

# An Exploration of Darwin's Finches

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STAT 5311: Multivariate and Nonparametric Statistics

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## Introduction

### Background

Charles Darwin is best known as the “Father of evolution.” His famous study took place in the Galapagos Islands where he observed birds, specifically finches over a span of five weeks. When he returned to London, he began to observe fascinating results. He realized that at least 13 species of finch were evolved from a single ancestor. This propelled Darwin’s idea of natural selection, the process through which populations of living organisms adapt and change. Through speciation, changes in related organisms to the point where they are different enough to be considered separate species, there were a total of 14 species of finches in the Galapagos Islands. Each finch species adapted to their environment based on their dietary needs. Although the finches were identical in nearly all ways to each other, their main differentiating factor was their beaks. Since Darwin, many scientists have spent years trying to understand the process of the finches evolving mainly in the size of their beaks.

The most recent scientists were Peter and Rosemary Grant. They spent 25 years in the Galapagos Islands, specifically on the smaller island of Daphne Major. They remained there, studying, and observing how climatic conditions drastically alter food supply. They focused their research on the Geospiza fortis species, otherwise known as medium ground finches. Having variability in size and shape, the medium ground finch made a good subject for studying evolution. Due to fewer predators or competitors, and its isolation, Daphne Major was selected as the ideal geographical area. They observed that the major factor influencing the medium ground finch’s survival was the weather and its effect on the availability of food. In 1977, a drought over 551 days resulted in plants wilting and the finch’s source of food became scarce as finches were accustomed to consuming the tiny seeds. The medium ground finches with larger beaks were able to open larger seeds and the smaller-beaked finches eventually died from starvation. When the Grants returned to Daphne Major in 1978, they observed the effect of the drought on the next generation of medium ground finches. When comparing beak sizes to the previous generation, they found the offspring’s beaks to be approximately 3% to 4% larger.

The Grants returned to Daphne Major over the course of the next 25 years to record their findings. The Grants’ work on the finches has been universally recognized as one of the most significant studies on the theory of evolution. Their findings have further cemented and expanded Darwin’s hypothesis of evolution and his idea of natural selection.

### Problem Description

There is comprehensive data available on the famous Darwin finches, collected by Peter and Rosemary Grant spanning approximately 40 years. These finches were famous in motivating and reinforcing Darwin’s original Theory of Evolution. We are setting out to explore the measurement differences in beak lengths and depths over the course of 1975 and 2012. By approaching this data, we seek to better understand if there is a significant difference or potential for evolving just over the span of 40 years.

### Features/Factors Description

Our finches dataset contains information about two different species of Finches gathered from 1975-2012. The dataset contains two files (one corresponding to the year 1975 and the other 2012). There are four features described in this dataset: Band, Species, Blength, and Bdepth. Band refers to the finch’s identity (the metal leg

band it was given), Blength refers to the Beak Length, and Bdepth refers to the Beak depth. Based on the research of Peter and Rosemary Grant, the beak shape (mainly their lengths and depths) was one of the main factors that contributed to the survival of the finches observed.

## **Information on Data Collection**

Peter and Rosemary Grant spent 37 years capturing, observing, tagging, and measuring medium ground finches' beaks. They documented environmental changes to better understand how the environment could potentially favor certain individuals and their traits within the population.

## **Hypothesis**

We will be comparing the medium ground finch's beak length and depth measurements collected in 1975 with 2012's data. We are looking to discover if there have been significant changes in the measures of the beak lengths and depths. Our working assumption is that there is no significant difference in beak length or depth between the years of 1975 and 2012.

## **Methods of Exploration**

We will do exploratory analysis of beak depths and lengths using statistical testing methods such as bootstrapping, permutation, Chi Square, and hypothesis.

## **Project Relevance**

Since Darwin's findings, scientists have been fascinated with the Theory of Evolution regarding natural selection. Analysis of this data is important as it may highlight the evolution of finches over 37 years due to adaptive requirements because of climate or nutritional source changes. If we were to find significant changes over the course of the 37-year period, we can confirm or reinforce the idea of natural selection within the Theory of Evolution.

