warmXtrophic Project: Greenup Analyses

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DATA INPUT: Data imported as csv files from shared Google drive "SpaCE_Lab_warmXtrophic" plant comp folder
DATA OUTPUT: a brief description of the data output from through the script, including what format it's in OVERVIEW: This script ... REQUIRES: any scripts or code sources that are required NOTES: The final_kbs and final_umbs dataframes contain data for greenup at each site.
"half_cover_date" is the date at which 50% of a species max cover was reached (per plot, per year)
"state" describes each treatment - warmed or ambient

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

#Load packages
library(tidyverse)
library(lme4)
library(olsrr)
library(predictmeans)
library(car)
library(fitdistrplus)
library(ggpubr)
library(rstatix)
library(vegan)

# Set working directory to Google Drive
# **** Update with the path to your Google drive on your computer
setwd("/Volumes/GoogleDrive/Shared drives/SpaCE_Lab_warmXtrophic/data/")

# Read in plant comp data
greenup <- read.csv("L1/greenup/final_greenup_L1.csv")
# check variable types
str(greenup)
```

```
## 'data.frame':    3419 obs. of  13 variables:
##  $ X              : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ species        : chr  "Acru" "Acru" "Acru" "Acru" ...
##  $ origin         : chr  "Native" "Native" "Native" "Native" ...
##  $ duration       : chr  "Perennial" "Perennial" "Perennial" "Perennial" ...
##  $ growth_habit   : chr  "Tree" "Tree" "Tree" "Tree" ...
##  $ plot           : chr  "A4" "B2" "B2" "B2" ...
##  $ state          : chr  "warmed" "warmed" "warmed" "warmed" ...
##  $ treatment_key  : chr  "W0" "W0" "W0" "W0" ...
##  $ insecticide    : chr  "no_insects" "no_insects" "no_insects" "no_insects" ...
##  $ half_cover_date: int  167 135 145 167 175 144 167 141 202 197 ...
##  $ site           : chr  "umbs" "umbs" "umbs" "umbs" ...
##  $ year           : int  2017 2016 2019 2017 2015 2018 2017 2015 2015 2016 ...
##  $ min_emerg_date : int  167 112 112 112 112 112 167 141 80 80 ...
```

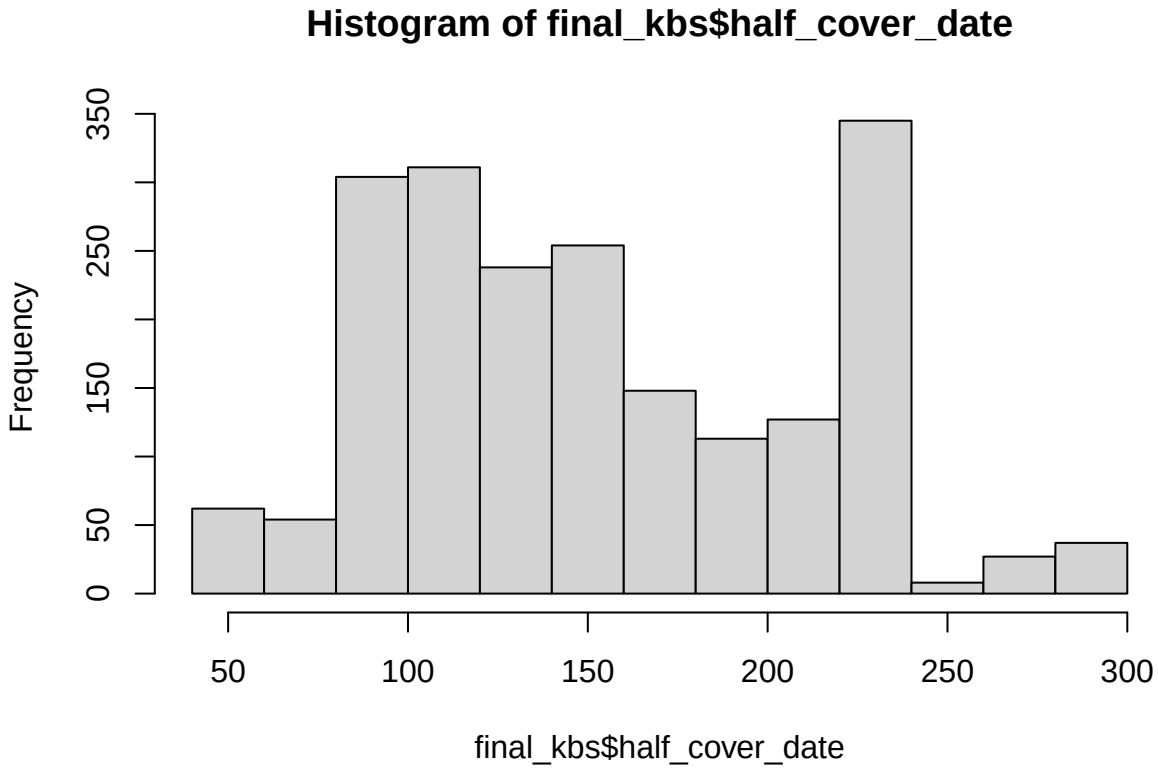
```r
# adding sequential year variable starting at 1
greenup$year1<-greenup$year
greenup$year[greenup$year == 2015] <- 1
greenup$year[greenup$year == 2016] <- 2
greenup$year[greenup$year == 2017] <- 3
greenup$year[greenup$year == 2018] <- 4
greenup$year[greenup$year == 2019] <- 5
greenup$year[greenup$year == 2020] <- 6

# create dataframes for kbs and umbs
final_kbs <- subset(greenup, site == "kbs")
final_umbs <- subset(greenup, site == "umbs")
```

Data Exploration: are there differences between warmed vs. ambient plots?

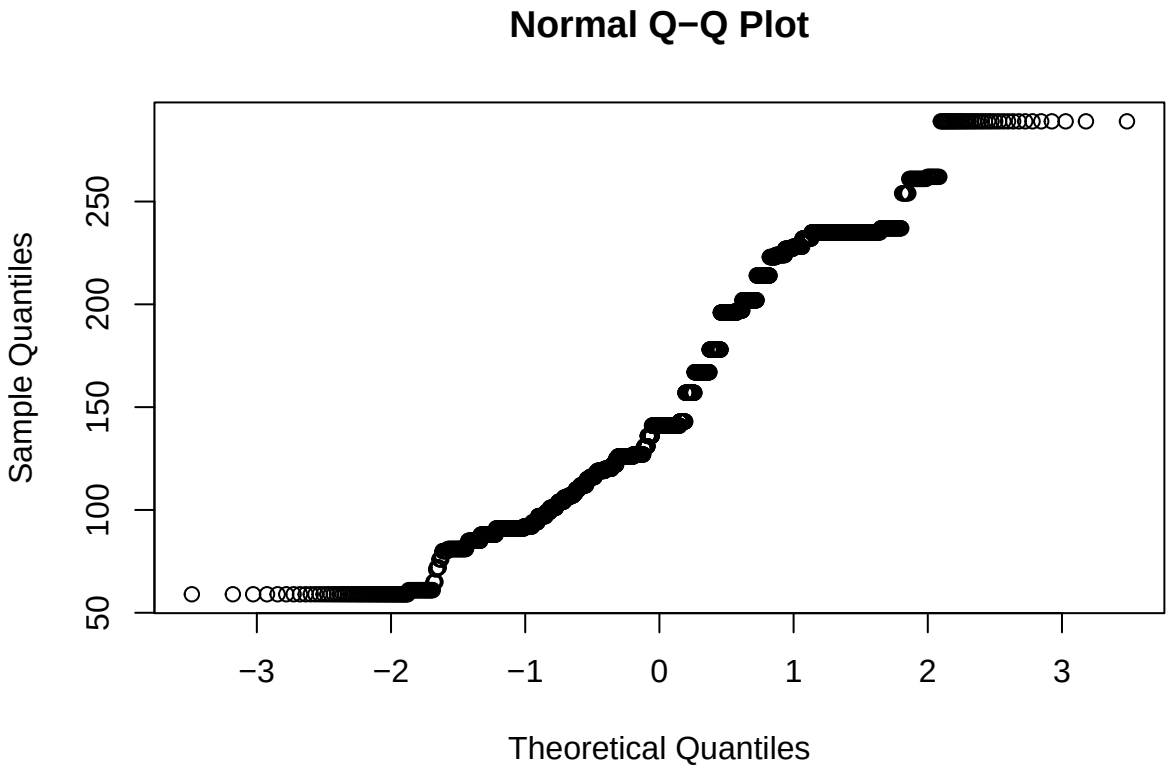
Starting with KBS

First, checking for normality in raw data

