

# warmXtrophic Project: Herbivory Analyses

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## Load in and prepare data for analyses

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

#Load packages
library(tidyverse)
library(lmerTest)
library(olsrr)
library(predictmeans)
library(car)
library(fitdistrplus)
library(MASS)
library(pscl)
library(lmtest)
library(emmeans)
library(bbmle)

# Get data
#Sys.getenv("L1DIR")
L1_dir<-Sys.getenv("L1DIR")
#list.files(L1_dir)
herb <- read.csv(file.path(L1_dir, "herbivory/final_herbivory_L1.csv"))

# changing scale of years
herb$year1<-herb$year
herb$year[herb$year == 2015] <- 1
herb$year[herb$year == 2016] <- 2
herb$year[herb$year == 2017] <- 3
herb$year[herb$year == 2018] <- 4
herb$year[herb$year == 2019] <- 5
herb$year[herb$year == 2020] <- 6

# Remove NAs
herb <- herb[complete.cases(herb),]

# create dataframes for kbs and umbs only for plots with no insecticide
herb_kbs <- subset(herb, site == "kbs" & insecticide == "insects")
herb_umbs <- subset(herb, site == "umbs" & insecticide == "insects")
herb_kbs_in <- subset(herb, site == "kbs")
herb_umbs_in <- subset(herb, site == "umbs")
```

```
# made separate dataframes for insects & no insects because the amount of herbivory measurements between
# each species differs with each, and is relevant for the below data checks
```

```
# only keep species that were recorded in both warmed and ambient plots
```

```
herb_kbs <- herb_kbs %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))
herb_umbs <- herb_umbs %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))
herb_kbs_in <- herb_kbs_in %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))
herb_umbs_in <- herb_umbs_in %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))
```

```
# checking to see if any species/state combos are all zeros
with(herb_kbs, table(species, state, p_eaten == 0))
```

```
## , , = FALSE
##
##      state
## species ambient warmed
##  Cest      78      39
##  Eugr      33      65
##  Hisp      27      11
##  Hype       0       5
##  Phpr      13      21
##  Popr      19      14
##  Soca     192     173
##
```

```
## , , = TRUE
##
##      state
## species ambient warmed
##  Cest      64      42
##  Eugr      44     103
##  Hisp     165     117
##  Hype       8      11
##  Phpr      27      51
##  Popr     183     176
##  Soca     217     244
```

```
with(herb_umbs, table(species, state, p_eaten == 0))
```

```
## , , = FALSE
##
##      state
## species ambient warmed
##  Cape      10      14
##  Cest     142     175
##  Dasp      49      65
##  Hype       9       8
```

```
## Poco      6    43
## Popr      1    11
## Posp     25    17
## Ptaq     27    39
## Ruac     80    98
```

```
##
```

```
## , , = TRUE
```

```
##
```

```
##      state
```

```
## species ambient warmed
```

```
## Cape      70    10
## Cest     182   153
## Dasp     131    87
## Hype      55    40
## Poco       6    21
## Popr     107    85
## Posp      23    47
## Ptaq      29    65
## Ruac      64   102
```

```
with(herb_kbs_in,table(species,state,p_eaten==0))
```

```
## , , = FALSE
```

```
##
```

```
##      state
```

```
## species ambient warmed
```

```
## Asun      23     9
## Brin       4     7
## Ceor       7     4
## Cest     136    68
## Dagl       6     0
## Eugr      78    89
## Hisp      42    22
## Hype       1     6
## Phpr      30    35
## Popr      37    21
## Pore      39     0
## Rual      16     7
## Soca     360   304
## Trpr      20     1
## Trre       0     2
```

```
##
```

```
## , , = TRUE
```

```
##
```

```
##      state
```

```
## species ambient warmed
```

```
## Asun      29     3
## Brin      16    13
## Ceor       5     4
## Cest     116    86
## Dagl      10     8
## Eugr     113   187
## Hisp     285   184
## Hype      31    22
## Phpr      82   129
```

```
##   Popr      388    327
##   Pore       67     4
##   Rual        4     5
##   Soca      466    547
##   Trpr       47     7
##   Trre       24    38
```

```
with(herb_umbs_in,table(species,state,p_eaten==0))
```

```
## , , = FALSE
##
##      state
## species ambient warmed
##   Anma        2      1
##   Cape       22     26
##   Cest      248    299
##   Dasp       74    129
##   Hica        2     10
##   Hype       13     18
##   Poco        6     43
##   Popr        9     15
##   Posp       38     25
##   Ptaq       45     49
##   Ruac      141    144
```

```
## , , = TRUE
##
##      state
## species ambient warmed
##   Anma        2     11
##   Cape      118     82
##   Cest     434    356
##   Dasp     242    228
##   Hica      10      6
##   Hype     147    122
##   Poco       6     33
##   Popr     243    177
##   Posp      70     79
##   Ptaq     111    126
##   Ruac     208    296
```

```
# number of observation per species/state combo (to find rare species)
herb_kbs %>% count(state, species)
```

```
## # A tibble: 14 x 3
## # Groups:   species [7]
##   species state      n
##   <chr>   <chr> <int>
## 1 Cest    ambient  142
## 2 Cest    warmed   81
## 3 Eugr    ambient   77
## 4 Eugr    warmed  168
## 5 Hisp    ambient  192
## 6 Hisp    warmed  128
## 7 Hype    ambient    8
```

```
## 8 Hype    warmed    16
## 9 Phpr    ambient    40
## 10 Phpr   warmed    72
## 11 Popr   ambient   202
## 12 Popr   warmed   190
## 13 Soca   ambient   409
## 14 Soca   warmed   417
```

```
herb_umbs %>% count(state, species)
```

```
## # A tibble: 18 x 3
## # Groups:   species [9]
##   species state     n
##   <chr>    <chr> <int>
## 1 Cape    ambient    80
## 2 Cape    warmed    24
## 3 Cest     ambient   324
## 4 Cest     warmed   328
## 5 Dasp     ambient   180
## 6 Dasp     warmed   152
## 7 Hype     ambient    64
## 8 Hype     warmed    48
## 9 Poco     ambient    12
## 10 Poco    warmed    64
## 11 Popr     ambient   108
## 12 Popr     warmed    96
## 13 Posp     ambient    48
## 14 Posp     warmed    64
## 15 Ptaq     ambient    56
## 16 Ptaq     warmed   104
## 17 Ruac     ambient   144
## 18 Ruac     warmed   200
```

```
herb_kbs_in %>% count(state, species)
```

```
## # A tibble: 30 x 3
## # Groups:   species [15]
##   species state     n
##   <chr>    <chr> <int>
## 1 Asun     ambient    52
## 2 Asun     warmed    12
## 3 Brin     ambient    20
## 4 Brin     warmed    20
## 5 Ceor     ambient    12
## 6 Ceor     warmed     8
## 7 Cest     ambient   252
## 8 Cest     warmed   154
## 9 Dagl     ambient    16
## 10 Dagl    warmed     8
## # ... with 20 more rows
```

```
herb_umbs_in %>% count(state, species)
```

```
## # A tibble: 22 x 3
## # Groups:   species [11]
##   species state     n
```

```
##      <chr>      <chr>      <int>
##  1 Anma      ambient         4
##  2 Anma      warmed        12
##  3 Cape      ambient       140
##  4 Cape      warmed       108
##  5 Cest      ambient       682
##  6 Cest      warmed       655
##  7 Dasp      ambient       316
##  8 Dasp      warmed       357
##  9 Hica      ambient        12
## 10 Hica      warmed         16
## # ... with 12 more rows
```

```
# removing rare species from KBS
```

```
herb_kbs <- herb_kbs[!grepl("Hype",herb_kbs$species),]
herb_kbs_in <- herb_kbs_in[!grepl("Ceor",herb_kbs_in$species),]
herb_kbs_in <- herb_kbs_in[!grepl("Dagl",herb_kbs_in$species),]
herb_kbs_in <- herb_kbs_in[!grepl("Pore",herb_kbs_in$species),]
herb_kbs_in <- herb_kbs_in[!grepl("Trpr",herb_kbs_in$species),]
```

```
# How much of the data is zeros?
```

```
100*sum(herb_kbs$p_eaten == 0)/nrow(herb_kbs) #68% - thats a lot! probably have to use a zero-inflated
```

```
## [1] 67.65817
```

```
# but I'll still check for normality & try some transformations below
```

```
100*sum(herb_umbs$p_eaten == 0)/nrow(herb_umbs) #61%
```

```
## [1] 60.92557
```

```
100*sum(herb_kbs_in$p_eaten == 0)/nrow(herb_kbs_in) #70.5%
```

```
## [1] 70.46903
```

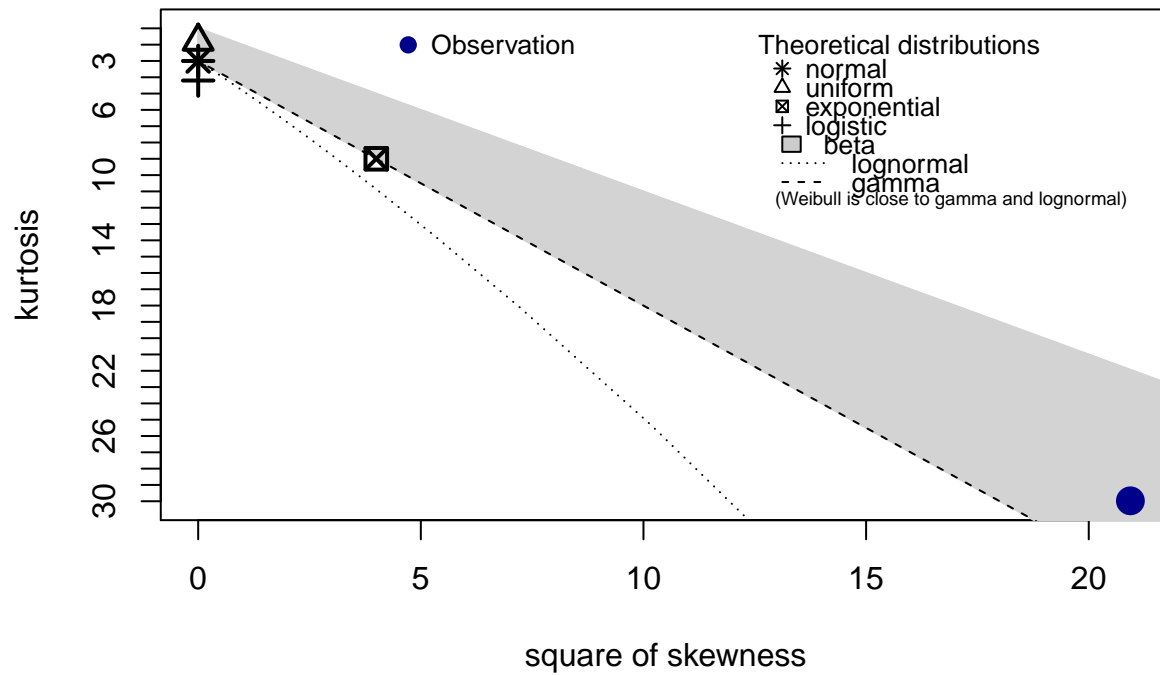
```
100*sum(herb_umbs_in$p_eaten == 0)/nrow(herb_umbs_in) #69.6%
```

```
## [1] 69.57009
```

## KBS Data Exploration

```
descdist(herb_kbs$p_eaten, discrete = FALSE)
```

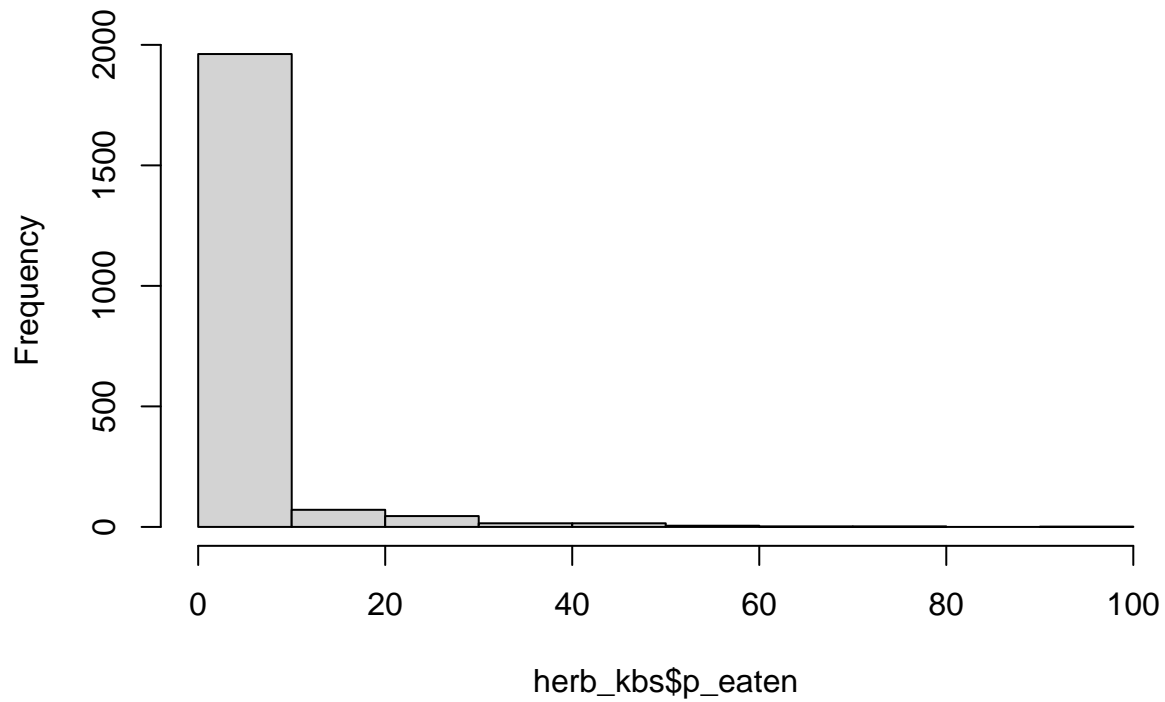
## Cullen and Frey graph



```
## summary statistics
## -----
## min: 0    max: 100
## median: 0
## mean: 3.1322
## estimated sd: 8.497325
## estimated skewness: 4.575498
## estimated kurtosis: 29.97498
```

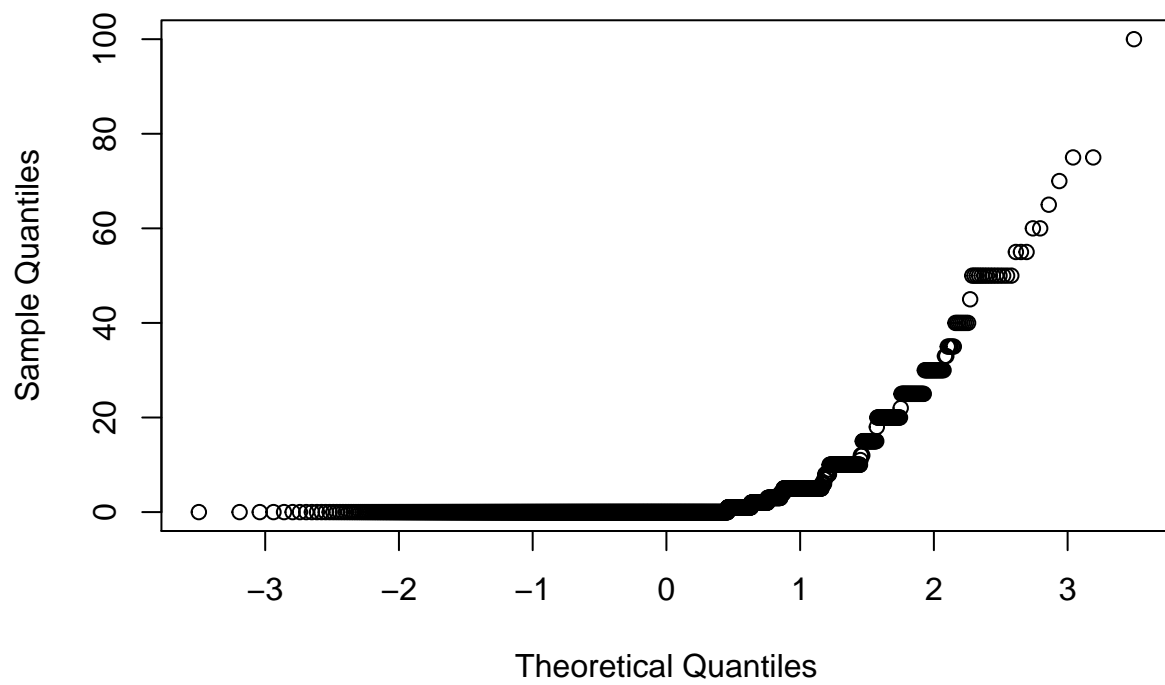
```
# normal distribution?
hist(herb_kbs$p_eaten)
```

Histogram of herb\_kbs\$p\_eaten



```
qqnorm(herb_kbs$p_eaten)
```

Normal Q-Q Plot

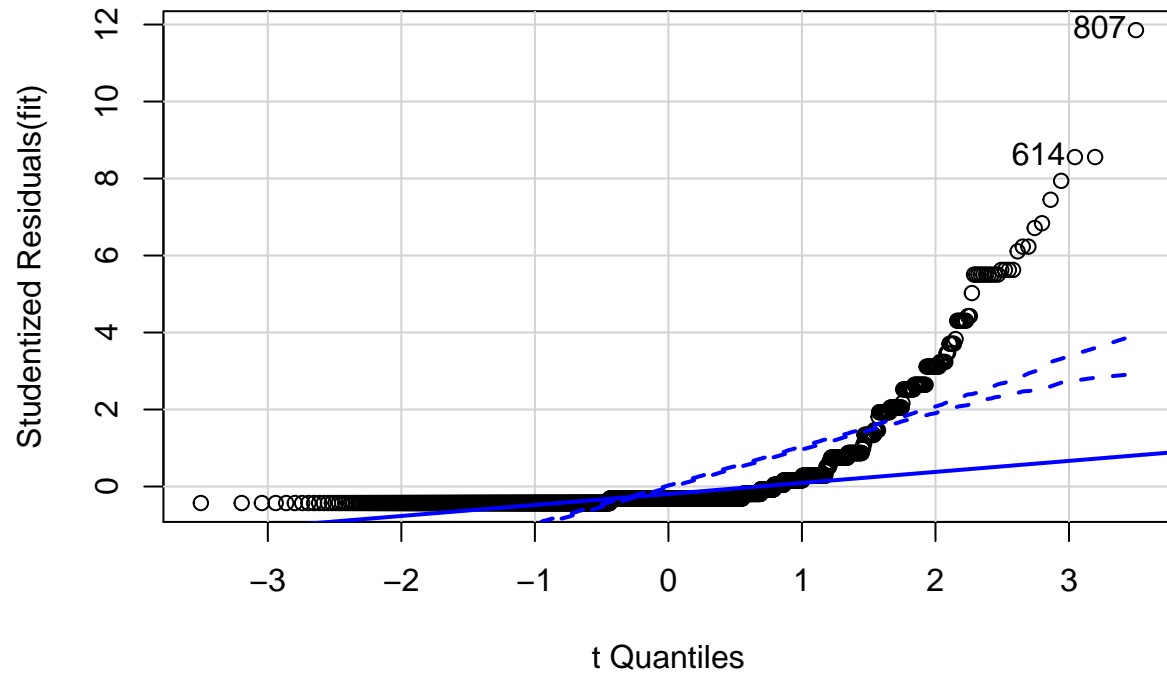


