Problem Set #4

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```
# load packages
library(foreign)
library(data.table)
library(knitr)
library(sandwich)
library(lmtest)
library(AER)
library(stargazer)
```

1. Potential Outcomes

Consider the following hypothetical schedule of potential outcomes.

- Amy, Brian, and Chris are *compliers*. This means they actually get the treatment if they are assigned to the treatment group. Their potential outcomes in the untreated state of the world are 11, 10, and 11 respectively.
- David, Erin, and Felipe are never-takers. (I.e. they do not get the treatment even if they are assigned to the treatment group.) Their potential outcomes in the untreated state of the world is 3, 2, and 4 respectively.

1. Make up a set of potential outcomes in the treated state of the world (i.e. $Y_i(1)$ for each of the individuals listed above) that would make both the ATE and the CACE positive.
   Ans: To make the ATE positive we can make the $Y_i(1)$ for each of the subject more than their $Y_i(0)$ this will also make the CACE positive as we have positive ATE for the compliers too

```
d <- data.table(id = c('Amy','Brian','Chris','David','Erin','Felipe'),
                y0 = c(11,10,11,3,2,4),
                y1 = c(13,12,13,5,4,6),
                status =c('compliers','compliers','compliers','noncompliers','noncompliers','noncomplie
knitr::kable(d)
```

id	y0	y1	status
Amy	11	13	compliers
Brian	10	12	compliers
Chris	11	13	compliers
David	3	5	noncompliers
Erin	2	4	noncompliers
Felipe	4	6	noncompliers

```
ATE <- d[,mean(y1-y0)]
paste('ATE = ',ATE)
```

```
## [1] "ATE =  2"
```

```
CACE <- d[status=='compliers',mean(y1-y0)]
paste('CACE = ',CACE)
```

```
## [1] "CACE =  2"
```

2. Make up a set of potential outcomes in the treated state of the world that would make the ATE positive but the CACE *negative*.
Ans: To make the ATE positive but the CACE negative we can make the $Y_i(1)$for the compliers less than their $Y_i(0)$ while making $Y_i(1)$ greater than their$Y_i(0)$for the never takers

```
d <- data.table(id = c('Amy','Brian','Chris','David','Erin','Felipe'),
                y0 = c(11,10,11,3,2,4),
                y1 = c(10,9,10,5,4,6),
                status =c('compliers','compliers','compliers','noncompliers','noncompliers','noncomplie
knitr::kable(d)
```

id	y0	y1	status
Amy	11	10	compliers
Brian	10	9	compliers
Chris	11	10	compliers
David	3	5	noncompliers
Erin	2	4	noncompliers
Felipe	4	6	noncompliers

```
ATE <- d[,mean(y1-y0)]
paste('ATE = ',ATE)
```

```
## [1] "ATE =  0.5"
```

```
CACE <- d[status=='compliers',mean(y1-y0)]
paste('CACE = ',CACE)
```

```
## [1] "CACE =  -1"
```

3. Suppose that you are conducting a trial for a new feature to be released in a product. From a limited point of view, if you are the person who wrote the *creative* content that is in the new feature, do you care more about the CACE or the ATE?
Ans: If I am the creative content writer then I would be interested in CACE as I would be interested to know what is the true effect of the creative content on subjects who actually were treated. Or in other words what is the causal effect of the creative content when its delivered as treatment which will be the testament for the creative content's efficacy.

4. Suppose that you are conducting a trial for a new feature to be released in the same product. From a limited point of view, compared to when you wrote the creative, if you are the product manager, do you care relatively **more** about the CACE or the ATE than before?
Ans: If I am the product manager then I would be more interested in ATE as I would be interested in knowing the treatment effect of the new feature on average in general overall on the audience rather than just on the compliers. I would be interested to know what will be the overall effect on audience when the product is rolled out. More than ATE I would be looking at ITT.

2. Noncompliance in Recycling Experiment

Suppose that you want to conduct a study of recycling behavior. A number of undergraduate students are hired to walk door to door and provide information about the benefits of recycling to people in the treatment group. 1,500 households are assigned to the treatment group. The undergrads tell you that they successfully managed to contact 700 households. The control group had 3,000 households (not contacted by

any undergraduate students). The subsequent recycling rates (i.e. the outcome variable) are computed and you find that 500 households in the treatment group recycled. In the control group, 600 households recycled.

1. What is the ITT?
   Ans: ITT is defined as the intent to treat effect. It is the mean of the difference between the outcomes of the treatment and control groups disregarding the fact if the treatment was actually delivered to treatment group. In other words ITT is the ATE calculation diregarding the non compliance.

```
treatment_group_outcome <- 500/1500
control_group_outcome <- 600/3000
ITT <- treatment_group_outcome - control_group_outcome
paste('ITT is =',ITT)
```

```
## [1] "ITT is = 0.133333333333333"
```

ITT is 0.1333333 which is 13.33%

2. What is the CACE? **Ans: CACE is defined as the treatment effects among the compliers. Which means comparing the potential outcome of the compliers in the treatment group with compliers in the control group. Without placebo design the compliers in the control group is just estimated from the control group. The formula for for calculating the CACE in one sided non-compliance is CACE = ITT/ITTd where ITTd is the proportion of compliers in the treatment group and ITT is the intent to treat effect which is the mean of the difference of potential outcome of treatment and control group disregarding the non-compliance issue**

```
treatment_group_outcome <- 500/1500
control_group_outcome <- 600/3000
ITT <- treatment_group_outcome - control_group_outcome
ITTd <- 700/1500
CACE <- ITT/ITTd
paste(' CACE is =',CACE)
```

