Phenology Analysis

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DATA INPUT: Cleaned phenology data csv from the shared Google drive
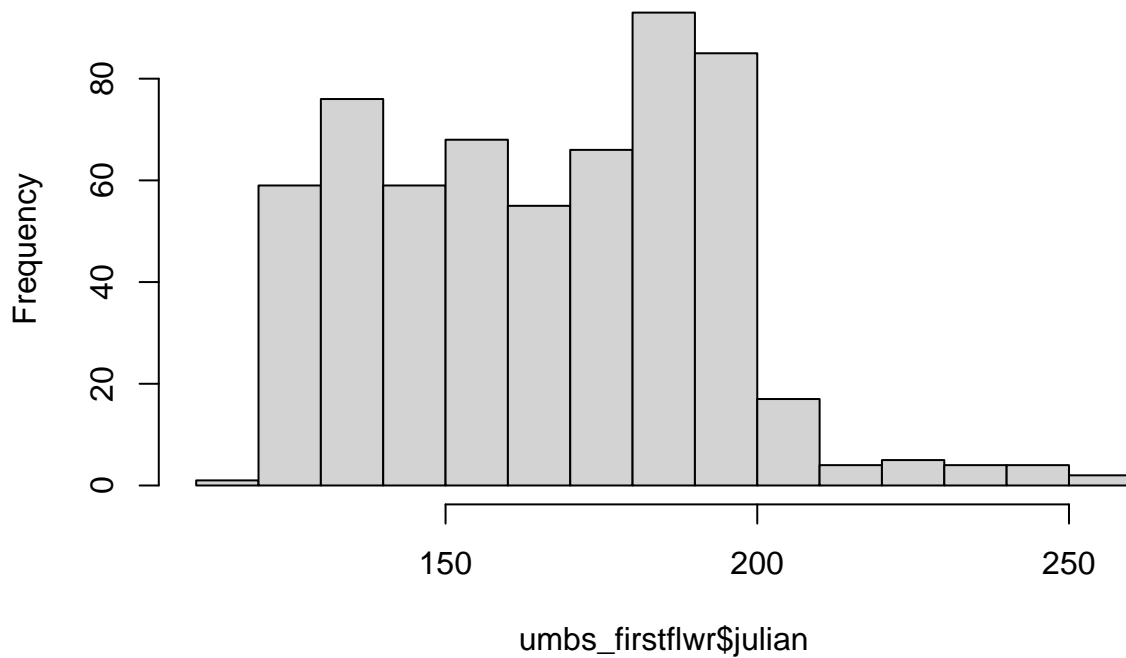DATA OUTPUT: Code and Rmd are in the scripts folder in Github
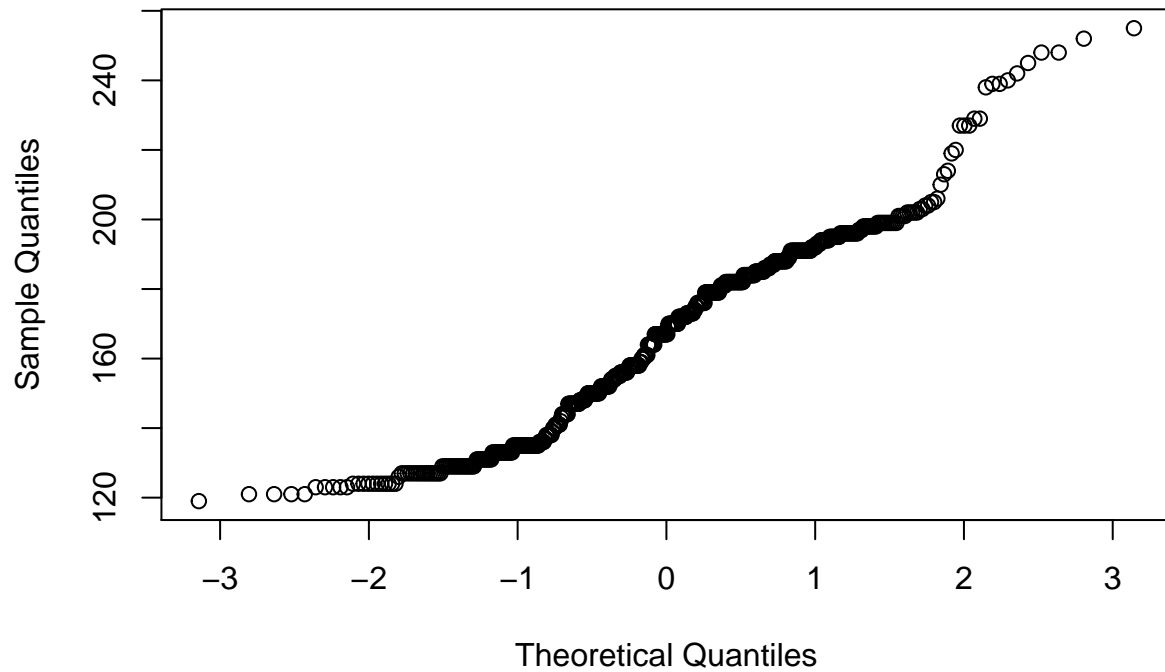PROJECT: warmXtrophic

UMBS Data

First Flower

```
umbs_firstflwr <- subset(FirstFlower_all, site == "umbs")  # pull out umbs only data

# first flower
hist(umbs_firstflwr$julian)  # poisson?
```

