Robust Inference Methods for Latent Group Panel Models under Possible Group Non-Separation[*]

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Abstract

This paper presents robust inference methods for general linear hypotheses in linear panel data models with latent group structure in the coefficients. We employ a selective conditional inference approach, deriving the conditional distribution of coefficient estimates given the group structure estimated from the data. Our procedure provides valid inference under possible violations of group separation, where distributional properties of group-specific coefficients remain unestablished. Furthermore, even when group separation does hold, our method demonstrates superior finite-sample properties compared to traditional asymptotic approaches. This improvement stems from our procedure's ability to account for statistical uncertainty in the estimation of group structure. We demonstrate the effectiveness of our approach through Monte Carlo simulations and apply the methods to two datasets on: (i) the relationship between income and democracy, and (ii) the cyclicality of firm-level R&D investment.

Keywords: Clustering; hypothesis testing; Kmeans; selective inference; latent group structure.

JEL classification: C12, C23, C38.

1. Introduction

Latent group structure has recently become a popular approach for analyzing panel data. A partial list of research articles on this topic includes Lin and Ng (2012), Bonhomme and Manresa (2015), Su et al. (2016), Lumsdaine et al. (2023). This specification assumes that the coefficients vary across individual units but are homogeneous within each group. This approach provides a flexible yet manageable way to model heterogeneity. Latent group structure can accommodate various forms of heterogeneity. Since there can be several units in a group, the parameters can be estimated with high precision.

This paper addresses an important yet under-explored issue: Conducting valid inference for general linear hypotheses on group-specific slope parameters when the groups are not well separated in the population (i.e., when their parameters are not sufficiently different from each other). Such tests are crucial in various applications. For instance, testing the homogeneity of the entire slope parameter vector serves as a general test of group separation. Specifically, we may want to determine whether two or more groups are identical and can be combined into a single group. Additionally, there are instances where we may be interested in the homogeneity of only a subset of parameters. For example, we may want to identify which aspects of the parameter vectors contribute to group heterogeneity and explore whether a specific group pair shares any coefficient values. However, we cannot be sure that group separation exists and that the groups are well-defined. Even if we are interested in the value of a particular parameter, it would be desirable to have a testing procedure that does not require group separation. Section 2 presents more concrete empirical examples that illustrate the importance of these considerations.

The primary challenge in testing general linear hypotheses in panels with latent group structures is that the groups are estimated using the same data as the coefficient parameters. Therefore, we must account for statistical uncertainty in a group-structure estimator. However, when group separation does not hold, the asymptotic distribution of the coefficient estimators may not be accessible, making it difficult to compute the null distribution. Only limited results are available in the literature; for example, Bonhomme and Manresa (2015) provide some findings in an elementary setting in their supplementary material. It is important to note that consistency holds even without group separation. However, to conduct statistical inferences, we require distributional results. When group separation holds, as in testing the homogeneity of a subset of parameters, these distributional results are available,

allowing us to perform standard Wald tests. This testing procedure is valid because the estimator for the group structure is super-consistent, meaning that the estimated group structure equals the true one with very high probability in large samples, and, asymptotically, we can disregard the statistical uncertainty behind the estimation of the group structure. Nevertheless, in finite samples, it is unusual to recover the entire group structure exactly, and the asymptotic result may not capture the finite-sample behavior of the Wald test statistic.

Our approach utilizes selective conditional inference. Specifically, we employ the polyhedral method (Lee et al., 2016; Gao et al., 2024; Chen and Witten, 2023). In our case, the polyhedral method involves calculating the distribution of statistics conditional on the estimated group structure. We derive the distribution of the Wald test statistic for the linear hypothesis, accounting for the estimated group structure. The key point is that, once we condition on the estimated group structure and nuisance terms, the distribution becomes known and is a truncated χ^2 distribution, which can be computed analytically. The main challenge is characterizing the estimated group structure as a subset of the data space. We provide the analytical formulas for computing the conditioning set for two different estimation algorithms of the group structure.

We provide theoretical justifications for the proposed method in Section 4, and Monte Carlo simulations presented in Section 6 demonstrate that our methods perform effectively in finite samples. Our testing procedure achieves the desired size conditional on the estimated group structure. The theory is developed under the assumptions of normally distributed errors and homoskedasticity. The theoretical results are exact and are valid in finite samples. To assess the robustness of our procedure against potential violations of these assumptions, we conduct Monte Carlo simulations. Our findings indicate that the method performs well, particularly when the sample size is large, even when errors deviate from normality or exhibit heteroskedasticity, and when serial or cross-sectional correlations are present.

Even when group separation is present and consistent group structure estimation is possible, our approach outperforms conventional methods in finite samples. Note that the latent group structure can be estimated super-consistently under group separation. While this result is theoretically impressive and helpful, it remains uncertain whether it accurately reflects statistical behavior in finite samples. The estimated group structure in finite samples may not perfectly match the true one. Additionally, it is essential to note that the super-consistency of the group structure estimator and the resulting asymptotic distributions of the coefficient estimator are obtained pointwise, meaning we fix the data-

generating process. Although there has been limited research explicitly addressing this issue, it is reasonable to expect that these asymptotic results will not be uniform and may not provide accurate approximations when group separation is weak.[1] Therefore, accounting for the statistical uncertainty surrounding the estimated group structure is crucial, an aspect that existing asymptotic distributional results often overlook. Our method addresses this issue effectively. Indeed, simulation studies in Section 6 show that our method provides better size control in finite samples without sacrificing power.

We present two empirical examples to illustrate our testing procedure. First, we examine the heterogeneity in firm-level R&D investment dynamics, following the work of Loyo and Boot (2025). Second, we explore the relationship between income and democracy, based on the research by Bonhomme and Manresa (2015). In both instances, the naive estimates reveal substantial heterogeneity. However, our testing procedures yield more nuanced results, underscoring the importance of accounting for group structure in our estimations.

Relation to the literature

Our study falls into two strands of the literature: latent group structure and selective conditional inference. We discuss how our study contributes to each strand.

Latent group structure: Models with latent group structures have long been studied as clustering problems in statistics. In the case of a single cross-section ($T = 1$), the regression model with group-specific coefficients is referred to as a clusterwise regression model by Späth (1979). The author built an algorithm similar to the Kmeans algorithm (MacQueen, 1967), applying the idea of grouping similar units to a regression model with general regressors. A large number of studies then proposed different estimation methods and algorithms to estimate the parameters of the model, and the research area in statistics and operations research is still active (see, for instance, D'Urso et al., 2010; Carbonneau et al., 2011, 2012, 2014; Ingrassia et al., 2014; Bagirov et al., 2015; Park et al., 2017; Bagirov and Ugon, 2018; Karmitsa et al., 2022).

The emergence of similar literature in econometrics has occurred more recently. A seminal contribution in this field is Lin and Ng (2012), which examines two types of estimators that we consider in

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[1]The importance of uniformity and the potential danger of relying on pointwise asymptotic results are discussed in Leeb and Pötscher (2005). Andrews et al. (2020) provide theoretical discussions on establishing uniform asymptotic results.

this paper. The first estimator uses a clustering algorithm on unit-specific time-series parameter estimates. Specifically, we estimate the coefficients for each unit individually and then apply the Kmeans algorithm, which we refer to as the Two-Step Kmeans (TSK) estimator. The second estimator expands on this approach by simultaneously estimating the clustering structure and the parameters. This method is particularly useful when the parameters are time-varying, making unit-by-unit estimation impossible. Bonhomme and Manresa (2015) extend the Kmeans algorithm to estimate models with group-specific but time-varying intercepts (such intercepts are called grouped fixed effects (GFE)). We label it Panel Clusterwise Regression (PCR).[2] Currently, the literature to extend the method to different directions of the model is growing rapidly (see, for example, Sarafidis and Weber, 2015; Ke et al., 2015, 2016; Qian and Su, 2016; Su et al., 2016; Ando and Bai, 2016; Su and Ju, 2018; Wang et al., 2018; Zhang et al., 2019; Su et al., 2019; Cytrynbaum, 2020; Huang et al., 2020; Okui and Wang, 2021; Wang and Su, 2021; Bonhomme et al., 2022; Chetverikov and Manresa, 2022; Mugnier, 2022; Cheng et al., 2025; Su et al., 2023; Lu and Su, 2023; Lumsdaine et al., 2023; Yu et al., 2024; Wang et al., 2024; Loyo and Boot, 2025).

This paper contributes to the literature on panel data models with latent group structures by developing methods that are robust to violations of the group-separation assumption. Traditionally, the literature on latent group structures has relied on this group-separation assumption. However, its validity is not always guaranteed. Therefore, it is essential to establish inference procedures that are resilient to potential group non-separation.

Our study is somewhat related to the question of testing the number of groups. When the number of groups is overspecified, the group separation assumption is violated by construction. Among the papers proposing sequential testing, Lin and Ng (2012) and Wang et al. (2024) advocate the use of homogeneity tests such as Pesaran and Yamagata (2008), Ando and Bai (2015) for subgroups, while Lu and Su (2017) propose a residual-based LM test to be used at each iteration. Raiola and Salish (2025) argue that homogeneity testing is useful for examining the existence of latent group structure. Patton and Weller (2023) employ the sample splitting technique to establish valid procedures for homogeneity testing. Because of the nature of sample splitting, their procedure cannot use the entire sample for the estimation and inference, which may result in a loss of statistical power. Other papers in the literature rely on information criteria (e.g., Lin and Ng (2012), Bonhomme and Manresa (2015), Su et al. (2016), Yu et al. (2024), Wang et al. (2024), Loyo and Boot (2025)). Lu and Su (2017) provide

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[2] In the literature, this estimator may be called the GFE estimator. Our primary model does not include GFE, and the coefficients exhibit a grouped structure of heterogeneity. We use a different term to avoid confusion.

some comparison of the two approaches. Our focus differs because they concentrate on the number of groups, while we examine whether (a subset of) parameters exhibit commonality within (a subset of) groups. Although these questions are closely related, they are distinct.

Another related but distinct question is how to perform statistical inferences on common parameters when group-specific nuisance parameters are present. Our focus is on group-specific coefficients that are directly influenced by the estimation of group structure. For instance, González-Casasús (2025) shows that the asymptotic results for the common coefficient are not affected by overspecifying the number of groups. Our research complements theirs.

Selective conditional inference: Selective conditional inference is a hot topic in recent statistics literature. See Taylor and Tibshirani (2015a), Benjamini (2020), Kuchibhotla et al. (2022). It is also gaining growing attention in recent econometrics literature. See Andrews et al. (2021), Andrews et al. (2024), Akgun et al. (2025). This paper extends the scope of this selective inference method. The main issue addressed in the selective inference literature is the complication arising from the fact that using a sample to choose a null hypothesis and consecutively testing it with the same sample conflicts with the mathematical foundations of the classical tests, such as Wald, LM, or LR. This issue is sometimes referred to as *double dipping* (Kriegeskorte et al., 2009). Kuchibhotla et al. (2022) reviews these efforts with a particular emphasis on inference following model selection. The main problem is that testing a null hypothesis on model fit, following a procedure that best fits the sample at hand, results in highly anti-conservative test statistics (see Chen and Witten, 2023; Patton and Weller, 2023; Gao et al., 2024, for the consequences of homogeneity testing post-clustering). Two of the most popular solutions for double dipping are sample splitting and selective inference. As mentioned above, Patton and Weller (2023) proposed a split-sample method. Although simple to implement, their methodology has important drawbacks, such as the question of how to split the sample, invalidity under general forms of time series dependence, and loss of power due to the reduction of the number of observations (see Kuchibhotla et al., 2022, for a more detailed discussion on sample splitting).

This paper employs the so-called polyhedral method for selective inference. It has been used for testing group separation in simple clustering settings by Gao et al. (2024); Chen and Witten (2023); Chen and Gao (2024). We extend their approach to panel data models. Our first proposed test is based on the Kmeans estimates of the group membership structure using unit-specific time-series estimates. In this case, we derive a novel decomposition of the vector of unit-specific estimates, expressing it

as a function of the constrained least-squares estimator and the deviation of the estimator under the alternative hypothesis from the constrained estimates. Besides being based on the unit-specific estimators of a panel data model, our decomposition is also the most general one in the literature and includes the special cases of Chen and Witten (2023), Gao et al. (2024), Chen and Gao (2024), and Yun and He (2024).

Our second test, which is a novel contribution to the literature, is based on the PCR estimator (Bonhomme and Manresa, 2015). Determining the conditioning set for selective inference in this case presents several technical challenges. The PCR estimator simultaneously estimates the coefficient parameters and the group memberships without relying on individual coefficient estimators. This characteristic of the PCR estimator makes it challenging to calculate the conditioning set, specifically in deriving the vector orthogonal to the parameter relevant to the null hypothesis. Nonetheless, we have successfully derived an appropriate conditioning set that enables the procedure to be feasible. This contribution and its insights are expected to broaden the application of the selective inference approach.

While preparing this paper, we became aware of the contemporaneous and independent work by Wan et al. (2025), which investigates a related problem. We note several key distinctions between our approaches. First, our framework addresses general linear hypotheses, whereas Wan et al. (2025) focuses specifically on homogeneity testing. Second, our procedure can accommodate parameters that cannot be estimated through unit-by-unit procedures, such as group fixed effects (GFE). Third, we employ Wald statistics, yielding a testing procedure based on a truncated χ^2 distribution, which is much simpler to implement. These differences make our methodology applicable to a broader class of inference problems in panel data models.

Organization of the paper

Section 2 provides the settings and discusses empirical examples where our testing could be relevant. Sections 3 and 4 outline a methodology that generalizes the framework of Chen and Witten (2023) to panel data settings. Section 5 discusses potential extensions of the main analysis. These include models with unit-specific heterogeneity (for instance, Extension 1 of Bonhomme and Manresa, 2015 and Example 1 of Su et al., 2016), models with interactive fixed effects (Su and Ju, 2018, among others), models with time-varying grouped fixed effects (Bonhomme and Manresa, 2015; Loyo and Boot, 2025), and models with group-specific structural breaks (Lumsdaine et al., 2023). The results

of Monte Carlo simulations are included in Section 6. Empirical illustrations are given in Section 7. Section 8 concludes the paper with directions to future research.

Notation

Random variables are denoted by uppercase letters, and their realizations by the corresponding lowercase letters. Further, $\| \cdot \|$ denotes Euclidean norm, $\mathbf{1}\{\cdot\}$ is the indicator function, $\mathrm{bdiag}(\cdot)$ forms a block-diagonal matrix by given elements, $\otimes$ denotes the Kronecker product, $\odot$ denotes element-wise multiplication applied row-wise. For any vector $\mathbf{v}$, $\mathrm{dir}(\mathbf{v})$ stands for its direction (i.e., $\mathrm{dir}(\mathbf{v}) = \mathbf{v}/\|\mathbf{v}\|$). Additionally, $[\mathbf{v}]_s^h$ represents the vector formed by the rows from $(1 + h(s-1))$ to hs of the vector $\mathbf{v}$.

2. Settings

In this section, we introduce panel data models with latent group structure and define the null hypotheses of our testing problem. We also list empirical examples where our testing procedure is relevant.

2.1. Panel data models with latent group structure

We consider panel data models with a grouped pattern of heterogeneity. Our primary focus is testing general linear hypotheses about the group-specific slope coefficients. The key issue is how to account for the fact that the unknown group structure must be estimated from the data.

Suppose we observe a panel data set $\mathcal{D} = \{(Y_{it}, \mathbf{X}_{it}); i = 1, \ldots, N, t = 1, \ldots, T\}$ where the subscripts i and t denote the observational unit and the time period, respectively, Y_{it} represents a scalar dependent variable for unit i at time t, and $\mathbf{X}_{it} = (X_{1,it}, \ldots, X_{K,it})'$ is a vector of explanatory variables for unit i at time t with $X_{k,it}$ being the scalar k-th explanatory variable.

Consider the following panel data model with heterogeneous coefficients:

$$Y_{it} = \mathbf{X}_{it}'\boldsymbol{\beta}_i + U_{it}, \ i = 1, \ldots, N, \ t = 1, \ldots, T, \tag{1}$$

where $\boldsymbol{\beta}_i = (\beta_{1,i}, \ldots, \beta_{K,i})'$ is a $K \times 1$ vector of unknown coefficients, and U_{it} is the error term. Note that $\boldsymbol{\beta}_i$ depends on i, meaning that the coefficients are potentially heterogeneous.

We assume a grouped pattern of heterogeneity, where each unit i is assigned to one of G groups. The membership indicator $g_i \in \{1, \ldots, G\}$ signifies the group assignment for unit i. The group membership variables g_i, $i = 1, \ldots, N$, are unobserved and need to be estimated from data. Every

unit belongs to exactly one group. Units within a group share the same coefficient values, while units in different groups may have distinct ones. Specifically, we assume that $\boldsymbol{\beta}_i = \boldsymbol{\alpha}_g$ if $g_i = g$ with $\boldsymbol{\alpha}_g = (\alpha_{1,g}, \ldots, \alpha_{K,g})'$ representing the underlying group-specific coefficients.