```
## [1] " CACE is = 0.285714285714286"
```

CACE is 0.2857143 which 28.57%

3. There appear to be some inconsistencies regarding how the undergraduates actually carried out the instructions they were given. One of the students, Mike, tells you that they actually lied about the the number of contacted treatment households. The true number was 500. Another student, Andy, tells you that the true number was actually 600.

   a. What is the CACE if Mike is correct?
      Ans: Mike tells that actual number of treated household were 500 instead of 700 which will decrease the ITTd and hence increase the CACE as CACE = ITT/ITTd

```
treatment_group_outcome <- 500/1500
control_group_outcome <- 600/3000
ITT <- treatment_group_outcome - control_group_outcome
ITTd <- 500/1500
CACE <- ITT/ITTd
paste('CACE if Mike is correct  =',CACE)
```

```
## [1] "CACE if Mike is correct  = 0.4"
```

   b. What is the CACE if Andy is correct?
      Ans: Andy tells that actual number of treated household were 600 instead of 700 which will decrease the ITTd and hence increase the CACE as CACE = ITT/ITTd but this CACE would be less than Mike's as Mike's ITTd is less than Andy's ITTd

```
treatment_group_outcome <- 500/1500
control_group_outcome <- 600/3000
ITT <- treatment_group_outcome - control_group_outcome
ITTd <- 600/1500
CACE <- ITT/ITTd
paste('CACE if Andy is correct  =',CACE)
```

```
## [1] "CACE if Andy is correct  = 0.333333333333333"
```

4. Suppose that Mike is correct.

a. What was the impact of the undergraduates's false reporting on our estimates of the treatment's effectiveness?
Ans: If Mike was correct then that would mean that proportion of subjects who got treated would be lesser and so the CACE would be higher as CACE = ITT/ITTd.

```
treatment_group_outcome <- 500/1500
control_group_outcome <- 600/3000
ITT <- treatment_group_outcome - control_group_outcome
ITTd <- 700/1500
ITTd_Mike <- 500/1500
CACE <- ITT/ITTd
CACE_Mike <- ITT/ITTd_Mike
paste('Difference in CACE if Mike is correct=',CACE_Mike - CACE)
```

```
## [1] "Difference in CACE if Mike is correct= 0.114285714285714"
```

b. Does your answer change depending on whether you choose to focus on the ITT or the CACE?
Ans:If we focus on ITT then there is no change to ITT if Mike is correct or wrong as ITT doesn't depend on the ratio of number of compliers to total number of subjects in treatment group. CACE changes if the ratio of number of compliers to total number of subjects in treatment group changes

3. Fun with the placebo

The table below summarizes the data from a political science experiment on voting behavior. Subjects were randomized into three groups: a baseline control group (not contacted by canvassers), a treatment group (canvassers attempted to deliver an encouragement to vote), and a placebo group (canvassers attempted to deliver a message unrelated to voting or politics).

Assignment	Treated?	N	Turnout
Baseline	No	2463	0.3008
Treatment	Yes	512	0.3890
Treatment	No	1898	0.3160
Placebo	Yes	476	0.3002
Placebo	No	2108	0.3145

1. Construct a data set that would reproduce the table.
Ans: To construct the dataset representing the aggregate as above we would need to create rows for each assignment status respecting the number of rows and proportion of the turnout. We would create a new variable voted which will be 0 or 1 if the subject didn't vote or voted respectively

```
df <- data.frame(matrix(ncol = 3, nrow = 0))
x <- c("Assignment", "Treated","Voted")
```

```
colnames(df) <- x
for (i in 1:nrow(d)){
  assignment_list <- rep(d[i,'Assignment'],d[i,'N'])
  treated_list <- rep(ifelse(d[i,'Treated?']=='No',0,1),d[i,'N'])
  voted_vector <- sample(x=c(rep(1,round(d[i,'N']*d[i,'Turnout'])),
                             rep(0, d[i,'N']-round(d[i,'N']*d[i,'Turnout']))))
                         )
  df_temp <- data.frame(unlist(assignment_list),unlist(treated_list),voted_vector)
  colnames(df_temp) <- x
  df <- rbind(df,df_temp)
}

dataset_turnout <- data.table(df)
#check the summary matches with original summary or not
dataset_turnout[,.(mean(Voted),.N),by=.(Assignment,Treated)]
```

```
##    Assignment Treated        V1    N
## 1:   Baseline       0 0.3008526 2463
## 2:  Treatment       1 0.3886719  512
## 3:  Treatment       0 0.3161222 1898
## 4:    Placebo       1 0.3004202  476
## 5:    Placebo       0 0.3145161 2108
```

2. Estimate the proportion of compliers by using the data on the treatment group.

```
(Complier_ratio_treatment_grp <- dataset_turnout[Assignment=='Treatment' & Treated ==1,.N] / dataset_tu
```

```
## [1] 0.2124481
```

Ans: The proportion of compliers in the treatment group is 0.2124481

3. Estimate the proportion of compliers by using the data on the placebo group.

```
(Complier_ratio_placebo_grp <- dataset_turnout[Assignment=='Placebo' & Treated ==1,.N] / dataset_turnou
```

```
## [1] 0.1842105
```

Ans: The proportion of compliers in the Placebo group is 0.1842105

4. Are the proportions in parts (1) and (2) statistically significantly different from each other? Provide *a test* and an description about why you chose that particular test, and why you chose that particular set of data.
   Ans: The proportions in (1) and (2) are different. To test if they are statistically different or not we can do chi square(χ^2) test of independence. Chi-Squared test tests if the categorical variables are independent of each other. We want to test if the treated proportions is independent of group (treatment or placebo) . So we take a contingency frquency table of the dataset which lists the frequency of treatment (yes or no) tabulated for Treatment and Placebo group and then run the chisq.test on this contigency table

```
(test_table <- table(dataset_turnout$Assignment,
                     dataset_turnout$Treated)[2:3,1:2])
```

