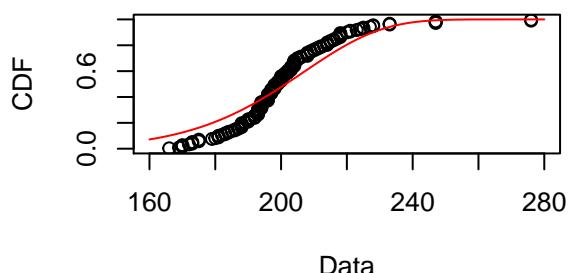
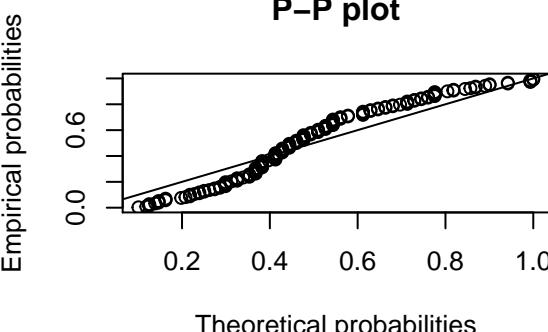
## summary statistics
## -----
## min: 166   max: 276
## median: 199
## mean: 200.8727
## estimated sd: 17.24966
## estimated skewness: 1.190949
## estimated kurtosis: 6.712314

# Gamma distribution
fit.gamma <- fitdist(kbs_sd_plot$julian_min, "gamma")
plot(fit.gamma)

```

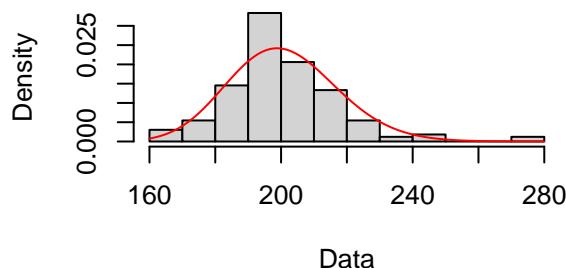
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

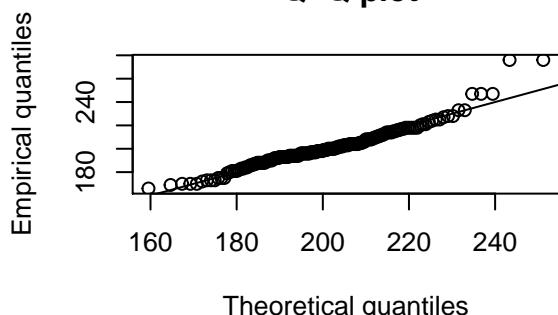
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

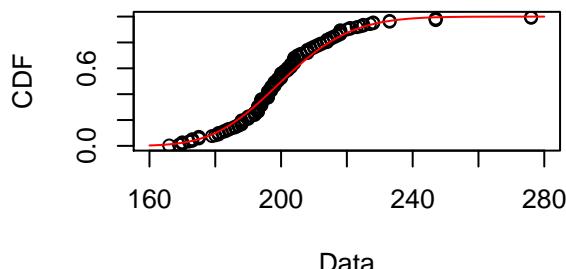
Empirical and theoretical dens.



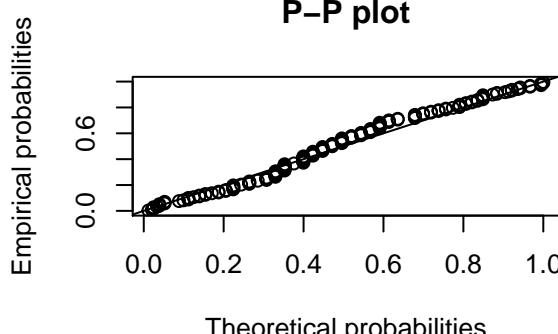
Q-Q plot



Empirical and theoretical CDFs

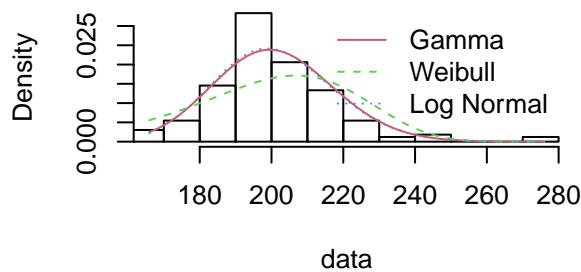


P-P plot

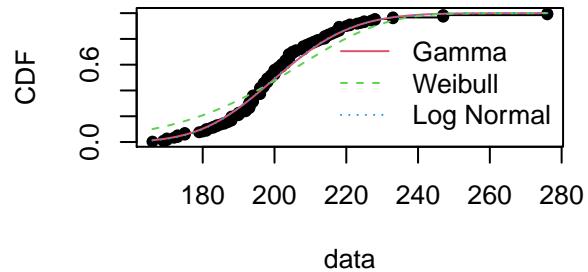


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

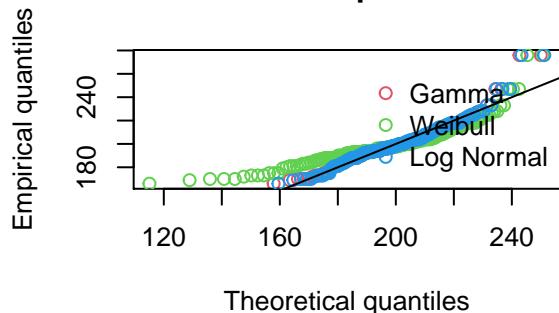
Histogram and theoretical densities



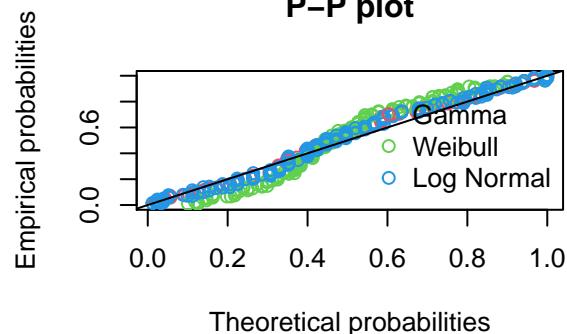
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

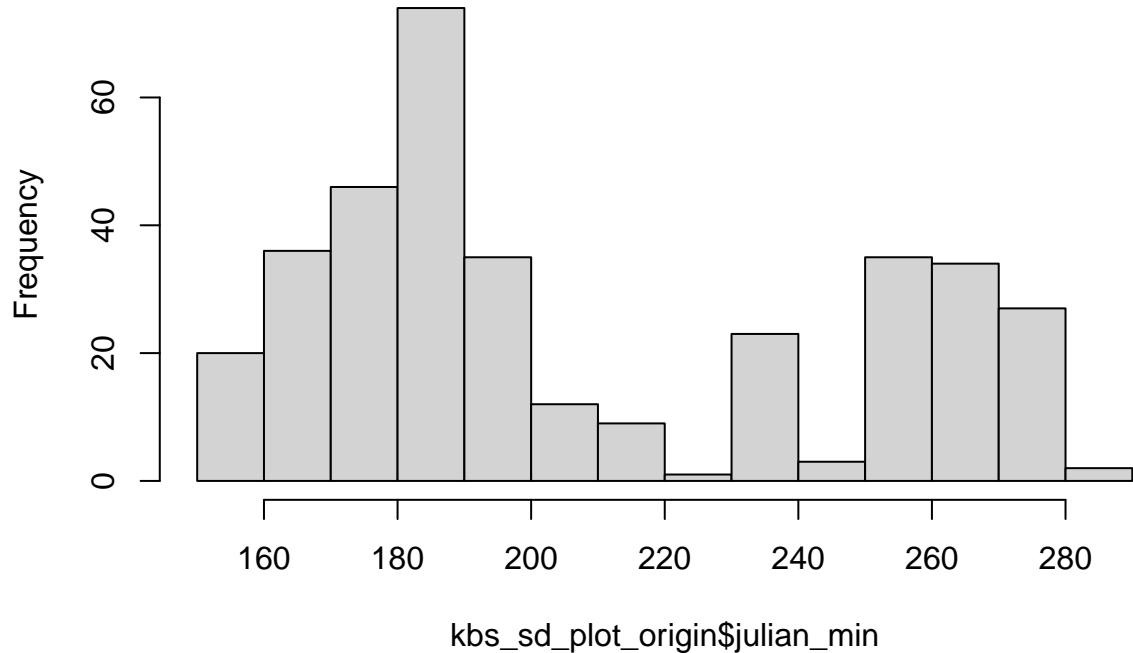
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1004296 0.1422884 0.09428196
## Cramer-von Mises statistic   0.2949814 1.3843015 0.25734148
## Anderson-Darling statistic   1.6842999 8.4222832 1.47267311
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 1402.059 1473.678 1398.466
## Bayesian Information Criterion 1408.271 1479.890 1404.678
```

```
# Lognormal is better - going with a lognormal transformation for kbs seed set at
# the plot level
```

KBS PLOT LEVEL ORIGIN - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

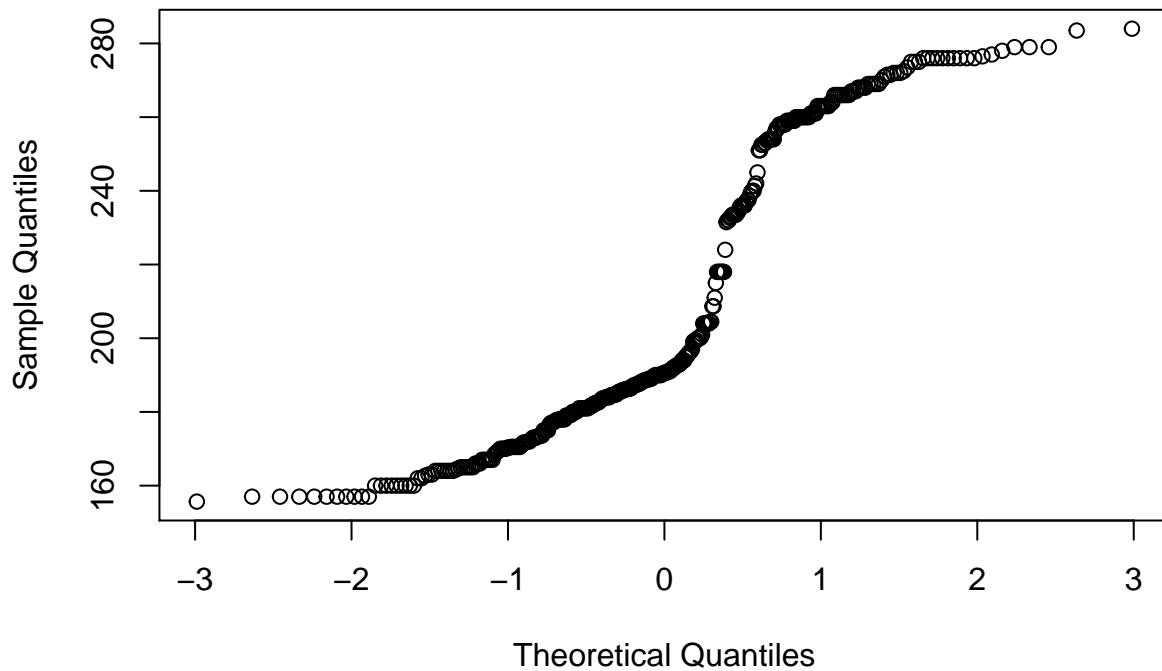
```
### KBS ####
hist(kbs_sd_plot_origin$julian_min)
```

Histogram of kbs_sd_plot_origin\$julian_min



```
qqnorm(kbs_sd_plot_origin$julian_min)
```

Normal Q-Q Plot



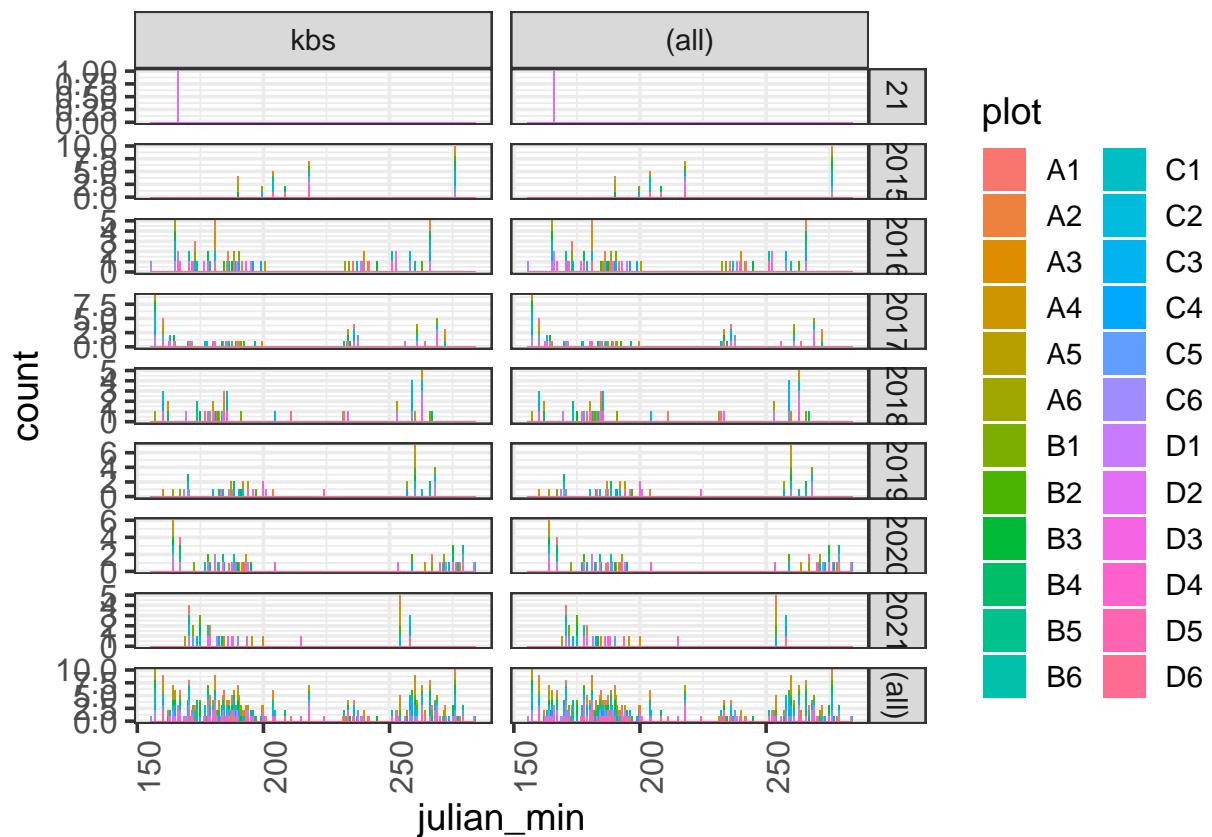
```

shapiro.test(kbs_sd_plot_origin$julian_min) # pvalue is < 0.05 so we reject the null hypothesis that t

## 
## Shapiro-Wilk normality test
## 
## data: kbs_sd_plot_origin$julian_min
## W = 0.87068, p-value < 2.2e-16

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

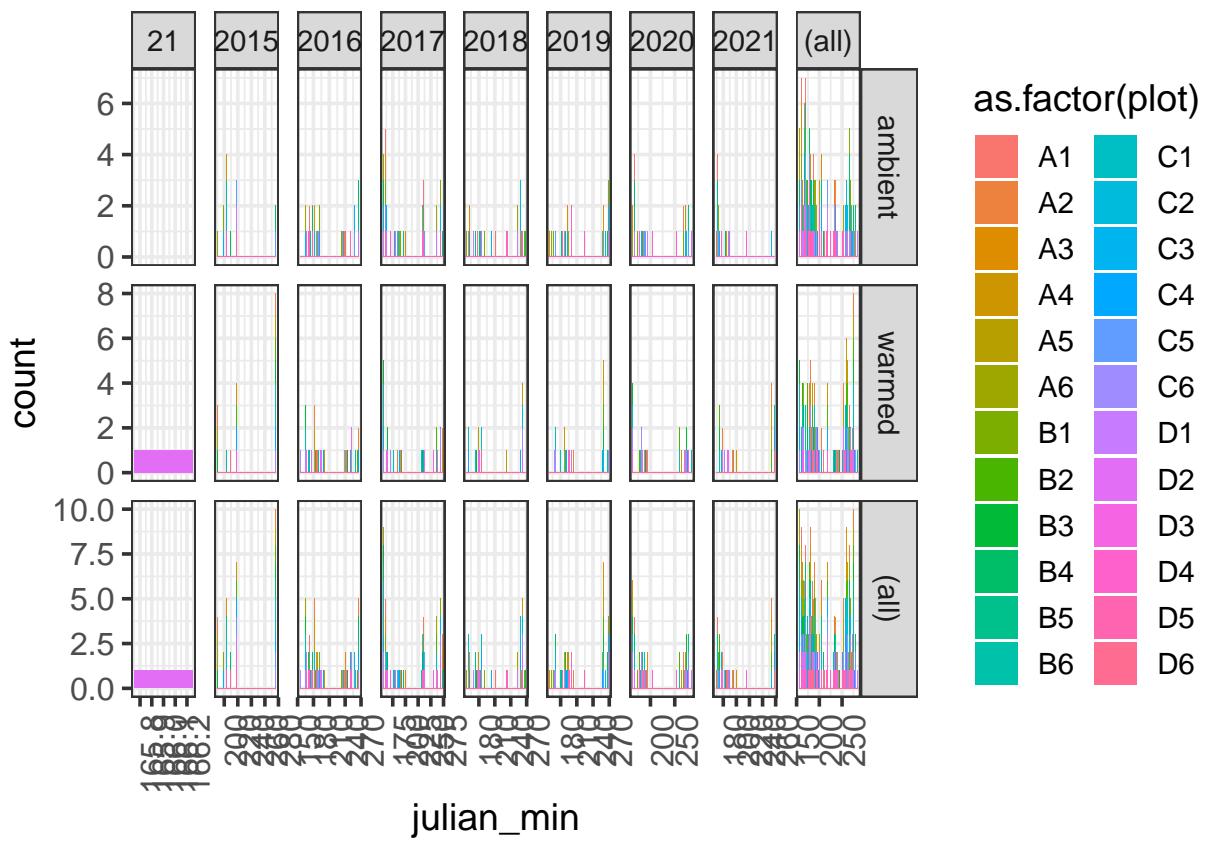
```



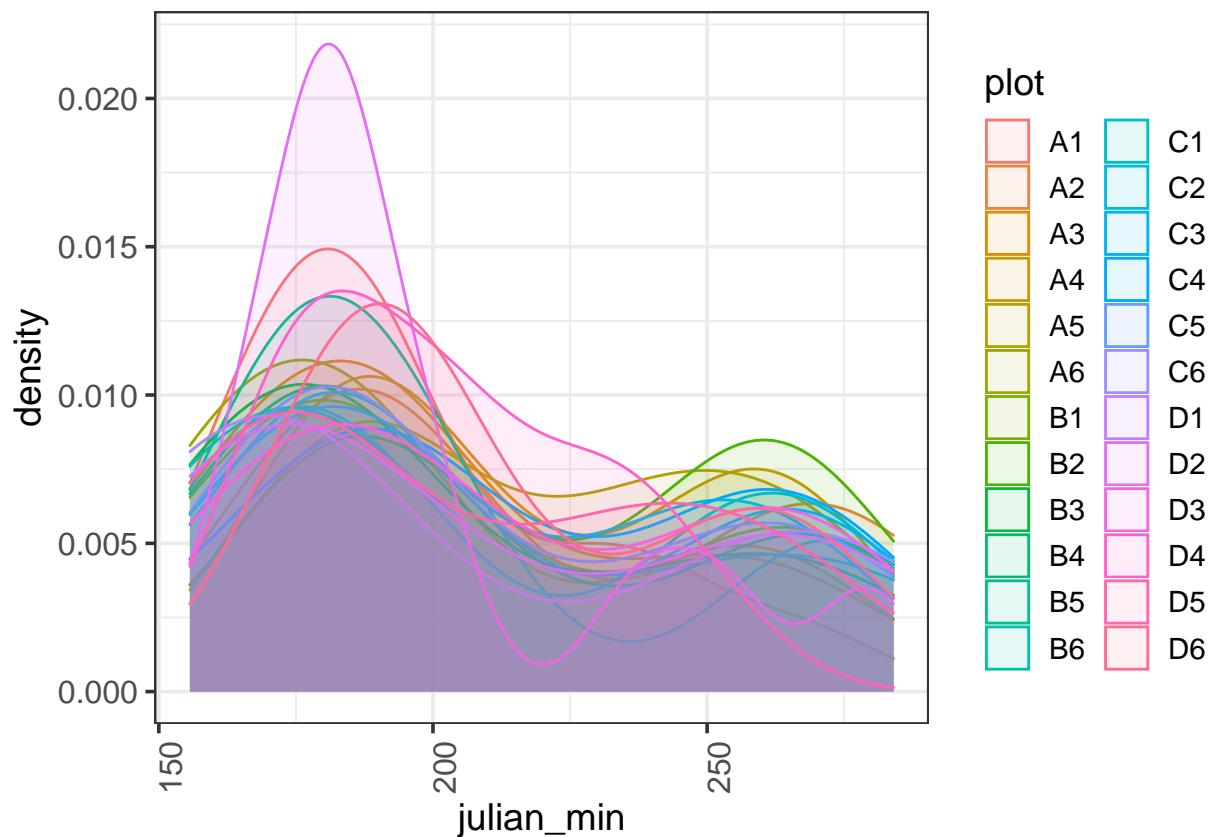
```

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

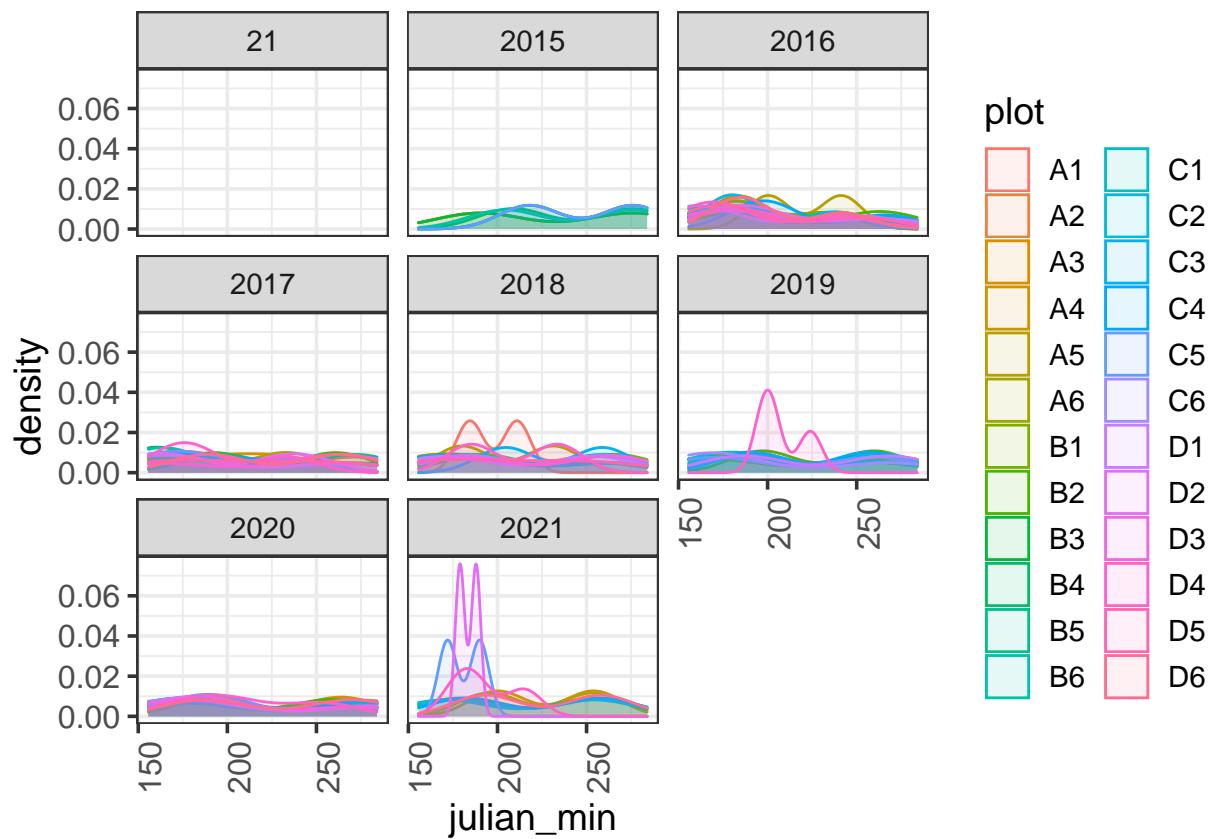
```



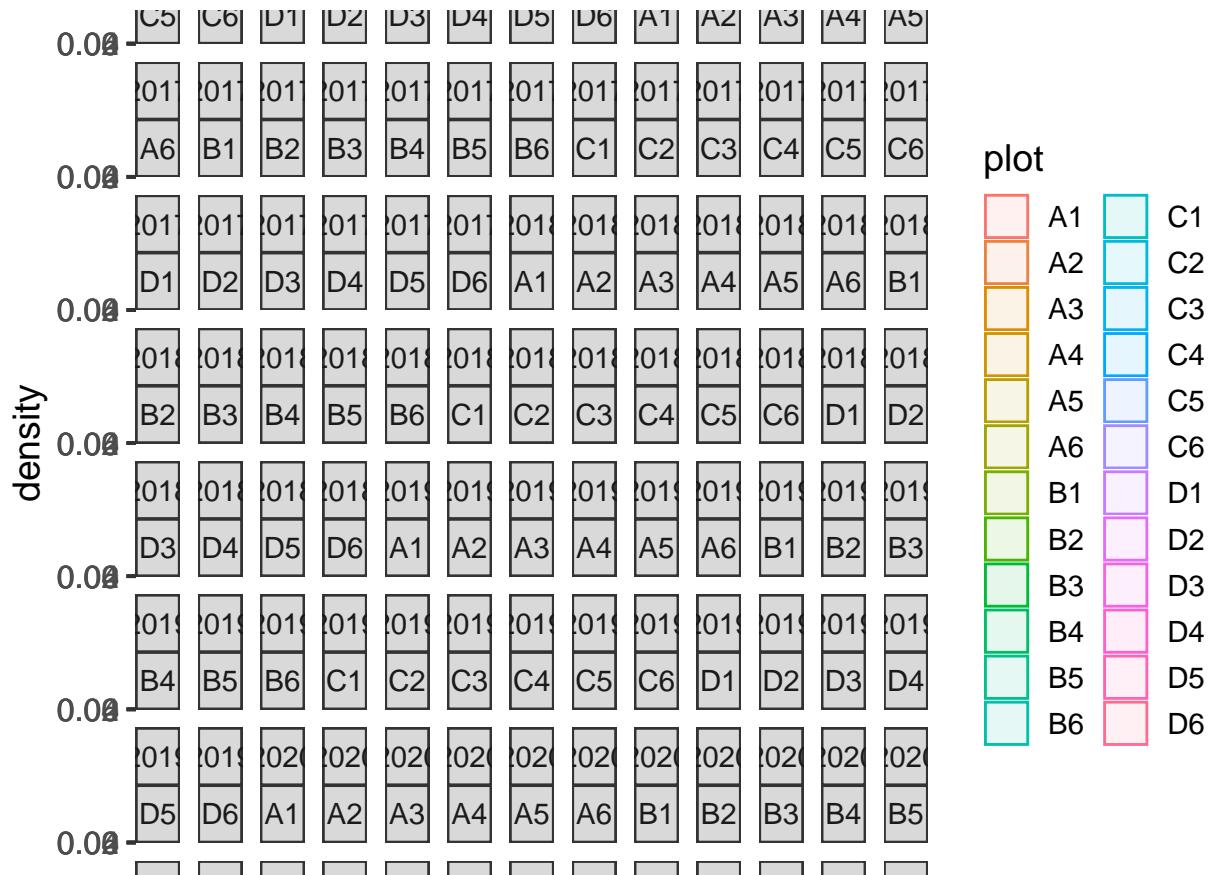
```
ggplot(kbs_sd_plot_origin, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

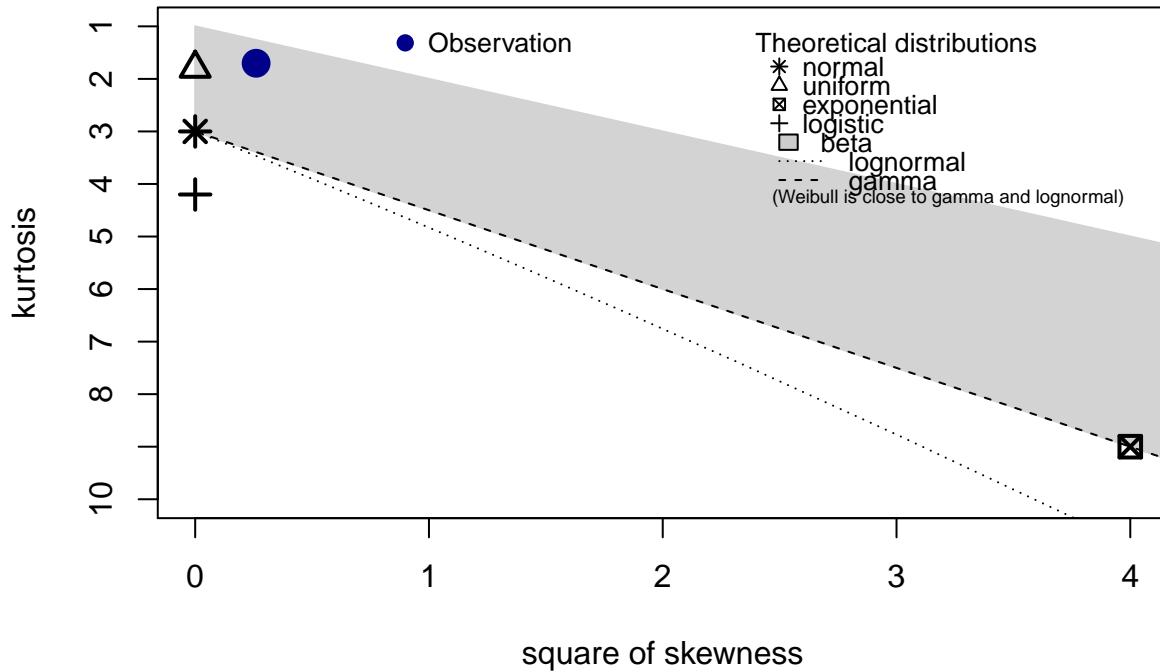


```
ggplot(kbs_sd_plot_origin, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these data:  
descdist(kbs_sd_plot_origin$julian_min, discrete = FALSE)
```

Cullen and Frey graph

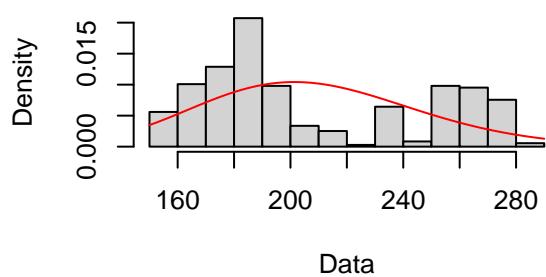
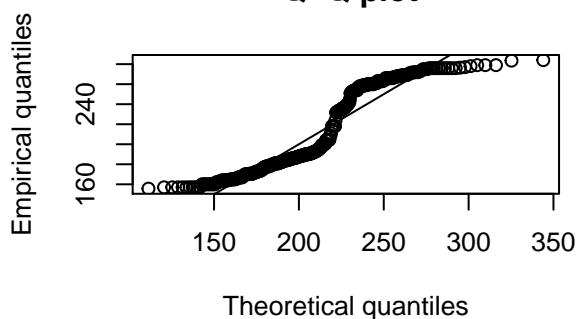
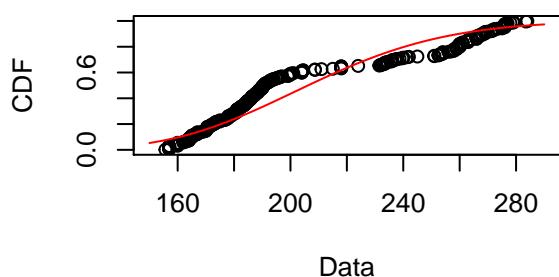
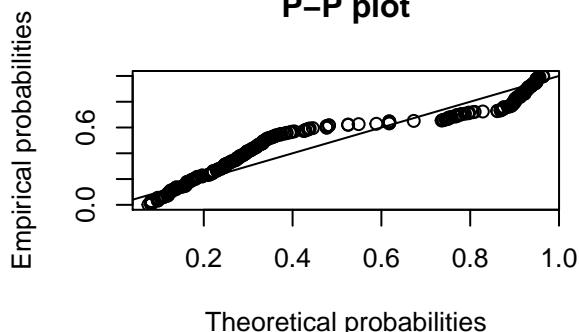


```

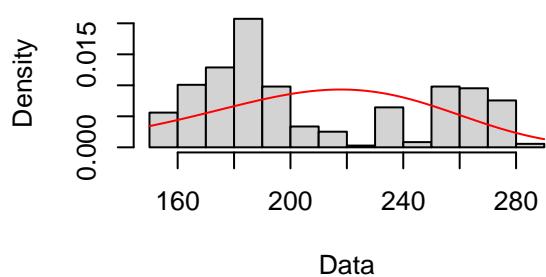
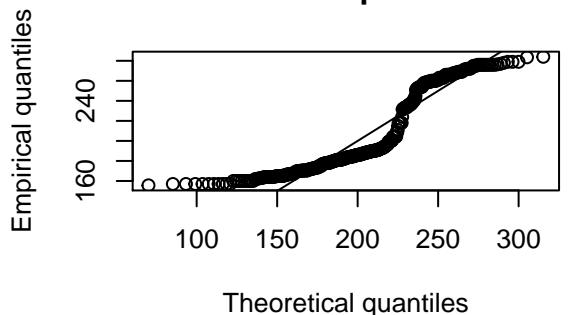
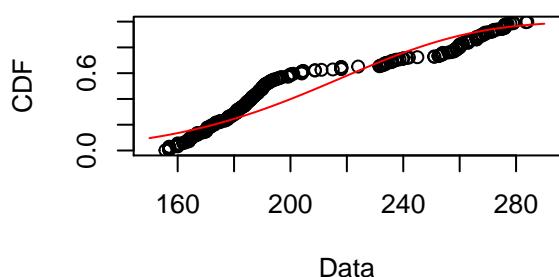
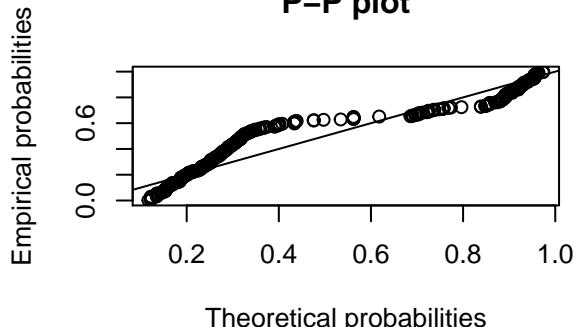
## summary statistics
## -----
## min: 155.6667  max: 284
## median: 190.5
## mean: 208.6387
## estimated sd: 39.75324
## estimated skewness: 0.5105558
## estimated kurtosis: 1.702394

# Gamma distribution
fit.gamma <- fitdist(kbs_sd_plot_origin$julian_min, "gamma")
plot(fit.gamma)

```

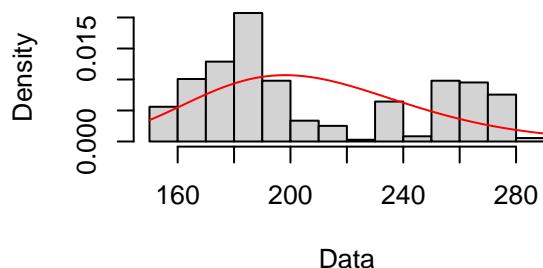
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

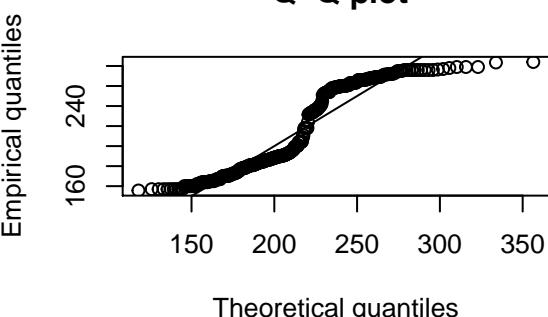
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

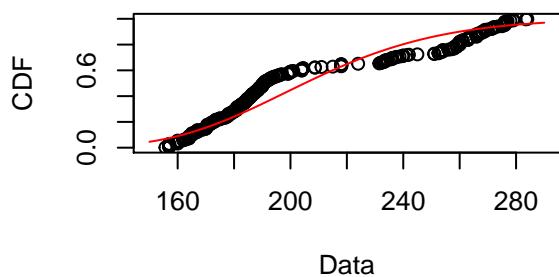
Empirical and theoretical dens.



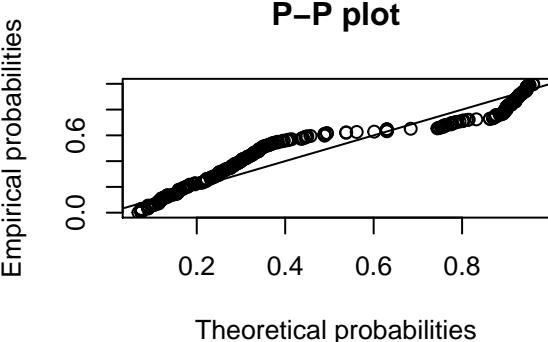
Q–Q plot



Empirical and theoretical CDFs

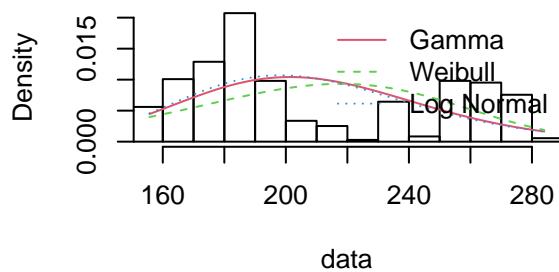


P–P plot

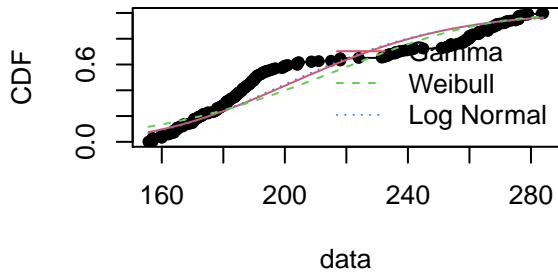


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

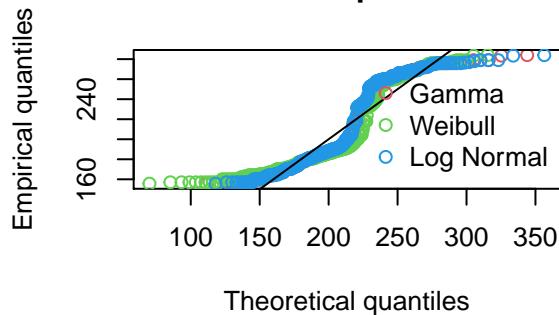
Histogram and theoretical densities



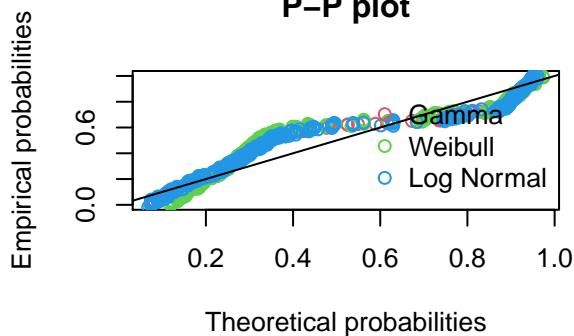
Empirical and theoretical CDFs



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"))
```

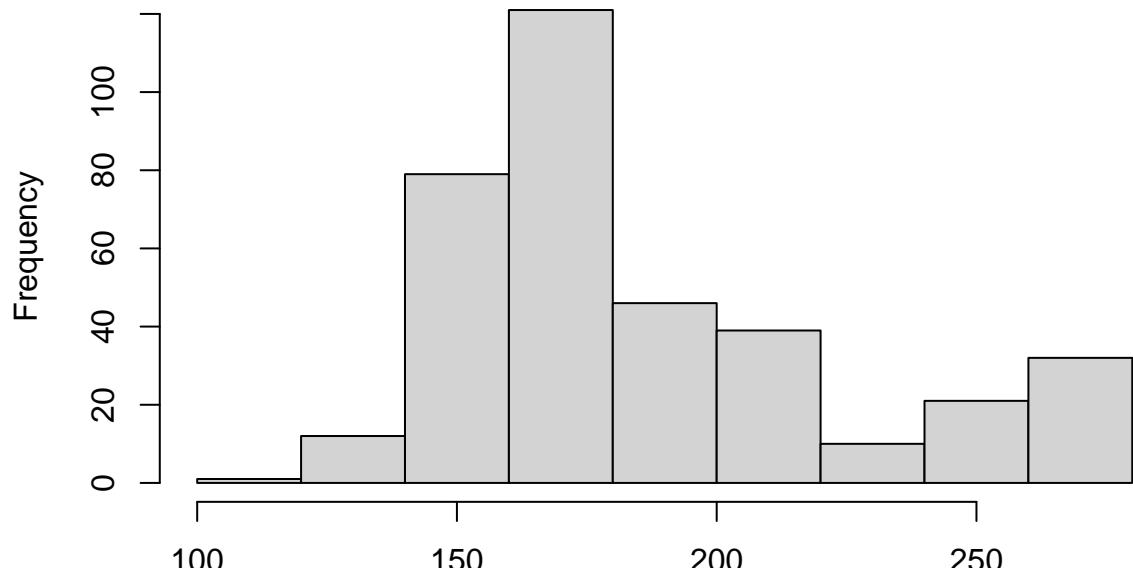
```
## Goodness-of-fit statistics
##                                     Gamma  Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1787132 0.20307 0.1693461
## Cramer-von Mises statistic   2.8784699 3.46052 2.6551340
## Anderson-Darling statistic  16.4100954 19.17250 15.2972231
##
## Goodness-of-fit criteria
##                                     Gamma  Weibull Log Normal
## Akaike's Information Criterion 3621.828 3668.628 3613.018
## Bayesian Information Criterion 3629.584 3676.384 3620.774
```

log normal looks like it's the best fit

KBS PLOT LEVEL GROWTH HABIT - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

```
### KBS ####
hist(kbs_sd_plot_growthhabit$julian_min)
```

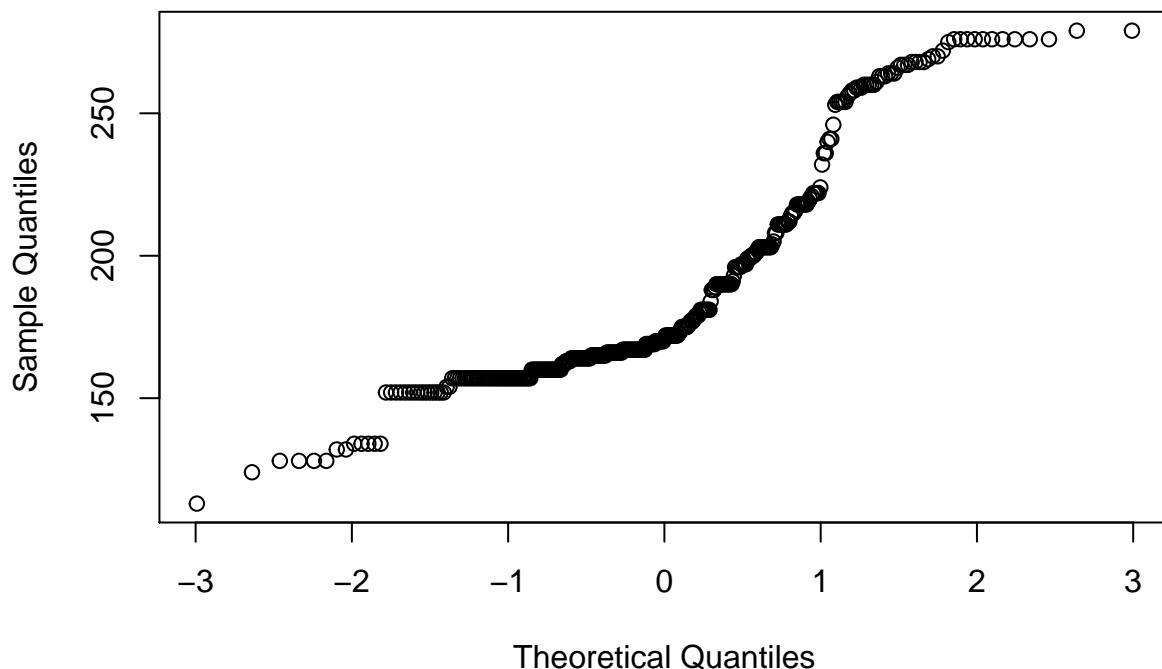
Histogram of kbs_sd_plot_growthhabit\$julian_min



```
kbs_sd_plot_growthhabit$julian_min
```

```
qqnorm(kbs_sd_plot_growthhabit$julian_min)
```

Normal Q-Q Plot



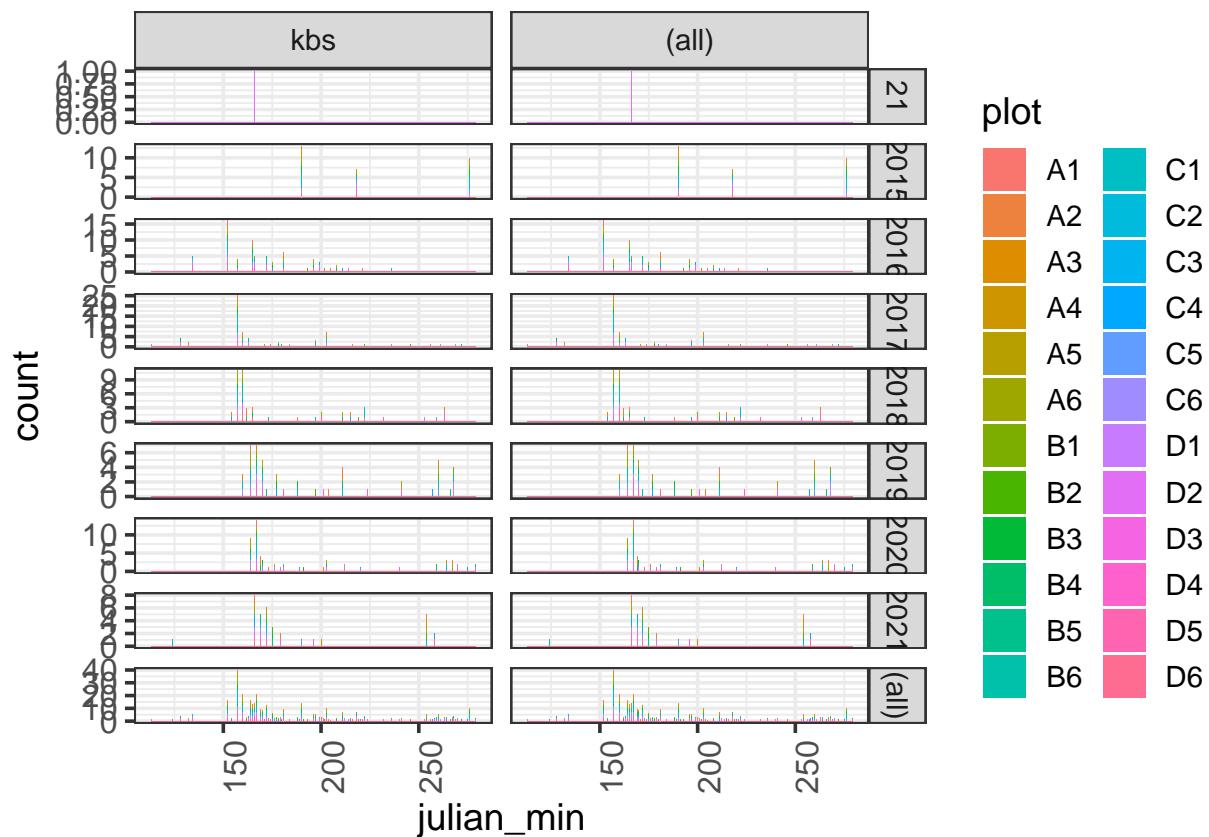
```

shapiro.test(kbs_sd_plot_growthhabit$julian_min) # pvalue is < 0.05 so we reject the null hypothesis that the Julian dates are normally distributed

## 
## Shapiro-Wilk normality test
## 
## data: kbs_sd_plot_growthhabit$julian_min
## W = 0.86086, p-value < 2.2e-16

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

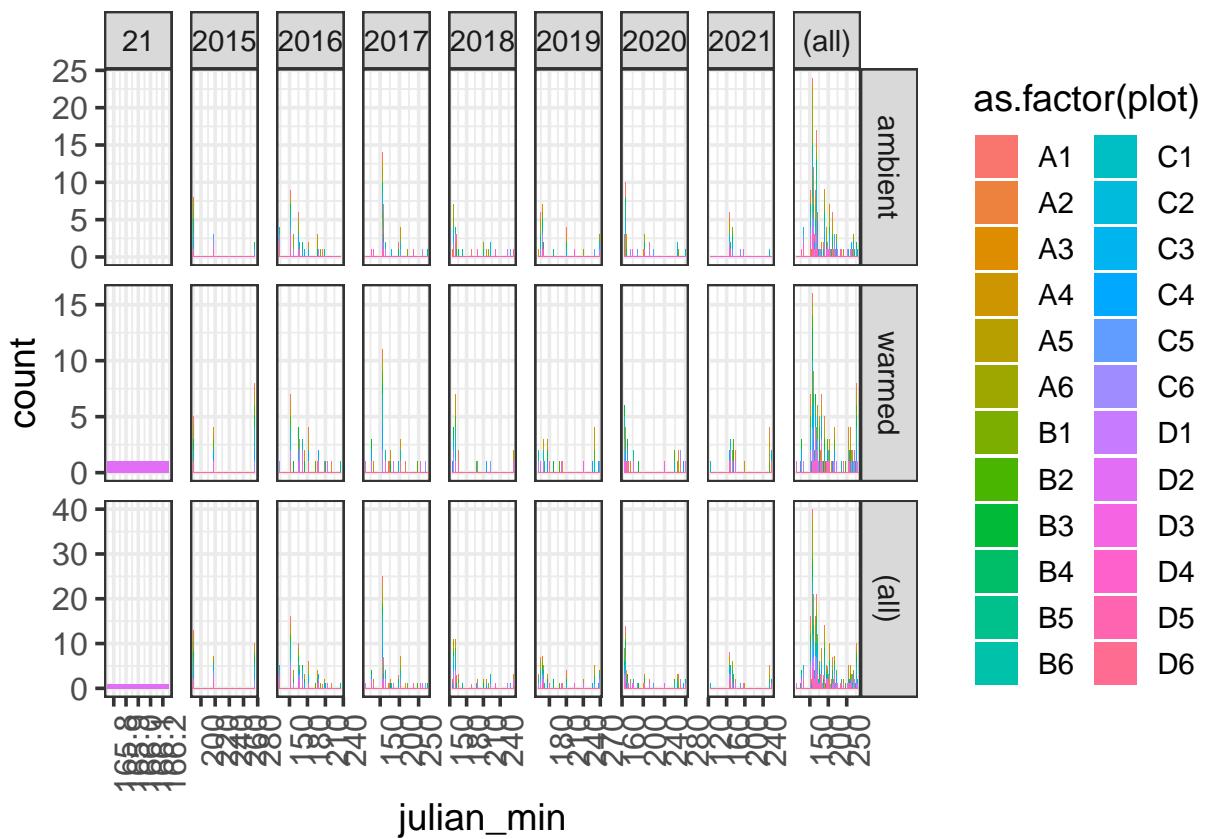
```



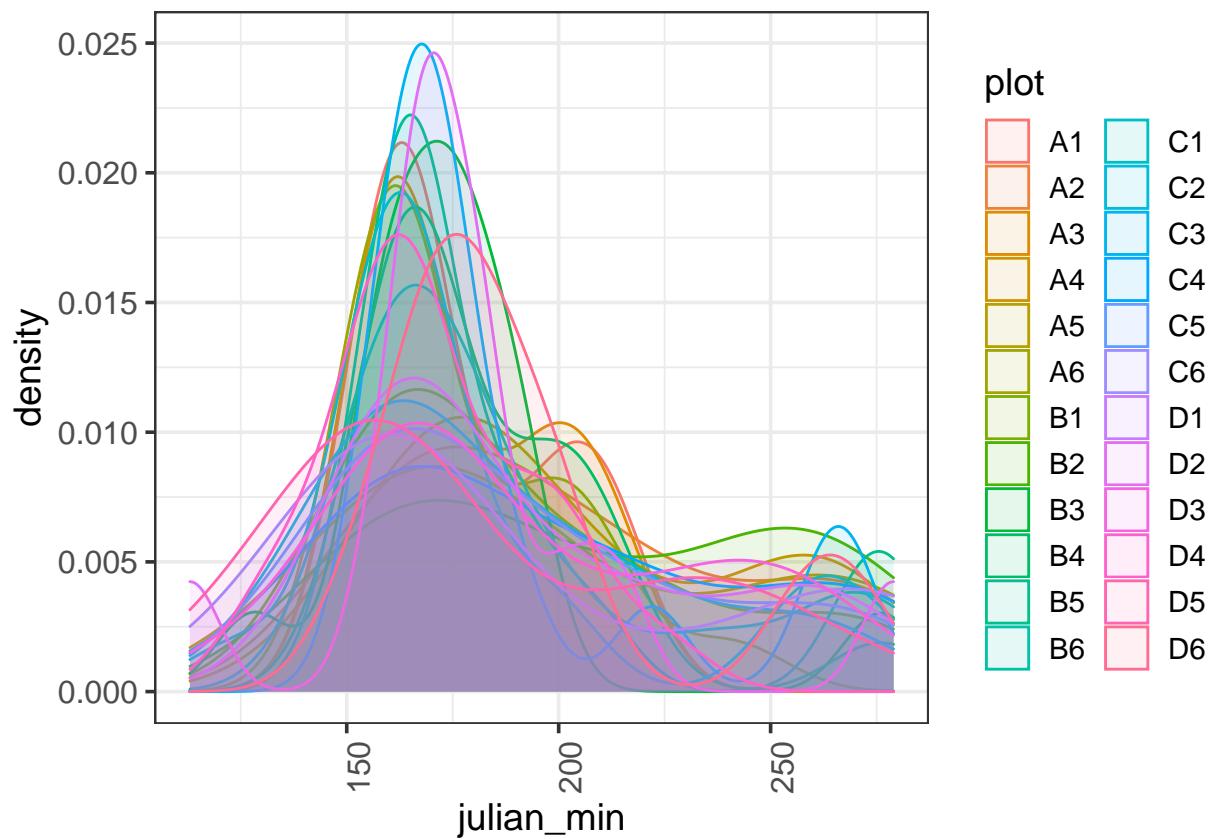
```

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

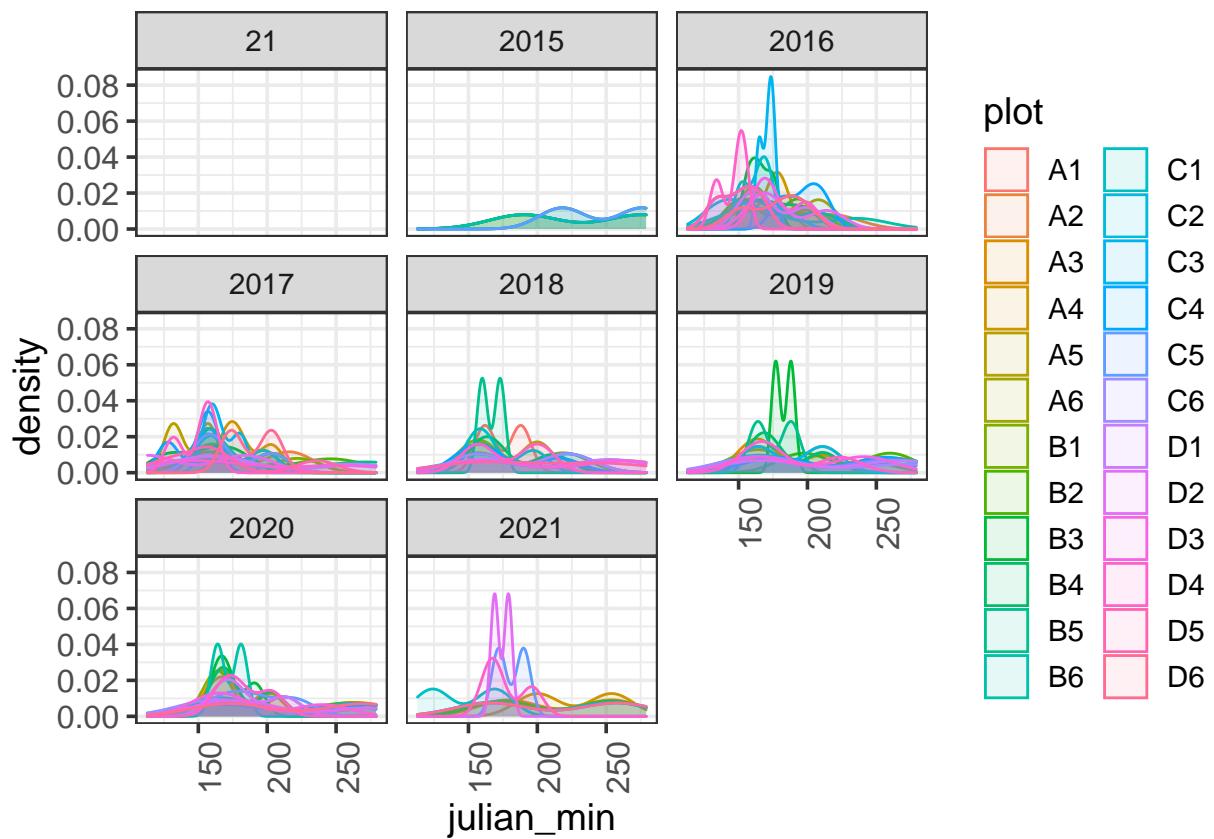
```



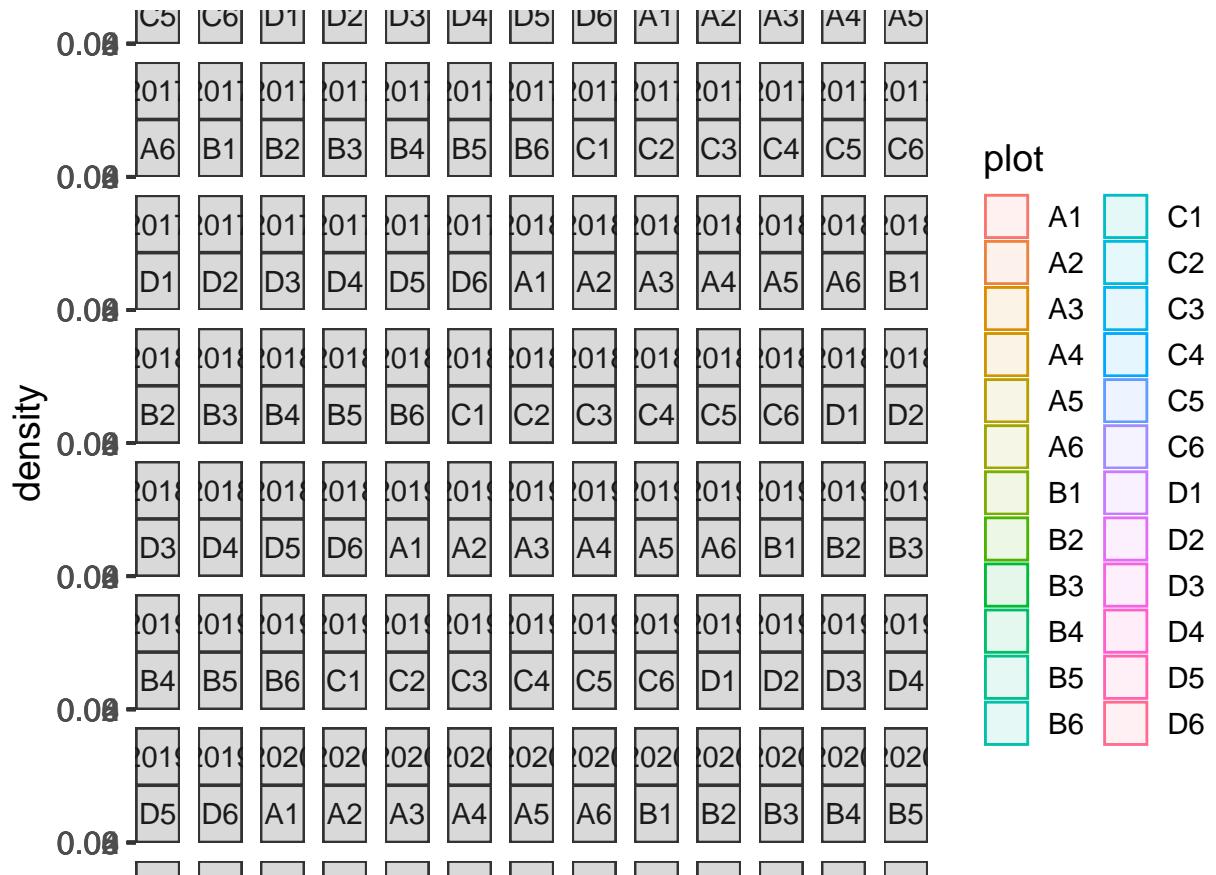
```
ggplot(kbs_sd_plot_growthhabit, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

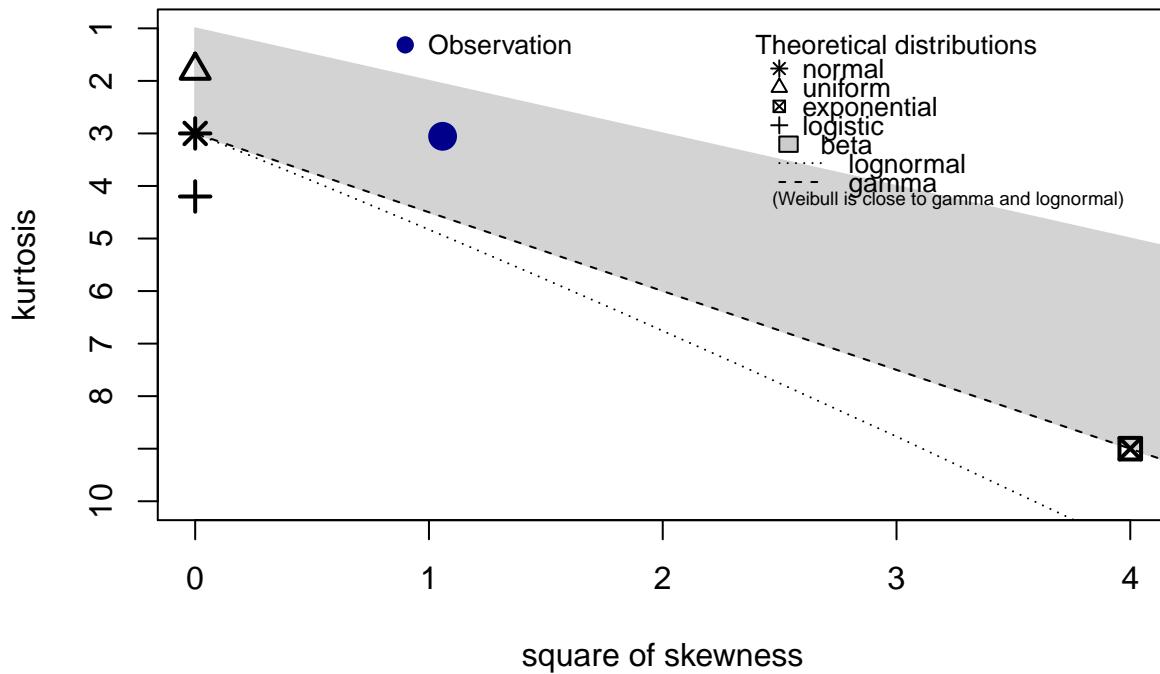