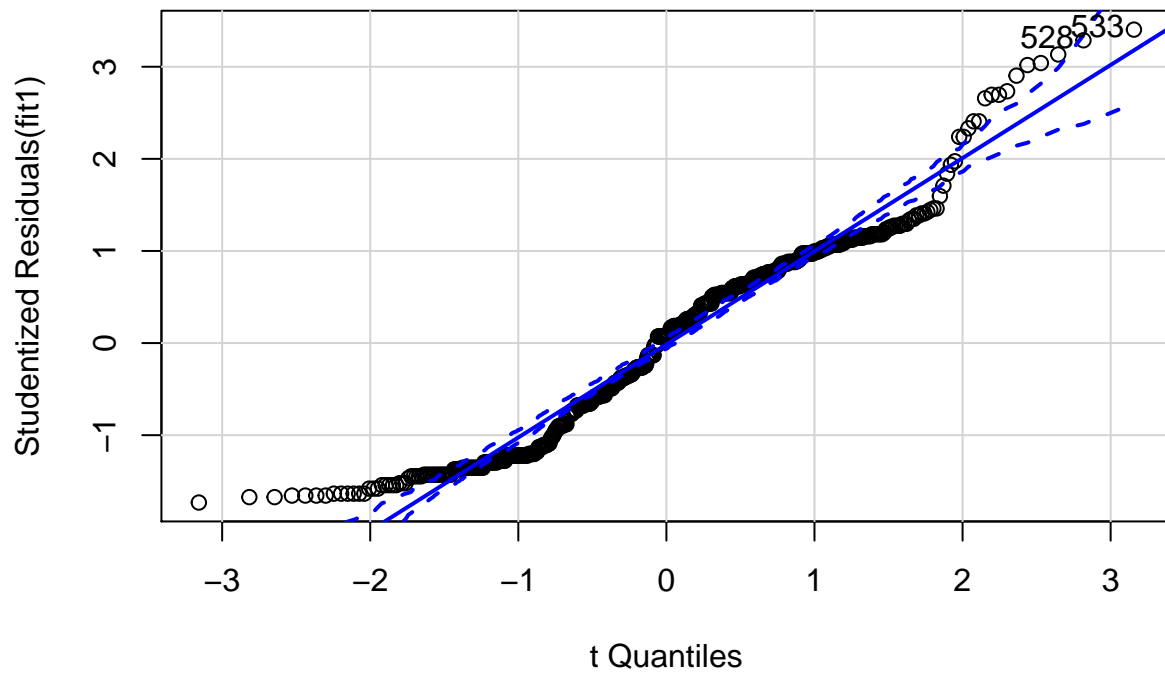## Histogram of umbs_firstflwr$julian

umbs_firstflwr$julian

```
qqnorm(umbs_firstflwr$julian)
```

Normal Q–Q Plot


```
fit1 <- lm(julian ~ state, data = umbs_firstflwr)
qqPlot(fit1)
```
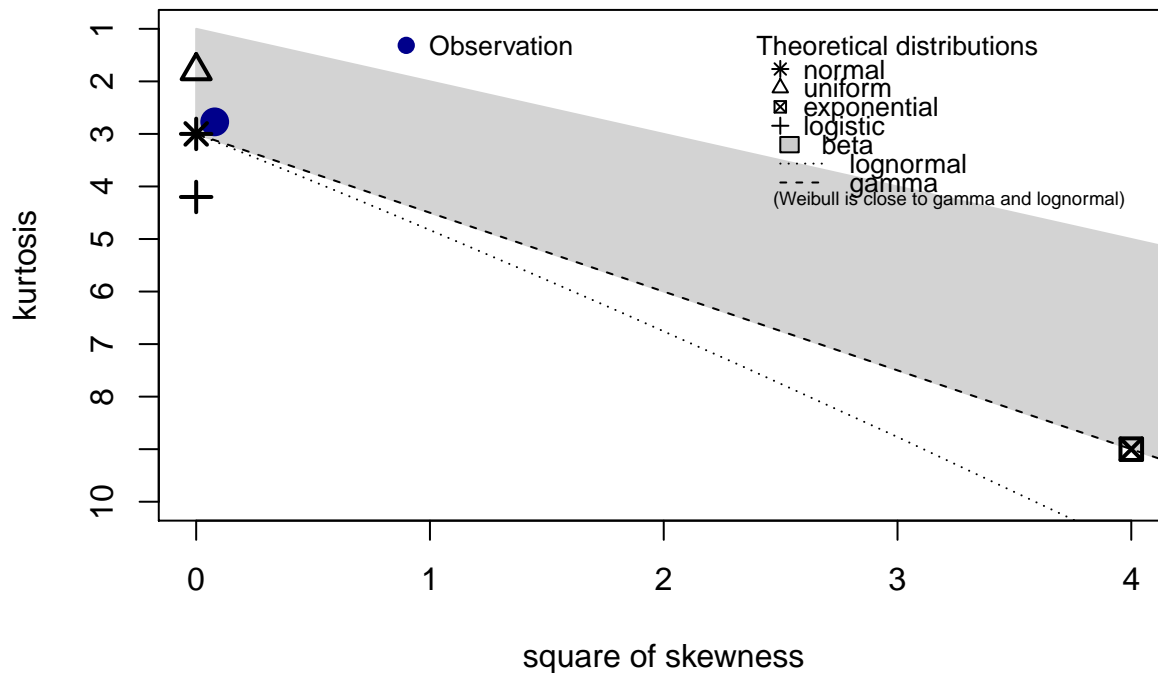


```
## [1] 528 533
```

```
shapiro.test(umbs_firstflwr$julian)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  umbs_firstflwr$julian
## W = 0.96131, p-value = 1.928e-11
```

```
descdist(umbs_firstflwr$julian, discrete = FALSE)  # uniform? normal?
```
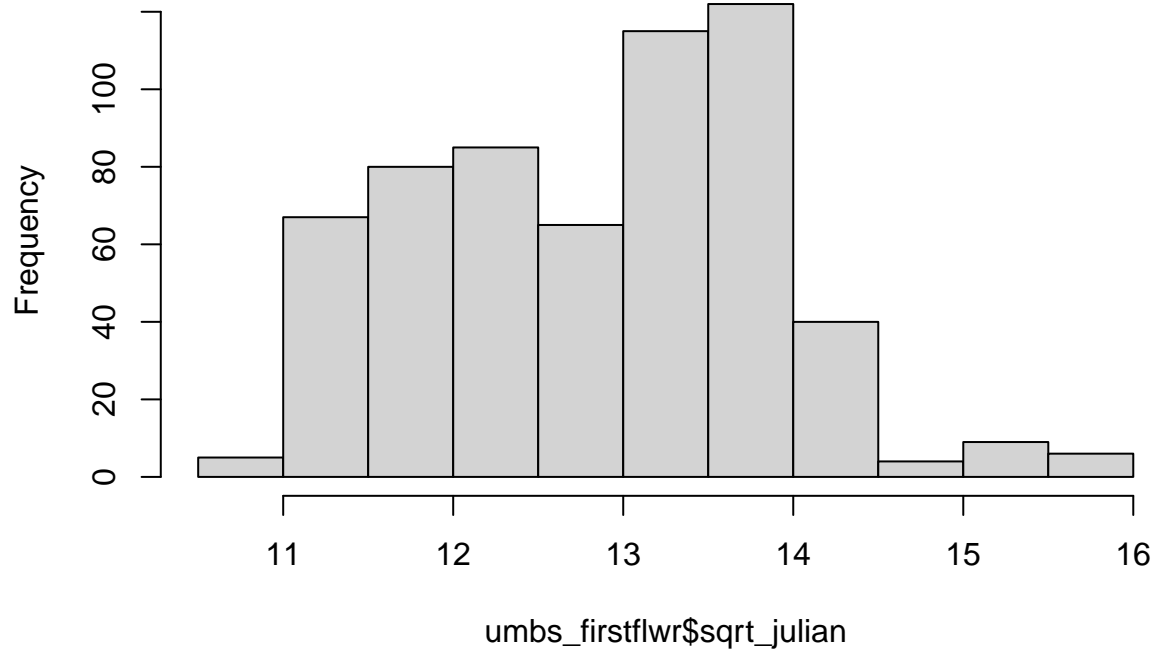
Cullen and Frey graph


```
## summary statistics
## ------
## min:  119    max:   255
## median:   167
## mean:  166.2709
## estimated sd:  26.70761
## estimated skewness:  0.281686
## estimated kurtosis:  2.770431
```

```
skewness(umbs_firstflwr$julian)
```

```
## [1] 0.2809789
```

```
umbs_firstflwr$sqrt_julian <- sqrt(umbs_firstflwr$julian)
hist(umbs_firstflwr$sqrt_julian)
```

Histogram of umbs_firstflwr$sqrt_julian
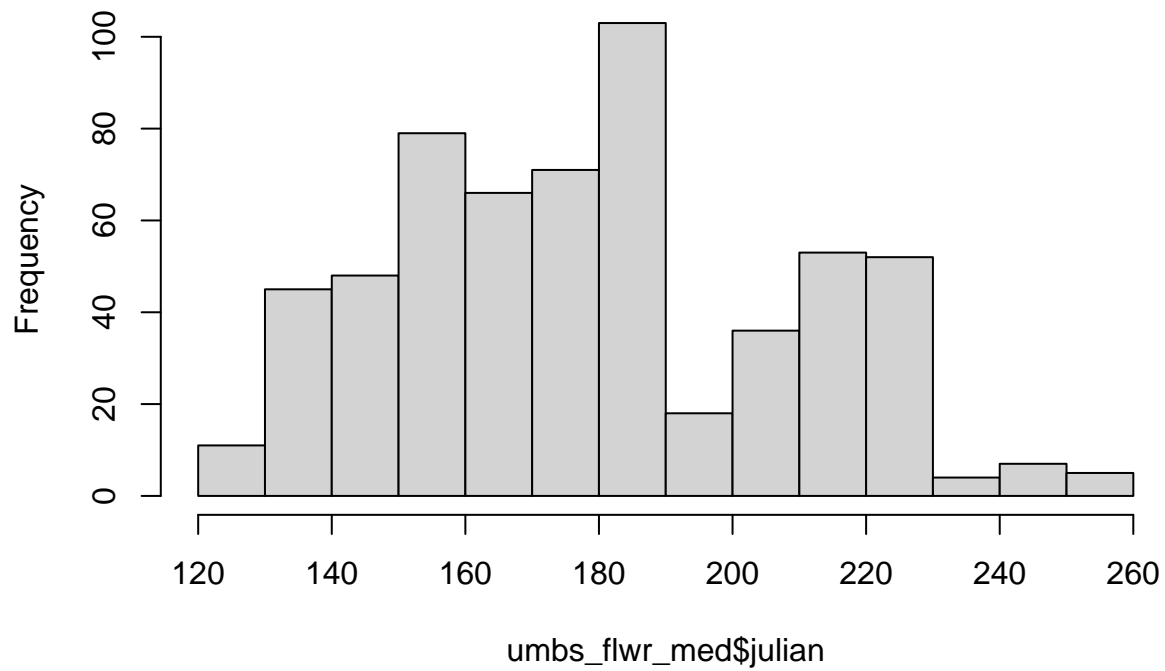

umbs_firstflwr$sqrt_julian

```
skewness(umbs_firstflwr$sqrt_julian, na.rm = TRUE)
```

```
## [1] 0.1021979
```

Median Flower

```
umbs_flwr_med <- subset(MedianFlwr_all, site == "umbs")  # pull out umbs only data

hist(umbs_flwr_med$julian)
```