```
shapiro.test(herb_kbs$p_eaten)
```

```
##
```

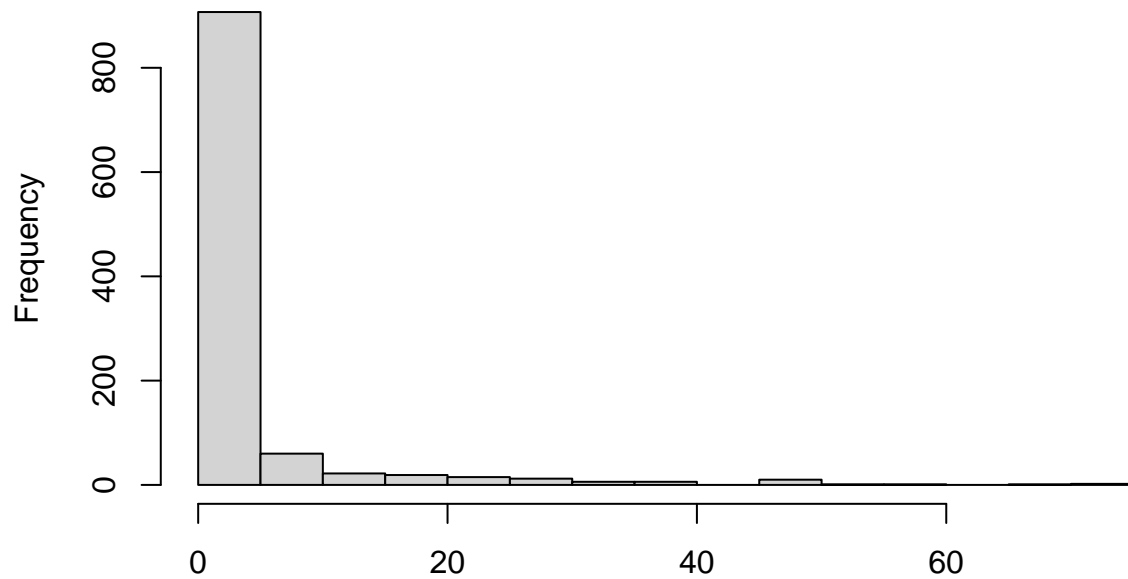


```
## Shapiro-Wilk normality test
##
## data: herb_kbs$p_eaten
## W = 0.41878, p-value < 2.2e-16
fit <- lm(p_eaten~state, data = herb_kbs)
qqPlot(fit)
```



```
## [1] 614 807
# looking at each treatment separately
hist(herb_kbs$p_eaten[herb_kbs$state == "ambient"])
```

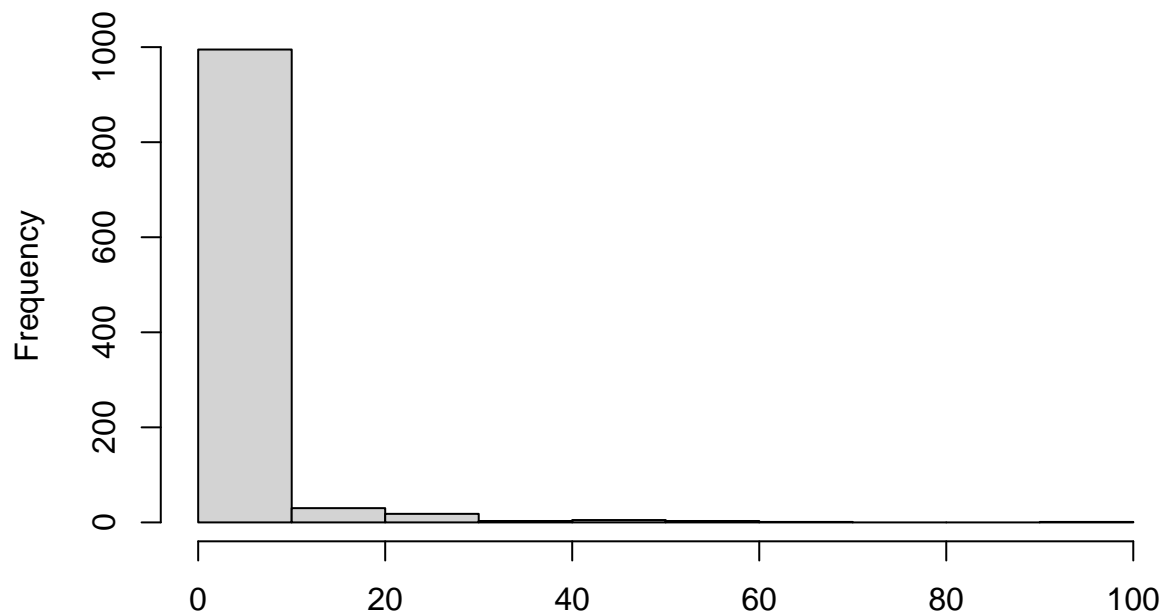
**Histogram of herb\_kbs\$p\_eaten[herb\_kbs\$state == "ambient"]**



`herb_kbs$p_eaten[herb_kbs$state == "ambient"]`

```
hist(herb_kbs$p_eaten[herb_kbs$state == "warmed"])
```

**Histogram of herb\_kbs\$p\_eaten[herb\_kbs\$state == "warmed"]**



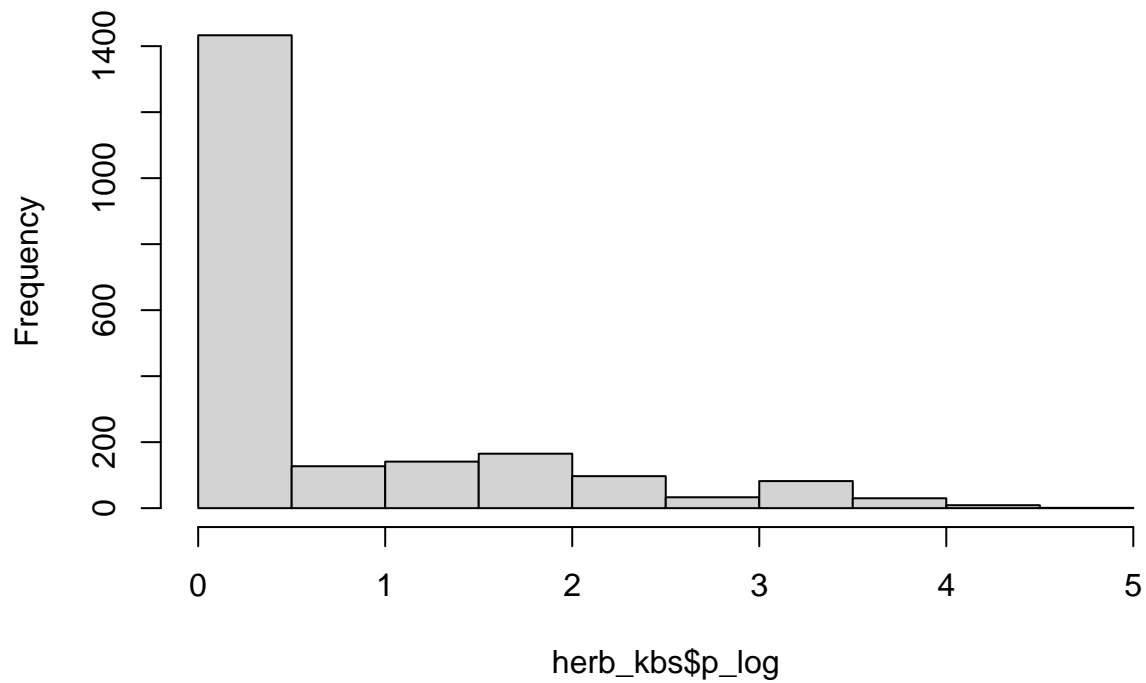
`herb_kbs$p_eaten[herb_kbs$state == "warmed"]`

```
# gamma distribution? - error message "the function mle failed to estimate the parameters"  
#fit.gamma <- fitdist(herb_kbs$p_eaten, "gamma")  
#plot(fit.gamma)
```

```
# lognormal distribution? - error message "values must be positive to fit a lognormal"
#fit.ln <- fitdist(herb_kbs$p_eaten, "lnorm")
#plot(fit.ln)

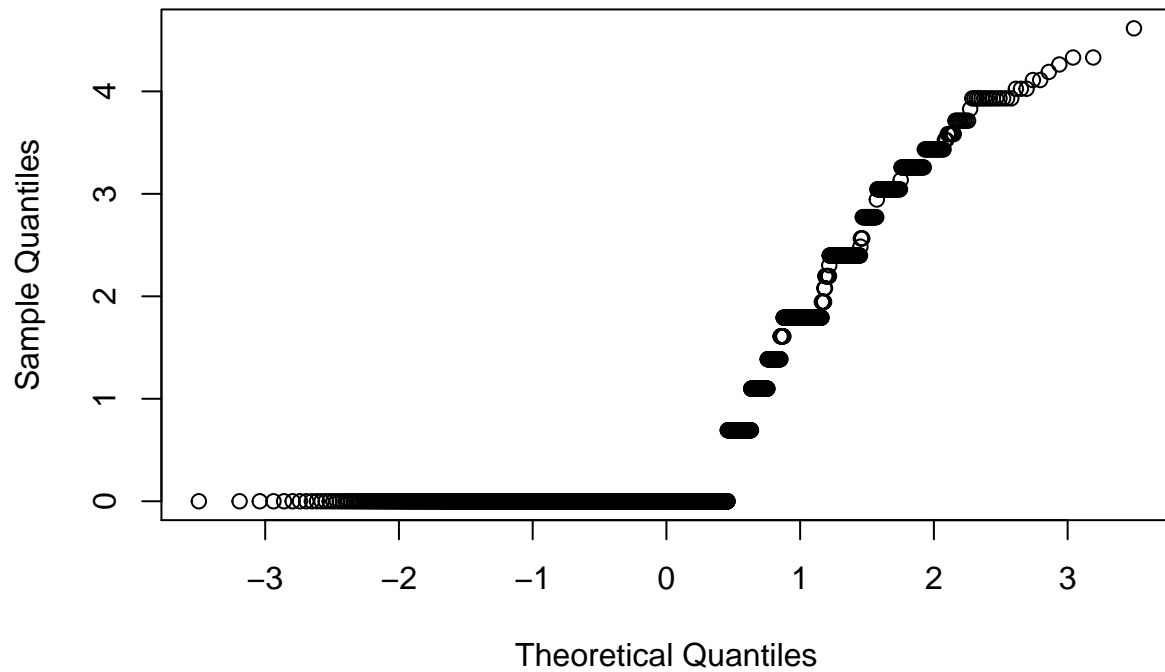
# log transform
herb_kbs$p_log <- log(herb_kbs$p_eaten+1)
hist(herb_kbs$p_log)
```

**Histogram of herb\_kbs\$p\_log**



```
qqnorm(herb_kbs$p_log)
```

## Normal Q-Q Plot



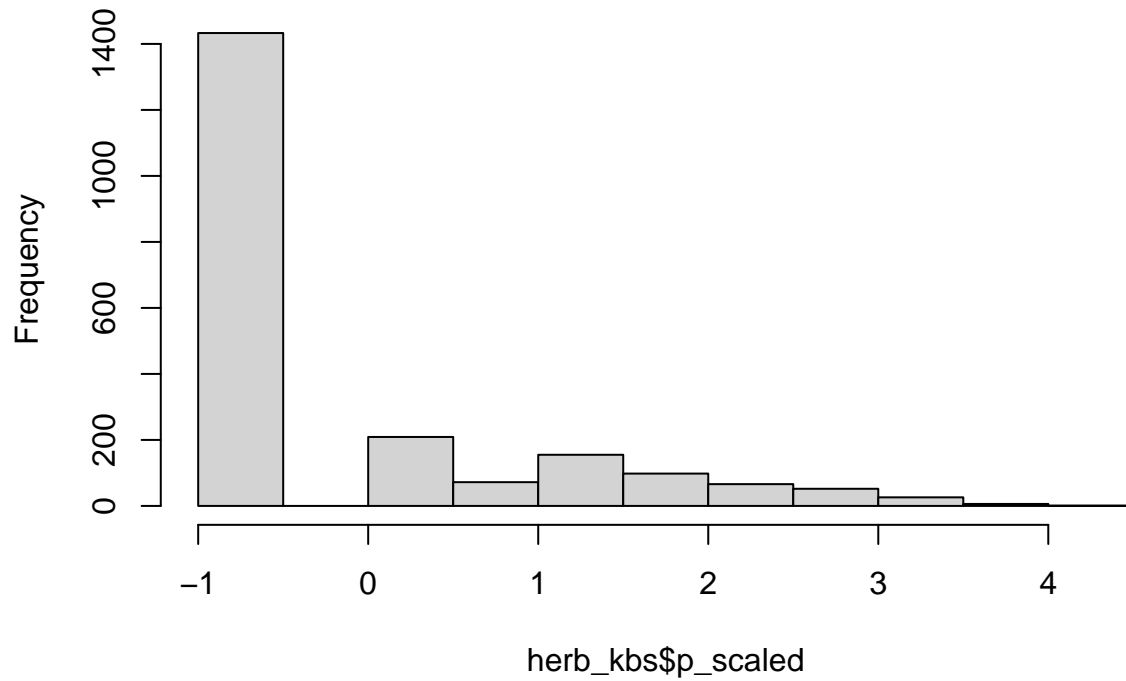
```
shapiro.test(herb_kbs$p_log) # NAs - data contains 0s
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: herb_kbs$p_log  
## W = 0.65296, p-value < 2.2e-16
```

```
# mean centering p_eaten
```

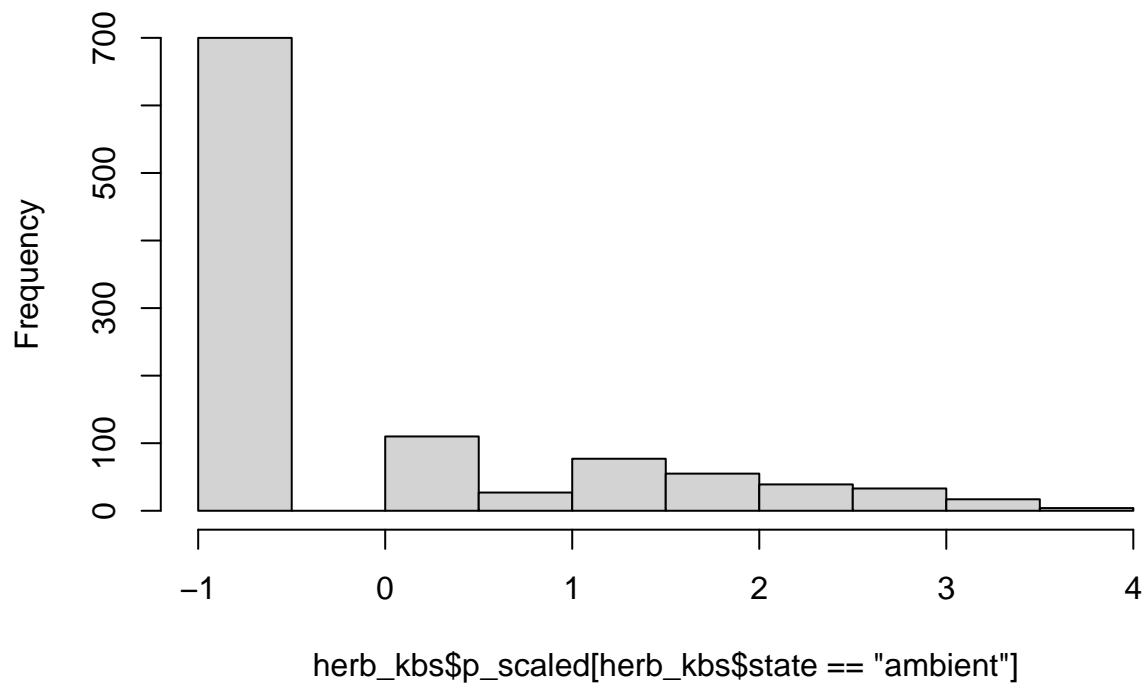
```
herb_kbs$p_scaled <- herb_kbs$p_log - mean(herb_kbs$p_log)  
hist(herb_kbs$p_scaled)
```

**Histogram of herb\_kbs\$p\_scaled**



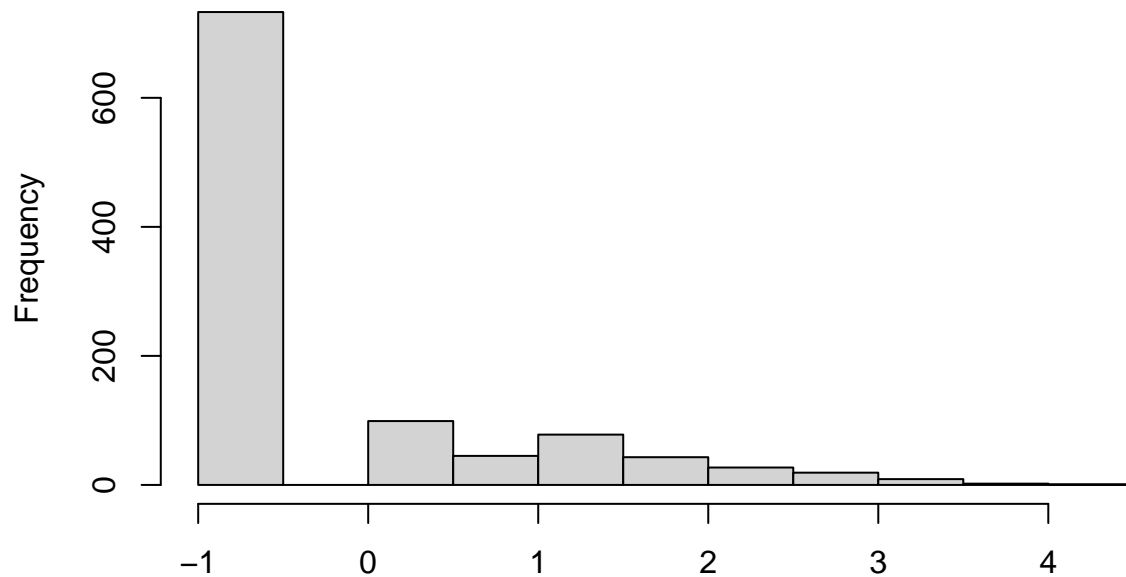
```
hist(herb_kbs$p_scaled[herb_kbs$state == "ambient"])
```

**Histogram of herb\_kbs\$p\_scaled[herb\_kbs\$state == "ambient"]**



