Problem Set 1 Final Product

Nathaniel Williams

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Simulation

Setup

```
set.seed(12345)
Population <- 1000000
Role <- c('Runeblade','Guardian','Wizard','Ranger')</pre>
#Add in probablity weights to better show convergence effect
Role_probs < c(0.4, 0.3, 0.2, 0.1)
P_Roles <- sample(Role, Population, replace = TRUE, prob = Role_probs)
Groups <- sample(c("Treatment", "Control"), Population, replace = TRUE)</pre>
## Df
Role_Data <- data.frame(</pre>
  ID = 1:Population,
  Role = P_Roles,
  Group = Groups
## parameters
n_{values} \leftarrow c(10, 25, 50, 100)
Repetitions <- 100
Overall_Results <- list()</pre>
```

The Simulation

```
## sim
for (n in n_values) {
    Simulation_results <- list()

for (i in 1:Repetitions) {

    #Rndm smple
    sample_indices <- sample(1:Population, n, replace = FALSE)
    sample_data <- Role_Data[sample_indices, ]

#Ovll role prop
    overall <- prop.table(table(sample_data$Role))
    overall_df <- as.data.frame(overall)
    overall_df$GroupType <- "Overall"

#Trtmnt grp prop</pre>
```

```
treat_props <- prop.table(table(sample_data$Role[sample_data$Group == "Treatment"]))</pre>
    treat_df <- as.data.frame(treat_props)</pre>
    treat_df$GroupType <- "Treatment"</pre>
    #Cntrl qrp prop
    control_props <- prop.table(table(sample_data$Role[sample_data$Group == "Control"]))</pre>
    control_df <- as.data.frame(control_props)</pre>
    control df$GroupType <- "Control"</pre>
    #Combine
    df <- rbind(overall_df, treat_df, control_df)</pre>
    df$Iteration <- i</pre>
    df$SampleSize <- n</pre>
    # put in list
    Simulation_results[[i]] <- df</pre>
  # Combine
  Overall_Results[[paste0("n_", n)]] <- do.call(rbind, Simulation_results)</pre>
## New df
simulation_df <- do.call(rbind, Overall_Results)</pre>
head(simulation df)
                Var1 Freq GroupType Iteration SampleSize
## n 10.1 Guardian 0.5
                            Overall
                                              1
## n_10.2 Runeblade 0.3
                            Overall
                                              1
                                                         10
                                                        10
## n_10.3
             Wizard 0.2 Overall
                                             1
## n 10.4 Guardian 0.6 Treatment
                                             1
                                                        10
## n 10.5 Runeblade 0.2 Treatment
                                              1
                                                         10
## n 10.6
             Wizard 0.2 Treatment
                                              1
                                                         10
```

Data Visualization

As n increases we get closer to the population distributions

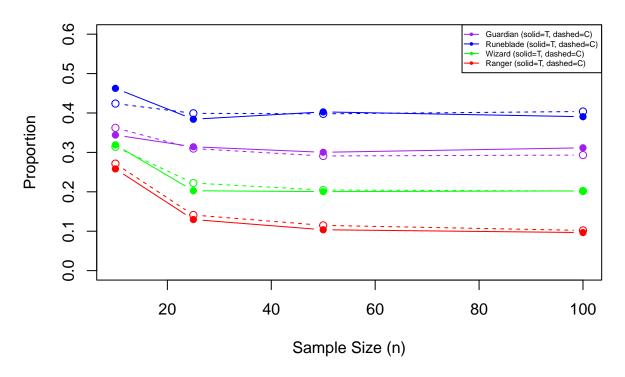
```
##
         Var1 GroupType SampleSize
                                      Freq
## 1 Guardian Control
                              10 0.3622869
## 2 Runeblade Control
                              10 0.4239418
## 3
       Wizard Control
                              10 0.3142507
               Control
## 4
       Ranger
                             10 0.2714866
## 5 Guardian Overall
                            10 0.2909091
```

```
## 6 Runeblade
                                  10 0.3930000
                 Overall
#Number table
smple poptble <- with(avg results[avg results$GroupType=="0verall", ],</pre>
                       tapply(Freq, list(Var1, SampleSize), mean))
print(round(smple_poptble, 2))
##
               10 25 50 100
## Guardian 0.29 0.31 0.3 0.3
## Runeblade 0.39 0.39 0.4 0.4
## Wizard
             0.22 0.20 0.2 0.2
             0.17 0.11 0.1 0.1
## Ranger
As we Increase the sample we converge onto the true values of .3, .4, .2, .1
```

```
As n increases the treatment and control group approach each other
```

```
#I like the graph visual here
plot(1, type='n', xlim=range(n_values),ylim=c(0,.6),
     xlab='Sample Size (n)', ylab='Proportion',
     main='Treatment vs Control Proportions by Sample Size')
roles<-unique(avg_results$Var1)</pre>
colors<-c('purple','blue','green','red')</pre>
for (i in seq_along(roles)) {
 treat_data<- avg_results[avg_results$Var1==roles[i] &</pre>
                              avg_results$GroupType=='Treatment',]
  control_data<- avg_results[avg_results$Var1==roles[i] &</pre>
                               avg_results$GroupType=='Control',]
 #line types
 lines(treat_data$SampleSize, treat_data$Freq, type='b',col=colors[i], pch=16)
 lines(control_data$SampleSize, control_data$Freq, type='b',col=colors[i], lty=2)
}
legend('topright',legend=paste(roles,'(solid=T, dashed=C)'),
       col=colors,lty=1, pch=16,cex=0.5)
```

