A BOOTSTRAP CO-INTEGRATION RANK TEST FOR PANELS OF VAR MODELS

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Abstract. This paper proposes a sequential procedure to determine the co-integration rank of panels of co-integrated VAR (PCVAR) models. The PCVAR model allows for multiple co-integration vectors and for cross sectional co-integration. The method proposed by Pesaran [2006] is used to control for cross section dependence and reduce the dimension of the parameter space by augmenting individual models with weighted averages of the rest of the panel. A bootstrap procedure derived from the bootstrap rank test of Cavaliere et al. [2012] is used to compute the empirical distribution of the trace test statistics and construct a panel trace test statistic based on pooling of the individual *p-values*. The small sample properties of these tests are documented by means of Monte Carlo experiments and an empirical application illustrates the use of this test.

JEL classification: C12, C32, C33

Keyword VAR, Large Panel, Cross section dependence, Co-integration.

1. Introduction

This paper proposes a panel co-integration rank test statistic using a bootstrap procedure to compute its empirical distribution under the null, and an associated sequential procedure to determine the co-integration rank in a Panel of Co-integrated Vector Autoregressive models (PCVAR).

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The co-integration rank is defined as the number of co-integrating relationships among the variables of a given unit of the panel, as well as between these variables and the rest of the panel. In an international macroeconomic setting this would correspond to the number of co-integrating relationships among the variables of country i and between country i and the $N-1$ countries of the rest of the world. It is of interest to be able to model the dynamics across units of the panel. Economic theory predicts many relations among variables from different countries, often driven by arbitrage. For instance, domestic and foreign prices are linked by purchasing power parity, interest rates are linked through the interest rate parity.

Determination of the co-integration rank is important to understand the long-run dynamics of a system of variables. The sequential likelihood-based procedure by Johansen [1995] is frequently used to estimate it. This procedure is based on a sequential likelihood ratio test, the so-called trace test, for the hypothesis that the true rank of the system, r_0, is less than or equal to r. The insufficient small sample performance of inference procedures based on the asymptotic distribution of the trace test have been documented, see among others Reinsel and Ahn [1992], Johansen [2002], Cavaliere et al. [2012].

Bootstrap methods are frequently used to compute empirical test statistic distributions that are closer to the finite sample distribution of the test statistic than their asymptotic counterparts, yielding tests with finite sample sizes closer to their nominal values. Cavaliere et al. [2012] propose a bootstrap algorithm to compute an empirical distribution of the trace test statistic and document the improved performances of this procedure.

Large panels composed of many countries, regions, or industries are frequently analysed in empirical economics. This has led to a vast literature on panels with a large cross section dimension, N, and a large time dimension, T. Two difficulties arise when working with large panels. First, the number of parameters in PCVAR models grows quadratically with the number of individuals. This is often referred to as the curse of dimensionality. In order to estimates panels with large N and T, one has to control the growth rate of the number of parameters with respect to N. Second, economic variables exhibit common patterns across individuals. If this is ignored, residuals display cross section dependence, leading to spurious inference when pooling individual statistics.

The main aim of the present paper is to implement the procedure of Cavaliere et al. [2012] in potentially high dimensional PCVAR models (in the sense of $Npk > T$ where k is the number of lags and p of variables) while explicitly modeling cross section dynamics.

Breitung and Pesaran [2008] review the literature on co-integration and rank testing in panels. Only a few procedures exist to that allow testing for a rank potentially greater than one in multivariate systems. Larsson et al. [2001] adapt the Johansen [1995] likelihood based framework to panels of VAR, using a standardized rank test statistic to obtain a normally distributed panel rank test statistic. The procedure by Larsson et al. [2001] has three major drawbacks: it assumes cross section independence, it requires the asymptotic distribution of the trace test statistic to be homogeneous across individuals, and it requires the first two moments of the asymptotic distribution of the trace test statistic to be simulated. The procedure proposed in this paper overcomes these limitations.

Pesaran [2006] and Kapetanios et al. [2011] propose a method to overcome the curse of dimensionality and model cross section dependence in order to obtain residuals that are cross-sectionally uncorrelated in large panels. This method is applied to non-stationary VAR models by Dees et al. [2007]. It is based on the use of weighted cross section averages of the data to construct a proxy for the unobserved common factors assumed to cause cross section dependence.

In the next section I introduce the PCVAR model and show how it can be transformed into a set of N independent models. I then introduce the bootstrap algorithm and the panel trace test statistic, and investigate its finite sample properties by means of Monte Carlo experiments. Follows an empirical application to interest rate dynamics in the Eurozone, intent on demonstrating potential applications of the panel rank test. All the results in this paper are easily reproducible using the supplementary material.

2. The Model

Consider a panel co-integrated VAR model with k lags, written in error correction form:

$$\Delta Y_t = \tilde{\alpha}\tilde{\rho}' d_t + \tilde{\psi}\delta_t + \tilde{\alpha}\tilde{\beta}' Y_{t-1} + \sum_{l=1}^{k} \tilde{\Gamma}_l \Delta Y_{t-l} + \tilde{\epsilon}_t \tag{1}$$

The variables are stacked $Y_t := (Y'_{1,t}, \ldots, Y'_{N,t})'$ in an $[Np \times 1]$ vector. $Y_{i,t}$ is the $p \times 1$ vector of variables for individual i. If there is co-integration among the variables of the model, it is useful to write the model in error correction form to highlight the matrix of co-integration vectors $\tilde{\beta}$, of dimension $Np \times R$, and the matrix of adjustment parameters $\tilde{\alpha}$ of dimension $Np \times R$. The co-integration rank of the system is R. The parameter matrices $\tilde{\Gamma}_l$ are of dimension $Np \times Np$. $\tilde{\epsilon}_t$ is an $Np \times 1$ vector of independent Gaussian shocks to the system, with mean 0 and variance-covariance matrix $\tilde{\Omega}$. The characteristic polynomial associated with model 1 has $Np - R$ roots equal to 1 and all the other roots are outside the unit circle.

The deterministic variables are separated between a component lying in the co-integration space d_t, and a component outside the co-integration space δ_t. They are assumed to fall in one of the three following categories defined in Johansen [1988]:

a) No deterministic components: $d_t = 0$, $\delta_t = 0$.
b) Restricted constant: $d_t = 1$, $\delta_t = 0$.
c) Restricted linear trend: $d_t = t$, $\delta_t = 1$.

The log-likelihood function for the model given in equation 1 is:

$$\mathcal{L}\left(\tilde{\alpha}, \tilde{\beta}, \tilde{\Gamma}_l, \tilde{\Omega}, \tilde{\rho}, \tilde{\psi}\right) = -\frac{T}{2} \ln\left(\det\left(\tilde{\Omega}\right)\right) - \frac{1}{2} \sum_t \left(\tilde{\epsilon}'_t \tilde{\Omega}^{-1} \tilde{\epsilon}_t\right). \tag{2}$$

The number of parameters in this model depends quadratically on N and p so that this model becomes impossible to estimate by maximum likelihood for a large range of values of N, p, and T. To overcome this problem we consider a constrained version of this model with restrictions close to those used in Dees et al. [2007].

Let $Y_i^* = \sum_{j=1}^N w_{ij} Y_j$ be a weighted average of the variables of the models with weights obeying the following conditions:

$$\begin{aligned} &i)\ \ w_{ii} = 0 && ii)\ w_{ij} \in]0,1[\quad \forall i \neq j \\ &iii)\ \sum_{j=1}^N w_{ij} = 1 && iv)\ w_{ij} \in O\left(N^{-1}\right) \end{aligned} \tag{3}$$

The three first conditions ensure that the weights for individual i construct a weighted average of $Y_{-i} := \{Y_j | j \neq i\}$. The last condition ensures that the average is not dominated

by a single individual, so that idiosyncratic dynamics cancel out when N grows large. Note that the weights may be time varying as long as they satisfy the conditions above, but for simplicity of exposition the weights are not be indexed by t.

