

COMPOSITIONAL DIFFERENCE-IN-DIFFERENCES FOR CATEGORICAL OUTCOMES

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ABSTRACT. In difference-in-differences (DiD) settings with categorical outcomes, such as voting decision, occupational choice, or field of study, treatment effects often act on both total quantities (e.g., turnout) and category shares (e.g., vote distribution). Linear DiD models can be problematic in this context: they are scale-dependent, can yield negative counterfactuals, and are inconsistent with discrete choice theory. We propose compositional DiD (CoDiD), a new extension of DiD, which identifies counterfactual totals and shares under a parallel growths assumption: absent treatment, each category’s size changes at the same proportional rate in treated and control groups. We show that, under a classical random utility framework, this implies that the relative preferences between any pair of categories (e.g., Democrats vs. Republicans) evolve similarly in both groups without treatment. Also geometrically, it implies a parallel evolution of the counterfactual trajectories of the groups’ probability distributions in their space (the simplex). We extend CoDiD to i) derive bounds under relaxed assumptions, ii) accommodate staggered treatment timing, and iii) construct a synthetic DiD analog. We illustrate the method’s empirical relevance through two applications: first, we examine how early voting reforms affect voter choice in U.S. presidential elections; second, we analyze how the regional greenhouse gas initiative (RGGI) affected the composition of electricity generation across sources such as coal, natural gas, nuclear, and renewables.

Keywords: categorical outcomes, difference-in-differences, causal inference, identification, changes-in-changes, compositional data.

JEL codes: C14, C23, C31

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INTRODUCTION

The classical difference-in-differences (DiD) framework identifies the average treatment effect on the treated under the parallel trends assumption for scalar outcomes. However, in many applications, the outcome of interest is categorical, and the notion of an average level is generally undefined. Examples include voting decision (democrat, republican, others), occupational sector (agriculture, manufacturing, and services) or field of study (stem, humanities, business, or others). For categorical outcomes, the key quantitative objects are the category-specific quantities, which jointly determine both the overall total quantity and the corresponding probability mass function across categories. In this case, we would like to analyze both absolute changes (how many units are added or removed in absolute terms for each category, and overall) and relative shifts (how the shares are reallocated across categories) in a consistent way. For example, a voting policy can differently affect both the total number of voters (turnout) and the share of votes for each party. A minimum wage policy can change both the number of people across all employment sectors and the probability of being in each of them. An education reform may reallocate students between fields, but policymakers may also care about the total number of new graduates overall.

The classical linear parallel trends assumption, which imposes a linear evolution in outcome levels, may be inappropriate in this context for several reasons already noted in the literature (see [Puhani \(2012\)](#); [Wooldridge \(2023\)](#)). A naive strategy would be to apply linear parallel trends separately to the raw quantities of each category, obtain counterfactual quantities, and then normalize them to form a counterfactual distribution. However, this approach is problematic for three main reasons. First, applying linear parallel trends to raw quantities is scale-dependent, as it ignores differences in group size. Transferring the same additive change from a large control group to a smaller treated group can distort counterfactual quantities, exaggerating or understating effects, and thus producing misleading totals and distributions. Second, this method can yield negative counterfactual quantities when a negative shift in the control group outweighs the pre-treatment value in the treated group. Finally, it can imply choice dynamics that lack any behavioral or structural justification from economic theory regarding how choices across categories evolve.

On top of that, applying parallel trends directly to probabilities is theoretically possible but often yields invalid counterfactuals, with values below zero or exceeding one. The

resulting counterfactual distribution can fall outside the probability simplex (the set of all vectors of positive numbers summing to one), rendering them invalid (see figure 1). Most existing nonlinear methods for categorical distributions require a natural ordering of the support because they rely on cumulative distribution functions, which are undefined for unordered outcomes. For such outcomes, only the probability mass function is well-defined, and importantly, these methods typically do not provide counterfactuals for the raw quantities.

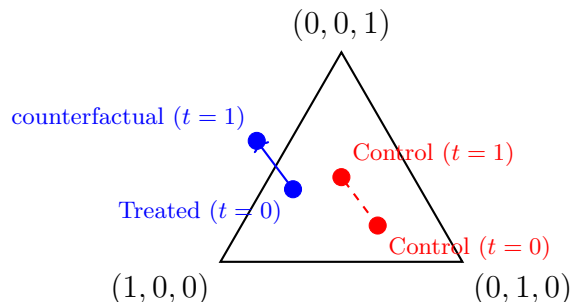


Figure 1. Illustration of how parallel trends can lead to invalid counterfactuals in the 2-dimensional probability simplex. The control group moves from $(0.7, 0.2, 0.1)$ to $(0.3, 0.3, 0.4)$, while applying the same linear shift to the treated group at $(0.2, 0.3, 0.5)$ produces an invalid counterfactual $(-0.2, 0.4, 0.8)$, shown above as lying outside the probability space.

Ideally, we would like to consider a nonlinear parallel trends assumption on quantities that has a clear economic meaning, resolves the scale-dependence problem, and ensures that the evolution of shares remains consistent with standard discrete choice theory. This paper introduces Compositional difference-in-differences (CoDiD), a new framework for analyzing categorical outcomes. The method is built on a nonlinear parallel trends assumption, which we call *parallel growths*, which allows us to point-identify the counterfactual categorical quantity, and thus the counterfactual total and probability mass functions within a DiD framework. We do so while addressing all the challenges outlined above. In addition, we define two treatment effect measures tailored to this context. The growth treatment effect on the treated (GTT) quantifies how each category’s absolute size changes as a result of treatment, and also how the total quantity has evolved as a result of treatment. The second is the compositional treatment effect on the treated (CTT), which captures how the probability mass is reallocated across categories in response to treatment.

We begin with the canonical 2×2 DiD setting. The parallel growths assumption is a parallel trends of log-transformed categorical quantities, meaning that the absolute size of each category would grow or shrink at the same proportional rate in both treated and control groups. We first show that this directly implies parallel trends in the log-odds of category shares. Economically, this connects to the random utility model ([McFadden \(1972\)](#)), where log-odds represent differences in utilities and reflect relative preferences. Under this interpretation, parallel growths mean that, absent treatment, the evolution of relative preferences between any pair of categories would be similar in both groups. In other words, the evolution of the way people chose between categories in the control group who did not experience treatment will be similar to what happens in the treated group if it did not have treatment. Also, without relying on a random utility framework, we can derive another economic meaning. In the control group, category shares naturally evolve over time, with some categories gaining mass at the expense of others. The assumption implies that, in the absence of treatment, the treatment group would have experienced the same reallocation pattern observed in the control group. This interpretation allows us to view the causal effect as the extent to which the treatment affects the way probability mass is redistributed across categories. Finally, in geometric terms, each probability mass function (PMF) corresponds to a point in the simplex, and its evolution traces a path within this space. The parallel growths assumption means that, in the absence of treatment, the treated group’s counterfactual path would be parallel to the control group’s path under Aitchison geometry, the standard geometry for the simplex in compositional data analysis ([Aitchison \(1982\)](#); [Egozcue et al. \(2003\)](#)).

We also discuss the connections and key differences between our approach and the multinomial logistic two-way fixed effects model. In the simple 2×2 case, we show that, when focusing solely on category shares, both methods yield the same counterfactual shares. The main distinction lies in the fact that our approach also recovers counterfactual quantities, which cannot be obtained directly from the logistic model. Moreover, our framework introduces a new treatment effect parameter that offers a more natural and interpretable measure than the change in log-odds implied by the logistic specification. Even when the analysis is limited to shares, the differences become more pronounced when extending the framework to multiple time periods (e.g. staggered adoption case) and relaxations of the identifying assumption. Our approach provides a more flexible and easily extendable foundation for such generalizations. Another comparison is made with the DiD and the changes-in-changes

(CiC) frameworks. While DiD focuses on expectations (points on the real line) and CiC on cumulative distribution functions (points in a space of CDFs), our method focuses on PMFs (points in the probability simplex). The underlying identification logic is consistent across all three methods: each characterizes the control group’s evolution via a translation mapping and applies that same mapping to the treated group’s initial state to recover its counterfactual. The fundamental distinction, therefore, lies not in the core logic but in the object being transported, expectations, CDFs, or PMFs, and the geometry that defines the translation. From this unified perspective, the CoDiD assumption emerges naturally as the DiD/CiC analogue for probability mass functions.

In a more general framework with multiple time periods, the parallel growths assumption can be assessed visually by plotting the log-transformed quantities. If the trends appear non-parallel in pre-treatment periods, the assumption becomes less credible. In this case, we first propose a set of relaxations of the assumption in the spirit of [Ban and Kédagni \(2022\)](#). Specifically, we bound the counterfactual log differences between groups by restricting their change to lie within the convex hull of observed changes across pre-treatment periods. This approach produces bounds for both counterfactual quantities and counterfactual distributions. When multiple potential control groups are available, we develop a synthetic DiD (see [Arkhangelsky et al. \(2021\)](#)) analog, synthetic CoDiD, that merges the flexibility of synthetic control methods with the causal logic of difference-in-differences. This extension constructs a weighted combination of control units whose pre-treatment log-trajectory closely matches that of the treated unit, while preserving the parallel growths structure in the post-treatment period. The resulting control group not only improves pre-treatment fit but also maintains interpretability within the CoDiD framework. Finally, we generalize the methodology to settings with staggered treatment adoption, where units receive treatment at different points in time. We follow the same assumptions as in [Callaway and Sant’Anna \(2021\)](#), propose two types of parallel growths assumption in this case, and derive the corresponding counterfactual in each case.

As applications, we first examine the impact of early voting programs on the distribution of voter support across political parties in U.S. presidential elections. These programs, allowing voters to cast ballots before election day, either in person or by mail, have been the subject of intense partisan debate. We revisit this question by analyzing both total turnout and

the compositional shift in voter preferences. As expected, the treatment increased overall turnout and the number of votes for all parties. However, our compositional treatment effect on the Treated (CTT) reveals a nuanced reallocation: a previously indifferent voter (assigning equal initial weight to all parties) would, after the treatment, shift support more toward alternative parties, with both major parties losing relative appeal, Republicans more so than Democrats. Secondly, we analyze the Regional Greenhouse Gas Initiative (RGGI) and its effects on the mix of electricity generation sources in participating states. RGGI, a cap-and-trade program designed to reduce carbon emissions from the power sector, is expected to shift the composition of electricity generation across coal, natural gas, nuclear, and renewable sources by promoting cleaner technologies and discouraging carbon-intensive ones. We assess how RGGI affected the size of each source in the electricity generation process over time. We find that RGGI sharply cut fossil fuel use, especially coal, by shifting generation to gas and nuclear rather than boosting renewables, underscoring the need for complementary policies to accelerate a truly renewable-driven energy transition.

RELATED LITERATURE

This paper makes some methodological contributions at the intersection of difference-in-differences and compositional data analysis.

First, it contributes to the extensive DiD literature. Classical DiD focuses on scalar outcomes, estimating treatment effects on the mean, with surveys and applications summarized in [Lechner \(2011\)](#); [Cafri et al. \(2019\)](#); [De Chaisemartin and d'Haultfoeuille \(2023\)](#); [Roth et al. \(2023\)](#); [Baker et al. \(2025\)](#). Recent works have extended DiD to more complex settings: [Callaway and Sant'Anna \(2020\)](#) develops methods for staggered treatment adoption, [Arkhangelsky et al. \(2021\)](#) combines DiD with synthetic controls, and [Manski and Pepper \(2018\)](#); [Rambachan and Roth \(2020\)](#); [Ban and Kédagni \(2022\)](#) relax the parallel trends assumption. A second wave of research extends DiD to entire outcome distributions. Early contributions include quantile DiD [Meyer et al. \(1990\)](#) and the changes-in-changes (CiC) approach [Athey and Imbens \(2006\)](#), which identifies counterfactual distributions non-parametrically. Subsequent work has generalized these ideas to multivariate outcomes [Torous et al. \(2021\)](#), settings where identifying assumptions apply to cumulative distribution functions [Havnes and Mogstad \(2015\)](#); [Roth and Sant'Anna \(2021\)](#), copula-based approaches

Callaway et al. (2018); Callaway and Li (2019); Ghanem et al. (2023), and methods using characteristic functions Bonhomme and Sauder (2011). However, these methods do not directly address categorical outcome distributions, which are probability mass functions. Graves et al. (2022) proposes a DiD for categorical outcomes while relying on parallel trends for proportions, which we explained earlier is not appropriate in general. Zhou et al. (2025) extend the difference-in-differences framework to non-Euclidean data, including probability mass functions, by employing Fréchet means and geodesic transport. While their approach is mathematically elegant, the identifying assumptions are primarily geometric and offer limited economic interpretability. In contrast, our framework delivers both counterfactual quantities and probability mass functions that retain economic intuition while incorporating a geometric perspective specifically designed for categorical outcomes. Another related paper is Tchetgen Tchetgen et al. (2024), who propose a general DiD framework applicable to count data in the binomial setting. Our analysis differs by focusing on the multinomial case, allowing for richer categorical structures and more general forms of distributional change. Second, the paper contributes to the compositional data analysis (CoDA) literature. CoDA, pioneered by Aitchison (1982, 1990, 1992, 2002), provides tools for analyzing data constrained to the simplex. Subsequent developments Egozcue et al. (2003); Billheimer et al. (2001); Barceló-Vidal et al. (2001) refine transformations and models that respect the geometric structure of compositional data. More recently, Arnold et al. (2020) connected CoDA to causal inference. We also combine compositional data methods with econometric identification strategies to analyze causal effects when outcomes are probability mass functions, providing a bridge between DiD and compositional statistics.

