

Effect of Wood Harvesting on the populations of *Bursera simaruba*

Jason Marcell Setiadi

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Introduction

Heritage tourism has opened up opportunities for local communities to sell handicrafts around heritage sites. Moreover, national and international development agencies and governments have begun to promote handicraft production as a strategy to help rural and indigenous communities gain social, cultural and economic benefits from tourism. However, social and environmental impacts are often overlooked in indigenous communities which depend on direct extraction of natural resources in order to produce such handicrafts.

In this consulting report, I will focus on analyzing the effects of wood harvesting on *Bursera simaruba* individuals and populations by comparing the basal area, stem density, and size population structure (stem densities of different size classes) in harvested and unharvested plots. I will also observe whether other factors (Milpa and Vegetation Type) have any significant effect on the response variables. Moreover, visualizations of the response across the 54 plots are also of interest.

Methods and Materials

The data is from an observational study since it is collected from June 6th-26th, 2017 in the community of Chimay, situated in Yaxcabá Municipality in the State of Yucatán, México. The way the data is collected is by first establishing circular plots of 10 m radius where all *Bursera simaruba* individuals with varying DBH and height are measured. Each plot is separated by a distance of 30 m so they don't overlap. 4 circular plots are chosen within each harvested and unharvested forest where each artisan harvest. There are 54 plots that ended up in our data, 28 are harvested while 26 aren't.

There are multiple measurements being taken, some of the important ones that will be analyzed are basal area of plots ($\frac{m^2}{ha}$), stem density ($\frac{\#stems}{ha}$) of each plot, and population size structure (stem densities within each size class) which are our response variables. The size classes of the population size structure are seedlings (<0.5 cm DBH), saplings (0.5-4 cm DBH), and adult trees (5-10 cm DBH, 11-15 cm DBH, 16-20 cm DBH, 21-25 cm DBH, 26-30 cm DBH), which amounts to a total of 7 classes. The predictors of interest in our analysis are Milpa (whether a plot implements the Milpa agricultural system (Yes/No)) and Vegetation Type (Ju'uche', Keelenche', Nuku'uch che').

The way I analyze the data was by using the analysis of variance (ANOVA) which allows us to perform hypothesis tests to check whether each predictor in the model has a significant effect on the response and to answer our research questions. It's also important to check model assumptions (Randomness, Independence, Normality, and Constant Variance) so that our results are reliable. To evaluate whether a predictor is significant or not, we will use 0.05 significance level as our cutoff. This implies that if the p-value is lower than the cutoff, then the predictor is significant, and vice versa. Furthermore, we can perform pairwise comparisons called Tukey HSD to gain more insight on the significant predictor (which level in the predictor is significant). We will also do some visualizations to gain more information from the data.

To visualize the basal area and stem density across our 54 plots, we can use the histogram which allows us to see the distribution across the plots. Therefore, we can see whether the distribution is uniform (equal

response across the different plots) or not. Furthermore, we will use the box-plot to visualize the population size structure between harvested and unharvested plots. Box-plots can show the mean, the variance, and outliers in the data which we can utilize to make comparisons.

Results

In this section, we will perform several analysis to answer our research questions. First, we want to test whether our predictors have a significant effect on the basal area of our 54 plots.

Table 1: P-values of Predictors

Predictors	P-Values
Harvested	0.8394
Milpa	0.0499
VegetationType	0.7481
Harvested:Milpa	0.8482
Harvested:VegetationType	0.852
Milpa:VegetationType	0.2103
Harvested:Milpa:VegetationType	0.6664

Based on Table 1, we can see that the Basal Area (m²/ha) is not statistically different between harvested and unharvested plots. However, although vegetation type don't have a significant effect on the response, we can see that Milpa has a really close p-value to 0.05. This is sometimes hard to conclude since the p-value is not significantly low. However at 0.05 level, we would say that Milpa has a significant effect on the response. Now let's visualize the Basal Area (m²/ha) among the 54 plots using the histogram.

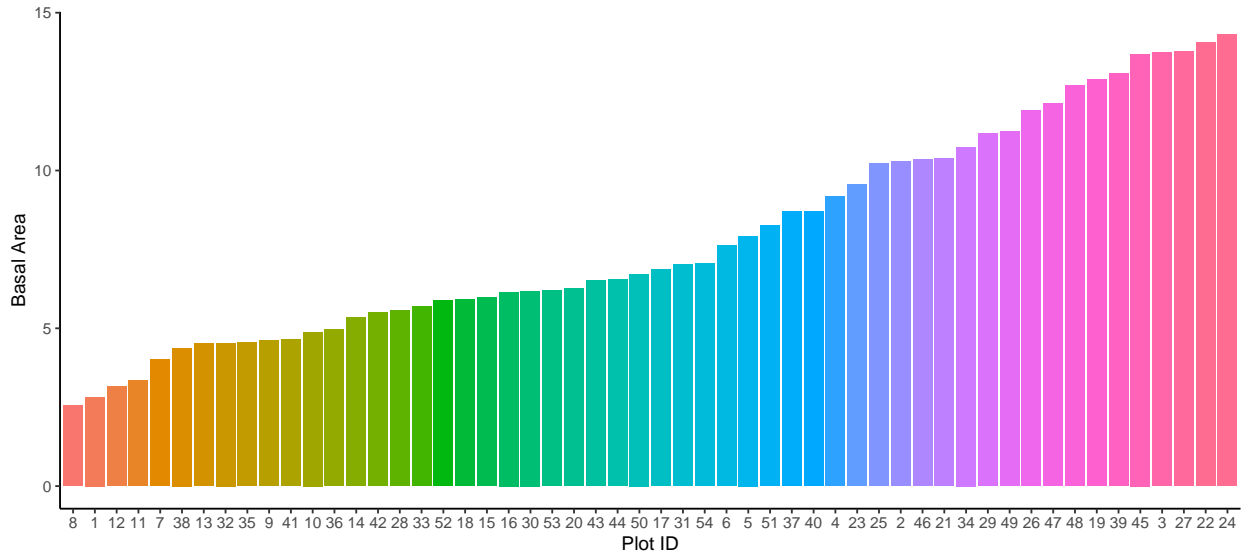


Figure 1: Basal Area Among the 54 Plots

We can see that the distribution is not uniform, meaning the Basal Area is different across the 54 plots. Plot 24 has the largest Basal Area while Plot 8 has the smallest Basal Area.

Next, we want to test whether our predictors have a significant effect on the stem density of our 54 plots.

Table 2: P-values of Predictors

Predictors	P-Values
Harvested	0.691
Milpa	0.5983
VegetationType	0.0013
Harvested:Milpa	0.7284
Harvested:VegetationType	0.32
Milpa:VegetationType	0.8517
Harvested:Milpa:VegetationType	0.3257

Based on Table 2, the stem density (#stems/ha) is not significantly different among harvested and unharvested plots. Milpa also doesn't have a significant effect on the stem density. However, Vegetation Type has a significant effect on stem density because the p-value is significantly lower than 0.05, so we can conclude that Vegetation Type has a significant effect on stem density. Let's visualize the Stem Density (#stems/ha) among the 54 plots using the histogram.

