When Can We Trust Cluster-Robust Inference?

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How can we decide whether various forms of cluster-robust inference can be relied upon in any given case?

There are G clusters, indexed by g. The g^{th} cluster has N_g observations, so the sample size is $N = \sum_{g=1}^G N_g$. The model can be written as

$$y_g = X_g \beta + u_g, \quad g = 1, \dots, G, \tag{1}$$

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$$\hat{\boldsymbol{\beta}} = (\boldsymbol{X}^{\top} \boldsymbol{X})^{-1} \boldsymbol{X}^{\top} \boldsymbol{y} = \boldsymbol{\beta}_0 + (\boldsymbol{X}^{\top} \boldsymbol{X})^{-1} \boldsymbol{X}^{\top} \boldsymbol{u}.$$
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The OLS estimator of β is

$$\hat{\beta} = (X^{\top} X)^{-1} X^{\top} y = \beta_0 + (X^{\top} X)^{-1} X^{\top} u.$$
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This assumes that the data are actually generated by (1) with $\beta = \beta_0$.

$$\hat{\beta} - \beta_0 = (X^{\top}X)^{-1} \sum_{g=1}^{G} X_g^{\top} u_g = \left(\sum_{g=1}^{G} X_g^{\top} X_g\right)^{-1} \sum_{g=1}^{G} s_g.$$
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Key assumptions:

$$E(s_g s_g^\top) = \Sigma_g$$
 and $E(s_g s_{g'}^\top) = \mathbf{0}$, $g, g' = 1, \dots, G$, $g' \neq g$, (4)

where Σ_g is the symmetric, positive semidefinite variance matrix of the scores for the g^{th} cluster. There are two assumptions here:

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- Within each cluster, there may be very general patterns of heteroskedasticity and/or intra-cluster correlation.
- The scores for every cluster are uncorrelated with the scores for every other cluster. This assumption is crucial!

$$\operatorname{Var}(\hat{\boldsymbol{\beta}}) = (\boldsymbol{X}^{\top} \boldsymbol{X})^{-1} \Big(\sum_{\sigma=1}^{G} \boldsymbol{\Sigma}_{g} \Big) (\boldsymbol{X}^{\top} \boldsymbol{X})^{-1}.$$
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Unfortunately, replacing the Σ_g in (6) by consistent estimates $\hat{\Sigma}_g$ may lead to seriously unreliable inferences.

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The simplest way is to replace Σ_g by $\hat{\mathbf{s}}_g\hat{\mathbf{s}}_g^{\top}$, where $\hat{\mathbf{s}}_g = X_g^{\top}\hat{\mathbf{u}}_g$ is the empirical score vector for the g^{th} cluster. Multiplying by a d-o-f correction, we obtain

CV₁:
$$\hat{V}_1(\hat{\beta}) = \frac{G(N-1)}{(G-1)(N-k)} (X^{\top}X)^{-1} \Big(\sum_{g=1}^{G} \hat{s}_g \hat{s}_g^{\top} \Big) (X^{\top}X)^{-1}.$$
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In general, $\hat{u} = M_X u$, where $M_X = \mathbf{I} - X(X^\top X)^{-1} X^\top$ projects u off X. This projection means that \hat{u} and u can have very different properties.

Depending on the X matrix and the u vector, the \hat{s}_g can sometimes differ greatly from the s_g , causing the middle factor in (7) to provide a poor estimate of $\sum_{g=1}^{G} \Sigma_g$. Thus CV₁ can perform very badly.

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• For HC₂, the \hat{u}_i are replaced by $\hat{u}_i/M_{ii}^{1/2}$, where M_{ii} is the i^{th} diagonal element of M_X . CV₂ is analogous; it involves the inverse symmetric square roots of the M_{gg} (diagonal blocks).

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- Better computational procedures (unless all the N_g are very small) are discussed in MacKinnon, Nielsen, and Webb (JAE 2023b).
- CV₃ is really a **cluster-jackknife** estimator.

$$\hat{\boldsymbol{\beta}}^{(g)} = (\boldsymbol{X}^{\top} \boldsymbol{X} - \boldsymbol{X}_{g}^{\top} \boldsymbol{X}_{g})^{-1} (\boldsymbol{X}^{\top} \boldsymbol{y} - \boldsymbol{X}_{g}^{\top} \boldsymbol{y}_{g}), \quad g = 1, \dots, G.$$
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To obtain the $\hat{\pmb{\beta}}^{(g)}$ efficiently, start by calculating

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The main cost, after $\hat{\beta}$ and its ingredients have been computed, is calculating the (generalized) inverse of a $k \times k$ matrix for each $\hat{\beta}^{(g)}$.