The paper is organized as follows. Section 1 introduces the canonical 2×2 case, presenting the main identifying assumption along with its economic and geometric interpretations. Section 2 generalizes the framework to settings with multiple time periods. Section 3 discusses the connection with existing approaches, and Section 4 illustrates the methodology through two empirical applications. Finally, Section 5 concludes.

1. CANONICAL 2×2 DiD CASE

In this section, we focus on the canonical, two-group, two-time period case in the DiD framework, and we clearly expose the assumptions and their implications. We will start

with the analytical framework, later discuss the main identifying assumption, and all the economic and geometric implications.

1.1. Analytical framework. In this section, we introduce the basic framework of our method. A categorical outcome Y takes values in a finite set of p mutually exclusive categories:

$$Y \in \{c_1, c_2, \dots, c_p\}.$$

We focus primarily on the absolute quantities for each category, which can appear in several empirical contexts. They can arise when the outcome is observed at the individual level. For example, in evaluating a job training program, individuals may be classified as unemployed, part-time employed, or full-time employed. The categorical quantity is obtained by aggregating individuals into these outcome categories. Sometimes, the data consist directly of quantities across categories rather than individual-level observations. For example, the number of votes each political party receives in an election. Unlike individual-level data, the identities or attributes of the units are not observed. In all these cases, the proposed method remains applicable, as it relies solely on knowledge of the categorical quantities.

We consider a setting with two groups, $g \in \{0, 1\}$, where $g = 1$ is the treated group and $g = 0$ is the control group. These groups are observed in two time periods, $t \in \{0, 1\}$, with $t = 0$ being the pre-treatment period and $t = 1$ the post-treatment period. Our object of interest is a categorical outcome. For any category c_k , we define $q_{g,t}^N(c_k)$: the potential untreated quantity (the quantity in c_k if the group g were untreated at time t). We also have $q_{g,t}^I(c_k)$: the potential treated quantity (the quantity in c_k if the group g were treated at time t). For the untreated potential outcomes, we aggregate across categories to define the total quantity for a group-period:

$$S_{g,t}^N = \sum_{k=1}^p q_{g,t}^N(c_k).$$

The share (or probability) for category c_k is then:

$$\pi_{g,t}^N(c_k) = \frac{q_{g,t}^N(c_k)}{S_{g,t}^N}.$$

The vector of quantities and the entire probability mass function are represented as:

$$q_{g,t}^N = [q_{g,t}^N(c_1), \dots, q_{g,t}^N(c_p)], \quad \pi_{g,t}^N = [\pi_{g,t}^N(c_1), \dots, \pi_{g,t}^N(c_p)], \quad \text{where} \quad \sum_{k=1}^p \pi_{g,t}^N(c_k) = 1.$$

All the same definitions apply to the treated potential quantities, $q_{g,t}^I(c_k)$, and their associated totals and shares. From the data, we can identify the vectors $q_{0,0}^N$ for the control group and $q_{1,0}^N$ for the treated group in the pre-treatment period. In the post-treatment period, we can identify from data the untreated vector of quantities for the control group, $q_{0,1}^N$, and the treated counterpart for the treated group, $q_{1,1}^I$. The counterfactual of interest is the vector of quantities that we would have observed for the treated group in the absence of treatment $q_{1,1}^N$. Identifying this missing object is the core challenge of our analysis. Once this is identified, we can consider the treatment effect parameters.

We introduce two treatment effect parameters to capture the impact of the intervention. The first is the growth treatment effect on the treated (GTT), which quantifies the causal effect on the absolute size of a category. For each category c_k (where $k = 1, \dots, q$), the GTT is defined as the proportional change in its quantity:

$$\text{GTT}(c_k) = \frac{q_{1,1}^I(c_k)}{q_{1,1}^N(c_k)} - 1, \quad GTT = \frac{S_{1,1}^I}{S_{1,1}^N} - 1.$$

This parameter has an intuitive interpretation: $GTT = 0$ implies the treatment had no effect on the absolute. $GTT > 0$ indicates that the treatment caused category c_k to grow in absolute terms. For example, a GTT of 0.15 means the category's size increased by 15% due to the treatment. $GTT < 0$ signifies that the treatment caused the category to shrink. A GTT of -0.10 , for instance, corresponds to a 10% decline.

The second parameter is the compositional treatment effect on the treated (CTT), which captures how treatment redistributes weight across categories. To measure this, we apply the compositional difference operator commonly used in compositional data analysis to compare probability mass functions. This operator quantifies how each category expands or contracts relative to all others. For intuition, fix a category c_k and consider its proportional change:

$$r_k = \frac{\pi_{1,1}^I(c_k)}{\pi_{1,1}^N(c_k)}, \quad \begin{cases} r_k > 1 & \text{category } k \text{ grew,} \\ r_k < 1 & \text{category } k \text{ shrunk,} \\ r_k = 1 & \text{no change.} \end{cases}$$

Dividing by the total change gives a vector showing each category's relative gain or loss. We obtain the compositional difference operation used in compositional data analysis for the

control group.

$$\pi_{1,1}^N \ominus \pi_{1,1}^N = \frac{1}{\sum_{k=1}^q r_k} [r_1, r_2, \dots, r_p] = \frac{1}{\sum_{k=1}^p \frac{\pi_{1,1}^I(c_k)}{\pi_{0,0}^N(c_k)}} \left[\frac{\pi_{1,1}^N(c_1)}{\pi_{1,1}^N(c_1)}, \dots, \frac{\pi_{1,1}^N(c_p)}{\pi_{1,1}^N(c_p)} \right]. \quad (1)$$

Each component then reflects how much a category's importance has shifted relative to the others. Components larger than $1/p$ indicate categories that gain relative importance, while components smaller than $1/p$ indicate categories that lose. If all ratios equal one and the operator yields the uniform composition $(1/p, \dots, 1/p)$, we therefore have:

$$CTT = \pi_{1,1}^I \ominus \pi_{1,1}^N. \quad (2)$$

A useful way to think about CTT is through a neutral individual who starts indifferent, assigning equal probability to all p categories, $(1/p)$. After treatment, this person updates their weights according to CTT. Components greater than $1/q$ indicate categories that gain relative importance, while smaller components indicate categories that lose. For example, in a three-party voting scenario, a neutral voter starts with $(1/3, 1/3, 1/3)$. After a campaign (treatment), CTT might imply $(0.5, 0.3, 0.2)$. This shows that support for the first party increased, while the other two declined, with the second party still stronger than the third.

1.2. parallel growths and Identification. This section develops the identification strategy and clarifies its implications for the probability mass function. We start with the following assumption.

Assumption 1 (Common Support). *The support, denoted by $\bar{\mathcal{Y}} = \{c_1, \dots, c_p\}$, is the same for all untreated potential categorical outcomes.*

This assumption ensures that all observed and counterfactual outcomes in the absence of treatment are defined over a common set of categories. It rules out situations where the support changes across groups or over time, which would make comparisons and counterfactual reasoning impossible. In practice, it implies that the set of possible outcomes is fixed. Such support conditions are standard in the literature. To introduce our main identifying assumption, we provide intuition for the DiD identification logic. The core idea is that, in the absence of treatment, the treated group would have followed the same trajectory as the

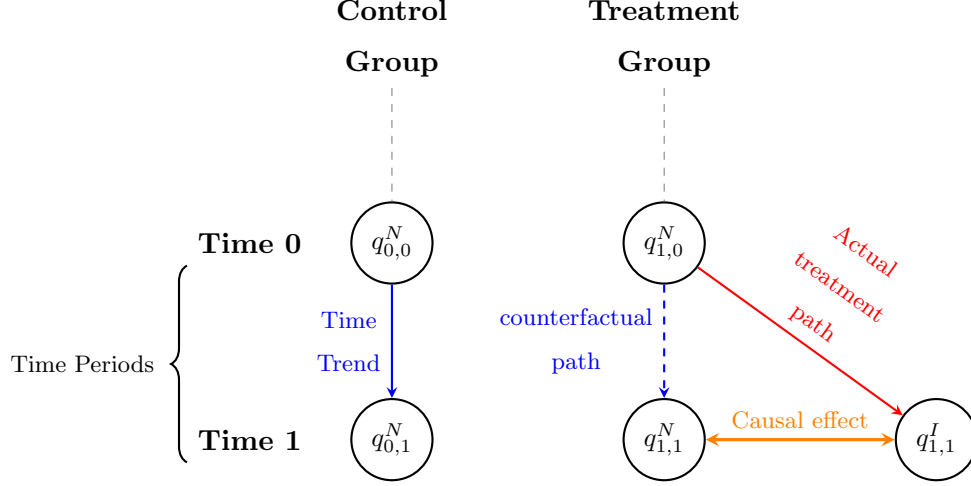


Figure 2. Visual representation of the DiD identification strategy. The counterfactual outcome for the treated group in the post-treatment period ($q_{1,1}^N$) is constructed by extrapolating the time trend observed in the control group (blue arrows) to the treated group’s pre-treatment level. The causal effect is the difference between the observed treated outcome ($q_{1,1}^I$) and this counterfactual ($q_{1,1}^N$), shown by the orange double-headed arrow.

control group. Figure 2 illustrates this DiD identification logic: the control group, unexposed to the treatment, serves as a counterfactual benchmark, mirroring what would have happened to the treated group had it not received the intervention.

As we said before, in many empirical settings, the sizes of the groups defined in each category can vary dramatically in scale. Therefore, a standard parallel trends assumption on the raw quantities is problematic in this context, as it would impose the same absolute change on both large and small groups, which is often unrealistic. To address this issue of scale and to formulate a more plausible identifying assumption, we instead consider parallel trends on the log transformation of the quantities. This approach focuses on proportional, rather than absolute, changes. For a given vector, define the functions $(\log \cdot)$ and $(\exp \cdot)$ which apply respectively the logarithm and the exponential functions component-wise to the vectors.

Assumption 2. (*parallel growths*)

$$\log \cdot (q_{1,1}^N) - \log \cdot (q_{1,0}^N) = \log \cdot (q_{0,1}^N) - \log \cdot (q_{0,0}^N).$$

Assumption 2 is the core identifying condition for our model. It states that, in the absence of treatment, the proportional growth (or decline) of each category in the treated group would have been the same as that of the control group. This reflects the intuitive idea that underlying trends affect all categories proportionally to their size. This may appear as a more realistic and flexible assumption than one based on raw quantities in many economic contexts, especially when the sizes of categories differ significantly. It captures the idea that trends often affect all units proportionally to their size. It is also possible to use discrete covariates to make the assumption more believable. We discuss this possibility in appendix B. From this assumption, the counterfactual quantity vector for the treated group can be easily recovered, and the corresponding counterfactual probability mass can be obtained by normalization, as we see in Theorem 1. Taken together, assumptions 1 and 2 impose sufficient structure to point-identify the counterfactual distributions. The following theorem 1 formalizes this result

Theorem 1. *Under assumptions 1 and 2, the counterfactual quantities are identified as:*

$$q_{1,1}^N = \exp \cdot (\log \cdot (q_{1,0}^N) + \log \cdot (q_{0,1}^N) - \log \cdot (q_{0,0}^N)), \quad (3)$$

$$S_{1,1}^N = \sum_{k=1}^p \exp \cdot (\log \cdot (q_{1,0}^N(c_k)) + \log \cdot (q_{0,1}^N(c_k)) - \log \cdot (q_{0,0}^N(c_k))), \quad (4)$$

$$\pi_{1,1}^N = \frac{1}{S_{1,1}^N} q_{1,1}^N. \quad (5)$$

This identification result is constructive and provides a straightforward way to implement the method. In the next section, we want to discuss further justifications for parallel growths using its economic and geometric implications.

1.3. Implications of parallel growths. Assumption 2 restricts the evolution of growth rates of quantities but also of shares. Using the constraints on the shares, we give further economic and geometric justifications for parallel growths.

Interpretation using the random utility model: To formalize that, let's define the multinomial logistic transform. For $\pi = [\pi(c_1), \dots, \pi(c_p)] \in \mathcal{S}^{p-1}$. The log-odds (or multinomial logit) transformation $\ell : \mathcal{S}^{p-1} \rightarrow \mathbb{R}^{p-1}$ maps probabilities to real-valued indices:

$$\ell(\pi) = \left[\log \left(\frac{\pi(c_1)}{\pi(c_p)} \right), \dots, \log \left(\frac{\pi(c_{p-1})}{\pi(c_p)} \right) \right]. \quad (6)$$

Each component of this vector is the log-odds of category c_k compared to the baseline category c_p . In fact, the ratio $\pi_{g,t}^N(c_k)/\pi_{g,t}^N(c_p)$ is the odds of category c_k relative to the reference category c_p and taking the logarithm gives the log-odds. The choice of the baseline category can be arbitrary. Its inverse is given by the softmax function: for any $y = (y_1, \dots, y_{p-1}) \in \mathbb{R}^{p-1}$,

$$\ell^{-1}(y) = \frac{1}{1 + \sum_{i=1}^{p-1} e^{y_i}} (e^{y_1}, \dots, e^{y_{p-1}}, 1). \quad (7)$$

The parallel growths assumption would imply a parallel trends assumption on the log-transformation of the probability distribution, as stated in this proposition.