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## **Results & Discussion**

### **Bootstrap test**

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*Donec egestas augue ut elit blandit tempus. Vivamus hendrerit dolor libero, in rutrum libero iaculis dignissim. Maecenas ac ipsum lobortis, pellentesque neque at, dignissim quam. Class aptent taciti sociosqu ad litora torquent per conubia nostra, per inceptos himenaeos. Integer ipsum dui, condimentum ac ipsum sit amet, facilisis malesuada leo. Aliquam ullamcorper urna et consequat suscipit. Suspendisse ut posuere velit. Ut facilisis eleifend sodales. Nam a leo lorem. Integer viverra sit amet mauris nec hendrerit. Suspendisse a tempus sem. Phasellus ut dolor dapibus, posuere augue eget, egestas massa.*

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### **Permutation test**

A permutation test is widely used when comparing the distributions or means of different datasets based on certain situations. Like the bootstrap testing method, we resample observed data, but unlike bootstrapping we skip replacement. Permutation tests are particularly useful when assessing the difference in treatment between groups. In our dataset, the weather/climate between the years of 1975 and 2012 would be considered the treatment. The null hypothesis for our permutation test is that there is no significant difference in beak length or beak depth in the finches between the years 1975 and 2012. The alternate being that there is a significant difference in beak length and depths between the years 1975 and 2012.

After running the permutation test on both beak depth and length, we obtained p-values of 2.2e-16 and 1e-04 for the beak length and depth respectively. At a 5% significance level, we can confidently reject the null hypothesis and conclude that there is a significant difference in finch beak length between the years 1975 and 2012.

### **Chi Square test**

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Cras a ex id mauris interdum molestie in efficitur augue. Donec mollis dictum odio in tincidunt. Aliquam vitae accumsan eros. Aenean fringilla convallis lorem sed mollis. Donec justo quam, ultricies ornare scelerisque ultrices, vulputate vulputate nulla. Proin pulvinar mi et euismod euismod. Maecenas efficitur tincidunt metus vitae vestibulum.

Donec egestas augue ut elit blandit tempus. Vivamus hendrerit dolor libero, in rutrum libero iaculis dignissim. Maecenas ac ipsum lobortis, pellentesque neque at, dignissim quam. Class aptent taciti sociosqu ad litora torquent per conubia nostra, per inceptos himenaeos. Integer ipsum dui, condimentum ac ipsum sit amet, facilisis malesuada leo. Aliquam ullamcorper urna et consequat suscipit. Suspendisse ut posuere velit. Ut facilisis eleifend sodales. Nam a leo lorem. Integer viverra sit amet mauris nec hendrerit. Suspendisse a tempus sem. Phasellus ut dolor dapibus, posuere augue eget, egestas massa.

Cras at massa metus. Aliquam lacinia interdum varius. Duis mollis dolor ut massa laoreet lobortis. Vivamus pulvinar est vel leo bibendum, sed laoreet tortor scelerisque. Fusce non pellentesque turpis. Vestibulum tincidunt maximus pulvinar. Praesent sit amet mauris ante. Pellentesque condimentum mi at mauris condimentum, eget mollis ligula lobortis. Curabitur fringilla mattis faucibus. Aenean varius sem id tellus mollis lobortis. Pellentesque sit amet rutrum diam, ut placerat nulla. Cras turpis sem, ornare nec tristique at, ullamcorper ut diam. Nullam in cursus purus.

### **Hypothesis test**

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Donec egestas augue ut elit blandit tempus. Vivamus hendrerit dolor libero, in rutrum libero iaculis dignissim. Maecenas ac ipsum lobortis, pellentesque neque at, dignissim quam. Class aptent taciti sociosqu ad litora torquent per conubia nostra, per inceptos himenaeos. Integer ipsum dui, condimentum ac ipsum sit amet, facilisis malesuada leo. Aliquam ullamcorper urna et consequat suscipit. Suspendisse ut posuere velit. Ut facilisis eleifend sodales. Nam a leo lorem. Integer viverra sit amet mauris nec hendrerit. Suspendisse a tempus sem. Phasellus ut dolor dapibus, posuere augue eget, egestas massa.

Cras at massa metus. Aliquam lacinia interdum varius. Duis mollis dolor ut massa laoreet lobortis. Vivamus pulvinar est vel leo bibendum, sed laoreet tortor scelerisque. Fusce non pellentesque turpis. Vestibulum tincidunt maximus pulvinar. Praesent sit amet mauris ante. Pellentesque condimentum mi at mauris condimentum, eget mollis ligula lobortis. Curabitur fringilla mattis faucibus. Aenean varius sem id tellus mollis lobortis. Pellentesque sit amet rutrum diam, ut placerat nulla. Cras turpis sem, ornare nec tristique at, ullamcorper ut diam. Nullam in cursus purus.