We can construct a set of N individual co-integrated VAR models using the weighted averages as weakly exogenous variables.

$$\begin{aligned} \Delta Y_{i,t} = \alpha_i \rho_i' d_{it} + \psi_i \delta_{it} \quad &+ \quad \alpha_i \beta_i' \left(Y_{i,t-1}', Y_{i,t-1}^{*\prime} \right)' + \Lambda_{i,0} \Delta Y_{i,t}^* \\ &+ \quad \sum_{l=1}^{k} \Gamma_{i,l} \Delta \left(Y_{i,t-l}', Y_{i,t-l}^{*\prime} \right)' + \epsilon_{i,t} \end{aligned} \tag{4}$$

The model for individual i given in (4) links Y_i to every other variable in the panel through the weighted averages Y_i^*. These weighted averages are treated as weakly exogenous and hence we allow for contemporaneous effect of these variables on Y_i. We can reformulate the model such that Y_i^* is expressed as a function of Y. For this purpose, define W_i such that

$$W_i Y_t = \left(Y_{i,t-1}', Y_{i,t-1}^{\prime *} \right)'.$$

The W_i matrix provides a link between the p variables of individual i and the $(N-1)p$ variables of the rest of the panel. W_i is composed of a first block of p rows with a identity matrix of dimension p between the columns ip and $(i+1)p-1$, and zeros elsewhere. The second block of p rows is composed of unit matrices multiplied by a weight scalar as defined above, except between column ip and $(i+1)p-1$ where it is equal to zero:

$$W_i = \begin{bmatrix} \mathtt{0_p} & \dots & \mathtt{0_p} & \mathtt{I_p} & \mathtt{0_p} & \dots & \mathtt{0_p} \\ w_{i1}\mathtt{I_p} & \dots & w_{ii-1}\mathtt{I_p} & \mathtt{0_p} & w_{ii+1}\mathtt{I_p} & \dots & w_{iN}\mathtt{I_p} \end{bmatrix}. \tag{5}$$

Similarly, define the matrix W_{i0}:

$$W_{i0} = \begin{bmatrix} w_{i1}\mathtt{I_p} & \dots & w_{ii-1}\mathtt{I_p} & \mathtt{0_p} & w_{ii+1}\mathtt{I_p} & \dots & w_{iN}\mathtt{I_p} \end{bmatrix}. \tag{6}$$

This matrix is used to extract Y_{it}^*: $Y_{it}^* = W_{i0} Y_t$. Define also $W = [W_1', \dots, W_N']'$, and similarly $W_0 = [W_{10}', \dots, W_{N0}']'$. These matrices are crucial in the formulation of the

PCVAR since they provide a link between every individual in the panel while reducing the dimension of the parameter space.

Using the notation introduced above we can reformulate the individual model given in equation 4:

$$\Delta Y_{it} = \alpha_i \beta_i' W_i Y_{t-1} + \Lambda_{i0} W_{i0} \Delta Y_t + \sum_{l=1}^{k} \Gamma_{il} \Delta W_i Y_{t-l} + \alpha_i \rho_i' d_t + \psi_i \delta_t + \epsilon_{it}. \tag{7}$$

The PCVAR can then be recovered by stacking the N individual models written as in 7:

$$\Delta Y_t = \alpha \beta' W Y_{t-1} + \Lambda_0 W_0 \Delta Y_t + \sum_{l=1}^{k} \Gamma_l \Delta W Y_{t-l} + \alpha \rho' d_t + \psi \delta_t + \epsilon_t, \tag{8}$$

where by construction:

$$\alpha = \begin{bmatrix} \alpha_1 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & \alpha_N \end{bmatrix}, \beta = \begin{bmatrix} \beta_1 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & \beta_N \end{bmatrix}. \tag{9}$$

Similarly, the lag matrices Γ_l and Λ_0 are also block diagonal. Assume that the covariance matrix Ω of the residuals is block diagonal with diagonal blocks Ω_{ii}. The log likelihood of the full panel given in equation 8 is the standard log likelihood function of the Gaussian VAR:

$$\begin{aligned} \mathcal{L}(\alpha, \beta, \Lambda_0, \Gamma_l, \Omega, \rho, \psi) &= -\frac{T}{2} \ln \det(\Omega) - \frac{1}{2} \sum_t \left(\epsilon_t' \Omega^{-1} \epsilon_t \right) \\ &= -\frac{T}{2} \sum_{i=1}^{N} \ln \det(\Omega_{ii}) - \frac{1}{2} \sum_{i=1}^{N} \sum_t \left(\epsilon_{it}' \Omega_{ii}^{-1} \epsilon_{it} \right) \\ &= \sum_{i=1}^{N} \mathcal{L}_i(\alpha_i, \beta_i, \Lambda_{0i}, \Gamma_{li}, \Omega_i, \rho_i, \psi_i). \end{aligned}$$

Under the assumption that the covariance matrix is block diagonal, each of the N individual models of the PCVAR can be estimated individually. The parameter matrices of the full PCVAR can then be constructed as above from the estimated parameter matrices of the individual models. Since the number of parameters of the individual model is not

function of N, we are not restricted in the number of cross section units that can be include in the panel.

The structure of the PCVAR is motivated by the results in Pesaran [2006] and Dees et al. [2007]. These results provide support for the assumption that the residual covariance matrix of the PCVAR is block diagonal. Consider the data generating process assumed by Dees et al. [2007]:

$$\begin{aligned} Y_{it} &= \delta_{i0} + \delta_{i1} t + \gamma_i \mathbf{f}_t + \xi_{it}, \\ \Delta \xi_{it} &= \mathbf{\Psi}_i (L) \nu_{it}, \quad \nu_{it} \sim \mathcal{N}(0, I_p), \\ \Delta \mathbf{f}_t &= \mathbf{\Lambda} (L) \eta_t, \quad \eta_t \sim \mathcal{N}(0, I_p), \end{aligned}$$

where $\mathbf{f}_t$ is a $m_f \times 1$ vector of common unobserved factors, with γ_i the associated $p \times m_f$ matrix of individual loadings. $\mathbf{\Psi}_i (L) = \sum_{l=0}^{\infty} \Psi_l L^l$ and $\mathbf{\Lambda}_i (L) = \sum_{l=0}^{\infty} \Lambda_l L^l$ are lag polynomials composed of absolute summable matrices Ψ_l and Λ_l such that $var(\Delta \xi_{it})$ and $var(\Delta \mathbf{f}_t)$ are positive definite and bounded.

This data generating process is a general dynamic common factor process allowing for m_f common factors and p individual variables integrated of order at most one, with the possibility of co-integration among the individual variables, and between these and the common factors. The cross section dependence in the observed data stems entirely from the unobserved common factors and can be approximated using cross sectional averages of the data.

Dees et al. [2007] shows that the unobserved common factors can be approximated by the observed cross sectional average of the data.

$$\begin{aligned} \sum_{j=1}^{N} w_{ij} Y_{jt} &= \sum_{j=1}^{N} w_{ij} (\delta_{j0} + \delta_{j1} t + \gamma_j \mathbf{f}_t + \xi_{jt}) \\ Y_{it}^* &= \delta_{i0}^* + \delta_{i1}^* t + \gamma_i^* \mathbf{f}_t + \xi_{it}^* \\ \mathbf{f}_t &\xrightarrow[N]{q.m.} \left(\gamma_i^{*\prime} \gamma_i^* \right)^{-1} \gamma_i^* (Y_{it}^* - \delta_{i0}^* - \delta_{i1}^* t - \xi_i^*) \end{aligned}$$

When the number of cross section units becomes large, the weighted averages of the observed variables converge in quadratic mean to the unobserved common factors.

The PCVAR is among the class of models considered by Dees et al. [2007] so that if we are willing to assume the cross section dependence stems from a limited number of factors the assumptions that the covariance matrix of the residuals is reasonable. Note that the block diagonality assumption is testable; Pesaran [2004] and Hsiao et al. [2012] provide tests for the assumptions that the residuals are cross sectionally independent.

