Inference in Difference-in-Differences with Few Treated Units and Spatial Correlation

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Abstract

We consider the problem of inference in Difference-in-Differences (DID) when there are few treated units and errors are spatially correlated. We first show that, when there is a single treated unit, some existing inference methods designed for settings with few treated and many control units remain asymptotically valid when errors are weakly dependent. However, these methods may be invalid with more than one treated unit. We propose alternatives that are asymptotically valid in this setting, even when the relevant distance metric across units is unavailable.

Keywords: hypothesis testing; causal inference; randomization inference; permutation tests

JEL Codes: C12; C21; C23; C33

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1 Introduction

Difference-in-Differences (DID) presents a series of challenges for inference. There is a large number of inference methods for DID. However, the effectiveness of different solutions depends crucially on the set of assumptions one is willing to make on the errors, and on many features of the empirical design, such as the number of treated and control units. A non-exhaustive list of papers that proposed and/or analyzed different inference methods for DID in different settings include Arellano (1987), Bertrand et al. (2004), Donald and Lang (2007), Cameron et al. (2008), Conley and Taber (2011), Bester et al. (2011), Ibragimov and Müller (2016), Brewer et al. (2017), Canay et al. (2017), Ferman and Pinto (2019), MacKinnon and Webb (2020), Ferman (2021a, 2023), Rambachan and Roth (2020), Athey and Imbens (2022) and Alvarez and Ferman (2023).

We consider a common setting in which a satisfactory solution is not yet available: when (i) there is a small number of treated units, (ii) the number of periods is fixed, and (iii) errors are possibly spatially correlated, but the relevant distance metric is not available to the applied researcher. Throughout, we refer to “spatial correlation” as any correlation in the cross section, not necessarily related to a geographical distance metric.

Conley and Taber (2011) (henceforth, CT) and Ferman and Pinto (2019) (henceforth, FP) proposed inference methods for settings with few treated and many control units, when there is a fixed number of pre-treatment periods. However, they derive the validity of these methods assuming independence across units (or a spatial correlation depending on an observed distance metric). Considering first a setting with a single treated unit, we derive conditions in which these methods remain asymptotically valid in the presence of spatial correlation, even when the relevant distance metric across units is not available. The main assumptions are that (i) the post-pre difference in average errors for each unit has the same marginal distribution for all units — we can relax this assumption by allowing for heteroskedasticity with a known structure that can be estimated —, and (ii) the cross-section distribution of this post-pre difference in average errors is weakly dependent for the control
units. Under these conditions, the asymptotic distribution of the DID estimator depends only on the post-pre difference in average errors of the treated unit. Moreover, the residuals of the control units asymptotically recover the distribution of the errors of the treated unit, even when there is spatial correlation.

However, when there is more than one treated unit, we show that these inference methods proposed by CT and FP may not be asymptotically valid if there is spatial correlation, and the applied researcher does not have information on the relevant distance metric. The intuition is clear: when we (mistakenly) assume that errors are independent across clusters, we underestimate the volatility of the average of the errors for the treated units if errors are positively correlated across the treated units.

We propose alternatives that are asymptotically valid, though generally conservative, in this setting. We first consider an aggregate of the treated units, and derive critical values based on a worst-case scenario for the spatial correlation. While this guarantees a test that is asymptotically valid when the number of control units increases (with the number of treated units fixed), the cost of being robust to unobserved spatial correlation among the treated units is a potential loss in terms of power. For settings in which the outcome variable is the aggregate of unit \( \times \) time individual-level observations, we consider a second alternative. We again consider the aggregation of the \( N_1 \) treated units. However, we show that, in this case, we can use information on the within-unit correlation to bound the spatial correlation between treated units. Under the assumption that two individuals within the same unit are relatively more correlated than two individuals in different units, we show that it is possible construct a test that is still robust to spatial correlation, but with a lower loss in terms of power.

Finally, we also consider a third alternative, where we consider separate regressions for each treated unit, and adjust the \( p \)-values using a multiple hypotheses testing (MHT) procedure that imposes few to no assumptions on the dependence between tests. In this case, one may invert the multiple testing procedure to produce valid confidence sets on the het-
erogeneous effects, and project these to obtain confidence sets on average effects. While this alternative imposes fewer assumptions on the errors, this comes at a cost: we show that this approach produces confidence sets that contain the confidence intervals obtained by our other alternatives.

We analyze a Monte Carlo simulation based on the spatial correlation structure of the American Community Survey (ACS). We then revisit the work by Sommers et al. (2014), who analyzed the effects of the Massachusetts 2006 health reform, in light of our results.

2 Setting

Let $Y_{st}(0)$ ($Y_{st}(1)$) be the potential outcome of unit $s$ at time $t$ when this unit is untreated (treated) at this period. We consider that potential outcomes are given by

$$\begin{cases} 
Y_{st}(0) = \theta_s + \gamma_t + \eta_{st} \\
Y_{st}(1) = \alpha_{st} + Y_{st}(0),
\end{cases}$$

(1)

where $\alpha_{st}$ is the (possibly heterogeneous) treatment effects for unit $s$ at time $t$, $\theta_s$ are time-invariant unobserved effects, and $\gamma_t$ are group-invariant unobserved effects. The error term $\eta_{st}$ represents unobserved determinants of $Y_{st}(0)$ that are not captured by the fixed effects. We observe $Y_{st} = d_{st}Y_{st}(1) + (1 - d_{st})Y_{st}(0)$, where $d_{st}$ is a dummy variable equal to one if unit $s$ is treated at time $t$. We can also consider the case in which we observe individual-level observations $Y_{ist}$. In this case, a solution to take within-(unit $\times$ time) correlations into account is to consider unit $\times$ time aggregates $Y_{st}$. Therefore, we focus on the unit $\times$ time aggregate setting.

We focus on the case in which treatment is non-reversible and starts for all treated units after date $t^*$ (see Remark 4.4 for the case with variation in adoption time). There are $N_1$ treated units, $N_0$ control units, and $T$ time periods. Let $\mathcal{I}_1$ ($\mathcal{I}_0$) be the set of indices for treated (control) units, while $\mathcal{T}_1$ ($\mathcal{T}_0$) be the set of indices for post- (pre-) treatment periods.
We treat the allocation of the treatment as fixed. We also treat \( \{ \alpha_{st} \}_{s \in \mathcal{I}_1, t \in \mathcal{T}_1} \) as fixed parameters, and define \( \alpha \equiv \frac{1}{N_1} \frac{1}{T-t^*} \sum_{s \in \mathcal{I}_1} \sum_{t \in \mathcal{T}_1} \alpha_{st} \), which is the average treatment effects across treated units and treated periods. Since \( \theta_s \) and \( \gamma_t \) are eliminated when we include the fixed effects, we do not need to impose any constrain on those variables, which can be treated either as fixed or stochastic. Therefore, the only relevant uncertainty in our setting comes from potentially different realizations of unobserved variables \( \eta_{st} \). This may include, for example, unit \( \times \) time specific weather or economics unobserved shocks. Moreover, it may be that such unobserved variables are serially correlated and/or correlated across units.

A framework in which treatment assignment and treatment effects are treated as fixed is common in the literature of DID with few treated clusters, as considered by CT, FP, and Alvarez and Ferman (2023). A similar framework is also considered in other settings in which the number of treated clusters is fixed, such as in the synthetic controls literature (Abadie et al., 2010; Arkhangelsky et al., 2021; Ben-Michael et al., 2021; Botosaru and Ferman, 2019; Chernozhukov et al., 2021; Ferman and Pinto, 2021; Ferman, 2021b; Zhang et al., 2022). In such settings, we want to learn about the realized treatment effects for the units that received treatment \( \{ \alpha_{st} \}_{s \in \mathcal{I}_1, t \in \mathcal{T}_1} \), while uncertainty comes from different realizations of unobserved variables, such as weather or economic unobserved shocks.

Let \( W_s = \frac{1}{T-t^*} \sum_{t \in \mathcal{T}_1} \eta_{st} - \frac{1}{t^*} \sum_{t \in \mathcal{T}_0} \eta_{st} \), which is the post-pre difference in average errors for each unit \( s \). In this case in which treatment starts at the same period for all treated units, the DID estimator is numerically equivalent to the two-way fixed effects (TWFE) estimator, which is given by

\[
\hat{\alpha} = \frac{1}{N_1} \sum_{s \in \mathcal{I}_1} \left[ \frac{1}{T-t^*} \sum_{t \in \mathcal{T}_1} Y_{st} - \frac{1}{t^*} \sum_{t \in \mathcal{T}_0} Y_{st} \right] - \frac{1}{N_0} \sum_{s \in \mathcal{I}_0} \left[ \frac{1}{T-t^*} \sum_{t \in \mathcal{T}_1} Y_{st} - \frac{1}{t^*} \sum_{t \in \mathcal{T}_0} Y_{st} \right] 
= \alpha + \frac{1}{N_1} \sum_{s \in \mathcal{I}_1} W_s - \frac{1}{N_0} \sum_{s \in \mathcal{I}_0} W_s. \tag{2}
\]

We consider the following identification assumption.

**Assumption 2.1.** \( \mathbb{E}[W_s] = 0 \) for all \( s \in \mathcal{I}_1 \cup \mathcal{I}_0 \).
We recall that treatment assignment is fixed, so this assumption means that the post-pre difference in average errors has the same mean for both treated and control units. This assumption is implied by a standard parallel trends assumption for all periods, and is equivalent to assuming a parallel trends assumption on the potential outcomes. We can extend our results to consider alternative parallel trends assumptions (Marcus and Sant’Anna, 2021) and alternative estimators.

Given Assumption 2.1, we have that $\mathbb{E}[\hat{\alpha}] = \alpha$, so the DID estimator is unbiased. However, in a setting in which $N_1$ is fixed and $N_0 \to \infty$, the DID estimator will not be consistent, and will not necessarily be asymptotically normal. In particular, CT show that, under a strong mixing condition on the errors, in this setting $\hat{\alpha}$ converges in probability to $\alpha + \tilde{W}$, where $\tilde{W} \equiv \frac{1}{N_1} \sum_{s \in I_1} W_s$. Therefore, if we want to test the null hypothesis $H_0 : \alpha = \alpha_0$ at the significance level $\tau$, this would pose some challenges for inference.

3 Inference with independent clusters

Before we move to the case in which errors may be spatially correlated, we start with a brief review of inference methods for settings with few treated clusters, when errors are independent in the cross-section. We focus on the inference approaches proposed by CT and FP for settings with few treated units and a fixed number of periods.

CT propose an interesting inference method in this setting by noting that the residuals $\hat{W}_s$ of the control units may be informative about the distribution of $W_s$ for the treated. In their running model, they assume that $W_s$ is iid across $s \in I_1 \cup I_0$ (Assumption 2 from CT). Note that, under this iid assumption, knowledge about the marginal distribution of $W_s$ for the control units implies knowledge about the distribution of $\tilde{W}$. Therefore, the main idea from CT is to use $\{\hat{W}_s\}_{s \in Z_0}$ to approximate the marginal distribution of $W_s$ for the treated, and then use that to calculate critical values. More specifically, they propose the following algorithm for testing the null $H_0 : \alpha = \alpha_0$ with a significance level $\tau$. 
Algorithm 1: Conley and Taber (2011)

1. Run the DID estimator, and store $\hat{\alpha}$ and the residuals $\hat{W}_s = \frac{1}{T-t^*} \sum_{t \in T_1} \hat{\eta}_{st} - \frac{1}{T} \sum_{t \in T_0} \hat{\eta}_{st}$ for all $s \in I_0$;

2. for $b=1, \ldots, B$ do
   
3. Sample with replacement $N_1$ values from $\{\hat{W}_s\}_{s \in I_0}$, $(\hat{W}_{1}^*, \ldots, \hat{W}_{N_1}^*)$;

4. Calculate $\hat{\alpha}_b = \frac{1}{N_1} \sum_{s=1}^{N_1} \hat{W}_s^*$;

5. Reject the null if $\frac{B}{B} \sum_{b=1}^{B} 1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\} > 1 - \tau$.

Let $\phi_{CT}$ be an indicator variable equal to one if we reject the null given the algorithm above. We summarize the results from CT in the following proposition.