```
ggplot(kbs_sd_plot_growthhabit, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these data:  
descdist(kbs_sd_plot_growthhabit$julian_min, discrete = FALSE)
```

Cullen and Frey graph

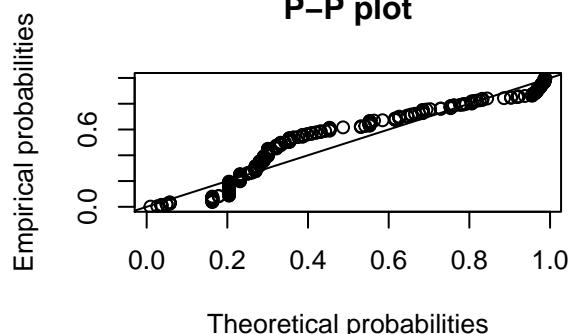
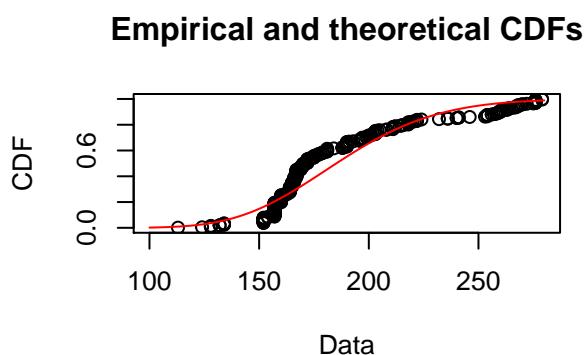
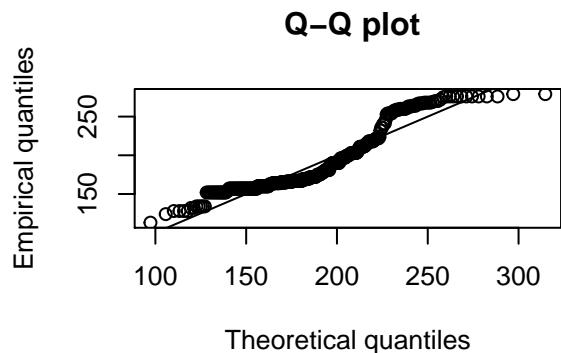
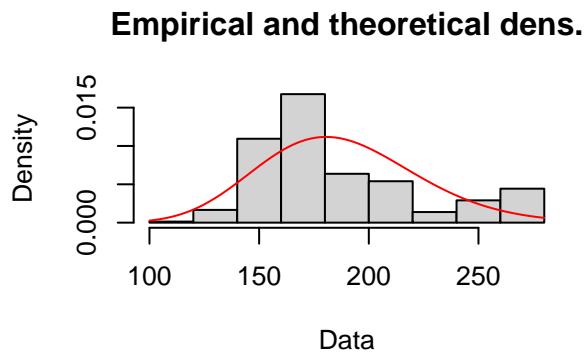


```

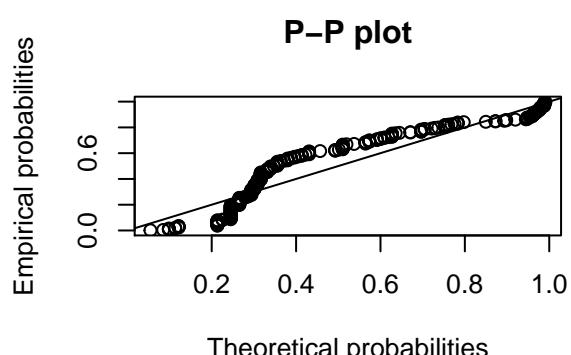
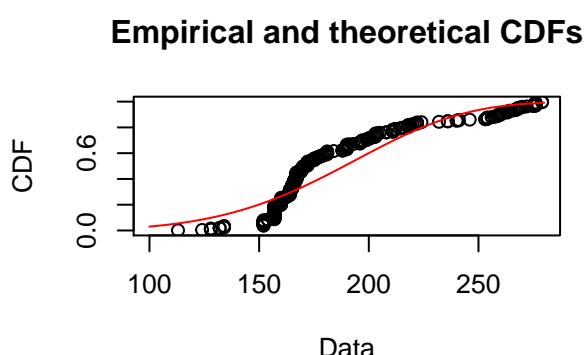
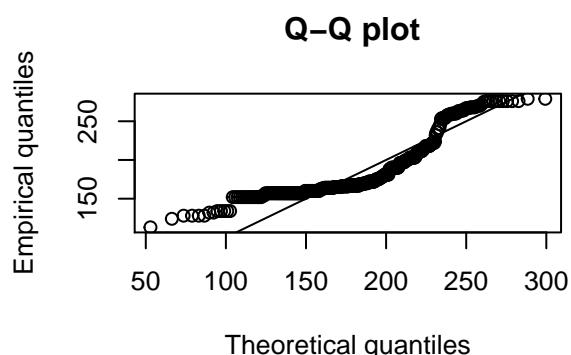
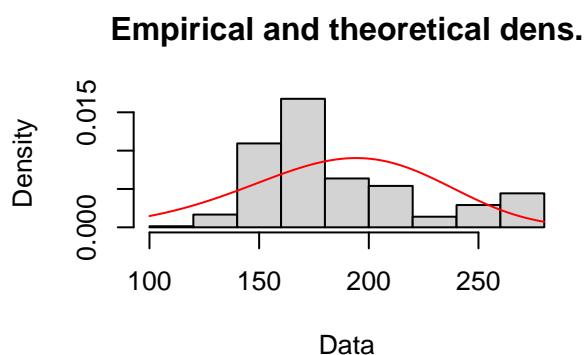
## summary statistics
## -----
## min: 113   max: 279
## median: 171
## mean: 187.5042
## estimated sd: 38.14505
## estimated skewness: 1.028789
## estimated kurtosis: 3.054855

# Gamma distribution
fit.gamma <- fitdist(kbs_sd_plot_growthhabit$julian_min, "gamma")
plot(fit.gamma)

```

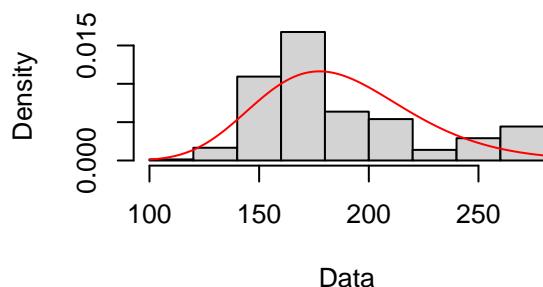


```
# Weibull distribution
fit.weibull <- fitdist(kbs_sd_plot_growthhabit$julian_min, "weibull")
plot(fit.weibull)
```

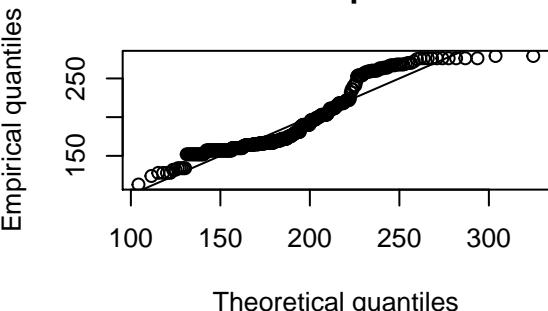


```
# Lognormal distribution
fit.ln <- fitdist(kbs_sd_plot_growthhabit$julian_min, "lnorm")
plot(fit.ln)
```

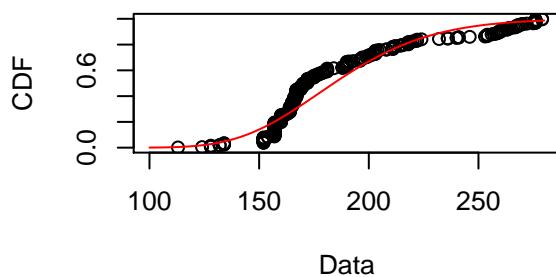
Empirical and theoretical dens.



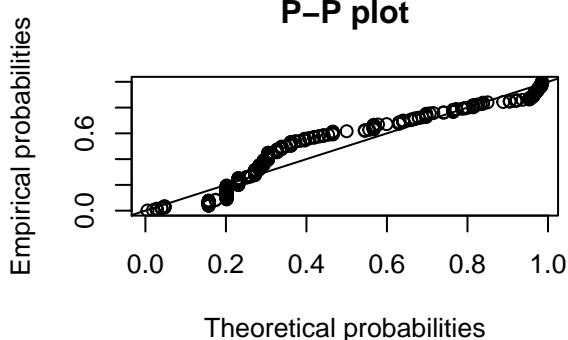
Q-Q plot



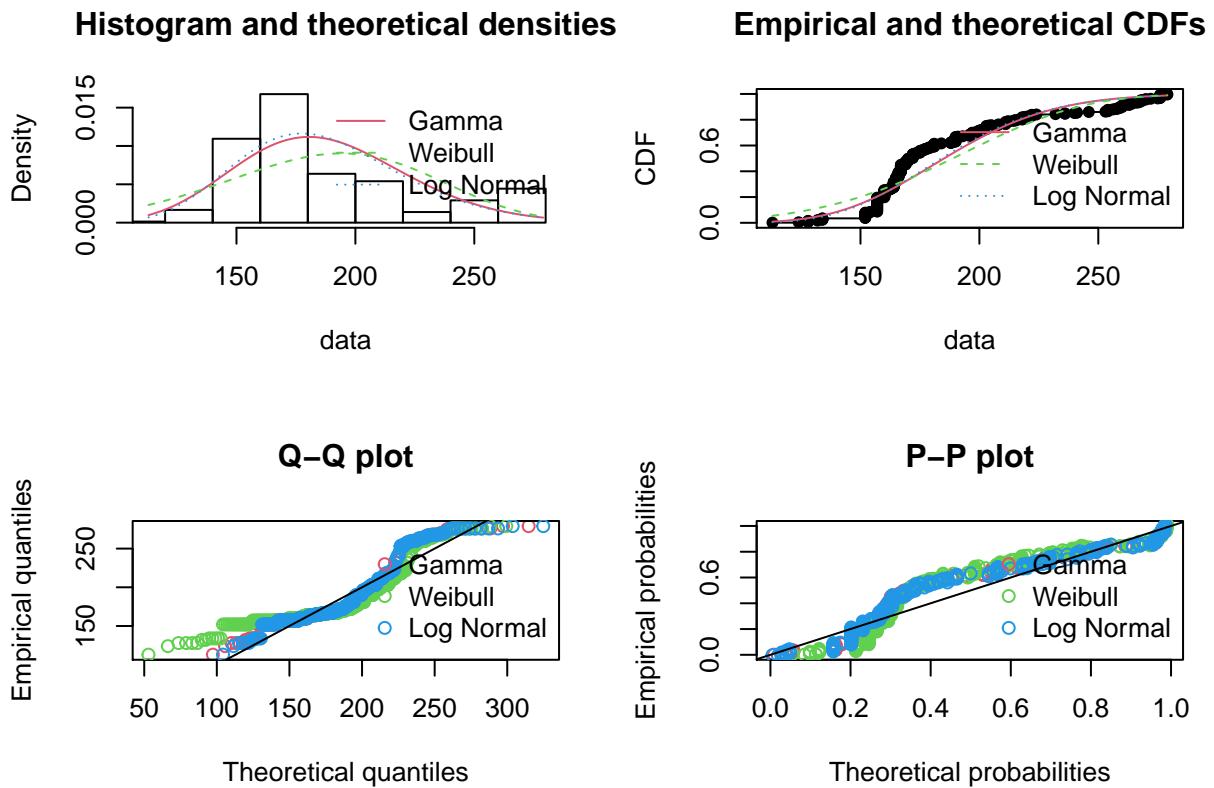
Empirical and theoretical CDFs



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"))

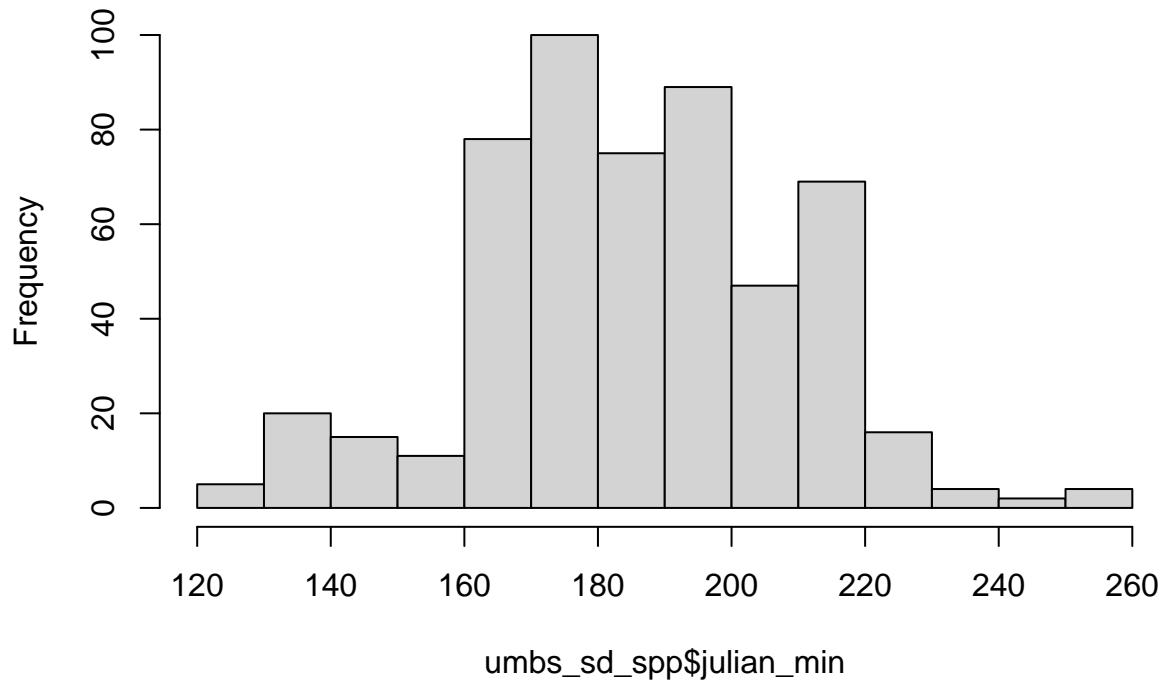
## Goodness-of-fit statistics
##                                     Gamma    Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.180911 0.1841854 0.1734767
## Cramer-von Mises statistic   2.814479 3.9664067 2.4803553
## Anderson-Darling statistic   16.284847 22.5165581 14.3842796
##
## Goodness-of-fit criteria
##                                     Gamma    Weibull Log Normal
## Akaike's Information Criterion 3611.901 3702.044 3594.292
## Bayesian Information Criterion 3619.678 3709.822 3602.070

# log normal looks like it's the best fit
```

UMBS SPECIES LEVEL - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

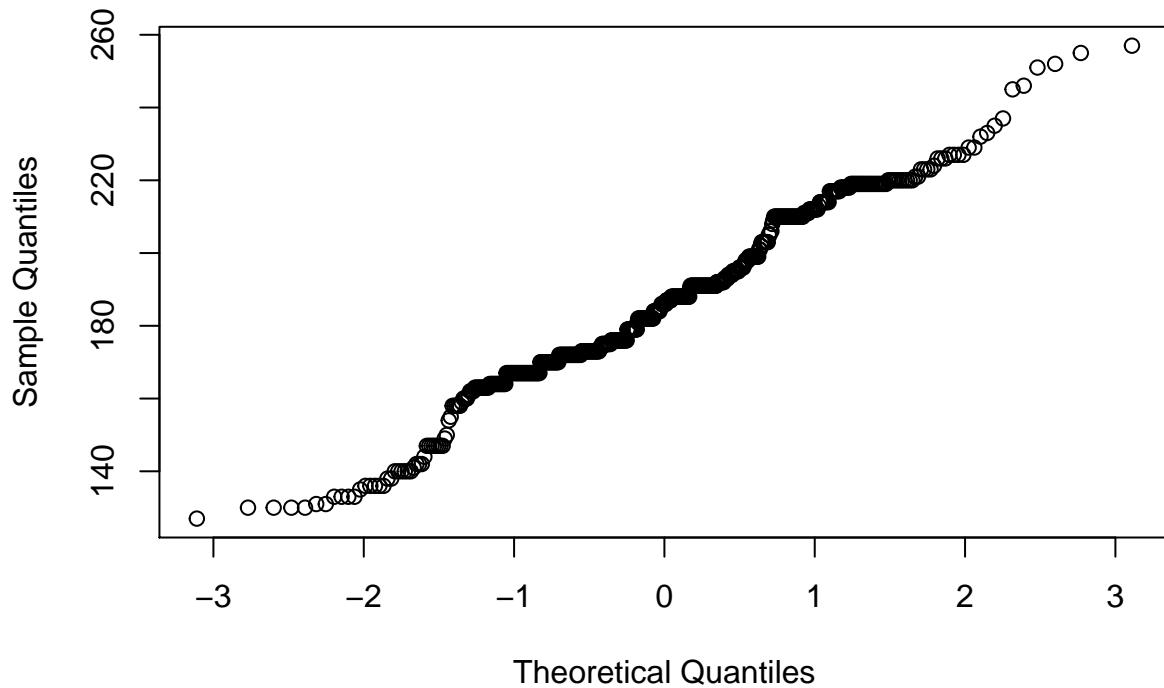
```
### UMBS ####
hist(umbs_sd_spp$julian_min)
```

Histogram of umbs_sd_spp\$julian_min



```
qqnorm(umbs_sd_spp$julian_min)
```

Normal Q-Q Plot



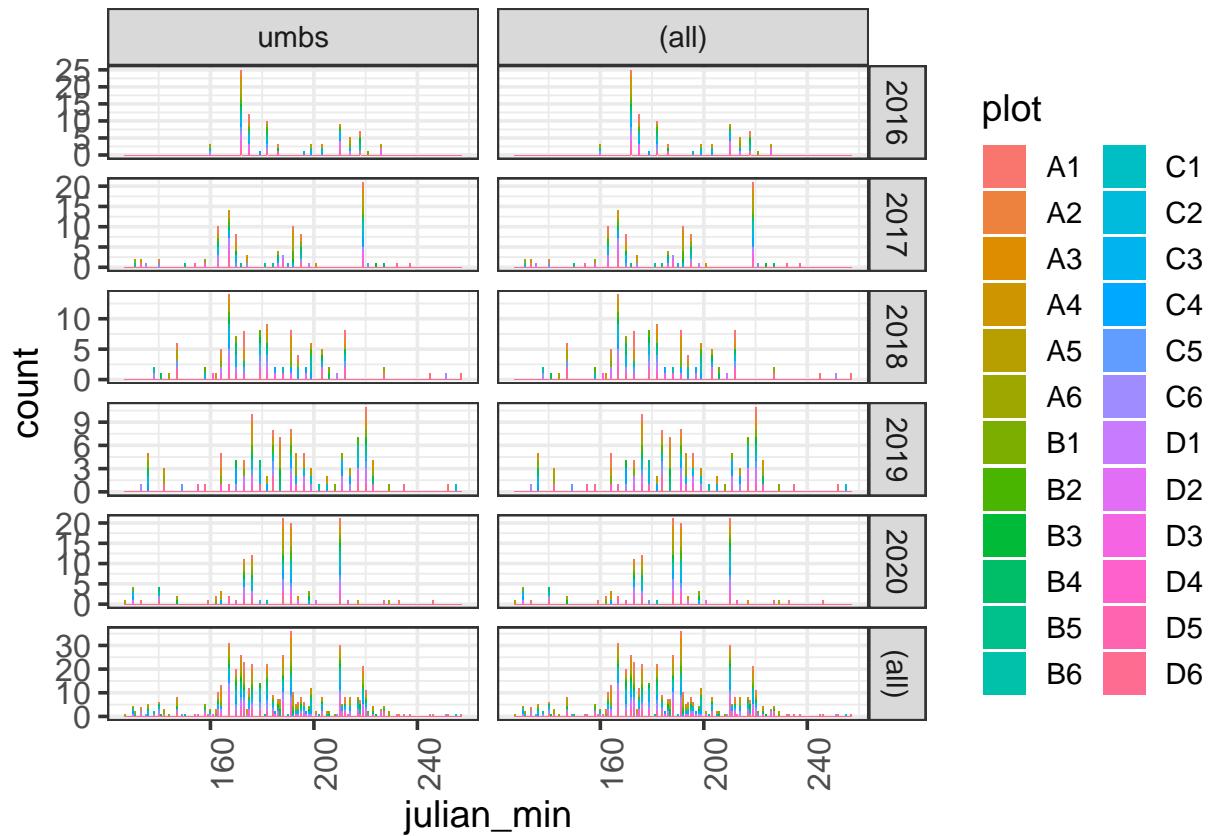
```

shapiro.test(umbs_sd_spp$julian_min) # pvalue is < 0.05 so we reject the null hypothesis that the data

## 
## Shapiro-Wilk normality test
## 
## data: umbs_sd_spp$julian_min
## W = 0.98284, p-value = 6.092e-06

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

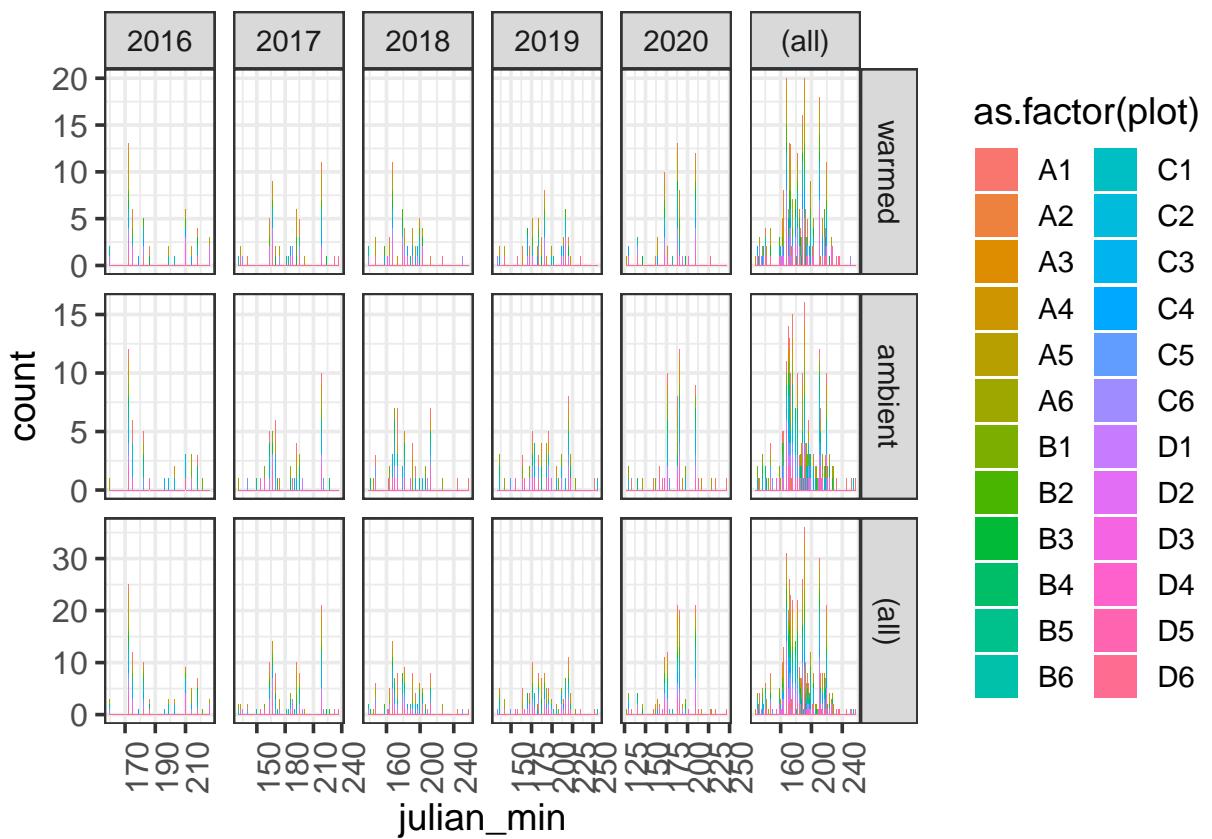
```



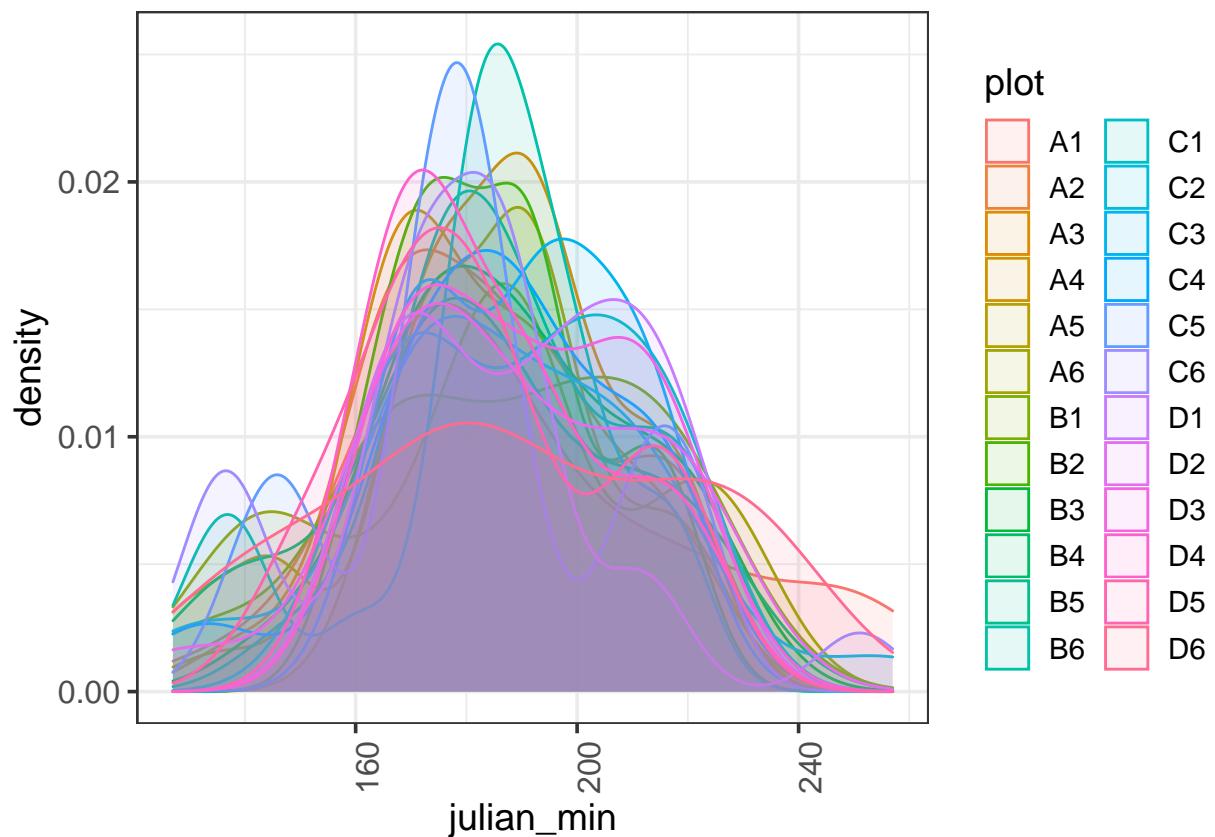
```

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

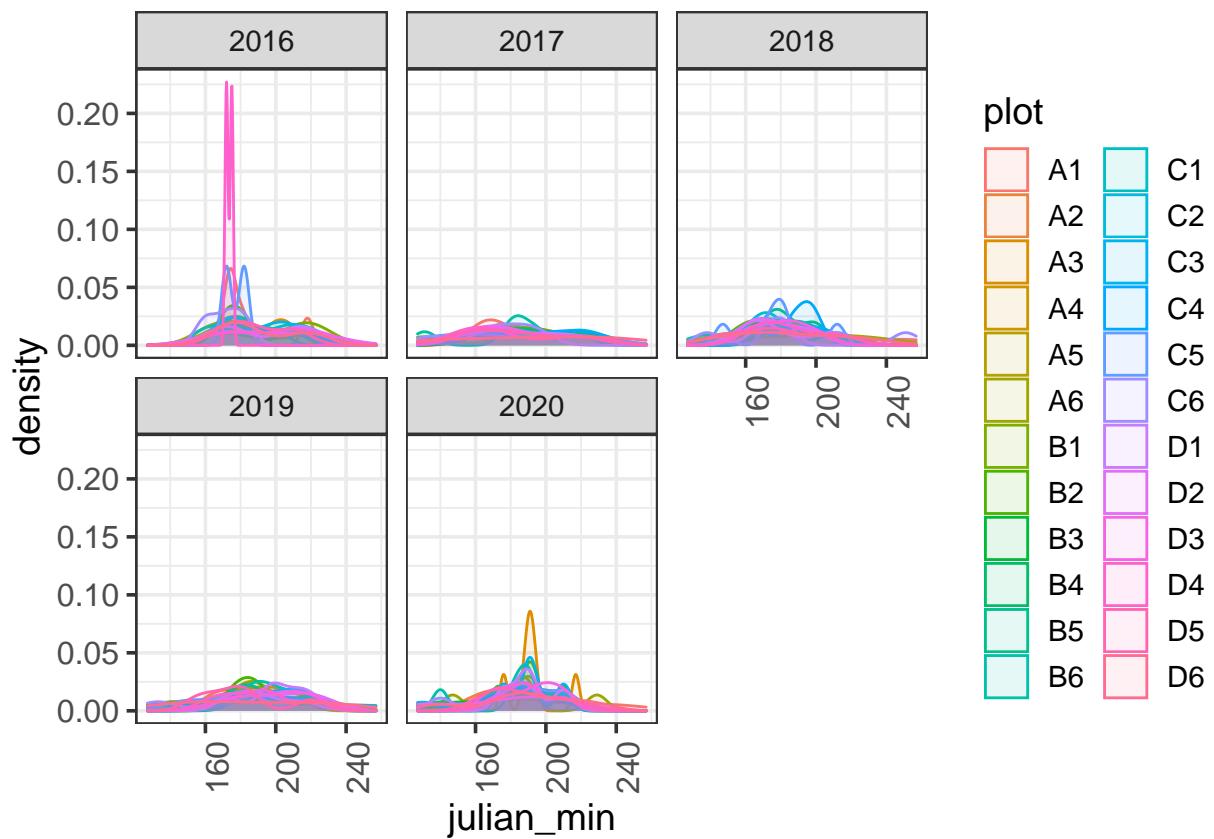
```



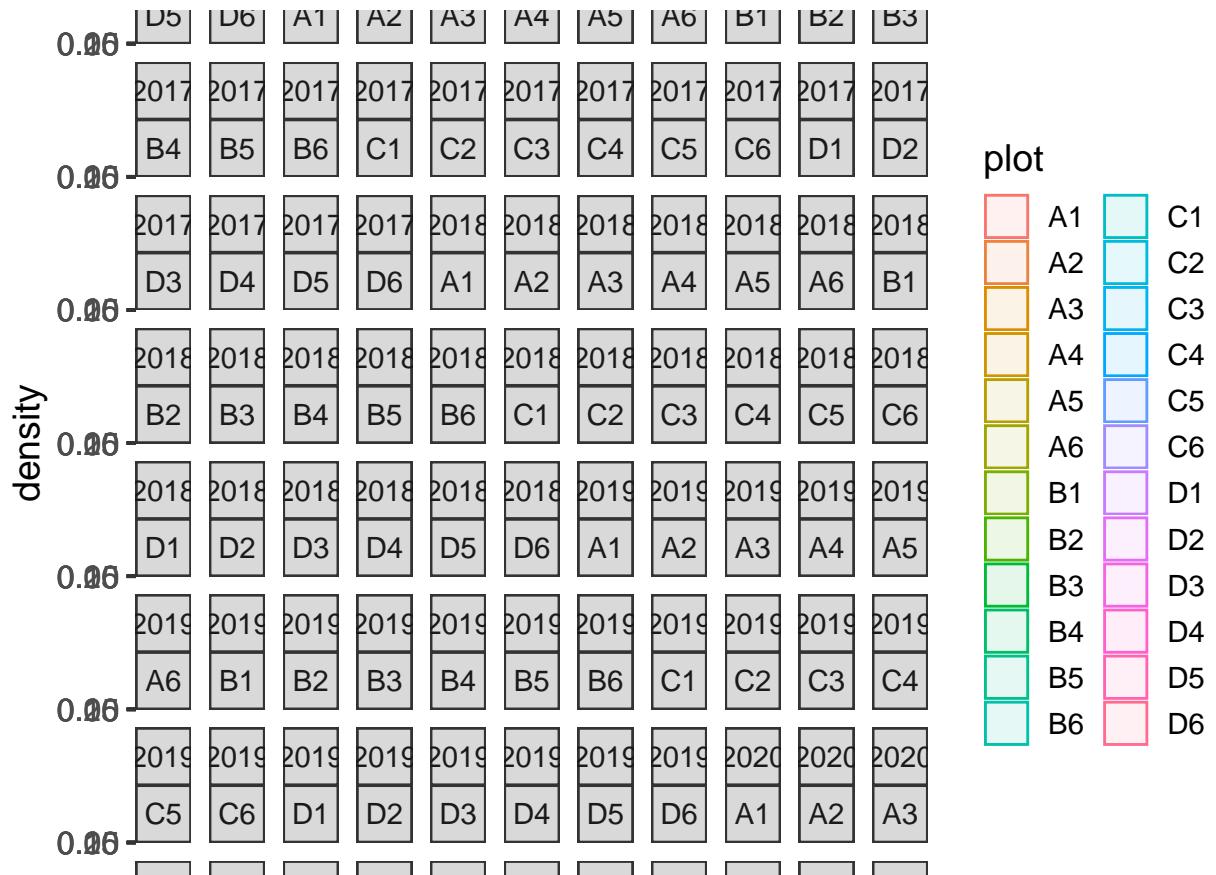
```
ggplot(umbs_sd_spp, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

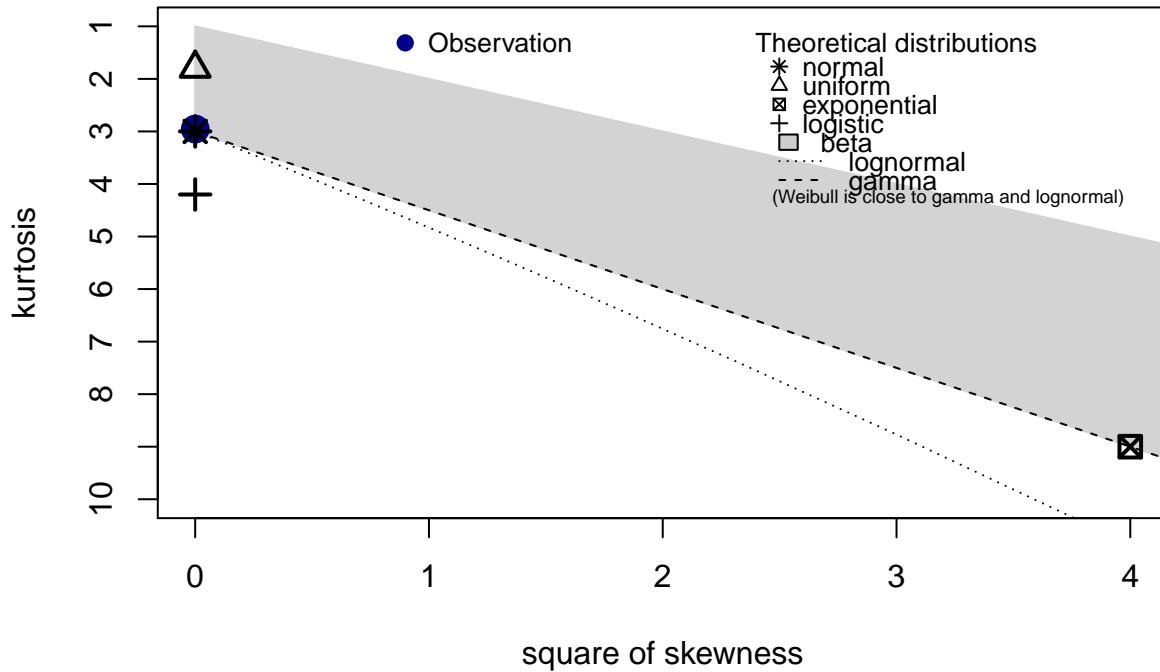


```
ggplot(umbs_sd_spp, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(umbs_sd_spp$julian_min, discrete = FALSE) # normal!
```

Cullen and Frey graph

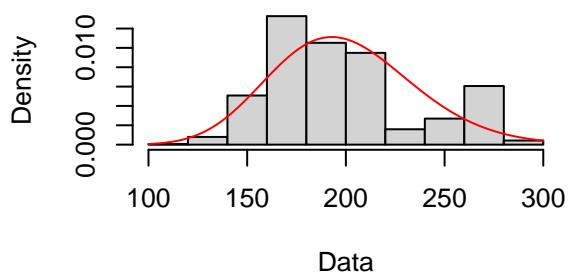
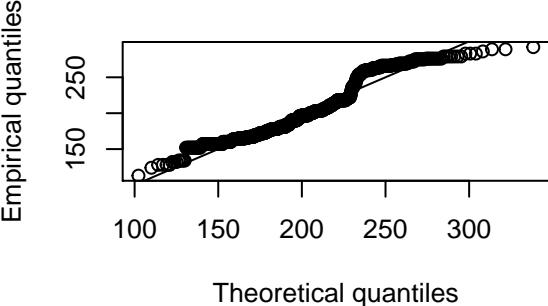
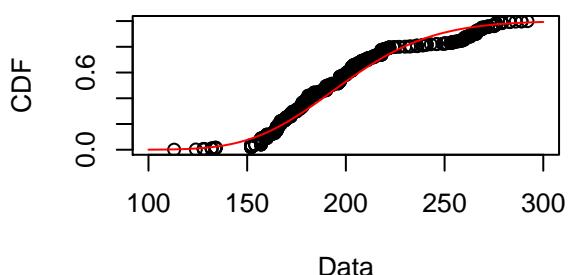
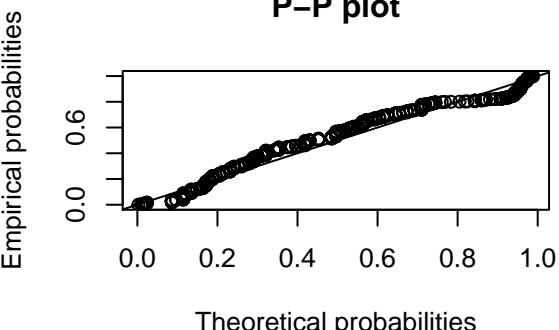


```

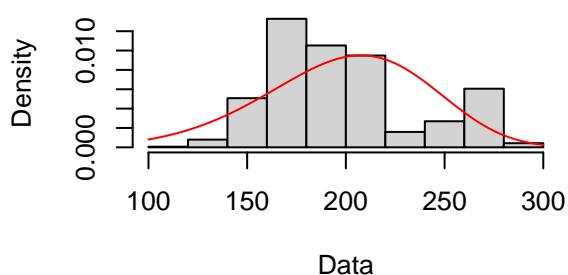
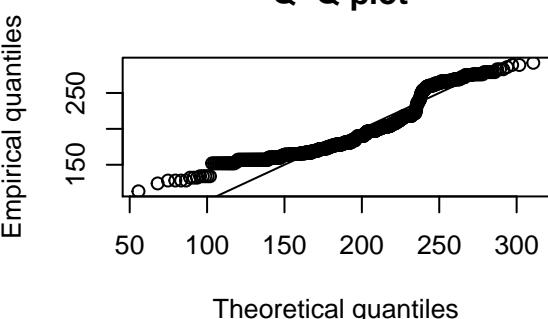
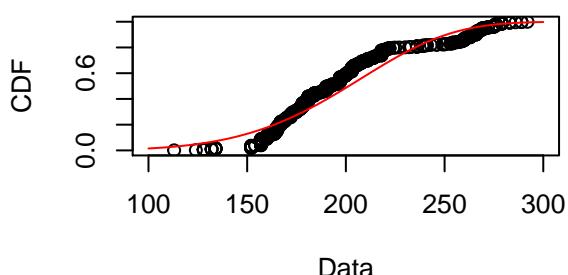
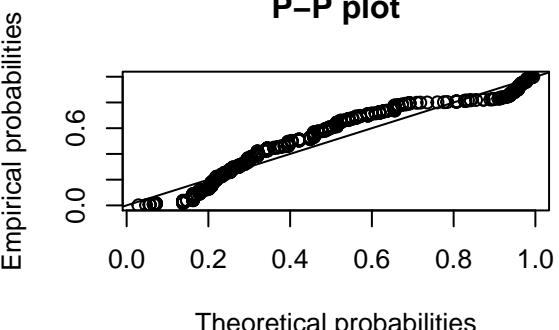
## summary statistics
## -----
## min: 127   max: 257
## median: 186
## mean: 186.2374
## estimated sd: 23.60302
## estimated skewness: 0.01509724
## estimated kurtosis: 2.954713

# Gamma distribution
fit.gamma <- fitdist(kbs_sd_spp$julian_min, "gamma")
plot(fit.gamma)

```

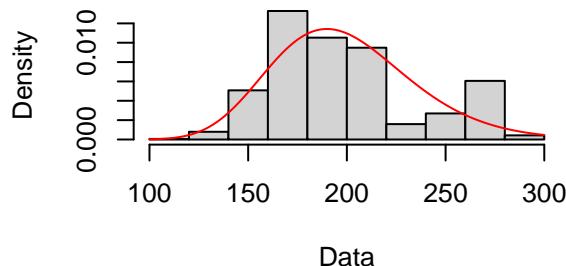
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

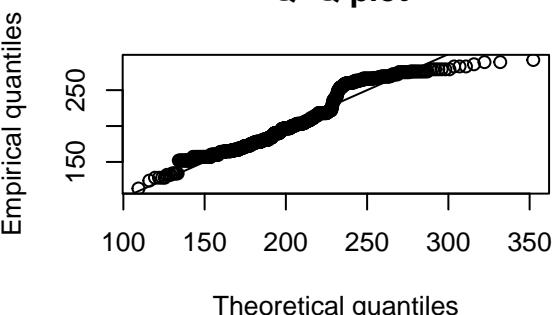
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

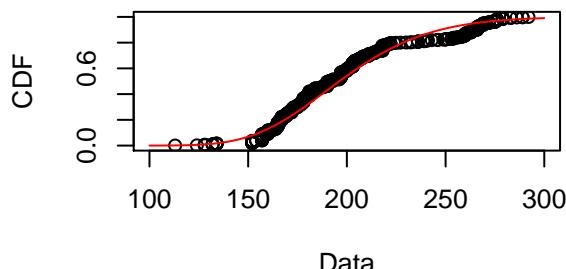
Empirical and theoretical dens.



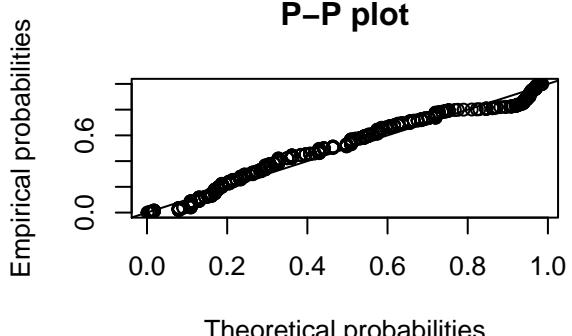
Q-Q plot



Empirical and theoretical CDFs

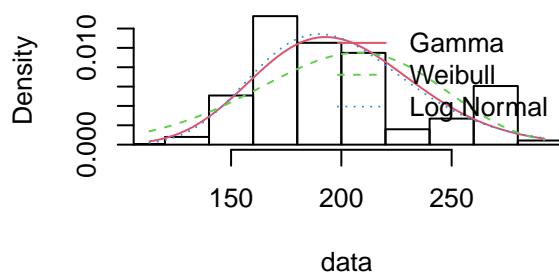


P-P plot

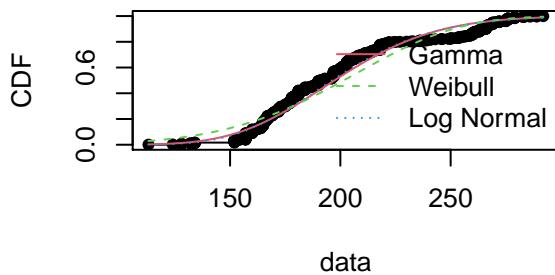


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

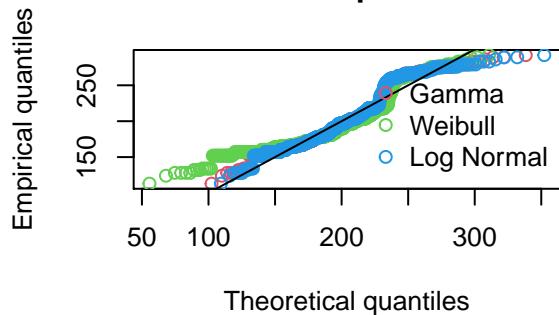
Histogram and theoretical densities



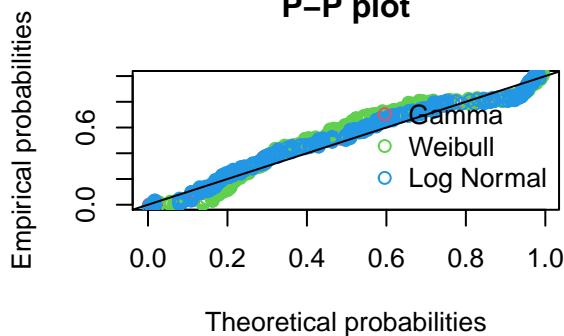
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```

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 0.09988396 0.1360783 0.09317306
## Cramer-von Mises statistic   2.41253973 5.0192692 1.88913912
## Anderson-Darling statistic   17.07536252 30.9119372 14.02047891
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull  Log Normal
## Akaike's Information Criterion 8177.095 8325.080 8155.683
## Bayesian Information Criterion 8186.506 8334.491 8165.094

# Lognormal is best - going with a lognormal transformation for umbs seed set at
# the species level

```

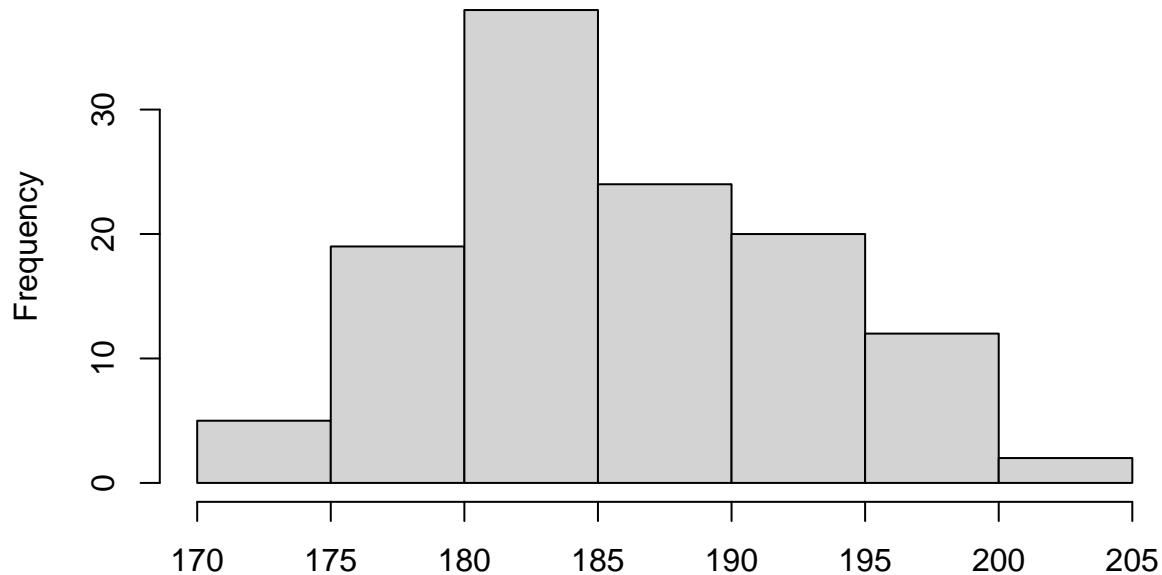
UMBS PLOT LEVEL - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

```

### UMBS ####
hist(umbs_sd_plot$julian_min)

```

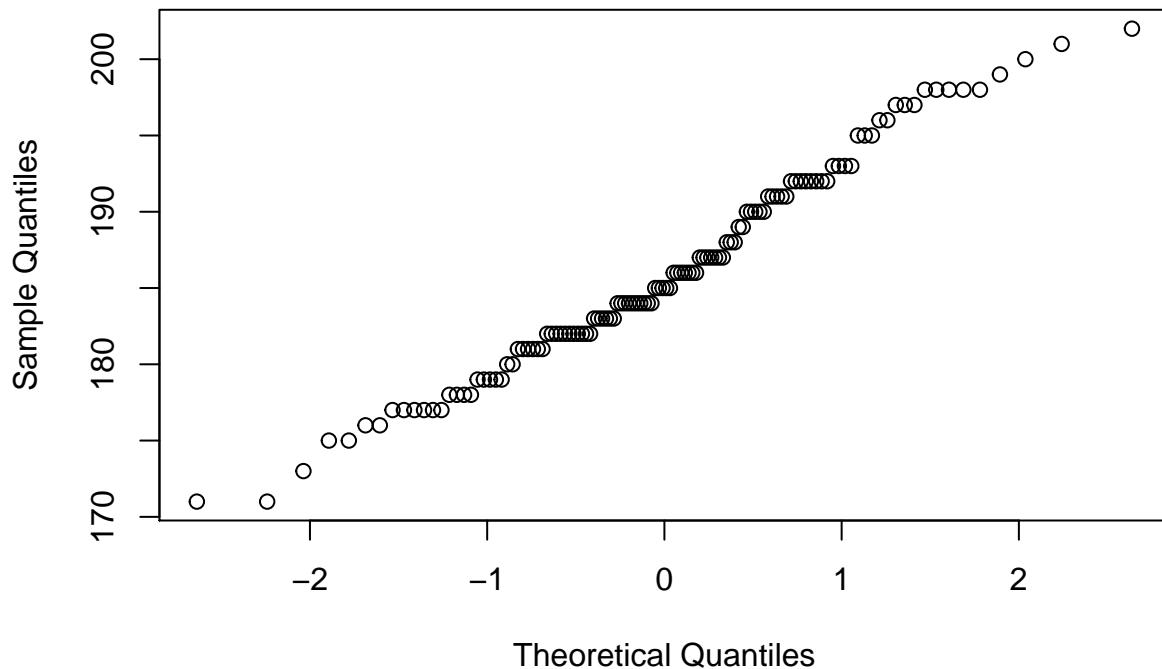
Histogram of umbs_sd_plot\$julian_min



umbs_sd_plot\$julian_min

```
qqnorm(umbs_sd_plot$julian_min)
```

Normal Q-Q Plot



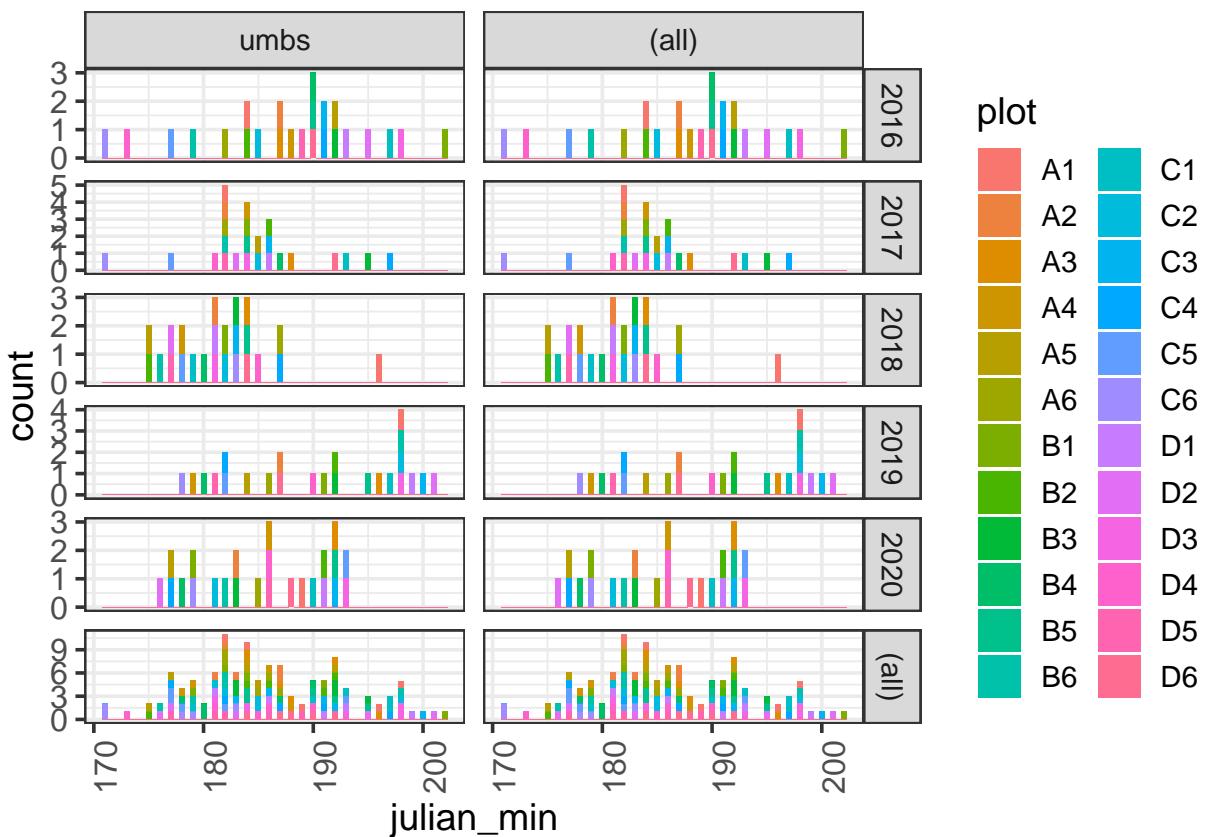
```

shapiro.test(umbs_sd_plot$julian_min) # pvalue is >0.05 so we accept the null hypothesis that the data

## 
## Shapiro-Wilk normality test
## 
## data: umbs_sd_plot$julian_min
## W = 0.98106, p-value = 0.08941

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

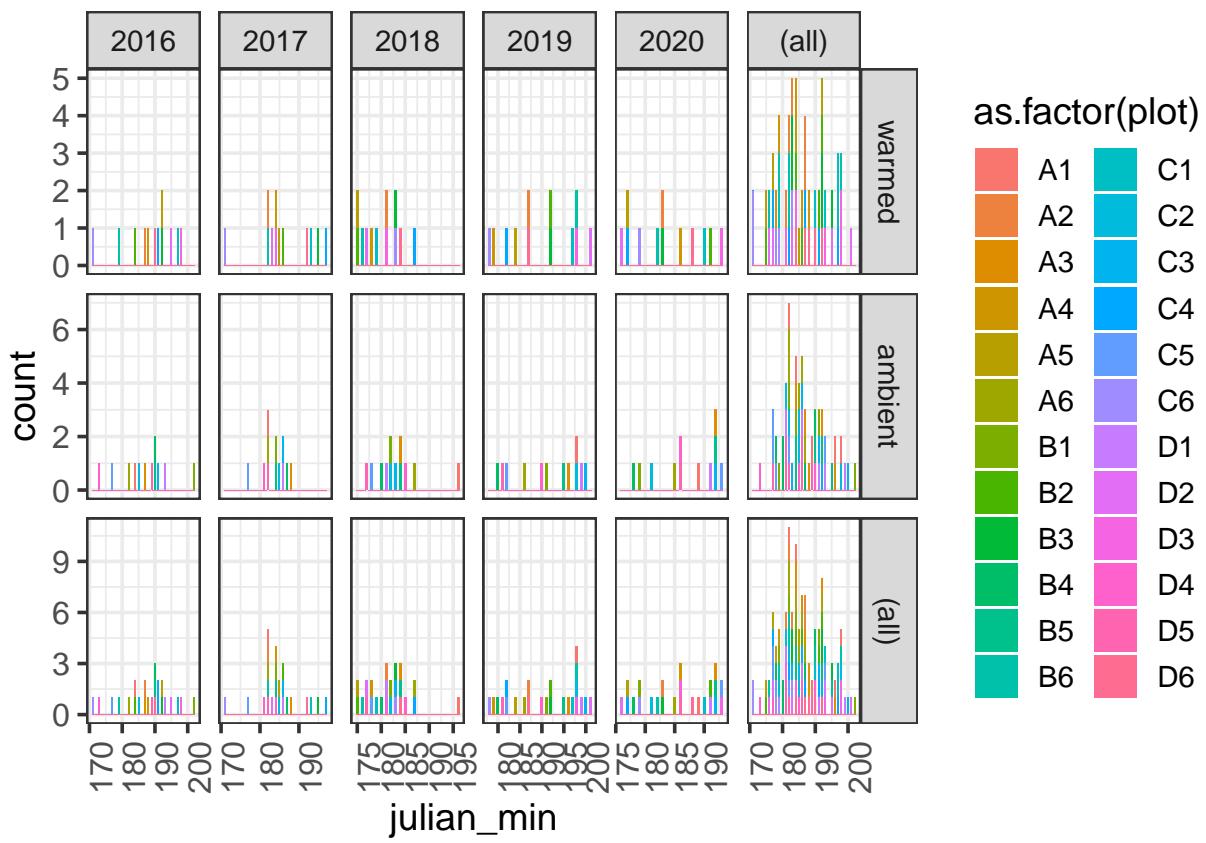
```



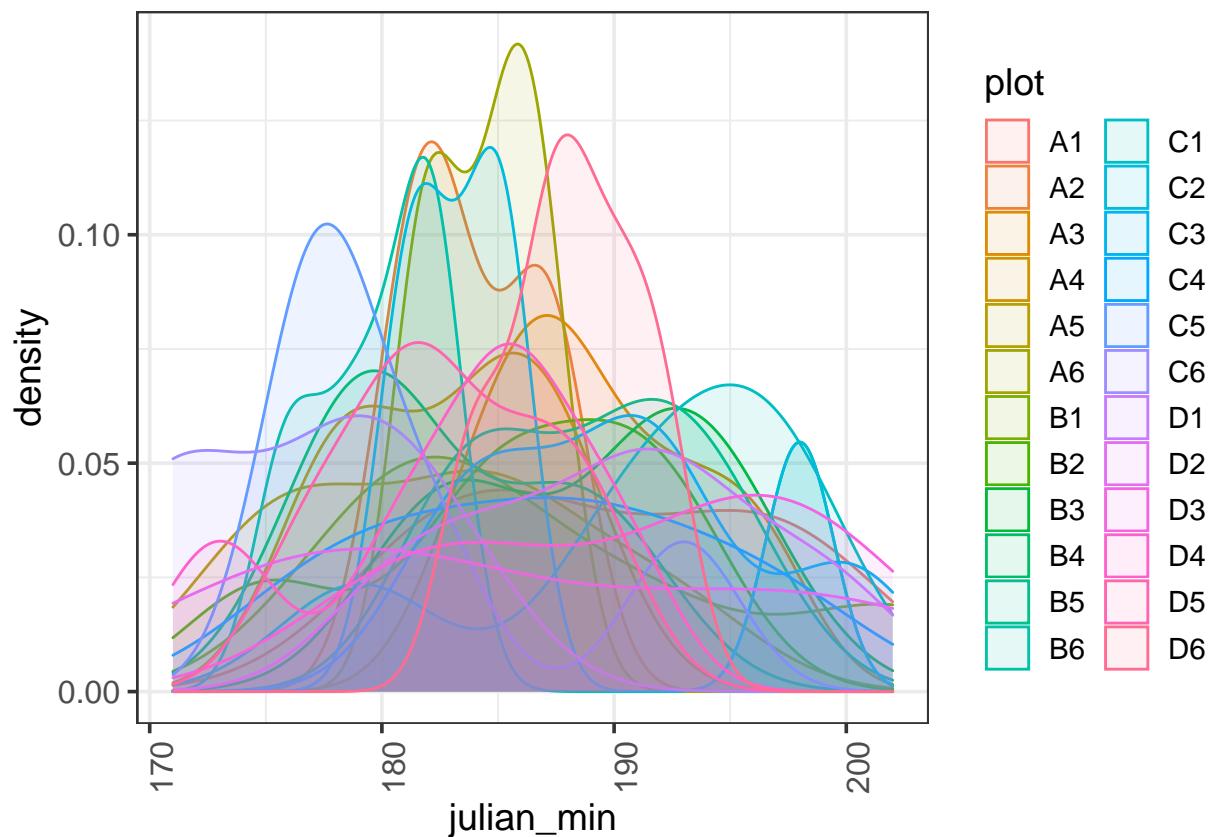
```

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

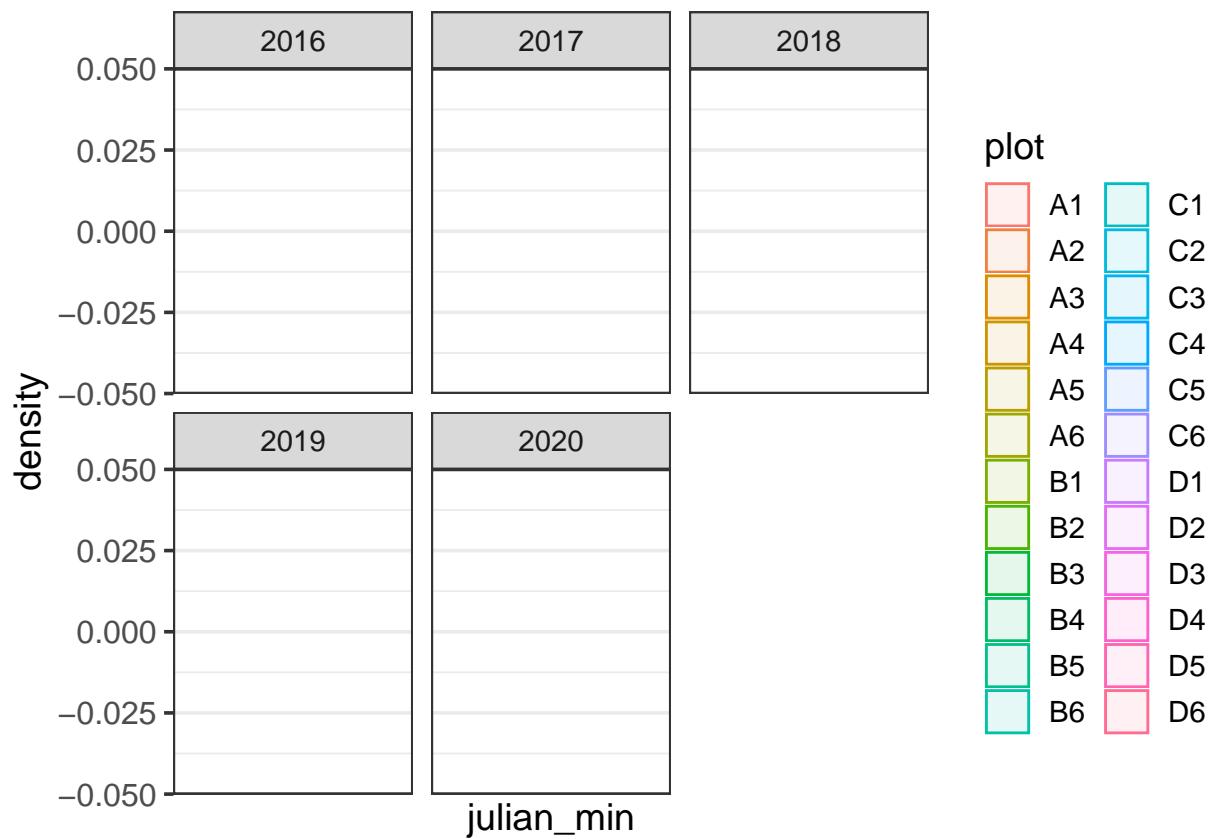
```



