

FEATURED ARTICLE

A sensitivity analysis for missing outcomes due to truncation by death under the matched-pairs design

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The matched-pairs design enables researchers to efficiently infer causal effects from randomized experiments. In this paper, we exploit the key feature of the matched-pairs design and develop a sensitivity analysis for missing outcomes due to truncation by death, in which the outcomes of interest (e.g., quality of life measures) are not even well defined for some units (e.g., deceased patients). Our key idea is that if 2 nearly identical observations are paired prior to the randomization of the treatment, the missingness of one unit's outcome is informative about the potential missingness of the other unit's outcome under an alternative treatment condition. We consider the average treatment effect among always-observed pairs (ATOP) whose units exhibit no missing outcome regardless of their treatment status. The naive estimator based on available pairs is unbiased for the ATOP if 2 units of the same pair are identical in terms of their missingness patterns. The proposed sensitivity analysis characterizes how the bounds of the ATOP widen as the degree of the within-pair similarity decreases. We further extend the methodology to the matched-pairs design in observational studies. Our simulation studies show that informative bounds can be obtained under some scenarios when the proportion of missing data is not too large. The proposed methodology is also applied to the randomized evaluation of the Mexican universal health insurance program. An open-source software package is available for implementing the proposed research.

KEYWORDS

average treatment effect, bounds, causal inference, observational studies, randomized experiments

1 | INTRODUCTION

As the well-known mantra “block what you can and randomize what you cannot”¹ (p 93) suggests, covariate adjustment prior to the randomization of treatment assignment is an effective strategy for ascertaining the treatment effects from randomized experiments.² In particular, it has been shown that the matched-pairs design, in which 2 similar observations are paired and the treatment assignment is randomized within each pair, can yield an efficient estimate of causal effects.³⁻⁵

However, it is well known that the validity of experimental findings can be compromised in the presence of missing outcomes, especially when the missingness pattern is affected by the treatment.^{6,7} In this paper, we exploit the key feature of the matched-pairs design and develop a sensitivity analysis for nonignorable missing outcomes due to truncation by death,^{8,9} in which the outcomes of interest are not even well defined for some units.

The so-called truncation-by-death problem originates from the scenario, in which researchers wish to evaluate the effect of a medical treatment on the quality of life measures but such measures are only defined for the individuals who are alive.¹⁰⁻¹² If the treatment affects patient survival, then the simple comparison between the treated and control groups among the surviving patients results in biased inference. The truncation-by-death problem also arises in other contexts. For example, the economic evaluation of a job-training program often involves the estimation of its effect on wages, which are defined only for those who are employed.^{13,14} The empirical application of this paper provides yet another example of the truncation-by-death problem in the field of public health research.

We consider the case of missing data mechanism, in which the treatment directly affects the missingness pattern. Under this scenario, it is important not to condition on observed outcomes because such an analysis may suffer from posttreatment bias. For this reason, the naive estimator based on available pairs, which is often used in practice, is likely to be invalid. However, the matched-pairs design can partially address this problem. The key idea is that if 2 nearly identical observations are paired prior to the randomization of the treatment, the missingness of one unit's outcome is informative about the potential missingness of the other unit's outcome. In particular, if matching is perfect so that 2 units of the same pair are identical in terms of their potential missingness patterns, then the naive estimator will be unbiased for the average treatment effect among always-observed pairs (ATOP) whose units exhibit no missing outcome regardless of their treatment status. This estimand is the matched-pairs design analogue of the the average treatment effect among always-observed units (ATOU) that is frequently studied in the literature on the truncation-by-death problem.⁷⁻⁹ In both cases, we condition on potential missingness indicators rather than observed ones so that we avoid posttreatment bias.

In practice, matching is never perfect and hence the naive estimator will be biased. We therefore propose a sensitivity analysis to characterize how the bounds of the ATOP widen as the degree of the within-pair similarity decreases. We further extend this sensitivity analysis to the matched-pairs design in observational studies, in which the treatment assignment is assumed to be unconfounded with respect to potential outcomes but not potential values of missingness indicators. Our simulation studies show that informative bounds can be obtained under some scenarios if the proportion of missing data is not too large. The analytical results and methodology presented in this paper complement the recent work by Fukumoto¹⁵ who examines the bias due to missing outcomes under the matched-pairs design. All the proposed methods are implemented via open-source R package, `experiment`.¹⁶

Finally, we apply the proposed methodology to the randomized evaluation of the Mexican universal health insurance program,¹⁷ in which randomly selected clusters of households are encouraged to enroll in the health insurance program, Seguro Popular. We examine the outcome variable measuring the satisfaction with Seguro Popular. This outcome variable suffers from the truncation-by-death problem because it is defined and hence measured only for those households who are enrolled in the program. We conduct the proposed sensitivity analysis for the ATOP.