```
##
##                0    1
##   Treatment 1898  512
##   Placebo   2108  476
```

```
chisq.test(test_table)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  test_table
## X-squared = 6.0887, df = 1, p-value = 0.0136
```

We see that the p-value is 0.0136 which means that we can reject the null hypothesis of treatment proportion being independent of the group. So the complier proportions are statistically different between treatment and placebo group

e. What critical assumption does this comparison of the two groups' compliance rates test?

Ans: This comaprison tests the assumption that proportions of compliers is same in the treatment and placebo group given the randomization is followed to place some one in treatment or placebo group. From the above test we can conclude that in this particular experiment it doesn't seem to obey theis assumption as the chi-square test rejects the null hypothesis of independence.

f. Estimate the CACE of receiving the placebo. Is the estimate consistent with the assumption that the placebo has no effect on turnout?

Ans:To estimate the CACE of receiving the placebo we will use 2SLS on the data set including the baseline and placebo group. We will then check if coefficient of treated variable is statistically significant or not.

```
lm_model <- dataset_turnout[Assignment!='Treatment',ivreg(Voted~Treated,~Assignment)]
coeftest(lm_model,vcovHC(lm_model))
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.300853   0.009245 32.5423   <2e-16 ***
## Treated     0.060077   0.070551  0.8515   0.3945
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model,se=list(sqrt(diag(vcovHC(lm_model)))),type='text',header=F)
```

```
##
## ================================================
##                          Dependent variable:
##                      ---------------------------
##                                 Voted
## ------------------------------------------------
## Treated                          0.060
##                                 (0.071)
##
## Constant                       0.301***
##                                 (0.009)
##
## ------------------------------------------------
## Observations                     5,047
## R2                              -0.002
## Adjusted R2                     -0.002
## Residual Std. Error       0.462 (df = 5045)
## ================================================
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

We see from the 2SLS that the CACE of the reciving placebo is .060077 with Std Error of

0.070551 and p value of 0.3945 which means that it is not statistically significant and hence the assumption that placebo has no affect on turnout cannot be rejected.

g. Estimate the CACE by first estimating the ITT and then dividing by ITT_D.

```
ITT <- dataset_turnout[Assignment=='Treatment',mean(Voted)]-dataset_turnout[Assignment=='Baseline',mean
ITTd <- dataset_turnout[Assignment=='Treatment' & Treated == 1,.N]/dataset_turnout[Assignment=='Treatme

(CACE_using_ITT <- ITT/ITTd)
```

```
## [1] 0.1444242
```

Ans: We see that CACE using the complier proportion from Treatment group and comparing treatment potential outcome to baseline potential outcome is 0.1444242

h. Estimate the CACE by comparing the turnout rates among the compliers in both the treatment and placebo groups. Interpret the results.

```
(CACE_using_placebo <- dataset_turnout[Assignment=='Treatment' & Treated == 1,mean(Voted)] - dataset_tu
```

```
## [1] 0.08825171
```

Ans: We see that the CACE by using the palcebo design is different from baseline design using ITT/ITTd this might be because the proportions of the compliers is different in treatment and placebo group as we saw earlier.

i. In class we discussed that the rate of compliance determines whether one or another design is more efficient. (You can review the paper here). Given the compliance rate in this study, which design *should* provide a more efficient estimate of the treatment effect?

Ans: Given the fact that the compliance rate is less than 0.5 the placebo design would provide more efficient estimate of the treatment effect

j. Does it?

Ans: To answer this let us do a 2SLS estimation of treatment effect to get CACE and Std Error and then another linear regression model only considering the treated rows for placebo and treatment group and check the Std error for the coefficient of the group .

```
lm_model2 <- dataset_turnout[Assignment!='Placebo',ivreg(Voted~Treated,~Assignment)]
(lm_model2.coeftest <- coeftest(lm_model2,vcovHC(lm_model2)))
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.300853   0.009245  32.542  < 2e-16 ***
## Treated     0.144424   0.062712   2.303  0.02132 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lm_model3 <- dataset_turnout[Treated==1,lm(Voted~Assignment)]
(lm_model3.coeftest <- coeftest(lm_model3,vcovHC(lm_model3)))
```

```
##
## t test of coefficients:
##
##                    Estimate Std. Error t value  Pr(>|t|)
## (Intercept)        0.388672   0.021585 18.0070 < 2.2e-16 ***
## AssignmentPlacebo -0.088252   0.030154 -2.9267  0.003505 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ans: We do see that the Std Error of the placebo design estimate is lesser than that of considering the estimate using ITT/ITT_d and hence it is more efficient. We see that the std error when using ITT/ITTd is 0.0627121 while the std error when using placebo design is 0.0301543. The placebo design has half the std error. As we saw in previous question that the proprtion of compliers and never takers are statistically different among placebo and treatment group the CACE calculated through ITT/ITTd and comparing placebo to treated gives different treatment effect estimate

4. Turnout in Dorms

Guan and Green report the results of a canvassing experiment conduced in Beijing on the eve of a local election. Students on the campus of Peking University were randomly assigned to treatment or control groups. Canvassers attempted to contact students in their dorm rooms and encourage them to vote. No contact with the control group was attempted. Of the 2,688 students assigned to the treatment group, 2,380 were contacted. A total of 2,152 students in the treatment group voted; of the 1,334 students assigned to the control group, 892 voted. One aspect of this experiment threatens to violate the exclusion restriction. At every dorm room they visited, even those where no one answered, canvassers left a leaflet encouraging students to vote.

