

# warmXtrophic Project: Flowering Phenology Analysis

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## Load in packages & data

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

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

# Set working directory
Sys.setenv("L1DIR")
```

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

```
L1_dir <- Sys.setenv("L1DIR")
L2_dir <- Sys.setenv("L2DIR")
list.files(L1_dir)
```

```
## [1] "ANPP"           "climate_data"    "CN"
## [4] "greenup"         "herbivory"       "HOBO_data"
## [7] "PAR"             "phenology"       "plant_composition"
## [10] "SLA"
```

```
# 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 cleaned phenology data from L1
phen_data <- read.csv(file.path(L1_dir, "phenology/final_flwr_sd_L1.csv"))
phen_data$X <- NULL # get rid of 'X' column that shows up
View(phen_data) # take a look at the data to see if looks good

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

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

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

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

```
# [1] 'warmed' 'ambient'

# Flowering data species level data for flowering
flwr_spp <- read.csv(file.path(L1_dir, "phenology/final_flwr_species_L1.csv"))
flwr_spp$X <- NULL

# plot level data for flowering
flwr_plot <- read_csv(file.path(L1_dir, "phenology/final_flwr_plot_L1.csv"))
```

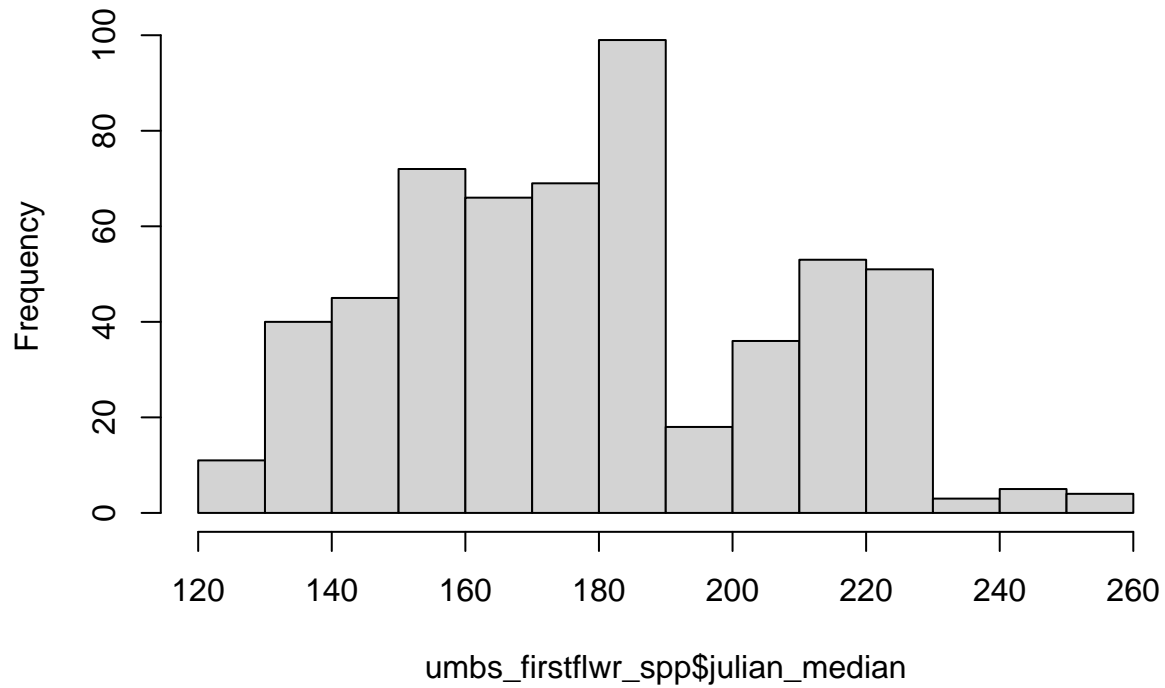
```
## Warning: Missing column names filled in: 'X1' [1]
```

```
flwr_plot$X1 <- NULL
```