Proposition 1 (Implication for shares). *Assumption 1, and assumption 2 implies the parallel trends of log-odds, which is: $\ell(\pi_{1,1}) - \ell(\pi_{1,0}) = \ell(\pi_{0,1}) - \ell(\pi_{0,0})$.*

This implication is important because it helps to better formalize the economic intuition behind our main assumption. In fact, it implies that, in the absence of treatment, the change in log-odds of each category (relative to a base category) would be the same across the treatment and control groups. To better explain the value of this implication, we analyze it through the lens of the random utility model (McFadden, 1972, 1974). In this foundational economic framework, individuals choose the option that provides the highest unobserved utility. The log-odds of choosing one category over another directly measure the difference in their underlying utilities (see appendix D), providing a direct measure of the underlying preference structure driving people’s choices. For example, in a voting context, the log-odds of choosing Democrat over Other (third parties) quantifies the relative preference for the Democratic party. Our parallel growths assumption, when viewed through this lens, implies that the relative preferences between any two categories would have evolved in parallel for the treated and control groups in the absence of the treatment. To illustrate: suppose the control group shows an increase in the log-odds of voting Democrat versus Other, indicating a growing preference for Democrats over third parties. Our assumption states that the treated group would have experienced this same evolution in relative preferences had they not been subjected to the treatment. This same logic applies to all category pairs, such as Republicans versus Other. This interpretation is important because it grounds our technical parallel growths condition to a clear behavioral story. It is no longer just an abstract statistical constraint, but an economic hypothesis about the stability of relative preference trends across

groups through the random utility model. From that, we can also identify the counterfactual distribution with an alternative formula:

$$\pi_{1,1}^N = \ell^{-1}(\ell(\pi_{1,0}) + \ell(\pi_{0,1}) - \ell(\pi_{0,0})). \quad (8)$$

Equation (8) represents a compositional DiD adjustment in the transformed space: the treatment-free evolution of the distribution is added to the initial treated distribution, and the result is mapped back to the simplex through the inverse transformation $\ell^{-1}(\cdot)$. This formulation not only preserves the probabilistic structure of the outcome (ensuring that $\pi_{1,1}^N$ remains a valid probability vector) but also provides an intuitive and computationally convenient way to estimate the counterfactual distribution when dealing with categorical or compositional outcomes.

Interpretation using the compositional difference interpretation: To further support the relevance of our assumption in this context, we provide an alternative interpretation that does not depend on the random utility framework or its underlying assumptions. Suppose our goal is to understand how the treatment redistributes probability mass across categories, that is, how each category gains or loses relative shares compared to the others as a consequence of treatment. An intuitive way of building the counterfactual would be to assume that the relative growth/decline in shares of each category in the control group reflects what would have happened in the treated group without treatment. The compositional difference operator (\ominus) defined in equation 1 provides the precise mathematical language to formalize this intuition. We now show that our parallel growths assumption can be interpreted using that intuition. Specifically, assumption 2 implies that, in the absence of treatment, the relative growth or decline of category shares would have been similar across the treated and control groups. This interpretation is formally established in the following proposition.

Proposition 2. *Assumption 1, assumption 2 implies that the compositional difference for the untreated potential categorical distributions is identical for the treated and control groups:*

$$\pi_{1,1}^N \ominus \pi_{1,0}^N = \pi_{0,1}^N \ominus \pi_{0,0}^N.$$

The equality states that these two compositional changes are identical. In essence, the underlying forces that caused shares in the control group to be reallocated in a particular

way would have produced the exact same pattern of reallocation within the treated group. This provides a clear, distributional interpretation of the parallel growths assumption.

Geometric interpretation parallel growths also imply parallel trajectories of probability mass functions in the probability simplex. Probability mass functions lie in the simplex \mathcal{S}^{p-1} , where movement can be meaningfully defined using the geometry introduced by [Aitchison \(1982\)](#). Unlike the Euclidean case, this geometry accounts for the simplex's constraints and forms the basis of compositional data analysis, redefining operations such as addition, scaling, and distance.

Proposition 3 ([Aitchison \(2002\)](#), [Egozcue et al. \(2003\)](#)). . *Let \mathcal{S}^{p-1} be the $p - 1$ simplex, define the following operations: for all $\pi_1, \pi_2 \in \mathcal{S}^{p-1}$, we have:*

$$\pi_1 \oplus \pi_2 = \left[\frac{\pi_1(c_1)\pi_2(c_1)}{\sum_{k=1}^q \pi_1(c_k)\pi_2(c_k)}, \dots, \frac{\pi_1(c_p)\pi_2(c_p)}{\sum_{k=1}^q \pi_1(c_k)\pi_2(c_k)} \right],$$

and for all $\pi_1 \in \mathcal{S}$ and $\alpha \in \mathbb{R}$,

$$\alpha \odot \pi_1 = \left[\frac{\pi_1^\alpha(c_1)}{\sum_{k=1}^q \pi_1^\alpha(c_k)}, \dots, \frac{\pi_1^\alpha(c_p)}{\sum_{k=1}^q \pi_1^\alpha(c_k)} \right], \quad \pi_1^\alpha \text{ is the usual powering.}$$

$(\mathcal{S}^{p-1}, \oplus, \odot)$ is a vector space of dimension $p - 1$ where \oplus denotes the perturbation operator (analogous to vector addition), \odot denotes the powering operator (analogous to scalar multiplication), and the uniform distribution $\left[\frac{1}{p}, \dots, \frac{1}{p}\right]$ acts as the zero element of the space.

The compositional difference between two distributions π_1 and π_2 can be redefined as:

$$\pi_1 \ominus \pi_2 = \pi_1 \oplus (-1 \odot \pi_2).$$

This formulation highlights that \ominus works like a genuine vector difference in this vector space: it represents the perturbation needed to move from π_2 to π_1 . In other words, it captures the direction and magnitude of the adjustment between the two points. Viewing \ominus this way makes the operator's mathematical structure natural. Under this structure, parallel growths implies that the movements of the two PMFs correspond to trajectories that remain at a constant separation without intersecting, having the same direction. Figure 3 illustrates this idea: in the Aitchison geometry of the simplex, the trajectories of two distributions evolve in parallel within the 2-dimensional simplex \mathcal{S}^2 , representing all valid probability distributions over three categories. In figure 3, each point in the triangle represents a distribution over three categories. As time evolves, distributions trace curves within the simplex. Although

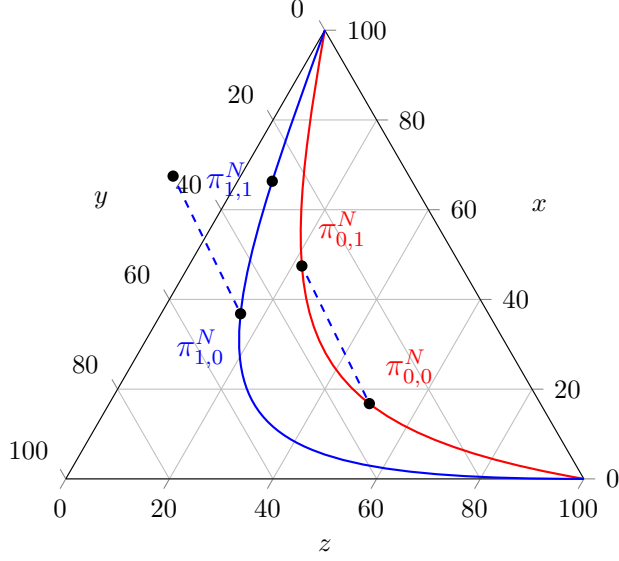


Figure 3. Illustration of parallel growths in the simplex. The red curve represents the trajectory of the control group from pre-treatment ($\pi_{0,0}^N$) to post-treatment ($\pi_{0,1}^N$), while the blue curve shows the counterfactual trajectory of the treated group from pre-treatment ($\pi_{1,0}^N$) to post-treatment ($\pi_{1,1}^N$). Dashed lines indicate the linear translation (parallel growths).

these paths may look non-linear in Euclidean space, in the simplex geometry, they are parallel, maintaining a consistent direction without intersecting. Here, we say that the implied evolution of the distributions is consistent with the nature of their space. Because of that, the compositional treatment effect on the treated can be written as:

$$CTT = \pi_{1,1} \ominus \pi_{1,0} \oplus \pi_{0,1} \ominus \pi_{0,0}. \quad (9)$$

This expression mirrors the structure of the standard average treatment effect on the treated (ATT) in difference-in-differences, but it operates in the probability simplex rather than in the real line. In the classical DiD, differences in means capture changes in average outcomes across time and groups. In contrast, the compositional DiD captures differences in entire categorical distributions: each component of the treated group's pre-treatment shares is rescaled by the corresponding ratio of control group shares, and the resulting vector is normalized to yield a valid probability distribution. Thus, (CTT) extends the ATT from the scalar outcome space to the compositional space, preserving the relative structure of category shares while identifying how treatment shifts the allocation of probability mass across categories.

All these perspectives reinforce the idea that imposing the parallel growths assumption on the quantities leads to desirable and interpretable restrictions on the evolution of category shares. It links the economic intuition of stable evolution of preferences with a geometric structure of parallel movements in the probability simplex.

2. EXTENSIONS WITH MULTIPLE TIME PERIODS

In this section, we propose several extensions of the method in the case where we have multiple time periods and possibly more potentially heterogeneous control groups.

2.1. Relaxations of parallel growths. When multiple pre-treatment periods are available, the plausibility of the parallel growths assumption can be evaluated by examining the pre-treatment trajectories of the log-quantities. If the estimated pre-treatment trends appear non-parallel, this raises concerns about the validity of the assumption. Rather than discarding the design altogether, one can relax the assumption in a way that delivers informative bounds on the treatment effect. In particular, we adopt a relaxation strategy closely related to the approach in [Ban and Kédagni \(2022\)](#). They relax the parallel trends assumption by allowing the counterfactual difference between treated and control units to lie within the convex hull of the differences observed in the two most recent pre-treatment periods ($t = 0$ and $t = -1$). By taking the convex hull of the last two differences, they are saying: the counterfactual evolution cannot jump outside the range spanned by recent dynamics. If the differences between groups have been changing slowly, then the most recent differences provide a plausible envelope for what would have happened in the absence of treatment. This is weaker than requiring parallelism and rules out wild deviations inconsistent with observed history. Analogously, in our setting, we extend this idea by applying the same type of convex-hull relaxation. We consider three main relaxations, where we can either only use the two most recent periods, all the past periods, or all the past periods with higher weights to the most recent ones. In all the cases, we provide the corresponding bounds. We keep the same notation as before, but now, we have that $t \in \{-T_1, \dots, 0, 1\}$. The three relaxations are given by the following assumptions:

Assumption 3. (*Relaxation I*)

For every category c_k where $k = 1, \dots, p$, we have:

$$\log(q_{1,1}^N(c_k)) - \log(q_{0,1}^N(c_k)) \in \text{Conv} \left\{ \log \left(\frac{q_{1,0}^N(c_k)}{q_{0,0}^N(c_k)} \right), \log \left(\frac{q_{1,-1}^N(c_k)}{q_{0,-1}^N(c_k)} \right) \right\}.$$

Assumption 4. (*Relaxation II*)

For every category c_k where $k = 1, \dots, p$, we have:

$$\log(q_{1,1}^N(c_k)) - \log(q_{0,1}^N(c_k)) \in \text{Conv} \left\{ \min_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \max_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\}.$$

Assumption 5. (*Relaxation III*)

For every category c_k where $k = 1, \dots, p$, we have for $\omega_t \geq 0, \omega_t > \omega_{t-1}$

$$\log(q_{1,1}^N(c_k)) - \log(q_{0,1}^N(c_k)) \in \text{Conv} \left\{ \min_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \max_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\}.$$

In all the cases, the assumption ensures that deviations from parallelism in the pre-treatment periods are accounted for, while still preserving enough structure to obtain informative bounds on the counterfactual. In practice, the researcher can consider only one of the case. Under Assumption 3, identification relies on a simple two-period comparison (the two most recent periods). Assumption 4 extends this logic to multiple pre-treatment periods, enabling the use of more temporal information, which may lead to wider bounds. Assumption 5 further introduces weighted relaxations through the parameters ω_t . For instance, periods closer to the treatment date might receive larger weights if they are believed to be more informative about counterfactual dynamics. The bounds for the quantities would also translate into bounds for the distributions. The key observation to derive the bounds for the counterfactual is that the convex hull of any two vectors in \mathbb{R}^p can be characterized componentwise by taking the minimum and maximum of each coordinate. Intuitively, this is because the convex hull is the smallest set containing both vectors and every possible weighted average of them. For each coordinate, all convex combinations lie between the smallest and largest value of that coordinate, so the lower and upper bounds are just the componentwise minimum and maximum. The identified set is the collection of all quantities that are consistent with the data and the model assumptions.

Theorem 2 (Partial Identification).

