Wild Bootstrap Inference for Wildly Different Cluster Sizes

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Introduction

- This paper is joint with:

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- Contributions:
  - Presents Monte Carlo evidence that overturns the 'rule of 42'
  - Shows that DiD and CRVE estimation works poorly when the proportion of clusters treated is very small or very large

Standard Method for Difference-in-Differences

- Suppose you want to estimate the following linear difference-in-differences equation

$$Y_{igt} = \beta_0 + \beta_1 * treat_g + \beta_2 * year_t + \beta_3 * treat_g * year_t + X_{igt}\gamma + \epsilon_{igt} \quad (1)$$

- Y_{igt} observation for person i in group g and time t
- $treat_g$ dummy for if the person is in the treatment group
- $year_t$ dummy if in time period after treatment
- X_{igt} other independent variables
- $treat_g * year_t$ is the DiD term

Estimating β

- We are interested in inference for the OLS estimate of $\hat{\beta}_3$
- With the assumptions that data are independent over g, but errors are correlated within cluster
- $E[u_g] = 0$
- $E[u_g u_g'] = \Sigma_g$, violates the i.i.d. assumption
- $E[u_g u_h'] = 0$ for cluster $h \neq g$
- When then have
- $\sqrt{N}(\hat{\beta} - \beta) \sim \aleph[0, NV[\hat{\beta}]]$

Cluster Robust Variance Estimator (CRVE)

$$\hat{V}_{CR}[\hat{\beta}] = (X'X)^{-1} \left(\sum_{g=1}^{G} X_g \tilde{u}_g \tilde{u}_g' X_g' \right) (X'X)^{-1}$$

- in the simplest case the OLS residuals are used $\tilde{u}_g = \hat{u}_g = y_g - X_g \beta$
- in other cases $\sum_{g=1}^{G} X_g \hat{u}_g \hat{u}_g' X_g'$, is replaced by $\sum_{g=1}^{G} \tilde{U}_g \tilde{U}_g'$
- Stata uses:

$$\tilde{U}_g = \sum_{i=1}^{N_g} \hat{u}_{ig} \begin{pmatrix} 1 \\ X_g \end{pmatrix},$$

Asymptotics Underlying CRVE

General results on covariance matrix estimation in White (1984) imply of the CRVE is consistent under three key assumptions:

A1. The number of clusters goes to infinity.
A2. The within-cluster correlation is constant across clusters.
A3. The individual clusters contain an equal number of observations.

Carter, Schnepel and Steigerwald (2012) relax A1 and A2.
This talk concerns A3.

Related Literature

- Clustered Errors
  - Kloek (1981)
  - Moulton (1990)
- Inference in Difference-in-Difference
  - Conley and Taber (2011)
  - Donald and Lang (2007)
- Bootstrap Inference in Difference-in-Differences
  - Bertrand, Duflo and Mullainathan (2004)
  - Cameron, Gelbach and Miller (2008)
  - Webb (2013)

Rejection Frequencies by Number of Clusters

	Number of Groups (G)					
	5	10	15	20	25	30
OLS $\sim N(0,1)$	0.468	0.486	0.493	0.494	0.489	0.499
CRVE $\sim N(0,1)$	0.211	0.133	0.108	0.094	0.084	0.080
CRVE $\sim T(G-1)$	**0.100**	**0.090**	**0.081**	**0.075**	**0.070**	**0.069**

Notes: Replication of simulations performed by CGM. Rejection frequencies estimated with 50,000 replications.

The "Rule of 42"

Claim: "In a DD scenario where you'd like to cluster on state or some other cross-sectional dimension, the relevant dimension for counting clusters is the number of states or cross-sectional groups. Therefore, following Douglas Adam's dictum that the answer to life, the universe, and everything is 42, we believe the question is: How many clusters are enough for reliable inference using the standard cluster adjustment?"
Angrist and Pischke, *Mostly Harmless Econometrics*, page 319.

Response:
True if clusters are of equal size, false otherwise.

The "Rule of 42"

	6	10	20	50
OLS	0.383	0.443	0.390	0.490
CRVE	0.153	0.105	0.080	0.055

Notes: Bertrand, Duflo and Mullainathan (2004) Monte Carlo Simulations using CPS aggregate data.