Histogram of umbs_flwr_med$julian


```
qqnorm(umbs_flwr_med$julian)
```

Normal Q–Q Plot

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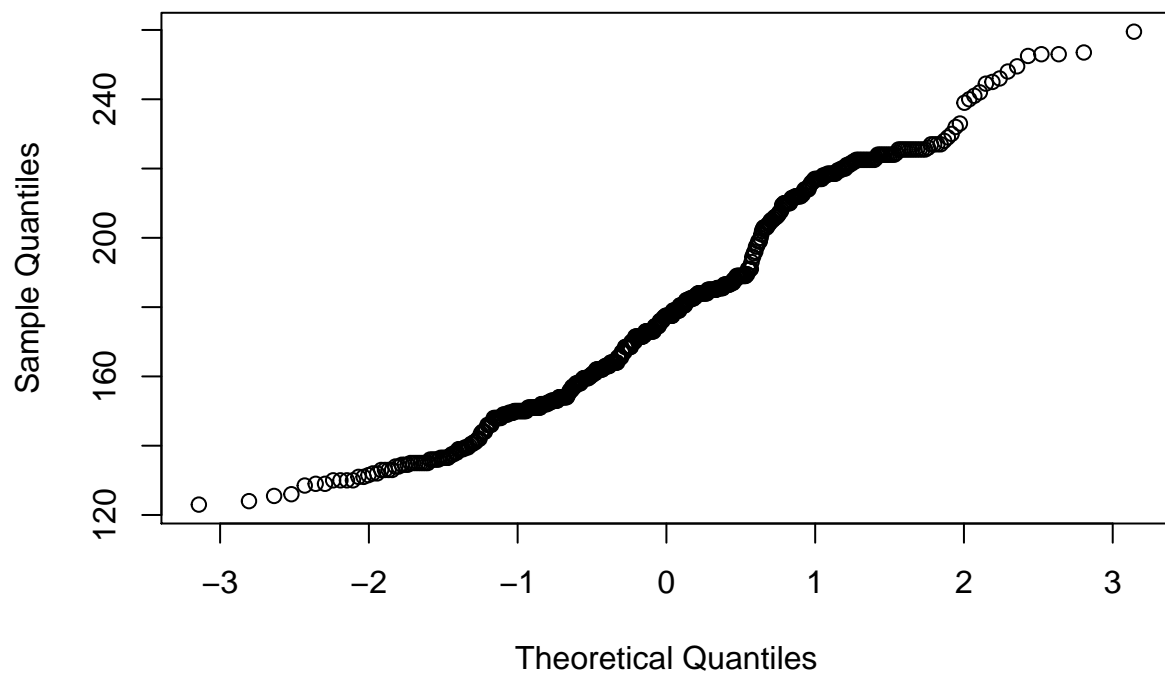
```
fit2 <- lm(julian ~ state, data = umbs_flwr_med)
qqPlot(fit2)
```



```
## [1] 528 533
```
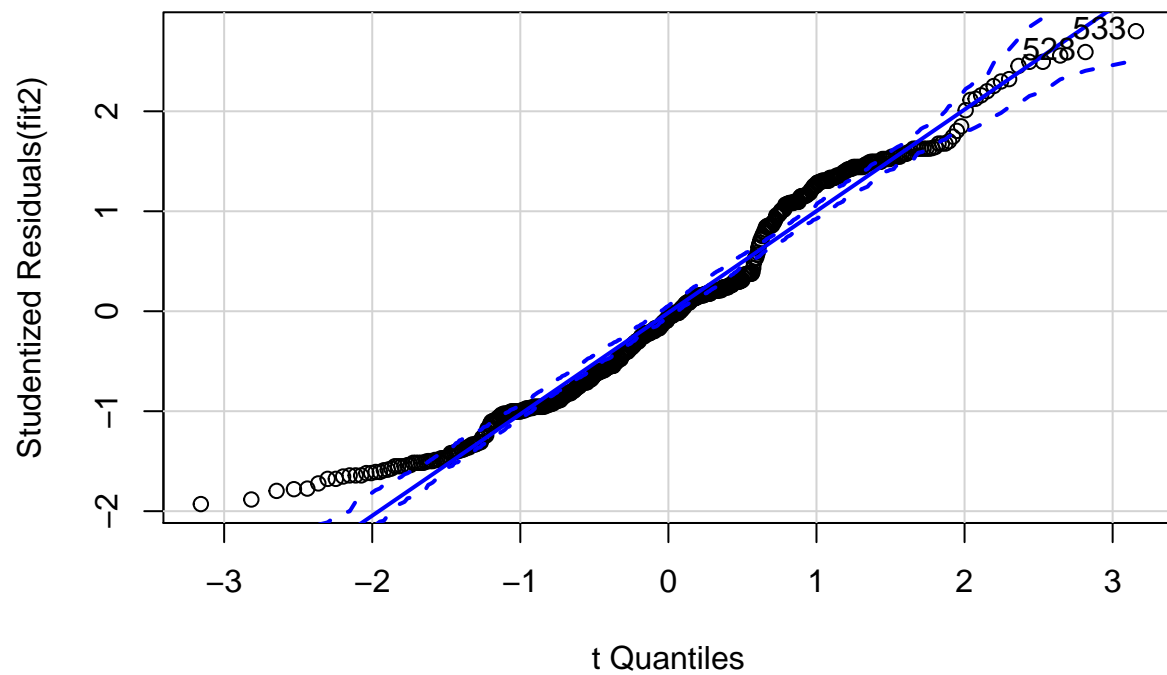
```
shapiro.test(umbs_flwr_med$julian)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  umbs_flwr_med$julian
## W = 0.96918, p-value = 6.893e-10
```

```
descdist(umbs_flwr_med$julian, discrete = FALSE)  # uniform?
```

Cullen and Frey graph
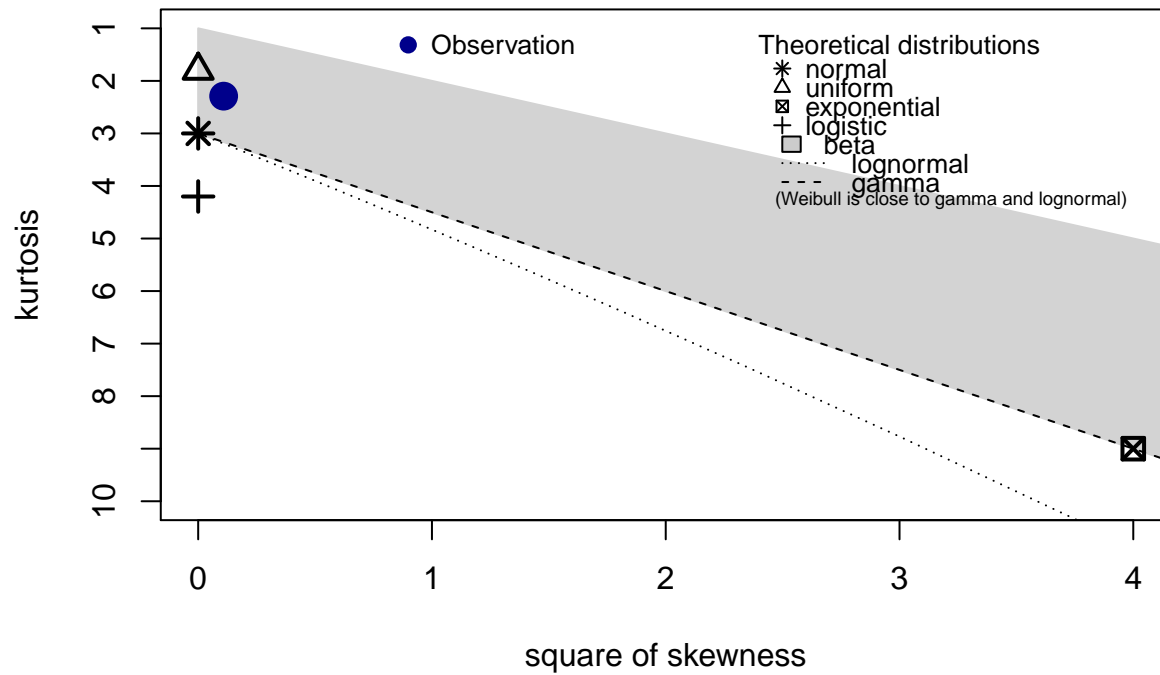

```
## summary statistics
## ------
## min:  123    max:  259.5
## median:  177.5
## mean:  179.1296
## estimated sd:  29.31017
## estimated skewness:  0.3300838
## estimated kurtosis:  2.290566
```

```
skewness(umbs_flwr_med$julian, na.rm = TRUE)  # slight positive skew
```

```
## [1] 0.3292553
```

```
# Because of slight positive skew I'm transforming the data by taking the square
# root.
umbs_flwr_med$sqrt_julian <- sqrt(umbs_flwr_med$julian)
hist(umbs_flwr_med$sqrt_julian)
```