Under assumptions 1, and 3, for all $\{c_k, k = 1, \dots, p\}$, we have:

$$b_{min}^k = \exp \left(\min \left\{ \log \left(\frac{q_{1,0}^N(c_k)}{q_{0,0}^N(c_k)} \right), \log \left(\frac{q_{1,-1}^N(c_k)}{q_{0,-1}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

$$b_{max}^k = \exp \left(\max \left\{ \log \left(\frac{q_{1,0}^N(c_k)}{q_{0,0}^N(c_k)} \right), \log \left(\frac{q_{1,-1}^N(c_k)}{q_{0,-1}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

Under assumptions 1, and 4, for all $\{c_k, k = 1, \dots, p\}$, we have:

$$b_{min}^k = \exp \left(\min \left\{ \min_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \min_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

$$b_{max}^k = \exp \left(\max \left\{ \min_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \min_{t < 0} \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

Under assumptions 1, and 5, for all $\{c_k, k = 1, \dots, p\}$, we have:

$$b_{min}^k = \exp \left(\min \left\{ \min_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \min_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

$$b_{max}^k = \exp \left(\max \left\{ \min_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right), \min_{t < 0} \omega_t \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) \right\} + \log(q_{0,1}^N(c_k)) \right),$$

In all the cases, we have the following bounds for the treatment effect:

$$GTT(c_k) \in \left[\frac{q_{1,1}^I(c_k)}{b_{max}^k} - 1, \frac{q_{1,1}^I(c_k)}{b_{min}^k} - 1 \right],$$

$$GTT \in \left[\frac{\sum_{k=1}^p q_{1,1}^I(c_k)}{\sum_{k=1}^p b_{max}^k} - 1, \frac{\sum_{k=1}^p q_{1,1}^I(c_k)}{\sum_{k=1}^p b_{min}^k} - 1, \right]$$

$$CTT \in \left\{ \pi \in \mathcal{S}^{p-1} : \pi = \pi_{1,1}^I \ominus s, s \in \ell^{-1} \left(\left\{ r \in \mathbb{R}^{p-1} \mid \log(b_{min}^k) \leq r_k \leq \log(b_{max}^k) \right\} \right) \right\}.$$

Theorem 2 provides a unified set of partial identification results for the counterfactual treatment effects under progressively different relaxations. Each set of assumptions 3, 4, and 5 represents a distinct way to relax the canonical parallel growths assumption, allowing for more flexibility while maintaining interpretability and structure in the evolution of shares across treatment and control groups. In all three cases, the bounds $[b_{min}^k, b_{max}^k]$ define the identified set for the counterfactual category-level quantities, which in turn determine bounds for three related treatment effect measures.

2.2. Staggered adoption. In this section, we extend the staggered treatment adoption framework of [Callaway and Sant’Anna \(2021\)](#), originally developed for scalar outcomes, to the setting of categorical outcomes. Such designs are increasingly common in applied policy evaluation, where reforms or programs are rolled out gradually across units rather than implemented simultaneously. We consider a panel of n units observed over periods $t = 0, 1, \dots, T$. Let $D_{i,t} \in \{0, 1\}$ indicate whether unit i is treated in period t . We impose the standard irreversibility assumption:

Assumption 6 (Irreversibility of Treatment). *No unit is treated at baseline: $D_{i,0} = 0$ almost surely. Moreover, treatment is permanent: if $D_{i,t-1} = 1$, then $D_{i,t} = 1$ for all $t = 1, \dots, T$.*

Under this assumption, each unit that ever receives treatment has a well-defined first treatment time, denoted $G_i = \min\{t : D_{i,t} = 1\}$. Units never treated are assigned $G_i = \infty$. This partitions the sample into cohorts: for each $g \in \{1, \dots, T\}$, group G_g consists of units first treated in period g ; the never-treated group is G_∞ . Our outcome of interest is categorical: for each group and time, we observe a vector of positive quantities $q_{G_g,t}$. We also work with the associated share vector $\pi_{G_g,t} = q_{G_g,t} / \sum_{k=1}^p q_{G_g,t}(c_k)$.

For each cohort G_g , we observe pre-treatment (untreated) outcomes for all $t < g$, and post-treatment (treated) outcomes for $t \geq g$. Our goal is to identify the counterfactual untreated quantity $q_{G_g,t}^N$ for $t \geq g$. Let $\bar{g} = \max\{G_i : G_i < \infty\}$ denote the last period in which any unit is first treated, and define $\mathcal{G} = \text{Supp}(G) \setminus \{\bar{g}\}$ as the set of all treated cohorts except the last one. (The last cohort cannot be used as a control for itself under our second identification strategy, as explained below). We propose two identification strategies, both generalizing the parallel growths assumption (assumption 2) to the staggered setting:

Assumption 7 (Parallel Growths : Never-Treated Control). *For every $g \in \mathcal{G}$ and every $t \geq g$,*

$$\log(q_{G_g,t}^N) - \log(q_{G_\infty,t}^N) = \log(q_{G_g,t-1}^N) - \log(q_{G_\infty,t-1}^N).$$

Assumption 8 (Parallel Growths : Not-Yet-Treated Controls). *For every $g \in \mathcal{G}$, and for all s, t such that $t \geq g$ and $t \leq s < \bar{g}$,*

$$\log(q_{G_g,t}^N) - \log(q_{G_s,t}^N) = \log(q_{G_g,t-1}^N) - \log(q_{G_s,t-1}^N).$$

Assumption 7 states that, in the absence of treatment, the log-quantity paths of cohort G_g and the never-treated group G_∞ evolve in parallel. Assumption 8 replaces the never-treated group with not-yet-treated cohorts G_s (those first treated after time t), which serve as internal controls. These conditions enable us to identify counterfactuals by extrapolating pre-treatment log-gaps into post-treatment periods. The resulting identification formulas are constructive, interpretable, and directly estimable from observed data, as formalized in the following theorem.

Theorem 3 (Identification). *Under Assumption 7, for every $g \in \{1, \dots, T\}$ and every $t \geq g$,*

$$q_{G_g,t}^N = \exp \left(\log q_{G_g,g-1}^N + \log q_{G_\infty,t}^N - \log q_{G_\infty,g-1}^N \right).$$

Under Assumption 8, for every $g \in \mathcal{G}$ and every $t \geq g$, and for any s such that $t < s \leq \bar{g}$ (i.e., G_s is not treated by time t),

$$q_{G_g,t}^N = \exp \left(\log q_{G_g,g-1}^N + \log q_{G_s,t}^N - \log q_{G_s,g-1}^N \right).$$

The corresponding distributions are obtained by normalizing the counterfactual quantities and the total by summing them.

2.3. Synthetic CoDiD. Now suppose we have a setting with $G > 2$ groups observed over $T > 2$ time periods. Only the first group ($g = 1$) receives treatment, beginning after period T_0 ; all other groups ($g = 2, \dots, G$) serve as never-treated controls. In this context, [Arkhangelsky et al. \(2021\)](#) propose the Synthetic difference-in-differences (SDID) method, an extension of the classic DiD framework that constructs a data-driven synthetic control by optimally reweighting the control units to best reproduce the pre-treatment trajectory of the treated unit. This improves the credibility of post-treatment comparisons by enforcing a stronger pre-treatment fit than standard DiD. In this section, we adapt SDID to settings where the outcome is a categorical quantity vector—for example, expenditures across categories, counts of events by type, or any positive-valued composition. For each group g and time t , let $q_{g,t}$ denote the vector of quantities across p categories, and let T_0 be the last pre-treatment period. Our objective is to estimate treatment effects on both GTT and CTT. The procedure is applied category by category; for clarity of exposition, we suppress the category index (c_k) in what follows, noting that all steps are repeated for each component of the quantity vector.

- **Find Unit Weights**(ω^*): We find weights for the control groups so that their weighted pre-treatment path best matches the pre-treatment path of the treated group.

$$\omega^* = \arg \min_{\omega \in \mathcal{S}^{J-1}} \sum_{t=1}^{T_0} \left\| \log(\mathbf{q}_{1,t}) - \sum_{g=2}^G \omega_g \log(\mathbf{q}_{g,t}) \right\|^2.$$

- **Find Time Weights** (λ^*): We find weights for the pre-treatment time periods so that the pre-treatment average of the controls best matches their post-treatment average.

$$\lambda^* = \arg \min_{\lambda \in \mathcal{S}^{T_0-1}} \sum_{g=2}^G \left\| \frac{1}{T-T_0} \sum_{t=T_0+1}^T \log(\mathbf{q}_{g,t}) - \sum_{t=1}^{T_0} \lambda_t \log(\mathbf{q}_{g,t}) \right\|^2.$$

The average categorical quantities are obtained by:

$$\begin{aligned} (\text{Treated, Before}) \quad \mathbf{q}_{\text{treated,pre}} &= \exp \left(\sum_{t=1}^{T_0} \lambda_t^* \log(\mathbf{q}_{1,t}) \right). \\ (\text{Treated, After}) \quad \mathbf{q}_{\text{treated,post}} &= \exp \left(\sum_{t=T_0+1}^T \frac{1}{T-T_0} \ell(\mathbf{q}_{1,t}) \right). \\ (\text{Control, Before}) \quad \mathbf{q}_{\text{control,pre}} &= \exp \left(\sum_{g=2}^G \sum_{t=1}^{T_0} \omega_g^* \lambda_t^* \log(\mathbf{q}_{g,t}) \right). \\ (\text{Control, After}) \quad \mathbf{q}_{\text{control,post}} &= \exp \left(\sum_{g=2}^G \sum_{t=T_0+1}^T \omega_g^* \frac{1}{T-T_0} \log(\mathbf{q}_{g,t}) \right). \end{aligned}$$

Finally, we calculate the average growth treatment effect.

$$\text{GTT} = \frac{\mathbf{q}_{\text{treated,post}}}{\mathbf{q}_{\text{treated,pre}} + \mathbf{q}_{\text{control,post}} - \mathbf{q}_{\text{control,pre}}} - 1.$$

We then construct four key average distributions by normalizing across categories, we obtain the corresponding distributions: $\boldsymbol{\pi}_{\text{treated,pre}}$, $\boldsymbol{\pi}_{\text{treated,post}}$, $\boldsymbol{\pi}_{\text{control,pre}}$, $\boldsymbol{\pi}_{\text{control,post}}$.

In our probability space, we use operations \ominus (perturbation-difference) and \oplus (perturbation-addition) instead of regular subtraction and addition. The Compositional Treatment Effect (CTT) is defined as:

$$\text{CTT} = (\boldsymbol{\pi}_{\text{treated,post}} \ominus \boldsymbol{\pi}_{\text{control,post}}) \oplus (\boldsymbol{\pi}_{\text{treated,pre}} \ominus \boldsymbol{\pi}_{\text{control,pre}}).$$

This effect shows how the treatment changed the probability distribution for the treated group, relative to the change experienced by the synthetic control group. It tells us which categories gained or lost probability mass because of the treatment.

3. CONNEXIONS WITH EXISTING APPROACHES

In this section, we discuss the link between our method and existing methods in the literature.

3.1. Connexion with Logistic model. Recall: $Y_{it} \in \{c_1, c_2, \dots, c_p\}$: outcome for unit i at time t , $G_i \in \{0, 1\}$: group indicator (1 = treated), $T_t \in \{0, 1\}$: time indicator (1 = post), Interaction: $D_{it} = G_i \cdot T_t$ (standard DiD treatment indicator). Pick category c_p as the baseline. The two-way fixed effects multinomial logit model without covariates is:

$$\mathbb{P}(Y_{it} = c_k \mid G_i, T_t) = \frac{\exp(\alpha_k + \delta_k G_i + \gamma_k T_t + \beta_k D_{it})}{1 + \sum_{g=1}^{p-1} \exp(\alpha_g + \beta_g G_i + \gamma_g T_t + \delta_g D_{it})}, \quad k = 1, \dots, p-1.$$

This specification is fully saturated: for each non-baseline outcome category c_k , the model includes four parameters, an intercept α_k , a group effect δ_k , a time effect γ_k , and an interaction term β_k , which together exactly span the log-odds in all four group–time cells. The interaction coefficient β_k captures the difference-in-differences contrast in log-odds and admits a causal interpretation under the assumption of parallel trends on the log-odds. Our compositional treatment effect parameter (CTT) can be linked to the coefficients of a multinomial logit model as follows:

$$CTT = \ell^{-1}(\beta_1, \beta_2, \dots, \beta_{p-1}),$$

where $\ell^{-1}(\cdot)$ denotes the inverse compositional log-ratio transformation, which maps the vector of log-odds coefficients back into category shares. Although using the multinomial logit representation coincides with our approach to modeling category shares in the simple (2×2) setup, several conceptual and practical differences are worth emphasizing.

The first key difference is that the multinomial logit model does not directly yield counterfactual quantities without imposing additional structural assumptions. In contrast, our approach provides these counterfactuals constructively, enabling the recovery of both treatment effects on quantities and on shares within a unified framework. Second, in settings with multiple time periods, the multinomial logit specification offers no straightforward way to

relax the identifying assumptions when they appear violated. Our framework, however, accommodates such relaxations naturally, formalized through assumptions 3, 4, and 5 allowing for partial identification. Third, when treatment timing varies across units (staggered adoption), the multinomial logit model requires estimating a full vector of time-varying treatment effect coefficients. By contrast, our method allows the estimation of treatment effect for each post-treatment period independently, without the need for joint optimization or functional minimization. This feature makes our approach computationally lighter. Finally, the Compositional Treatment Effect (CTT) parameter provides a direct and interpretable measure of the treatment’s impact on category shares. Operating within the space of compositional data, it connects naturally to discrete choice theory and can be naturally used in applications where proportions or probabilities, rather than levels, constitute the primary outcomes of interest.

3.2. Unified view with DiD and CiC. Our method identifies the counterfactual probability mass function for unordered categorical outcomes. We show how the identifying assumption relates to parallel trends (DiD) and rank invariance (CiC). DiD targets objects like expectations, CiC targets the CDF for ordered outcomes, and CoDiD extends the same logic to the PMF for unordered outcomes. We proceed in two steps. First, we show that DiD and CiC, although targeting different objects (means versus CDFs), share the same geometric identification logic. Second, we show how CoDiD applies that logic to probability mass functions. A recall of the setup: we consider two groups $g \in 0, 1$ (treatment and control), observed in two periods $t \in 0, 1$. Let $m_{g,t}^N$ denote the potential parameter of interest for unit g at time t in the absence of treatment.