Simulations such as these, and those by Cameron, Gelbach and Miller (2008) have led to a shorthand 'rule of 42', when A1 is approximately satisfied. "Current consensus appears to be that $G = 50$ is enough for state-year panel data." Cameron and Miller (2013)

Procedure for Wild Cluster Bootstrap-t

1. estimate equation 1 and obtain estimates of $\hat{\beta}$, $\hat{\gamma}$ and $\hat{\epsilon}_{igt}$

1a. estimate a restricted version of equation 1 which imposes the null hypothesis, obtain $\tilde{\epsilon}_{igt}$ and equivalent

2. we are interested in the significance of $\hat{\beta}_3$ so calculate the t-statistic, $\hat{t}$, using cluster robust standard errors

3. choose a number of bootstraps, B, and for each iteration generate a new bootstrap sample from the bootstrap DGP:

$$y^*_{igt} = \tilde{\beta}_0 + \tilde{\beta}_1 * treat_g + \tilde{\beta}_2 * year_t + \tilde{\beta}_3 * treat_g * year_t + X_{igt}\tilde{\gamma} + f(\tilde{u}_{igt})v^*_g, \quad (2)$$

where $f(\tilde{u}_{igt})$ transforms the i^{th} residual in time t from group g, $\tilde{u}_{igt}$, and v_g is a bootstrap weight. Impose the null by setting $\tilde{\beta}_3 = 0$

Procedure for Wild Cluster Bootstrap-t

4. estimate equation 1 again using the bootstrap sample
5. calculate the t-statistic, t_j^* on $\hat{\beta}_3$ by using the cluster robust standard errors
6. after the B^{th} iteration calculate the bootstrap p-value by

$$\hat{p}^*(\hat{t}) = 2\text{min}\left(\frac{1}{B}\sum_{j=1}^{B} I(t_j^* \leq \hat{t}), \frac{1}{B}\sum_{j=1}^{B} I(t_j^* > \hat{t})\right). \tag{3}$$

Bootstrap Weight Distribution

- Consider the $f(\tilde{u}_{igt})v_g^*$ term in equation 2
- With the bootstrap techniques considered here $f(\tilde{u}_{igt}) = \tilde{u}_{igt}$
- However, v_g changes according to the bootstrap weight distribution
- One common distribution is the Mammen distribution

$$v_g = -\frac{\sqrt{5}-1}{2} \text{ w.p. } p = \frac{\sqrt{5}+1}{2\sqrt{5}}$$

$$\text{and } v_g = \frac{\sqrt{5}+1}{2} \text{ w.p. } 1-p$$

- The other common distribution, with preferable characteristics, is the Rademacher distribution

$$v_g = \pm 1 \text{ w.p. } 0.5$$

- **However,** both of these result in only 2^G possible bootstrap samples

Monte Carlo Simulation Design

The model is:

$$y_{ig} = \beta_1 + \beta_2 X_{ig} + \epsilon_{ig}, \quad i = 1, \ldots, N_g, \quad g = 1, \ldots, G. \tag{4}$$

Each simulation proceeds as follows:

1. Specify $\rho_x \in \{0, 0.2, \ldots, 0.8, 1\}$ and $\rho_\epsilon \in \{0, 0.1, \ldots, 0.8, 0.9\}$.
2. For each simulated sample, generate X_{ig} and ϵ_{ig} and use equation (4) to compute y_{ig}, with $\beta_1 = 0$ and $\beta_2 = 0$.
3. Estimate equation (4) by OLS.
4. Test the hypothesis that $\beta_2 = 0$, using either a t test based on the CRVE or a wild bootstrap test, as discussed above.
5. Repeat steps 2, 3, and 4 100,000 times, and estimate the rejection frequencies of each test at the .01, .05, and .10 levels.