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The simplest version of the cluster-jackknife variance matrix is

CV₃:
$$\hat{V}_3(\hat{\beta}) = \frac{G-1}{G} \sum_{g=1}^{G} (\hat{\beta}^{(g)} - \hat{\beta}) (\hat{\beta}^{(g)} - \hat{\beta})^{\top}$$
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This matrix is numerically identical to the original CV₃ matrix. However, it is usually very much cheaper to compute.

What about CV_2 standard errors?

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- In contrast, the diagonal elements of CV₃ and HC₃ are generally biased upwards in the special case of i.i.d. disturbances.
- However, because the numerators of cluster-robust *t*-statistics are not independent of the denominators, using the square root of an unbiased variance estimator in the denominator does *not* guarantee that inference will be reliable.
- Simulations suggest that CV_3 usually outperforms CV_2 , so I won't say any more about the latter.



Suppose we wish to test the hypothesis that $\beta_j = \beta_{0j}$ or construct a confidence interval for β_j . We start with the *t*-statistic

$$t_j^m = \frac{\hat{\beta}_j - \beta_{0j}}{\text{se}_m(\hat{\beta}_j)}, \quad m = 1, 2, 3,$$
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where $se_m(\hat{\beta}_j)$ is the square root of the j^{th} diagonal element of CV_m .

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where $se_m(\hat{\beta}_j)$ is the square root of the j^{th} diagonal element of CV_m .

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The asymptotic theory of Bester, Conley, and Hansen (2011) holds G fixed, with the N_g increasing and intra-cluster correlation diminishing. For CV_1 , (11) is then asymptotically distributed as t(G-1).

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These two approaches are combined in Hansen's two papers. His Stata package jregress rescales each CV₃ standard error differently and computes d_i , often much less than G-1, for each coefficient.



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This is testing the hypothesis that $\beta_j = \hat{\beta}_j$, not that $\beta_j = \beta_{0j}$.



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vce(bootstrap) with cluster(cvar) calculates PCB standard errors, but not P values like (14) or intervals like (15). It is very expensive, and it can be unreliable if many bootstrap samples are omitted.



The wild cluster bootstrap (WCB) often works much better than the PCB. It was proposed in Cameron, Gelbach, and Miller (2008), proved to be valid in Djogbenou, MacKinnon, and Nielsen (2019), and improved in MacKinnon, Nielsen, and Webb (JAE 2023b).

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Consider the unrestricted empirical score vectors

$$\hat{\mathbf{s}}_{g} = \mathbf{X}_{g}^{\top} \hat{\mathbf{u}}_{g} = \mathbf{X}_{g}^{\top} \mathbf{y}_{g} - \mathbf{X}_{g}^{\top} \mathbf{X}_{g} \hat{\boldsymbol{\beta}}, \quad g = 1, \dots, G.$$
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We then obtain bootstrap estimates of the vector $\delta \equiv \beta - \hat{\beta}$:

$$\hat{\delta}^{*b} = (X^{\top}X)^{-1} \sum_{g=1}^{G} s_g^{*b}, \quad s_g^{*b} = v_g^{*b} \hat{s}_g.$$
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Imposing restrictions on the bootstrap samples makes bootstrapping more complicated, but it often improves performance.

$$\tilde{\mathbf{s}}_{g} = \mathbf{X}_{g}^{\top} \tilde{\mathbf{u}}_{g} = \mathbf{X}_{g}^{\top} \mathbf{y}_{g} - \mathbf{X}_{g}^{\top} \mathbf{X}_{g} \tilde{\boldsymbol{\beta}}, \quad g = 1, \dots, G.$$
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Happily, boottest does this incredibly quickly. See Roodman, MacKinnon, Nielsen, and Webb (2019) and MacKinnon (2023).

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Recall that $\hat{u} = M_X u$. We can partly undo the ill effects of this by using

$$\hat{\mathbf{s}}_{g} = \mathbf{X}_{g}^{\top} \mathbf{M}_{gg}^{-1} \hat{\mathbf{u}}_{g}, \tag{21}$$

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Thus computing the \dot{s}_g is almost costless once the jackknife estimates, which are needed for CV₃, have been computed.