In DiD, the parameter of interest $m_{g,t}^N$ is the expectation of some individual-level outcome, $m_{g,t}^N = E(Y_{g,t}^N)$. The construction of the counterfactual is given by:

$$E(Y_{1,1}^N) = E(Y_{1,0}^N) \underbrace{- E(Y_{0,0}^N) + E(Y_{0,1}^N)}_{\text{control group change over time}}.$$

In CiC, the parameter of interest $m_{g,t}^N$ is the cumulative distribution function of some individual-level outcome, $m_{g,t}^N = F_{Y_{g,t}^q}$. The construction of the counterfactual is given by:

$$F_{Y_{1,1}^N} = F_{Y_{1,0}^N} \circ \underbrace{F_{Y_{0,0}^N}^{-1} \circ F_{Y_{0,1}^N}}_{\text{control group change over time}}.$$

DiD and CiC share a simple underlying idea: the object of interest exists within a space where the notion of movement can be well-defined, and there is a transformation that characterizes how the control group evolves within this space. To obtain the counterfactual for the treated group, we then apply the same transformation to the treated group. Mathematically, if the control group moves from $m_{0,0}^N$ to $m_{0,1}^N$, we write:

$$m_{0,1}^N = \varphi^c(m_{0,0}^N),$$

where φ^c captures the change or movement in the control group. The counterfactual for the treated group is then obtained by applying the same transformation to the initial state of the treated group $m_{1,0}^N$:

$$m_{1,1}^N = \varphi^c(m_{1,0}^N).$$

In DiD:

$$\forall m \in \mathbb{R}, \quad \varphi^c(m) = m - E_{Y_{0,0}^N} + E_{Y_{0,1}^N}. \quad (10)$$

In CiC:

$$\forall F \in \mathcal{F}, \quad \varphi^c(F) = F \circ F_{Y_{0,0}^N}^{-1} \circ F_{Y_{0,1}^N}. \quad (11)$$

where \mathcal{F} is the space of cumulative distribution functions. The map φ^c has the same interpretation in both methods and can be understood as a translation map. If we want to use a map to define the idea of movement within a space. A natural way to formalize that is through the concept of translation. A translation operator is defined as an operator that shifts points by a certain amount in a certain direction. We consider a general definition of this operator. Intuitively, suppose the outcome space forms a group, meaning it is a set of objects equipped with a binary operation that can help define the idea of movement (moves that can be combined, reversed, and have a neutral element that does nothing). These moves can be addition (for numeric outcomes) or function composition (for distributional transformations). Let's start with the formal definition of a group.

Definition 1 (Group). *A group (G, \wedge) consists of a set G and a binary operation*

$$\wedge : G \times G \rightarrow G, \quad (a, b) \mapsto a \wedge b,$$

satisfying the following axioms: i) Associativity: $(a \wedge b) \wedge c = a \wedge (b \wedge c)$ for all $a, b, c \in G$. ii) Identity: There exists $e \in G$ such that $e \wedge a = a \wedge e = a$ for all $a \in G$. iii) Inverses: For each $a \in G$, there exists $a^{-1} \in G$ such that $a^{-1} \wedge a = a \wedge a^{-1} = e$.

For example, in DiD, the outcome space is \mathbb{R} with addition $+$ as the group operation, identity $e = 0$, and inverse given by negation $-a$. In CiC, the outcome space is the set of cumulative distribution functions, the operation is composition \circ , the identity is the identity function $Id(x) = x$, and the inverse is the quantile function. Once the group structure is defined, we can formalize the idea of a movement using translations.

Definition 2 (Right Translation Operator ([Hamilton, 2017](#))). *Let (G, \wedge) be a group with identity element e . For a fixed $h \in G$, the left translation by h is the map:*

$$R_h : G \rightarrow G, \quad R_h(m) := m \wedge h, \quad \forall h \in G.$$

If you start at m , you then apply h on the right, ending at $m \wedge h$. Think of shifting relative to where you already are, like taking your current position and then performing the move locally. This formalizes the notion of a shift or transformation acting consistently across the entire outcome space. From this perspective, the map φ^c can be identified as the unique right translation that captures how the control group evolves over time.

In DiD, φ^c is the right translation operator defining how the control group has moved from its initial state. We have that:

$$\varphi^c(m) = R_h(m) = m + h.$$

Since $\varphi^c(E(Y_{0,0}^N)) = E(Y_{0,1}^N)$, it implies that $h = E(Y_{0,1}^N) - E(Y_{0,0}^N)$. We therefore obtain that:

$$\varphi^c(m) = m + E(Y_{0,1}^N) - E(Y_{0,0}^N).$$

Graphically, it can be represented in figure [4](#)

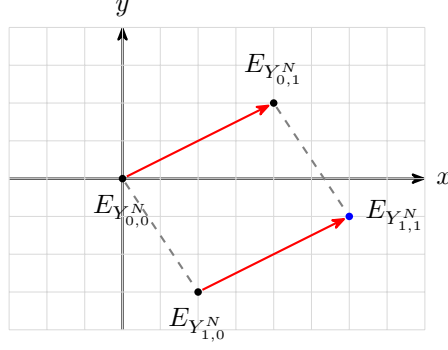


Figure 4. Geometric Illustration of parallel trends

In CiC, φ^c is also the left translation operator defining how the control group has moved from its initial state. We have that:

$$\varphi^c(F) = R_h(F) = F \circ h.$$

Since $\varphi^c(F_{Y_{0,0}^N}) = F_{Y_{0,1}^N}$, it implies that $h = F_{Y_{0,0}^N}^{-1} \circ F_{Y_{0,1}^N}$. We therefore obtain that:

$$\varphi^c(F) = F \circ F_{Y_{0,0}^N}^{-1} \circ F_{Y_{0,1}^N}.$$

Graphically, we can illustrate through figure 5. The uniqueness of φ^c is what guarantees

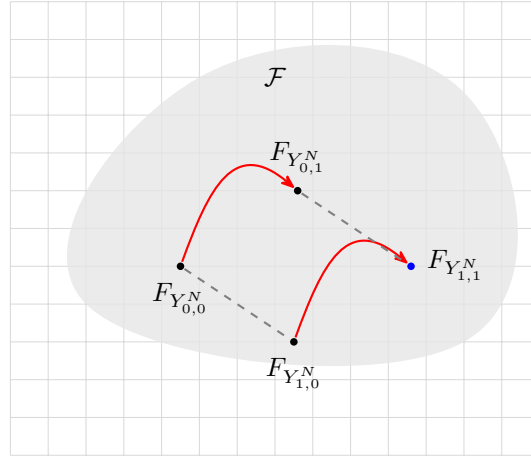


Figure 5. Geometric illustration of Rank invariance

point identification. If multiple transformations could map the control group across periods, the counterfactual is no longer unique. In that case, we have identified a set of feasible outcomes, as in the case of Changes-in-Changes (CiC) with a discrete ordered outcome.

CoDiD shares this same logic, but for probability mass functions, where the space is the simplex. Here, the parameter of interest $m_{g,t}^N$ is the probability mass function, $m_{g,t}^N = \pi_{g,t}^N$.

The construction of the counterfactual is given by:

$$\pi_{1,1}^N = \pi_{1,0}^N \underbrace{\ominus \pi_{0,0}^N \oplus \pi_{0,1}^N}_{\text{control group change over time}}.$$

The control group map is therefore defined in this way:

$$\forall \pi \in \mathcal{S}^{p-1}, \quad \varphi^c(\pi) = \pi \ominus \pi_{0,0}^N \oplus \pi_{0,1}^N. \quad (12)$$

In CoDiD, the group is the simplex equipped with the perturbation operator (\oplus). In that method, φ^c is also a right translator operator defined as:

$$\varphi^c(\pi) = R_h(\pi) = \pi \oplus h.$$

Since $\varphi^c(\pi_{0,0}^N) = \pi_{0,1}^N$, it implies that $h = \ominus \pi_{0,0}^N \oplus \pi_{0,1}^N$. We therefore obtain that:

$$\varphi^c(\pi) = \pi \ominus \pi_{0,0}^N \oplus \pi_{0,1}^N$$

That unified logic breaks down if we use the Euclidean group structure for the simplex (doing parallel trends on proportions). In fact, when we restrict to the simplex, the structure no longer forms a group since the neutral element would have to be the zero vector (which is not part of the simplex). In contrast, under our formulation, the group structure is preserved, ensuring consistency with DiD and CiC. Table 1 summarizes this comparison. Let \mathcal{F} , be the space of non-decreasing real functions.

Table 1. Comparison of Identification Strategies

Method	Outcome Type	Geometric Space	Control group map
parallel trends (DiD)	Expectation	\mathbb{R} (Euclidean)	$m \mapsto m - E_{Y_{0,0}^N} + E_{Y_{0,1}^N}$
Rank Invariance (CiC)	CDF	\mathcal{F}	$F \mapsto F \circ F_{Y_{0,0}^N}^{-1} \circ F_{Y_{0,1}^N}$
parallel growths (CoDiD)	PMF	Aitchison simplex	$\pi \mapsto \pi \ominus \pi_{0,0}^N \oplus \pi_{0,1}^N$

4. APPLICATIONS

This section presents two empirical applications. The first examines the effect of early voting policies on voter support decisions in U.S. presidential elections. The second evaluates the impact of the regional greenhouse gas initiative (RGGI) on the composition of electricity generation across energy sources.

4.1. Impact of early voting law on distributions of voters’ support across parties.

Early voting allows registered voters to cast their ballots in person or by mail before Election Day. We evaluate the effect of this policy on voter decisions using the compositional difference-in-differences (CoDiD) framework. A credible analysis requires comparing states with similar political, social, and demographic characteristics so that observed differences in voter participation can be attributed to early voting rather than to preexisting trends. The treatment group includes Maryland and New Jersey, which introduced early voting before 2008, while Pennsylvania and New York serve as the control group. These states are geographically close, share comparable demographic and political profiles, and consistently supported Democratic presidential candidates from 1992 to 2004, indicating similar partisan alignment and voting behavior during the pre-treatment period. Table 2 reports their racial and ethnic composition around 2007 to further contextualize the comparison. This

Table 2. Population Composition in 2007

State/Group	Total Pop. (2007)	White	Black/ Afr. Am.	Am. Ind./ Alaska Nat.	Asian	Two or More Races	Hispanic Latino	White, not Hisp.
Maryland	5,618,344	63.6%	29.5%	0.3%	5.0%	1.6%	6.3%	58.1%
New Jersey	8,685,920	76.3%	14.5%	0.3%	7.5%	1.3%	15.9%	62.2%
MD+NJ	14,304,264	71.3%	20.8%	0.3%	6.5%	1.4%	12.1%	60.5%
New York	19,297,729	73.6%	17.3%	0.5%	6.9%	1.5%	16.4%	60.3%
Pennsylvania	12,432,792	85.6%	10.8%	0.2%	2.4%	1.0%	4.5%	81.8%
NY+PA	31,730,521	78.0%	14.5%	0.4%	5.0%	1.3%	11.7%	69.9%

Source: U.S. Census Bureau, Population Division, released May 1, 2008

table shows that the two groups have almost similar racial compositions. Combined with their geographic proximity and political alignment over the study period, this makes them well-suited for causal analysis. The outcome of interest is the voter’s support across three categories, Democrats, Republicans, and Others. We consider that from 1992 elections to 2008. These data are publicly available and consistently reported across states. We start by plotting the log-counts to assess the plausibility of parallel growths. Figure 6 displays the evolution of log transformations of each party vote counts across 5 presidential elections. The dotted red line denotes the pre-treatment elections, while the purple line indicates the

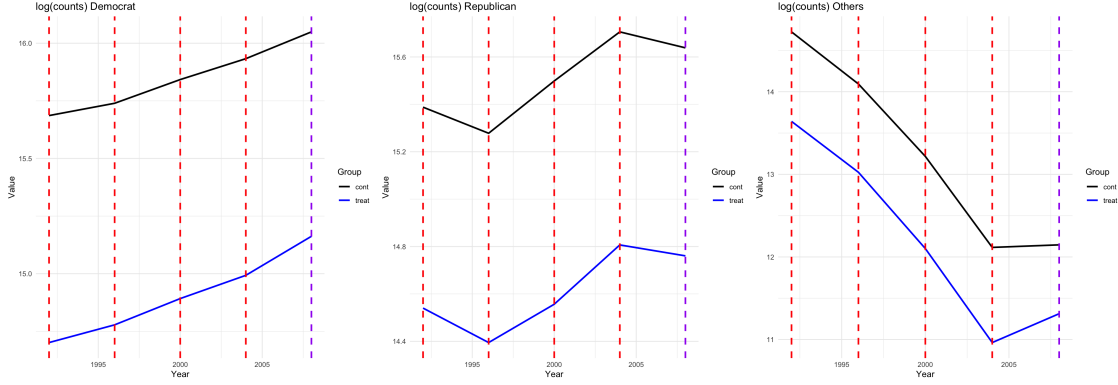


Figure 6. log-ratios evolution 1992-2008 (treated vs. control)

post-treatment election. In the pre-treatment period, both states exhibit broadly parallel trajectories in log-counts, suggesting comparable underlying voter dynamics before the policy change. This visual similarity reinforces the plausibility of the identification strategy. In this empirical illustration, neither parallel trends on raw proportions nor parallel trends on quantity data provide an appropriate comparison, as evidenced by figure 7 and figure 8

