# Frontier Topics in Empirical Economics: Week 11 Standard Error Issues

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#### Introduction: Nonstandard Standard Error Issues

- Inference is important in practice: Data ⇒ Target distribution
- How accurate is our estimate? How confident are we on our results?
- In traditional inference of econometrics, we have two assumptions:
  - Uncertainty comes from random-sampling, asymptotics when  $n \to \infty$
  - i.i.d. sample, no correlations
- What if these two assumptions are violated?

#### Introduction: Nonstandard Standard Error Issues

- In this lecture, we consider two cases
- First, when n is naturally limited (e.g. number of provinces)
- Another type of uncertainty becomes important: Design-based uncertainty
- Second, when i.i.d. fails and errors are clustered
- We have to incorporate this structure in inference
- Angrist calls them "Nonstandard Standard Error Issues"

- In usual case, when we talk about inference, what is that?
- We have a target parameter: "estimand"  $\beta$  (Target)
- We want to recover it using an "estimator" (Method)  $\hat{\beta}$  with a sample from the population, which gives you a result called "estimate"  $\hat{\beta} = 0.5$  (Result)
- This process is called *estimation*, or statistical inference (Process)

- Usually, we consider sampling-based uncertainty
- Each time you draw a new sample, it gives you a new estimate from your estimation process
- When sample changes, your estimation result changes
- Uncertainty comes from sampling process
- Thus, you have a standard error for your estimation
- But is this the only uncertainty in empirical research?
- Today, we are going to introduce the second source of uncertainty

- Design-based uncertainty, introduced by Abadie et al. (2020)
- It is the uncertainty coming from the treatment assignment
- Treatment X<sub>i</sub> is no longer considered fixed
- In some cases, person 1 is treated; in other cases, person 1 is not treated
- The potential outcome you observed is different when treatment is randomly changed
- We show that this helps you to understand uncertainty of estimation when you have non-negligible sample size

- To visually explain the difference between traditional sampling-based uncertainty and design-based uncertainty
- Let's take a look at two tables from Abadie et al. (2020)
- $\blacksquare$   $R_i$  is an indicator of whether this observation is included in the sample

#### Sampling-based uncertainty

TABLE I SAMPLING-BASED UNCERTAINTY ( $\checkmark$  IS OBSERVED, ? IS MISSING)

Unit	Actual Sample			Alternative Sample I			Alternative Sample II			
	$Y_i$	$Z_i$	$R_i$	$Y_i$	$Z_i$	$R_i$	$Y_i$	$Z_i$	$R_i$	
1	<b>√</b>	<b>√</b>	1	?	?	0	?	?	0	
2	?	?	0	?	?	0	?	?	0	
3	?	?	0	✓	$\checkmark$	1	✓	✓	1	
4	?	?	0	$\checkmark$	$\checkmark$	1	?	?	0	
	:	:	:	:	:	:	:	:	:	
n	· /	· /	i	$\dot{?}$	$\dot{?}$	0	$\dot{?}$	?	0	

Unit	Actual Sample			Alternative Sample I			Alternative Sample II			
	$Y_i^*(1)$	$Y_i^*(0)$	$X_i$	$Y_{i}^{*}(1)$	$Y_i^*(0)$	$X_i$	$Y_i^*(1)$	$Y_i^*(0)$	$X_i$	
1	✓	?	1	✓	?	1	?	✓	0	
2	?	✓	0	?	✓	0	?	✓	0	
3	?	<b>√</b>	0	✓	?	1	✓	?	1	
4	?	✓	0	?	✓	0	✓	?	1	
:	:	:	:	:	:	:	:	:	:	
		•			•					
n	✓	?	1	?	✓	0	?	✓	0	

- Sampling-based uncertainty
  - Treatment is fixed, sampling observation is random
  - For non-sampled individuals, we cannot observe anything
  - Source of uncertainty: in each sample, we have different observations
- Design-based uncertainty
  - Treatment is random, sampling observation is fixed (e.g. all provinces in China)
  - For each individual, we only observe potential outcome in the realized status (but not counterfactual status)
  - Source of uncertainty: in each sample, we have different treatment status for each individual