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## Conclusion

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---

## Appendices

### Bootstrap analysis

```
t.test(bdepth_1975, bdepth_2012)$conf
```

---

```
## [1] 0.1058994 0.3403661
## attr(,"conf.level")
## [1] 0.95
```

```
# Bootstrap test

thetahat <- mean(bdepth_1975) - mean(bdepth_2012)
nx <- length(bdepth_1975) #nx
ny <- length(bdepth_2012) #ny=23
SE <- sqrt(var(bdepth_1975)/nx + var(bdepth_2012)/ny)

N <- 10000
Tstar <- numeric(N)
set.seed(0)

for(i in 1:N)
{
  bootx <- sample(bdepth_1975, nx, replace = TRUE)
  booty <- sample(bdepth_2012, ny, replace = TRUE)
  Tstar[i] <- (mean(bootx) - mean(booty) - thetahat) /
    sqrt(var(bootx)/nx + var(booty)/ny)
}

thetahat - quantile(Tstar, c(.975, .025)) * SE
```

---

```
##      97.5%      2.5%
## 0.1052585 0.3414293
```

```

# Bootstrapping confidence interval shows on average beak depth 2012 is higher
# than beak depth in 1975

thetahat <- mean(blength_1975) - mean(blength_2012)
nx <- length(blength_1975) #nx
ny <- length(blength_2012) #ny
SE <- sqrt(var(blength_1975)/nx + var(blength_2012)/ny)

N <- 10000
Tstar <- numeric(N)
set.seed(0)

for(i in 1:N)
{
  bootx <- sample(blength_1975, nx, replace = TRUE)
  booty <- sample(blength_2012, ny, replace = TRUE)
  Tstar[i] <- (mean(bootx) - mean(booty) - thetahat) /
    sqrt(var(bootx)/nx + var(booty)/ny)
}

thetahat - quantile(Tstar, c(.975, .025)) * SE

```

---

```

##      97.5%      2.5%
## -0.9245327 -0.4119528

```

---

```

t.test(blength_1975, blength_2012)$conf

```

---

```

## [1] -0.9305010 -0.4125201
## attr(),"conf.level")
## [1] 0.95

```

## Permutation test

```
# Permutation testing

finch_1975 <- read.csv('finch_beaks_1975.csv', sep = ',', header = TRUE)
finch_2012 <- read.csv('finch_beaks_2012.csv', sep = ',', header = TRUE)

blength_1975 <- finch_1975[, 3]
blength_2012 <- finch_2012[, 3]
bdepth_1975 <- finch_1975[, 4]
bdepth_2012 <- finch_2012[, 4]

# Difference in means
blength_diff <- mean(blength_1975) - mean(blength_2012)
blength_diff

## [1] -0.6715105

bdepth_diff <- mean(bdepth_1975) - mean(bdepth_2012)
bdepth_diff

## [1] 0.2231328
```

```
# Running permutation test for beak lengths
library(MKinfer)
perm.t.test(blength_1975, blength_2012, mu = 0, conf.level = 0.95)

##
##  Permutation Welch Two Sample t-test
##
##  data:  blength_1975 and blength_2012
##  (Monte-Carlo) permutation p-value < 2.2e-16
##  95 percent (Monte-Carlo) permutation percentile confidence interval:
##  -0.9332475 -0.4057007
##
##  Results without permutation:
##  t = -5.0937, df = 517.19, p-value = 4.928e-07
##  alternative hypothesis: true difference in means is not equal to 0
##  95 percent confidence interval:
##  -0.9305010 -0.4125201
##  sample estimates:
##  mean of x mean of y
##  11.33280 12.00431
```

```
# Running permutation test for beak depths
perm.t.test(bdepth_1975, bdepth_2012, mu = 0, conf.level = 0.95)

##
##  Permutation Welch Two Sample t-test
##
## data: bdepth_1975 and bdepth_2012
## (Monte-Carlo) permutation p-value = 2e-04
## 95 percent (Monte-Carlo) permutation percentile confidence interval:
##  0.1051979 0.3413990
##
## Results without permutation:
## t = 3.7396, df = 496.29, p-value = 0.0002058
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1058994 0.3403661
## sample estimates:
## mean of x mean of y
##  9.125955 8.902823
```