A similar procedure can be used to compute restricted score vectors \dot{s} that "correct" for the distortions caused by estimating the restricted model. The \dot{s} are used in the bootstrap DGP for the WCR-S bootstrap, which otherwise is computed just like the WCR-C bootstrap.

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WCR[U/R]-[C/S] are implemented in current versions of boottest. It computes both bootstrap confidence intervals and bootstrap P values, including for tests of several linear restrictions. In most cases, this is inexpensive, even when B is chosen to be a large number like 99,999.

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We need $\frac{1}{G}\sum_{g=1}^{G} \hat{s}_g \hat{s}_g^{\top}$ in (7), and its analog for the other CRVEs, to converge to the same matrix as $\frac{1}{G}\sum_{g=1}^{G} s_g s_g^{\top}$.



The sample size N also matters, but not much once N/G is moderately large. We cannot simply hold G fixed and let $N \to \infty$.

Any sort of heterogeneity in the $X_g^{\top}X_g$ and the $X_g^{\top}y_g$ matters.

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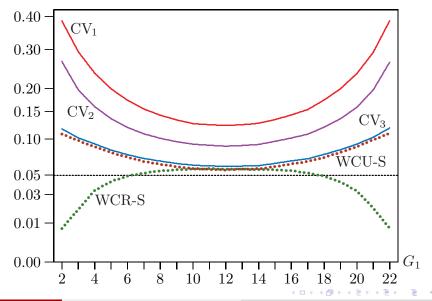
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Otherwise, cluster-robust standard errors are too small, pairs cluster and WCU bootstraps over-reject, and WCR bootstraps under-reject. See MacKinnon and Webb (JAE 2017, EJ 2018).

Figure 1. Rejection frequencies as functions of G_1 for G=24





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- Perhaps there is a fine level (say, schools) and a coarser level (say school districts).
- When there are many fine clusters, inference is likely to be reliable if fine clustering is appropriate.
- But it will be invalid if coarse clustering is appropriate.

MacKinnon, Nielsen, and Webb (JoE, 2023d) proposes both asymptotic and wild bootstrap tests based on elements of the score vectors after regressors that are not of primary interest have been partialed out. These are called **score-variance tests**.

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- \bullet Even without testing, we should cluster at the coarse level if se_c , the coarse standard error, is noticeably larger than se_f , the fine one.
- ullet However, we should probably not cluster at the coarse level if se_c is smaller, even "significantly" smaller, than se_f .

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Anything that causes inference to be unreliable for one-way clustering also causes it to be unreliable for two-way clustering.

For two-way clustering, the filling in the sandwich for the true variance matrix is

$$\Sigma = \sum_{g=1}^{G} \Sigma_g + \sum_{h=1}^{H} \Sigma_h - \sum_{g=1}^{G} \sum_{h=1}^{H} \Sigma_{gh}.$$
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MacKinnon, Nielsen, and Webb (2024) and Davezies et al. (2025) suggested computing both one-way standard errors, along with two-way ones (if defined) and using whichever is largest.

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Sample 2: 19 clusters each with $N_g = 500$, 1 cluster with $N_{20} = 10,000$. Thus $N_{20} > \sum_{g=1}^{19} N_g$. Inference is likely to be dreadful!

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Since the L_{gj} sum to unity, their average is 1/G. Thus, if cluster h has $L_{hi} >> 1/G$, it has high partial leverage for the j^{th} coefficient.

When *G* is not small, graph them or report summary measures of how much they vary across clusters. One such measure is the scaled variance

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It also calculates both CV_1 and CV_3 variance matrices, along with the associated P values and confidence intervals.

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This typically harms performance of every method, expecially all variants of the wild cluster bootstrap. イロティボチィミティミテー 第

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- But if the regressors include cluster fixed effects, they completely explain the v_g , so there is no within-cluster correlation.
- There are many ways to generate the u_{gi} for models with cluster fixed effects, and it is not clear how much it matters.

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Can we model heteroskedasticity related to treatment?