- Next, the authors construct a simple model and make the following four points:
  - 1. Show how design-based uncertainty affects the variance of the regression estimator
  - 2. Show White estimator remains conservative when we consider design-based uncertainty
  - 3. We can derive a finite-population correction for White estimator
  - 4. Discuss two sources of uncertainty and external/internal validity

- Assume that we have a finite population of size n
- We randomly sample N from n
- $R_i \in \{0,1\}$  as an indicator of whether i is sampled or not
- There is a random binary treatment regressor  $X_i$
- $\blacksquare$   $n_1, N_1$  are treated,  $n_0, N_0$  are not treated
- We have observed and potential outcome as:

$$Y_i = Y_i^*(X_i) = \begin{cases} Y_i^*(1) & \text{if } X_i = 1, \\ Y_i^*(0) & \text{if } X_i = 0 \end{cases}$$

Potential outcomes are assumed to be non-stochastic

- We use bold letters to represent vector of the whole sample  $(\mathbf{Y}, \mathbf{Y}_{i}^{*}(1), \mathbf{Y}_{i}^{*}(0), \mathbf{R})$
- We define three estimands as our proposed targets
  - Descriptive estimand: free of **R** and potential outcome (population mean difference)  $\theta^{descr} = \frac{1}{n_1} \sum_{i=1}^{n} X_i Y_i \frac{1}{n_0} \sum_{i=1}^{n} (1 X_i) Y_i$
  - Causal estimand: parameter depending on potential outcome  $\mathbf{Y}_{i}^{*}(1), \mathbf{Y}_{i}^{*}(0)$   $\theta^{causal,sample} = \frac{1}{N} \sum_{i=1}^{n} R_{i}(Y_{i}^{*}(1) Y_{i}^{*}(0))$   $\theta^{causal} = \frac{1}{n} \sum_{i=1}^{n} (Y_{i}^{*}(1) Y_{i}^{*}(0))$
- ullet  $\theta^{causal,sample}$  is the average causal effect of the current sample
- $m{\theta}^{causal}$  is the average causal effect of the whole population

- lacktriangledown When estimating  $heta^{descr}$ , we do not care about design-based uncertainty Nothing about treatment or potential outcome
- When estimating  $\theta^{causal,sample}$ , we do not care about sampling-based uncertainty Nothing about sampling process (given current sample)
- lacktriangle When estimating  $heta^{causal}$ , we do care about both types of uncertainty

■ To estimate these estimands, we use a simple OLS regression of  $Y_i$  on  $X_i$  to have:

$$\hat{\theta} = \frac{1}{N_1} \sum_{i=1}^{n} R_i X_i Y_i - \frac{1}{N_0} \sum_{i=1}^{n} R_i (1 - X_i) Y_i$$

- Sampling-based uncertainty comes from the randomness of R
- Design-based uncertainty comes from the randomness of X
- We further assume that both sampling and treatment assignment are random

It is shown that:

$$E[\hat{\theta}|\mathbf{X}, N_1, N_0] = \theta^{descr}$$

$$E[\hat{\theta}|\mathbf{R}, N_1, N_0] = \theta^{causal, sample}$$

$$E[\hat{\theta}|N_1, N_0] = \theta^{causal}$$

- $\blacksquare$  Conditioning on (fix) treatment,  $\theta$  is unbiased for descriptive estimand
- lacktriangle Conditioning on (fix) sampling, heta is unbiased for causal sample estimand
- lacktriangle Conditioning on none of them, heta is unbiased for causal estimand