Rejection Frequencies with 50 Equal-Sized Clusters

		ρ_x					
ρ_ϵ		**0**	**0.2**	**0.4**	**0.6**	**0.8**	**1**
0	**t(G-1)**	0.0512	0.0502	0.0512	0.0509	0.0572	0.0663
	wild	0.0510	0.0495	0.0505	0.0483	0.0505	0.0503
0.3	**t(G-1)**	0.0501	0.0518	0.0536	0.0568	0.0616	0.0667
	wild	0.0496	0.0508	0.0504	0.0504	0.0505	0.0503
0.5	**t(G-1)**	0.0506	0.0502	0.0543	0.0581	0.0634	0.0662
	wild	0.0497	0.0495	0.0506	0.0500	0.0501	0.0501
0.7	**t(G-1)**	0.0507	0.0521	0.0543	0.0590	0.0637	0.0676
	wild	0.0498	0.0502	0.0500	0.0500	0.0507	0.0515
0.9	**t(G-1)**	0.0503	0.0517	0.0545	0.0578	0.0641	0.0657
	wild	0.0498	0.0509	0.0498	0.0494	0.0509	0.0495

Notes: Rejection frequencies at the 5% level are based on 100,000 replications. There are 50 equal-sized clusters with 2000 observations. Wild bootstrap P values are based on 399 bootstraps using the Rademacher distribution.

Rejection Frequencies with 50 State-Sized Clusters

		ρ_x					
ρ_ϵ		**0**	**0.2**	**0.4**	**0.6**	**0.8**	**1**
0	**t(G-1)**	0.0583	0.0596	0.0600	0.0612	0.0684	0.0818
	wild	0.0489	0.0503	0.0506	0.0498	0.0515	0.0518
0.3	**t(G-1)**	0.0581	0.0639	0.0706	0.0815	0.0970	0.1051
	wild	0.0498	0.0512	0.0513	0.0519	0.0533	0.0518
0.5	**t(G-1)**	0.0586	0.0652	0.0746	0.0865	0.0975	0.1064
	wild	0.0506	0.0503	0.0516	0.0538	0.0518	0.0509
0.7	**t(G-1)**	0.0575	0.0666	0.0771	0.0871	0.0995	0.1086
	wild	0.0494	0.0502	0.0530	0.0522	0.0520	0.0520
0.9	**t(G-1)**	0.0570	0.0674	0.0769	0.0868	0.0983	0.1077
	wild	0.0519	0.0520	0.0527	0.0519	0.0515	0.0521

Notes: Rejection frequencies at the 5% level are based on 100,000 replications. There are 50 clusters proportional to US state populations with 2000 observations. Wild bootstrap P values are based on 399 bootstraps using the Rademacher distribution.

Set up for Percentage Treated Monte Carlo

- Many applications to clustered data involve treatment effects at the cluster level.
- We conduct another set of experiments in which the test regressor is a dummy variable that equals one for some proportion P of the clusters.
- The limitations of the CRVE when P is low were presented in Conley and Taber (2011)
- We report results for 50 clusters with 1000 observations, $\rho_\epsilon = 0.50$, and P that varies between 0.02 and 0.98 at intervals of 0.02.
- In "cluster indicator" experiments all observations in a cluster are "treated".
- In "DiD" experiments one half of observations in a cluster are "treated".
- The CRVE rejection frequencies are presented in figures 1, 3.
- The Wild bootstrap rejection frequencies are presented in figures 2, 4.

Figure : 1 - CRVE rejection frequencies and proportion treated (cluster indicators)