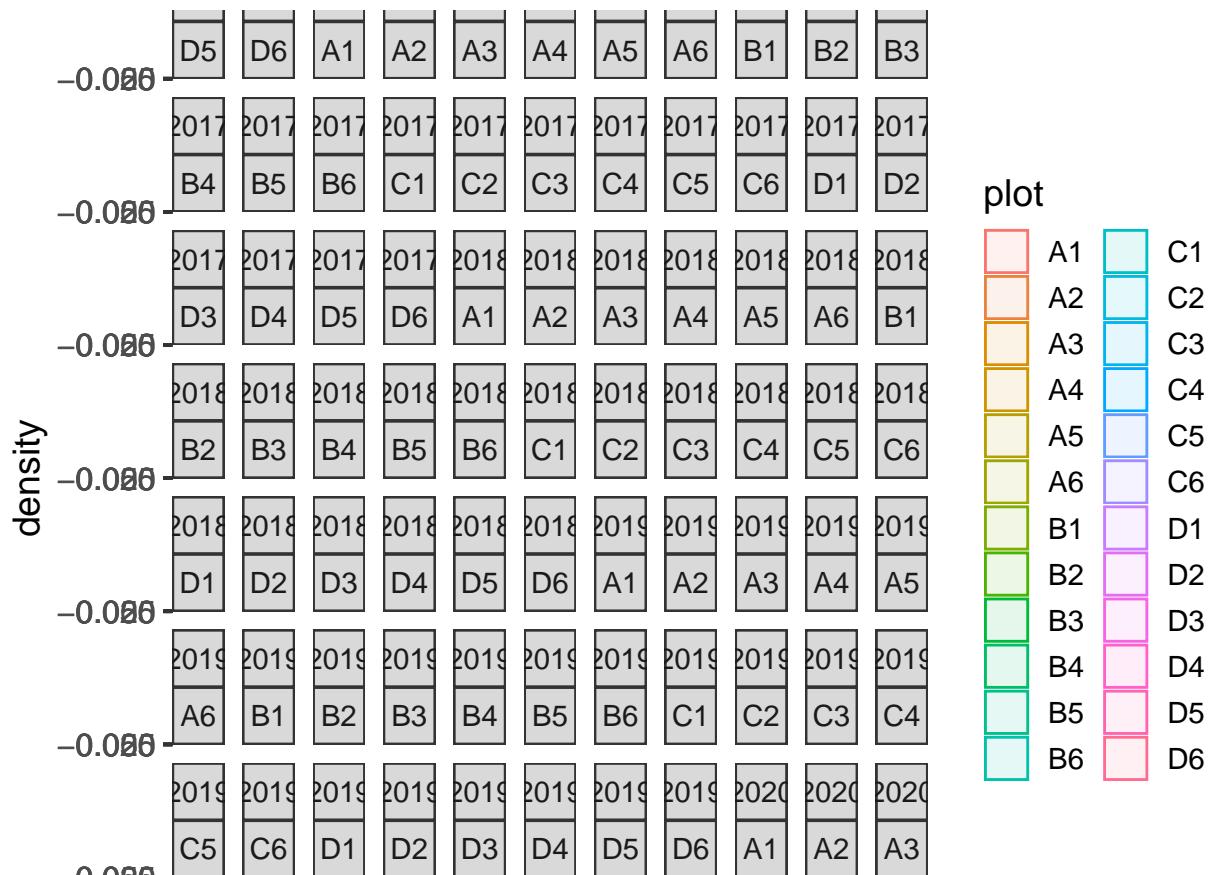
```
ggplot(umbs_sd_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

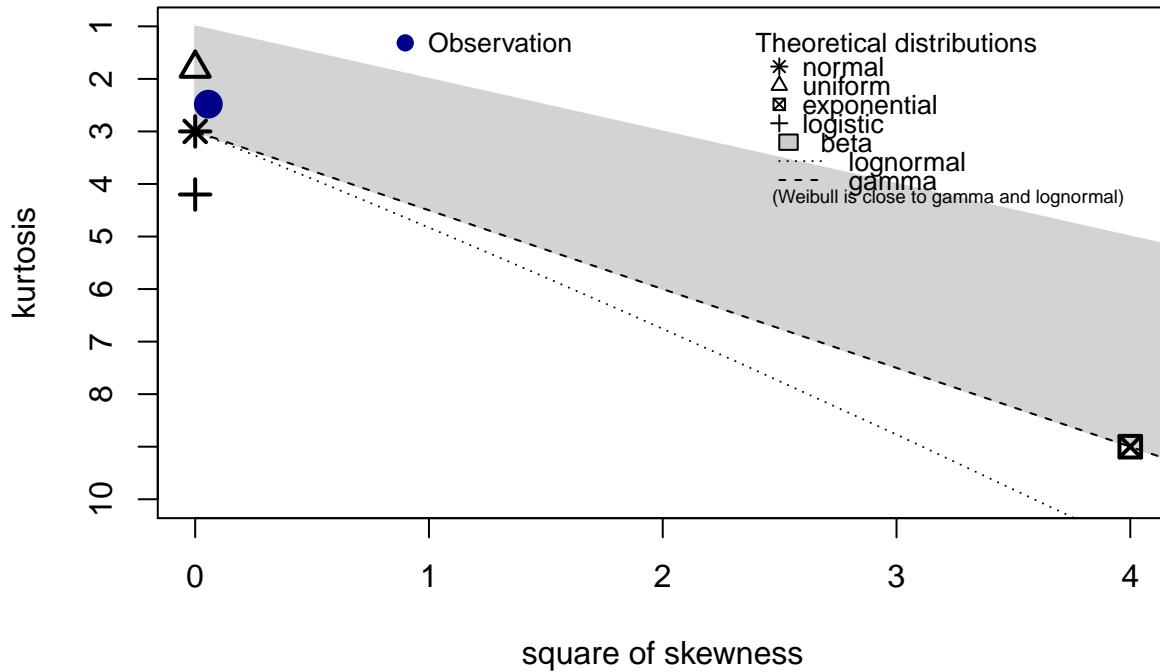


```
ggplot(umbs_sd_plot, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(umbs_sd_plot$julian_min, discrete = FALSE) # normal
```

Cullen and Frey graph



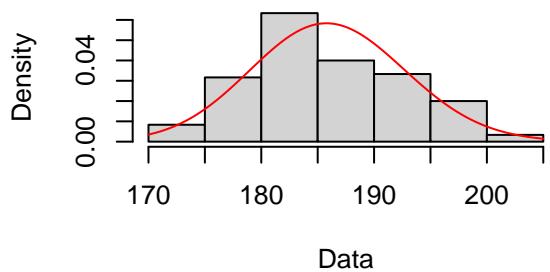
```

## summary statistics
## -----
## min: 171   max: 202
## median: 185
## mean: 186.025
## estimated sd: 6.886185
## estimated skewness: 0.2371013
## estimated kurtosis: 2.480561

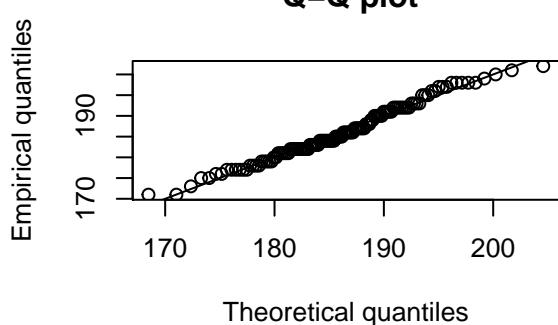
# Gamma distribution
fit.gamma <- fitdist(umbs_sd_plot$julian_min, "gamma")
plot(fit.gamma)

```

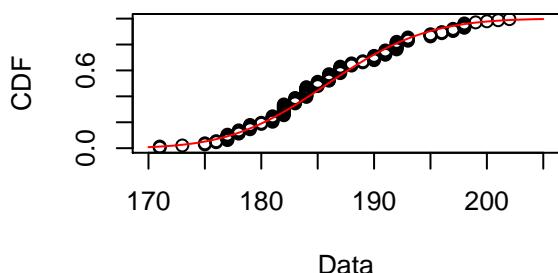
Empirical and theoretical dens.



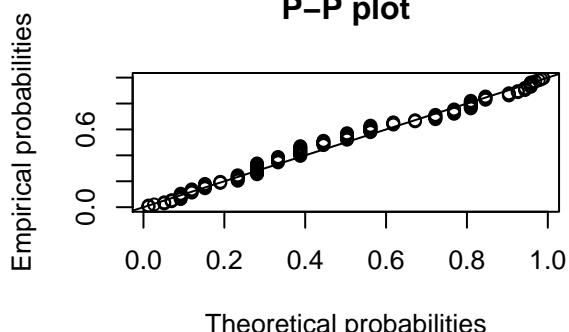
Q-Q plot



Empirical and theoretical CDFs

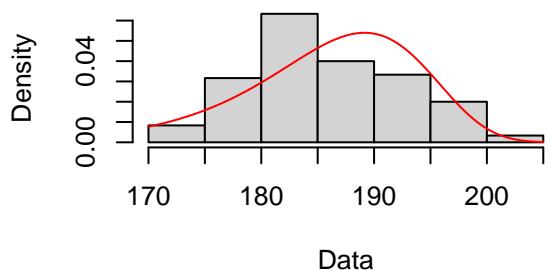


P-P plot

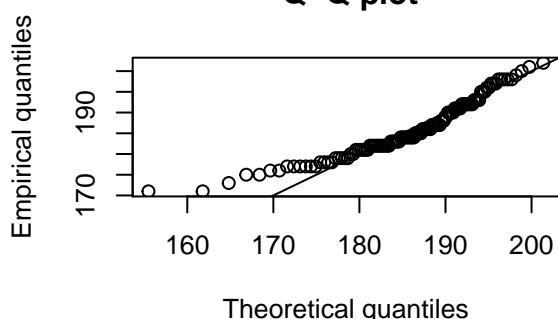


```
# Weibull distribution
fit.weibull <- fitdist(umbs_sd_plot$julian_min, "weibull")
plot(fit.weibull)
```

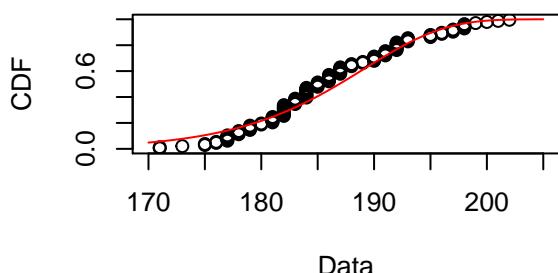
Empirical and theoretical dens.



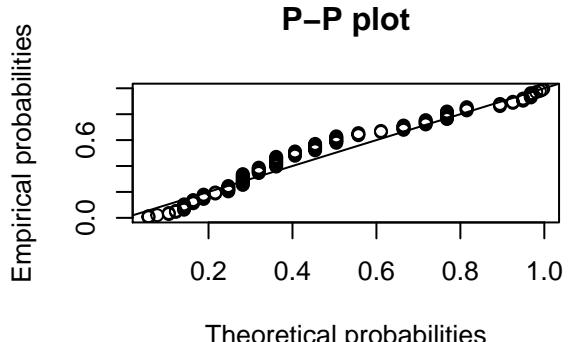
Q-Q plot



Empirical and theoretical CDFs

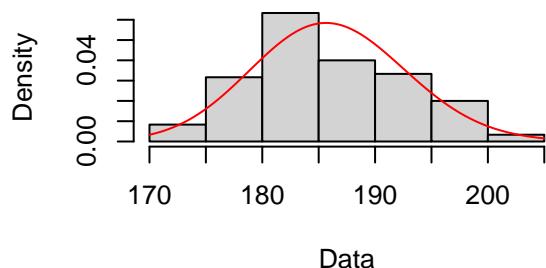


P-P plot

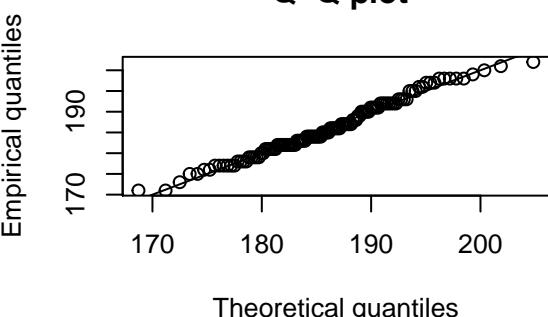


```
# Lognormal distribution
fit.ln <- fitdist(umbss_sd_plot$julian_min, "lnorm")
plot(fit.ln)
```

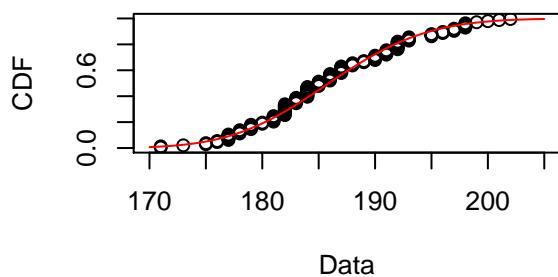
Empirical and theoretical dens.



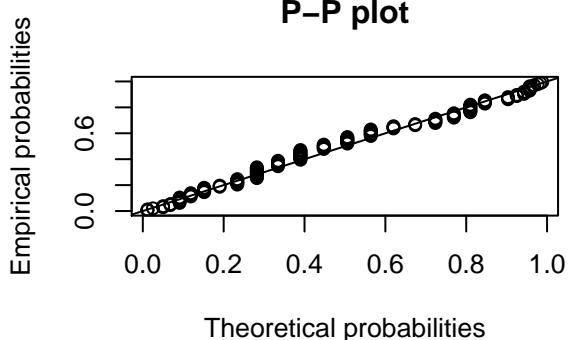
Q-Q plot



Empirical and theoretical CDFs

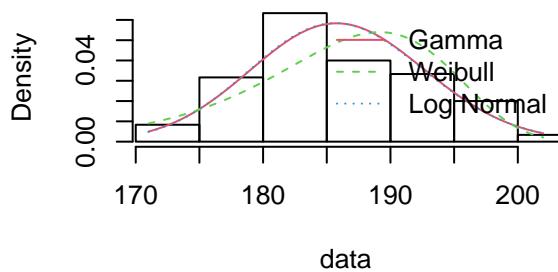


P-P plot

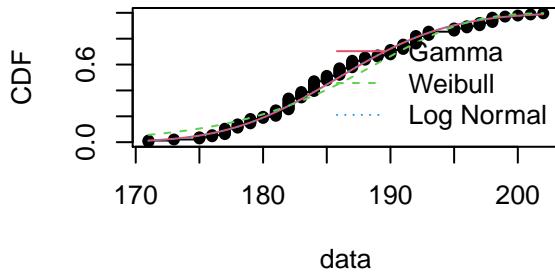


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

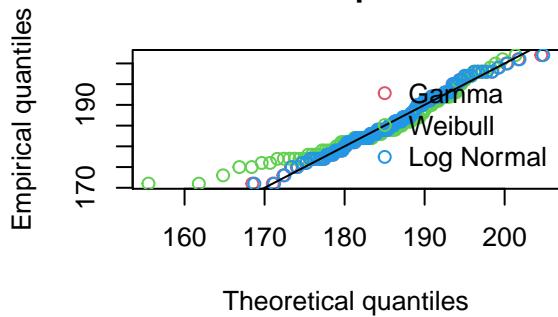
Histogram and theoretical densities



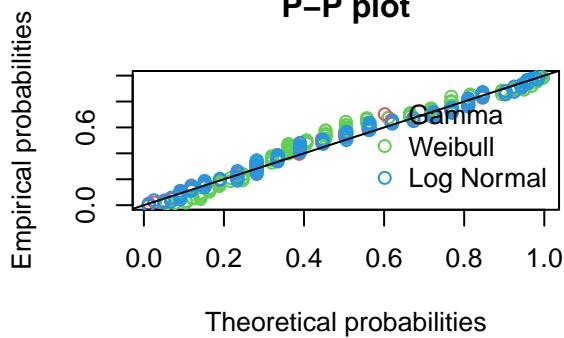
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

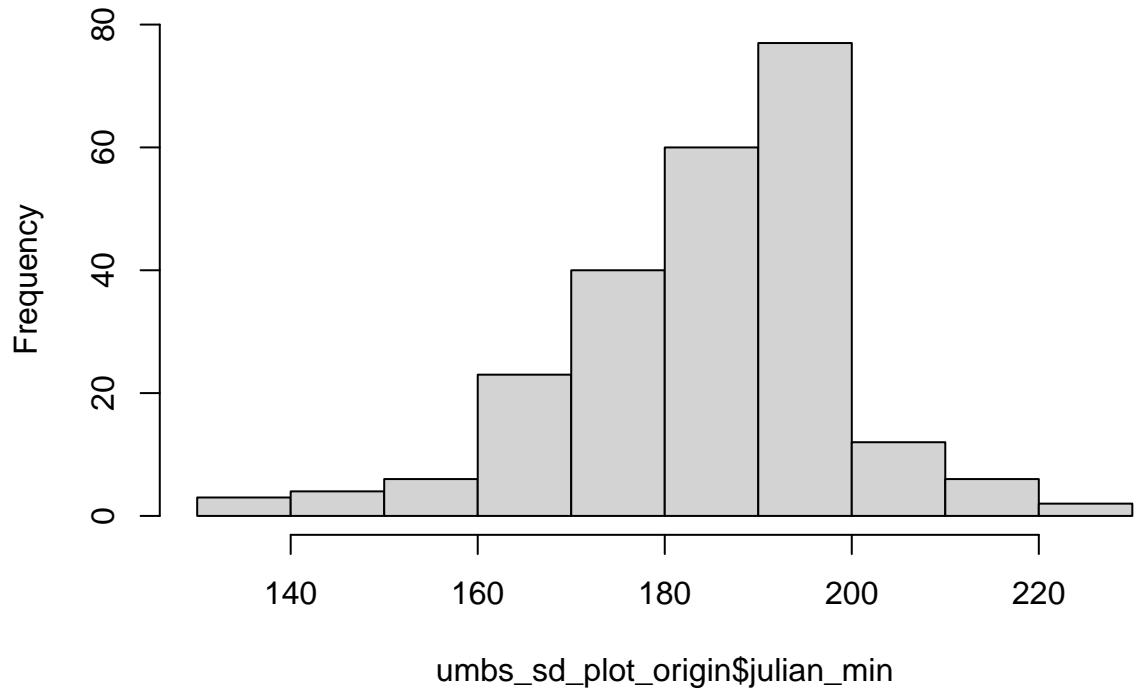
```
## Goodness-of-fit statistics
##                               Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.08708919 0.1288883 0.08502908
## Cramer-von Mises statistic   0.12292058 0.3832521 0.11613520
## Anderson-Darling statistic   0.70871844 2.3005633 0.67294119
##
## Goodness-of-fit criteria
##                               Gamma   Weibull Log Normal
## Akaike's Information Criterion 805.9965 824.5308 805.7474
## Bayesian Information Criterion 811.5715 830.1058 811.3224
```

```
# log normal is slightly better here but going to go with a normal transformation
# for umbs seed set at the plot level based on graphs and shapiro test above
```

UMBS PLOT LEVEL ORIGIN - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

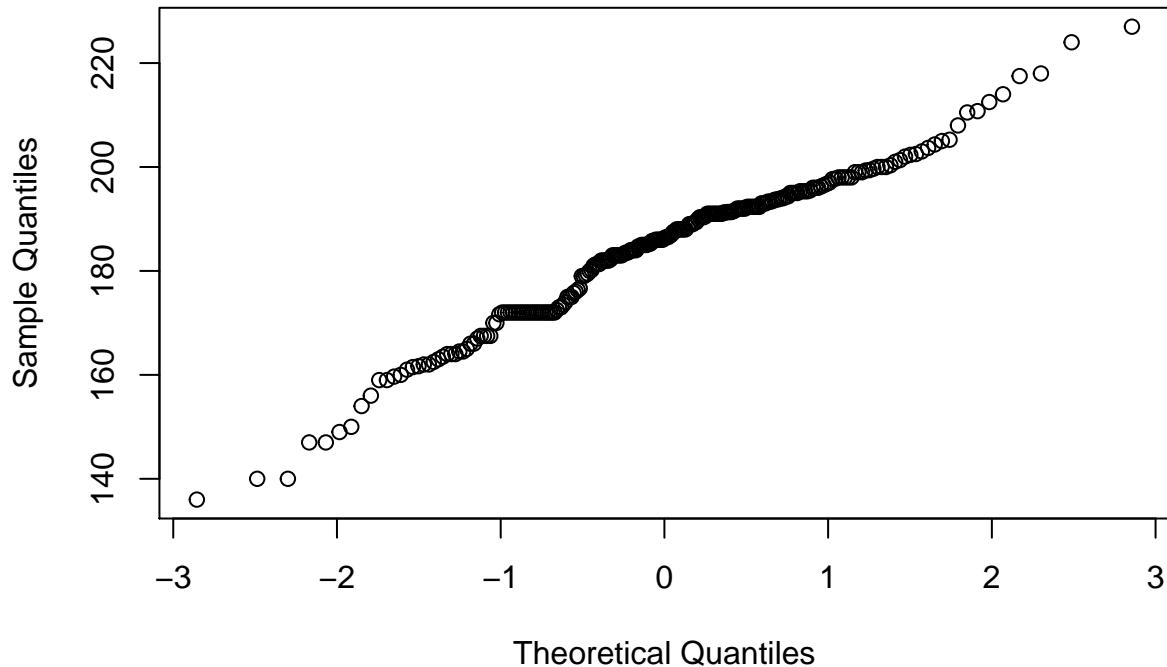
```
### UMBS ####
hist(umbs_sd_plot_origin$julian_min)
```

Histogram of umbs_sd_plot_origin\$julian_min



```
qqnorm(umbs_sd_plot_origin$julian_min)
```

Normal Q-Q Plot



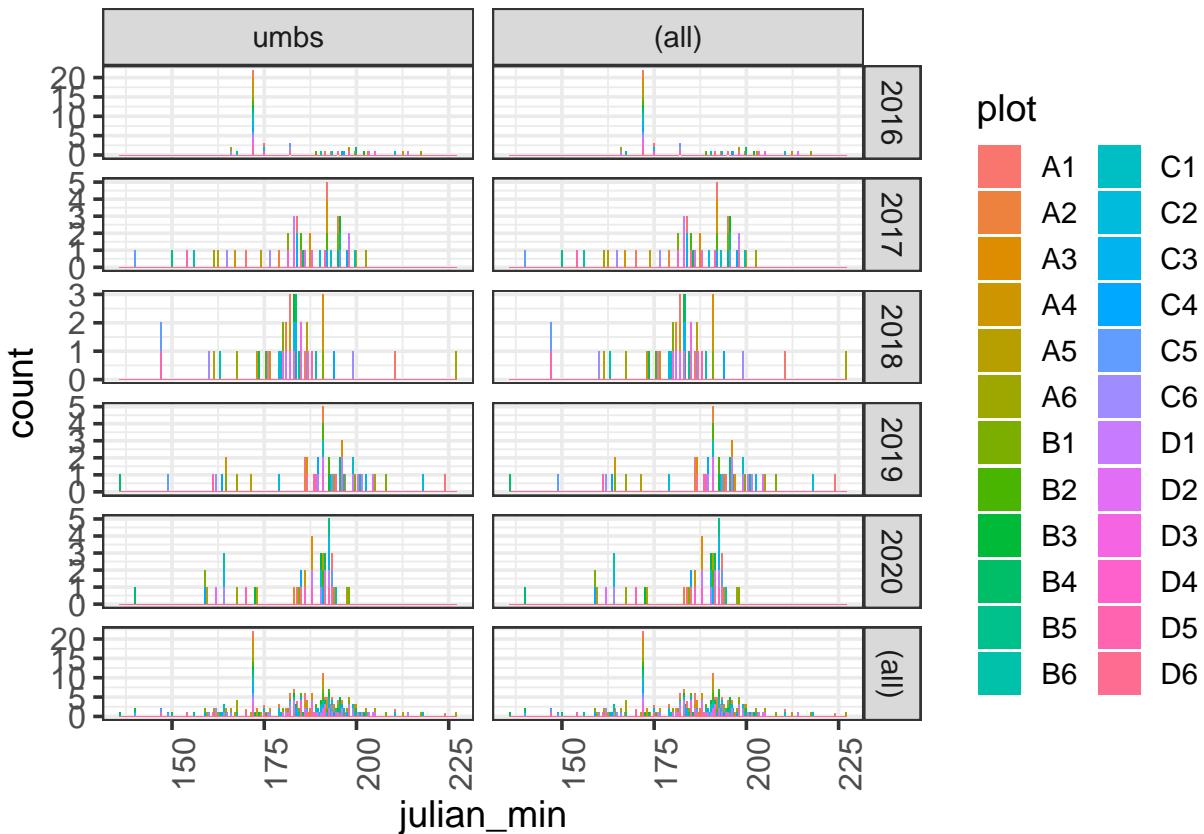
```

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

##
## Shapiro-Wilk normality test
##
## data: umbs_sd_plot_origin$julian_min
## W = 0.97337, p-value = 0.000226

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

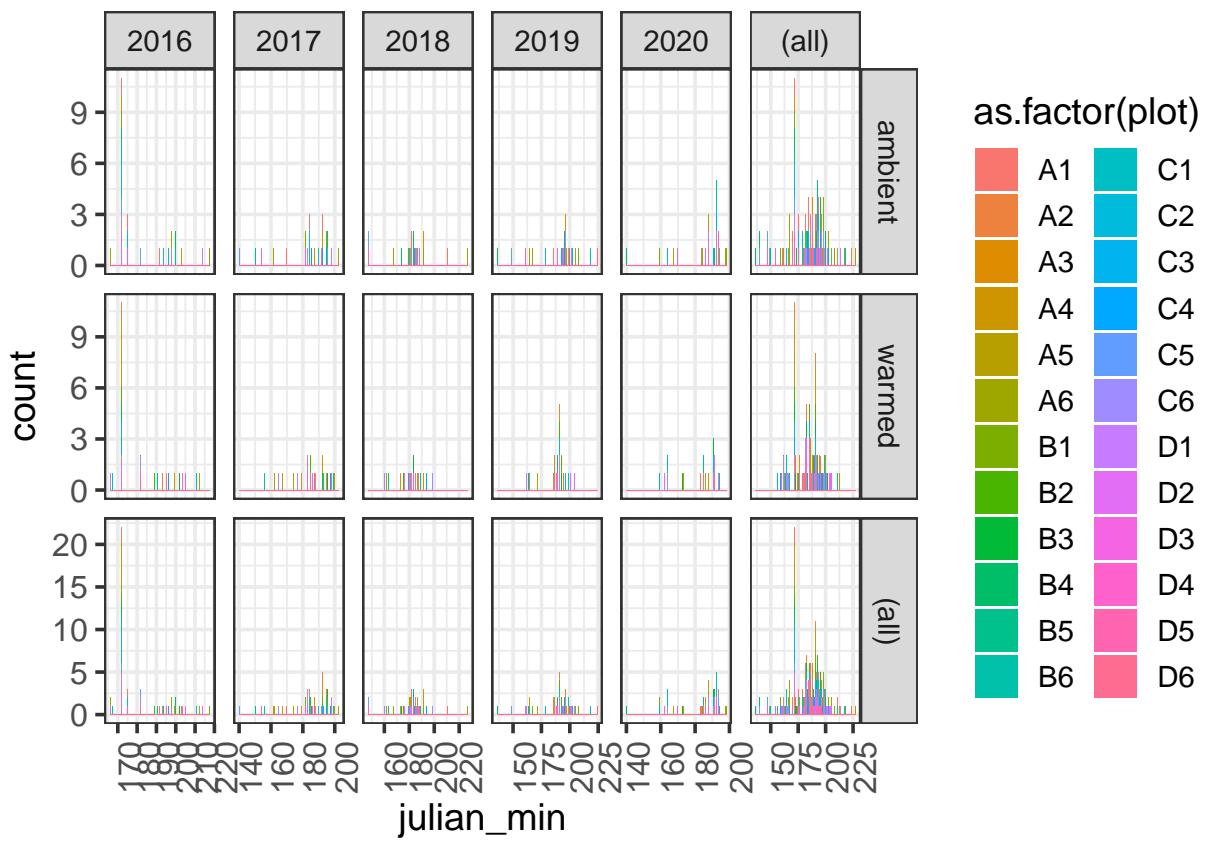
```



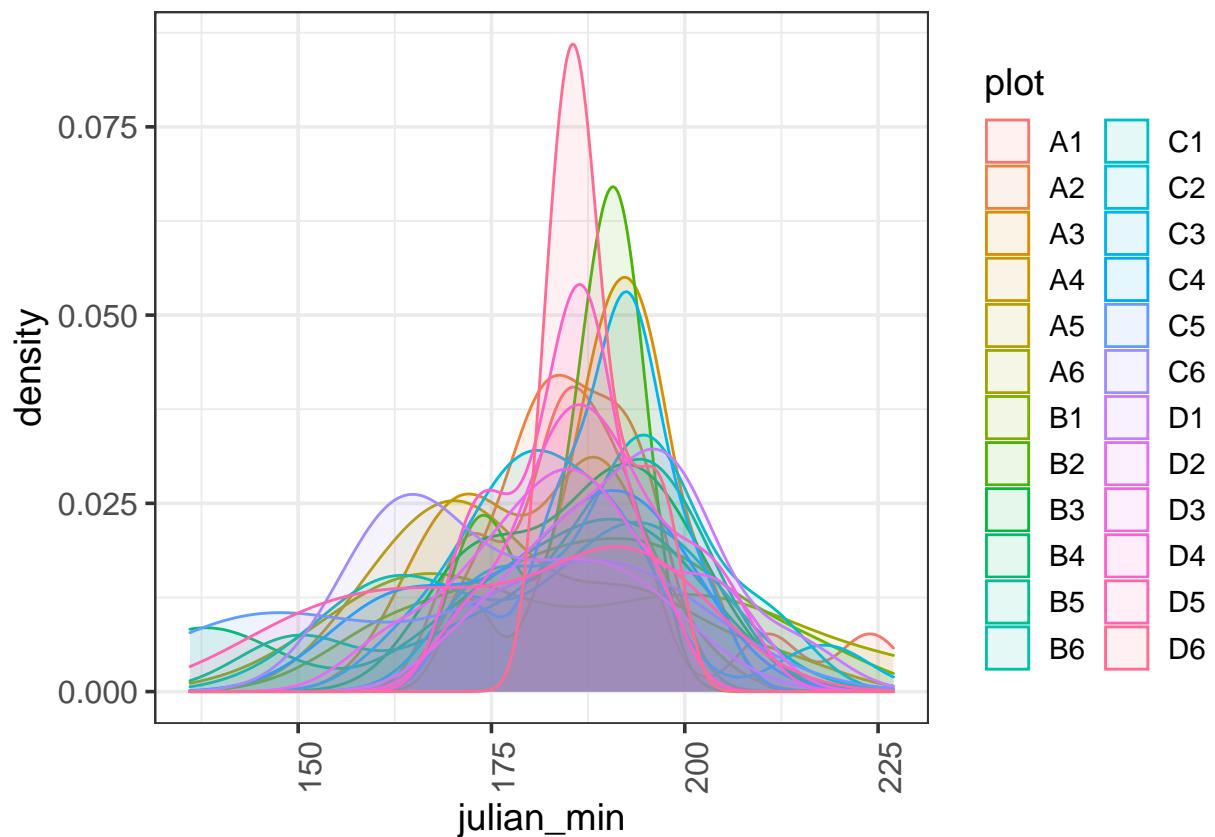
```

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

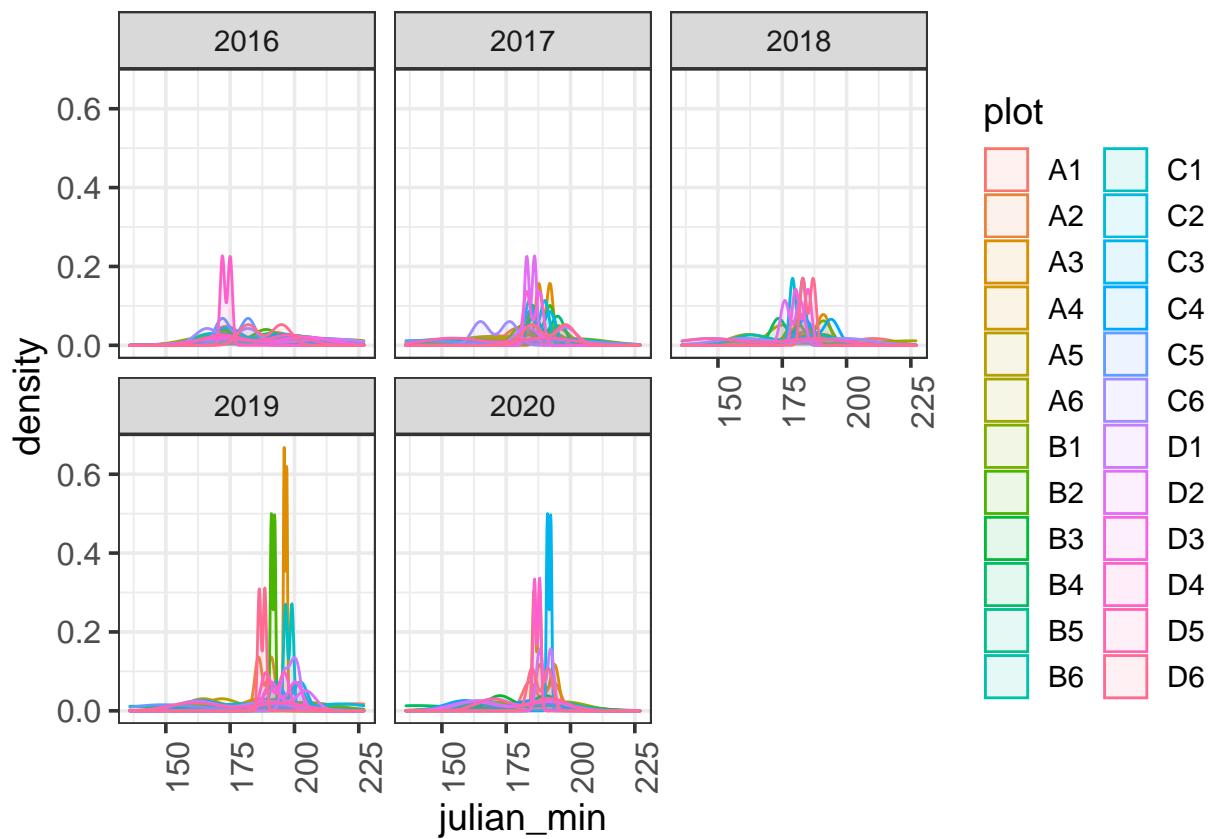
```



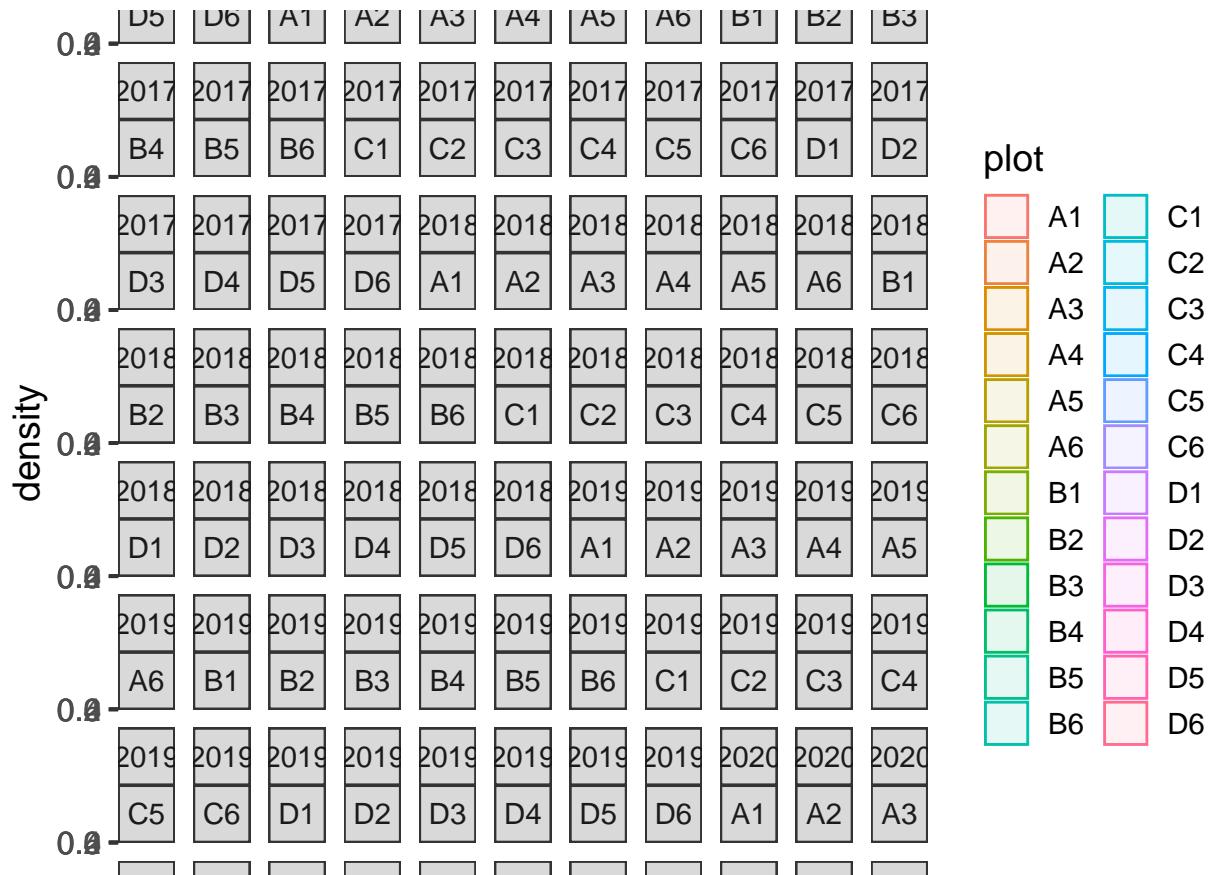
```
ggplot(umbs_sd_plot_origin, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

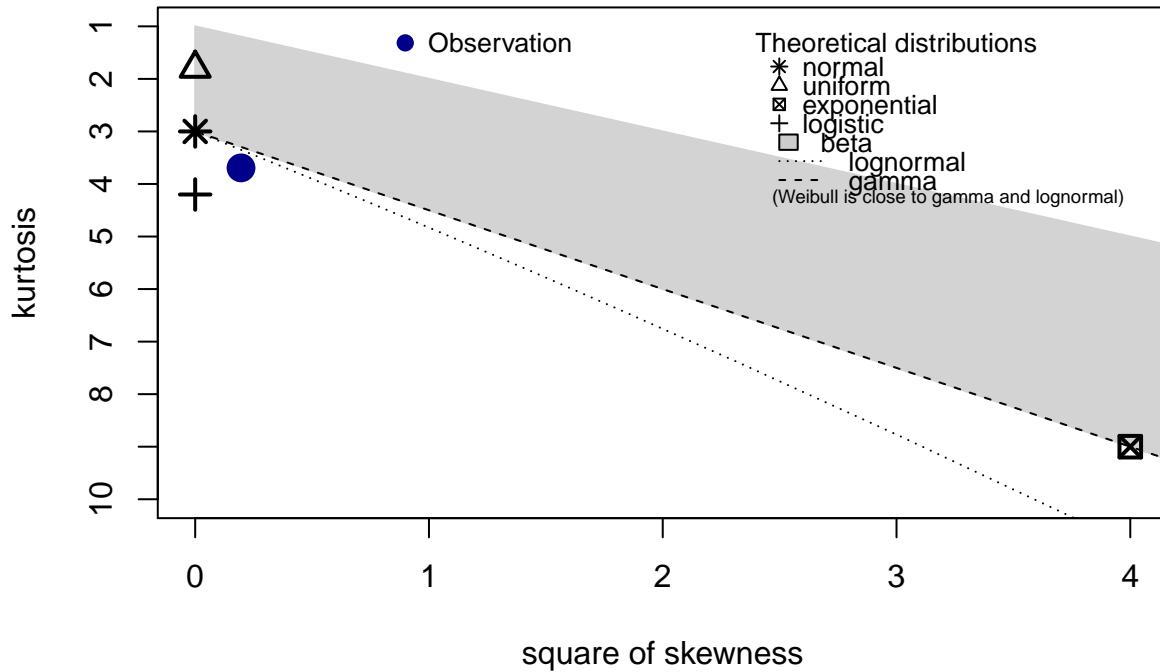


```
ggplot(umbs_sd_plot_origin, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these data:  
descdist(umbs_sd_plot_origin$julian_min, discrete = FALSE)
```

Cullen and Frey graph

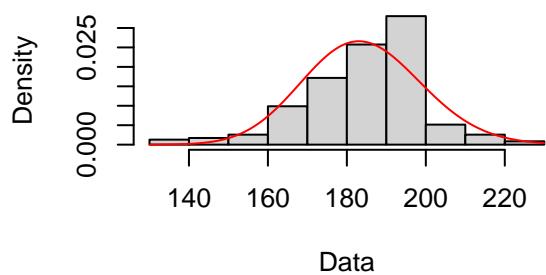
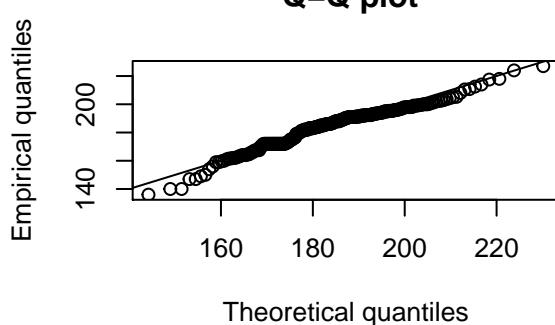
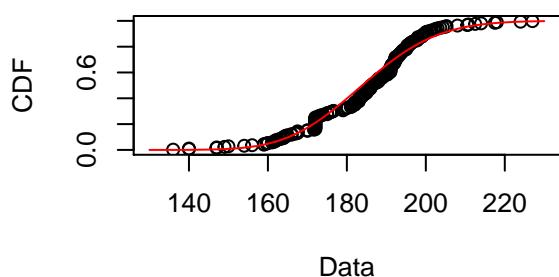
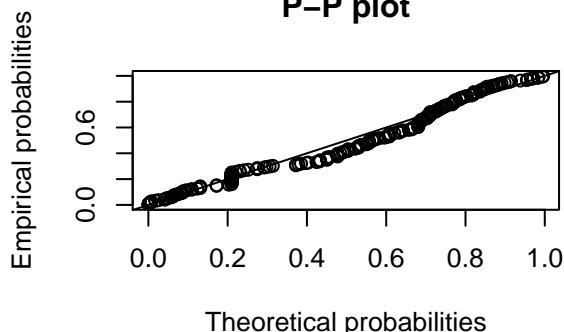


```

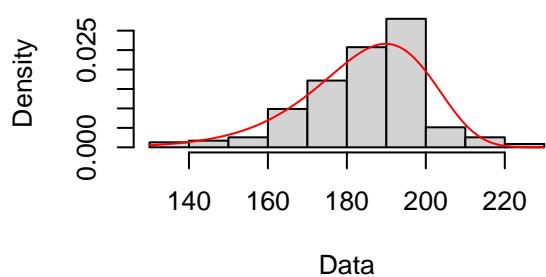
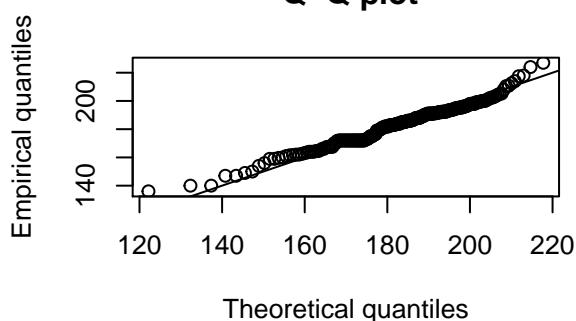
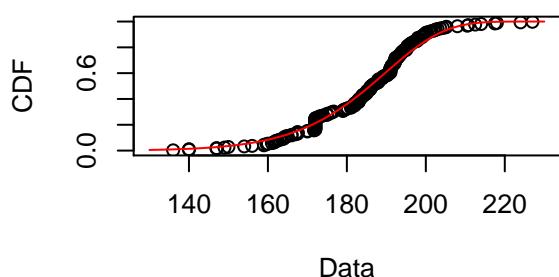
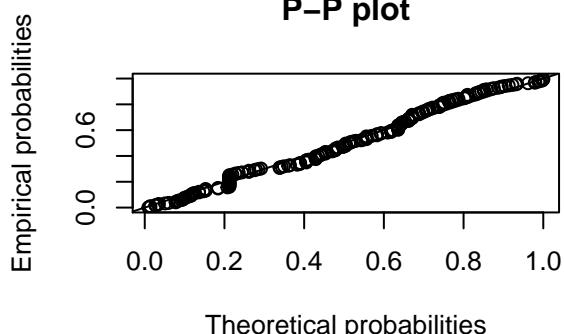
## summary statistics
## -----
## min: 136   max: 227
## median: 186.3333
## mean: 184.2609
## estimated sd: 14.82065
## estimated skewness: -0.4428369
## estimated kurtosis: 3.693731

# Gamma distribution
fit.gamma <- fitdist(umbs_sd_plot_origin$julian_min, "gamma")
plot(fit.gamma)

```

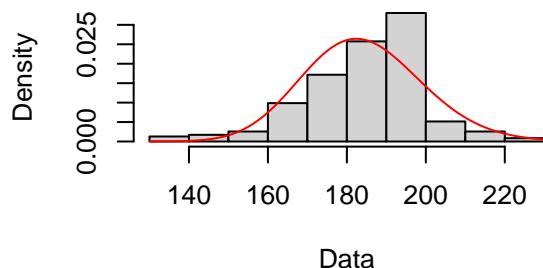
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

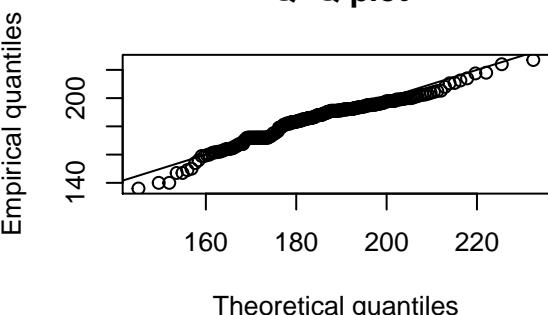
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

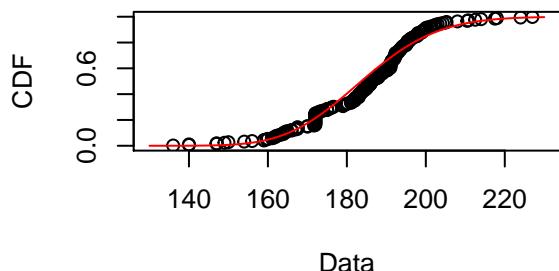
Empirical and theoretical dens.



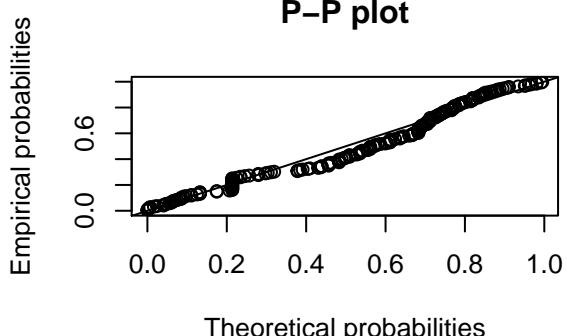
Q-Q plot



Empirical and theoretical CDFs

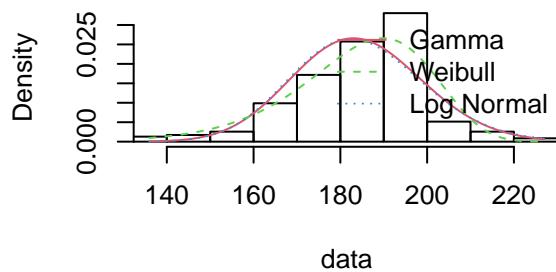


P-P plot

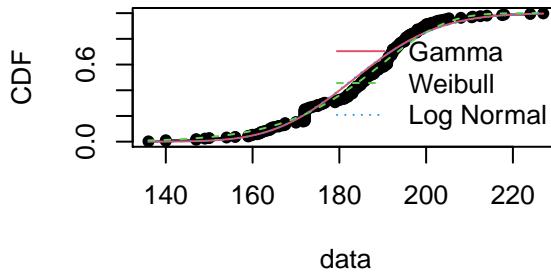


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

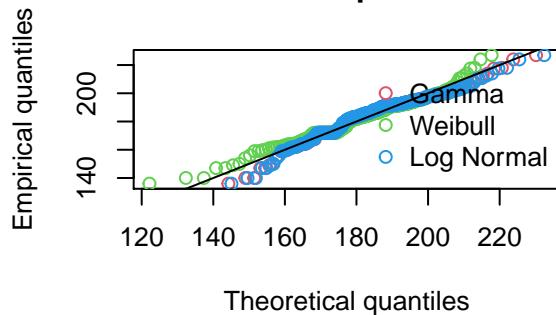
Histogram and theoretical densities



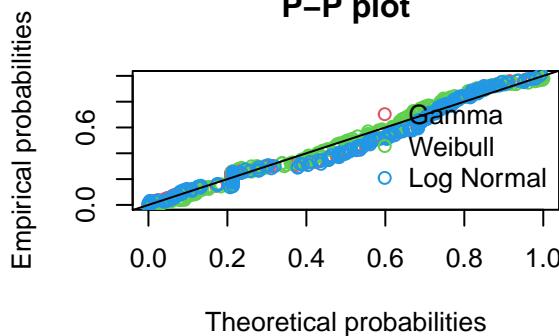
Empirical and theoretical CDFs



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"))

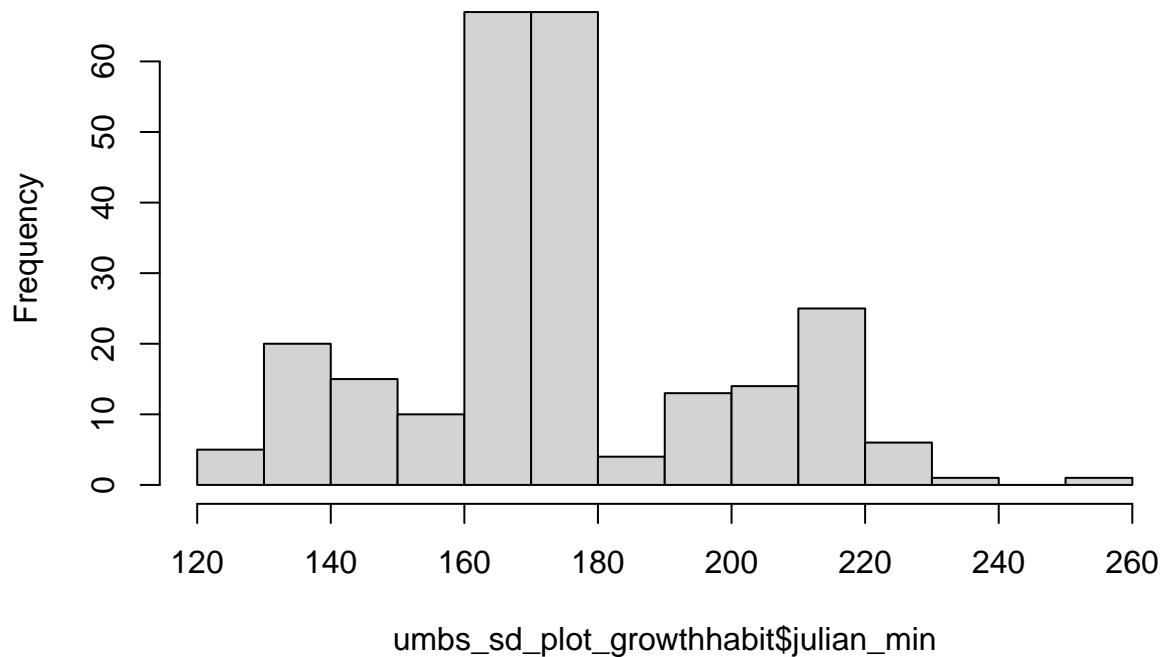
## Goodness-of-fit statistics
##                                     Gamma    Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.1039092 0.06597959 0.1095598
## Cramer-von Mises statistic   0.5724530 0.26609180 0.6386879
## Anderson-Darling statistic   3.0359342 1.87536361 3.3972035
##
## Goodness-of-fit criteria
##                                     Gamma    Weibull Log Normal
## Akaike's Information Criterion 1927.599 1924.254 1932.034
## Bayesian Information Criterion 1934.501 1931.156 1938.937

# log normal looks like it's the best fit
```

UMBS PLOT LEVEL GROWTH HABIT - Looking at MINIMUM JULIAN DAY (aka date of observed first seed set)

```
### UMBS ####
hist(umbs_sd_plot_growthhabit$julian_min)
```

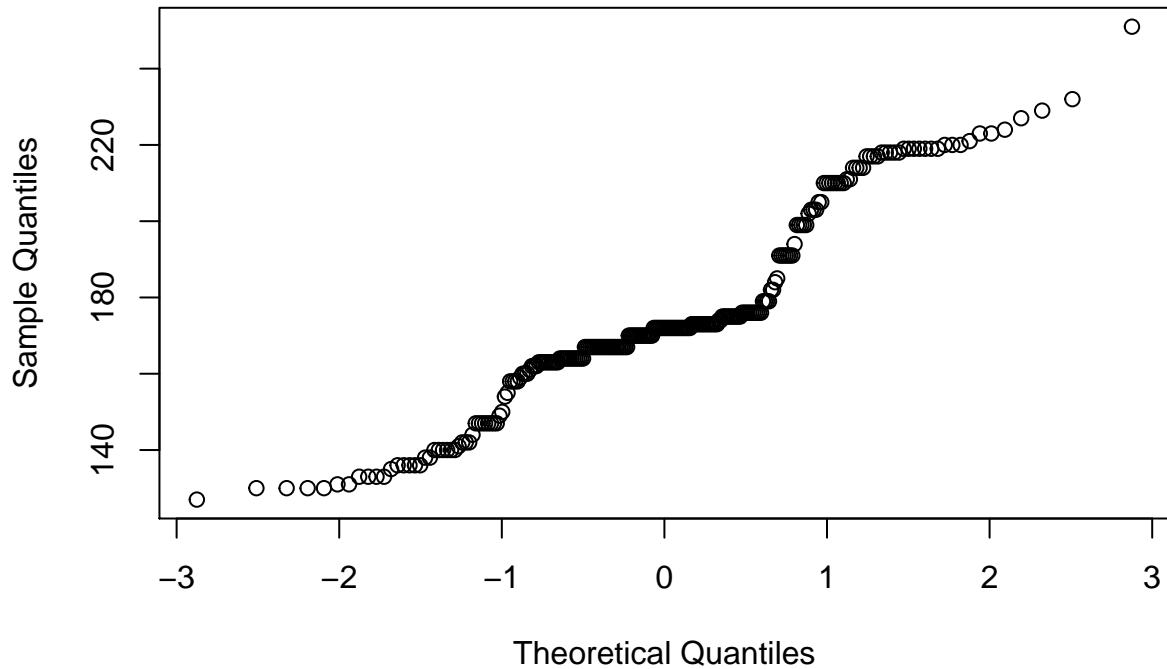
Histogram of umbs_sd_plot_growthhabit\$julian_min



umbs_sd_plot_growthhabit\$julian_min

```
qqnorm(umbss_sd_plot_growthhabit$julian_min)
```

Normal Q-Q Plot



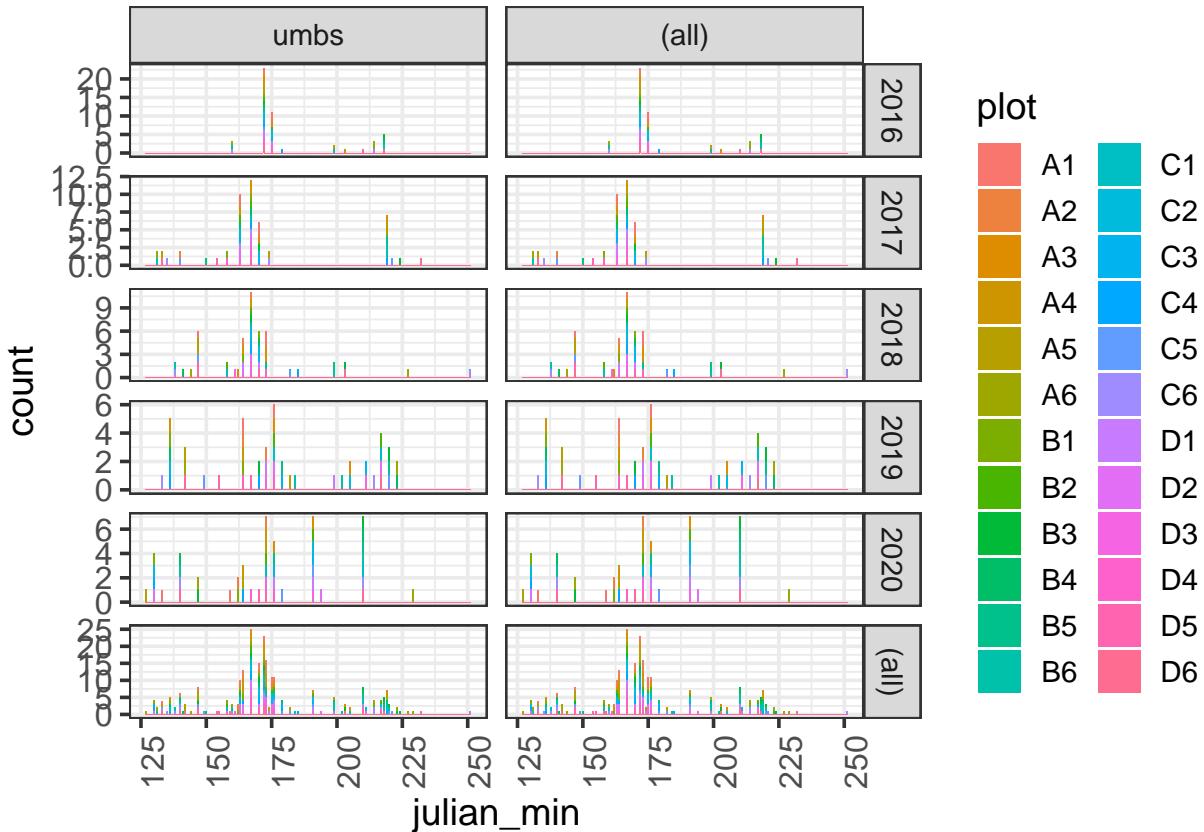
```

shapiro.test(umbs_sd_plot_growthhabit$julian_min) # pvalue is < 0.05 so we reject the null hypothesis

