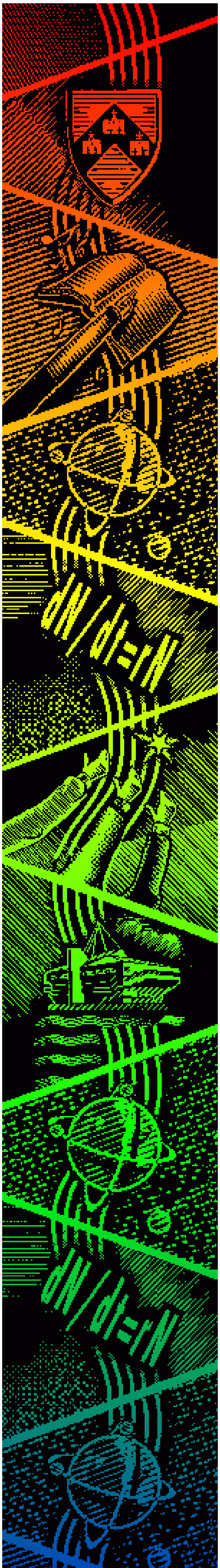

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By

Leslie Godfrey, University of York; Takashi Yamagata, University of York

Department of Economics and Related Studies
University of York
Heslington
York, YO10 5DD

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Leslie Godfrey and Takashi Yamagata*

Abstract

A wild bootstrap test of the null hypothesis that the errors of a panel data model are not correlated over cross-section units is proposed. The new test is more generally applicable than others that use the restrictive assumptions of normality and homoskedasticity. Monte Carlo results indicate that the new test is reliable.

Keywords: Cross-section correlation; Wild bootstrap; Robust test

JEL classification: C12; C52

* Corresponding author. Tel: +44-1904-43-3758; fax: +44-1904-43-3759
E-mail address: ty509@york.ac.uk (Takashi Yamagata)

Department of Economics and Related Studies,
University of York,
Heslington,
York YO10 5DD,
UK.

1 Introduction

As discussed in Moscone and Tosetti (2009), there is considerable interest in the problem of checking for cross-section dependence in panel data. Following Pesaran et al. (2008), the panel data model is written as

$$y_{it} = \beta_i' x_{it} + u_{it}, \text{for } i = 1, 2, ..., N \text{ and } t = 1, 2, ..., T, \tag{1}$$

in which: i and t index the cross-section and time-series dimensions, respectively; x_{it} is a k-dimensional vector with its first element always equal to unity and all other elements being observations on strictly exogenous regressors; and the errors u_{it} are serially independent over time periods with common zero mean.

The null hypothesis to be tested is $H_0 : \rho_{ij} = Corr(u_{it}, u_{jt}) = 0$, for all t and $i \neq j$, where $Corr(.,.)$ denotes a population correlation coefficient. If all the errors are assumed to have normal distributions, H_0 implies cross-section independence. The assumption of normality is used in Breusch and Pagan (1980) to obtain a Lagrange multiplier (LM) test of H_0. Under normality and H_0, maximum likelihood estimation of parameters reduces to applying ordinary least squares (OLS) estimation to

$$y_{it} = \beta_i' x_{it} + u_{it}, \ \ t = 1, 2, ..., T, \tag{2}$$

for each cross-section unit. Let a typical OLS residual be denoted by $\hat{u}_{it}$. The OLS residuals can be used to estimate ρ_{ij} by

$$\hat{\rho}_{ij} = \frac{\sum \hat{u}_{it}\hat{u}_{jt}}{\sqrt{[\sum \hat{u}_{it}^2][\sum \hat{u}_{jt}^2]}}, i = 1, 2, ..., (N-1) \text{ and } j > i.$$

Under the classical assumptions in Breusch and Pagan (1980), i.e., with u_{it} being normally distributed, homoskedastic over t and serially independent, the LM statistic is

$$BP = T \sum_{i=1}^{N-1} \sum_{j=i+1}^{N} \hat{\rho}_{ij}^2. \tag{3}$$

When H_0 is true and $T \to \infty$, with N fixed, BP is asymptotically distributed as χ^2_ν with $\nu = N(N-1)/2$ degrees of freedom. Large values of the test statistic are interpreted as strong evidence against the null hypothesis. This test is now widely used and is discussed in standard textbooks.

However, as pointed out in Pesaran et al. (2008), the Breusch-Pagan test based upon asymptotic critical values from the χ^2_ν distribution can suffer from serious size distortion, especially when N/T is not small. Pesaran et al. make use of analytical adjustments in order to correct the bias of the LM statistic. These analytical adjustments are derived under the strong assumptions that the errors of (2) are normally distributed and homoskedastic for each cross-section unit. As explained by Beran, an alternative to the derivation of analytical adjustments based upon restrictive assumptions is to employ bootstrap methods that have the great practical advantage of allowing "direct nonanalytical implementation"; see Beran (1988).