Proposition (CT). Suppose we have data on $\{Y_{s1}, \ldots, Y_{sT}\}_{I_1 \cup I_0}$, and that Assumption 2.1 holds. Assume also that $W_s$ is iid across $s$, with a common distribution function $F_W$ that has bounded second moment and is absolutely continuous with bounded density. Then, as $N_0 \to \infty$ and $N_1$ is fixed, (i) $\hat{\alpha}$ converges in probability to $\alpha + \tilde{W}$, and (ii) if the null is true, then $E[\phi_{CT}] \to \tau$ as $N_0, B \to \infty$ at any rate.

Note that CT provide a proof of result (i) under less restrictive conditions (their Proposition 1). Proposition 2 from CT presents result (ii) under similar conditions as we consider here. In particular, assuming that errors are iid in the cross section. CT also consider another alternative for inference in their appendix, in which they relax the iid assumptions, allowing for spatial correlation and heteroskedasticity with a known structure. However, this alternative relies on a known distance metric. It also requires parametrization/estimation of the serial correlation structure, and relies on normality.

FP builds on CT to propose an alternative that allows for heteroskedasticity with a known structure that can be estimated, without requiring parametrization/estimation of the serial correlation structure, and without relying on normality. They consider a setting in which we also observe a vector of covariates $Z_s$, and assume that $W_s = h(Z_s, \delta)\xi_s$, where $h(\cdot, \delta)$ is a known function with $\delta$ being an unknown parameter, and $\xi_s$ is iid for all $s$. In Appendix A.3, we provide evidence that, under the assumption that heteroskedasticity is a
sole function of \( Z_s \), our adopted parametric form for \( h \) is reasonable for the dataset used to base our simulations in Section 5, and for the dataset of our empirical illustration in Section 6. Throughout, we consider that the sequence \( \{ Z_s \} \cup \{0\} \) is fixed. This allows for treated and control units to be arbitrarily different with respect to \( Z_s \). Therefore, this allows for heteroskedasticity with a known structure (up to a parameter that can be estimated), but still relies on independence across units. In this case, instead of directly sampling from \( \{ \hat{W}_s \} \), we re-scale the residuals taking into account that they may have different variances. The algorithm to implement their inference method for testing the null hypothesis \( H_0 : \alpha = \alpha_0 \) with a significance level \( \tau \) is the following.

**Algorithm 2:** Ferman and Pinto (2019)

1. Run the DID estimator, and store \( \hat{\alpha} \) and the residuals \( \hat{W}_s = \frac{1}{T-T} \sum_{t \in T_1} \hat{\eta}_{st} - \frac{1}{T} \sum_{t \in T_0} \hat{\eta}_{st} \) for all \( s \in I_0 \);
2. Estimate \( \hat{\delta} \) using the residuals from the controls (see example below);
3. Compute the normalized residuals \( \hat{\xi}_s = \hat{W}_s / h(Z_s, \hat{\delta}) \), for \( s \in I_0 \);
4. for \( b=1, \ldots, B \) do
   5. Sample with replacement \( N_1 \) values from \( \{ \hat{\xi}_s \} \cup \{ \hat{\xi}_1^*, \ldots, \hat{\xi}_{N_1}^* \} \);
   6. Calculate \( \hat{\alpha}_b = \frac{1}{N_1} \sum_{s=1}^{N_1} h(Z_s, \hat{\delta})\hat{\xi}_s^* \);
6. Reject the null if \( \frac{1}{B} \sum_{b=1}^{B} |\hat{\alpha}_b - \alpha_0| > |\hat{\alpha}| > 1 - \tau \).

Let \( \phi_{FP} \) be an indicator variable equal to one if we reject the null given the algorithm above.

**Proposition** (FP). Suppose we have data on \( \{Y_s, Z_s\} \cup \{0\} \), and that Assumption 2.1 holds. Assume also that \( W_s = h(Z_s, \delta)\xi_s \), where \( \xi_s \) is iid across \( s \), with a common distribution function \( F_\xi \) that has bounded second moment and is absolutely continuous with bounded density. Assume there exist constants \( 0 < h \leq \overline{h} < \infty \), not depending on \( N_0 \), such that \( h \leq h(Z_s, \delta) \leq \overline{h} \) for all \( s \in I_0 \cup I_1 \), uniformly as \( N_0 \to \infty \). Assume also that we have an estimator \( \hat{\delta} \) of \( \delta \) such that \( \max_{s \in I_0 \cup I_1} |h(Z_s, \hat{\delta}) - h(Z_s, \delta)| = o_p(1) \) as \( N_0 \to \infty \). Then, (i) \( \hat{\alpha} \) converges in probability to \( \alpha + \overline{W} \), and (ii) if the null is true, then \( \mathbb{E}[\phi_{FP}] \to \tau \) as \( N_0, B \to \infty \) at any rate.
This approach is well-suited for settings in which \( Y_{st} \) is the state \( \times \) time aggregate of individual-level observations \( Y_{ist} \). Let \( Z_s \) be the number of individual-level observations in state \( s \). FP consider the case in which heteroskedasticity arises only from variation in the number of observations per unit. In this case, we should expect \( \mathbb{V}(W_s) \) to be a decreasing function of \( Z_s \). In such cases, the approach from CT would tend to (over-) under-reject when the treated units are (larger) smaller relative to the control units. FP show that, under a wide range of structures on the within-unit correlations, \( \mathbb{V}(W_s) \) would be given by \( A + B/Z_s \), for parameters \( A, B \geq 0 \). Note that the bounding conditions on \( h(Z_s, \delta) \) are satisfied in this setting if either \( A > 0 \), or \( B > 0 \) and the sequence \( (Z_s)_{s \in I_0 \cup I_1} \) is bounded uniformly as \( N_0 \to \infty \). In this case, the idea is to estimate \( A \) and \( B \) using the residuals from the control units, and then re-scale the residuals to the control units in order to approximate the marginal distributions of \( W_s \) for the treated. Then we can use these distributions to compute critical values. This approach can be used when we have access to the individual-level data, or when we have only aggregate data (provided that we have access to information on the number of observations per unit). FP also consider another alternative that allows for spatial correlation, but in this case they would need an asymptotic theory in which the number of pre-treatment periods goes to infinity (see Remark 4.2).

There are other alternatives that are valid with few treated clusters in settings where clusters are independent. Canay et al. (2017) and Hagemann (2023) propose randomization tests that remain valid under heteroskedasticity, whenever approximate symmetry of the \( \{W_s\}_{s \in I_1} \) holds. However, in the limiting case where \( N_1 = 1 \), these tests have either low power or are not defined. MacKinnon and Webb (2020) propose alternative randomization inference tests for few clusters. However, they show in simulations that their method may severely overreject when there is a single treated unit and heteroskedasticity. Hagemann (2020) introduces a procedure that is valid under heteroskedasticity when \( N_1 = 1 \) and the \( \{W_s\}_{s \in I_0 \cup I_1} \) are approximately normal. His approach requires the user pre-specifying an upper bound for the relative variance of the treated \( W \) vis-à-vis the variance of the \( W \) in
the control group. Finally, the wild bootstrap is another common alternative in settings with few independent clusters. However, this method can have poor power when there are few treated units (see, for example, the simulations in Appendix A.7). See Canay et al. (2021) for further discussion on the validity of the wild bootstrap with few clusters.

4 Inference with spatial correlation

We consider now the case in which errors may be spatially correlated. We consider the following assumptions.

Assumption 4.1. (i) $W_s = h(Z_s; \delta)\xi_s$, where $\xi_s$ is equally distributed for all $s \in I_1 \cup I_0$, with a common distribution function $F_\xi$ that is absolutely continuous with bounded density; (ii) there exists a constant $h > 0$ not depending on $N_0$ such that $\min_{s \in I_0 \cup I_1} h(Z_s; \delta) \geq h$ for all $N_0 \in \mathbb{N}$; (iii) $\frac{1}{N_0} \sum_{s \in I_0} W_s \overset{p}{\rightarrow} 0$ and $\frac{1}{N_0} \sum_{s \in I_0} 1\{\xi_s \leq c\} \overset{p}{\rightarrow} F_\xi(c)$ for every $c \in \mathbb{R}$ when $N_0 \rightarrow \infty$; and (iv) the estimator $\hat{\delta}$ for $\delta$ is such that $\max_{s \in I_1 \cup I_0} |h(Z_s; \hat{\delta}) - h(Z_s; \delta)| = o_p(1)$ when $N_0 \rightarrow \infty$.

Assumptions 4.1(i) and 4.1(ii) restrict the marginal distribution of the treated and control units, as in FP. With this assumption, the residuals of the control units become informative about the distribution of the errors of the treated units, which is the main insight from CT. If we set $h(Z_s, \delta)$ constant, then these assumptions imply that the marginal distribution $W_s$ is the same for both treated and control units, as considered by CT in their running model.

Assumption 4.1(iii) is a high-level assumption that allows for spatially correlated shocks, but restricts such dependence so that we can apply a law of large numbers when we consider the control units. This will be satisfied, for example, if we assume strong mixing conditions in the cross section (see Theorem 3 from Jenish and Prucha (2009)). More generally, however, laws of large numbers are known to hold for a wide range of spatially dependent processes (Jenish and Prucha, 2012). For simplicity, we refer to this assumption in the text as a weak dependence assumption. Importantly, Assumption 4.1 allows for arbitrary spatial correlation.
among the treated units. Finally, Assumption 4.1(iv) states that we can consistently estimate
the parameters of the heteroskedasticity.

Since we focus on settings in which researchers do not have information on what generates
the spatial correlation or they are not willing to assume such structure, we do not need to
model in detail the sources of spatial correlation. As a concrete example, we can consider a
setting in which the \( N_1 \) treated units are closely located geographically, but we have a larger
number of control units in different locations. In this case, if spatial correlation goes to zero
when geographical distance increases, then we would have Assumption 4.1(iii) satisfied, even
though we may have arbitrarily strong spatial correlation among the \( N_1 \) treated units. While
it is natural to think about spatial correlation based on geographical distance, this may not
be the case in relevant empirical applications. For example, we may have that units with
similar industry shares have more correlated errors. Importantly, we consider a setting in
which the applied researcher may be unaware or may not have information on the relevant
distance metrics in the cross section, which is common in DID applications (Ferman, 2023).
We further discuss this assumption in Remark 4.3.

Under Assumptions 2.1 and 4.1, it follows again that \( \hat{\alpha} \) is unbiased, and that, when \( N_1 \)
is fixed and \( N_0 \to \infty \), \( \hat{\alpha} \) converges in probability to \( \alpha + \tilde{W} \). We now consider different
approaches for testing the null \( H_0 : \alpha = \alpha_0 \).