## Chi Square test

```
library(dbplyr)

# Importing and Cleaning data
F1975 <-read.csv('finch_beaks_1975.csv')

# Separate into beak length and depth for each species

# Fortis 1975
blfort75<-subset(F1975, species == 'fortis', select = Beak.length..mm)

bdfort75 <-subset(F1975, species == 'fortis', select = Beak.depth..mm)

# Scandens 1975
blscan75<-subset(F1975, species == 'scandens', select = Beak.length..mm)

bdscan75 <-subset(F1975, species == 'scandens', select = Beak.depth..mm)

# Fortis 2012
F2012 <-read.csv('finch_beaks_2012.csv')
blfort12<-subset(F2012, species == 'fortis', select = blength)

bdfort12 <-subset(F2012, species == 'fortis', select = bdepth)

# Scandens 2012
blscan12<-subset(F2012, species == 'scandens', select = blength)

bdscan12 <-subset(F2012, species == 'scandens', select = bdepth)

# Data Table with Fortis Beak Length comparison
Fort.BLength1975 <-c(sum(blfort75[, 1] >= 8.5 & blfort75[, 1] <= 9.625),
                      sum(blfort75[,1] >=9.63 & blfort75[, 1] <= 10.745),
                      sum(blfort75[,1] >=10.75 & blfort75[, 1] <= 11.87),
                      sum(blfort75[,1] >= 11.875 & blfort75[,1]<= 13))

Fort.BLength2012 <-c(sum(blfort12[, 1] >= 8.5 & blfort12[, 1] <= 9.625),
                      sum(blfort12[, 1] >= 9.63 & blfort12[, 1]<= 10.745),
                      sum(blfort12[,1] >= 10.75 & blfort12[, 1] <= 11.87),
                      sum(blfort12[,1] >= 11.875 & blfort12[,1]<= 13))

chiblfort <-data.frame(Fort.BLength1975,Fort.BLength2012)
rownames(chiblfort) <-c("8.5-9.625mm", "9.63-10.745mm",
                       "10.75-11.87mm", "11.875-13mm")
```

```

# Data Table with Fortis Beak Depth comparison
Fort.BDepth1975 <-c(sum(bdfort75[, 1] >= 7 & bdfort75[, 1] <= 8.12),
                     sum(bdfort75[, 1] >= 8.125 & bdfort75[, 1] <= 9.245),
                     sum(bdfort75[, 1] >= 9.25 & bdfort75[, 1] <= 10.37),
                     sum(bdfort75[, 1] >= 10.375 & bdfort75[, 1] <= 11.5))

Fort.BDepth2012 <-c(sum(bdfort12[, 1] >= 7 & bdfort12[, 1] <= 8.12),
                      sum(bdfort12[, 1] >= 8.125 & bdfort12[, 1] <= 9.245),
                      sum(bdfort12[, 1] >= 9.25 & bdfort12[, 1] <= 10.37),
                      sum(bdfort12[, 1] >= 10.375 & bdfort12[, 1] <= 11.5))

chibdfort <-data.frame(Fort.BDepth1975,Fort.BDepth2012)
rownames(chibdfort) <-c("7-8.12mm", "8.125-9.245mm",
                       "9.25-10.37mm", "10.375-11.5mm")

```

```

# Data Table with Scandens Beak Length comparison
Scan.BLength1975 <-c(sum(blscan75[, 1] >= 11 & blscan75[, 1] <= 12.2),
                      sum(blscan75[, 1] >= 12.25 & blscan75[, 1] <= 13.45),
                      sum(blscan75[, 1] >= 13.5 & blscan75[, 1] <= 14.7),
                      sum(blscan75[, 1] >= 14.75 & blscan75[, 1] <= 16))

Scan.BLength2012 <-c(sum(blscan12[, 1] >= 11 & blscan12[, 1] <= 12.2),
                      sum(blscan12[, 1] >= 12.25 & blscan12[, 1] <= 13.45),
                      sum(blscan12[, 1] >= 13.5 & blscan12[, 1] <= 14.7),
                      sum(blscan12[, 1] >= 14.75 & blscan12[, 1] <= 16))

chiblscan <-data.frame(Scan.BLength1975,Scan.BLength2012)
rownames(chiblscan) <-c("11-12.2mm", "12.25-13.45mm",
                        "13.5-14.7mm", "14.75-16mm")