```
d <- fread('./data/Guan_Green_CPS_2006.csv')
d
```

```
##       turnout treated   dormid treatment_group
##    1:       0       0  1010101               0
##    2:       0       0  1010101               0
##    3:       0       0  1010101               0
##    4:       0       0  1010102               0
##    5:       0       0  1010102               0
##   ---
## 4020:       1       1 24033067               1
## 4021:       1       1 24033068               1
## 4022:       1       1 24033068               1
## 4023:       1       1 24033068               1
## 4024:       1       1 24033068               1
```

Here's what is in that data:

- `turnout` did the person turn out to vote?
- `treated` did someone at the dorm open the door?
- `dormid` a unique ID for the door of the dorm
- `treatment_group` whether the dorm door was assigned to be treated or not

1. Using the data set from the book's website, estimate the ITT. First, estimate the ITT using the difference in two-group means. Then, estimate the ITT using a linear regression on the appropriate subset of data. *Heads up: There are two NAs in the data frame. Just na.omit to remove these rows.*

```
(ITT_using_group_mean <- d[treatment_group==1,mean(turnout,na.rm = T)] - d[treatment_group==0,mean(turn
```

```
## [1] 0.1319296
```

```
lm_model4 <- d[,lm(turnout~treatment_group,na.action=na.omit)]
coeftest(lm_model4,vcovCL(lm_model4,cluster=d[,dormid]))
```

```
##
## t test of coefficients:
##
##                 Estimate Std. Error t value  Pr(>|t|)
```

```
## (Intercept)     0.668666   0.020241 33.0349 < 2.2e-16 ***
## treatment_group 0.131930   0.023271  5.6692 1.536e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model4,se=list(sqrt(diag(vcovCL(lm_model4,cluster=d[,dormid])))),type='text',header=F)
```

```
##
## ================================================
##                          Dependent variable:
##                      ---------------------------
##                                turnout
## ------------------------------------------------
## treatment_group              0.132***
##                               (0.023)
##
## Constant                     0.669***
##                               (0.020)
##
## ------------------------------------------------
## Observations                   4,022
## R2                             0.021
## Adjusted R2                    0.021
## Residual Std. Error      0.425 (df = 4020)
## F Statistic          86.082*** (df = 1; 4020)
## ================================================
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

ITT using group means is 0.1319296 and ITT using linear regression is 0.1319296

2. Use randomization inference to test the sharp null hypothesis that the ITT is zero for all observations, taking into account the fact that random assignment was clustered by dorm room. Interpret your results – in particular, are you surprised at your result when you compare it to the p-value in part (1)? (This is a 2 point question, because there's quite a bit of work here.)

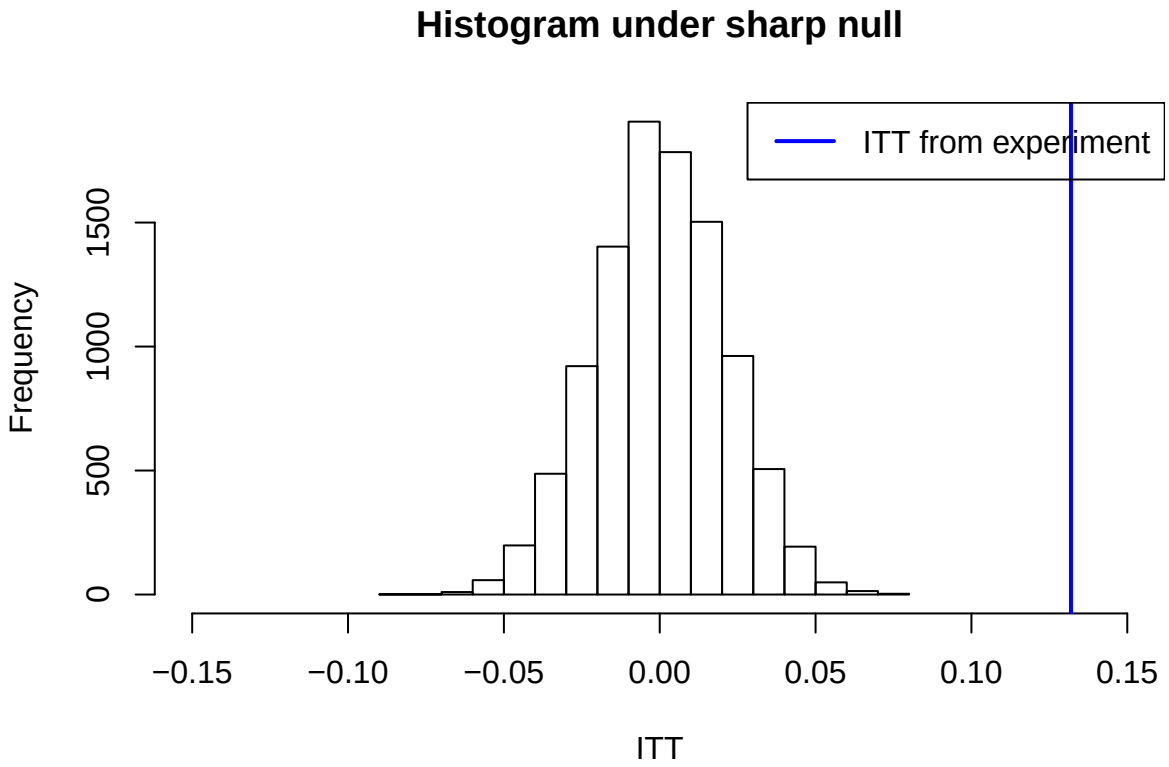
```
#get the unique clusters i.e. dormids
unique_dormids <- d[,unique(dormid)]
randomize_clustered <- function(){
                                treat_dormids <- sample(x = unique_dormids,
                                                        size = length(unique_dormids)/2,
                                                        replace = FALSE)
                                return(as.numeric(d$dormid %in% treat_dormids))
                                }
#function for estimated ITT
est_ate <- function(outcome, treat) {
  mean(outcome[treat==1],na.rm = T) - mean(outcome[treat==0],na.rm = T)
}
(ITT <- est_ate(d$turnout,d$treatment_group))
```

```
## [1] 0.1319296
```

```
distribution_under_sharp_null <- replicate(10000, est_ate(d$turnout, randomize_clustered()))

hist(distribution_under_sharp_null,
     main='Histogram under sharp null',
     xlab= 'ITT',
     xlim=c(-.15,.15))
```

```
abline(v=ITT, lwd = 2, col = "blue")
legend("topright", legend = "ITT from experiment",
       lwd = 2, lty = 1, col = "blue")
```




```
#calculate P vaue
(p_val <- mean(distribution_under_sharp_null>ATE))
```

```
## [1] 0
```