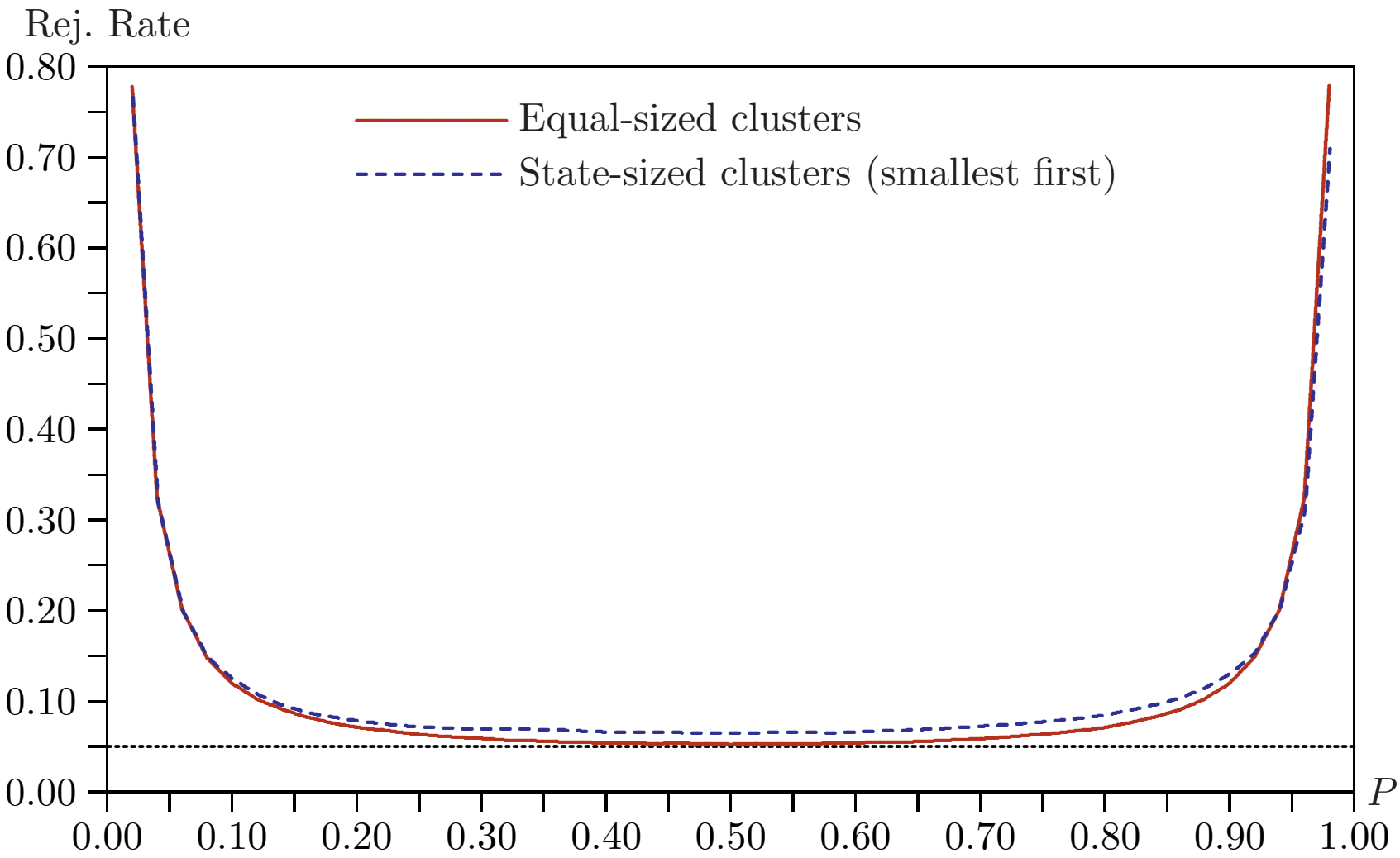


Figure : 2 - Wild bootstrap rejection frequencies and proportion treated (cluster indicators)