```

```

# Data Table with Scandens Beak Depth comparison
Scan.BDepth1975 <-c(sum(bdscan75[, 1] >= 7.5 & bdscan75[, 1] <= 8.37),
                     sum(bdscan75[, 1] >= 8.375 & bdscan75[, 1] <= 9.245),
                     sum(bdscan75[, 1] >= 9.25 & bdscan75[, 1] <= 10.12),
                     sum(bdscan75[, 1] >= 10.125 & bdscan75[, 1] <= 11))

Scan.BDepth2012 <-c(sum(bdscan12[, 1] >= 7.5 & bdscan12[, 1] <= 8.37),
                     sum(bdscan12[, 1] >= 8.375 & bdscan12[, 1] <= 9.245),
                     sum(bdscan12[, 1] >= 9.25 & bdscan12[, 1] <= 10.12),
                     sum(bdscan12[, 1] >= 10.125 & bdscan12[, 1] <= 11))

chibdscan <-data.frame(Scan.BDepth1975,Scan.BDepth2012)
rownames(chibdscan) <-c("7.5-8.37mm", "8.375-9.245mm",
                        "9.25-10.12mm", "10.125-11mm")

```

```

listofDF <-list(
  "Beak Length of Fortis 1972 & 2012"=chiblfort,
  "Beak Depth of Fortis 1972 & 2012"=chibdfort,
  "Beak Length of Scandens 1972 & 2012"=chiblscan,
  "Beak Depth of Scandens 1972 & 2012"=chibdscan
)

listofDF

```

```

## $`Beak Length of Fortis 1972 & 2012`
##           Fort.BLength1975 Fort.BLength2012
## 8.5-9.625mm          25          12
## 9.63-10.745mm        157         74
## 10.75-11.87mm        127         26
## 11.875-13mm          7          9
##
## $`Beak Depth of Fortis 1972 & 2012`
##           Fort.BDepth1975 Fort.BDepth2012
## 7-8.12mm              29          33
## 8.125-9.245mm         137         66
## 9.25-10.37mm          134         21
## 10.375-11.5mm         16          1
##
## $`Beak Length of Scandens 1972 & 2012`
##           Scan.BLength1975 Scan.BLength2012
## 11-12.2mm              0          6
## 12.25-13.45mm          17         59
## 13.5-14.7mm             47         58
## 14.75-16mm              22         4
##
## $`Beak Depth of Scandens 1972 & 2012`
##           Scan.BDepth1975 Scan.BDepth2012
## 7.5-8.37mm              13         13
## 8.375-9.245mm           52         53
## 9.25-10.12mm             19         50
## 10.125-11mm              3          11

```

```
lapply(listofDF, fisher.test)
```

```

## $`Beak Length of Fortis 1972 & 2012`
##
## Fisher's Exact Test for Count Data
##
## data: X[[i]]
## p-value = 0.0003546
## alternative hypothesis: two.sided
##
##
## $`Beak Depth of Fortis 1972 & 2012`
##
## Fisher's Exact Test for Count Data
##
## data: X[[i]]
## p-value = 2.605e-09
## alternative hypothesis: two.sided
##
```

```

## 
## $`Beak Length of Scandens 1972 & 2012`
## 
## Fisher's Exact Test for Count Data
## 
## data: X[[i]]
## p-value = 1.832e-08
## alternative hypothesis: two.sided
## 
## 
## $`Beak Depth of Scandens 1972 & 2012`
## 
## Fisher's Exact Test for Count Data
## 
## data: X[[i]]
## p-value = 0.009121
## alternative hypothesis: two.sided