## Data exploration

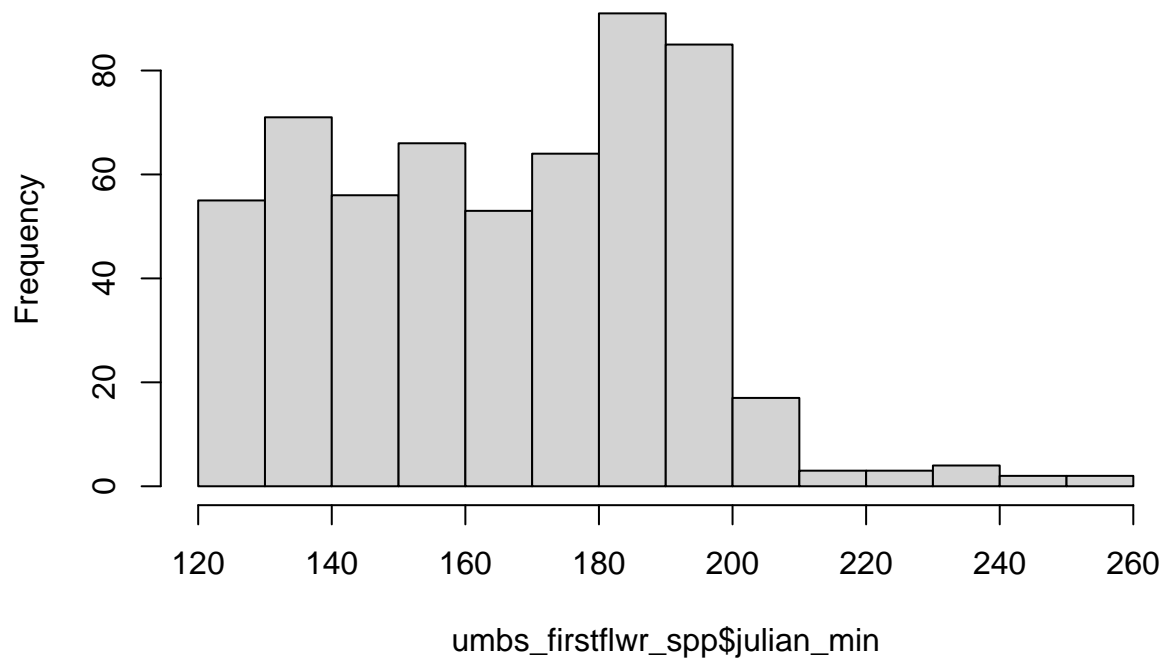
```
## UMBS ##
umbs_firstflwr_spp <- subset(flwr_spp, site == "umbs") # pull out umbs only data
hist(umbs_firstflwr_spp$julian_median)
```