## 
## Shapiro-Wilk normality test
## 
## data: umbs_sd_plot_growthhabit$julian_min
## W = 0.9322, p-value = 2.951e-09

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

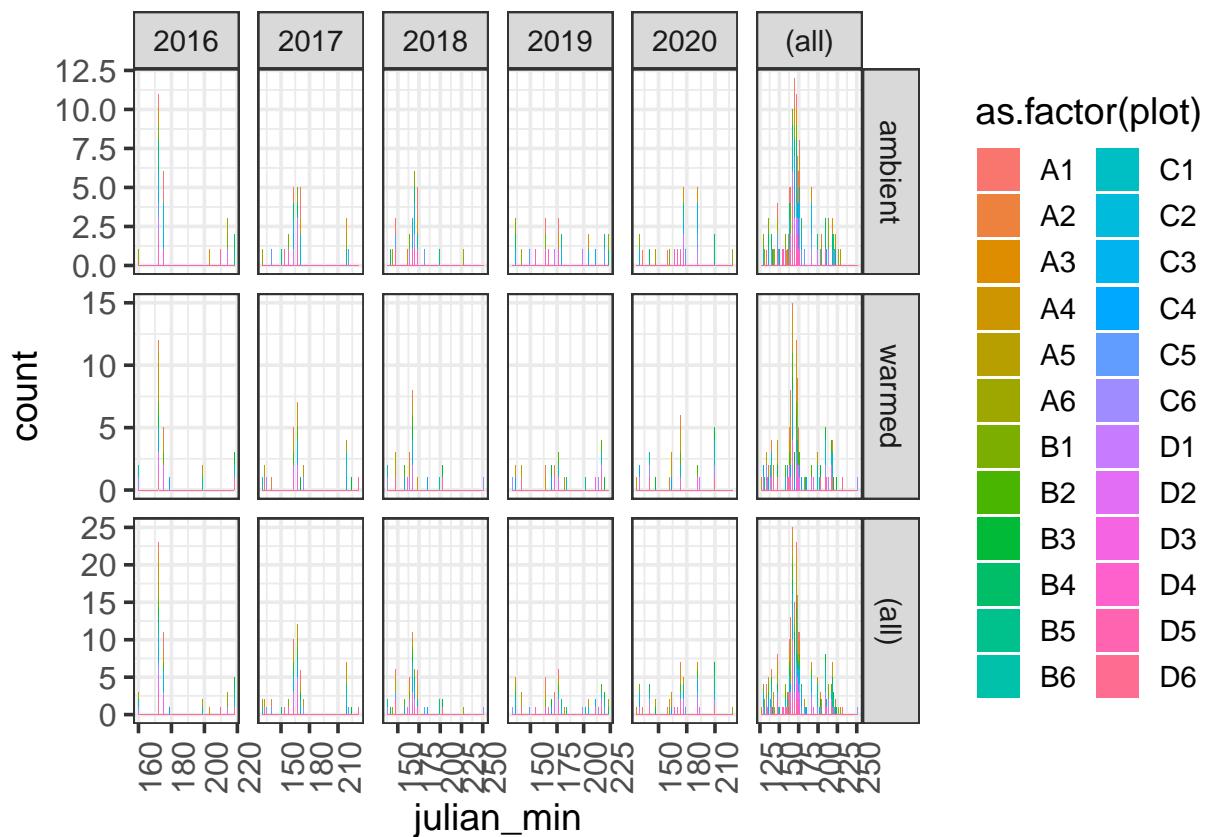
```



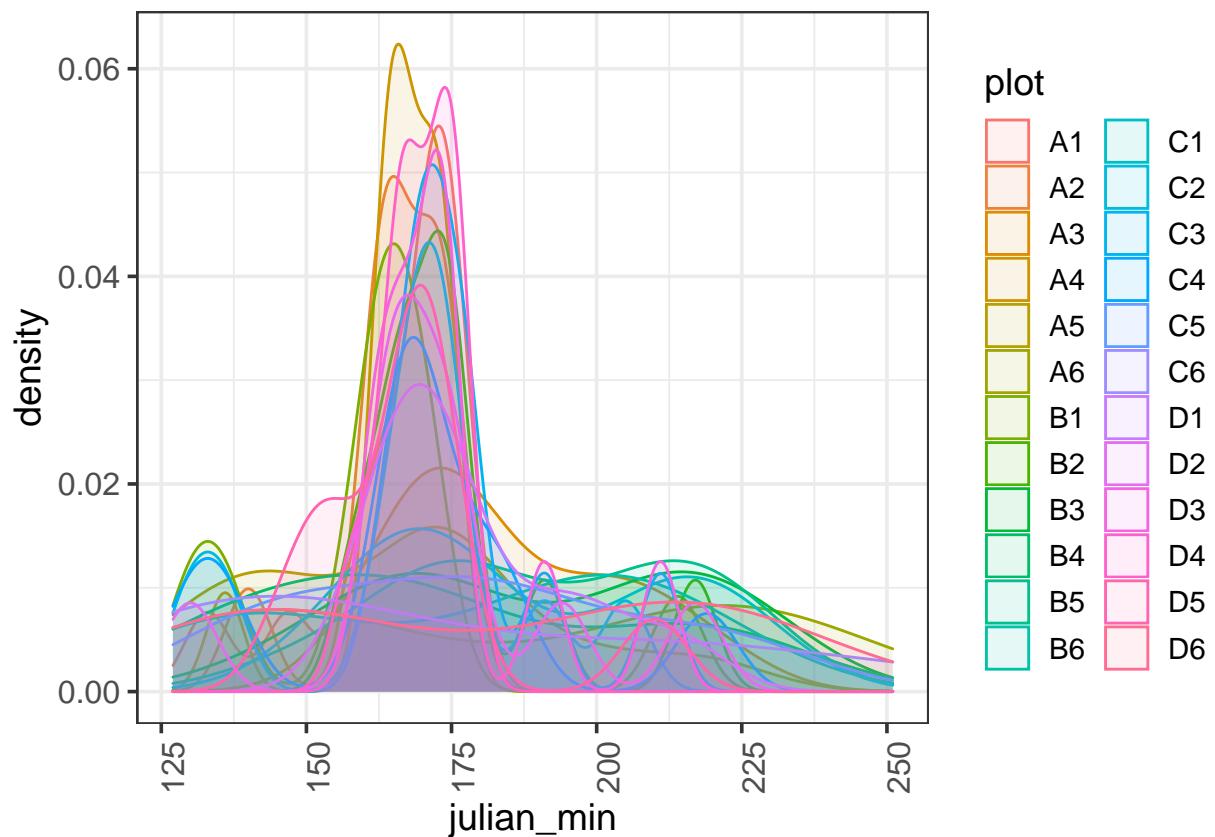
```

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

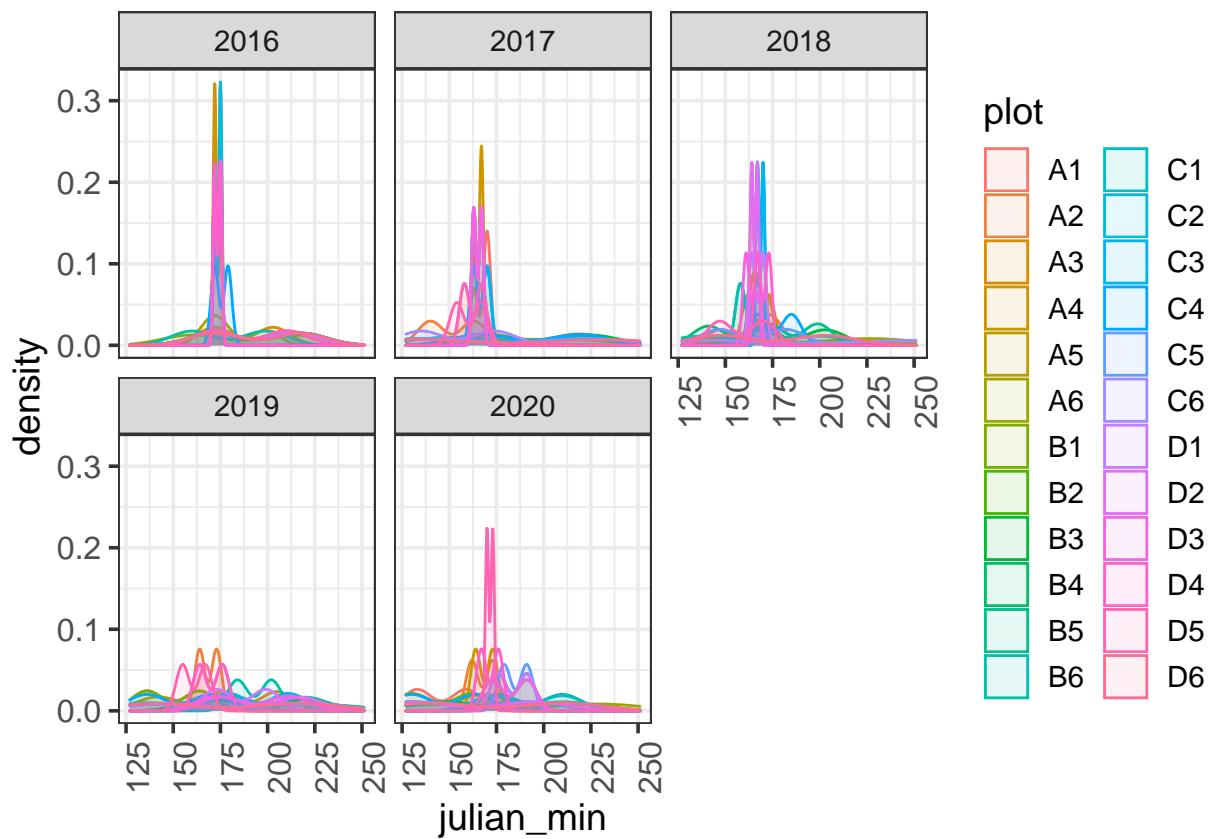
```



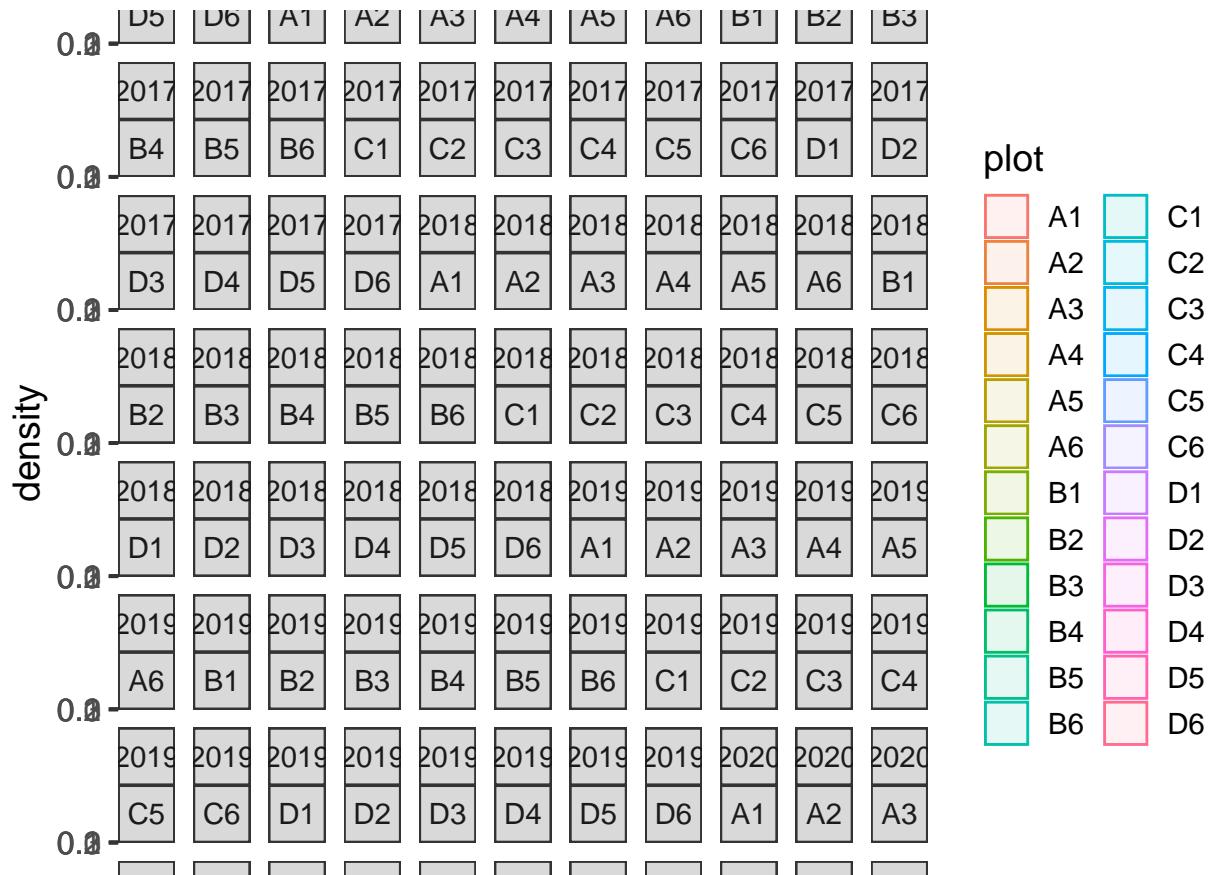
```
ggplot(umbs_sd_plot_growthhabit, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



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

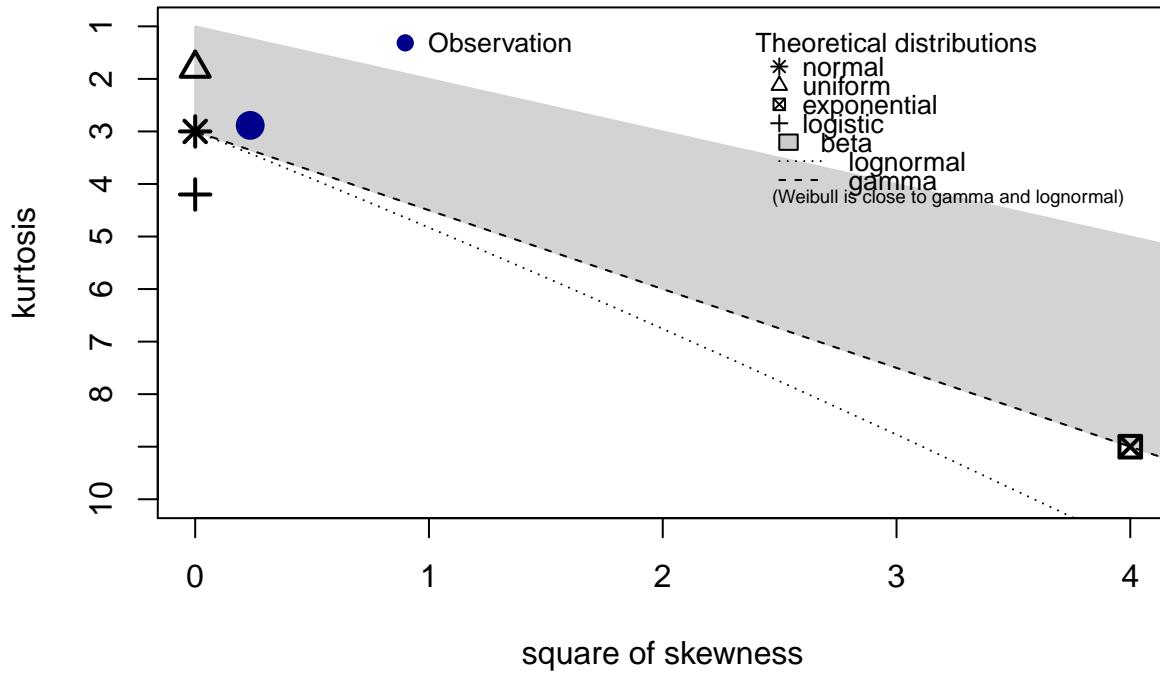


```
ggplot(umbs_sd_plot_growthhabit, aes(julian_min, fill = plot, color = plot)) + geom_density(alpha = 0.1)
  facet_wrap(~year + plot)
```



```
# Exploring distributions for these data:  
descdist(umbs_sd_plot_growthhabit$julian_min, discrete = FALSE)
```

Cullen and Frey graph



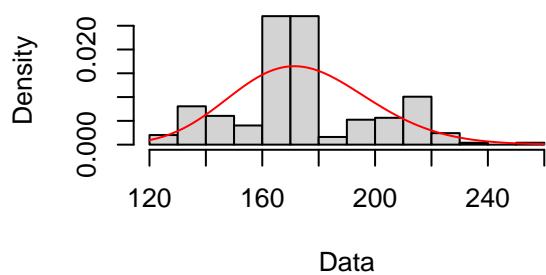
```

## summary statistics
## -----
## min: 127   max: 251
## median: 172
## mean: 174.7581
## estimated sd: 24.71714
## estimated skewness: 0.4851066
## estimated kurtosis: 2.884973

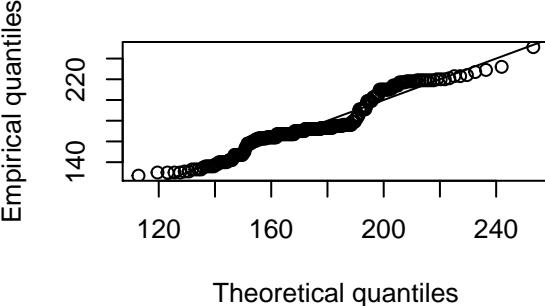
# Gamma distribution
fit.gamma <- fitdist(umbs_sd_plot_growthhabit$julian_min, "gamma")
plot(fit.gamma)

```

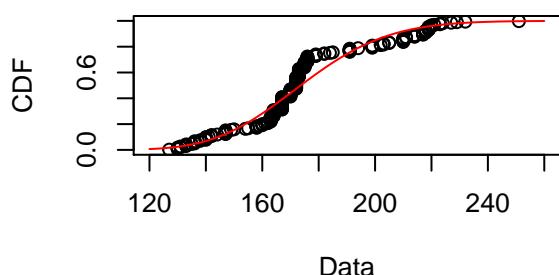
Empirical and theoretical dens.



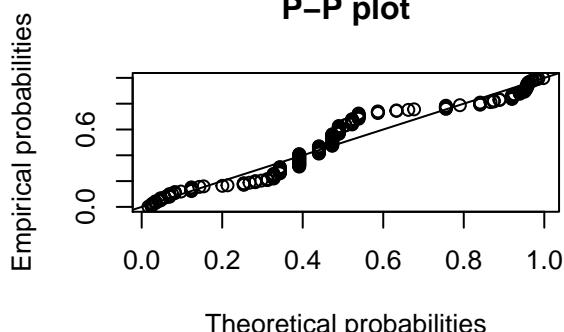
Q-Q plot



Empirical and theoretical CDFs

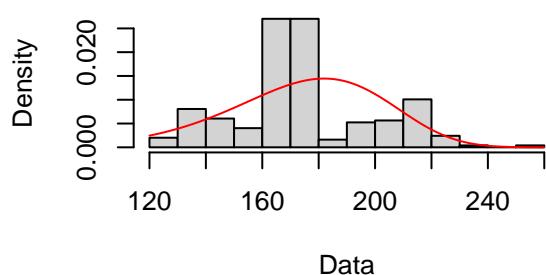


P-P plot

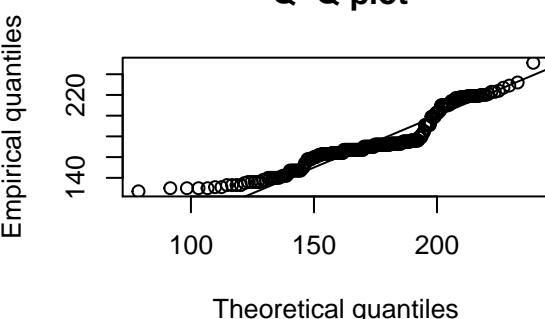


```
# Weibull distribution
fit.weibull <- fitdist(umbs_sd_plot_growthhabit$julian_min, "weibull")
plot(fit.weibull)
```

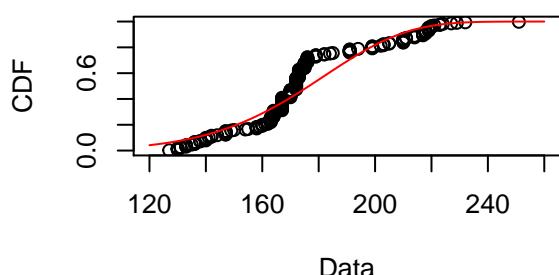
Empirical and theoretical dens.



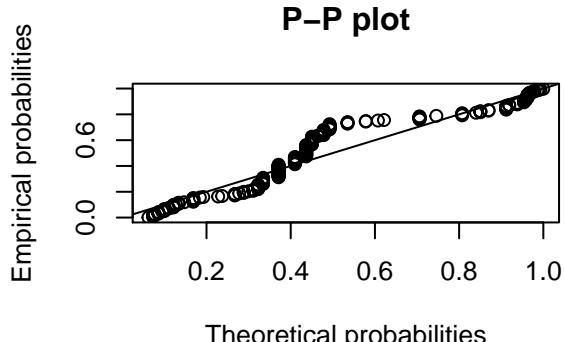
Q-Q plot



Empirical and theoretical CDFs

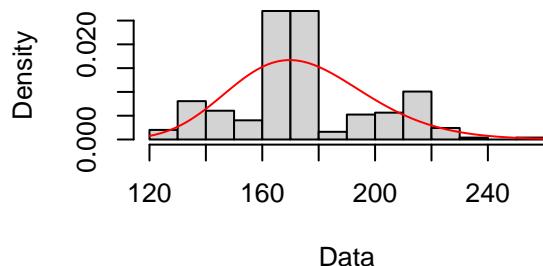


P-P plot

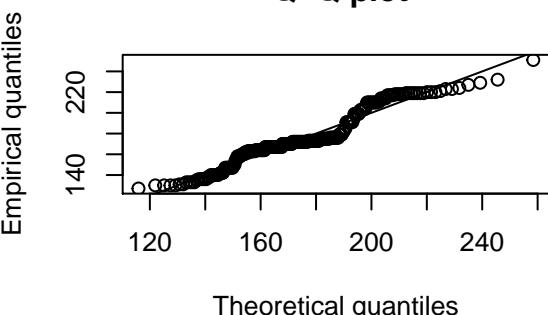


```
# Lognormal distribution
fit.ln <- fitdist(umbs_sd_plot_growthhabit$julian_min, "lnorm")
plot(fit.ln)
```

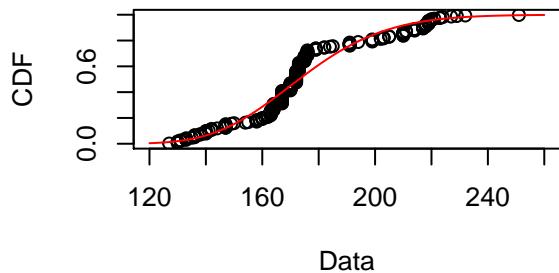
Empirical and theoretical dens.



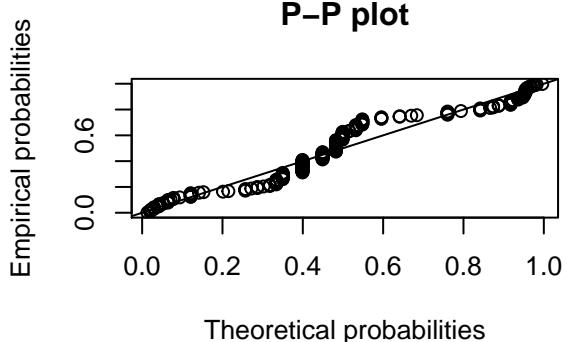
Q-Q plot



Empirical and theoretical CDFs

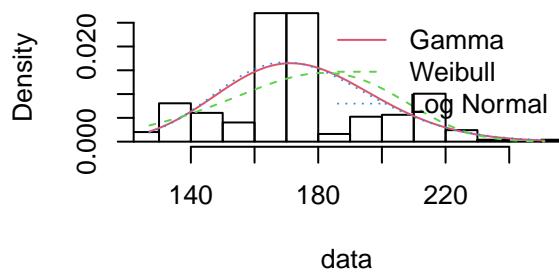


P-P plot

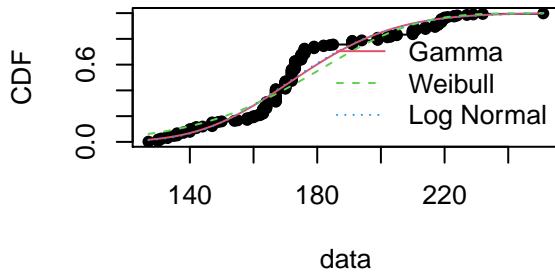


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

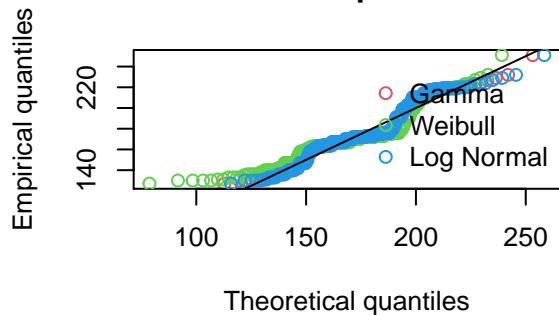
Histogram and theoretical densities



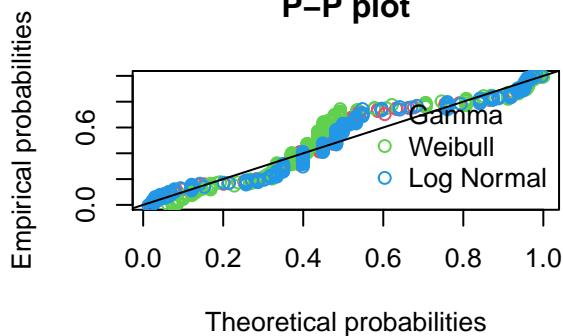
Empirical and theoretical CDFs



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 0.1870698 0.2335321 0.1776961
## Cramer-von Mises statistic   1.3110891 2.1292901 1.2248073
## Anderson-Darling statistic   6.6239300 10.5105885 6.2406073
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 2289.017 2328.736 2286.855
## Bayesian Information Criterion 2296.044 2335.763 2293.882
```

```
# Log normal looks like it's the best fit
```

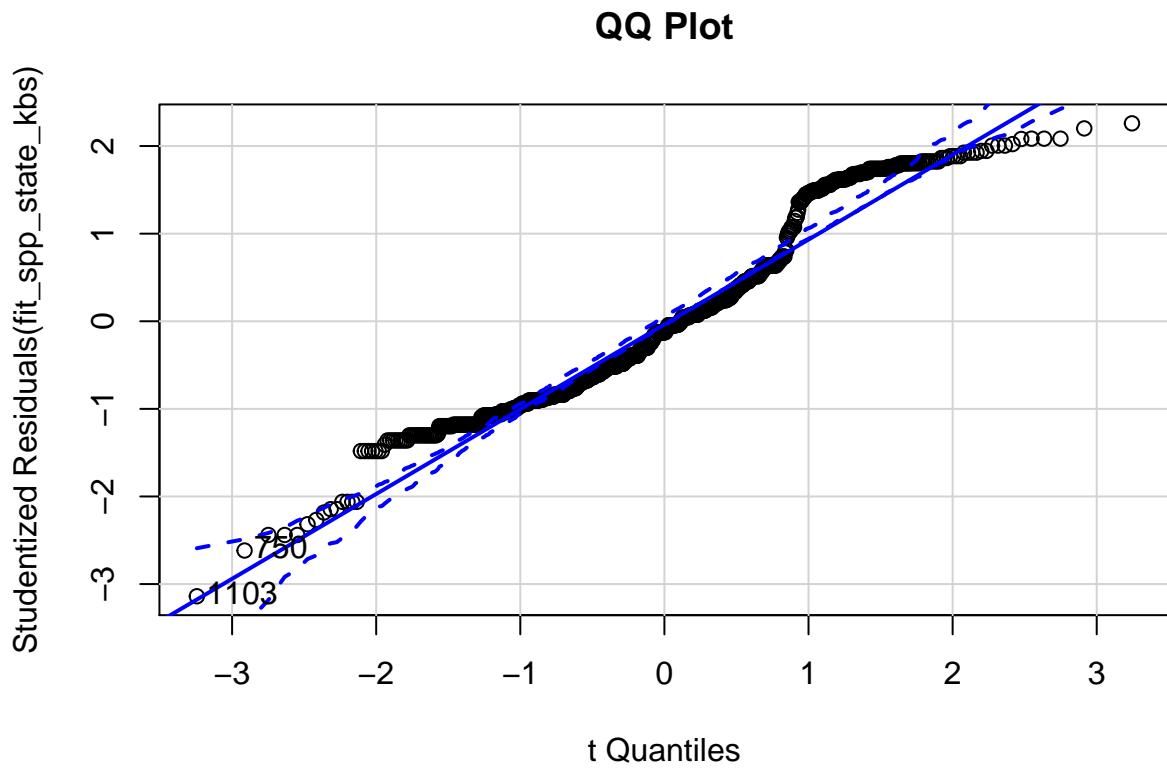
Leverage plots and detecting Outliers. <https://www.statmethods.net/stats/rdiagnostics.html>

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>

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

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1103 -3.139037      0.0017562        NA
```

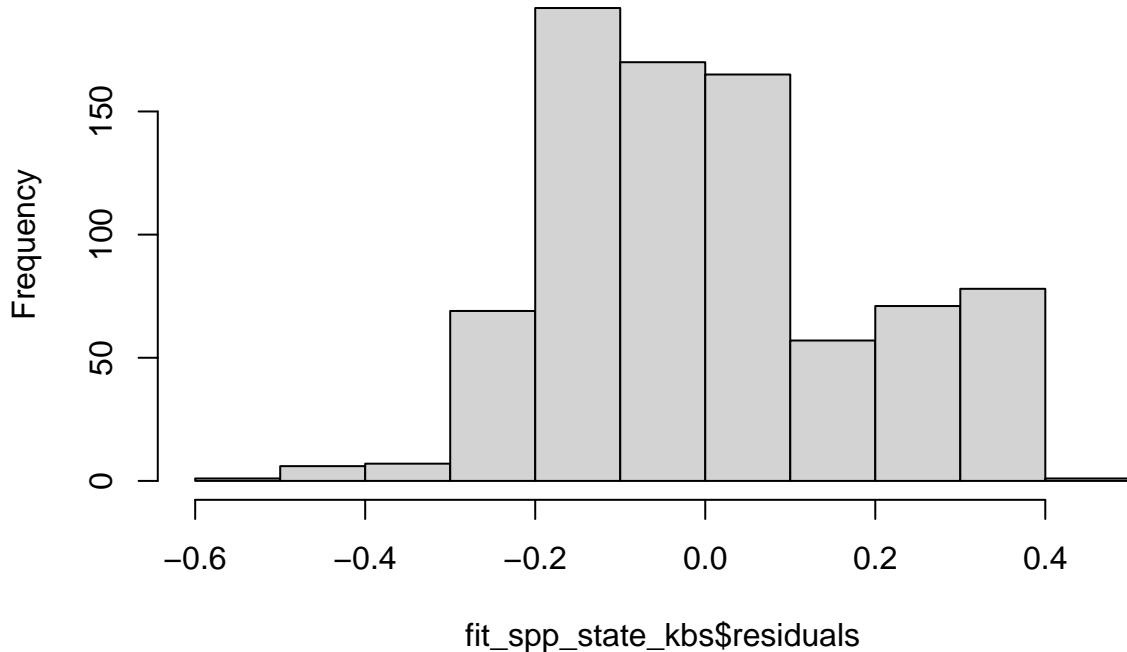
```
qqPlot(fit_spp_state_kbs, main = "QQ Plot")
```



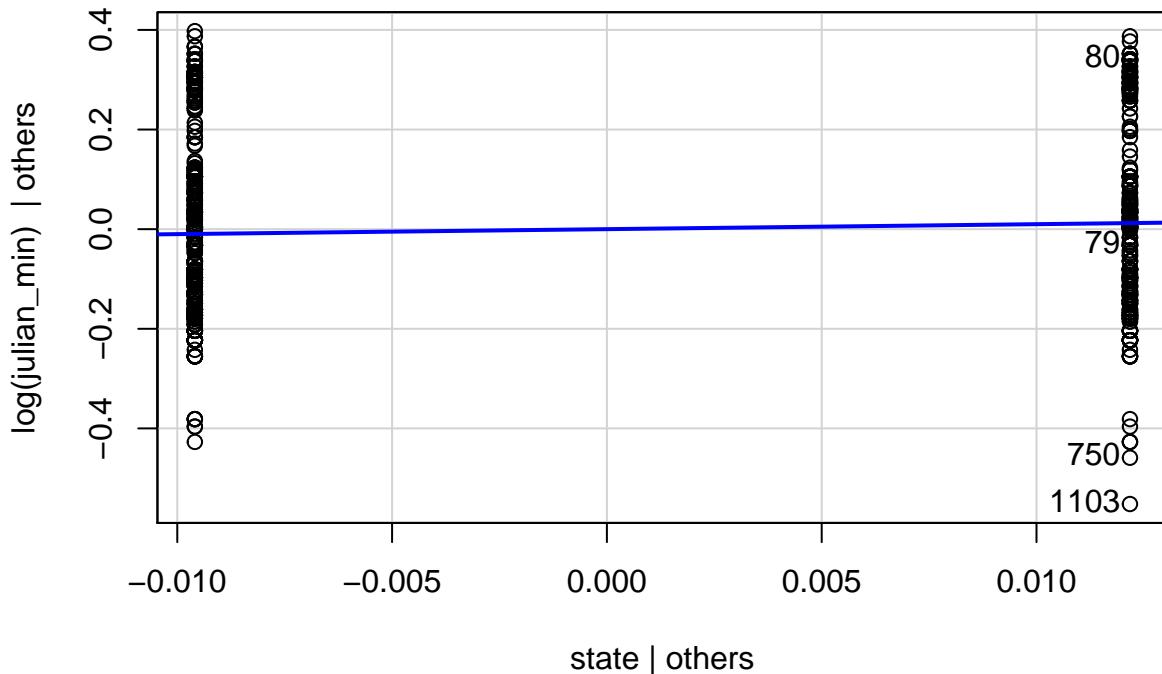
```
##   750 1103
##   433 642
```

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

Histogram of fit_spp_state_kbs\$residuals



```
leveragePlots(fit_spp_state_kbs)
```



```
ols_test_normality(fit_spp_state_kbs)
```

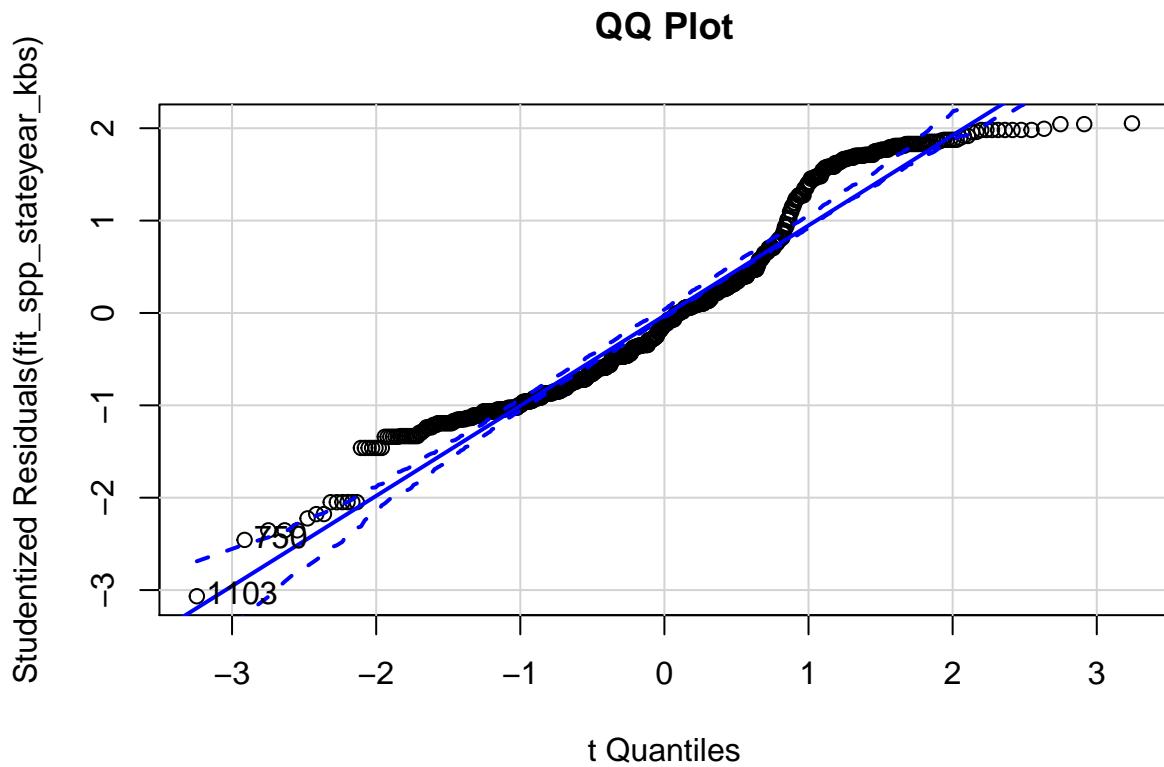
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9542       0.0000
## Kolmogorov-Smirnov 0.0901       0.0000
## Cramer-von Mises 183.3113      0.0000
## Anderson-Darling 13.2382       0.0000
## -----
```

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

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##           rstudent unadjusted p-value Bonferroni p
## 1103 -3.066819             0.0022357        NA
```

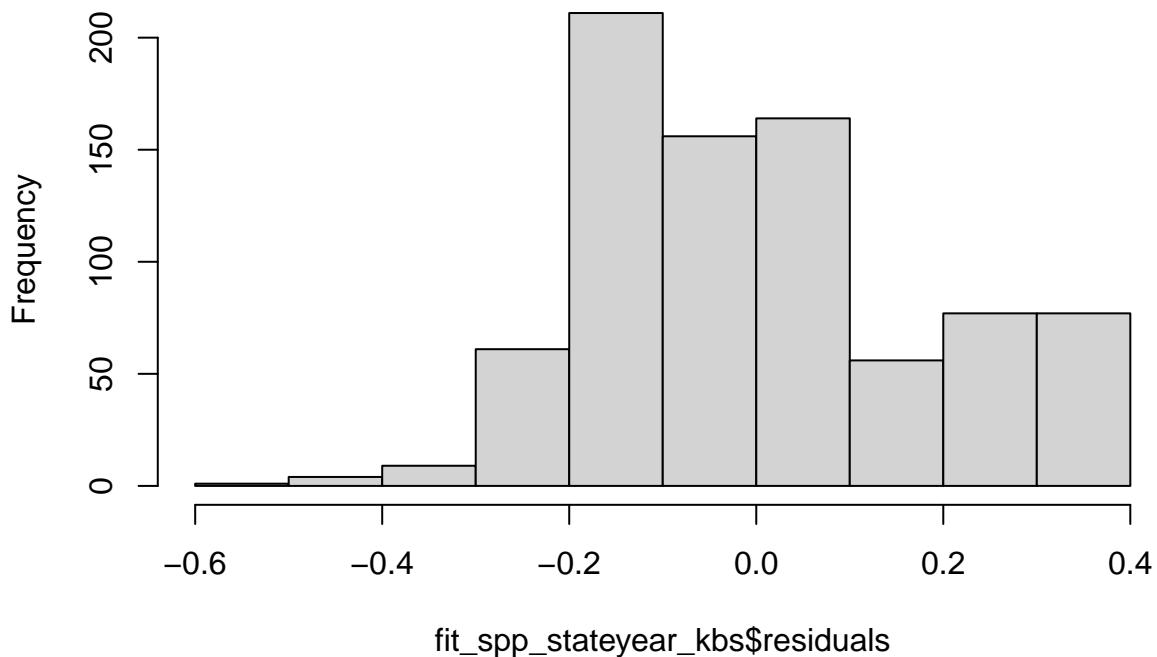
```
qqPlot(fit_spp_stateyear_kbs, main = "QQ Plot")
```



```
##   750 1103
##   433 642
```

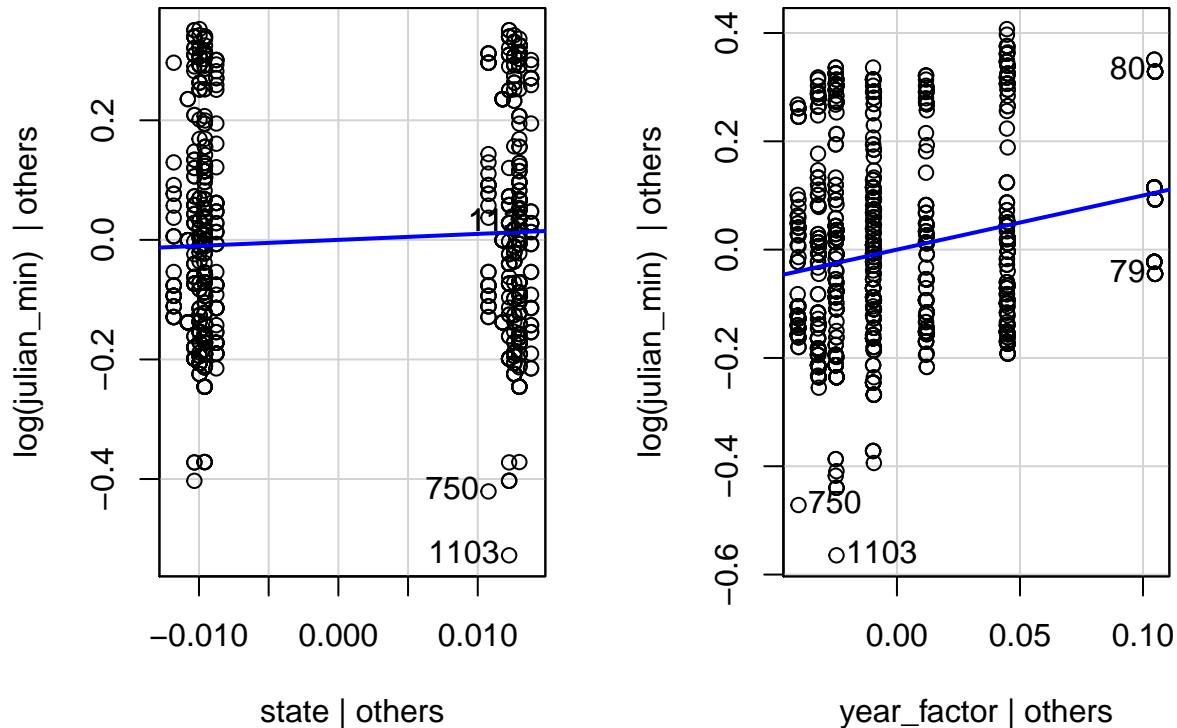
```
hist(fit_spp_stateyear_kbs$residuals)
```

Histogram of 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      0.9499    0.0000
## Kolmogorov-Smirnov 0.0903    0.0000
## Cramer-von Mises   184.0438   0.0000
## Anderson-Darling    14.1724    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/
```

```
# these wont work below
fit3 <- lm(log(julian_min) ~ state + year_factor + species, data = kbs_sd_spp)
interact_plot(fit3, pred = year_factor, modx = state)
```

```
## Using data kbs_sd_spp from global environment. This could cause incorrect
## results if kbs_sd_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.

## Error in interact_plot(fit3, pred = year_factor, modx = state): Focal predictor ("pred") cannot be a

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

## Using data kbs_sd_spp from global environment. This could cause incorrect
## results if kbs_sd_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.

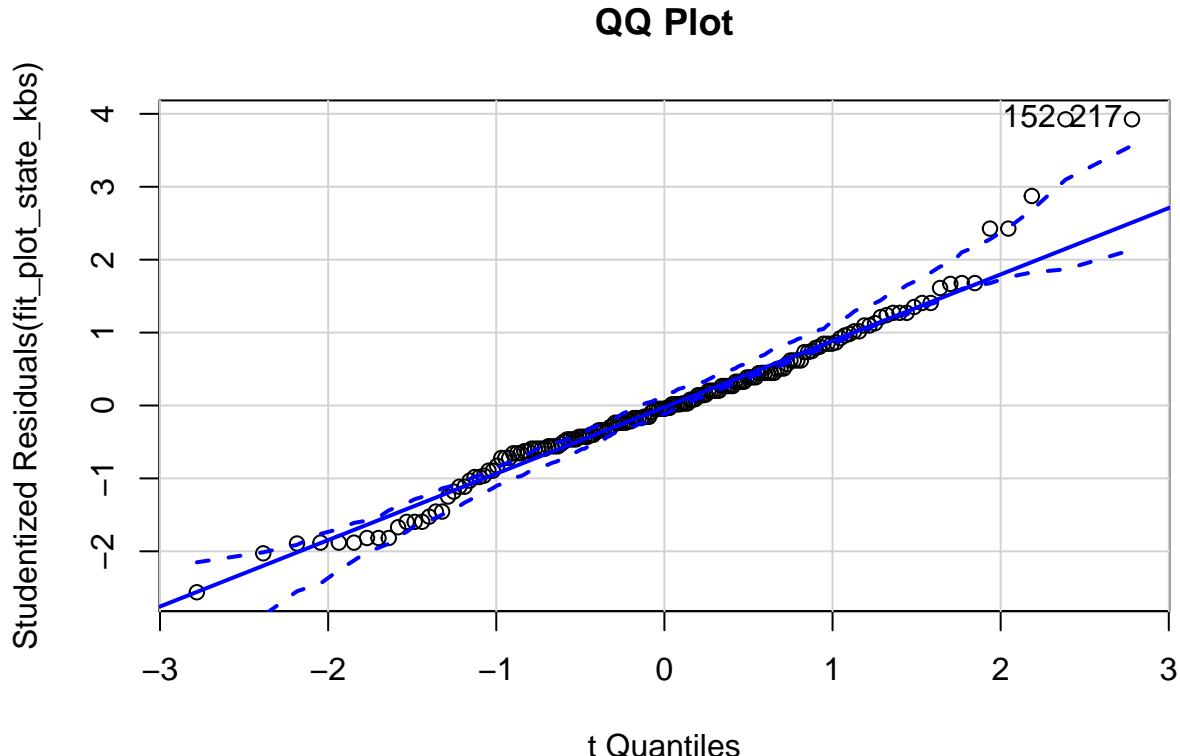
## Error in interact_plot(fit4, pred = year_factor, modx = state, mod2 = species): Focal predictor ("pred")

# KBS Plot level data KBS State-only model
fit_plot_state_kbs <- lm(log(julian_min) ~ state, data = kbs_sd_plot)
outlierTest(fit_plot_state_kbs) # outliers - 152, 217

##      rstudent unadjusted p-value Bonferroni p
## 152 3.924672      0.00012813     0.021141
## 217 3.924672      0.00012813     0.021141

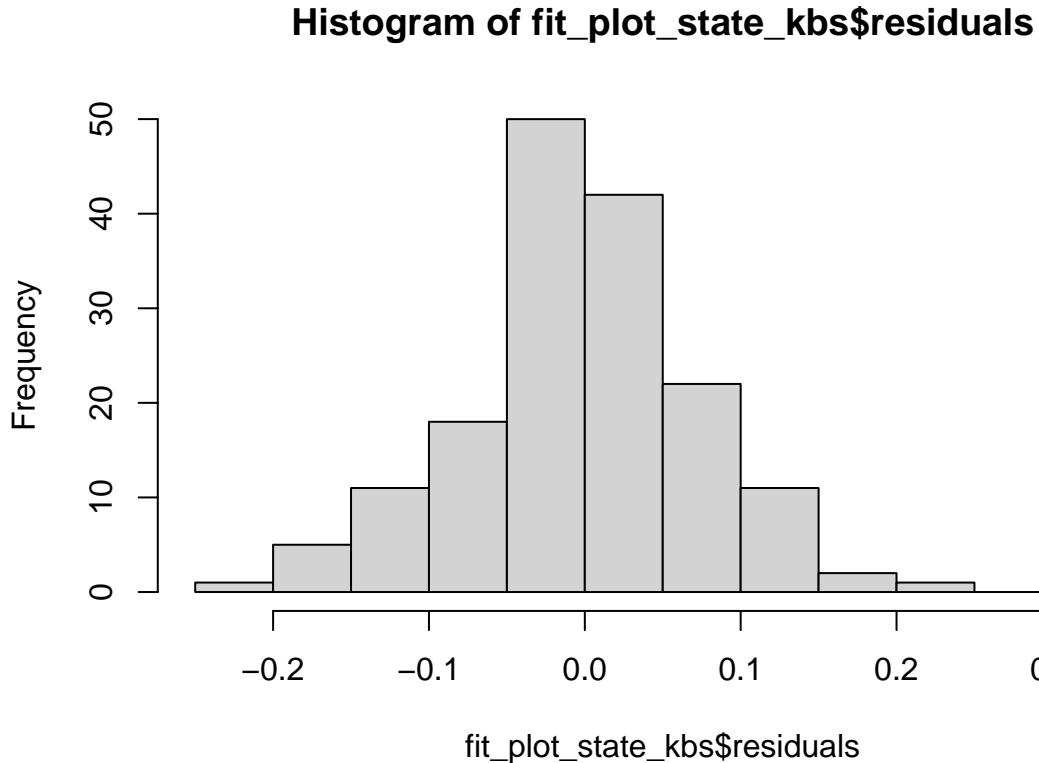
qqPlot(fit_plot_state_kbs, main = "QQ Plot")

```

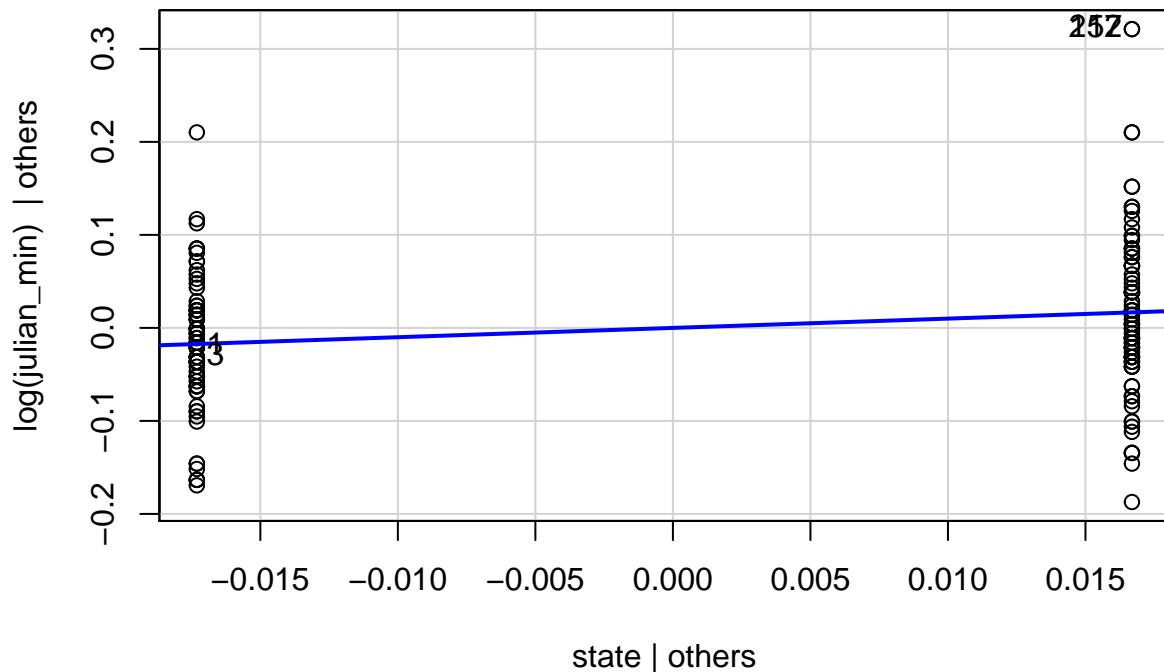


```
## 152 217  
## 84 119
```

```
hist(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      0.9648    3e-04
## Kolmogorov-Smirnov   0.0744    0.3205
## Cramer-von Mises    46.9551   0.0000
## Anderson-Darling     1.1738    0.0045
## -----
# KBS State and year model
fit_plot_stateyear_kbs <- lm(log(julian_min) ~ state + year_factor, data = kbs_sd_plot)
outlierTest(fit_spp_stateyear_kbs) # no outliers

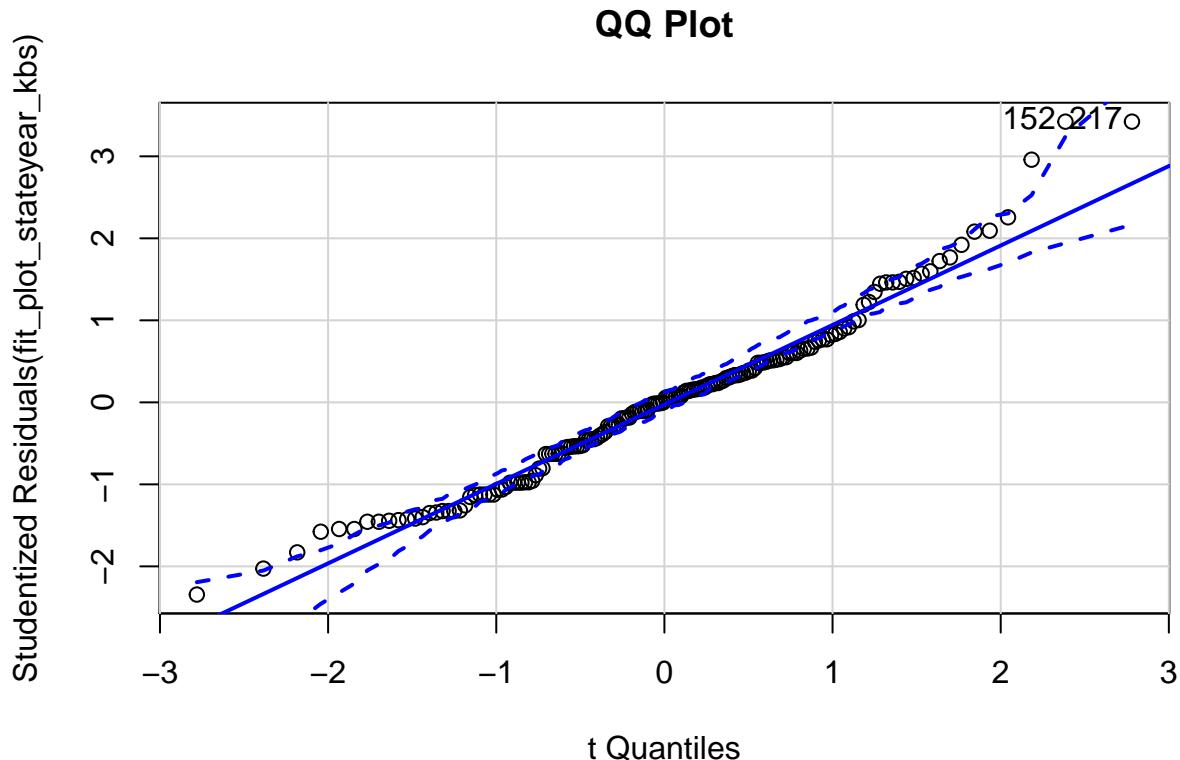
```

```

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##           rstudent unadjusted p-value Bonferroni p
## 1103 -3.066819            0.0022357        NA

```

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



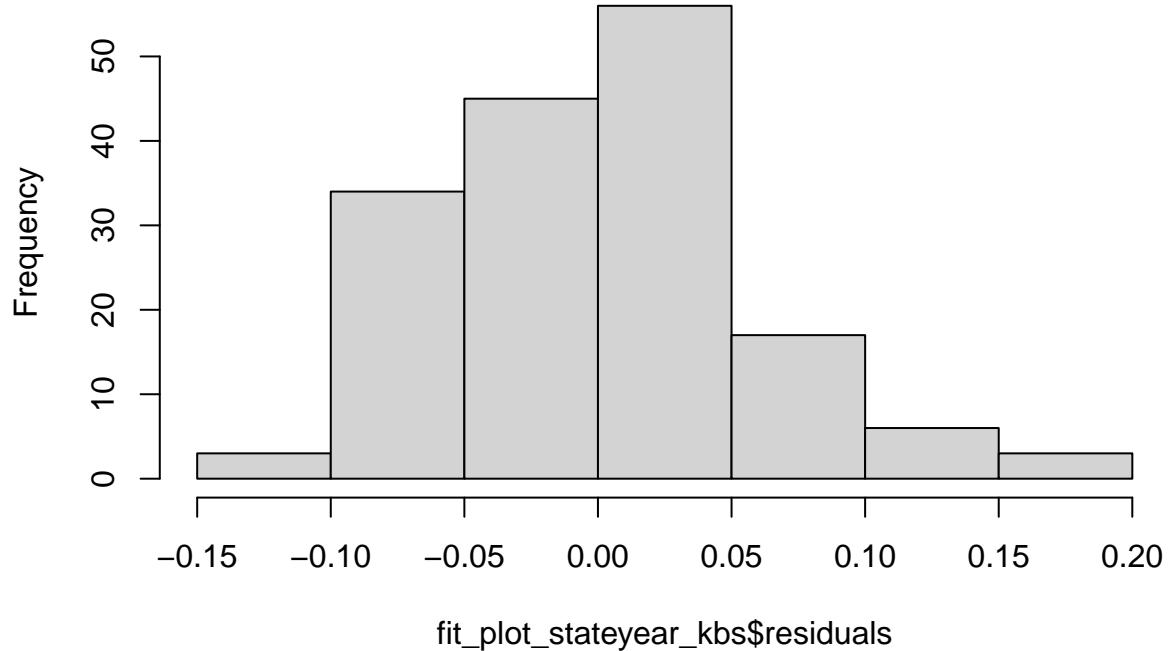
```

## 152 217
## 84 119

```

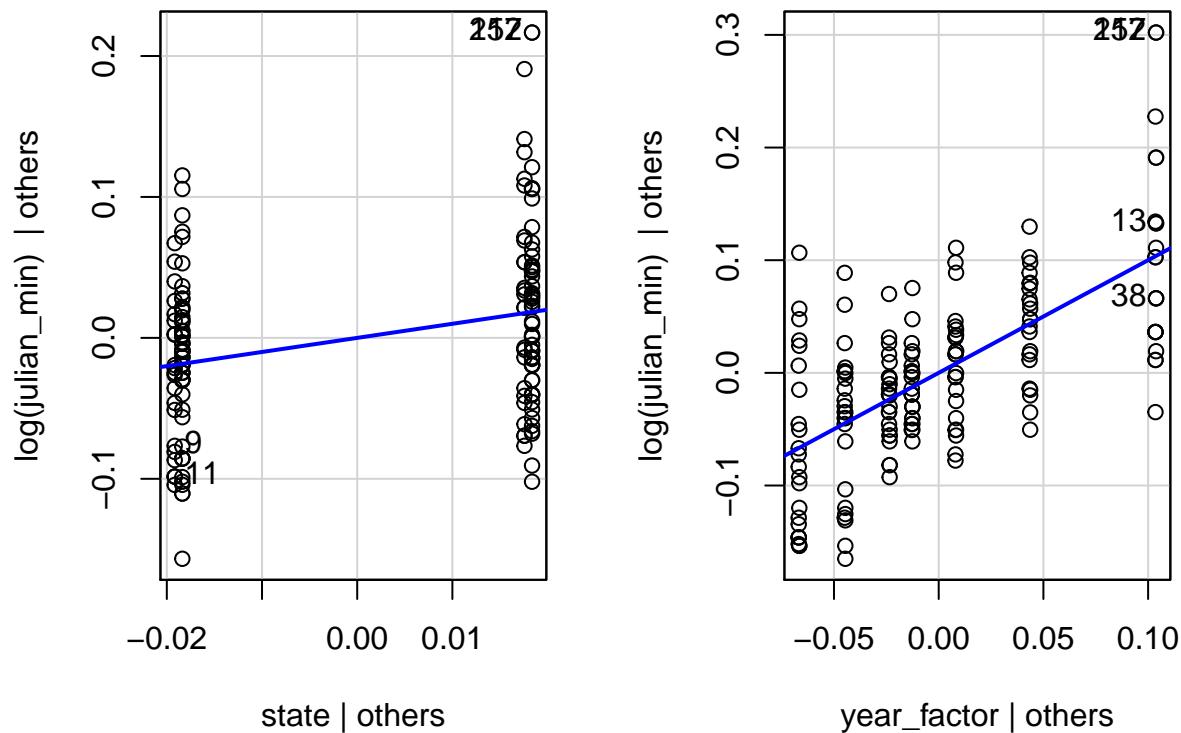
```
hist(fit_plot_stateyear_kbs$residuals)
```

Histogram of fit_plot_stateyear_kbs\$residuals



```
leveragePlots(fit_plot_stateyear_kbs)
```

Leverage Plots



```
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      0.9747    0.0042
## Kolmogorov-Smirnov   0.0632    0.5286
## Cramer-von Mises  48.4006    0.0000
## Anderson-Darling   0.8621    0.0263
## -----
```

```
# 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_min) ~ state * year_factor, data = kbs_sd_plot)
interact_plot(fit3, pred = year_factor, modx = state) # this doesn't work
```

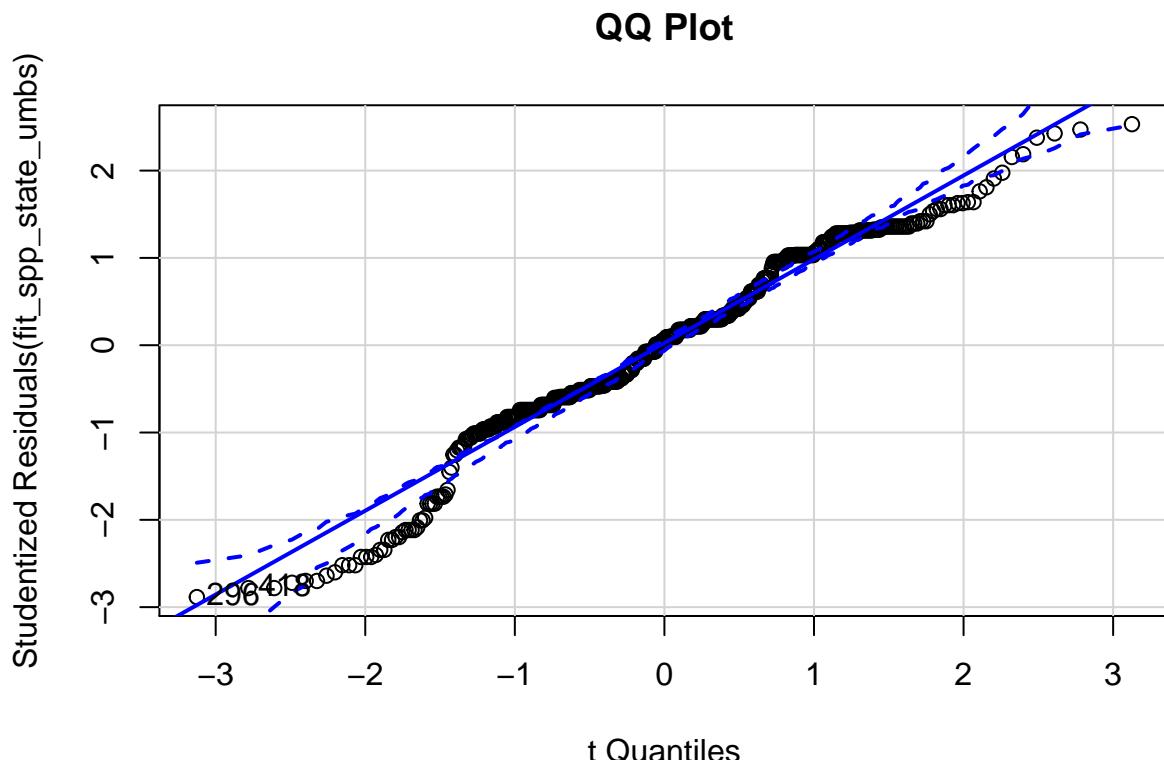
```
## Using data kbs_sd_plot from global environment. This could cause incorrect
## results if kbs_sd_plot has been altered since the model was fit. You can
## manually provide the data to the "data =" argument.
```

```
## Error in interact_plot(fit3, pred = year_factor, modx = state): Focal predictor ("pred") cannot be a
```