2 | THE PROPOSED METHODOLOGY

2.1 | The setup

Following Imai,¹⁸ we consider a randomized experiment with the standard matched-pairs design. Suppose that we have a sample of n pairs. Each pair consists of 2 units that are similar to one another in terms of their pretreatment covariates \mathbf{X} , which is a K -dimensional vector. To create such pairs, for example, researchers may employ multivariate matching based on the Mahalanobis distance measure.⁴ The treatment assignment is completely randomized within each pair where one unit receives the treatment and the other unit does not. Let T_{ij} represent the binary treatment variable for unit i of pair j where $i = 1, 2$ and $j = 1, 2, \dots, n$. Then, under the matched-pairs design, we have $T_{1j} + T_{2j} = 1$ for each pair j and $\Pr(T_{ij} = 1) = 1/2$.

Our analysis is based on the potential outcomes framework,^{19,20} and throughout this paper, we maintain the stable unit treatment value assumption (SUTVA). That is, we assume that there is only one version of treatment and there is no interference between units.²¹ The SUTVA allows us to uniquely define the potential outcomes $Y_{ij}(t)$ under the treatment condition $T_{ij} = t$ for unit i of pair j where $t = 0, 1, i = 1, 2$, and $j = 1, 2, \dots, J$. Since we only observe one of the 2 potential outcomes, we write the observed outcome as $Y_{ij} = T_{ij}Y_{ij}(1) + (1 - T_{ij})Y_{ij}(0)$.

In this paper, we consider the setting where the outcome variable is missing for some units due to the truncation-by-death problem, in which the outcome variable may not even be well defined under a certain circumstance. For example, in a medical trial, the quality of life measure is not well defined for deceased patients. Let $R_{ij}(t)$ represent the potential value of response indicator for the outcome variable where $R_{ij}(t) = 1$ ($R_{ij}(t) = 0$) implies that the outcome is observed (missing) for unit i of pair j under the treatment condition $T_{ij} = t$. This notation relies on the SUTVA but allows

the treatment to directly affect missing data pattern. Like the outcome variable, we only observe one of the 2 potential values of the response indicator, and hence, we write the observed value of this indicator as $R_{ij} = T_{ij}R_{ij}(1) + (1 - T_{ij})R_{ij}(0)$. Under the truncation-by-death problem, the potential outcome $Y_{ij}(t)$ is not well defined when $R_{ij}(t) = 0$.

The randomization of treatment assignment within each pair implies the following independence relationship between the treatment assignment and the potential values of outcome and response indicator,

Assumption 1. (Within-pair randomization of treatment assignment)

Within each pair $j = 1, 2, \dots, J$,

$$T_{ij} \perp\!\!\!\perp \{Y_{1j}(1), Y_{1j}(0), Y_{2j}(1), Y_{2j}(0), R_{1j}(1), R_{1j}(0), R_{2j}(1), R_{2j}(0)\},$$

and $\Pr(T_{ij} = 1) = 1/2$ where $i = 1, 2$.

In observational studies, researchers often match a treated unit with a control unit based on the similarity of pretreatment characteristics X . In this case, there are 2 types of confounders: the variables that confound the causal relationship between the treatment and outcome variables, and those that confound the relationship between the treatment and response indicator variables. Assumption 1 implies that neither type of confounders exists.

Without loss of generality, we assume that within each pair the unit labels, $i = 1, 2$, are arbitrarily assigned and hence, these 2 units are exchangeable.¹⁸ Formally, we write this assumption as the following set of equalities since the potential outcomes $Y_{ij}(t)$ may be defined only when $R_{ij}(t) = 1$,

$$\begin{aligned} P\{R_{1j}(1), R_{1j}(0), R_{2j}(1), R_{2j}(0)\} &= P\{R_{2j}(1), R_{2j}(0), R_{1j}(1), R_{1j}(0)\}, \\ P\{Y_{1j}(1), Y_{1j}(0) \mid R_{1j}(1) = 1, R_{1j}(0) = 1\} &= P\{Y_{2j}(1), Y_{2j}(0) \mid R_{2j}(1) = 1, R_{2j}(0) = 1\}, \\ P\{Y_{1j}(t) \mid R_{1j}(t) = 1, R_{1j}(1-t) = 1\} &= P\{Y_{2j}(t) \mid R_{2j}(t) = 1, R_{2j}(1-t) = 1\}. \end{aligned}$$

We will maintain this exchangeability assumption throughout this paper. In practice, the randomization of unit labels within each pair is sufficient to ensure that the assumption holds.