```r
hist(final_kbs$half_cover_date)
```



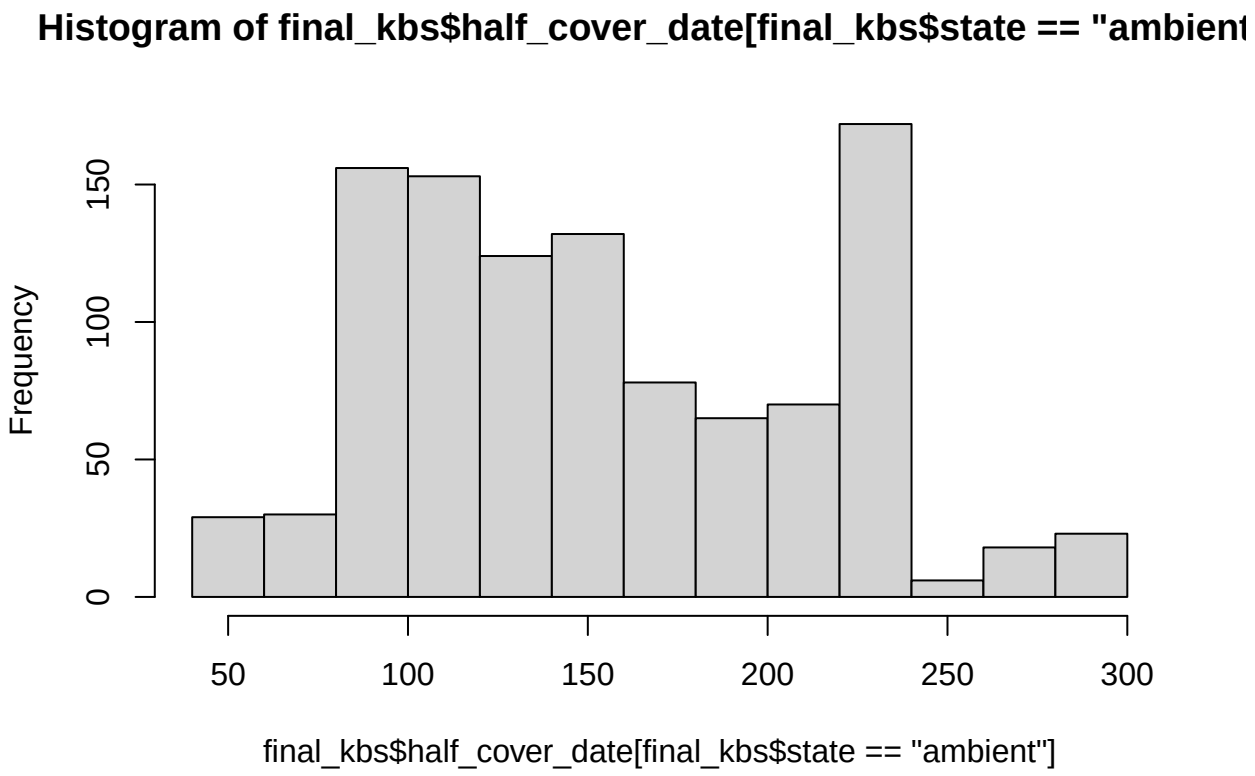

```r
qqnorm(final_kbs$half_cover_date)
```



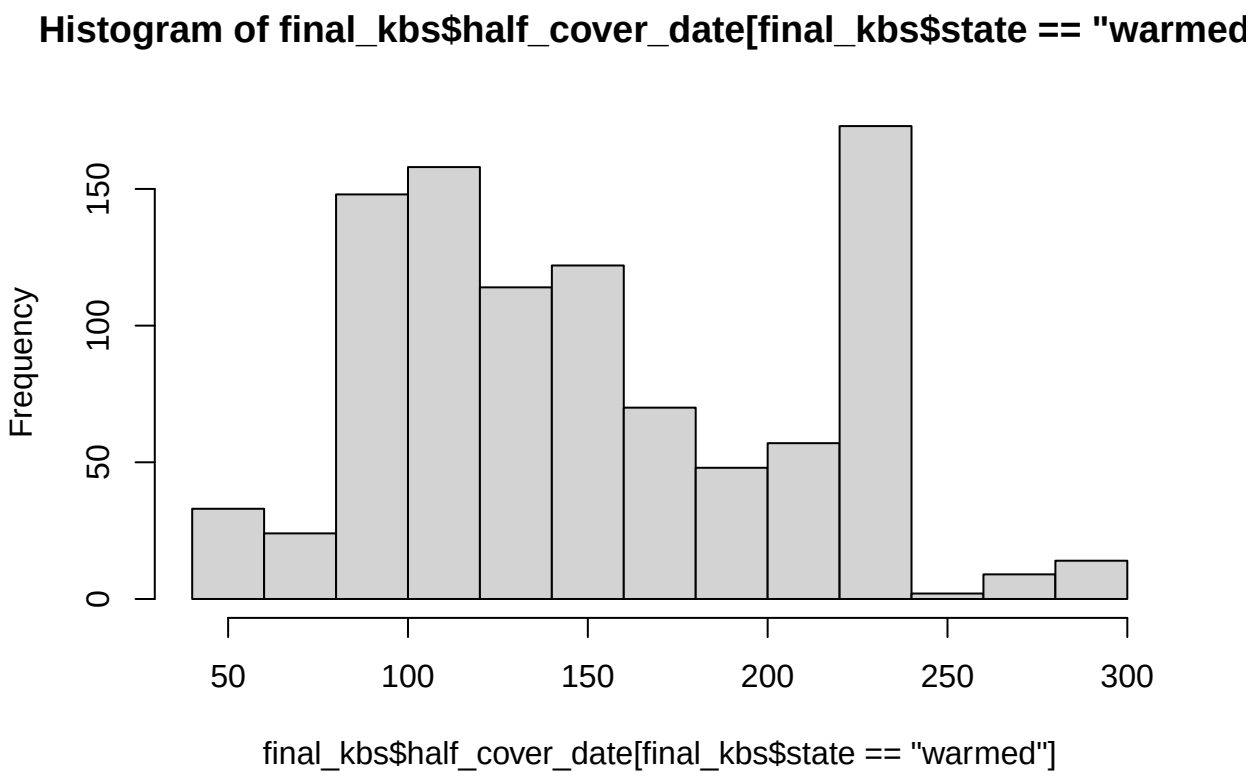

```
shapiro.test(final_kbs$half_cover_date)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  final_kbs$half_cover_date
## W = 0.94273, p-value < 2.2e-16
```

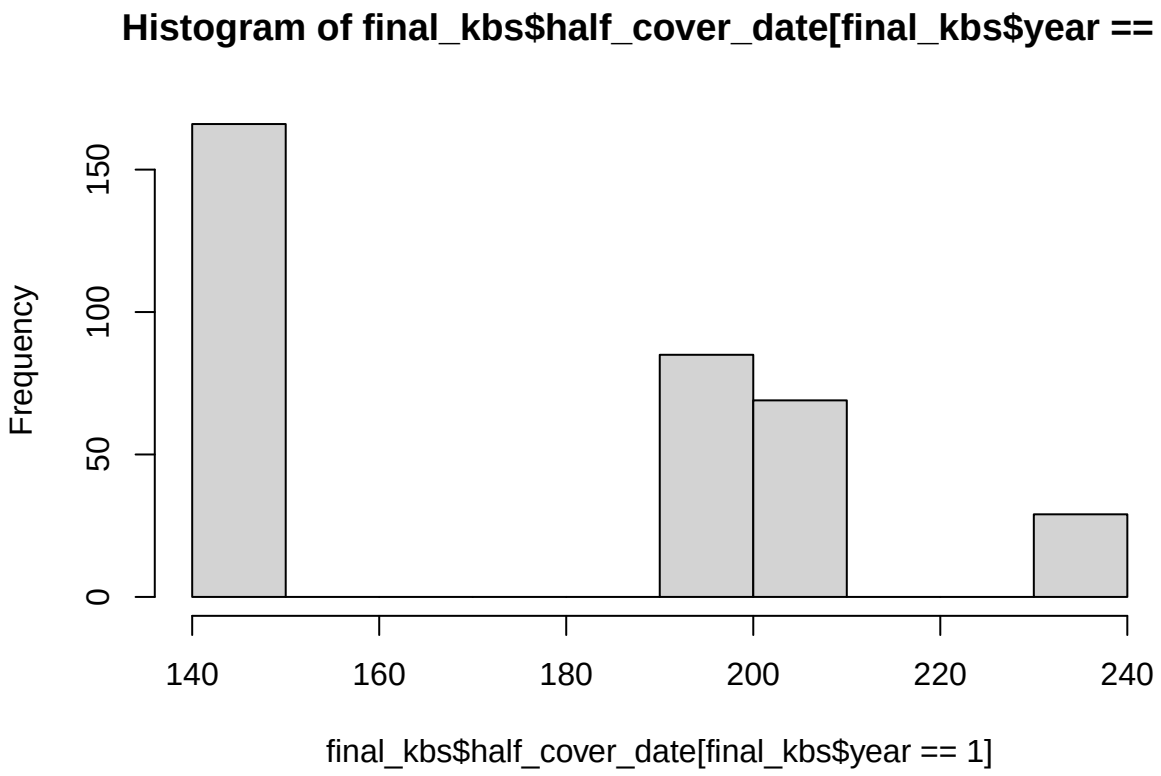
```
# histograms for each treatment separately - look almost identical
hist(final_kbs$half_cover_date[final_kbs$state == "ambient"])
```



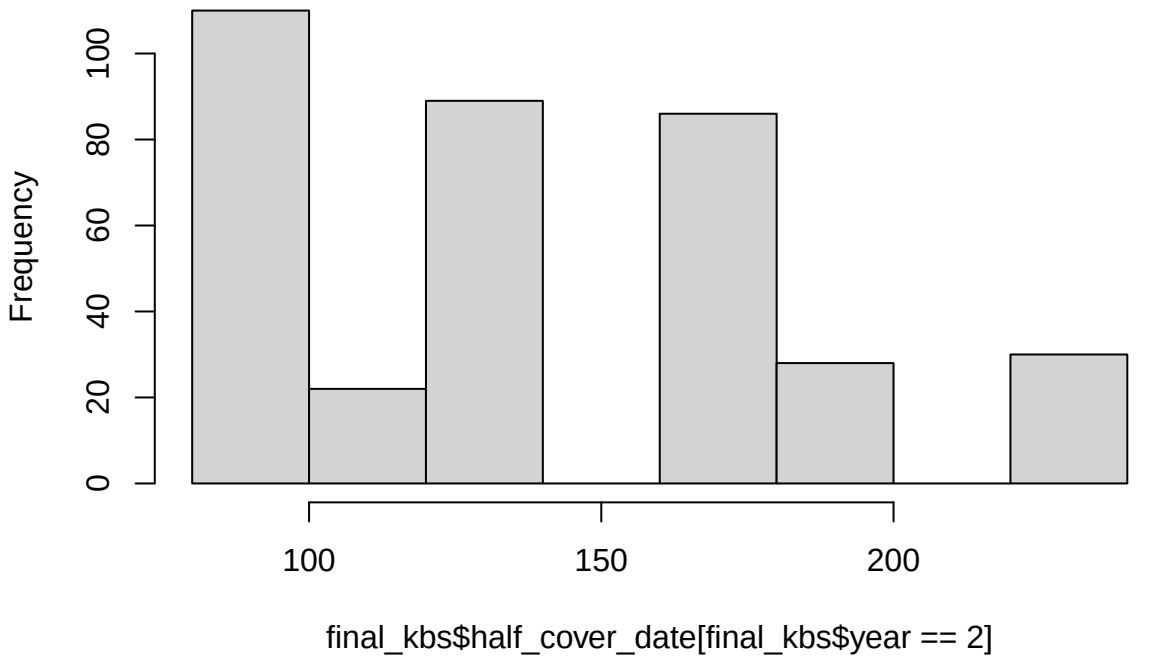

