# RHW3

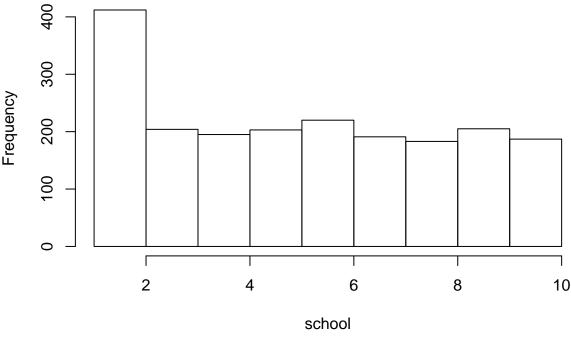
Rabia Suleiman 8/23/2019

#### R Markdown

Schools are a stabilizing feature in the unsettled lives of immigrant youth. They provide a safe space, learning opportunities, and diverse interactions. Extensive research indicares that educators and the school environment are important components in promoting socialization and acculturation of immigrant youth. The question I have stems from a current research project which seeks to determine the effectiveness of a specific intervention method. My population consists of school aged immigrants and whether the educational intervention led to better grade outcomes in their first year of schooling in Houston. The dependent variable is a cumulative grade (0 < y < 100) the independent variable is their enrollment into the program. control variables include school choice, English language ability and socioeconomic status. First we create Variables

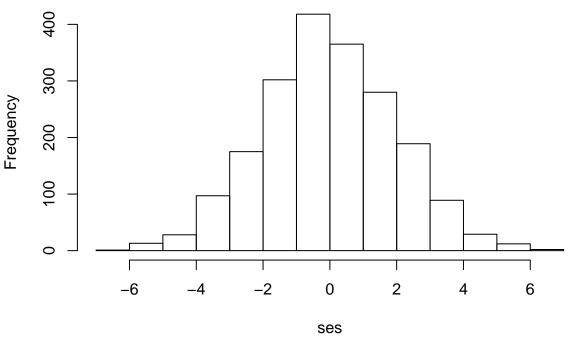
```
rm(list=ls())
set.seed(648057)
N = 2000
N_samp <- 50
#covariates
school=sample(1:10, N, replace=TRUE) # School ID (10 total)
hist(school)</pre>
```

## **Histogram of school**



```
ela <- rbinom(n=N, 1, 0.2)  # English Language ability
ses <- rnorm(n=N, mean=0, sd=2)  # Socio economic status
hist (ses)</pre>
```

### Histogram of ses



```
a = 55.5
b = 5
b2 = 3.5
b3= .4
tau = 6
e = rnorm(n=N, mean=0, sd=1)

#no intervention possible outcomes
Y_0 <- a + tau*0 + (b*ela) + (b2*ses) + (b3*school) + e

#intervention outcomes
Y_1 <- a + tau*1 + (b*ela) + (b2*ses) + (b3*school) + e # intervention possible outcomes</pre>
```

### **Including Plots**

You can also embed plots, for example:

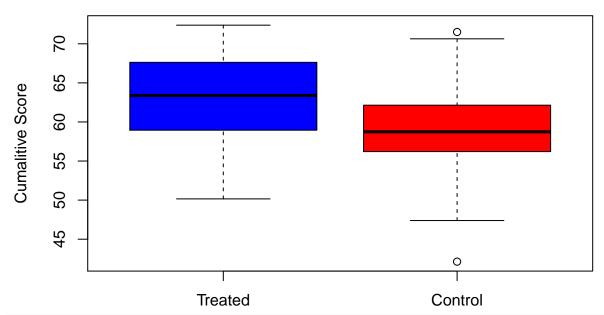
sample\_ind <- sample(1:nrow(pop\_dat), size=N\_samp)</pre>

```
pop_dat <- data.frame(Y_0, Y_1, ela, ses, school)</pre>
head(pop_dat)
##
          Y 0
                   Y_1 ela
                                   ses school
## 1 62.97775 68.97775
                         1 0.3646740
## 2 45.19290 51.19290
                        0 -3.7789375
                                            6
## 3 66.79468 72.79468
                         0 2.4982980
                                            6
## 4 51.73052 57.73052
                         0 -1.3000532
                                            1
## 5 56.96641 62.96641
                         1 -1.1379328
                                            1
## 6 62.23956 68.23956
                         0 0.3860879
                                            8
# Now, we consider our sample from here #GIVEN this vector I want to randomly
```