```

## Hypothesis test

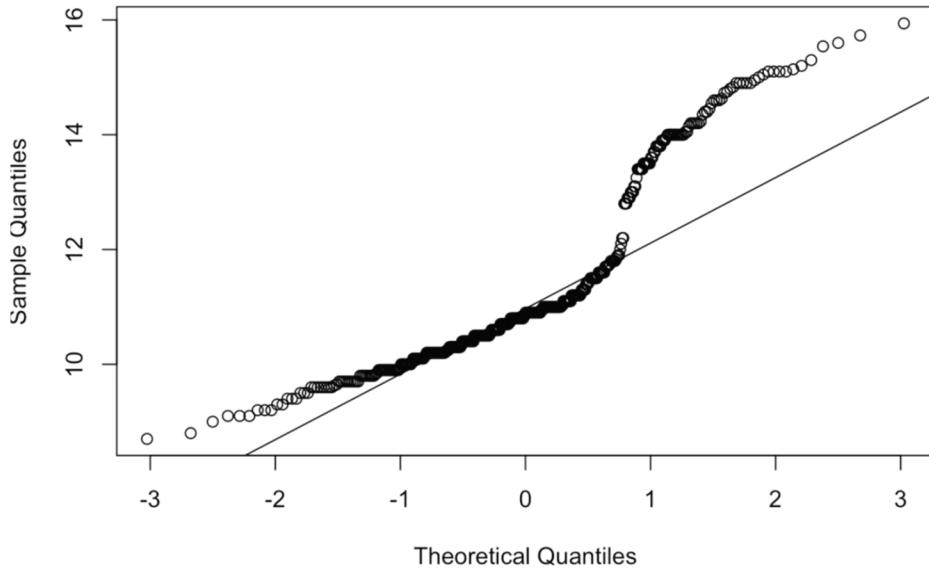
```

# Hypothesis Testing

# Checking normality
qqnorm(blength_1975)
qqline(blength_1975)

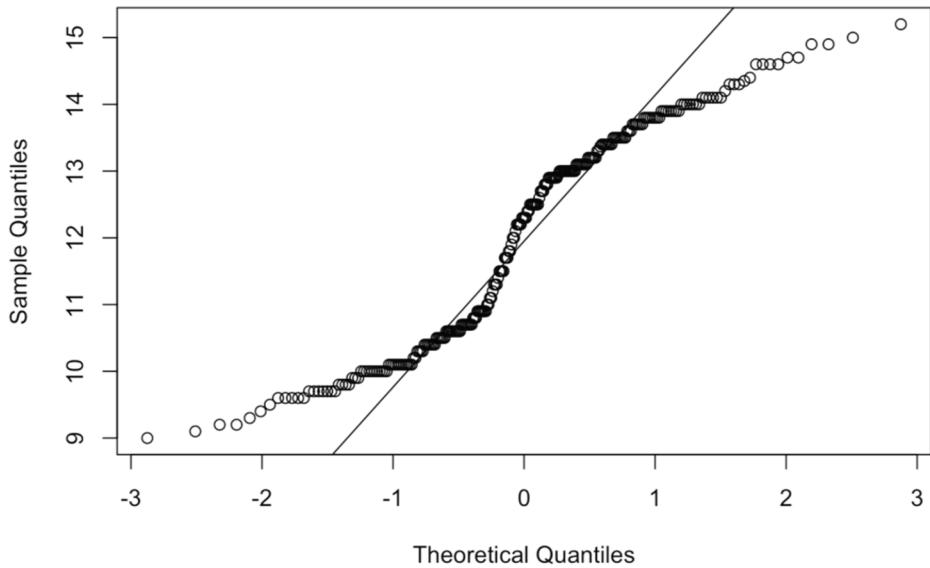
```

Normal Q-Q Plot



```
qqnorm(blength_2012)
qqline(blength_2012)
```

Normal Q-Q Plot



```
t.test(blength_1975, blength_2012, alternative =
  "two.sided", var.equal = TRUE)
```