**Histogram of umbs\_firstflwr\_spp\$julian\_median**



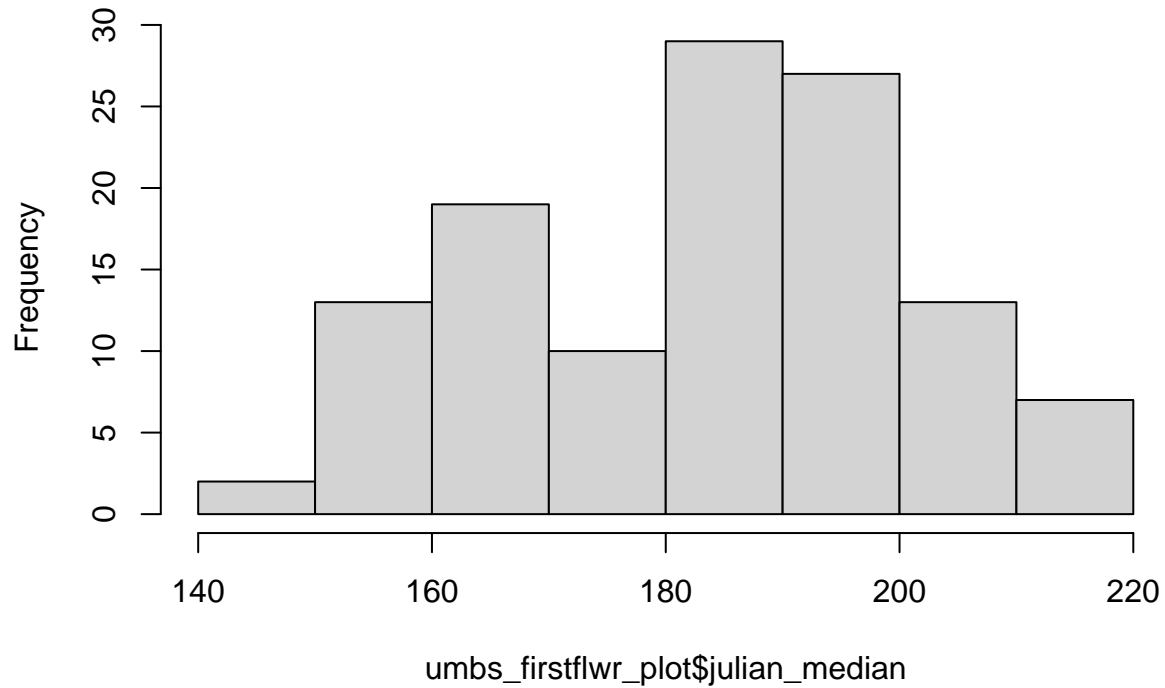
```
hist(umbs_firstflwr_spp$julian_min)
```

**Histogram of umbs\_firstflwr\_spp\$julian\_min**



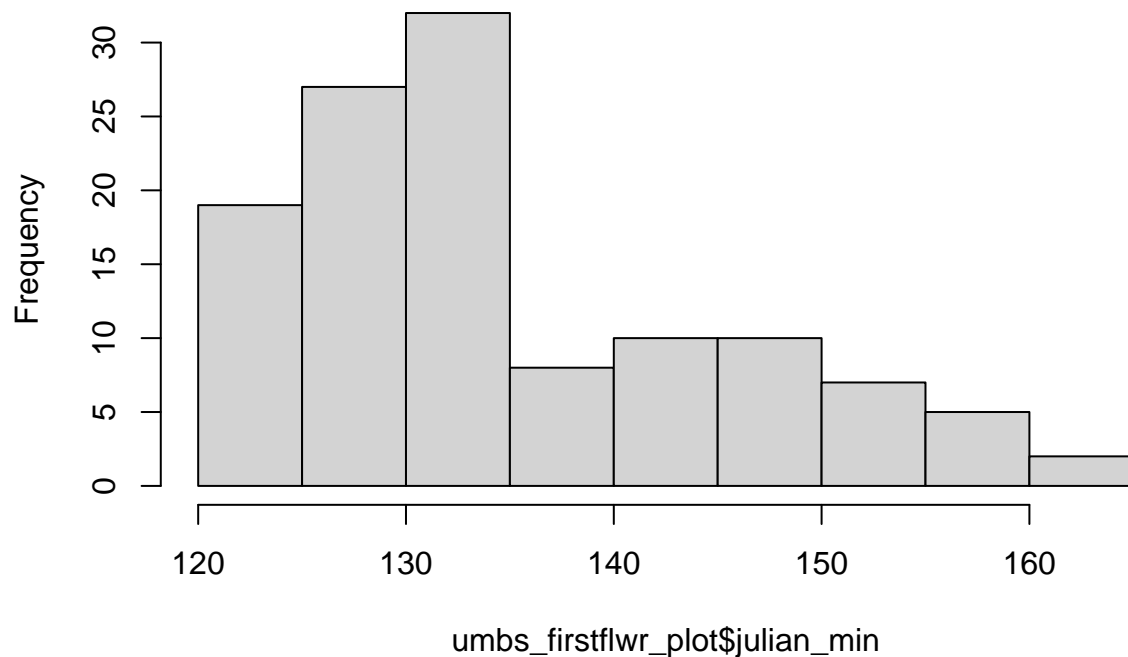
```
umbs_firstflwr_plot <- subset(flwr_plot, site == "umbs") # pull out umbs only data
hist(umbs_firstflwr_plot$julian_median)
```