Ans: We see that we can reject the sharp null hypothesis of no treatment effect using randomization inference. We see for the ITT: 0.1319296 we get pval as: 0 . This confirms that we get the same results from linear regression model and randomization ineference. The randomization inference is underlying model free.

3. Assume that the leaflet had no effect on turnout. Estimate the CACE. Do this in two ways:

a. First, estimate the CACE using means.

```
(ITT_using_mean <- d[treatment_group==1,mean(turnout,na.rm=T)] - d[treatment_group==0,mean(turnout,na.r
```

```
## [1] 0.1319296
```

```
(ITTd <- d[treatment_group==1 & treated==1 & !is.na(turnout),.N]/d[treatment_group==1 & !is.na(turnout)
```

```
## [1] 0.8857887
```

```
(CACE <- ITT_using_mean / ITTd)
```

```
## [1] 0.1489402
```

b. Second, use some form of linear model to estimate this as well. If you use a 2SLS, then report the standard errors and draw inference about whether contact had any causal effect among compliers.

```
lm_model5 <- d[,ivreg(turnout~treated,~treatment_group)]
coeftest(lm_model5,vcovCL(lm_model5,cluster=d[,dormid]))
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value  Pr(>|t|)
## (Intercept) 0.668666   0.020239 33.0390 < 2.2e-16 ***
## treated     0.148940   0.026308  5.6614 1.607e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model5,se=list(sqrt(diag(vcovCL(lm_model5,cluster=d[,dormid])))),type='text',header=F)
```

```
##
## ================================================
##                          Dependent variable:
##                      ---------------------------
##                                turnout
## ------------------------------------------------
## treated                       0.149***
##                                (0.026)
##
## Constant                      0.669***
##                                (0.020)
##
## ------------------------------------------------
## Observations                    4,022
## R2                              0.016
## Adjusted R2                     0.016
## Residual Std. Error       0.426 (df = 4020)
## ================================================
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

Ans: We see from the coeftest that Estimate of CACE is .148940 with std Error as 0.026308 with p value as 1.607e-08 . The standard errors are calculated using clustered std error on dormid using vcovCL function. 2SLS (using ivreg) is used for estimating the CACE. The pvalue is less than 0.05 which means there is evidence of causal effect of contact on voter turnout

5. Another Turnout Question

We're sorry; it is just that the outcome and treatment spaces are so clear!

Hill and Kousser (2015) report that it is possible to increase the probability that someone votes in the California *Primary Election* simply by sending them a letter in the mail. This is kind of surprising, because who even reads the mail anymore anyways? (Actually, if you talk with folks who work in the space, they'll say, "We know that everybody throws our mail away; we just hope they see it on the way to the garbage.")

Can you replicate their findings? Let's walk through them.

```
#d <- fread('http://ischool.berkeley.edu/~d.alex.hughes/data/hill_kousser_analysisFile.csv')
#head(d)
```

You'll note that this takes some time to download. Probably best to save a copy locally, and keep from reading this off the internet. In your project structure, create a folder called `./data/raw/` and write this

file to the folder. Data that is in this raw folder *never* gets modified; instead, any changes that you make should be reflected into either an `./data/interim/` or `./data/analysis/` folder. You might consider using the function `fwrite` from data.table.

```
#fwrite(d,"./data/raw/hill_kousser_analysisFile.csv")
d <- fread('./data/raw/hill_kousser_analysisFile.csv')
#head(d)
```

Here's what is in that data.

- `age.bin` a bucketed version of the `age.in.14` variable
- `party.bin` a bucketed version of the `Party` variable
- `in.toss.up.dist` whether the voter lives in a close race
- `minority.dist` whether the voter lives in a majority minority district
- `Gender` voter file reported gender
- `Dist1-8` congressional and data districts
- `reg.date.pre.08` whether the voter has been registered since before 2008
- `vote.xx.gen` whether the voter voted in the `xx` general election
- `vote.xx.gen.pri` whether the voter voted in the `xx` general primary election
- `vote.xx.pre.pri` whether the voter voted in the `xx` presidential primary election
- `block.num` a block indicator for blocked random assignment.
- `treatment.assign` either "Control", "Election Info", "Partisan Cue", or "Top-Two Info"
- `yvar` the outcome variable: did the voter vote in the 2014 primary election

These variable names are horrible. Do two things:

- Rename the smallest set of variables that you think you might use to something more useful
- For the variables that you think you might use; check that the data makes sense;

```
d[,AnyLetter:= ifelse(treatment.assign == 'Control',0,1)]
d[,treatment_type:= as.factor(treatment.assign)]
d[,Control:= ifelse(treatment.assign == 'Control',1,0)]
d[,Top.two.info:= ifelse(treatment.assign == 'Top-two info',1,0)]
d[,Partisan:= ifelse(treatment.assign == 'Partisan',1,0)]
d[,Election.info:= ifelse(treatment.assign == 'Election info',1,0)]
fwrite(d,"./data/analysis/modified_hill_kousser_analysisFile.csv")
```

Then, save this data to `./data/analysis/`.

Well, while you're at it, you might as well also modify your `.gitignore` to ignore the data folder. Because you're definitely going to have the data rejected when you try to push it to github.

1. **A Simple Treatment Effect**: Load the data from `./data/analysis/` and estimate a model that compares the rates of turnout in the control group to the rate of turnout among *anybody* who received a letter. Report robust standard errors.