Before discussing the bootstrap panel rank test applied to the PCVAR, it is convenient to write the model in levels since it will be used to generate bootstrap data in the following section.

$$
\begin{aligned}
\left(I_{Np} - \Lambda_0 W_0\right) \Delta Y_t &= \alpha\beta' W Y_{t-1} + \sum_{l=1}^{k} \Gamma_l \Delta W Y_{t-l} + \alpha\rho' d_t + \psi\delta_t + \epsilon_t \\
A Y_t &= \left(A + \alpha\beta' W\right) Y_{t-1} + \sum_{l=1}^{k} \Gamma_l \Delta W Y_{t-l} + \alpha\rho' d_t + \psi\delta_t + \epsilon_t \\
Y_t &= (A)^{-1} \left(A + \alpha\beta' W\right) Y_{t-1} + \sum_{l=1}^{k} (A)^{-1} \Gamma_l \Delta W Y_{t-l} \\
&\quad + (A)^{-1} \alpha\rho' d_t + (A)^{-1} \psi\delta_t + (A)^{-1} \epsilon_t. \qquad (10)
\end{aligned}
$$

3. Bootstrap Panel Rank Test

The likelihood ratio test of Johansen [1995] is a test for the hypothesis that the true co-integration rank r_0 is less than or equal to some rank r, against the hypothesis that the system has full rank. For a VAR with p variables the test statistics are computed as $Q_{r,T} := -T \sum_{i=r+1}^{p} \log\left(1 - \hat{\lambda}_i\right)$, where $\hat{\lambda}_1 > \cdots > \hat{\lambda}_p$ are the solutions of the following eigenvalue problem:

$$
\left|\lambda S_{11} - S_{10} S_{00}^{-1} S_{01}\right| = 0. \qquad (11)
$$

The matrices S_{ij} are defined as $S_{ij} := T^{-1} \sum_{t=1}^{T} R_{it} R_{jt}'$, with R_{0t} and R_{1t} being ΔY_{t-1} and (Y_{t-1}, d_t) corrected for the short run dynamics $(\Delta Y_{t-1}, \cdots, \Delta Y_{t-k+1})$ and the short run deterministic component δ_t. The test rejects for large values of the $Q_{r,T}$ statistics, that is, if some of the λ_i, $i = r+1, \cdots, p$ are close to 1.

This likelihood ratio test is embedded in a sequential procedure to select the rank of a VAR. The procedure starts by testing the hypothesis that $r = 0$, then $r \leq 1$ up to

$r \leq p-1$, until the test fails to reject one of the hypotheses. If $r = p-1$ is rejected, the rank is set to p. This paper will construct a panel version of the sequential procedure using the bootstrap to compute p-values associated with the rank test statistics.

The bootstrap is expected to yield more accurate finite sample performances than an approach based on the asymptotic distribution of the trace statistic. Cavaliere et al. [2012] shows that it is indeed the case in co-integrated VAR models. Since the test proposed in this paper is based on pooling individual tests, it is likely to be the case that the bootstrap delivers more accurate inference than an approach based on asymptotic distributions.

The trace test statistic's asymptotic distribution depends on the deterministic components as well as the number of weakly exogenous variables. This distribution needs to be simulated for every specification of the model. The bootstrap procedure does not require simulation of the asymptotic distribution of the trace test statistic for the model under investigation, but instead provides an approximation of the cumulative density function of the statistics conditional on the original data. This enables me to construct a test that can accommodate a wide degree of heterogeneity in the structure of the individual models.

Assume a co-integrated VAR of the form of (7) with a co-integration rank r_0. Let the parameters of this model be estimated under an assumed rank $r < r_0$. Denote these parameters $\hat{\theta}^r := \left\{\hat{\alpha}^r, \hat{\beta}^r, \hat{\Gamma}_l^r, \hat{\rho}^r, \hat{\delta}^r\right\}$. One important result of Cavaliere et al. [2012] is to show that bootstrap data generated using the estimated parameters $\hat{\theta}^r$ are integrated of order at most 1 and have r co-integrating relations in the limit. This is an asymptotic result; in finite samples the $I(1,r)$ condition could be violated and thus it needs to be verified, which is the purpose of the second step of the bootstrap algorithm. Below I show how their results are applicable to the PCVAR model.

A few assumptions on the dynamics of the model have to be made. First, assumptions on the dynamics of the individual models.

Assumption 1. *For every individual $i \in 1, \cdots, N$:*

a) The co-integration rank of model 4 is equal to $r_0 \in 0, \cdots, p$.

b) The characteristic polynomial of the model described by equation 4 has r_0 roots on the unit circle and $p - r_0$ roots outside.

c) The limiting non-zero eigenvalue solutions of problem 11 are distinct.

Assumption 1*a* implies that the full PCVAR has rank Nr_0. Homogeneity of the co-integration rank across individuals is not a testable assumption but, since every individual model contains the same set of variables, it could be reasonable to postulate that each individual model also possesses the same number of long run equilibrium relations. 1*b* ensures that the model is at most $I(1)$.

Assumption 2. *The innovations follow an* i.i.d. *sequence* $\{\epsilon_{it}\}$ *satisfying:*

$$a)\ E(\epsilon_{it}) = 0 \qquad c)\ E||\epsilon_{it}||^4 \leq K < \infty$$

$$b)\ E(\epsilon_{it}\epsilon_{it}') = \Omega_i \qquad d)\ E(\epsilon_{it}'\epsilon_{jt}) = 0_p,\ i \neq j.$$

Assumptions 2*a* to 2*c* are as in Cavaliere et al. [2012] and ensure well behaved residuals. 2*d* assumes a block diagonal structure of the variance covariance matrix and hence innovations that are independent across individuals.

Assumption 3. *Assumptions on the full panel.*

a) $I_{Np} - \Gamma_0 W_0$ *is invertible.*

b) The $Np - Nr$ *non-zero eigenvalues of model 10 written in companion form are on or inside the unit circle.*

Assumption 3*b* is equivalent to assuming that the roots of the characteristic polynomial of the PCVAR are on or outside the unit circle. It is a sufficient condition for assumptions 1*b* to hold for every i. This assumption will be tested for each bootstrap data generating process. 3*a* ensures that we can write the PCVAR in levels.

I can now state the bootstrap algorithm to compute the p-value of the likelihood ratio test for the hypothesis $\mathcal{H}_r$ against $\mathcal{H}_p$. .

Algorithm 1. *(1) Under the assumption that* $r_0 = r$*, estimate by Gaussian quasi-maximum likelihood the set of parameters* θ_i^r *and the residuals* $\hat{\epsilon}_{r,i,t}$ *of equation (4) for each individual model. Compute the individual trace test statistic* $Q_{r,i}$ *by solving the eigenvalue problem (11).*

(2) Verify that the characteristic polynomial $|\hat{A}^r(z)| = 0$ *with:*

$$\hat{A}^r(z) = (1-z)I_{Np} - \hat{\alpha}^r\hat{\beta}^{r\prime}Wz - \sum_{l=1}^{k-1}\Gamma_l^{r\prime}W(1-z)z^l,$$

has no roots inside the unit circle. Verify that $I_{Np} - \hat{\Lambda}_0 W_0$ *is invertible. If both conditions are satisfied proceed to the next step, otherwise exit the algorithm.*

(3) Recenter the residuals $\hat{\epsilon}^c_{r,i,t} = \hat{\epsilon}_{r,i,t} - \frac{1}{T}\sum_t \hat{\epsilon}_{r,i,t}$ *and construct a bootstrap matrix of residuals by resampling from* $\hat{\epsilon}^c_{r,i,t}$*. Define the bootstrap residuals as* $\hat{\epsilon}^\dagger_{r,i,t}$*. Using the parameter matrix* $\hat{\theta}^r$ *and the bootstrap residuals, generate* B *bootstrap samples for the full panel using the recursion given in (10).*

(4) Using the bootstrap sample $Y_t^\dagger$*, apply the procedure in the previous section to transform the panel in a set of* N *independent models. Solve the eigenvalue problem (11) for each individual model and compute the LR statistics*

$$Q^{\dagger,b}_{r,i,T} = -T\sum_{v=r+1}^{p}\log\left(1-\hat{\lambda}^{\dagger,b}_{v,i}\right),$$

where $b \in 1,\cdots,B$ *indexes the bootstrap iterations.*

(5) Compute the p-value for every individual i*:*

$$p^\dagger_{i,r} = \frac{1}{B}\sum_{b=1}^{B}\mathbb{1}_{\{Q_{i,r}<Q^{\dagger,b}_{i,r}\}}.$$

Pool the individual p-values to obtain a bootstrap panel test statistic:

$$\bar{P}_r = \frac{\sum_{i=1}^{N}\left(-2log(p^\dagger_{i,r})-2\right)}{\sqrt{4N}}.$$

The asymptotic behavior of this test is discussed in theorem 1.