**Histogram of umbs\_firstflwr\_plot\$julian\_median**



```
hist(umbs_firstflwr_plot$julian_min)
```

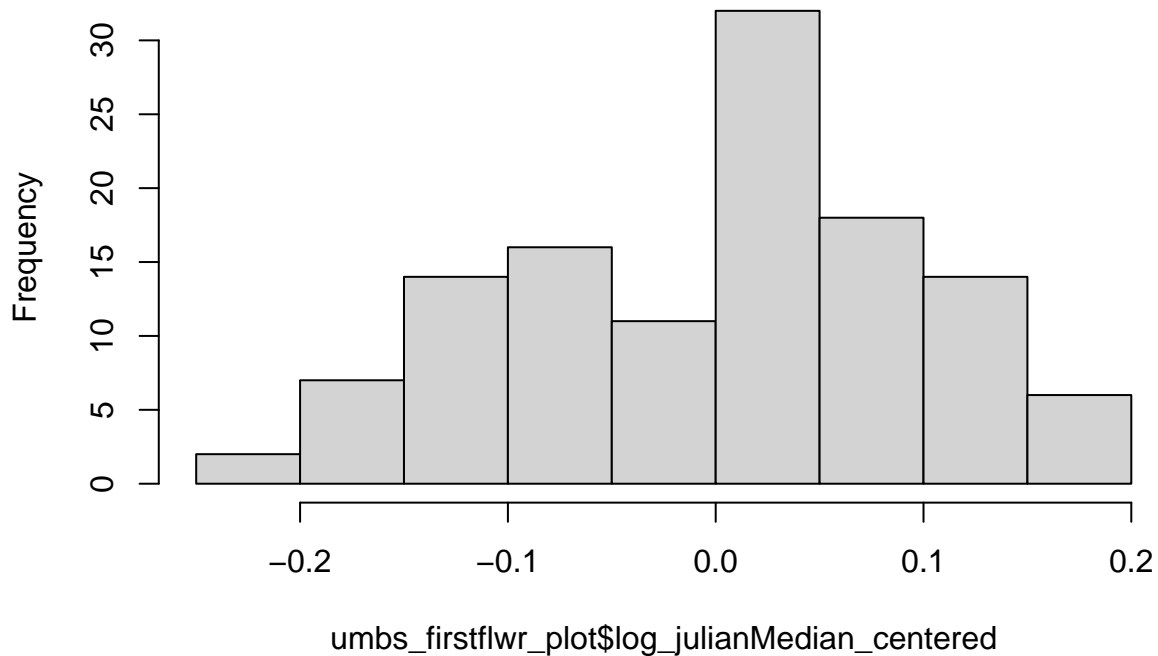
**Histogram of umbs\_firstflwr\_plot\$julian\_min**