# Sampling index

```
sample_dat <- pop_dat[sample_ind, ] #the sample is the population data # Only keep obs that match t
head(sample_dat)
##
             Y 0
                      Y_1 ela
                                     ses school
## 189 58.19481 64.19481 0 0.2186004
                                              3
                          1 0.3956277
## 1405 62.32110 68.32110
                                              4
## 810 57.30187 63.30187 0 -0.2899689
                                              3
## 727 53.90615 59.90615 0 -0.8675956
                                              6
## 1198 62.00015 68.00015 0 2.0371102
                                              2
## 525 42.13054 48.13054
                           0 -4.2900712
                                              2
d <- ifelse(runif(N samp)<=0.2, 1, 0)</pre>
# Treatment assignment indicator (1=Treated, O=Controlled) the .2 is the indicator
sample_dat$Y_obs <- d*sample_dat$Y_1 + (1-d)*sample_dat$Y_0 # Observed outcomes</pre>
                                                             \# Y_obs = d*Y_1 + (1-d)*Y_0
                                                             # Copying the treatment status into sample
sample_dat$Status <- ifelse(d==1, "Treated", "Control")</pre>
head(sample_dat)
##
             Y_0
                                     ses school
                                                   Y_obs Status
                      Y_1 ela
## 189 58.19481 64.19481 0 0.2186004
                                             3 58.19481 Control
                                              4 62.32110 Control
## 1405 62.32110 68.32110
                          1 0.3956277
## 810 57.30187 63.30187 0 -0.2899689
                                              3 57.30187 Control
## 727 53.90615 59.90615 0 -0.8675956
                                             6 53.90615 Control
## 1198 62.00015 68.00015
                          0 2.0371102
                                             2 62.00015 Control
## 525 42.13054 48.13054
                           0 -4.2900712
                                              2 42.13054 Control
t.test(Y_obs ~ Status, data=sample_dat)
##
## Welch Two Sample t-test
##
## data: Y_obs by Status
## t = -1.1534, df = 7.2415, p-value = 0.2854
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -10.580430
                3.611118
## sample estimates:
## mean in group Control mean in group Treated
                59.23857
                                      62.72322
# Estimating the average treatment effect
tau_ate <- mean(sample_dat$Y_obs[sample_dat$Status=="Treated"]) -</pre>
        mean(sample_dat$Y_obs[sample_dat$Status=="Control"])
tau_ate
## [1] 3.484656
Now we visualize the impact of the treatment
boxplot(sample_dat$Y_obs[sample_dat$Status=="Treated"],
        sample_dat$Y_obs[sample_dat$Status=="Control"],
       names=c("Treated", "Control"), ylab="Cumalitive Score",
       main="Distribution of Grades",
        col=c("blue", "red"))
```

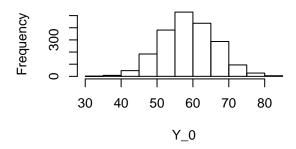
#### **Distribution of Grades**

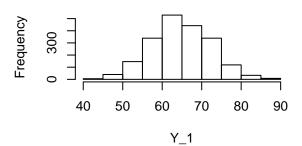


```
par(mfrow=c(2,2)) # Specify the graphic parameter
hist(Y_0, xlab=deparse(substitute(Y_0)),
    main=paste0("Histogram of", sep=" Control Group", substitute()))
hist(Y_1, xlab=deparse(substitute(Y_1)),
    main=paste0("Histogram of", sep=" Treatment Group", substitute()))
```

#### **Histogram of Control Group**

#### **Histogram of Treatment Group**



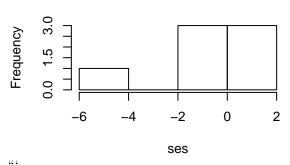


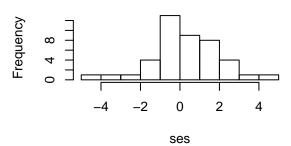
Now we can see the variation in contol variables between the two groups.

```
par(mfrow=c(2,2))
hist(sample_dat$ses[sample_dat$Status=="Treated"],
    main= "Distribution of SES in treatment group ", xlab="ses")
hist(sample_dat$ses[sample_dat$Status=="Control"],
    main= "Distribution of SES in control group",
    xlab="ses")
```

#### Distribution of SES in treatment group

#### **Distribution of SES in control group**

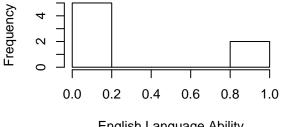




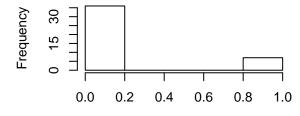
"

#### Distribution of ELA in treatment group

### Distribution of ELA in control group





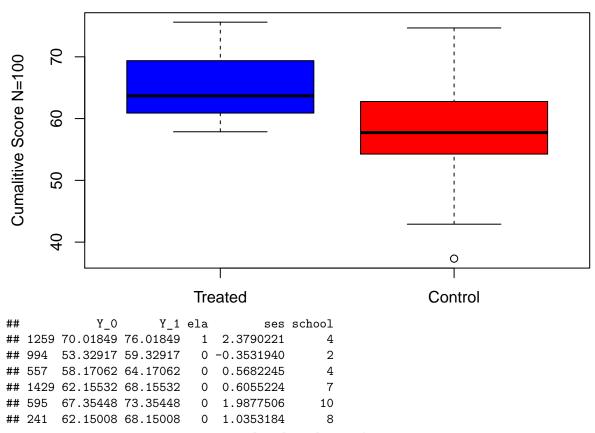


**English Language Ability** 

Now we replicate with other sample sizes

#	#	Y_0	Y_1	ela	ses	school
#	# 1083	57.70080	63.70080	1	-1.4321008	4
#	# 261	62.03209	68.03209	0	0.7911216	9
#	# 80	57.76423	63.76423	0	0.6413876	1
#	# 467	67.32541	73.32541	0	2.6987369	5
#	# 1995	64.63977	70.63977	0	1.7390773	8
#	# 970	66.75029	72.75029	0	2.6359049	7

## **Distribution of Grades**



## **Distribution of Grades**