Histogram of umbs_flwr_med$sqrt_julian

umbs_flwr_med$sqrt_julian
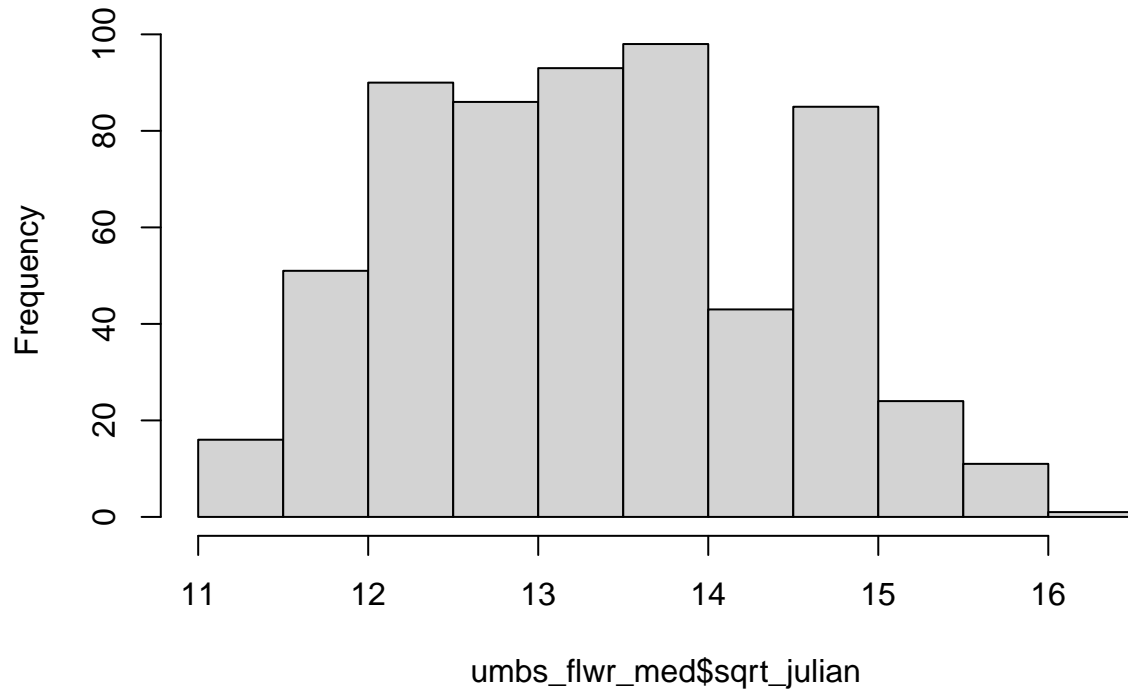
```
skewness(umbs_flwr_med$sqrt_julian, na.rm = TRUE)
```

```
## [1] 0.187288
```

```
ggdensity(umbs_flwr_med, x = "sqrt_julian", fill = "lightgray", title = "CONT") +
    stat_overlay_normal_density(color = "red", linetype = "dashed")
```
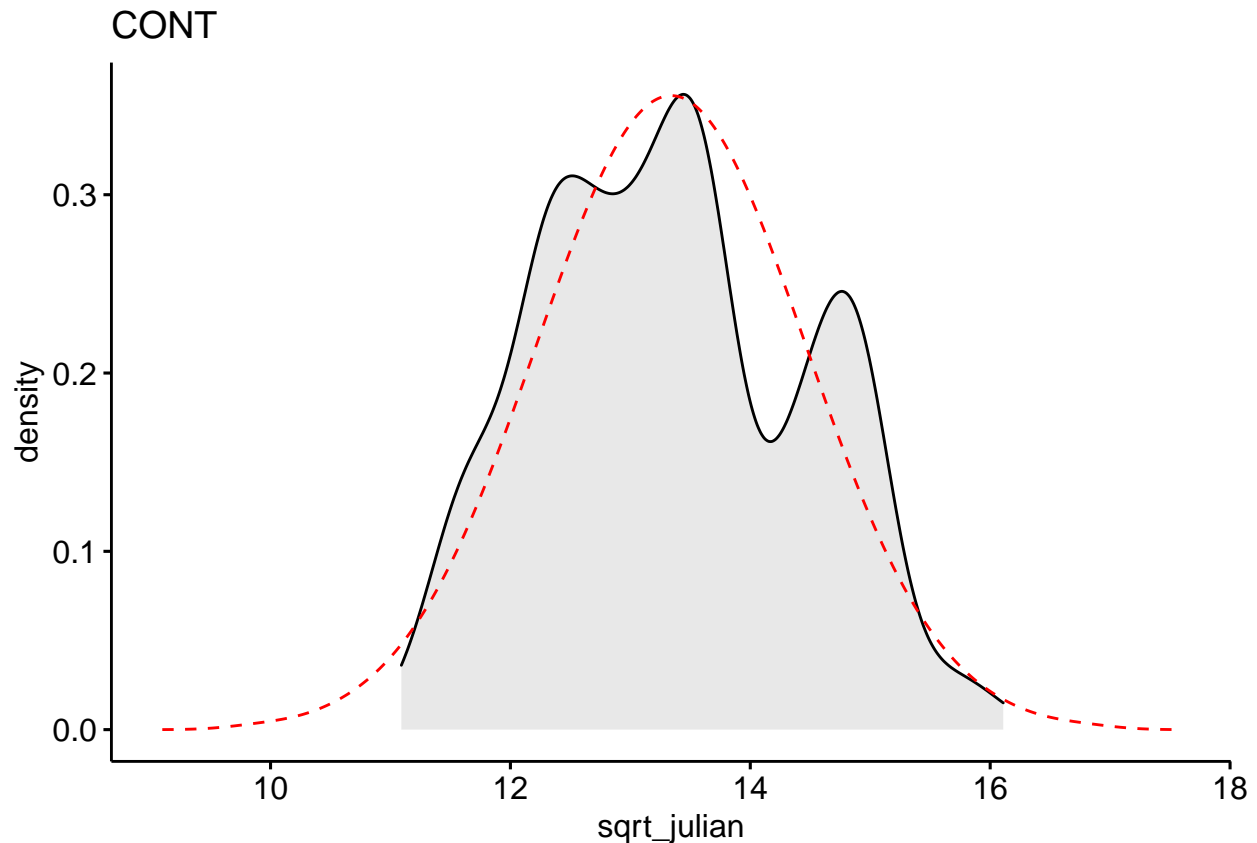
```
# there's that weird dip around 14 on the x-axis
```

Models! What is the effect of warming (state) on the median date of flower?

```
# state, year and insecticide are fixed effects with interaction btw state and
# year - species and plot are random effects

# normal dist
umbsMED_norm <- lmer(sqrt_julian ~ state * year_factor + insecticide + (1 | species) +
    (1 | plot), data = umbs_flwr_med, REML = FALSE)
```

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

```
summary(umbsMED_norm)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state * year_factor + insecticide + (1 | species) +
##     (1 | plot)
##    Data: umbs_flwr_med
##
##      AIC      BIC   logLik deviance df.resid
##    556.1    617.6   -264.1    528.1      584
##
## Scaled residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -5.9560 -0.5553 -0.0481  0.6076  3.1940
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  species   (Intercept) 1.4509   1.2045
##  plot      (Intercept) 0.0000   0.0000
##  Residual              0.1144   0.3383
## Number of obs: 598, groups:  species, 30; plot, 24
##
## Fixed effects:
##                           Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)              13.284926   0.229672  33.417175  57.843  < 2e-16 ***
## statewarmed              -0.076647   0.070570 569.956854  -1.086  0.27788
## year_factor3              0.185417   0.068576 571.254488   2.704  0.00706 **
## year_factor4              0.271762   0.068068 569.218046   3.993 7.39e-05 ***
## year_factor5              0.481660   0.066097 569.834495   7.287 1.06e-12 ***
## year_factor6              0.377016   0.065514 569.588411   5.755 1.42e-08 ***
## insecticideno_insects    -0.037231   0.028926 569.953425  -1.287  0.19857
## statewarmed:year_factor3  0.009110   0.095666 570.804816   0.095  0.92417
## statewarmed:year_factor4 -0.070302   0.095122 569.440556  -0.739  0.46017
## statewarmed:year_factor5 -0.003494   0.092306 569.861732  -0.038  0.96982
## statewarmed:year_factor6 -0.014094   0.091263 569.429882  -0.154  0.87732
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttwrm yr_fc3 yr_fc4 yr_fc5 yr_fc6 insct_ stt:_3 stt:_4
## statewarmed -0.155
## year_factr3 -0.169  0.508
## year_factr4 -0.159  0.511  0.538
## year_factr5 -0.168  0.526  0.551  0.563
## year_factr6 -0.171  0.534  0.560  0.573  0.591
## insctcdn_ns -0.091  0.022  0.014  0.009  0.028  0.029
## sttwrmd:y_3  0.115 -0.732 -0.701 -0.374 -0.382 -0.387 -0.034
## sttwrmd:y_4  0.110 -0.737 -0.372 -0.702 -0.388 -0.390 -0.009  0.545
## sttwrmd:y_5  0.118 -0.759 -0.383 -0.390 -0.702 -0.401 -0.041  0.558  0.566
## sttwrmd:y_6  0.121 -0.771 -0.389 -0.395 -0.407 -0.693 -0.038  0.566  0.570
##            stt:_5
## statewarmed
## year_factr3
## year_factr4
## year_factr5
## year_factr6
## insctcdn_ns
## sttwrmd:y_3
## sttwrmd:y_4
## sttwrmd:y_5
## sttwrmd:y_6  0.587
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```r
umbsFF_norm <- lmer(sqrt_julian ~ state * year_factor + insecticide + (1 | species) +
    (1 | plot), data = umbs_firstflwr, REML = FALSE)
```

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

```
summary(umbsFF_norm)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state * year_factor + insecticide + (1 | species) +
##     (1 | plot)
##    Data: umbs_firstflwr
##
##      AIC      BIC   logLik deviance df.resid
##    833.4    894.9   -402.7    805.4      584
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.4481 -0.4587 -0.0401  0.4855  3.8916
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  species  (Intercept) 1.3916   1.180
##  plot     (Intercept) 0.0000   0.000
##  Residual             0.1866   0.432
## Number of obs: 598, groups:  species, 30; plot, 24
##
## Fixed effects:
##                           Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)              13.020511   0.231268  35.666865  56.301  < 2e-16 ***
## statewarmed              -0.176740   0.090072 571.144985  -1.962 0.050223 .
## year_factor3             -0.006892   0.087495 573.056632  -0.079 0.937240
## year_factor4              0.290144   0.086898 569.919464   3.339 0.000896 ***
## year_factor5              0.511511   0.084367 570.875961   6.063 2.43e-09 ***
## year_factor6              0.355532   0.083629 570.527942   4.251 2.48e-05 ***
## insecticideno_insects    -0.048498   0.036919 571.163350  -1.314 0.189505
## statewarmed:year_factor3  0.128240   0.122074 572.401094   1.051 0.293927
## statewarmed:year_factor4  0.047980   0.121428 570.304058   0.395 0.692892
## statewarmed:year_factor5  0.102263   0.117818 570.987523   0.868 0.385773
## statewarmed:year_factor6  0.082943   0.116502 570.286883   0.712 0.476790
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm yr_fc3 yr_fc4 yr_fc5 yr_fc6 insct_ stt:_3 stt:_4
## statewarmed -0.197
## year_factr3 -0.214  0.509
## year_factr4 -0.202  0.511  0.538
## year_factr5 -0.213  0.526  0.551  0.563
## year_factr6 -0.217  0.534  0.561  0.573  0.591
## insctcdn_ns -0.115  0.022  0.014  0.009  0.028  0.029
## sttwrmd:y_3  0.146 -0.733 -0.701 -0.374 -0.382 -0.387 -0.034
## sttwrmd:y_4  0.140 -0.737 -0.373 -0.702 -0.388 -0.390 -0.009  0.545
## sttwrmd:y_5  0.150 -0.759 -0.383 -0.389 -0.702 -0.401 -0.041  0.559  0.565
## sttwrmd:y_6  0.153 -0.771 -0.389 -0.394 -0.407 -0.694 -0.038  0.566  0.570
##             stt:_5
## statewarmed
```

```
## year_factr3
## year_factr4
## year_factr5
## year_factr6
## insctcdn_ns
## sttwrmd:y_3
## sttwrmd:y_4
## sttwrmd:y_5
## sttwrmd:y_6  0.587
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
#### More models! This needs more work, I need to write out what each model is doing
#### Models using median flowering julian date

# Null model?
model0 <- lmer(sqrt_julian ~ 1  # This means median flower date (julian) is predicted by the intercept
 +
    (1 | plot), data = umbs_flwr_med, REML = FALSE)  # each plot gets its own intercept
```