The primary objective of this paper is to develop tests for general linear hypotheses that account for estimation uncertainty in the group assignments. To state the null hypothesis of interest, we need extra notation. We denote the data-dependent vector of group assignment variables as $\boldsymbol{\gamma}_{\mathcal{D}} = (g_{1,\mathcal{D}}, \ldots, g_{N,\mathcal{D}})'$. That is, $\boldsymbol{\gamma}_{\mathcal{D}}$ is an estimator of $\boldsymbol{\gamma} = (g_1, \ldots, g_N)$ based on the data set $\mathcal{D}$. We also define the vector of group specific coefficients as $\boldsymbol{\alpha}(\boldsymbol{\gamma}_{\mathcal{D}}) = [\boldsymbol{\alpha}_1'(\boldsymbol{\gamma}_{\mathcal{D}}), \ldots, \boldsymbol{\alpha}_G'(\boldsymbol{\gamma}_{\mathcal{D}})]'$, where $\boldsymbol{\alpha}_g(\boldsymbol{\gamma}_{\mathcal{D}}) = [\alpha_{1,g}(\boldsymbol{\gamma}_{\mathcal{D}}), \ldots, \alpha_{K,g}(\boldsymbol{\gamma}_{\mathcal{D}})]'$ with $\alpha_{k,g}(\boldsymbol{\gamma}_{\mathcal{D}})$ being the population slope coefficient for the k-th explanatory variable of the g-th estimated group, associated with the group estimates implied by the vector $\boldsymbol{\gamma}_{\mathcal{D}}$. We state the null hypothesis as follows:

$$\mathcal{H}_0 : R\boldsymbol{\alpha}(\boldsymbol{\gamma}_{\mathcal{D}}) = \mathbf{r} \tag{2}$$

where R is an $r \times GK$ nonrandom matrix with $\text{rank}(R) = r$ and $\mathbf{r}$ is an $r \times 1$ nonrandom vector.

Despite appearing to be a standard testing problem, the null hypothesis $\mathcal{H}_0$ presents several challenges, and testing it is nonstandard. These challenges arise because the null hypothesis depends on the group structure, $\boldsymbol{\gamma}$, which is unknown and needs to be estimated. When they are known, the usual Wald test statistic is applicable to $\mathcal{H}_0$ and is considered a standard testing problem. However, the Wald test statistic may lose its validity when the group structure is unobserved and estimated from the dataset before testing $\mathcal{H}_0$. A particularly important example is the homogeneity hypothesis, which posits that all or a subset of groups share the values of all or a subset of coefficients. The following subsection argues that this testing issue is practically relevant.

2.2. Examples

In this section, we demonstrate the practical importance of having valid tests of the null hypothesis $\mathcal{H}_0$ in three empirical examples.

Example 1: Convergence clubs. The literature on economic growth suggests that it may exhibit convergence properties. Furthermore, it has been noted that convergence patterns may exhibit heterogeneity across countries, which is hypothesized to be due to the presence of convergence clubs. Various methods for testing the hypothesis of convergence clubs are proposed by Canova (2004) and Phillips and Sul (2007), among others. Let the first difference of the natural logarithm of per capita

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GDP be given by

$$\Delta \log GDP_{it} = \rho_{g_i} \log GDP_{i,t-1} + \mathbf{W}'_{it}\boldsymbol{\psi}_{g_i} + U_{it}$$

where $\mathbf{W}_{it}$ is a vector of conditioning variables, t typically represents years, and i may denote countries or regions. Our model is derived by setting $Y_{it} = \Delta \log GDP_{it}$, $\mathbf{X}_{it} = (\log GDP_{i,t-1}, \mathbf{W}'_{it})'$ and $\boldsymbol{\alpha}_g = (\rho_g, \boldsymbol{\psi}'_g)'$ in (1). For example, assume that $K = 3$ and $G = 2$. In this case, the null hypothesis of a single convergence club is represented as the single restriction $\rho_1 = \rho_2$ and obtained by setting $\mathbf{r} = 0$ and $R = (1, 0, 0, -1, 0, 0)$ in (2), where the non-zero entries of R correspond to the regressors of interest and the zeros indicate the control variables. Note that the model of Canova (2004) includes unit-specific intercepts, an extension discussed in Section 5.1.

Example 2: Firm level R&D investment and the business cycle. The literature on the relationship between output and the R&D investment provides mixed evidence concerning the effect of output on R&D. As the evidence in Bachmann and Bayer (2014) suggests, a particular question pertains to its heterogeneity. A version of the model estimated by Loyo and Boot (2025) is

$$\Delta \log RD_{it} = \psi_{1,g_i}\Delta \log X_{st} + \mathbf{W}'_{it}\psi_{2,g_i} + U_{it},$$

where RD_{it} is the R&D investment of firm i in year t and X_{st} is the output of industry s. Setting $Y_{it} = \Delta \log RD_{it}$, $\mathbf{X}_{it} = (\Delta \log X_{st}, \mathbf{W}'_{it})'$ and $\boldsymbol{\alpha}_g = (\psi_{1,g}, \boldsymbol{\psi}'_{2,g})'$ corresponds to the model in (1). Loyo and Boot (2025) argues that group heterogeneity in the effect of output on the R&D investment may not be substantial. To address this issue, they propose an estimation method that incorporates information on variance heterogeneity, but they do not formally assess the extent of heterogeneity in the coefficients across groups. Supposing for simplicity that $K = 3$ and $G = 2$, this claim can be represented as $\psi_{1,1} = \psi_{1,2}$ such that $\mathbf{r} = 0$ and $R = (1, 0, 0, -1, 0, 0)$ in (2) as in the previous example. Note that the model estimated by Loyo and Boot (2025) incorporates time-varying grouped fixed effects. This extension of the main model is discussed in Section 5.2.

Example 3: Income and democracy. A typical application of panel models with latent group structure is the estimation of the relationship between income and democracy. Bonhomme and Manresa (2015) (See also Okui and Wang, 2021) estimate a model similar to

$$DEM_{it} = \rho_{g_i} DEM_{i,t-1} + \psi_{g_i} \log GDP_{i,t-1} + U_{it}$$

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where DEM_{it} is the Freedom House indicator of democracy and GDP_{it} is the per capita GDP of country i at year t. The model is obtained by setting $Y_{it} = DEM_{it}$, $\mathbf{X}_{it} = (DEM_{i,t-1}, \log GDP_{i,t-1})'$ and $\boldsymbol{\alpha}_g = (\rho_g, \psi_g)'$ in (1). Here, $K = 2$ and the authors choose $G = 4$. In their exercise with heterogeneous coefficients, they estimate two models: first, ψ_{g_i} is partially heterogeneous while $\rho_{g_i} = \rho$ for all i, and second, both are partially heterogeneous. To determine whether the coefficient of lagged democracy is equal across all groups, one may set

$$R = \begin{pmatrix} 1,0,0,0,0,0,-1,0 \\ 0,0,1,0,0,0,-1,0 \\ 0,0,0,0,1,0,-1,0 \end{pmatrix} \text{ and } \mathbf{r} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix},$$

whereas to test whether the coefficient of lagged income is equal for groups 3 and 4, we can select $R = (0,0,0,0,0,1,0,-1)$ and $\mathbf{r} = 0$.

3. Estimators

In this section, we discuss the estimation of the group membership variables g_i, $i = 1, \ldots, N$. The TSK estimator defined in Section 3.1 utilizes unit-specific estimates of model parameters to cluster the units into G groups. Section 3.2 introduces the PCR estimator that simultaneously estimates the coefficient parameters and the group memberships.

3.1. Two-Step Kmeans estimator

A straightforward method for estimating the group memberships and the group-specific slope parameters involves applying the standard Kmeans algorithm to unit-specific estimates of the slope parameters. Several studies in the literature employ this strategy. For instance, Patton and Weller (2023) and Wang et al. (2024) use unit-specific slope parameter estimates to cluster the units into different groups using Kmeans.

The TSK estimator of the group membership variables g_i, $i = 1, \ldots, N$, and the group-specific slopes $\boldsymbol{\alpha}_g$, is defined as

$$(\widetilde{\boldsymbol{\alpha}}_{1,\mathcal{D}}, \ldots, \widetilde{\boldsymbol{\alpha}}_{G,\mathcal{D}}, \tilde{g}_{1,\mathcal{D}}, \ldots, \tilde{g}_{N,\mathcal{D}}) = \underset{(\boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_G, g_1, \ldots, g_N)}{\arg\min} \sum_{i=1}^{N} \left\| \widehat{\boldsymbol{\beta}}_{i,\mathcal{D}} - \boldsymbol{\alpha}_{g_i} \right\|^2 \tag{3}$$

where $\widehat{\boldsymbol{\beta}}_{i,\mathcal{D}} = \left(\sum_{t=1}^{T} \mathbf{X}_{it} \mathbf{X}_{it}' \right)^{-1} \sum_{t=1}^{T} \mathbf{X}_{it} Y_{it}$ represents the unit-by-unit OLS estimator of $\boldsymbol{\beta}_i$. For any given $\boldsymbol{\gamma} = (g_1, \ldots, g_N)'$, this definition implies $\widetilde{\boldsymbol{\alpha}}_{g,\mathcal{D}}(\boldsymbol{\gamma}) = \arg\min_{(\boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_G)} \sum_{i=1}^{N} \|\widehat{\boldsymbol{\beta}}_{i,\mathcal{D}} - \boldsymbol{\alpha}_g\|^2$, and

for any given $\{\boldsymbol{\alpha}_g, g = 1, \ldots, G\}$, $\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}(\boldsymbol{\alpha}) = (\tilde{g}_{1,\mathcal{D}}, \ldots, \tilde{g}_{N,\mathcal{D}})' = \arg\min_{(g_1,\ldots,g_N)} \sum_{i=1}^{N} \|\widehat{\boldsymbol{\beta}}_{i,\mathcal{D}} - \boldsymbol{\alpha}_{g_i}\|^2$. Algorithm 1 which takes a realization of $\{\widehat{\boldsymbol{\beta}}_{i,\mathcal{D}}; i = 1, \ldots, N\}$ as input summarizes the steps of the standard iterative Kmeans algorithm associated with the above estimator.

Algorithm 1: Two-Step Kmeans

Input: Realization $\{\widehat{\boldsymbol{\beta}}_{i,\text{\scriptsize$\not$}}; i = 1, \ldots, N\}$ of $\{\widehat{\boldsymbol{\beta}}_{i,\mathcal{D}}; i = 1, \ldots, N\}$; number of groups G
Output: Group assignment vector $\widetilde{\boldsymbol{\gamma}}_{\text{\scriptsize$\not$}}$; group means $\widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}(\widetilde{\boldsymbol{\gamma}}_{\text{\scriptsize$\not$}})$; number of iterations M

1 Initialize $\widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}^{(0)}$ for all $g = 1, \ldots, G$; set $m = 0$

2 **repeat**

3   **for** $i = 1$ **to** N **do**

4   Assign cluster: $\tilde{g}_{i,\text{\scriptsize$\not$}}^{(m+1)} = \arg\min_{g \in \{1,\ldots,G\}} \left\| \widehat{\boldsymbol{\beta}}_{i,\text{\scriptsize$\not$}} - \widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}^{(m)} \right\|^2$

5   **end**

6   **for** $g = 1$ **to** G **do**

7   Compute:

$$\widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}^{(m+1)} = \frac{1}{\tilde{n}_{g,\text{\scriptsize$\not$}}^{(m+1)}} \sum_{i=1}^{N} \widehat{\boldsymbol{\beta}}_{i,\text{\scriptsize$\not$}} \cdot \mathbf{1}\left\{ \tilde{g}_{i,\text{\scriptsize$\not$}}^{(m+1)} = g \right\}$$

        where $\tilde{n}_{g,\text{\scriptsize$\not$}}^{(m+1)} = \sum_{i=1}^{N} \mathbf{1}\left\{ \tilde{g}_{i,\text{\scriptsize$\not$}}^{(m+1)} = g \right\}$

8   **end**

9   Update $m \leftarrow m + 1$

10 **until** $\tilde{g}_{i,\text{\scriptsize$\not$}}^{(m+1)} = \tilde{g}_{i,\text{\scriptsize$\not$}}^{(m)}$ *for all* $i = 1, \ldots, N$

11 Set $M = m$; $\widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}(\widetilde{\boldsymbol{\gamma}}_{\text{\scriptsize$\not$}}) = \widetilde{\boldsymbol{\alpha}}_{g,\text{\scriptsize$\not$}}^{(M)}$; $\widetilde{\boldsymbol{\gamma}}_{\text{\scriptsize$\not$}} = (\tilde{g}_{1,\text{\scriptsize$\not$}}^{(M)}, \ldots, \tilde{g}_{N,\text{\scriptsize$\not$}}^{(M)})'$

It is easily seen that $\widetilde{\boldsymbol{\alpha}}_{g,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \tilde{n}_{g,\mathcal{D}}^{-1} \sum_{i=1}^{N} \widehat{\boldsymbol{\beta}}_{i,\mathcal{D}} \mathbf{1}\{\tilde{g}_{i,\mathcal{D}} = g\}$ where $\tilde{n}_{g,\mathcal{D}} = \sum_{i=1}^{N} \mathbf{1}\{\tilde{g}_{i,\mathcal{D}} = g\}$. While $\widetilde{\boldsymbol{\alpha}}_{g,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ is not obtained as the least squares estimator applied to the set of observations in group g, it can be shown under mild conditions that $\widetilde{\boldsymbol{\alpha}}_{g,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \xrightarrow{p} \boldsymbol{\alpha}_g$ as $(T, N) \to \infty$. This estimator is the Mean Group estimator applied to each group. The advantages of the Mean Group estimator in short dynamic panels with heterogeneous coefficients are well documented in the early literature (Pesaran and Smith, 1995).

Algorithm 1 is easy to implement. It is the Kmeans clustering, which is commonly available in most statistical software packages, with initial values obtained by least squares. Additionally, to examine some basic sub-cases of the null hypothesis $\mathcal{H}_0$ regarding parameter homogeneity across groups, a simple adjustment to the computational procedures outlined by Chen and Witten (2023) and Chen and Gao (2024) can be utilized. However, these studies focus on a narrow null hypothesis of equality between two cluster centers and operate under restrictive assumptions that may not hold in typical economic panel data settings. Our work expands the scope of the test by introducing a more realistic

set of assumptions for economic applications.

3.2. Panel Clusterwise Regression estimator

Next, we discuss an alternative estimator, the panel clusterwise regression (PCR) estimator. This estimator has gained popularity in the econometrics literature with the work of Bonhomme and Manresa (2015). The main advantage is that it can accommodate a broader class of models. Algorithm 1 requires unit-by-unit coefficient estimates. It results in the shortcoming of not being able to accommodate important generalizations of the model in (1), such as grouped fixed effects (Bonhomme and Manresa, 2015) or group-specific structural breaks (Okui and Wang, 2021). In addition, it is unfeasible when $T < K$. The PCR estimator can be used to estimate these models.

Consider the following least squares estimator of the group membership variables and the group-specific parameters:

$$(\widehat{\boldsymbol{\alpha}}_{1,\mathcal{D}}, \ldots, \widehat{\boldsymbol{\alpha}}_{G,\mathcal{D}}, \hat{g}_{1,\mathcal{D}}, \ldots, \hat{g}_{N,\mathcal{D}}) = \underset{(\boldsymbol{\alpha}_1,\ldots,\boldsymbol{\alpha}_G,g_1,\ldots,g_N)}{\arg\min} \sum_{i=1}^{N} \sum_{t=1}^{T} (Y_{it} - \mathbf{X}'_{it}\boldsymbol{\alpha}_{g_i})^2. \quad (4)$$

The estimator and its numerical implementations are well-studied in the literature. We rely on the following algorithm, which is a panel data generalization of the clusterwise regression algorithm (Späth, 1979), similar to the main algorithm of Bonhomme and Manresa (2015). It iterates between two optimizations: for any given $\boldsymbol{\gamma}$, we have $\widehat{\boldsymbol{\alpha}}_{g,\mathcal{D}}(\boldsymbol{\gamma}) = \arg\min_{(\boldsymbol{\alpha}_1,\ldots,\boldsymbol{\alpha}_G)} \sum_{i=1}^{N} \sum_{t=1}^{T}(Y_{it} - \mathbf{X}'_{it}\boldsymbol{\alpha}_{g_i})^2$, and for any given $\{\boldsymbol{\alpha}_g, g = 1,\ldots,G\}$, $\widehat{\boldsymbol{\gamma}}_{\mathcal{D}} = (\hat{g}_{1,\mathcal{D}},\ldots,\hat{g}_{N,\mathcal{D}}) = \arg\min_{(g_1,\ldots,g_N)} \sum_{i=1}^{N}(Y_{it} - \mathbf{X}'_{it}\boldsymbol{\alpha}_g)^2$. Apart from the absence of grouped fixed effects and the presence of group-specific slope coefficients in our main model, Algorithm 2, which takes a realization of the original data set $\mathcal{D}$ as input, is equivalent to the main iterative algorithm of Bonhomme and Manresa (2015). In Section 5.2, we discuss the extension to the models with grouped fixed effects.

4. Test Statistics

In this section, we propose two main test statistics, each corresponding to one of the estimators discussed in the previous section. In Section 4.1, we introduce the selective Type I error rate and other preliminary definitions. In Section 4.2, the tests based on the TSK estimator are derived, and Section 4.3 is concerned with the derivation of the PCR estimator-based tests.

