

3. Turnout in Dorms

Guan and Green report the results of a canvassing experiment conducted 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.

```
# install.packages("ri2")
# install.packages("tidyverse")
# install.packages("ivreg")
# install.packages("stargazer")
# install.packages("sandwich")
# install.packages("ghostscript")

library(ri2)
library(stats)
library(tidyverse)
require(lmtest)
require(sandwich)
library(ivreg)
library(data.table)
library(stargazer)
library(tinytex)

if (!require('ivreg'))
{
  install.packages('ivreg');
  library(ivreg);
}

d <- fread('https://ucb-mids-w241.s3-us-west-1.amazonaws.com/Guan_Green_CPS_2006.csv')
head(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
## 6:         0         1 1010103              1

# Custom function to calculate and return clustered std errors
clustered_se <- function(mod){
  mod$vcovCL_ <- NULL
  mod$vcovCL_ <- vcovCL(mod, cluster = d[, dormid])
  return(sqrt(diag(mod$vcovCL_)))
}
```

Here are definitions for 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

Use Linear Regressions

1. Estimate the ITT using a linear regression on the appropriate subset of data. Notice that there are two NA in the data. Just `na.omit` to remove these rows so that we are all working with the same data. Given the ways that randomization was conducted, what is the appropriate way to construct the standard errors?

```
d <- na.omit(d)
dorm_model <- lm(turnout ~ treatment_group, data = d)

#Print out the model summary with clustered std errors
coeftest(dorm_model, vcov = vcovCL(dorm_model, d$dormid))[2:1,]

##              Estimate Std. Error   t value    Pr(>|t|)
## treatment_group 0.1319296 0.02327136  5.669182 1.535511e-08
## (Intercept)     0.6686657 0.02024116 33.034940 6.022303e-212

#Print out descriptive model summary with clustered std errors
stargazer(
  dorm_model,
  se = list(clustered_se(dorm_model)[2]),
  type='text',
  add.lines = list(c('SE Flavor','Clustered')),
  column.labels = c("dorm_model"),
  header = F
)
```

```
##
## =====
##              Dependent variable:
##              -----
##              turnout
##              dorm
## -----
## treatment_group          0.132
##                          (0.023)
##
## Constant                 0.669***
##
## -----
## SE Flavor                Clustered
## 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
```

We see that the treatment assignment was done at the student level, with students at each dorm room being assigned to the treatment or control (and hence clustering happening at the dorm room level and

randomization assignment happening at the clustered dorm room level). Therefore it is appropriate to have clustered standard errors here, as a measure of standard error.

Use Randomization Inference

1. How many people are in treatment and control? Does this give you insight into how the scientists might have randomized? As usual, include a narrative sentence after your code.

```
# Here we calculate absolute number of people in treatment and control
n_treatment <- d[treatment_group == 1, .N]
n_control <- d[treatment_group == 0, .N]
```

```
n_treatment
```

```
## [1] 2688
```

```
n_control
```

```
## [1] 1334
```

Total number of people in treatment: 2688

Total number of people in control : 1334

We see a roughly 2:1 randomization ratio for treatment and control (2.0149925 to be precise using formula `n_treatment/ n_control`)