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

```
summary(model0)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##    method [lmerModLmerTest]
## Formula: sqrt_julian ~ 1 + (1 | plot)
##    Data: umbs_flwr_med
##
##      AIC      BIC   logLik deviance df.resid
##    1804.3   1817.5   -899.1   1798.3      595
##
## Scaled residuals:
##     Min      1Q   Median      3Q      Max
## -2.06653 -0.85446 -0.01534  0.83449  2.54463
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  plot     (Intercept) 0.000    0.000
##  Residual             1.184    1.088
## Number of obs: 598, groups:  plot, 24
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept) 13.33961    0.04451 598.00000   299.7   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
# The effects of warming/ambient (state) on median date of flowering (julian)
# with species (species) as a random effect.
```

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```
model1 <- lmer(sqrt_julian ~ state + (1 | species), data = umbs_flwr_med, REML = FALSE)
summary(model1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state + (1 | species)
##    Data: umbs_flwr_med
##
##      AIC       BIC    logLik deviance df.resid
##    648.2     665.7    -320.1    640.2      594
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.5254 -0.5318  0.0406  0.6138  2.4795
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  species  (Intercept) 1.4988   1.224
##  Residual             0.1391   0.373
## Number of obs: 598, groups:  species, 30
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)  13.52959    0.22835 30.34706  59.249  < 2e-16 ***
## statewarmed  -0.09338    0.03156 570.78158  -2.959  0.00321 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## statewarmed -0.073
```

```
# The effects of warming/ambient on median date of flowering (julian - response
# variable) with an interaction between warming and native vs exotic species
# (origin) with species and year as a random effect.
model2 <- lmer(sqrt_julian ~ state * origin + (1 | species) + (1 | year_factor),
    data = umbs_flwr_med, REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
summary(model2)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state * origin + (1 | species) + (1 | year_factor)
##    Data: umbs_flwr_med
##
##      AIC       BIC    logLik deviance df.resid
##    567.6     611.5    -273.8    547.6      588
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -5.9549 -0.5468 -0.0301  0.6294  3.1709
##
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  species      (Intercept) 1.40248  1.1843
##  year_factor (Intercept) 0.03124  0.1768
##  Residual                0.11576  0.3402
## Number of obs: 598, groups:  species, 30; year_factor, 5
##
## Fixed effects:
##                            Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                 12.6337     1.2350 33.3720  10.229 8.05e-12 ***
## statewarmed                  0.9949     1.7426 33.0719   0.571    0.572
## originBoth                  -0.5580     1.5047 32.6813  -0.371    0.713
## originExotic                 0.8079     1.2802 32.8323   0.631    0.532
## originNative                 1.0517     1.2740 32.9241   0.826    0.415
## statewarmed:originExotic    -1.0931     1.7429 33.0972  -0.627    0.535
## statewarmed:originNative    -1.0772     1.7434 33.1343  -0.618    0.541
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm orgnBt orgnEx orgnNt sttw:E
## statewarmed -0.705
## originBoth  -0.001 -0.579
## originExotc -0.961  0.681  0.001
## originNativ -0.965  0.684  0.001  0.931
## sttwrmd:rgE  0.705 -1.000  0.579 -0.681 -0.684
## sttwrmd:rgN  0.705 -1.000  0.579 -0.680 -0.684  0.999
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
# The effects of warming/ambient on median date of flowering with origin and
# insecticide as fixed effects and species and year_factor as random effects
model3 <- lmer(sqrt_julian ~ state + origin + insecticide + (1 | species) + (1 |
    year_factor), data = umbs_flwr_med, REML = FALSE)
summary(model3)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state + origin + insecticide + (1 | species) +
##     (1 | year_factor)
##    Data: umbs_flwr_med
##
##      AIC      BIC   logLik deviance df.resid
##    564.4    604.0   -273.2    546.4      589
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.8967 -0.5476 -0.0320  0.5882  3.1268
##
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  species      (Intercept) 1.42474  1.1936
```

```
##  year_factor (Intercept) 0.03122  0.1767
##  Residual                 0.11543  0.3398
## Number of obs: 598, groups:  species, 30; year_factor, 5
##
## Fixed effects:
##                      Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)          13.19483    0.88179  33.58537  14.964  < 2e-16 ***
## statewarmed          -0.09227    0.02878 566.28188  -3.206  0.00142 **
## originBoth           -0.01387    1.23579  32.40580  -0.011  0.99111
## originExotic          0.26894    0.94461  32.51523   0.285  0.77767
## originNative          0.52359    0.93594  32.65702   0.559  0.57969
## insecticideno_insects -0.03684   0.02901 566.00521  -1.270  0.20464
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Correlation of Fixed Effects:
##            (Intr) sttwrm orgnBt orgnEx orgnNt
## statewarmed -0.016
## originBoth  -0.707 -0.012
## originExotc -0.925  0.000  0.661
## originNativ -0.934  0.001  0.667  0.872
## insctcdn_ns -0.015 -0.031  0.000 -0.006 -0.009
```

```
summ(model3)
```

```
## MODEL INFO:
## Observations: 598
## Dependent Variable: sqrt_julian
## Type: Mixed effects linear regression
##
## MODEL FIT:
## AIC = 564.44, BIC = 603.98
## Pseudo-R² (fixed effects) = 0.01
## Pseudo-R² (total) = 0.93
##
## FIXED EFFECTS:
## ----------------------------------------------------------------------
##                                Est.    S.E.   t val.     d.f.       p
## -------------------------- ------- ------ -------- -------- ------
## (Intercept)                   13.19   0.88    14.96    33.59   0.00
## statewarmed                   -0.09   0.03    -3.21   566.28   0.00
## originBoth                    -0.01   1.24    -0.01    32.41   0.99
## originExotic                   0.27   0.94     0.28    32.52   0.78
## originNative                   0.52   0.94     0.56    32.66   0.58
## insecticideno_insects         -0.04   0.03    -1.27   566.01   0.20
## ----------------------------------------------------------------------
##
## p values calculated using Satterthwaite d.f.
##
## RANDOM EFFECTS:
## -----------------------------------------
##     Group        Parameter     Std. Dev.
## ------------- ------------- -----------
##    species      (Intercept)     1.19
```

```
## year_factor    (Intercept)      0.18
##    Residual                     0.34
## ---------------------------------------
##
## Grouping variables:
## -------------------------------
##     Group       # groups   ICC
## ------------ ---------- ------
##    species        30      0.91
##  year_factor       5      0.02
## -------------------------------
```

Permanova

```
# perma1 <- adonis2(julian ~ state + (1|species), data = umbs_flwr_med,
# permutations = 999, by = 'terms') summary(perma1)

permanova.lmer(model1)
```

```
## Analysis of Variance Table of type I with Kenward-Roger
## approximation for degrees of freedom
##        Sum Sq Mean Sq NumDF  DenDF F value     Pr(>F)    DDf p.value Perm.p
## state  1.2179  1.2179     1 570.78  8.7555 0.0032146 569.63 0.00325  0.002
```

Updated from Kileigh's script

```
# should plot be a random effect?
moda <- lmer(sqrt_julian ~ state * origin + insecticide + (1 | species) + (1 | plot),
    umbs_flwr_med, REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

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

```
mod1 <- lmer(sqrt_julian ~ state * origin + insecticide + (1 | species), umbs_flwr_med,
    REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
anova(mod1, moda)
```

```
## Data: umbs_flwr_med
## Models:
## mod1: sqrt_julian ~ state * origin + insecticide + (1 | species)
## moda: sqrt_julian ~ state * origin + insecticide + (1 | species) +
## moda:     (1 | plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod1   10 657.62 701.56 -318.81   637.62
## moda   11 659.62 707.95 -318.81   637.62     0  1          1
```

```
AIC(mod1, moda)
```

```
##      df      AIC
## mod1 10 657.6214
## moda 11 659.6214
```

```
# Do we need insects?
mod2 <- lmer(sqrt_julian ~ state * origin + (1 | species), umbs_flwr_med, REML = FALSE)
```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
anova(mod2, mod1)
```

```
## Data: umbs_flwr_med
## Models:
## mod2: sqrt_julian ~ state * origin + (1 | species)
## mod1: sqrt_julian ~ state * origin + insecticide + (1 | species)
##      npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod2    9 657.08 696.62 -319.54   639.08
## mod1   10 657.62 701.56 -318.81   637.62 1.4592  1     0.2271
```

```
# Do we need interaction term?
mod3 <- lmer(sqrt_julian ~ state + origin + (1 | species), umbs_flwr_med, REML = FALSE)
anova(mod3, mod2)
```

```
## Data: umbs_flwr_med
## Models:
## mod3: sqrt_julian ~ state + origin + (1 | species)
## mod2: sqrt_julian ~ state * origin + (1 | species)
##      npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## mod3    7 653.49 684.25 -319.75   639.49
## mod2    9 657.08 696.62 -319.54   639.08 0.4101  2     0.8146
```