```
hist(final_kbs$half_cover_date[final_kbs$state == "warmed"])
```



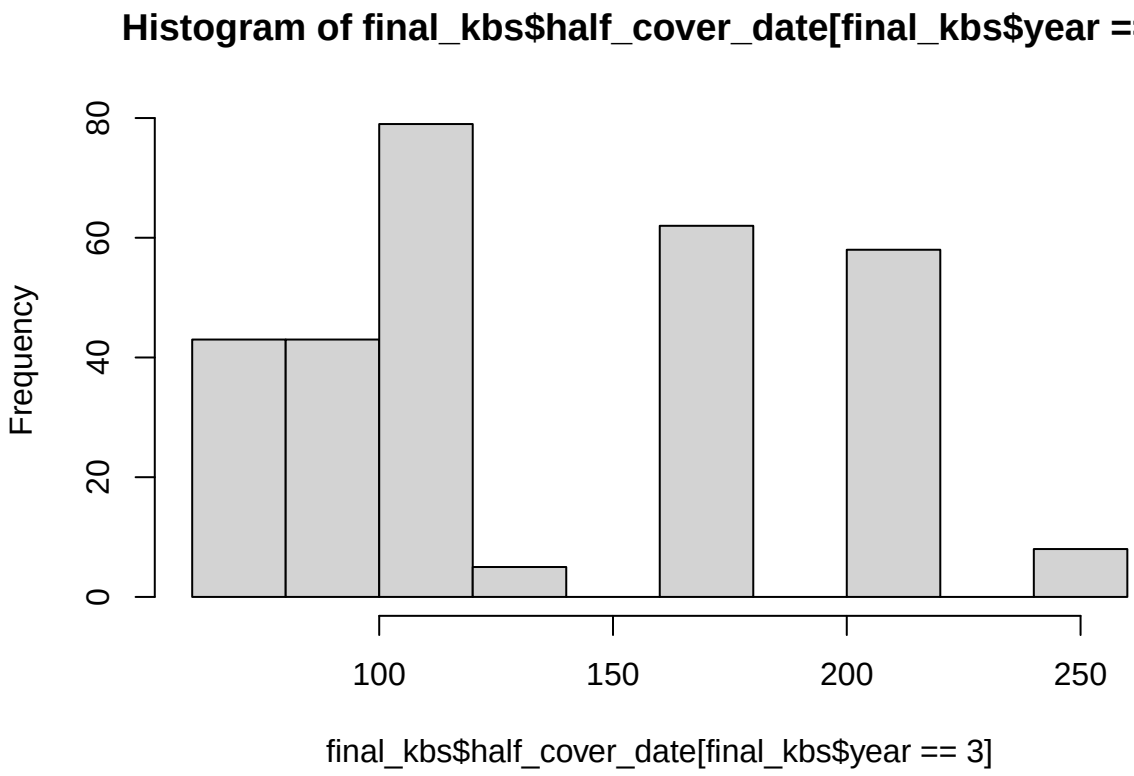

```
# histograms for each year
hist(final_kbs$half_cover_date[final_kbs$year == 1])
```



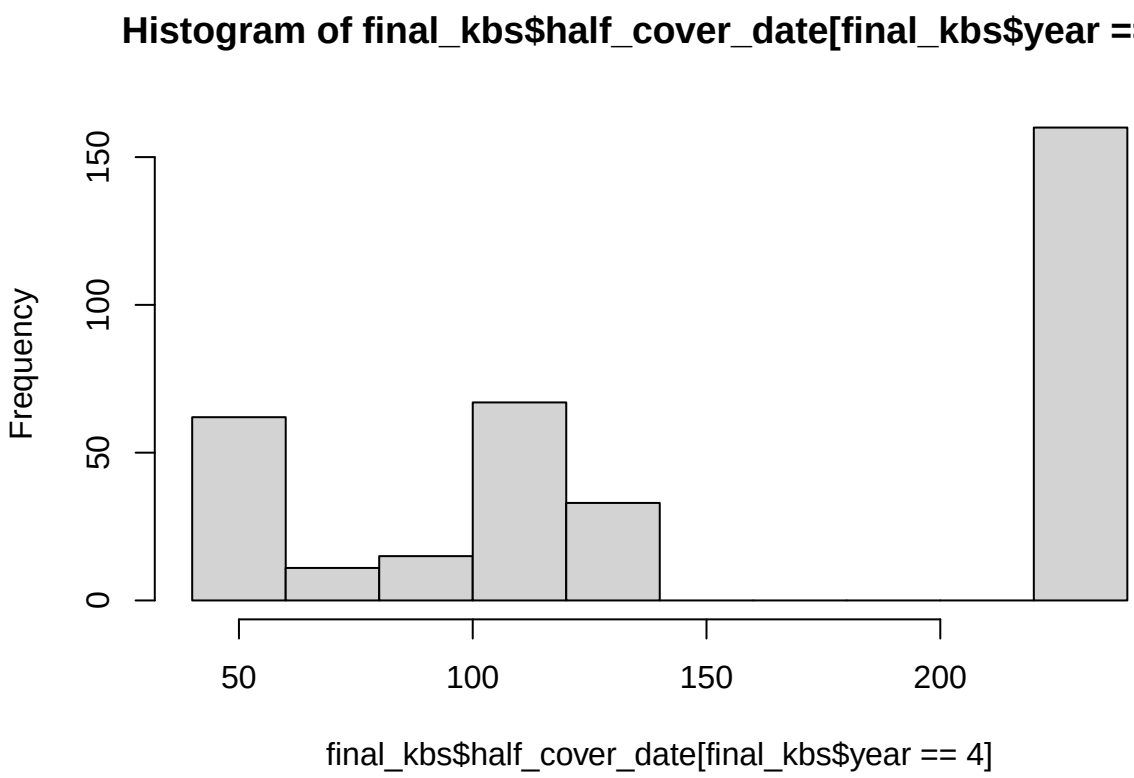

```
hist(final_kbs$half_cover_date[final_kbs$year == 2])
```



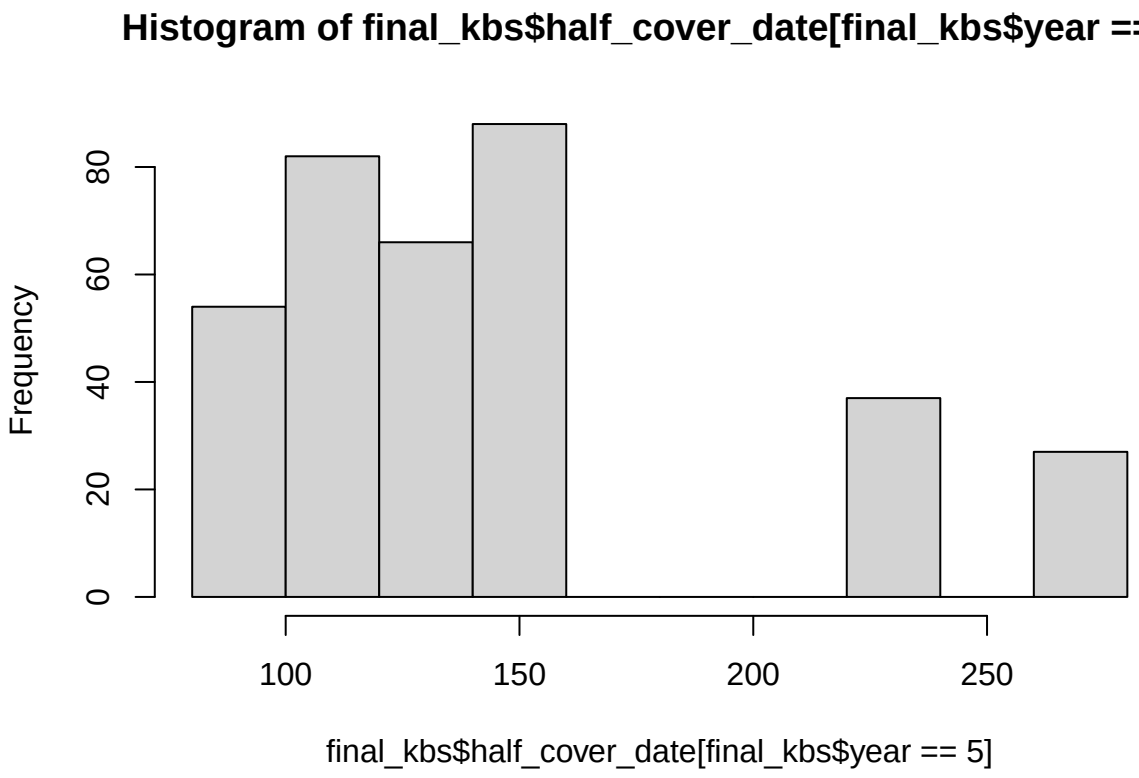