```
# UMBS species level data UMBS State-only model
fit_spp_state_umbs <- lm(log(julian_min) ~ state, data = umbs_sd_spp)
outlierTest(fit_spp_state_umbs) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 296 -2.8848          0.0040754        NA
```

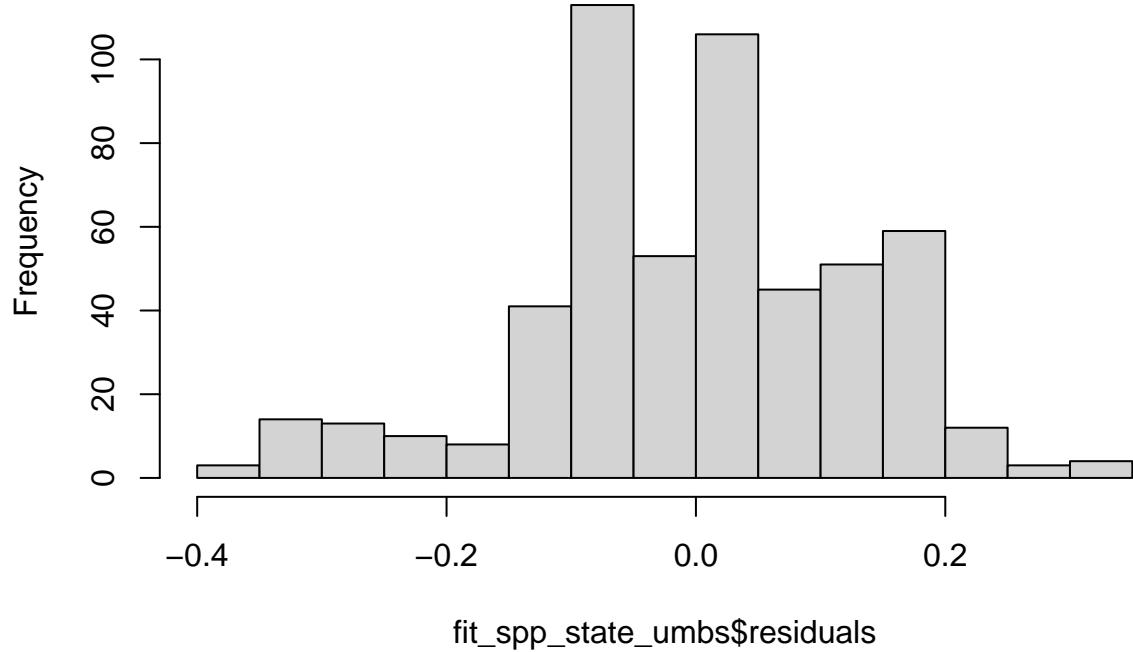
```
qqPlot(fit_spp_state_umbs, main = "QQ Plot")
```



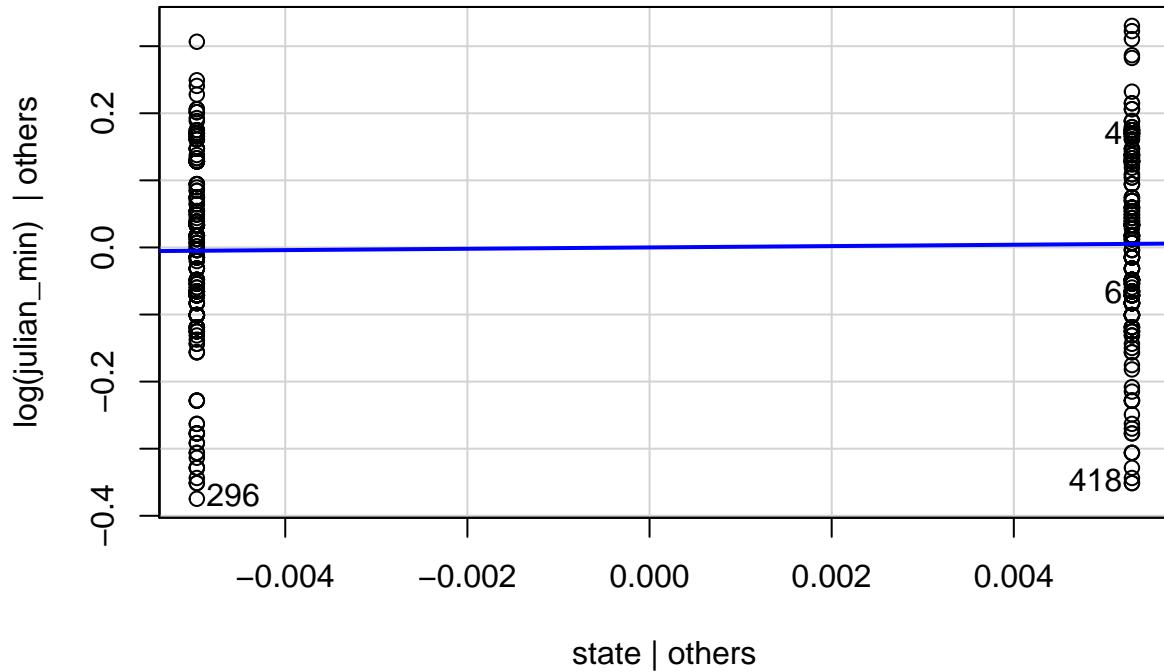
```
## 296 418
## 132 180
```

```
hist(fit_spp_state_umbs$residuals)
```

Histogram of fit_spp_state_umbs\$residuals



```
leveragePlots(fit_spp_state_umbs)
```



```
ols_test_normality(fit_spp_state_umbs)
```

```
## 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      0.9754    0.0000
## Kolmogorov-Smirnov 0.0632    0.0278
## Cramer-von Mises   136.2309   0.0000
## Anderson-Darling    3.4524    0.0000
## -----

```

```

# UMBS State and year model
fit_spp_stateyear_umbs <- lm(log(julian_min) ~ state + year_factor, data = umbs_sd_spp)
outlierTest(fit_spp_stateyear_umbs) # no outliers

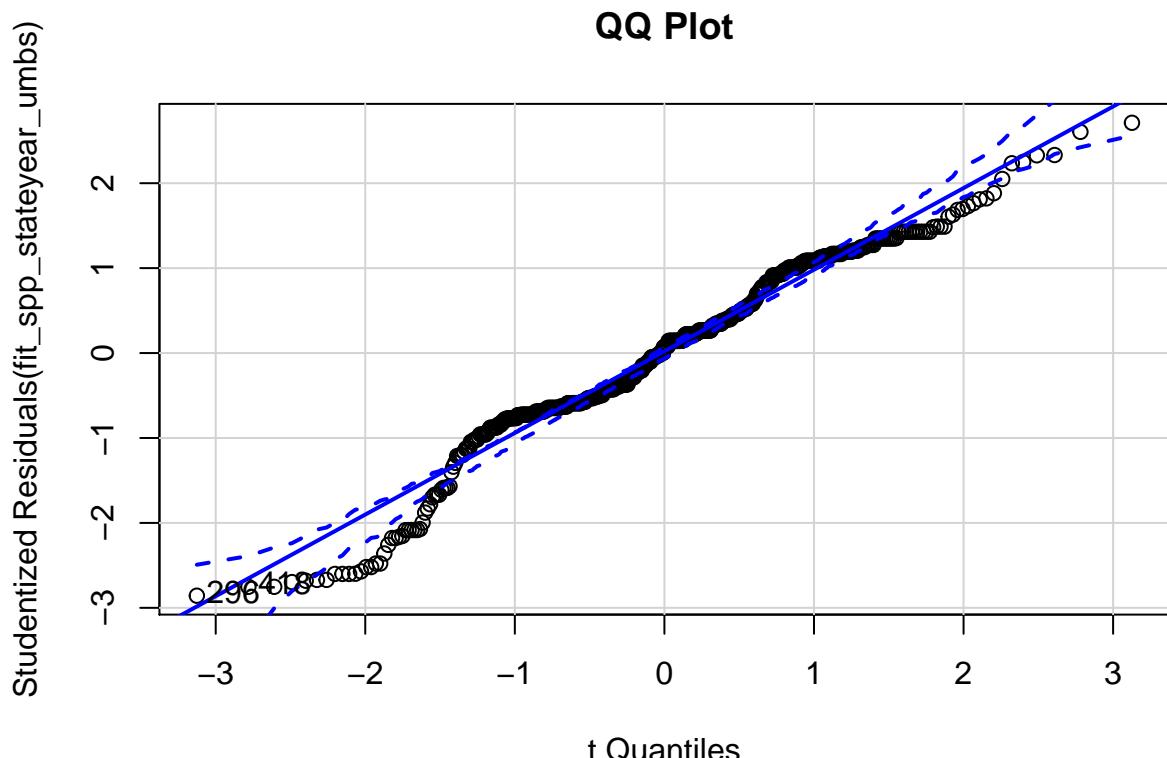
```

```

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##           rstudent unadjusted p-value Bonferroni p
## 296 -2.856926          0.0044463            NA

```

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



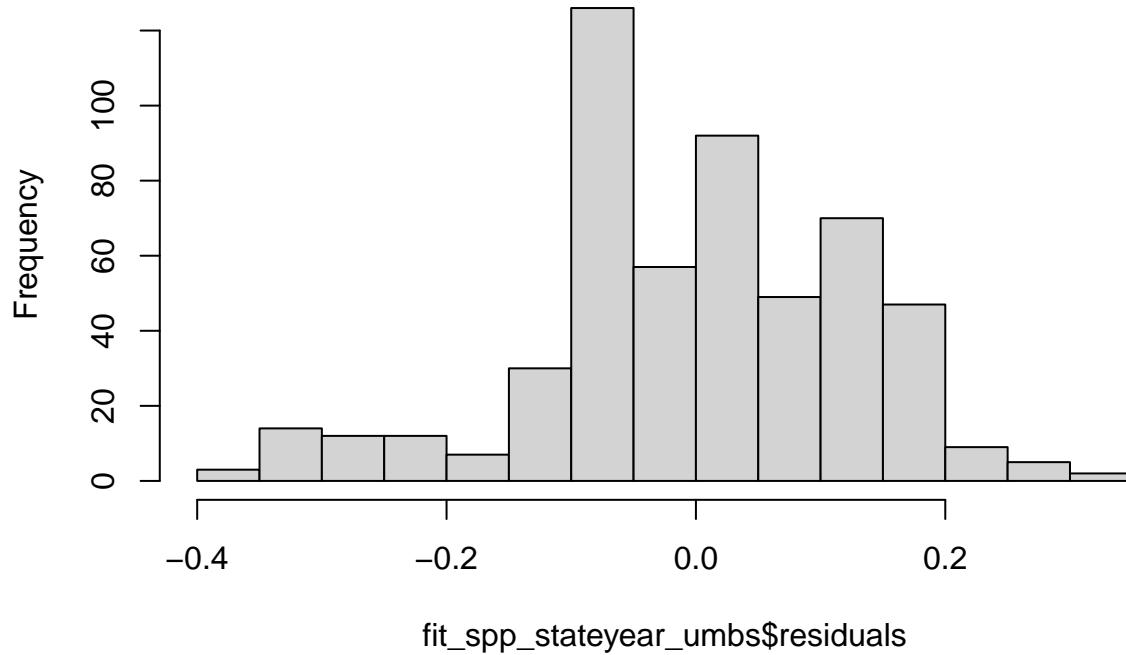
```

## 296 418
## 132 180

```

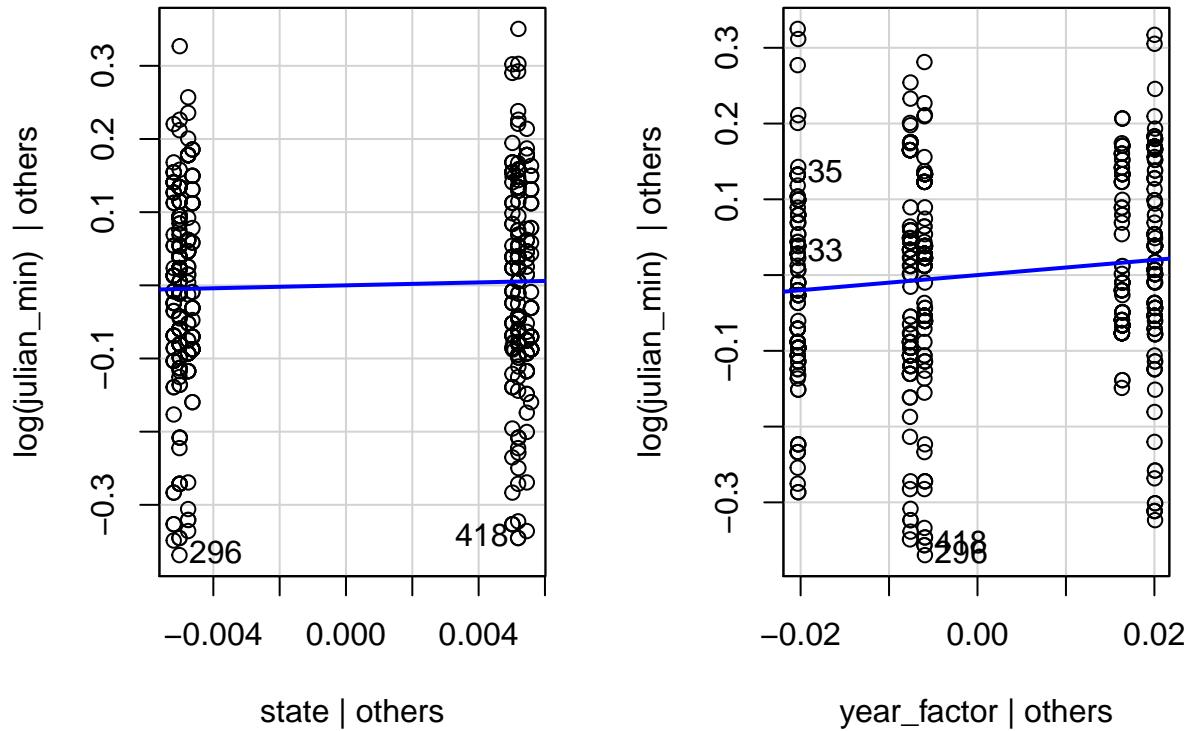
```
hist(fit_spp_stateyear_umbs$residuals)
```

Histogram of fit_spp_stateyear_umbs\$residuals



```
leveragePlots(fit_spp_stateyear_umbs)
```

Leverage Plots



```

ols_test_normality(fit_spp_stateyear_umbs)

## 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      0.9747    0.0000
## Kolmogorov-Smirnov   0.0754    0.0046
## Cramer-von Mises   136.3144   0.0000
## Anderson-Darling    3.7057    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/

# these wont work below
fit3_spp_umbs <- lm(log(julian_min) ~ state + year_factor + species, data = umbs_sd_spp)
interact_plot(fit3, pred = year_factor, modx = state)

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

## Error in interact_plot(fit3, pred = year_factor, modx = state): Focal predictor ("pred") cannot be a

fit4_spp_umbs <- lm(log(julian_min) ~ state * year_factor + species, data = umbs_sd_spp)
interact_plot(fit4, pred = year_factor, modx = state, mod2 = species)

## Using data kbs_sd_spp from global environment. This could cause incorrect
## results if kbs_sd_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.

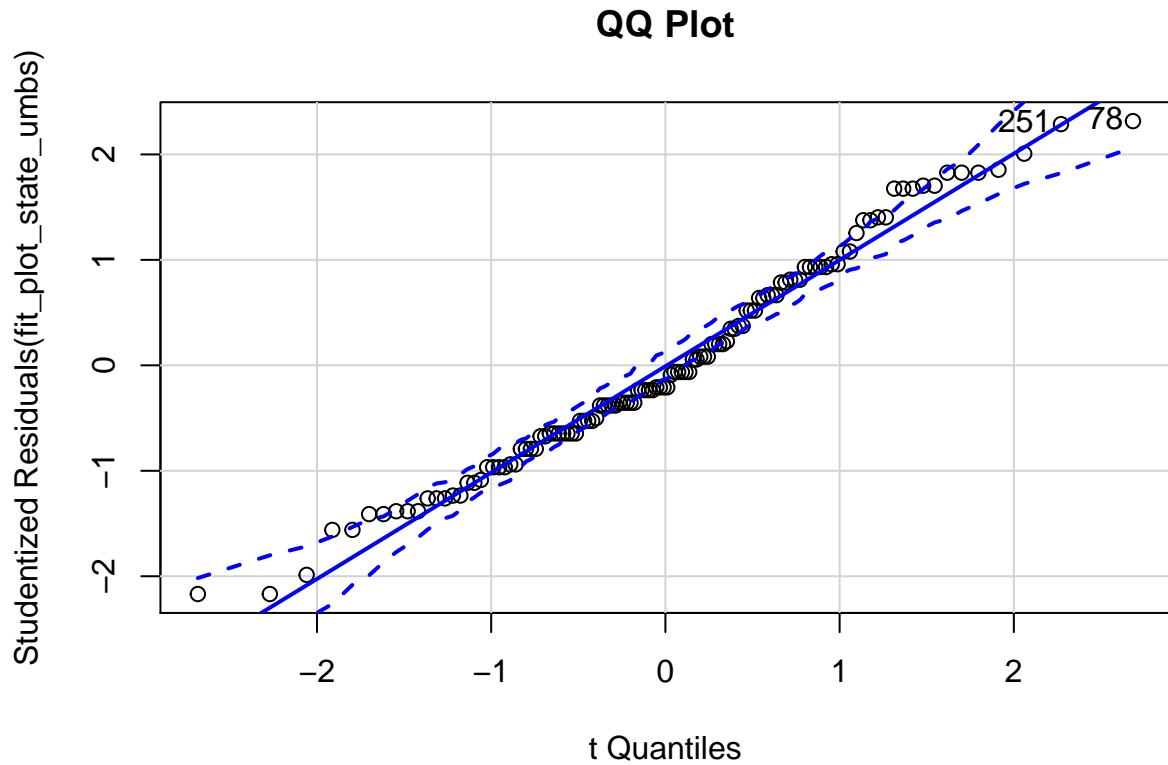
## Error in interact_plot(fit4, pred = year_factor, modx = state, mod2 = species): Focal predictor ("pr

# Plot level data UMBS State-only model
fit_plot_state_umbs <- lm(julian_min ~ state, data = umbs_sd_plot)
outlierTest(fit_plot_state_umbs) # no outliers

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 78  2.315735        0.022315       NA

```

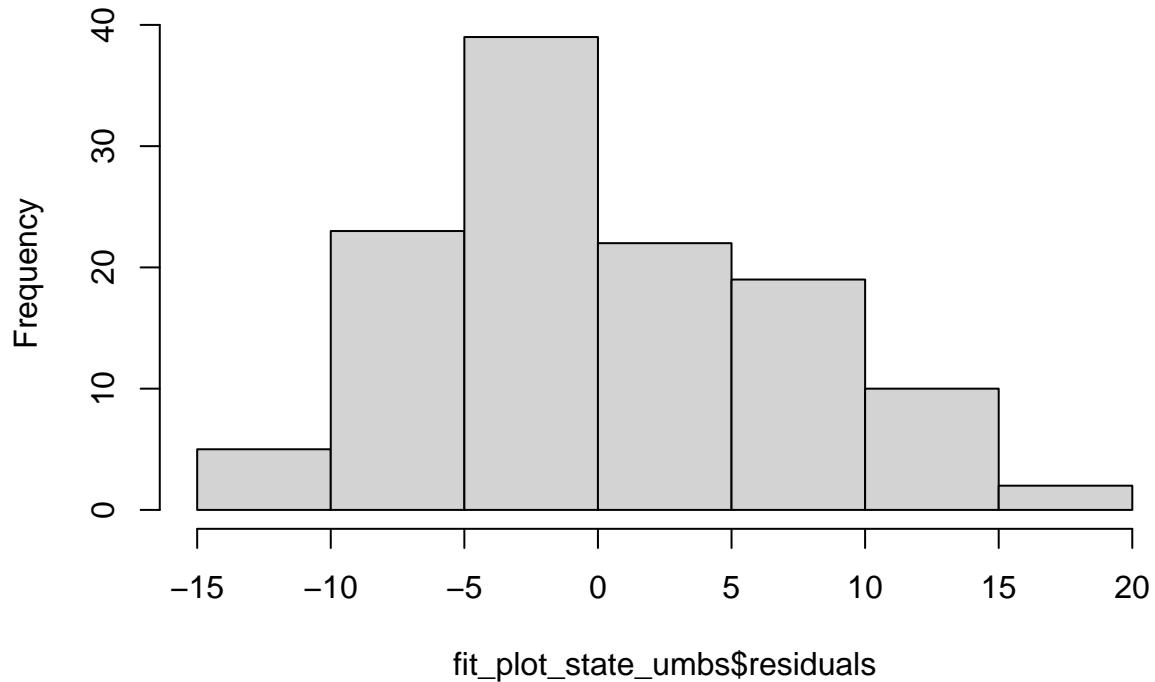
```
qqPlot(fit_plot_state_umbs, main = "QQ Plot")
```



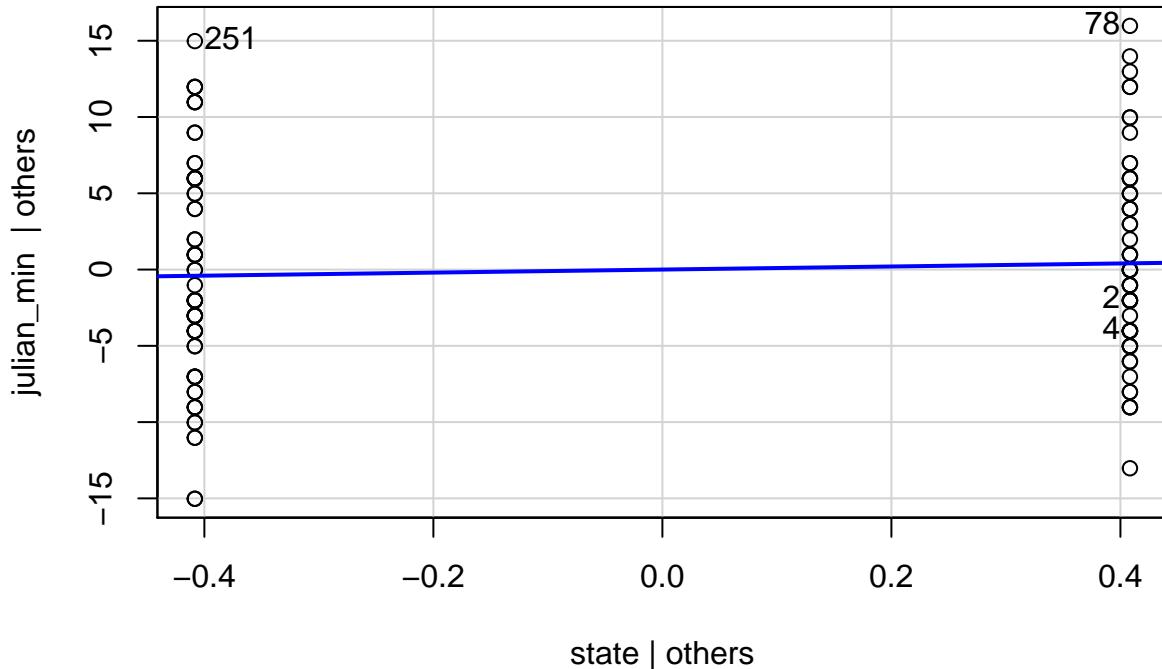
```
## 78 251  
## 31 99
```

```
hist(fit_plot_state_umbs$residuals)
```

Histogram of fit_plot_state_umbs\$residuals



```
leveragePlots(fit_plot_state_umbs)
```



```
ols_test_normality(fit_plot_state_umbs)
```

```
## 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    0.0623
## Kolmogorov-Smirnov 0.0909    0.2744
## Cramer-von Mises   9.5908    0.0000
## Anderson-Darling   0.7846    0.0406
## -----
# UMBS State and year model
fit_plot_stateyear_umbs <- lm(julian_min ~ state + year_factor, data = umbs_sd_plot)
outlierTest(fit_plot_stateyear_umbs)

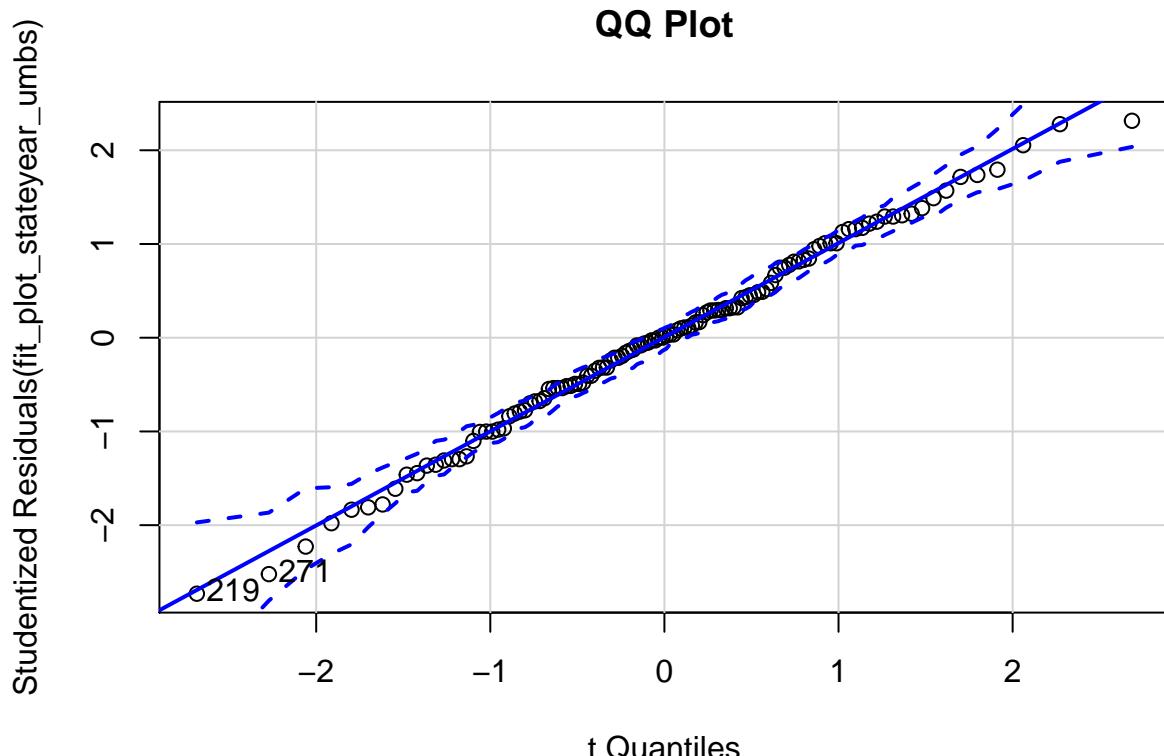
```

```

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##           rstudent unadjusted p-value Bonferroni p
## 219 -2.731017        0.0073274       0.87928

```

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



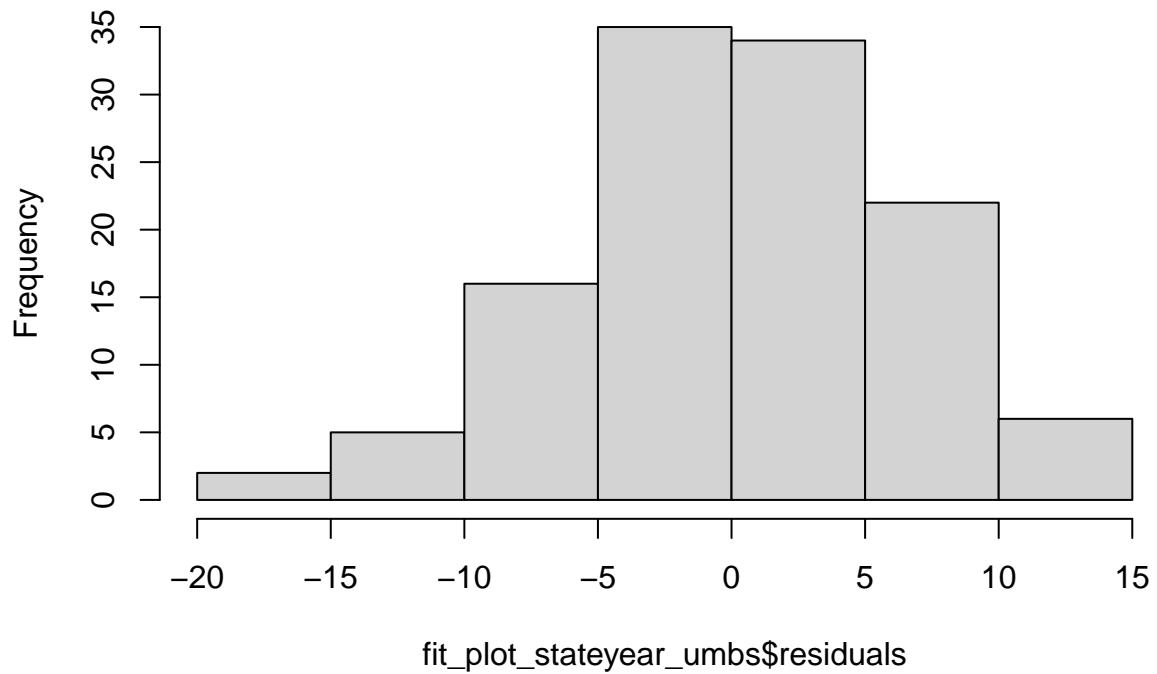
```

## 219 271
## 86 106

```

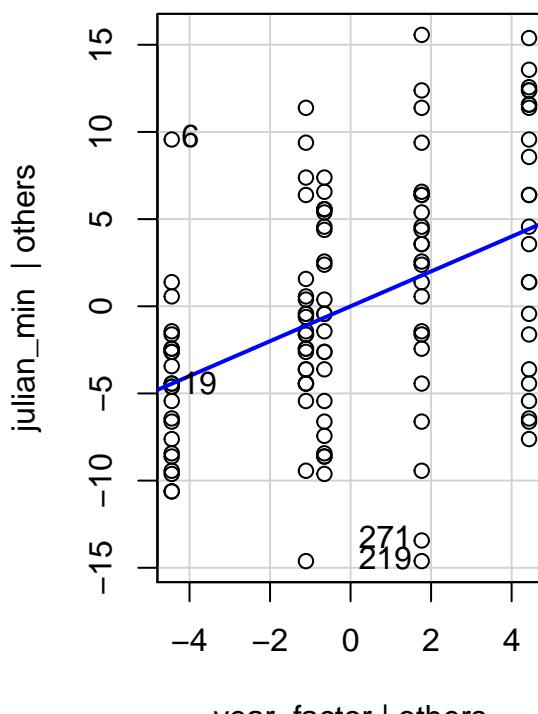
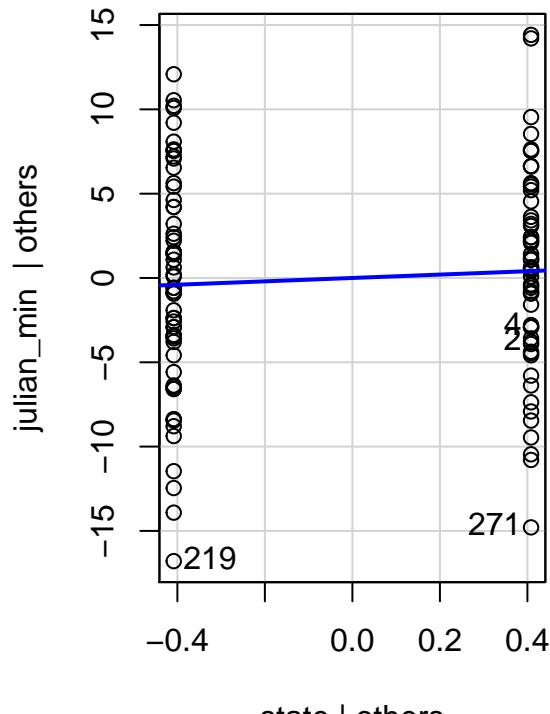
```
hist(fit_plot_stateyear_umbs$residuals)
```

Histogram of fit_plot_stateyear_umbs\$residuals



```
leveragePlots(fit_plot_stateyear_umbs)
```

Leverage Plots



```

ols_test_normality(fit_plot_stateyear_umbs)

## 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      0.9939      0.8870
## Kolmogorov-Smirnov 0.0424      0.9822
## Cramer-von Mises   8.6515      0.0000
## Anderson-Darling    0.1808      0.9128
## -----
```

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_umbs <- lm(julian_min ~ state * year_factor, data = umbs_sd_plot)
interact_plot(fit3_plot_umbs, pred = year_factor, modx = state)
```

Error in interact_plot(fit3_plot_umbs, pred = year_factor, modx = state): Focal predictor ("pred") c

MODEL BUILDING

KBS Species-level Mixed Effects Models

Start by replicating (almost) what we did in the Decologia 2018 paper. The only
difference here is that we have multiple years, so we are also including year
as a fixed effect and as an interactive term. Our goal here is to find a model
that is the best fit to the data. We also want to find a model that is the most
parsimonious (one that has the fewest parameters).

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

boundary (singular) fit: see ?isSingular

```

mod2 <- lmer(log(julian_min) ~ state * year_factor + insecticide * year_factor +  

(1 | species), kbs_sd_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)
```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
## state	0.00671	0.006706	1	794.06	2.8796	0.0901 .
## year_factor	0.72591	0.120986	6	794.41	51.9480	<2e-16 ***
## insecticide	0.00474	0.004742	1	794.09	2.0359	0.1540

```

## state:year_factor      0.00928 0.001546      6 794.03  0.6640 0.6789
## year_factor:insecticide 0.01238 0.002063      6 794.06  0.8857 0.5048
## ---
## 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                      0.00671 0.006706      1 794.06  2.8796 0.0901 .
## year_factor                 0.72591 0.120986      6 794.41 51.9480 <2e-16 ***
## insecticide                  0.00474 0.004742      1 794.09  2.0359 0.1540
## state:year_factor          0.00928 0.001546      6 794.03  0.6640 0.6789
## year_factor:insecticide    0.01238 0.002063      6 794.06  0.8857 0.5048
## ---
## 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) # models are not different from each other so go with simpler model = model 2
```

```

## Data: kbs_sd_spp
## Models:
## mod2: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##       (1 | species)
## mod1: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##       (1 | species) + (1 | plot)
##       npar   AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2  23 -2458.1 -2349.9 1252.1 -2504.1
## mod1  24 -2456.1 -2343.2 1252.1 -2504.1      0  1           1

```

```
summary(mod1)
```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##           (1 | species) + (1 | plot)
## Data: kbs_sd_spp
##
##       AIC     BIC logLik deviance df.resid
##   -2456.1 -2343.2 1252.1 -2504.1      792
##
## Scaled residuals:
##       Min     1Q Median     3Q    Max
## -4.5749 -0.5062 -0.0168  0.4582  7.6160
##
## Random effects:

```

```

## Groups      Name          Variance Std.Dev.
## plot        (Intercept) 0.0000000 0.00000
## species     (Intercept) 0.040350 0.20087
## Residual    0.002329 0.04826
## Number of obs: 816, groups: plot, 24; species, 22
##
## Fixed effects:
##                               Estimate Std. Error      df t value
## (Intercept)                5.36220  0.04483 25.74146 119.607
## stateambient               0.02061  0.01433 793.79819   1.438
## year_factor2              -0.09614  0.01421 793.86859  -6.768
## year_factor3              -0.10098  0.01466 794.21173  -6.887
## year_factor4              -0.10740  0.01515 793.88740  -7.088
## year_factor5              -0.07735  0.01543 793.82667  -5.014
## year_factor6              -0.06531  0.01461 793.84647  -4.470
## year_factor7              -0.07777  0.01661 793.88823  -4.683
## insecticideno_insects     0.03017  0.01427 793.79100   2.114
## stateambient:year_factor2 -0.02182  0.01594 793.83440  -1.369
## stateambient:year_factor3 -0.01223  0.01638 793.87744  -0.747
## stateambient:year_factor4 -0.02685  0.01700 793.95450  -1.580
## stateambient:year_factor5 -0.01148  0.01751 793.81399  -0.656
## stateambient:year_factor6 -0.01401  0.01666 793.96220  -0.841
## stateambient:year_factor7 -0.01151  0.01871 793.82712  -0.615
## year_factor2:insecticideno_insects -0.03334  0.01584 793.79868  -2.105
## year_factor3:insecticideno_insects -0.03443  0.01634 793.99170  -2.107
## year_factor4:insecticideno_insects -0.02605  0.01686 794.01578  -1.545
## year_factor5:insecticideno_insects -0.02812  0.01734 793.80149  -1.622
## year_factor6:insecticideno_insects -0.02782  0.01656 793.81823  -1.680
## year_factor7:insecticideno_insects -0.02310  0.01887 793.87303  -1.224
##                               Pr(>|t|)
## (Intercept)                < 2e-16 ***
## stateambient               0.1507
## year_factor2              2.53e-11 ***
## year_factor3              1.16e-11 ***
## year_factor4              3.01e-12 ***
## year_factor5              6.59e-07 ***
## year_factor6              8.95e-06 ***
## year_factor7              3.32e-06 ***
## insecticideno_insects     0.0348 *
## stateambient:year_factor2 0.1714
## stateambient:year_factor3 0.4555
## stateambient:year_factor4 0.1146
## stateambient:year_factor5 0.5123
## stateambient:year_factor6 0.4006
## stateambient:year_factor7 0.5388
## year_factor2:insecticideno_insects 0.0356 *
## year_factor3:insecticideno_insects 0.0354 *
## year_factor4:insecticideno_insects 0.1228
## year_factor5:insecticideno_insects 0.1053
## year_factor6:insecticideno_insects 0.0934 .
## year_factor7:insecticideno_insects 0.2212
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it

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

summary(mod2)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##           (1 | species)
## Data: kbs_sd_spp
##
##      AIC      BIC  logLik deviance df.resid
## -2458.1 -2349.9  1252.1 -2504.1     793
## 
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.5749 -0.5062 -0.0168  0.4582  7.6160
## 
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   species (Intercept) 0.040350 0.20087
##   Residual            0.002329 0.04826
## Number of obs: 816, groups: species, 22
## 
## Fixed effects:
##                               Estimate Std. Error      df t value
## (Intercept)                5.36220  0.04483 25.74146 119.607
## stateambient               0.02061  0.01433 793.79818   1.438
## year_factor2              -0.09614  0.01421 793.86859  -6.768
## year_factor3              -0.10098  0.01466 794.21173  -6.887
## year_factor4              -0.10740  0.01515 793.88740  -7.088
## year_factor5              -0.07735  0.01543 793.82667  -5.014
## year_factor6              -0.06531  0.01461 793.84647  -4.470
## year_factor7              -0.07777  0.01661 793.88823  -4.683
## insecticideno_insects     0.03017  0.01427 793.79100   2.114
## stateambient:year_factor2 -0.02182  0.01594 793.83440  -1.369
## stateambient:year_factor3 -0.01223  0.01638 793.87744  -0.747
## stateambient:year_factor4 -0.02685  0.01700 793.95450  -1.580
## stateambient:year_factor5 -0.01148  0.01751 793.81399  -0.656
## stateambient:year_factor6 -0.01401  0.01666 793.96220  -0.841
## stateambient:year_factor7 -0.01151  0.01871 793.82712  -0.615
## year_factor2:insecticideno_insects -0.03334  0.01584 793.79868  -2.105
## year_factor3:insecticideno_insects -0.03443  0.01634 793.99170  -2.107
## year_factor4:insecticideno_insects -0.02605  0.01686 794.01578  -1.545
## year_factor5:insecticideno_insects -0.02812  0.01734 793.80149  -1.622
## year_factor6:insecticideno_insects -0.02782  0.01656 793.81823  -1.680
## year_factor7:insecticideno_insects -0.02310  0.01887 793.87303  -1.224
## Pr(>|t|)
```

```

## (Intercept) < 2e-16 ***
## stateambient 0.1507
## year_factor2 2.53e-11 ***
## year_factor3 1.16e-11 ***
## year_factor4 3.01e-12 ***
## year_factor5 6.59e-07 ***
## year_factor6 8.95e-06 ***
## year_factor7 3.32e-06 ***
## insecticideno_insects 0.0348 *
## stateambient:year_factor2 0.1714
## stateambient:year_factor3 0.4555
## stateambient:year_factor4 0.1146
## stateambient:year_factor5 0.5123
## stateambient:year_factor6 0.4006
## stateambient:year_factor7 0.5388
## year_factor2:insecticideno_insects 0.0356 *
## year_factor3:insecticideno_insects 0.0354 *
## year_factor4:insecticideno_insects 0.1228
## year_factor5:insecticideno_insects 0.1053
## year_factor6:insecticideno_insects 0.0934 .
## year_factor7:insecticideno_insects 0.2212
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

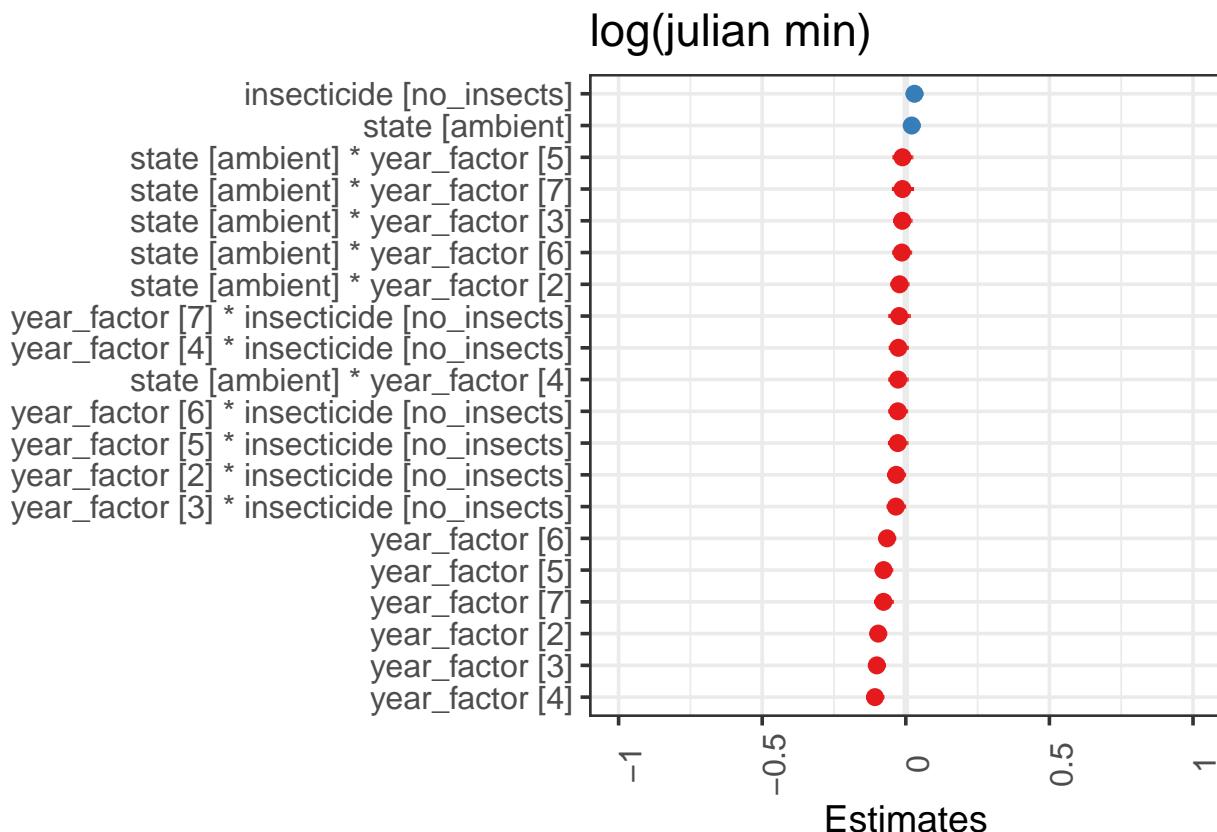
##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it

```

```

# 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
plot_model(mod2, sort.est = TRUE)

```

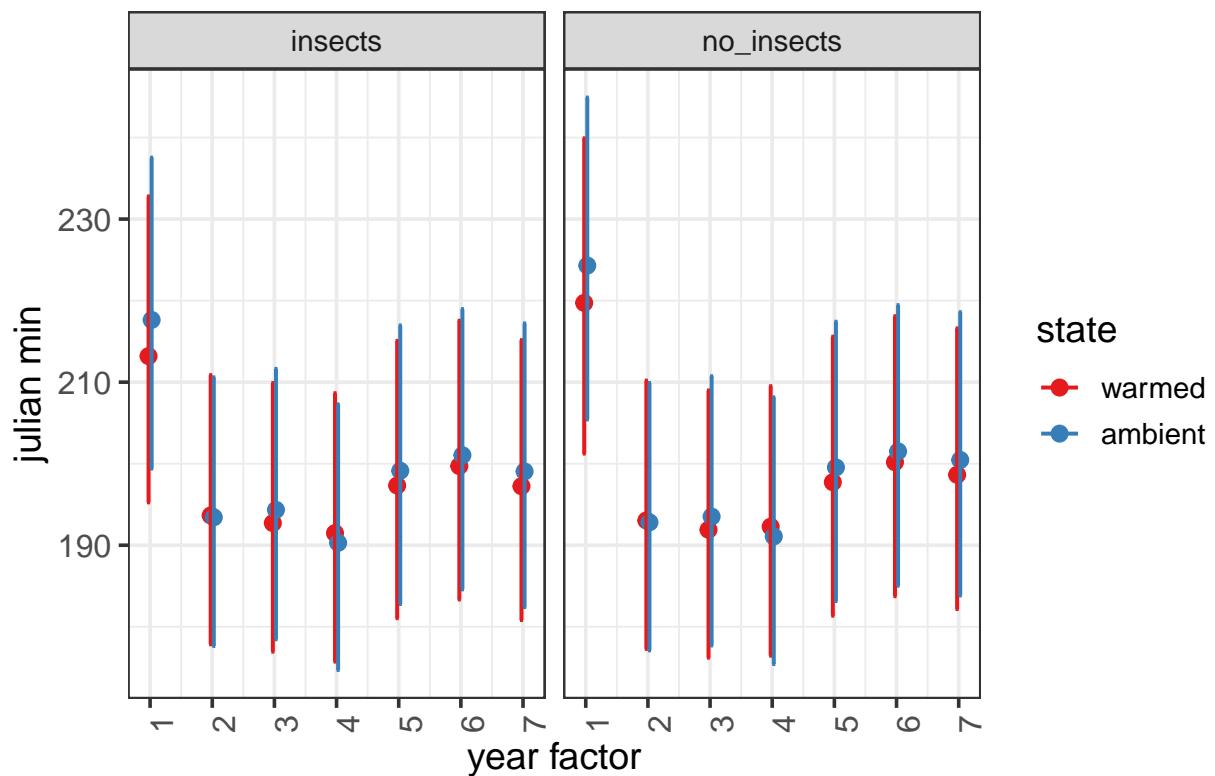


```
# these are the fixed predicted values:
```

```
plot_model(mod2, type = "pred", terms = c("year_factor", "state", "insecticide"))
```

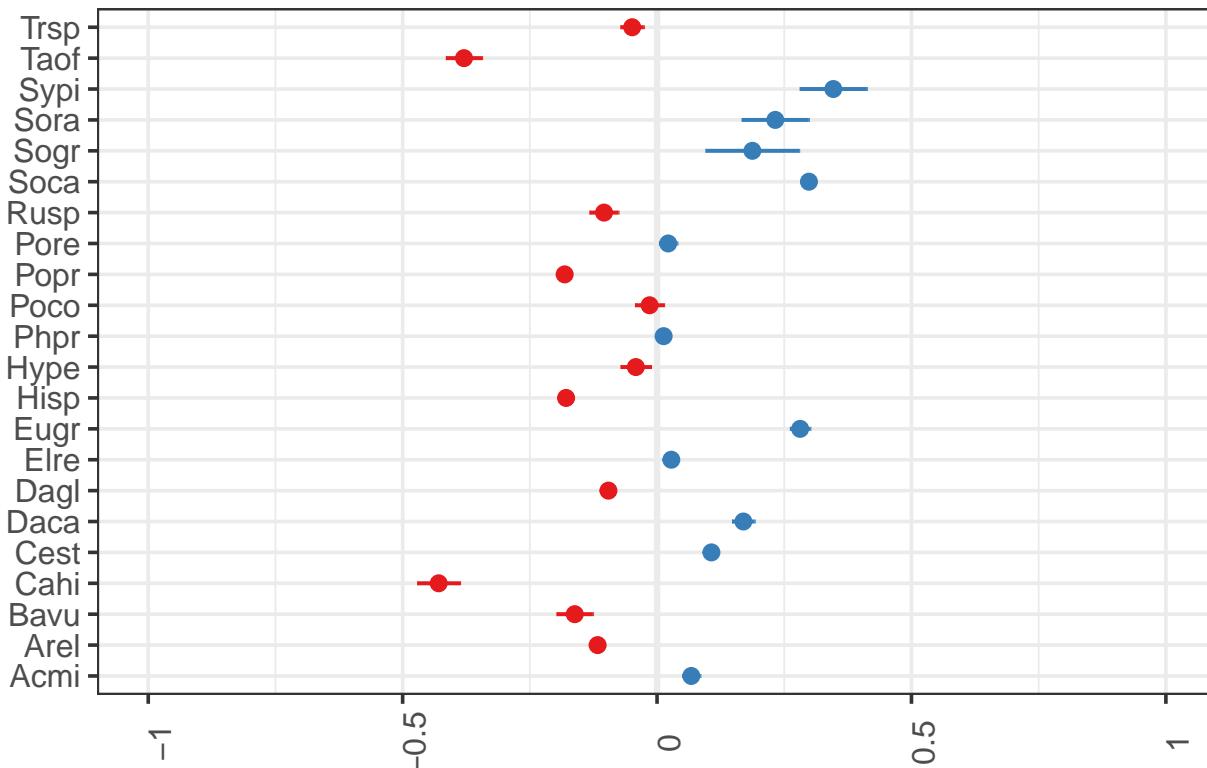
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized
```

Predicted values of julian min



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

Random effects



```
# Do we need to include insecticide?
mod3 <- lmer(log(julian_min) ~ state * year_factor + (1 | species), kbs_sd_spp, REML = FALSE)
anova(mod2, mod3) # Don't need insecticide, continue with mod3
```

```
## Data: kbs_sd_spp
## Models:
## mod3: log(julian_min) ~ state * year_factor + (1 | species)
## mod2: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##        (1 | species)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3   16 -2466.5 -2391.2 1249.3   -2498.5
## mod2   23 -2458.1 -2349.9 1252.1   -2504.1 5.6243  7     0.5842
```

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

```
# Does year need to be interactive with state?
mod5 <- lmer(log(julian_min) ~ state + year_factor + (1 | species) + (1 | plot),
             kbs_sd_spp, REML = FALSE)
```

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

```
anova(mod3, mod5)
```

```

## Data: kbs_sd_spp
## Models:
## mod5: log(julian_min) ~ state + year_factor + (1 | species) + (1 |
## mod5:     plot)
## mod3: log(julian_min) ~ state * year_factor + (1 | species)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5   11 -2472.7 -2420.9 1247.3   -2494.7
## mod3   16 -2466.5 -2391.2 1249.3   -2498.5 3.8516  5       0.571

```

```
AICctab(mod3, mod5, weights = T) # go with mod5
```

```

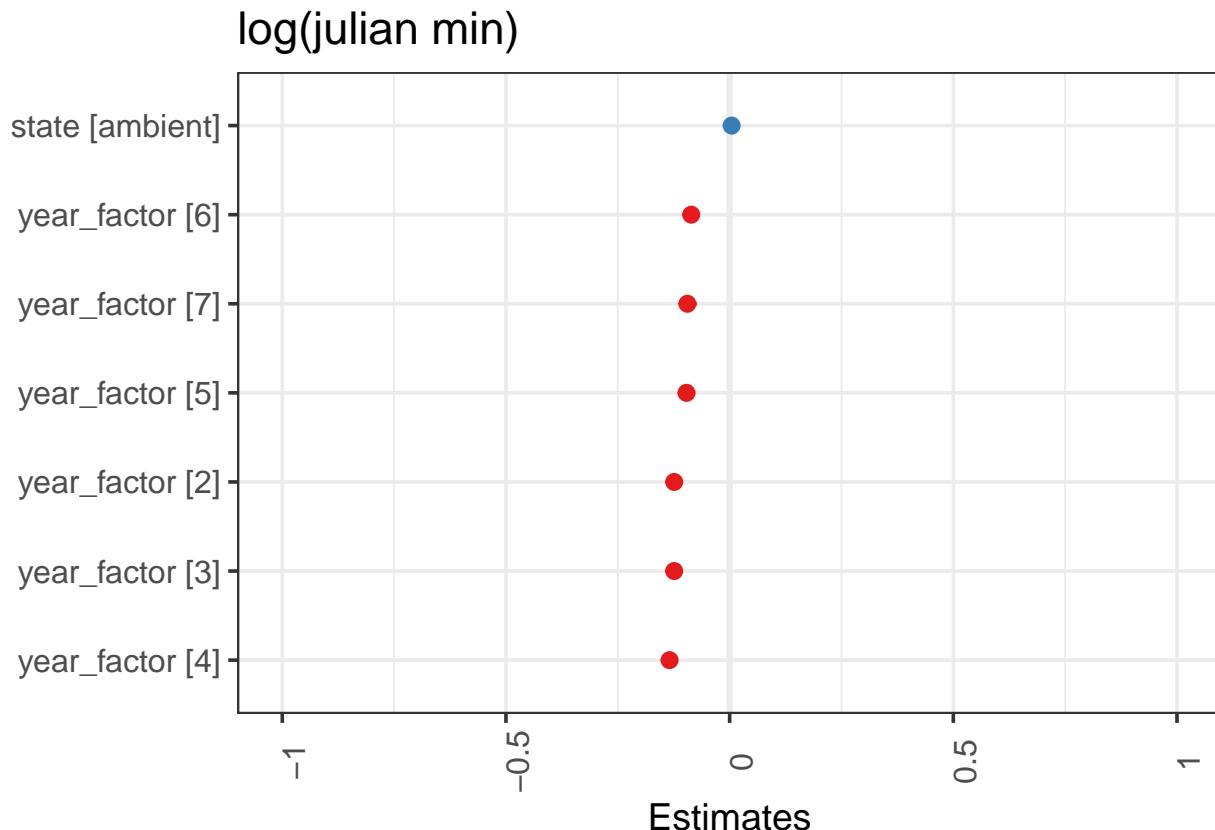
##      dAICc df weight
## mod5  0.0  11  0.963
## mod3  6.5  16  0.037

```

```

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

```



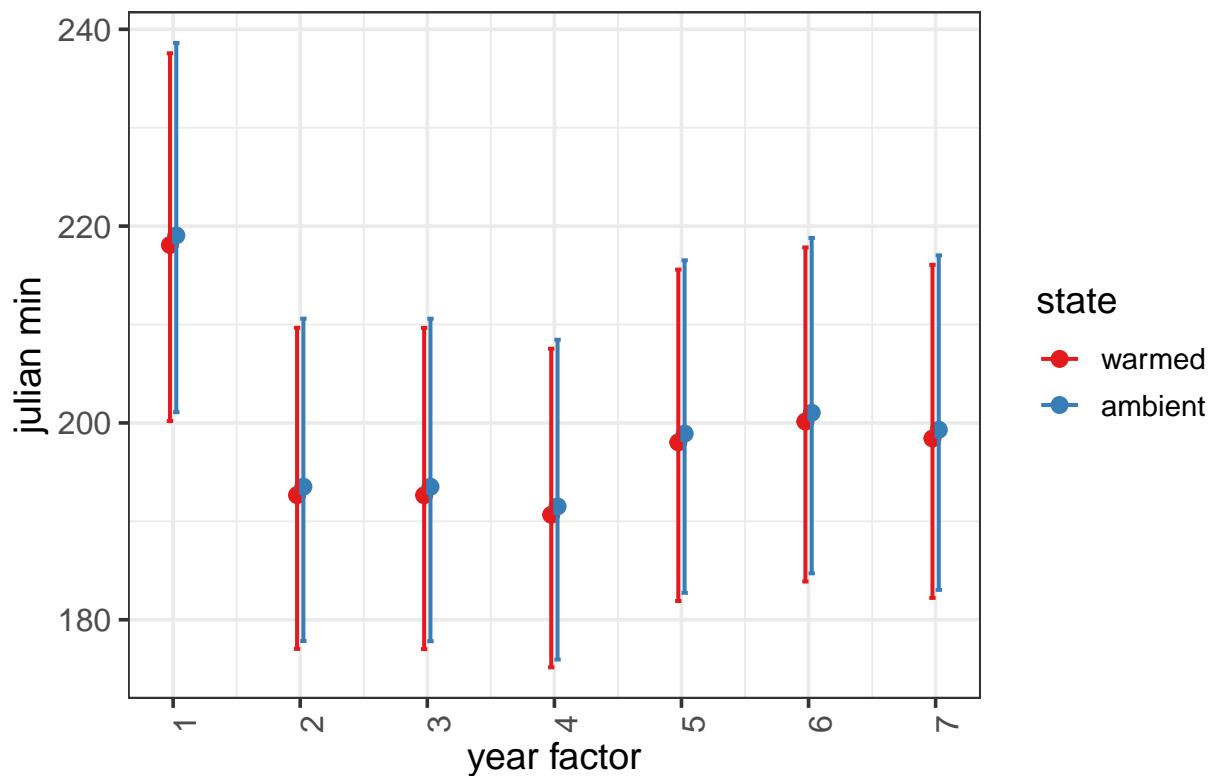
```

# 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
```

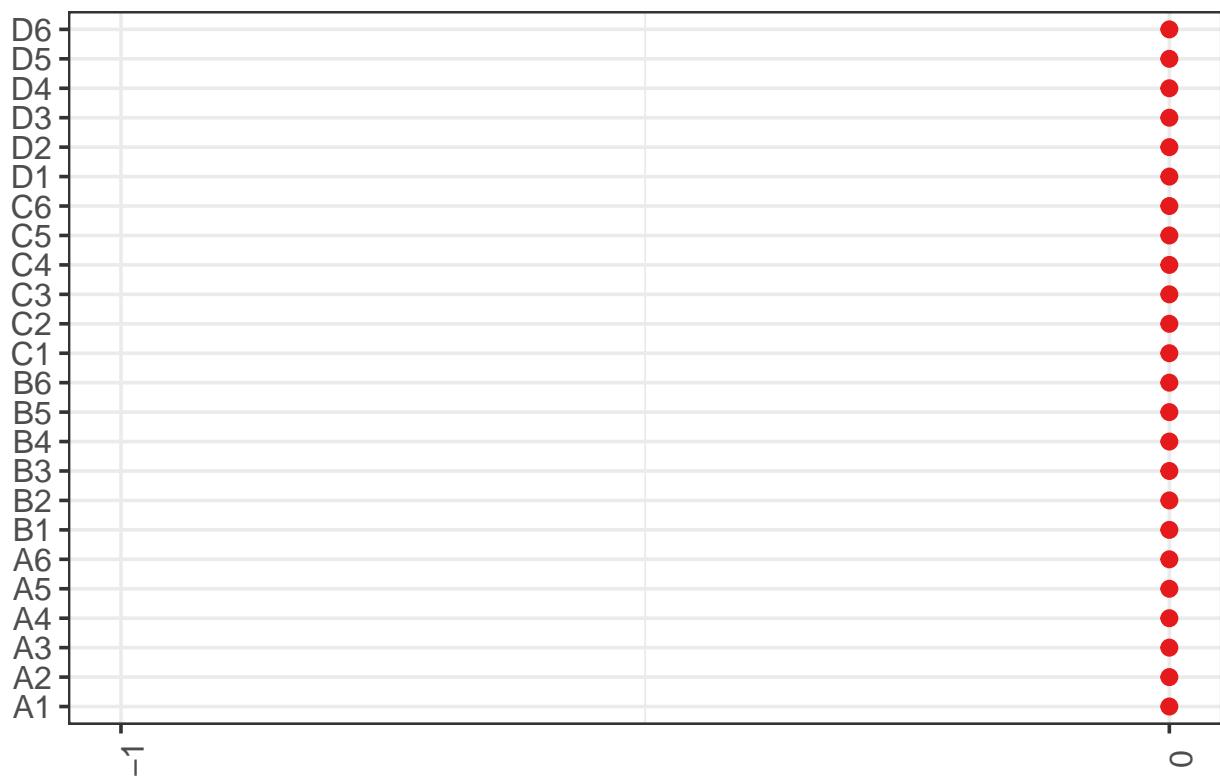
Predicted values of julian min



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

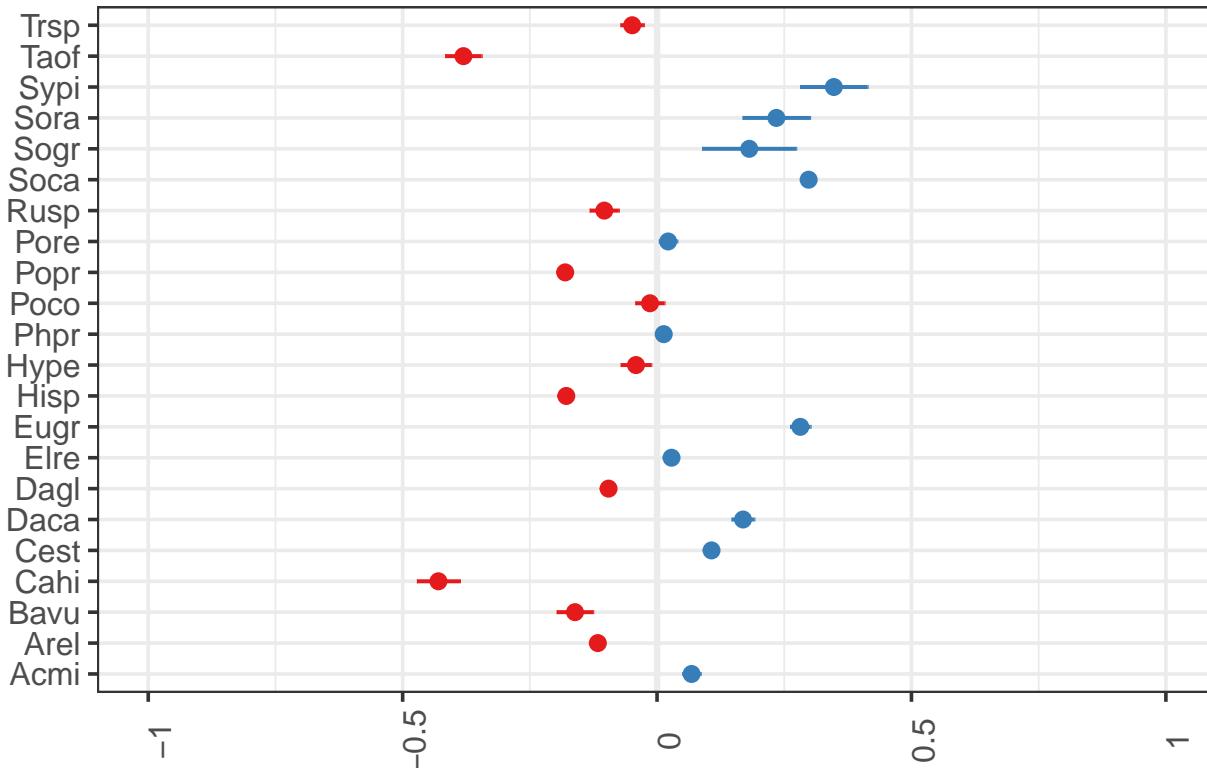
```
## [[1]]
```

Random effects



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

Random effects



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

```
## boundary (singular) fit: see ?isSingular
## Warning: Model failed to converge with 1 negative eigenvalue: -2.5e-01
anova(mod5, mod6) #stick with mod5
```

```
## Data: kbs_sd_spp
## Models:
## mod5: log(julian_min) ~ state + year_factor + (1 | species) + (1 |
## mod5:   plot)
## mod6: log(julian_min) ~ state + year_factor + (1 | species) + (1 +
## mod6:   year | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5    11 -2472.7 -2420.9 1247.3   -2494.7
## mod6    13 -2379.0 -2317.8 1202.5   -2405.0     0  2          1
```

```
anova(mod5)
```