■ We define the population variances as follows:

$$S_{x}^{2} = \frac{1}{n-1} \sum_{i=1}^{n} \left( Y_{i}^{*}(x) - \frac{1}{n} \sum_{j=1}^{n} Y_{j}^{*}(x) \right)^{2}, \text{ for } x = 0, 1$$

$$S_{\theta}^{2} = \frac{1}{n-1} \sum_{i=1}^{n} \left( Y_{i}^{*}(1) - Y_{i}^{*}(0) - \frac{1}{n} \sum_{j=1}^{n} (Y_{j}^{*}(1) - Y_{j}^{*}(0)) \right)^{2}$$

- $S_x^2$  is the variance of potential outcomes for population
- ullet  $S_{ heta}^2$  is the variance of treatment effect for population

Based on the defined population variance, we can derive three variances

$$V^{total}(N_{1}, N_{0}, n_{1}, n_{0}) = var(\hat{\theta}|N_{1}, N_{0}) = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{n_{0} + n_{1}}$$

$$V^{sampling}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{X}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} \left(1 - \frac{N_{1}}{n_{1}}\right) + \frac{S_{0}^{2}}{N_{0}} \left(1 - \frac{N_{0}}{n_{0}}\right)$$

$$V^{design}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{R}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{N_{0} + N_{1}}$$

■ Now let's analyze them one by one

- $V^{total}$  is the total variance, considering both sampling-based and design-based uncertainty:  $var(\hat{\theta}|N_1, N_0)$
- It is the variance we want to capture in inference for causal estimator
- $V^{sampling}$  is the variance from only sampling-based uncertainty, by conditioning on treatment assignment:  $E[var(\hat{\theta}|\mathbf{X}, N_1, N_0)|N_1, N_0]$
- It is the variance in inference for descriptive estimator
- $V^{design}$  is the variance from only design-based uncertainty, by conditioning on current sample:  $E[var(\hat{\theta}|\mathbf{R}, N_1, N_0)|N_1, N_0]$
- It is the variance in inference for causal sample estimator

$$V^{total}(N_{1}, N_{0}, n_{1}, n_{0}) = var(\hat{\theta}|N_{1}, N_{0}) = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{n_{0} + n_{1}}$$

$$V^{sampling}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{X}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} \left(1 - \frac{N_{1}}{n_{1}}\right) + \frac{S_{0}^{2}}{N_{0}} \left(1 - \frac{N_{0}}{n_{0}}\right)$$

$$V^{design}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{R}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{N_{0} + N_{1}}$$

■ 1. Generally,  $V^{sampling}$  and  $V^{design}$  cannot be ranked, depending on the sampling rates  $\frac{N}{n}$ . A very large sampling rate means a very small  $V^{sampling}$ .

$$V^{total}(N_{1}, N_{0}, n_{1}, n_{0}) = var(\hat{\theta}|N_{1}, N_{0}) = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{n_{0} + n_{1}}$$

$$V^{sampling}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{X}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} \left(1 - \frac{N_{1}}{n_{1}}\right) + \frac{S_{0}^{2}}{N_{0}} \left(1 - \frac{N_{0}}{n_{0}}\right)$$

$$V^{design}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{R}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{N_{0} + N_{1}}$$

■ 2. When  $n \to \infty$ ,  $V^{sampling} = V^{total}$ If the population is infinite, then design-based uncertainty is ignorable and traditional inference for causal estimand (without considering design-based uncertainty) is fine

$$V^{total}(N_{1}, N_{0}, n_{1}, n_{0}) = var(\hat{\theta}|N_{1}, N_{0}) = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{n_{0} + n_{1}}$$

$$V^{sampling}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{X}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} \left(1 - \frac{N_{1}}{n_{1}}\right) + \frac{S_{0}^{2}}{N_{0}} \left(1 - \frac{N_{0}}{n_{0}}\right)$$

$$V^{design}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{R}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{N_{0} + N_{1}}$$

■ 3. Consider estimating  $\theta^{descr}$  or  $\theta^{causal}$ :