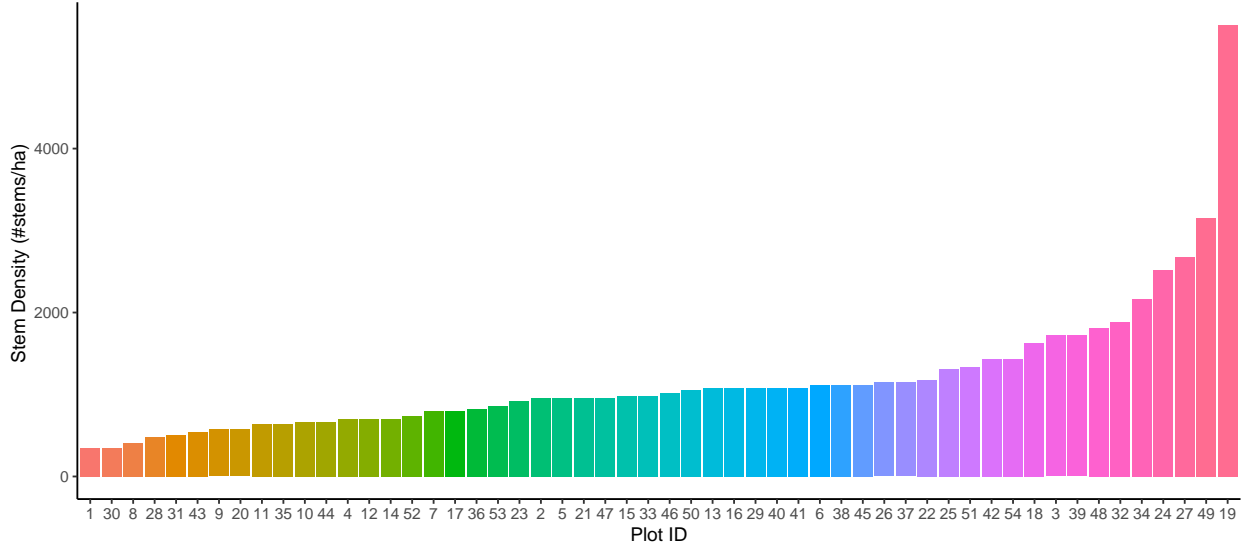


Figure 2: Stem Density Among the 54 Plots

We can see again the stem density is not uniform across the different plots. Plot 19 has the largest stem density while most of the other plots have lower stem density such as Plot 1 and 30.

Next, we can analyze the population size structure in harvested and unharvested plots. We will use the box-plot to visualize each of the size classes and make comparisons between them. We can check number of plots where each size class is present.

Table 3: Number of Plots where the Size Class is Present

Size Class	Plot Frequency
Seedlings	54
Saplings	54
Adult 5-10 cm	54

Size Class	Plot Frequency
Adult 11-15 cm	53
Adult 16-20 cm	41
Adult 21-25 cm	15
Adult 26- 30 cm	1

Based on Table 3, we can observe that the Adult size classes aren't present in all 54 plots except Adult 5-10 cm DBH class. Therefore, the comparisons for those size classes won't be that reliable. Moreover, we can observe that Adult 26-30 cm class is only present in one plot. This means it doesn't make sense to do the analysis for that size class, since our goal is to compare the density among harvested and unharvested plots.

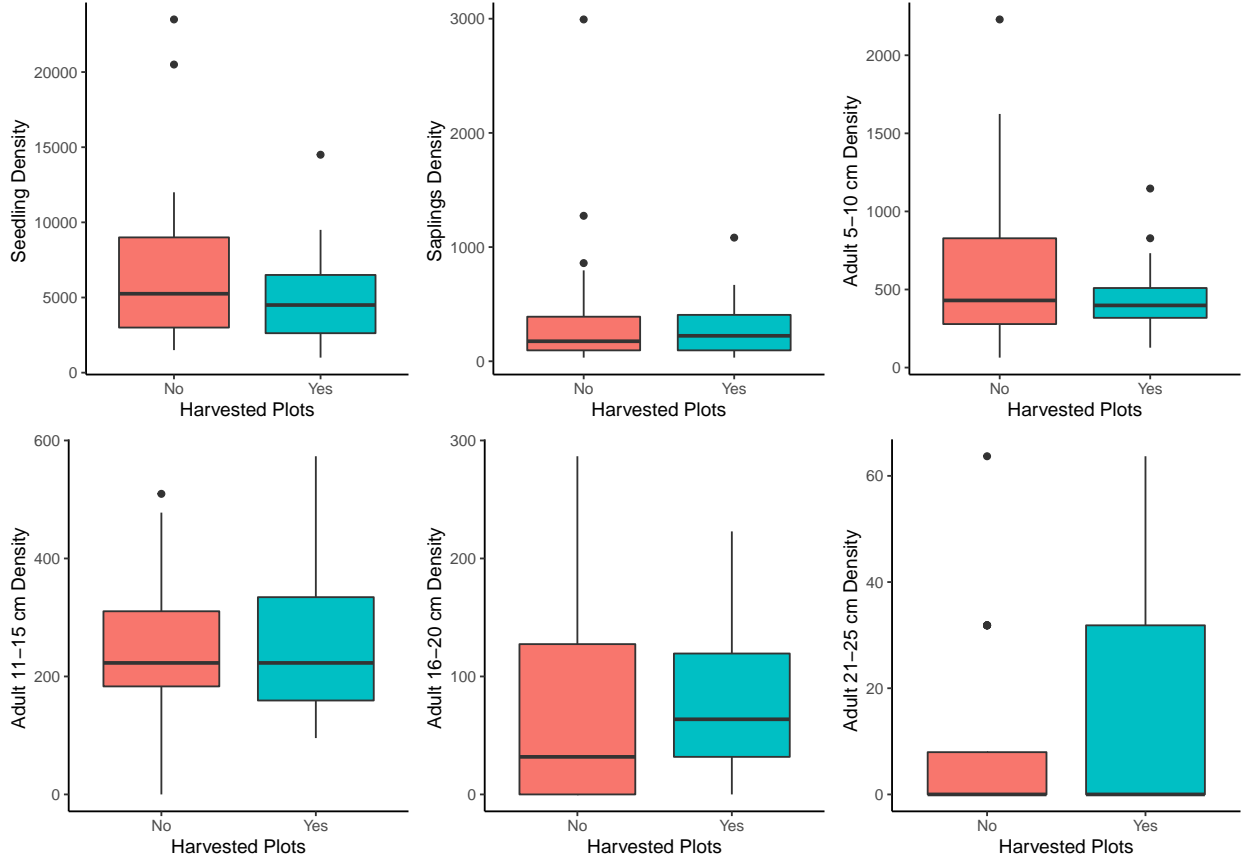


Figure 3: Population Size Structure in Harvested and Unharvested Plots

Notice that seedlings, saplings, and adults with 5-10 cm DBH has a larger density in unharvested plots than harvested plots which makes sense. As we have stated earlier, the plots for the other size classes maybe unreliable due to the number of missing values (not present in all 54 plots).

In order to test this observation statistically, we can perform ANOVA to conclude whether the population size structure is affected by harvesting as well as the other predictors.