Algorithm 2: Panel Clusterwise Regression

Input: Realization $\mathpzc{d} = \{(y_{it}, \mathbf{x}_{it}); i = 1, \ldots, N, t = 1, \ldots, T\}$ of $\mathpzc{D}$; number of groups G

Output: Group assignment vector $\widehat{\boldsymbol{\gamma}}_{\mathpzc{d}}$; group means $\widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}(\widehat{\boldsymbol{\gamma}}_{\mathpzc{d}})$; number of iterations M

1 Initialize $\widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}^{(0)}$ for all $g = 1, \ldots, G$; set $m = 0$

2 repeat

3 $\quad$ **for** $i = 1$ **to** N **do**

4 $\quad\quad$ Assign group:

$$\hat{g}_{i,\mathpzc{d}}^{(m+1)} = \underset{g \in \{1, \ldots, G\}}{\arg\min} \sum_{t=1}^{T} \left(y_{it} - \mathbf{x}_{it}' \widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}^{(m)} \right)^2$$

5 $\quad$ **end**

6 $\quad$ **for** $g = 1$ **to** G **do**

7 $\quad\quad$ Update group parameters:

$$\widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}^{(m+1)} = \left(\sum_{i=1}^{N} \sum_{t=1}^{T} \mathbf{x}_{it}\mathbf{x}_{it}' \cdot \mathbf{1}\left\{ \hat{g}_{i,\mathpzc{d}}^{(m+1)} = g \right\} \right)^{-1} \sum_{i=1}^{N} \sum_{t=1}^{T} \mathbf{x}_{it}y_{it} \cdot \mathbf{1}\left\{ \hat{g}_{i,\mathpzc{d}}^{(m+1)} = g \right\}$$

8 $\quad$ **end**

9 $\quad$ Update $m \leftarrow m + 1$

10 until $\hat{g}_{i,\mathpzc{d}}^{(m+1)} = \hat{g}_{i,\mathpzc{d}}^{(m)}$ *for all* $i = 1, \ldots, N$

11 Set $M = m$; $\widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}(\widehat{\boldsymbol{\gamma}}_{\mathpzc{d}}) = \widehat{\boldsymbol{\alpha}}_{g,\mathpzc{d}}^{(M)}$; $\widehat{\boldsymbol{\gamma}}_{\mathpzc{d}} = (\hat{g}_{1,\mathpzc{d}}^{(M)}, \ldots, \hat{g}_{N,\mathpzc{d}}^{(M)})'$

4.1. Conditional inference in panel models

In this section, we establish the testing situation and define the Type I error rate we aim to control. The construction of the null hypothesis (2) indicates that the group structure is estimated from the data and may differ from the population's group structure. Under (2), the group separation may not hold, and the number of groups may be overspecified.

The null hypothesis (2) is random because $\boldsymbol{\gamma}_{\mathpzc{D}}$ is computed from the data. The matrix R and the vector $\mathbf{r}$ in (2) are non-random. Thus, the coefficients being tested are fixed for any *given* $\boldsymbol{\gamma}$. However, when the groups are unknown and estimated from the data, the coefficients become random because they depend on $\mathpzc{D}$. At first glance, the randomness of the null hypothesis may seem counterintuitive. Nonetheless, introducing this randomness is important for handling situations in which the groups are not well-defined under the null hypothesis. Failing to acknowledge the randomness in the estimated group structure undermines the conventional outcomes related to the null distribution of the test statistics for $\mathcal{H}_0$ in (2), such as the use of a χ^2 distribution to compute the critical value for the Wald test, as shown in Section 6.

We design tests that control the Type I error conditional on the estimated group structure. This approach eliminates the randomness in the null hypothesis. Below, we define the concept of selective Type I error rate.

Definition 1. A test of $\mathcal{H}_0$ controls the selective Type I error rate at level $\alpha \in (0,1)$ if

$$\mathbb{P}_{\mathcal{H}_0}\left[\text{Reject } \mathcal{H}_0 \text{ at level } \alpha \mid \boldsymbol{\gamma}_{\mathcal{D}} = \boldsymbol{\gamma}_{\mathscr{d}}\right] \leq \alpha, \tag{5}$$

where $\boldsymbol{\gamma}_{\mathcal{D}}$, is a data dependent choice for $\boldsymbol{\gamma}$, such as the output of Algorithm 1 or Algorithm 2, and $\boldsymbol{\gamma}_{\mathscr{d}}$ is its sample counterpart associated to the realization $\mathscr{d}$ of $\mathcal{D}$.

The definition states that a test controls for the selective Type I error rate if the probability of rejecting $\mathcal{H}_0$ when it is true is at most α across all realizations of the data set $\mathcal{D}$, which results in the same group membership estimates. Below, we demonstrate how to construct tests by conditioning on the estimated groups, which asymptotically control for the selective Type I error rate.

4.2. Tests based on the Two-Step Kmeans estimator

We now discuss our testing procedures. First, we consider the circumstances under which the TSK estimator is used. Our test statistic is based on the conditional distribution of the quadratic form of the constrained estimator given the estimated group structure. The conditional distribution follows a truncated χ^2 distribution.

The test statistic we consider is the Wald test statistic based on the TSK estimator associated with the null hypothesis $\mathcal{H}_0$, whose conditional distribution is used for testing. It is defined as

$$H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = [R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}]'\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}] \tag{6}$$

where $\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = [\widetilde{\boldsymbol{\alpha}}'_{1,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}), \ldots, \widetilde{\boldsymbol{\alpha}}'_{G,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})]'$, $\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = R\widetilde{\Sigma}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})R'$ with $\widetilde{\Sigma}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ being an estimator of the variance of $\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$, denoted as $\Sigma_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$.

We assume that $\widehat{\mathbf{B}}_{\mathcal{D}} \sim N(\mathbf{B}, \sigma^2 I_N \otimes \Sigma^{-1})$ where $\widehat{\mathbf{B}}_{\mathcal{D}} = (\widehat{\boldsymbol{\beta}}'_{1,\mathcal{D}}, \ldots, \widehat{\boldsymbol{\beta}}'_{N,\mathcal{D}})'$ be the $NK \times 1$ vector of estimated slope coefficients, $\mathbf{B}$ is an $NK \times 1$ vector of the true values of the coefficients, $\sigma^2 > 0$ is a constant, and Σ is an invertible $K \times K$ matrix. Here, we implicitly assume that the regression error is normally distributed and homoskedastic, and that $\sum_{t=1}^{T} \mathbf{X}_{it}\mathbf{X}'_{it} = \Sigma$ for all i. In this setting, we have $\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \sigma^2 R\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}R'$, where $\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \text{diag}(\widetilde{n}_{1,\mathcal{D}}, \ldots, \widetilde{n}_{G,\mathcal{D}}) \otimes \Sigma$.

We examine the conditional distribution of $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ under the assumption that the estimator of the group structure is $\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}$. However, obtaining this distribution is quite challenging. Therefore, we

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condition on additional random variables that are independent of $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$. We decompose $\widehat{\mathbf{B}}_{\mathcal{D}}$ into two components: one that is related to $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ and another that is independent of it.

Our derivation of the conditional distribution is based on the deviations from the constrained estimator of $\boldsymbol{\alpha}$. Describing the constrained estimator, denoted as $\tilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$, requires newly introduced notation. Define $\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = D(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \otimes I_K$ where $D(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ is the $N \times G$ matrix of group dummies based on the TSK estimator $\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}$ and I_K is the K-dimensional identity matrix. The TSK estimator of the group-specific slope coefficients can be written as $\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = (\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})'\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}))^{-1}\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})'\widehat{\mathbf{B}}_{\mathcal{D}}$. The constrained estimator is then given by

$$\widetilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}R'[R\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}R']^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}] \tag{7}$$

which follows from the standard textbook formula of the constrained least squares estimator (see Greene, 2011, p 122, for instance).

We now obtain the following decomposition:

$$\widehat{\mathbf{B}}_{\mathcal{D}} = \mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})\widetilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) + P_{(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}),R)}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}] + M_{\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})}\widehat{\mathbf{B}}_{\mathcal{D}} \tag{8}$$

where

$$P_{(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}),R)} = \mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}R'[R\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}R']^{-1},$$

$$\text{and } M_{\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})} = I_{NK} - (I_N \otimes \Sigma^{-1})\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})'\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}))^{-1}\widetilde{n}_{\Sigma}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})'\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}))^{-1}\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})'$$

The first term in (8) is the vector of constrained estimates of the group means under $\mathcal{H}_0$. The second term is the deviations of the unconstrained grouped means from the constrained estimates. The third term is the vector of deviations of the unit-specific estimates from the unconstrained group means. The decomposition in Equation (8) is important because it allows us to measure the distance of the unconstrained estimates from the constrained estimates of the group means through the second term of the right-hand side. The test statistic $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ can easily be expressed in the second term of (8). To see this, first note that $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \left\| \widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1/2}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}] \right\|^2$. Since for any vector $\mathbf{v}$ we have $\mathbf{v} = \|\mathbf{v}\|\text{dir}(\mathbf{v})$, applying this identity to $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$, we obtain

$$\widehat{\mathbf{B}}_{\mathcal{D}} = \sqrt{H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})}P_{(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}),R)}\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{1/2}\widetilde{\mathbf{J}}_R(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) + \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \tag{9}$$

where

$$\widetilde{\mathbf{J}}_R(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \text{dir}\{\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1/2}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}]\},$$

$$\mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})\widetilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) + M_{\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})}\widehat{\mathbf{B}}_{\mathcal{D}}.$$

To the best of our knowledge, ours is the first paper in the literature that considers a decomposition at this level of generality. For instance, Chen and Witten (2023) consider the equality of the centers of only two clusters, Yun and He (2024) focused on the equality of all cluster centers, and Chen and Gao (2024) developed a test for the equality of the mean of a single feature. Our decomposition enables consideration of general linear constraints by selecting different matrices R. Furthermore, all the decompositions proposed in the aforementioned literature are special cases of (9).

Lastly, given the estimated group structure, we derive the conditional distribution of the quadratic form defined above. Let $\widetilde{\Sigma}_{R,\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})$ be the realization of $\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ associated with the realization $\mathcal{d}$ of $\mathcal{D}$, $\widetilde{\boldsymbol{\alpha}}_{\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})$ that of $\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$, and $\mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})$ that of $\mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$. Define the conditioning set:

$$\mathcal{A}_{TSK} = \left\{ \bigcap_{m=0}^{M} \left\{ \widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}^{(m)} = \widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}^{(m)} \right\}, \widetilde{\mathbf{J}}_R(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \tilde{\mathbf{j}}_R(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}), \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) \right\}$$

where $\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}^{(m)} = (\tilde{g}_{1,\mathcal{d}}^{(m)}, \ldots, \tilde{g}_{N,\mathcal{d}}^{(m)})'$ and $\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}^{(m)}$ is its population counterpart. The conditioning set $\mathcal{A}_{TSK}$ contains more information than the condition in Definition 1. The first term implies that we focus on the realizations of $\mathcal{D}$ that produce the same group membership estimates at each iteration of Algorithm 1 as the current realization. Although this is more restrictive than conditioning solely on the final group membership estimates, it greatly simplifies the analytical formulas for the truncation set (Chen and Witten, 2023). Moreover, to obtain a nuisance-free conditional distribution of the test statistic, we need the second and third terms (see also a related discussion in Gao et al., 2024). By the law of iterated expectations, conditioning on these additional terms does not affect the Type I error rate (see also Taylor and Tibshirani, 2015b).

Now we can state the following result, which shows that the asymptotic conditional distribution of the test statistic $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ is truncated χ_r^2.

Theorem 1. Suppose that $\widehat{\mathbf{B}}_{\mathcal{D}} \sim N(\mathbf{B}, \sigma^2 I_N \otimes \Sigma^{-1})$, $\sigma^2 > 0$, and Σ is nonsingular. Then, under H_0, $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \mid \mathcal{A}_{TSK} \sim \chi_r^2|_{\mathcal{S}_{TSK}}$ with $\chi_r^2|_{\mathcal{S}_{TSK}}$ a χ_r^2 random variable truncated to the set $\mathcal{S}_{TSK}$ which is given by

$$\mathcal{S}_{TSK} = \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{m=0}^{M} \{ \widetilde{\boldsymbol{\gamma}}_{\mathcal{d}(\phi)}^{(m)} = \widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}^{(m)} \} \right\} \tag{10}$$

where $\mathcal{d}(\phi) = \{ \widehat{\boldsymbol{\beta}}_{i,\mathcal{d}}(\phi); i = 1, \ldots, N \}$ with $\widehat{\boldsymbol{\beta}}_{i,\mathcal{d}}(\phi) = [\widehat{\mathbf{b}}_{\mathcal{d}}(\phi)]_i^K$ and

$$\widehat{\mathbf{b}}_{\mathcal{d}}(\phi) = \phi P_{(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}),R)} \widetilde{\Sigma}_{R,\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})^{1/2} \tilde{\mathbf{j}}_R(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) + \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}). \tag{11}$$

Equation (11) defines a perturbation of the vector $\widehat{\mathbf{b}}$ as a function of the scalar ϕ. Let $h_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})$ be the realization of $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$ associated with the data $\mathcal{d}$. When $\phi = \sqrt{h_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})}$, the original vector $\widehat{\mathbf{b}}_{\mathcal{d}}$ is obtained. If $\phi > \sqrt{h_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})}$, the data set is perturbed so that its deviation from the null hypothesis becomes more pronounced. Conversely, if $\phi < \sqrt{h_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})}$, the data is perturbed to bring it closer to the null hypothesis. The theorem states that the truncation set $\mathcal{S}_{TSK}$ consists of the values of ϕ for which Algorithm 1 yields the same groups when applied to $\widehat{\mathbf{b}}_{\mathcal{d}}(\phi)$ as it does with the original vector $\widehat{\mathbf{b}}$. The analytical formulas for computing the truncation set $\mathcal{S}_{TSK}$ will be derived in Section A.

4.3. Tests based on the Panel Clusterwise estimator

Next, we examine the scenario where the parameters are estimated using the PCR estimator. The process of constructing the test is similar to that of the TSK estimator, although there are subtle differences. Specifically, a different decomposition is needed to derive the conditional distribution of the estimator.

In this case, the test statistic is given by

$$H_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = [R\widehat{\boldsymbol{\alpha}}_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}]'\widehat{\Sigma}_{R,\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) - \mathbf{r}] \tag{12}$$

where $\widehat{\boldsymbol{\alpha}}_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = [\widehat{\boldsymbol{\alpha}}'_{1,\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}), \ldots, \widehat{\boldsymbol{\alpha}}'_{G,\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})]'$, $\widehat{\Sigma}_{R,\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = R\widehat{\Sigma}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})R'$ with $\widehat{\Sigma}_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})$ being an estimator of $\Sigma_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = \mathrm{V}[\widehat{\boldsymbol{\alpha}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})]$. To provide the explicit formula of $\Sigma_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})$, we introduce the following notation: $\mathbb{X}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = [\mathbb{D}_{T,1}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \odot X, \ldots, \mathbb{D}_{T,G}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \odot X]$. Using this notation, we write $\Sigma_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = \sigma^2[\mathbb{X}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})'\mathbb{X}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}})]^{-1}$.

We derive a decomposition of observations. Note that in this design, all statistics depend on data only through $\mathbf{s}_i = \sum_{t=1}^{T} \mathbf{X}_{it} Y_{it}$. $\mathbf{s}_i$ is $K \times 1$. Let $\mathbf{s} = (\mathbf{s}'_1, \ldots, \mathbf{s}'_N)'$. Thus, $\mathbf{s}$ is $NK \times 1$. Let $\mathbb{X}$ be defined as follows. $X_i = (\mathbf{X}_{i1}, \ldots, \mathbf{X}_{iT})'$ is a $T \times K$ matrix. Then $\mathbb{X}$ is the $NT \times NK$ block diagonal matrix whose i-th block is X_i. Note that $\mathbb{X}(\boldsymbol{\gamma})$ is an $NT \times GK$ matrix. We write

$$\mathbf{s} = \mathbb{X}'\mathbf{Y}.$$

The formula of the group-specific coefficient can also be written in terms of $\mathbf{s}$ such that

$$\widehat{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) = [\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbf{s},$$

where $\mathbb{D}(\boldsymbol{\gamma}) = D(\boldsymbol{\gamma}) \otimes I_K$ and is an $NK \times GK$ matrix. The decomposition also depends on the constrained PCR estimator of $\boldsymbol{\alpha}(\boldsymbol{\gamma}) = [\boldsymbol{\alpha}_1(\boldsymbol{\gamma})', \ldots, \boldsymbol{\alpha}_G(\boldsymbol{\gamma})']'$ obtained by imposing $\mathcal{H}_0$, denoted $\widehat{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\boldsymbol{\gamma})$

is given by

$$\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma}) = \widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - [\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}].$$

We use the following decomposition.

$$\begin{aligned}
\mathbf{s} &= \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}] + \mathbf{W}_{PCR}(\boldsymbol{\gamma}) \\
&= \widehat{\mathbb{P}}(\boldsymbol{\gamma})j_{\mathscr{D}}(\boldsymbol{\gamma}) + \mathbf{W}_{PCR}(\boldsymbol{\gamma}),
\end{aligned}$$

where

$$\begin{aligned}
\widehat{\mathbb{P}}(\boldsymbol{\gamma}) &= \mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1} \\
&\quad \times (R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})\mathbb{D}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R')^{1/2},
\end{aligned}$$

$$j_{\mathscr{D}}(\boldsymbol{\gamma}) = (R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}R')^{-1/2}\left[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}\right],$$

and

$$\mathbf{W}_{PCR}(\boldsymbol{\gamma}) = \mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma}) + \mathbb{X}(\boldsymbol{\gamma})'\widehat{\mathbf{U}}(\boldsymbol{\gamma})$$

noting that $\widehat{\mathbf{U}}(\boldsymbol{\gamma}) = \mathbf{Y} - \mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma})$. Note that this decomposition is purely algebraic and holds for any $\boldsymbol{\gamma}$. So, it is valid for $\boldsymbol{\gamma} = \widehat{\boldsymbol{\gamma}}_{\mathscr{d}}$.