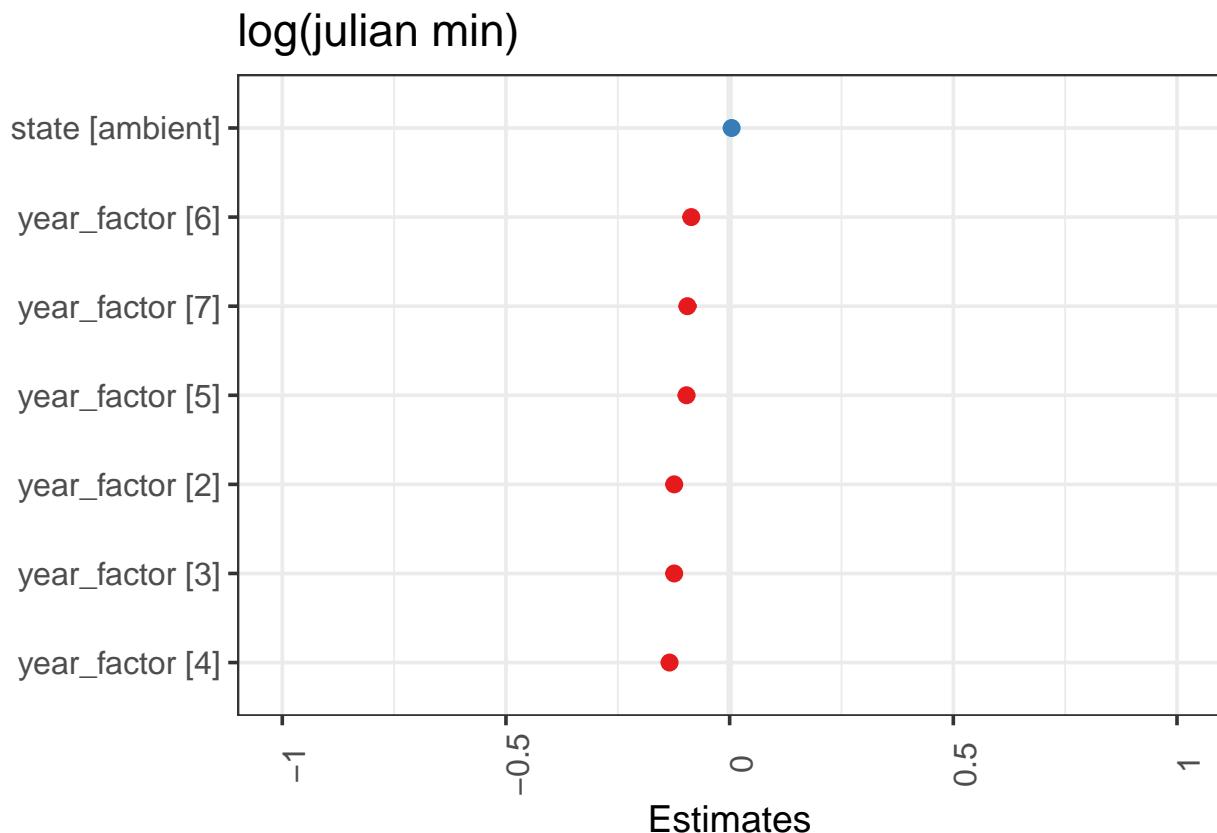
```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq  Mean Sq NumDF DenDF F value Pr(>F)
## state      0.00370 0.003698     1 794.25  1.569 0.2107
```

```

## year_factor 0.73853 0.123088      6 794.44  52.223 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

plot_model(mod5, sort.est = TRUE)

```



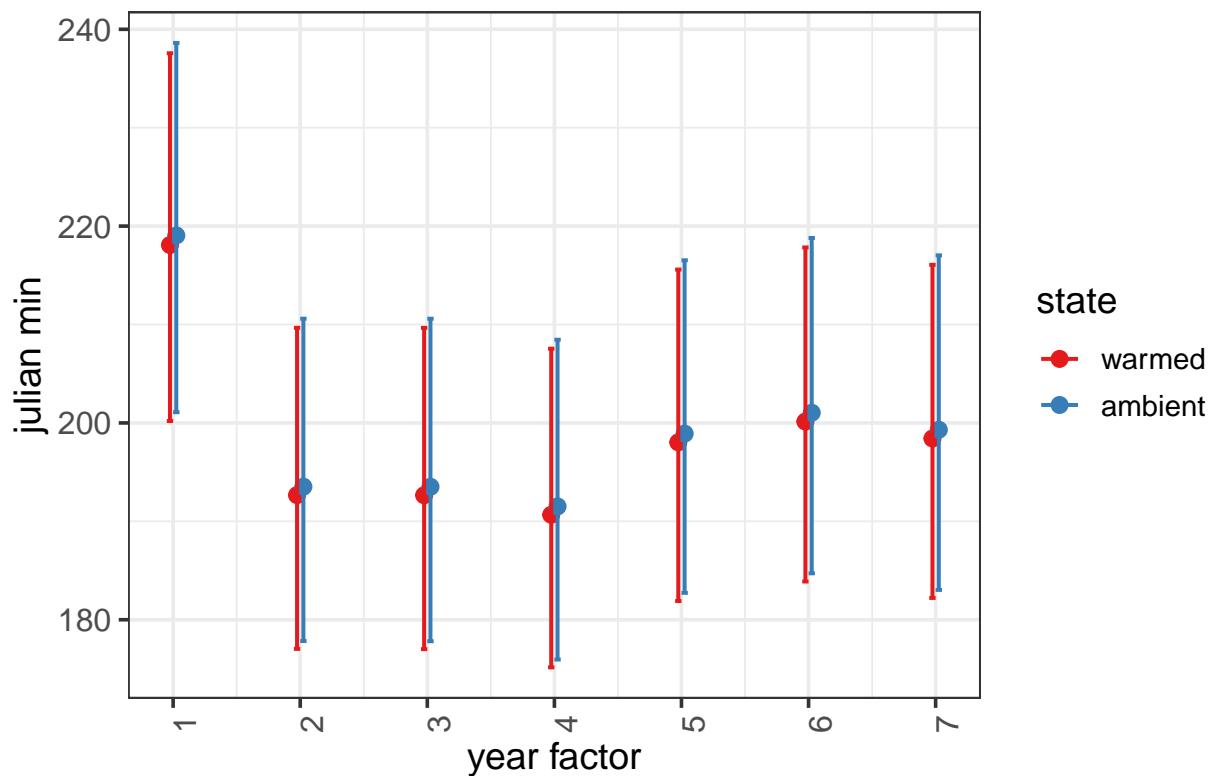
```

# 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. Standardized residuals.

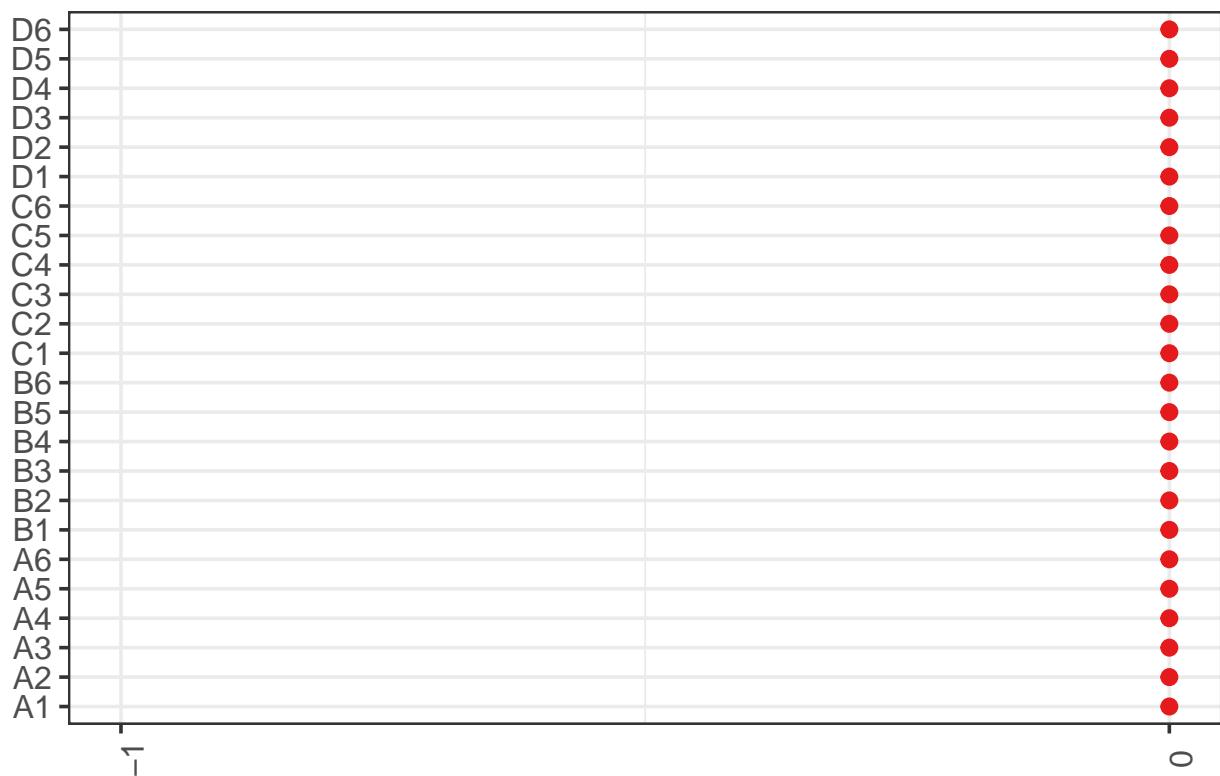
Predicted values of julian min



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

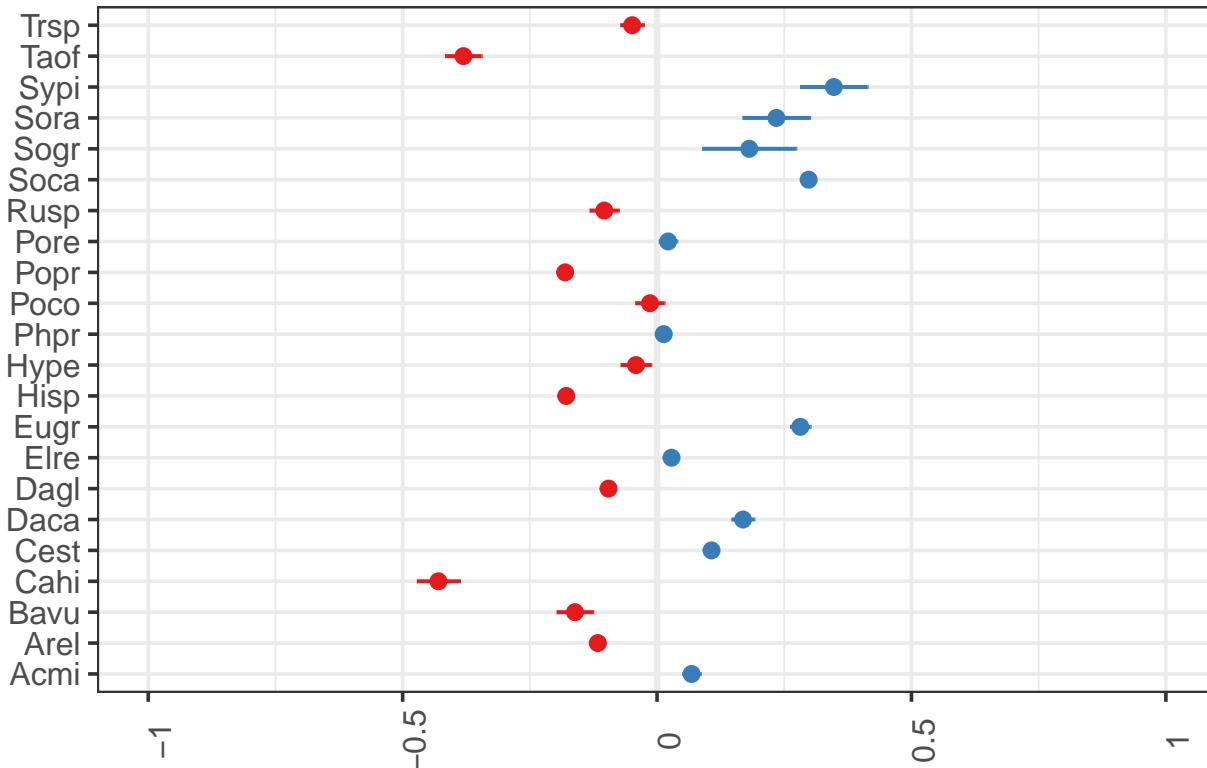
```
## [[1]]
```

Random effects



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

Random effects



```
# 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_min) ~ state + species + (1 + year_factor | plot), kbs_sd_spp,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 2 negative eigenvalues: -3.4e-02 -3.2e+00

mod7a <- lmer(log(julian_min) ~ state + species + year_factor + (1 | plot), kbs_sd_spp,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

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

```

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

## Data: kbs_sd_spp
## Models:
## mod5: log(julian_min) ~ state + year_factor + (1 | species) + (1 |
## mod5:      plot)
## mod7: log(julian_min) ~ state + species + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5    11 -2472.7 -2420.9 1247.3   -2494.7
## mod7    52 -2485.0 -2240.4 1294.5   -2589.0 94.377 41  4.315e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

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

```

## Data: kbs_sd_spp
## Models:
## mod7a: log(julian_min) ~ state + species + year_factor + (1 | plot)
## mod7: log(julian_min) ~ state + species + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a   31 -2581.8 -2436.0 1321.9   -2643.8
## mod7    52 -2485.0 -2240.4 1294.5   -2589.0      0 21           1

```

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

```

## Data: kbs_sd_spp
## Models:
## mod7a: log(julian_min) ~ state + species + year_factor + (1 | plot)
## mod7b: log(julian_min) ~ state * year_factor + species + (1 | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a   31 -2581.8 -2436.0 1321.9   -2643.8
## mod7b   37 -2573.8 -2399.7 1323.9   -2647.8 3.9597  6     0.6821

```

```
anova(mod7a, mod7c) #mod7a
```

```

## Data: kbs_sd_spp
## Models:
## mod7a: log(julian_min) ~ state + species + year_factor + (1 | plot)
## mod7c: log(julian_min) ~ state + species + year_factor + insecticide +
## mod7c:      (1 | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7a   31 -2581.8 -2436.0 1321.9   -2643.8
## mod7c   32 -2580.2 -2429.6 1322.1   -2644.2 0.3422  1     0.5586

```

```
summary(mod7a)
```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + species + year_factor + (1 | plot)
## Data: kbs_sd_spp

```

```

##
##      AIC      BIC logLik deviance df.resid
## -2581.8 -2436.0   1321.9 -2643.8      785
##
## Scaled residuals:
##      Min     1Q Median     3Q    Max
## -4.5921 -0.5306 -0.0049  0.4909  7.6708
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0000000 0.00000
## Residual           0.002293 0.04789
## Number of obs: 816, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)  5.452875  0.011990 816.00000 454.793 < 2e-16 ***
## stateambient 0.004370  0.003507 816.00000  1.246 0.213101  
## speciesArel -0.184443  0.010465 816.00000 -17.624 < 2e-16 ***
## speciesBavu -0.230672  0.020305 816.00000 -11.360 < 2e-16 ***
## speciesCahi -0.502774  0.023467 816.00000 -21.425 < 2e-16 ***
## speciesCest  0.039215  0.011618 816.00000  3.375 0.000772 ***
## speciesDaca  0.101541  0.014495 816.00000  7.005 5.16e-12 ***
## speciesDagl -0.163366  0.010831 816.00000 -15.083 < 2e-16 ***
## speciesElre -0.039521  0.011372 816.00000 -3.475 0.000537 ***
## speciesEugr  0.214379  0.013900 816.00000 15.422 < 2e-16 ***
## speciesHisp -0.246588  0.011127 816.00000 -22.161 < 2e-16 ***
## speciesHype -0.109633  0.017723 816.00000 -6.186 9.75e-10 ***
## speciesPhpr -0.054832  0.010547 816.00000 -5.199 2.54e-07 ***
## speciesPoco -0.082002  0.017606 816.00000 -4.658 3.73e-06 ***
## speciesPopr -0.248610  0.010203 816.00000 -24.368 < 2e-16 ***
## speciesPore -0.046105  0.013012 816.00000 -3.543 0.000418 ***
## speciesRusp -0.172216  0.017181 816.00000 -10.024 < 2e-16 ***
## speciesSoca  0.230129  0.010169 816.00000 22.630 < 2e-16 ***
## speciesSogr  0.123923  0.048964 816.00000  2.531 0.011564 *  
## speciesSora  0.173318  0.035168 816.00000  4.928 1.00e-06 ***
## speciesSypi  0.289872  0.035383 816.00000  8.192 9.86e-16 ***
## speciesTaof -0.451748  0.020315 816.00000 -22.237 < 2e-16 ***
## speciesTrsp -0.117081  0.014949 816.00000 -7.832 1.49e-14 ***
## year_factor2 -0.123848  0.008143 816.00000 -15.210 < 2e-16 ***
## year_factor3 -0.123874  0.008310 816.00000 -14.906 < 2e-16 ***
## year_factor4 -0.134431  0.008450 816.00000 -15.909 < 2e-16 ***
## year_factor5 -0.096438  0.008651 816.00000 -11.148 < 2e-16 ***
## year_factor6 -0.086017  0.008330 816.00000 -10.327 < 2e-16 ***
## year_factor7 -0.094345  0.009449 816.00000 -9.985 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 29 > 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) # investigates whether at least one of the levels within each factor is significantly dif

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.0036 0.00356     1    816  1.5527 0.2131
## species    23.6339 1.12542    21    816 490.7854 <2e-16 ***
## year_factor 0.7373 0.12289     6    816  53.5895 <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 min
# first seed dates).
emmeans(mod7a, 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 1          5.386 0.008638 731.1   5.369   5.403
##   ambient 1         5.390 0.008527 717.0   5.373   5.407
##   warmed 2          5.262 0.005434 323.6   5.251   5.273
##   ambient 2         5.266 0.005230 282.4   5.256   5.277
##   warmed 3          5.262 0.005630 346.9   5.251   5.273
##   ambient 3         5.266 0.005453 302.0   5.255   5.277
##   warmed 4          5.251 0.006294 469.0   5.239   5.264
##   ambient 4         5.256 0.006062 404.7   5.244   5.268
##   warmed 5          5.289 0.006753 535.0   5.276   5.303
##   ambient 5         5.294 0.006446 460.0   5.281   5.306
##   warmed 6          5.300 0.005916 451.5   5.288   5.311
##   ambient 6         5.304 0.005715 378.3   5.293   5.315
##   warmed 7          5.291 0.007527 606.6   5.277   5.306
##   ambient 7         5.296 0.007543 571.4   5.281   5.311
##
## 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 1 - ambient 1 -4.37e-03 0.00358 25.9 -1.220 0.9914
##   warmed 1 - warmed 2  1.24e-01 0.00830 840.6 14.917 <.0001
##   warmed 1 - ambient 2  1.19e-01 0.00903 509.1 13.235 <.0001
##   warmed 1 - warmed 3  1.24e-01 0.00847 841.6 14.618 <.0001
##   warmed 1 - ambient 3  1.20e-01 0.00920 517.6 12.994 <.0001
##   warmed 1 - warmed 4  1.34e-01 0.00861 839.0 15.606 <.0001
##   warmed 1 - ambient 4  1.30e-01 0.00928 528.5 14.018 <.0001
##   warmed 1 - warmed 5  9.64e-02 0.00882 838.2 10.937 <.0001
##   warmed 1 - ambient 5  9.21e-02 0.00940 540.7  9.789 <.0001
##   warmed 1 - warmed 6  8.60e-02 0.00849 838.6 10.131 <.0001

```

```

## warmed 1 - ambient 6 8.16e-02 0.00919 516.5 8.882 <.0001
## warmed 1 - warmed 7 9.43e-02 0.00964 843.5 9.789 <.0001
## warmed 1 - ambient 7 9.00e-02 0.01039 597.9 8.663 <.0001
## ambient 1 - warmed 2 1.28e-01 0.00906 509.1 14.156 <.0001
## ambient 1 - ambient 2 1.24e-01 0.00830 840.6 14.917 <.0001
## ambient 1 - warmed 3 1.28e-01 0.00920 524.6 13.934 <.0001
## ambient 1 - ambient 3 1.24e-01 0.00847 841.6 14.618 <.0001
## ambient 1 - warmed 4 1.39e-01 0.00938 555.2 14.796 <.0001
## ambient 1 - ambient 4 1.34e-01 0.00861 839.0 15.606 <.0001
## ambient 1 - warmed 5 1.01e-01 0.00963 581.7 10.469 <.0001
## ambient 1 - ambient 5 9.64e-02 0.00882 838.2 10.937 <.0001
## ambient 1 - warmed 6 9.04e-02 0.00924 547.9 9.783 <.0001
## ambient 1 - ambient 6 8.60e-02 0.00849 838.6 10.131 <.0001
## ambient 1 - warmed 7 9.87e-02 0.01018 610.2 9.700 <.0001
## ambient 1 - ambient 7 9.43e-02 0.00964 843.5 9.789 <.0001
## warmed 2 - ambient 2 -4.37e-03 0.00358 25.9 -1.220 0.9914
## warmed 2 - warmed 3 2.51e-05 0.00547 841.2 0.005 1.0000
## warmed 2 - ambient 3 -4.35e-03 0.00656 228.8 -0.663 1.0000
## warmed 2 - warmed 4 1.06e-02 0.00591 839.9 1.792 0.8797
## warmed 2 - ambient 4 6.21e-03 0.00686 258.7 0.906 0.9998
## warmed 2 - warmed 5 -2.74e-02 0.00624 844.9 -4.392 0.0011
## warmed 2 - ambient 5 -3.18e-02 0.00707 269.7 -4.497 0.0008
## warmed 2 - warmed 6 -3.78e-02 0.00568 846.0 -6.664 <.0001
## warmed 2 - ambient 6 -4.22e-02 0.00670 225.3 -6.298 <.0001
## warmed 2 - warmed 7 -2.95e-02 0.00749 845.3 -3.937 0.0068
## warmed 2 - ambient 7 -3.39e-02 0.00845 392.3 -4.008 0.0056
## ambient 2 - warmed 3 4.40e-03 0.00652 232.8 0.674 1.0000
## ambient 2 - ambient 3 2.51e-05 0.00547 841.2 0.005 1.0000
## ambient 2 - warmed 4 1.50e-02 0.00696 288.4 2.149 0.6665
## ambient 2 - ambient 4 1.06e-02 0.00591 839.9 1.792 0.8797
## ambient 2 - warmed 5 -2.30e-02 0.00733 321.8 -3.145 0.0982
## ambient 2 - ambient 5 -2.74e-02 0.00624 844.9 -4.392 0.0011
## ambient 2 - warmed 6 -3.35e-02 0.00673 252.2 -4.976 0.0001
## ambient 2 - ambient 6 -3.78e-02 0.00568 846.0 -6.664 <.0001
## ambient 2 - warmed 7 -2.51e-02 0.00816 394.8 -3.080 0.1159
## ambient 2 - ambient 7 -2.95e-02 0.00749 845.3 -3.937 0.0068
## warmed 3 - ambient 3 -4.37e-03 0.00358 25.9 -1.220 0.9914
## warmed 3 - warmed 4 1.06e-02 0.00615 831.5 1.716 0.9100
## warmed 3 - ambient 4 6.19e-03 0.00706 295.2 0.877 0.9998
## warmed 3 - warmed 5 -2.74e-02 0.00649 843.2 -4.228 0.0021
## warmed 3 - ambient 5 -3.18e-02 0.00727 301.0 -4.375 0.0014
## warmed 3 - warmed 6 -3.79e-02 0.00600 845.5 -6.309 <.0001
## warmed 3 - ambient 6 -4.22e-02 0.00696 258.5 -6.066 <.0001
## warmed 3 - warmed 7 -2.95e-02 0.00767 846.0 -3.851 0.0094
## warmed 3 - ambient 7 -3.39e-02 0.00859 424.8 -3.944 0.0070
## ambient 3 - warmed 4 1.49e-02 0.00718 320.8 2.079 0.7155
## ambient 3 - ambient 4 1.06e-02 0.00615 831.5 1.716 0.9100
## ambient 3 - warmed 5 -2.31e-02 0.00755 348.2 -3.055 0.1246
## ambient 3 - ambient 5 -2.74e-02 0.00649 843.2 -4.228 0.0021
## ambient 3 - warmed 6 -3.35e-02 0.00702 282.6 -4.773 0.0002
## ambient 3 - ambient 6 -3.79e-02 0.00600 845.5 -6.309 <.0001
## ambient 3 - warmed 7 -2.52e-02 0.00833 423.0 -3.019 0.1355
## ambient 3 - ambient 7 -2.95e-02 0.00767 846.0 -3.851 0.0094
## warmed 4 - ambient 4 -4.37e-03 0.00358 25.9 -1.220 0.9914

```

```

##  warmed 4 - warmed 5 -3.80e-02 0.00672 836.3 -5.653 <.0001
##  warmed 4 - ambient 5 -4.24e-02 0.00754 350.2 -5.620 <.0001
##  warmed 4 - warmed 6 -4.84e-02 0.00634 837.9 -7.633 <.0001
##  warmed 4 - ambient 6 -5.28e-02 0.00732 319.3 -7.211 <.0001
##  warmed 4 - warmed 7 -4.01e-02 0.00789 841.4 -5.078 <.0001
##  warmed 4 - ambient 7 -4.45e-02 0.00885 479.0 -5.025 0.0001
##  ambient 4 - warmed 5 -3.36e-02 0.00769 372.8 -4.371 0.0013
##  ambient 4 - ambient 5 -3.80e-02 0.00672 836.3 -5.653 <.0001
##  ambient 4 - warmed 6 -4.40e-02 0.00725 320.3 -6.076 <.0001
##  ambient 4 - ambient 6 -4.84e-02 0.00634 837.9 -7.633 <.0001
##  ambient 4 - warmed 7 -3.57e-02 0.00849 457.5 -4.208 0.0025
##  ambient 4 - ambient 7 -4.01e-02 0.00789 841.4 -5.078 <.0001
##  warmed 5 - ambient 5 -4.37e-03 0.00358 25.9 -1.220 0.9914
##  warmed 5 - warmed 6 -1.04e-02 0.00660 835.6 -1.580 0.9511
##  warmed 5 - ambient 6 -1.48e-02 0.00762 360.1 -1.941 0.8023
##  warmed 5 - warmed 7 -2.09e-03 0.00812 837.5 -0.258 1.0000
##  warmed 5 - ambient 7 -6.46e-03 0.00911 518.6 -0.709 1.0000
##  ambient 5 - warmed 6 -6.05e-03 0.00739 338.9 -0.819 0.9999
##  ambient 5 - ambient 6 -1.04e-02 0.00660 835.6 -1.580 0.9511
##  ambient 5 - warmed 7 2.28e-03 0.00863 481.4 0.264 1.0000
##  ambient 5 - ambient 7 -2.09e-03 0.00812 837.5 -0.258 1.0000
##  warmed 6 - ambient 6 -4.37e-03 0.00358 25.9 -1.220 0.9914
##  warmed 6 - warmed 7 8.33e-03 0.00767 839.7 1.087 0.9984
##  warmed 6 - ambient 7 3.96e-03 0.00861 464.4 0.460 1.0000
##  ambient 6 - warmed 7 1.27e-02 0.00831 437.8 1.529 0.9618
##  ambient 6 - ambient 7 8.33e-03 0.00767 839.7 1.087 0.9984
##  warmed 7 - ambient 7 -4.37e-03 0.00358 25.9 -1.220 0.9914
##
## 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 14 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
##  1            5.388 0.008394 821.4    5.371   5.404
##  2            5.264 0.005023 519.7    5.254   5.274
##  3            5.264 0.005245 537.0    5.254   5.274
##  4            5.253 0.005914 655.2    5.242   5.265
##  5            5.291 0.006353 701.1    5.279   5.304
##  6            5.302 0.005534 656.2    5.291   5.313
##  7            5.294 0.007319 747.7    5.279   5.308
##
## 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  1.24e-01 0.00830 841 14.917 <.0001
## 1 - 3  1.24e-01 0.00847 842 14.618 <.0001
## 1 - 4  1.34e-01 0.00861 839 15.606 <.0001
## 1 - 5  9.64e-02 0.00882 838 10.937 <.0001
## 1 - 6  8.60e-02 0.00849 839 10.131 <.0001
## 1 - 7  9.43e-02 0.00964 843  9.789 <.0001
## 2 - 3  2.51e-05 0.00547 841  0.005 1.0000
## 2 - 4  1.06e-02 0.00591 840  1.792 0.5542
## 2 - 5 -2.74e-02 0.00624 845 -4.392 0.0003
## 2 - 6 -3.78e-02 0.00568 846 -6.664 <.0001
## 2 - 7 -2.95e-02 0.00749 845 -3.937 0.0017
## 3 - 4  1.06e-02 0.00615 832  1.716 0.6053
## 3 - 5 -2.74e-02 0.00649 843 -4.228 0.0005
## 3 - 6 -3.79e-02 0.00600 846 -6.309 <.0001
## 3 - 7 -2.95e-02 0.00767 846 -3.851 0.0024
## 4 - 5 -3.80e-02 0.00672 836 -5.653 <.0001
## 4 - 6 -4.84e-02 0.00634 838 -7.633 <.0001
## 4 - 7 -4.01e-02 0.00789 841 -5.078 <.0001
## 5 - 6 -1.04e-02 0.00660 836 -1.580 0.6954
## 5 - 7 -2.09e-03 0.00812 838 -0.258 1.0000
## 6 - 7  8.33e-03 0.00767 840  1.087 0.9321
##
## 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(mod7a, list(pairwise ~ species), adjust = "tukey")
```

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

```

## $`emmeans of species`
##   species emmean      SE  df lower.CL upper.CL
##   Acmi    5.361 0.009503 766.2    5.342    5.380
##   Arel    5.176 0.004916 533.2    5.167    5.186
##   Bavu    5.130 0.018595 821.7    5.094    5.167
##   Cahí    4.858 0.022232 845.8    4.815    4.902
##   Cest    5.400 0.007665 754.1    5.385    5.415
##   Daca    5.462 0.011681 820.5    5.440    5.485
##   Dagl    5.198 0.005888 667.2    5.186    5.209
##   Elre    5.321 0.006853 758.1    5.308    5.335
##   Eugr    5.575 0.010748 820.3    5.554    5.596
##   Hisp    5.114 0.006754 722.6    5.101    5.128
##   Hype    5.251 0.015643 829.6    5.221    5.282
##   Phpr    5.306 0.005261 567.8    5.296    5.316
##   Poco    5.279 0.015173 839.7    5.249    5.309
##   Popr    5.112 0.004615 543.9    5.103    5.121
##   Pore    5.315 0.009684 827.1    5.296    5.334
##   Rusp    5.189 0.014945 781.0    5.159    5.218
##   Soca    5.591 0.004507 525.4    5.582    5.600
##   Sogr    5.485 0.049100 846.1    5.388    5.581
##   Sora    5.534 0.034789 846.0    5.466    5.603

```

```

##   Sypi      5.651 0.034843 846.0      5.582      5.719
##   Taof      4.909 0.018683 844.5      4.873      4.946
##   Trsp      5.244 0.012360 845.0      5.220      5.268
##
## 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  0.18444 0.01071 840  17.228 <.0001
##   Acmi - Bavu  0.23067 0.02071 844  11.137 <.0001
##   Acmi - Cahи  0.50277 0.02395 846  20.993 <.0001
##   Acmi - Cest -0.03921 0.01188 843  -3.300 0.1254
##   Acmi - Daca -0.10154 0.01480 846  -6.863 <.0001
##   Acmi - Dagl  0.16337 0.01106 846  14.768 <.0001
##   Acmi - Elre  0.03952 0.01163 839   3.398 0.0948
##   Acmi - Eugr -0.21438 0.01419 846  -15.105 <.0001
##   Acmi - Hisp  0.24659 0.01137 845  21.687 <.0001
##   Acmi - Hype  0.10963 0.01812 838   6.051 <.0001
##   Acmi - Phpr  0.05483 0.01079 839   5.083 0.0001
##   Acmi - Poco  0.08200 0.01796 845   4.565 0.0012
##   Acmi - Popr  0.24861 0.01044 838  23.809 <.0001
##   Acmi - Pore  0.04611 0.01328 846   3.471 0.0762
##   Acmi - Rusp  0.17222 0.01756 843   9.809 <.0001
##   Acmi - Soca -0.23013 0.01040 843  -22.127 <.0001
##   Acmi - Sogr -0.12392 0.05001 846  -2.478 0.6494
##   Acmi - Sora -0.17332 0.03591 845  -4.826 0.0004
##   Acmi - Sypi -0.28987 0.03612 846  -8.025 <.0001
##   Acmi - Taof  0.45175 0.02074 846  21.779 <.0001
##   Acmi - Trsp  0.11708 0.01524 841   7.681 <.0001
##   Arel - Bavu  0.04623 0.01925 835   2.402 0.7067
##   Arel - Cahи  0.31833 0.02282 844  13.950 <.0001
##   Arel - Cest -0.22366 0.00911 842  -24.561 <.0001
##   Arel - Daca -0.28598 0.01266 846  -22.581 <.0001
##   Arel - Dagl -0.02108 0.00767 846  -2.748 0.4375
##   Arel - Elre -0.14492 0.00847 846  -17.106 <.0001
##   Arel - Eugr -0.39882 0.01181 845  -33.777 <.0001
##   Arel - Hisp  0.06214 0.00833 846   7.457 <.0001
##   Arel - Hype -0.07481 0.01642 844  -4.557 0.0012
##   Arel - Phpr -0.12961 0.00720 840  -17.991 <.0001
##   Arel - Poco -0.10244 0.01588 846  -6.449 <.0001
##   Arel - Popr  0.06417 0.00672 845   9.551 <.0001
##   Arel - Pore -0.13834 0.01080 843  -12.804 <.0001
##   Arel - Rusp -0.01223 0.01569 812  -0.779 1.0000
##   Arel - Soca -0.41457 0.00669 846  -62.011 <.0001
##   Arel - Sogr -0.30837 0.04934 846  -6.250 <.0001
##   Arel - Sora -0.35776 0.03516 846  -10.175 <.0001
##   Arel - Sypi -0.47431 0.03516 846  -13.492 <.0001
##   Arel - Taof  0.26730 0.01930 846  13.847 <.0001
##   Arel - Trsp -0.06736 0.01329 844  -5.068 0.0001
##   Bavu - Cahи  0.27210 0.02883 846   9.439 <.0001
##   Bavu - Cest -0.26989 0.02005 836  -13.458 <.0001

```

```

##  Bavu - Daca -0.33221 0.02185 845 -15.206 <.0001
##  Bavu - Dagl -0.06731 0.01948 839 -3.456 0.0798
##  Bavu - Elre -0.19115 0.01975 838 -9.679 <.0001
##  Bavu - Eogr -0.44505 0.02136 845 -20.836 <.0001
##  Bavu - Hisp 0.01592 0.01969 843 0.808 1.0000
##  Bavu - Hype -0.12104 0.02416 842 -5.010 0.0001
##  Bavu - Phpr -0.17584 0.01931 836 -9.109 <.0001
##  Bavu - Poco -0.14867 0.02396 842 -6.206 <.0001
##  Bavu - Popr 0.01794 0.01914 835 0.937 1.0000
##  Bavu - Pore -0.18457 0.02092 841 -8.824 <.0001
##  Bavu - Rusp -0.05846 0.02374 844 -2.463 0.6613
##  Bavu - Soca -0.46080 0.01908 839 -24.149 <.0001
##  Bavu - Sogr -0.35460 0.05258 846 -6.744 <.0001
##  Bavu - Sora -0.40399 0.03937 845 -10.261 <.0001
##  Bavu - Sypi -0.52054 0.03952 845 -13.172 <.0001
##  Bavu - Taof 0.22108 0.02625 846 8.420 <.0001
##  Bavu - Trsp -0.11359 0.02220 845 -5.118 0.0001
##  Cah - Cest -0.54199 0.02341 845 -23.156 <.0001
##  Cah - Daca -0.60431 0.02495 845 -24.224 <.0001
##  Cah - Dagl -0.33941 0.02295 844 -14.789 <.0001
##  Cah - Elre -0.46325 0.02318 846 -19.985 <.0001
##  Cah - Eogr -0.71715 0.02471 845 -29.019 <.0001
##  Cah - Hisp -0.25619 0.02309 843 -11.097 <.0001
##  Cah - Hype -0.39314 0.02698 844 -14.574 <.0001
##  Cah - Phpr -0.44794 0.02283 843 -19.621 <.0001
##  Cah - Poco -0.42077 0.02700 845 -15.585 <.0001
##  Cah - Popr -0.25416 0.02267 845 -11.212 <.0001
##  Cah - Pore -0.45667 0.02419 844 -18.878 <.0001
##  Cah - Rusp -0.33056 0.02676 846 -12.351 <.0001
##  Cah - Soca -0.73290 0.02261 845 -32.419 <.0001
##  Cah - Sogr -0.62670 0.05393 843 -11.621 <.0001
##  Cah - Sora -0.67609 0.04085 839 -16.550 <.0001
##  Cah - Sypi -0.79265 0.04141 846 -19.142 <.0001
##  Cah - Taof -0.05103 0.02900 844 -1.760 0.9804
##  Cah - Trsp -0.38569 0.02546 843 -15.150 <.0001
##  Cest - Daca -0.06233 0.01375 842 -4.533 0.0014
##  Cest - Dagl 0.20258 0.00956 844 21.197 <.0001
##  Cest - Elre 0.07874 0.01016 844 7.749 <.0001
##  Cest - Eogr -0.17516 0.01305 843 -13.420 <.0001
##  Cest - Hisp 0.28580 0.00991 845 28.830 <.0001
##  Cest - Hype 0.14885 0.01727 840 8.617 <.0001
##  Cest - Phpr 0.09405 0.00918 846 10.250 <.0001
##  Cest - Poco 0.12122 0.01716 846 7.065 <.0001
##  Cest - Popr 0.28782 0.00877 844 32.832 <.0001
##  Cest - Pore 0.08532 0.01205 846 7.080 <.0001
##  Cest - Rusp 0.21143 0.01676 787 12.614 <.0001
##  Cest - Soca -0.19091 0.00876 844 -21.794 <.0001
##  Cest - Sogr -0.08471 0.04962 846 -1.707 0.9862
##  Cest - Sora -0.13410 0.03555 846 -3.773 0.0284
##  Cest - Sypi -0.25066 0.03567 846 -7.027 <.0001
##  Cest - Taof 0.49096 0.01999 845 24.556 <.0001
##  Cest - Trsp 0.15630 0.01415 840 11.048 <.0001
##  Daca - Dagl 0.26491 0.01299 844 20.400 <.0001
##  Daca - Elre 0.14106 0.01345 846 10.487 <.0001

```

```

## Daca - Eugr -0.11284 0.01574 846 -7.170 <.0001
## Daca - Hisp 0.34813 0.01326 846 26.248 <.0001
## Daca - Hype 0.21117 0.01938 844 10.894 <.0001
## Daca - Phpr 0.15637 0.01273 846 12.284 <.0001
## Daca - Poco 0.18354 0.01924 844 9.541 <.0001
## Daca - Popr 0.35015 0.01246 845 28.099 <.0001
## Daca - Pore 0.14765 0.01493 846 9.886 <.0001
## Daca - Rusp 0.27376 0.01885 845 14.520 <.0001
## Daca - Soca -0.12859 0.01243 846 -10.347 <.0001
## Daca - Sogr -0.02238 0.05045 846 -0.444 1.0000
## Daca - Sora -0.07178 0.03657 846 -1.963 0.9389
## Daca - Sypi -0.18833 0.03672 845 -5.128 0.0001
## Daca - Taof 0.55329 0.02189 846 25.274 <.0001
## Daca - Trsp 0.21862 0.01677 843 13.034 <.0001
## Dagl - Elre -0.12384 0.00900 846 -13.758 <.0001
## Dagl - Eugr -0.37774 0.01214 846 -31.108 <.0001
## Dagl - Hisp 0.08322 0.00884 846 9.416 <.0001
## Dagl - Hype -0.05373 0.01664 842 -3.229 0.1520
## Dagl - Phpr -0.10853 0.00784 839 -13.846 <.0001
## Dagl - Poco -0.08136 0.01632 844 -4.985 0.0002
## Dagl - Popr 0.08524 0.00744 846 11.463 <.0001
## Dagl - Pore -0.11726 0.01121 841 -10.465 <.0001
## Dagl - Rusp 0.00885 0.01602 830 0.553 1.0000
## Dagl - Soca -0.39349 0.00736 846 -53.485 <.0001
## Dagl - Sogr -0.28729 0.04944 846 -5.811 <.0001
## Dagl - Sora -0.33668 0.03524 846 -9.553 <.0001
## Dagl - Sypi -0.45324 0.03530 846 -12.840 <.0001
## Dagl - Taof 0.28838 0.01954 846 14.758 <.0001
## Dagl - Trsp -0.04628 0.01358 838 -3.407 0.0923
## Elre - Eugr -0.25390 0.01265 846 -20.077 <.0001
## Elre - Hisp 0.20707 0.00952 846 21.749 <.0001
## Elre - Hype 0.07011 0.01699 836 4.128 0.0075
## Elre - Phpr 0.01531 0.00855 846 1.790 0.9763
## Elre - Poco 0.04248 0.01678 846 2.531 0.6078
## Elre - Popr 0.20909 0.00820 844 25.505 <.0001
## Elre - Pore 0.00658 0.01184 843 0.556 1.0000
## Elre - Rusp 0.13269 0.01648 831 8.051 <.0001
## Elre - Soca -0.26965 0.00810 843 -33.294 <.0001
## Elre - Sogr -0.16344 0.04955 846 -3.299 0.1258
## Elre - Sora -0.21284 0.03543 846 -6.008 <.0001
## Elre - Sypi -0.32939 0.03552 846 -9.274 <.0001
## Elre - Taof 0.41223 0.01990 846 20.720 <.0001
## Elre - Trsp 0.07756 0.01406 841 5.516 <.0001
## Eugr - Hisp 0.46097 0.01248 846 36.940 <.0001
## Eugr - Hype 0.32401 0.01872 844 17.307 <.0001
## Eugr - Phpr 0.26921 0.01188 844 22.667 <.0001
## Eugr - Poco 0.29638 0.01864 845 15.902 <.0001
## Eugr - Popr 0.46299 0.01164 846 39.764 <.0001
## Eugr - Pore 0.26048 0.01424 846 18.298 <.0001
## Eugr - Rusp 0.38659 0.01824 844 21.189 <.0001
## Eugr - Soca -0.01575 0.01153 846 -1.366 0.9993
## Eugr - Sogr 0.09046 0.05030 846 1.798 0.9751
## Eugr - Sora 0.04106 0.03643 846 1.127 1.0000
## Eugr - Sypi -0.07549 0.03626 846 -2.082 0.8961

```

```

##  Eogr - Taof  0.66613 0.02138 845  31.152 <.0001
##  Eogr - Trsp  0.33146 0.01604 845  20.669 <.0001
##  Hisp - Hype -0.13695 0.01687 842  -8.118 <.0001
##  Hisp - Phpr -0.19176 0.00846 843 -22.660 <.0001
##  Hisp - Poco -0.16459 0.01669 846  -9.864 <.0001
##  Hisp - Popr  0.00202 0.00803 845   0.252 1.0000
##  Hisp - Pore -0.20048 0.01149 844 -17.444 <.0001
##  Hisp - Rusp -0.07437 0.01629 818  -4.565 0.0012
##  Hisp - Soca -0.47672 0.00797 844 -59.780 <.0001
##  Hisp - Sogr -0.37051 0.04954 846  -7.479 <.0001
##  Hisp - Sora -0.41991 0.03533 846 -11.886 <.0001
##  Hisp - Sypi -0.53646 0.03541 846 -15.151 <.0001
##  Hisp - Taof  0.20516 0.01971 845  10.410 <.0001
##  Hisp - Trsp -0.12951 0.01382 840  -9.374 <.0001
##  Hype - Phpr -0.05480 0.01644 845 -3.333 0.1144
##  Hype - Poco -0.02763 0.02187 843  -1.263 0.9998
##  Hype - Popr  0.13898 0.01627 842  8.543 <.0001
##  Hype - Pore -0.06353 0.01827 838  -3.477 0.0749
##  Hype - Rusp  0.06258 0.02155 837  2.905 0.3255
##  Hype - Soca -0.33976 0.01618 843 -21.003 <.0001
##  Hype - Sogr -0.23356 0.05159 846  -4.527 0.0014
##  Hype - Sora -0.28295 0.03801 845  -7.444 <.0001
##  Hype - Sypi -0.39950 0.03811 846 -10.482 <.0001
##  Hype - Taof  0.34211 0.02424 843  14.114 <.0001
##  Hype - Trsp  0.00745 0.01972 843  0.378 1.0000
##  Phpr - Poco  0.02717 0.01613 845  1.684 0.9882
##  Phpr - Popr  0.19378 0.00694 845  27.927 <.0001
##  Phpr - Pore -0.00873 0.01093 844  -0.799 1.0000
##  Phpr - Rusp  0.11738 0.01585 818  7.407 <.0001
##  Phpr - Soca -0.28496 0.00686 846 -41.513 <.0001
##  Phpr - Sogr -0.17876 0.04935 846  -3.622 0.0472
##  Phpr - Sora -0.22815 0.03517 846  -6.487 <.0001
##  Phpr - Sypi -0.34470 0.03522 846  -9.787 <.0001
##  Phpr - Taof  0.39692 0.01938 846  20.477 <.0001
##  Phpr - Trsp  0.06225 0.01333 839  4.669 0.0007
##  Poco - Popr  0.16661 0.01588 846  10.494 <.0001
##  Poco - Pore -0.03590 0.01806 843  -1.988 0.9313
##  Poco - Rusp  0.09021 0.02104 845  4.288 0.0039
##  Poco - Soca -0.31213 0.01590 846 -19.628 <.0001
##  Poco - Sogr -0.20593 0.05147 846  -4.001 0.0123
##  Poco - Sora -0.25532 0.03801 846  -6.716 <.0001
##  Poco - Sypi -0.37187 0.03796 845  -9.797 <.0001
##  Poco - Taof  0.36975 0.02405 846  15.376 <.0001
##  Poco - Trsp  0.03508 0.01970 840  1.781 0.9776
##  Popr - Pore -0.20250 0.01059 845 -19.127 <.0001
##  Popr - Rusp -0.07639 0.01561 803  -4.895 0.0003
##  Popr - Soca -0.47874 0.00638 830 -74.980 <.0001
##  Popr - Sogr -0.37253 0.04927 846  -7.561 <.0001
##  Popr - Sora -0.42193 0.03506 846 -12.035 <.0001
##  Popr - Sypi -0.53848 0.03512 846 -15.333 <.0001
##  Popr - Taof  0.20314 0.01918 846  10.590 <.0001
##  Popr - Trsp -0.13153 0.01309 841 -10.046 <.0001
##  Pore - Rusp  0.12611 0.01766 829   7.143 <.0001
##  Pore - Soca -0.27623 0.01058 845 -26.104 <.0001

```

```

## Pore - Sogr -0.17003 0.05000 846 -3.400 0.0941
## Pore - Sora -0.21942 0.03603 846 -6.090 <.0001
## Pore - Sypi -0.33598 0.03602 846 -9.328 <.0001
## Pore - Taof 0.40564 0.02084 846 19.468 <.0001
## Pore - Trsp 0.07098 0.01535 838 4.624 0.0009
## Rusp - Soca -0.40234 0.01559 817 -25.802 <.0001
## Rusp - Sogr -0.29614 0.05135 846 -5.768 <.0001
## Rusp - Sora -0.34553 0.03783 846 -9.134 <.0001
## Rusp - Sypi -0.46209 0.03781 842 -12.221 <.0001
## Rusp - Taof 0.27953 0.02373 846 11.778 <.0001
## Rusp - Trsp -0.05513 0.01923 845 -2.867 0.3513
## Soca - Sogr 0.10621 0.04931 846 2.154 0.8627
## Soca - Sora 0.05681 0.03504 846 1.621 0.9926
## Soca - Sypi -0.05974 0.03510 846 -1.702 0.9866
## Soca - Taof 0.68188 0.01917 846 35.562 <.0001
## Soca - Trsp 0.34721 0.01305 839 26.605 <.0001
## Sogr - Sora -0.04939 0.06011 837 -0.822 1.0000
## Sogr - Sypi -0.16595 0.06019 846 -2.757 0.4309
## Sogr - Taof 0.57567 0.05249 842 10.967 <.0001
## Sogr - Trsp 0.24100 0.05064 846 4.759 0.0005
## Sora - Sypi -0.11655 0.04926 846 -2.366 0.7327
## Sora - Taof 0.62507 0.03941 843 15.859 <.0001
## Sora - Trsp 0.29040 0.03693 846 7.864 <.0001
## Sypi - Taof 0.74162 0.03952 846 18.766 <.0001
## Sypi - Trsp 0.40695 0.03697 846 11.007 <.0001
## Taof - Trsp -0.33467 0.02198 844 -15.224 <.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 22 estimates

```

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

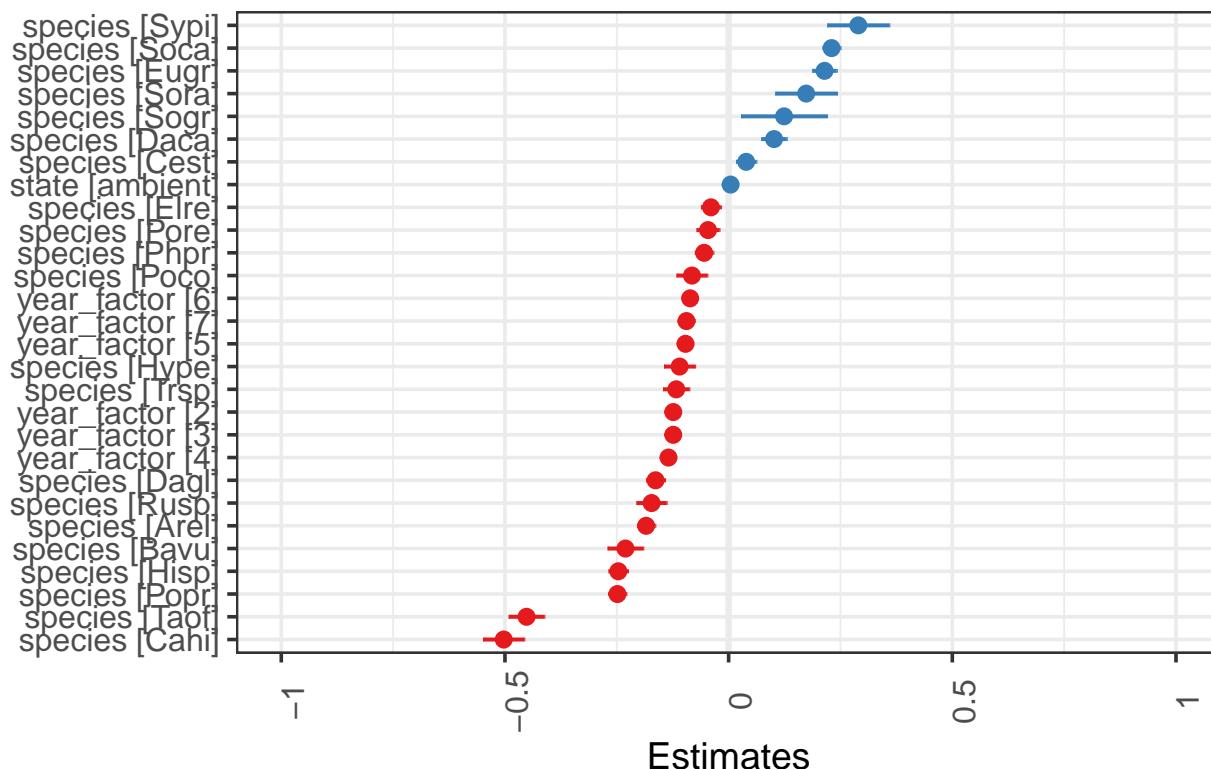
```
## boundary (singular) fit: see ?isSingular
```

```
## 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).*

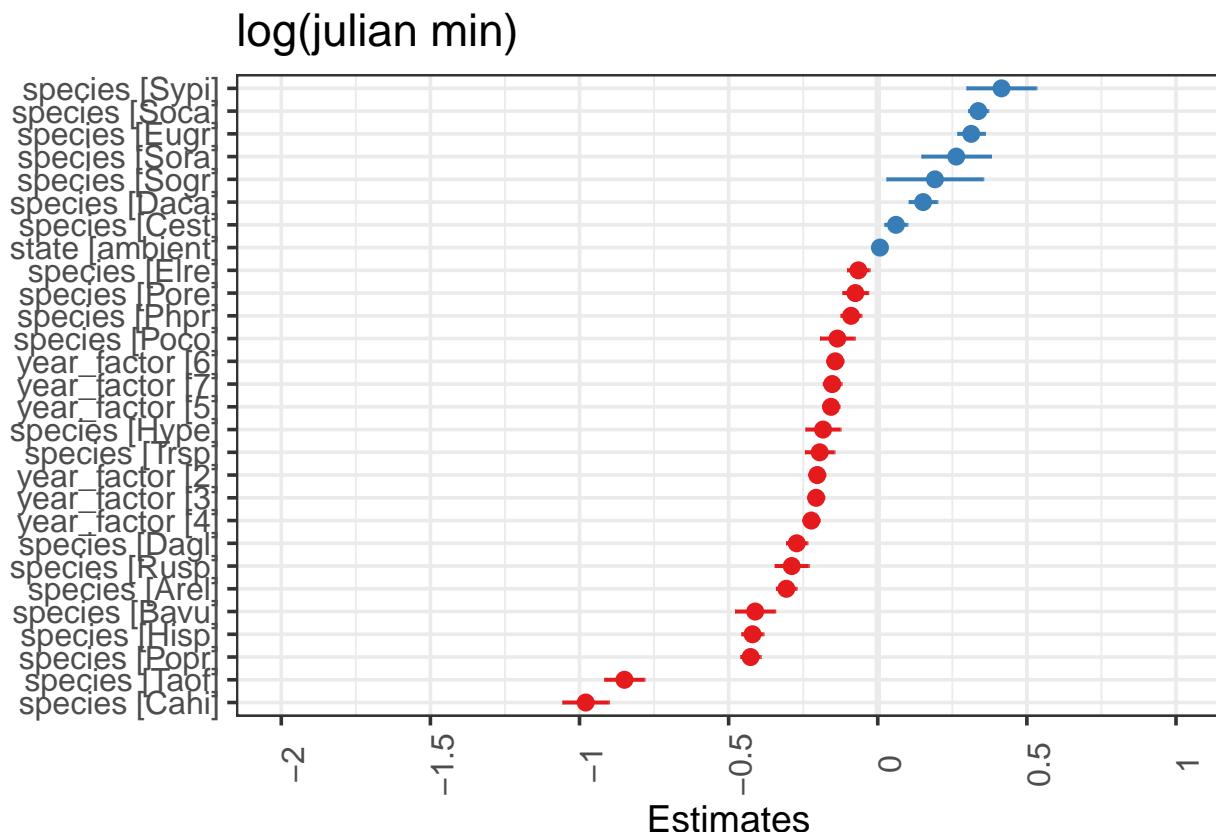
```
plot_model(mod7a, sort.est = TRUE)
```

log(julian min)



```
# 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
```

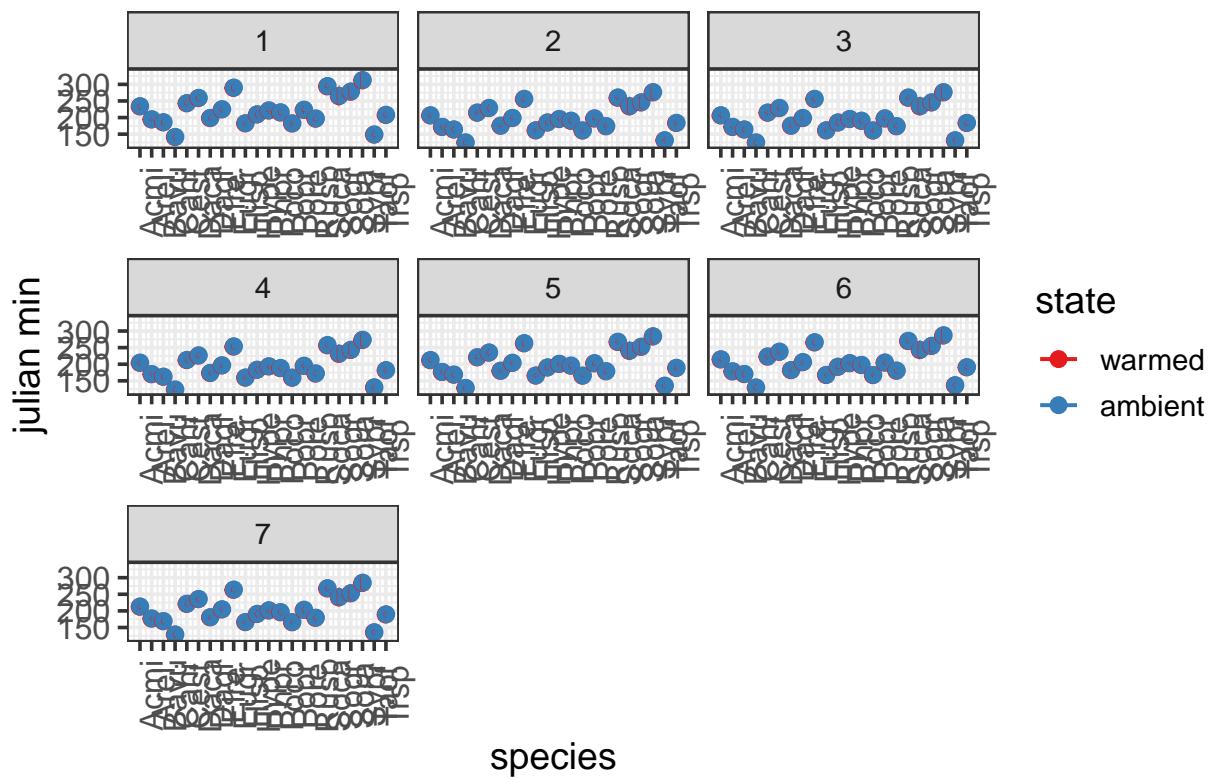


these are the fixed predicted values: - note this is a new plot

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

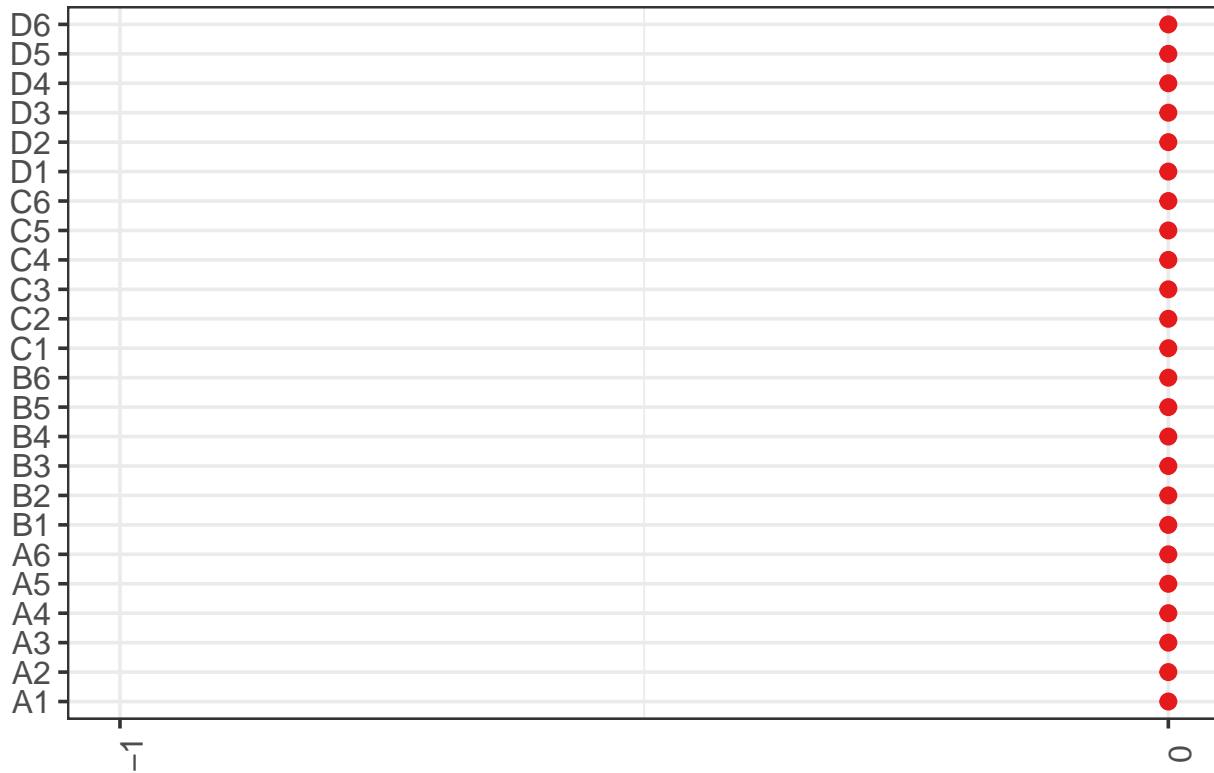
Model has log-transformed response. Back-transforming predictions to original response scale. Standardized predictions are back-transformed using the mean residual standard deviation.

Predicted values of julian min



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

Random effects



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

## boundary (singular) fit: see ?isSingular

mod9 <- lmer(log(julian_min) ~ state + origin + (1 + year_factor | plot), kbs_sd_spp,
              REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9a <- lmer(log(julian_min) ~ state + origin + year_factor + (1 | plot), kbs_sd_spp,
               REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod8, mod9) # model 8 is a better fit to data

## Data: kbs_sd_spp
## Models:
## mod9: log(julian_min) ~ state + origin + (1 + year_factor | plot)
## mod8: log(julian_min) ~ state * origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9   33 -1154.2 -999.03 610.08   -1220.2
## mod8   35 -1151.1 -986.56 610.54   -1221.1 0.9268  2     0.6291
```

```

anova(mod8, mod9a) # mod 8

## Data: kbs_sd_spp
## Models:
## mod9a: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## mod8: log(julian_min) ~ state * origin + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9a    12 -1237.6 -1181.16 630.78   -1261.6
## mod8     35 -1151.1  -986.56 610.54   -1221.1      0 23           1

summary(mod8)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * origin + (1 + year_factor | plot)
## Data: kbs_sd_spp
##
##      AIC      BIC      logLik deviance df.resid
## -1151.1  -986.6    610.5   -1221.1      778
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.0296 -0.5743  0.0208  0.6870  3.3227
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## plot     (Intercept) 0.005363 0.07324
##         year_factor2 0.006936 0.08328 -1.00
##         year_factor3 0.011825 0.10874 -1.00  1.00
##         year_factor4 0.009032 0.09504 -1.00  1.00  1.00
##         year_factor5 0.003570 0.05975 -1.00  1.00  1.00  1.00
##         year_factor6 0.002650 0.05148 -1.00  1.00  1.00  1.00  1.00
##         year_factor7 0.007075 0.08411 -1.00  1.00  1.00  1.00  1.00
## Residual          0.012630 0.11238
## Number of obs: 813, groups: plot, 24
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)  5.55011   0.01202 787.41127 461.566 <2e-16 ***
## stateambient -0.01382   0.01717 783.92132 -0.805   0.421    
## originBoth   -0.41492   0.02452 794.37409 -16.919 <2e-16 ***
## originExotic -0.33135   0.01410 793.37366 -23.506 <2e-16 ***
## stateambient:originBoth  0.01734   0.03125 793.27064  0.555   0.579    
## stateambient:originExotic 0.01890   0.01971 793.86699  0.958   0.338    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn orgnBt orgnEx sttm:B
## stateambient -0.700
## originBoth   -0.492  0.344
## originExotic -0.855  0.599  0.424