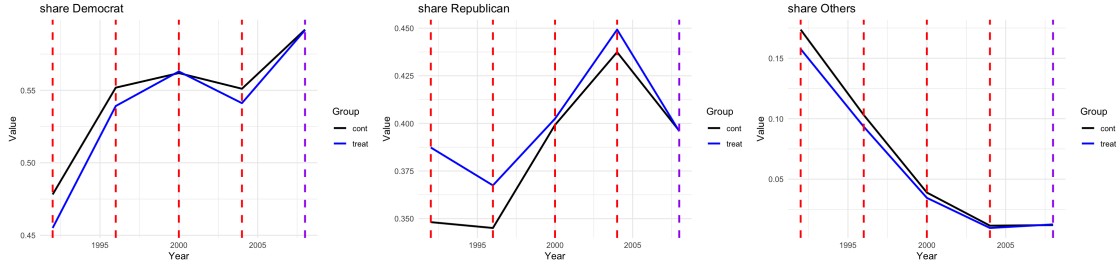


Figure 7. shares evolution 1992-2008 (treated vs. control)

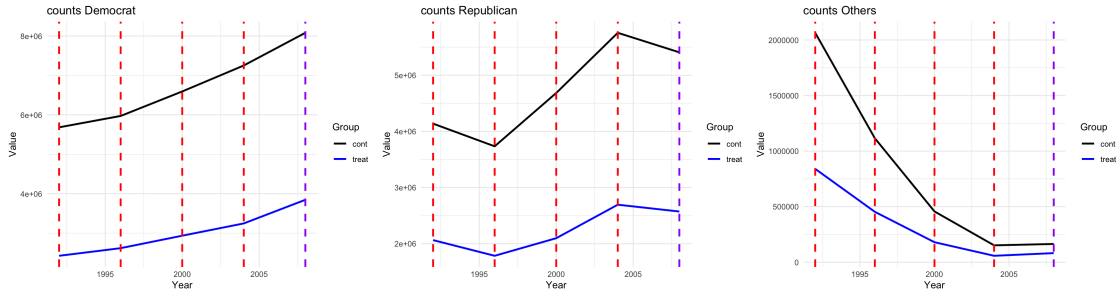


Figure 8. quantities evolution 1992-2008 (treated vs. control)

Our method appears to be the most appropriate in this context, as it relies on the visual assessment of parallel trends between the treatment and control groups. The observed

similarity in pre-treatment trajectories provides reassuring evidence that the identifying assumptions are reasonable, thereby strengthening the credibility of the causal analysis.

Empirical findings We begin by examining how the treatment affected the total number of votes cast for each party. Table 3 reports the estimated Growth Treatment Effects (GTT), that is, the proportional increase in votes due to the treatment, along with 95% confidence intervals obtained via the bootstrap procedure described in appendix C. Overall, the policy

Table 3. Estimated growth treatment effects

Party	Estimate [95% CI]
Democrat	0.0545 [0.0533, 0.0557]
Republican	0.0214 [0.0199, 0.0230]
Other	0.3747 [0.3578, 0.3915]
Total	0.0441 [0.0441, 0.0443]

increased turnout by around 4.4%, demonstrating that early voting can mobilize more voters. This finding is consistent with the existing literature on the effects of early voting. All three categories experienced a statistically significant increase in votes, although the magnitude of the effect varies considerably. The Democratic Party saw a modest 5.5% increase, while the Republican Party experienced a smaller rise of about 2.1%. In contrast, support for Other parties, which includes third-party and independent candidates, grew by nearly 37.5%, representing a much larger relative gain. Importantly, because “Other” parties started from a much smaller base, even a modest absolute increase translates into a large percentage change. Focusing on the two major parties, the Democratic Party benefited more from the policy than the Republican Party. This aligns with the results in [Berry et al. \(2025\)](#), which also found that such policies tend to favor Democrats over Republicans. However, we exercise caution in interpreting these results, as the states we selected were already Democratic-leaning during this period.

The next table presents the results for the compositional treatment effects (CTT). Table 4 presents the estimated CTT for the 2008 election. Each entry represents the post-treatment

Table 4. Estimated CTT for 2008 elections

Party	Estimate	95% CI Lower	95% CI Upper
Democrat	0.3136	0.3119	0.3151
Republican	0.2998	0.2982	0.3012
Other	0.3867	0.3838	0.3898

probability of selecting a given party, under a counterfactual scenario where, before treatment, all parties were equally likely (i.e., each had a baseline probability of 1/3). The results show a clear reallocation of voter preference. After the treatment: the probability of voting for “Other” rises to 38.7%, up from the baseline of 33.3%. The probability of voting Republican falls to 30.0%. The probability of voting Democratic also declines slightly, to 31.4%, but remains higher than that of Republicans. Thus, while both major parties lose relative appeal, Republicans lose more ground than Democrats, and third-party candidates gain the most in relative terms. This suggests the treatment not only increased overall turnout but also reshaped the internal composition of voter choice, pulling support more toward alternative options. This finding is interesting because most prior work focuses exclusively on the two major parties. Our analysis reveals that policy interventions or informational treatments can meaningfully affect the electoral relevance of minor parties, a dimension often overlooked in the literature. It is worth emphasizing that this shift is purely relative: the overall ranking of parties by actual vote share in the treated states remains unchanged (Democrats first, Republicans second, Others third). Hence, the treatment does not overturn the existing political hierarchy, but it does narrow the gap between major and minor parties in terms of voter consideration.

4.2. Impact of RGGI on electricity generation composition. In this section, we study how the Regional Greenhouse Gas Initiative (RGGI) affected the mix of electricity generation in participating states. RGGI, launched in 2009, is a cooperative, market-based program among Connecticut, Delaware, Maine, Maryland, Massachusetts, New Hampshire, New York, Rhode Island, and Vermont. Its goal is to cap and reduce carbon emissions from the power sector. The program works by setting a regional cap on total carbon dioxide emissions from power plants and issuing a limited number of tradable allowances. Each

allowance gives a power plant the right to emit one short ton of carbon dioxide. States distribute these allowances through quarterly auctions. The revenue from these auctions is reinvested in energy efficiency, renewable energy, and other programs that benefit consumers. Evaluating the impact of the Regional Greenhouse Gas Initiative (RGGI) on electricity generation is an interesting causal question because it reveals whether the policy effectively shifts energy production toward cleaner sources and reduces carbon emissions. We analyze U.S. electricity generation data, which is publicly available on the U.S. Energy Information Administration’s website (<https://www.eia.gov/electricity/data/state/>). This dataset provides annual electricity generation figures in megawatts by energy source for each state. We consider the following four categories of energy sources: gas (combining natural gas and other gases), coal and oil (combining coal and petroleum), nuclear (corresponding solely to the nuclear category), and renewables (combining hydroelectric, conventional, solar thermal and photovoltaic, geothermal, wind, and wood and wood-derived fuel). For each state and year, we observe the number of megawatts generated by different sources, and we aggregate these into two groups: the treated group and the control group. In constructing the control group, we exclude states that either joined RGGI, are strongly affected by leakage through electricity market integration, or implemented their own carbon pricing policies. In particular, Pennsylvania, West Virginia, Virginia, and Ohio are excluded due to their geographic proximity and electricity market linkages with RGGI states, which expose them to leakage and anticipatory effects. In fact, electricity markets in the U.S. Northeast and Mid-Atlantic are highly integrated (PJM, NYISO, ISO-NE), including these states in the control group risks contamination. California, Washington, and Oregon are also excluded, since those states adopted cap-and-trade or cap-and-invest programs that constitute carbon pricing mechanisms similar in nature to RGGI. Including them in the control pool would compromise the validity of the counterfactual by mixing treated and untreated units. The program was organized into three-year compliance periods, with the first spanning January 1, 2009, to December 31, 2011. We focus our analysis on this initial period because the parallel growth assumption becomes progressively less plausible over longer time horizons. Here, we also assess the validity of the parallel growths assumption by plotting both the raw quantities and their logarithmic transformations over the study period (2000-2011). As shown in Figure 10, the log-quantity trajectories for the treated and control groups move approximately in parallel during the pre-treatment period, supporting the plausibility of the

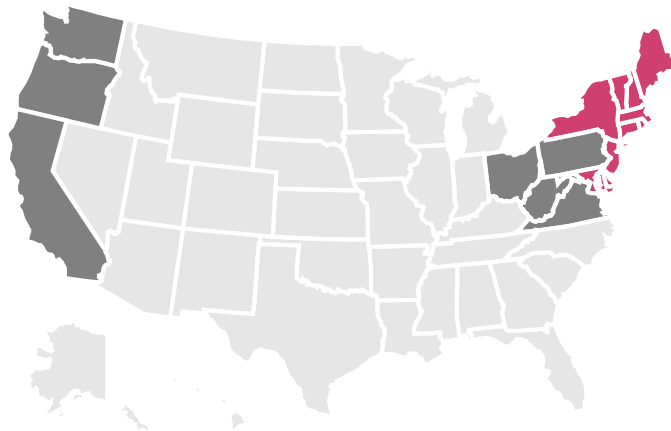


Figure 9. Map of the United States showing the nine RGGI states in purple and six excluded control states (due to market leakage or carbon pricing policies) in dark gray, and the control group consists of the gray states.

assumption. We examine the impact of RGGI over the first three years of implementation

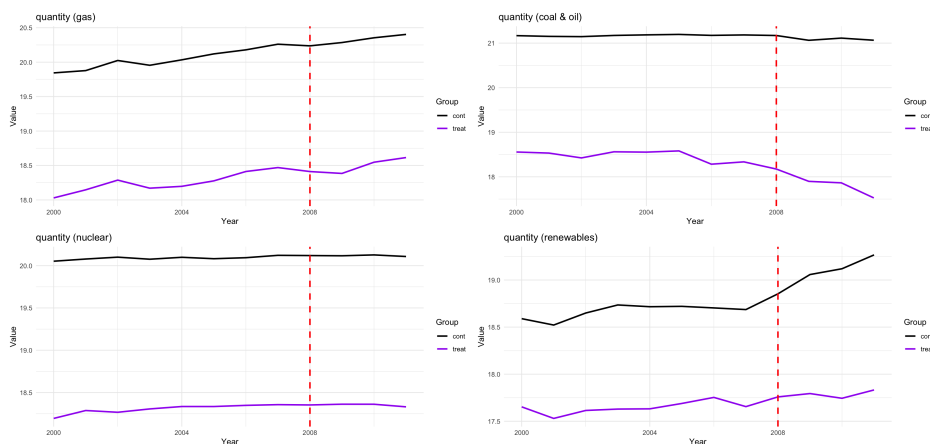
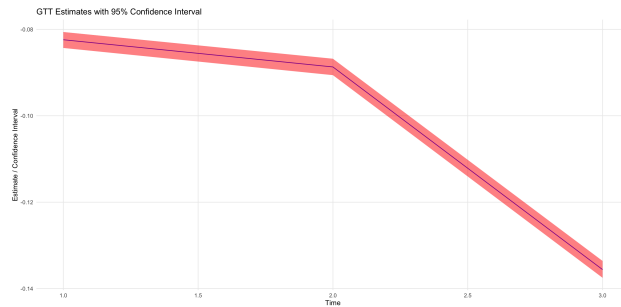


Figure 10. log-quantity evolution 2000-2011 (treated vs control group)

(2009–2011), corresponding to the program’s initial compliance period. As shown in the dynamic estimates below, the policy induced a statistically significant and growing reduction in total electricity generation (see figure 11). These results show an 8.2% decline in total electricity generation in the first year, increasing to 8.9% in the second year, and reaching 13.6% by the end of the initial compliance period in 2011. The growing effect suggests that RGGI not only reduced generation in the short term but also triggered accelerating adjustments over time, potentially through coal plant retirements, fuel switching, or improvements in demand-side efficiency.

**Figure 11.** GTT on total electricity production

While total output fell, the composition of generation shifted, as we can see in table 5.

Table 5. Observed and Counterfactual Shares Across Three Years

Year	Category	Observed			Counterfactual		
		Estimate	2.5%	97.5%	Estimate	2.5%	97.5%
2009	Gas	0.3179	0.3178	0.3179	0.3146	0.3130	0.3161
	coal & oil	0.1954	0.1953	0.1954	0.2123	0.2113	0.2132
	Nuclear	0.3107	0.3106	0.3107	0.2818	0.2802	0.2833
	Renewables	0.1761	0.1761	0.1762	0.1914	0.1896	0.1932
2010	Gas	0.3594	0.3593	0.3594	0.3215	0.3199	0.3231
	coal & oil	0.1815	0.1815	0.1816	0.2127	0.2117	0.2137
	Nuclear	0.2982	0.2982	0.2983	0.2716	0.2701	0.2731
	Renewables	0.1609	0.1608	0.1609	0.1942	0.1924	0.1960
2011	Gas	0.3927	0.3927	0.3928	0.3272	0.3257	0.3289
	coal & oil	0.1322	0.1322	0.1322	0.1965	0.1956	0.1974
	Nuclear	0.2955	0.2954	0.2955	0.2583	0.2568	0.2597
	Renewables	0.1796	0.1795	0.1796	0.2180	0.2161	0.2199

Over the first three years of RGGI (2009–2011), coal and oil generation fell sharply, dropping from a counterfactual share of about 21% to just 13.2% by 2011, a decline of over 8 percentage points, or nearly 40% relative to the counterfactual. Interestingly, this reduction was not primarily offset by renewables, as one might expect, but by natural gas.