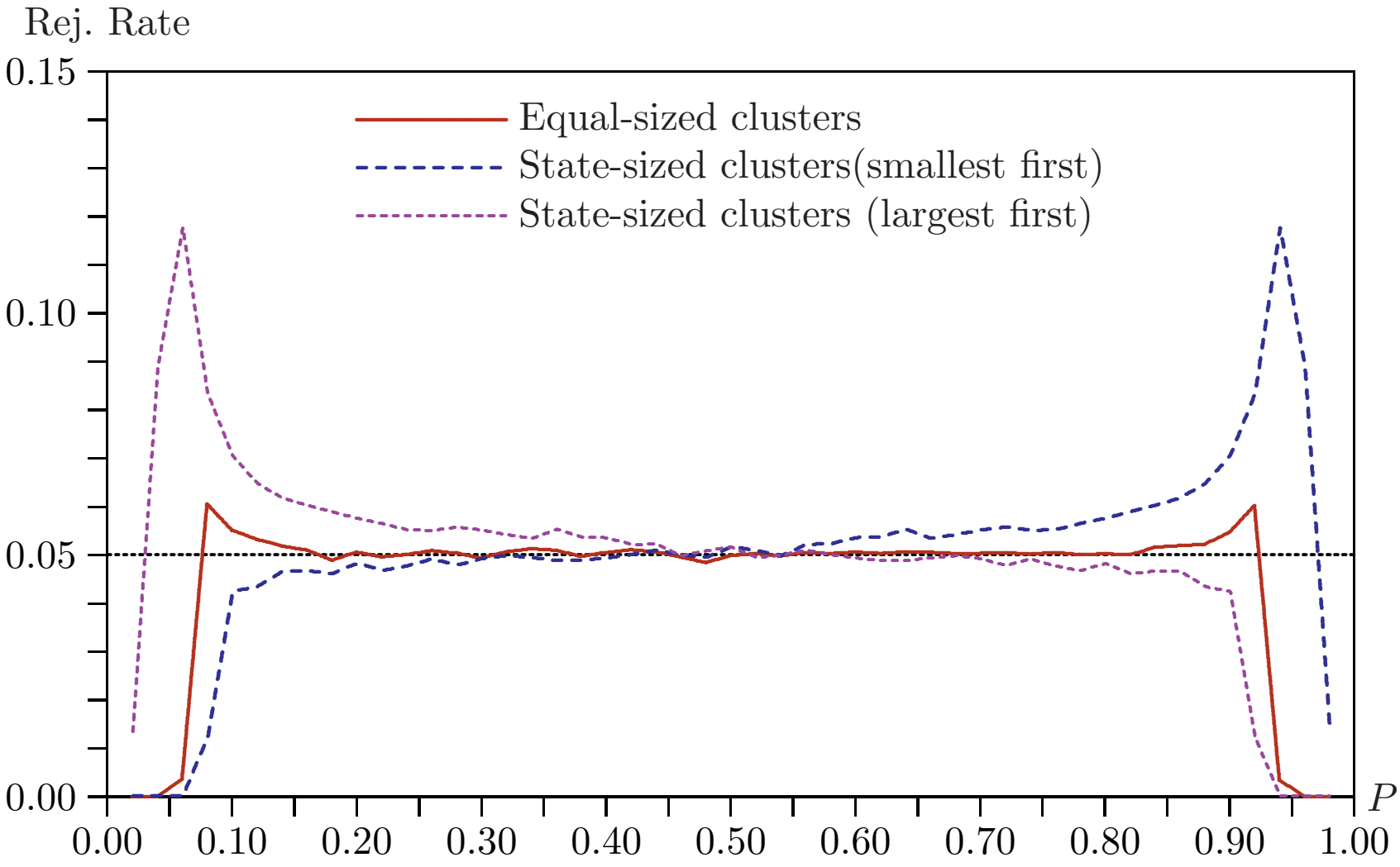


Figure : 3 - Rejection frequencies and proportion treated - DiD