```
hist(final_kbs$half_cover_date[final_kbs$year == 3])
```



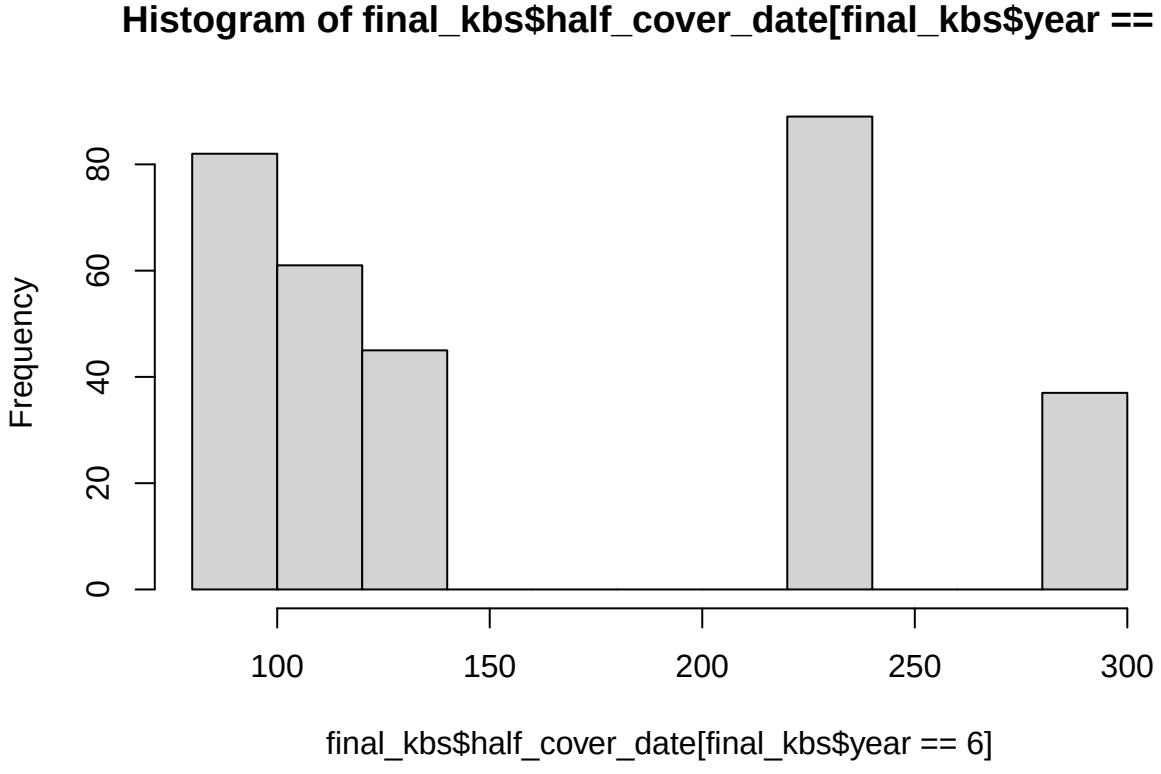

```
hist(final_kbs$half_cover_date[final_kbs$year == 4])
```




```
hist(final_kbs$half_cover_date[final_kbs$year == 5])
```



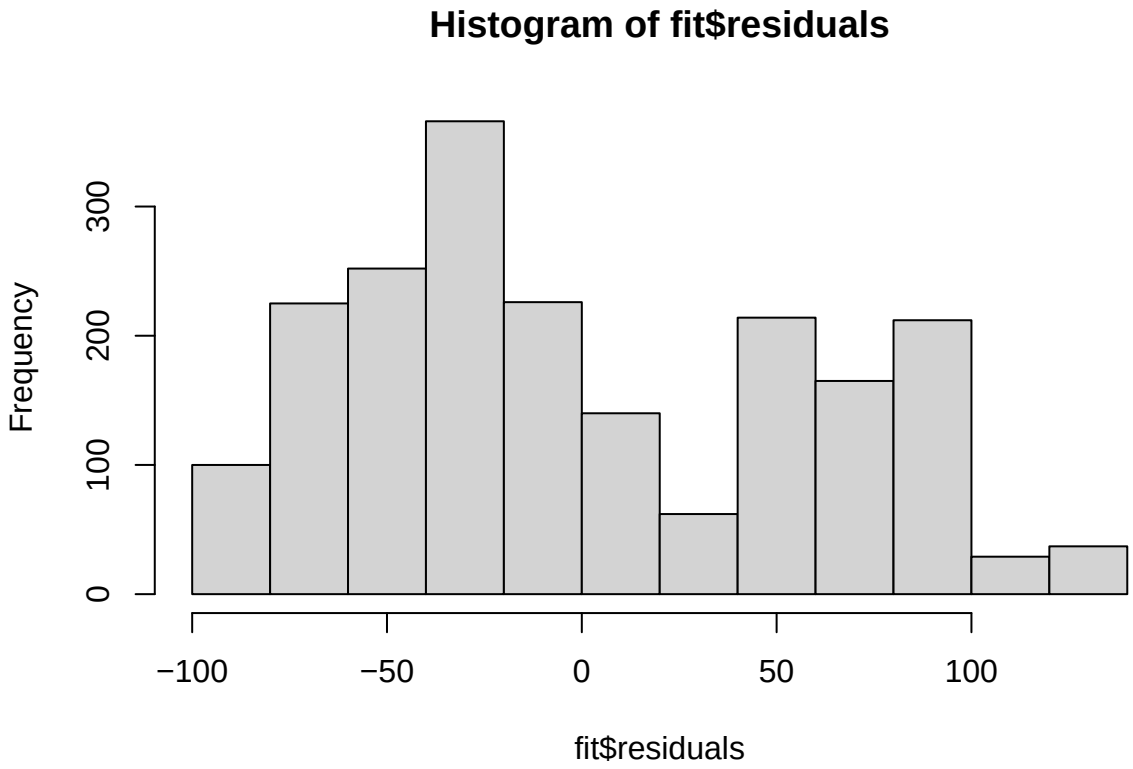

```r
hist(final_kbs$half_cover_date[final_kbs$year == 6])
```



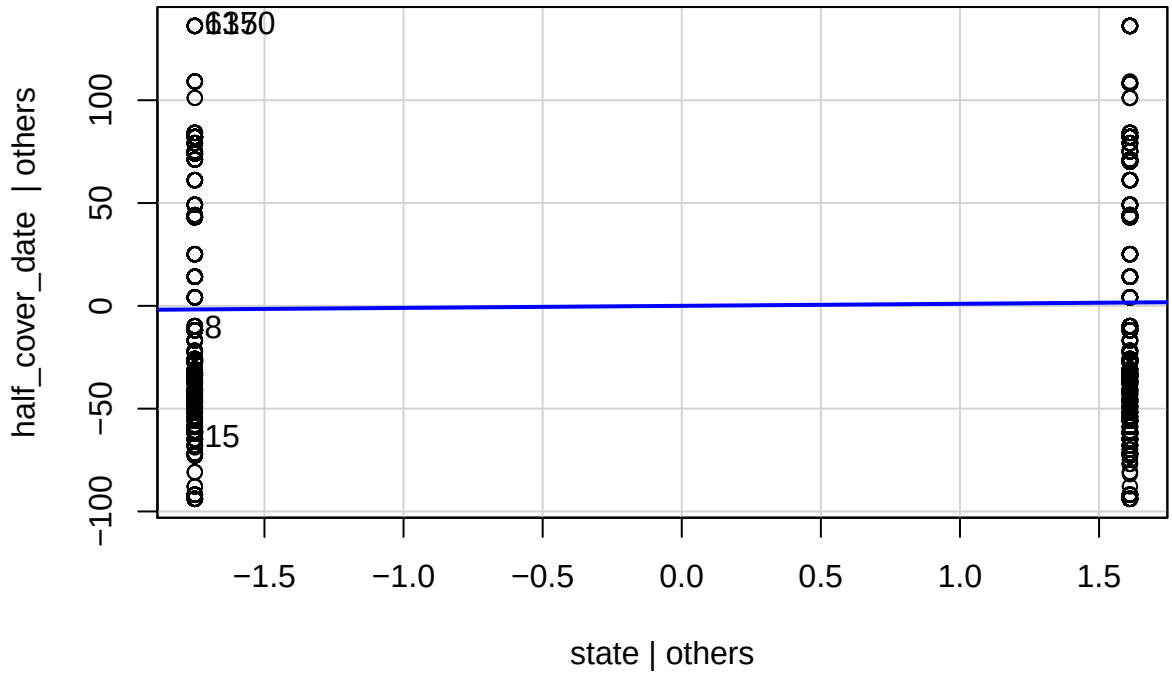

