Econometrics II - Assignment 4

Uncensored sloths

30 Jan 2022

Question 1

a) Despite having exactly the same pre-treatment outcomes, it happens to be the case that parallel trends assumption is violated. How is this possible? Explain what it means for parallel trends assumption to be violated, and give an example of how it could be violated.

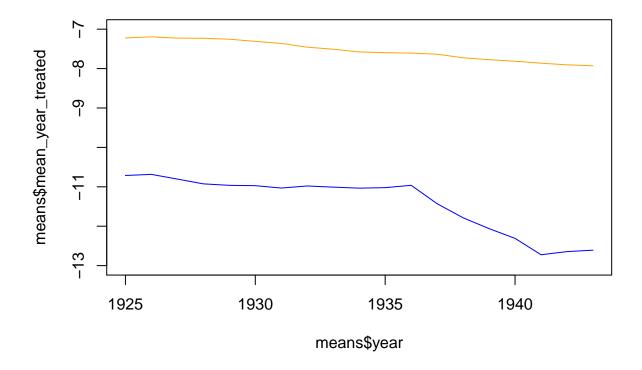
parallel trend assumption: The selection bias should be constant over time (eta_t - eta_c) it is an identifying assumption so we cannot test for it

Example: employment in brger restaurants - treatment is the minimum income - but we include taxes into the group specific effects (beforehand the same and after increase in Penselvenia)

b) biased estimation (which direction depends on the change in eta) as part of the change in the eta is part of the estimation

Question 2

```
# Load data
data <- read.csv("assignment5.csv")</pre>
  a)
ex1 <- data[data$treated == 1,] %>%
    group by(year) %>%
          summarise(mean_year_treated = mean(lnm_rate))
ex2 <- data[data$treated == 0,] %>%
    group_by(year) %>%
          summarise(mean_year_untreated = mean(lnm_rate))
means = merge(x=ex1,y=ex2,by="year")
head(means)
##
     year mean_year_treated mean_year_untreated
                  -10.71272
## 1 1925
                                       -7.222623
## 2 1926
                  -10.68480
                                       -7.194308
## 3 1927
                  -10.80431
                                       -7.226814
## 4 1928
                  -10.92541
                                       -7.231104
## 5 1929
                  -10.96293
                                       -7.254658
## 6 1930
                  -10.97147
                                       -7.309226
plot(means$year, means$mean_year_treated,type="1",col="blue", ylim=c(-13,-7))
points(means$year, means$mean_year_untreated,type="l",col="orange")
```



Generally, there seems to be a common downward trend which can be explained by advancement of treatment methods, diet and hygiene and is independent from the Sulfa drug. However, in 1937 you can see a substantial drop in mortality due to scarlet fever which stabilizes around 1942, increasing even a little bit (probably due to war and shortage in medicine).

b) Using only data for the years 1936 and 1937, make a table with the mean log mortality rate for treated and control diseases before and after the introduction of sulfa drugs. Use the numbers from the table to calculate the difference-in-differences estimator.

c) Using only data for the years 1936 and 1937, estimate a difference-in-difference regression. Comment on your results.

```
data$year_control <- ifelse(data$year == 1937, 1, 0)
data$post <- ifelse(data$year >= 1937, 1, 0)
data$D <- data$post*data$treated</pre>
```

```
m1 <- feols(lnm_rate ~ D | treated + year, data = subset(data, data$year == 1936| data$year == 1937),
            se = 'standard')
summary(m1)
## OLS estimation, Dep. Var.: lnm_rate
## Observations: 192
## Fixed-effects: treated: 2, year: 2
## Standard-errors: IID
      Estimate Std. Error t value Pr(>|t|)
                 0.218887 -2.00564 0.046329 *
## D -0.439008
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.750306
                      Adj. R2: 0.848869
##
                    Within R2: 0.020948
  d) Using all years, estimate a difference-in-difference regression. To do that, you need to create an indicator
     variable equal to 1 for the years 1937-1943 and equal to 0 for the years 1925-
1936. What is the interpretation of the difference-in-differences coefficients? What do you conclude about the
     effect of sulfa drugs on mortality rates?
m2 <- feols(lnm_rate ~ D | treated + year, data,</pre>
            se = 'standard')
summary(m2)
## OLS estimation, Dep. Var.: lnm_rate
## Observations: 1,721
## Fixed-effects: treated: 2, year: 19
## Standard-errors: IID
##
      Estimate Std. Error t value Pr(>|t|)
                 0.060468 -14.3336 < 2.2e-16 ***
## D -0.866724
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.605666
                      Adj. R2: 0.914713
##
                    Within R2: 0.107824
As it will be discussed later, we first assume that there is no clustering in sample and treatment.
  e) Estimate an event-study specification. Comment on your results.
m3 <- feols(lnm rate ~ treated*i(year, ref = 1936) | treated + year, data,
 se = 'standard')
## Variables 'treated', 'year::1925' and 17 others have been removed because of collinearity (see $coll
summary(m3)
## OLS estimation, Dep. Var.: lnm_rate
## Observations: 1,721
## Fixed-effects: treated: 2, year: 19
## Standard-errors: IID
##
                       Estimate Std. Error t value
                                                        Pr(>|t|)
## treated:year::1926 -0.135567
                                  0.187186 -0.724239 4.6902e-01
## treated:year::1927 -0.222575
                                 0.180546 -1.232787 2.1783e-01
## treated:year::1928 -0.339383
                                 0.177195 -1.915308 5.5623e-02 .
## treated:year::1929 -0.353351
                                 0.175174 -2.017141 4.3839e-02 *
```