Remark 1. The trace test statistic $Q_{r,i,T}$ is similar with respect to ρ_i and asymptotically similar with respect to ψ_i. That is, the rejection frequency of the test does not depend on the value of ρ_i nor, asymptotically, on the value of ψ_i (see Nielsen and Rahbek [2000] and Cavaliere et al. [2012], remark 2). Hence the recursion in step 3 of algorithm 1 can be used excluding the estimated deterministic terms $\hat{\alpha}^r_i\hat{\rho}'_{it}d_t + \hat{\psi}_i\delta_{it}$ and setting the initial values $Y_{i,1-k} = \cdots = Y_{i,0} = 0$.

Remark 2. In step 3 of the algorithm, the bootstrap residuals can also be constructed using the Wild bootstrap instead of *i.i.d.* resampling. To do so, multiply the recentered residuals by random draws from a $\mathcal{N}(0,1)$ to obtain a set of wild bootstrap residuals.

Theorem 1. *Under assumptions 1 to 3 we have*

- *if* $r = r_0$*:* $\bar{P}_r \xrightarrow[(N,T)_j]{w} \mathcal{N}(0,1)$,
- *if* $r < r_0$*:* $\bar{P}_r \xrightarrow[(N,T)_j]{} \infty$,

where $\xrightarrow[(N,T)_j]{}$ *stands for a limit when* N *and* T *tend jointly to infinity with no restrictions on their relative rates of divergence.*

The $\bar{P}$ statistic is based on the Fisher test, as discussed in Maddala and Wu [1999]. We rely on large N asymptotics for pooling and the fact that the logarithm of the individual p-values (multiplied by -2) is χ^2 distributed since the bootstrap p-value are uniformly distributed between 0 and 1 under the null.

Remark 3. The p-values associated with each test statistics $Q_{r,i,T}$ are computed independently based on the B bootstrap statistics $Q^{\dagger,b}_{r,i,T}$ generated with algorithm 1. The trace test statistics is known to have different limiting distributions for different d_t, δ_t, and different numbers of weakly exogenous variables. The p-values obtained at step 5 of algorithm 1 are *i.i.d.* so that the panel statistic is still valid when different deterministic components are used for different individuals. This is particularly useful when dummy variables are required to account for an exceptional event impacting a limited number of series.

I now introduce the sequential procedure to determine the co-integration rank of the panel.

Algorithm 2. *Initialize the algorithm with* $r = 0$.

(1) Perform steps 1 to 5 of algorithm 1.

(2) If $p^{\dagger}\left(\bar{P}_r\right)$ *exceeds the selected significance level, set* $\hat{r} = r$. *Otherwise repeat the previous steps for* $r+1$ *if* $r+1 < p$, *else set* $\hat{r} = p$.

The sequential rank test procedure yields an estimator of the co-integration rank with the following properties:

Theorem 2. *Let $\hat{r}$ be the rank selected by the sequential procedure of algorithm 2 and η the selected significance level. Then under assumptions 1, 2, and 3:*

$$\begin{aligned}
\lim_{(N,T)_j\to\infty} P\left(\hat{r}=r\right) &= 0,\ \forall r<r_0 \\
\lim_{(N,T)_j\to\infty} P(\hat{r}=r_0) &= \begin{cases} 1-\eta \ \textit{if}\ r_0<p \\ 1 \ \textit{if}\ r_0=p \end{cases} \\
\lim_{(N,T)_j\to\infty} \sup_{r\in\{r_0+1,\cdots,p\}} P(\hat{r}=r) &\leq \eta \ \textit{for}\ r>r_0.
\end{aligned}$$

Theorem 2 shows that the sequential procedure selects a rank below the true rank with probability tending to zero. At the true rank, the procedure has size η if the system is not full rank and 0 otherwise.

The remark below discusses the impact of cross sectional co-integration on the number of unit roots of the PCVAR model.

Remark 4. Consider a bi-variate system with a single co-integration vector $\beta_i=[1,-1,0,0]'$ and $\alpha_i=[-0.5,0]'$ for all $i=1,\cdots,N$. Further assume that the model as no cross sectional co-integration, no short run dynamics or deterministic components, and the weights are uniform: $w_{ij}=\frac{1}{N-1}\ \forall i\neq j$. The resulting individual model is

$$\Delta Y_{it}=\begin{bmatrix}\Delta Y_{it}^1\\ \Delta Y_{it}^2\end{bmatrix}=\begin{bmatrix}-0.5\\ 0\end{bmatrix}\begin{bmatrix}1,-1,0,0\end{bmatrix}W_iY_{t-1}+\epsilon_{it}.$$

The corresponding PCVAR has N eigenvalues equal to 1 and N eigenvalues equal to 0.5. Consider a similar model with a different co-integration vector $\beta_i'^*=[1,0,-1,0]$. Each individual model has one eigenvalue equal to 1 and one eigenvalue smaller than 1. However the PCVAR has $N+1$ unit roots and $N-1$ stationary ones. The variable Y_i^2 has an idiosyncratic unit root for all i, and Y_{it}^1 share the same unit root by cross sectional co-integrations. In a model with p variables and an individual model rank equal to r_0, if the cross section parameters of β_i are not zero the PCVAR has $Np-(N-1)r_0$ eigenvalues equal to 1 and $(N-1)r_0$ eigenvalues lower than one.

The existence of these *global* unit roots, at most r_0 unit roots caused by cross sectional co-integration, does not undermine the results of theorems 1 and 2. Each individual model

has exactly r_0 co-integration vectors since the weighted averages are weakly exogenous to the individual model, and the co-integration vectors of the PCVAR are partially identified by the block diagonal restriction on α. This ensures that the bootstrap DGP has the desired properties and the tests are as in the case of no cross sectional co-integration.

4. Monte Carlo

The results presented in this section and the following application section are fully reproducible as advocated in the academic literature by Koenker and Zeileis [2009] for example. All the computations are carried using `R` and the `pcvar` package available in the supplementary material. Replication files are provided to reproduce the computations and output using the `knitr` package, a tool similar to the one described by Meredith and Racine [2009] to facilitate the reproducibility of research. The choice of the random number generator's seeds is made so as to ensure reproducibility on systems with a different number of cores as described by Delgado and Parmeter [2013].

The Monte Carlo study below aims at documenting the performances of the bootstrap rank test for the PCVAR along three axis. First, benchmark the performances of the test on simple models satisfying the assumptions stated above. Second, document the behaviour of the test when the co-integration rank is heterogeneous across individuals. Third, investigate the behaviour of the test when the innovations follow a Student distribution or follow a GARCH process.

4.1. **Benchmark models.**

Start by considering a simple model, already exposed in Remark 4, where for all i:

$$DGPA1 : \Delta Y_{it} = \begin{bmatrix} \Delta Y_{it}^1 \\ \Delta Y_{it}^2 \end{bmatrix} = \begin{bmatrix} -0.5 \\ 0 \end{bmatrix} \Big[1, -1, 0, 0\Big] W_i Y_{t-1} + \epsilon_{it}. \tag{12}$$

The weights are uniform ($w_{ij} = \frac{1}{N-1} \forall\ i \neq j$), and $\epsilon_{it} \sim \mathcal{N}(0, \mathtt{1}_p)$ in this experiment and all subsequent ones unless specified otherwise. I use 199 bootstrap replications and 1000 Monte Carlo replications in this experiment. Exploratory experiments conducted with much higher numbers of bootstrap replications showed that it did not modify the performances of the test.

Table 1 reports statistics from experiment A1. The shaded rows report the frequency at which each rank is selected by the sequential procedure. The *Average* $p(\bar{P}_r)$ rows report the average bootstrap p-value for the panel rank test. The third row reports the p-value of the (individual) bootstrap trace test averaged across individuals and Monte Carlo iterations.

[Table 1 about here.]

Table 1 shows that the sequential procedure selects the correct rank in every iteration. The average p-value on the last line of the first panel ($T = 50$) is above the selected significance level of 5% implying that the individual test fails to reject the incorrect hypothesis $\mathcal{H}_0$ at least some time. However the pooling of the individual p-values gives the panel tests extra power to consistently reject this hypothesis. When T increases, the average p-value of the individual statistic decreases rapidly below the selected significance level.