If the binary variable y_{gi} is the response for observation i in cluster g,

$$\Pr(y_{gi} = 1 \mid X_{gi}) = \Lambda(X_{gi}\beta), \quad g = 1, \dots, G, \quad i = 1, \dots, N_g.$$
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The pseudo-loglikelihood function for (30) is

$$\ell(\boldsymbol{y}, \boldsymbol{\beta}) = \sum_{g=1}^{G} \sum_{i=1}^{N_g} (y_{gi} \log \Lambda(\boldsymbol{X}_{gi} \boldsymbol{\beta}) + (1 - y_{gi}) \log \Lambda(-\boldsymbol{X}_{gi} \boldsymbol{\beta})).$$
 (32)

There are other ways to write this.

$$s_g(\beta) = \sum_{i=1}^{N_g} s_{gi}(\beta) = \sum_{i=1}^{N_g} (y_{gi} - \Lambda(X_{gi}\beta)) X_{gi}.$$
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$$\hat{\mathbf{V}}(\hat{\boldsymbol{\beta}}) = (\mathbf{X}^{\top} \mathbf{Y}(\hat{\boldsymbol{\beta}}) \mathbf{X})^{-1}, \tag{35}$$

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where $\mathbf{Y}(\boldsymbol{\beta})$ is an $N \times N$ diagonal matrix with typical diagonal element

$$Y_i(\boldsymbol{\beta}) = \Lambda(X_i \boldsymbol{\beta}) \Lambda(-X_i \boldsymbol{\beta}). \tag{36}$$

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The usual CRVE is

$$CV_{1\mathcal{I}}: \quad \hat{\mathbf{V}}_{1\mathcal{I}} = \frac{G}{G-1} \frac{N-1}{N-k} (\mathbf{X}^{\top} \hat{\mathbf{Y}} \mathbf{X})^{-1} \left(\sum_{g=1}^{G} \hat{\mathbf{s}}_{g} \hat{\mathbf{s}}_{g}^{\top} \right) (\mathbf{X}^{\top} \hat{\mathbf{Y}} \mathbf{X})^{-1}. \quad (37)$$

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If $\hat{\beta}^{(g)}$ is the vector of delete-one estimates when cluster g is deleted, we obtain the cluster-jackknife CRVE

CV₃:
$$\hat{V}_3(\hat{\beta}) = \frac{G-1}{G} \sum_{g=1}^{G} (\hat{\beta}^{(g)} - \hat{\beta}) (\hat{\beta}^{(g)} - \hat{\beta})^{\top}.$$
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Computing CV₃ requires G + 1 nonlinear estimations.



For the logit model, the contributions to the information matrix are

$$J_{g}(\boldsymbol{\beta}) = \sum_{i=1}^{N_g} \Lambda_{gi}(\boldsymbol{\beta}) \Lambda_{gi}(-\boldsymbol{\beta}) \boldsymbol{X}_{gi}(\boldsymbol{\beta})^{\top} \boldsymbol{X}_{gi}(\boldsymbol{\beta}), \quad g = 1, \dots, G.$$
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The estimates from linearizing the model around β are then

$$\boldsymbol{b}(\boldsymbol{\beta}) = \left(\sum_{g=1}^{G} J_{g}(\boldsymbol{\beta})\right)^{-1} \sum_{g=1}^{G} s_{g}(\boldsymbol{\beta}) = J(\boldsymbol{\beta})^{-1} s(\boldsymbol{\beta}). \tag{41}$$

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After we estimate the logit model, we form the cluster-level vectors $\hat{\mathbf{s}}_g = \mathbf{s}_g(\hat{\boldsymbol{\beta}})$ and matrices $\hat{\boldsymbol{J}}_g = \boldsymbol{J}_g(\hat{\boldsymbol{\beta}})$ for $g = 1, \ldots, G$.

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We can use these approximations to compute cluster-jackknife variance matrices. The one comparable to (10) is

$$CV_{3L}: \quad \hat{\mathbf{V}}_{3L}(\hat{\boldsymbol{\beta}}) = \frac{G-1}{G} \sum_{g=1}^{G} \hat{\boldsymbol{b}}^{(g)} \hat{\boldsymbol{b}}^{(g)\top}.$$
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Once the logit model has been estimated (possibly subject to the restrictions to be tested) and linearized, computations are identical to those for the WCR/WCU bootstraps for linear regression models.

$$\ddot{\mathbf{s}}_{g}^{*b} = v_{g}^{*b} \ddot{\mathbf{s}}_{g}, \quad g = 1, \dots, G.$$
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Then the bootstrap model is estimated by OLS, yielding

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We can also transform the empirical scores, as proposed in MacKinnon, Nielsen, and Webb (JAE 2023b), to undo some of the deleterious effects of ML estimation.

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We can also transform the empirical scores, as proposed in MacKinnon, Nielsen, and Webb (JAE 2023b), to undo some of the deleterious effects of ML estimation.