2. Write an algorithm to conduct the Randomization Inference. Be sure to take into account the fact that random assignment was clustered by dorm room.

```
# We use ri2 package as an efficient way of implementing randomization inference.
```

```
# STEPS:
```

```
# First we define the experiment in the declaration
```

```
# Then we pass on hyperparameters along with the experiment design (declaration)
```

```
# in the 2nd step (ri2_out_at)
```

```
# We also illustrate a method of running custom formula (code commented) to
```

```
# show how ri2 package can be used to provide various statistics on
```

```
# a custom formula
```

```
# Here we get total number of clusters for treatment and control
```

```
n_treatment_cluster <- d[treatment_group == 1, .N, by=dormid][, .N]
```

```
n_control_cluster <- d[treatment_group == 0, .N, by=dormid][, .N]
```

```
# Declare the type of design we need for our experiment in the ri2 package
```

```
declaration <-
```

```
  with(d,{
```

```
    declare_ra(
```

```
      clusters = dormid,
```

```
      m_each = c(n_treatment_cluster, n_control_cluster))
```

```
  })
```

```
# Print out the design of the experiment here (FOR DEBUGGING)
```

```
# note the probability of assignment of clusters for treatment and control
```

```
declaration
```

```
## Random assignment procedure: Cluster random assignment
```

```
## Number of units: 4022
```

```

## Number of clusters: 1004
## Number of treatment arms: 2
## The possible treatment categories are 0 and 1.
## The number of possible random assignments is approximately infinite.
## The probabilities of assignment are constant across units:
##   prob_0   prob_1
## 0.6673307 0.3326693

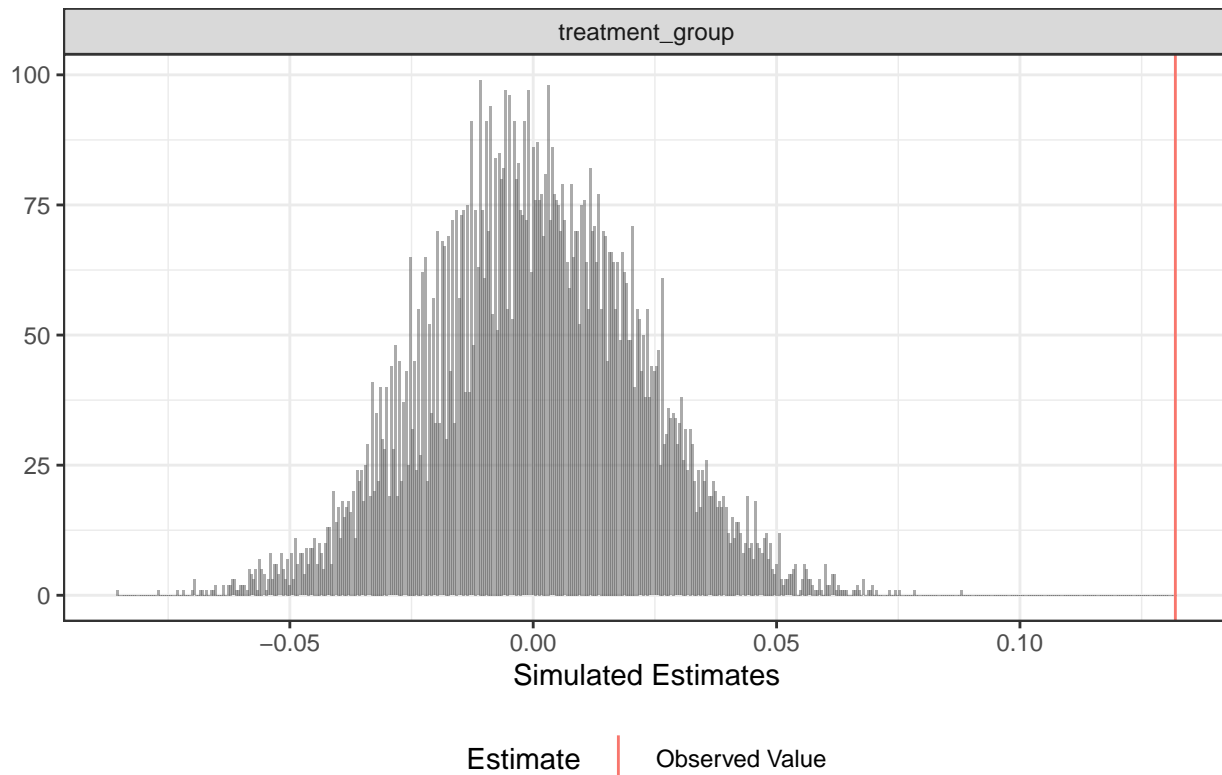
# Finally running randomization inference for 10000 steps using sharp_null_hyp = 0
ri2_out_ate <- conduct_ri(
  formula = d[, lm(turnout ~ treatment_group)],
  assignment = "treatment_group",
  sharp_hypothesis = 0, # means we assume there is no effect of treatment
  declaration = declaration, # passing model design here
  data = d,
  sims = 10000, # running for 10000 simulations,
  progress_bar = TRUE
)

# Below code commented: but could be used (IN A SIMILAR PROJECT SETTING)
# for returning a custom statistic (such as standard error)
# for a given formula (using ri2)
# stderr_fun <- function(data) {
#   model <- lm(turnout ~ treatment_group, data = d)
#   se <- sqrt(diag(vcovCL(model)))[2]
#   names(se) <- NULL
#   return(se)
# }
#
# stderr_fun(d)
#
# ri2_out_stderr <- conduct_ri(
#   test_function = stderr_fun,
#   assignment = "treatment_group",
#   sharp_hypothesis = 0,
#   declaration = declaration,
#   data = d,
#   sims = 1000,
#   progress_bar = TRUE
# )

plot(ri2_out_ate)