Now consider a variation on DGPA1, replacing co-integration between the variables of a unit by a cross sectional co-integration vector.

$$DGPA2 : \Delta Y_{it} = \begin{bmatrix} \Delta Y_{it}^1 \\ \Delta Y_{it}^2 \end{bmatrix} = \begin{bmatrix} -0.5 \\ 0 \end{bmatrix} \Big[1, 0, -1, 0\Big] W_i Y_{t-1} + \epsilon_{it}. \tag{13}$$

In experiment A2 each individual model is of rank 1, the resulting PCVAR however has $N + 1$ unit roots and $N - 1$ eigenvalues below zero. The purpose of this experiment is to investigate the impact of this *global* unit root on the test. Table 2 reports the same statistics as table 1 for experiment A2.

[Table 2 about here.]

Table 2 shows that the individual rank test performs worse for $T = 50$ in this experiment than in experiment $A1$. The panel rank test to fail to reject $\mathcal{H}_0$ 28% of the time when $N = 5$. The power of the test increases with N so that the rejection rate is of 2% when $N = 10$ and negligible when $N = 20$. Increasing T also improves the performance of the individual rank statistic, so that the panel rank test performs as well as in experiment $A1$ for $T \geq 100$.

[Figure 1 about here.]

Figure 1 plots the average absolute eigenvalues of DGP A2 and of the bootstrap data generating process under each rank hypothesis. The vertical bar in each panel separates the eigenvalues by blocks of N. The top left panel, $T = 50$ and $N = 5$, illustrates most clearly the presence of the *global* unit root in DGP A2, dotted line. Notice that bootstrap DGP under the assumption that the rank is 1 has exactly N unit roots. When $T = 500$, bottom left panel, the eigenvalue $N+1$ of DGP for $\mathcal{H}_1$ is not one, as in the original DGP, but is very close to it.

Before investigating the robustness of the panel rank test to departures from the assumptions, I consider a third well specified DGP. Experiment A3 has 4 variables and 2 co-integration vectors per individual model. Specifically, the individual DGP is:

$$\text{DGP A3} : \Delta Y_{it} = \begin{bmatrix} -0.5 & 0 \\ 0 & 0 \\ 0 & -0.5 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 \end{bmatrix} W_i Y_{t-1} + \epsilon_{it} \tag{14}$$

The results of experiment A3 are presented in table 3; the test consistently rejects the hypothesis of no co-integration, however it lacks power to reject the (incorrect) hypothesis $\mathcal{H}_1$ when $T = 50$. Power increases with N but only moderately, the rejection frequency of $\mathcal{H}_1$ goes from 0.23 for $N = 5$ to 0.41 for $N = 20$. Increasing T to 100 increases the power of the test so that the correct rank is always selected.

[Table 3 about here.]

4.2. **Heterogeneous co-integration rank experiment.** The purpose of experiment B1 is to investigate the impact of heterogeneous co-integration ranks in the individual models on the panel rank test. To do so, I consider a DGP in which a fraction f of

individual models have a rank of 2 and a fraction $1-f$ have rank 1.

$$\text{(15)}\quad \text{DGP B1}: \begin{cases} f: \Delta Y_{it} &= \begin{bmatrix} -0.5 & 0 \\ 0 & 0 \\ 0 & -0.5 \end{bmatrix} \begin{bmatrix} 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & -1 \end{bmatrix} W_i Y_{t-1} + \epsilon_{it} \\ 1-f: \Delta Y_{it} &= \begin{bmatrix} -0.5 \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} 1 & -1 & 0 & 0 & 0 & 0 \end{bmatrix} W_i Y_{t-1} + \epsilon_{it} \end{cases}.$$

[Figure 2 about here.]

I focus on the rank selected by the sequential procedure[1]. Figure 2 plots the co-integration rank selected by the sequential procedure for all possible values of f between 0 and 1 by steps of $1/N$. The experiments are conducted with sample sizes $T = 100, 500$, $N = 5, 20$, and 100 Monte Carlo iterations.

The top left panel of figure 2 shows that the sequential test selects correctly a rank of 1 when every individual has rank 1, this is in line with the results of experiment $A1$. When a single individual has rank 2 the sequential procedure selects a rank 2 in approximately 5% of the iterations. The frequency at which the procedure selects a rank of 2 increases rapidly, when 3 individuals have rank 2 the procedure selects this rank in around 95% of the iterations.

Increasing both N or T decreases the share of models with rank 2 required for the procedure to begin selecting a rank of 2. Increasing the dimensions of the model also makes the share of experiments for which rank 1 is selected fall more rapidly. This appears clearly in the bottom right panel ($N = 20$, $T = 500$) where the two lines are very steep and rank 2 is selected 50% of the time with a share of only 15% (3 out of 20) individuals with rank 2.

4.3. **Misspecified residuals experiments.** In this section I consider departures from the assumption that the innovations are *i.i.d.* gaussian. Exploratory experiments[2] with

[1]The full detail of the experiments as well as plots of the eigenvalues are available in the supplementary material.

[2]Results of these experiments are available as experiment $C1$ and $C2$ in the supplementary material.

residual cross section dependence showed that it did not impact the test, the weighted averages appear to perform satisfyingly in capturing cross section dependence. I consider both the effect of fat tails by using innovations following a Student t distribution with 4 degrees of freedom, $t(4)$, as well as innovations following a GARCH(1,1) process. I also investigate the performances of the wild bootstrap on a process with GARCH errors.

To investigate the effect of these departures from the assumptions I consider a bi-variate DGP:

$$DGPD : \Delta Y_{it} = \begin{bmatrix} \Delta Y_{it}^1 \\ \Delta Y_{it}^2 \end{bmatrix} = \begin{bmatrix} -0.5 \\ 0 \end{bmatrix} \Big[1, -1, -1, 0\Big] W_i Y_{t-1} + \epsilon_{it}. \tag{16}$$

This particular co-integration vector is chosen to induce both co-integration among on units variables and cross sectional co-integration, giving rise to more complex dynamics than in experiment $A1$ and $A2$. This better highlights the effect of the different residual specifications on the sequential test procedure.

[Table 4 about here.]

Table 4 presents the performance of the sequential rank test procedure for 6 residual specifications in $DGPD$, experiments $D1$ to $D6$. The top panel reports the rank selected by the sequential procedure for standard normal and $t(4)$ distributed innovations. The central and lower panels report the performance of the test for residuals following a GARCH(1,1) process parametrized as follows:

$$\epsilon_{it} = \sigma_{it}\nu_{it}, \qquad \sigma_{it}^2 = 1 + 0.1\epsilon_{it-1}^2 + 0.85\sigma_{it-1}^2,$$

where ν_{it} is either $\mathcal{N}(0,1)$, left column, or $t(4)$, right column. In the lower panel a wild bootstrap is used instead of a resampling based bootstrap.

In these experiments it appears that the test rejects $\mathcal{H}_1$ more frequently than the nominal 5% rate. In every panel, $t(4)$ residuals deteriorates the performance of the test relative to gaussian residuals. Keeping N constant, an increase in T deteriorates the perfomance of the test in this setting. It appears that increasing N, from 5 to 10, improves greatly the performances of the test with a correct selection rate between .83 and .99.

The test appears robust to GARCH effects, only a modest deterioration of at most 0.15 of the selection rate of $\mathcal{H}_1$ is observed. The wild bootstrap does not seem to bring significant improvements, in fact it performs slightly worse than resampling except for $T = 500$ and $N = 5$.

5. An application to Eurozone countries' interest rates and prices.

To illustrate the potential applications of the panel rank test presented in this paper, I propose an empirical application investigating the co-integration properties of a set of monthly interest rates and inflation rates for 10 Eurozone countries from January 1995 to May 2012 (T=209). The data is retrieved from the OECD statistical database, details on the data is available in the supplementary material.

[Figure 3 about here.]

In 1993 the Maastricht Treaty was ratified and enforced by a number of European states. It provided for the establishment of a common currency among countries of the European Union that was to be launched on 1 January 1999. Interest rates reacted to this fact by converging but rates of inflation did not despite a Eurozone wide inflation target. Figure 3 illustrates this; CPI is the consumer price index, LIR the 10-year state obligation rate and SIR the 3-month interest rate.