4.1 Case with \( N_1 = 1 \)

When \( N_1 = 1 \), the inference methods proposed by CT and FP can remain valid even
if we allow for spatial correlation, and even when we do not have information on the relevant
distance metric. The main intuition is that, under Assumption 4.1, the asymptotic
distribution of \( \hat{\alpha} \) depends only on \( W_1 \), and the distribution of \( W_1 \) can still be asymptotically
approximated using the residuals from the controls, so we can use that to construct critical
values.

Let \( \hat{F}_c(c) = N_0^{-1} \sum_{s \in Z_0} \mathbb{1}\{\hat{W}_s / h(Z_s, \hat{\delta}) \leq c\} \), where \( \hat{\delta} \) is an estimator for \( \delta \). We first show
that \( \hat{F}_\xi(c) \) approximates the distribution of \( \xi_s \) if \( \hat{\delta} \) is consistent.

**Proposition 4.1.** Suppose Assumptions 2.1 and 4.1 hold. Then, as \( N_0 \rightarrow \infty \), \( \hat{F}_\xi(c) \) converges in probability to \( F_\xi(c) \), uniformly over \( c \in \mathbb{R} \).

The proof of Proposition 4.1 is similar to the proof of Proposition 2 from CT. We present details in Appendix A.1.1. In this setting with \( N_1 = 1 \), the inference method proposed by FP would approximate the asymptotic distribution of \( \hat{\alpha} \) with the empirical distribution of \( \{h(Z_1, \hat{\delta})\hat{W}_s/h(Z_s, \hat{\delta})\}_{s \in I_0} \), to construct the critical values. It immediately follows from Proposition 4.1 that the inference method proposed by FP remains valid for the case with \( N_1 = 1 \), even when we may have spatial correlation.

**Corollary 4.1.** Suppose we have data on \( \{Y_{s1}, ..., Y_{sT}, Z_s\}_{I_1 \cup I_0} \), and that Assumptions 2.1 and 4.1 hold. Then, if \( N_1 = 1 \) and the null is true, \( \mathbb{E}[^{\phi_{FP}}] \rightarrow \tau \) as \( N_0, B \rightarrow \infty \) at any rate.

Note that if we set \( h(Z_s, \delta) \) constant, and \( h(Z_s, \hat{\delta}) = 1 \), then Proposition 4.1 and Corollary 4.1 imply that the standard procedure proposed by CT in their running model is also asymptotically valid when \( N_1 = 1 \) and \( N_0 \rightarrow \infty \), even when we have spatial correlation. The proof of Corollary 4.1 is presented in Appendix A.1.2.

### 4.2 Case with \( N_1 > 1 \): inference problems

When \( N_1 > 1 \), spatial correlation can lead to relevant size distortions if we rely on the methods proposed by CT and FP. For simplicity, consider the case in which \( N_1 = 2 \), and \( \{W_1, W_2\} \) is multivariate normally distributed with correlation \( \rho \). Consider also the case in which \( h(Z_s, \delta) \) is constant. Under Assumption 4.1, \( \hat{\alpha} \xrightarrow{p} \alpha + \hat{W} \), where \( \hat{W} \sim N(0, 2^{-1}(1 + \rho)\nabla(W_s)) \). However, if \( W_s \) is weakly dependent for the control units, when we consider two random draws from \( \{\hat{W}_s\}_{s \in I_0} \) to recover the distribution of \( \hat{W} \), the correlation between these draws would converge to zero when \( N_0 \rightarrow \infty \). As a consequence, the approach proposed by CT would recover a distribution for \( \hat{W} \) that is normal with a variance \( 2^{-1}\nabla(W_s) \). In this
case, critical values would be too small, leading to over-rejection. The same problem applies for the inference method proposed by FP.

The other alternatives for inference discussed in Section 3 would also lead to over-rejection in case the errors of the treated units are positively correlated.

4.3 Case with $N_1 > 1$: alternatives

We consider different alternatives that allows for spatial correlation, even when the applied researcher does not have information on the relevant source of spatial correlation.

4.3.1 Conservative Test 1: worst-case scenario for spatial correlation

We consider first the case in which the errors of all treated units are perfectly correlated as a worst-case scenario to provide an asymptotically valid, though possibly conservative, inference method in this setting. In this case, instead of considering Algorithm 1 or 2, we consider the following alternative.

\begin{algorithm}
\caption{Conservative Test 1}
\begin{algorithmic}[1]
1. Run the DID estimator, and store $\hat{\alpha}$ and the residuals $\hat{W}_s = \frac{1}{T-t^*} \sum_{t \in T_1} \hat{\eta}_{st} - \frac{1}{T} \sum_{t \in T_0} \hat{\eta}_{st}$ for all $s \in I_0$;
2. Estimate $\hat{\delta}$ using the residuals from the controls, and compute the normalized residuals $\hat{\xi}_s = \hat{W}_s / h(Z_s, \hat{\delta})$, $s \in I_0$;
3. for $b=1, \ldots, B$ do
4. \quad Sample one value from $\{\hat{\xi}_s\}_{s \in I_0}$, $\hat{\xi}^*$;
5. \quad Calculate $\hat{\alpha}_b = \frac{1}{N_1} \sum_{s=1}^{N_1} h(Z_s, \hat{\delta})\hat{\xi}^*$;
6. Reject the null if $\frac{1}{B} \sum_{b=1}^{B} 1\{ |\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b| \} > 1 - \tau$.
\end{algorithmic}
\end{algorithm}

Let $\phi_{\text{cons}}$ be an indicator variable equal to one if we reject the null given the algorithm above. More specifically, we consider the empirical distribution

$$\hat{H}(c) = \frac{1}{N_0} \sum_{s' \in I_0} 1\{N_1^{-1} \sum_{s \in I_1} h(Z_s, \hat{\delta})\hat{\xi}_{s'} < c \}.$$
This would recover the asymptotic distribution of $\hat{\alpha}$ if $\{W_s\}_{s \in \mathcal{I}_1}$ were perfectly correlated. When treated units are not perfectly correlated, though, we would recover a distribution for $\hat{\alpha}$ that has a higher variance relative to the true distribution of $\hat{\alpha}$. Therefore, we can use this distribution to construct critical values that guarantee that, under some assumptions, the test will asymptotically be level $\tau$ regardless of the spatial correlation. To formalize this idea, we consider the following high-level assumption.

**Assumption 4.2.** $Pr\left(|\tilde{W}| > c_{1-\tau}\right) \leq \tau$, where $c_{1-\tau}$ is the $(1 - \tau)$-quantile of the distribution of $N_1^{-1} \sum_{s \in \mathcal{I}_1} h(Z_s, \delta)|\xi|$.

Consider the simpler case in which $h(Z_s, \delta)$ is constant. Then this regularity condition simply means that, regardless of the spatial correlation among the treated units, the probability of having extreme values for the average of the treated units, $\tilde{W}$, is weakly smaller than the probability of having extreme values for a single draw of $W_s$.

Note that Assumption 4.2 is satisfied if $\{W_s\}_{s \in \mathcal{I}_1}$ is multivariate normal. In this case, $\tilde{W}$ would also be normally distributed, and we have that $\nabla(\tilde{W}) \leq \nabla(W_s)$ irrespectively of the spatial correlation among the treated units. Therefore, $\tilde{W}$ will be less likely to attain extreme values than $W_s$. This is valid for any value of the spatial correlation, even when treated units are negatively correlated. The same intuition remains valid if $h(Z_s, \delta)$ is not constant.

If we relax the condition that $\{W_s\}_{s \in \mathcal{I}_1}$ is multivariate normal, then we still have that $\nabla(\tilde{W}) \leq \nabla(W_s)$. However, this does not necessarily guarantee that Assumption 4.2 holds in this case. Still, since the marginal distributions of $\{W_s\}_{s \in \mathcal{I}_1}$ are identified (Proposition 4.1), it is possible to check whether Assumption 4.2 is reasonable in a given empirical setting. We show in Appendix A.4 that it is possible to search over the space of copulas for the worst-case scenario for $Pr\left(|\tilde{W}| > c_{1-\tau}\right)$, given the marginal distributions of $\{W_s\}_{s \in \mathcal{I}_1}$. For the dataset we used to base our simulations from Section 5, we searched over 100,000 Gaussian copulas, holding fixed the marginal distributions of $W_s$, and we show that in all of those cases the joint distribution of $\{W_1, ..., W_{N_1}\}$ would satisfy Assumption 4.2. In those
simulations, we allow for complex dependencies between treated units, in which, for example, the conditional expectation function (CEF) of $W_1$ given $W_2$ is non-monotonic (in contrast to the setting with $\{W_1, ..., W_N\}$ multivariate normal, in which this CEF would necessarily be linear). Therefore, these simulations provide evidence that Assumption 4.2 is a reasonable approximation to the data used to construct our simulations. We find a similar conclusion in the dataset used in our empirical illustration in Section 6. In case we find copulas such that $Pr\left(\left|\tilde{W}\right| > c_{1-\tau}\right) > \tau$, so Assumption 4.2 would not necessarily be satisfied, we also show how one could correct critical values so that the test remains valid whenever the true dependence structure is less conservative than the most conservative copula considered.

It follows directly from Proposition 4.1 and Assumption 4.2 that this modified test asymptotically controls for size under these assumptions.

**Proposition 4.2.** Suppose we have data on $\{Y_{s1}, ..., Y_{sT}, Z_s\}_{I_1 \cup I_0}$, and that Assumptions 2.1, 4.1, and 4.2 hold. Then, if the null is true, $\limsup_{N_0, B \to \infty} \mathbb{E}[\phi_{cons}] \leq \tau$, where $N_0, B \to \infty$ at any rate.

Therefore, this conservative test provides a viable alternative in settings where $N_1 << N_0$ that is robust to weakly dependent spatial correlation. While we guarantee that this modified test does not over-reject (asymptotically), it will generally be conservative when $N_1 > 1$, unless the errors of treated units are perfectly correlated.

**Remark 4.1.** If a distance metric is available and the researcher is willing to assume such distance metric is the relevant one for the spatial correlation, then other available alternatives might present better power (for example, the inference method proposed in the Appendix of CT). In this case, there would be a trade-off between a test that is more powerful but requires correct specification of the spatial correlation, versus a test that is less powerful, but does not require correct specification of the spatial correlation (or even the observation of a distance metric in the cross section).
Remark 4.2. Related to Remark 4.1, another alternative to provide a more powerful test may be to infer about the spatial correlation using the time series. For example, Vogelsang (2012) and Chernozhukov et al. (2021). FP also propose an alternative inference method in their section IV (not the one we reviewed in Section 3) that allows for spatial correlation. However, such alternatives would require a large time series, while the alternatives we propose remain valid even when we have only one pre- and one post-treatment period. Given the survey from Roth (2022), settings in which the time series dimension is short are prevalent in DID applications.

Remark 4.3. The assumption that $W_s$ is weakly dependent would not be satisfied if there are unobserved shocks affecting a non-negligible fraction of the controls (so that $\frac{1}{N_0} \sum_{s \in Z_0} W_s$ converges in probability to a non-degenerate random variable). In this case, the DID residuals $\hat{W}_s$ would not capture these shocks, and $\hat{F}_\xi(c)$ would underestimate the dispersion of the marginal distribution of $\xi_s$. As a consequence, even the conservative test may over-reject. Importantly, however, since the critical values of our conservative test are weakly larger relative to CT or FP, the over-rejection would be no larger than the over-rejection for these other methods. In contrast, a weak dependence assumption may be reasonable when units closer in some distance metric have more correlated errors, but such correlation goes to zero when this distance increases. Such distance metric does not need to coincide with geographical distance (for example, we may have that units with similar industry shares have more correlated errors), and we do not even need to have information on the relevant distance metrics.