Table 4: P-value for each Size Class

Predictors	Seedlings	Saplings	Adult 5-10	Adult 11-15	Adult 16-20	Adult 21-25
Harvested	0.2079	0.7269	0.6214	0.2982	0.331	0.6762
Milpa	0.5532	0.0314	0.7189	0.9364	0.0098	0.1894
VegetationType	0.0166	1e-04	0.0033	0.009	0.0281	0.0082
Harvested:Milpa	0.3821	0.3093	0.89	0.788	0.6734	0.9501
Harvested:VegetationType	0.7182	0.2173	0.24	0.2844	0.8927	0.2751
Milpa:VegetationType	0.8242	0.504	0.958	0.9353	0.5941	0.0733
Harvested:Milpa:VegetationType	0.0135	0.3259	0.5649	0.663	0.4812	0.2056

Based on Table 4, there is no significant difference between harvested and unharvested plots in every size class analyzed. However, we see that vegetation type has a significant effect on the population size structure. Milpa also has quite a significant effect in some classes such as Saplings and Adult 16-20 at 0.05 level. We can conclude that Vegetation Type has a significant effect on the population size structure.

Discussion and Summary

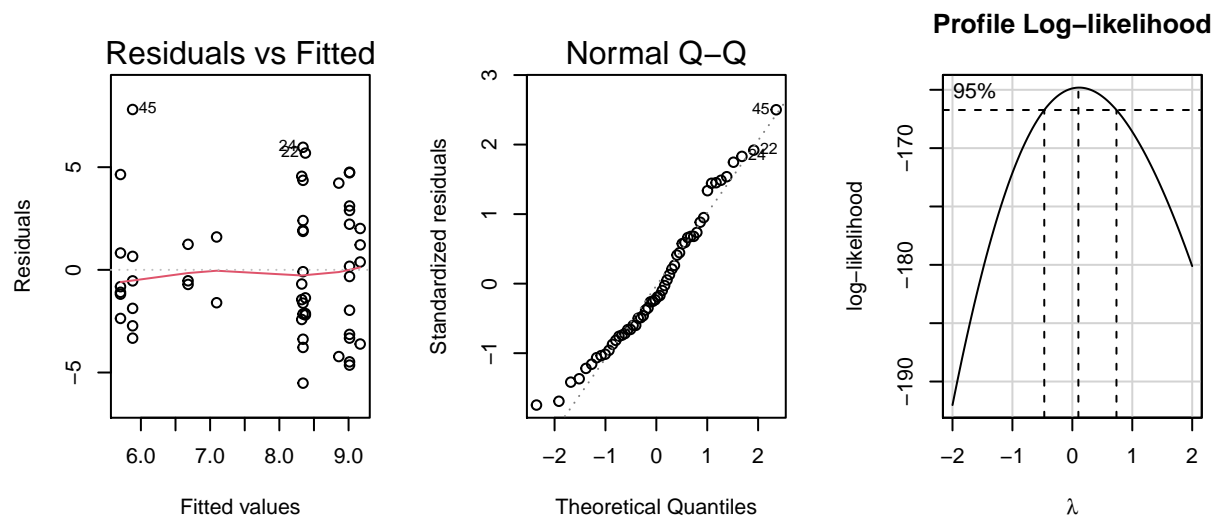
Based on our analysis results, there is no significant evidence to conclude that harvesting negatively impacts *Bursera simaruba* population as measured by basal area, stem density, and population size structure. However, we found out that there are other factors that impact the *Bursera simaruba* population. Plots with Milpa agricultural system may have larger basal area than plots without Milpa. We cannot conclude surely since our findings doesn't show confident statistical significance. Moreover, vegetation type does have a significant effect on stem density and population size structure. In general, we can conclude that Nuku'uch che' vegetation type would produce the highest stem density and population size structure compared to the other vegetation types (Keelenche' and Ju'uche'). For future work, I would recommend to get samples with a more uniform stem density and population size structure to obtain a more confident and reliable statistical result.

Appendix

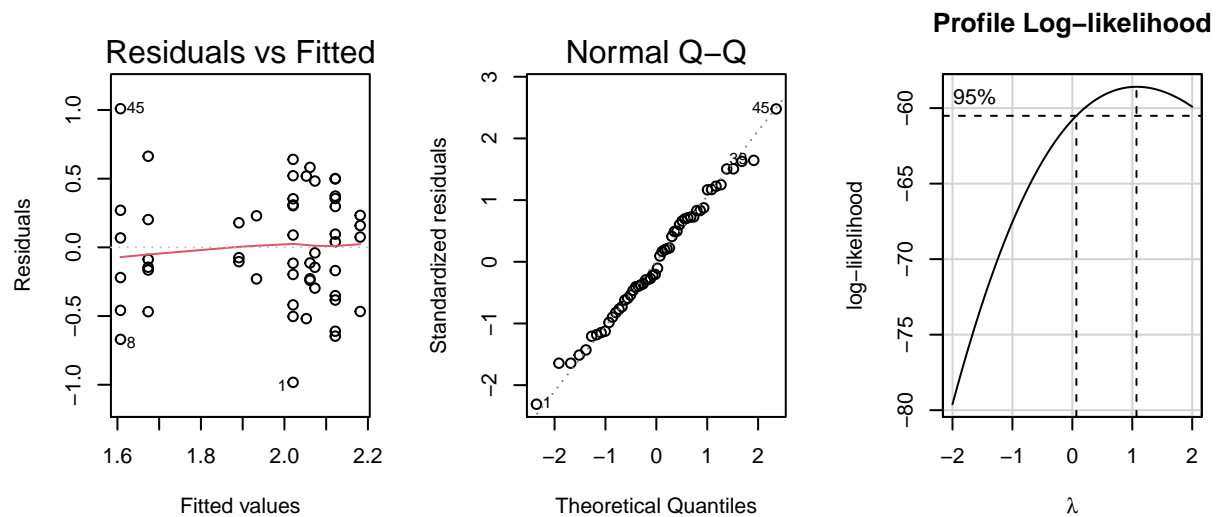
```
analysis = read.csv('Analysis_Revisado_RM.csv', stringsAsFactors = T)
plots = read.csv('Plots_data.csv', stringsAsFactors = T)
plots$PlotID = as.factor(plots$PlotID)
plots$Milpa[plots$Milpa == "Maybe"] = as.factor("No")
seedlings = read.csv('Seedlings_cut_sprouting_together.csv', stringsAsFactors = T)

##### QUESTION 1 #####

# part a
library(car)
mod = lm(plots$Basal.Area~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod) #log transformation
```



```
mod = lm(log(plots$Basal.Area)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
Anova(mod)
```

```
## Anova Table (Type II tests)
##
## Response: log(plots$Basal.Area)
##
## plots$Harvested      Sum Sq Df F value  Pr(>F)
## plots$Milpa          0.8098  1  4.0669 0.04986 *
## plots$VegetationType  0.1163  2  0.2921 0.74810
## plots$Harvested:plots$Milpa  0.0074  1  0.0371 0.84819
## plots$Harvested:plots$VegetationType  0.0640  2  0.1608 0.85197
## plots$Milpa:plots$VegetationType  0.3217  1  1.6159 0.21035
```

```
## plots$Harvested:plots$Milpa:plots$VegetationType 0.0375 1 0.1883 0.66642
## Residuals 8.7608 44
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(aov(mod))$`plots$Milpa`
```