The convergence of nominal interest rates is predicted by simple no-arbitrage conditions. However, the sustained divergence in inflation rates ensured that real interest rates were not converging in the Eurozone, as illustrated by figure 4, where $DCPI$ is the monthly inflation rate, $RSIR$ and $RLIR$ are the real 3-month and 10-years monthly interest rates, respectively. The series are smoothed for readability.

I consider 4 different models. Model 1 includes domestic and foreign $DCPI$, SIR, and LIR. Model 2 includes the domestic and foreign real interest rates, $RSIR$ and $RLIR$. Model 3 and 4 include $DCPI$ and either $RSIR$ or $RLIR$. All models are estimated with 1 lagged first difference, a restricted constant and monthly dummies. The results presented below are robust to specification changes, details of all computations can be found in the supplementary material.

[Figure 4 about here.]

[Table 5 about here.]

The results of the sequential panel rank test procedure are presented in table 5. For every model the rank selected is unambiguously equal to 1, which is compatible with interest rate parity and arbitrage conditions. To further interpret the co-intergation properties of these models one would need to test structural hypotheses on the co-integration vectors, this is the object of further work.

6. Conclusion

The aim of this paper is to propose a sequential bootstrap co-integration rank test procedure for panels of co-integrated VAR models with a large cross-section dimension and cross section dependence. The test is based on the bootstrap sequential rank test procedure by Cavaliere et al. [2012]. I introduced a bootstrap panel test statistic, the $\bar{P}_r$ statistic, which allows for a great amount of heterogeneity across models both in terms of parameter values and in the specification of deterministic components.

The test relies on the rather restrictive assumption that the co-integration rank is homogeneous across units of the panel. The Monte Carlo study documents the effect of departures from this assumption, as well as departures from the assumptions of independence (cross sectional and dynamic) of the residuals.

An illustration of potential applications of this test is presented using data from the Eurozone. Further work is required in order to develop inference procedures in PCVAR that would render the co-integration vectors and the parameters of the model interpretable.

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Appendix A. Supplementary material

All supplementary material is contained in the `pcvar_rank.zip` file. It contains at its root at `README.pdf` file with details of the content. Summary of the content:

- The `MC` folder contains the replication files for each experiment. The cached output is not included due to its size, larger than 10 Go.
- The `pcvar` package for `R` which is used for all computations.
- The `EZ` folder containing all the replication material for the empirical application.

Appendix B. Proofs

Proof. Proof of Theorem 1:

Consider the recursion used in step 3 of algorithm 1:

$$\begin{aligned} Y_t = (A)^{-1}(A+\alpha\beta' W)\,Y_{t-1}, + \sum_{l=1}^{k}(A)^{-1}\Gamma_l \Delta W Y_{t-l} \\ + (A)^{-1}\alpha\rho' d_t + (A)^{-1}\psi\delta_t + (A)^{-1}\epsilon_t \end{aligned} \tag{17}$$

with $A = I_{Np} - \Lambda_0$ where A is invertible by assumption 3a. As shown in section 2, and under assumption 2, this recursion is equivalent to N independent models of the form:

$$\begin{aligned} \Delta Y_{i,t} = \alpha_i\rho_i' d_{it} + \psi_i\delta_{it} \quad + \quad \alpha_i\beta_i' W_i Y_{t-1} + \Lambda_{i,0}\Delta W_{i0} Y_t \\ + \quad \sum_{l=1}^{k}\Gamma_{i,l}\Delta W_i Y_{t-l} + \epsilon_{i,t}. \end{aligned} \tag{18}$$

By estimating model 18 under the assumptions $r_0 = r$, for $i = 1, \cdots, N$, we get a set of PCVAR parameters: $\hat{\theta}_i^r = \left(\hat{\alpha}^r, \hat{\beta}^r, \hat{\Lambda}_0^r, \hat{\Gamma}_1^r, \cdots, \hat{\Gamma}_k^r\right)$. Dees et al. [2007][3] shows that $\hat{\beta}^r$ is super-consistently estimated and that the other parameters of $\hat{\theta}^r$ are consistently estimated.

Lemma 1 of Cavaliere et al. [2012] shows that as $T \to \infty$, $\hat{\theta}_i^r \to \theta_i^r$ where θ_i^r satisfy the $I(1,r)$ condition for all $i \in 1, \cdots, N$. Hence bootstrap data generated according to 17, and for any $r \leq r_0$, satisfies the $I(1, Nr)$ condition asymptotically.

[3] Appendix, section 2.

By proposition 2 in Cavaliere et al. [2012], $Q^{\dagger}_{r,i,T} \xrightarrow{w.p.} tr(Q_{i,r,\infty})$ where

$$Q_{r,i,\infty} := \int_0^1 dB_{p-r}(u)F_{p-r}(u)' \left(\int_0^1 dF_{p-r}(u)F_{p-r}(u)'du \right) \int_0^1 dF_{p-r}(u)B_{p-r}(u)'$$

with B_{p-r} being a standard Brownian motion of dimension $p-r$ and:

$$\begin{aligned} F_{p-r} &:= B_{p-r} && \text{no deterministics} \\ F_{p-r} &:= (B'_{p-r}, 1)' && \text{restricted constant} \\ F_{p-r} &:= (B'_{p-r}, u|1)' && \text{restricted linear trend} \end{aligned}$$

where $x|y$ denotes the projection of the residuals of x on y. Since $Q_{r,i,T} \to \infty$ if $r < r_0$ and $Q_{r_0,i,T} \xrightarrow{w} tr\left(Q_{i,r_0,\infty}\right)$ it follows that for $p^{\dagger}_{i,r} = \frac{1}{B}\sum_{b=1}^{B} \mathbb{1}_{\{Q_{i,r,T} < Q^{\dagger,b}_{i,r,T}\}}$ we have:

$$\begin{aligned} p^{\dagger}(Q_{i,r,T}) &\xrightarrow{p} 0 && \text{if } r < r_0 \\ p^{\dagger}(Q_{i,r,T}) &\sim \mathcal{U}[0,1] && \text{if } r = r_0 \end{aligned}$$

The logarithm of the $p-values$ (scaled by -2) are χ^2 distributed. Since $p^{\dagger}_{i,r}$ is $i.i.d.$ $\forall i$, we can be pool the individual p-values:

$$\bar{P}_r = \frac{\sum_{i=1}^{N}\left(-2log(p^{\dagger}_{i,r}) - 2\right)}{\sqrt{4N}}.$$

Using the Lindeberg-Lévy central limit theorem, it follows that:

$$\begin{aligned} \bar{P}_r &\xrightarrow[(N,T)_j]{p} \infty \\ \bar{P}_r &\xrightarrow[(N,T)_j]{w} \mathcal{N}(0,1) \end{aligned}$$

□

Proof. Proof of Theorem 2: Let η be the chosen significance level of the LR test. To prove theorem 2, three cases have to be considered:

(1) $\hat{r} < r_0$: from theorem 1, $\bar{P}_r \xrightarrow[(N,T)_j]{} \infty$.

(2) $\hat{r} = r_0$: from theorem 1, $\bar{P}_r \xrightarrow[(N,T)_j]{w} \mathcal{N}(0,1)$. In this case, if $r_0 < p$ it follows that $P(\hat{r} = r_0) = 1 - \eta$. If $r_0 = p$, and since $P(\hat{r} < r_0) \xrightarrow[(N,T)_j]{p} 0$ it follows that $P(\hat{r} = r_0) \xrightarrow[(N,T)_j]{} 1$.

(3) $\hat{r} > r_0$ and $r_0 < p$: $\sup_{p \geq r > r_0} P(\hat{r} = r) \xrightarrow[(N,T)_j]{} \eta$ follows from the previous point.