The purpose of this paper is to propose bootstrap methods for testing H_0 that are based upon much weaker assumptions than those used in Pesaran et al. (2008). Consequently the procedures of this paper are more widely applicable. First, for the test of this paper, the strong assumption of normality can be replaced simply by the requirement that each error have a finite fourth-order moment. Second, the assumption that the errors of (2) are homoskedastic is dropped and heteroskedasticity is permitted with variance terms $\sigma_{it}^2 = E(u_{it}^2)$ varying with t and only having to be finite and positive, i.e.,

$$0 < \min_t(\sigma_{it}^2) \leq \max_t(\sigma_{it}^2) < \infty, \text{ for each } i,$$

which covers both homoskedasticity and unspecified forms of heteroskedasticity. Since heteroskedasticity is allowed, a wild bootstrap is adopted, with the external distribution being as recommended in Davidson and Flachaire (2008). Thus the only classical assumption about the errors that is not relaxed is serial independence.

The plan of the paper is as follows. The bootstrap test is described in Section 2. Monte Carlo evidence is reported in Section 3. This evidence indicates that the wild bootstrap test works well. Section 4 contains some concluding remarks.

2 The wild bootstrap test

The wild bootstrap data process that corresponds to (1) can be written as

$$y_{it}^* = \beta_i^{*\prime} x_{it} + u_{it}^*, \text{for } i = 1, 2, ..., N \text{ and } t = 1, 2, ..., T, \tag{4}$$

in which β_i^* is specified by the user and $u_{it}^* = \hat{u}_{it}\epsilon_{it}$, where the variates ϵ_{it} are independent drawings from an external distribution with zero mean and variance equal to unity. While $\beta_i^* = \hat{\beta}_i$ is an obvious choice, it is easy to show that $\beta_i^* = 0$ yields exactly the same residuals after OLS estimation of

$$y_{it}^* = \beta_i^{*\prime} x_{it} + u_{it}^*, \ t = 1, 2, ..., T. \tag{5}$$

Hence $\beta_i^* = \hat{\beta}_i$ and $\beta_i^* = 0$ produce the same value of the Breusch-Pagan statistic that is the bootstrap sample counterpart of BP in (3). It is, therefore, convenient to generate bootstrap data using $y_{it}^* = u_{it}^* = \hat{u}_{it}\epsilon_{it}$ and, in view of the results in Davidson and Flachaire (2008), the external distribution is defined by $\Pr(\epsilon_{it} = 1) = \Pr(\epsilon_{it} = -1) = 0.5$.

The test is implemented as follows.

Step 1 Use the actual data to estimate (2) for $i = 1, 2, ..., N$ to obtain the OLS residuals $\{\hat{u}_{it}; i = 1, 2, ..., N; t = 1, 2, ..., T\}$ and the statistic BP of (3).

Step 2 (which is repeated B times) Use the OLS residuals from Step 1 with the wild bootstrap data process described above to generate artificial data $\{y_{it}^* = \hat{u}_{it}\epsilon_{it}; i = 1, 2, ..., N; t = 1, 2, ..., T\}$. Next estimate (5) by OLS for $i = 1, 2, ..., N$ and calculate the implied value of the bootstrap counterpart of BP in (3). Let the bootstrap test statistic be denoted by BP^*.

Step 3 Calculate the proportion of bootstrap test statistics from the B repetitions of Step 2 that are at least as large as the actual value of BP. Let this proportion be denoted by $\tilde{p}$ and the desired significance level be denoted by α. The asymptotically valid rejection rule is that H_0 is rejected if $\tilde{p} \leq \alpha$.

Standard regularity conditions are required to justify the bootstrap approach above; see, e.g., Mammen (1993). It is assumed here that, for each i, $T^{1/2}(\hat{\beta}_i - \beta_i)$ is asymptotically normally distributed with zero mean vector and finite positive-definite covariance matrix as $T \to \infty$. It is not necessary to regard N as fixed. The analysis in Mammen (1993) suggests that it is only necessary to restrict the rate at which N grows, so that $N^{3/2}/T \to 0$ as $T \to \infty$.