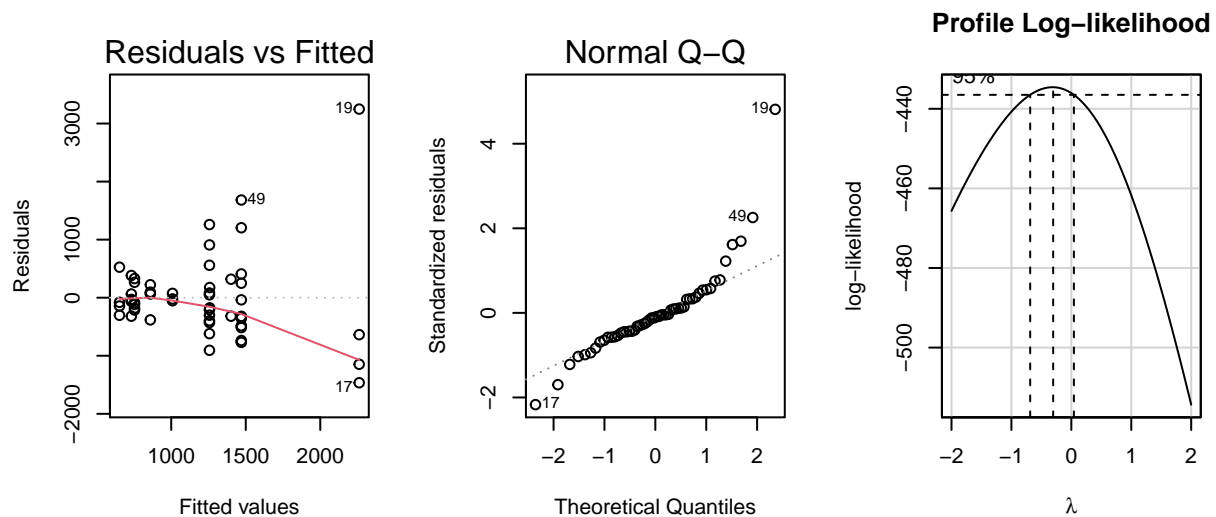
```
##          diff          lwr          upr          p adj
## Yes-No 0.3397467 0.07174029 0.6077531 0.01415883
```

```
# part b
library(ggplot2)
plots$ordered = reorder(plots$PlotID, plots$Basal.Area)
# ggplot(plots)+geom_col(aes(x=ordered, y=Basal.Area, fill=ordered)) + theme_classic() +
#   theme(legend.position="none")+labs(x="Plot ID", y="Basal Area")

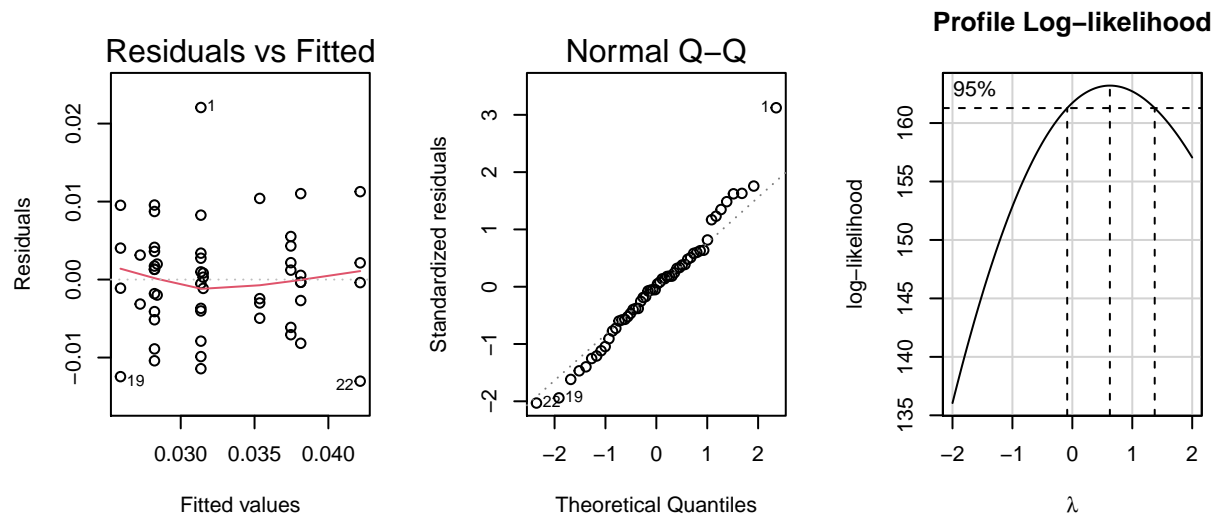
##### QUESTION 2 #####

# part a
library(plyr)
num_stem = count(analysis$Plot)$freq
plots$Stem.density.ha = num_stem*10000/314

mod = lm(plots$Stem.density.ha~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2))
boxCox(mod) #perform reciprocal of square root transformation
```



```
mod = lm(1/sqrt(plots$Stem.density.ha)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
Anova(mod)
```

```
## Anova Table (Type II tests)
##
## Response: 1/sqrt(plots$Stem.density.ha)
##
##               Sum Sq Df F value    Pr(>F)
## plots$Harvested    0.00000878  1  0.1601 0.691006
## plots$Milpa        0.00001545  1  0.2816 0.598291
## plots$VegetationType 0.00085199  2  7.7638 0.001295
## plots$Harvested:plots$Milpa 0.00000670  1  0.1221 0.728382
## plots$Harvested:plots$VegetationType 0.00012832  2  1.1694 0.320030
## plots$Milpa:plots$VegetationType 0.00000194  1  0.0353 0.851734
## plots$Harvested:plots$Milpa:plots$VegetationType 0.00005420  1  0.9877 0.325733
## Residuals        0.00241425 44
##
## plots$Harvested
## plots$Milpa
## plots$VegetationType
## plots$Harvested:plots$Milpa
## plots$Harvested:plots$VegetationType
## plots$Milpa:plots$VegetationType
## plots$Harvested:plots$Milpa:plots$VegetationType
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

```
##               diff          lwr          upr      p adj
## Keelenche'-Ju'uche' 0.000492465 -0.0071278241 0.008112754 0.98655006
## Nuku'uch che'-Ju'uche' 0.007441169 -0.0004488996 0.015331237 0.06812853
## Nuku'uch che'-Keelenche' 0.006948704 0.0016482267 0.012249180 0.00746308
```



```

# part b
plots$ordered = reorder(plots$PlotID, plots$Stem.density.ha)
# ggplot(plots)+geom_col(aes(x=ordered, y=Stem.density.ha, fill=ordered)) + theme_classic() +
#   theme(legend.position="none")+labs(x="Plot ID", y="Stem Density (#stems/ha) ")

##### QUESTION 3 #####

#function to get density of 54 plots
full_vec = function(count_data){
  if (nrow(count_data) < 54){
    vec = rep(0,54)
    vec[count_data$x] = (count_data$freq)*10000/314
    return(vec)
  }
  else{
    return((count_data$freq)*10000/314)
  }
}

analysis$Plot = as.factor(analysis$Plot)
plots$Seedling.density.ha = seedlings$Seedlings.per.Ha
plots$Saplings.density.ha = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 0.5) & (analysis$DBH_cm <= 10)])
plots$Adult.5.10.density = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 5) & (analysis$DBH_cm <= 10)])
plots$Adult.11.15.density = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 11) & (analysis$DBH_cm <= 15)])
plots$Adult.16.20.density = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 16) & (analysis$DBH_cm <= 20)])
plots$Adult.21.25.density = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 21) & (analysis$DBH_cm <= 25)])
plots$Adult.26.30.density = full_vec(count(analysis$Plot[(analysis$DBH_cm >= 26) & (analysis$DBH_cm <= 30)])

#Seedling Density
seedling = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Seedling.density.ha,
                                           fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Seedling Density ")

#Sapling density
sapling = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Saplings.density.ha,
                                           fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Saplings Density ")