```r
# looks like the 225 spike is from 2018 and 2020
kbs_2018 <- subset(final_kbs, year == 4) # many records on 235
kbs_2020 <- subset(final_kbs, year == 6) # records from 227 & 228
```

Leverage plots?

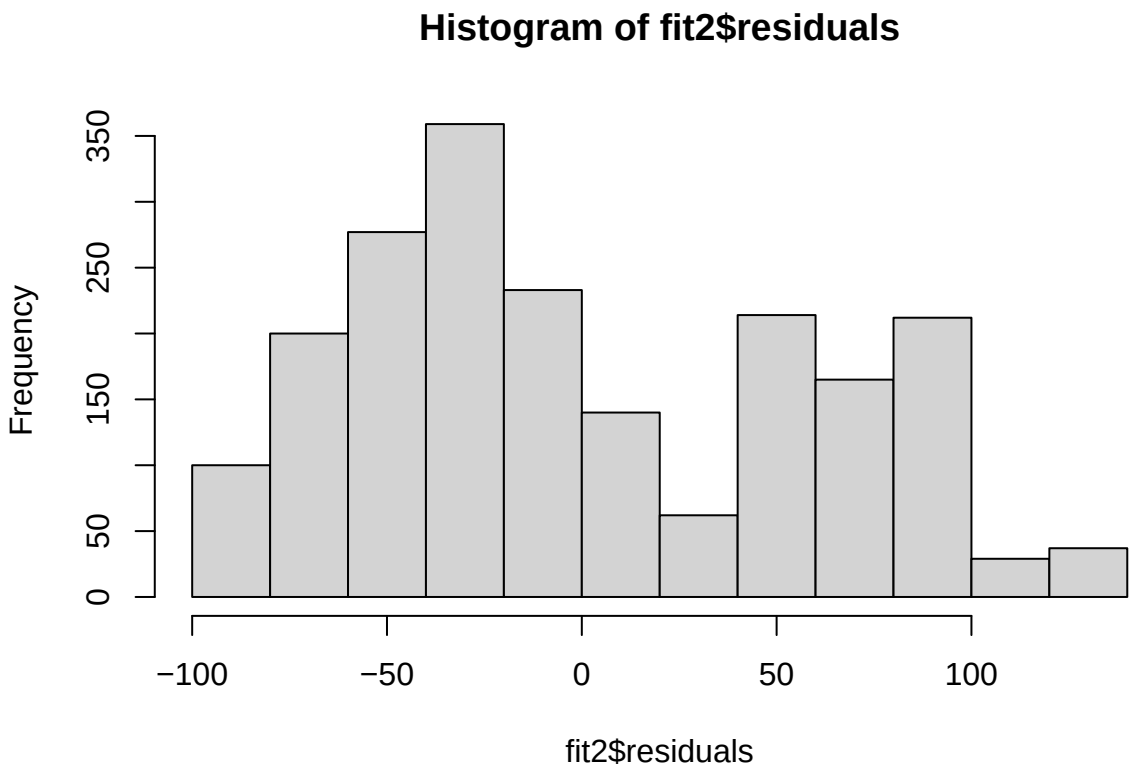
```
# checking fit for date as a function of state
fit <- lm(half_cover_date~state, data = final_kbs)
hist(fit$residuals)
```



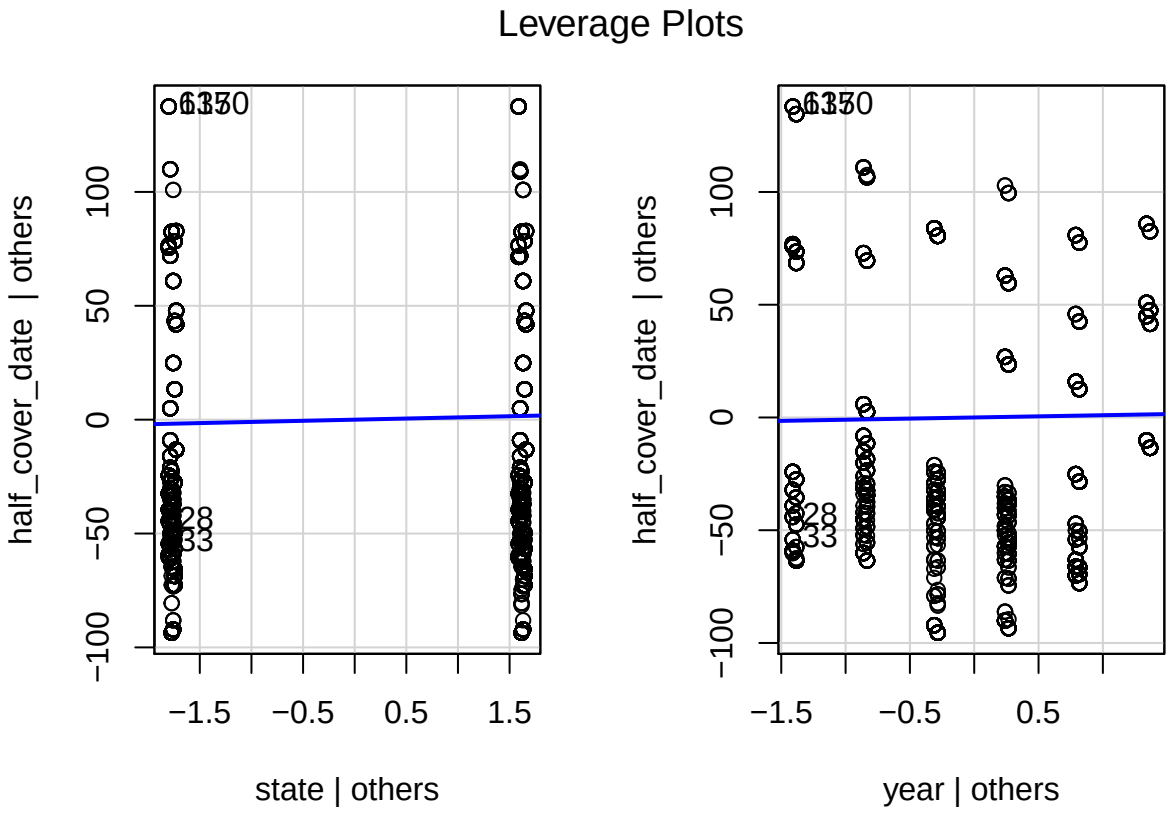

```
leveragePlots(fit)
```



```r
# checking fit for date as a function of state and year
fit2 <- lm(half_cover_date~state+year, data = final_kbs)
hist(fit2$residuals)
```



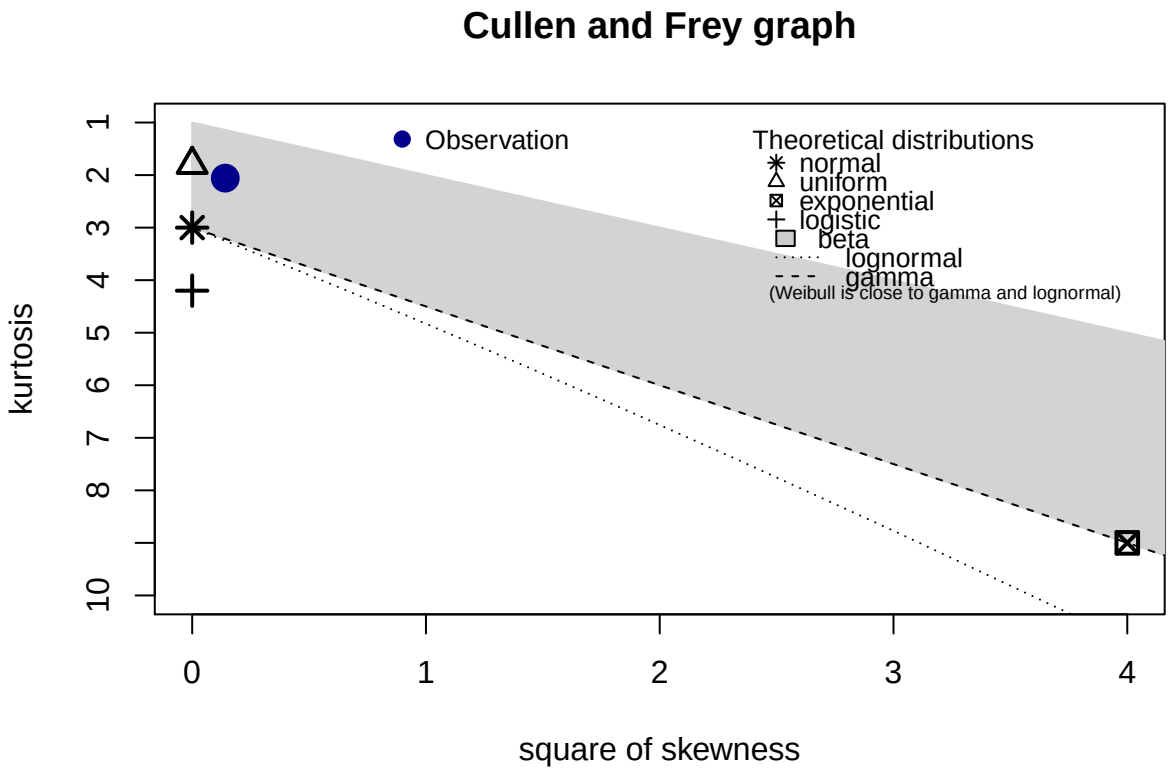