2.2 | The quantities of interest

Typically, researchers are interested in the average treatment effect (ATE), which is defined as follows:

$$\text{ATE} = \mathbb{E}\{Y_{ij}(1) - Y_{ij}(0)\}.$$

As briefly discussed in Section 1, under the problem of truncation by death, the outcome variables (eg, quality-of-life measures) may not be well defined for some units (eg, deceased patients). Thus, in the literature, scholars focus on a subpopulation of units whose outcome would be observed regardless of their treatment status (eg, patients who would survive under both conditions).²²⁻²⁴ This is essential for avoiding posttreatment bias since the treatment may affect the missingness pattern. For this reason, researchers focus on the average treatment effect for always-observed units (ATOU), which is defined as

$$\text{ATOU} = \mathbb{E}\{Y_{ij}(1) - Y_{ij}(0) \mid R_{ij}(1) = R_{ij}(0) = 1\}.$$

In this paper, we take advantage of the matched-pairs design and consider the average treatment effect for always-observed pairs (ATOP), which is a quantity analogous to the ATOU under this design. The idea is that we preserve the key feature of the experimental design and focus on a subset of pairs, in which the outcome variable is well defined for both units regardless of their treatment status. Formally, the ATOP is defined as follows:

$$\text{ATOP} = \mathbb{E}\{Y_{ij}(1) - Y_{ij}(0) \mid R_{1j}(1) = R_{1j}(0) = R_{2j}(1) = R_{2j}(0) = 1\}. \quad (1)$$

Now, consider the following naive difference-in-means estimator, applied to all the pairs without missing outcomes,

$$\hat{\tau}_{\text{ATOP}} = \frac{1}{\sum_{j=1}^J R_{1j}R_{2j}} \sum_{j=1}^J R_{1j}R_{2j}(2T_{1j} - 1)(Y_{1j} - Y_{2j}). \quad (2)$$

This estimator is unbiased for ATOP if the missingness pattern does not depend on the treatment, ie, $R_{ij}(1) = R_{ij}(0)$ for all i and j , or matching is perfect so that the potential response indicators are identical between units within the same

pair, $R_{1j}(t) = R_{2j}(t)$ for each $t = 0, 1$ and $j = 1, 2, \dots, J$. However, in practice, the treatment often affects the missingness pattern and matching is imperfect. Thus, in what follows, we characterize the bias that arises when these conditions are violated and develop a sensitivity analysis.

2.3 | No-assumption bounds

We begin by deriving the bounds for the ATOP without an additional assumption. First, the following quantities are identified from the observed data,

$$\pi = P(R_{1j} = R_{2j} = 1) = P(R_{1j}(t) = R_{2j}(1-t) = 1), \quad (3)$$

$$\alpha_t = P(R_{ij} = 1 \mid T_{1j} = t) = P(R_{1j}(t) = 1), \quad (4)$$

$$\psi_t = \mathbb{E}(Y_{ij} \mid R_{ij} = 1, T_{ij} = t) = \mathbb{E}(Y_{ij}(t) \mid R_{ij}(t) = 1), \quad (5)$$

$$\omega_t = \mathbb{E}(Y_{ij} \mid T_{ij} = t, R_{1j} = R_{2j} = 1) = \mathbb{E}(Y_{ij}(t) \mid R_{1j}(t) = R_{2j}(1-t) = 1) \quad (6)$$

for $i = 1, 2$ and $t = 0, 1$ where in Equations 3 to 6 the equalities hold due to the exchangeability of unit labels and Assumption 1. Then, the following theorem establishes the sharp bounds for the ATOP.

Theorem 1. (Sharp bounds for the average treatment effect for always-observed pairs)

Suppose that the outcome variable is bounded such that $Y_{ij} \in [l, u]$ where $l < u$. Then, under Assumption 1, the sharp bounds for the average treatment effect for always-observed pairs (ATOP) defined in Equation 1 are given by

$$ATOP \in \begin{cases} \left[f^{[l,u]} \left(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi} \right), g^{[l,u]} \left(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi} \right) \right] & \text{if } \pi > \frac{1}{2} \\ [l - u, u - l] & \text{if } \pi \leq \frac{1}{2} \end{cases},$$

where

$$f^{[l,u]}(x_1, y_1, x_0, y_0) = \max \left\{ l, u - \frac{u - x_1}{y_1} \right\} - \min \left\{ u, \frac{x_0 - l}{y_0} + l \right\},$$

$$g^{[l,u]}(x_1, y_1, x_0, y_0) = \min \left\{ u, \frac{x_1 - l}{y_1} + l \right\} - \max \left\{ l, u - \frac{u - x_0}{y_0} \right\}.$$