Treatment vs Control Proportions by Sample Size



Data Analysis

```
#Read In data
setwd('C:/Users/natha/OneDrive/Documents/GitHub/NBW Pols 602 Work/Problem Set 1')
df <- read.csv('data/voting.csv')
voting<- df</pre>
```

Question 1: Observations

1a. The Treatment variable is whether or not they received the message or not.

1b. It is a discrete Variable

1c.The data type is Character, it is the word "yes" or "no"

Question 2: Binary Variable Assignment

```
#New binary Variable
#use ifelse for vectors
#not If()
#else()
voting$treated<- ifelse(voting$message == "yes",1,0)</pre>
```

Question 3: Average Group Outcomes

```
#Need to subset the groups to get the means
Treated<-voting[voting$treated==1, ]</pre>
Control<-voting[voting$treated==0, ]</pre>
#now can look at group outcome
mean(Treated$voted)
## [1] 0.3779482
mean(Control$voted)
## [1] 0.2966383
#quick table
aggregate(voted ~ treated, data = voting, mean)
##
     treated
                  voted
## 1
           0 0.2966383
## 2
           1 0.3779482
#difference
treated_mean <- mean(Treated$voted)</pre>
control_mean <- mean(Control$voted)</pre>
Effect<- treated_mean - control_mean</pre>
Effect
```

[1] 0.08130991

The likelihood that somebody voted, on average, if they received the experimental treatment (a mailed message) was 37.8 percent.

For the control group (those who did not receive a message) the likelihood the voted on average was 29.7 percent.

Question 4: Creating new Data Frames from Subsets

```
#New treatment df
TreatmentGroup_df<- voting[voting$treated == 1,]
#new control df
ControlGroup_df<- voting[voting$treated== 0, ]
#check that no data dropped
nrow(voting)
## [1] 229444
nrow(TreatmentGroup_df)
## [1] 38201
nrow(ControlGroup_df)
## [1] 191243
nrow(ControlGroup_df) + nrow(TreatmentGroup_df)
## [1] 229444</pre>
```

Question 5: Average Birth Years

```
mean(TreatmentGroup_df$birth)
```

[1] 1956.147

mean(ControlGroup_df\$birth)

[1] 1956.186

Average Birth year for the treated group is 1956.147

Average Birth Year for the control group is 1956.186

Question 6: Estimated Average Causal Effect

```
\#Did\ this\ code\ already\ for\ question\ 3 so just display results Effect
```

[1] 0.08130991

There is a roughly 8 percentage point increase in the likelihood that an individual will vote if they received the message (treatment) compared to those who did not (control).

This would signal that social pressure does contribute to increased voting likelihood, at least under the design of this papers experiment.

Question 7: Generalizing these results

In order for us to be able to generalize these results to the entire U.S population we would need to be able to assume that the survey population is not systematically different than the U.S. population.

Some concerns then are that the experiment surveys only households, completely ignoring the large number of individuals who live in apartments or other dwellings. Other factors such as whether the survey was conducted only in one or few states, and whether those state populations generalize.

Based solely off the knowledge that this was a survey of households we can say this systematically discriminates against apartment dwellers and other home types. Which raises concerns about generalization.