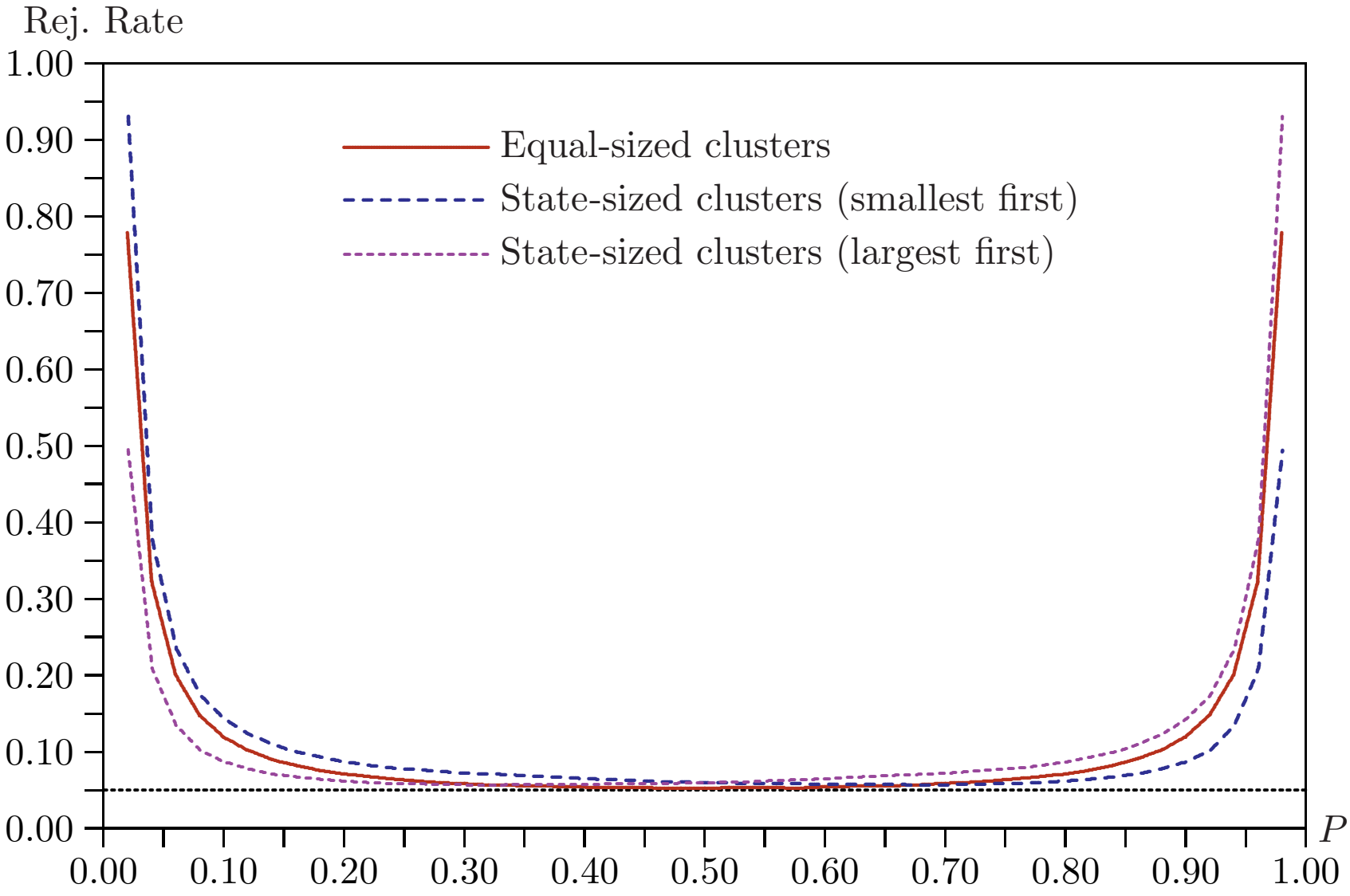


Figure : 4 - Wild bootstrap rejection frequencies DID