Remark 4.4. Constructing a conservative test becomes more complicated if treated units start treatment at different periods, as we discuss in Appendix A.5.

4.3.2 Conservative Test 2: bounding the across-unit correlations

For settings in which $Y_{st}$ represents averages of $M_{st}$ individual-level observations $Y_{ist}$, we show that it is possible to construct an alternative test that will generally be less conservative.
than the Conservative Test 1. The idea is again to consider worst-case scenarios for the spatial
correlation, through aggregation of the treated units. In this case, however, we assume that
individual-level observations within the same unit are weakly more spatially correlated than
individual-level observations in different units. Then, we can use information on the within-
unit spatial correlation to bound the across-units spatial correlation. We can consider either
the case in which the econometrician observes only unit aggregates \(Y_{st}\) (but has information
on \(M_{st}\)) or the case in which individual-level data \(Y_{ist}\) is observed. For simplicity, consider
the case in which \(M_{st} = M_s\) for all \(t\). We treat the sequence \(\{M_s\}_{s \in \mathcal{I}_0 \cup \mathcal{I}_1}\) as fixed.

In this setting, FP show that, under a wide range of structures on the within-unit cor-
relations for the individual-level errors, we have that \(\mathbb{V}(W_s) = A + B/M_s\) for constants
\(A, B \geq 0\). Importantly, these parameters are informative about the within-unit correlations,
and can be used to bound the across-unit correlations, under the assumption that within-unit
correlations are stronger than the across unit ones.

Let \(M_T = \sum_{s \in \mathcal{I}_1} M_s\) be the total number of individual-level observations in the treated
units. We consider in this case the DID estimator weighted by \(M_s\), \(\tilde{\alpha}\), so that

\[
\tilde{\alpha} = \alpha' + \frac{1}{M_T} \sum_{s \in \mathcal{I}_1} M_s W_s - \frac{1}{M_T} \sum_{s \in \mathcal{I}_0} M_s W_s,
\]

(3)

where \(\alpha' \equiv \frac{1}{M_T} \sum_{s \in \mathcal{I}_1} M_s \left(\frac{1}{T-t} \sum_{t \in \mathcal{T}_1} \alpha_{st}\right)\) is the weighted average treatment effect across
units and treated periods. The weighted DID estimator in this case is numerically the same
as the DID estimator using the individual-level data (note that all our results are valid
whether we have access to the individual-level data, or only to the aggregate data).

We consider a version of Assumption 4.1 for this specific setting. In particular, we
consider that the observed covariate driving the heteroskedasticity is \(M_s\) (the number of
individual-level observations), and that \(\mathbb{V}(W_s) = A + B/M_s\).

**Assumption 4.3.**

(i) \(W_s = (A + B/M_s)^{1/2} \xi_s\) for nonnegative constants \(A, B\), where \(\xi_s\) is
equally distributed for all \(s \in \mathcal{I}_1 \cup \mathcal{I}_0\), with a distribution \(F_\xi\) that is absolutely continuous with
bounded density; there exists $h > 0$, not depending on $N_0$, such that $\min_{j \in \mathcal{I}_0 \cup \mathcal{I}_1} \{A + B/M_j\} \geq h$, for all $N_0 \in \mathbb{N}$; (iii) $\sum_{s \in \mathcal{I}_0} M_s W_s \overset{p}{\to} 0$ and $\frac{1}{N_0} \sum_{s \in \mathcal{I}_0} 1\{\xi_s \leq c\} \overset{p}{\to} F(\xi(c))$ for every $c \in \mathbb{R}$; (iv) the (nonnegative) least squares estimators of $\hat{W}_s^2$ on a constant and $1/M_s$ using only the control units are consistent for $A$ and $B$ as $N_0 \to \infty$.

Given Assumption 4.3, we have that $\hat{\alpha} \overset{p}{\to} \alpha + W$, where $W = \frac{1}{M_T} \sum_{s \in \mathcal{I}_1} M_s W_s$. We propose the following idea for inference: we consider an aggregate treated unit that is the weighted average of the treated units. Then we run FP inference method using this aggregate treated unit and the controls, considering that it has $M_T$ observations. We refer to this test as “Conservative Test 2”. More specifically, we consider the following algorithm.

**Algorithm 4: Conservative Test 2**

1. Run the weighted DID estimator, and store $\hat{\alpha}$ and the residuals $\hat{W}_s = \frac{1}{T-1} \sum_{t \in \mathcal{T}_1} \hat{\eta}_{st} - \frac{1}{T} \sum_{t \in \mathcal{T}_0} \hat{\eta}_{st}$ for all $s \in \mathcal{I}_0$;
2. Run a (nonnegative) least squares regression of $\hat{W}_s^2$ on a constant and $1/M_s$, to estimate $\hat{A}$ and $\hat{B}$;
3. Compute the normalized residuals $\hat{\xi}_s = \hat{W}_s / \sqrt{\hat{A} + \hat{B}/M_s}$, for $s \in \mathcal{I}_0$;
4. for $b=1, \ldots, B$ do
   5. Sample 1 value from $\{\hat{\xi}_s\}_{s \in \mathcal{I}_0}, \hat{\xi}^*$;
   6. Calculate $\hat{\alpha}_b = \left(\hat{A} + \hat{B}/M_T\right)^{1/2} \hat{\xi}_s^*$;
7. Reject the null if $\frac{1}{B} \sum_{b=1}^B 1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\} > 1 - \tau$.

Let $\phi_{\text{cons2}}$ be an indicator variable equal to one if we reject the null given the algorithm above.

We assume that individual-level observations within the same unit are weakly more spatially correlated than individual-level observations in different units, which is summarized in the following assumption.

**Assumption 4.4.** $\mathcal{V}(W) \leq A + B/M_T$.

If we assume that $(W_1, \ldots, W_{N_1})$ is multivariate normal, then this would be sufficient to guarantee that the Conservative Test 2 would be asymptotically conservative. More generally, we consider the following assumption, which is similar to Assumption 4.2.
Assumption 4.5. \( Pr (|W| > c_{1-\tau}) \leq \tau \), where \( c_{1-\tau} \) is the \((1-\tau)\)-quantile of the distribution of \([A + B/M_T]^{1/2}|\xi|\)

Similarly to the discussion in Section 4.3.1, Assumption 4.5 is satisfied under joint normality, if Assumption 4.4 holds. More generally, we can also evaluate whether this assumption is plausible by searching over the space of copulas, as we did when evaluating Assumption 4.2. For the datasets we used to base our MC simulations and empirical illustration, we again find that this assumption holds for all the simulated distributions for \((W_1, \ldots, W_{N_1})\), providing evidence that this assumption is reasonable in these applications (details in Appendix A.4).

Proposition 4.3. Suppose we have data on \( \{Y_{s1}, \ldots, Y_{sT}, Z_s\}_{I_1 \cup I_0} \), and that Assumptions 2.1, 4.3, 4.4, and 4.5 hold. Then, if the null is true, \( \lim \sup_{N_0, B \to \infty} \mathbb{E}[\phi_{cons2}] \leq \tau \), where \( N_0, B \to \infty \) at any rate.

Importantly, since we are bounding the across-unit correlations using information on the within-unit correlations, we expect that this test will be less conservative (and, therefore, have more power) than the Conservative Test 1.

Remark 4.5. We consider the case in which \( M_{st} \) varies across \( t \) in Appendix A.2.

4.3.3 Running \( N_1 \) tests, and correcting for multiple testing

Since CT and FP are valid when \( N_1 = 1 \) (Corollary 4.1), another alternative for the case with \( N_1 > 1 \) is to consider \( N_1 \) separate DID regressions — one for each treated unit —, and adjust the inference for multiple testing. In this case, each of the \( N_1 \) hypotheses being tested concerns a treated unit post-treatment average effect, i.e. the \( \alpha_s = \frac{1}{T-t^*} \sum_{t \in T} \alpha_{st} \) for \( s \in I_1 \). Since we wish to remain agnostic about spatial correlation, we should use a method that imposes few or no assumptions on the dependence structure between the test statistics. Methods that remain agnostic about the dependence between the tests and that control the family-wise error rate (FWER) involved in multiple testing are provided by the Bonferroni, Holm (1979) and Hochberg (1988) corrections. Benjamini and Yekutieli (2001) show that
the method provided in Benjamini and Hochberg (1995) for controlling the false discovery rate (FDR) in a setting where tests are independent remains valid under positive dependence of the p-values used; they also show that a simple modification of the procedure produces a test that controls FDR and remains valid under arbitrary dependence of the p-values. By combining any of these methods with the results from Section 4.1, we are able to conduct valid inference for each \( \alpha_s, s \in I_1 \), while taking into account that we are testing multiple hypotheses.

Once a procedure that controls either the FWER or the FDR is selected, we can also compute a valid \((1 - \tau)\) confidence set for the vector of individual treatment effects \((\alpha_s)_{s \in I_1}\) by test inversion: one collects each vector \((a_s)_{s \in I_1} \in \mathbb{R}^{N_1}\) such that the procedure does not reject any null when testing the nulls \(\alpha_s = a_s, s \in N_1\), at significance \(\tau\).

Moreover, we can also construct a valid confidence set for the weighted average effect \(\alpha_\omega = \sum_{s \in N_1} \omega_s \alpha_s\), where \((\omega_s)\) are a set of pre-specified weights. Specifically, we construct this set via projection: we calculate and store \(\sum_{s \in I_1} \omega_s a_s\) for each \((a_s)_{s \in I_1}\) in the confidence set for individual effects (Scheffe, 1953; Dufour, 1990; Gafarov et al., 2016; Freyberger and Rai, 2018). This is equivalent to constructing a confidence set by considering all values \(a \in \mathbb{R}\), such that there are null hypotheses \(\alpha_s = a_s\) for \(s \in \{1, ..., N_1\}\) with \(\sum_{s \in N_1} \omega_s \alpha_s = a\), where the multiple hypothesis testing procedure would not reject the null for any null hypotheses \(\alpha_s = a_s, s \in \{1, ..., N_1\}\).

Considering confidence intervals for weighted averages of the treatment effects is interesting, because then we can compare those confidence intervals to the ones generated using the approaches from Sections 4.3.1 and 4.3.2. Whilst the format of the resulting set for average effects is dependent on the correction being employed, when the Bonferroni correction is used, a simple expression is available. In this case, the resulting confidence set is given by:

\[
I_{\text{Bonferroni}}(\alpha_\omega; 1-\tau) = \left[ \hat{\alpha}_\omega - \left( \sum_{s \in I_1} \omega_s h(Z_s, \hat{\delta}) \right) \hat{q}(1 - \tau/N_1), \hat{\alpha}_\omega + \left( \sum_{s \in I_1} \omega_s h(Z_s, \hat{\delta}) \right) \hat{q}(1 - \tau/N_1) \right],
\]
where $\hat{\alpha}_\omega$ is the weighted TWFE estimator and $\hat{q}_{|\xi|}$ is the empirical quantile function of the absolute value of the rescaled residuals in the control group. In contrast, the confidence set obtained by inverting Conservative Test 1 is given by:

$$I_{\text{Conservative} 1(\alpha_\omega; 1-\tau)} = \left[ \hat{\alpha}_\omega - \left( \sum_{s \in s \in I_1} \omega_s h(Z_s, \hat{\delta}) \right) \hat{q}_{|\xi|}(1-\tau), \hat{\alpha}_\omega + \left( \sum_{s \in I_1} \omega_s h(Z_s, \hat{\delta}) \right) \hat{q}_{|\xi|}(1-\tau) \right],$$

which shows that the Conservative Test 1 will always lead to tighter intervals.