Proof is given in Appendix A.2. Theorem 1 shows that if the proportion of the observed pairs, ie, π , is high, then the bounds will be informative. The informativeness of the bounds also depends on the (expected) magnitude of naive ATOP estimator $\hat{\tau}_{ATOP}$ given in Equation 2, which is equal to $\omega_1 - \omega_0$. To see this, we note that the definitions of $f^{[l,u]}$ and $g^{[l,u]}$ imply

$$f^{[l,u]} \left(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi} \right) \geq \frac{\pi(\omega_1 - \omega_0)}{2\pi - 1} - \frac{(1 - \pi)(u - l)}{2\pi - 1},$$

$$g^{[l,u]} \left(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi} \right) \leq \frac{\pi(\omega_1 - \omega_0)}{2\pi - 1} + \frac{(1 - \pi)(u - l)}{2\pi - 1}.$$

Therefore, when the naive estimator has a value away from zero, then the bounds are less likely to contain zero. The above inequalities further imply that the width of the bounds is less than or equal to

$$\frac{2(1 - \pi)}{2\pi - 1}(u - l).$$

Thus, as expected, when the proportion of observed pairs is greater, the bound is narrower.

We now compare the bounds for the ATOP with those for the ATOU. Zhang and Rubin⁸ derived the no-assumption bounds for the ATOU and the bounds under the monotonicity assumption $R(1) \geq R(0)$. Imai⁹ proved that these bounds are sharp. The bounds for the ATOU below are expressed differently from those presented in the literature, but they are identical to each other.

Theorem 2. (Sharp bounds for the average treatment effect for always-observed units)

If the outcome is bounded such that $Y_{ij} \in [l, u]$ where $l < u$, then under Assumption 1, the lower and upper bounds for the the average treatment effect for always-observed units (ATOu) are given by

$$ATOUE \in \begin{cases} \left[f^{[l,u]} \left(\psi_1, \frac{\Gamma}{\alpha_1}, \psi_0, \frac{\Gamma}{\alpha_0} \right), g^{[l,u]} \left(\psi_1, \frac{\Gamma}{\alpha_1}, \psi_0, \frac{\Gamma}{\alpha_0} \right) \right] & \text{if } \Gamma > 0 \\ [l - u, u - l] & \text{if } \Gamma \leq 0 \end{cases},$$

where $\Gamma = \alpha_1 + \alpha_0 - 1$.

Proof is given in Appendix A.3. Similar to the case of ATOP, the width of the bounds critically depends on Γ with a greater missing proportion leading to wider bounds. By definition, we have $\alpha_i \geq \pi$ for $i = 0, 1$, which implies $\pi \leq (\alpha_1 + \alpha_0)/2$. Thus, if $\alpha_1 + \alpha_0 \leq 1$, then $\pi \leq 1/2$. As a result, the bounds for the ATOP given in Theorem 1 are more likely to be noninformative, i.e., $[l - u, u - l]$, than those for the ATOU in Theorem 2. Note that the widths of both bounds are written in the form of $g^{[l,u]}(x_1, y_1, x_0, y_0) - f^{[l,u]}(x_1, y_1, x_0, y_0)$, which is decreasing in y_0 and y_1 . In Appendix A.4, we show that $\Gamma/\alpha_i > 2 - 1/\pi$, and thus, the ATOP bounds are always wider than the ATOU bounds.

In a similar setting, Ding et al¹¹ point out that, even under the monotonicity assumption ($R(1) \leq R(0)$ or $R(1) \geq R(0)$), the bounds for the ATOU may be too wide to be useful. Therefore, the bounds in Theorem 1 may give us little information about the ATOP. To address this issue, we next develop a sensitivity analysis. In particular, we exploit the fact that the assumption about within-pair similarity can be used to narrow the bounds for the ATOP.