0.175174 -1.754360 7.9551e-02 .

treated:year::1930 -0.307318

```
## treated:year::1940 -1.139170 0.174240 -6.537948 8.2465e-11 ***
## treated:year::1942 -1.384778   0.174240 -7.947544 3.4544e-15 ***
## treated:year::1943 -1.323763
             0.174739 -7.575677 5.8611e-14 ***
## ... 19 variables were removed because of collinearity (treated, year::1925 and 17 others [full set in
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.593665
         Adj. R2: 0.917231
        Within R2: 0.142828
```

f) Argue at which level you need to cluster standard errors. Implement your suggested clusterrobust standard errors. Comment on your results.

state level - as there is potential heterogeneity on state level - states with higher scarlet fever rate receive

```
m1_clustered <- feols(lnm_rate ~ D | treated + year, data = subset(data, data$year == 1936| data$year =
           cluster = 'state')
summary(m1 clustered)
## OLS estimation, Dep. Var.: lnm rate
## Observations: 192
## Fixed-effects: treated: 2, year: 2
## Standard-errors: Clustered (state)
     Estimate Std. Error t value Pr(>|t|)
## D -0.439008   0.250152 -1.75497   0.082489 .
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.750306
                     Adj. R2: 0.848869
                   Within R2: 0.020948
m2_clustered <- feols(lnm_rate ~ D | treated + year, data,</pre>
           cluster = 'state')
summary(m2_clustered)
## OLS estimation, Dep. Var.: lnm_rate
## Observations: 1,721
## Fixed-effects: treated: 2, year: 19
## Standard-errors: Clustered (state)
     Estimate Std. Error t value
                                  Pr(>|t|)
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.605666
                    Adj. R2: 0.914713
                   Within R2: 0.107824
m3_clustered <- feols(lnm_rate ~ treated*i(year, ref = 1936) | treated + year, data,
cluster = 'state')
```

```
## Variables 'treated', 'year::1925' and 17 others have been removed because of collinearity (see $coll
summary(m3_clustered)
## OLS estimation, Dep. Var.: lnm_rate
## Observations: 1,721
## Fixed-effects: treated: 2, year: 19
## Standard-errors: Clustered (state)
               Estimate Std. Error
                             t value
## treated:year::1926 -0.135567   0.149337 -0.907792 3.6629e-01
## treated:year::1934 -0.102580 0.115933 -0.884816 3.7849e-01
## treated:year::1937 -0.439008   0.250893 -1.749783 8.3385e-02 .
## treated:year::1941 -1.505930
                     0.229506 -6.561604 2.7862e-09 ***
## treated:year::1942 -1.384778
                      0.237230 -5.837276 7.3536e-08 ***
## treated:year::1943 -1.323763
                     0.231502 -5.718148 1.2412e-07 ***
## ... 19 variables were removed because of collinearity (treated, year::1925 and 17 others [full set i
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.593665
              Adj. R2: 0.917231
             Within R2: 0.142828
year as we choose turbocolosis as a control based on the argumentation that at that point of time there was
no medication against it - treatment level
 g) Do a test of whether the prior trends differ between the treated and control groups. What do you
   conclude?
linearHypothesis(m3_clustered, c("treated:year::1925=0", "treated:year::1926=0", "treated:year::1927=0"
                      "treated:year::1929=0", "treated:year::1930=0", "treated:year::1931=0
## Warning: In vcov.fixest(model, complete = FALSE):
## 'complete' is not a valid argument of function vcov.fixest (fyi, some of
```

its main arguments are 'vcov' and 'ssc').

Linear hypothesis test

treated:year::1925 = 0
treated:year::1926 = 0
treated:year::1927 = 0
treated:year::1928 = 0
treated:year::1929 = 0
treated:year::1930 = 0
treated:year::1931 = 0
treated:year::1932 = 0

Hypothesis:

##

```
## treated:year::1933 = 0
## treated:year::1934 = 0
## treated:year::1935 = 0
##
## Model 1: restricted model
## Model 2: lnm_rate ~ treated * i(year, ref = 1936) | treated + year
##
## Df Chisq Pr(>Chisq)
## 1
## 2 11 38.547 6.322e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```