□

List of Figures

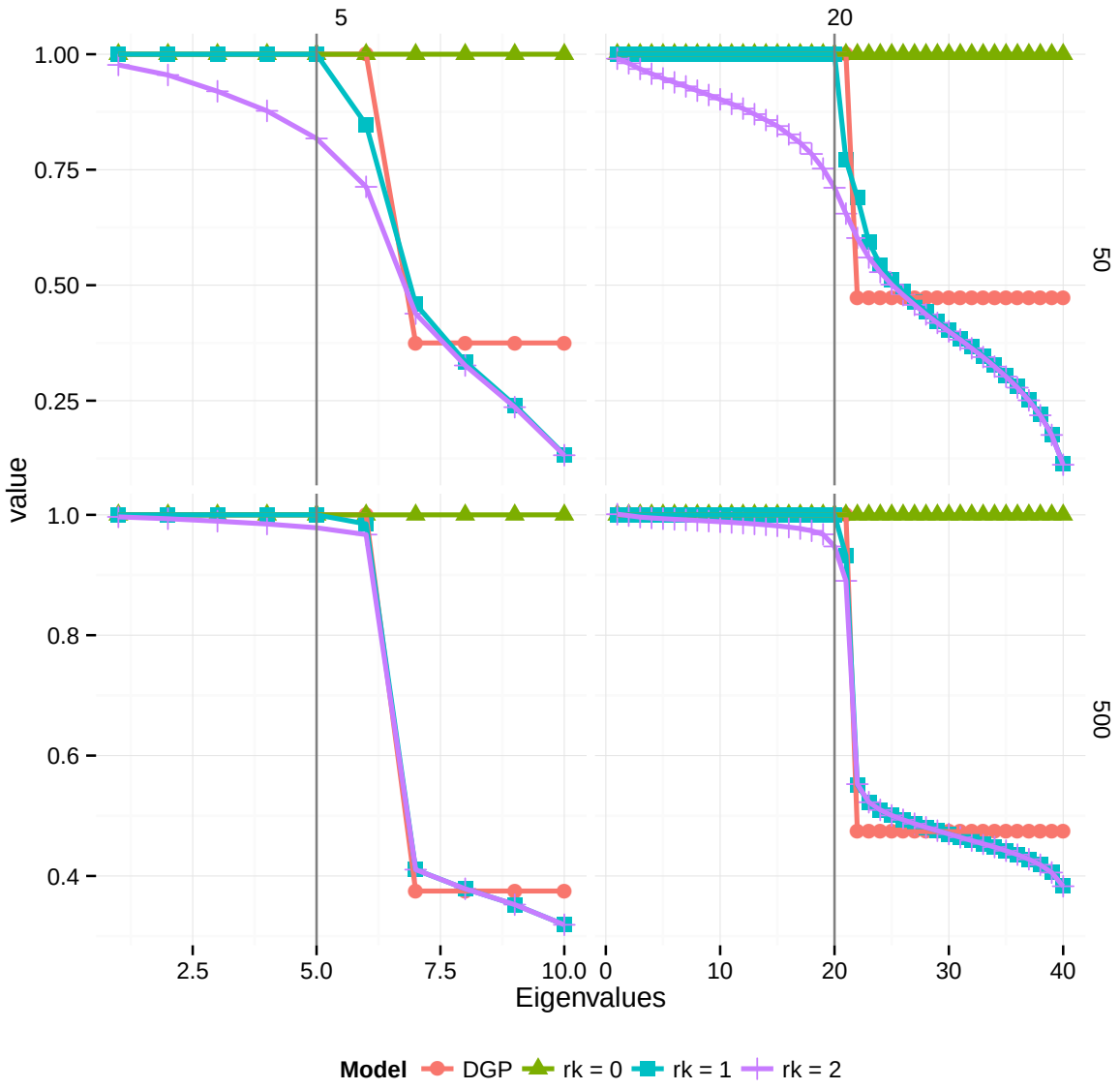

FIGURE 1. Eigenvalues of the Monte Carlo and Bootstrap DGP for experiment A2.

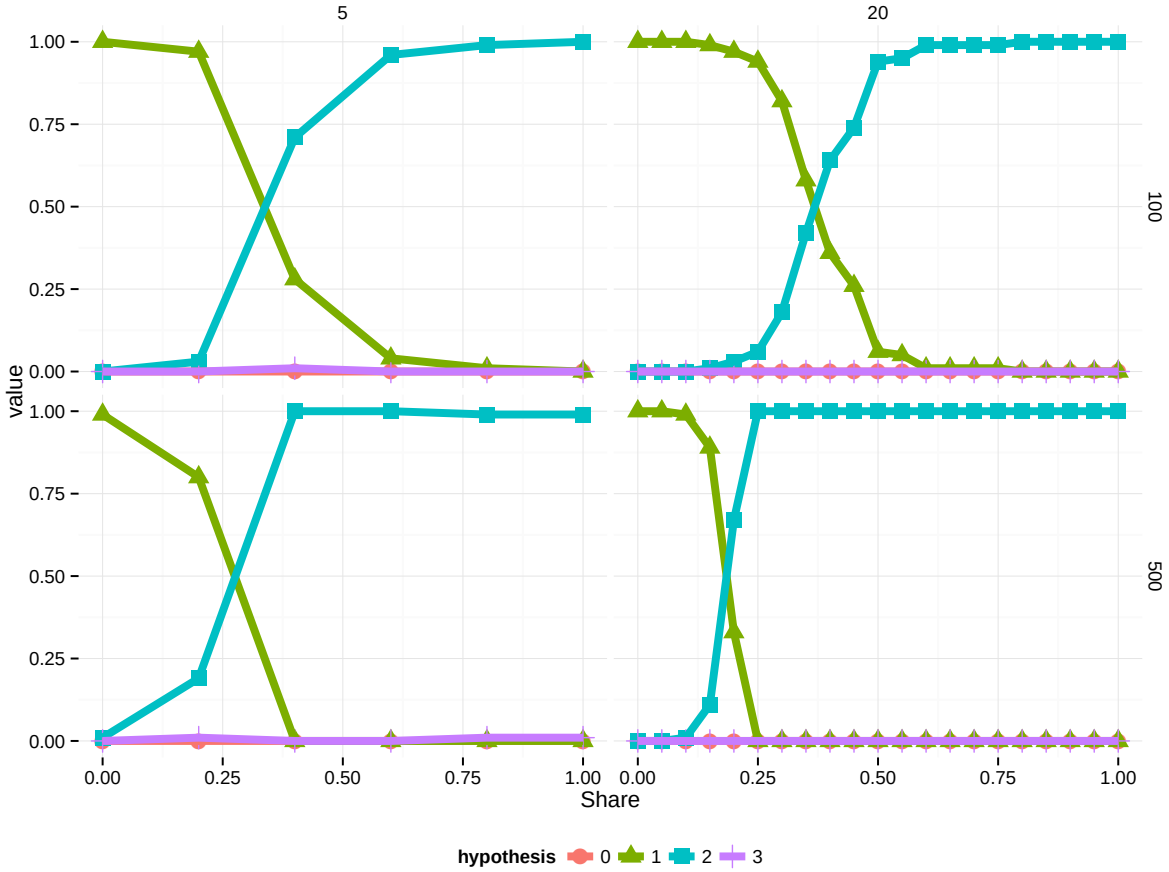

FIGURE 2. Experiment B1: rank selected by the sequential procedure as a function of the share of individuals with rank 2. 100 Monte Carlo replication, 199 bootstrap iterations.

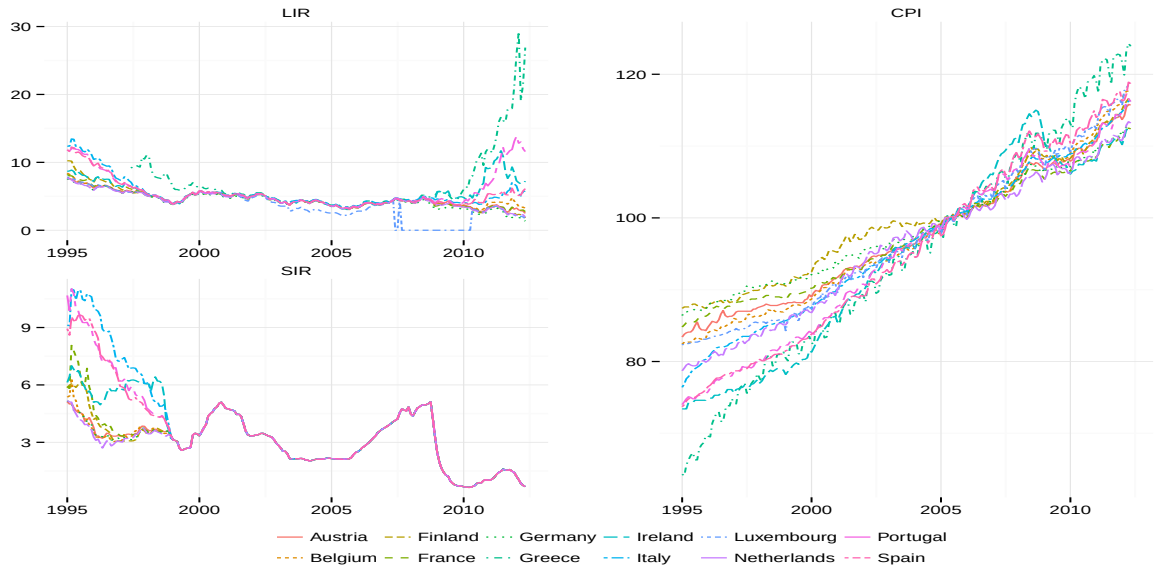

FIGURE 3. Interest Rates and Consumer Price Index.