```
hist(herb_kbs$p_scaled[herb_kbs$state == "warmed"])
```

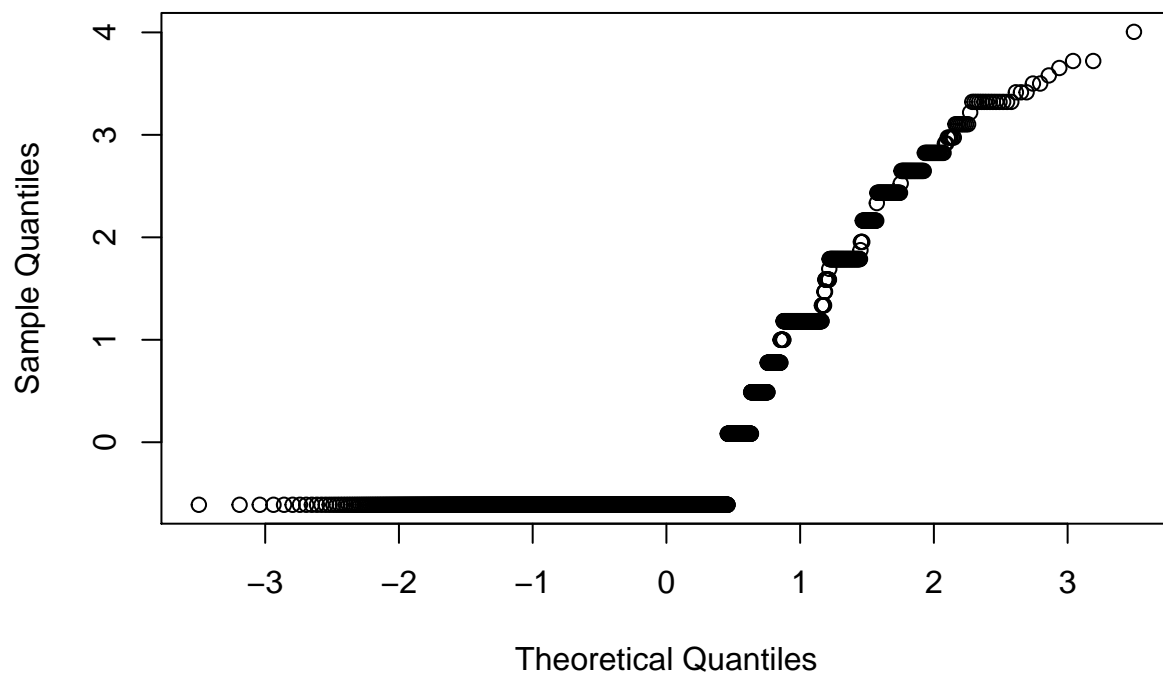
**Histogram of herb\_kbs\$p\_scaled[herb\_kbs\$state == "warmed"]**



herb\_kbs\$p\_scaled[herb\_kbs\$state == "warmed"]

```
qqnorm(herb_kbs$p_scaled)
```

**Normal Q-Q Plot**

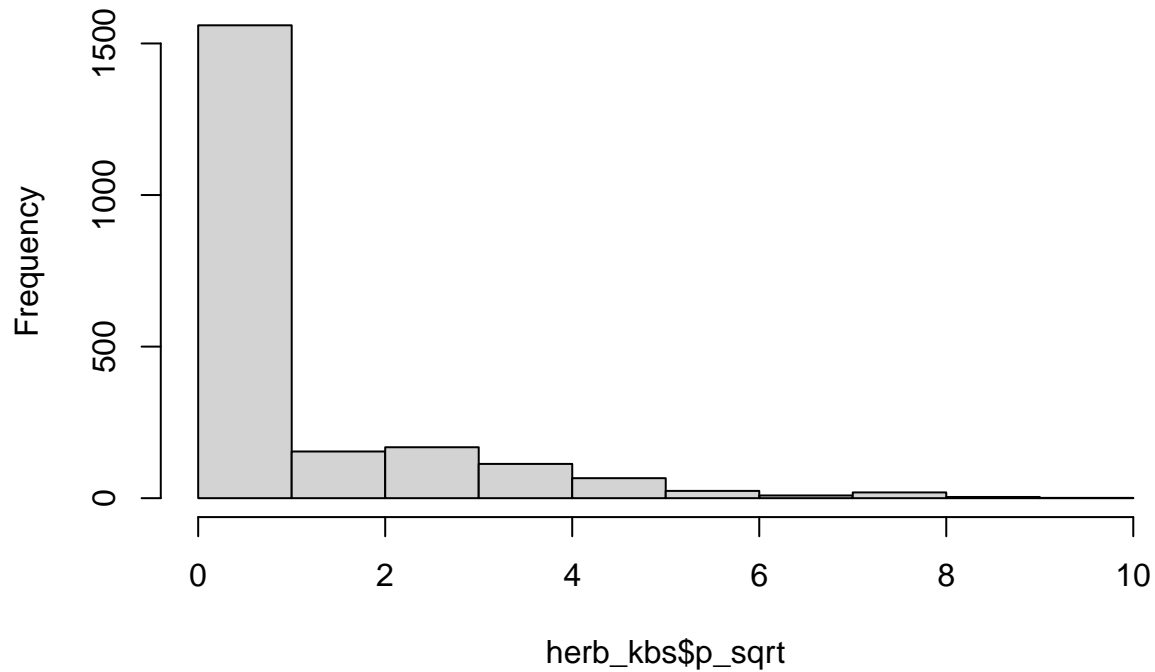


```
shapiro.test(herb_kbs$p_scaled)
```

```
##
```

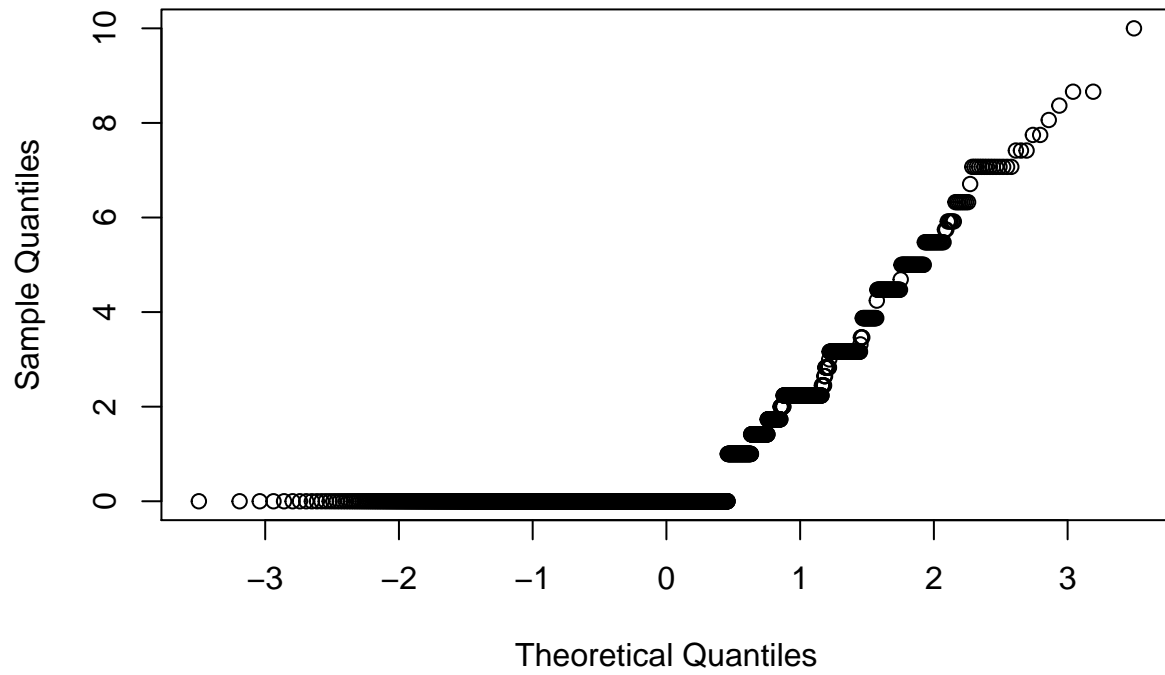
```
## Shapiro-Wilk normality test
##
## data: herb_kbs$p_scaled
## W = 0.65296, p-value < 2.2e-16
# square root?
herb_kbs$p_sqrt <- sqrt(herb_kbs$p_eaten)
hist(herb_kbs$p_sqrt)
```

**Histogram of herb\_kbs\$p\_sqrt**



```
qqnorm(herb_kbs$p_sqrt)
```

## Normal Q-Q Plot



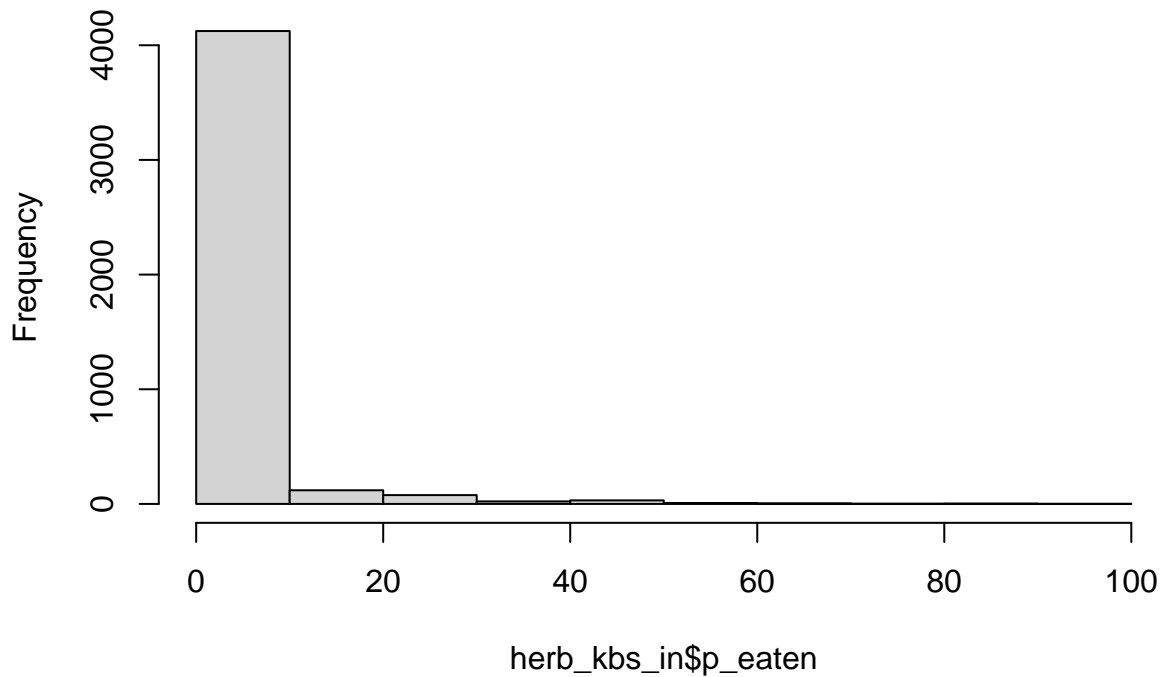
```
shapiro.test(herb_kbs$p_sqrt)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  herb_kbs$p_sqrt  
## W = 0.62798, p-value < 2.2e-16
```

```
# quick look at insecticide plots  
hist(herb_kbs_in$p_eaten)
```



## Histogram of herb\_kbs\_in\$p\_eaten



Transformations are a no-go

Going to try a zero-inflated model due to the excess number of zeros in the data

```
# mean and var of non-zero counts
herb_kbs %>%
  dplyr::filter(p_eaten != "0") %>%
  dplyr::summarize(mean_eaten = mean(p_eaten, na.rm=T), var_eaten = var(p_eaten, na.rm=T))

## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 6 x 3
##   species mean_eaten var_eaten
##   <chr>      <dbl>    <dbl>
## 1 Cest        9.41     156.
## 2 Eugr        6.60      66.3
## 3 Hisp       10.9     210.
## 4 Phpr       14.3     445.
## 5 Popr       17.8     455.
## 6 Soca        9.31     120.

herb_kbs_in %>%
  dplyr::filter(p_eaten != "0") %>%
  dplyr::summarize(mean_eaten = mean(p_eaten, na.rm=T), var_eaten = var(p_eaten, na.rm=T))

## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 11 x 3
##   species mean_eaten var_eaten
##   <chr>      <dbl>    <dbl>
## 1 Asun       14.2     153.
```

```
## 2 Brin      34.6    555.
## 3 Cest      9.78    169.
## 4 Eugr      4.89     47.4
## 5 Hisp     11.1    215.
## 6 Hype      4.71     8.24
## 7 Phpr     14.9    551.
## 8 Popr     18.5    407.
## 9 Rual      4.04    16.2
## 10 Soca     8.10    97.0
## 11 Trre     5.5     40.5
```

```
# variance is also > mean, so can't be poisson
# I'll try zero-inflated negative binomial due to an excess of zeros
```

## Models for non-insecticide plots (KBS)

```
# zero-inflated negative binomial
# state as a fixed effect
k.m1 <- zeroinfl(p_eaten ~ state,
                 dist = 'negbin',
                 data = herb_kbs)
#summary(k.m1)

# state and year as fixed effects
k.m2 <- zeroinfl(p_eaten ~ state + as.factor(year),
                 dist = 'negbin',
                 data = herb_kbs)
#summary(k.m2)
lrtest(k.m1, k.m2) # model 2
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state
## Model 2: p_eaten ~ state + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1    5 -3478.4
## 2   15 -3324.2 10  308.54 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# state and growth habit as fixed effects
herb_kbs <- within(herb_kbs, growth_habit <- relevel(factor(growth_habit), ref = "Forb")) # releveling
k.m3 <- zeroinfl(p_eaten ~ state + growth_habit,
                 dist = 'negbin',
                 data = herb_kbs)
#summary(k.m3)
lrtest(k.m2, k.m3) # model 2
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + as.factor(year)
## Model 2: p_eaten ~ state + growth_habit
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   15 -3324.2
## 2    9 -3340.4 -6  32.431  1.349e-05 ***
```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# state, growth habit, and year as fixed effects
k.m4 <- zeroinfl(p_eaten ~ state + growth_habit + as.factor(year),
                dist = 'negbin',
                data = herb_kbs)

#summary(k.m4)
lrtest(k.m2, k.m4) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + as.factor(year)
## Model 2: p_eaten ~ state + growth_habit + as.factor(year)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   15 -3324.2
## 2   19 -3155.4  4 337.52 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and growth habit as fixed effects
k.m5 <- zeroinfl(p_eaten ~ state * growth_habit,
                dist = 'negbin',
                data = herb_kbs)

#summary(k.m5)
lrtest(k.m4, k.m5) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   19 -3155.4
## 2   13 -3339.4 -6 367.97 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and growth habit as fixed effects, plus year
k.m6 <- zeroinfl(p_eaten ~ state * growth_habit + as.factor(year),
                dist = 'negbin',
                data = herb_kbs)

summary(k.m6)

##
## Call:
## zeroinfl(formula = p_eaten ~ state * growth_habit + as.factor(year),
##          data = herb_kbs, dist = "negbin")
##
## Pearson residuals:
##      Min       1Q   Median       3Q      Max
## -0.7380 -0.4559 -0.2932 -0.1375  24.8209
##
## Count model coefficients (negbin with log link):
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.470803   0.149260   3.154  0.00161 **
## statewarmed    -0.155999   0.095415  -1.635  0.10206