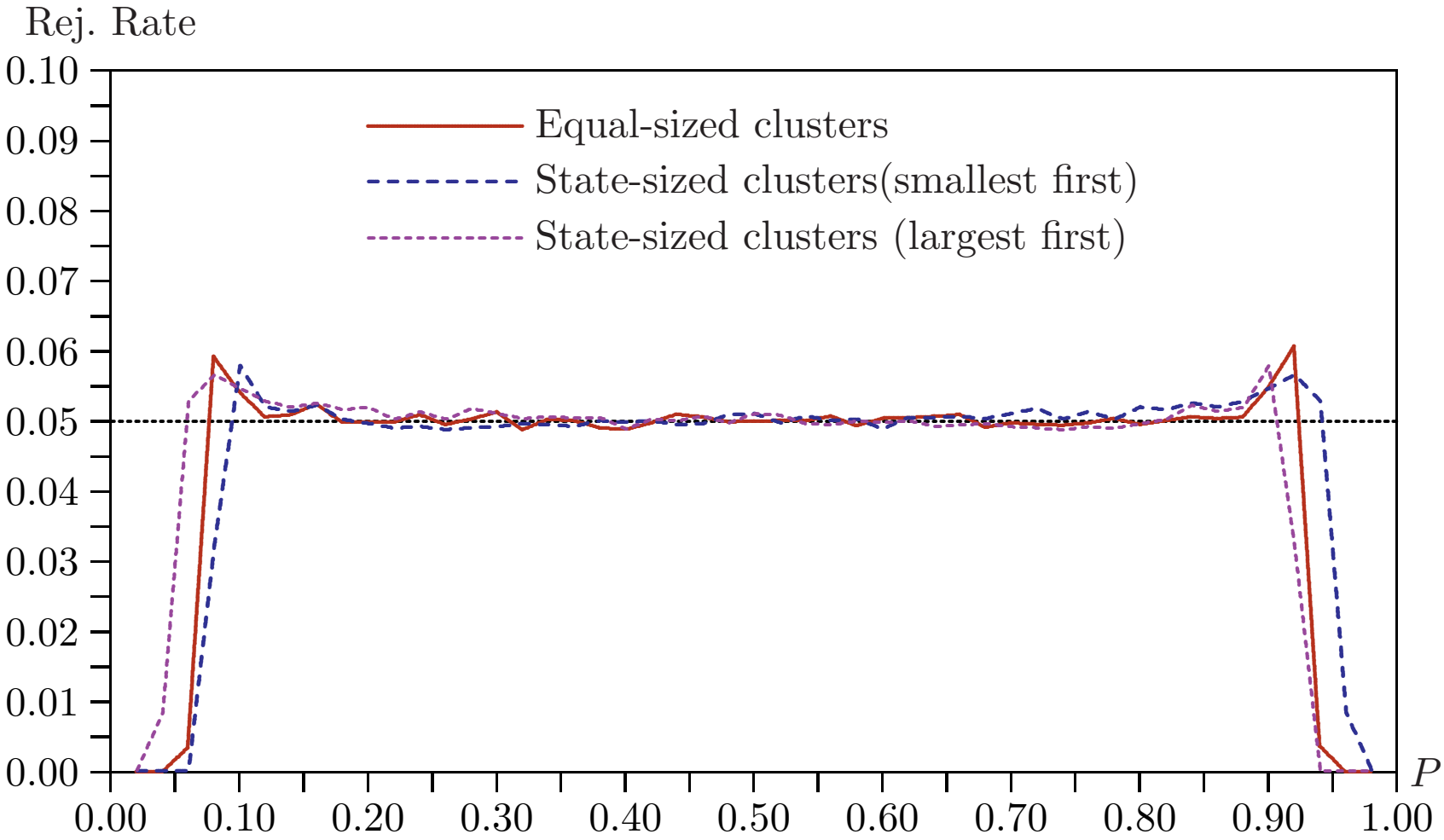
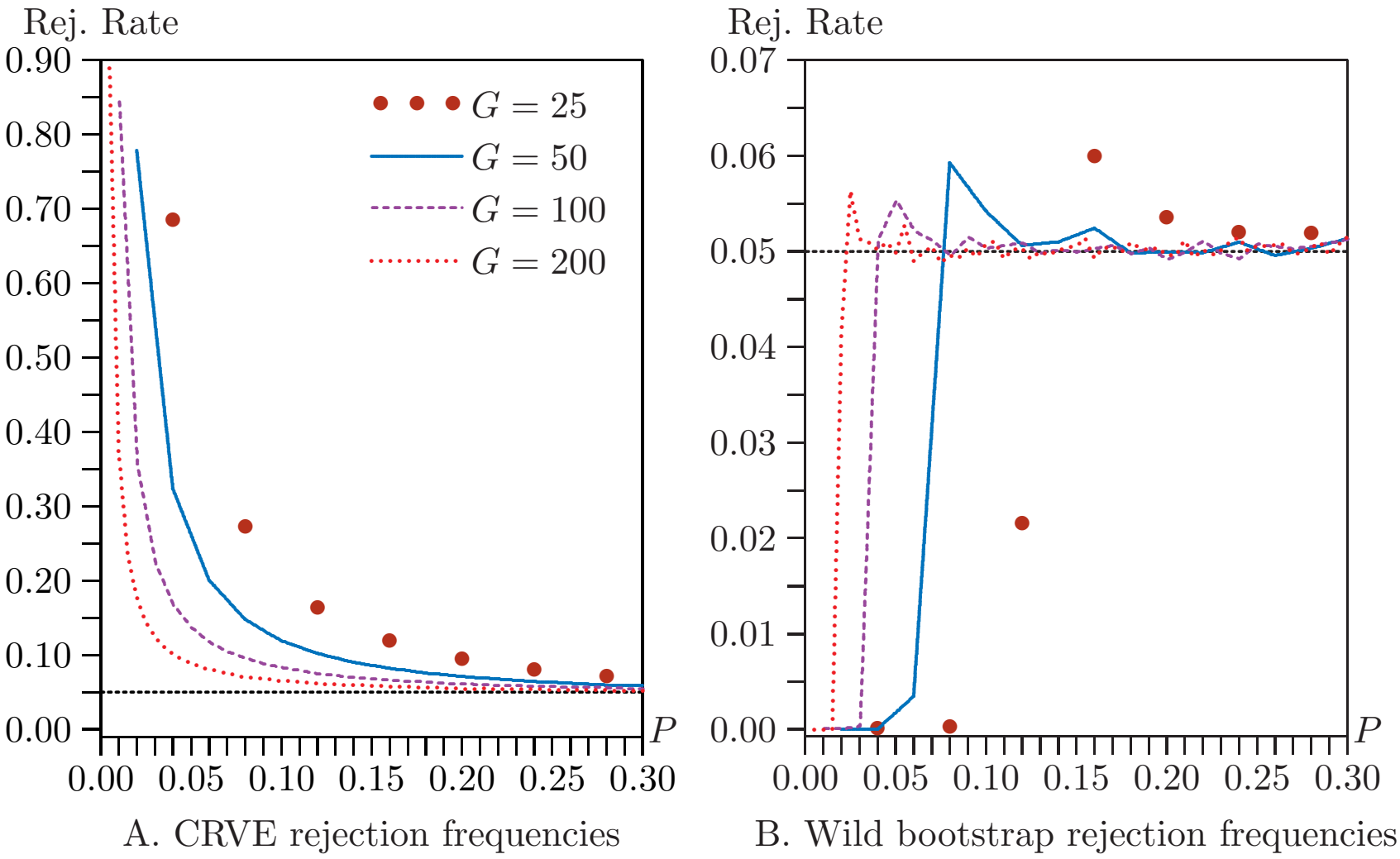