```
d <- fread('./data/analysis/modified_hill_kousser_analysisFile.csv')
head(d)
```

```
##    LocalityCode age.bin party.bin in.toss.up.dist minority.dist
## 1:            1       2         1               0             0
## 2:            1       5         3               0             0
## 3:            1       6         2               0             0
## 4:            1       5         1               1             1
## 5:            1       5         2               0             0
## 6:            1       6         3               0             0
##    vote.10.gen vote.08.gen Party age.in.14 Gender Dist1 Dist2 Dist3 Dist4
## 1:           0           0   REP        32      F CG015 SA020 SE002 SS010
## 2:           0           1   NPP        61      F CG013 SA018 SE002 SS009
```

```
## 3:           0           1   DEM        77      M CG013 SA015 SE002 SS009
## 4:           0           1   REP        62      M CG017 SA025 SE002 SS010
## 5:           1           1   DEM        60      M CG015 SA020 SE002 SS010
## 6:           1           1   NPP        81        CG015 SA020 SE002 SS010
##    Dist5 Dist6 Dist7 Dist8 reg.date.pre.08 reg.date.pre.10 vote.12.gen
## 1:    NA    NA    NA    NA               1               1           1
## 2:    NA    NA    NA    NA               0               0           1
## 3:    NA    NA    NA    NA               1               1           1
## 4:    NA    NA    NA    NA               0               0           1
## 5:    NA    NA    NA    NA               1               1           1
## 6:    NA    NA    NA    NA               1               1           1
##    vote.12.pre.pri vote.10.gen.pri vote.08.pre.pri vote.08.gen.pri
## 1:               0               0               0               0
## 2:               0               0               0               0
## 3:               0               0               0               0
## 4:               0               0               0               0
## 5:               0               0               0               0
## 6:               0               0               0               0
##    block.num leftover.case treatment.assign yvar matched.to.post
## 1:        91             0          Control    0               1
## 2:       316             0          Control    0               1
## 3:       364             0          Control    1               1
## 4:       296             0          Control    0               1
## 5:       302             0          Control    0               1
## 6:       382             0          Control    0               1
##    vote.14.gen AnyLetter treatment_type Control Top.two.info Partisan
## 1:           0         0       Control       1            0        0
## 2:           0         0       Control       1            0        0
## 3:           1         0       Control       1            0        0
## 4:           0         0       Control       1            0        0
## 5:           1         0       Control       1            0        0
## 6:           0         0       Control       1            0        0
##    Election.info
## 1:             0
## 2:             0
## 3:             0
## 4:             0
## 5:             0
## 6:             0
```

```
lm_model6 <- d[,lm(yvar~AnyLetter)]
(coeftest.model <- coeftest(lm_model6,vcovHC(lm_model6)))
```

```
##
## t test of coefficients:
##
##               Estimate Std. Error  t value  Pr(>|t|)
## (Intercept) 0.09312478 0.00015062 618.2813 < 2.2e-16 ***
## AnyLetter   0.00489923 0.00078340   6.2538 4.007e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model6,se=list(sqrt(diag(vcovHC(lm_model6)))),type='text',header=F)
```

```
##
```

```
## ================================================
##                         Dependent variable:
##                     ---------------------------
##                                   yvar
## ------------------------------------------------
## AnyLetter                      0.005***
##                                 (0.001)
##
## Constant                       0.093***
##                                (0.0002)
##
## ------------------------------------------------
## Observations                   3,872,268
## R2                              0.00001
## Adjusted R2                     0.00001
## Residual Std. Error     0.291 (df = 3872266)
## F Statistic          40.801*** (df = 1; 3872266)
## ================================================
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

Ans: We see that the rate of turnout difference between control and anybody who received letter is 0.0048992 . The robust std error is 7.8340355×10^{-4}

2. **Specific Treatment Effects**: Suppose that you want to know whether different letters have different effects. To begin, what are the effects of each of the letters, as compared to control? Report robust standard errors on a linear model.

```
lm_model7 <- d[,lm(yvar~treatment_type)]
(coeftest.model <- coeftest(lm_model7,vcovHC(lm_model7)))
```

```
##
## t test of coefficients:
##
##                               Estimate Std. Error  t value  Pr(>|t|)
## (Intercept)                 0.09312478 0.00015062 618.2813 < 2.2e-16 ***
## treatment_typeElection info 0.00498464 0.00172734   2.8857 0.0039050 **
## treatment_typePartisan      0.00525971 0.00122666   4.2878 1.804e-05 ***
## treatment_typeTop-two info  0.00449610 0.00122250   3.6778 0.0002353 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model7,se=list(sqrt(diag(vcovHC(lm_model7)))),type='text',header=F)
```

```
##
## ======================================================
##                                 Dependent variable:
##                             ---------------------------
##                                       yvar
## ------------------------------------------------------
## treatment_typeElection info          0.005***
##                                       (0.002)
##
## treatment_typePartisan               0.005***
##                                       (0.001)
##
## treatment_typeTop-two info           0.004***
```

```
##                                      (0.001)
##
## Constant                            0.093***
##                                     (0.0002)
##
## ------------------------------------------------------
## Observations                        3,872,268
## R2                                   0.00001
## Adjusted R2                          0.00001
## Residual Std. Error            0.291 (df = 3872264)
## F Statistic                 13.670*** (df = 3; 3872264)
## ======================================================
## Note:                        *p<0.1; **p<0.05; ***p<0.01
```