Gas generation surged from a counterfactual 32.7% to an observed 39.3%, a 6.6-point increase, reflecting rapid fuel switching to a lower-carbon, flexible source. Nuclear output also rose above its counterfactual, increasing by 3.7 percentage points, suggesting that RGGI enhanced the economic value of existing zero-carbon baseload capacity. Renewables, in contrast, underperformed: despite national trends favoring wind and solar, their share in RGGI states remained below the counterfactual in all three years, ending 2011 at 18.0% versus a counterfactual of 21.8%. These patterns indicate that the early RGGI-driven transition was led by natural gas rather than renewables.

Overall, RGGI effectively reduced coal and oil dependence, achieving substantial emissions reductions, as reflected in a 13.6% decline in total generation, but primarily through fuel switching to gas and increased nuclear output, rather than new renewable deployment. This highlights the role of existing infrastructure in shaping the composition of the clean energy transition. It also reveals the importance of complementary policies, such as renewable subsidies, to accelerate the shift toward truly clean energy sources. The results are consistent with several other studies (see [Yan \(2021\)](#)).

5. CONCLUSION

This paper introduces compositional difference-in-differences (CoDiD), a causal inference framework for analyzing how treatments and policies affect entire categorical outcome quantities and distributions. It is especially suited to settings with discrete, unordered outcomes, such as employment status (employed, unemployed, out of the labor force), voting choice, or health categories, where the policy-relevant question is not whether a single average has changed, but how the composition of all categories has been reconfigured. CoDiD addresses a dual objective: it quantifies both absolute changes in total counts and relative shifts in shares (i.e., the probability mass function). This allows researchers and policymakers to identify which categories expanded or contracted, by how much, and in what combination of scale and composition. The framework is built on a parallel growths assumption, a multiplicative analog of standard parallel trends, which posits that, in the absence of treatment, the ratios of category sizes evolve proportionally over time. This assumption has a natural interpretation in random utility models: it corresponds to stable relative utility differences across categories, so that estimated effects map directly to shifts in underlying preferences. CoDiD is designed for practical use and naturally extends to richer settings, including relaxations of the identifying assumption, staggered treatment adoption, and a synthetic DiD analog for richer data contexts. A key direction for future work is the incorporation of continuous covariates, enabling adjustment for confounders and the estimation of heterogeneous treatment effects across subpopulations.

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APPENDIX A. PROOFS OF THE RESULTS IN THE MAIN TEXT

A.1. **Proof of Theorem 1.** Start from assumption 2:

$$\log \cdot (q_{1,1}^N) - \log \cdot (q_{1,0}^N) = \log \cdot (q_{0,1}^N) - \log \cdot (q_{0,0}^N).$$

Add $\log \cdot (q_{1,0}^N)$ to both sides:

$$\log \cdot (q_{1,1}^N) = \log \cdot (q_{1,0}^N) + \log \cdot (q_{0,1}^N) - \log \cdot (q_{0,0}^N). \quad (1)$$

Since all vectors are strictly positive (by Assumption 1), the logarithm is defined component-wise, and we can apply the component-wise exponential function $\exp \cdot$ to both sides of (1). Because $\exp \cdot$ and $\log \cdot$ are inverses on $\mathbb{R}_{>0}^p$, we obtain:

$$q_{1,1}^N = \exp \cdot (\log \cdot (q_{1,0}^N) + \log \cdot (q_{0,1}^N) - \log \cdot (q_{0,0}^N)).$$

By definition (implied by the structure of the model and assumption 1, the scalar $S_{1,1}^N$ is the sum of the components of the vector $q_{1,1}^N$. Let the components be indexed by c_k , for $k = 1, \dots, p$. Then:

$$S_{1,1}^N = \sum_{k=1}^p q_{1,1}^N(c_k) = \sum_{k=1}^p \exp (\log q_{1,0}^N(c_k) + \log q_{0,1}^N(c_k) - \log q_{0,0}^N(c_k)),$$

By definition (again, standard in compositional or share-based models),

$$\pi_{1,1}^N = \frac{q_{1,1}^N}{S_{1,1}^N},$$

where the division is component-wise (i.e., normalizing the vector $q_{1,1}^N$ to sum to 1). Since both numerator and denominator are identified in Steps 1 and 2, $\pi_{1,1}^N$ is identified as stated.

A.2. **Proof of proposition 1.** We consider the untreated counterfactual quantities $q_{g,t}^N(c_k) > 0$ for groups $g \in 0, 1$, times $t \in 0, 1$. Pick a baseline category c_p . Let $S_{g,t}^N = \sum_{k=1}^p q_{g,t}^N(c_k)$ be the counterfactual total for all category for group g at time t . We know that $\pi(c_k) = \frac{q_{g,t}^N(c_k)}{S_{g,t}^N}$. The log-odds for each category can be written as :

$$\log \left(\frac{\pi_{g,t}^N(c_k)}{\pi_{g,t}^N(c_p)} \right) = \log \left(\frac{q_{g,t}^N(c_k)}{S_{g,t}^N} \times \frac{S_{g,t}^N}{q_{g,t}^N(c_p)} \right) = \log(q_{g,t}^N(c_k)) - \log(q_{g,t}^N(c_p)).$$

Parallel growths implies hold for each category, so we have :

$$\log(q_{1,1}^N(c_k)) - \log(q_{1,0}^N(c_k)) = \log(q_{0,1}^N(c_k)) - \log(q_{0,0}^N(c_k)),$$

and also

$$\log(q_{1,1}^N(c_p)) - \log(q_{1,0}^N(c_p)) = \log(q_{0,1}^N(c_p)) - \log(q_{0,0}^N(c_p)).$$

Taking the difference between the two equalities gives:

$$\begin{aligned} & \{ \log(q_{1,1}^N(c_k)) - \log(q_{1,1}^N(c_p)) \} - \{ \log(q_{1,0}^N(c_k)) - \log(q_{1,0}^N(c_p)) \} = \\ & \{ \log(q_{0,1}^N(c_k)) - \log(q_{0,1}^N(c_p)) \} - \{ \log(q_{0,0}^N(c_k)) - \log(q_{0,0}^N(c_p)) \}. \end{aligned}$$

This is exactly parallel trends in log-odds :

$$\log \left(\frac{\pi_{1,1}^N(c_k)}{\pi_{1,1}^N(c_p)} \right) - \log \left(\frac{\pi_{0,1}^N(c_k)}{\pi_{0,1}^N(c_p)} \right) = \log \left(\frac{\pi_{1,0}^N(c_k)}{\pi_{1,0}^N(c_p)} \right) - \log \left(\frac{\pi_{0,0}^N(c_k)}{\pi_{0,0}^N(c_p)} \right).$$

A.3. Proof of Proposition 2. We aim to show that the parallel growths assumption in compositional form is equivalent to a parallel trends condition in log-ratio coordinates. Specifically, we prove the equivalence of the following two statements:

$$(i) \pi_{1,1}^N \ominus \pi_{0,1}^N = \pi_{1,0}^N \ominus \pi_{0,0}^N$$

$$(ii) \text{ for all } k = 1, \dots, p-1, \log \left(\frac{\pi_{1,1}^N(c_k)}{\pi_{1,1}^N(c_p)} \right) - \log \left(\frac{\pi_{0,1}^N(c_k)}{\pi_{0,1}^N(c_p)} \right) = \log \left(\frac{\pi_{1,0}^N(c_k)}{\pi_{1,0}^N(c_p)} \right) - \log \left(\frac{\pi_{0,0}^N(c_k)}{\pi_{0,0}^N(c_p)} \right).$$

Here, all share vectors π belong to the interior of the $(p-1)$ -dimensional simplex \mathcal{S}^{p-1} , and the operation \ominus denotes compositional subtraction (perturbation inverse), defined for any two compositions $\pi_1, \pi_2 \in \mathcal{S}^{p-1}$ as:

$$\pi_1 \ominus \pi_2 := \frac{1}{\sum_{k=1}^p \frac{\pi_1(c_k)}{\pi_2(c_k)}} \left(\frac{\pi_1(c_1)}{\pi_2(c_1)}, \dots, \frac{\pi_1(c_p)}{\pi_2(c_p)} \right).$$

We know that $\ell : \text{int}(\mathcal{S}^{p-1}) \rightarrow \mathbb{R}^{p-1}$ defined by:

$$\ell(\pi) = \left[\log \left(\frac{\pi(c_1)}{\pi(c_p)} \right), \dots, \log \left(\frac{\pi(c_{p-1})}{\pi(c_p)} \right) \right].$$

This map is a bijection: for any $x = (x_1, \dots, x_{p-1}) \in \mathbb{R}^{p-1}$, define $r_j = e^{x_j}$ for $j = 1, \dots, p-1$, and set

$$\pi(c_j) = \frac{r_j}{1 + \sum_{g=1}^{p-1} r_g}, \quad j = 1, \dots, p-1, \quad \pi(c_p) = \frac{1}{1 + \sum_{g=1}^{p-1} r_g}.$$

A key property of that transformation is that it linearizes the Aitchison geometry of the simplex. In particular, for any $\pi_1, \pi_2 \in \text{int}(\mathcal{S}^{p-1})$,

$$\ell(\pi_1 \ominus \pi_2) = \ell(\pi_1) - \ell(\pi_2).$$

By definition of \ominus , the k -th component of $\pi_1 \ominus \pi_2$ is proportional to $\pi_1(c_k)/\pi_2(c_k)$.

$$\begin{aligned} \ell_k(\pi_1 \ominus \pi_2) &= \log \left(\frac{(\pi_1 \ominus \pi_2)(c_k)}{(\pi_1 \ominus \pi_2)(c_p)} \right) \\ &= \log \left(\frac{\pi_1(c_k)/\pi_2(c_k)}{\pi_1(c_p)/\pi_2(c_p)} \right) \\ &= \log \left(\frac{\pi_1(c_k)}{\pi_1(c_p)} \right) - \log \left(\frac{\pi_2(c_k)}{\pi_2(c_p)} \right) \\ &= \ell_k(\pi_1) - \ell_k(\pi_2). \end{aligned}$$

Because ℓ is bijective, we have:

$$\pi_{1,1}^N \ominus \pi_{0,1}^N = \pi_{1,0}^N \ominus \pi_{0,0}^N \iff \ell(\pi_{1,1}^N \ominus \pi_{0,1}^N) = \ell(\pi_{1,0}^N \ominus \pi_{0,0}^N).$$

Using the linearity property, this becomes:

$$\ell(\pi_{1,1}^N) - \ell(\pi_{0,1}^N) = \ell(\pi_{1,0}^N) - \ell(\pi_{0,0}^N),$$

which holds if and only if the equality in (ii) holds component-wise for all $k = 1, \dots, p-1$.

A.4. Proof of Theorem 2. Define the log cross-group ratio at time t for category c_k :

$$\Delta_t^k := \log \left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)} \right) = \log(q_{1,t}^N(c_k)) - \log(q_{0,t}^N(c_k)).$$

The unobserved quantity of interest is $q_{1,1}^N(c_k)$, or equivalently Δ_1^k , since:

$$q_{1,1}^N(c_k) = \exp \left(\Delta_1^k + \log(q_{0,1}^N(c_k)) \right). \quad (1)$$

Thus, bounding Δ_1^k yields bounds on $q_{1,1}^N(c_k)$.

Assumption 3 states:

$$\Delta_1^k \in \text{Conv} \{ \Delta_0^k, \Delta_{-1}^k \} = [\min\{\Delta_0^k, \Delta_{-1}^k\}, \max\{\Delta_0^k, \Delta_{-1}^k\}].$$

Therefore, the sharp bounds on Δ_1^k are:

$$\underline{\Delta}_1^k = \min\{\Delta_0^k, \Delta_{-1}^k\}, \quad \overline{\Delta}_1^k = \max\{\Delta_0^k, \Delta_{-1}^k\}.$$

Plugging into (1), we obtain sharp bounds on $q_{1,1}^N(c_k)$:

$$b_{\min}^k := \exp(\underline{\Delta}_1^k + \log(q_{0,1}^N(c_k))) = \exp\left(\min\left\{\log\left(\frac{q_{1,0}^N(c_k)}{q_{0,0}^N(c_k)}\right), \log\left(\frac{q_{1,-1}^N(c_k)}{q_{0,-1}^N(c_k)}\right)\right\} + \log(q_{0,1}^N(c_k))\right),$$

$$b_{\max}^k := \exp(\overline{\Delta}_1^k + \log(q_{0,1}^N(c_k))) = \exp\left(\max\left\{\log\left(\frac{q_{1,0}^N(c_k)}{q_{0,0}^N(c_k)}\right), \log\left(\frac{q_{1,-1}^N(c_k)}{q_{0,-1}^N(c_k)}\right)\right\} + \log(q_{0,1}^N(c_k))\right).$$

Assumption 4 states:

$$\Delta_1^k \in \text{Conv}\left\{\min_{t < 0} \Delta_t^k, \max_{t < 0} \Delta_t^k\right\} = [\underline{\Delta}^k, \overline{\Delta}^k],$$

where

$$\underline{\Delta}^k := \min_{t < 0} \Delta_t^k, \quad \overline{\Delta}^k := \max_{t < 0} \Delta_t^k.$$