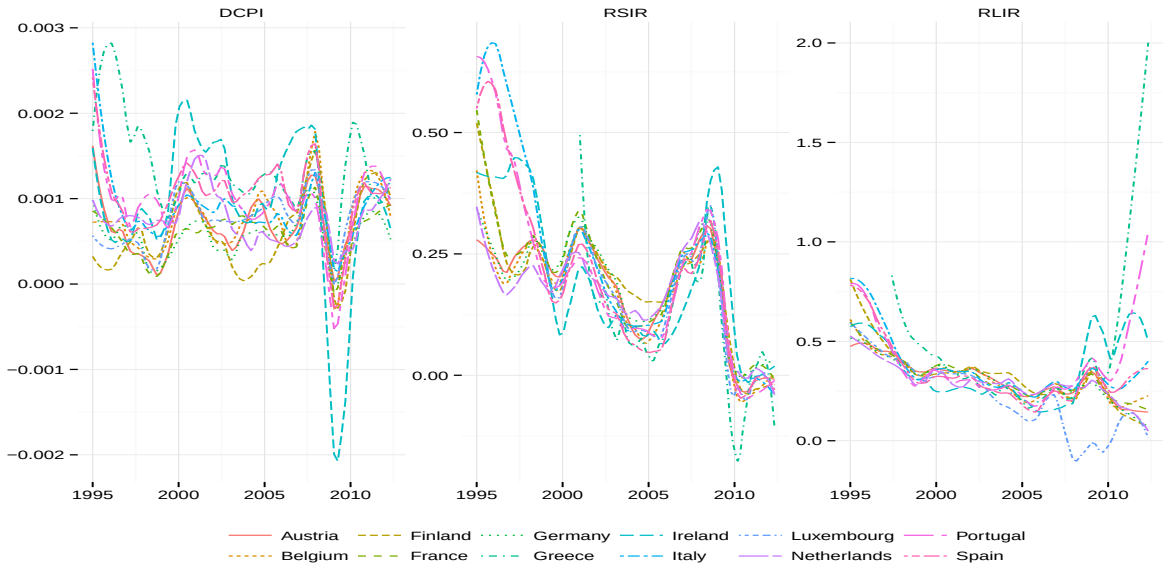

FIGURE 4. Real Monthly Interest and Inflation Rates.

List of Tables

T = 50	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	1	0	0	1	0	0	1	0
Average $p(\bar{P}_r)$	0	0.81	1	0	0.93	1	0	0.98	1
Average $p^{\dagger}_{i,r}$	0.06	0.67	1	0.06	0.72	1	0.06	0.72	1
T = 100	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	1	0	0	1	0	0	1	0
Average $p(\bar{P}_r)$	0	0.78	1	0	0.92	1	0	0.98	1
Average $p^{\dagger}_{i,r}$	0.01	0.65	1	0.01	0.7	1	0.01	0.73	1
T = 500	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	1	0	0	1	0	0	1	0
Average $p(\bar{P}_r)$	0	0.72	1	0	0.92	1	0	0.98	1
Average $p^{\dagger}_{i,r}$	0.01	0.61	1	0.01	0.7	1	0.01	0.7	1

TABLE 1. Experiment A1, 1000 Monte Carlo replications, 199 Bootstrap iterations.

T = 50	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0.28	0.72	0	0.02	0.97	0	0	0.99	0
Average $p(\bar{P}_r)$	0.05	0.78	1	0.01	0.85	1	0	0.88	1
Average $p^{\dagger}_{i,r}$	0.21	0.65	1	0.18	0.66	1	0.2	0.63	1
T = 100	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	1	0	0	1	0	0	1	0
Average $p(\bar{P}_r)$	0	0.74	1	0	0.86	1	0	0.88	1
Average $p^{\dagger}_{i,r}$	0.03	0.63	1	0.02	0.65	1	0.02	0.63	1
T = 500	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	0.99	0.01	0	1	0	0	1	0
Average $p(\bar{P}_r)$	0	0.68	1	0	0.86	1	0	0.88	1
Average $p^{\dagger}_{i,r}$	0.01	0.59	1	0.01	0.65	1	0.01	0.62	1

TABLE 2. Experiment A2, 1000 Monte Carlo replications, 199 Bootstrap iterations.

T = 50	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	0.77	0.22	0	0.69	0.31	0	0.59	0.41
Average $p(\bar{P}_r)$	0	0.22	0.81	0	0.21	0.92	0	0.19	0.95
Average $p^{\dagger}_{i,r}$	0.07	0.35	0.67	0.06	0.36	0.7	0.07	0.38	0.69
T = 100	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	0	1	0	0	1	0	0	1
Average $p(\bar{P}_r)$	0	0	0.8	0	0	0.94	0	0	0.98
Average $p^{\dagger}_{i,r}$	0.01	0.05	0.66	0.01	0.05	0.72	0.01	0.05	0.73
T = 500	N = 5			N = 10			N = 20		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
Selected rank	0	0	1	0	0	1	0	0	1
Average $p(\bar{P}_r)$	0	0	0.74	0	0	0.94	0	0	0.98
Average $p^{\dagger}_{i,r}$	0	0	0.62	0	0	0.72	0	0	0.71

TABLE 3. Experiment A3, 1000 Monte Carlo replications, 199 Bootstrap iterations.

	$\mathcal{N}(0,1)$						$t(4)$					
i.i.d.												
Resampling	N = 5			N = 10			N = 5			N = 10		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
T = 100	0	0.86	0.14	0	1	0	0	0.79	0.21	0	0.99	0.01
T = 500	0	0.46	0.54	0	0.99	0.01	0	0.48	0.52	0	0.98	0.02
$GARCH(1,1)$												
Resampling	N = 5			N = 10			N = 5			N = 10		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
T = 100	0	0.84	0.16	0	0.99	0.01	0	0.81	0.19	0	0.97	0.03
T = 500	0	0.45	0.55	0	0.97	0.03	0	0.36	0.64	0	0.83	0.17
$GARCH(1,1)$												
Wild	N = 5			N = 10			N = 5			N = 10		
	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$
T=100	0	0.78	0.22	0	0.99	0.01	0	0.78	0.22	0	0.95	0.05
T=500	0	0.57	0.43	0	0.89	0.11	0	0.49	0.51	0	0.83	0.17

TABLE 4. DGP D1-6. Sequential test procedure selection rate, 1000 Monte Carlo, 199 bootstrap iterations.

		Panel Rank Test			
		$\mathcal{H}_0$	$\mathcal{H}_1$	$\mathcal{H}_2$	$\mathcal{H}_3$
Model 1	$\bar{P}_r$	138.2	0.008	0.218	0
	$p\left(\bar{P}_r\right)$	0	1	1	1
Model 2	$\bar{P}_r$	125.2	1.407	0	
	$p\left(\bar{P}_r\right)$	0	1	1	
Model 3	$\bar{P}_r$	138.2	0.006	0	
	$p\left(\bar{P}_r\right)$	0	1	1	
Model 4	$\bar{P}_r$	123	0.736	0	
	$p\left(\bar{P}_r\right)$	0	1	1	

TABLE 5. Panel rank test statistics for each of the 4 specifications considered. 999 Bootstrap iterations, restricted constant, seasonal dummies, and 1 lagged first difference.