We consider the following conditioning set:

$$\mathscr{A}_{PCR} = \left\{ \bigcap_{m=0}^{M}\left\{\widehat{\boldsymbol{\gamma}}_{\mathscr{D}}^{(m)} = \widehat{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)}\right\}, \widehat{\mathbf{J}}_{R}(\widehat{\boldsymbol{\gamma}}_{\mathscr{D}}) = \widehat{\mathbf{j}}_{R}(\widehat{\boldsymbol{\gamma}}_{\mathscr{d}}), \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathscr{D}}) = \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\}$$

where $\widehat{\Sigma}_{R,\mathscr{d}}(\widehat{\boldsymbol{\gamma}}_{\mathscr{d}})$ be the realization of $\widehat{\Sigma}_{R,\mathscr{D}}(\widehat{\boldsymbol{\gamma}}_{\mathscr{D}})$ associated with the realization $\mathscr{d}$ of $\mathscr{D}$, $\widehat{\boldsymbol{\alpha}}_{\mathscr{d}}(\widehat{\boldsymbol{\gamma}}_{\mathscr{d}})$ that of $\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\widehat{\boldsymbol{\gamma}}_{\mathscr{D}})$, and $\mathbf{w}_{TSK}(\widehat{\boldsymbol{\gamma}}_{\mathscr{d}})$ that of $\mathbf{W}_{TSK}(\widehat{\boldsymbol{\gamma}}_{\mathscr{D}})$, and $\widehat{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)} = (\hat{g}_{1,\mathscr{d}}^{(m)}, \ldots, \hat{g}_{N,\mathscr{d}}^{(m)})'$ and $\widehat{\boldsymbol{\gamma}}_{\mathscr{D}}^{(m)}$ is its population counterpart.

The following result summarizes how to construct a test statistic that successfully controls the Type I error rate.

Theorem 2. Suppose that $\mathbf{X}_{it}$ is non-random, $\mathbf{s} \sim N(\mathbb{X}'\mathbf{XB}, \sigma^2\mathbb{X}'\mathbb{X})$ and $\sum_{t=1}^{T}\mathbf{X}_{it}\mathbf{X}_{it}' = \Sigma$ for any i, where Σ is nonsingular. Then, under H_0, $H_{PCR}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{D}}) \mid \mathscr{A}_{PCR} \sim \chi_r^2|_{\mathscr{S}_{PCR}}$ with $\chi_r^2|_{\mathscr{S}_{PCR}}$ a χ_r^2 random variable truncated to the set $\mathscr{S}_{PCR}$ which is given by

$$\mathscr{S}_{PCR} = \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{m=0}^{M}\{\widehat{\boldsymbol{\gamma}}_{\mathscr{d}(\phi)}^{(m)} = \widehat{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)}\} \right\} \tag{13}$$

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where

$$\mathbf{s}(\phi) = \phi P_{(\mathbf{x}(\widehat{\boldsymbol{\gamma}}_{\mathscr{A}}),R)}\widehat{\mathbf{j}}_R(\widehat{\boldsymbol{\gamma}}_{\mathscr{A}}) + \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathscr{A}}). \tag{14}$$

The theorem assumes that $\mathbf{s} \sim N(\mathbb{X}'\mathbf{X}\mathbf{B}, \sigma^2\mathbb{X}'\mathbb{X})$. This assumption holds when the regression errors are normally distributed and homoskedastic. Moreover, the data matrix is identical across i ($\sum_{t=1}^{T}\mathbf{X}_{it}\mathbf{X}'_{it} = \Sigma$ for any i). A representative example is $\Sigma = I_K$, that is, the data matrix for each i is normalized. Note that we make similar assumptions for the TSK procedure.

4.4. Variance estimation

We now describe the variance estimators used for the TSK and PCR procedures. In the theoretical results presented above, we assume that the variances are known. However, in practice, they are usually unknown and need to be estimated. In the simulations presented later, we examine the performance of our procedures with estimated variances. Note that while both TSK and PCR estimators have different variances. Hence, we use different estimators for the two methods.

The TSK estimator is based on unit-level time-series regressions. Since the group estimator is simply the average of these unit-specific slope estimates, its sampling variation is driven by the cross-sectional dispersion of the individual OLS coefficients. This insight underlies the non-parametric variance estimator of Pesaran (2006), later shown by Pesaran and Tosetti (2011) to be robust to both spatial and serial dependence under mild conditions on the error structure. For group g, the estimator takes the form

$$\widetilde{\Sigma}_{g,\mathscr{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{D}}) = \frac{1}{\tilde{n}_{g,\mathscr{D}}(\tilde{n}_{g,\mathscr{D}} - 1)}\sum_{i=1}^{N}\mathbf{1}\{\tilde{g}_{i,\mathscr{D}} = g\}\left[\widehat{\boldsymbol{\beta}}_{i,\mathscr{D}} - \widetilde{\boldsymbol{\alpha}}_{g,\mathscr{D}}(\boldsymbol{\gamma})\right]\left[\widehat{\boldsymbol{\beta}}_{i,\mathscr{D}} - \widetilde{\boldsymbol{\alpha}}_{g,\mathscr{D}}(\boldsymbol{\gamma})\right]'. \tag{15}$$

This expression is the sample covariance matrix of the unit-level slope estimators within group g, scaled appropriately by the group size. It is non-parametric and places no restrictions on how U_{it} may be correlated both across units and over time, provided that a suitable law of large numbers holds in the cross-section.

In contrast, the PCR estimator relies on a pooled regression within each group, which aggregates information across units. Its variance, therefore, depends on the long-run covariance structure of the group-level score process. To estimate this object, we use the Driscoll-Kraay estimator (Driscoll and Kraay, 1998), which is designed precisely for panels exhibiting arbitrary cross-sectional dependence

and serial correlation. Let $\widehat{U}_{it}$ denote the pooled residuals and define the Bartlett weights

$$
w_{ts} = k_T\left(\frac{|t-s|}{L_T}\right), \qquad k_T(x) = \begin{cases} 1-x, & 0 \le x \le 1, \\ \\ 0, & \text{otherwise.} \end{cases}
$$

For each group g, the Driscoll–Kraay covariance estimator is

$$
\widehat{\Sigma}_{g,\mathcal{D}}(\widehat{\gamma}_{\mathcal{D}}) = Q_g^{-1}\left[\frac{1}{T^2}\sum_{i,j=1}^{N}\sum_{t,s=1}^{T}\frac{w_{ts}}{\hat{n}_{g,\mathcal{D}}^2}\mathbf{X}_{it}\mathbf{X}_{js}'\widehat{U}_{it}\widehat{U}_{js}\mathbf{1}\{\hat{g}_{i,\mathcal{D}}=g\}\mathbf{1}\{\hat{g}_{j,\mathcal{D}}=g\}\right]Q_g^{-1}, \tag{16}
$$

with

$$
Q_g = \frac{1}{\hat{n}_{g,\mathcal{D}}T}\sum_{i=1}^{N}\sum_{t=1}^{T}\mathbf{X}_{it}\mathbf{X}_{it}'\mathbf{1}\{\hat{g}_{i,\mathcal{D}}=g\}.
$$

Here, Q_g is the normalized regressor second-moment matrix for group g, and the inner sum is a HAC-type estimator of the long-run covariance of the group score.

Finally, since the group-specific slope estimates are computed independently across groups, the overall estimator of the covariance matrix is obtained by block-diagonalizing the group-wise estimators:

$$
\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\gamma}_{\mathcal{D}}) = \text{bdiag}[\widetilde{\Sigma}_{1,\mathcal{D}}(\widetilde{\gamma}_{\mathcal{D}}),\ldots,\widetilde{\Sigma}_{G,\mathcal{D}}(\widetilde{\gamma}_{\mathcal{D}}],
$$

and

$$
\widehat{\Sigma}_{R,\mathcal{D}}(\widehat{\gamma}_{\mathcal{D}}) = \text{bdiag}[\widehat{\Sigma}_{1,\mathcal{D}}(\widehat{\gamma}_{\mathcal{D}}),\ldots,\widehat{\Sigma}_{G,\mathcal{D}}(\widehat{\gamma}_{\mathcal{D}})].
$$

This matrix serves as the key input in the construction of the Wald statistics in our selective inference procedures.

5. Extensions

This section discusses how the proposed methods can be extended to more general models. We consider models with unit-specific intercepts and those with grouped fixed effects.

5.1. Unit-specific heterogeneity

We consider a model with additive unit-specific unobserved heterogeneity and group-specific slope parameters. Unit-specific effects, referred to as one-way fixed effects (FE), control for time-invariant unobserved heterogeneity that may be correlated with the regressors. Incorporating such effects is standard practice in panel data analysis, as it mitigates omitted variable bias arising from unobserved

heterogeneity that does not vary over time. When the regressors are strictly exogenous, accounting for one-way FE is straightforward: we apply the unit within transformation and then apply the proposed methods to the transformed data.

The model with one-way FE is

$$Y_{it} = \mathbf{X}'_{it}\boldsymbol{\alpha}_{g_i} + \mu_i + U_{it}, \tag{17}$$

where μ_i denotes the unobserved time-invariant unit-specific effect. The regressor vector $\mathbf{X}_{it}$ is assumed to be strictly exogenous, that is, $E(U_{it} \mid \mathbf{X}_{i1}, \ldots, \mathbf{X}_{iT}) = 0$ for all i, t. Moreover, $\mathbf{X}_{it}$ must exhibit sufficient time variation to ensure identification after the within transformation.

To eliminate the fixed effects, we apply the one-way within transformation, which removes the unit means. For any variable a_{it}, let

$$\dot{a}_{it} = a_{it} - \bar{a}_{i\cdot}, \quad \bar{a}_{i\cdot} = \frac{1}{T}\sum_{s=1}^{T} a_{is}.$$

Applying this transformation to equation (17) yields

$$\dot{Y}_{it} = \dot{\mathbf{X}}'_{it}\boldsymbol{\alpha}_{g_i} + \dot{U}_{it}. \tag{18}$$

We then apply the proposed methods to equation (18). The inference procedures remain valid provided that the transformed variables satisfy the assumptions stated earlier. In particular, strict exogeneity and sufficient time variation of $\mathbf{X}_{it}$ are essential. Under strict exogeneity, the OLS estimator applied to each unit in the case of the TSK estimator or to each group in the case of the PCR estimator retains its desirable properties after the unit within transformation. If, however, $\mathbf{X}_{it}$ is only predetermined (i.e. $E(U_{it} \mid \mathbf{X}_{i1}, \ldots, \mathbf{X}_{it}) = 0$ but $E(U_{it} \mid \mathbf{X}_{i1}, \ldots, \mathbf{X}_{iT}) \neq 0$), alternative estimation procedures would be required. Finally, the requirement that $\mathbf{X}_{it}$ be time-varying ensures that the within-transformed regressors $\dot{\mathbf{X}}_{it}$ are not constant, preventing collinearity after the one-way transformation.

5.2. Grouped fixed effects

We now extend the analysis to models with grouped fixed effects (GFE) and group-specific slope parameters. Whereas the two-way fixed effects model in Section 5.1 controls for additive unit and time effects that are common across groups, it cannot capture unobserved shocks that vary over time in a group-specific way. The grouped fixed effects specification relaxes this restriction by allowing the intercept to vary over time within each group while preserving the grouped pattern of heterogeneity.

The model with grouped fixed effects is given by

$$Y_{it} = \mathbf{X}'_{it}\boldsymbol{\alpha}_{g_i} + \eta_{g_i t} + U_{it}, \tag{19}$$

where $\eta_{g_i t}$ denotes the fixed effect specific to group g_i at time t. Compared with the model in Section 5.1, this specification accommodates time-varying unobserved confounders that may differ systematically across groups. The grouped structure ensures parsimony by restricting the heterogeneity to evolve along G latent trajectories rather than across N individual units. A similar model, though with homogeneous slopes, appears as Extension 2 in the supplementary material of Bonhomme and Manresa (2015).

Because $\eta_{g_i t}$ varies over time, the Two-Step Kmeans (TSK) estimator is no longer applicable. We therefore extend the Panel Clusterwise Regression (PCR) estimator to jointly estimate group-specific slopes and group-time fixed effects. This is done by applying Algorithm 2 by extending the explanatory variables vector $\mathbf{X}_{it}$ with time dummies. The rest of the procedure for GFE remains identical to PCR.

6. Monte Carlo

In this section, we examine the finite-sample performance of the proposed selective inference procedures and illustrate the impact of ignoring the estimation uncertainty of the group structure. As emphasized in Patton and Weller (2023), Chen and Witten (2023), and Gao et al. (2024), post-clustering inference based on estimated groups may lead to substantial size distortions, particularly when group separation is weak. Another purpose of these simulation exercises is to examine the robustness of our procedures to potential violations of the assumptions underlying the theoretical justification. While we assume that the errors are normal, this assumption may be violated in real applications. To investigate this potential issue, we conduct Monte Carlo simulations.

All experiments are based on $N = 120$ units and $T \in \{50, 100\}$ time periods, with 1000 Monte Carlo replications. The data are generated according to

$$Y_{it} = \mathbf{X}'_{it}\boldsymbol{\alpha}_{g_i} + \xi_{it} + U_{it}, \quad i = 1, \ldots, N, \ t = 1, \ldots, T, \tag{20}$$

where the true group membership is $g_i = 1$ for $i \leq 40$ and $g_i = 2$ for $i > 40$. Hence, the first cluster contains 40 units and the second cluster 80 units.

Regressors and errors. The regressors are $\mathbf{X}_{it} = (X_{1,it}, X_{2,it})'$ and the errors U_{it} follow weakly stationary AR(1) processes in time,

$$U_{it} = \rho_U U_{i,t-1} + \sqrt{1 - \rho_U^2}\, \varepsilon_{it}, \quad \rho_U = 0.5.$$

The innovation vector $\varepsilon_t = (\varepsilon_{1t}, \ldots, \varepsilon_{Nt})'$ is spatially correlated across units with an exponential kernel within each cluster:

$$\Sigma_S = \begin{bmatrix} \rho_S \exp(-D_1/\ell) + (1 - \rho_S)I_{40} & 0 \\ 0 & \rho_S \exp(-D_2/\ell) + (1 - \rho_S)I_{80} \end{bmatrix}, \quad \rho_S = 0.2,\ \ell = 0.3,$$

where D_g is the $n_g \times n_g$ matrix of pairwise distances between the locations of the units in cluster g. Units within each cluster are placed at equally spaced points on the unit interval, so that for $i, j \in g$,

$$(D_g)_{ij} = |s_{i,g} - s_{j,g}|, \qquad s_{i,g} = \frac{i-1}{n_g - 1}.$$

Thus, D_g captures the absolute distance between unit locations on a one-dimensional grid: nearby units have small distances and therefore exhibit stronger spatial correlation, while distant units have weaker correlation. The block-diagonal structure of Σ_S ensures cross-sectional dependence within clusters while maintaining independence across clusters.

The regressor processes follow AR(1) dynamics,

$$X_{i,t,k} = \rho_X X_{i,t-1,k} + \sqrt{1 - \rho_X^2}\, \eta_{i,t,k}, \quad \rho_X = 0.5, \quad k = 1, 2,$$

where the innovation vectors $(\eta_{i,t,1}, \eta_{i,t,2})'$ are jointly normal with $\mathrm{Corr}(\eta_{\cdot,t,1}, \eta_{\cdot,t,2}) = 0.4$ and share the same within-cluster spatial covariance Σ_N. Thus, both regressors are persistent, spatially dependent, and contemporaneously correlated.

To introduce controlled deviations from Gaussianity, the error innovations are Gaussian during the first half of the sample and $t(6)$-distributed in the second half, scaled to have equal variance:

$$\varepsilon_t \sim \begin{cases} N(0, \Sigma_S), & t \leq T/2, \\ t_6(0, \Sigma_S), & t > T/2, \end{cases}$$

where $t_6(0, \Sigma_S)$ denotes a standardized multivariate t distribution with six degrees of freedom and covariance Σ_S.

Parametrization. We consider three data-generating processes for the slope parameters:

$$\text{DGP1: } \boldsymbol{\alpha}_1 = \boldsymbol{\alpha}_2 = (2, 1)',$$

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$$\text{DGP2: } \boldsymbol{\alpha}_1 = (2,1)', \quad \boldsymbol{\alpha}_2 = (4,1)',$$
$$\text{DGP3: } \boldsymbol{\alpha}_1 = (2,1)', \quad \boldsymbol{\alpha}_2 = (4,2)'.$$

DGP1 is homogeneous and violates the group separation condition. DGP2 has one heterogeneous coefficient and exhibits partial separation. DGP3 has two heterogeneous coefficients and exhibits full separation.

In terms of the model intercept, we consider three data-generating cases:

- **Case 1–Baseline:** As in Model (20), with $\xi_{it} = 0$ for all i and t.

- **Case 2–Unit-specific heterogeneity:** As in Model (20), with $\xi_{it} = \mu_i$ where $\mu_i \sim N(0, 0.5^2)$.

- **Case 3–Grouped fixed effects:** As in Model (20), with $\xi_{it} = \mu_i + \eta_{gt}$ where $\eta_{1t} = 0.8\sin(2\pi t/T)$, $\eta_{2t} = 2 + \sin(2\pi t/T + \pi/4)$ and $\mu_i \sim N(0, 0.5^2)$.

The first two cases preserve the group separation structure implied by the slope parameters, since the intercept component does not contribute to cross-group differences beyond idiosyncratic variation. In contrast, Case 3 introduces systematic time-varying differences in group intercepts, so that clusters remain separated even when the slope parameters coincide.

Hypotheses and procedures. For each design, we test the following null hypotheses:

$$\mathcal{H}_{0,1} : \boldsymbol{\alpha}_1(\boldsymbol{\gamma}_{\mathcal{D}}) - \boldsymbol{\alpha}_2(\boldsymbol{\gamma}_{\mathcal{D}}) = \mathbf{0},$$
$$\mathcal{H}_{0,2} : \alpha_{2,1}(\boldsymbol{\gamma}_{\mathcal{D}}) - \alpha_{2,2}(\boldsymbol{\gamma}_{\mathcal{D}}) = 0,$$
$$\mathcal{H}_{0,3} : \alpha_{1,1}(\boldsymbol{\gamma}_{\mathcal{D}}) = \alpha_{1,2}(\boldsymbol{\gamma}_{\mathcal{D}}) = 0,$$

using both the Two-Step Kmeans (TSK) and the Panel Clusterwise Regression (PCR) algorithms with $G = 2$, where $\boldsymbol{\gamma}_{\mathcal{D}}$ denotes the estimated group assignment obtained from data $\mathcal{D}$. All standard errors and Wald statistics are computed using the Driscoll-Kraay covariance estimator, which accommodates serial correlation and within-cluster cross-sectional dependence. The simulation results below report empirical rejection frequencies at the 5% level.