At first sight, the result on the conservativeness of the Bonferroni confidence set may appear to be restricted to this correction, and one may wonder whether considering alternative MHT corrections may produce tighter confidence intervals than Conservative Test 1. However, as we show in Appendix A.6, the confidence interval for the average effect constructed using the Benjamini and Hochberg (1995) approach – which is the least conservative method discussed in this section and valid under positive dependence of the p-values used in the tests – contains the confidence interval constructed using Conservative Test 1. This reveals an interesting tradeoff between the methods proposed in Sections 4.3.1 and 4.3.2 and MHT corrections: while agnostic MHT procedures have the advantage of not requiring Assumption 4.2 or 4.5, this comes at a cost of larger confidence intervals.

Finally, we note that, for settings with variation in treatment timing, MHT would have the advantage of circumventing the challenges of implementing Conservative Tests 1 and 2 discussed in Remark 4.4.

## 5 Simulations with Real Datasets

We analyze the spatial correlation problem, and the proposed conservative tests, in simulations based on the ACS (Ruggles et al., 2015), at the Public Use Microdata Area (PUMA). We estimate a model for the spatial correlation in which the covariance between two PUMAs may depend on whether they belong to the same state, and on the similarity between their
industry compositions. We also allow for heteroskedasticity depending on population sizes (details in Appendix A.7). This way, we can analyze three scenarios: (i) when the applied researcher ignores all spatial correlation; (ii) when he/she considers spatial correlation arising from geographical distance; and (iii) when he/she correctly considers that spatial correlation may arise from both geographical distance and industry composition.

If we consider all pairs of PUMAs, the correlation between their errors in this estimated model is greater (in absolute value) than 0.05 in only 2.5% of the cases. Therefore, the weak dependence condition we consider seems reasonable in this setting. Still, we have PUMAs with spatial correlation as strong as 0.125. Therefore, we may have a setting in which the $N_1$ treated PUMAs exhibit relevant spatial correlation.

In line with our theoretical model, we consider a setting in which we fix $N_1 \in \{1, 2, \ldots, 9, 10\}$ PUMAs as the treated ones, and generate multivariate normal draws of $W_s$ with this estimated spatial dependence. To illustrate issues related to spatial correlation, we choose the PUMA with the strongest spatial correlation with some other PUMA in our dataset to be treated, and then iteratively assign treatment to $N_1 - 1$ PUMAs in the same state that are most similar in industry composition to previously selected PUMAs. Treatment effects are assumed to be zero. We consider six different inference procedures: (i) the naive version of FP approach (which assumes errors are independent across PUMAs); (ii) a parametric bootstrap that correctly specifies and estimates the heteroskedasticity structure and both sources of spatial correlation (this procedure is similar to the parametric bootstrap suggested in the Appendix of CT); (iii) a misspecified parametric bootstrap that estimates the heteroskedasticity structure due to group sizes and spatial correlation due to being in the same state, but ignores spatial correlation due to industry similarity; (iv) the conservative test presented in Section 4.3.1 (which we refer to as “Conservative Test 1”); (v) the conservative test proposed in Section 4.3.2 (which we refer to as “Conservative Test 2”); and the test function stemming from a CI for the average effect obtained by inversion and projection of the Benjamini and Hochberg (1995) MHT procedure discussed in Section 4.3.3. In Appendix
A.7, we consider other alternatives, such as inference based on a cluster robust variance estimator (CRVE) and on the wild cluster bootstrap (WCB). These alternatives perform poorly in our setting, both because the number of treated units is very small, and because we have spatial correlation from multiple sources (see, for example, MacKinnon and Webb (2017) and Djogbenou et al. (2019) for discussions on asymptotic approximations for CRVE and WCB).

Figure 1.A presents rejection rates, as a function of $N_1$, of tests of the null of no average effect conducted nominally at the 5% significance level, while Figure 1.B presents the ratio between the length of nominal 95% confidence intervals obtained by inverting the corresponding test procedures and the length of a 95% unfeasible confidence interval which uses the true sampling variance of $\hat{\alpha}$ in the simulations.
Figure 1: MC simulations

A: test size

B: length of CI / length of unfeasible CI

Notes: Figure A presents rejection rates for the six different inference methods we discussed in Section 5, for different values of $N_1$. Tests are conducted nominally at the 5% level. Figure B presents information on the ratios between the average length of nominal 95% CIs obtained by test inversion relative to the length of the CI which uses the true sampling variance of $\hat{\alpha}$.

Overall, these simulations highlight the main messages of the paper: (1) the inference methods proposed by CT and FP remain valid when we have a single treated unit, even when errors are spatially correlated; (2) with $N_1 > 1$, these inference methods over-reject when errors are spatially correlated, and the over-rejection is increasing with $N_1$; (3) only accounting for the known sources of spatial correlation, e.g. only controlling for state correlation as the misspecified parametric bootstrap does, may not be sufficient to control size; (4) the proposed conservative tests control for size, although they may be conservative when $N_1 > 1$; (5) we are able to provide a less conservative test exploiting the structure of common empirical applications in which units are aggregates of individual-level observations to construct a more powerful test (even if we do not have information on the individual-level
We note that, when $N_1 = 5$, the length of the confidence interval obtained by inverting Conservative Test 2 is only 22% larger than the length of the unfeasible confidence interval. In contrast, Conservative Test 1 has an 85% larger confidence interval than the unfeasible procedure. When $N_1 = 10$, Conservative Test 2 has 33% larger confidence intervals, whereas confidence intervals with Conservative Test 1 are more than 120% larger. The MHT procedure is even more conservative, with confidence intervals 111% (166%) larger when $N_1 = 5$ ($N_1 = 10$). Overall, these numbers illustrate the gains of considering the information on the within-unit correlation to bound the between-unit correlation. Of course, if we have information on all relevant distance metrics in the cross section, then it is possible to correct for spatial correlation with a more powerful test, as the correctly specified parametric bootstrap shows. Still, these simulations illustrate that it is possible to construct valid tests even when such information is unavailable or the researcher is not willing to impose a structure on the spatial correlation.

6 Empirical Illustration

We also illustrate our findings analyzing the effects of the Massachusetts 2006 health care reform. This reform was analyzed by Sommers et al. (2014) using a DID design comparing 14 Massachusetts counties with 513 control counties from 45 different states that were selected based on a propensity score to be more similar with the treated counties (we find similar results if we consider a DID regression using all counties, so that there is no pre-selection of control counties). Sommers et al. (2014) find a reduction of 2.9%-4.2% in mortality in Massachusetts relative to the controls after the reform (depending on whether covariates are included).

As shown in Figure 1 from Sommers et al. (2014), the outcome variables in the pre-treatment periods followed parallel trajectories when we compare Massachusetts and the
control groups. This provides some evidence in favor of Assumption 2.1, although it does not guarantee that. While we do not have strong reasons to believe the parallel trends assumption is violated in this application, we note that this is not crucial for our purposes, since our goal is to analyze alternative inference methods. If we believed there were relevant departures from parallel trends, then, for our purposes, we can simply redefine the target parameters as the treatment effect plus the departure of parallel trends. In this case, for this redefined parameter, Assumption 2.1 would be trivially satisfied, and we can contrast the results from different inference methods.

Sommers et al. (2014) relied on standard errors clustered at the state level, which does not work well in this setting with a single treated state. Their inference procedures were then re-analyzed by Kaestner (2016), who considered permutation tests at the county level. While permutation tests are usually considered in a design-based framework, if we consider this approach in our framework, it is asymptotically equivalent to CT at the county level. Therefore, this would also be problematic if counties within the same state are spatially correlated, as we show in Section 4.2. In Appendix A.8, we propose a test for the null that there are relevant state-level shocks. We provide evidence that such spatial correlation is indeed relevant in this application.

We note that this is a setting in which (i) we have only a single treated state, (ii) errors are likely correlated across counties within the same state, and (iii) there is variation in population sizes across counties/states that may lead to heteroskedasticity. If we assume that errors are independent across states, then FP at the state level would be an appropriate inference method in this setting. Moreover, given Corollary 4.1, this inference method remains valid even if we assume that state-level errors are weakly dependent, since in this case we have only a single treated state. We consider, therefore, p-values and CI’s from FP at the state-level as a benchmark. As presented in Table 1, in this case we fail to reject the null of no effect, for the two outcomes we considered.

While in this application we have a well-defined distance measure for the spatial cor-
relation (which, in this case, is the information on the states), we consider a “thought experiment” in which the applied researcher does not have such information, in order to illustrate our main results. The main advantage is that, in this case, we can contrast our findings with the conclusions based on FP at the state level, which we use as a benchmark.

First, note that we would reject the null if we relied on most of the inference methods that ignore spatial correlation (FP, CRVE and WCB at county level), contrasting with our benchmark results using FP at the state level. This happens because, as discussed in Section 4.2, spatial correlation among the treated units leads to over-rejection. The only exception is CT at the county level. This happens because, while spatial correlation induces over-rejection in this case, the fact that treated counties are relatively larger induces under-rejections. Appendix A.9 reports the results for alternative inference methods at both the state and county levels.

We also consider how our conservative tests would perform in this case (again, considering this “thought experiment” in which information on states is unavailable). The conservative tests we propose in Sections 4.3.1 and 4.3.2 present p-values similar to the ones from FP at the state level (our benchmark). When we consider the conservative test proposed in Section 4.3.2, the length of the 95% confidence interval is 43% larger for all cause mortality, and 23% larger for healthcare amenable mortality. Therefore, there is some loss in terms of power, but in settings in which a distance metric is not available, this may be a cost we would have to pay to provide a test that controls for size in the presence of spatial correlation. Moreover, Conservative Tests 1 and 2 offer clear improvements over the procedure based on inverting and projecting the Benjamini and Hochberg (1995) correction discussed in Section 4.3.3. Indeed, this procedure leads to CI length around 90% larger than FP at the state level. Overall, results indicate that Conservative Tests 1 and 2 would perform well even if we did not have information on a distance metric, and despite the fact that we have spatial correlation across counties.
Table 1: Alternative inference methods for Sommers et al. (2014)

|                          | All cause mortality (deaths per 100,000 adults) | Health care-amenable mortality (deaths per 100,000 adults) |
|--------------------------|-----------------------------------------------|----------------------------------------------------------|
|                          | p-value (1) length of 95% CI (2)              | p-value (3) length of 95% CI (4)                          |
| CT and FP at state level | CT 0.430 128.98                               | CT 0.342 59.97                                           |
|                          | FP (benchmark) 0.339 59.81                    | FP (benchmark) 0.196 32.11                               |
| CRVE and WCB at county level | CRVE 0.002 16.08                                    | CRVE 0.001 11.36                                         |
|                          | WCB 0.046 20.53                                | WCB 0.028 14.36                                         |
| CT and FP at county level | CT 0.320 55.76                                | CT 0.266 39.54                                          |
|                          | FP 0.069 28.11                                 | FP 0.010 15.15                                          |
| Conservative tests       | Conservative Test 1 0.470 92.15               | Conservative Test 1 0.331 48.46                           |
|                          | Conservative Test 2 0.456 85.74                | Conservative Test 2 0.264 40.89                           |
|                          | MHT (Benjamini and Hochberg) 1.000 116.20      | MHT (Benjamini and Hochberg) 1.000 61.00                  |

Notes: This table presents p-values and lengths of confidence intervals for a series of alternative inference methods for the application from Sommers et al. (2014). We consider a DID estimator based on OLS TWFE regression with no covariates. Point estimates are slightly different than reported in the original paper because we use the publicly available data set (so we do not have death counts for cells with fewer than 10 deaths), and because we weight observations by population mean across years to avoid problems with TWFE estimand highlighted in recent papers. See, for example, Goodman-Bacon (2021), de Chaisemartin and D’Haultfoeuille (2020), and Callaway and Sant’Anna (2021). We also restrict to counties with non-missing information for all years. We end up with 485 control counties, as compared to 513 from the original study. The point estimates are $-12.77$ for all cause mortality and $-9.94$ for health care-amenable mortality.