When population is finite,  $V^{total}$  and  $V^{sampling}$  are overstated if we think it is infinite  $V^{total}(N_1, N_0, \infty, \infty) - V^{total}(N_1, N_0, n_1, n_0) = \frac{S_\theta^2}{n_0 + n_1} \ge 0$ ,

$$V = (N_1, N_0, \infty, \infty) - V = (N_1, N_0, n_1, n_0) = \frac{s_0}{n_0 + n_1} \ge 0,$$

$$V^{sampling}(N_1, N_0, \infty, \infty) - V^{sampling}(N_1, N_0, n_1, n_0) = \frac{S_1^2}{n_1} + \frac{S_0^2}{n_0} \ge 0$$

$$V^{total}(N_{1}, N_{0}, n_{1}, n_{0}) = var(\hat{\theta}|N_{1}, N_{0}) = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{n_{0} + n_{1}}$$

$$V^{sampling}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{X}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} \left(1 - \frac{N_{1}}{n_{1}}\right) + \frac{S_{0}^{2}}{N_{0}} \left(1 - \frac{N_{0}}{n_{0}}\right)$$

$$V^{design}(N_{1}, N_{0}, n_{1}, n_{0}) = E[var(\hat{\theta}|\mathbf{R}, N_{1}, N_{0})|N_{1}, N_{0}] = \frac{S_{1}^{2}}{N_{1}} + \frac{S_{0}^{2}}{N_{0}} - \frac{S_{\theta}^{2}}{N_{0} + N_{1}}$$

• 4. Consider estimating  $\theta^{causal,sample}$ :

When population is finite,  $V^{design}$  is fine even if we think it is infinite  $V^{design}(N_1, N_0, \infty, \infty) = V^{design}(N_1, N_0, n_1, n_0)$ Relative sample size does not affect variance conditional on current sample

- In practice, we usually use White estimator of the variance matrix
- It is calculated without considering design-based uncertainty<sup>1</sup>

$$\hat{V}^{w} = \frac{\hat{S}_{1}^{2}}{N_{1}} + \frac{\hat{S}_{0}^{2}}{N_{0}}, \text{ where } \hat{S}_{1}^{2} = \frac{1}{N_{1} - 1} \sum_{i=1}^{n} R_{i} X_{i} \left( Y_{i} - \frac{1}{N_{1}} \sum_{i=1}^{n} R_{i} X_{i} Y_{i} \right)^{2}$$

- It is unbiased for  $V^{total}$  when n is infinite
- The small population bias is  $E[\hat{V}^w|N] V^{total} = S_\theta^2/n$

 $<sup>^{1}\</sup>hat{\mathcal{S}}_{0}^{2}$  is defined analogously

- We can see that if we ignore design-based uncertainty in inference
- It is fine if we have a small sample compared with a massive population
- Like you have a CFPS dataset to represent all families in China
- But the positive bias will become large if we have a large sample size compared with a limited population
- Like you have a province-level regression
- In this case, traditional variance estimation can be too large and too conservative
- Because you ignore the fact that you already have a large part of the population

- But fortunately, we can derive a bias-corrected estimator
- By taking into consideration
  - You have a large sample relative to a small population
  - You have uncertainty in treatment assignment
- The derivation of this estimator is technical
- Read Abadie et al. (2020) if you are interested

#### Clustered Standard Errors: Motivating Example

- Next, let's consider the clustering issue
- Many scholars claim that smaller classes are better
- What is the impact of class size on students' achievement?
- Hard to identify using observational data (selection problem)
- STAR is a RCT to answer this question

#### Clustered Standard Errors: Motivating Example

- It involves 11,600 children in TN
- Kids are randomly assigned to two kinds of classes
   (1) Small class with 13-17 children;
   (2) Regular class with 22-25 children
- Then we can identify the treatment effect of class size
- One assumption we always make is i.i.d.
- However, students in the same class are of course not independently sampled
- What will happen if we have correlations at class/school/district... level?