```

Randomization Inference



```
summary(ri2_out_ate, p = "two-tailed")
```

```
##           term estimate two_tailed_p_value
## 1 treatment_group 0.1319296                0
```

3. What is the value that you estimate for the treatment effect?

```
dorm_room_ate <- summary(ri2_out_ate, p = "two-tailed")[2]
dorm_room_ate
```

```
##      estimate
## 1 0.1319296
```

We get an estimate of the treatment effect from the RI process as: 0.1319295709 (using the formula: `summary(ri2_out_ate, p = "two-tailed")[2]`)

4. What are the 2.5% and 97.5% quantiles of this distribution?

```
dorm_room_ci <- quantile(ri2_out_ate$sims_df[, 1], prob = c(0.025, 0.975))
dorm_room_ci
```

```
##           2.5%           97.5%
## -0.04274158  0.04395124
```

5. What is the p-value that you generate for the test: How likely is this treatment effect to have been generated if the sharp null hypothesis were true.

```
p_value <- summary(ri2_out_ate, p = "two-tailed")[3]
p_value
```

```
##      two_tailed_p_value
## 1                      0
```

The likelihood of treatment effect to have been generated if the sharp null hypothesis were true is the p-value of 0 calculated in the above section.

6. Assume that the leaflet (which was left in case nobody answered the door) had no effect on turnout. Estimate the CACE either using ITT and ITT_d or using a set of linear models. What is the CACE, the estimated standard error of the CACE, and the p-value of the test you conduct?

```
#Calculating CACE using 2SLS (ivreg) and displaying results:
dorm_room_cace <- d[, ivreg(turnout ~ treated, ~ treatment_group)]
dorm_room_cace$coefficients[2]
```

```
##      treated
## 0.1489402
```

```
#Clustered standard errors of the CACE:
clustered_se(dorm_room_cace)[2]
```

```
##      treated
## 0.02630817
```

```
#p-value of the CACE
summary(dorm_room_cace)$coefficients[2,4]
```

```
## [1] 3.355883e-20
```

```
# Finally, displaying model summary:
stargazer(
  dorm_room_cace,
  se = list(clustered_se(dorm_room_cace)[2]
    #sqrt(diag(vcovHC(dorm_room_cace, type = 'HCO'))))
  ),
  type='text',
  add.lines = list(c('SE Flavor','Clustered')),
  column.labels = c("dorm_room_cace"),
  header = F
)
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               turnout
##                               dorm
## -----
## treated                      0.149
##                               (0.026)
##
## Constant                     0.669***
##
## -----
## SE Flavor                    Clustered
## 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
```

We conduct a two-stage least square regression test to find the CACE of our experiment.

CACE: 0.1489402

Clustered Standard Error of the CACE: 0.0263082

P-value: $3.3558829 \times 10^{-20}$

7. What if the leaflet that was left actually *did* have an effect? Is it possible to estimate a CACE in this case? Why or why not?

If dropping a leaflet had an effect, this would mean that dropping a leaflet was equal to providing treatment to those subjects where we dropped those leaflets. Therefore, we would have essentially provided treatment to all those who were assigned treatment. This would imply that there was no one who left without compliance (and equal to knocking on all doors and finding all those assigned to treatment and giving them the same treatment).

Thus in this case, with 100% compliance, CACE (or the complier ATE) would equal to ITT. Therefore calculating CACE in this case would be equal to calculating ITT.