```r
leveragePlots(fit2)
```


Leverage Plots
half_cover_date | others
state | others
year | others
−100
−50
0
50
100
−1.5
−0.5
0.5
1.5
28
33

Not normal, and previously attempted transformations don't help (in R script)

Seeing what other distribution could fit

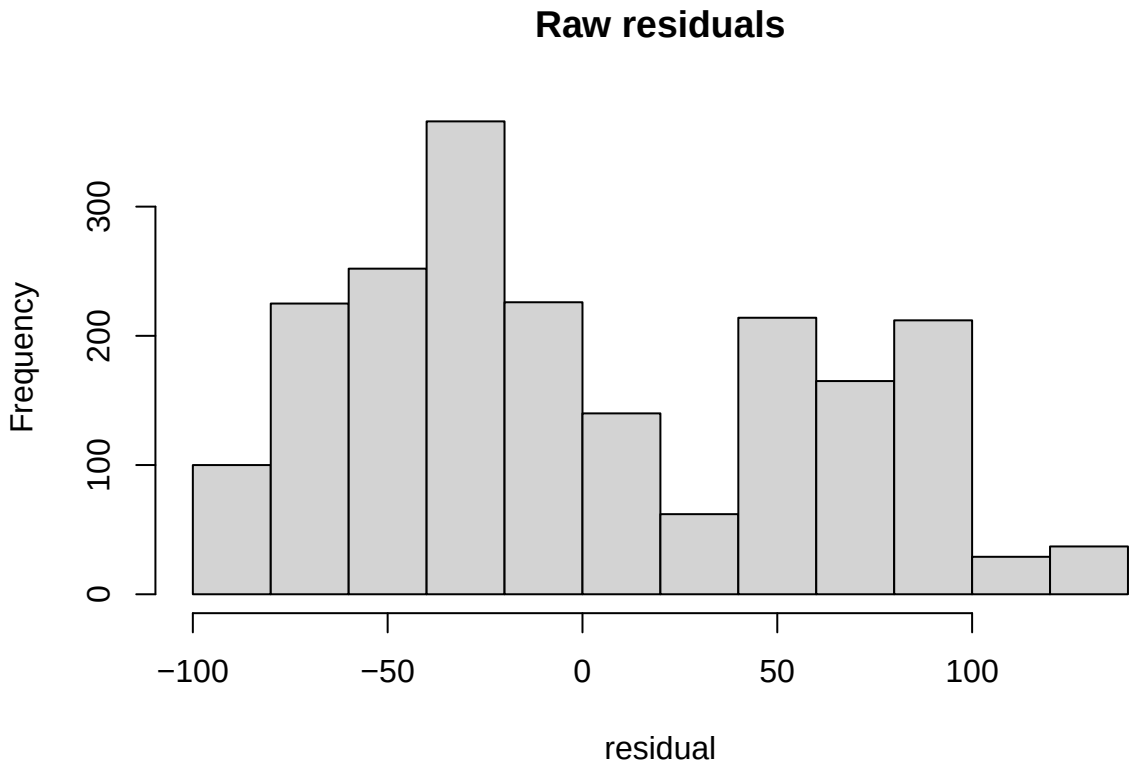
```
descdist(final_kbs$half_cover_date, discrete = FALSE)
```



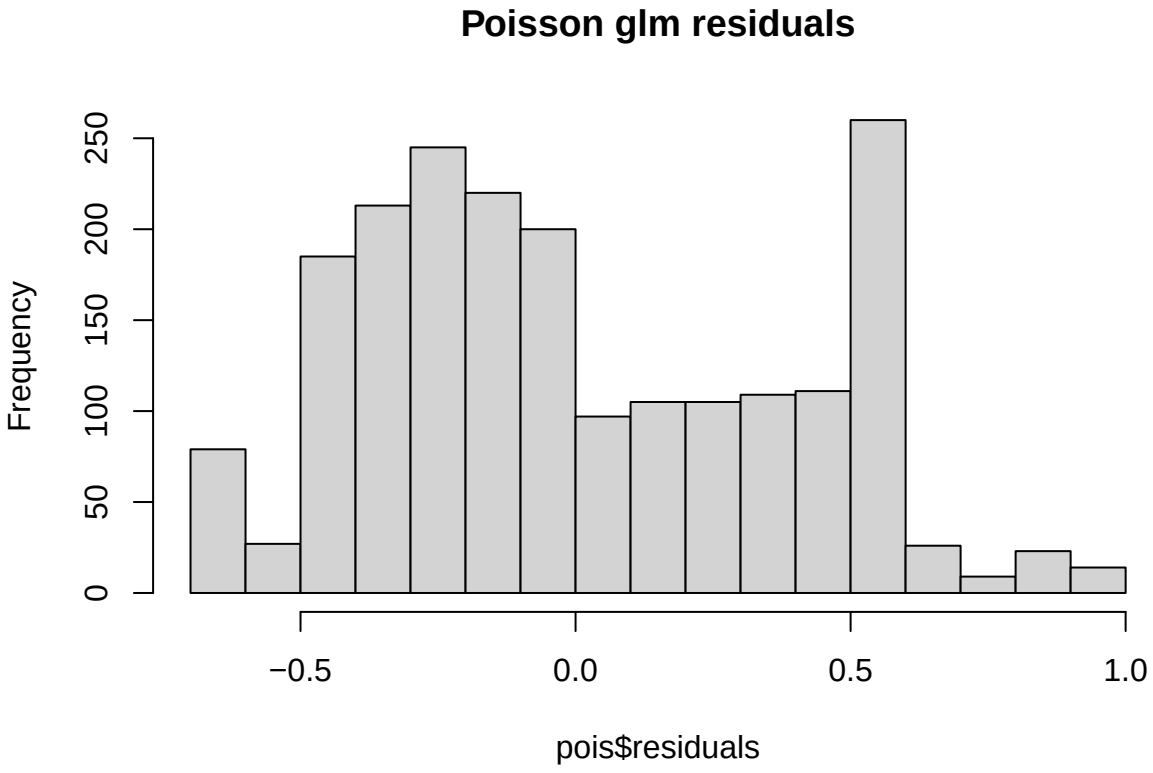

```
## summary statistics
## ------
## min:  59   max:  289
## median:  141
## mean:  152.8644
## estimated sd:  57.73216
## estimated skewness:  0.3763172
## estimated kurtosis:  2.058193
```

While uniform looks the closest, I'll try poisson

```
fit <- lm(half_cover_date~state, data = final_kbs)
residual <- fit$residuals
hist(residual, main="Raw residuals")
```




```
pois <- glm(half_cover_date~state, data = final_kbs, family="poisson")
hist(pois$residuals, main="Poisson glm residuals")
```



Below I try a few different generalized linear models with poisson distribution:

An interaction between state and year, plus insecticide as a fixed effect and species and plot as random effects

```
moda <- glmer(half_cover_date ~ state*year + insecticide + (1|species) + (1|plot),
              data=final_kbs, family = poisson)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unider
##  - Rescale variables?
```

```
summary(moda)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: half_cover_date ~ state * year + insecticide + (1 | species) +
##     (1 | plot)
##    Data: final_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  42924.6  42963.9 -21455.3  42910.6     2021
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -9.0161 -2.8352 -0.6425  2.3763 14.4656
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  species (Intercept) 0.069953 0.26449
##  plot    (Intercept) 0.001848 0.04299
## Number of obs: 2028, groups:  species, 55; plot, 24
##
## Fixed effects:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             5.020672   0.039631 126.686  < 2e-16 ***
## statewarmed             0.009389   0.019347   0.485   0.6275
## year                    0.003600   0.001520   2.368   0.0179 *
## insecticideno_insects   0.028935   0.017936   1.613   0.1067
## statewarmed:year       -0.009698   0.002116  -4.584 4.57e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm year   insct_
## statewarmed -0.243
## year        -0.130  0.249
## insctcdn_ns -0.227 -0.002  0.008
## statwrmd:yr  0.089 -0.375 -0.648  0.006
## convergence code: 0
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

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

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

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unide
##  - Rescale variables?
```

```
summary(modb)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: half_cover_date ~ state + year + insecticide + (1 | species) +
##     (1 | plot)
##    Data: final_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  42943.6  42977.3 -21465.8  42931.6     2022
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -9.0054 -2.8448 -0.6575  2.3929 14.2130
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  species (Intercept) 0.069954 0.26449
##  plot    (Intercept) 0.001847 0.04297
## Number of obs: 2028, groups:  species, 55; plot, 24
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)             5.0367370  0.0394718 127.603   <2e-16 ***
## statewarmed            -0.0238778  0.0179289  -1.332    0.183
## year                   -0.0009129  0.0011579  -0.788    0.430
## insecticideno_insects   0.0294349  0.0179300   1.642    0.101
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm year
## statewarmed -0.227
## year        -0.096  0.007
## insctcdn_ns -0.228  0.001  0.015
## convergence code: 0
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

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

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

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: half_cover_date ~ state + insecticide + (1 | year) + (1 | species) +
##     (1 | plot)
##    Data: final_kbs
##
##      AIC      BIC   logLik deviance df.resid
##  41436.8  41470.5 -20712.4  41424.8     2022
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -9.3418 -2.8134 -0.5215  2.1783 13.1976
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  species (Intercept) 0.068408 0.26155
##  plot    (Intercept) 0.001820 0.04266
##  year    (Intercept) 0.005867 0.07659
## Number of obs: 2028, groups:  species, 55; plot, 24; year, 6
##
## Fixed effects:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            5.01945    0.04991 100.577   <2e-16 ***
## statewarmed           -0.02683    0.01781  -1.507   0.1319
## insecticideno_insects  0.03093    0.01781   1.737   0.0824 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sttwrm
## statewarmed -0.178
## insctcdn_ns -0.178  0.001
```

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

```
#friedman_kbs <- final_kbs %>%
#  friedman_test(half_cover_date ~ state)
```

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

Can't figure out what this means

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