#### Clustered Standard Errors: Motivating Example

- The short answer is: we may underestimate the standard error
- Let's see why it is and how to fix this issue

#### Clustered Standard Errors: Setting

- Let's go on with the STAR experiment
- Consider the following regression for student i in class g:

$$y_{ig} = \beta_0 + \beta_1 x_g + e_{ig}$$

- $y_{ig}$  test score;  $x_g$  class size (randomly assigned);  $e_{ig}$  error term
- This is a special case when x is fixed at g level (same treatment for the whole class)
- Test scores in the same class tend to be correlated (Same environment, teacher...)

## Clustered Standard Errors: Setting

■ Thus, we give up i.i.d. assumption and assume that for student i and j:

$$E[e_{ig}e_{jg}] = \rho_e\sigma_e^2 > 0$$

- Assume that we can decompose error into

$$e_{ig} = \nu_g + \eta_{ig}, \quad \nu_g \perp \eta_{ig}$$

- We assume that  $\nu_g$  captures all within class correlations  $(\eta_{ig} \perp \!\!\! \perp \eta_{jg})$
- lacktriangle Also assume homoskedasticity for both  $u_{oldsymbol{g}}$  and  $\eta_{ioldsymbol{g}}$
- Then we can prove that

$$\rho_e = \frac{\sigma_\nu^2}{\sigma_\nu^2 + \sigma_n^2} \tag{1}$$

Intraclass correlation is the share of intraclass uncertainty in the total uncertainty

#### Clustered Standard Errors: Setting

- Equation (1) is called "intraclass correlation coefficient"
- Homework: Derive equation (1) from the previous setting

#### Clustered Standard Errors: Bias and Moulton Factor

- Let  $V_c(\hat{\beta}_1)$  be the conventional OLS variance,  $V(\hat{\beta}_1)$  be the correct variance
- $\blacksquare$  Assume we have classes with equal size n, then

$$\frac{V(\hat{\beta}_1)}{V_c(\hat{\beta}_1)} = 1 + (n-1)\rho_e$$

- We call this Moulton factor
- $n, \rho_e \uparrow \Rightarrow$  Bias of conventional variance  $\uparrow$
- Larger n means fewer groups  $\Rightarrow$  less information
- What will happen if  $\rho_e = 1?$  ⇒ variance is biased by 1/n
- Students in the same class do not provide additional information

#### Clustered Standard Errors: Bias and Moulton Factor

- Previous setting assumes fixed  $x_g$  within each group
- Let's see Moulton factor in a more general case when  $x_{ig}$  can vary across i in the same group

$$\frac{V(\hat{\beta}_1)}{V_c(\hat{\beta}_1)} = 1 + \left[\frac{V(n_g)}{\bar{n}} + \bar{n} - 1\right] \rho_{\times} \rho_e \tag{2}$$

■  $\bar{n}$  is average group size;  $V(n_g)$  is variance of group sizes;  $\rho_x$  is intraclass correlation of  $x_{ig}$ 

#### Clustered Standard Errors: Bias and Moulton Factor

- In general, bias from within class correlation is larger when
  - (1) Average group size ↑
  - (2) Variance of group size ↑
  - (3) Intraclass correlation of treatment  $x_{ig} \uparrow$
  - (4) Error intraclass correlation ↑
- The implication of (3)
  - lacksquare Bias can be very large in the fixed group treatment  $x_g$  case
  - No need to cluster anything if the assignment is totally random for every individual
- The implication of (4): Naturally, no bias when  $\rho_e = 0$

#### Clustered Standard Errors: Fix the Bias

- Now we know that std error estimation can be biased when we have correlation within classes
- What we should do? Several methods are available
  - (1) Use Moulton factor equation (2) to correct
     Not that good: error structure assumptions (homoskedasticity)
  - (2) Recommended: Liang and Zeger (1986) clustering estimator Generally consistent as number of groups  $\rightarrow \infty$  (In stata, use option *cluster*)
  - (3) Running group-level regressions  $\bar{y}_g = \beta_0 + \beta_1 x_g + \bar{e}_g$  using WLS (group size as weights)
    - Better finite-sample properties, but  $x_g$  has to be group-fixed
  - Other methods: Block bootstrap, MLE...