#Adult 5-10 density
adult.5.10 = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Adult.5.10.density,
                                           fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Adult 5-10 cm Density ")

#Adult 11-15 density
adult.11.15 = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Adult.11.15.density,
                                           fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Adult 11-15 cm Density ")

#Adult 16-20 density
adult.16.20 = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Adult.16.20.density,
                                           fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Adult 16-20 cm Density ")

```

```

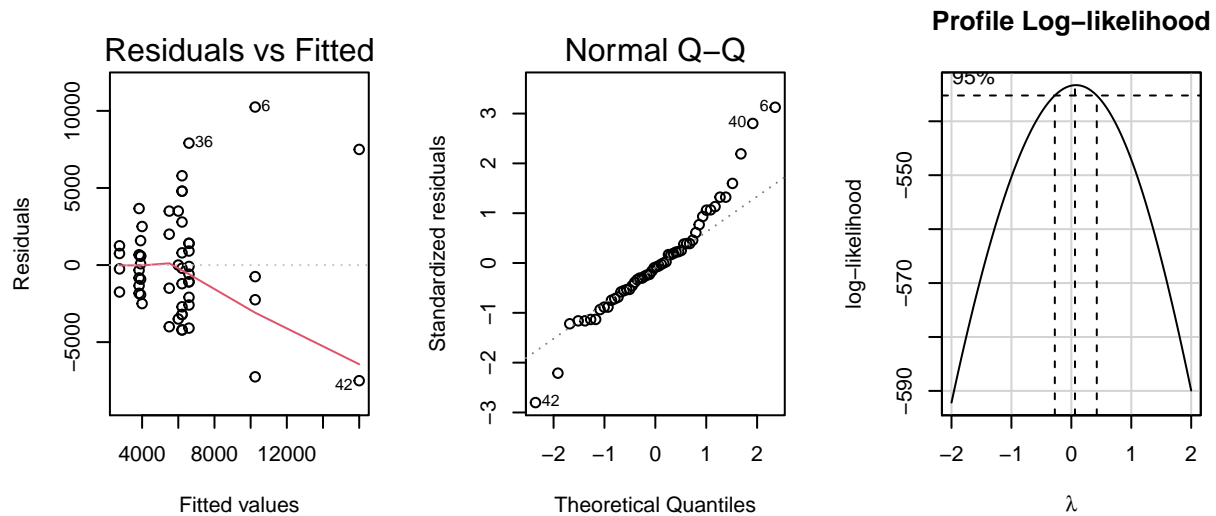
#Adult 21-25 density
adult.21.25 = ggplot(plots)+geom_boxplot(aes(x=Harvested, y=Adult.21.25.density,
                                             fill=Harvested)) + theme_classic() +
  theme(legend.position="none")+labs(x="Harvested Plots", y="Adult 21-25 cm Density ")

library(ggpubr)
# ggarrange(seedling,sapling,adult.5.10,adult.11.15,adult.16.20,adult.21.25,nrow=2,ncol=3)

##### QUESTION 4 #####

# test seedlings size structure
mod = lm(plots$Seedling.density.ha~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)

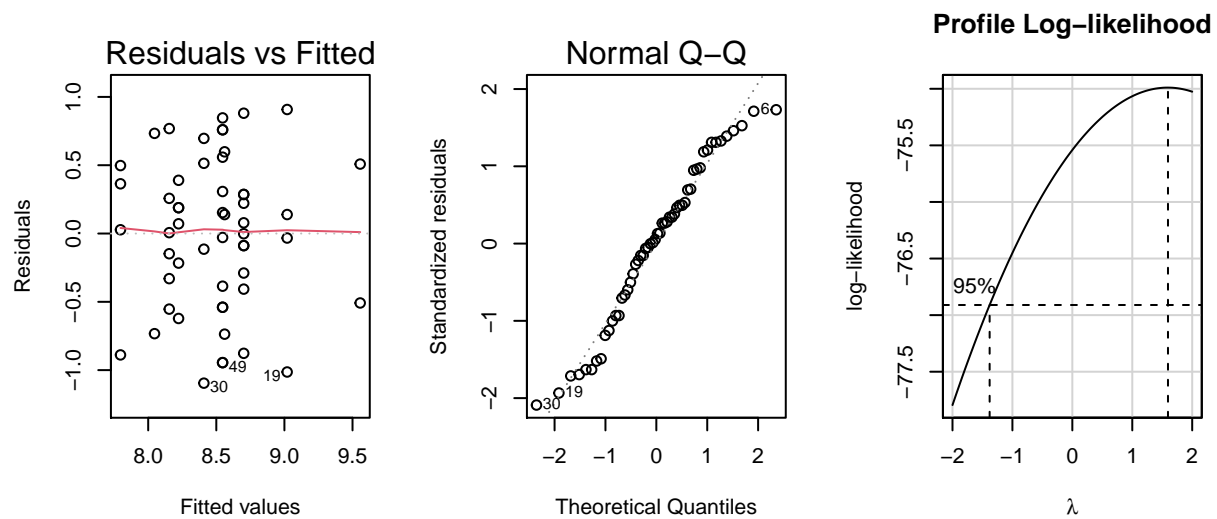
```



```

mod = lm(log(plots$Seedling.density.ha)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)

```

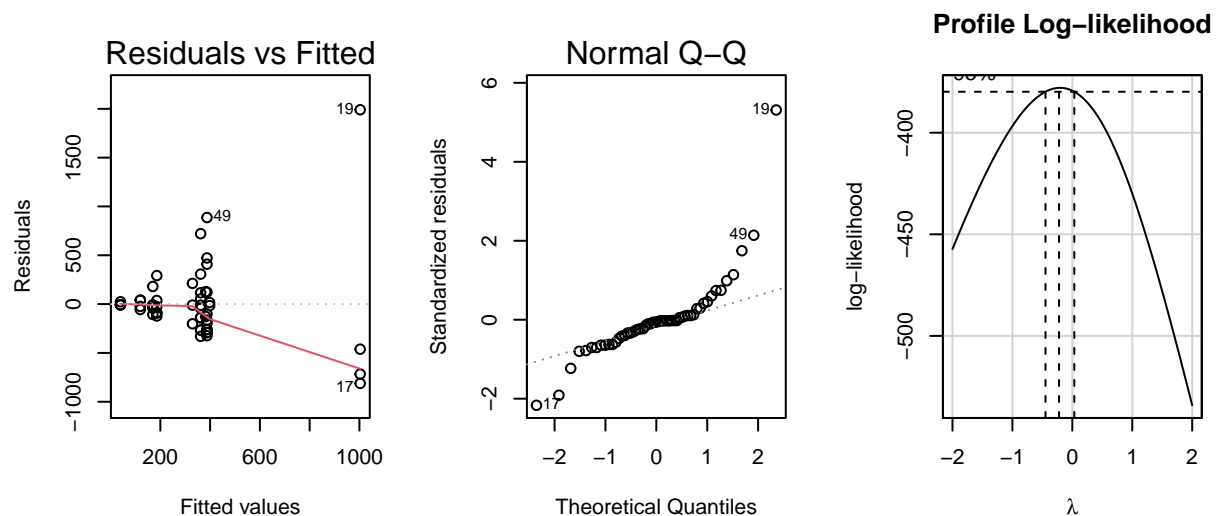