3 Monte Carlo experiments

The data generating process is specified by

$$y_{it} = \sum\nolimits_{\ell=1}^{3} \beta_{\ell i} x_{\ell it} + u_{it},\ i = 1, 2, ..., N \text{ and } t = 1, 2, ..., T, \tag{6}$$

where, without loss of generality, $\beta_{\ell i} = 0$ for all ℓ and i. The six values of (N, T) used are obtained by taking all combinations of $N = 25, 50$ and $T = 25, 50, 100$. The regression model (6) has an intercept with $x_{1it} = 1$ for all i and t. The two non-constant regressors, denoted by x_{2it} and x_{3it}, are generated for $(N = 25, T = 25)$ as independent random draws from the standard lognormal distribution. This block of regressor values is then reused as necessary to build up data for the other combinations (N, T). Clearly the values of (N, T) include cases in which T is not large and N/T is not small; so that the experiments provide a stringent check of the usefulness of the wild bootstrap method.

The error term in (6) is written as

$$u_{it} = \sigma_{it}\varepsilon_{it},\ i = 1, 2, ..., N \text{ and } t = 1, 2, ..., T. \tag{7}$$

Four models for σ_{it} are considered. First, there is homoskedasticity under scheme VAR1, with $\sigma_{it} = 1$ for all t. Second, a one-break-in-volatility model, henceforth scheme VAR2, is employed with $\sigma_{it} = 1$ for $t = 1, 2, ..., m = \lfloor T/2 \rfloor$ and $\sigma_{it} = 1.2$ for $t = m, m+1, ..., T$, where $\lfloor A \rfloor$ is the largest integer part of A. Third, scheme VAR3 is a trending volatility model, with $\sigma_{it} = \sigma_0 - (\sigma_1 - \sigma_0)\left(\frac{t-1}{T-1}\right)$; see "Model 2" in Cavaliere and Taylor (2008), where $\sigma_0 = 1$ and $\sigma_1 = 1.2$. Fourth, there is conditional heteroskedasticity under scheme VAR4, with $\sigma_{it} = \sqrt{\exp\{cx_{2it}\}}$, $t = 1, ..., T$; this sort of skedastic function is discussed in Lima et al.

(2010). The value of c in VAR4 is chosen to be 0.5; so that $\max(\sigma_{it}^2)/\min(\sigma_{it}^2)$, which is a well-known measure of the strength of heteroskedasticity, is 22.29.

The term ε_{it} in (7) is generated as

$$\varepsilon_{it} = \sqrt{1-\rho^2}\xi_{it} + \rho\zeta_t$$

where $\xi_{it} \sim iid(0,1)$ and $\zeta_t \sim iid(0,1)$, which are independent of each other. For estimating significance levels, the value of ρ is set to zero. Power is investigated using $\rho = 0.2$. Three distributions are used to obtain the *iid* standardized errors for ξ_{it} and ζ_t: the standard normal distribution; the t-distribution with five degrees of freedom (t_5); and the chi-square distribution with two degrees of freedom (χ_2^2).

Samples are simulated for all combinations of $N = 25, 50$ and $T = 25, 50, 100$. Rejection frequencies are based upon 2000 replications and 400 wild bootstrap samples are used. All tests are implemented with a nominal significance level of 5 per cent.

Additional estimates are obtained with serially correlated regressors, as in Pesaran et al. (2008), in order to see how sensitive findings are to changes in the experimental design. Serial correlation of the regressors is generated using the first-order autoregressive model $x_{\ell it} = 0.8x_{\ell it-1} + v_{\ell it}$, with $v_{\ell it} \sim iidN(0, 1/(1-0.8^2))$ for all i, t and $\ell = 2, 3$.

The Breusch-Pagan LM test (BP), the bias-adjusted LM test proposed by Pesaran et al. (2008) (BP_{adj}) and the proposed wild-bootstrap LM test (BP_{WB}) are all considered in the experiments. Table 1 reports the rejection frequencies of tests at a nominal 5 per cent significance level with homoskedastic standard normal errors. The use of critical values from a χ_ν^2, $\nu = N(N-1)/2$, distribution in the BP test leads to the true null hypothesis being rejected more frequently than is predicted by asymptotic theory. The size-distortion decreases as T increases, but the best size result is 6.4 per cent when $N = 25$ and $T = 100$. On the other hand, the bias-adjusted version of the BP test, BP_{adj}, and the wild-bootstrap BP test, BP_{WB}, both perform very well for all combinations of N and T.