```

```
## growth_habit -0.312403 0.228490 -1.367 0.17155
## growth_habitGraminoid 1.234010 0.214060 5.765 8.18e-09 ***
## as.factor(year)2 1.041649 0.164115 6.347 2.19e-10 ***
## as.factor(year)3 2.069581 0.192776 10.736 < 2e-16 ***
## as.factor(year)4 2.216598 0.177989 12.454 < 2e-16 ***
## as.factor(year)5 2.207352 0.169315 13.037 < 2e-16 ***
## as.factor(year)6 -0.487341 0.237227 -2.054 0.03994 *
## statearmed:growth_habit -0.001963 0.407694 -0.005 0.99616
## statearmed:growth_habitGraminoid -0.504858 0.287675 -1.755 0.07927 .
## Log(theta) -0.129596 0.101683 -1.275 0.20248
##
## Zero-inflation model coefficients (binomial with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.6332 3.3116 -1.097 0.273
## statearmed 0.2195 0.1603 1.369 0.171
## growth_habit 2.1203 0.2563 8.272 <2e-16 ***
## growth_habitGraminoid 2.4782 0.2395 10.346 <2e-16 ***
## as.factor(year)2 2.6837 3.2845 0.817 0.414
## as.factor(year)3 3.9208 3.3036 1.187 0.235
## as.factor(year)4 3.6122 3.3012 1.094 0.274
## as.factor(year)5 3.0516 3.2986 0.925 0.355
## as.factor(year)6 3.4608 3.2955 1.050 0.294
## statearmed:growth_habit 0.3307 0.4308 0.767 0.443
## statearmed:growth_habitGraminoid -0.3176 0.3139 -1.012 0.312
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8785
## Number of iterations in BFGS optimization: 34
## Log-likelihood: -3153 on 23 Df
```

```
lrtest(k.m4, k.m6) # virtually the same, keeping model 4 because its simpler
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit + as.factor(year)
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 23 -3153.0 4 4.7846 0.3101
```

```
# calculating effect size of graminoids vs forb herbivory - accounting for log link
exp(0.470803 + 1.234010*0) # 1.60128
```

```
## [1] 1.60128
```

```
exp(0.470803 + 1.234010*1) # 5.500357
```

```
## [1] 5.500357
```

```
# effect of herbivory:
5.500357 - 1.60128 # 3.899077
```

```
## [1] 3.899077
```

```
# interaction between state, growth habit, and year (year as a factor wouldn't work - non-finite value)
k.m7 <- zeroinfl(p_eaten ~ state * growth_habit * year,
  dist = 'negbin',
```

```

data = herb_kbs)
#summary(k.m7)
lrtest(k.m4, k.m7) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit * year
##   #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 25 -3266.0 6 221.1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# state and origin as fixed effects
herb_kbs <- within(herb_kbs, origin <- relevel(factor(origin), ref = "Native")) # releveling so native
k.m8 <- zeroinfl(p_eaten ~ state + origin,
                 dist = 'negbin',
                 data = herb_kbs)

#summary(k.m8)
lrtest(k.m4, k.m8) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + origin
##   #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 9 -3398.8 -10 486.71 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# state, origin, and year as fixed effects
k.m9 <- zeroinfl(p_eaten ~ state + origin + as.factor(year),
                 dist = 'negbin',
                 data = herb_kbs)

summary(k.m9)

##
## Call:
## zeroinfl(formula = p_eaten ~ state + origin + as.factor(year), data = herb_kbs,
##   dist = "negbin")
##
## Pearson residuals:
##      Min       1Q   Median       3Q      Max
## -0.7219 -0.4221 -0.3205 -0.1137  24.9342
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.45619    0.13519   3.375 0.000739 ***
## statewarmed   -0.15828    0.08981  -1.762 0.078000 .
## originBoth    -0.31058    0.19804  -1.568 0.116816
## originExotic   0.30246    0.10637   2.843 0.004462 **
## as.factor(year)2 1.30567    0.15286   8.542 < 2e-16 ***
## as.factor(year)3 2.06704    0.18635  11.092 < 2e-16 ***

```

```
## as.factor(year)4 2.12925 0.16958 12.556 < 2e-16 ***
## as.factor(year)5 2.22129 0.15866 14.000 < 2e-16 ***
## as.factor(year)6 -0.48355 0.23247 -2.080 0.037519 *
## Log(theta) -0.15767 0.09422 -1.673 0.094258 .
##
## Zero-inflation model coefficients (binomial with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.1976 0.8412 -3.801 0.000144 ***
## statearmed 0.2822 0.1211 2.331 0.019764 *
## originBoth 2.1256 0.2095 10.146 < 2e-16 ***
## originExotic 1.4067 0.1408 9.989 < 2e-16 ***
## as.factor(year)2 2.4214 0.8309 2.914 0.003565 **
## as.factor(year)3 3.2969 0.8462 3.896 9.77e-05 ***
## as.factor(year)4 3.1316 0.8380 3.737 0.000186 ***
## as.factor(year)5 2.7791 0.8364 3.323 0.000892 ***
## as.factor(year)6 2.9608 0.8787 3.370 0.000753 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8541
## Number of iterations in BFGS optimization: 27
## Log-likelihood: -3229 on 19 Df
```

```
lrtest(k.m4, k.m9) # model 4
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + origin + as.factor(year)
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 19 -3229.1 0 147.37 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# interaction between state and origin as fixed effects
```

```
k.m10 <- zeroinfl(p_eaten ~ state * origin,
  dist = 'negbin',
  data = herb_kbs)
```

```
#summary(k.m10)
```

```
lrtest(k.m4, k.m10) # model 4
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * origin
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 13 -3398.6 -6 486.43 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# interaction between state and origin as fixed effects, plus year
```

```
k.m11 <- zeroinfl(p_eaten ~ state * origin + as.factor(year),
  dist = 'negbin',
  data = herb_kbs)
```

```
summary(k.m11)
```

```
##
## Call:
## zeroinfl(formula = p_eaten ~ state * origin + as.factor(year), data = herb_kbs,
##   dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.7179 -0.4281 -0.3252 -0.1216 24.4702
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.43056    0.13973   3.081  0.00206 **
## statewarmed      -0.11188    0.10810  -1.035  0.30070
## originBoth       -0.28071    0.23332  -1.203  0.22893
## originExotic      0.37613    0.13409   2.805  0.00503 **
## as.factor(year)2    1.30898    0.15326   8.541 < 2e-16 ***
## as.factor(year)3    2.08185    0.18733  11.113 < 2e-16 ***
## as.factor(year)4    2.12297    0.16979  12.504 < 2e-16 ***
## as.factor(year)5    2.22721    0.15904  14.004 < 2e-16 ***
## as.factor(year)6   -0.49356    0.23250  -2.123  0.03377 *
## statewarmed:originBoth -0.07068    0.41642  -0.170  0.86521
## statewarmed:originExotic -0.17972    0.20005  -0.898  0.36899
## Log(theta)       -0.15837    0.09430  -1.679  0.09307 .
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -3.1704     0.8721  -3.635  0.000277 ***
## statewarmed      0.1815     0.1675   1.084  0.278495
## originBoth       1.9865     0.2571   7.727 1.10e-14 ***
## originExotic     1.3201     0.1846   7.149 8.73e-13 ***
## as.factor(year)2    2.4473     0.8574   2.854  0.004312 **
## as.factor(year)3    3.3156     0.8726   3.800  0.000145 ***
## as.factor(year)4    3.1585     0.8639   3.656  0.000256 ***
## as.factor(year)5    2.8081     0.8626   3.255  0.001132 **
## as.factor(year)6    2.9887     0.9019   3.314  0.000920 ***
## statewarmed:originBoth 0.3577     0.4303   0.831  0.405808
## statewarmed:originExotic 0.1720     0.2586   0.665  0.505956
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8535
## Number of iterations in BFGS optimization: 31
## Log-likelihood: -3228 on 23 Df
lrtest(k.m4, k.m11) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * origin + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   19 -3155.4
```

```

## 2 23 -3228.1 4 145.36 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

exp(0.43056 + 0.37613*0) # 1.538119

## [1] 1.538119

exp(0.43056 + 0.37613*1) # 2.24048

## [1] 2.24048

# effect of herbivory:
2.24048 - 1.538119 # 0.702361

## [1] 0.702361

# interaction between state, origin, and year
k.m12 <- zeroinfl(p_eaten ~ state * origin * year,
                 dist = 'negbin',
                 data = herb_kbs)

#summary(k.m12)
lrtest(k.m4, k.m12) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * origin * year
##   #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 25 -3332.6 6 354.47 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# just origin - testing to see w/o state
k.m12.2 <- zeroinfl(p_eaten ~ origin,
                   dist = 'negbin',
                   data = herb_kbs)

#summary(k.m12.2)

# state and species as fixed effects
k.m13 <- zeroinfl(p_eaten ~ state + species,
                 dist = 'negbin',
                 data = herb_kbs)

#summary(k.m13)
lrtest(k.m4, k.m13) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + species
##   #Df LogLik Df Chisq Pr(>Chisq)
## 1 19 -3155.4
## 2 15 -3318.4 -4 326.01 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



```

# state, species and year as fixed effects
k.m14 <- zeroinfl(p_eaten ~ state + species + as.factor(year),
                 dist = 'negbin',
                 data = herb_kbs)

summary(k.m14)

##
## Call:
## zeroinfl(formula = p_eaten ~ state + species + as.factor(year), data = herb_kbs,
##          dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.7568 -0.4595 -0.2437 -0.1264 24.5632
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.27490    0.14310   1.921  0.0547 .
## statearmed     -0.22879    0.08973  -2.550  0.0108 *
## speciesEugr     0.30066    0.17100   1.758  0.0787 .
## speciesHisp    -0.08568    0.21913  -0.391  0.6958
## speciesPhpr     0.96249    0.23019   4.181 2.90e-05 ***
## speciesPopr     1.45768    0.23949   6.087 1.15e-09 ***
## speciesSoca     0.27379    0.12256   2.234  0.0255 *
## as.factor(year)2 1.00539    0.14799   6.794 1.09e-11 ***
## as.factor(year)3 2.11838    0.17565  12.060 < 2e-16 ***
## as.factor(year)4 2.25866    0.15781  14.313 < 2e-16 ***
## as.factor(year)5 2.18186    0.14707  14.835 < 2e-16 ***
## as.factor(year)6 -0.53881    0.23597  -2.283  0.0224 *
## Log(theta)     -0.16853    0.09807  -1.718  0.0857 .
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -16.0545  1638.7804  -0.010  0.9922
## statearmed     0.1933    0.1357   1.425  0.1542
## speciesEugr     0.5715    0.3900   1.465  0.1429
## speciesHisp     2.8006    0.3579   7.825 5.09e-15 ***
## speciesPhpr     1.7573    0.4182   4.202 2.64e-05 ***
## speciesPopr     3.4030    0.3744   9.090 < 2e-16 ***
## speciesSoca     0.6532    0.3048   2.143  0.0321 *
## as.factor(year)2 14.6235  1638.7802   0.009  0.9929
## as.factor(year)3 15.8370  1638.7802   0.010  0.9923
## as.factor(year)4 15.4532  1638.7802   0.009  0.9925
## as.factor(year)5 14.7907  1638.7803   0.009  0.9928
## as.factor(year)6 15.2518  1638.7804   0.009  0.9926
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8449
## Number of iterations in BFGS optimization: 50
## Log-likelihood: -3135 on 25 Df

```

```

lrtest(k.m4, k.m14) # model 14

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + species + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   19 -3155.4
## 2   25 -3135.2  6 40.308  3.962e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# calculating effect size - accounting for log link
exp(0.27490 + -0.22879*0) # 1.316399

## [1] 1.316399

exp(0.27490 + -0.22879*1) # 1.04719

## [1] 1.04719

# effect of herbivory:
1.04719 - 1.316399 # -0.269209

## [1] -0.269209

# interaction between state and species as fixed effects, plus year
k.m15 <- zeroinfl(p_eaten ~ state * species + as.factor(year),
                  dist = 'negbin',
                  data = herb_kbs)

summary(k.m15)

##
## Call:
## zeroinfl(formula = p_eaten ~ state * species + as.factor(year), data = herb_kbs,
##   dist = "negbin")
##
## Pearson residuals:
##      Min       1Q   Median       3Q      Max
## -0.7484 -0.4512 -0.2436 -0.1453  24.4209
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.28180    0.16239   1.735   0.0827 .
## statearmed     -0.30056    0.21826  -1.377   0.1685
## speciesEugr     0.18694    0.23344   0.801   0.4232
## speciesHispr   -0.11739    0.26062  -0.450   0.6524
## speciesPhpr     1.38715    0.35200   3.941 8.12e-05 ***
## speciesPopr     1.52144    0.30340   5.015 5.32e-07 ***
## speciesSoca     0.24827    0.15802   1.571   0.1162
## as.factor(year)2  0.98047    0.15108   6.490 8.61e-11 ***
## as.factor(year)3  2.18486    0.18141  12.044 < 2e-16 ***
## as.factor(year)4  2.25850    0.15994  14.121 < 2e-16 ***
## as.factor(year)5  2.18045    0.14810  14.723 < 2e-16 ***
## as.factor(year)6 -0.63192    0.25350  -2.493   0.0127 *
## statearmed:speciesEugr 0.28197    0.32875   0.858   0.3910
## statearmed:speciesHispr 0.15699    0.45694   0.344   0.7312

```

```
## statearmed:speciesPhpr -0.76163    0.46758  -1.629   0.1033
## statearmed:speciesPopr -0.04837    0.45134  -0.107   0.9147
## statearmed:speciesSoca  0.11182    0.24880   0.449   0.6531
## Log(theta)              -0.17952    0.10189  -1.762   0.0781 .
##
## Zero-inflation model coefficients (binomial with logit link):
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -16.0304  1675.9445  -0.010  0.992368
## statearmed      -0.1854    0.7459  -0.249  0.803662
## speciesEugr      0.2039    0.5995   0.340  0.733823
## speciesHisp      2.6398    0.4045   6.526  6.75e-11 ***
## speciesPhpr      2.0039    0.5328   3.761  0.000169 ***
## speciesPopr      3.3475    0.4313   7.761  8.45e-15 ***
## speciesSoca      0.6303    0.3477   1.812  0.069910 .
## as.factor(year)2  14.6149  1675.9445   0.009  0.993042
## as.factor(year)3  15.8883  1675.9445   0.009  0.992436
## as.factor(year)4  15.4714  1675.9445   0.009  0.992634
## as.factor(year)5  14.8115  1675.9446   0.009  0.992949
## as.factor(year)6  15.1591  1675.9447   0.009  0.992783
## statearmed:speciesEugr  0.8375    0.9352   0.895  0.370542
## statearmed:speciesHisp  0.7449    0.8458   0.881  0.378501
## statearmed:speciesPhpr -0.1405    0.8682  -0.162  0.871399
## statearmed:speciesPopr  0.4300    0.8348   0.515  0.606460
## statearmed:speciesSoca  0.3230    0.7660   0.422  0.673285
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8357
## Number of iterations in BFGS optimization: 59
## Log-likelihood: -3131 on 35 Df
```

```
lrtest(k.m14, k.m15) # model 15 slightly better, going with 14 because its simpler
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + species + as.factor(year)
## Model 2: p_eaten ~ state * species + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1  25 -3135.2
## 2  35 -3131.5 10  7.5151    0.6761
```

```
# checking models again
```

```
lrtest(k.m2, k.m4, k.m9, k.m14) # model 14 best - with species
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + as.factor(year)
## Model 2: p_eaten ~ state + growth_habit + as.factor(year)
## Model 3: p_eaten ~ state + origin + as.factor(year)
## Model 4: p_eaten ~ state + species + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1  15 -3324.2
## 2  19 -3155.4  4 337.52 < 2.2e-16 ***
## 3  19 -3229.1  0 147.37 < 2.2e-16 ***
## 4  25 -3135.2  6 187.68 < 2.2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.k <- AIC(k.m1, k.m2, k.m3, k.m4, k.m5, k.m6, k.m7, k.m8, k.m9, k.m10, k.m11,k.m12,k.m13,k.m14,k.m15)

## interaction between state, species, and year - doesn't run
#m8 <- zeroinfl(p_eaten ~ state * species * as.factor(year),
#             dist = 'negbin',
#             data = herb_kbs)
#summary(m8)

# check dispersion
E <- resid(k.m14, type = "pearson")
N <- nrow(herb_kbs)
p <- length(coef(k.m14)) + 1 # '+1' is due to theta
sum(E^2) / (N - p) # a little overdispersed - is that okay?

## [1] 1.302343

# pairwise comparisons
emmmeans(k.m14, ~ state + species + as.factor(year))
```

##	state	species	year	emmean	SE	df	asympt.LCL	asympt.UCL
##	ambient	Cest	1	1.3164	0.1884	Inf	0.9472	1.6856
##	warmed	Cest	1	1.0472	0.1557	Inf	0.7420	1.3524
##	ambient	Eugr	1	1.7781	0.2968	Inf	1.1964	2.3598
##	warmed	Eugr	1	1.4145	0.2252	Inf	0.9731	1.8559
##	ambient	Hisp	1	1.2083	0.2732	Inf	0.6728	1.7438
##	warmed	Hisp	1	0.9612	0.2238	Inf	0.5226	1.3998
##	ambient	Phpr	1	3.4466	0.8260	Inf	1.8277	5.0655
##	warmed	Phpr	1	2.7417	0.6480	Inf	1.4716	4.0118
##	ambient	Popr	1	5.6552	1.3852	Inf	2.9403	8.3701
##	warmed	Popr	1	4.4987	1.0871	Inf	2.3681	6.6292
##	ambient	Soca	1	1.7310	0.2164	Inf	1.3069	2.1551
##	warmed	Soca	1	1.3770	0.1689	Inf	1.0459	1.7081
##	ambient	Cest	2	2.9035	0.3731	Inf	2.1722	3.6348
##	warmed	Cest	2	2.2184	0.3164	Inf	1.5983	2.8386
##	ambient	Eugr	2	3.4141	0.5006	Inf	2.4328	4.3953
##	warmed	Eugr	2	2.5539	0.3823	Inf	1.8046	3.3032
##	ambient	Hisp	2	0.6693	0.1600	Inf	0.3557	0.9829
##	warmed	Hisp	2	0.4550	0.1163	Inf	0.2271	0.6830
##	ambient	Phpr	2	3.9480	0.8915	Inf	2.2007	5.6953
##	warmed	Phpr	2	2.7945	0.6450	Inf	1.5303	4.0586
##	ambient	Popr	2	1.8882	0.5015	Inf	0.9053	2.8711
##	warmed	Popr	2	1.2652	0.3471	Inf	0.5850	1.9455
##	ambient	Soca	2	3.2414	0.3388	Inf	2.5775	3.9054
##	warmed	Soca	2	2.4163	0.2771	Inf	1.8732	2.9595
##	ambient	Cest	3	6.0676	1.1547	Inf	3.8043	8.3308
##	warmed	Cest	3	4.4077	0.8975	Inf	2.6487	6.1666
##	ambient	Eugr	3	6.0994	1.4558	Inf	3.2460	8.9527
##	warmed	Eugr	3	4.3118	1.0325	Inf	2.2882	6.3354
##	ambient	Hisp	3	0.7058	0.2249	Inf	0.2649	1.1467
##	warmed	Hisp	3	0.4686	0.1546	Inf	0.1655	0.7717
##	ambient	Phpr	3	5.0615	1.6185	Inf	1.8893	8.2337
##	warmed	Phpr	3	3.4250	1.0997	Inf	1.2697	5.5803