Thus, the bounds are:

$$b_{\min}^k = \exp(\underline{\Delta}^k + \log(q_{0,1}^N(c_k))) = \exp\left(\min_{t < 0} \log\left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)}\right) + \log(q_{0,1}^N(c_k))\right),$$

$$b_{\max}^k = \exp(\overline{\Delta}^k + \log(q_{0,1}^N(c_k))) = \exp\left(\max_{t < 0} \log\left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)}\right) + \log(q_{0,1}^N(c_k))\right).$$

Assumption 5 states:

$$\Delta_1^k \in \text{Conv}\left\{\min_{t < 0} \omega_t \Delta_t^k, \max_{t < 0} \omega_t \Delta_t^k\right\} = [\underline{\Delta}_\omega^k, \overline{\Delta}_\omega^k],$$

where

$$\underline{\Delta}_\omega^k := \min_{t < 0} \omega_t \Delta_t^k, \quad \overline{\Delta}_\omega^k := \max_{t < 0} \omega_t \Delta_t^k.$$

Hence:

$$b_{\min}^k = \exp(\underline{\Delta}_\omega^k + \log(q_{0,1}^N(c_k))) = \exp\left(\min_{t < 0} \omega_t \log\left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)}\right) + \log(q_{0,1}^N(c_k))\right),$$

$$b_{\max}^k = \exp(\overline{\Delta}_\omega^k + \log(q_{0,1}^N(c_k))) = \exp\left(\max_{t < 0} \omega_t \log\left(\frac{q_{1,t}^N(c_k)}{q_{0,t}^N(c_k)}\right) + \log(q_{0,1}^N(c_k))\right).$$

Let $q_{1,1}^I(c_k)$ denote the observed outcome for group 1 in period 1 (i.e., the treated outcome). The causal effect is often defined as the ratio of observed to counterfactual (in multiplicative models):

$$\text{GTT}(c_k) := \frac{q_{1,1}^I(c_k)}{q_{1,1}^N(c_k)}.$$

Since $q_{1,1}^N(c_k) \in [b_{\min}^k, b_{\max}^k]$, and the function $x \mapsto 1/x$ is decreasing for $x > 0$, we have:

$$\frac{q_{1,1}^I(c_k)}{b_{\max}^k} - 1 \leq \text{GTT}(c_k) \leq \frac{q_{1,1}^I(c_k)}{b_{\min}^k} - 1.$$

Define total observed outcome: $S_{1,1}^I = \sum_{k=1}^p q_{1,1}^I(c_k)$. The counterfactual total is $S_{1,1}^N = \sum_{k=1}^p q_{1,1}^N(c_k) \in [\sum_k b_{\min}^k, \sum_k b_{\max}^k]$. Then the aggregate treatment effect (e.g., ratio of totals) satisfies:

$$\frac{S_{1,1}^I}{\sum_k b_{\max}^k} - 1 \leq \text{GTT} \leq \frac{S_{1,1}^I}{\sum_k b_{\min}^k} - 1.$$

Let $\pi_{1,1}^I = q_{1,1}^I / S_{1,1}^I$ be the observed share vector (in the simplex \mathcal{S}^{p-1}). The counterfactual share is $\pi_{1,1}^N = q_{1,1}^N / S_{1,1}^N$. The set of possible $\pi_{1,1}^N$ is:

$$\left\{ \pi \in \mathcal{S}^{p-1} : \pi_k = \frac{q_k}{\sum_j q_j}, q_k \in [b_{\min}^k, b_{\max}^k] \text{ for all } k \right\}.$$

This can be expressed via the log-ratio transformation ℓ . Then the set of possible log-ratios satisfies:

$$\log(b_{\min}^k) - \log(b_{\max}^p) \leq \ell(\pi)_k \leq \log(b_{\max}^k) - \log(b_{\min}^p),$$

$$\text{CTT} \in \left\{ \pi \in \mathcal{S}^{p-1} : \pi = \pi_{1,1}^I \ominus s, s \in \ell^{-1}(\{r \in \mathbb{R}^{p-1} : \log(b_{\min}^k) \leq r_k \leq \log(b_{\max}^k)\}) \right\},$$

= The key idea is that the uncertainty in each component $q_{1,1}^N(c_k) \in [b_{\min}^k, b_{\max}^k]$ translates into a set-identified region for the share vector $\pi_{1,1}^N$. The bounds $[b_{\min}^k, b_{\max}^k]$ are sharp under each relaxation, because the convex hull assumption allows Δ_1^k to attain any value in the interval, including the endpoints. The treatment effect bounds follow directly from monotonicity of the ratio function.

A.5. Proof of Theorem 3. Strategy 1: Use the never-treated group (G_∞) as control, it requires assumption 7: parallel growth (in logs) between each cohort G_g and the never-treated group G_∞ .

Strategy 2: Use not-yet-treated groups as controls, it requires assumption 8: parallel growth (in logs) between cohort G_g and any cohort G_s that is not yet treated at time t (i.e., $s > t$).

Because \mathcal{G} excludes \bar{g} , for every $g \in \mathcal{G}$ and $t \geq g$, there exists at least one $s > t$ such that G_s is not yet treated at time t (since $s \leq \bar{g}$ and $\bar{g} > g$). Assumption 7 states: for all g and $t \geq g$,

$$\log q_{G_g,t}^N - \log q_{G_\infty,t}^N = \log q_{G_g,t-1}^N - \log q_{G_\infty,t-1}^N.$$

This implies the difference is constant over time for $t \geq g$. In particular, it equals its value at $t = g - 1$ (the last pre-treatment period):

$$\log q_{G_g,t}^N - \log q_{G_\infty,t}^N = \log q_{G_g,g-1}^N - \log q_{G_\infty,g-1}^N.$$

Rearranging:

$$\log q_{G_g,t}^N = \log q_{G_g,g-1}^N + \log q_{G_\infty,t}^N - \log q_{G_\infty,g-1}^N.$$

Exponentiating both sides gives the result. Assumption 8 states: for all $g \in \mathcal{G}$, and for all s, t such that $t \geq g$ and $t < s \leq \bar{g}$,

$$\log q_{G_g,t}^N - \log q_{G_s,t}^N = \log q_{G_g,t-1}^N - \log q_{G_s,t-1}^N.$$

Again, this implies the log-difference is time-invariant from period $g - 1$ onward (since G_s is untreated at all times $\leq t < s$, so $q_{G_s,\tau}^N = q_{G_s,\tau}^I$ is observed for $\tau \leq t$). Thus, for any $t \geq g$ and any valid $s > t$,

$$\log q_{G_g,t}^N - \log q_{G_s,t}^N = \log q_{G_g,g-1}^N - \log q_{G_s,g-1}^N.$$

Rearranging and exponentiating gives the result.

APPENDIX B. ADDING COVARIATES

This section extends our main identification results to incorporate covariates. Let $X \in \mathcal{X}$ denote a vector of covariates, which may be endogenous. For this analysis, we restrict our attention to the case where X is discrete. In this setting, we can redefine all relevant quantities by stratifying on X . This yields a set of new estimands, each conditional on a specific covariate profile x . Provided that the untreated potential quantities $q_{g,t}^N(x)$ are strictly positive for all groups, time periods, and values $x \in \mathcal{X}$, we can formulate the following conditional assumption:

Assumption 9. (*Conditional parallel growths*)

$$\log \cdot (q_{1,1,x}^N) - \log \cdot (q_{1,0,x}^N) = \log \cdot (q_{0,1,x}^N) - \log \cdot (q_{0,0,x}^N).$$

The conditional parallel growths assumption is often more plausible in practice. The corresponding counterfactuals are derived in the same way as in the unconditional case.

$$q_{1,1,x}^N = \exp \cdot (\log \cdot (q_{1,0,x}^N) + \log \cdot (q_{0,1,x}^N) - \log \cdot (q_{0,0,x}^N)) \quad (13)$$

$$q_{1,1}^N = \sum_{x \in \mathcal{X}} \mathbb{P}(X = x) q_{1,1,x}^N \quad (14)$$

And the corresponding counterfactual probability mass can be obtained by: for each category $c_k, k = 1, \dots, p$

$$\pi_{1,1,x}^N(c_k) = \frac{\exp(\log(q_{1,0,x}^N(c_k)) + \log(q_{0,1,x}^N(c_k)) - \log(q_{0,0,x}^N(c_k)))}{\sum_{g=1}^p \exp(\log(q_{1,0,x}^N(c_g)) + \log(q_{0,1,x}^N(c_g)) - \log(q_{0,0,x}^N(c_g)))} \quad (15)$$

$$\pi_{1,1}^N(c_k) = \sum_{x \in \mathcal{X}} \mathbb{P}(X = x) \pi_{1,1,x}^N(c_k) \quad (16)$$

The main challenge arises when X includes continuous variables, as it becomes necessary to model or approximate the conditional distribution in a flexible way, rather than relying on simple stratification. We do not explicitly discuss this case here.

APPENDIX C. IMPLEMENTATION OF CoDiD AND INFERENCE PROCEDURE

For each group g and each time period t , we have a random sample of $q_{g,t}$ individuals. Define $\hat{q}_{g,t}(c_k)$ as the number of individuals in group g at time t in category c_k . The estimated counterfactual is given by:

$$\hat{g}_{1,1}^N = \exp \cdot (\log \cdot (\hat{q}_{1,0}^N) + \log \cdot (\hat{q}_{0,1}^N) - \log \cdot (\hat{q}_{0,0}^N))$$

The total and shares are obtained using the estimated counterfactual quantities. The estimated treatment effects are given by:

$$G\hat{T}T(c_k) = \frac{\hat{q}_{1,1}^I(c_k)}{\hat{q}_{1,1}^N(c_k)} - 1$$

$$G\hat{T}T = \frac{\hat{S}_{1,1}^I}{\hat{S}_{1,1}^N} - 1$$

$$C\hat{T}T = \hat{\pi}_{1,1}^I \ominus \hat{\pi}_{1,1}^N$$

For inference, we use the parametric bootstrap to approximate the sampling distribution of the parameters. The parametric bootstrap is a resampling technique designed for situations where the data-generating process can be modeled parametrically. Instead of drawing resamples directly from the observed data, the procedure assumes a parametric model for the data and uses estimated parameters to generate new synthetic samples. For a detailed treatment of the method, see [Horowitz \(2019\)](#). In our case, the procedure proceeds as follows. For each bootstrap iteration $b = 1, \dots, B$, where B is the total number of iterations, we:

- Resample quantities for each group-time pair (g, t) using a multinomial distribution:

$$q_{g,t}^{(b)}(c_1, \dots, c_p) \sim \text{Multinomial}(S_{g,t}, \hat{\pi}_{g,t}(c_1), \dots, \hat{\pi}_{g,t}(c_p)).$$

- Compute counterfactual total quantities and category shares based on the bootstrap samples.
- Calculate the bootstrap treatment effects: $G\hat{T}T^b$ and $C\hat{T}T^b$.

The 95% confidence interval for each category c_k is then obtained from the 2.5% and 97.5% quantiles of the bootstrap distribution in each case.

APPENDIX D. RANDOM UTILITY MODEL AND LOG ODDS

Consider a standard *Random Utility Model* (RUM), in which a decision-maker selects one alternative from a finite set of mutually exclusive choices $\{c_1, c_2, \dots, c_p\}$. The utility that the individual derives from alternative c_k is modeled as:

$$U_k = V_k + \varepsilon_k,$$

where V_k denotes the deterministic (systematic) component of utility—typically specified as a function of observable attributes of alternative k and characteristics of the decision-maker, and ε_k represents the random (idiosyncratic) component, capturing unobserved preference heterogeneity and measurement error. The individual is assumed to choose the alternative that yields the highest realized utility:

$$\text{Choice} = \arg \max_{k \in \{1, \dots, p\}} U_k.$$

Consequently, the probability that alternative c_k is selected is given by

$$\pi(c_k) = \Pr(\text{Choice} = c_k) = \Pr(U_k \geq U_j \text{ for all } j \neq k).$$

Substituting the utility decomposition, this becomes

$$\pi(c_k) = \Pr(V_k + \varepsilon_k \geq V_j + \varepsilon_j \text{ for all } j \neq k) = \Pr(\varepsilon_j - \varepsilon_k \leq V_k - V_j \text{ for all } j \neq k).$$

A closed-form expression for $\pi(c_k)$ is obtained under the assumption that the stochastic components $\{\varepsilon_k\}_{k=1}^p$ are independent and identically distributed according to the Type I extreme value (Gumbel) distribution. Under this assumption, the choice probabilities follow the *multinomial logit* (MNL) model:

$$\pi(c_k) = \frac{\exp(V_k)}{\sum_{j=1}^p \exp(V_j)}.$$

An important implication of the MNL structure is that the relative odds of choosing any two alternatives depend only on their systematic utilities. Specifically, for any pair of alternatives c_k and c_ℓ , the odds ratio is

$$\frac{\pi(c_k)}{\pi(c_\ell)} = \frac{\exp(V_k)}{\exp(V_\ell)} = \exp(V_k - V_\ell).$$

Taking natural logarithms yields the familiar linear-in-parameters form:

$$\log\left(\frac{\pi(c_k)}{\pi(c_\ell)}\right) = V_k - V_\ell.$$

Thus, the log-odds of selecting alternative c_k over c_ℓ are exactly equal to the difference in their deterministic utilities. This property implies that an increase in V_k relative to V_ℓ , for example, due to a favorable change in the attributes of c_k , monotonically increases the probability that c_k is chosen, holding all else constant. This tractable relationship underpins much of the empirical appeal of the multinomial logit model in applied choice analysis.