- How to choose the level of clustering?
- In STAR experiment, why not boy/girl, black/white/asian...?
- Clustering in more dimensions/higher level gives you larger std errs
- Is that OK to always cluster in more and more dimensions (be conservative)? NO. You can be too conservative ⇒ Overestimate std err
- Similarly, not always good to cluster at higher and higher level

- This is because when you cluster in more and more dimensions
- Or at higher and higher level
- Your effective sample size compared with effective population becomes larger and larger
- As Abadie et al. (2020) has shown, it leads to overestimation of the std err
- For example, you have data of 10,000 firms in 20 provinces
- 10,000 can be a very small proportion of all firms in mainland China
- When you cluster at province level, effective sample rate becomes 20/31!

- Thus, two issues remains
  - How to choose cluster level reasonably?
  - How to incorporate design-based uncertainty?
- Abadie et al. (2023) considers clustering as a sampling/design problem
- Cluster level depends on how you get your samples/assign your treatment
- It comes from the basic idea of Abadie et al. (2020)
- You have to consider both sampling-based and design-based uncertainty
- This is more to the core of the clustering problem

- There are three misconceptions they want to clarity
- 1. The need for clustering hinges on the presence of a correlation between residuals
  - No. The essence is the clustering of sampling or treatment assignment
  - Even if students' scores are correlated within classroom, there is no need to cluster when sampling and treatment are totally random
- 2. No harm in using clustered std err when they are not required
  - Confidence intervals will be unnecessarily conservative
- 3. Researchers either fully adjust for clustering by using Liang and Zeger (1986) or not do that at all
  - Not really. They propose a new estimator CCV/TSCB to correct for large effective sample rate in clustering

Here are some empirical suggestions from Abadie et al. (2023)

- 1. If sampling and treatment are both random
  - Do not cluster!
  - In this case, if sample represents a large fraction of the population, even White estimator is too conservative (Abadie et al., 2020)
- 2. If random sampling but clustered treatment assignment
  - Cluster at the treatment level.
  - In the fuzzy design case, using CCV/TSCB estimator

- 3. If clustered sampling, random treatment assignment
  - Cluster at the sampling level, if you have small fraction of sampled clusters or small fraction of sampled units within each cluster
  - This is specifically important in panel data analysis
  - Do not cluster in other cases
- 4. If clustered sampling, clustered treatment assignment
  - Cluster at the higher level to be conservative

- Let us go over two practical examples
- Case 1: (Sampling cluster) Some household/firm survey will
  - (1) Randomly select 50/350 prefectures in China
  - (2) Randomly select 100 households/firms in each sampled prefecture
- It gives you a natural stratified data set
- Just cluster at city level (in general, first sampling stage level)
- Case 2: (Treatment cluster) STAR assigns treatment at class level
- Then just cluster at class level

#### Clustered Standard Errors: DID and Serial Correlation

- One special case we must underscore is panel data analysis
- When using panel data, we usually employ time variation for identification
- You draw people, but not people in a specific year ⇒ serial correlation
- You are drawing samples/assign treatment clustered at individual level
- Thus, DID gives a natural clustering structure of error
- One-level-up principle:
   Cluster at individual/province/city level, but NEVER individual-year/province-year/city-year level!!

#### Conclusion

- Today we discuss two nonstandard standard error issues
  - When sample is large compared with population
  - When errors are not i.i.d. but clustered
- In the first issue, we claim that we need to consider both sampling-based and design-based uncertainty
- Using traditional inference will have too large and conservative std err

#### Conclusion

- In the second case, we find that not adjusting for cluster will generate a too small std err
- We can use LZ estimator to fix it (consistent as #groups→ ∞)
- Clustering at higher level is not always good
- Clustering comes from either clustered sampling or clustered treatment
- Cluster at the first sampling stage, or treatment assignment level
- Do NOT cluster if you have a totally random sample and random treatment
- In DID, cluster one level up to take care of the serial correlation

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