```
## ambient Popr      3  1.8680 0.6456 Inf      0.6027      3.1334
## warmed Popr       3  1.2335 0.4317 Inf      0.3874      2.0795
## ambient Soca      3  5.6547 0.9788 Inf      3.7362      7.5732
## warmed Soca       3  3.9826 0.7048 Inf      2.6012      5.3640
## ambient Cest      4  8.1379 1.2603 Inf      5.6679     10.6080
## warmed Cest       4  6.0193 1.0445 Inf      3.9721      8.0665
## ambient Eugr      4  8.6354 1.7680 Inf      5.1703     12.1006
## warmed Eugr       4  6.2166 1.3059 Inf      3.6571      8.7760
## ambient Hisp      4  1.1542 0.3137 Inf      0.5393      1.7691
## warmed Hisp       4  0.7703 0.2217 Inf      0.3358      1.2048
## ambient Phpr      4  7.8965 2.4273 Inf      3.1390     12.6540
## warmed Phpr       4  5.4050 1.6927 Inf      2.0873      8.7227
## ambient Popr      4  3.0976 0.9735 Inf      1.1895      5.0056
## warmed Popr       4  2.0517 0.6605 Inf      0.7571      3.3462
## ambient Soca      4  8.0681 1.1531 Inf      5.8080     10.3281
## warmed Soca       4  5.7853 0.8888 Inf      4.0432      7.5274
## ambient Cest      5  9.0964 1.3647 Inf      6.4216     11.7712
## warmed Cest       5  6.9115 1.0704 Inf      4.8135      9.0094
## ambient Eugr      5 10.5031 1.7037 Inf      7.1638     13.8424
## warmed Eugr       5  7.8004 1.2141 Inf      5.4209     10.1800
## ambient Hisp      5  1.8954 0.4566 Inf      1.0005      2.7903
## warmed Hisp       5  1.2827 0.3231 Inf      0.6494      1.9160
## ambient Phpr      5 11.5792 3.1964 Inf      5.3144     17.8439
## warmed Phpr       5  8.1342 2.2605 Inf      3.7037     12.5647
## ambient Popr      5  5.2800 1.5475 Inf      2.2469      8.3130
## warmed Popr       5  3.5273 1.0419 Inf      1.4853      5.5693
## ambient Soca      5  9.9422 1.2088 Inf      7.5731     12.3114
## warmed Soca       5  7.3569 0.8802 Inf      5.6317      9.0821
## ambient Cest      6  0.5304 0.1100 Inf      0.3147      0.7461
## warmed Cest       6  0.3958 0.0820 Inf      0.2350      0.5565
## ambient Eugr      6  0.5784 0.1050 Inf      0.3726      0.7843
## warmed Eugr       6  0.4204 0.0725 Inf      0.2783      0.5626
## ambient Hisp      6  0.0842 0.0275 Inf      0.0302      0.1381
## warmed Hisp       6  0.0564 0.0190 Inf      0.0191      0.0936
## ambient Phpr      6  0.5589 0.1820 Inf      0.2022      0.9157
## warmed Phpr       6  0.3853 0.1264 Inf      0.1375      0.6331
## ambient Popr      6  0.2280 0.0826 Inf      0.0661      0.3900
## warmed Popr       6  0.1514 0.0553 Inf      0.0431      0.2597
## ambient Soca      6  0.5426 0.0936 Inf      0.3592      0.7260
## warmed Soca       6  0.3929 0.0661 Inf      0.2633      0.5225
##
## Confidence level used: 0.95
```

## Insecticide plots included (KBS)

```
# zero-inflated negative binomial
# insecticide as fixed effect
k.m1.i <- zeroinfl(p_eaten ~ insecticide,
                  dist = 'negbin',
                  data = herb_kbs_in)
summary(k.m1.i)
```

```
##
## Call:
```

```
## zeroinfl(formula = p_eaten ~ insecticide, data = herb_kbs_in, dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.3557 -0.3557 -0.3243 -0.1781 12.8354
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.57267    0.12638  12.444  <2e-16 ***
## insecticideno_insects -0.21098    0.09725  -2.169    0.03 *
## Log(theta)       -1.55091    0.17411  -8.908  <2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.6864    0.3384  -2.029  0.04248 *
## insecticideno_insects  0.4117    0.1513   2.721  0.00652 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.2121
## Number of iterations in BFGS optimization: 23
## Log-likelihood: -6614 on 5 Df

# full model
k.m2.i <- zeroinfl(p_eaten ~ insecticide + state + species + as.factor(year),
                  dist = 'negbin',
                  data = herb_kbs_in)
#summary(k.m2.i)

# full model w/ interaction term
k.m3.i <- zeroinfl(p_eaten ~ insecticide * state + species + as.factor(year),
                  dist = 'negbin',
                  data = herb_kbs_in)
summary(k.m3.i)

##
## Call:
## zeroinfl(formula = p_eaten ~ insecticide * state + species + as.factor(year),
##      data = herb_kbs_in, dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.8197 -0.4452 -0.2613 -0.1379 29.9850
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.70150    0.23831   2.944  0.00324 **
## insecticideno_insects -0.23501    0.08314  -2.827  0.00470 **
## statewarmed       -0.15813    0.08499  -1.861  0.06280 .
## speciesBrin        0.89092    0.40270   2.212  0.02694 *
## speciesCest       -0.13747    0.22031  -0.624  0.53263
## speciesEugr       -0.26237    0.23814  -1.102  0.27056
## speciesHispr       0.08018    0.25256   0.317  0.75088
## speciesHype       -1.43449    0.49511  -2.897  0.00376 **
## speciesPhpr        0.51902    0.26033   1.994  0.04618 *
```

```

## speciesPopr          1.04482      0.26430      3.953 7.71e-05 ***
## speciesRual         -0.38645      0.33338     -1.159 0.24637
## speciesSoca         -0.01575      0.21709     -0.073 0.94216
## speciesTrre          0.02785      0.84832      0.033 0.97381
## as.factor(year)2      0.90799      0.10417      8.716 < 2e-16 ***
## as.factor(year)3      2.09935      0.12018     17.469 < 2e-16 ***
## as.factor(year)4      2.06207      0.11469     17.979 < 2e-16 ***
## as.factor(year)5      1.89641      0.11352     16.705 < 2e-16 ***
## as.factor(year)6     -0.89374      0.17420     -5.131 2.89e-07 ***
## insecticideno_insects:statearmed 0.14365      0.12780      1.124 0.26100
## Log(theta)          -0.11722      0.06824     -1.718 0.08586 .
##
## Zero-inflation model coefficients (binomial with logit link):
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.5355    139.2849   -0.104 0.916885
## insecticideno_insects      0.2448      0.1245      1.966 0.049263 *
## statearmed           0.1297      0.1277      1.016 0.309796
## speciesBrin          1.1588      0.4872      2.379 0.017376 *
## speciesCest          0.2184      0.3376      0.647 0.517787
## speciesEugr          0.1337      0.3613      0.370 0.711351
## speciesHisp          2.4609      0.3309      7.437 1.03e-13 ***
## speciesHype          1.9728      0.5833      3.382 0.000719 ***
## speciesPhpr          1.6665      0.3511      4.746 2.08e-06 ***
## speciesPopr          3.0460      0.3338      9.125 < 2e-16 ***
## speciesRual         -2.4441      2.8620     -0.854 0.393117
## speciesSoca          0.6303      0.3071      2.053 0.040092 *
## speciesTrre          3.9317      0.8118      4.843 1.28e-06 ***
## as.factor(year)2     13.4316    139.2845      0.096 0.923177
## as.factor(year)3     13.9078    139.2845      0.100 0.920462
## as.factor(year)4     14.0348    139.2845      0.101 0.919738
## as.factor(year)5     13.7528    139.2845      0.099 0.921346
## as.factor(year)6     13.4117    139.2848      0.096 0.923291
## insecticideno_insects:statearmed 0.4721      0.1849      2.553 0.010677 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.8894
## Number of iterations in BFGS optimization: 55
## Log-likelihood: -5929 on 39 Df

# calculating effect size - accounting for log link
exp(0.70150 + -0.23501*0) # 2.016776

## [1] 2.016776

exp(0.70150 + -0.23501*1) # 1.594388

## [1] 1.594388

# effect of herbivory:
1.594388 - 2.016776 # -0.422388

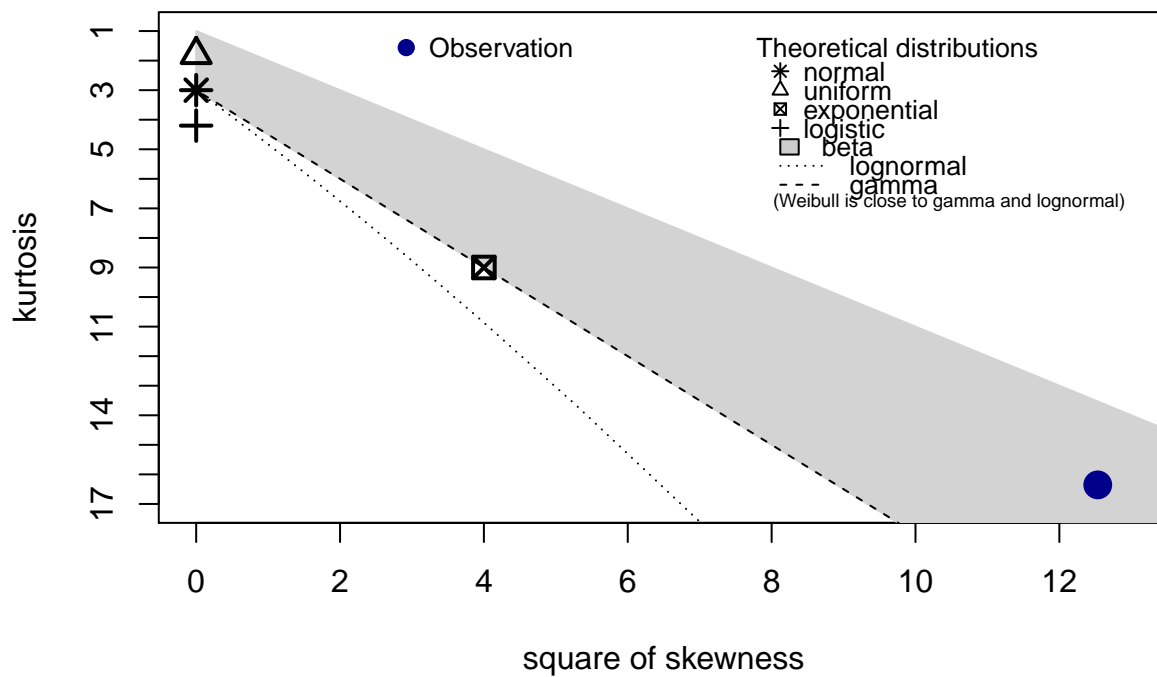
## [1] -0.422388

```

## UMBS - Data Exploration

```
descdist(herb_umbs$p_eaten, discrete = FALSE)
```

### Cullen and Frey graph

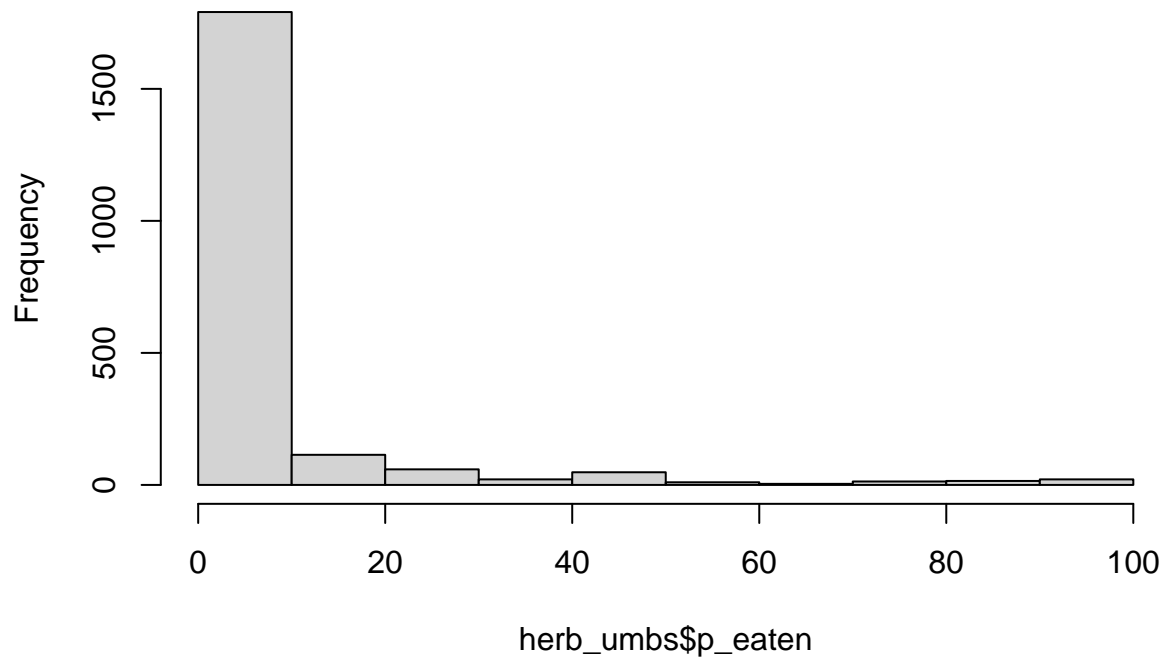


```
## summary statistics
## -----
## min: 0    max: 100
## median: 0
## mean: 6.87166
## estimated sd: 16.80741
## estimated skewness: 3.540296
## estimated kurtosis: 16.35555
```

```
# normal distribution?
hist(herb_umbs$p_eaten)
```

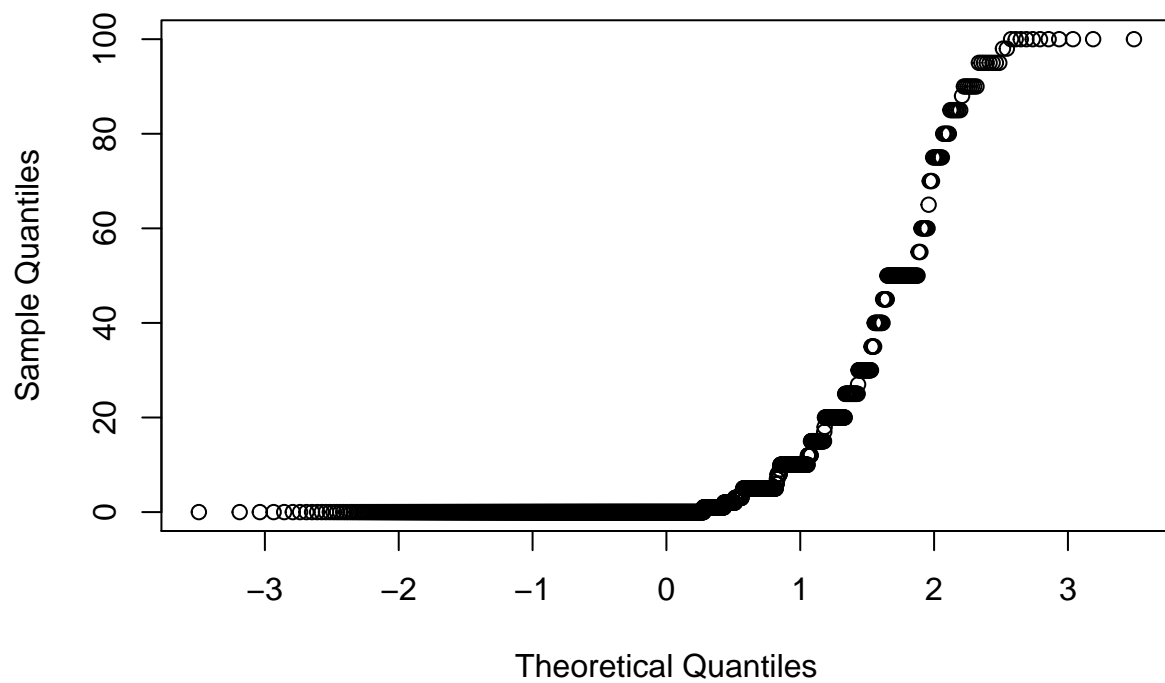


**Histogram of herb\_umbs\$p\_eaten**



```
qqnorm(herb_umbs$p_eaten)
```

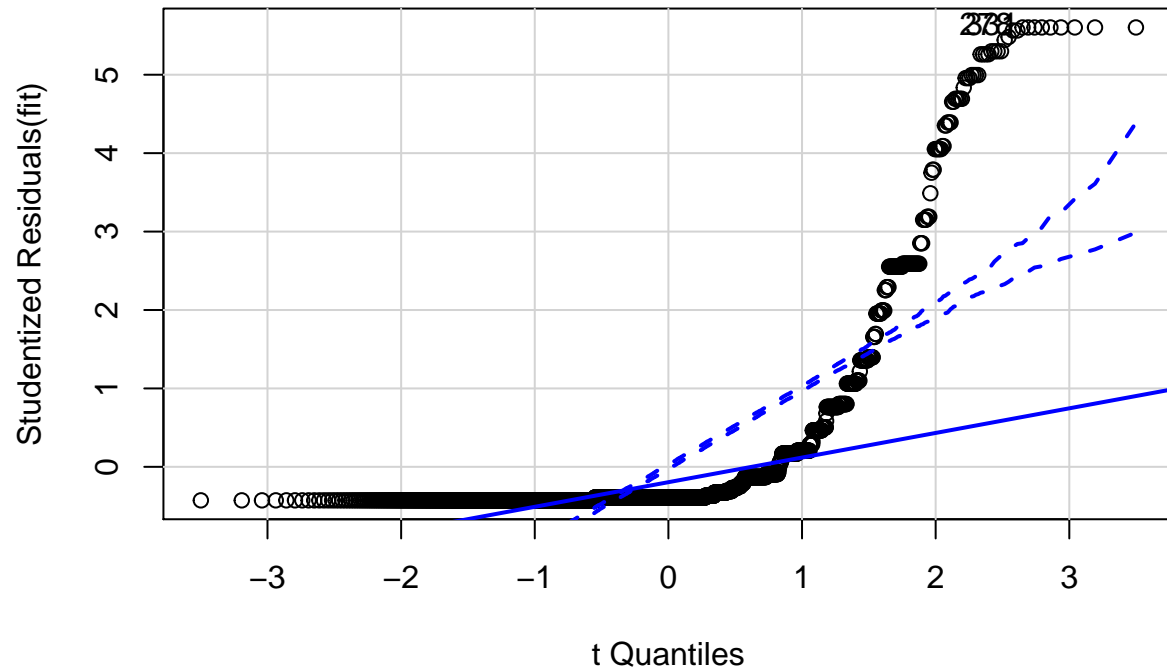
**Normal Q-Q Plot**