```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

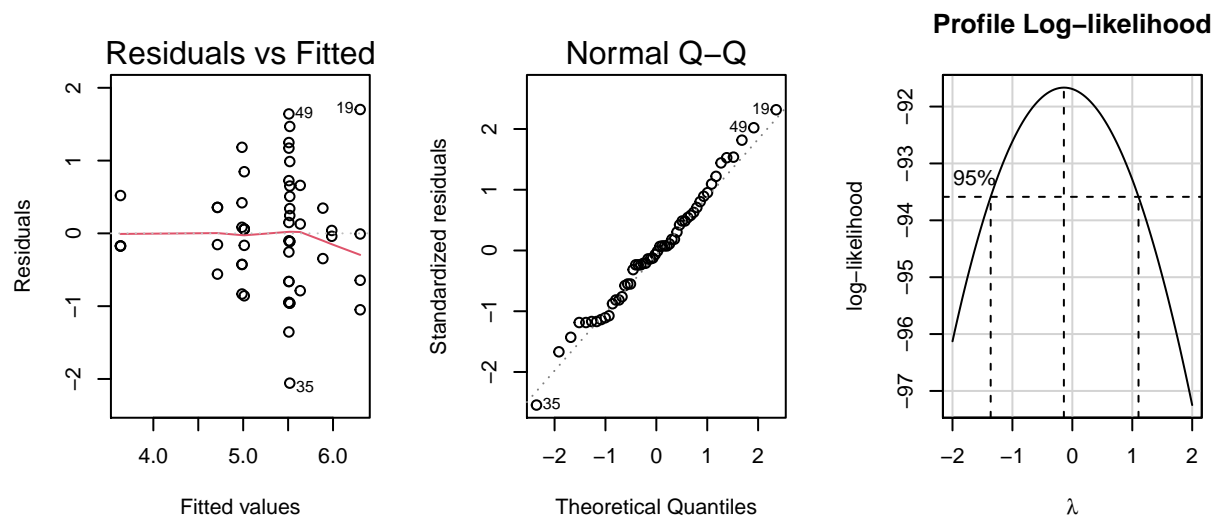
```
##               diff      lwr      upr      p adj
## Keelenche'-Ju'uche' -0.1346000 -0.7573258 0.48812575 0.85991493
## Nuku'uch che'-Ju'uche' -0.5325067 -1.1772787 0.11226530 0.12336439
## Nuku'uch che'-Keelenche' -0.3979066 -0.8310587 0.03524537 0.07750452
```

```
# test saplings size structure
```

```
mod = lm(log(plots$Saplings.density.ha)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
mod = lm(log(plots$Saplings.density.ha)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



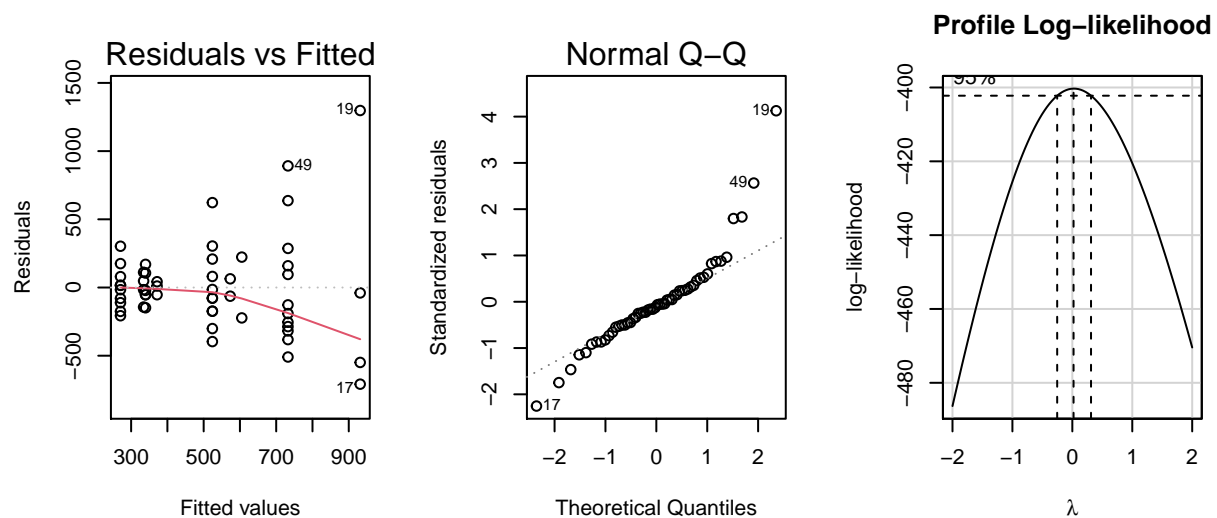
```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

```
##               diff      lwr      upr      p adj
## Keelenche'-Ju'uche' -0.4291696 -1.301720  0.4433810 0.463598244
## Nuku'uch che'-Ju'uche' -1.2955780 -2.199019 -0.3921367 0.003234279
## Nuku'uch che'-Keelenche' -0.8664084 -1.473332 -0.2594847 0.003383831
```

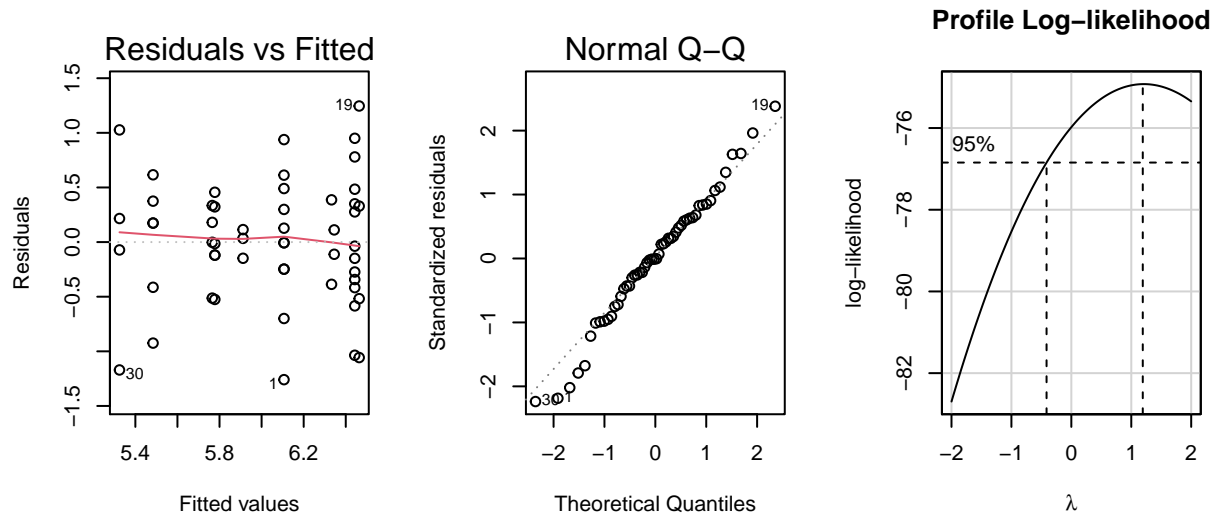
```
TukeyHSD(aov(mod))$`plots$Milpa`
```

```
##               diff      lwr      upr      p adj
## Yes-No 0.09176687 -0.4176618 0.6011955 0.7183118
```

```
# test adult 5-10 cm size structure
mod = lm(plots$Adult.5.10.density~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



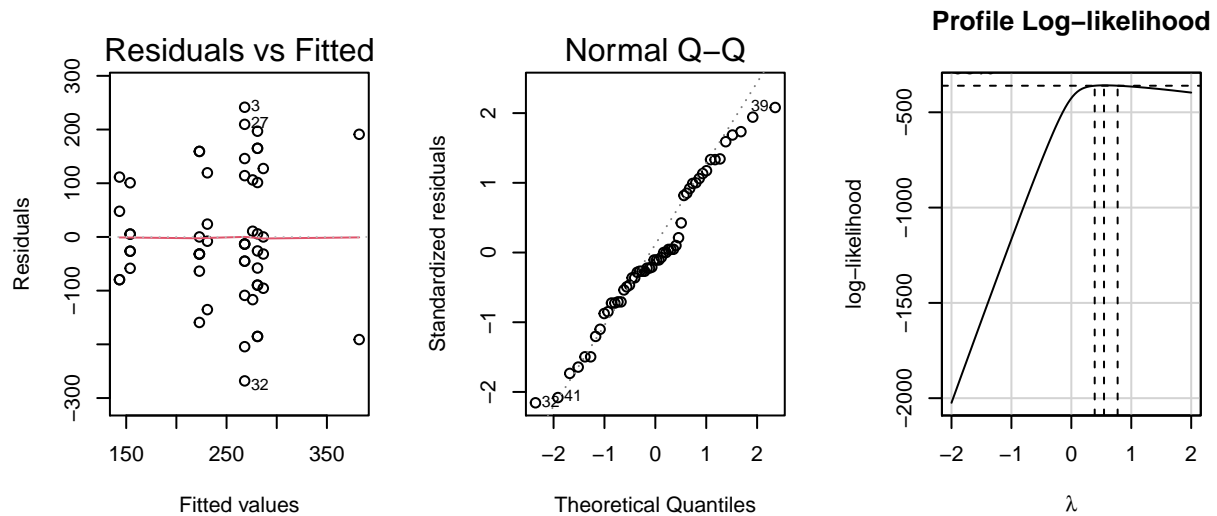
```
mod = lm(log(plots$Adult.5.10.density)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