7 Conclusion

We consider the problem of inference in DID when there are few treated units and errors are spatially correlated. We first show that, when there is a single treated unit, the main inference methods proposed by CT and FP, which were designed for settings with few treated and many control units, remain asymptotically valid when errors are weakly dependent (even when the relevant distance metric is unspecified). This extends the set of possible applications in which the tests proposed by CT and FP can be reliably used when there is only a single treated unit. However, these methods can lead to over-rejection with more than one treated unit. We propose three alternative inference methods that are
asymptotically valid, though generally conservative, in the presence of spatial correlation. These tests provide interesting alternatives when spatial correlation is likely relevant, but the researcher does not have information on a distance metric or is not willing to impose a structure on the spatial correlation.

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A Appendix

A.1 Proof of main results

This Appendix presents the proofs of the main results of the paper.

A.1.1 Proof of Proposition 4.1

**Proof.** Fix \( c \in \mathbb{R} \). We first show that \( \hat{F}_\xi(c) \xrightarrow{p} F_\xi(c) \). Recall we estimate the distribution function of shocks by:

\[
\hat{F}_\xi(c) = \frac{1}{N_0} \sum_{i \in I_0} \mathbb{1} \left\{ \frac{\hat{W}_i}{h(Z_i; \hat{\delta})} \leq c \right\},
\]

where, for \( i \in I_0 \), \( \hat{W}_i = W_i - \frac{1}{N_0} \sum_{i \in I_0} W_i \). Let:

\[
\lambda_i(c; a, b) = \mathbb{1} \{ \xi_i \leq ac + b \},
\]

and \( \tilde{\lambda}(c; a, b) = F_\xi(ac + b) \). Observe that:

\[
\hat{F}_\xi(c) = \frac{1}{N_0} \sum_{i \in I_0} \lambda_i(c; \hat{a}_i, \hat{b}_i),
\]

where \( \hat{a}_i = h(Z_i; \hat{\delta})/h(Z_i; \delta) \) and \( \hat{b}_i = \frac{1}{N_0} \sum_{s \in I_0} \frac{W_s}{h(Z_s; \delta)} \). Furthermore, by Assumptions 4.1.(ii)-(iv), \( \max_{i \in I_0} |\hat{a}_i - 1| = o_p(1) \) and \( \max_{i \in I_0} |\hat{b}_i| = o_p(1) \). Since \( F_\xi \) is continuous, this implies:

\[
\frac{1}{N_0} \sum_{i \in I_0} \tilde{\lambda}(c; \hat{a}_i, \hat{b}_i) \xrightarrow{p} F_\xi(c).
\]

Therefore, to show that \( \hat{F}_\xi(c) \xrightarrow{p} F_\xi(c) \), it suffices to show that:

\[
\frac{1}{N_0} \left| \sum_{i \in I_0} (\lambda_i(c; \hat{a}_i, \hat{b}_i) - \tilde{\lambda}(c; \hat{a}_i, \hat{b}_i)) \right| = o_p(1).
\]

Fix \( \epsilon > 0 \). It is easy to see that:
\[
\frac{1}{N_0} \left| \sum_{i \in \mathcal{I}_0} (\lambda_i(c; \hat{a}_i, \hat{b}_i) - \bar{\lambda}(c; \hat{a}_i, \hat{b}_i)) \right| \leq \frac{1}{N_0} \sup_{a_i \in [1-\epsilon, 1+\epsilon], b_i \in [-\epsilon, \epsilon]} \left| \sum_{i \in \mathcal{I}_0} (\lambda_i(c; a_i, b_i) - \bar{\lambda}(c; a_i, b_i)) \right| + o_p(1).
\]

We will bound the first term on the right-hand side. Suppose \( c \geq 0 \) (the argument is similar for \( c < 0 \)). Note that:

\[
\sum_{i \in \mathcal{I}_0} (\lambda_i(c; a_i, b_i) - \bar{\lambda}(c; a_i, b_i)) \leq \frac{1}{N_0} \sum_{i \in \mathcal{I}_0} (\lambda_i(c; (1+\epsilon), \epsilon) - \bar{\lambda}(c; (1+\epsilon), \epsilon)) + \sup_{a \in [1-\epsilon, 1+\epsilon], b \in [-\epsilon, \epsilon]} |\bar{\lambda}(c; a, b) - \bar{\lambda}(c; (1+\epsilon), \epsilon)| \leq o_p(1) + \mathcal{F}^2(c \lor 1) \epsilon,
\]

where, in the last inequality, the \( o_p(1) \) term is due to Assumption 4.1.(ii) and \( \mathcal{F} \) is the upper bound on the density of \( \xi \), which follows from application of the mean-value theorem. An analogous lower bound applies to \( \sum_{i \in \mathcal{I}_0} (\lambda_i(c; a_i, b_i) - \bar{\lambda}(c; a_i, b_i)) \). We then conclude that:

\[
\frac{1}{N_0} \left| \sum_{i \in \mathcal{I}_0} (\lambda_i(c; \hat{a}_i, \hat{b}_i) - \bar{\lambda}(c; \hat{a}_i, \hat{b}_i)) \right| \leq o_p(1) + 2\mathcal{F}(c \lor 1) \epsilon.
\]

Now, since the choice of \( \epsilon \) was arbitrary, it follows that \( \frac{1}{N_0} \left| \sum_{i \in \mathcal{I}_0} (\lambda_i(c; \hat{a}_i, \hat{b}_i) - \bar{\lambda}(c; \hat{a}_i, \hat{b}_i)) \right| = o_p(1) \), and therefrom \( \hat{F}_\xi(c) \overset{p}{\to} F_\xi(c) \). Since the choice of \( c \) was arbitrary and \( F_\xi \) is a continuous distribution function, it follows that the convergence is uniform, i.e. \( \sup_{c \in \mathbb{R}} |\hat{F}_\xi(c) - F_\xi(c)| = o_p(1) \) (van der Vaart, 1998, page 339).

A.1.2 Proof of Corollary 4.1

**Proof.** Let \( \mathbb{E}_* \) denote the expectation with respect to the resampling law of the FP algorithm, conditional on the data. Observe that, under the null:

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\[
\frac{1}{B} \sum_{b=1}^{B} \mathbb{E}_s[1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\}] = \hat{F}_\xi \left( \frac{|\hat{\alpha} - \alpha_0|}{h(Z_1, \delta)} \right) - \hat{F}_\xi \left( -\frac{|\hat{\alpha} - \alpha_0|}{h(Z_1, \delta)} \right) \xrightarrow{p} F_\xi(|\xi_1|) - F_\xi(-|\xi_1|),
\]
where the convergence in probability follows from Assumption 4.1 and Proposition 4.1. Next, observe that, since \( B \to \infty \):

\[
\mathbb{E}_s \left[ \left( \frac{1}{B} \sum_{b=1}^{B} (1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\} - \mathbb{E}_s[1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\}]) \right)^2 \right] = o_p(1).
\]

It then follows by the conditional Markov inequality and bounded convergence that

\[
\frac{1}{B} \sum_{b=1}^{B} 1\{|\hat{\alpha} - \alpha_0| > |\hat{\alpha}_b|\} \xrightarrow{p} F_\xi(|\xi_1|) - F_\xi(-|\xi_1|) = F_{\xi|\xi}(|\xi_1|). \]

Since \( F_{\xi|\xi}(|\xi_1|) \) is uniformly distributed, the continuous mapping theorem implies \( \phi_{FP} \xrightarrow{p} 1 \{ F_{\xi|\xi}(|\xi_1|) > 1 - \tau \} \). It then follows by bounded convergence that:

\[
\mathbb{E}[\phi_{FP}] \to \mathbb{P}[F_{\xi|\xi}(|\xi_1|) > 1 - \tau] = \tau,
\]
which establishes the desired result.

### A.2 Conservative Test 2 with variation in observations per cell across time

If the number of observations per cell, \( M_{st} \), varies with \( t \), then the original DID estimator would not be numerically the same as the one using an aggregate treated unit \( \tilde{y}_t \). In this case, we recommend first aggregating the data at the unit \( \times \) time level, and then estimating the DID estimator using sampling weights \( M_{s}^\text{min} = \min_{t \in T_0 \cup T_1} \{ M_{st} \} \) (or \( M_{s}^\text{mean} = T^{-1} \sum_{t=1}^{T} M_{st} \)).

Then we can conduct the conservative inference method proposed above based on this alternative DID estimator. The advantage of using \( M_{s}^\text{min} \) is that we guarantee a conservative estimator for the variance of \( W \), which in this case will be a weighted average of \( W_s \) of the treated units using \( M_{s}^\text{min} \). The reason is that for each \( t \) we will calculate \( \tilde{y}_t = \sum_{s \in I_1} \frac{M_{s}^\text{min}}{M_{s}^\text{min}} Y_{st}, \)
where $M_{st} \geq M_s^{\text{min}}$ for all $t \in T_0 \cup T_1$ and $s \in I_1$. Note that this way we would also have that the estimand is a well-defined weighted average of the heterogeneous treatment effects, avoiding the problems highlighted by de Chaisemartin and D’Haultfoeuille (2020) for the TWFE estimator in settings in which we have variation in the number of observations per cell. Moreover, if $M_{st}$ does not vary much on $t$, then the estimand and the resulting estimator should be close to the original DID estimator using individual-level data.

### A.3 Assessing the plausibility of Assumption 4.1.(i)

Observe that an implication of Assumption 4.1.(i) is that there exist a quantile function $h : (0,1) \rightarrow \mathbb{R}$, such that

$$Q_s(u) = h(u), \quad \forall s \in I_0, u \in (0,1), \quad (5)$$

where $Q_s$ is the quantile function of $|W_s|/h(Z_s; \delta)$. This suggests the following procedure to assess the plausibility of a proposed heteroskedasticity correction in accounting for distribution differences across units. Using the rescaled residuals in the control group, we may perform a quantile regression of $\hat{\xi}_s$ on a transformation of $Z_s$, for different quantiles $u$. Given (5), we would not expect estimated quantiles to vary as a function of the $Z_s$, for any of the $u$.