```
shapiro.test(herb_umbs$p_eaten)
```

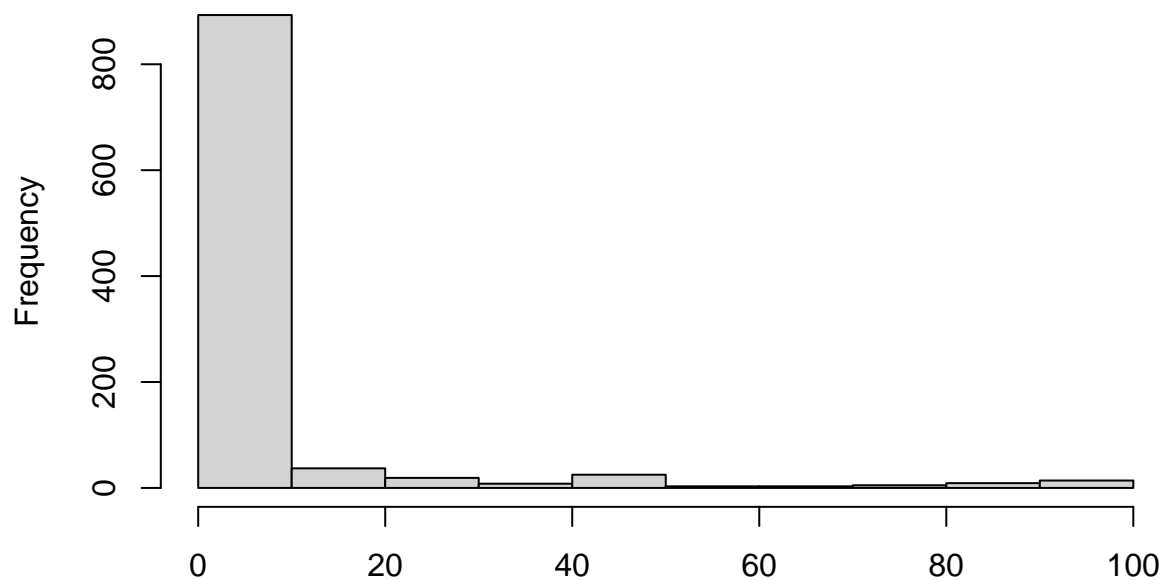
```
##
```

```
## Shapiro-Wilk normality test
##
## data: herb_umbs$p_eaten
## W = 0.46641, p-value < 2.2e-16
fit <- lm(p_eaten ~ state, data = herb_umbs)
qqPlot(fit)
```



```
## [1] 278 331
# looking at each treatment separately
hist(herb_umbs$p_eaten[herb_umbs$state == "ambient"])
```

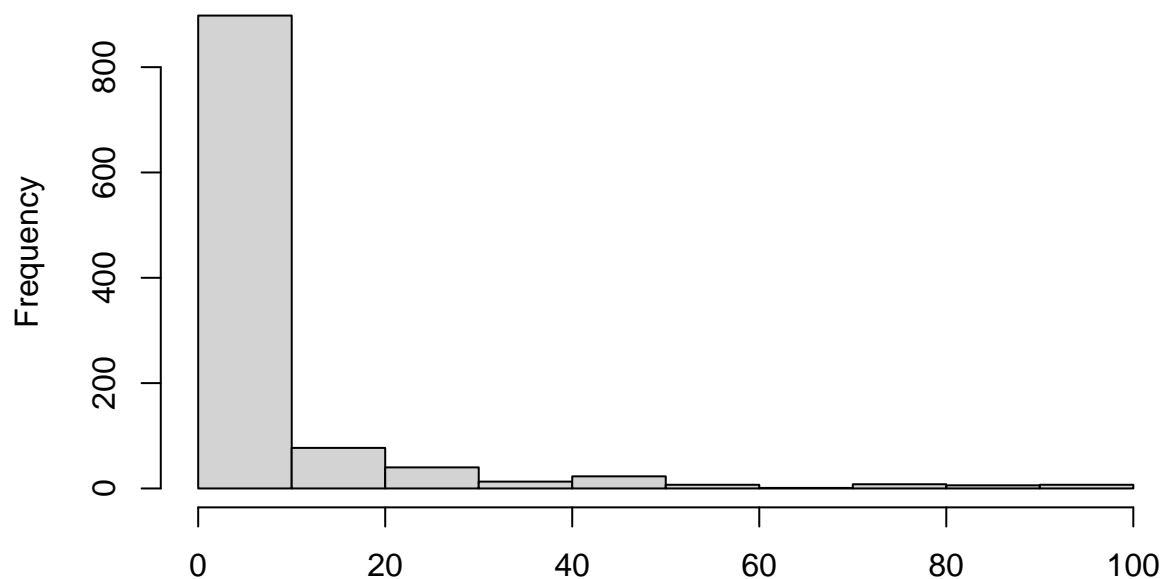
## Histogram of herb\_umbs\$p\_eaten[herb\_umbs\$state == "ambient"]



herb\_umbs\$p\_eaten[herb\_umbs\$state == "ambient"]

```
hist(herb_umbs$p_eaten[herb_umbs$state == "warmed"])
```

## Histogram of herb\_umbs\$p\_eaten[herb\_umbs\$state == "warmed"]



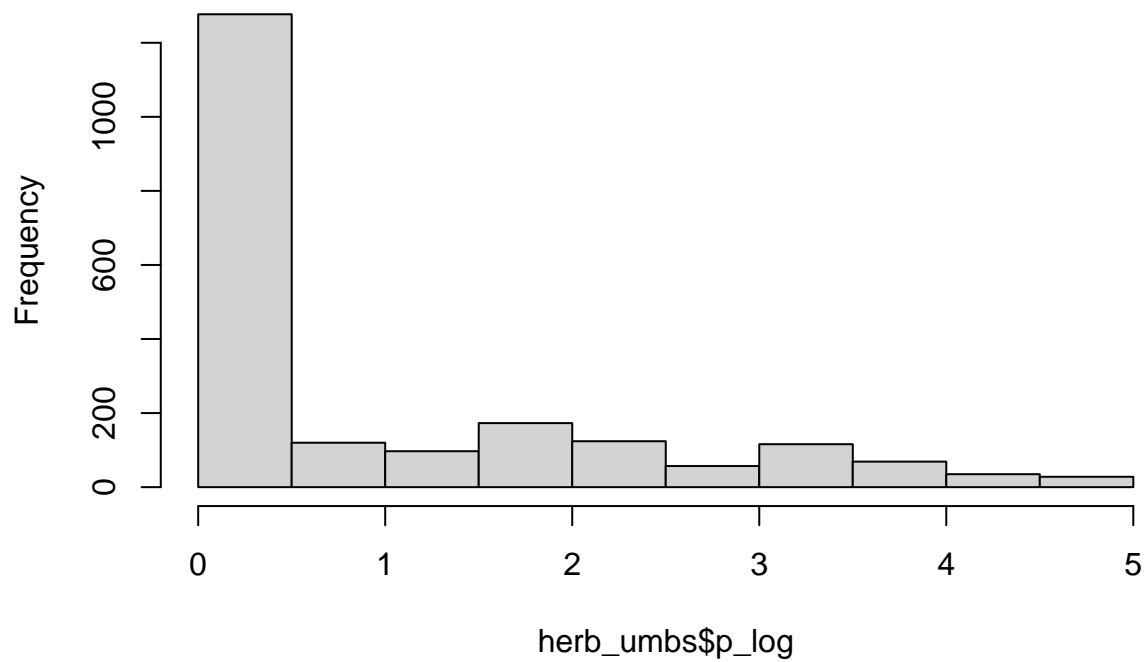
herb\_umbs\$p\_eaten[herb\_umbs\$state == "warmed"]

```
# gamma distribution? - error message "the function mle failed to estimate the parameters"  
#fit.gamma <- fitdist(herb_umbs$p_eaten, "gamma")  
#plot(fit.gamma)
```

```
# lognormal distribution? - error message "values must be positive to fit a lognormal"
#fit.ln <- fitdist(herb_umbs$p_eaten, "lnorm")
#plot(fit.ln)

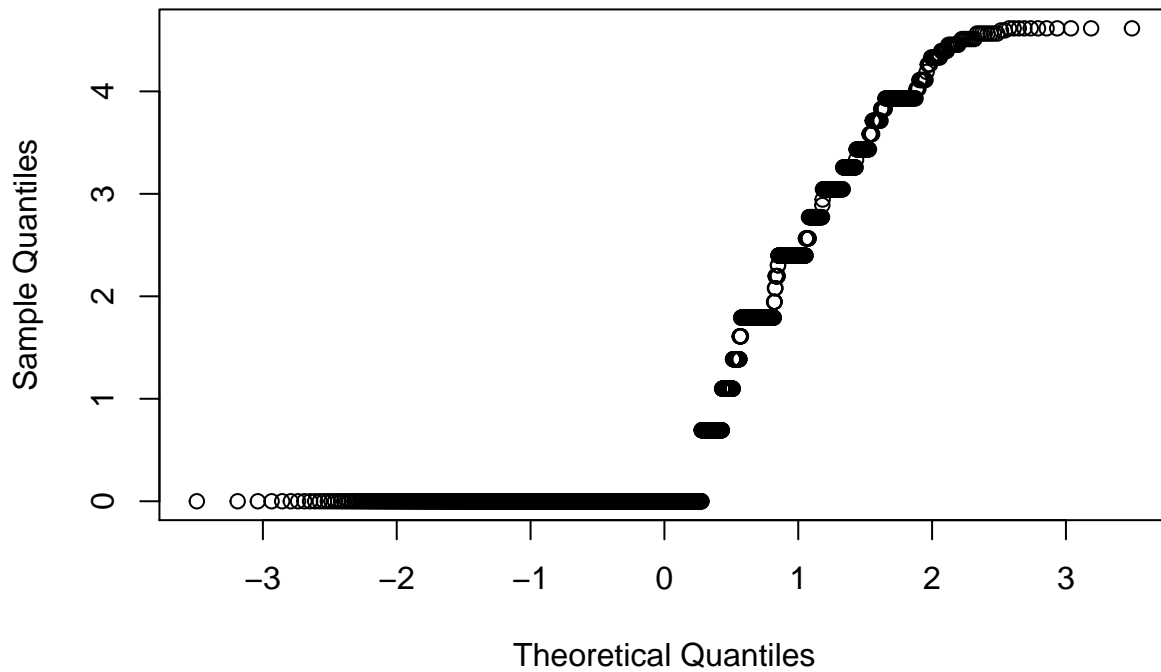
# log transform
herb_umbs$p_log <- log(herb_umbs$p_eaten+1)
hist(herb_umbs$p_log)
```

**Histogram of herb\_umbs\$p\_log**



```
qqnorm(herb_umbs$p_log)
```

## Normal Q-Q Plot

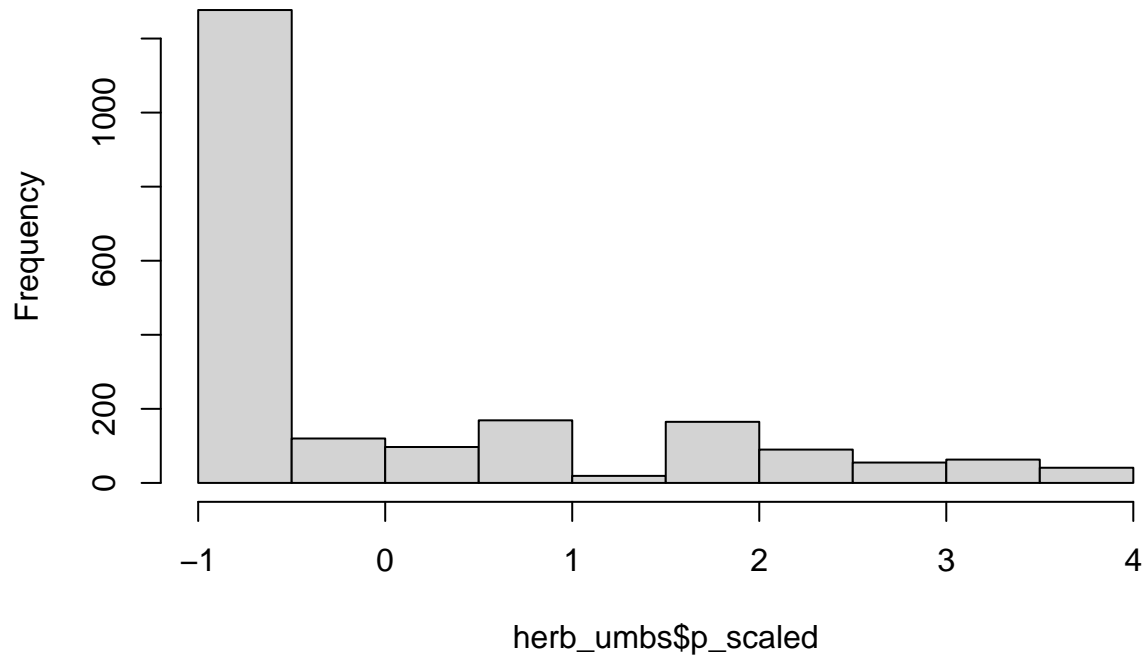


```
shapiro.test(herb_umbs$p_log) # NAs - data contains 0s
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: herb_umbs$p_log  
## W = 0.71293, p-value < 2.2e-16
```

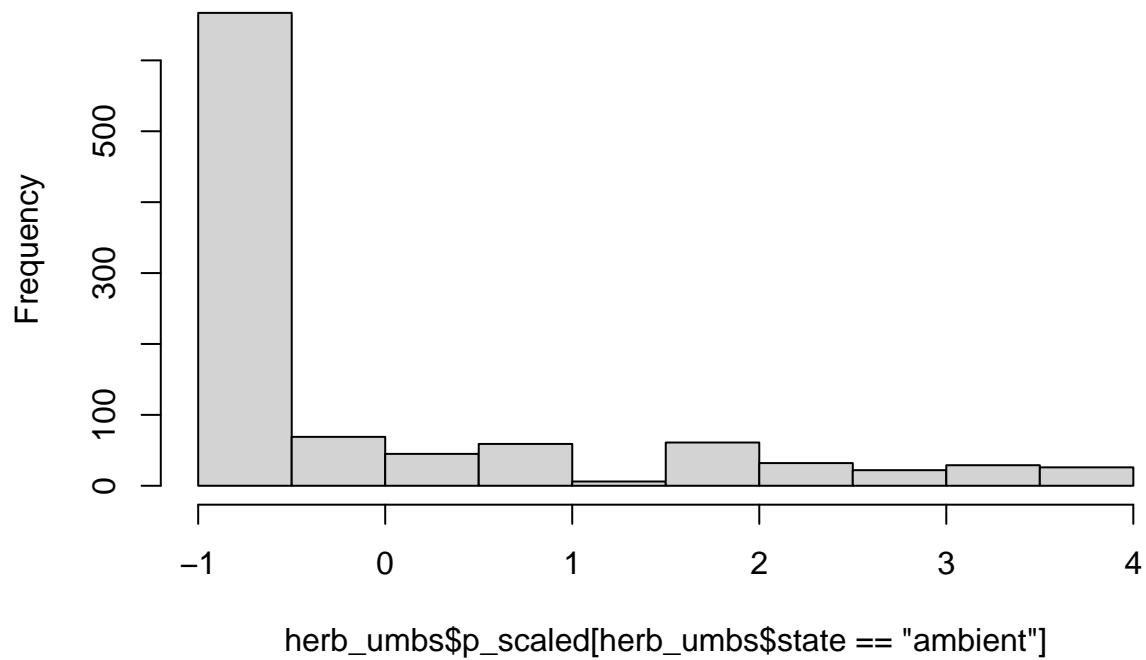
```
# mean centering p_eaten  
herb_umbs$p_scaled <- herb_umbs$p_log - mean(herb_umbs$p_log)  
hist(herb_umbs$p_scaled)
```

**Histogram of herb\_umbs\$p\_scaled**



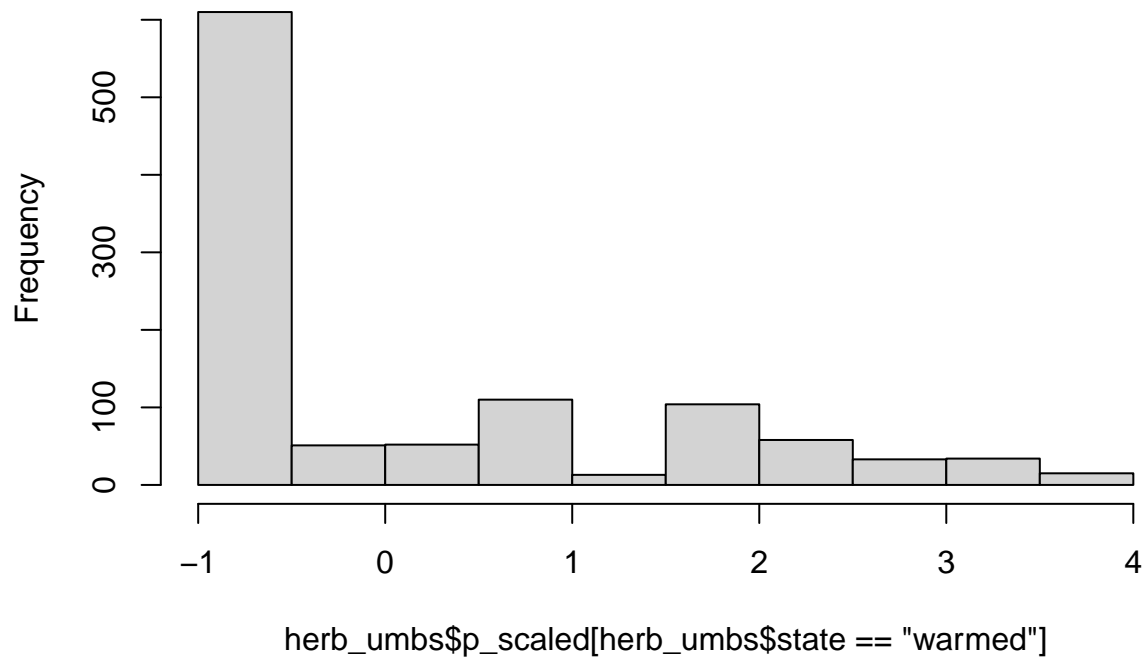
```
hist(herb_umbs$p_scaled[herb_umbs$state == "ambient"])
```

**Histogram of herb\_umbs\$p\_scaled[herb\_umbs\$state == "ambient"]**



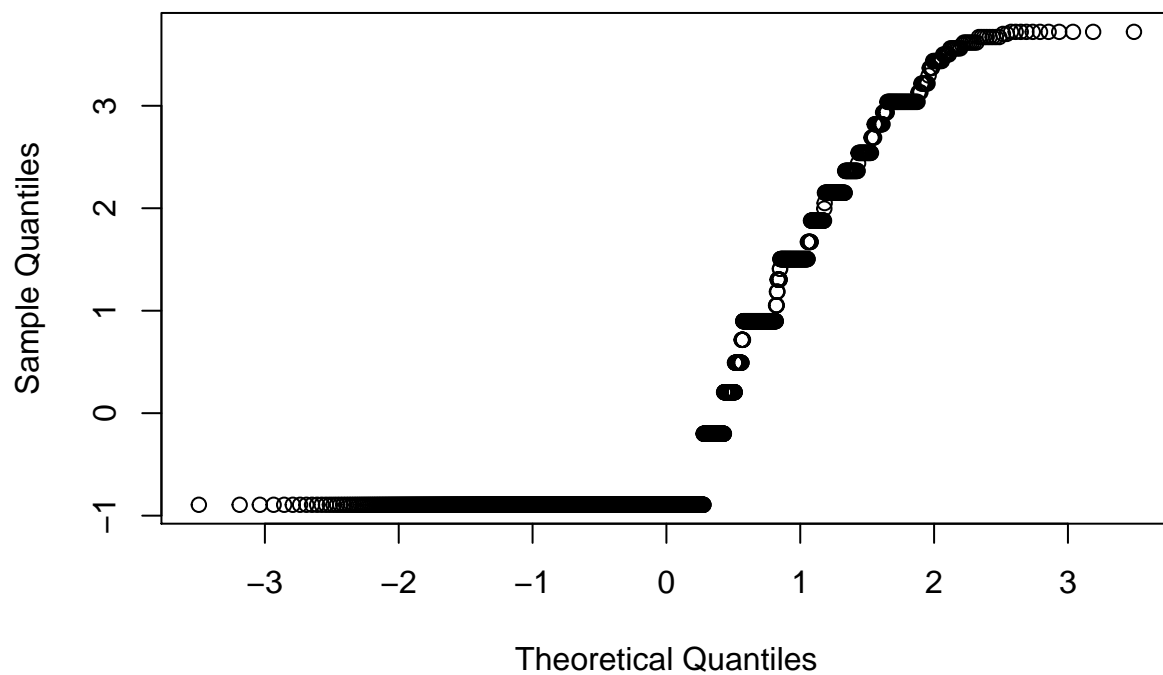
```
hist(herb_umbs$p_scaled[herb_umbs$state == "warmed"])
```

## Histogram of herb\_umbs\$p\_scaled[herb\_umbs\$state == "warmed"]