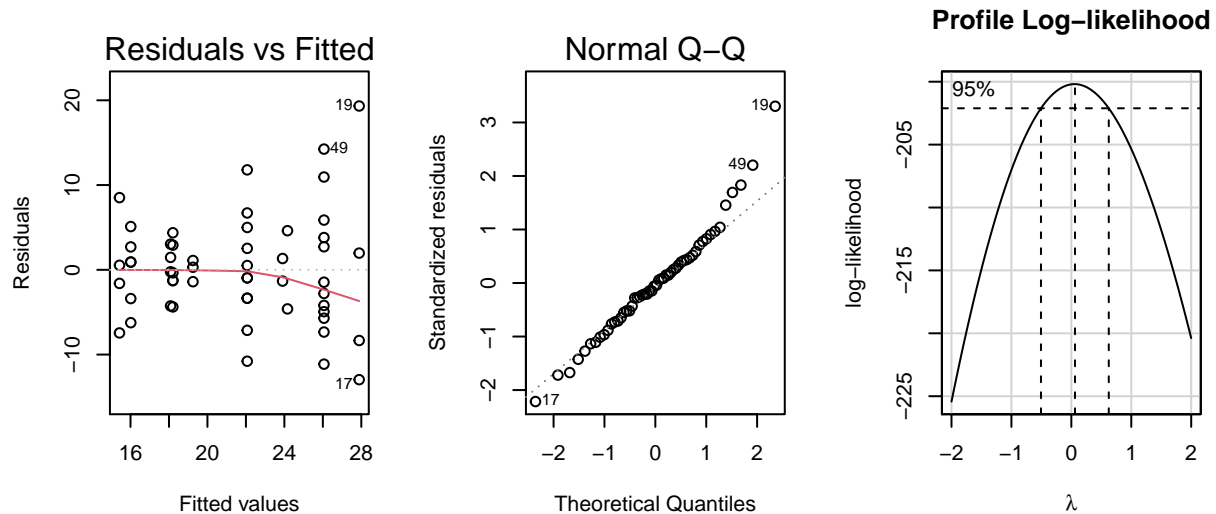
```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

	diff	lwr	upr	p adj
## Keelenche'-Ju'uche'	0.1133968	-0.5080556	0.7348493	0.897913091
## Nuku'uch che'-Ju'uche'	-0.4402131	-1.0836667	0.2032404	0.232188093
## Nuku'uch che'-Keelenche'	-0.5536100	-0.9858763	-0.1213437	0.009105962

```
# test adult 11-15 cm size structure
mod = lm(log(plots$Adult.11.15.density+1e-5)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



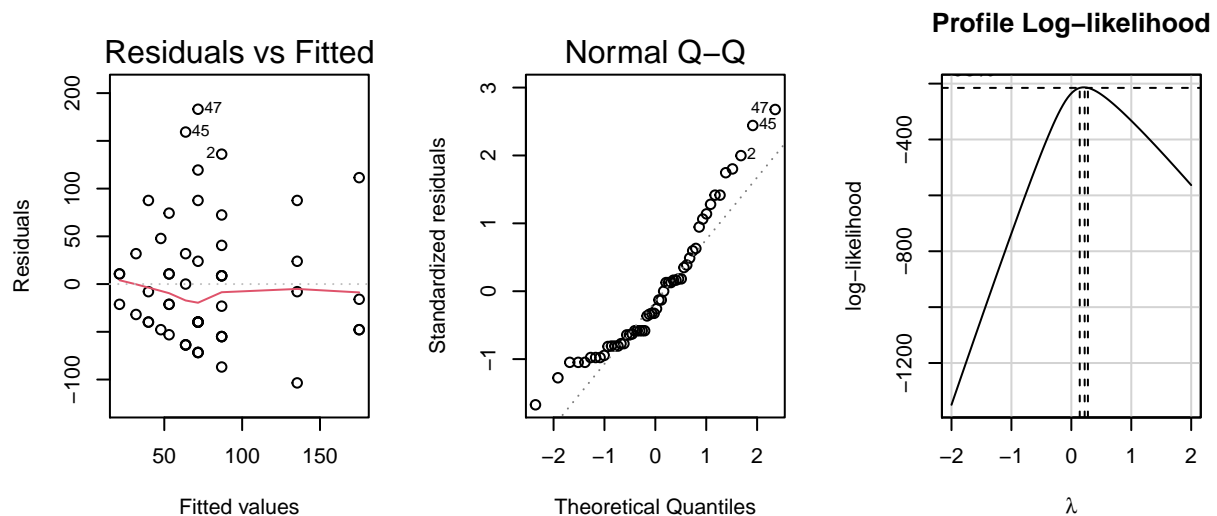
```
mod = lm(sqrt(plots$Adult.5.10.density+1e-5)~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



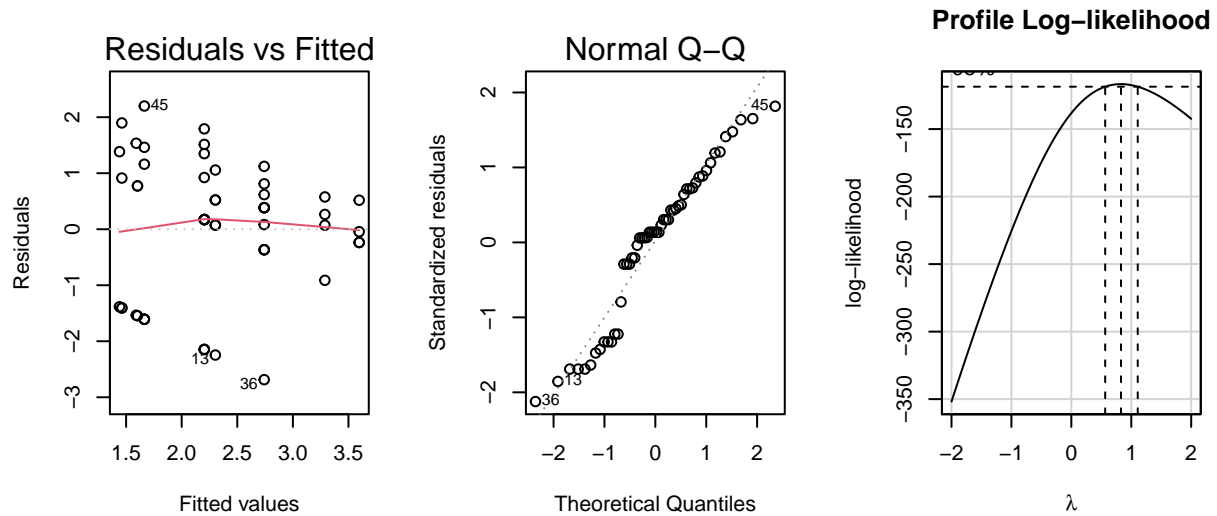
```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