The rejection frequencies for a nominal value of 5% are reported in Tables 2–4. We examine seven procedures. The first procedure involves using the "Predetermined" group structure, which is incorrect for DGP1 and correct for DGP2 and DGP3. We then examine the rejection frequencies of the Wald test based on the estimated group structure, which is determined using PCR, TSK,

Table 1: Truth of Null Hypotheses under Different DGPs

Null	Constraint	DGP1 No Group Separation	DGP2 Partial Group Separation	DGP3 Full Group Separation
$\mathcal{H}_{0,1}$	$\boldsymbol{\alpha}_1 = \boldsymbol{\alpha}_2$	✓	×	×
$\mathcal{H}_{0,2}$	$\alpha_{2,1} = \alpha_{2,2}$	✓	✓	×
$\mathcal{H}_{0,3}$	$\alpha_{1,1} = \alpha_{1,2} = 0$	×	×	×

and GFE ("Naive PCR", "Naive TSK", "Naive GFE"). Lastly, we evaluate the performance of our conditioning approaches, specifically the conditional TSK, conditional PCR, and conditional GFE methods ("Conditional TSK", "Conditional PCR", "Conditional GFE"). The results are discussed below for each experimental case.

Table 2 (Baseline case). Table 2 reports the rejection rates of the various tests in the baseline setting, where the model contains no fixed effects and the disturbance term exhibits both serial and spatial dependence. Since such dependence invalidates classical variance formulas, all procedures rely on the Driscoll–Kraay long-run variance estimator, which remains consistent under general forms of cross-sectional and temporal correlation. The predetermined test, which uses the true group structure, therefore serves as a benchmark: it isolates the effect of group selection uncertainty from the effect of dependence-robust variance estimation.

The results reveal the dramatic size distortions of the naive tests, which reuse the data to estimate the group partition and then test hypotheses as if the groups were known. Across all DGPs and for both null hypotheses $\mathcal{H}_{0,1}$ and $\mathcal{H}_{0,2}$, the naive TSK and PCR tests reject almost with probability one, even when the null is true. This is fully consistent with our theoretical discussion: ignoring the selection step induces a bias, inflating the appearance of cross-group differences and leading to spurious evidence against the null.

By contrast, the conditional tests that apply our selective inference correction display substantially improved size properties. Their rejection rates remain close to the nominal level for all cases with weak or partial group separation. In several designs, particularly when T is small, the conditional tests are somewhat more conservative than the predetermined test, indicating that the conditioning step may mildly over-correct. This behavior is expected: the DK adjustment already widens the variance under spatial and serial dependence, and the selective correction adds a further correction against false discoveries. Nevertheless, relative to the naive tests, the improvement is large and systematic.

Table 2: Rejection rates of naive tests and proposed tests under different null hypotheses
Case 1: Baseline results

T	Test	DGP	Predetermined	Naive TSK	Naive PCR	Naive GFE	Conditional TSK	Conditional PCR	Conditional GFE
Panel (a): Size									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,1}$	DGP1	0.12	1.00	1.00	0.35	0.13	0.06	0.06
20	$\mathcal{H}_{0,2}$	DGP1	0.08	1.00	0.86	0.25	0.12	0.06	0.05
50	$\mathcal{H}_{0,1}$	DGP1	0.11	1.00	1.00	0.21	0.14	0.06	0.05
50	$\mathcal{H}_{0,2}$	DGP1	0.08	1.00	0.83	0.16	0.12	0.05	0.04
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,2}$	DGP2	0.11	0.14	0.11	0.11	0.10	0.08	0.09
50	$\mathcal{H}_{0,2}$	DGP2	0.08	0.15	0.09	0.08	0.11	0.07	0.08
Panel (b): Power									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.88	0.93	0.97
50	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.86	0.97	0.99
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.84	0.95	0.94
20	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.89	1.00	1.00
50	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.84	0.99	0.99
50	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.86	1.00	1.00
DGP3: Full Group Separation									
20	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.82	0.99	0.98
20	$\mathcal{H}_{0,2}$	DGP3	1.00	1.00	1.00	1.00	0.83	0.92	0.91
20	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.86	1.00	0.99
50	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.85	1.00	0.99
50	$\mathcal{H}_{0,2}$	DGP3	1.00	1.00	1.00	1.00	0.53	0.93	0.98
50	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.83	1.00	1.00

Notes: This table reports rejection frequencies in Case 1 (Baseline). $\mathcal{H}_{0,1}$ tests equality of all group-specific slopes; $\mathcal{H}_{0,2}$ tests equality of a subset of slopes; $\mathcal{H}_{0,3}$ corresponds to violations of the null (power). "Predetermined" uses the true group structure. "Naive" tests ignore group selection uncertainty. "Conditional" tests apply our selective inference correction.

Panel (b) demonstrates that these size corrections do not come at the expense of power. When the null hypothesis is false, all tests, including the conditional ones, exhibit high rejection rates, especially under partial or full group separation (DGP2 and DGP3). The conditional procedures incur only modest power losses relative to the predetermined benchmark, confirming that the selective adjustment works well against size inflation without sacrificing sensitivity to true cross-group heterogeneity.

Table 3 (Unit-specific heterogeneity). Table 3 reports the rejection rates when the model is augmented with unit-specific heterogeneity in the form of individual intercepts. In this case, we implement all tests after applying the within-transformation to all observed variables. The Driscoll–Kraay variance estimator remains valid and provides an appropriate benchmark for evaluating the behavior of the different testing procedures.

As in the baseline design, the naive tests display severe size distortions. Under both $\mathcal{H}_{0,1}$ and $\mathcal{H}_{0,2}$, the naive TSK and PCR procedures reject with probability close to one across all DGPs. Although the predetermined test itself exhibits modest over-rejection in some cases (a consequence of the additional unit-level heterogeneity and the presence of strong temporal and spatial dependence), the naive tests amplify these distortions dramatically by failing to adjust for the uncertainty in the estimated group structure.

The conditional procedures again restore size control, with rejection rates close to the nominal level throughout DGP1 and DGP2. In fact, relative to the predetermined test, the conditional tests tend to be slightly conservative, particularly for small T. Notably, this conservativeness remains acceptable and does not undermine the overall performance of the tests.

Panel (b) shows that the conditional procedures retain high power under $\mathcal{H}_{0,3}$, even in the presence of strong cross-sectional heterogeneity. Under both partial and full group separation (DGP2 and DGP3), conditional TSK and PCR achieve rejection probabilities close to one, closely mirroring the performance of the predetermined benchmark. This confirms that the selective adjustment primarily corrects the size distortions without materially sacrificing the ability to detect true group heterogeneity.

Table 4 (Grouped fixed effects). Table 4 reports rejection rates when the data are generated according to a GFE structure. This design differs fundamentally from the two previous cases: the disturbance term now includes latent time-varying group-specific intercepts, and correct specification requires accounting for these grouped fixed effects. Since Predetermined, TSK, and PCR do not incorporate such intercepts, these procedures are inherently misspecified in this setting. Hence, the

Table 3: Rejection rates of naive tests and proposed tests under different null hypotheses
Case 2: Unit-specific heterogeneity

T	Test	DGP	Predetermined	Naive TSK	Naive PCR	Naive GFE	Conditional TSK	Conditional PCR	Conditional GFE
Panel (a): Size									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,1}$	DGP1	0.15	1.00	1.00	0.38	0.10	0.07	0.06
20	$\mathcal{H}_{0,2}$	DGP1	0.09	1.00	0.89	0.25	0.10	0.06	0.06
50	$\mathcal{H}_{0,1}$	DGP1	0.10	1.00	1.00	0.24	0.17	0.05	0.05
50	$\mathcal{H}_{0,2}$	DGP1	0.08	1.00	0.85	0.15	0.13	0.05	0.06
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,2}$	DGP2	0.11	0.11	0.11	0.10	0.08	0.08	0.08
50	$\mathcal{H}_{0,2}$	DGP2	0.08	0.15	0.06	0.07	0.16	0.06	0.06
Panel (b): Power									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.89	0.93	0.99
50	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.84	0.97	0.99
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.84	0.95	0.94
20	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.87	1.00	0.99
50	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.84	0.99	0.98
50	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.85	1.00	1.00
DGP3: Full Group Separation									
20	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.84	0.97	0.97
20	$\mathcal{H}_{0,2}$	DGP3	1.00	1.00	1.00	1.00	0.82	0.91	0.93
20	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.85	1.00	1.00
50	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.83	1.00	0.99
50	$\mathcal{H}_{0,2}$	DGP3	1.00	1.00	1.00	1.00	0.51	0.91	0.97
50	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.86	1.00	1.00

Notes: This table reports rejection frequencies in Case 2 (Unit-specific heterogeneity). See also Table 2 notes.

Table 4: Rejection rates of naive tests and proposed tests under different null hypotheses
Case 3: Grouped fixed effects

T	Test	DGP	Predetermined	Naive TSK	Naive PCR	Naive GFE	Conditional TSK	Conditional PCR	Conditional GFE
Panel (a): Size									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,1}$	DGP1	0.30	1.00	1.00	0.32	0.14	0.04	0.06
20	$\mathcal{H}_{0,2}$	DGP1	0.19	1.00	0.86	0.22	0.14	0.06	0.07
50	$\mathcal{H}_{0,1}$	DGP1	0.22	1.00	1.00	0.15	0.18	0.04	0.05
50	$\mathcal{H}_{0,2}$	DGP1	0.15	1.00	0.81	0.11	0.14	0.04	0.06
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,2}$	DGP2	0.21	0.26	0.20	0.11	0.13	0.12	0.09
50	$\mathcal{H}_{0,2}$	DGP2	0.13	0.28	0.14	0.10	0.21	0.11	0.08
Panel (b): Power									
DGP1: No Group Separation									
20	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.85	0.87	0.98
50	$\mathcal{H}_{0,3}$	DGP1	1.00	1.00	1.00	1.00	0.89	0.93	0.99
DGP2: Partial Group Separation									
20	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.72	0.79	0.93
20	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.90	0.97	0.99
50	$\mathcal{H}_{0,1}$	DGP2	1.00	1.00	1.00	1.00	0.84	0.97	0.98
50	$\mathcal{H}_{0,3}$	DGP2	1.00	1.00	1.00	1.00	0.84	1.00	1.00
DGP3: Full Group Separation									
20	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.83	0.92	0.97
20	$\mathcal{H}_{0,2}$	DGP3	0.99	1.00	1.00	1.00	0.73	0.81	0.92
20	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.85	0.99	1.00
50	$\mathcal{H}_{0,1}$	DGP3	1.00	1.00	1.00	1.00	0.83	0.99	0.99
50	$\mathcal{H}_{0,2}$	DGP3	1.00	1.00	1.00	1.00	0.80	0.92	0.97
50	$\mathcal{H}_{0,3}$	DGP3	1.00	1.00	1.00	1.00	0.83	1.00	1.00

Notes: This table reports rejection frequencies in Case 3 (Grouped fixed effects). See also Table 2 notes.

predetermined test does not provide a correct benchmark in this case, and is expected to over-reject under the null.

Panel (a) shows that the predetermined procedure exhibits noticeable over-rejection under $\mathcal{H}_{0,1}$ and $\mathcal{H}_{0,2}$, even for moderate sample sizes. This is consistent with the fact that the grouped intercepts induce additional variation that is not absorbed by the TSK or PCR regression structures, inflating the apparent cross-group differences in slope estimates. The naive tests suffer from the same problem, compounded by the fact that they fail to adjust for selection of the estimated groups; as in previous cases, they reject almost deterministically.

The conditional TSK and PCR procedures again substantially reduce size distortions, but they remain imperfect in this setting because the underlying estimators do not model grouped intercepts. Indeed, their rejection rates under $\mathcal{H}_{0,1}$ and $\mathcal{H}_{0,2}$ tend to be higher than in Cases 1 and 2, reflecting an inherent model-misspecification rather than a failure of the selective inference correction itself.

In contrast, the conditional GFE test displays the best size performance. This is particularly visible in DGP2 and DGP3, where group separation is partial or strong: the conditional GFE test maintains rejection frequencies close to the nominal level, even when the corresponding TSK and PCR tests remain somewhat inflated.

Panel (b) shows that the power properties of all procedures remain strong when $\mathcal{H}_{0,3}$ is false, with rejection rates close to one in DGP2 and DGP3. Importantly, the conditional GFE test achieves these high power levels while simultaneously offering the best size control in Panel (a). This reinforces its suitability for settings with grouped intercept heterogeneity: incorporating the correct mean structure not only mitigates size distortions but also ensures that the selective adjustment does not compromise power.

These Monte Carlo experiments illustrate how using the same data both to estimate groups and to test $\mathcal{H}_0$ can severely distort inference. When the data are homogeneous, as in DGP1, the clustering step selects group partitions that maximize between-group differences in each replication, thereby inflating the Wald statistic and causing the naive TSK and PCR tests to over-reject far beyond the nominal level. The predetermined test shows that, if the true groups were known, such distortions would disappear; and even without knowledge of the true partition, our conditioning methods restore the intended size across all designs. Although the conditional procedures can be somewhat less powerful when group separation is strong, they retain high power in larger samples, and they provide valid size control, which is the primary objective of formal statistical inference.

7. Empirical Applications

This section presents two empirical applications to illustrate our procedures. The first application focuses on R&D dynamics, while the second explores the relationship between income and democracy. In both cases, the initial analyses reveal clear heterogeneity. However, using our proposed methods, this evidence becomes more nuanced when we incorporate the effects of estimating group structures.

7.1. Firm level R&D investment and the business cycle

The model of Loyo and Boot (2025) is particularly relevant for illustrating the challenges of inference under latent grouping. In their setting, firm-level R&D responses to industry output are modeled with group-specific coefficients and controls for balance sheet characteristics. The data, originally compiled by Fabrizio and Tsolmon (2014) and made available by van Ophem et al. (2019), consist of yearly information on U.S. firms over the period 1975–2002. When balanced over time, the sample spans 28 years and includes 291 firms without controls and 176 firms with balance-sheet variables incorporated. While the estimation strategy in Loyo and Boot (2025) incorporates heteroskedasticity across groups, their analysis leaves open the question of whether the apparent heterogeneity in slopes is genuine or spurious. By testing between-group linear restrictions within our conditional inference approach, we are able to assess whether group distinctions in the cyclicality of R&D are statistically significant.

To illustrate our testing framework, we estimate a simplified dynamic specification of firm-level R&D expenditures following Loyo and Boot (2025):

$$\Delta \log RD_{it} = \rho_{g_i} \log RD_{i,t-1} + \psi_{g_i} \Delta \log X_{st} + \lambda_t + \mu_i + U_{it}, \ N = 176, \ T = 26,$$

where $\Delta \log RD_{it}$ is the growth of firm i's R&D expenditure, $\log RD_{i,t-1}$ its lag, $\Delta \log X_{st}$ the industry-level output growth, λ_t time fixed effects, and μ_i firm-specific effects. Group heterogeneity is captured through the slope parameters (ρ_{g_i}, ψ_{g_i}).

Table 5 reports the estimation outcomes using both PCR and TSK procedures, together with homogeneity tests. For the lagged R&D term, both methods reveal economically meaningful persistence, with stronger convergence effects in Group 3. Industry output growth is positively associated with Group 1 but negatively with Group 2, suggesting substantial heterogeneity in cyclical sensitivities. However, the formal homogeneity tests yield high p-values: for instance, the joint null of

Table 5: Firm-Level R&D Regressions and Heterogeneity Tests Results

| | Group 1 | | Group 2 | | Group 3 | | Coef. Het. | Het. |
	Coef.	SE	Coef.	SE	Coef.	SE	Test p-val	Test p-val
				PCR				
$\log RD_{i,t-1}$	-0.07	0.01	-0.21	0.01	-0.66	0.04	0.36	0.43
$\Delta \log X_{st}$	0.46	0.07	-0.42	0.11	0.13	0.20	0.36	
				TSK				
$\log RD_{i,t-1}$	-0.19	0.03	-0.25	0.02	-0.19	0.01	0.98	0.09
$\Delta \log X_{st}$	2.53	0.36	-1.11	0.16	0.34	0.06	0.08	

coefficient equality across groups cannot be rejected at conventional levels under PCR ($p = 0.43$). The TSK procedure indicates somewhat sharper contrasts in output elasticities, yet the corresponding test still yields borderline evidence ($p = 0.09$). Taken together, these results indicate that while latent grouping uncovers heterogeneous point estimates, the evidence for statistically significant group-level differences remains weak. This result underscores the importance of conducting valid inference: without adjustment, the striking variation in estimated coefficients might be mistaken for strong evidence of heterogeneity.

7.2. Income and democracy

We next consider the classical application of grouped fixed effects models to the relationship between income and democracy. Following Bonhomme and Manresa (2015), we estimate a dynamic panel specification of the form

$$DEM_{it} = \rho_{g_i} DEM_{i,t-1} + \psi_{g_i} \log GDP_{i,t-1} + \lambda_t + \mu_i + U_{it}, \ N = 74, \ T = 7,$$

where DEM_{it} denotes the Freedom House democracy indicator, GDP_{it} is per capita income, λ_t captures time shocks, and μ_i unit-specific effects. Group-specific coefficients (ρ_{g_i}, ψ_{g_i}) allow the persistence of democracy and its dependence on lagged income to vary across clusters of countries. This model provides a useful benchmark for assessing whether latent group structures reveal systematic heterogeneity in the political economy of democratization.