## Centering and transforming data

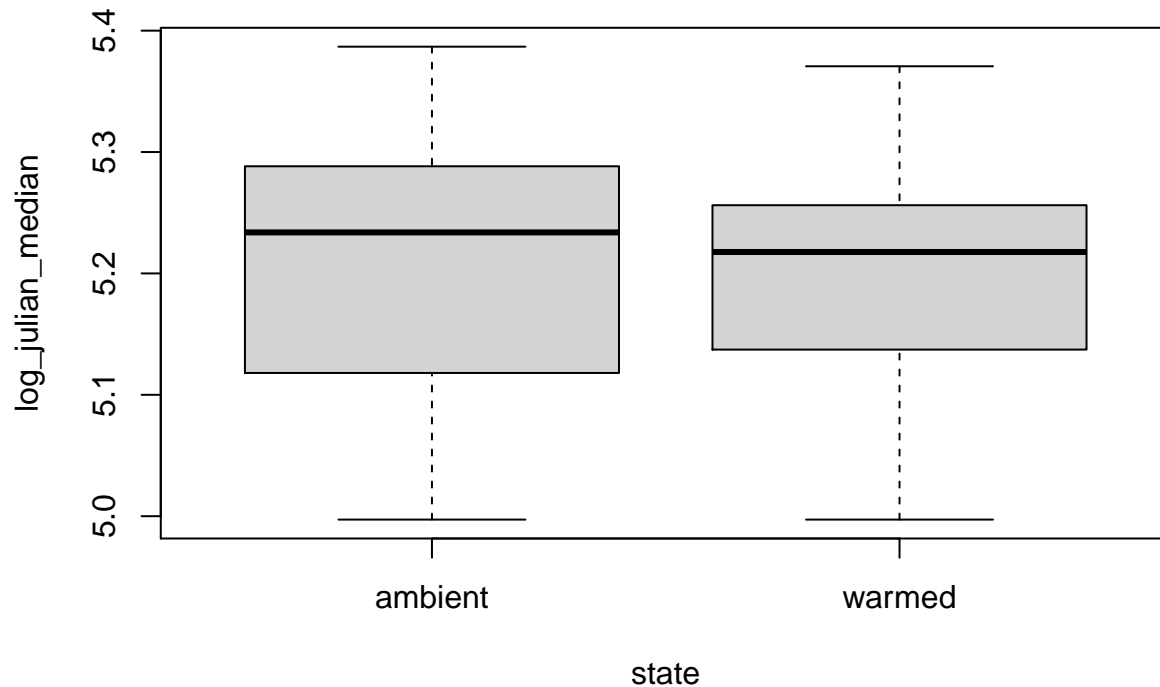
```
umbs_firstflwr_plot$log_julian_median <- log(umbs_firstflwr_plot$julian_median)
umbs_firstflwr_plot$log_julianMedian_centered = umbs_firstflwr_plot$log_julian_median -
  mean(umbs_firstflwr_plot$log_julian_median)
hist(umbs_firstflwr_plot$log_julianMedian_centered)
```

### Histogram of umbs\_firstflwr\_plot\$log\_julianMedian\_centered



## Plot key relationships

```
# Convert all columns to factor first
umbs_firstflwr_plot <- as.data.frame(unclass(umbs_firstflwr_plot), stringsAsFactors = TRUE)
plot(log_julian_median ~ state, data = umbs_firstflwr_plot)
```



## Fit models

```
m0 <- lmer(log_julian_median ~ 1, data = umbs_firstflwr_plot)
```

```
## Error: No random effects terms specified in formula
```

```
m1 <- lmer(log_julian_median ~ state, data = umbs_firstflwr_plot)
```

```
## Error: No random effects terms specified in formula
```

```
m2 <- lmer(log_julian_median ~ state + insecticide, data = umbs_firstflwr_plot)
```

```
## Error: No random effects terms specified in formula
```

```
m3 <- lmer(log_julian_median ~ state * insecticide, data = umbs_firstflwr_plot)
```

```
## Error: No random effects terms specified in formula
```

```
m4 <- lmer(log_julian_median ~ state * insecticide + (1 | species), data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'species' not found
```

```
m5 <- lmer(log_julian_median ~ state + insecticide + (1 | species), data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'species' not found
```

```
m6 <- lmer(log_julian_median ~ state * insecticide + (1 | species) + (1 | year_factor),  
  data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'species' not found
```

```
m7 <- lmer(log_julian_median ~ state + insecticide + (1 | species) + (1 | year_factor),  
  data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'species' not found
```

```
m8 <- lmer(log_julian_median ~ state + insecticide + origin + (1 | species) + (1 |  
  year_factor), data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'origin' not found
```

```
m9 <- lmer(log_julian_median ~ state + insecticide + origin + (1 | species) + (1 |  
  year_factor) + (1 | plot), data = umbs_firstflwr_plot)
```

```
## Error in eval(predvars, data, env): object 'origin' not found
```

## Compare models

```
# AICtab(m0,m1,m2,m3,m4,m5, weights=TRUE)
```

## Evaluate models using residuals