```
#friedman_kbs <- final_kbs %>%
#  friedman_test(half_cover_date ~ state | plot)
```

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

Permanova?

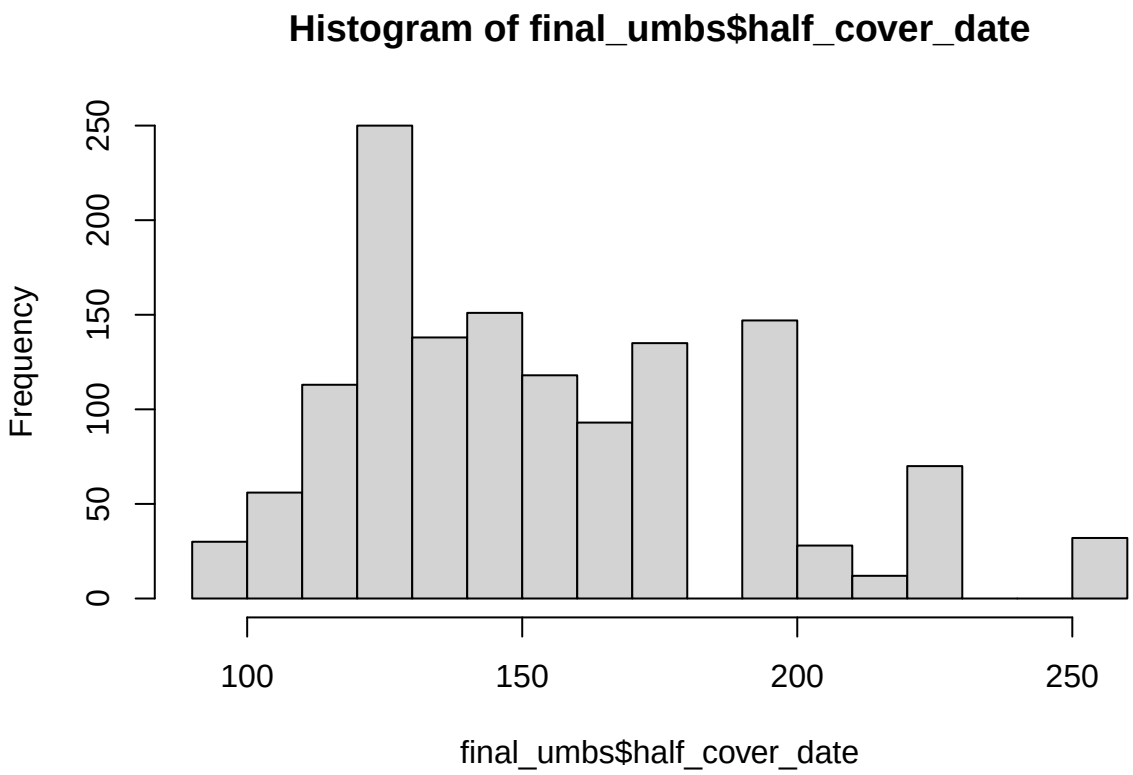
```
per1 <- adonis2(final_kbs$half_cover_date ~ state*year + insecticide, data = final_kbs)
per1
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = final_kbs$half_cover_date ~ state * year + insecticide, data = final_kbs)
##               Df SumOfSqs      R2       F Pr(>F)
## state          1    0.051 0.00074  1.5046  0.212
## year           1    0.487 0.00698 14.2700  0.001 ***
## insecticide    1    0.168 0.00241  4.9326  0.021 *
## state:year     1    0.025 0.00036  0.7290  0.405
## Residual    2023   69.058 0.98951
## Total       2027   69.790 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

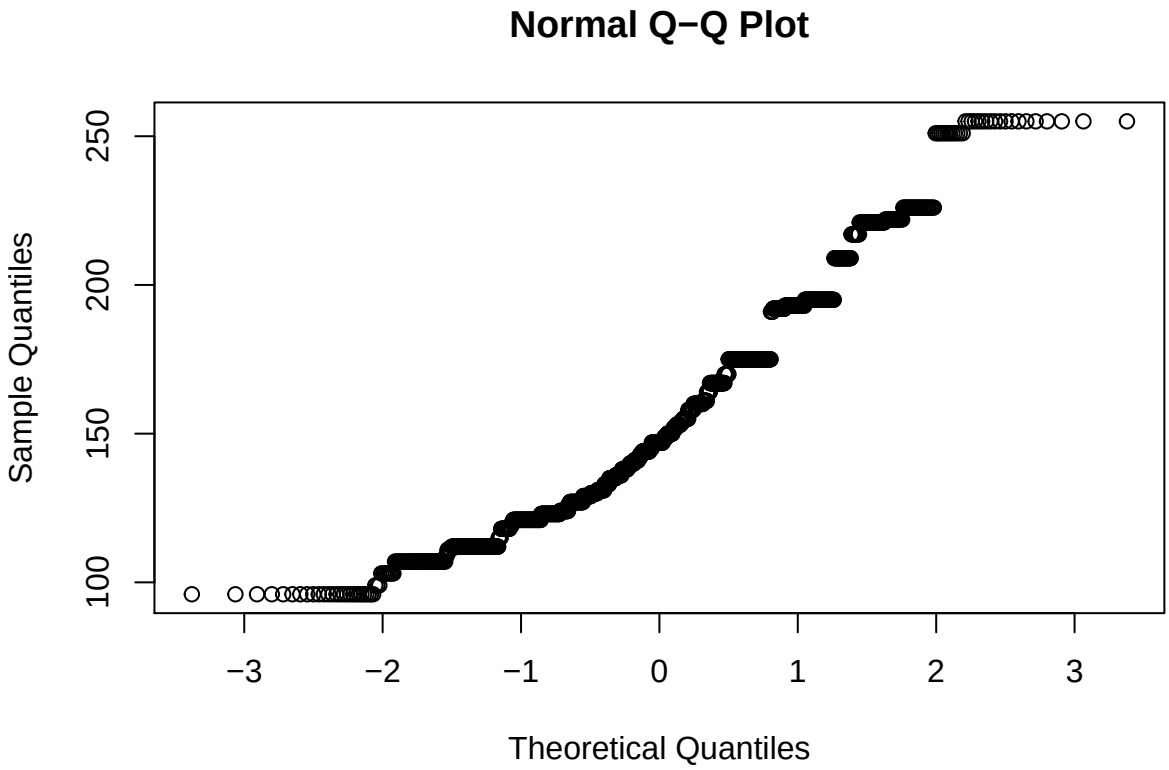
UMBS

Checking for normality

```
hist(final_umbs$half_cover_date)
```



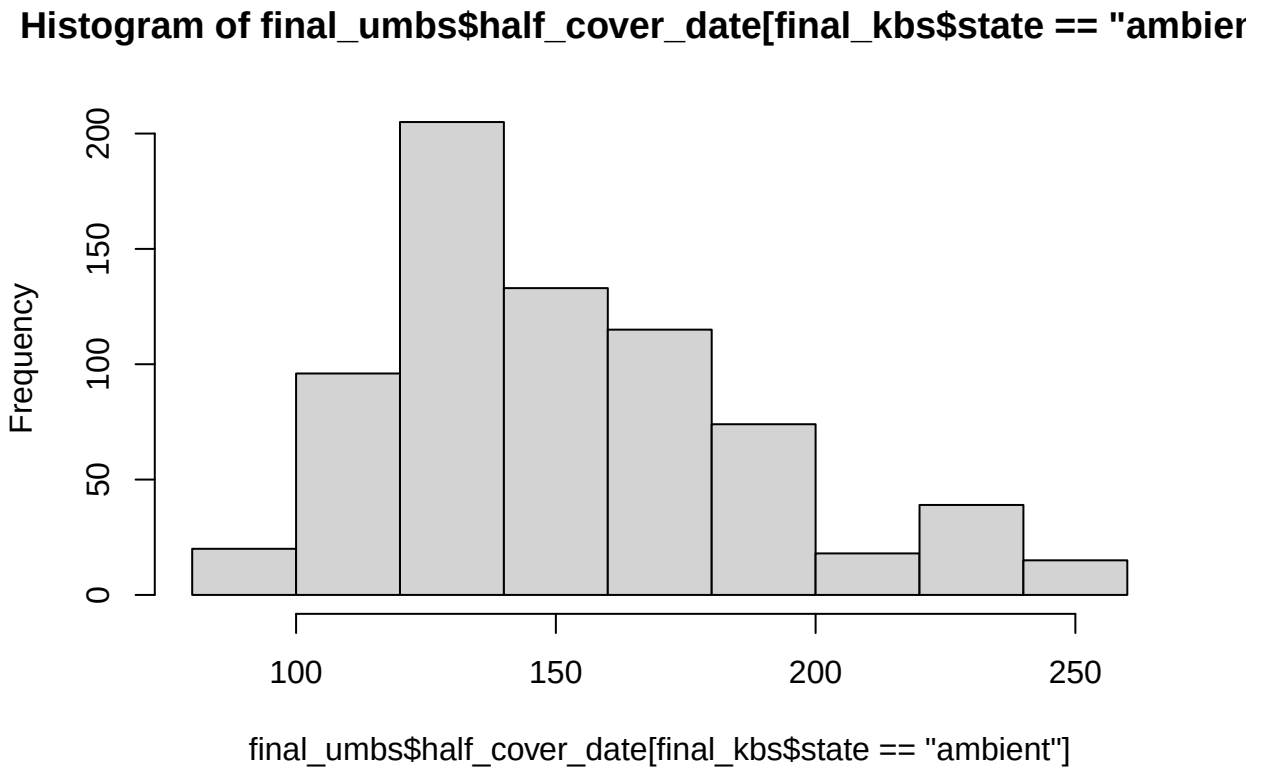

```
qqnorm(final_umbs$half_cover_date)
```