Ans: We see the different letters do have different treatment effects as they have different coefficients and each of the coeffcient are statistically significant with robust std errors being used to report the p value

3. Then, test, using an F-test, whether the increased flexibility of the model estimated in part (2) has improved the performance of the model over that estimated in part (1). What does the evidence suggest?

```
( anova_test_report <- anova(lm_model6,lm_model7,test='F') )
```

```
## Analysis of Variance Table
##
## Model 1: yvar ~ AnyLetter
## Model 2: yvar ~ treatment_type
##    Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1 3872266 327616
## 2 3872264 327616  2  0.017723 0.1047 0.9006
```

Ans: We see from the anova test when comparing the more flexible model which have different treatment levels with the less flexible model which clubs all treatments into one group that the F ststistics is not significant. We get the F stats pvalue as 0.9005593 . So this added flexibility doesn't increase the performance of the causal model.

4. **More Specific Treatment Effects** Is one message more effective than the others? The authors have drawn up this design as a full-factorial design. Write a *specific* test for the difference between the *Partisan* message and the *Election Info* message. Write a *specific* test for the difference between *Top-Two Info* and the *Election Info* message. Report robust standard errors on both tests.

```
lm_model_partisan_election <- d[treatment.assign %in%c('Control','Partisan','Election info'),lm(yvar~Any
(partisan_elec_test <- coeftest(lm_model_partisan_election,vcovHC(lm_model_partisan_election)))
```

```
##
## t test of coefficients:
##
##               Estimate Std. Error  t value  Pr(>|t|)
## (Intercept) 0.09312478 0.00015062 618.2813 < 2.2e-16 ***
## AnyLetter   0.00498464 0.00172734   2.8857  0.003905 **
## Partisan    0.00027506 0.00210785   0.1305  0.896175
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lm_model_toptwo_election <- d[treatment.assign %in%c('Control','Top-two info','Election info'),lm(yvar~A
(top_two_elec_test <- coeftest(lm_model_toptwo_election,vcovHC(lm_model_toptwo_election)))
```

```
##
```

```
## t test of coefficients:
##
##                 Estimate  Std. Error  t value  Pr(>|t|)
## (Intercept)   0.09312478  0.00015062 618.2813 < 2.2e-16 ***
## AnyLetter     0.00498464  0.00172734   2.8857  0.003905 **
## Top.two.info -0.00048854  0.00210543  -0.2320  0.816508
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stargazer(lm_model_partisan_election,lm_model_toptwo_election,se=list(sqrt(diag(vcovHC(lm_model_partisa
```

```
##
## ===============================================================================
##                                       Dependent variable:
##                     ------------------------------------------------------
##                                             yvar
##                                (1)                          (2)
## -------------------------------------------------------------------------------
## AnyLetter                    0.005***                     0.005***
##                               (0.002)                      (0.002)
##
## Partisan                      0.0003
##                               (0.002)
##
## Top.two.info                                               -0.0005
##                                                            (0.002)
##
## Constant                     0.093***                     0.093***
##                              (0.0002)                     (0.0002)
##
## -------------------------------------------------------------------------------
## Observations                 3,812,414                    3,812,411
## R2                            0.00001                      0.00001
## Adjusted R2                   0.00001                      0.00001
## Residual Std. Error    0.291 (df = 3812411)         0.291 (df = 3812408)
## F Statistic         13.850*** (df = 2; 3812411) 11.276*** (df = 2; 3812408)
## ===============================================================================
## Note:                                           *p<0.1; **p<0.05; ***p<0.01
```

Ans: To test the hypothesis that different treatment types have different treatment effect we would run the linear regression model on subset of data including the control and treatments of interest. In the linear model we would include the AnyLetter and one of the treatment variable. If the coefficient of the treatment variable comes out to be non 0 and statistically significant then we can conclude that there is different treatment affect between the treatment type of interest. For the first one we will have model as Yvar ~ AnyLetter + Partisan for the subset of data including control,Partisan and Election info. If the coefficient of Partisan comes different than 0 and if its statistically significant then we can conclude that the treatment effect is different for Partisan and Election Info . We find that the estimate of the difference between the treatment effect is 2.7506358×10^{-4} and the robust std error for this is 0.0021078 and the p value is 0.8961747 so we can conclude that the difference is not statistically significant. Similarly for testing if the Election info and Top-Two info have different treatment effects we create a model with Yvar ~ AnyLetter + Top.two.info . We find that the difference in treatment effect is $-4.8854197 \times 10^{-4}$ and the robust std error for this is 0.0021054 and the p value is 0.8165075 so we can conclude that the difference is not statistically significant.

5. **Blocks?** There are a *many* of blocks in this data. How many?

```
(num_blocks = length(d[,unique(block.num)]))
```

```
## [1] 382
```

Ans:There are 382 blocks in this data inside which random assignment to treatments were done