The estimates for the original form of the Breusch-Pagan test when the null hypothesis is untrue are not included in Table 1. The over-rejection under the null that is associated with BP makes "power" comparisons with the two well-behaved procedures BP_{WB} and BP_{adj} inappropriate. Given the results in Table 1 that correspond to significance levels, BP_{WB} and BP_{adj} can, however, be compared. The rejection frequencies of these tests differ by small amounts when the null hypothesis is false; so that there is evidence that, under homoskedastic and normal errors, BP_{WB} and BP_{adj} have similar levels of power. Hence the results suggest that, when the restrictive classical assumptions hold, the use of the wild bootstrap test, while unnecessary, does not harm sampling properties under either the null or alternative hypothesis. No attempt is made to use Monte Carlo results to derive "size-corrections" to allow inclusion of BP in power comparisons because, as argued persuasively in Horowitz and Savin (2000), such corrections are not relevant to empirical research.

Table 2 reports the rejection frequencies of tests at a nominal 5 per cent significance level with various skedastic schemes under standardized χ^2_2 errors; so that classical assumptions do not hold.[1] The BP test rejects the true null hypothesis too frequently relative to the

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[1] To save the space, we do not report the results under standardised t_5 errors nor with serially correlated regressors since these were similar. A full set of results is available upon request from the corresponding author.

nominal significance level for all the variances schemes that are considered. Under VAR1, i.e., homoskedastic errors, BP_{adj} is subject to mild size-distortion, which is not accentuated as N increases, and the size of BP_{WB} is close to the nominal size. Under the time-series heteroskedastic schemes of VAR2, VAR3 and VAR4, BP_{adj} tends to be over-sized and the size-distortion becomes more substantial as N increases. In contrast, the wild bootstrap works well for all skedastic schemes and the finite sample significance levels of BP_{WB} appear to be much better controlled than those of BP_{adj}.

4 Conclusions

A wild bootstrap method has been proposed that allows applied workers to carry out a new test for error cross-section correlation in panel models. The wild bootstrap procedure, like other tests in the literature, requires serial independence of the errors and strict exogeneity of the regressors. However, in contrast to checks described in, e.g., Pesaran et al. (2008), the wild bootstrap test is asymptotically valid in the presence of time-variation in error variances, as well as nonnormality. Monte Carlo results suggest that the wild bootstrap procedure is well-behaved in finite samples under heteroskedasticity and matches the performance of less robust tests under classical assumptions.

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Table 1: Rejection frequencies of tests at a nominal 5% significance level with homoskedastic standard normal errors

	BP		BP_{adj}		BP_{WB}	
	$N = 25$	$N = 50$	$N = 25$	$N = 50$	$N = 25$	$N = 50$
Null hypothesis is true						
$T = 25$	10.3	25.7	5.0	6.7	4.6	5.4
$T = 50$	8.1	13.4	5.5	5.2	4.4	5.1
$T = 100$	6.4	8.8	5.6	5.1	4.7	5.2
Null hypothesis is untrue						
$T = 25$	n/a	n/a	20.5	44.4	18.5	40.1
$T = 50$	n/a	n/a	49.5	83.9	46.2	82.1
$T = 100$	n/a	n/a	87.2	99.7	85.6	99.7

Notes: BP denotes the Breusch-Pagan LM test; BP_{adj} denotes the bias-adjusted LM test proposed by Pesaran et al. (2008); BP_{WB} is the wild-bootstrap LM test. Also "n/a" denotes that "power" comparisons of the asymptotic BP test with either BP_{adj} or BP_{WB} are not appropriate; see the discussion in the text.

Table 2: Rejection frequencies with a nominal 5% significance level with various skedastic schemes under standardized χ^2_2 errors

	BP		BP_{adj}		BP_{WB}	
	$N = 25$	$N = 50$	$N = 25$	$N = 50$	$N = 25$	$N = 50$
VAR1						
$T = 25$	12.2	28.6	6.1	6.3	4.9	4.7
$T = 50$	9.9	12.9	6.8	5.3	5.2	4.8
$T = 100$	7.1	9.1	6.3	6.1	4.5	4.6
VAR2						
$T = 25$	17.9	44.2	10.5	15.9	5.1	5.2
$T = 50$	16.7	29.5	12.1	15.5	5.6	5.2
$T = 100$	13.4	24.1	11.6	18.2	4.9	5.1
VAR3						
$T = 25$	14.5	33.5	7.9	9.6	4.8	4.9
$T = 50$	11.6	17.3	8.3	8.2	5.5	5.1
$T = 100$	8.8	13.9	7.6	9.8	4.8	4.7
VAR4						
$T = 25$	12.0	29.7	6.0	7.0	4.1	4.4
$T = 50$	9.5	17.4	7.0	7.5	5.0	5.3
$T = 100$	7.5	14.4	6.6	10.1	4.3	5.1

Notes: BP denotes the Breusch-Pagan LM test; BP_{adj} denotes the bias-adjusted LM test proposed by Pesaran et al. (2008); BP_{WB} is the wild-bootstrap LM test.