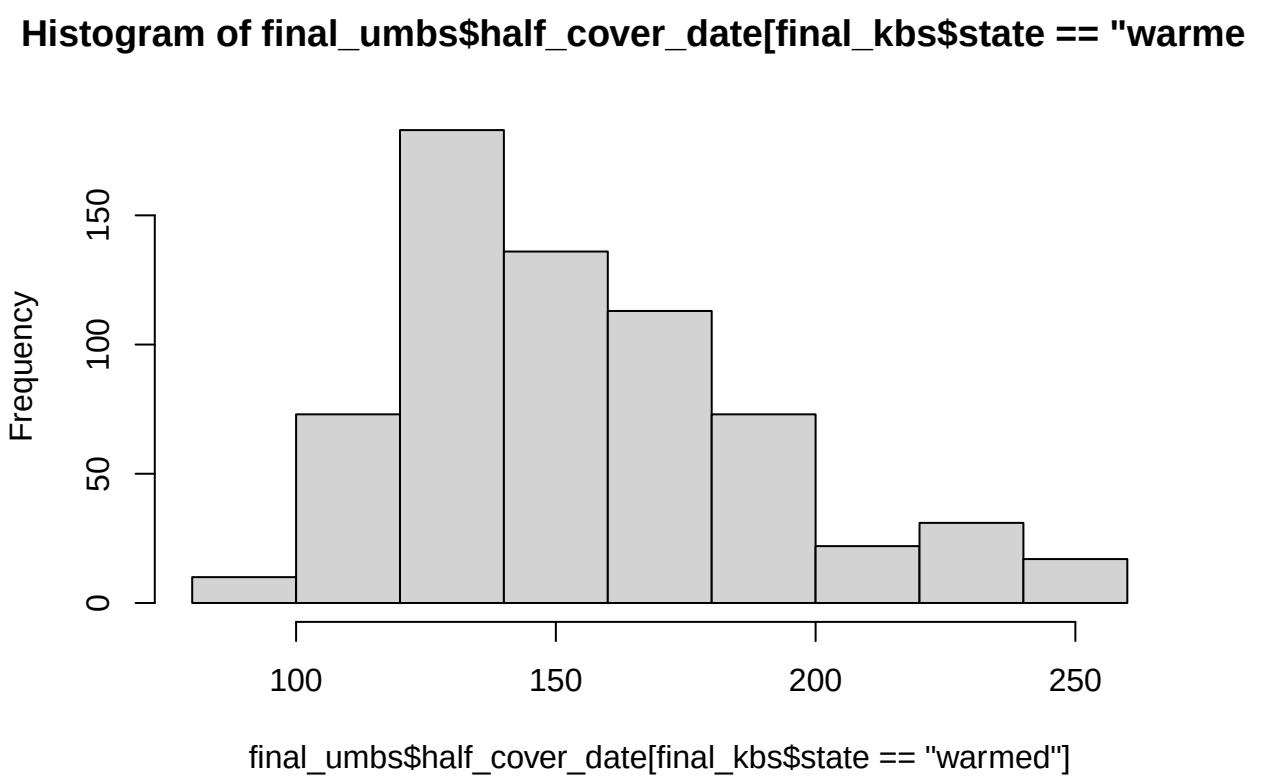

```
shapiro.test(final_umbs$half_cover_date)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  final_umbs$half_cover_date
## W = 0.94754, p-value < 2.2e-16
```

```
hist(final_umbs$half_cover_date[final_kbs$state == "ambient"])
```



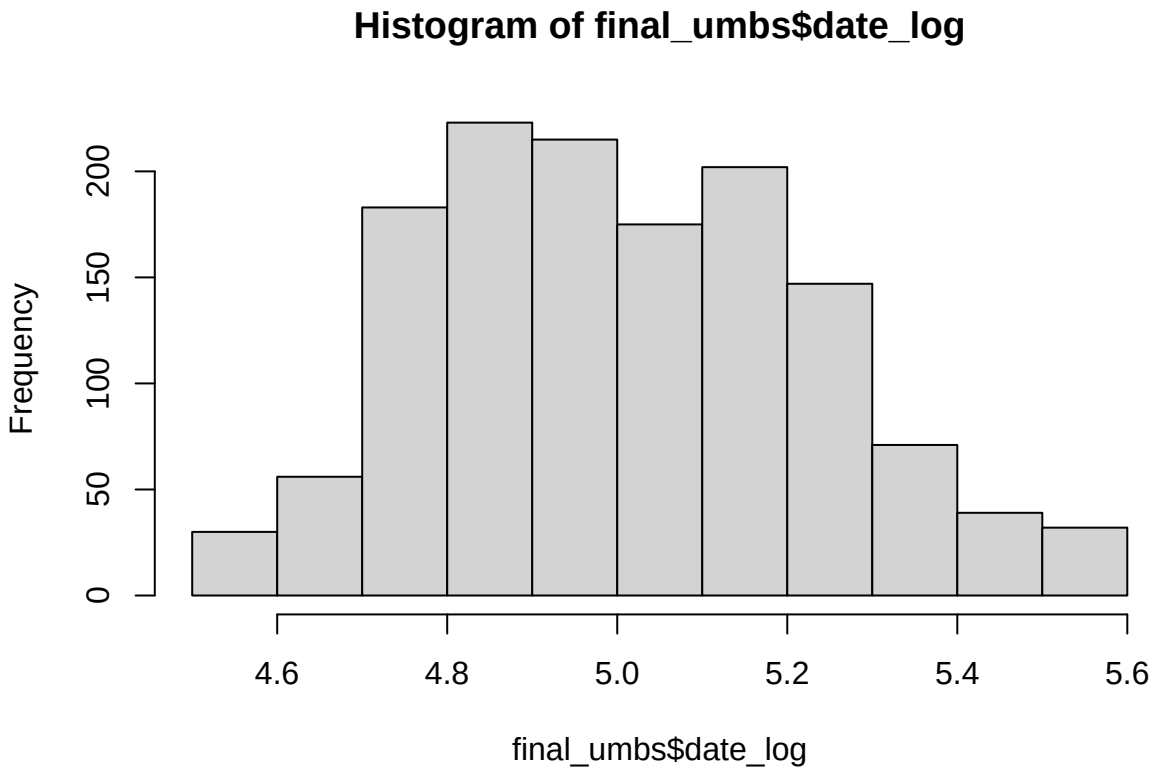

```
hist(final_umbs$half_cover_date[final_kbs$state == "warmed"])
```



These look pretty good

Trying log transformation

```
final_umbs$date_log <- log(final_umbs$half_cover_date)
hist(final_umbs$date_log)
```



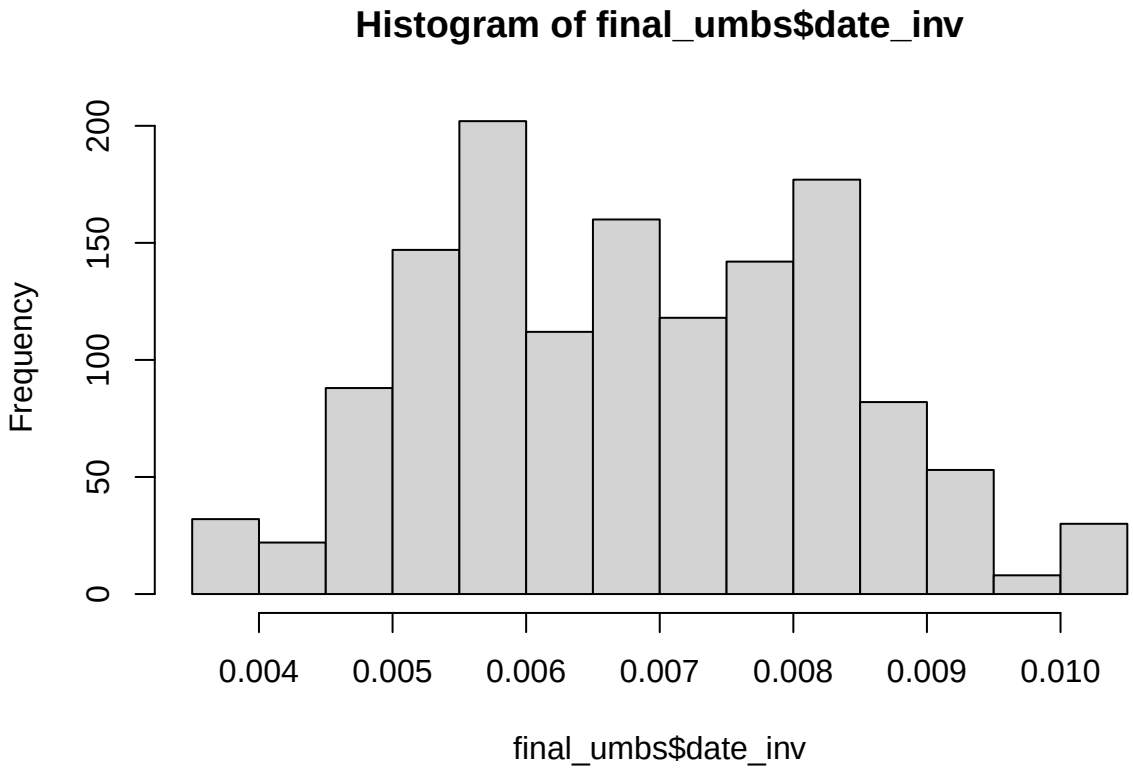

```
shapiro.test(final_umbs$date_log)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  final_umbs$date_log
## W = 0.97728, p-value = 6.765e-14
```

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

Trying inverse tranformation

```
final_umbs$date_inv <- 1/(final_umbs$half_cover_date)
hist(final_umbs$date_inv)
```




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

```
##
##  Shapiro-Wilk normality test
##
## data:  final_umbs$date_inv
## W = 0.97993, p-value = 6.679e-13
```

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