```
qqnorm(herb_umbs$p_scaled)
```

## Normal Q-Q Plot

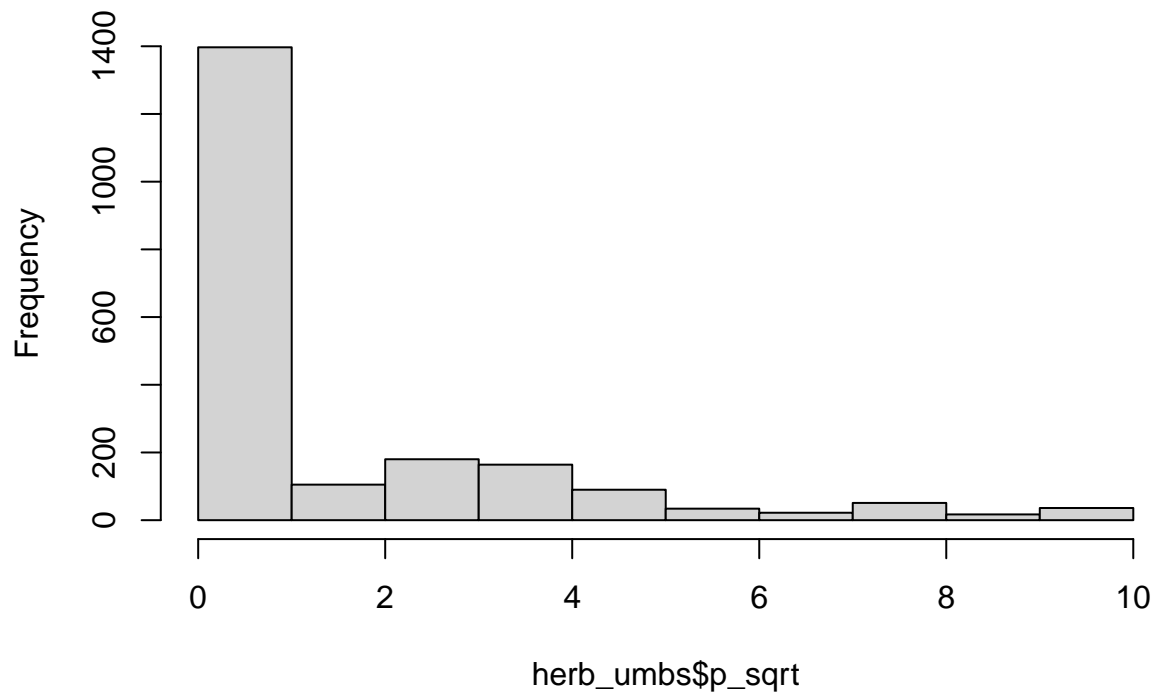


```
shapiro.test(herb_umbs$p_scaled)
```

```
##
```

```
## Shapiro-Wilk normality test
##
## data: herb_umbs$p_scaled
## W = 0.71293, p-value < 2.2e-16
# square root?
herb_umbs$p_sqrt <- sqrt(herb_umbs$p_eaten)
hist(herb_umbs$p_sqrt)
```

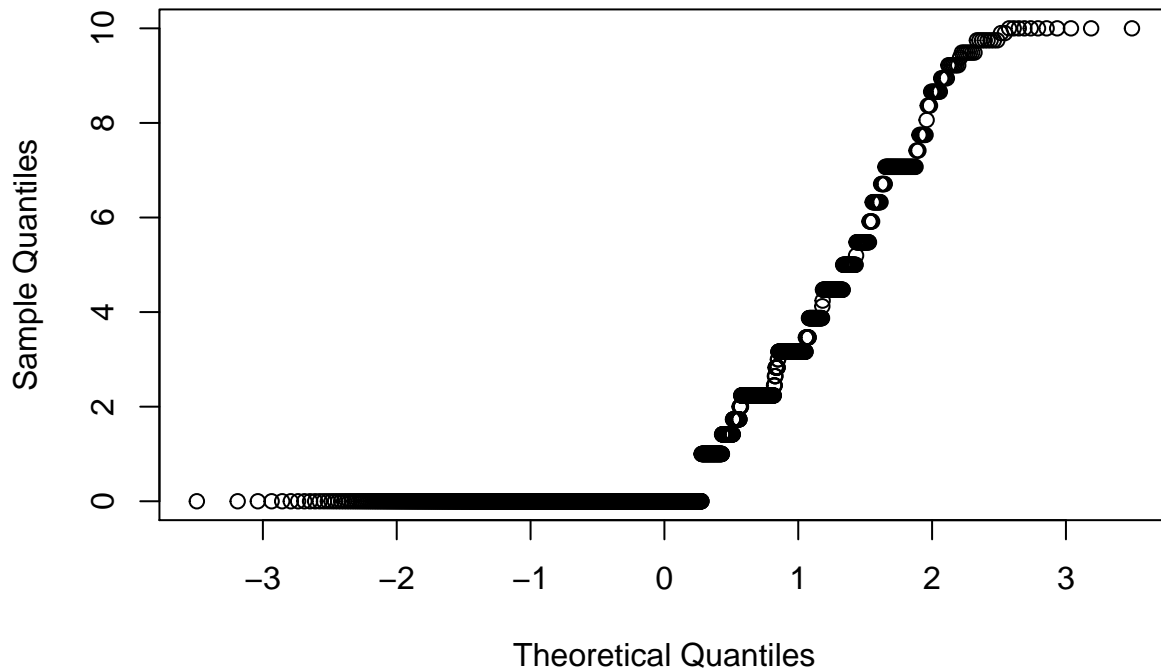
**Histogram of herb\_umbs\$p\_sqrt**



```
qqnorm(herb_umbs$p_sqrt)
```



## Normal Q-Q Plot



```
shapiro.test(herb_umbs$p_sqrt)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  herb_umbs$p_sqrt
## W = 0.67356, p-value < 2.2e-16
```

Transformations are a no-go

Going to try a zero-inflated model due to the excess number of zeros in the data

```
# mean and var of non-zero counts
herb_umbs %>%
  dplyr::filter(p_eaten != "0") %>%
  dplyr::summarize(mean_eaten = mean(p_eaten, na.rm=T), var_eaten = var(p_eaten, na.rm=T))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 9 x 3
##   species mean_eaten var_eaten
##   <chr>      <dbl>      <dbl>
## 1 Cape      5.62      96.2
## 2 Cest      16.9      562.
## 3 Dasp      16.4      578.
## 4 Hype      27.5      622.
## 5 Poco       5.65      40.3
## 6 Popr      20.6      445.
## 7 Posp      37.1      654.
## 8 Ptaq       8.27      52.3
```

```
## 9 Ruac          22.3      606.
```

```
# variance is also > mean, so can't be poisson  
# I'll try zero-inflated negative binomial due to an excess of zeros
```

```
# zero-inflated negative binomial  
# state as a fixed effect
```

```
u.m1 <- zeroinfl(p_eaten ~ state,  
                 dist = 'negbin',  
                 data = herb_umbs)
```

```
#summary(u.m1)
```

```
# state and year as fixed effects
```

```
u.m2 <- zeroinfl(p_eaten ~ state + as.factor(year),  
                 dist = 'negbin',  
                 data = herb_umbs)
```

```
#summary(u.m2)
```

```
lrtest(u.m1, u.m2) # model 2
```

```
## Likelihood ratio test
```

```
##
```

```
## Model 1: p_eaten ~ state
```

```
## Model 2: p_eaten ~ state + as.factor(year)
```

```
##   #Df LogLik Df  Chisq Pr(>Chisq)
```

```
## 1    5 -4445.5
```

```
## 2   15 -4260.0 10 370.95 < 2.2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# state and growth habit as fixed effects
```

```
herb_umbs <- within(herb_umbs, growth_habit <- relevel(factor(growth_habit), ref = "Forb")) # releveling
```

```
u.m3 <- zeroinfl(p_eaten ~ state + growth_habit,  
                 dist = 'negbin',  
                 data = herb_umbs)
```

```
#summary(u.m3)
```

```
lrtest(u.m2, u.m3) # model 2
```

```
## Likelihood ratio test
```

```
##
```

```
## Model 1: p_eaten ~ state + as.factor(year)
```

```
## Model 2: p_eaten ~ state + growth_habit
```

```
##   #Df LogLik Df  Chisq Pr(>Chisq)
```

```
## 1   15 -4260.0
```

```
## 2    7 -4415.4 -8 310.84 < 2.2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# state, growth habit, and year as fixed effects
```

```
u.m4 <- zeroinfl(p_eaten ~ state + growth_habit + as.factor(year),  
                 dist = 'negbin',  
                 data = herb_umbs)
```

```
#summary(u.m4)
```

```
lrtest(u.m2, u.m4) # model 4
```

```
## Likelihood ratio test
```

```
##
```

```

## Model 1: p_eaten ~ state + as.factor(year)
## Model 2: p_eaten ~ state + growth_habit + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   15 -4260.0
## 2   17 -4218.9  2 82.184 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and growth habit as fixed effects
u.m5 <- zeroinfl(p_eaten ~ state * growth_habit,
  dist = 'negbin',
  data = herb_umbs)

#summary(u.m5)
lrtest(u.m4, u.m5) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   17 -4218.9
## 2    9 -4407.2 -8 376.53 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and growth habit as fixed effects, plus year
u.m6 <- zeroinfl(p_eaten ~ state * growth_habit + as.factor(year),
  dist = 'negbin',
  data = herb_umbs)

summary(u.m6)

##
## Call:
## zeroinfl(formula = p_eaten ~ state * growth_habit + as.factor(year),
##   data = herb_umbs, dist = "negbin")
##
## Pearson residuals:
##      Min      1Q   Median      3Q      Max
## -0.65834 -0.47972 -0.32606 -0.01636 11.83813
##
## Count model coefficients (negbin with log link):
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.270199   0.220072  -1.228  0.21953
## statewarmed      0.296797   0.106514   2.786  0.00533 **
## growth_habitGraminoid 0.254834   0.164301   1.551  0.12090
## as.factor(year)2    1.061158   0.245930   4.315 1.60e-05 ***
## as.factor(year)3    3.226367   0.239076  13.495 < 2e-16 ***
## as.factor(year)4    2.289732   0.245551   9.325 < 2e-16 ***
## as.factor(year)5    3.125807   0.245176  12.749 < 2e-16 ***
## as.factor(year)6    3.300644   0.244568  13.496 < 2e-16 ***
## statewarmed:growth_habitGraminoid 0.003845   0.204963   0.019  0.98503
## Log(theta)      -0.469147   0.102137  -4.593 4.36e-06 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -13.5562   323.7932  -0.042  0.967

```

```
## statearmed -0.1634 0.1515 -1.079 0.281
## growth_habitGraminoid 1.5102 0.2045 7.384 1.53e-13 ***
## as.factor(year)2 11.6530 323.7933 0.036 0.971
## as.factor(year)3 13.1255 323.7932 0.041 0.968
## as.factor(year)4 13.9538 323.7932 0.043 0.966
## as.factor(year)5 13.5468 323.7932 0.042 0.967
## as.factor(year)6 13.7481 323.7932 0.042 0.966
## statearmed:growth_habitGraminoid -0.5139 0.2450 -2.097 0.036 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.6255
## Number of iterations in BFGS optimization: 40
## Log-likelihood: -4217 on 19 Df
```

```
lrtest(u.m4, u.m6) # almost the same, going with model 4 because its simpler
```

```
## Likelihood ratio test
##
```

```
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit + as.factor(year)
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 17 -4218.9
## 2 19 -4216.7 2 4.5081 0.105
```

```
# interaction between state, growth habit, and year (year as a factor wouldn't woru - non-finite value)
```

```
u.m7 <- zeroinfl(p_eaten ~ state * growth_habit * year,
  dist = 'negbin',
  data = herb_umbs)
```

```
#summary(u.m7)
```

```
lrtest(u.m4, u.m7) # model 4
```

```
## Likelihood ratio test
##
```

```
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * growth_habit * year
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 17 -4218.9
## 2 17 -4240.7 0 43.623 < 2.2e-16 ***
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# state and origin as fixed effects
```

```
herb_umbs <- within(herb_umbs, origin <- relevel(factor(origin), ref = "Native")) # releveling so native
```

```
u.m8 <- zeroinfl(p_eaten ~ state + origin,
  dist = 'negbin',
  data = herb_umbs)
```

```
#summary(u.m8)
```

```
lrtest(u.m4, u.m8) # model 4
```

```
## Likelihood ratio test
##
```

```
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + origin
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 17 -4218.9
```

```

## 2    9 -4428.5 -8 419.15 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# state, origin, and year as fixed effects
u.m9 <- zeroinfl(p_eaten ~ state + origin + as.factor(year),
                 dist = 'negbin',
                 data = herb_umbs)

#summary(u.m9)
lrtest(u.m4, u.m9) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + origin + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   17 -4218.9
## 2   19 -4249.6  2 61.362  4.736e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and origin as fixed effects
u.m10 <- zeroinfl(p_eaten ~ state * origin,
                  dist = 'negbin',
                  data = herb_umbs)

#summary(u.m10)
lrtest(u.m4, u.m10) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * origin
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   17 -4218.9
## 2   13 -4417.6 -4 397.42 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# interaction between state and origin as fixed effects, plus year
u.m11 <- zeroinfl(p_eaten ~ state * origin + as.factor(year),
                  dist = 'negbin',
                  data = herb_umbs)

summary(u.m11)

##
## Call:
## zeroinfl(formula = p_eaten ~ state * origin + as.factor(year), data = herb_umbs,
##          dist = "negbin")
##
## Pearson residuals:
##      Min       1Q   Median       3Q      Max
## -0.65417 -0.46593 -0.36493 -0.02109  9.47634
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.26760    0.25243  -1.060 0.289103

```

```

## statearmed          0.09681    0.17695    0.547 0.584294
## origin              0.57712    0.27344    2.111 0.034807 *
## originExotic        -0.02525    0.15781   -0.160 0.872890
## as.factor(year)2     1.38107    0.23181    5.958 2.56e-09 ***
## as.factor(year)3     3.31051    0.22899   14.457 < 2e-16 ***
## as.factor(year)4     2.38935    0.23691   10.085 < 2e-16 ***
## as.factor(year)5     3.15962    0.23432   13.484 < 2e-16 ***
## as.factor(year)6     3.33175    0.23351   14.268 < 2e-16 ***
## statearmed:origin    -0.27675    0.41098   -0.673 0.500709
## statearmed:originExotic 0.24530    0.19903    1.232 0.217762
## Log(theta)          -0.32561    0.08377   -3.887 0.000102 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -15.3960  1295.7168  -0.012  0.99052
## statearmed     -0.8763    0.2186  -4.008 6.12e-05 ***
## origin        -0.8079    0.3537  -2.284  0.02235 *
## originExotic  -0.6378    0.1835  -3.476  0.00051 ***
## as.factor(year)2  15.3288  1295.7168   0.012  0.99056
## as.factor(year)3  15.9936  1295.7168   0.012  0.99015
## as.factor(year)4  16.9728  1295.7168   0.013  0.98955
## as.factor(year)5  16.6761  1295.7168   0.013  0.98973
## as.factor(year)6  16.3750  1295.7168   0.013  0.98992
## statearmed:origin   2.0110    0.4785   4.202 2.64e-05 ***
## statearmed:originExotic 0.5053    0.2553   1.979  0.04779 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.7221
## Number of iterations in BFGS optimization: 45
## Log-likelihood: -4239 on 23 Df

lrtest(u.m4, u.m11) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state * origin + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1  17 -4218.9
## 2  23 -4238.8  6 39.822  4.938e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

exp(-0.26760 + 0.37613*0) # 1.538119

## [1] 0.7652138

exp(-0.26760 + 0.37613*1) # 2.24048

## [1] 1.114638
# effect of herbivory:
2.24048 - 1.538119 # 0.702361

## [1] 0.702361

```

```

## interaction between state, origin, and year - doesn't work
#u.m12 <- zeroinfl(p_eaten ~ state * origin * as.factor(year),
#               dist = 'negbin',
#               data = herb_umbs)
#summary(u.m12)