Table 6 reports the estimated coefficients and the results of homogeneity tests. The PCR estimates suggest moderate variation across groups: democracy persistence is negative in Group 1 but positive in Groups 2 and 3, while the income coefficient switches sign across groups. However, the corresponding

Table 6: Democracy Regressions and Heterogeneity Tests Results

	Group 1		Group 2		Group 3		Coef. Het.	Het.
	Coef.	SE	Coef.	SE	Coef.	SE	Test p-val	Test p-val
PCR								
$DEM_{i,t-1}$	-0.18	0.07	0.33	0.07	0.24	0.06	0.21	0.08
$\log GDP_{i,t-1}$	-0.15	0.05	-0.66	0.09	0.23	0.05	0.18	
TSK								
$DEM_{i,t-1}$	-0.19	0.13	0.14	0.05	0.02	0.09	0.08	0.03
$\log GDP_{i,t-1}$	3.05	0.33	0.03	0.03	-1.40	0.15	0.03	

p-values indicate that such differences are not strongly significant ($p = 0.08$ for joint heterogeneity). In contrast, the TSK procedure uncovers sharper contrasts, with implausibly large positive and negative income effects, and its homogeneity test rejects equality more decisively ($p = 0.03$). These findings illustrate a recurrent pattern: latent group methods can generate striking cross-group variation in point estimates, yet careful inference is essential to distinguish genuine heterogeneity from overfitting. In this application, the evidence for robust group-level differences in the income–democracy relationship remains relatively weak after selective testing.

8. Concluding Remarks

This paper presents methods for robust statistical inference in the presence of potential violations of group-separation conditions. We propose a selective conditional inference approach that conditions on the estimated group structure and other nuisance parameters. Our methods yield valid inferences even without group separation, as demonstrated by theoretical analysis and numerical simulations. Specifically, our methods can be used to test whether two groups are identical and to determine whether a subset of coefficient parameters is equal across groups. It is important to note that existing asymptotic results can be used to test the homogeneity of a subset of coefficients. However, they require that the coefficients unrelated to the null hypothesis satisfy the group separation condition. Our method addresses this limitation by providing valid inferences even without group separation. Additionally, we allow for general linear hypotheses. Even when there is group separation or when the null hypothesis is not directly related to the group separation condition, our procedure demonstrates superior performance by effectively accounting for the impact of group-structure estimation.

There are several avenues for future research. First, it is crucial to incorporate dependence struc-

tures into panel data analysis. The work by González-Delgado et al. (2023) focuses on dependent observations and highlights the limitations of selective inference. We may consider conducting an asymptotic analysis to address this issue effectively. Second, while our simulation results indicate that our procedure has strong power, a theoretical examination of its power properties would be desired. Third, we have focused on linear panel data models; however, the clustering method could also be applied to nonlinear models, such as binary choice models. Exploring extensions to these models would be of great interest and would expand the scope of selective inferences.

Appendices

A. Calculation of the Truncation Sets

In this section, we develop the analytical formulas for the calculation of the truncation sets of Sections 4.2 and 4.3. The sets are polygons in the data space. Furthermore, they can have representations characterized by quadratic functions of ϕ in (10) and (13). Before proceeding with our derivations, we discuss some preliminary aspects of Algorithms 1 and 2, and the associated truncation sets $\mathcal{S}_{TSK}$ and $\mathcal{S}_{PCR}$.

Preliminaries. The truncation sets characterize the conditioning event that covers not only the estimated group membership assignment but also all the iterations from the initial values to the final estimated group structure. The conditioning event defined in (5) is equivalent of $\mathcal{S} = \left\{ \bigcap_{i=1}^{N} \{g_{i,\mathcal{D}} = g_{i,\mathscr{d}}\} \right\}$ where $g_{i,\mathcal{D}}$ is the i-th element of $\boldsymbol{\gamma}_{\mathcal{D}}$ and $g_{i,\mathscr{d}}$ is the associated realization. The truncation sets in (10) and (13) can be similarly written as

$$\mathcal{S}_{TSK} = \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{m=0}^{M} \bigcap_{i=1}^{N} \{\tilde{g}_{i,\mathscr{d}(\phi)}^{(m)} = \tilde{g}_{i,\mathscr{d}}^{(m)}\} \right\}, \tag{21}$$

$$\mathcal{S}_{PCR} = \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{m=0}^{M} \bigcap_{i=1}^{N} \{\hat{g}_{i,\mathscr{d}(\phi)}^{(m)} = \hat{g}_{i,\mathscr{d}}^{(m)}\} \right\}, \tag{22}$$

where $\mathscr{d}(\phi) = \{\widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi); i = 1, \ldots, N\}$ with $\widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi) = [\widehat{\mathbf{b}}_{\mathscr{d}}(\phi)]_i^K$ for TSK with $\widehat{\mathbf{b}}_{\mathscr{d}}(\phi)$ defined in (11) and $\mathscr{d}(\phi) = \{[y_{it}(\phi), \mathbf{x}_{it}]; i = 1, \ldots, N, t = 1, \ldots, T\}$ for PCR with $y_{it}(\phi)$ being the it-th element of the

vector defined in (14). Now it is seen that

$$\mathcal{S}_{TSK} = \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{i=1}^{N} \{ \tilde{g}_{i,\mathcal{J}(\phi)}^{(0)} = \tilde{g}_{i,\mathcal{J}}^{(0)} \} \right\} \bigcap \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \bigcap_{m=1}^{M} \bigcap_{i=1}^{N} \{ \tilde{g}_{i,\mathcal{J}(\phi)}^{(m)} = \tilde{g}_{i,\mathcal{J}}^{(m)} \} \right\}$$

$$\equiv \mathcal{S}_{TSK}^{(0)} \bigcap \left(\bigcap_{m=1}^{M} \mathcal{S}_{TSK}^{(m)} \right)$$

and similarly

$$\mathcal{S}_{PCR} \equiv \mathcal{S}_{PCR}^{(0)} \bigcap \left(\bigcap_{m=1}^{M} \mathcal{S}_{PCR}^{(m)} \right).$$

This simple decomposition of the truncation sets will prove useful because different initialization methods for Algorithms 1 and 2 yield different formulas for their analytical calculations. We discuss below two different methods.

Initialization of algorithms. The characterization of the initial value sets, specifically $\mathcal{S}_{TSK}^{(0)}$ and $\mathcal{S}_{PCR}^{(0)}$, requires different derivations compared to the other sets. These characterizations are specifically designed based on the methods used for selecting the initial values. For both algorithms, we explore two alternative methods for selecting these initial values. These are:

1. random initialization, and

2. Kmeans++ (as a potential extension for future analysis).

In the first method, implemented in our results, the initial group assignment for each unit is randomly selected from the set $\{1, \ldots, G\}$ with equal probability. The initial parameter values for each cluster are then calculated using least squares. However, as is well-known, Algorithms 1 and 2 may converge to local minima. To address this issue, we utilize a large number of random initial values and select the final estimates that yield the minimum value of the objective function.

In the second method, the initial group centers would be determined using the Kmeans++ algorithm (Arthur and Vassilvitskii, 2007), which is directly applicable to Algorithm 1. To the best of our knowledge, Kmeans++ initialization has not yet been extended to PCR. For the Kmeans++ initialization of Algorithm 2, one could use the same Kmeans++ initial values as in Algorithm 1. We leave the full development and analysis of this extension for future work.

When the random initialization method is employed, there is no need to consider $\mathcal{S}_{TSK}^{(0)}$ and $\mathcal{S}_{PCR}^{(0)}$ since the group assignments are not data-dependent. However, if Kmeans++ initialization were to be used, these sets would have to be taken into account.

A.1. Calculation of $\mathcal{S}_{\text{TSK}}^{(m)}$ for $m \geq 1$

We derive the analytical formulas for the calculation of the truncation set $\mathcal{S}_{TSK}^{(m)}$, $m \geq 1$, which will also serve as a useful basis for the calculation of $\mathcal{S}_{PCR}^{(m)}$, $m \geq 1$.

We start by characterizing the second term in the equation above, which is common to both initialization methods. To this end, following Proposition 2 of Chen and Witten (2023), we note that

$$\mathcal{S}_{TSK}^{(m)} = \bigcap_{i=1}^{N} \bigcap_{g=1}^{G} \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \left\| \widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi) - A_{\tilde{g}_{i,\mathscr{d}}^{(m)}}^{(m-1)} \widehat{\mathbf{b}}_{\mathscr{d}}(\phi) \right\|^2 \leq \left\| \widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi) - A_g^{(m-1)} \widehat{\mathbf{b}}_{\mathscr{d}}(\phi) \right\|^2 \right\}$$

where

$$A_g^{(m-1)} = (\mathbf{e}_g' \otimes I_K) \widetilde{\mathcal{n}}_\Sigma [\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m-1)}]^{-1} \mathbb{D}[\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m-1)}]'.$$

Now, according to Equation (11), the vector $\widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi)$ is defined as the $(1 + K(i-1)) : Ki$-th block of the rows of $\widehat{\mathbf{b}}_{\mathscr{d}}(\phi) = \phi \mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) + \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})$ where

$$\mathbf{v}_{TSK} = P_{(\mathbb{D}(\widetilde{\boldsymbol{\gamma}}_{\widetilde{\mathcal{D}}}), R)} \widetilde{\Sigma}_{R,\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})^{1/2} \text{dir}\{\widetilde{\Sigma}_{R,\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})^{-1/2}[R\widetilde{\boldsymbol{\alpha}}_{\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) - \mathbf{r}]\}.$$

We thus obtain $\widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi) = \phi [\mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K + [\mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K$. The following result follows immediately from this expression.

Proposition A.1. For all $i \in \{1, \ldots, N\}$, $g \in \{1, \ldots, G\}$ and $m \in \{1, \ldots, M\}$,

$$\left\| \widehat{\boldsymbol{\beta}}_{i,\mathscr{d}}(\phi) - A_g^{(m)} \widehat{\mathbf{b}}_{\mathscr{d}}(\phi) \right\|^2 = \lambda_{i,g,1}^{(m)} \phi^2 + \lambda_{i,g,2}^{(m)} \phi + \lambda_{i,g,3}^{(m)}$$

where

$$\lambda_{i,g,1}^{(m)} = \left\| [\mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K - A_g^{(m)} \mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\|^2,$$

$$\lambda_{i,g,2}^{(m)} = 2 \left\{ [\mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K - A_g^{(m)} \mathbf{v}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\}' \left\{ [\mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K - A_g^{(m)} \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\},$$

$$\lambda_{i,g,3}^{(m)} = \left\| [\mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})]_i^K - A_g^{(m)} \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\|^2.$$

This result now serves as a basis for the calculation of $\mathcal{S}_{TSK}^{(m)}$ and hence of $\mathcal{S}_{TSK}$ in the case of random initialization. This is because, in this case, we have

$$\mathcal{S}_{TSK} = \bigcap_{m=1}^{M} \bigcap_{i=1}^{N} \bigcap_{g=1}^{G} \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \Lambda_{i,g}^{(m)}(\phi) \leq 0 \right\}$$

where

$$\Lambda_{i,g}^{(m)}(\phi) = [\lambda_{i,\tilde{g}_{i,\mathscr{d}}^{(m)},1}^{(m)} - \lambda_{i,g,1}^{(m)}] \phi^2 + [\lambda_{i,\tilde{g}_{i,\mathscr{d}}^{(m)},2}^{(m)} - \lambda_{i,g,2}^{(m)}] \phi + [\lambda_{i,\tilde{g}_{i,\mathscr{d}}^{(m)},3}^{(m)} - \lambda_{i,g,3}^{(m)}],$$

and all the coefficients can be calculated from the data.

A.2. Calculation of $\mathcal{S}_{\mathrm{PCR}}^{(m)}$ for $m \geq 1$

We now derive the formulas for the truncation set $\mathcal{S}_{PCR}^{(m)}$, $m \geq 1$, following broadly the derivation of $\mathcal{S}_{TSK}$. The representation of the set $\mathcal{S}_{PCR}$ analogous to (A.1) is given by

$$\mathcal{S}_{PCR}^{(m)} = \bigcap_{i=1}^{N} \bigcap_{g=1}^{G} \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \left\| [\mathbf{y}(\phi)]_i^T - X_i B_{i,\hat{g}_{i,\mathcal{I}}}^{(m-1)} \mathbf{y}(\phi) \right\|^2 \leq \left\| [\mathbf{y}(\phi)]_i^T - X_i B_{i,g}^{(m-1)} \mathbf{y}(\phi) \right\|^2 \right\} \quad (23)$$

where

$$B_{i,g}^{(m-1)} = (\mathbf{e}_g' \otimes I_T)\{\mathbb{X}[\hat{\gamma}_{\mathcal{D}}^{(m-1)}]'\mathbb{X}[\hat{\gamma}_{\mathcal{D}}^{(m-1)}]\}^{-1}\mathbb{X}[\hat{\gamma}_{\mathcal{D}}^{(m-1)}]'.$$

Now, we write the vector $[\mathbf{y}(\phi)]_i^T = \phi[\mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T + [\mathbf{w}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T$, where

$$\mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}}) = P_{(\mathbf{x}(\hat{\gamma}_{\mathcal{I}}),R)}\widehat{\Sigma}_{R,\mathcal{I}}(\hat{\gamma}_{\mathcal{I}})^{1/2}\mathrm{dir}\{\widehat{\Sigma}_{R,\mathcal{I}}(\hat{\gamma}_{\mathcal{I}})^{-1/2}[R\widehat{\alpha}_{\mathcal{I}}(\hat{\gamma}_{\mathcal{I}}) - \mathbf{r}]\}.$$

We have the following result.

Proposition A.2. For all $i \in \{1,\ldots,N\}$, $g \in \{1,\ldots,G\}$ and $m \in \{1,\ldots,M\}$,

$$\left\| [\mathbf{y}(\phi)]_i^T - X_i B_{i,g}^{(m)} \mathbf{y}(\phi) \right\|^2 = \psi_{i,g,1}^{(m)} \phi^2 + \psi_{i,g,2}^{(m)} \phi + \psi_{i,g,3}^{(m)},$$

where

$$\psi_{i,g,1}^{(m)} = \left\| [\mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T - X_i B_{i,g}^{(m)} \mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}}) \right\|^2,$$

$$\psi_{i,g,2}^{(m)} = 2\left\{ [\mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T - X_i B_{i,g}^{(m)} \mathbf{v}_{PCR}(\hat{\gamma}_{\mathcal{I}}) \right\}' \left\{ [\mathbf{w}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T - X_i B_{i,g}^{(m)} \mathbf{w}_{PCR}(\hat{\gamma}_{\mathcal{I}}) \right\},$$

$$\psi_{i,g,3}^{(m)} = \left\| [\mathbf{w}_{PCR}(\hat{\gamma}_{\mathcal{I}})]_i^T - X_i B_{i,g}^{(m)} \mathbf{w}_{PCR}(\hat{\gamma}_{\mathcal{I}}) \right\|^2.$$

This result now serves as a basis for the calculation of $\mathcal{S}_{PCR}^{(m)}$ and hence of $\mathcal{S}_{PCR}$ in the case of random initialization because

$$\mathcal{S}_{PCR} = \bigcap_{m=1}^{M} \bigcap_{i=1}^{N} \bigcap_{g=1}^{G} \left\{ \phi^2 \in \mathbb{R}_{\geq 0} : \Psi_{i,g}^{(m)}(\phi) \leq 0 \right\}$$

where

$$\Psi_{i,g}^{(m)}(\phi) = [\psi_{i,\hat{g}_{i,\mathcal{I}}^{(m)},1}^{(m)} - \psi_{i,g,1}^{(m)}]\phi^2 + [\psi_{i,\hat{g}_{i,\mathcal{I}}^{(m)},2}^{(m)} - \psi_{i,g,2}^{(m)}]\phi + [\psi_{i,\hat{g}_{i,\mathcal{I}}^{(m)},3}^{(m)} - \psi_{i,g,3}^{(m)}],$$

and all the coefficients can be calculated from the data.

B. Technical appendix for TSK

This appendix provides the proof of Theorem 1. We first recall the notation and introduce new ones. Then, we establish several lemmas. Finally, we present the proof of Theorem 1.

B.1. Notation

We first recall the notation established in the main text. $\widehat{\mathbf{B}}_{\mathcal{D}} = (\widehat{\boldsymbol{\beta}}'_{1,\mathcal{D}}, \ldots, \widehat{\boldsymbol{\beta}}'_{N,\mathcal{D}})'$ denotes the $NK \times 1$ vector of estimated slope coefficients. $\mathbb{D}(\boldsymbol{\gamma}) = D(\boldsymbol{\gamma}) \otimes I_K$ where $D(\boldsymbol{\gamma})$ is the $N \times G$ matrix of group dummies based on $\boldsymbol{\gamma}$ and I_K is the K-dimensional identity matrix. The TSK estimator of the group-specific slope coefficients under group structure $\boldsymbol{\gamma}$ can be written as $\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) = (\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\widehat{\mathbf{B}}_{\mathcal{D}}$.

We now consider the setting with Gaussian, homoskedastic errors and provide the formula for the test statistic under this condition. Assume that

$$\widehat{\mathbf{B}}_{\mathcal{D}} \sim N(\mathbf{B}, \sigma^2 I_N \otimes \Sigma^{-1}).$$

Under this condition, the test statistic under group structure $\boldsymbol{\gamma}$ is

$$H_{TSK}(\boldsymbol{\gamma}) = [R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \mathbf{r}]'(\sigma^2 R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R')^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \mathbf{r}],$$

where $\widetilde{n}_{\Sigma}(\boldsymbol{\gamma}) = \mathrm{diag}(\tilde{n}_1, \ldots, \tilde{n}_G) \otimes \Sigma$. Note that the variance of $R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma})$, $\widetilde{\Sigma}_{R,\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$, is

$$R(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\sigma^2(I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R' = \sigma^2 R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'.$$

The test statistic we actually compute in the sample is $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})$.