```

```

## sttmbnt:rgB  0.386 -0.547 -0.785 -0.333
## sttmbnt:rgE  0.611 -0.870 -0.303 -0.715  0.479
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

anova(mod8)

## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.0003  0.0003     1 466.06  0.0254 0.8735
## origin     15.2258  7.6129     2 794.07 602.7549 <2e-16 ***
## state:origin 0.0118  0.0059     2 794.07  0.4653 0.6281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod8, 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  5.550 0.012960 282.83    5.525  5.576
##   ambient Native  5.536 0.013434 275.92    5.510  5.563
##   warmed Both    5.135 0.022426 574.17    5.091  5.179
##   ambient Both   5.139 0.016618 377.46    5.106  5.171
##   warmed Exotic  5.219 0.008588  57.14    5.202  5.236
##   ambient Exotic 5.224 0.008141  33.56    5.207  5.240
##
## 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  0.01382 0.0187 291  0.741  0.9767
##   warmed Native - warmed Both    0.41492 0.0253 745 16.404 <.0001
##   warmed Native - ambient Both  0.41141 0.0211 356 19.522 <.0001
##   warmed Native - warmed Exotic 0.33135 0.0145 742 22.790 <.0001
##   warmed Native - ambient Exotic 0.32628 0.0153 152 21.318 <.0001
##   ambient Native - warmed Both  0.40110 0.0261 495 15.343 <.0001
##   ambient Native - ambient Both 0.39758 0.0199 728 19.952 <.0001
##   ambient Native - warmed Exotic 0.31752 0.0159 176 19.915 <.0001
##   ambient Native - ambient Exotic 0.31245 0.0142 740 21.965 <.0001
##   warmed Both - ambient Both   -0.00352 0.0279 508 -0.126  1.0000
##   warmed Both - warmed Exotic  -0.08358 0.0233 747 -3.582  0.0049
##   warmed Both - ambient Exotic -0.08865 0.0239 449 -3.716  0.0031
##   ambient Both - warmed Exotic -0.08006 0.0187 260 -4.280  0.0004
##   ambient Both - ambient Exotic -0.08513 0.0171 741 -4.989 <.0001
##   warmed Exotic - ambient Exotic -0.00507 0.0118  45 -0.429  0.9980
##
## 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
kbs_sd_spp <- within(kbs_sd_spp, growth_habit <- relevel(factor(growth_habit), ref = "Forb")) # relevance
mod10 <- lmer(log(julian_min) ~ state * growth_habit + (1 + year_factor | plot),
               kbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11 <- lmer(log(julian_min) ~ state + growth_habit + (1 + year_factor | plot),
               kbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11a <- lmer(log(julian_min) ~ state + growth_habit + year_factor + (1 | plot),
                kbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod10, mod11) # model 10 is a better fit to data

## Data: kbs_sd_spp
## Models:
## mod11: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
## mod10: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11    33 -936.63 -781.50 501.31   -1002.6
## mod10    35 -933.15 -768.62 501.57   -1003.1 0.5171  2     0.7722

anova(mod10, mod11a) # model 10 is still a better fit to data

## Data: kbs_sd_spp
## Models:
## mod11a: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
## mod10: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11a   12 -1031.46 -975.05 527.73   -1055.5
## mod10    35  -933.15 -768.62 501.57   -1003.1      0 23           1

summary(mod10)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
## Data: kbs_sd_spp
##
##      AIC      BIC logLik deviance df.resid
## -933.1   -768.6   501.6   -1003.1      778
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max

```

```

## -5.2893 -0.5948 -0.0447  0.7358  3.3214
##
## Random effects:
##   Groups   Name        Variance Std.Dev. Corr
##   plot     (Intercept) 0.014278 0.11949
##             year_factor2 0.022088 0.14862 -1.00
##             year_factor3 0.029850 0.17277 -1.00  1.00
##             year_factor4 0.018353 0.13547 -1.00  1.00  1.00
##             year_factor5 0.008688 0.09321 -1.00  1.00  1.00  1.00
##             year_factor6 0.006839 0.08270 -1.00  1.00  1.00  1.00  1.00
##             year_factor7 0.013298 0.11532 -1.00  1.00  1.00  1.00  1.00
##   Residual          0.016274 0.12757
## Number of obs: 813, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value
##   (Intercept)            5.457672 0.011340 629.699469 481.265
##   stateambient         -0.019374 0.015268 536.457793 -1.269
##   growth_habit          -0.313710 0.026717 790.823951 -11.742
##   growth_habitGraminoid -0.248169 0.014541 791.768914 -17.067
##   stateambient:growth_habit 0.020874 0.033254 790.785548  0.628
##   stateambient:growth_habitGraminoid -0.002254 0.019705 792.800826 -0.114
##                               Pr(>|t|)
##   (Intercept)            <2e-16 ***
##   stateambient          0.205
##   growth_habit          <2e-16 ***
##   growth_habitGraminoid <2e-16 ***
##   stateambient:growth_habit 0.530
##   stateambient:growth_habitGraminoid 0.909
##   ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##   (Intr) sttmbn grwth_ grwt_G sttm:_ stateambint
##   stateambint -0.743
##   growth_habt -0.417  0.310
##   grwth_hbtGr -0.783  0.581  0.324
##   sttmbnt:gr_  0.335 -0.446 -0.803 -0.260
##   sttmbnt:g_G  0.578 -0.779 -0.239 -0.738  0.344
##   optimizer (nloptwrap) convergence code: 0 (OK)
##   boundary (singular) fit: see ?isSingular

```

`anova(mod10)`

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state              0.0199  0.0199     1 448.56  1.2205 0.2699
## growth_habit       12.0940  6.0470     2 789.85 371.5814 <2e-16 ***
## state:growth_habit 0.0084  0.0042     2 789.85  0.2590 0.7719
##   ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

emmeans(mod10, list(pairwise ~ factor(year_factor) * growth_habit), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

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

# 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_min) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), kbs_sd_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_min) ~ state * factor(year_factor) + (1 | species), kbs_sd_spp)

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -2.5e-01

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

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 2 negative eigenvalues: -3.4e-02 -3.2e+00

```

```

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

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

## boundary (singular) fit: see ?isSingular

```

```

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

## boundary (singular) fit: see ?isSingular

mod13 <- lmer(log(julian_min) ~ state * factor(year_factor) + (1 | species), kbs_sd_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

## Error in ICtab(..., mnames = mnames, type = "AICc"): nobs different: must have identical data for all

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + species + factor(year_factor) + (1 |
##   plot)
## Data: kbs_sd_spp
##
##      AIC      BIC      logLik deviance df.resid
## -2581.8 -2436.0    1321.9   -2643.8      785
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.5921 -0.5306 -0.0049  0.4909  7.6708
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.000000 0.00000
## Residual           0.002293 0.04789
## Number of obs: 816, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) 5.452875  0.011990 816.000000 454.793 < 2e-16 ***
## stateambient 0.004370  0.003507 816.000000  1.246 0.213101    
## speciesArel -0.184443  0.010465 816.000000 -17.624 < 2e-16 ***
## speciesBavu -0.230672  0.020305 816.000000 -11.360 < 2e-16 ***
## speciesCahi -0.502774  0.023467 816.000000 -21.425 < 2e-16 ***
## speciesCest  0.039215  0.011618 816.000000  3.375 0.000772 ***
## speciesDaca  0.101541  0.014495 816.000000  7.005 5.16e-12 ***
## speciesDagl -0.163366  0.010831 816.000000 -15.083 < 2e-16 ***
## speciesElre -0.039521  0.011372 816.000000 -3.475 0.000537 ***
## speciesEugr  0.214379  0.013900 816.000000 15.422 < 2e-16 ***
## speciesHisp -0.246588  0.011127 816.000000 -22.161 < 2e-16 ***
## speciesHype -0.109633  0.017723 816.000000 -6.186 9.75e-10 ***
## speciesPhpr -0.054832  0.010547 816.000000 -5.199 2.54e-07 ***
## speciesPoco -0.082002  0.017606 816.000000 -4.658 3.73e-06 ***
## speciesPopr -0.248610  0.010203 816.000000 -24.368 < 2e-16 ***
## speciesPore -0.046105  0.013012 816.000000 -3.543 0.000418 ***
## speciesRusp -0.172216  0.017181 816.000000 -10.024 < 2e-16 ***

```

```

## speciesSoca      0.230129  0.010169 816.000000 22.630 < 2e-16 ***
## speciesSogr     0.123923  0.048964 816.000000  2.531 0.011564 *
## speciesSora     0.173318  0.035168 816.000000  4.928 1.00e-06 ***
## speciesSypi     0.289872  0.035383 816.000000  8.192 9.86e-16 ***
## speciesTaof     -0.451748 0.020315 816.000000 -22.237 < 2e-16 ***
## speciesTrsp     -0.117081 0.014949 816.000000 -7.832 1.49e-14 ***
## factor(year_factor)2 -0.123848 0.008143 816.000000 -15.210 < 2e-16 ***
## factor(year_factor)3 -0.123874 0.008310 816.000000 -14.906 < 2e-16 ***
## factor(year_factor)4 -0.134431 0.008450 816.000000 -15.909 < 2e-16 ***
## factor(year_factor)5 -0.096438 0.008651 816.000000 -11.148 < 2e-16 ***
## factor(year_factor)6 -0.086017 0.008330 816.000000 -10.327 < 2e-16 ***
## factor(year_factor)7 -0.094345 0.009449 816.000000 -9.985 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 29 > 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                      0.0036 0.00356     1    816   1.5527 0.2131
## species                     23.6339 1.12542    21    816 490.7854 <2e-16 ***
## factor(year_factor) 0.7373 0.12289     6    816  53.5895 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

KBS Plot-level Mixed Effects Models

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

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

```
mod2p <- lmer(log(julian_min) ~ insecticide + (1 | plot), kbs_sd_plot, REML = FALSE)
mod3p <- lmer(log(julian_min) ~ insecticide + state + (1 | plot), kbs_sd_plot, REML = FALSE)
```

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

```
mod4p <- lmer(log(julian_min) ~ insecticide * state + (1 | plot), kbs_sd_plot, REML = FALSE)
```

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

```

mod5p <- lmer(log(julian_min) ~ state + year_factor + (1 | plot), kbs_sd_plot, REML = FALSE)
mod6p <- lmer(log(julian_min) ~ state + year_factor + insecticide + (1 | plot), kbs_sd_plot,
               REML = FALSE)
mod7p <- lmer(log(julian_min) ~ state * year_factor + (1 | plot), kbs_sd_plot, REML = FALSE)
mod8p <- lmer(log(julian_min) ~ state * year_factor + insecticide + (1 | plot), kbs_sd_plot,
               REML = FALSE)
mod9p <- lmer(log(julian_min) ~ state * insecticide + year_factor + (1 | plot), kbs_sd_plot,
               REML = FALSE)
mod10p <- lmer(log(julian_min) ~ state + insecticide * year_factor + (1 | plot),
                 kbs_sd_plot, REML = FALSE)
mod11p <- lmer(log(julian_min) ~ state * year_factor * insecticide + (1 | plot),
                 kbs_sd_plot, REML = FALSE)
AICctab(mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p, mod8p, mod9p, mod10p, mod11p,
        weights = T) # model 11p and 10p the same

```

Error in ICtab(..., mnames = mnames, type = "AICc"): nobs different: must have identical data for all

```
anova(mod5p, mod6p) #6p just barely better, going with 5p because it's simpler though
```

```

## Data: kbs_sd_plot
## Models:
## mod5p: log(julian_min) ~ state + year_factor + (1 | plot)
## mod6p: log(julian_min) ~ state + year_factor + insecticide + (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5p   10 -438.38 -407.38 229.19  -458.38
## mod6p   11 -438.77 -404.67 230.38  -460.77 2.3927  1     0.1219

```

```
summary(mod5p)
```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + year_factor + (1 | plot)
##   Data: kbs_sd_plot
##
##      AIC      BIC    logLik deviance df.resid
## -438.4   -407.4    229.2    -458.4      154
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.2394 -0.6911  0.0559  0.5012  3.3777
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot     (Intercept) 0.0001572 0.01254
##   Residual           0.0034388 0.05864
## Number of obs: 164, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  5.42170   0.01382 139.00228 392.403 < 2e-16 ***
## stateambient -0.03685   0.01050  24.17695 -3.510 0.001783 **

```

```

## year_factor2 -0.11588  0.01732 141.71838 -6.689 4.80e-10 ***
## year_factor3 -0.12674  0.01732 141.71838 -7.316 1.73e-11 ***
## year_factor4 -0.14791  0.01732 141.71838 -8.538 1.91e-14 ***
## year_factor5 -0.09502  0.01732 141.71838 -5.485 1.84e-07 ***
## year_factor6 -0.05978  0.01751 142.51177 -3.414 0.000833 ***
## year_factor7 -0.17002  0.01751 142.51177 -9.710 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) sttmbn yr_fc2 yr_fc3 yr_fc4 yr_fc5 yr_fc6
## stateambint -0.380
## year_factr2 -0.655  0.000
## year_factr3 -0.655  0.000  0.522
## year_factr4 -0.655  0.000  0.522  0.522
## year_factr5 -0.655  0.000  0.522  0.522  0.522
## year_factr6 -0.652  0.011  0.517  0.517  0.517  0.517
## year_factr7 -0.652  0.011  0.517  0.517  0.517  0.517  0.512

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

## $`emmeans of state, year_factor`
##   state    year_factor emmean     SE  df lower.CL upper.CL
##   warmed    1        5.42 0.0142 148     5.39    5.45
##   ambient   1        5.38 0.0142 148     5.36    5.41
##   warmed    2        5.31 0.0137 144     5.28    5.33
##   ambient   2        5.27 0.0137 144     5.24    5.30
##   warmed    3        5.29 0.0137 144     5.27    5.32
##   ambient   3        5.26 0.0137 144     5.23    5.29
##   warmed    4        5.27 0.0137 144     5.25    5.30
##   ambient   4        5.24 0.0137 144     5.21    5.26
##   warmed    5        5.33 0.0137 144     5.30    5.35
##   ambient   5        5.29 0.0137 144     5.26    5.32
##   warmed    6        5.36 0.0139 146     5.33    5.39
##   ambient   6        5.33 0.0140 146     5.30    5.35
##   warmed    7        5.25 0.0139 146     5.22    5.28
##   ambient   7        5.21 0.0140 146     5.19    5.24
##
## 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 1 - ambient 1  0.03685 0.0110 26.1  3.359  0.1000
##   warmed 1 - warmed 2  0.11588 0.0177 147.8  6.541 <.0001
##   warmed 1 - ambient 2  0.15273 0.0208 154.8  7.329 <.0001
##   warmed 1 - warmed 3  0.12674 0.0177 147.8  7.154 <.0001
##   warmed 1 - ambient 3  0.16359 0.0208 154.8  7.850 <.0001
##   warmed 1 - warmed 4  0.14791 0.0177 147.8  8.349 <.0001
##   warmed 1 - ambient 4  0.18476 0.0208 154.8  8.866 <.0001
##   warmed 1 - warmed 5  0.09502 0.0177 147.8  5.364 <.0001
##   warmed 1 - ambient 5  0.13187 0.0208 154.8  6.328 <.0001
##   warmed 1 - warmed 6  0.05978 0.0179 148.7  3.337  0.0617

```

```

##  warmed 1 - ambient 6  0.09664 0.0211 155.4  4.578  0.0008
##  warmed 1 - warmed 7  0.17002 0.0179 148.7  9.491  <.0001
##  warmed 1 - ambient 7  0.20687 0.0211 155.4  9.801  <.0001
##  ambient 1 - warmed 2  0.07903 0.0208 154.9  3.793  0.0148
##  ambient 1 - ambient 2  0.11588 0.0177 147.8  6.541  <.0001
##  ambient 1 - warmed 3  0.08988 0.0208 154.9  4.314  0.0022
##  ambient 1 - ambient 3  0.12674 0.0177 147.8  7.154  <.0001
##  ambient 1 - warmed 4  0.11106 0.0208 154.9  5.330  <.0001
##  ambient 1 - ambient 4  0.14791 0.0177 147.8  8.349  <.0001
##  ambient 1 - warmed 5  0.05817 0.0208 154.9  2.792  0.2400
##  ambient 1 - ambient 5  0.09502 0.0177 147.8  5.364  <.0001
##  ambient 1 - warmed 6  0.02293 0.0209 155.2  1.097  0.9980
##  ambient 1 - ambient 6  0.05978 0.0179 148.7  3.337  0.0617
##  ambient 1 - warmed 7  0.13317 0.0209 155.2  6.371  <.0001
##  ambient 1 - ambient 7  0.17002 0.0179 148.7  9.491  <.0001
##  warmed 2 - ambient 2  0.03685 0.0110 26.1   3.359  0.1000
##  warmed 2 - warmed 3  0.01086 0.0173 146.3  0.628  1.0000
##  warmed 2 - ambient 3  0.04771 0.0205 153.4  2.329  0.5367
##  warmed 2 - warmed 4  0.03203 0.0173 146.3  1.851  0.8485
##  warmed 2 - ambient 4  0.06888 0.0205 153.4  3.362  0.0572
##  warmed 2 - warmed 5  -0.02086 0.0173 146.3  -1.205  0.9950
##  warmed 2 - ambient 5  0.01599 0.0205 153.4  0.781  1.0000
##  warmed 2 - warmed 6  -0.05609 0.0175 147.1  -3.205  0.0892
##  warmed 2 - ambient 6  -0.01924 0.0208 154.2  -0.927  0.9997
##  warmed 2 - warmed 7  0.05414 0.0175 147.1  3.094  0.1193
##  warmed 2 - ambient 7  0.09100 0.0208 154.2  4.383  0.0017
##  ambient 2 - warmed 3  -0.02599 0.0205 153.4  -1.269  0.9919
##  ambient 2 - ambient 3  0.01086 0.0173 146.3  0.628  1.0000
##  ambient 2 - warmed 4  -0.00482 0.0205 153.4  -0.235  1.0000
##  ambient 2 - ambient 4  0.03203 0.0173 146.3  1.851  0.8485
##  ambient 2 - warmed 5  -0.05771 0.0205 153.4  -2.817  0.2275
##  ambient 2 - ambient 5  -0.02086 0.0173 146.3  -1.205  0.9950
##  ambient 2 - warmed 6  -0.09295 0.0206 153.9  -4.522  0.0010
##  ambient 2 - ambient 6  -0.05609 0.0175 147.1  -3.205  0.0892
##  ambient 2 - warmed 7  0.01729 0.0206 153.9  0.841  0.9999
##  ambient 2 - ambient 7  0.05414 0.0175 147.1  3.094  0.1193
##  warmed 3 - ambient 3  0.03685 0.0110 26.1   3.359  0.1000
##  warmed 3 - warmed 4  0.02117 0.0173 146.3  1.224  0.9942
##  warmed 3 - ambient 4  0.05802 0.0205 153.4  2.832  0.2201
##  warmed 3 - warmed 5  -0.03172 0.0173 146.3  -1.833  0.8574
##  warmed 3 - ambient 5  0.00514 0.0205 153.4  0.251  1.0000
##  warmed 3 - warmed 6  -0.06695 0.0175 147.1  -3.825  0.0134
##  warmed 3 - ambient 6  -0.03010 0.0208 154.2  -1.450  0.9741
##  warmed 3 - warmed 7  0.04329 0.0175 147.1  2.473  0.4338
##  warmed 3 - ambient 7  0.08014 0.0208 154.2  3.860  0.0118
##  ambient 3 - warmed 4  -0.01568 0.0205 153.4  -0.765  1.0000
##  ambient 3 - ambient 4  0.02117 0.0173 146.3  1.224  0.9942
##  ambient 3 - warmed 5  -0.06857 0.0205 153.4  -3.347  0.0598
##  ambient 3 - ambient 5  -0.03172 0.0173 146.3  -1.833  0.8574
##  ambient 3 - warmed 6  -0.10380 0.0206 153.9  -5.050  0.0001
##  ambient 3 - ambient 6  -0.06695 0.0175 147.1  -3.825  0.0134
##  ambient 3 - warmed 7  0.00643 0.0206 153.9  0.313  1.0000
##  ambient 3 - ambient 7  0.04329 0.0175 147.1  2.473  0.4338
##  warmed 4 - ambient 4  0.03685 0.0110 26.1   3.359  0.1000

```

```

##  warmed 4 - warmed 5  -0.05289 0.0173 146.3 -3.057  0.1309
##  warmed 4 - ambient 5 -0.01604 0.0205 153.4 -0.783  0.9999
##  warmed 4 - warmed 6 -0.08812 0.0175 147.1 -5.035  0.0001
##  warmed 4 - ambient 6 -0.05127 0.0208 154.2 -2.470  0.4359
##  warmed 4 - warmed 7  0.02211 0.0175 147.1  1.263  0.9922
##  warmed 4 - ambient 7  0.05897 0.0208 154.2  2.840  0.2161
##  ambient 4 - warmed 5 -0.08974 0.0205 153.4 -4.380  0.0017
##  ambient 4 - ambient 5 -0.05289 0.0173 146.3 -3.057  0.1309
##  ambient 4 - warmed 6 -0.12498 0.0206 153.9 -6.080  <.0001
##  ambient 4 - ambient 6 -0.08812 0.0175 147.1 -5.035  0.0001
##  ambient 4 - warmed 7 -0.01474 0.0206 153.9 -0.717  1.0000
##  ambient 4 - ambient 7  0.02211 0.0175 147.1  1.263  0.9922
##  warmed 5 - ambient 5  0.03685 0.0110 26.1   3.359  0.1000
##  warmed 5 - warmed 6  -0.03524 0.0175 147.1 -2.013  0.7570
##  warmed 5 - ambient 6  0.00162 0.0208 154.2  0.078  1.0000
##  warmed 5 - warmed 7  0.07500 0.0175 147.1  4.285  0.0026
##  warmed 5 - ambient 7  0.11185 0.0208 154.2  5.388  <.0001
##  ambient 5 - warmed 6 -0.07209 0.0206 153.9 -3.507  0.0371
##  ambient 5 - ambient 6 -0.03524 0.0175 147.1 -2.013  0.7570
##  ambient 5 - warmed 7  0.03815 0.0206 153.9  1.856  0.8462
##  ambient 5 - ambient 7  0.07500 0.0175 147.1  4.285  0.0026
##  warmed 6 - ambient 6  0.03685 0.0110 26.1   3.359  0.1000
##  warmed 6 - warmed 7  0.11024 0.0177 146.3  6.237  <.0001
##  warmed 6 - ambient 7  0.14709 0.0208 155.6  7.070  <.0001
##  ambient 6 - warmed 7  0.07339 0.0208 155.6  3.528  0.0348
##  ambient 6 - ambient 7  0.11024 0.0177 146.3  6.237  <.0001
##  warmed 7 - ambient 7  0.03685 0.0110 26.1   3.359  0.1000
##
## 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

```

```

# including native vs. exotic
kbs_sd_plot_origin <- within(kbs_sd_plot_origin, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
mod12p <- lmer(log(julian_min) ~ state * origin + (1 + year_factor | plot), kbs_sd_plot_origin,
  REML = FALSE)

```

```

## boundary (singular) fit: see ?isSingular

```

```

mod13p <- lmer(log(julian_min) ~ state + origin + (1 + year_factor | plot), kbs_sd_plot_origin,
  REML = FALSE)

```

```

## boundary (singular) fit: see ?isSingular

```

```

mod14p <- lmer(log(julian_min) ~ state + origin + year_factor + (1 | plot), kbs_sd_plot_origin,
  REML = FALSE)
anova(mod12p, mod13p) # go with model 13pu

```

```

## Data: kbs_sd_plot_origin
## Models:
## mod13p: log(julian_min) ~ state + origin + (1 + year_factor | plot)

```

```

## mod12p: log(julian_min) ~ state * origin + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod13p     8 -953.81 -922.88 484.90 -969.81
## mod12p    10 -951.67 -913.00 485.83 -971.67 1.8597  2      0.3946

anova(mod13p, mod14p)  # mod 14pu

## Data: kbs_sd_plot_origin
## Models:
## mod14p: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## mod13p: log(julian_min) ~ state + origin + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod14p     7 -959.48 -932.41 486.74 -973.48
## mod13p     8 -953.81 -922.88 484.90 -969.81      0  1          1

summary(mod14p)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + origin + year_factor + (1 | plot)
##   Data: kbs_sd_plot_origin
##
##      AIC      BIC      logLik deviance df.resid
## -959.5   -932.4    486.7   -973.5      346
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.2397 -0.5653  0.0968  0.6404  2.9846
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot     (Intercept) 1.423e-05 0.003772
##   Residual            3.700e-03 0.060830
## Number of obs: 353, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) 5.566419  0.009448 223.083716 589.180 <2e-16 ***
## statewarmed 0.006302  0.006692  23.289336  0.942  0.3560    
## originBoth  -0.429279  0.009280 344.456110 -46.259 <2e-16 ***
## originExotic -0.326543  0.007266 333.981948 -44.942 <2e-16 ***
## year_factor -0.004011  0.001753 338.187599 -2.288  0.0227 *  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) sttwrm orgnBt orgnEx
## statewarmed -0.367
## originBoth  -0.402  0.093
## originExotic -0.418  0.021  0.443
## year_factor -0.722 -0.005  0.038 -0.034

```

```
anova(mod14p)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF   F value Pr(>F)
## state       0.0033  0.0033     1  23.29    0.8869 0.35599
## origin      10.6672  5.3336     2 341.59 1441.3991 < 2e-16 ***
## year_factor  0.0194  0.0194     1 338.19    5.2358 0.02274 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod14p, list(pairwise ~ state + origin + year_factor), adjust = "tukey")
```

```
## $`emmeans of state, origin, year_factor`
##   state origin year_factor emmean      SE   df lower.CL upper.CL
##   ambient Native      3.929  5.551 0.006725 88.41   5.537   5.564
##   warmed  Native      3.929  5.557 0.006567 80.45   5.544   5.570
##   ambient Both       3.929  5.121 0.008139 148.17   5.105   5.137
##   warmed  Both       3.929  5.128 0.008713 174.38   5.110   5.145
##   ambient Exotic     3.929  5.224 0.006084  62.19   5.212   5.236
##   warmed  Exotic     3.929  5.230 0.006079  62.28   5.218   5.243
##
## 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, year_factor`
##   estimate
##   1
##   ambient Native 3.92917847025496 - warmed Native 3.92917847025496 -0.0063
##   ambient Native 3.92917847025496 - ambient Both 3.92917847025496  0.4293
##   ambient Native 3.92917847025496 - warmed Both 3.92917847025496  0.4230
##   ambient Native 3.92917847025496 - ambient Exotic 3.92917847025496  0.3265
##   ambient Native 3.92917847025496 - warmed Exotic 3.92917847025496  0.3202
##   warmed Native 3.92917847025496 - ambient Both 3.92917847025496  0.4356
##   warmed Native 3.92917847025496 - warmed Both 3.92917847025496  0.4293
##   warmed Native 3.92917847025496 - ambient Exotic 3.92917847025496  0.3328
##   warmed Native 3.92917847025496 - warmed Exotic 3.92917847025496  0.3265
##   ambient Both 3.92917847025496 - warmed Both 3.92917847025496 -0.0063
##   ambient Both 3.92917847025496 - ambient Exotic 3.92917847025496 -0.1027
##   ambient Both 3.92917847025496 - warmed Exotic 3.92917847025496 -0.1090
##   warmed Both 3.92917847025496 - ambient Exotic 3.92917847025496 -0.0964
##   warmed Both 3.92917847025496 - warmed Exotic 3.92917847025496 -0.1027
##   ambient Exotic 3.92917847025496 - warmed Exotic 3.92917847025496 -0.0063
##
##   SE   df t.ratio p.value
##   0.00702 26.4 -0.898 0.9436
##   0.00935 348.0 45.891 <.0001
##   0.01219 179.0 34.706 <.0001
##   0.00731 337.4 44.697 <.0001
##   0.01023 115.2 31.300 <.0001
##   0.01118 144.0 38.957 <.0001
##   0.00935 348.0 45.891 <.0001
##   0.01003 106.7 33.184 <.0001
##   0.00731 337.4 44.697 <.0001
```

```

##  0.00702 26.4 -0.898 0.9436
##  0.00897 350.5 -11.449 <.0001
##  0.01096 134.5 -9.951 <.0001
##  0.01181 162.3 -8.164 <.0001
##  0.00897 350.5 -11.449 <.0001
##  0.00702 26.4 -0.898 0.9436
##
## 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
kbs_sd_plot_growthhabit <- within(kbs_sd_plot_growthhabit, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
mod15p <- lmer(log(julian_min) ~ state * growth_habit + (1 + year_factor | plot),
  kbs_sd_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod16p <- lmer(log(julian_min) ~ state + growth_habit + (1 + year_factor | plot),
  kbs_sd_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod17p <- lmer(log(julian_min) ~ state + growth_habit + year_factor + (1 | plot),
  kbs_sd_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod15p, mod16p) # go with model 16pu

## Data: kbs_sd_plot_growthhabit
## Models:
## mod16p: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
## mod15p: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod16p     8 -339.15 -308.12 177.57   -355.15
## mod15p    10 -335.65 -296.87 177.82   -355.65 0.5005  2      0.7786

anova(mod16p, mod17p) # mod 17pu

## Data: kbs_sd_plot_growthhabit
## Models:
## mod17p: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
## mod16p: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod17p     7 -344.60 -317.46 179.30   -358.60
## mod16p     8 -339.15 -308.12 177.57   -355.15      0  1           1

```

```
summary(mod17p)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
##   Data: kbs_sd_plot_growthhabit
##
##          AIC      BIC  logLik deviance df.resid
## -344.6   -317.5   179.3   -358.6     350
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.4528 -0.3872 -0.0961  0.5183  2.0152
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot     (Intercept) 0.00000  0.0000
##   Residual           0.02144  0.1464
## Number of obs: 357, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 5.321938  0.022476 357.000000 236.785 <2e-16 ***
## statewarmed 0.033945  0.015576 357.000000   2.179  0.0300 *
## growth_habit -0.251555  0.022191 357.000000 -11.336 <2e-16 ***
## growth_habitGraminoid -0.240385  0.017326 357.000000 -13.875 <2e-16 ***
## year_factor   0.007848  0.004211 357.000000   1.864  0.0632 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttwrm grwth_ grwt_G
## statewarmed -0.355
## growth_habit -0.400  0.089
## grwth_hbtGr -0.415  0.014  0.436
## year_factor  -0.735 -0.003  0.043 -0.028
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
anova(mod17p)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state       0.1018 0.10183     1    357  4.7491 0.02997 *
## growth_habit 4.8685 2.43423     2    357 113.5215 < 2e-16 ***
## year_factor  0.0745 0.07447     1    357  3.4729 0.06320 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod17p, list(pairwise ~ state + growth_habit + year_factor), adjust = "tukey")
```

```
## $`emmeans of state, growth_habit, year_factor`
```

```

##  state   growth_habit year_factor emmean      SE    df lower.CL upper.CL
##  ambient  Forb          3.94  5.35 0.0155  84.0     5.32    5.38
##  warmed   Forb          3.94  5.39 0.0153  78.0     5.36    5.42
##  ambient          3.94  5.10 0.0193 146.8     5.06    5.14
##  warmed          3.94  5.14 0.0206 172.4     5.09    5.18
##  ambient  Graminoid     3.94  5.11 0.0142  61.0     5.08    5.14
##  warmed   Graminoid     3.94  5.15 0.0142  61.5     5.12    5.17
##
## 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, year_factor'
## 1
## ambient Forb 3.93837535014006 - warmed Forb 3.93837535014006
## ambient Forb 3.93837535014006 - ambient 3.93837535014006
## ambient Forb 3.93837535014006 - warmed 3.93837535014006
## ambient Forb 3.93837535014006 - ambient Graminoid 3.93837535014006
## ambient Forb 3.93837535014006 - warmed Graminoid 3.93837535014006
## warmed Forb 3.93837535014006 - ambient 3.93837535014006
## warmed Forb 3.93837535014006 - warmed 3.93837535014006
## warmed Forb 3.93837535014006 - ambient Graminoid 3.93837535014006
## warmed Forb 3.93837535014006 - warmed Graminoid 3.93837535014006
## ambient 3.93837535014006 - warmed 3.93837535014006
## ambient 3.93837535014006 - ambient Graminoid 3.93837535014006
## ambient 3.93837535014006 - warmed Graminoid 3.93837535014006
## warmed 3.93837535014006 - ambient Graminoid 3.93837535014006
## warmed 3.93837535014006 - warmed Graminoid 3.93837535014006
## ambient Graminoid 3.93837535014006 - warmed Graminoid 3.93837535014006
##
## estimate      SE    df t.ratio p.value
## -0.0339 0.0161 24.6 -2.115  0.3127
##  0.2516 0.0224 354.6 11.234 <.0001
##  0.2176 0.0287 175.8  7.590 <.0001
##  0.2404 0.0174 341.8 13.788 <.0001
##  0.2064 0.0239 112.9  8.655 <.0001
##  0.2855 0.0264 142.7 10.822 <.0001
##  0.2516 0.0224 354.6 11.234 <.0001
##  0.2743 0.0235 105.5 11.651 <.0001
##  0.2404 0.0174 341.8 13.788 <.0001
## -0.0339 0.0161 24.6 -2.115  0.3127
## -0.0112 0.0216 356.6 -0.517  0.9955
## -0.0451 0.0259 134.3 -1.745  0.5048
##  0.0228 0.0279 160.8  0.816  0.9643
## -0.0112 0.0216 356.6 -0.517  0.9955
## -0.0339 0.0161 24.6 -2.115  0.3127
##
## 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

```

```

# Do we need to include plot as a random effect with the UMBS models?
mod1u <- lmer(log(julian_min) ~ state * year_factor + insecticide * year_factor +
  (1 | species) + (1 | plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2u <- lmer(log(julian_min) ~ state * year_factor + insecticide * year_factor +
  (1 | species), umbs_sd_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(mod1u)

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq  Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.002117 0.0021175     1   522.35  0.7065  0.40099
## year_factor                 0.086462 0.0216156     4   522.10  7.2121 1.172e-05 ***
## insecticide                  0.000282 0.0002819     1   522.72  0.0941  0.75920
## state:year_factor           0.026659 0.0066647     4   521.99  2.2237  0.06531 .
## year_factor:insecticide     0.010509 0.0026273     4   522.09  0.8766  0.47767
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod2u)

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq  Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.002117 0.0021175     1   522.35  0.7065  0.40099
## year_factor                 0.086462 0.0216156     4   522.10  7.2121 1.172e-05 ***
## insecticide                  0.000282 0.0002819     1   522.72  0.0941  0.75920
## state:year_factor           0.026659 0.0066647     4   521.99  2.2237  0.06531 .
## year_factor:insecticide     0.010509 0.0026273     4   522.09  0.8766  0.47767
## ---
## 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(mod1u, mod2u) # models are not different from each other so go with simpler model = model 2

## Data: umbs_sd_spp
## Models:
## mod2u: log(julian_min) ~ state * year_factor + insecticide * year_factor +
## mod2u:      (1 | species)
## mod1u: log(julian_min) ~ state * year_factor + insecticide * year_factor +
## mod1u:      (1 | species) + (1 | plot)
##      npar   AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod2u   17 -1492 -1419.2 762.99    -1526
## mod1u   18 -1490 -1412.9 762.99    -1526      0   1             1

```

```
summary(mod1u)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##           (1 | species) + (1 | plot)
## Data: umbs_sd_spp
##
##          AIC      BIC  logLik deviance df.resid
## -1490.0 -1412.9    763.0   -1526.0      517
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.0351 -0.4932 -0.0655  0.4447  6.9115
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.000000 0.00000
## species  (Intercept) 0.020042 0.14157
## Residual            0.002997 0.05475
## Number of obs: 535, groups: plot, 24; species, 13
##
## Fixed effects:
##                               Estimate Std. Error      df t value
## (Intercept)                  5.257377  0.040910 14.608317 128.511
## stateambient                 -0.019454  0.011885 521.845430 -1.637
## year_factor3                 -0.026413  0.014079 521.854144 -1.876
## year_factor4                 -0.049132  0.013845 521.925762 -3.549
## year_factor5                 -0.016187  0.013953 521.944380 -1.160
## year_factor6                 -0.019020  0.013772 521.941571 -1.381
## insecticideno_insects       -0.005013  0.012044 522.112659 -0.416
## stateambient:year_factor3   0.016609  0.016110 521.838764  1.031
## stateambient:year_factor4   0.035078  0.015885 522.035413  2.208
## stateambient:year_factor5   0.042685  0.015724 521.967300  2.715
## stateambient:year_factor6   0.023213  0.015595 522.015769  1.488
## year_factor3:insecticideno_insects 0.012964  0.016137 521.859176  0.803
## year_factor4:insecticideno_insects 0.007544  0.015930 522.073920  0.474
## year_factor5:insecticideno_insects 0.008673  0.015819 522.132214  0.548
## year_factor6:insecticideno_insects -0.011677 0.015699 522.226885 -0.744
##                               Pr(>|t|)    
## (Intercept)                  < 2e-16 ***
## stateambient                 0.102267
## year_factor3                 0.061214 .
## year_factor4                 0.000422 ***
## year_factor5                 0.246527
## year_factor6                 0.167866
## insecticideno_insects        0.677402
## stateambient:year_factor3   0.303014
## stateambient:year_factor4   0.027664 *
## stateambient:year_factor5   0.006853 **
## stateambient:year_factor6   0.137245
## year_factor3:insecticideno_insects 0.422133
## year_factor4:insecticideno_insects 0.635988
```

```

## year_factor5:insecticideno_insects 0.583751
## year_factor6:insecticideno_insects 0.457340
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

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

summary(mod2u)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * year_factor + insecticide * year_factor +
##           (1 | species)
## Data: umbs_sd_spp
##
##       AIC     BIC   logLik deviance df.resid
## -1492.0 -1419.2    763.0   -1526.0      518
## 
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.0351 -0.4932 -0.0655  0.4447  6.9115
## 
## Random effects:
## Groups   Name        Variance Std.Dev.
## species (Intercept) 0.020042 0.14157
## Residual            0.002997 0.05475
## Number of obs: 535, groups: species, 13
## 
## Fixed effects:
##                               Estimate Std. Error      df t value
## (Intercept)                  5.257377  0.040910 14.608310 128.511
## stateambient                 -0.019454  0.011885 521.845433 -1.637
## year_factor3                 -0.026413  0.014079 521.854146 -1.876
## year_factor4                 -0.049132  0.013845 521.925764 -3.549
## year_factor5                 -0.016187  0.013953 521.944382 -1.160
## year_factor6                 -0.019020  0.013772 521.941574 -1.381
## insecticideno_insects       -0.005013  0.012044 522.112661 -0.416
## stateambient:year_factor3   0.016609  0.016110 521.838767  1.031
## stateambient:year_factor4   0.035078  0.015885 522.035416  2.208
## stateambient:year_factor5   0.042685  0.015724 521.967303  2.715
## stateambient:year_factor6   0.023213  0.015595 522.015772  1.488
## year_factor3:insecticideno_insects 0.012964  0.016137 521.859178  0.803
## year_factor4:insecticideno_insects 0.007544  0.015930 522.073922  0.474
## year_factor5:insecticideno_insects 0.008673  0.015819 522.132216  0.548
## year_factor6:insecticideno_insects -0.011677 0.015699 522.226887 -0.744
##                               Pr(>|t|)
## (Intercept) < 2e-16 ***

```

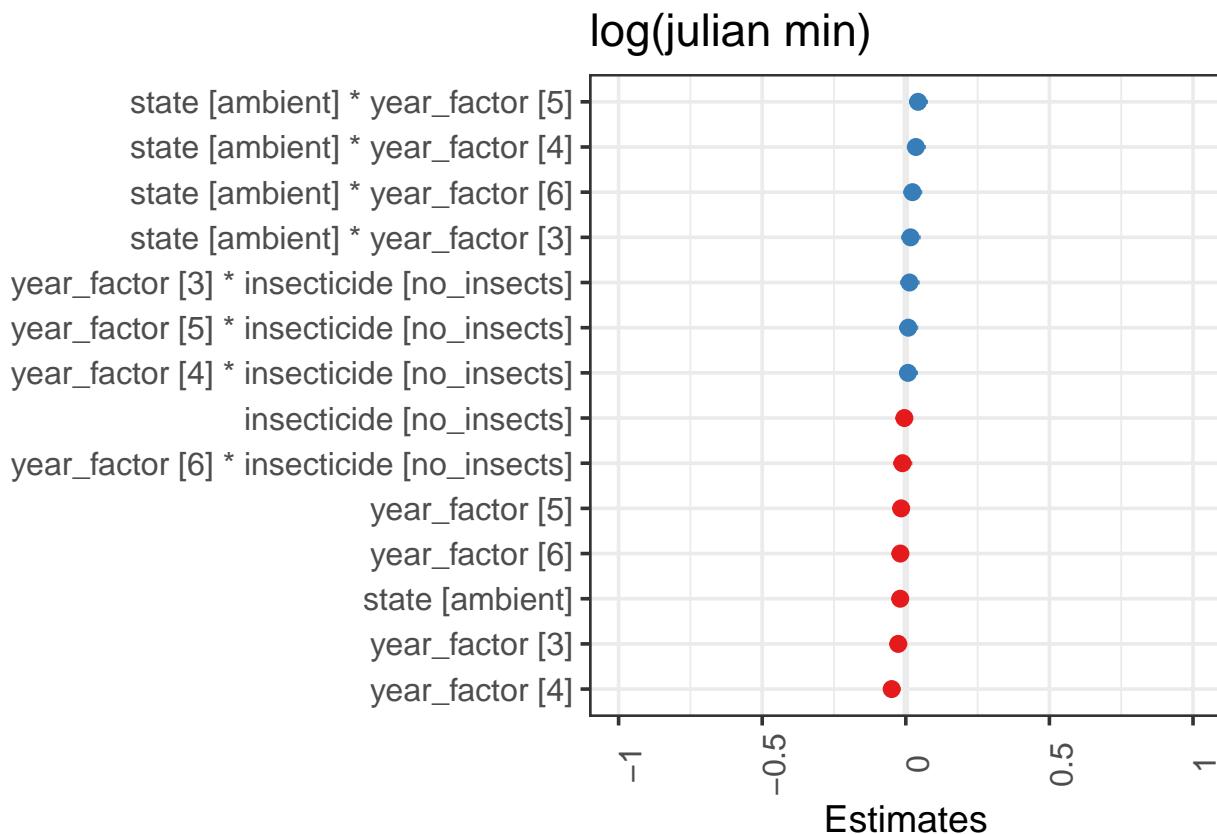
```

## stateambient          0.102267
## year_factor3         0.061214 .
## year_factor4         0.000422 ***
## year_factor5         0.246527
## year_factor6         0.167866
## insecticideno_insects 0.677402
## stateambient:year_factor3 0.303014
## stateambient:year_factor4 0.027664 *
## stateambient:year_factor5 0.006853 **
## stateambient:year_factor6 0.137245
## year_factor3:insecticideno_insects 0.422133
## year_factor4:insecticideno_insects 0.635988
## year_factor5:insecticideno_insects 0.583751
## year_factor6:insecticideno_insects 0.457340
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

# Next, plot the model. There are multiple variables but here's one way to do it
# based on this package sjPlot:
# https://strengejacke.github.io/sjPlot/articles/plot\_model\_estimates.html
# Annoyingly, this package somehow overwrites the factor order in its plotting so
# we will have to modify the code to get warmed = red. I haven't figured this out
# yet. It does seem to work on some of the plots. hmm. ?plot_model Plot the fixed
# effects estimates for different models these are the fixed effects estimates
plot_model(mod2u, sort.est = TRUE)

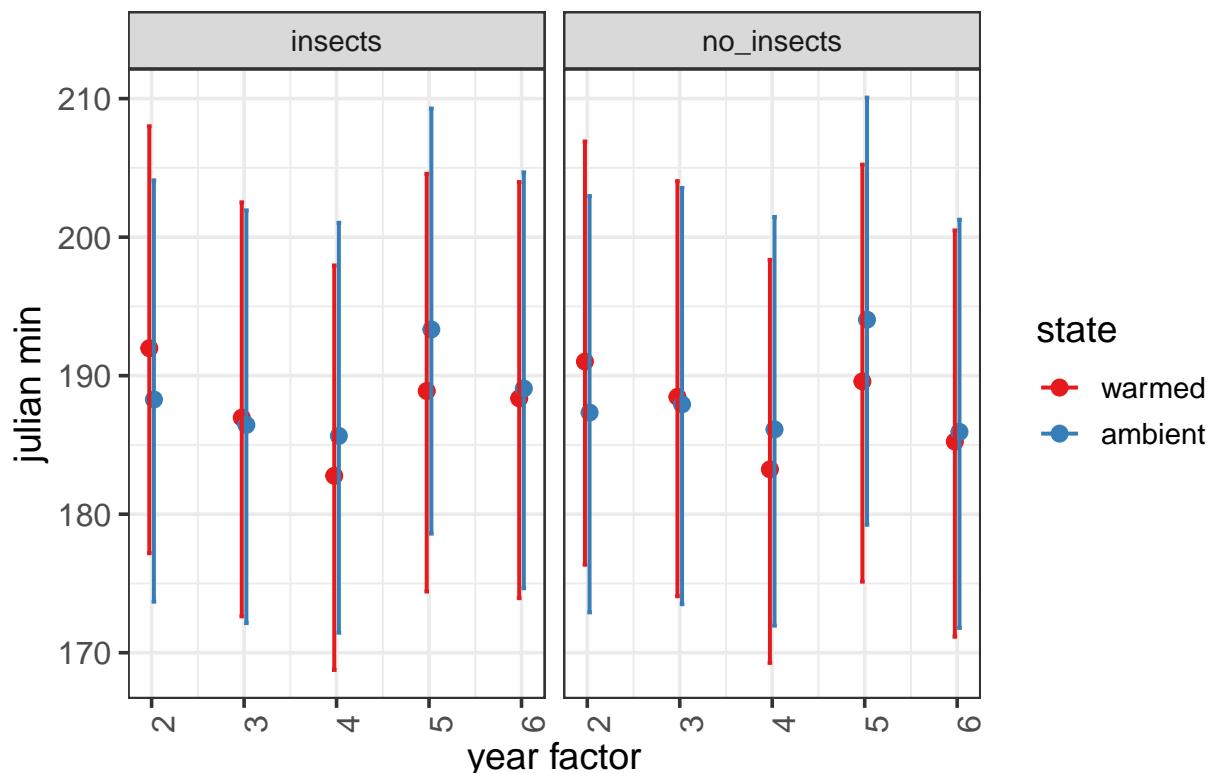
```



```
# these are the fixed predicted values:
plot_model(mod2u, type = "pred", terms = c("year_factor", "state", "insecticide"))
```

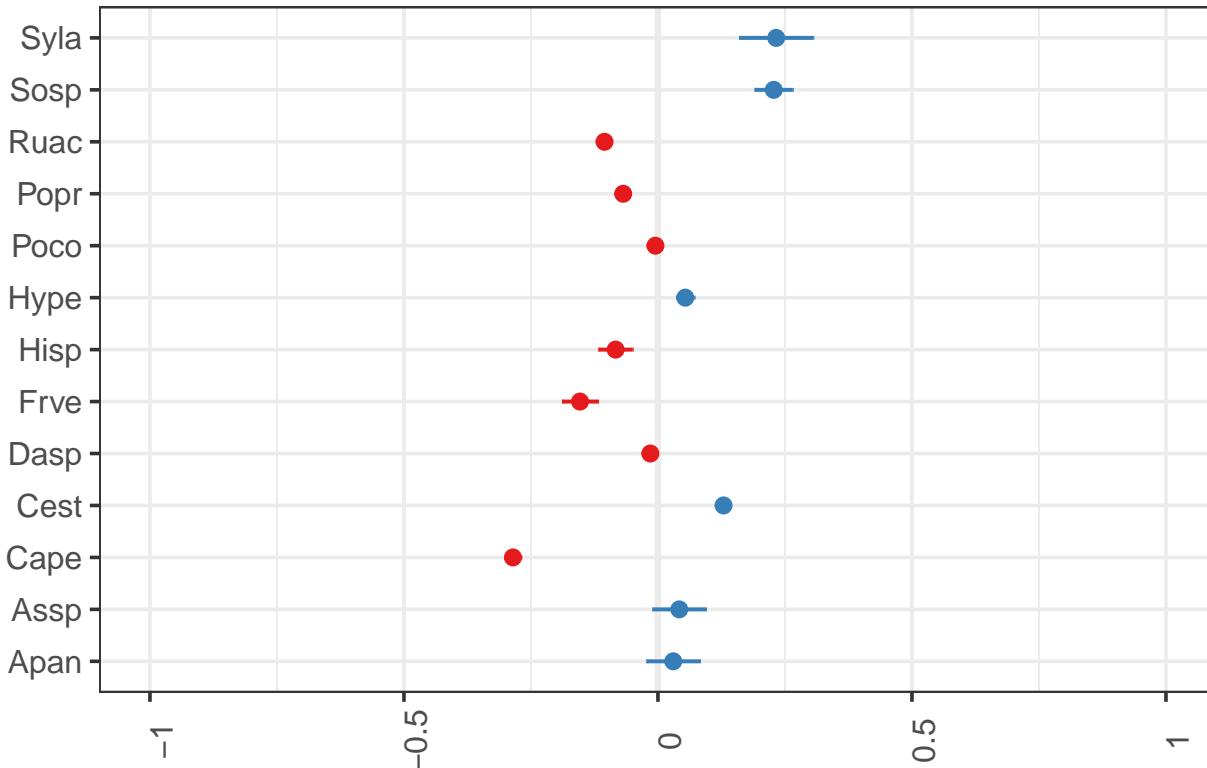
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized
```

Predicted values of julian min



```
# these are the random effects estimates
plot_model(mod2u, type = "re", terms = c("species"))
```

Random effects



```
# Do we need to include insecticide?
mod3u <- lmer(log(julian_min) ~ state * year_factor + (1 | species), umbs_sd_spp,
  REML = FALSE)
anova(mod1u, mod3u) # Don't need insecticide, continue with mod3
```

```
## Data: umbs_sd_spp
## Models:
## mod3u: log(julian_min) ~ state * year_factor + (1 | species)
## mod1u: log(julian_min) ~ state * year_factor + insecticide * year_factor +
## mod1u:   (1 | species) + (1 | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3u    12 -1498.4 -1447.0 761.19   -1522.4
## mod1u    18 -1490.0 -1412.9 762.99   -1526.0 3.6031  6     0.7302
```

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

```
# Does year need to be interactive with state?
mod5u <- lmer(log(julian_min) ~ state + year_factor + (1 | species) + (1 | plot),
  umbs_sd_spp, REML = FALSE)
```

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

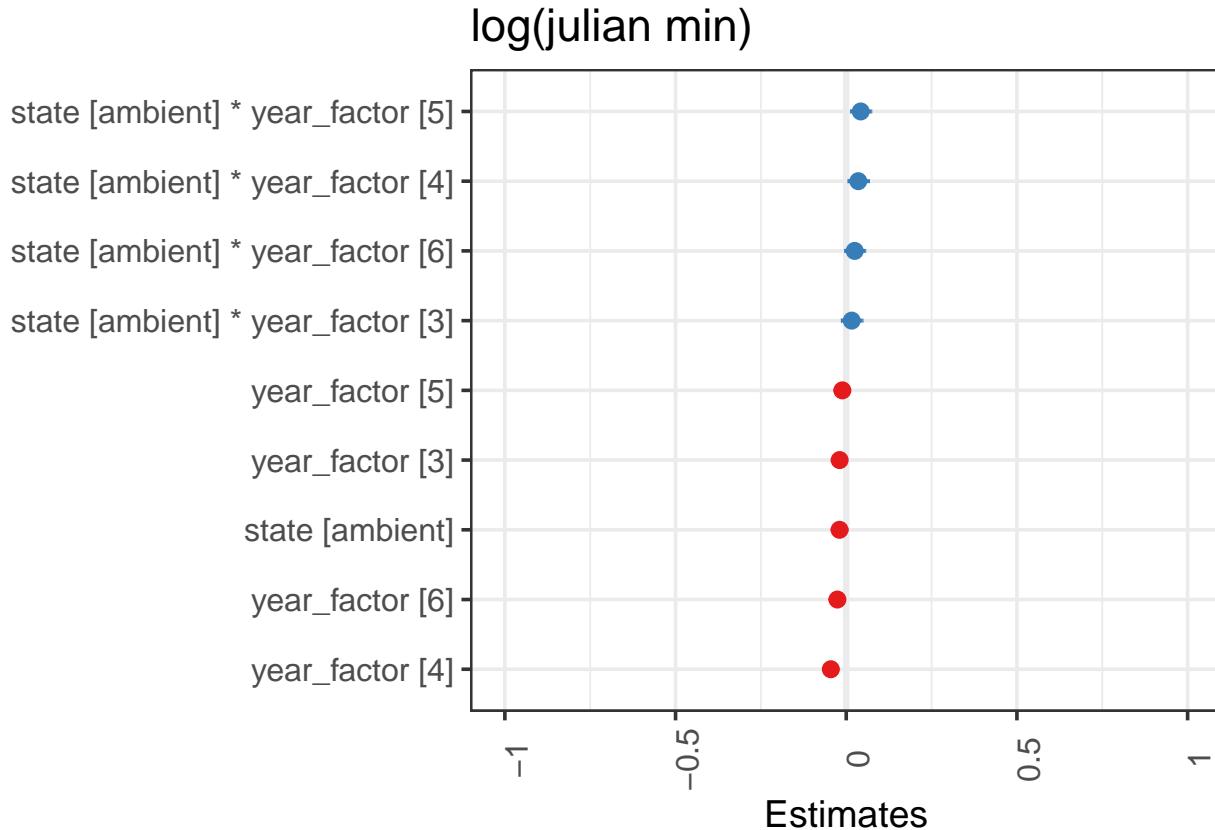
```
anova(mod3u, mod5u) # more complex model is better so go with mod3u
```

```
## Data: umbs_sd_spp
## Models:
## mod5u: log(julian_min) ~ state + year_factor + (1 | species) + (1 | 
## mod5u:     plot)
## mod3u: log(julian_min) ~ state * year_factor + (1 | species)
##      npar    AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5u     9 -1495.6 -1457 756.78 -1513.6
## mod3u    12 -1498.4 -1447 761.19 -1522.4 8.8273  3     0.03168 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AICctab(mod3u, mod5u, weights = T) # go with mod3u
```

```
##          dAICc df weight
## mod3u     0.0   12  0.78
## mod5u    2.6    9  0.22
```

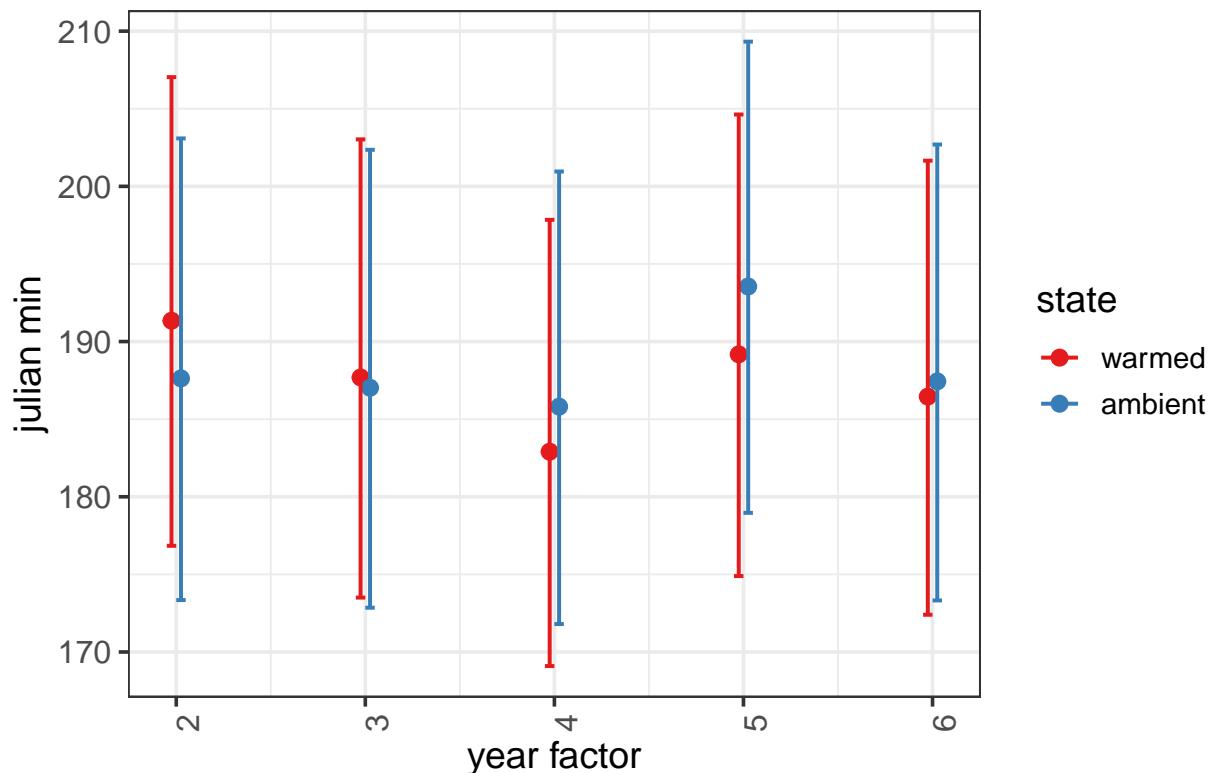
```
# Plot the fixed effects estimates for different models these are the fixed
# effects estimates from summary(mod5)
plot_model(mod3u, sort.est = TRUE)
```



```
# these are the fixed predicted values:  
plot_model(mod3u, type = "pred", terms = c("year_factor", "state"))
```

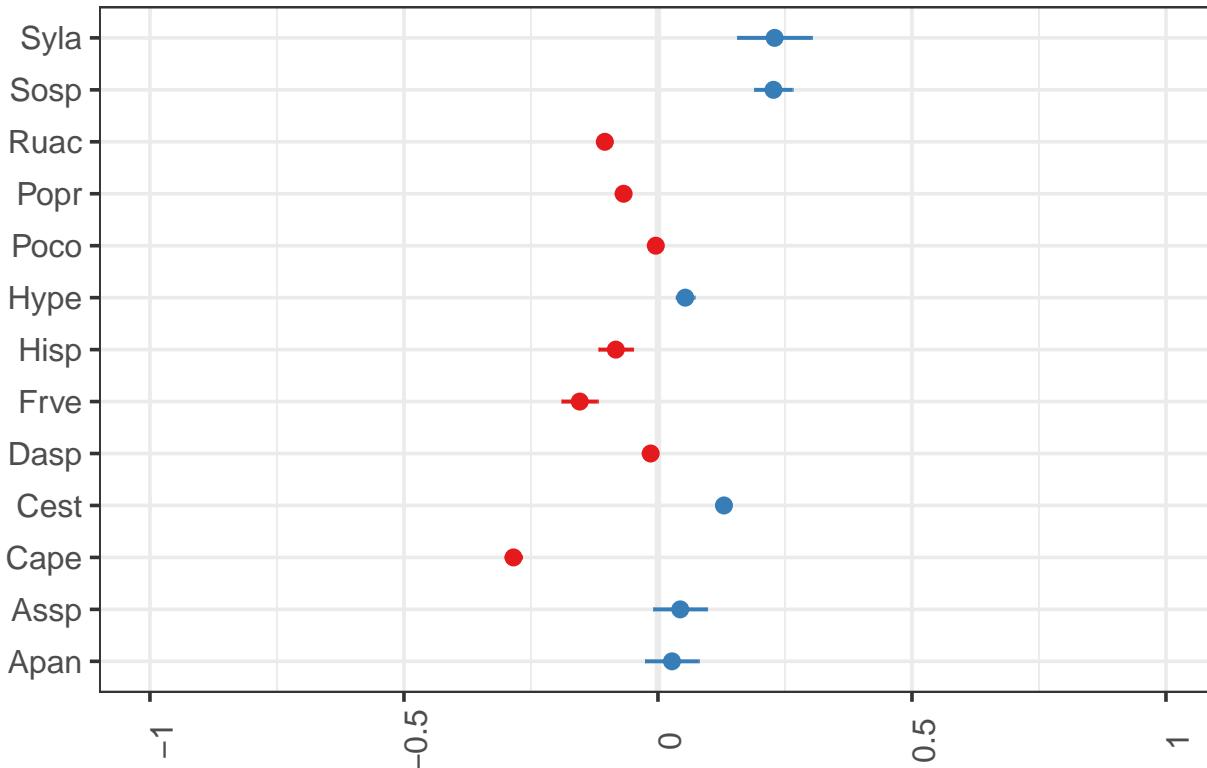
Model has log-transformed response. Back-transforming predictions to original response scale. Standard errors are back-transformed and may not be accurate.