# state and species as fixed effects
u.m13 <- zeroinfl(p_eaten ~ state + species,
                 dist = 'negbin',
                 data = herb_umbs)
#summary(u.m13)
lrtest(u.m4, u.m13) # model 4

## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + species
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   17 -4218.9
## 2   21 -4292.4  4 146.98 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# state, species and year as fixed effects
u.m14 <- zeroinfl(p_eaten ~ state + species + as.factor(year),
                 dist = 'negbin',
                 data = herb_umbs)
summary(u.m14)

##
## Call:
## zeroinfl(formula = p_eaten ~ state + species + as.factor(year), data = herb_umbs,
##          dist = "negbin")
##
## Pearson residuals:
##      Min      1Q   Median      3Q      Max
## -0.70260 -0.49987 -0.32878 -0.01447 11.66668
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.40972    0.35052  -1.169  0.242448
## statewarmed     0.26343    0.09307   2.830  0.004650 **
## speciesCest     0.15545    0.28274   0.550  0.582459
## speciesDasp     0.41035    0.29147   1.408  0.159171
## speciesHype     0.38761    0.40744   0.951  0.341443
## speciesPoco     0.43451    0.31758   1.368  0.171253
## speciesPopr     0.29092    0.44567   0.653  0.513902
## speciesPosp     0.80799    0.34166   2.365  0.018035 *
## speciesPtaq    -0.01442    0.30768  -0.047  0.962609
## speciesRuac     0.49122    0.28612   1.717  0.086013 .
## as.factor(year)2 1.17523    0.24755   4.748 2.06e-06 ***
## as.factor(year)3 3.06518    0.24034  12.754 < 2e-16 ***
## as.factor(year)4 2.28318    0.24552   9.299 < 2e-16 ***
## as.factor(year)5 2.99940    0.24663  12.161 < 2e-16 ***

```

```
## as.factor(year)6 3.28438 0.23403 14.034 < 2e-16 ***
## Log(theta) -0.33330 0.08651 -3.853 0.000117 ***
##
## Zero-inflation model coefficients (binomial with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -14.9891 1547.7505 -0.010 0.99227
## statearmed -0.2966 0.1191 -2.490 0.01277 *
## speciesCest -1.4338 0.3093 -4.635 3.57e-06 ***
## speciesDasp -0.4142 0.2989 -1.386 0.16583
## speciesHype 0.6283 0.3917 1.604 0.10871
## speciesPoco -1.8193 0.7522 -2.419 0.01558 *
## speciesPopr 1.3788 0.4077 3.382 0.00072 ***
## speciesPosp -0.4734 0.3713 -1.275 0.20228
## speciesPtaq -1.0125 0.3584 -2.825 0.00473 **
## speciesRuac -1.4319 0.3053 -4.690 2.73e-06 ***
## as.factor(year)2 15.2197 1547.7505 0.010 0.99215
## as.factor(year)3 16.0462 1547.7505 0.010 0.99173
## as.factor(year)4 16.7231 1547.7505 0.011 0.99138
## as.factor(year)5 16.1363 1547.7505 0.010 0.99168
## as.factor(year)6 16.5355 1547.7505 0.011 0.99148
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.7166
## Number of iterations in BFGS optimization: 53
## Log-likelihood: -4154 on 31 Df
```

```
lrtest(u.m4, u.m14) # model 14
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + growth_habit + as.factor(year)
## Model 2: p_eaten ~ state + species + as.factor(year)
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 17 -4218.9
## 2 31 -4153.7 14 130.54 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# calculating effect size - accounting for log link
exp(-0.40972 + 0.26343*0) # 0.6638361
```

```
## [1] 0.6638361
```

```
exp(-0.40972 + 0.26343*1) # 0.8639071
```

```
## [1] 0.8639071
```

```
# effect of herbivory:
0.8639071 - 0.6638361 # 0.200071
```

```
## [1] 0.200071
```

```
# interaction between state and species as fixed effects, plus year
u.m15 <- zeroinfl(p_eaten ~ state * species + as.factor(year),
  dist = 'negbin',
  data = herb_umbs)
summary(u.m15)
```



```
##
## Call:
## zeroinfl(formula = p_eaten ~ state * species + as.factor(year), data = herb_umbs,
##   dist = "negbin")
##
## Pearson residuals:
##      Min      1Q   Median      3Q      Max
## -0.71759 -0.50964 -0.31412 -0.05114 10.77704
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.56238    0.46370  -1.213 0.225209
## statearmed      0.49483    0.52624   0.940 0.347058
## speciesCest     0.23959    0.42534   0.563 0.573242
## speciesDasp     0.67525    0.45045   1.499 0.133859
## speciesHype    -0.02343    0.56353  -0.042 0.966841
## speciesPoco    -0.04919    0.67903  -0.072 0.942252
## speciesPopr     0.46320    1.27083   0.364 0.715497
## speciesPosp     1.17204    0.48351   2.424 0.015348 *
## speciesPtaq     0.38266    0.47107   0.812 0.416613
## speciesRuac     0.77307    0.43323   1.784 0.074354 .
## as.factor(year)2  1.19443    0.24644   4.847 1.26e-06 ***
## as.factor(year)3  3.01325    0.24087  12.510 < 2e-16 ***
## as.factor(year)4  2.27642    0.24396   9.331 < 2e-16 ***
## as.factor(year)5  2.96236    0.24562  12.061 < 2e-16 ***
## as.factor(year)6  3.30472    0.23268  14.203 < 2e-16 ***
## statearmed:speciesCest -0.09171    0.54453  -0.168 0.866259
## statearmed:speciesDasp -0.38308    0.57492  -0.666 0.505211
## statearmed:speciesHype  0.79783    0.77615   1.028 0.303981
## statearmed:speciesPoco  0.45497    0.77816   0.585 0.558771
## statearmed:speciesPopr -0.20828    1.36477  -0.153 0.878705
## statearmed:speciesPosp -0.67450    0.64178  -1.051 0.293267
## statearmed:speciesPtaq -0.63943    0.60653  -1.054 0.291767
## statearmed:speciesRuac -0.41412    0.55624  -0.744 0.456576
## Log(theta)      -0.30399    0.08523  -3.567 0.000361 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -13.70447  1126.42094  -0.012 0.990293
## statearmed     -2.54202    0.67898  -3.744 0.000181 ***
## speciesCest    -1.97446    0.40609  -4.862 1.16e-06 ***
## speciesDasp    -0.79081    0.41200  -1.919 0.054930 .
## speciesHype    -0.15737    0.54007  -0.291 0.770755
## speciesPoco    -2.58422    2.17122  -1.190 0.233961
## speciesPopr     2.48657    1.07616   2.311 0.020855 *
## speciesPosp    -1.90334    0.50200  -3.792 0.000150 ***
## speciesPtaq    -2.04852    0.51673  -3.964 7.36e-05 ***
## speciesRuac    -2.43632    0.41879  -5.818 5.97e-09 ***
## as.factor(year)2  14.64934  1126.42090   0.013 0.989624
## as.factor(year)3  15.40399  1126.42088   0.014 0.989089
## as.factor(year)4  16.12980  1126.42088   0.014 0.988575
## as.factor(year)5  15.44148  1126.42088   0.014 0.989063
```

```
## as.factor(year)6      15.89701 1126.42088    0.014 0.988740
## statearmed:speciesCest 2.04479    0.71433    2.863 0.004203 **
## statearmed:speciesDaspr 1.68122    0.73296    2.294 0.021805 *
## statearmed:speciesHype 2.47526    0.88283    2.804 0.005051 **
## statearmed:speciesPoco 2.24483    2.35794    0.952 0.341083
## statearmed:speciesPopr -0.04895    1.26292   -0.039 0.969080
## statearmed:speciesPosp 3.67473    0.80065    4.590 4.44e-06 ***
## statearmed:speciesPtaq 2.83563    0.80840    3.508 0.000452 ***
## statearmed:speciesRuac 2.90264    0.72344    4.012 6.01e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.7379
## Number of iterations in BFGS optimization: 69
## Log-likelihood: -4123 on 47 Df
```

```
lrtest(u.m14, u.m15) # model 15 - might go with 14 because its simpler
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + species + as.factor(year)
## Model 2: p_eaten ~ state * species + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1  31 -4153.7
## 2  47 -4123.0 16 61.233 3.239e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## interaction between state, species, and year - doesn't run
```

```
#m8 <- zeroinfl(p_eaten ~ state * species * year,
#               dist = 'negbin',
#               data = herb_umbs)
#summary(m8)
```

```
# checking models again
```

```
lrtest(u.m2, u.m4, u.m9, u.m14) # model 14 best - with species
```

```
## Likelihood ratio test
##
## Model 1: p_eaten ~ state + as.factor(year)
## Model 2: p_eaten ~ state + growth_habit + as.factor(year)
## Model 3: p_eaten ~ state + origin + as.factor(year)
## Model 4: p_eaten ~ state + species + as.factor(year)
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1  15 -4260.0
## 2  17 -4218.9  2  82.184 < 2.2e-16 ***
## 3  19 -4249.6  2  61.362 4.736e-14 ***
## 4  31 -4153.7 12 191.904 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
res.u <- AIC(u.m1, u.m2, u.m3, u.m4, u.m5, u.m6, u.m7, u.m9, u.m10, u.m11, u.m13, u.m14, u.m15)
```

```
# check dispersion - chose lowest loglik model for example
```

```
E <- resid(u.m14, type = "pearson")
```

```
N <- nrow(herb_umbs)
```

```
p <- length(coef(u.m14)) + 1 # '+1' is due to theta
sum(E^2) / (N - p) # pretty close to one
```

```
## [1] 1.033222
```

```
# pairwise comparisons
emmmeans(u.m14, ~ state + species + as.factor(year))
```

##	state	species	year	emmean	SE	df	asympt.LCL	asympt.UCL
##	ambient	Cape	1	0.664	0.233	Inf	0.2078	1.120
##	warmed	Cape	1	0.864	0.307	Inf	0.2628	1.465
##	ambient	Cest	1	0.775	0.163	Inf	0.4552	1.096
##	warmed	Cest	1	1.009	0.213	Inf	0.5917	1.427
##	ambient	Dasp	1	1.001	0.256	Inf	0.4990	1.502
##	warmed	Dasp	1	1.302	0.336	Inf	0.6427	1.962
##	ambient	Hype	1	0.978	0.364	Inf	0.2651	1.691
##	warmed	Hype	1	1.273	0.474	Inf	0.3438	2.202
##	ambient	Poco	1	1.025	0.312	Inf	0.4139	1.636
##	warmed	Poco	1	1.334	0.403	Inf	0.5442	2.124
##	ambient	Popr	1	0.888	0.371	Inf	0.1601	1.616
##	warmed	Popr	1	1.156	0.479	Inf	0.2165	2.095
##	ambient	Posp	1	1.489	0.451	Inf	0.6044	2.374
##	warmed	Posp	1	1.938	0.594	Inf	0.7729	3.103
##	ambient	Ptaq	1	0.654	0.178	Inf	0.3054	1.003
##	warmed	Ptaq	1	0.852	0.238	Inf	0.3845	1.319
##	ambient	Ruac	1	1.085	0.262	Inf	0.5707	1.599
##	warmed	Ruac	1	1.412	0.348	Inf	0.7292	2.095
##	ambient	Cape	2	0.952	0.283	Inf	0.3973	1.506
##	warmed	Cape	2	1.445	0.417	Inf	0.6288	2.262
##	ambient	Cest	2	1.932	0.263	Inf	1.4167	2.447
##	warmed	Cest	2	2.672	0.311	Inf	2.0620	3.283
##	ambient	Dasp	2	1.769	0.275	Inf	1.2294	2.308
##	warmed	Dasp	2	2.606	0.366	Inf	1.8892	3.322
##	ambient	Hype	2	0.943	0.343	Inf	0.2710	1.614
##	warmed	Hype	2	1.497	0.524	Inf	0.4700	2.523
##	ambient	Poco	2	2.757	0.518	Inf	1.7424	3.772
##	warmed	Poco	2	3.751	0.616	Inf	2.5449	4.958
##	ambient	Popr	2	0.479	0.221	Inf	0.0461	0.913
##	warmed	Popr	2	0.794	0.354	Inf	0.0991	1.488
##	ambient	Posp	2	2.703	0.691	Inf	1.3481	4.058
##	warmed	Posp	2	3.965	0.955	Inf	2.0933	5.837
##	ambient	Ptaq	2	1.454	0.257	Inf	0.9510	1.957
##	warmed	Ptaq	2	2.058	0.346	Inf	1.3798	2.736
##	ambient	Ruac	2	2.701	0.396	Inf	1.9260	3.477
##	warmed	Ruac	2	3.737	0.498	Inf	2.7606	4.714
##	ambient	Cape	3	3.670	1.236	Inf	1.2473	6.093
##	warmed	Cape	3	5.900	1.997	Inf	1.9853	9.815
##	ambient	Cest	3	9.860	1.299	Inf	7.3152	12.405
##	warmed	Cest	3	14.328	1.947	Inf	10.5120	18.145
##	ambient	Dasp	3	7.393	1.230	Inf	4.9822	9.803
##	warmed	Dasp	3	11.566	1.948	Inf	7.7487	15.384
##	ambient	Hype	3	3.280	1.244	Inf	0.8412	5.718
##	warmed	Hype	3	5.448	2.048	Inf	1.4340	9.461
##	ambient	Poco	3	14.985	3.934	Inf	7.2748	22.695

##	warmed	Poco	3	21.235	5.105	Inf	11.2293	31.241
##	ambient	Popr	3	1.532	0.709	Inf	0.1430	2.921
##	warmed	Popr	3	2.610	1.196	Inf	0.2652	4.954
##	ambient	Posp	3	11.433	2.550	Inf	6.4349	16.431
##	warmed	Posp	3	17.814	3.921	Inf	10.1281	25.500
##	ambient	Ptaq	3	6.858	1.350	Inf	4.2110	9.504
##	warmed	Ptaq	3	10.272	2.064	Inf	6.2263	14.318
##	ambient	Ruac	3	13.784	1.803	Inf	10.2503	17.318
##	warmed	Ruac	3	20.033	2.768	Inf	14.6081	25.458
##	ambient	Cape	4	0.977	0.344	Inf	0.3039	1.650
##	warmed	Cape	4	1.626	0.565	Inf	0.5195	2.733
##	ambient	Cest	4	3.236	0.513	Inf	2.2318	4.241
##	warmed	Cest	4	4.940	0.696	Inf	3.5761	6.304
##	ambient	Dasp	4	2.069	0.446	Inf	1.1955	2.943
##	warmed	Dasp	4	3.377	0.680	Inf	2.0444	4.710
##	ambient	Hype	4	0.826	0.338	Inf	0.1629	1.489
##	warmed	Hype	4	1.404	0.560	Inf	0.3076	2.501
##	ambient	Poco	4	5.241	1.852	Inf	1.6107	8.872
##	warmed	Poco	4	7.777	2.374	Inf	3.1242	12.429
##	ambient	Popr	4	0.371	0.170	Inf	0.0376	0.704
##	warmed	Popr	4	0.640	0.287	Inf	0.0782	1.202
##	ambient	Posp	4	3.226	1.004	Inf	1.2584	5.194
##	warmed	Posp	4	5.248	1.538	Inf	2.2346	8.262
##	ambient	Ptaq	4	2.099	0.454	Inf	1.2091	2.989
##	warmed	Ptaq	4	3.302	0.659	Inf	2.0108	4.593
##	ambient	Ruac	4	4.523	0.774	Inf	3.0059	6.040
##	warmed	Ruac	4	6.905	1.083	Inf	4.7825	9.027
##	ambient	Cape	5	3.212	1.079	Inf	1.0961	5.327
##	warmed	Cape	5	5.191	1.714	Inf	1.8304	8.551
##	ambient	Cest	5	8.891	1.439	Inf	6.0706	11.712
##	warmed	Cest	5	13.002	1.867	Inf	9.3427	16.661
##	ambient	Dasp	5	6.519	1.379	Inf	3.8172	9.221
##	warmed	Dasp	5	10.263	2.028	Inf	6.2875	14.239
##	ambient	Hype	5	2.845	1.057	Inf	0.7731	4.916
##	warmed	Hype	5	4.743	1.698	Inf	1.4139	8.072
##	ambient	Poco	5	13.622	3.970	Inf	5.8416	21.403
##	warmed	Poco	5	19.412	4.988	Inf	9.6352	29.188
##	ambient	Popr	5	1.320	0.581	Inf	0.1821	2.458
##	warmed	Popr	5	2.254	0.965	Inf	0.3616	4.145
##	ambient	Posp	5	10.094	3.026	Inf	4.1641	16.024
##	warmed	Posp	5	15.827	4.457	Inf	7.0917	24.563
##	ambient	Ptaq	5	6.126	1.440	Inf	3.3037	8.948
##	warmed	Ptaq	5	9.237	2.046	Inf	5.2271	13.247
##	ambient	Ruac	5	12.429	2.002	Inf	8.5056	16.352
##	warmed	Ruac	5	18.178	2.678	Inf	12.9296	23.426
##	ambient	Cape	6	3.112	1.138	Inf	0.8806	5.343
##	warmed	Cape	6	5.136	1.885	Inf	1.4421	8.831
##	ambient	Cest	6	9.768	1.342	Inf	7.1370	12.399
##	warmed	Cest	6	14.705	2.017	Inf	10.7518	18.658
##	ambient	Dasp	6	6.511	1.503	Inf	3.5643	9.457
##	warmed	Dasp	6	10.514	2.393	Inf	5.8234	15.204
##	ambient	Hype	6	2.665	1.066	Inf	0.5751	4.754
##	warmed	Hype	6	4.506	1.783	Inf	1.0113	8.001
##	ambient	Poco	6	15.537	5.141	Inf	5.4605	25.614

##	warmed	Poco	6	22.742	6.708	Inf	9.5950	35.890
##	ambient	Popr	6	1.207	0.580	Inf	0.0709	2.343
##	warmed	Popr	6	2.077	0.988	Inf	0.1412	4.012
##	ambient	Posp	6	10.130	3.148	Inf	3.9602	16.301
##	warmed	Posp	6	16.301	4.910	Inf	6.6784	25.924
##	ambient	Ptaq	6	6.456	1.579	Inf	3.3603	9.551
##	warmed	Ptaq	6	10.023	2.404	Inf	5.3104	14.735
##	ambient	Ruac	6	13.652	2.389	Inf	8.9700	18.334
##	warmed	Ruac	6	20.555	3.636	Inf	13.4285	27.681
##								
##	Confidence level used: 0.95							