```
anova(mod3)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##         Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## state  1.2126 1.21257     1 570.62  8.7183 0.00328 **
## origin 0.0940 0.03133     3  31.58  0.2253 0.87810
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mod3)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: sqrt_julian ~ state + origin + (1 | species)
##    Data: umbs_flwr_med
##
```

```
##      AIC      BIC   logLik deviance df.resid
##    653.5    684.2   -319.7    639.5      591
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.5266 -0.5311  0.0436  0.6151  2.4797
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  species  (Intercept) 1.4679   1.2116
##  Residual             0.1391   0.3729
## Number of obs: 598, groups:  species, 30
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)  13.11383    0.89652  33.57863  14.627 3.97e-16 ***
## statewarmed  -0.09319    0.03156 570.61566  -2.953  0.00328 **
## originBoth    0.21597    1.26075  32.81637   0.171  0.86504
## originExotic  0.30173    0.96384  32.94953   0.313  0.75621
## originNative  0.59840    0.95519  33.12020   0.626  0.53530
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm orgnBt orgnEx
## statewarmed -0.018
## originBoth  -0.711 -0.013
## originExotc -0.930 -0.001  0.661
## originNativ -0.938  0.001  0.667  0.873
```

```r
confint(mod3, method = "boot", nsim = 999)
```

```
## Computing bootstrap confidence intervals ...
```

```
##                     2.5 %       97.5 %
## .sig01          0.7980652  1.45508619
## .sigma          0.3508487  0.39047481
## (Intercept)    11.2926971 14.86940453
## statewarmed    -0.1568170 -0.03005389
## originBoth     -2.4034447  2.49773195
## originExotic   -1.5993888  2.24917933
## originNative   -1.3197531  2.50859422
```

```r
difflsmeans(mod3, test.effs = NULL, ddf = "Satterthwaite")
```
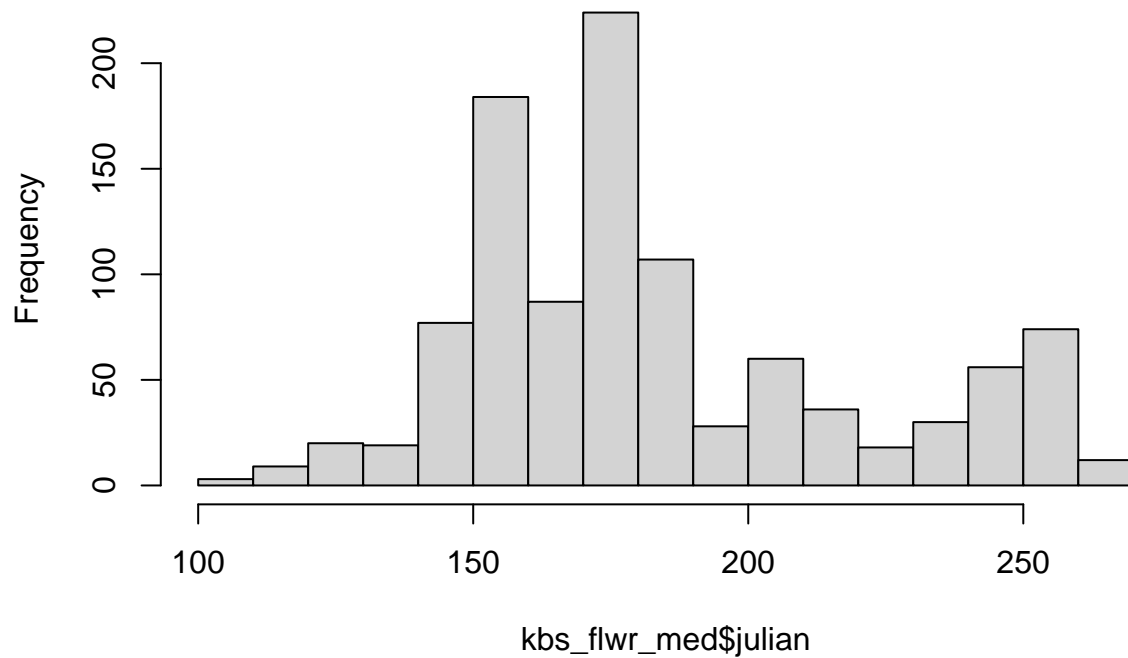
```
## Least Squares Means table:
##
##      Estimate Std. Error df t value lower upper Pr(>|t|)
##
##   Confidence level: 95%
##   Degrees of freedom method: Satterthwaite
```
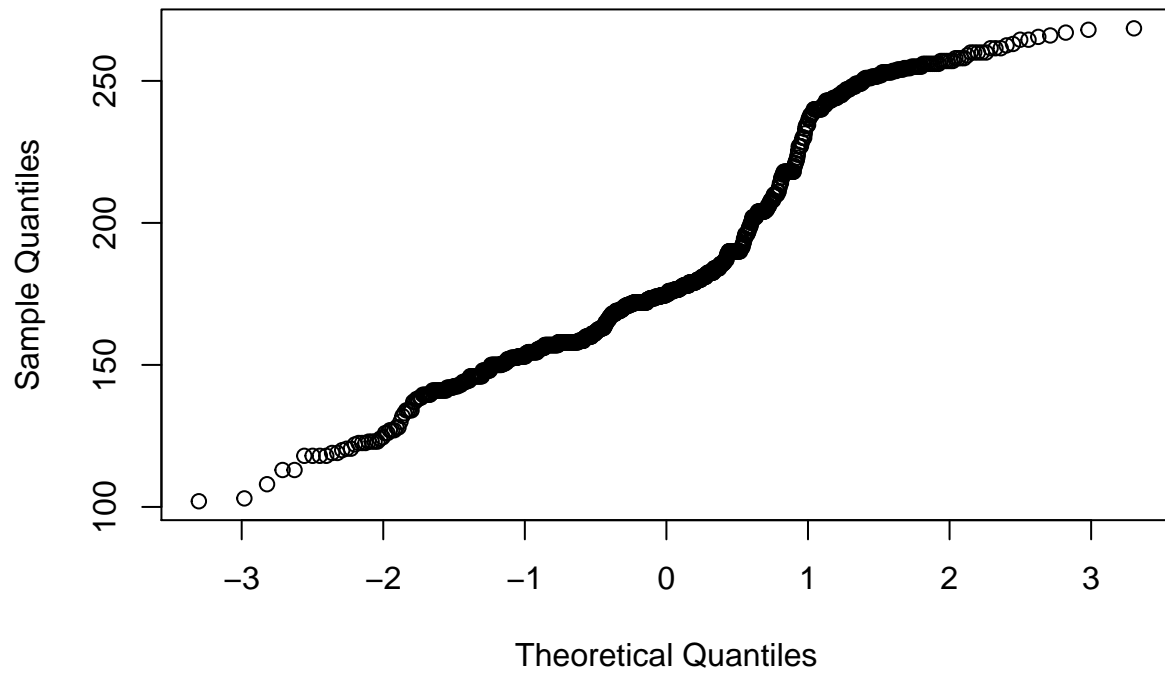
KBS Data

```
kbs_firstflwr <- subset(FirstFlower_all, site == "kbs")  # pull out kbs only data

kbs_flwr_med <- subset(MedianFlwr_all, site == "kbs")  # pull out kbs only data

hist(kbs_flwr_med$julian)
```
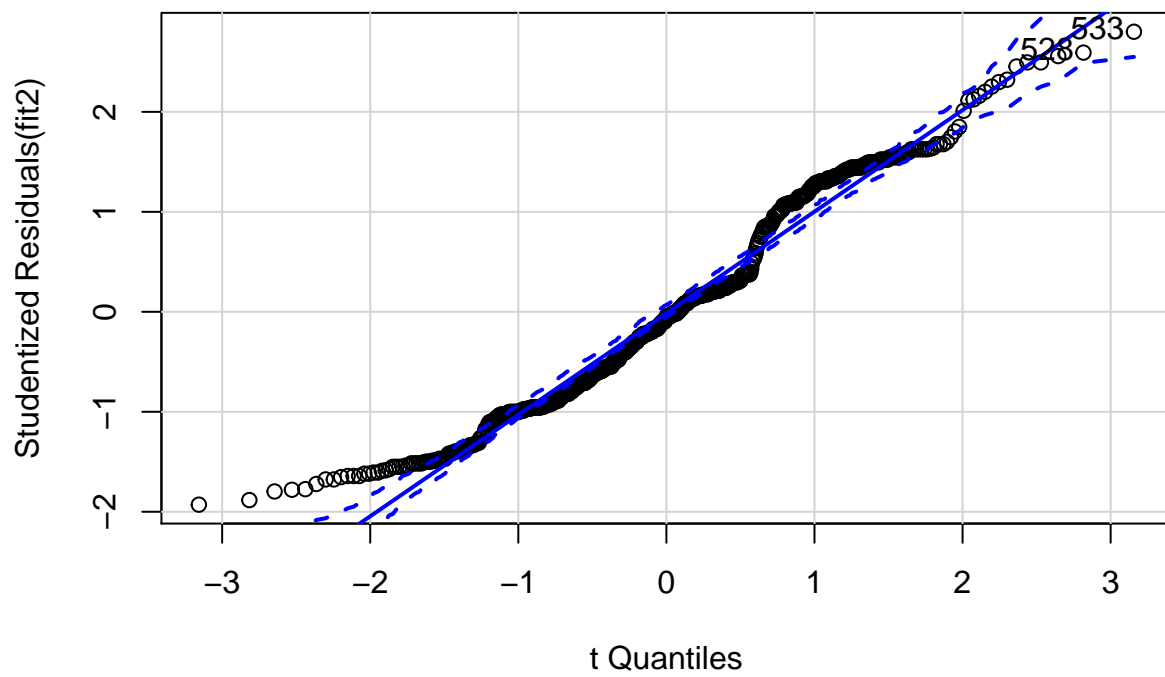
Histogram of kbs_flwr_med$julian