We apply the proposed test to the data used to construct our Monte Carlo exercise in Section 5. Specifically, we consider $u \in \{0.9, 0.95\}$, and perform quantile regression of the $\hat{\xi}_s$ on quintile indicators of the $M_s$. We also consider a similar procedure on the standardized residuals $\hat{W}_s / \text{sd}(\hat{W}_s)$. In this case, if variation in $M_s$ has a meaningful effect on the variance of $W_s$, then we should expect this quantile function not to be constant.

Figure A.1 presents the estimated quantile regressions, along with 95% confidence intervals computed under the assumption of independent observations. Clearly, adopting the parametric form of heteroskedasticity offers improvements over using the $\hat{W}_s$, as regards the
plausibility of Assumption 4.1.(i). Indeed, the quantiles of $\hat{\xi}$ vary less than those of $\hat{W}$, especially at $u = 0.9$. To further present evidence of this improvement, Table A.1 reports, for each $u$, the p-values of the null that there is no variation of the conditional quantile function across quintiles of $M$. We report p-values under the assumption of independence, as well as p-values clustered at the state level, which we compute using the bootstrap procedure in Hagemann (2017) as implemented in R package quantreg (Koenker, 2022). We see that adopting the proposed parametric correction leads to improved credibility of Assumption 4.1.(i).

Figure A.1: Quantiles of residuals as a function of PUMA size

A: $u = 0.9$

90th quantiles as a function of $M$

B: $u = 0.95$

95th quantiles as a function of $M$
We conducted a similar exercise for the data used in our empirical illustration of Section 6 and also found suggestive evidence of the appropriateness of the heteroskedasticity correction in this setting. Specifically, at the $u = 0.95$ quantile, the p-value clustered at state level of the null that the quantile function does not vary across quintiles of county size is 0 for the unrescaled residuals $\hat{W}_s$ of both outcomes considered; and 0.20 and 0.26 for the rescaled residuals of, respectively, all-cause and healthcare-amenable mortality.

### A.4 Assessing the plausibility of Assumptions 4.2 and 4.5

Observe that, under either Assumption 4.1 or 4.3, the marginal distribution of the $W_s$, $s \in I_1$, is identified. Indeed, since the normalized distribution of residuals in the control group is a consistent estimator of $F_\xi$ (Proposition 4.1), and given that $W_s = h(Z_s; \hat{\delta})\xi_s$ and the parametric estimator of the heteroskedasticity is consistent, it follows that the marginal distribution of the $W_s$ is consistently estimated as $\hat{F}_W(x) = \hat{F}_\xi(x/h(Z_s; \hat{\delta}))$, $x \in \mathbb{R}$. Using this fact, we propose a method to assess the plausibility of Assumptions 4.2 or 4.5 under a wide range of dependence structures for the $W_s$.

The proposed method proceeds as follows. Let $\hat{q}_\xi$ denote the empirical quantile functions of the normalized residuals in the control group. Let $H$ be a $N_1$-dimensional copula, a cdf on $[0, 1]^{N_1}$ with uniform marginals. For $b = 1, \ldots, B$, we may construct samples:
\((W_1^b, \ldots, W_{N_1}^b) = \left( h(Z_1; \hat{\delta})\hat{q}_\xi(U_1^b), \ldots, h(Z_{N_1}; \hat{\delta})\hat{q}_\xi(U_{N_1}^b) \right), \quad (U_1^b, \ldots, U_{N_1}^b) \sim H.\)

Observe that, as \(N_0 \to \infty\), observations in each of these samples have marginal distributions equal to the marginals of the \(\{W_s\}_{s \in I_1}\), with dependence structure dictated by \(H\).

We can then use these \(B\) samples to verify the validity of Assumptions 4.2 and 4.5 under dependence structure \(H\). For example, we will say dependence structure \(H\) satisfies 4.2 if:

\[
\hat{p}_H = \frac{1}{B} \sum_{b=1}^{B} \left\{ \left| \frac{1}{N_1} \sum_{i=1}^{N_1} W_i^b \right| > \left( \frac{1}{N_1} \sum_{i=1}^{N_1} h(Z_s, \delta) \right) \hat{q}_\xi(1 - \alpha) \right\} \leq \tau,
\]

and similarly for Assumption 4.5. By varying \(H\), we may then assess the validity of the assumptions under different dependence structures.

For the procedure to convey meaningful information, we must find a method to vary \(H\) in a principled manner. One alternative is to sample \(H\) from a nonparametric class of copulas. When \(N_1 = 2\), Guillotte and Perron (2012) provides a sampler from a Jeffrey’s prior on a nonparametric class of bivariate copulas. For \(N_1 > 2\), one may use one of the priors available in nonparametric Bayesian Statistics (e.g. Ghosal and Van der Vaart, 2017) to sample from a nonparametric class of multivariate cdfs, which can then be normalized to have uniform marginals. However, it should be noted that the computational cost of these approaches is increasing in \(N_1\) and can be quite large even for few treated units.

Another alternative is to consider parametric classes of copulas. This is the approach we undertake when verifying the plausibility of Assumptions 4.2 and 4.5 on the data used to construct our simulations in Section 5. Specifically, we vary \(H\) over the class of Gaussian copulas, which are able in our data to produce non-monotone conditional expectations between the treated units’ \(\xi_s\). This class is given as follows. For a given positive semidefinite \(N_1 \times N_1\) matrix \(\Sigma\) with trace equal to \(N_1\), the draws \((U_i^b)_{i=1}^{N_1}\) are given by:
\[(U_1^b, \ldots, U_{N_1}^b) = \left( \Phi \left( \frac{Z_1^b}{\Sigma_{11}} \right), \ldots, \Phi \left( \frac{Z_{N_1}^b}{\Sigma_{N_1N_1}} \right) \right), \quad (Z_1, \ldots, Z_{N_1}) \sim \mathcal{N}(0, \Sigma). \]

We can then span this class of copulas by sampling from the class of \(N_1 \times N_1\) positive semidefinite matrices with trace equal to \(N_1\). In R, we may do this by first sampling an \(N_1 \times N_1\) orthogonal matrix using the \texttt{rorth} function available in package \texttt{ICtest}, which generates draws with respect to the Haar measure on the space of orthogonal \(N_1 \times N_1\) matrices (Nordhausen et al., 2022). We then sample a \(N_1\)-dimensional vector uniformly from the \(N_1 - 1\) simplex, and multiply the draw by \(N_1\). Finally, we can use the spectral decomposition to construct the resulting matrix \(\Sigma\). Using this procedure, and for different values of \(N_1\) and the chosen treated units in Section 5, we consider 100,000 Gaussian copulas drawn at random. We verify that all such dependence structures satisfy Assumption 4.2. Once we discard copulas that do not satisfy Assumption 4.4 (i.e. we discard those structures where within-state correlation between individuals is smaller than between-state correlation), we also verify that Assumption 4.5 is always satisfied.

We conduct a similar exercise on the dataset used in our empirical illustration, and verify that Assumptions 4.2 and 4.5 are always satisfied for all simulated copulas and both outcomes considered.

If in a given empirical application this simulation procedure detects violations of the required assumptions, a simple correction is available. Let \(\mathcal{H}\) be the set of copulas for which the assumptions were verified. We can then consider the corrected critical value \(\tilde{\tau} := \sup_{h \in \mathcal{H}} \tilde{p}_H\) when conducting inference. The resulting procedure will be asymptotically valid whenever the true dependence structure is less conservative than the most conservative element in \(\mathcal{H}\).
A.5 Conservative Tests 1 and 2 with variation in treatment timing

Constructing a conservative test as proposed in Sections 4.3.1 or 4.3.2 becomes more complicated if treated units start treatment at different periods. For example, consider that unit 1 starts treatment after $t_1$, while unit 2 starts treatment after $t_2$. In this case, the asymptotic distribution of $\hat{\alpha}$ would depend on the linear combinations of the errors $W_1(1) = \frac{1}{T-t_1} \sum_{t=t_1+1}^{T} \eta_{1t} - \frac{1}{t_1} \sum_{t=1}^{t_1} \eta_{1t}$, and $W_2(2) = \frac{1}{T-t_2} \sum_{t=t_2+1}^{T} \eta_{2t} - \frac{1}{t_2} \sum_{t=1}^{t_2} \eta_{2t}$. We can still consistently estimate the marginal distributions of $W_1(1)$ and $W_2(2)$ by considering the appropriate linear combination of the residuals from the control units. This is what CT and FP do, and works well in a setting in which $W_1(1)$ and $W_2(2)$ are independent. When we allow for spatial dependence, however, it becomes harder to define a worst case scenario. The worst case scenario will generally not be such that $\text{corr}(\eta_{1t}, \eta_{2t}) = 1$. To see that, suppose there are 3 time periods, with $t_1 = 1$ and $t_2 = 2$. In this case, $\hat{\alpha} - \alpha \xrightarrow{p} 0.5(0.5\eta_{13} + 0.5\eta_{12} - \eta_{11}) + 0.5(\eta_{23} - 0.5\eta_{22} - 0.5\eta_{21})$. Therefore, assuming $\text{corr}(\eta_{1t}, \eta_{2t}) = 1$ will lead to a lower variance relative to the case with no spatial dependence if $\mathbb{V}(\eta_{ij})$ is substantially larger than the variance at the two other periods. A possible alternative in this case could be to first estimate the variance/covariance matrix of the marginal distribution of $(\eta_{1t}, \ldots, \eta_{st})$ for the treated units using the residuals of the control units. These estimated marginal distributions would be the same for all treated units under the stationarity assumption from CT, or will vary depending on the estimated heteroskedascity as considered by FP. Then we can calculate the spatial correlation parameters among the treated units (which will be $N_1(N_1-1)$ symmetric $T \times T$ matrices) that maximizes the variance of $\hat{\alpha}$ to construct a worst case scenario. To implement that, we could follow a similar strategy as the one considered by CT to deal with spatial correlation in their appendix. The difference is that, since we cannot estimate the spatial dependence because there is no distance metric in our setting, we would have to do a grid search over the possible variance-covariance matrices that are consistent with the marginal distributions of the errors, and consider the worst case scenario.
A.6 Confidence intervals for average effects based on the Benjamini and Hochberg (1995) approach

The procedure proposed by Benjamini and Hochberg (1995) for controlling the FDR is as follows. For testing the nulls $\alpha_s = a_s, s \in I_1$, with control of the FDR at level $\tau$, we first compute $N_1$ p-values for the tests, which in our setting are given by:

$$\hat{p}_s = 1 - \hat{F}_{\xi_s} \left( \frac{\hat{\alpha}_s - a_s}{h(Z_s; \hat{\delta})} \right),$$

where $\hat{\alpha}_s$ is the DID estimator that only uses treated unit $s$ and the controls. We then order the nulls and corresponding p-values from smallest to largest, $\hat{p}(1) \leq \hat{p}(2) \leq ... \leq \hat{p}(N_1)$, and compute:

$$k = \max \left\{ i \leq N_1 : \hat{p}(i) < \frac{i}{N_1} \tau \right\}.$$

We then reject the first $k$ nulls. If no $k$ satisfies the above requirement, we do not reject any null.