The selective inference and its theoretical result crucially depend on the decomposition of the individual-specific coefficient estimators. For this, we first consider the constrained estimator of $\boldsymbol{\alpha}$:

$$\widetilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\boldsymbol{\gamma}) = \widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \mathbf{r}]$$

It holds that

$$\widehat{\mathbf{B}}_{\mathcal{D}} = \mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \mathbf{r}] + \mathbf{W}_{TSK}(\boldsymbol{\gamma}),$$

where

$$\mathbf{W}_{TSK}(\boldsymbol{\gamma}) = \mathbb{D}(\boldsymbol{\gamma})\widetilde{\boldsymbol{\alpha}}_{R,\mathcal{D}}(\boldsymbol{\gamma}) + (I_{NK} - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})')\widehat{\mathbf{B}}_{\mathcal{D}}$$

Note that this decomposition is algebraic and holds for any choice of $\boldsymbol{\gamma}$.

B.2. Lemma

The following lemmas establish the independence conditions needed to prove the main theorem. We fix $\boldsymbol{\gamma}$, and the results below hold. Note that we eventually set $\boldsymbol{\gamma}$ to $\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}$.

Lemma B.1. *Suppose that* $\widehat{\mathbf{B}}_{\mathcal{D}} \sim N(\mathbf{B}, \sigma^2 I_N \otimes \Sigma^{-1})$ *and* $\boldsymbol{\gamma}$ *is fixed. Then, it holds that*

$$R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) \perp \mathbf{W}_{TSK}(\boldsymbol{\gamma}).$$

Proof. Note that

$$R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) = R(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\widehat{\mathbf{B}}_{\mathcal{D}}$$

and

$$
\begin{aligned}
\mathbf{W}_{TSK}(\boldsymbol{\gamma}) =& \mathbb{D}(\boldsymbol{\gamma})\left(\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}[R\widetilde{\boldsymbol{\alpha}}_{\mathcal{D}}(\boldsymbol{\gamma}) - \mathbf{r}]\right) \\
&+ \left(I_{NK} - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right)\widehat{\mathbf{B}}_{\mathcal{D}} \\
=& \left(I_{NK} - \mathbb{D}(\boldsymbol{\gamma})(I_{GK} - \widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}R)(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right. \\
&\left. - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right)\widehat{\mathbf{B}}_{\mathcal{D}} \\
&+ \mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}\mathbf{r}.
\end{aligned}
$$

The last term, $\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}\mathbf{r}$ is a constant and thus does not affect the independence.

Because $\widehat{\mathbf{B}}_{\mathcal{D}} \sim N(\mathbf{B}, \sigma^2(I_N \otimes \Sigma^{-1}))$, by the properties of the multivariate normal distributions, it is sufficient to show that

$$
\begin{aligned}
&\left(I_{NK} - \mathbb{D}(\boldsymbol{\gamma})(I_{GK} - \widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}R)(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right. \\
&\left. - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right) \\
&\times (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R' = 0.
\end{aligned}
$$

We observe that

$$
\begin{aligned}
&\left(I_{NK} - \mathbb{D}(\boldsymbol{\gamma})(I_{GK} - \widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}R)(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right. \\
&\left. - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\right) \\
&\quad \times (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R' \\
=& (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R' \\
&- \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R' \\
&+ \mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}_{\Sigma}(\boldsymbol{\gamma})^{-1}R']^{-1}R(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1}R'
\end{aligned}
$$

$$- (I_N \otimes \Sigma^{-1}) \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} \widetilde{n}_\Sigma(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} \mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma^{-1}) \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} R'$$

$$= (I_N \otimes \Sigma^{-1}) \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} R'$$

$$- \mathbb{D}(\boldsymbol{\gamma}) \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R'$$

$$+ \mathbb{D}(\boldsymbol{\gamma}) \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R'[R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R']^{-1} R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R'$$

$$- (I_N \otimes \Sigma^{-1}) \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} \widetilde{n}_\Sigma(\boldsymbol{\gamma}) \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R'$$

$$= (I_N \otimes \Sigma)^{-1} \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} R' - (I_N \otimes \Sigma)^{-1} \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} R'$$

$$- \mathbb{D}(\boldsymbol{\gamma}) \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R' + \mathbb{D}(\boldsymbol{\gamma}) \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R'$$

$$= 0,$$

where the first and second equalities are based on the fact that

$$(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} \mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma^{-1}) \mathbb{D}(\boldsymbol{\gamma})(\mathbb{D}(\boldsymbol{\gamma})'\mathbb{D}(\boldsymbol{\gamma}))^{-1} = \widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}.$$

$\square$

Note that this lemma holds regardless of whether the null hypothesis holds.

The following lemma requires the null hypothesis to be true, unlike the above lemma.

Lemma B.2. *Suppose that $\widehat{\mathbf{B}}_{\mathscr{D}} \sim N(\mathbf{B}, \sigma^2 I_N \otimes \Sigma^{-1})$ and $\boldsymbol{\gamma}$ is fixed. Under H_0,*

$$(R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}} - \mathbf{r})(R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R')^{-1}(R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}} - \mathbf{r}) \perp \mathrm{dir}\left\{ (R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R')^{-1/2} [R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}] \right\}$$

Proof. Because

$$R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r} \sim N(0, \sigma^2 R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R')$$

under H_0, it holds that

$$(R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1} R')^{-1/2} [R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}] \sim N(0, \sigma^2 I_q).$$

Thus, by Proposition 4.11 and Corollary 4.3 of Bilodeau and Brenner (1999), its norm and direction are independent. $\square$

B.3. Proof of the theorem

Let

$$\mathcal{G}_{\mathscr{D}}(\boldsymbol{\gamma}) = [R\widetilde{n}(\boldsymbol{\gamma})^{-1} R']^{-1/2} [R\widetilde{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}].$$

Consider an event $H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E$ for some E. We observe that

$$\Pr_{H_0}\left(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \mathscr{A}_{TSK}\right)$$

$$=\Pr_{H_0}\left(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \bigcap_{m=0}^{M}\left\{\widetilde{\gamma}_{\mathcal{D}}^{(m)} = \widetilde{\gamma}_{\mathcal{d}}^{(m)}\right\},\right.$$

$$\left.\mathrm{dir}\left\{\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}})\right\} = \mathrm{dir}\left\{\mathcal{G}_{\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right\}, \quad \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) = \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right)$$

$$=\Pr_{H_0}\left(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) \in E \mid \bigcap_{m=0}^{M}\left\{\widetilde{\gamma}_{\mathcal{D}}^{(m)} = \widetilde{\gamma}_{\mathcal{d}}^{(m)}\right\},\right.$$

$$\left.\mathrm{dir}\left\{\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right\} = \mathrm{dir}\left\{\mathcal{G}_{\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right\}, \quad \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) = \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right).$$

The first equality follows by the definition of $\mathscr{A}_{TSK}$. The second equality uses the fact that $\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}} = \widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}$ in this conditioning set.

We use the following decomposition.

$$\widehat{\mathbf{B}}_{\mathcal{D}} = \mathbb{P}(\boldsymbol{\gamma})\mathcal{G}_{\mathcal{D}}(\boldsymbol{\gamma}) + \mathbf{W}_{TSK}(\boldsymbol{\gamma}),$$

where

$$\mathbb{P}(\boldsymbol{\gamma}) = \mathbb{D}(\boldsymbol{\gamma})\widetilde{n}(\boldsymbol{\gamma})^{-1}R'[R\widetilde{n}(\boldsymbol{\gamma})^{-1}R']^{-1/2}.$$

Note that this decomposition holds for any $\boldsymbol{\gamma}$ so is valid for $\boldsymbol{\gamma} = \widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}$.

We write

$$\widetilde{\gamma}_{\mathcal{D}}^{(m)} = \widetilde{\gamma}^{(m)}(\widehat{\mathbf{B}}_{\mathcal{D}})$$

$$= \widetilde{\gamma}^{(m)}\left(\mathbb{P}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) + \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right)$$

$$= \widetilde{\gamma}^{(m)}\left(\sqrt{H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})}\mathbb{P}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\mathrm{dir}(\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})) + \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right).$$

Using this decomposition, we write

$$\Pr_{H_0}\left(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \mathscr{A}_{TSK}\right)$$

$$=\Pr_{H_0}\left(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) \in E \mid\right.$$

$$\bigcap_{m=0}^{M}\left\{\widetilde{\gamma}^{(m)}\left(\sqrt{H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})}\mathbb{P}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\mathrm{dir}(\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})) + \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right) = \widetilde{\gamma}_{\mathcal{d}}^{(m)}\right\},$$

$$\left.\mathrm{dir}\left\{\mathcal{G}_{\mathcal{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right\} = \mathrm{dir}\left\{\mathcal{G}_{\mathcal{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right\}, \quad \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}}) = \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathcal{d}})\right).$$

We insert the latter two conditions into the argument of $\widetilde{\boldsymbol{\gamma}}^{(m)}$, and the probability becomes

$$
= \Pr_{H_0} \bigg(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \in E \mid
$$
$$
\bigcap_{m=0}^{M} \Big\{ \widetilde{\boldsymbol{\gamma}}^{(m)} \Big(\sqrt{H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})} \mathbb{P}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \mathrm{dir}(\mathscr{G}_{\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})) + \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \Big) = \widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)} \Big\},
$$
$$
\mathrm{dir}\left\{ \mathscr{G}_{\mathscr{D}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\} = \mathrm{dir}\left\{ \mathscr{G}_{\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \right\}, \quad \mathbf{W}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) = \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \bigg).
$$

The latter two conditions in the conditioning set can be dropped because of the independence properties established in Lemmas B.1 and B.2. So we obtain

$$
= \Pr_{H_0} \bigg(H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \in E \mid
$$
$$
\bigcap_{m=0}^{M} \Big\{ \widetilde{\boldsymbol{\gamma}}^{(m)} \Big(\sqrt{H_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})} \mathbb{P}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \mathrm{dir}(\mathscr{G}_{\mathscr{d}}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}})) + \mathbf{w}_{TSK}(\widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}) \Big) = \widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)} \Big\} \bigg)
$$
$$
= \Pr_{H_0} \bigg(\phi^2 \in E \mid \Big\{ \widetilde{\boldsymbol{\gamma}}^{(m)} \Big(\widehat{\mathbf{b}}_{\mathscr{d}}(\phi) \Big) = \widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}^{(m)} \Big\} \bigg)
$$
$$
= \Pr_{H_0} \bigg(\phi^2 \in E \mid \mathscr{S}_{TSK} \bigg)
$$

where $\phi^2 \sim \chi^2_{\mathrm{rank}(R)}$.

C. Technical appendix for PCR

This appendix contains the proof of Theorem 2 and related technical details. We first review the notation and discuss various theoretical properties of the random variable underlying the test statistics. The proof follows similar steps to those of Theorem 1.

C.1. Notation and lemmas

We recall that in this design, all statistics depend on data only through $\mathbf{s} = (\mathbf{s}_1', \ldots, \mathbf{s}_N')'$, where $\mathbf{s}_i = \sum_{t=1}^{T} X_{it} Y_{it}$. Note that $\mathbf{s}_i$ is $K \times 1$ and that $\mathbf{s}$ is $NK \times 1$. Recall also the definition of $\mathbb{X}$. It is the $NT \times NK$ block diagonal matrix whose i-th block is X_i, where $X_i = (\mathbf{X}_{i1}, \ldots, \mathbf{X}_{iT})'$ is a $T \times K$ matrix. Note that $\mathbb{X}(\boldsymbol{\gamma})$ is an $NT \times GK$ matrix. We write

$$
\mathbf{s} = \mathbb{X}' \mathbf{Y}.
$$

The constrained PCR estimator of $\boldsymbol{\alpha}(\boldsymbol{\gamma}) = [\boldsymbol{\alpha}_1(\boldsymbol{\gamma})', \ldots, \boldsymbol{\alpha}_G(\boldsymbol{\gamma})']'$ obtained by imposing $\mathcal{H}_0$, denoted

as $\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma})$, is given by

$$\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma}) = \widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - [\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}].$$

We use the following decomposition.

$$\begin{aligned}
\mathbf{s} =& \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}] + \mathbf{W}_{PCR}(\boldsymbol{\gamma}) \\
=& \widehat{\mathbb{P}}(\boldsymbol{\gamma})j_{\mathscr{D}}(\boldsymbol{\gamma}) + \mathbf{W}_{PCR}(\boldsymbol{\gamma}),
\end{aligned}$$

where

$$\begin{aligned}
\widehat{\mathbb{P}}(\boldsymbol{\gamma}) =& \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1} \\
& \times (R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbb{X}'\mathbb{X}\mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}R')^{1/2},
\end{aligned}$$

$$j_{\mathscr{D}}(\boldsymbol{\gamma}) = (R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbb{X}'\mathbb{X}\mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}R')^{-1/2}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}],$$

and

$$\mathbf{W}_{PCR}(\boldsymbol{\gamma}) = \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma}) + \mathbb{X}'\widehat{\mathbf{U}}(\boldsymbol{\gamma})$$

noting that $\widehat{\mathbf{U}}(\boldsymbol{\gamma}) = \mathbf{Y} - \mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma})$. The formula of the group-specific coefficient can also be written in terms of $\mathbf{s}$ such that

$$\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) = (\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbf{s},$$

where $\mathbb{D}(\boldsymbol{\gamma}) = D(\boldsymbol{\gamma}) \otimes I_K$ and is an $NK \times GK$ matrix. Note that this decomposition is purely algebraic and holds for any $\boldsymbol{\gamma}$. So, it is valid for $\boldsymbol{\gamma} = \widehat{\boldsymbol{\gamma}}_{\mathscr{d}}$.

We make the following assumptions. We assume that

$$\mathbf{s} \sim N(\mathbb{X}'\mathbf{X}\mathbf{B}, \sigma^2\mathbb{X}'\mathbb{X}).$$

Moreover, the data matrix is identical across i such that

$$\sum_{t=1}^{T}\mathbf{X}_{it}\mathbf{X}_{it}' = \Sigma$$

for any i. A representative example is $\Sigma = I_K$, that is, the data matrix for each i is normalized.

We now establish several lemmas. They hold for fixed $\boldsymbol{\gamma}$. Eventually, we consider the case with $\boldsymbol{\gamma} = \widetilde{\boldsymbol{\gamma}}_{\mathscr{d}}$.

Lemma C.1. *Suppose that $\mathbf{s} \sim N(\mathbb{X}'\mathbf{XB}, \sigma^2\mathbb{X}'\mathbb{X})$ and $\sum_{t=1}^{T} \mathbf{X}_{it}\mathbf{X}'_{it} = \Sigma$ for any i. Then, it holds that*

$$R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) \perp \mathbf{W}_{PCR}(\boldsymbol{\gamma}).$$

Proof. Note that

$$R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) = R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbf{s}$$

and

$$
\begin{aligned}
\mathbf{W}_{PCR}(\boldsymbol{\gamma}) =& \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{R,\mathscr{D}}(\boldsymbol{\gamma}) + \mathbb{X}'\widehat{\mathbf{U}}(\boldsymbol{\gamma}) \\
=& \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) \\
& - \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}[R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) - \mathbf{r}] \\
& + \mathbb{X}'\mathbf{Y} - \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) \\
=& - \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}R\widehat{\boldsymbol{\alpha}}_{\mathscr{D}}(\boldsymbol{\gamma}) \\
& + \mathbb{X}'\mathbf{Y} \\
& + \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}\mathbf{r} \\
=& - \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbf{s} \\
& + \mathbf{s} \\
& + \mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}\mathbf{r}.
\end{aligned}
$$

The last term, $\mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}\mathbf{r}$ is a constant and thus does not affect the independence.

Because $\mathbf{s} \sim N(\mathbb{X}'\mathbf{XB}, \sigma^2\mathbb{X}'\mathbb{X})$, by the properties of the multivariate normal distributions, it is sufficient to show that

$$
\begin{aligned}
& \left(\mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})' - \mathbf{I}\right) \\
& \times (\mathbb{X}'\mathbb{X}) \\
& \times \mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}R' = 0.
\end{aligned}
$$

To show this equality, we use the normalization that

$$\sum_{t=1}^{T} \mathbf{X}_{it}\mathbf{X}'_{it} = \Sigma$$

for any i. Under this normalization, $\mathbb{X}'\mathbb{X} = I_N \otimes \Sigma$, $\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}) = \widetilde{n}_{\Sigma}(\boldsymbol{\gamma}) = \mathrm{diag}(n_1, \ldots, n_G) \otimes \Sigma$ and

$\mathbb{X}'\mathbb{X}(\boldsymbol{\gamma}) = \mathbb{X}'\mathbb{X}\mathbb{D}(\boldsymbol{\gamma}) = (I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma})$. Thus, we have

$$
\begin{aligned}
&\left(\mathbb{X}'\mathbb{X}(\boldsymbol{\gamma})[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\{R[\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma})]^{-1}R'\}^{-1}R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})' - \mathbf{I}\right)\\
&\quad \times (\mathbb{X}'\mathbb{X})\\
&\quad \times \mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})\mathbb{X}(\boldsymbol{\gamma})')^{-1}R'\\
&=(I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\{R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\}^{-1}\\
&\quad \times R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}\mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\\
&\quad - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\\
&=(I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\{R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\}^{-1}R\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}\widetilde{n}_\Sigma(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\\
&\quad - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\\
&=(I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R' - (I_N \otimes \Sigma^{-1})\mathbb{D}(\boldsymbol{\gamma})\widetilde{n}_\Sigma(\boldsymbol{\gamma})^{-1}R'\\
&=0,
\end{aligned}
$$

where we use the fact that $\mathbb{D}(\boldsymbol{\gamma})'(I_N \otimes \Sigma)\mathbb{D}(\boldsymbol{\gamma}) = \widetilde{n}_\Sigma(\boldsymbol{\gamma})$. $\qquad\square$

Note that this lemma holds regardless of whether the null hypothesis holds.