```
qqnorm(kbs_flwr_med$julian)
```

Normal Q–Q Plot


```
fit2 <- lm(julian ~ state, data = umbs_flwr_med)
qqPlot(fit2)
```
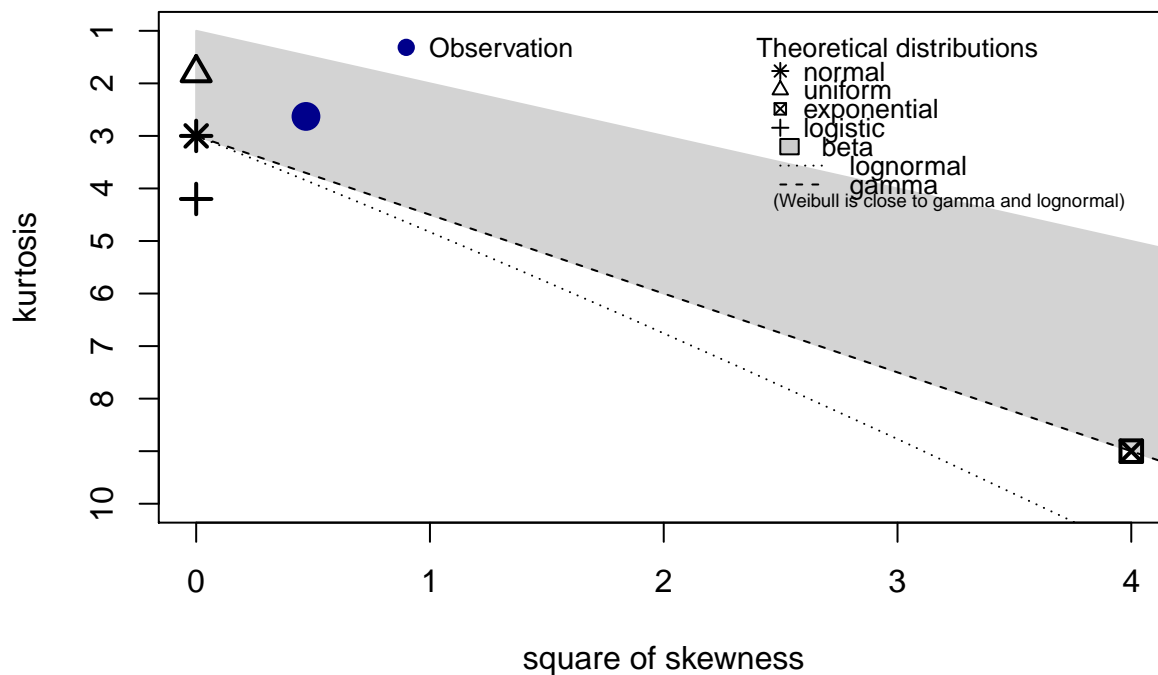


```
## [1] 528 533
```

```r
shapiro.test(kbs_flwr_med$julian)  #not normal
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  kbs_flwr_med$julian
## W = 0.92382, p-value < 2.2e-16
```

```r
descdist(kbs_flwr_med$julian, discrete = FALSE)  # beta?
```
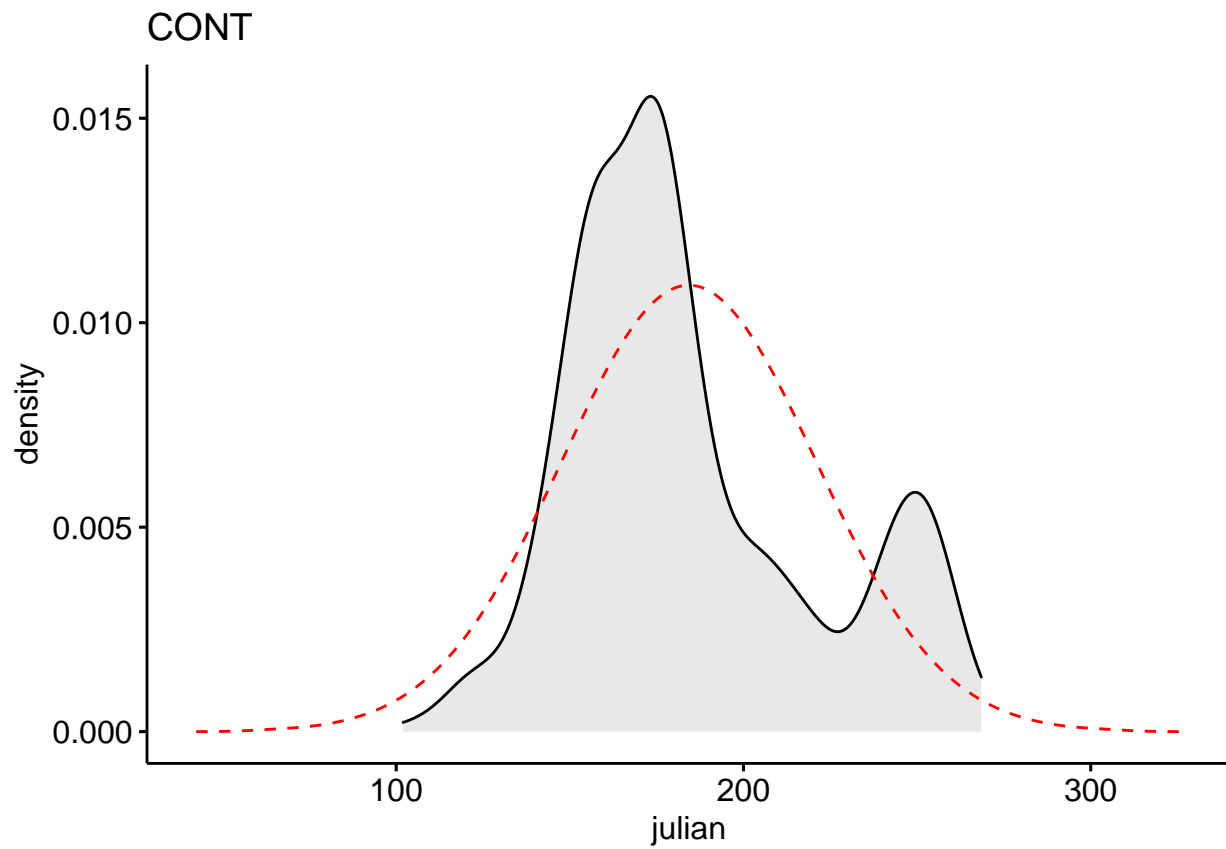
Cullen and Frey graph


```
## summary statistics
## ------
## min:  102    max:   268.5
## median:  175
## mean:  184.2926
## estimated sd:  35.68827
## estimated skewness:  0.6852815
## estimated kurtosis:  2.629031
```

```r
skewness(kbs_flwr_med$julian, na.rm = TRUE)  # slight positive skew
```
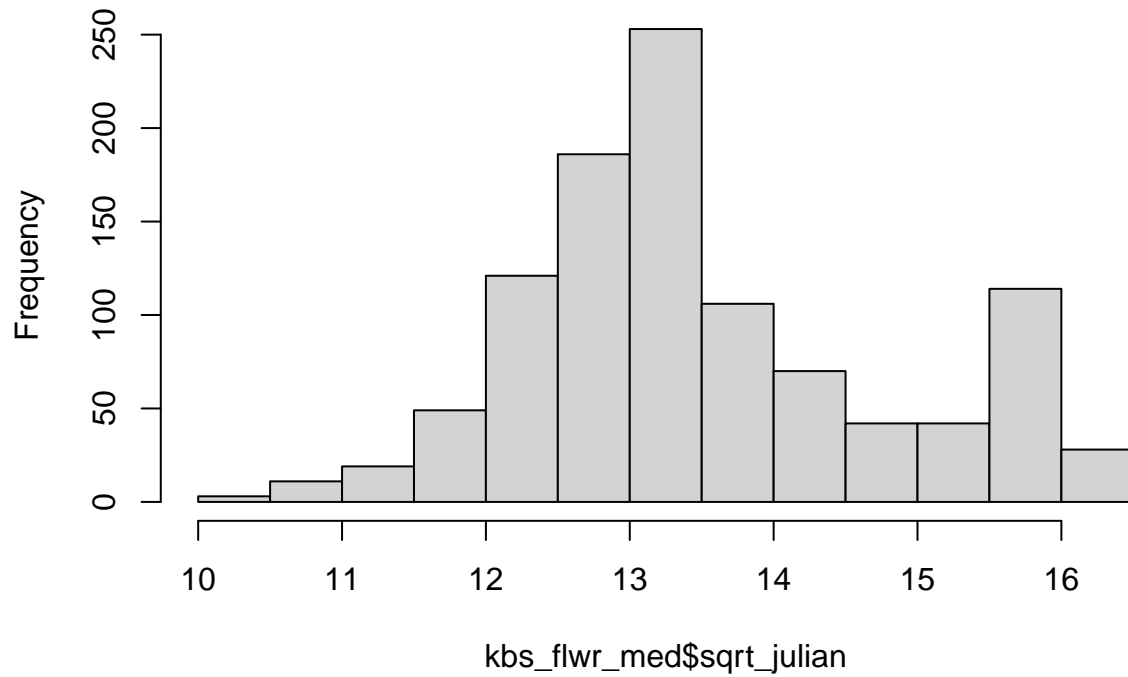
```
## [1] 0.6842965
```