From the above description, it is clear that the set of null hypotheses for which no elements are rejected must satisfy $\hat{p}(i) \geq \frac{i}{N_1} \alpha$ for all $i \leq N_1$. Let $P_{N_1}$ denote the set of bijective functions from $\{1, \ldots, N_1\}$ to $I_1$. It follows that the confidence set for heterogeneous effects is given by:

$$I_{BH}((\alpha_s)_{s \in I_1}; 1 - \tau) = \bigcup_{\rho \in P_{N_1}} \left( \bigcup_{s_1 \leq s_2 \leq s_3 \leq s_4 \leq \hat{q}_{\xi_1}} \left( 1 - \frac{1}{N_1} \tau \right) \left\{ (\hat{\alpha}_{\rho(i)} \pm h(Z_{\rho(i)}; \hat{\delta}) s_{i=1}^{N_1} \right\} \right).$$

Since, for each $\rho \in P_{N_1}$, the set inside the outermost union is connected, it follows that its projection is an interval. A simple argument reveals that the union of these intervals as $\rho$ ranges $P_{N_1}$ is also an interval, which establishes that the confidence set for average effects is given by:
\[ I_{BH}(\alpha_w; 1 - \alpha) = [\hat{\alpha}_w - c^*, \hat{\alpha}_w + c^*], \]

where \( c^* = \max_{\rho \in \mathcal{P}_1} \sum_{i=1}^{N_1} \omega_{\rho(i)} h(Z_{\rho(i)}; \hat{\delta}) \hat{q}_{\xi}(1 - \frac{i}{N_1}) \). Clearly, this confidence interval contains the confidence interval obtained from Conservative Test 1. The constant \( c^* \) can be quickly computed by ordering \( \hat{m}_s := \omega_s h(Z_s; \hat{\delta}) \) from largest to smallest, \( \hat{m}_1 \geq \hat{m}_2 \geq \ldots \geq \hat{m}_{N_1} \) and noting that \( c^* = \sum_{i=1}^{N_1} \hat{m}_i \hat{q}_{\xi}(1 - \frac{i}{N_1}) \).

A.7 Details on the MC simulation

We construct our MC simulations based on the American Community Survey (ACS). We restrict our sample to individuals on the workforce, and consider log wages as the outcome variable. With data from 2014 to 2017, we estimate the residuals \( \hat{W}_s \) at the PUMA level, considering a setting in which treatment starts after 2015. More specifically, we compute the residuals from a PUMA \( \times \) year regression. We then calculate \( \hat{W}_s = (\hat{e}_{s,2017} + \hat{e}_{s,2016})/2 - (\hat{e}_{s,2015} + \hat{e}_{s,2014})/2. \)

Given \( \hat{W}_s \) for all PUMAs, we estimate a model for the spatial correlation in which the covariance between two PUMAs may depend on the similarity between their industry compositions, on whether they belong to the same state, and on their workforce sizes. More specifically, letting \( M_s \) denote the (average) workforce size at PUMA \( s \), we assume that \( (W_1, \ldots, W_N) \) is multivariate normally distributed with mean zero and variance/covariance matrix given by:

\[
\text{cov}(W_s, W_h) = \begin{cases} 
\sigma_p^2 + \sigma_{M_s}^2 + \sigma_S^2 + \sigma_I^2 & \text{if } s = h \\
\sigma_S^2 + \sigma_I^2 \mu_s \mu_h & \text{if } s \neq h \text{ and state}_s = \text{state}_h \\
\mu_s \mu_h & \text{if state}_s \neq \text{state}_h 
\end{cases}
\]

where \( \mu_s \) is a \( 12 \times 1 \) vector of PUMA industry composition measures normalized so \( \mu_s \mu_s =
1. These industry measures are obtained by performing principal component analysis on the PUMA sector shares computed according to the Census 1990 industry classification. Parametrization (6) can be motivated by the following factor model for the $W_s$ (Ferman, 2023):

$$W_s = \omega_s + \frac{1}{M_s} \sum_{i=1}^{M_s} \epsilon_{i,s} + \gamma_{\text{State}_s} + \mu_s' \psi,$$

where $\omega_s$ is a PUMA-level shock, $\epsilon_{i,s}$ are individual-level shocks, $\gamma_{\text{State}_s}$ is a state shock, and $\psi$ is a vector of industry shocks with common variance. If shocks are assumed to be uncorrelated, then this factor model leads to parametrization (6).

We estimate (6) by nonnegative least-squares. We find that:

$$(\hat{\sigma}_P^2, \hat{\sigma}_\epsilon^2, \hat{\sigma}_S^2, \hat{\sigma}_I^2) = (6.627967 \times 10^{-4}, 2.400695 \times 10^2, 2.022981 \times 10^{-4}, 1.870911 \times 10^{-4}).$$

For the MC simulations presented in Section 5 we first selected a PUMA that exhibits a strong spatial correlation with some other PUMAs to be treated. Then we sequentially pick $N_1 - 1$ PUMAs in the same state that are most similar in industry composition with previously selected PUMAs. Given this treatment assignment, we draw random normal variables ($W_1, ..., W_N$) from the estimated DGP. We note that all simulations are invariant to the choice of unit and time fixed effects. Moreover, we consider simulations in which the treated units are fixed, treatment effects are also fixed (and equal to zero), and the only stochastic components are the $W_s$. Therefore, these simulations are based on the exact same framework as in the theoretical part of the paper. All TWFE regressions are weighted by workforce size.

We present in the main text the results for a naive FP, Conservative Tests 1 and 2, a correctly specified parametric bootstrap, and a parametric bootstrap that estimates the heteroskedasticity and state correlation structures, but ignores correlation due to industry shares. We present in Appendix Figure A.2 the results using alternative inference methods.
For inference based on CRVE at the state level and on Conley (1999) heteroskedasticity- and spatial-correlation-robust standard errors using a geographical distance metric, we have over-rejection for two reasons: because we have few treated units and because we have spatial correlation from other dimensions other than geographic distance. This is why rejection rates do not become close to 5% even when $N_1$ increases. For the Wild Bootstrap at the state level with null imposed (Canay et al., 2021), tests exhibit strong underrejection, which is reflected in confidence intervals whose length can be over 20 times larger than the unfeasible CI. Finally, the CT procedure exhibits underrejection for small $N_1$ – which stems from the fact that treated units exhibit larger group size than controls –, but overrejection for large $N_1$ due to the effect of spatial correlation.
Figure A.2: **MC simulations - alternative inference methods**

- **A:** test size
- **B:** length of CI / length of unfeasible CI

**Notes:** This figure replicates Figure 1 for alternative inference methods. We consider inference based on CRVE at the state level, Conley (1999) standard errors based on geographical distance, WCB at the state level with the null imposed, and the CT approach. We report rejection rates of tests conducted nominally at the 5% significance level, and the relative length of nominal 95% confidence levels, vis-à-vis the length of the unfeasible confidence interval constructed using the true sampling variance.

**A.8 Testing for Spatial Correlation**

It is common in empirical applications to have settings in which, for example, there are only a few states that are treated, but we observe subgroups (e.g., counties) within each state. Consider a setting in which there is only one treated state, and assume spatial correlation is restricted within states. In this case, the researcher could decide between using CRVE at the county level or a method such as CT and FP at the aggregate level. There is a trade off in terms of assumptions for these different type of methods. The first one relies on no spatial correlation within states, while the former relies on homoskedasticity (or heteroskedasticity
with a structure as considered by FP). See Ferman (2021a) for a more thorough comparison among different inference methods.

In this setting, we can consider a simple way to assess whether spatial correlation poses a problem for CRVE at the county level. Let \( \hat{W}_{cs} \) be the post-pre different in the residuals of county \( c \) in state \( s \). Under the assumption that errors are independent across counties, and given that \( \hat{W}_{cs} \overset{p}{\rightarrow} W_{cs} \), we should expect that the proportion of residuals \( \hat{W}_{cs} \) that is positive to be uniform across states (if \( W_{cs} \) is symmetric, then we should expect that to be approximately 1/2 for all states). In contrast, if there are state shocks, then we should expect positive residuals concentrated in some states, and negative residuals concentrated in others.

This suggests the following test. We calculate the proportion of positive residuals for each state \( \hat{p}_s \), and construct a test statistic \( t = \sum_{s=1}^{S} (\hat{p}_s - \bar{p})^2 \), where \( S \) is the number of states and \( \bar{p} = S^{-1} \sum_{s=1}^{S} \hat{p}_s \). Then we can consider permutations of \( \hat{W}_{cs} \), and reconstruct \( \hat{p}_s^b \). With that, we then calculate \( t^b \) for each permutation, and check whether \( t \) is extreme in the distribution of permutations. The distribution of the permutations would recover the discrepancies between \( \hat{p}_s \) and \( \bar{p} \) that we should expect when errors are independent, given that we have only a finite number of counties per state. If \( t \) is extreme in this distribution, then this would indicate relevant within-state spatial correlation.

This idea is similar in spirit to the test for appropriate level of clustering proposed by MacKinnon et al. (2023). Note, however, that CRVE at the state level would not be consistent in our setting, so their test would not be valid. Following the work by Roth (2022), we consider such test with caution, as we may fail to reject the null of no spatial correlation due to sampling variation. Still, such test may be very informative about when we cannot rely on CRVE and, therefore, should focus on alternatives such as CT and FP. If we consider this test for the empirical illustration in Section 6, the p-value is virtually equal to zero, providing strong evidence that spatial correlation is problematic in this setting.

When we consider this test for the empirical application considered in Section 6, we find
a p-value of zero. This provides strong evidence that spatial correlation is important in this setting.

### A.9 Empirical illustration: alternative inference methods

Table A.2 reports the results of alternative inference methods for the empirical application in Section 6. These include Conley (1999) robust standard errors based on the geographical county distance; the cluster robust variance estimator and the wild bootstrap with null imposed at the state level; and a parametric bootstrap that specifies and then estimates heteroskedasticity due to population size and spatial correlation due to county distance. Conley (1999) standard errors perform poorly in this setting because there are few treated units. Similarly, cluster robust standard errors and the wild bootstrap at the state level perform poorly because there is a single treated state. The parametric bootstrap appears to work well, especially for health care-amenable mortality, where it closely tracks FP at the state level, though it is more conservative than Conservative Tests 1 and 2 with regards to all cause mortality.
Table A.2: **Other inference methods for Sommers et al. (2014)**

| Method                                | All cause mortality (deaths per 100,000 adults) | Health care-amenable mortality (deaths per 100,000 adults) |
|---------------------------------------|-----------------------------------------------|------------------------------------------------------------|
|                                       | p-value | length of 95% CI | p-value | length of 95% CI |
| Conley (1999) (county distance)       | 0.066   | 27.19            | 0.022   | 17.07            |
| CRVE and WCB at state level          |         |                  |         |                  |
| CRVE                                 | 0.030   | 22.34            | 0.002   | 11.61            |
| WCB                                  | 0.465   | 220.44           | 0.440   | 117.38           |
| Parametric bootstrap (county distance)| 0.619   | 102.47           | 0.283   | 35.03            |

Notes: This table presents p-values and lengths of confidence intervals for a series of alternative inference methods for the application from Sommers et al. (2014). We consider a DID estimator based on OLS TWFE regression with no covariates. Point estimates are slightly different than reported in the original paper because we use the publicly available data set (so we do not have death counts for cells with fewer than 10 deaths), and because we weight observations by population mean across years to avoid problems with TWFE estimand highlighted in recent papers. See, for example, Goodman-Bacon (2021), de Chaisemartin and D'Haultfoeuille (2020), and Callaway and Sant’Anna (2021). We also restrict to counties with non-missing information for all years. We end up with 485 control counties, as compared to 513 from the original study. The point estimates are $-12.77$ for all cause mortality and $-9.94$ for health care-amenable mortality.