The following, in contrast, requires that the null hypothesis be true.

Lemma C.2. *Under H_0,*

$$
j_\mathscr{D}(\boldsymbol{\gamma})' \, j_\mathscr{D}(\boldsymbol{\gamma}) \perp \mathrm{dir}\{j_\mathscr{D}(\boldsymbol{\gamma})\}.
$$

Proof. Because

$$
R\widehat{\boldsymbol{\alpha}}_\mathscr{D}(\boldsymbol{\gamma}) - \mathbf{r} \sim N(0, \sigma^2 R(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}\mathbb{D}(\boldsymbol{\gamma})'\mathbb{X}'\mathbb{X}\mathbb{D}(\boldsymbol{\gamma})(\mathbb{X}(\boldsymbol{\gamma})'\mathbb{X}(\boldsymbol{\gamma}))^{-1}R')
$$

under H_0, it holds that

$$
j_\mathscr{D}(\boldsymbol{\gamma}) \sim N(0, \sigma^2 I_q).
$$

Therefore, its norm and the direction are independent by Proposition 4.11 and Corollary 4.3 of Bilodeau and Brenner (1999). $\qquad\square$

C.2. Proof of the theorem for PCR

Recall that

$$
\widehat{\mathbf{s}}_\mathscr{d}(\phi) = \phi\widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_\mathscr{d})\mathrm{dir}(j_\mathscr{d}(\widehat{\boldsymbol{\gamma}}_\mathscr{d})) + \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_\mathscr{d})
$$

Consider an event $H_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E$ for some E. We observe that

$$\Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \mathscr{A}_{PCR} \right)$$

$$= \Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \bigcap_{m=0}^{M} \left\{ \widehat{\boldsymbol{\gamma}}_{\mathcal{D}}^{(m)} = \widehat{\boldsymbol{\gamma}}_{d}^{(m)} \right\}, \right.$$

$$\left. \operatorname{dir} \left\{ j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) \right\} = \operatorname{dir} \left\{ j_{d}(\widehat{\boldsymbol{\gamma}}_{d}) \right\}, \quad \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) = \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right)$$

$$= \Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \in E \mid \bigcap_{m=0}^{M} \left\{ \widehat{\boldsymbol{\gamma}}_{\mathcal{D}}^{(m)} = \widehat{\boldsymbol{\gamma}}_{d}^{(m)} \right\}, \right.$$

$$\left. \operatorname{dir} \left\{ j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d}) \right\} = \operatorname{dir} \left\{ j_{d}(\widehat{\boldsymbol{\gamma}}_{d}) \right\}, \quad \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) = \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right).$$

The first equality follows by the definition of $\mathscr{A}_{PCR}$. The second equality uses the fact that $\widehat{\boldsymbol{\gamma}}_{\mathcal{D}} = \widehat{\boldsymbol{\gamma}}_{d}$ in this conditioning set.

We write

$$\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}^{(m)} = \widehat{\boldsymbol{\gamma}}^{(m)}(\mathbf{s})$$

$$= \widehat{\boldsymbol{\gamma}}^{(m)} \left(\widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_{d}) j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d}) + \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right)$$

$$= \widehat{\boldsymbol{\gamma}}^{(m)} \left(\sqrt{H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d})} \widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_{d}) \operatorname{dir}(j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d})) + \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right).$$

Using this decomposition, we write

$$\Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{\mathcal{D}}) \in E \mid \mathscr{A}_{PCR} \right)$$

$$= \Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \in E \mid \right.$$

$$\bigcap_{m=0}^{M} \left\{ \widehat{\boldsymbol{\gamma}}^{(m)} \left(\sqrt{H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d})} \widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_{d}) \operatorname{dir}(j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d})) + \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right) = \widehat{\boldsymbol{\gamma}}_{d}^{(m)} \right\},$$

$$\left. \operatorname{dir} \left\{ j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d}) \right\} = \operatorname{dir} \left\{ j_{d}(\widehat{\boldsymbol{\gamma}}_{d}) \right\}, \quad \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) = \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right).$$

We insert the latter two conditions into the argument of $\widehat{\boldsymbol{\gamma}}^{(m)}$, and the probability becomes

$$= \Pr_{H_0} \left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \in E \mid \right.$$

$$\bigcap_{m=0}^{M} \left\{ \widehat{\boldsymbol{\gamma}}^{(m)} \left(\sqrt{H_{PCR}(\widehat{\boldsymbol{\gamma}}_{d})} \widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_{d}) \operatorname{dir}(j_{d}(\widehat{\boldsymbol{\gamma}}_{d})) + \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right) = \widehat{\boldsymbol{\gamma}}_{d}^{(m)} \right\},$$

$$\left. \operatorname{dir} \left\{ j_{\mathcal{D}}(\widehat{\boldsymbol{\gamma}}_{d}) \right\} = \operatorname{dir} \left\{ j_{d}(\widehat{\boldsymbol{\gamma}}_{d}) \right\}, \quad \mathbf{W}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) = \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_{d}) \right).$$

The latter two conditions can be dropped from the conditioning set because of the independence

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properties established in Lemmas C.1 and C.2. So we obtain

$$
\begin{aligned}
&= \Pr_{H_0}\left(H_{PCR}(\widehat{\boldsymbol{\gamma}}_\partial) \in E \mid \right. \\
&\qquad \left. \bigcap_{m=0}^{M} \left\{ \widehat{\boldsymbol{\gamma}}^{(m)}\left(\sqrt{H_{PCR}(\widehat{\boldsymbol{\gamma}}_\partial)}\widehat{\mathbb{P}}(\widehat{\boldsymbol{\gamma}}_\partial)\mathrm{dir}(j_\partial(\widehat{\boldsymbol{\gamma}}_\partial)) + \mathbf{w}_{PCR}(\widehat{\boldsymbol{\gamma}}_\partial) \right) = \widehat{\boldsymbol{\gamma}}_\partial^{(m)} \right\} \right) \\
&= \Pr_{H_0}\left(\phi^2 \in E \mid \left\{ \widehat{\boldsymbol{\gamma}}^{(m)}\left(\widehat{\mathbf{s}}_\partial(\phi) \right) = \widehat{\boldsymbol{\gamma}}_\partial^{(m)} \right\} \right) \\
&= \Pr_{H_0}\left(\phi^2 \in E \mid \mathcal{S}_{PCR} \right)
\end{aligned}
$$

where $\phi^2 \sim \chi^2_{\mathrm{rank}(R)}$.

References

Akgun, O., Pirotte, A., Urga, G., and Yang, Z. (2025). Testing clustered equal predictive ability with unknown clusters.

Ando, T. and Bai, J. (2015). A simple new test for slope homogeneity in panel data models with interactive effects. *Economics Letters*, 136:112–117.

Ando, T. and Bai, J. (2016). Panel data models with grouped factor structure under unknown group membership. *Journal of Applied Econometrics*, 31(1):163–191.

Andrews, D. W. K., Cheng, X., and Guggenberger, P. (2020). Generic results for establishing the asymptotic size of confidence sets and tests. *Journal of Econometrics*, 218:496–531.

Andrews, I., Kitagawa, T., and McCloskey, A. (2021). Inference after estimation of breaks. *Journal of Econometrics*, 224(1):39–59.

Andrews, I., Kitagawa, T., and McCloskey, A. (2024). Inference on winners. *The Quarterly Journal of Economics*, 139(1):305–358.

Arthur, D. and Vassilvitskii, S. (2007). k-means++: The advantages of careful seeding. In *Proceedings of the eighteenth annual ACM-SIAM symposium on Discrete algorithms*, pages 1027–1035. Society for Industrial and Applied Mathematics Philadelphia, PA, USA.

Bachmann, R. and Bayer, C. (2014). Investment dispersion and the business cycle. *American Economic Review*, 104(4):1392–1416.

Bagirov, A. and Ugon, J. (2018). Nonsmooth DC programming approach to clusterwise linear regression: optimality conditions and algorithms. *Optimization Methods and Software*, 33(1):194–219.

Bagirov, A. M., Ugon, J., and Mirzayeva, H. G. (2015). An algorithm for clusterwise linear regression based on smoothing techniques. *Optimization Letters*, 9(2):375–390.

Benjamini, Y. (2020). Selective inference: The silent killer of replicability. *Harvard Data Science Review*, 2(4).

Bonhomme, S., Lamadon, T., and Manresa, E. (2022). Discretizing unobserved heterogeneity. *Econometrica*, 90(2):625–643.

Bonhomme, S. and Manresa, E. (2015). Grouped patterns of heterogeneity in panel data. *Econometrica*, 83(3):1147–1184.

Canova, F. (2004). Testing for convergence clubs in income per capita: a predictive density approach. *International Economic Review*, 45(1):49–77.

Carbonneau, R. A., Caporossi, G., and Hansen, P. (2011). Globally optimal clusterwise regression by mixed logical-quadratic programming. *European Journal of Operational Research*, 212(1):213–222.

Carbonneau, R. A., Caporossi, G., and Hansen, P. (2012). Extensions to the repetitive branch and bound algorithm for globally optimal clusterwise regression. *Computers & Operations Research*, 39(11):2748–2762.

Carbonneau, R. A., Caporossi, G., and Hansen, P. (2014). Globally optimal clusterwise regression by column generation enhanced with heuristics, sequencing and ending subset optimization. *Journal of Classification*, 31(2):219–241.

Chen, Y. T. and Gao, L. L. (2024). Testing for a difference in means of a single feature after clustering. *Biostatistics*, 26(1):kxae046.

Chen, Y. T. and Witten, D. M. (2023). Selective inference for k-means clustering. *Journal of Machine Learning Research*, 24(152):1–41.

Cheng, X., Schorfheide, F., and Shao, P. (2025). Clustering for multi-dimensional heterogeneity with an application to production function estimation. mimeo.

Chetverikov, D. and Manresa, E. (2022). Spectral and post-spectral estimators for grouped panel data models. arXiv:2212.13324 [econ, stat].

Cytrynbaum, M. (2020). Blocked clusterwise regression. arXiv:2001.11130 [econ, stat].

Driscoll, J. C. and Kraay, A. C. (1998). Consistent covariance matrix estimation with spatially dependent panel data. *Review of Economics and Statistics*, 80(4):549–560.

D'Urso, P., Massari, R., and Santoro, A. (2010). A class of fuzzy clusterwise regression models. *Information Sciences*, 180(24):4737–4762.

Fabrizio, K. R. and Tsolmon, U. (2014). An empirical examination of the procyclicality of r&d investment and innovation. *Review of Economics and Statistics*, 96(4):662–675.

Gao, L. L., Bien, J., and Witten, D. (2024). Selective inference for hierarchical clustering. *Journal of the American Statistical Association*, 119(545):332–342.

González-Delgado, J., Cortés, J., and Neuvial, P. (2023). Post-clustering inference under dependency. *arXiv preprint arXiv:2310.11822*.

González-Casasús, O. (2025). Grouped fixed-effects estimation is more robust than you think. mimeo.

Greene, W. (2011). *Econometric Analysis*. Pearson Education.

Huang, W., Jin, S., and Su, L. (2020). Identifying latent grouped patterns in cointegrated panels. *Econometric Theory*, 36(3):410–456.

Ingrassia, S., Minotti, S. C., and Punzo, A. (2014). Model-based clustering via linear cluster-weighted models. *Computational Statistics & Data Analysis*, 71:159–182.

Karmitsa, N., Taheri, S., Bagirov, A., and Mäkinen, P. (2022). Missing value imputation via clusterwise linear regression. *IEEE Transactions on Knowledge and Data Engineering*, 34(4):1889–1901. Conference Name: IEEE Transactions on Knowledge and Data Engineering.

Ke, Y., Li, J., and Zhang, W. (2016). Structure identification in panel data analysis. *The Annals of Statistics*, 44(3):1193–1233.

Ke, Z. T., Fan, J., and Wu, Y. (2015). Homogeneity pursuit. *Journal of the American Statistical Association*, 110(509):175–194.

Kriegeskorte, N., Simmons, W. K., Bellgowan, P. S., and Baker, C. I. (2009). Circular analysis in systems neuroscience: the dangers of double dipping. *Nature Neuroscience*, 12(5):535–540.

Kuchibhotla, A. K., Kolassa, J. E., and Kuffner, T. A. (2022). Post-selection inference. *Annual Review of Statistics and Its Application*, 9:505–527.

Lee, J. D., Sun, D. L., Sun, Y., and Taylor, J. E. (2016). Exact post-selection inference, with application to the Lasso. *The Annals of Statistics*, 44(3):907–927.

Leeb, H. and Pötscher, B. M. (2005). Model Selection and Inference: Facts and Fiction. *Econometric Theory*, 21(1):21–59. Publisher: Cambridge University Press.

Lin, C.-C. and Ng, S. (2012). Estimation of panel data models with parameter heterogeneity when group membership is unknown. *Journal of Econometric Methods*, 1(1):42–55.

Loyo, J. A. and Boot, T. (2025). Grouped heterogeneity in linear panel data models with heterogeneous error variances. *Journal of Business & Economic Statistics*, 43(1):68–80.

Lu, X. and Su, L. (2017). Determining the number of groups in latent panel structures with an application to income and democracy. *Quantitative Economics*, 8(3):729–760.

Lu, X. and Su, L. (2023). Uniform inference in linear panel data models with two-dimensional heterogeneity. *Journal of Econometrics*, 235(2):694–719.

Lumsdaine, R. L., Okui, R., and Wang, W. (2023). Estimation of panel group structure models with structural breaks in group memberships and coefficients. *Journal of Econometrics*, 233(1):45–65.

MacQueen, J. (1967). Some methods for classification and analysis of multivariate observations. In *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability*, volume 1, pages 281–297. Oakland, CA, USA.

Mugnier, M. (2022). Unobserved clusters of time-varying heterogeneity in nonlinear panel data models.

Okui, R. and Wang, W. (2021). Heterogeneous structural breaks in panel data models. *Journal of Econometrics*, 220(2):447–473.

Park, Y. W., Jiang, Y., Klabjan, D., and Williams, L. (2017). Algorithms for generalized clusterwise linear regression. *INFORMS Journal on Computing*, 29(2):301–317. Publisher: INFORMS.

Patton, A. J. and Weller, B. M. (2023). Testing for unobserved heterogeneity via *k-means* clustering. *Journal of Business & Economic Statistics*, 41(3):737–751.

Pesaran, H. M. and Yamagata, T. (2008). Testing slope homogeneity in large panels. *Journal of Econometrics*, 142(1):50–93.

Pesaran, M. H. (2006). Estimation and inference in large heterogeneous panels with a multifactor error structure. *Econometrica*, 74(4):967–1012.

Pesaran, M. H. and Smith, R. (1995). Estimating long-run relationships from dynamic heterogeneous panels. *Journal of Econometrics*, 68(1):79–113.

Pesaran, M. H. and Tosetti, E. (2011). Large panels with common factors and spatial correlation. *Journal of Econometrics*, 161(2):182–202.

Phillips, P. C. and Sul, D. (2007). Transition modeling and econometric convergence tests. *Econometrica*, 75(6):1771–1855.

Qian, J. and Su, L. (2016). Shrinkage estimation of common breaks in panel data models via adaptive group fused Lasso. *Journal of Econometrics*, 191(1):86–109.

Raiola, A. and Salish, N. (2025). Testing for grouped patterns in panel data models. mimeo.

Sarafidis, V. and Weber, N. (2015). A partially heterogeneous framework for analyzing panel data. *Oxford Bulletin of Economics and Statistics*, 77(2):274–296.

Späth, H. (1979). Algorithm 39: Clusterwise linear regression. *Computing*, 22:367–373.

Su, L. and Ju, G. (2018). Identifying latent grouped patterns in panel data models with interactive fixed effects. *Journal of Econometrics*, 206(2):554–573.

Su, L., Shi, Z., and Phillips, P. C. B. (2016). Identifying latent structures in panel data. *Econometrica*, 84(6):2215–2264.

Su, L., Wang, W., and Xu, X. (2023). Identifying latent group structures in spatial dynamic panels. *Journal of Econometrics*, 235(2):1955–1980.

Su, L., Wang, X., and Jin, S. (2019). Sieve Estimation of Time-Varying Panel Data Models With Latent Structures. *Journal of Business & Economic Statistics*, 37(2):334–349.

Taylor, J. and Tibshirani, R. J. (2015a). Statistical learning and selective inference. *Proceedings of the National Academy of Sciences*, 112(25):7629–7634.

Taylor, J. and Tibshirani, R. J. (2015b). Statistical learning and selective inference. *Proceedings of the National Academy of Sciences*, 112(25):7629–7634.

van Ophem, H., van Giersbergen, N., van Garderen, K. J., and Bun, M. (2019). The cyclicality of r&d investment revisited. *Journal of Applied Econometrics*, 34(2):315–324.

Wan, C., Sun, J., and Xu, X. (2025). Conditional selective inference for the selected groups in panel data. mimeo.

Wang, W., Phillips, P. C. B., and Su, L. (2018). Homogeneity pursuit in panel data models: Theory and application. *Journal of Applied Econometrics*, 33(6):797–815.

Wang, W. and Su, L. (2021). Identifying latent group structures in nonlinear panels. *Journal of Econometrics*, 220(2):272–295.

Wang, Y., Phillips, P. C. B., and Su, L. (2024). Panel data models with time-varying latent group structures. *Journal of Econometrics*, 240(1):105685.

Yu, L., Gu, J., and Volgushev, S. (2024). Spectral clustering with variance information for group structure estimation in panel data. *Journal of Econometrics*, 241(1):105709.

Yun, Y. and He, Y. (2024). Selective inference for multiple pairs of clusters after k-means clustering. *arXiv preprint arXiv:2405.16379*.

Zhang, Y., Wang, H. J., and Zhu, Z. (2019). Quantile-regression-based clustering for panel data. *Journal of Econometrics*, 213(1):54–67.