```r
ggdensity(kbs_flwr_med, x = "julian", fill = "lightgray", title = "CONT") + stat_overlay_normal_density
    linetype = "dashed")
```

CONT

```
# Because of positive skew I'm transforming the data by taking the square root
kbs_flwr_med$sqrt_julian <- sqrt(kbs_flwr_med$julian)
hist(kbs_flwr_med$sqrt_julian)
```

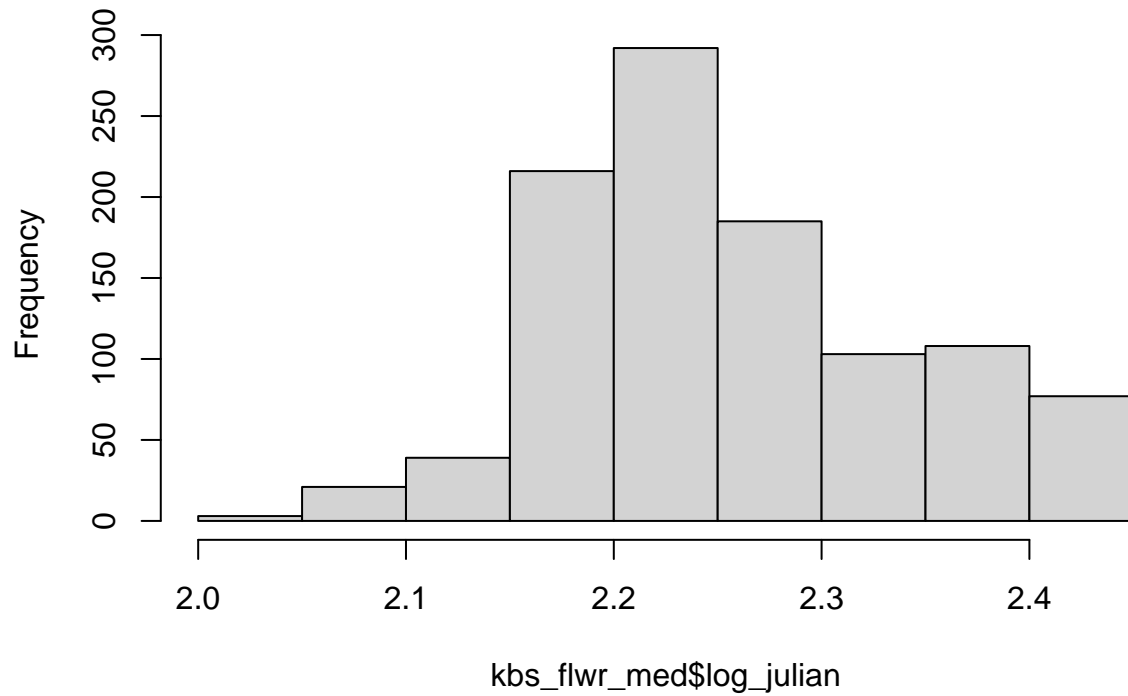**Histogram of kbs_flwr_med$sqrt_julian**


```r
skewness(kbs_flwr_med$sqrt_julian, na.rm = TRUE)
```

```
## [1] 0.5060672
```

```r
# Now try the log of julian dates
kbs_flwr_med$log_julian <- log10(kbs_flwr_med$julian)
hist(kbs_flwr_med$log_julian)
```

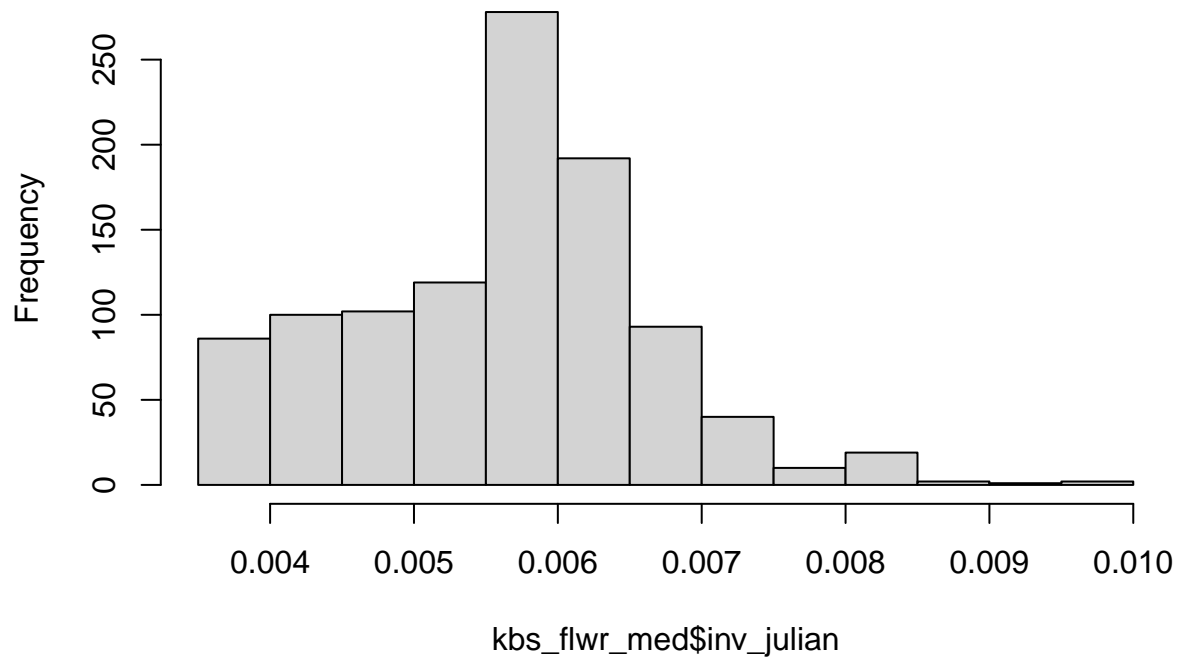## Histogram of kbs_flwr_med$log_julian


```
skewness(kbs_flwr_med$log_julian, na.rm = TRUE)
```

```
## [1] 0.3024989
```

```
# Ok now try the inverse
kbs_flwr_med$inv_julian <- 1/(kbs_flwr_med$julian)
hist(kbs_flwr_med$inv_julian)
```
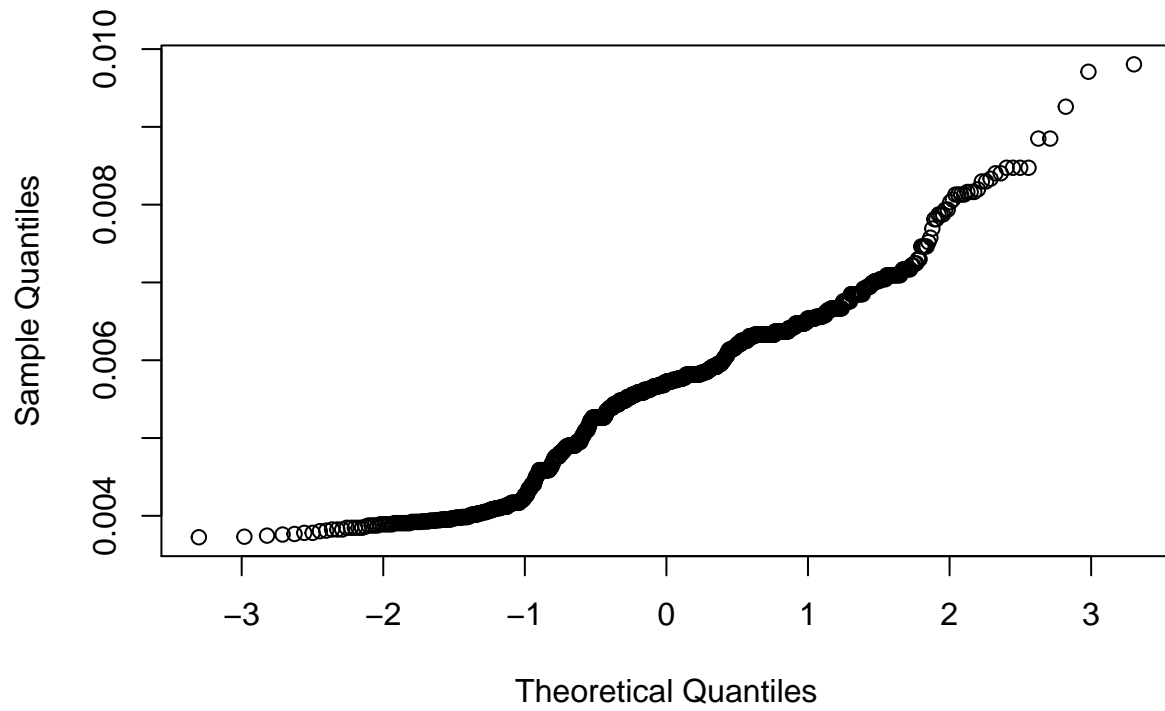
Histogram of kbs_flwr_med$inv_julian


```
skewness(kbs_flwr_med$inv_julian, na.rm = TRUE)
```

```
## [1] 0.1989016
```

```
# taking the inverse of the julian dates made the data the least skewed
qqnorm(kbs_flwr_med$inv_julian)
```

Normal Q–Q Plot


```r
shapiro.test(kbs_flwr_med$inv_julian)  #still not normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  kbs_flwr_med$inv_julian
## W = 0.96541, p-value = 4.803e-15
```

```r
# pois <- glm(julian ~ state, data = kbs_flwr_med, family='poisson')
# hist(pois$residuals)
```