

Assignment 1

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Prepare the dataset:

```
library(foreign)
library(Hmisc)
rm(list = ls())
```

Modify this to your path

```
setwd("/Users/Alfonso/Google Drive/UT/Fall 2017/RD")
```

Load Dataset:

```
students <- read.dta("students.dta")
```

Load Variable Labels:

```
var.labels <- attr(students, "var.labels")
data.key <- data.frame(var.name=names(students), var.labels)
```

Clear Missing gkschid:

```
STAR_kindergarteners <- students[!(is.na(students$gkschid)),]
```

Population Parameters:

```
mu <- mean(STAR_kindergarteners$gktreadss)
mu

## [1] 436.7253

sigma <- sd(STAR_kindergarteners$gktreadss)
sigma

## [1] 31.70626
```

Set Sample Size:

```
n <- 160
```

Take Sample 1

```
sample1 <- STAR_kindergarteners[sample(nrow(STAR_kindergarteners), n),]  
  
xbar1 <- mean(sample1$gktreadss)  
xbar1  
  
## [1] 439.8375  
  
sigma1 <- sd(sample1$gktreadss)  
sigma1  
  
## [1] 31.22809
```

Sampling Error:

```
diff1 <- mu - xbar1  
diff1  
  
## [1] -3.112159
```

Confidence Interval:

```
c1 <- xbar1 - qnorm(0.975) * sigma1/sqrt(n)  
c2 <- xbar1 + qnorm(0.975) * sigma1/sqrt(n)  
  
sample1_CI <- c(c1, c2)  
sample1_CI  
  
## [1] 434.9987 444.6763
```

Hypothesis test:

```
z1 <- (xbar1 - mu)/(sigma1/sqrt(n))  
z1  
  
## [1] 1.260597
```

```
alpha <- 0.05
critical_values <- c(-qnorm(1-alpha/2), qnorm(1-alpha/2))
reject1 <- isTRUE(!-qnorm(1-alpha/2) < z1 & z1 < qnorm(1-alpha/2))
reject1

## [1] FALSE
```

Take Sample 2

```
sample2 <- STAR_kindergarteners[sample(nrow(STAR_kindergarteners), n),]
xbar2 <- mean(sample2$gktreadss)
xbar2

## [1] 440.5063

sigma2 <- sd(sample2$gktreadss)
sigma2

## [1] 35.33381
```

Sampling Error:

```
diff2 <- mu - xbar2
diff2

## [1] -3.780909
```

Sample Variation:

```
sample_variation <- xbar1 - xbar2
sample_variation

## [1] -0.66875
```

Confidence Interval:

```
c1 <- xbar2 - qnorm(0.975) * sigma2/sqrt(n)
c2 <- xbar2 + qnorm(0.975) * sigma2/sqrt(n)

sample2_CI <- c(c1, c2)
sample2_CI

## [1] 435.0313 445.9812
```

Hypothesis test:

```
z2 <- (xbar2 - mu)/(sigma2/sqrt(n))
z2

## [1] 1.353523

alpha <- 0.05
critical_values <- c(-qnorm(1-alpha/2), qnorm(1-alpha/2))
reject2 <- isTRUE(!-qnorm(1-alpha/2) < z2 & z2 < qnorm(1-alpha/2))
reject2

## [1] FALSE
```

Bootstrap Method