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The logitjack package computes CV_3 , CV_{3L} , all four bootstrap P values, and confidence intervals based on WCLU-C and WCLU-S.



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Dependent variable is 1 if a student took another economics class. Only 21.7% did.

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- $G^*(0) = 8.490$ and $G^*(1) = 5.978$.



Table 1: Effects of Treatment on Taking Another Economics Course

Method	Coef.	Std. error	t-stat.	P value	Lower	Upper
LPM HC_1	0.1389	0.0673	2.0632	0.0395	0.0067	0.2710
LPM HC ₃	0.1389	0.0680	2.0431	0.0415	0.0054	0.2723
LPM CV_1	0.1389	0.0518	2.6791	0.0214	0.0248	0.2529
LPM CV ₃	0.1389	0.0646	2.1505	0.0546	-0.0033	0.2810
jregress	0.1389	0.0674	2.0589	0.0504	-0.0004	0.2781
Logit (default)	0.8739	0.4071	2.1467	0.0318	0.0760	1.6717
Logit CV ₁ Nml.	0.8739	0.3087	2.8306	0.0046	0.2688	1.4790
Logit $CV_1 t(11)$	0.8739	0.3112	2.8079	0.0170	0.1889	1.5589
Logit CV ₃	0.8739	0.3905	2.2380	0.0469	0.0144	1.7333
Logit CV _{3L}	0.8739	0.3875	2.2554	0.0455	0.0211	1.7266

Table 2: Effects of Treatment Using Bootstrap Methods

Method	Coef.	t-stat.	P value	Lower	Upper
LPM Pairs (stud-boot)	0.1389	2.6791	0.1019	-0.0087	0.3796
LPM Pairs (boot s.e.)	0.1389	2.3108	0.0412	0.0066	0.2711
LPM WCU-C	0.1389	2.6791	0.0332	0.0103	0.2674
LPM WCU-S	0.1389	2.6791	0.0443	0.0034	0.2743
LPM WCR-C	0.1389	2.6791	0.0345	0.0133	0.2617
LPM WCR-S	0.1389	2.6791	0.0404	0.0079	0.2573
Logit WCLU-C (boot s.e.)	0.8739	2.9575	0.0114	0.2235	1.5242
Logit WCLU-S (boot s.e.)	0.8739	2.1602	0.0212	-0.0165	1.7642
Logit WCLR-C	0.8739	2.8079	0.0294		
Logit WCLR-S	0.8739	2.8079	0.0346		

B = 999,999; Webb (6-point) weights.

LPM results from boottest; Logit results from logitjack.

Some reported *t*-statistics use bootstrap standard errors, but *P* values are for actual ones.

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Of these, 33, 38, 38, and 21 are treated.

Figure 2. Monte Carlo rejection frequencies as functions of ρ

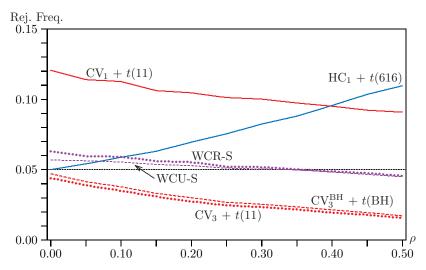


Table 3: *P* Values and Rejection Frequencies

Method	P value	M.C. ($\rho = 0$)	M.C. ($\rho = 0.25$)	Placebo Reg.
$HC_1 + t(616)$	0.0395	0.0500	0.0754	0.0528
$CV_1 + t(11)$	0.0214	0.1206	0.1012	0.1866
$CV_3 + t(11)$	0.0546	0.0437	0.0243	0.0933
$CV_3^{BH} + t(BH)$	0.0504	0.0469	0.0266	0.0457
WCU-S	0.0443	0.0567	0.0509	0.0773
WCR-S	0.0404	0.0627	0.0517	0.0613
Pairs Cluster	0.1019	0.0241	0.0158	0.0245
Logit (default)	0.0318	0.0507	0.0769	0.0465
Logit $CV_1 t(11)$	0.0170	0.0853	0.0745	0.1492
Logit $CV_{3L} t(11)$	0.0455	0.0421	0.0252	0.0895
Logit WCLR-S	0.0346	0.0610	0.0538	0.0558

Rejection frequencies are based on 100,000 replications.

Actual bootstrap tests use B = 999,999; simulations use B = 999.



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- Targeted Monte Carlo experiments and placebo regressions can tell us which *P* values or confidence intervals to believe.



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