Predicted values of julian min



```
# these are the random effects estimates  
plot_model(mod3u, type = "re", terms = c("species"))
```

Random effects



```
# If we wanted to include plots nested within year it would look like this:
mod6u <- lmer(log(julian_min) ~ state + year_factor + (1 | species) + (1 + year |
  plot), umbs_sd_spp, REML = FALSE)
```

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

```
# model failed to converge
anova(mod3u, mod6u) #stick with mod3
```

```
## Data: umbs_sd_spp
## Models:
## mod6u: log(julian_min) ~ state + year_factor + (1 | species) + (1 +
## mod6u:      year | plot)
## mod3u: log(julian_min) ~ state * year_factor + (1 | species)
##      npar    AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod6u   11 -1490.6 -1443.5 756.30  -1512.6
## mod3u   12 -1498.4 -1447.0 761.19  -1522.4 9.7818  1  0.001763 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod3u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq  Mean Sq NumDF DenDF F value    Pr(>F)
## state     0.002204 0.0022043     1 522.37  0.7302  0.39320
```

```

## year_factor      0.086777 0.0216943      4 522.13  7.1871 1.225e-05 ***
## state:year_factor 0.026867 0.0067169      4 522.00  2.2252  0.06515 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# 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:
mod7u <- lmer(log(julian_min) ~ state + species + (1 + year_factor | plot), umbs_sd_spp,
               REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.2e+00

mod7au <- lmer(log(julian_min) ~ state + species + year_factor + (1 | plot), umbs_sd_spp,
                REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7bu <- lmer(log(julian_min) ~ state * year_factor + species + (1 | plot), umbs_sd_spp,
                REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7cu <- lmer(log(julian_min) ~ state + species + year_factor + insecticide + (1 |
                plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod3u, mod7u) # model 3u is a better fit to data

## Data: umbs_sd_spp
## Models:
## mod3u: log(julian_min) ~ state * year_factor + (1 | species)
## mod7u: log(julian_min) ~ state + species + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3u    12 -1498.4 -1447.0 761.19   -1522.4
## mod7u    30 -1511.0 -1382.6 785.51   -1571.0 48.642 18  0.0001208 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod3u, mod7au) #mod 7au

## Data: umbs_sd_spp
## Models:
## mod3u: log(julian_min) ~ state * year_factor + (1 | species)
## mod7au: log(julian_min) ~ state + species + year_factor + (1 | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod3u    12 -1498.4 -1447 761.19   -1522.4
## mod7au   20 -1550.7 -1465 795.33   -1590.7 68.279  8  1.081e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
anova(mod7au, mod7bu) #mod7bu
```

```
## Data: umbs_sd_spp
## Models:
## mod7au: log(julian_min) ~ state + species + year_factor + (1 | plot)
## mod7bu: log(julian_min) ~ state * year_factor + species + (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7au    20 -1550.7 -1465.0 795.33   -1590.7
## mod7bu    24 -1551.6 -1448.8 799.79   -1599.6 8.9236  4     0.06304 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod7au, mod7cu) #mod7bu
```

```
## Data: umbs_sd_spp
## Models:
## mod7au: log(julian_min) ~ state + species + year_factor + (1 | plot)
## mod7cu: log(julian_min) ~ state + species + year_factor + insecticide +
## mod7cu:      (1 | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod7au    20 -1550.7 -1465 795.33   -1590.7
## mod7cu    21 -1548.9 -1459 795.45   -1590.9 0.2351  1     0.6278
```

```
summary(mod7bu)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state * year_factor + species + (1 | plot)
## Data: umbs_sd_spp
##
##      AIC      BIC logLik deviance df.resid
## -1551.6 -1448.8    799.8   -1599.6      511
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -4.1550 -0.5527 -0.0629  0.4432  7.0147
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.000000 0.00000
## Residual           0.002945 0.05426
## Number of obs: 535, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)  5.28289  0.02854 535.00000 185.083 < 2e-16 ***
## stateambient -0.01955  0.01177 535.00000 -1.661 0.097341 .
## year_factor3 -0.01927  0.01087 535.00000 -1.773 0.076780 .
## year_factor4 -0.04506  0.01085 535.00000 -4.155 3.79e-05 ***
## year_factor5 -0.01139  0.01083 535.00000 -1.051 0.293680
## year_factor6 -0.02584  0.01070 535.00000 -2.415 0.016073 *
## speciesAssp   0.01690  0.03845 535.00000  0.440 0.660384
```

```

## speciesCape      -0.31422   0.02853 535.00000 -11.012 < 2e-16 ***
## speciesCest      0.10129   0.02775 535.00000  3.651 0.000287 ***
## speciesDasp     -0.04317   0.02798 535.00000 -1.543 0.123428
## speciesFrve     -0.18526   0.03267 535.00000 -5.670 2.34e-08 ***
## speciesHisp     -0.11307   0.03239 535.00000 -3.491 0.000521 ***
## speciesHype      0.02521   0.02879 535.00000  0.876 0.381501
## speciesPoco     -0.03305   0.02816 535.00000 -1.174 0.241086
## speciesPopr     -0.09651   0.02776 535.00000 -3.476 0.000550 ***
## speciesRuac     -0.13369   0.02830 535.00000 -4.724 2.96e-06 ***
## speciesSosp      0.20294   0.03333 535.00000  6.088 2.18e-09 ***
## speciesSyla      0.21856   0.04713 535.00000  4.637 4.44e-06 ***
## stateambient:year_factor3 0.01613   0.01594 535.00000  1.012 0.312092
## stateambient:year_factor4 0.03495   0.01574 535.00000  2.221 0.026788 *
## stateambient:year_factor5 0.04234   0.01554 535.00000  2.724 0.006660 **
## stateambient:year_factor6 0.02444   0.01543 535.00000  1.584 0.113748
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

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

```

```

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

```

```
anova(mod7bu) # 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                      0.0021 0.00208     1    535  0.7066  0.40096
## year_factor                 0.0873 0.02183     4    535  7.4124 8.15e-06 ***
## species                     7.1803 0.59836    12    535 203.2001 < 2.2e-16 ***
## state:year_factor           0.0265 0.00662     4    535  2.2496  0.06261 .
## ---
## 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 min
# first seed dates).
emmeans(mod7bu, 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 2          5.256 0.009589 412.2   5.237   5.275
##   ambient 2         5.236 0.010386 388.6   5.216   5.257
##   warmed 3          5.236 0.009017 341.6   5.219   5.254
##   ambient 3         5.233 0.009529 384.0   5.214   5.252
##   warmed 4          5.211 0.008914 339.7   5.193   5.228
##   ambient 4         5.226 0.008579 283.9   5.209   5.243
##   warmed 5          5.244 0.008930 324.7   5.227   5.262

```

```

## ambient 5          5.267 0.008508 287.9    5.250   5.284
## warmed  6          5.230 0.008573 303.8    5.213   5.247
## ambient 6          5.235 0.008356 250.1    5.218   5.251
##
## 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  0.019554 0.0120 383  1.624  0.8358
## warmed 2 - warmed 3  0.019275 0.0111 542  1.735  0.7750
## warmed 2 - ambient 3 0.022701 0.0114 371  1.983  0.6117
## warmed 2 - warmed 4  0.045059 0.0111 540  4.066  0.0022
## warmed 2 - ambient 4 0.029659 0.0112 345  2.642  0.2025
## warmed 2 - warmed 5  0.011386 0.0111 541  1.029  0.9904
## warmed 2 - ambient 5 -0.011404 0.0110 339 -1.033  0.9901
## warmed 2 - warmed 6  0.025841 0.0109 542  2.363  0.3504
## warmed 2 - ambient 6 0.020956 0.0110 329  1.896  0.6715
## ambient 2 - warmed 3 -0.000279 0.0117 363 -0.024  1.0000
## ambient 2 - ambient 3 0.003147 0.0121 542  0.261  1.0000
## ambient 2 - warmed 4  0.025505 0.0117 366  2.175  0.4757
## ambient 2 - ambient 4 0.010105 0.0119 549  0.852  0.9977
## ambient 2 - warmed 5 -0.008168 0.0117 360 -0.698  0.9995
## ambient 2 - ambient 5 -0.030958 0.0117 549 -2.651  0.1969
## ambient 2 - warmed 6  0.006287 0.0116 354  0.543  0.9999
## ambient 2 - ambient 6 0.001401 0.0117 550  0.120  1.0000
## warmed 3 - ambient 3  0.003426 0.0110 338  0.312  1.0000
## warmed 3 - warmed 4  0.025784 0.0105 540  2.445  0.3012
## warmed 3 - ambient 4  0.010384 0.0107 309  0.966  0.9939
## warmed 3 - warmed 5 -0.007889 0.0105 540 -0.749  0.9992
## warmed 3 - ambient 5 -0.030679 0.0105 303 -2.921  0.1043
## warmed 3 - warmed 6  0.006566 0.0104 540  0.634  0.9998
## warmed 3 - ambient 6  0.001681 0.0105 295  0.159  1.0000
## ambient 3 - warmed 4  0.022358 0.0110 341  2.042  0.5703
## ambient 3 - ambient 4 0.006958 0.0111 542  0.628  0.9998
## ambient 3 - warmed 5 -0.011316 0.0109 335 -1.033  0.9900
## ambient 3 - ambient 5 -0.034105 0.0109 542 -3.126  0.0580
## ambient 3 - warmed 6  0.003139 0.0108 329  0.291  1.0000
## ambient 3 - ambient 6 -0.001746 0.0109 544 -0.160  1.0000
## warmed 4 - ambient 4 -0.015400 0.0107 310 -1.443  0.9125
## warmed 4 - warmed 5 -0.033673 0.0105 540 -3.222  0.0437
## warmed 4 - ambient 5 -0.056463 0.0104 301 -5.421 <.0001
## warmed 4 - warmed 6 -0.019218 0.0103 540 -1.869  0.6899
## warmed 4 - ambient 6 -0.024103 0.0104 293 -2.311  0.3851
## ambient 4 - warmed 5 -0.018273 0.0107 307 -1.711  0.7887
## ambient 4 - ambient 5 -0.041063 0.0106 547 -3.892  0.0044
## ambient 4 - warmed 6 -0.003818 0.0105 297 -0.364  1.0000
## ambient 4 - ambient 6 -0.008703 0.0105 544 -0.828  0.9981
## warmed 5 - ambient 5 -0.022790 0.0104 295 -2.199  0.4601
## warmed 5 - warmed 6  0.014455 0.0102 538  1.412  0.9233
## warmed 5 - ambient 6  0.009570 0.0104 287  0.922  0.9957
## ambient 5 - warmed 6  0.037245 0.0102 284  3.657  0.0112

```

```

##  ambient 5 - ambient 6  0.032359 0.0103 540  3.155  0.0533
##  warmed 6 - ambient 6 -0.004885 0.0102 277 -0.479  1.0000
##
## 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(mod7bu, list(pairwise ~ year_factor), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## NOTE: Results may be misleading due to involvement in interactions

## $`emmeans of year_factor`
##   year_factor emmean      SE   df lower.CL upper.CL
##   2            5.246 0.007979 408.9    5.230    5.262
##   3            5.235 0.007472 378.1    5.220    5.249
##   4            5.218 0.006933 312.9    5.205    5.232
##   5            5.256 0.007015 313.6    5.242    5.269
##   6            5.232 0.006756 276.2    5.219    5.246
##
## 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  0.01121 0.00824 542   1.360  0.6537
##   2 - 4  0.02758 0.00819 545   3.368  0.0072
##   2 - 5 -0.00979 0.00814 546  -1.202  0.7505
##   2 - 6  0.01362 0.00811 548   1.679  0.4480
##   3 - 4  0.01637 0.00766 541   2.138  0.2056
##   3 - 5 -0.02100 0.00761 541  -2.759  0.0471
##   3 - 6  0.00241 0.00757 542   0.318  0.9978
##   4 - 5 -0.03737 0.00745 544  -5.018 <.0001
##   4 - 6 -0.01396 0.00737 542  -1.895  0.3211
##   5 - 6  0.02341 0.00724 539   3.231  0.0114
##
## 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(mod7bu, list(pairwise ~ species), adjust = "tukey")

```

```

## boundary (singular) fit: see ?isSingular

## $`emmeans of species`
##   species emmean      SE   df lower.CL upper.CL
##   Apan    5.265 0.028140 494.6    5.209    5.320

```

```

## Assp      5.281 0.028123 555.5    5.226   5.337
## Cape     4.950 0.008781 428.0    4.933   4.968
## Cest     5.366 0.005172 309.4    5.356   5.376
## Dasp     5.221 0.006097 371.3    5.209   5.233
## Frve     5.079 0.018801 440.1    5.042   5.116
## Hisp     5.152 0.017852 470.9    5.116   5.187
## Hype     5.290 0.009682 459.4    5.271   5.309
## Poco     5.232 0.007333 426.3    5.217   5.246
## Popr     5.168 0.005270 317.4    5.158   5.178
## Ruac     5.131 0.007701 393.6    5.116   5.146
## Sosp     5.468 0.019969 352.8    5.428   5.507
## Syla     5.483 0.039851 538.6    5.405   5.561
##
## 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'
##   estimate      SE  df t.ratio p.value
## Apan - Assp -0.01690 0.03961 527 -0.427 1.0000
## Apan - Cape  0.31422 0.02941 513 10.686 <.0001
## Apan - Cest -0.10129 0.02860 512 -3.542 0.0253
## Apan - Dasp  0.04317 0.02885 509  1.497 0.9565
## Apan - Frve  0.18526 0.03375 477  5.489 <.0001
## Apan - Hisp  0.11307 0.03341 518  3.384 0.0420
## Apan - Hype -0.02521 0.02966 517 -0.850 0.9998
## Apan - Poco  0.03305 0.02905 494  1.138 0.9957
## Apan - Popr  0.09651 0.02862 510  3.372 0.0438
## Apan - Ruac  0.13369 0.02916 522  4.585 0.0004
## Apan - Sosp -0.20294 0.03449 450 -5.885 <.0001
## Apan - Syla -0.21856 0.04865 522 -4.493 0.0006
## Assp - Cape  0.33113 0.02941 556 11.259 <.0001
## Assp - Cest -0.08438 0.02858 558 -2.952 0.1424
## Assp - Dasp  0.06007 0.02880 558  2.086 0.6741
## Assp - Frve  0.20216 0.03369 545  6.000 <.0001
## Assp - Hisp  0.12998 0.03341 556  3.891 0.0073
## Assp - Hype -0.00831 0.02966 557 -0.280 1.0000
## Assp - Poco  0.04995 0.02904 556  1.720 0.8859
## Assp - Popr  0.11341 0.02860 558  3.965 0.0055
## Assp - Ruac  0.15059 0.02914 558  5.169 <.0001
## Assp - Sosp -0.18603 0.03439 540 -5.409 <.0001
## Assp - Syla -0.20166 0.04849 557 -4.159 0.0025
## Cape - Cest -0.41551 0.01018 553 -40.820 <.0001
## Cape - Dasp -0.27105 0.01073 557 -25.272 <.0001
## Cape - Frve -0.12896 0.02068 495 -6.235 <.0001
## Cape - Hisp -0.20115 0.01997 515 -10.074 <.0001
## Cape - Hype -0.33943 0.01299 530 -26.138 <.0001
## Cape - Poco -0.28118 0.01129 558 -24.903 <.0001
## Cape - Popr -0.21771 0.01023 552 -21.286 <.0001
## Cape - Ruac -0.18054 0.01174 499 -15.375 <.0001
## Cape - Sosp -0.51716 0.02175 440 -23.780 <.0001
## Cape - Syla -0.53278 0.04081 541 -13.055 <.0001
## Cest - Dasp  0.14446 0.00801 549  18.038 <.0001

```

```

##  Cest - Frve  0.28655 0.01948 487  14.708 <.0001
##  Cest - Hisp  0.21436 0.01860 516  11.525 <.0001
##  Cest - Hype  0.07608 0.01096 556   6.939 <.0001
##  Cest - Poco  0.13433 0.00895 556  15.012 <.0001
##  Cest - Popr  0.19780 0.00738 539  26.799 <.0001
##  Cest - Ruac  0.23497 0.00927 557  25.336 <.0001
##  Cest - Sosp -0.10165 0.02063 395  -4.928 0.0001
##  Cest - Syla -0.11727 0.04018 543  -2.919 0.1548
##  Dasp - Frve  0.14209 0.01982 484   7.170 <.0001
##  Dasp - Hisp  0.06990 0.01880 531   3.718 0.0137
##  Dasp - Hype -0.06838 0.01146 557  -5.969 <.0001
##  Dasp - Poco -0.01012 0.00961 558  -1.053 0.9979
##  Dasp - Popr  0.05334 0.00807 552   6.607 <.0001
##  Dasp - Ruac  0.09052 0.00984 558   9.203 <.0001
##  Dasp - Sosp -0.24611 0.02090 398  -11.775 <.0001
##  Dasp - Syla -0.26173 0.04034 546  -6.488 <.0001
##  Frve - Hisp -0.07218 0.02588 550  -2.789 0.2103
##  Frve - Hype -0.21047 0.02107 488  -9.988 <.0001
##  Frve - Poco -0.15221 0.02010 509  -7.574 <.0001
##  Frve - Popr -0.08875 0.01951 490  -4.549 0.0005
##  Frve - Ruac -0.05157 0.02033 457  -2.537 0.3528
##  Frve - Sosp -0.38820 0.02736 450  -14.189 <.0001
##  Frve - Syla -0.40382 0.04378 552  -9.224 <.0001
##  Hisp - Hype -0.13828 0.02040 520  -6.778 <.0001
##  Hisp - Poco -0.08003 0.01939 515  -4.127 0.0029
##  Hisp - Popr -0.01657 0.01862 516  -0.890 0.9996
##  Hisp - Ruac  0.02061 0.01938 534   1.064 0.9977
##  Hisp - Sosp -0.31601 0.02675 484  -11.815 <.0001
##  Hisp - Syla -0.33164 0.04354 558  -7.617 <.0001
##  Hype - Poco  0.05826 0.01208 528   4.824 0.0001
##  Hype - Popr  0.12172 0.01101 555  11.054 <.0001
##  Hype - Ruac  0.15890 0.01242 557  12.794 <.0001
##  Hype - Sosp -0.17773 0.02219 369  -8.008 <.0001
##  Hype - Syla -0.19335 0.04099 536  -4.717 0.0002
##  Poco - Popr  0.06346 0.00901 556   7.047 <.0001
##  Poco - Ruac  0.10064 0.01067 532  9.428 <.0001
##  Poco - Sosp -0.23598 0.02121 420  -11.125 <.0001
##  Poco - Syla -0.25161 0.04052 543  -6.210 <.0001
##  Popr - Ruac  0.03718 0.00932 558   3.988 0.0050
##  Popr - Sosp -0.29945 0.02063 404  -14.512 <.0001
##  Popr - Syla -0.31507 0.04019 544  -7.840 <.0001
##  Ruac - Sosp -0.33662 0.02140 397  -15.728 <.0001
##  Ruac - Syla -0.35225 0.04052 549  -8.694 <.0001
##  Sosp - Syla -0.01562 0.04429 557  -0.353 1.0000
##
## 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 13 estimates

```

```
emmeans(mod7bu, list(pairwise ~ insecticide), adjust = "tukey")
```

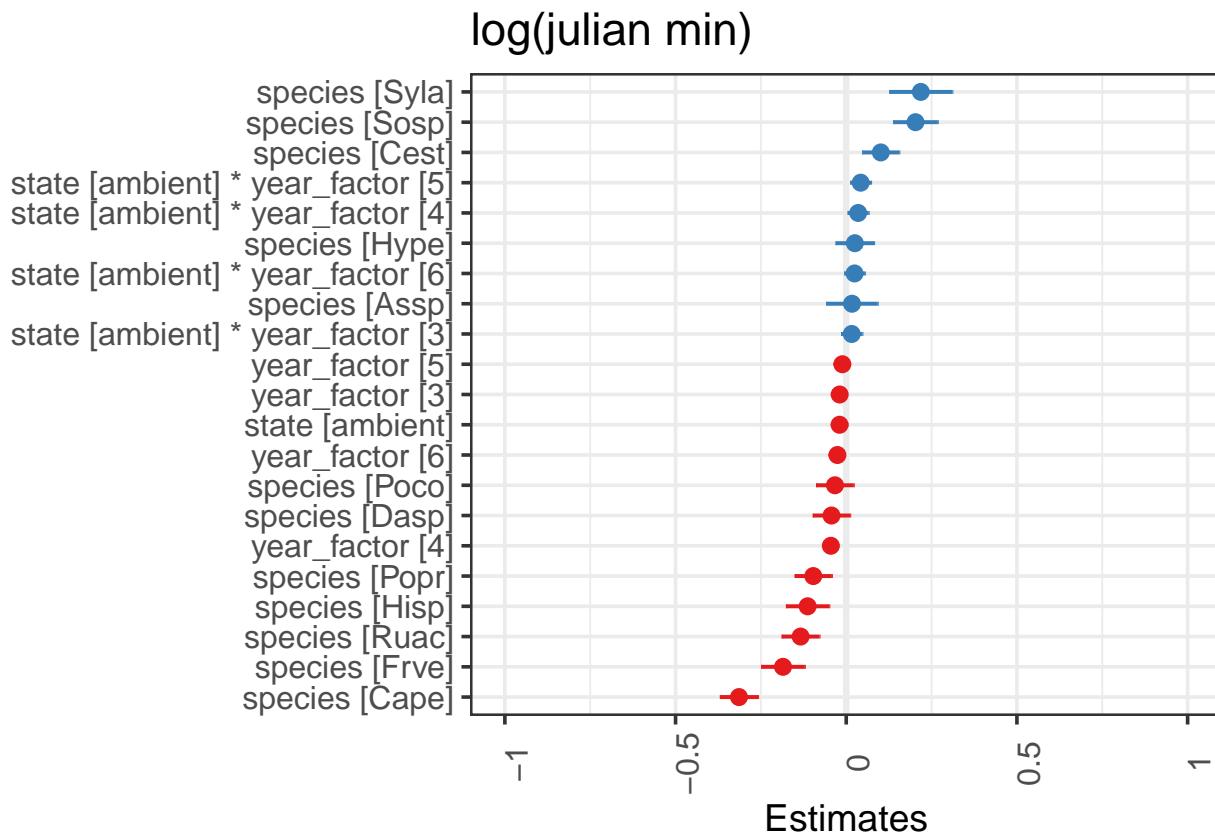
```
## boundary (singular) fit: see ?isSingular
```

```

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

# 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(mod7bu, sort.est = TRUE)

```



```

# if you want to standardize the estimates:
plot_model(mod7bu, sort.est = TRUE, type = "std")

```

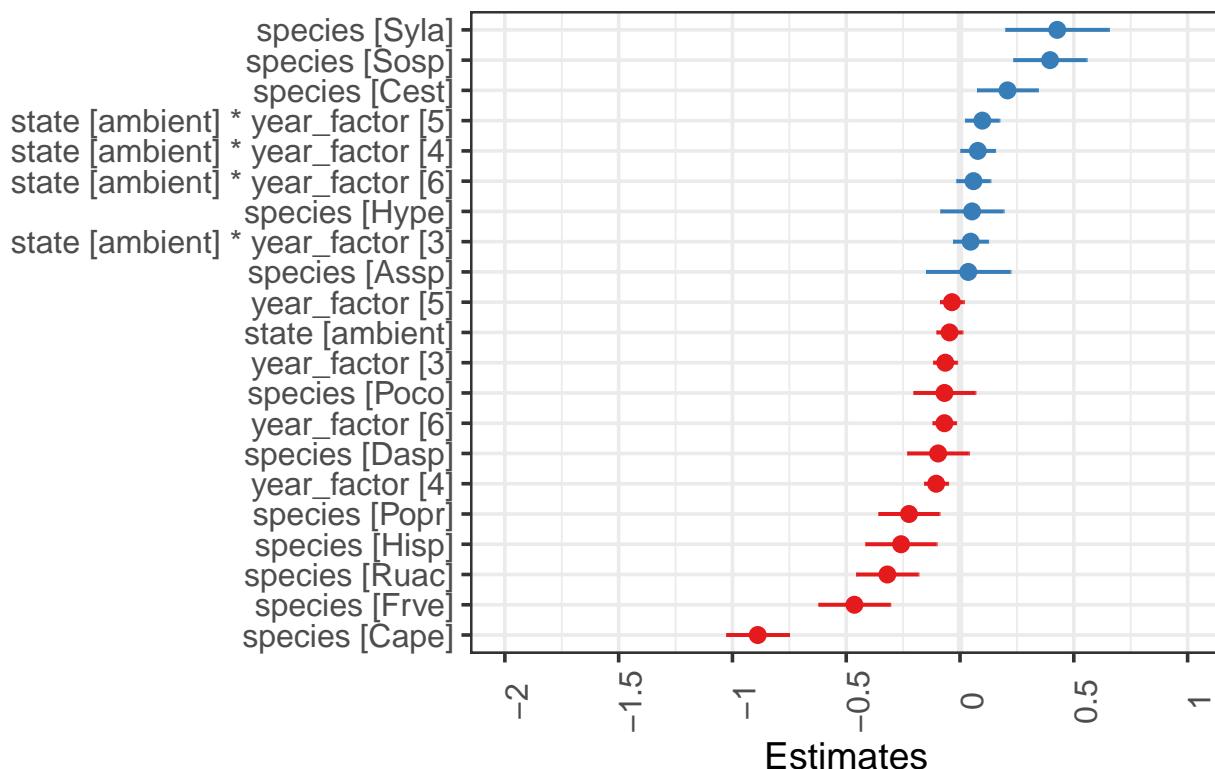
```

## Formula contains log- or sqrt-terms. See help("standardize") for how such terms are standardized.

## boundary (singular) fit: see ?isSingular

```

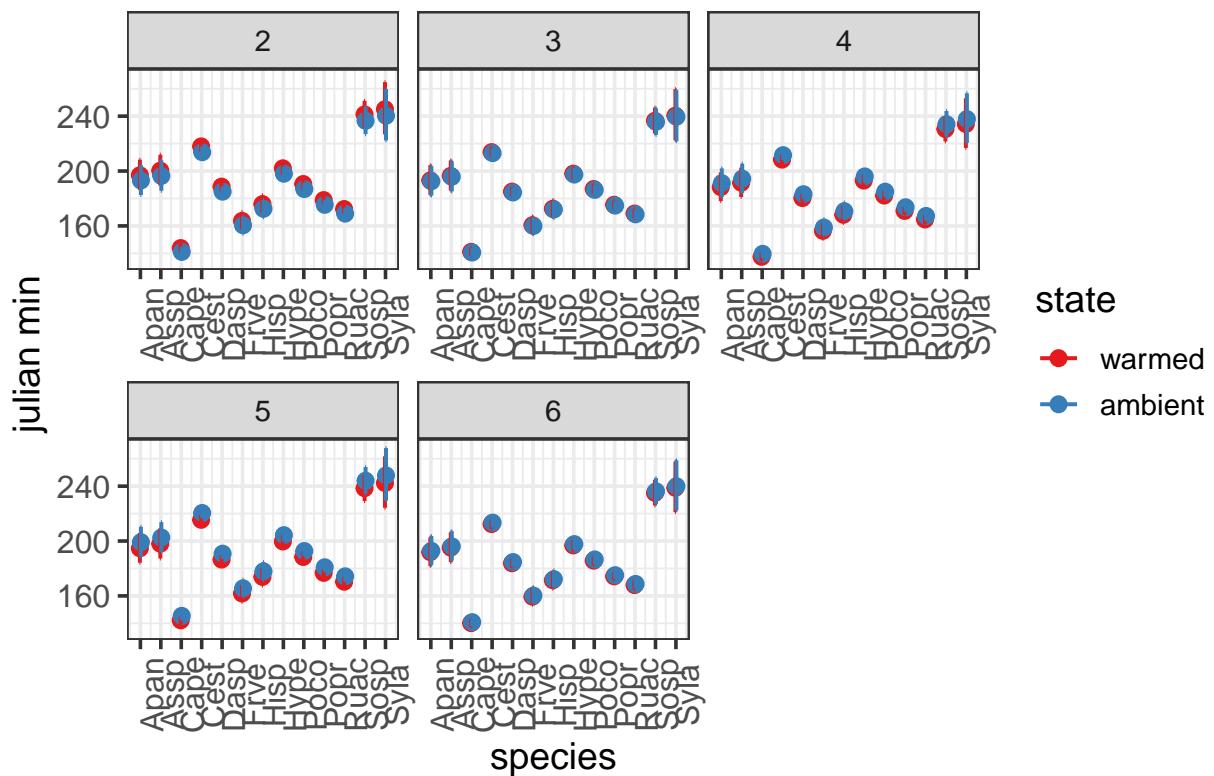
log(julian min)



```
# these are the fixed predicted values: - note this is a new plot
plot_model(mod7bu, type = "pred", terms = c("species", "state", "year_factor"))
```

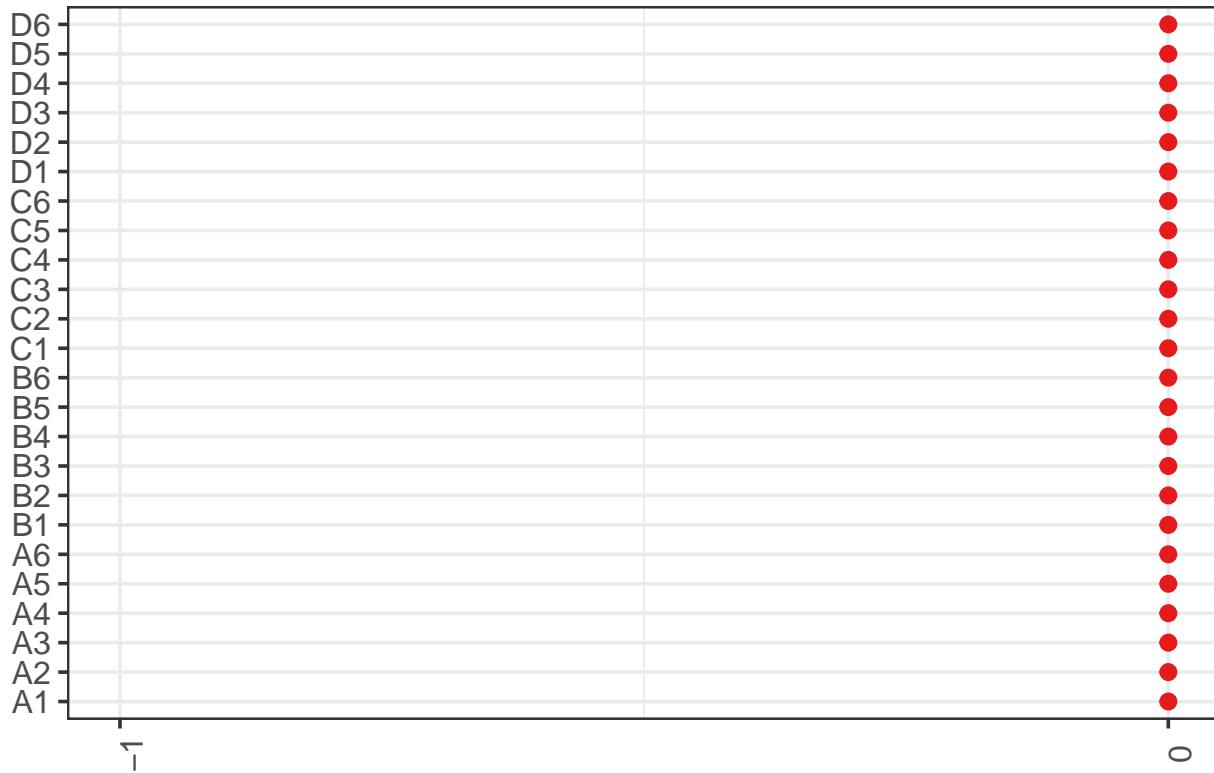
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standard
```

Predicted values of julian min



```
# these are the random effects estimates  
plot_model(mod7bu, type = "re")
```

Random effects



```
# including native vs. exotic
umbss_sd_spp <- within(kbs_sd_spp, origin <- relevel(factor(origin), ref = "Native")) # releveling so no NA's
mod8u <- lmer(log(julian_min) ~ state * origin + (1 + year_factor | plot), umbss_sd_spp,
               REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9u <- lmer(log(julian_min) ~ state + origin + (1 + year_factor | plot), umbss_sd_spp,
               REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9au <- lmer(log(julian_min) ~ state + origin + year_factor + (1 | plot), umbss_sd_spp,
                REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod8u, mod9u) # model 9u is a better fit to data

## Data: umbss_sd_spp
## Models:
## mod9u: log(julian_min) ~ state + origin + (1 + year_factor | plot)
## mod8u: log(julian_min) ~ state * origin + (1 + year_factor | plot)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9u   33 -1154.2 -999.03 610.08 -1220.2
## mod8u   35 -1151.1 -986.56 610.54 -1221.1 0.9268  2     0.6291
```

```

anova(mod9u, mod9au) # mod 9au

## Data: umbs_sd_spp
## Models:
## mod9au: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## mod9u: log(julian_min) ~ state + origin + (1 + year_factor | plot)
##      npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9au    12 -1237.6 -1181.16 630.78   -1261.6
## mod9u     33 -1154.2  -999.03 610.08   -1220.2      0 21          1

summary(mod9au)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## Data: umbs_sd_spp
##
##      AIC      BIC      logLik deviance df.resid
## -1237.6 -1181.2     630.8   -1261.6      801
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max
## -4.1280 -0.6127  0.0255  0.6215  3.4904
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.00000  0.0000
## Residual           0.01241  0.1114
## Number of obs: 813, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 5.636e+00 1.848e-02 8.130e+02 304.969 < 2e-16 ***
## stateambient 3.164e-05 7.921e-03 8.130e+02   0.004 0.996814
## originBoth   -4.029e-01 1.497e-02 8.130e+02 -26.905 < 2e-16 ***
## originExotic -3.207e-01 9.782e-03 8.130e+02 -32.786 < 2e-16 ***
## year_factor2 -1.036e-01 1.836e-02 8.130e+02  -5.640 2.35e-08 ***
## year_factor3 -1.281e-01 1.883e-02 8.130e+02  -6.803 1.99e-11 ***
## year_factor4 -1.178e-01 1.940e-02 8.130e+02  -6.070 1.96e-09 ***
## year_factor5 -7.814e-02 1.994e-02 8.130e+02  -3.919 9.63e-05 ***
## year_factor6 -6.981e-02 1.906e-02 8.130e+02  -3.662 0.000266 ***
## year_factor7 -1.135e-01 2.149e-02 8.130e+02  -5.284 1.63e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttmbn orgnBt orgnEx yr_fc2 yr_fc3 yr_fc4 yr_fc5 yr_fc6
## stateambint -0.198
## originBoth   -0.183 -0.092
## originExotic -0.401 -0.061  0.491
## year_factr2 -0.803 -0.016 -0.093  0.029
## year_factr3 -0.784 -0.004 -0.060  0.023  0.791

```

```

## year_factr4 -0.740 -0.017 -0.039 -0.020  0.761  0.741
## year_factr5 -0.722 -0.032 -0.041 -0.006  0.743  0.722  0.699
## year_factr6 -0.780 -0.013 -0.040  0.042  0.780  0.758  0.731  0.713
## year_factr7 -0.671  0.021 -0.048 -0.030  0.687  0.669  0.648  0.631  0.660
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

anova(mod9au)

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state      0.0000  0.0000     1   813    0.00  0.9968
## origin     15.2484  7.6242     2   813  614.58 < 2.2e-16 ***
## year_factor 0.7868  0.1311     6   813   10.57 2.546e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod9au, 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  5.549 0.009663 172.72    5.530    5.568
##   ambient Native  5.549 0.009794 163.67    5.529    5.568
##   warmed Both     5.146 0.013849 433.30    5.119    5.173
##   ambient Both    5.146 0.013141 336.34    5.120    5.172
##   warmed Exotic   5.228 0.006725  46.92    5.214    5.241
##   ambient Exotic   5.228 0.006168  30.62    5.215    5.241
##
## 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 -3.16e-05 0.00800 22.9 -0.004  1.0000
##   warmed Native - warmed Both    4.03e-01 0.01510 821.8 26.689 <.0001
##   warmed Native - ambient Both   4.03e-01 0.01644 273.4 24.507 <.0001
##   warmed Native - warmed Exotic 3.21e-01 0.00986 822.6 32.518 <.0001
##   warmed Native - ambient Exotic 3.21e-01 0.01231 116.9 26.051 <.0001
##   ambient Native - warmed Both   4.03e-01 0.01771 362.6 22.756 <.0001
##   ambient Native - ambient Both   4.03e-01 0.01510 821.8 26.689 <.0001
##   ambient Native - warmed Exotic 3.21e-01 0.01308 140.0 24.530 <.0001
##   ambient Native - ambient Exotic 3.21e-01 0.00986 822.6 32.518 <.0001
##   warmed Both - ambient Both    -3.16e-05 0.00800 22.9 -0.004  1.0000
##   warmed Both - warmed Exotic   -8.22e-02 0.01339 823.1 -6.134 <.0001
##   warmed Both - ambient Exotic   -8.22e-02 0.01598 274.6 -5.144 <.0001
##   ambient Both - warmed Exotic   -8.21e-02 0.01521 209.6 -5.398 <.0001
##   ambient Both - ambient Exotic   -8.22e-02 0.01339 823.1 -6.134 <.0001
##   warmed Exotic - ambient Exotic -3.16e-05 0.00800 22.9 -0.004  1.0000

```

```

##  

## 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
umbss_sd_spp <- within(umbss_sd_spp, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
mod10u <- lmer(log(julian_min) ~ state * growth_habit + (1 + year_factor | plot),
  umbss_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11u <- lmer(log(julian_min) ~ state + growth_habit + (1 + year_factor | plot),
  umbss_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11au <- lmer(log(julian_min) ~ state + growth_habit + year_factor + (1 | plot),
  umbss_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod10u, mod11u) # model 11u is a better fit to data

## Data: umbss_sd_spp
## Models:
## mod11u: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
## mod10u: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11u   33 -936.63 -781.50 501.31   -1002.6
## mod10u   35 -933.15 -768.62 501.57   -1003.1 0.5171  2      0.7722

anova(mod11u, mod11au) # model 11u is still a better fit to data

## Data: umbss_sd_spp
## Models:
## mod11au: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
## mod11u: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod11au   12 -1031.46 -975.05 527.73   -1055.5
## mod11u    33 -936.63 -781.50 501.31   -1002.6      0 21           1

summary(mod11u)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)

```

```

##      Data: umbs_sd_spp
##
##      AIC      BIC  logLik deviance df.resid
## -936.6   -781.5   501.3   -1002.6      780
##
## Scaled residuals:
##      Min     1Q Median     3Q    Max
## -5.2851 -0.5989 -0.0475  0.7416  3.3066
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## plot     (Intercept) 0.014242 0.11934
##          year_factor2 0.022091 0.14863 -1.00
##          year_factor3 0.029831 0.17272 -1.00  1.00
##          year_factor4 0.018320 0.13535 -1.00  1.00  1.00
##          year_factor5 0.008661 0.09306 -1.00  1.00  1.00  1.00
##          year_factor6 0.006836 0.08268 -1.00  1.00  1.00  1.00  1.00
##          year_factor7 0.013196 0.11487 -1.00  1.00  1.00  1.00  1.00
## Residual           0.016284 0.12761
## Number of obs: 813, groups: plot, 24
##
## Fixed effects:
##                   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      5.457329  0.009114 606.673254 598.794 <2e-16 ***
## stateambient    -0.018677  0.009135 586.364698 -2.045  0.0413 *
## growth_habit     -0.299861  0.015877 790.434459 -18.887 <2e-16 ***
## growth_habitGraminoid -0.249369  0.009817 792.730576 -25.402 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttmbn grwth_
## stateambient -0.553
## growth_habit -0.351 -0.062
## grwth_hbtGr -0.656  0.014  0.355
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod11u)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state             0.0681  0.0681     1 586.36   4.1801 0.04135 *
## growth_habit    12.3186  6.1593     2 789.42 378.2403 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
emmeans(mod11u, list(pairwise ~ growth_habit), adjust = "tukey")
```

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

```
## $`emmeans of growth_habit`
```

```

##  growth_habit emmean      SE   df lower.CL upper.CL
##  Forb          5.448 0.008641 133.39    5.431    5.465
##              5.148 0.015138 493.51    5.118    5.178
##  Graminoid     5.199 0.007251  65.85    5.184    5.213
##
## 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 growth_habit'
##  1             estimate      SE  df t.ratio p.value
##  Forb -           0.2999 0.0163 736 18.365 <.0001
##  Forb - Graminoid  0.2494 0.0102 749 24.424 <.0001
##  - Graminoid     -0.0505 0.0161 751 -3.143  0.0049
##
## 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 3 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
mod12u <- lmer(log(julian_min) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), umbs_sd_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
mod13u <- lmer(log(julian_min) ~ state * factor(year_factor) + (1 | species), umbs_sd_spp)

# All the models ran:
mod1u <- lmer(log(julian_min) ~ state * year_factor + insecticide * year_factor +
  (1 | species) + (1 | plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2u <- lmer(log(julian_min) ~ state * year_factor + insecticide * year_factor +
  (1 | species), umbs_sd_spp, REML = FALSE)
mod3u <- lmer(log(julian_min) ~ state * year_factor + (1 | species), umbs_sd_spp,
  REML = FALSE)
mod4u <- lmer(log(julian_min) ~ state * year_factor + insecticide + (1 | species) +
  (1 | plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

mod5u <- lmer(log(julian_min) ~ state + year_factor + (1 | species), umbs_sd_spp,
  REML = FALSE)
mod6u <- lmer(log(julian_min) ~ state + year_factor + (1 | species) + (1 + year |
  plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -2.5e-01

mod7u <- lmer(log(julian_min) ~ state + species + (1 + factor(year_factor) | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 2 negative eigenvalues: -3.4e-02 -3.2e+00

mod7au <- lmer(log(julian_min) ~ state + species + factor(year_factor) + (1 | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7bu <- lmer(log(julian_min) ~ state * factor(year_factor) + species + (1 | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7cu <- lmer(log(julian_min) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod8u <- lmer(log(julian_min) ~ state * origin + (1 + factor(year_factor) | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9u <- lmer(log(julian_min) ~ state + origin + (1 + factor(year_factor) | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9au <- lmer(log(julian_min) ~ state + origin + factor(year_factor) + (1 | plot),
  umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

mod10u <- lmer(log(julian_min) ~ state * growth_habit + (1 + factor(year_factor) |
  plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11u <- lmer(log(julian_min) ~ state + growth_habit + (1 + factor(year_factor) |
  plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11au <- lmer(log(julian_min) ~ state + growth_habit + factor(year_factor) + (1 |
  plot), umbs_sd_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod12u <- lmer(log(julian_min) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), umbs_sd_spp)

## boundary (singular) fit: see ?isSingular

mod13u <- lmer(log(julian_min) ~ state * factor(year_factor) + (1 | species), umbs_sd_spp)
AICctab(mod1u, mod2u, mod3u, mod5u, mod6u, mod7u, mod7au, mod7bu, mod7cu, mod8u,
  mod9u, mod9au, mod10u, mod11u, mod11au, mod13u, weights = T) # idk why this wont run

## Error in ICtab(..., mnames = mnames, type = "AICc"): nobs different: must have identical data for all

AICctab(mod3u, mod9au, mod11u, weights = T)

## Error in ICtab(..., mnames = mnames, type = "AICc"): nobs different: must have identical data for all

summary(mod7au)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + species + factor(year_factor) + (1 |
##   plot)
## Data: umbs_sd_spp
##
##      AIC      BIC    logLik deviance df.resid
## -2581.8 -2436.0  1321.9   -2643.8      785
##
## Scaled residuals:
##      Min      1Q Median      3Q     Max
## -4.5921 -0.5306 -0.0049  0.4909  7.6708
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.000000 0.000000

```

```

## Residual           0.002293 0.04789
## Number of obs: 816, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                5.452875  0.011990 816.000000 454.793 < 2e-16 ***
## stateambient               0.004370  0.003507 816.000000   1.246 0.213101
## speciesArel                -0.184443  0.010465 816.000000 -17.624 < 2e-16 ***
## speciesBavu                 -0.230672  0.020305 816.000000 -11.360 < 2e-16 ***
## speciesCahi                 -0.502774  0.023467 816.000000 -21.425 < 2e-16 ***
## speciesCest                 0.039215  0.011618 816.000000   3.375 0.000772 ***
## speciesDaca                 0.101541  0.014495 816.000000   7.005 5.16e-12 ***
## speciesDagl                 -0.163366  0.010831 816.000000 -15.083 < 2e-16 ***
## speciesElre                 -0.039521  0.011372 816.000000 -3.475 0.000537 ***
## speciesEugr                 0.214379  0.013900 816.000000  15.422 < 2e-16 ***
## speciesHisp                 -0.246588  0.011127 816.000000 -22.161 < 2e-16 ***
## speciesHype                 -0.109633  0.017723 816.000000 -6.186 9.75e-10 ***
## speciesPhpr                 -0.054832  0.010547 816.000000 -5.199 2.54e-07 ***
## speciesPoco                 -0.082002  0.017606 816.000000 -4.658 3.73e-06 ***
## speciesPopr                 -0.248610  0.010203 816.000000 -24.368 < 2e-16 ***
## speciesPore                 -0.046105  0.013012 816.000000 -3.543 0.000418 ***
## speciesRusp                 -0.172216  0.017181 816.000000 -10.024 < 2e-16 ***
## speciesSoca                 0.230129  0.010169 816.000000  22.630 < 2e-16 ***
## speciesSogr                 0.123923  0.048964 816.000000   2.531 0.011564 *
## speciesSora                 0.173318  0.035168 816.000000   4.928 1.00e-06 ***
## speciesSypi                 0.289872  0.035383 816.000000   8.192 9.86e-16 ***
## speciesTaof                 -0.451748  0.020315 816.000000 -22.237 < 2e-16 ***
## speciesTrsp                 -0.117081  0.014949 816.000000 -7.832 1.49e-14 ***
## factor(year_factor)2        -0.123848  0.008143 816.000000 -15.210 < 2e-16 ***
## factor(year_factor)3        -0.123874  0.008310 816.000000 -14.906 < 2e-16 ***
## factor(year_factor)4        -0.134431  0.008450 816.000000 -15.909 < 2e-16 ***
## factor(year_factor)5        -0.096438  0.008651 816.000000 -11.148 < 2e-16 ***
## factor(year_factor)6        -0.086017  0.008330 816.000000 -10.327 < 2e-16 ***
## factor(year_factor)7        -0.094345  0.009449 816.000000 -9.985 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

##
## Correlation matrix not shown by default, as p = 29 > 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(mod7au)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state                      0.0036 0.00356     1    816   1.5527 0.2131
## species                     23.6339 1.12542    21    816 490.7854 <2e-16 ***
## factor(year_factor)        0.7373 0.12289     6    816  53.5895 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

UMBS Plot-level Mixed Effects Models

```

mod1pu <- lmer(julian_min ~ state + (1 | plot), umbs_sd_plot, REML = FALSE)
mod2pu <- lmer(julian_min ~ insecticide + (1 | plot), umbs_sd_plot, REML = FALSE)
mod3pu <- lmer(julian_min ~ insecticide + state + (1 | plot), umbs_sd_plot, REML = FALSE)
mod4pu <- lmer(julian_min ~ insecticide * state + (1 | plot), umbs_sd_plot, REML = FALSE)
mod5pu <- lmer(julian_min ~ state + year_factor + (1 | plot), umbs_sd_plot, REML = FALSE)
mod6pu <- lmer(julian_min ~ state + year_factor + insecticide + (1 | plot), umbs_sd_plot,
    REML = FALSE)
mod7pu <- lmer(julian_min ~ state * year_factor + (1 | plot), umbs_sd_plot, REML = FALSE)
mod8pu <- lmer(julian_min ~ state * year_factor + insecticide + (1 | plot), umbs_sd_plot,
    REML = FALSE)
mod9pu <- lmer(julian_min ~ state * insecticide + year_factor + (1 | plot), umbs_sd_plot,
    REML = FALSE)
mod10pu <- lmer(julian_min ~ state + insecticide * year_factor + (1 | plot), umbs_sd_plot,
    REML = FALSE)
mod11pu <- lmer(julian_min ~ state * year_factor * insecticide + (1 | plot), umbs_sd_plot,
    REML = FALSE)
AICctab(mod1pu, mod2pu, mod3pu, mod4pu, mod5pu, mod6pu, mod7pu, mod8pu, mod9pu, mod10pu,
    mod11pu, weights = T) # model 11p and 10p the same

```

```

##          dAICc df weight
## mod5pu    0.0   8  0.6144
## mod6pu    2.3   9  0.1908
## mod7pu    3.6  12  0.1026
## mod9pu    4.7  10  0.0600
## mod8pu    6.1  13  0.0291
## mod10pu   10.9 13  0.0027
## mod11pu   15.1 22 <0.001
## mod1pu    19.9  4  <0.001
## mod2pu    20.2  4  <0.001
## mod3pu    22.1  5  <0.001
## mod4pu    24.2  6  <0.001

```

```
anova(mod5pu, mod6pu) #5pu just barely better, going with 5pu because it's simpler though
```

```

## Data: umbs_sd_plot
## Models:
## mod5pu: julian_min ~ state + year_factor + (1 | plot)
## mod6pu: julian_min ~ state + year_factor + insecticide + (1 | plot)
##      npar   AIC   BIC logLik deviance Chisq Df Pr(>Chisq)
## mod5pu     8 787.59 809.89 -385.8   771.59
## mod6pu     9 789.59 814.68 -385.8   771.59 1e-04  1      0.9909

```

```
summary(mod5pu)
```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: julian_min ~ state + year_factor + (1 | plot)
##   Data: umbs_sd_plot
##
##      AIC      BIC   logLik deviance df.resid

```

```

##      787.6     809.9    -385.8     771.6      112
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.39707 -0.61543  0.03155  0.61564  2.35330
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 6.536   2.557
## Residual            31.490   5.612
## Number of obs: 120, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 187.3833    1.4557 75.9400 128.719 < 2e-16 ***
## stateambient 0.8167    1.4625 24.0000  0.558 0.581754
## year_factor3 -2.8750    1.6199 96.0000 -1.775 0.079108 .
## year_factor4 -6.2083    1.6199 96.0000 -3.832 0.000227 ***
## year_factor5  2.6667    1.6199 96.0000  1.646 0.103003
## year_factor6 -2.4167    1.6199 96.0000 -1.492 0.139024
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn yr_fc3 yr_fc4 yr_fc5
## stateambint -0.502
## year_factr3 -0.556  0.000
## year_factr4 -0.556  0.000  0.500
## year_factr5 -0.556  0.000  0.500  0.500
## year_factr6 -0.556  0.000  0.500  0.500  0.500

emmeans(mod5pu, list(pairwise ~ state + year_factor), adjust = "tukey")

## $`emmeans of state, year_factor`
##   state year_factor emmean   SE   df lower.CL upper.CL
##   warmed 2           187 1.5 82.1     184    190
##   ambient 2          188 1.5 82.1     185    191
##   warmed 3          185 1.5 82.1     182    188
##   ambient 3          185 1.5 82.1     182    188
##   warmed 4          181 1.5 82.1     178    184
##   ambient 4          182 1.5 82.1     179    185
##   warmed 5          190 1.5 82.1     187    193
##   ambient 5          191 1.5 82.1     188    194
##   warmed 6          185 1.5 82.1     182    188
##   ambient 6          186 1.5 82.1     183    189
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of state, year_factor`
##   1             estimate   SE   df t.ratio p.value
##   warmed 2 - ambient 2    -0.817 1.53 26.2 -0.535  0.9999
##   warmed 2 - warmed 3     2.875 1.65 100.2  1.737  0.7715
##   warmed 2 - ambient 3    2.058 2.25  93.2  0.914  0.9957

```

```

## warmed 2 - warmed 4      6.208 1.65 100.2  3.752  0.0105
## warmed 2 - ambient 4    5.392 2.25  93.2   2.394  0.3414
## warmed 2 - warmed 5     -2.667 1.65 100.2  -1.611  0.8395
## warmed 2 - ambient 5    -3.483 2.25  93.2  -1.547  0.8694
## warmed 2 - warmed 6     2.417 1.65 100.2   1.460  0.9042
## warmed 2 - ambient 6    1.600 2.25  93.2   0.710  0.9994
## ambient 2 - warmed 3    3.692 2.25  93.2   1.639  0.8253
## ambient 2 - ambient 3   2.875 1.65 100.2   1.737  0.7715
## ambient 2 - warmed 4    7.025 2.25  93.2   3.119  0.0695
## ambient 2 - ambient 4   6.208 1.65 100.2   3.752  0.0105
## ambient 2 - warmed 5    -1.850 2.25  93.2  -0.821  0.9981
## ambient 2 - ambient 5   -2.667 1.65 100.2  -1.611  0.8395
## ambient 2 - warmed 6    3.233 2.25  93.2   1.436  0.9126
## ambient 2 - ambient 6   2.417 1.65 100.2   1.460  0.9042
## warmed 3 - ambient 3    -0.817 1.53  26.2  -0.535  0.9999
## warmed 3 - warmed 4     3.333 1.65 100.2   2.014  0.5912
## warmed 3 - ambient 4    2.517 2.25  93.2   1.117  0.9817
## warmed 3 - warmed 5     -5.542 1.65 100.2  -3.349  0.0363
## warmed 3 - ambient 5    -6.358 2.25  93.2  -2.823  0.1439
## warmed 3 - warmed 6     -0.458 1.65 100.2  -0.277  1.0000
## warmed 3 - ambient 6    -1.275 2.25  93.2  -0.566  0.9999
## ambient 3 - warmed 4    4.150 2.25  93.2   1.843  0.7065
## ambient 3 - ambient 4   3.333 1.65 100.2   2.014  0.5912
## ambient 3 - warmed 5    -4.725 2.25  93.2  -2.098  0.5336
## ambient 3 - ambient 5   -5.542 1.65 100.2  -3.349  0.0363
## ambient 3 - warmed 6    0.358 2.25  93.2   0.159  1.0000
## ambient 3 - ambient 6   -0.458 1.65 100.2  -0.277  1.0000
## warmed 4 - ambient 4    -0.817 1.53  26.2  -0.535  0.9999
## warmed 4 - warmed 5     -8.875 1.65 100.2  -5.363  <.0001
## warmed 4 - ambient 5    -9.692 2.25  93.2  -4.303  0.0016
## warmed 4 - warmed 6     -3.792 1.65 100.2  -2.291  0.4038
## warmed 4 - ambient 6    -4.608 2.25  93.2  -2.046  0.5693
## ambient 4 - warmed 5    -8.058 2.25  93.2  -3.578  0.0187
## ambient 4 - ambient 5   -8.875 1.65 100.2  -5.363  <.0001
## ambient 4 - warmed 6    -2.975 2.25  93.2  -1.321  0.9463
## ambient 4 - ambient 6   -3.792 1.65 100.2  -2.291  0.4038
## warmed 5 - ambient 5    -0.817 1.53  26.2  -0.535  0.9999
## warmed 5 - warmed 6     5.083 1.65 100.2   3.072  0.0777
## warmed 5 - ambient 6    4.267 2.25  93.2   1.895  0.6726
## ambient 5 - warmed 6    5.900 2.25  93.2   2.620  0.2234
## ambient 5 - ambient 6   5.083 1.65 100.2   3.072  0.0777
## warmed 6 - ambient 6    -0.817 1.53  26.2  -0.535  0.9999
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 10 estimates

# including native vs. exotic
umbs_sd_plot_origin <- within(umbs_sd_plot_origin, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
mod12pu <- lmer(log(julian_min) ~ state * origin + (1 + year_factor | plot), umbs_sd_plot_origin,
  REML = FALSE)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00645698 (tol = 0.002, component 1)

```

```

mod13pu <- lmer(log(julian_min) ~ state + origin + (1 + year_factor | plot), umbs_sd_plot_origin,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -6.7e-02

mod14pu <- lmer(log(julian_min) ~ state + origin + year_factor + (1 | plot), umbs_sd_plot_origin,
  REML = FALSE)
anova(mod12pu, mod13pu) # go with model 13pu

## Data: umbs_sd_plot_origin
## Models:
## mod13pu: log(julian_min) ~ state + origin + (1 + year_factor | plot)
## mod12pu: log(julian_min) ~ state * origin + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod13pu     8 -560.91 -533.30 288.45   -576.91
## mod12pu    10 -560.82 -526.31 290.41   -580.82 3.9164  2      0.1411

anova(mod13pu, mod14pu) # mod 14pu

## Data: umbs_sd_plot_origin
## Models:
## mod14pu: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## mod13pu: log(julian_min) ~ state + origin + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod14pu     7 -561.62 -537.47 287.81   -575.62
## mod13pu     8 -560.91 -533.30 288.45   -576.91 1.2848  1      0.257

summary(mod14pu)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + origin + year_factor + (1 | plot)
## Data: umbs_sd_plot_origin
##
##          AIC      BIC      logLik deviance df.resid
## -561.6   -537.5    287.8    -575.6       226
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max
## -3.4958 -0.6412 -0.0811  0.7023  3.3251
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0003208 0.01791
## Residual           0.0046986 0.06855
## Number of obs: 233, groups: plot, 24
##
## Fixed effects:
```

```

##             Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) 5.167399  0.015657 174.152793 330.049 <2e-16 ***
## statewarmed -0.003980  0.011631  23.706415 -0.342   0.735
## originBoth   0.018679  0.020883 232.702099  0.894   0.372
## originExotic 0.086444  0.009319 213.578718  9.276 <2e-16 ***
## year_factor   0.000469  0.003149 211.921877  0.149   0.882
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttwrm orgnBt orgnEx
## statewarmed -0.372
## originBoth   -0.179  0.011
## originExotic -0.291 -0.017  0.235
## year_factor   -0.788  0.013  0.044 -0.036

anova(mod14pu)

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.00055 0.000550     1  23.706  0.1171 0.7352
## origin     0.41245 0.206226     2 225.309 43.8910 <2e-16 ***
## year_factor 0.00010 0.000104     1 211.922  0.0222 0.8817
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod14pu, list(pairwise ~ state + origin + year_factor), adjust = "tukey")

## $`emmeans of state, origin, year_factor`
##    state origin year_factor emmean       SE      df lower.CL upper.CL
##    ambient Native      3.936  5.169 0.010006  48.02    5.149   5.189
##    warmed  Native      3.936  5.165 0.010196  50.54    5.145   5.186
##    ambient Both       3.936  5.188 0.021400 198.82    5.146   5.230
##    warmed  Both       3.936  5.184 0.021629 197.81    5.141   5.227
##    ambient Exotic    3.936  5.256 0.009660  42.42    5.236   5.275
##    warmed  Exotic    3.936  5.252 0.009657  42.08    5.232   5.271
##
## 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, year_factor` 
##   estimate
## 1
##    ambient Native 3.93562231759657 - warmed Native 3.93562231759657  0.00398
##    ambient Native 3.93562231759657 - ambient Both 3.93562231759657 -0.01868
##    ambient Native 3.93562231759657 - warmed Both 3.93562231759657 -0.01470
##    ambient Native 3.93562231759657 - ambient Exotic 3.93562231759657 -0.08644
##    ambient Native 3.93562231759657 - warmed Exotic 3.93562231759657 -0.08246
##    warmed Native 3.93562231759657 - ambient Both 3.93562231759657 -0.02266
##    warmed Native 3.93562231759657 - warmed Both 3.93562231759657 -0.01868
##    warmed Native 3.93562231759657 - ambient Exotic 3.93562231759657 -0.09042
##    warmed Native 3.93562231759657 - warmed Exotic 3.93562231759657 -0.08644
##    ambient Both 3.93562231759657 - warmed Both 3.93562231759657  0.00398

```

```

## ambient Both 3.93562231759657 - ambient Exotic 3.93562231759657 -0.06777
## ambient Both 3.93562231759657 - warmed Exotic 3.93562231759657 -0.06379
## warmed Both 3.93562231759657 - ambient Exotic 3.93562231759657 -0.07175
## warmed Both 3.93562231759657 - warmed Exotic 3.93562231759657 -0.06777
## ambient Exotic 3.93562231759657 - warmed Exotic 3.93562231759657 0.00398
##      SE   df t.ratio p.value
## 0.0122 25.9  0.326  0.9994
## 0.0213 237.3 -0.878  0.9516
## 0.0247 170.1 -0.596  0.9912
## 0.0094 216.5 -9.199 <.0001
## 0.0153 64.3 -5.401 <.0001
## 0.0244 171.5 -0.928  0.9387
## 0.0213 237.3 -0.878  0.9516
## 0.0155 67.3 -5.825 <.0001
## 0.0094 216.5 -9.199 <.0001
## 0.0122 25.9  0.326  0.9994
## 0.0212 238.1 -3.196  0.0195
## 0.0243 166.2 -2.630  0.0959
## 0.0247 166.0 -2.909  0.0466
## 0.0212 238.1 -3.196  0.0195
## 0.0122 25.9  0.326  0.9994
##
## 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
umbssdplot_growthhabit <- within(umbssdplot_growthhabit, growth_habit <- relevel(factor(growth_habit,
  ref = "Forb")) # releveling so forb is the reference
mod15pu <- lmer(log(julian_min) ~ state * growth_habit + (1 + year_factor | plot),
  umbssdplot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod16pu <- lmer(log(julian_min) ~ state + growth_habit + (1 + year_factor | plot),
  umbssdplot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod17pu <- lmer(log(julian_min) ~ state + growth_habit + year_factor + (1 | plot),
  umbssdplot_growthhabit, REML = FALSE)
anova(mod15pu, mod16pu) # go with model 16pu

## Data: umbssdplot_growthhabit
## Models:
## mod16pu: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
## mod15pu: log(julian_min) ~ state * growth_habit + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod16pu    8 -355.85 -327.75 185.93  -371.85
## mod15pu   10 -354.67 -319.53 187.33  -374.67 2.811   2     0.2452

```

```

anova(mod16pu, mod17pu) # mod 17pu

## Data: umbs_sd_plot_growthhabit
## Models:
## mod17pu: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
## mod16pu: log(julian_min) ~ state + growth_habit + (1 + year_factor | plot)
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## mod17pu     7 -356.19 -331.60 185.09   -370.19
## mod16pu     8 -355.85 -327.75 185.93   -371.85 1.6653  1      0.1969

summary(mod17pu)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(julian_min) ~ state + growth_habit + year_factor + (1 | plot)
## Data: umbs_sd_plot_growthhabit
##
##          AIC      BIC      logLik deviance df.resid
## -356.2    -331.6    185.1    -370.2      241
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.0682 -0.9016  0.2706  0.7563  2.6865
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0008765 0.02961
## Residual           0.0124843 0.11173
## Number of obs: 248, groups: plot, 24
##
## Fixed effects:
##                   Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)      5.271908  0.025405 181.439771 207.517 <2e-16 ***
## statewarmed     -0.004444  0.018670  23.023443 -0.238  0.8140  
## growth_habit    -0.066348  0.038721 247.308775 -1.713  0.0879 .  
## growth_habitGraminoid -0.157582  0.014489 223.325999 -10.876 <2e-16 ***
## year_factor     -0.009070  0.005067 223.719202 -1.790  0.0748 .  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttwrm grwth_ grwt_G
## statewarmed -0.363
## growth_habit -0.196 -0.028
## grwth_hbtGr -0.298  0.000  0.190
## year_factor -0.803 -0.006  0.123  0.012

anova(mod17pu)

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

```

```

## state      0.00071 0.00071      1 23.023 0.0567 0.81397
## growth_habit 1.47825 0.73913      2 236.227 59.2044 < 2e-16 ***
## year_factor  0.04000 0.04000      1 223.719 3.2040 0.07481 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod17pu, list(pairwise ~ state + growth_habit + year_factor), adjust = "tukey")

## $`emmeans of state, growth_habit, year_factor`
##   state   growth_habit year_factor emmean     SE    df lower.CL upper.CL
##   ambient   Forb          Forb    3.98  5.24 45.1    5.20  5.27
##   warmed   Forb          Forb    3.98  5.23 45.3    5.20  5.26
##   ambient           Forb    3.98  5.17 40.2 221.5    5.09  5.25
##   warmed            Forb    3.98  5.17 39.7 218.4    5.09  5.24
##   ambient  Graminoid    Graminoid 3.98  5.08 44.5    5.05  5.11
##   warmed  Graminoid    Graminoid 3.98  5.07 44.6    5.04  5.11
##
## 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, year_factor`
## 1
##   ambient Forb 3.97983870967742 - warmed Forb 3.97983870967742
##   ambient Forb 3.97983870967742 - ambient   3.97983870967742
##   ambient Forb 3.97983870967742 - warmed   3.97983870967742
##   ambient Forb 3.97983870967742 - ambient Graminoid 3.97983870967742
##   ambient Forb 3.97983870967742 - warmed Graminoid 3.97983870967742
##   warmed Forb 3.97983870967742 - ambient   3.97983870967742
##   warmed Forb 3.97983870967742 - warmed   3.97983870967742
##   warmed Forb 3.97983870967742 - ambient Graminoid 3.97983870967742
##   warmed Forb 3.97983870967742 - warmed Graminoid 3.97983870967742
##   ambient   Forb 3.97983870967742 - warmed   3.97983870967742
##   ambient   Forb 3.97983870967742 - ambient Graminoid 3.97983870967742
##   ambient   Forb 3.97983870967742 - warmed Graminoid 3.97983870967742
##   warmed   Forb 3.97983870967742 - ambient Graminoid 3.97983870967742
##   warmed   Forb 3.97983870967742 - warmed Graminoid 3.97983870967742
##   ambient   Graminoid 3.97983870967742 - warmed Graminoid 3.97983870967742
##   estimate     SE    df t.ratio p.value
##   0.00444 0.0196 26.3  0.227  0.9999
##   0.06635 0.0395 253.2 1.678  0.5476
##   0.07079 0.0437 187.7 1.621  0.5856
##   0.15758 0.0146 226.9 10.806 <.0001
##   0.16203 0.0244 64.8  6.636 <.0001
##   0.06190 0.0446 194.7 1.389  0.7338
##   0.06635 0.0395 253.2 1.678  0.5476
##   0.15314 0.0244 64.8  6.271 <.0001
##   0.15758 0.0146 226.9 10.806 <.0001
##   0.00444 0.0196 26.3  0.227  0.9999
##   0.09123 0.0395 253.2 2.309  0.1941
##   0.09568 0.0445 194.3 2.148  0.2674
##   0.08679 0.0436 187.2 1.989  0.3526
##   0.09123 0.0395 253.2 2.309  0.1941
##   0.00444 0.0196 26.3  0.227  0.9999

```

```
##  
## 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
```