	diff	lwr	upr	p adj
## Keelenche'-Ju'uche'	0.6050367	-6.345687	7.5557605	0.9757393
## Nuku'uch che'-Ju'uche'	-4.8481280	-12.044926	2.3486703	0.2423486
## Nuku'uch che'-Keelenche'	-5.4531648	-10.287909	-0.6184204	0.0238134

```
# test adult 16-20 cm size structure
mod = lm(plots$Adult.16.20.density+1e-5~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
mod = lm((plots$Adult.16.20.density+1e-5)^.25~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



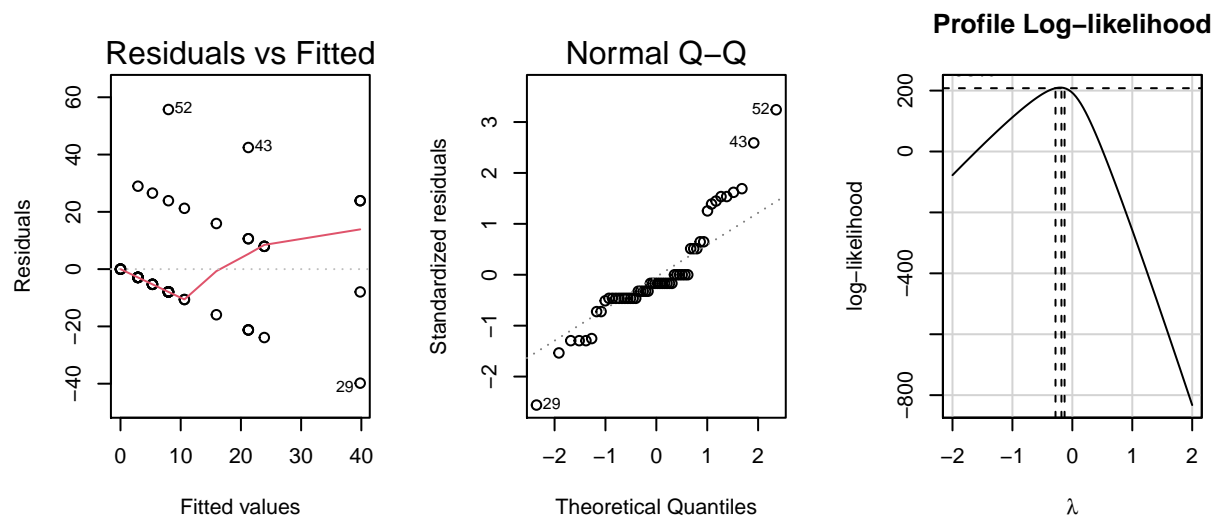
```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

	diff	lwr	upr	p adj
## Keelenche'-Ju'uche'	0.8726157	-0.4923604	2.237592	0.27773195
## Nuku'uch che'-Ju'uche'	1.3997727	-0.0135273	2.813073	0.05271991
## Nuku'uch che'-Keelenche'	0.5271570	-0.4222852	1.476599	0.37747594

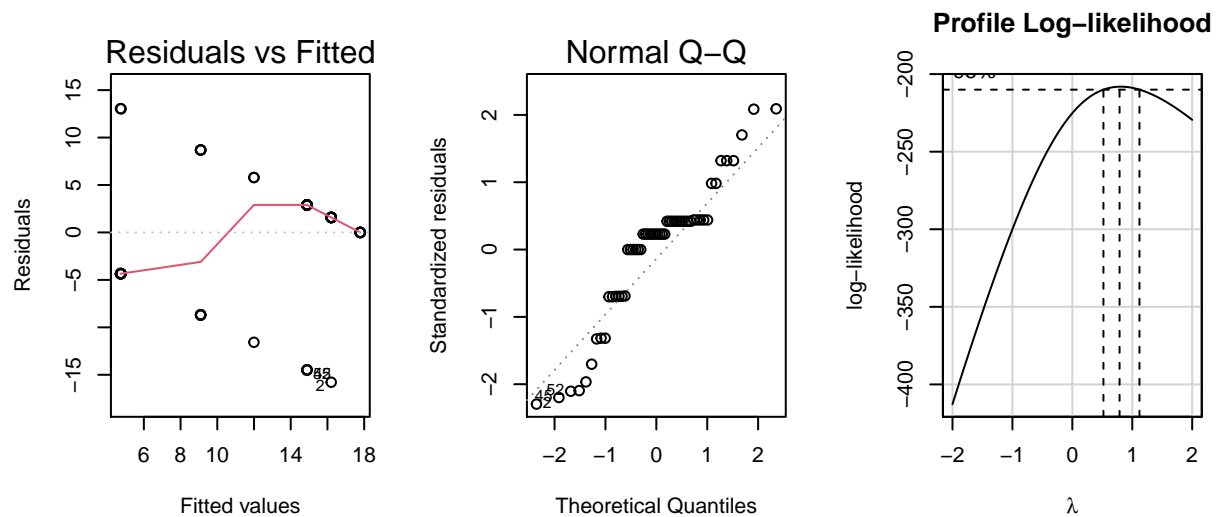
```
TukeyHSD(aov(mod))$`plots$Milpa`
```

	diff	lwr	upr	p adj
## Yes-No	0.6379648	-0.1589608	1.43489	0.1138149

```
# test adult 21-25 cm size structure
mod = lm(plots$Adult.21.25.density+1e-5~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
mod = lm((plots$Adult.21.25.density+1e-5)^-.25~plots$Harvested*plots$Milpa*plots$VegetationType)
par(mfrow = c(1, 3)); plot(mod, which=c(1,2)); boxCox(mod)
```



```
TukeyHSD(aov(mod))$`plots$VegetationType`
```

	diff	lwr	upr	p adj
## Keelenche'-Ju'uche'	0.08086869	-7.337277	7.499014	0.99961462
## Nuku'uch che'-Ju'uche'	-5.64235014	-13.323118	2.038418	0.18748356
## Nuku'uch che'-Keelenche'	-5.72321882	-10.883090	-0.563348	0.02664703