Figure : 5 - Rejection frequencies and proportion treated - equal sized clusters DiD



Placebo Law Design

- Replication of Bertrand, Duflo and Mullainathan (2004)
- Estimate DiD coefficients on fake laws for women's wages
- Data from US Current Population Survey, for women aged 25-50 from 1979 to 1999
- For each replication generate a fake treatment which starts in a random year between 1985 - 1995

The regression for the log of women's wages is

$$\begin{aligned}\ln(\text{wage}) =& \beta_1 + \beta_{treat}\text{TREAT} + \text{YEARS}\,\boldsymbol{\beta}_{years} + \text{STATES}\,\boldsymbol{\beta}_{states} \\ &+ \text{controls} + \epsilon,\end{aligned} \tag{5}$$

where YEARS and STATES are full sets of fixed effects, and the controls are a quadratic in age and a set of education dummy variables.

Rejection Frequencies of Placebo Law Monte Carlo Simulations Using Current Population Survey Data

		HCCME	t(G-1)	Wild
level 0.10	**Random 25**	0.706	0.182	0.143
level 0.10	**Random 10**	0.754	0.222	0.106
level 0.10	**Random 1**	0.712	0.804	0.000
		HCCME	**t(G-1)**	**Wild**
level 0.05	**Random 25**	0.652	0.118	0.059
level 0.05	**Random 10**	0.713	0.134	0.049
level 0.05	**Random 1**	0.640	0.762	0.000
		HCCME	**t(G-1)**	**Wild**
level 0.01	**Random 25**	0.560	0.023	0.011
level 0.01	**Random 10**	0.618	0.052	0.012
level 0.01	**Random 1**	0.498	0.709	0.000

Notes: Rejection frequencies based on 1000 replications.

Conclusions

- Even with many clusters, CRVE inference can be unreliable, especially when:
  - Clusters are of wildly different sizes
  - The proportion of clusters treated is either very large or very small
- The wild cluster bootstrap allows for reliable inference with variable cluster sizes
- The wild cluster bootstrap will underreject when the proportion treated is very large of very small

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