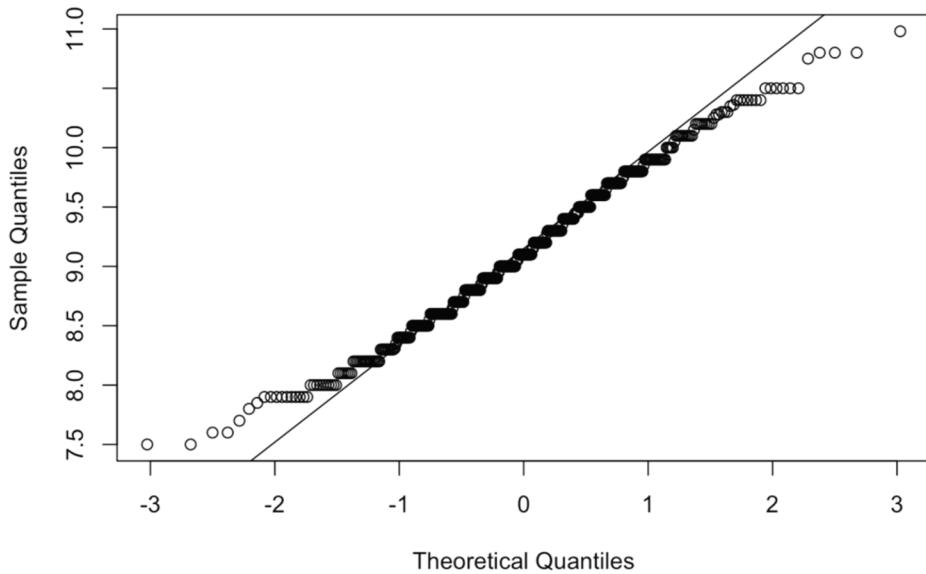
```
##
##  Two Sample t-test
##
## data:  blength_1975 and blength_2012
## t = -5.1109, df = 649, p-value = 4.222e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.9295056 -0.4135155
## sample estimates:
## mean of x mean of y
## 11.33280 12.00431
```

```
# Testing equality of variances
library(testequavar)
equa2vartest(blength_1975, blength_2012, 0.05, B = 5000)
```

```
## [[1]]
## [1] "Decision: Fail to Reject the Null"
##
## $Alpha
## [1] 0.05
##
## $NumberOfBootSamples
## [1] 5000
```

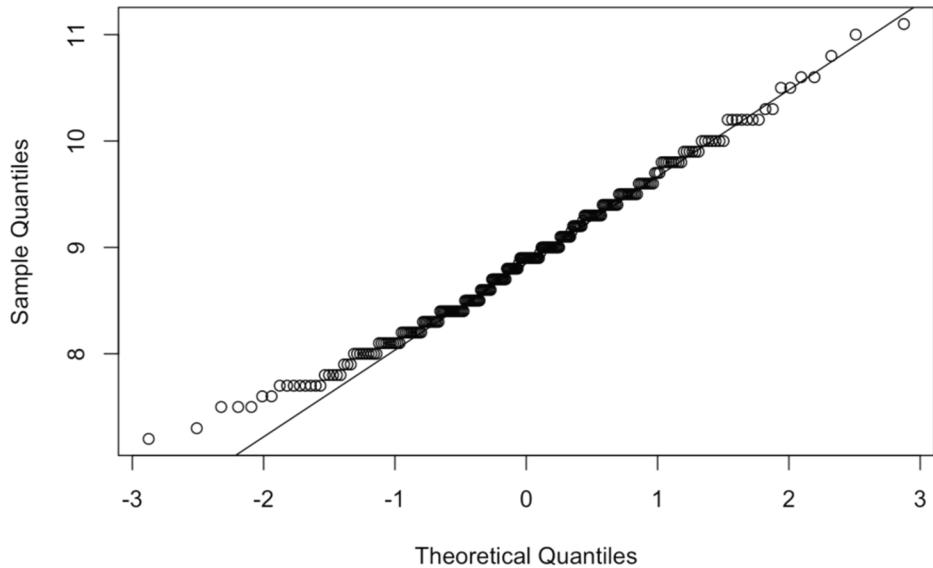
```
# Checking normality
qqnorm(bdepth_1975)
qqline(bdepth_1975)
```

Normal Q-Q Plot



```
qqnorm(bdepth_2012)
qqline(bdepth_2012)
```

**Normal Q-Q Plot**



```

t.test(bdepth_1975, bdepth_2012, alternative =
  "two.sided", var.equal = TRUE)

## 
## Two Sample t-test
##
## data: bdepth_1975 and bdepth_2012
## t = 3.7993, df = 649, p-value = 0.0001587
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.1078095 0.3384560
## sample estimates:
## mean of x mean of y
## 9.125955 8.902823

# Testing equality of variances
library(testequavar)
equa2vartest(bdepth_1975, bdepth_2012, 0.05, B = 5000)

## [[1]]
## [1] "Decision: Fail to Reject the Null"
##
## $Alpha
## [1] 0.05
##
## $NumberOfBootSamples
## [1] 5000

```

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## References

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