6. Create a new indicator that is the *average turnout within a block* and attach this back to the data.table. Use this new indicator in a regression that predicts the difference between Control and Any Letter. Then, using an F-test, does the increased information from all these blocks improve the performance of the *causal* model? Use an F-test to check.

```
d[,avg_turn_out_block:= mean(yvar),by=block.num]
lm_shorter_model <- d[,lm(yvar~AnyLetter)]
lm_longer_model <- d[,lm(yvar~AnyLetter+avg_turn_out_block)]
se_shorter_model <- sqrt(diag(vcovHC(lm_shorter_model)))
se_longer_model <- sqrt(diag(vcovHC(lm_longer_model)))

stargazer(lm_shorter_model,lm_longer_model,se=list(se_shorter_model,se_longer_model),type='text',header=
```

```
##
## ===============================================================================
##                                        Dependent variable:
##                     ---------------------------------------------------------
##                                              yvar
##                                (1)                           (2)
## -------------------------------------------------------------------------------
## AnyLetter                    0.005***                      0.005***
##                               (0.001)                       (0.001)
##
## avg_turn_out_block                                         1.000***
##                                                             (0.003)
##
## Constant                     0.093***                       -0.0002
##                              (0.0002)                      (0.0003)
##
## -------------------------------------------------------------------------------
## Observations                 3,872,268                     3,872,268
## R2                            0.00001                       0.038
## Adjusted R2                   0.00001                       0.038
## Residual Std. Error    0.291 (df = 3872266)          0.285 (df = 3872265)
## F Statistic         40.801*** (df = 1; 3872266) 76,106.350*** (df = 2; 3872265)
## ===============================================================================
## Note:                                            *p<0.1; **p<0.05; ***p<0.01
```

```
anovatest_result <- anova(lm_shorter_model,lm_longer_model,test='F')
anovatest_result
```

```
## Analysis of Variance Table
##
## Model 1: yvar ~ AnyLetter
## Model 2: yvar ~ AnyLetter + avg_turn_out_block
##    Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1 3872266 327616
## 2 3872265 315228  1     12388 152170 < 2.2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ans: We see from the stargazer and anova test that the long form of the model which has the average turnout per block as an extra information do fit the data better as the adjusted R2 is higher in the long ferm and the residual std error is less. The F statistics p value is 0 which means that longer form is statistically significant. The stargazer report also tells that adding the extra information doesn't change the estimate of treatment effect of any letter and also doesn't impact the standard error much

7. **HTES?** Do you think that there are features of the data that might systematically predict that people will respond strongly or weakly to the treatment effect? List two that you think might be there, in the order that you would like to test them. Then, test for these heterogeneities. What do you learn? What is the right way to adjust your p-values, given that you're testing twice?

```
#test the heterogeneity for vote.14.gen
lm_vote.14.gen.hte <- d[,lm(yvar~AnyLetter+vote.14.gen+vote.14.gen*AnyLetter)]
lm_vote.14.gen.hte.se <- sqrt(diag(vcovHC(lm_vote.14.gen.hte)))
coeftest.lm_vote.14.gen.hte <- coeftest(lm_vote.14.gen.hte,vcovHC(lm_vote.14.gen.hte))
#test the heterogeneity for gender
d[,Female := ifelse(Gender=='F',1,0)]
lm_gender.hte <- d[,lm(yvar~AnyLetter+Female+Female*AnyLetter)]
lm_gender.hte.se <- sqrt(diag(vcovHC(lm_gender.hte)))
coeftest.lm_gender.hte <- coeftest(lm_gender.hte,vcovHC(lm_gender.hte))
stargazer(lm_vote.14.gen.hte,lm_gender.hte,se=list(lm_vote.14.gen.hte.se,lm_gender.hte.se),type='text',
```

```
##
## ===============================================================
##                                        Dependent variable:
##                                    ---------------------------
##                                                yvar
##                                          (1)            (2)
## ---------------------------------------------------------------
## AnyLetter                              0.002***       0.006***
##                                        (0.001)        (0.001)
##
## vote.14.gen                            0.220***
##                                        (0.0004)
##
## AnyLetter:vote.14.gen                  0.010***
##                                        (0.002)
##
## Female                                                -0.011***
##                                                       (0.0003)
##
## AnyLetter:Female                                       -0.002
##                                                        (0.002)
##
## Constant                               0.033***       0.097***
##                                        (0.0001)       (0.0002)
##
## ---------------------------------------------------------------
## Observations                         3,872,268      3,872,268
## R2                                     0.114          0.0003
## Adjusted R2                            0.114          0.0003
## Residual Std. Error (df = 3872264)     0.274          0.291
## F Statistic (df = 3; 3872264)       165,794.600***  444.227***
```

```
## ================================================================
## Note:                                *p<0.1; **p<0.05; ***p<0.01
```

Ans: Yes there are several features of the data such as vote.xx features and gender which might predict treatment effect strongly or weakly. I would like to test the features vote.14.gen and then being Female. Since we are testing one hypothesis after the other we should look to adjust the rejection p-value according to some family wise error rate (FWER) such as Bonferroni in which since we are testing twice we should reject if the p-value $<$ .05/2 which is p-value $<$ 0.025. We see that there is a hetrogeneous effect of treatment on vote.14.gen while there is no heterogenous effect of treatment on being Female

8. Summarize these results in a short paragraph that includes inline reports from your estimated models. (This can be integrated into your last response, if that works better for you.)

   The first test on treatment effect of AnyLetter we see that we have a positive treatment effect of 0.00489923 (about .5% increase in turnout) with robust std error of 0.00078340 and a p-value of 4.007e-10. This tells us that we indeed have a positive treatment effect on voter turnout. From the above tests for heterogeneous treatment effects we find that feature vote.14.gen has statistically significant heterogeneous treatment effect . The effect is 0.0095421 and the robust std error is 0.002294 and the p-value associated is 3.1881807×10^{-5} which means that this statistically significant result event after Bonferroni correction to critical p-value as 0.025 . For the heterogeneous treatment effect for Female we find that the heterogeneous treatment effect is not statistically significant. We find that the effect is -0.0019109 and the robust std error is 0.0016098 and the p-value associated is 0.2352197 which means its not statistically significant HTE.

9. Cheating? Suppose that you didn't write down your testing plan. How risky is the false discovery problem in this data set?
   Ans: There are many covariates in the dataset and if we don't write the testing plan we will get heterogeneous effect or significant effect on some covariate just by random chance as we would be doing a fishing exercise. So we should make sure to use some family wise error rate correction such as Bonferroni