2.4 | Sensitivity analysis

Because the above no-assumption bounds are often too wide, we develop a sensitivity analysis. Specifically, we consider the case, in which the missingness depends on the treatment, ie, $R_{ij}(1) \neq R_{ij}(0)$ for some i and j . Under this setting, we exploit the experimental design and base our sensitivity analysis on the quality of matches under the matched-pairs design rather than the dependence between the treatment and the missingness pattern. If matching is perfectly done such that 2 observations within each pair are perfect substitutes, then we have $R_{1j}(t) = R_{2j}(t)$ for each $t = 0, 1$ and $j = 1, 2, \dots, J$. And, under this perfect matching assumption, ATOP is identifiable. However, since in practice the quality of matches is unlikely to be perfect, the observed value of one unit's response indicator is only an approximation to the unobserved value of the response indicator for the other unit within the same pair, ie, $R_{1j}(t) \approx R_{2j}(t)$. We formalize this scenario as follows:

Assumption 2. (Similarity of missingness pattern within a pair)

$$P\{R_{2j}(t) = r \mid R_{1j}(t) = r\} = P\{R_{1j}(t) = r \mid R_{2j}(t) = r\} \geq \gamma$$

for $r = 0, 1$ and $t = 0, 1$.

Under Assumption 2, if $\gamma = 1$, then we have perfect matches, ie, $R_{1j}(t) = R_{2j}(t)$ for $t = 0, 1$ and all $j = 1, 2, \dots, J$, and therefore, the naive estimator $\hat{\tau}_{ATOP}$ given in Equation 2 is unbiased for the ATOP. By moving the sensitivity parameter γ away from 1, we can characterize the maximal magnitude of bias induced in the estimation of the ATOP. The next theorem formally characterizes the bounds for the ATOP as a function of the sensitivity parameter γ :

Theorem 3. (Sensitivity analysis for the average treatment effect for always-observed pairs)

Under Assumptions 1 and 2, the sharp bounds for the ATOP are

$$ATOP \in \begin{cases} \left[f^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta), g^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta) \right] & \text{if } \Delta > 0 \\ [l - u, u - l] & \text{if } \Delta \leq 0 \end{cases},$$

where $\Delta = \max_{i \in \{0,1\}} \{2\pi - 1 + \gamma(1 - \alpha_i), \pi - (1 - \gamma)(\alpha_1 + \alpha_0), 2\pi - (2 - \gamma)\alpha_i, \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0), \pi - (1 - \gamma)(1 - |\alpha_1 - \alpha_0|)\} / \pi$.

Proof is given in Appendix A.5. In typical situations with $\alpha_i > 1/2$ for $i = 0, 1$, we can simplify the expression of Δ as $\Delta = \max_{i \in \{0,1\}} \{2\pi - 1 + \gamma(1 - \alpha_i), \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0)\} / \pi$.

From the expressions of the bounds, we have

$$\begin{aligned} f^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta) &\geq \frac{\omega_1 - \omega_0}{\Delta} - \left(\frac{1}{\Delta} - 1\right)(u - l), \\ g^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta) &\leq \frac{\omega_1 - \omega_0}{\Delta} + \left(\frac{1}{\Delta} - 1\right)(u - l). \end{aligned}$$

Thus, similar to Theorem 1, the informativeness of these sensitivity bounds depends on the (expected) magnitude of the naive ATOP estimator $\hat{\tau}_{ATOP}$. In addition, the width of the bounds is less than or equal to

$$2(u - l) \left(\frac{1}{\Delta} - 1 \right),$$

which is decreasing in Δ . When $\gamma = 1$, we have $\Delta = 1$, reducing the bounds to a point and identifying the ATOP as $\omega_1 - \omega_0$. When $\alpha_i > 1/2$ for $i = 0, 1$, the width of the bounds is decreasing in γ . This is consistent with our expectation that when the units within each pair are similar, the bounds should be narrower. Interestingly, the width of the bounds is not necessarily decreasing in α_i unless the within-pair similarity is high as indicated by a large value of γ .

2.5 | Extension to observational studies

Finally, we extend our results to observational studies and develop a sensitivity analysis for pair-matching. We consider the setting where a set of observed confounders are used to create pairs of similar observations. A variety of matching methods such as Mahalanobis and propensity score matching can be used for the construction of pairs, and we make the standard within-pair unconfoundedness assumption.²⁵⁻²⁷

Assumption 3. (Within-pair unconfoundedness of treatment assignment)

Within each pair, $j = 1, 2, \dots, J$,

$$T_{ij} \perp\!\!\!\perp \{Y_{1j}(0), Y_{1j}(1), Y_{2j}(0), Y_{2j}(1)\}$$

and $\Pr(T_{ij} = 1) = 1/2$ where $i = 1, 2$.

Unlike Assumption 1, we do not assume that the treatment assignment is independent of potential response indicator variables. This allows for the possible existence of unobserved confounders that are associated with the treatment assignment and potential response indicators even within each pair.

Assumption 3 alone leads to noninformative bounds, and yet researchers may feel that Assumption 1 is not credible in observational studies. Thus, we consider the following conditional independence assumption, which still allows for the correlation between T_{ij} and $\{R_{1j}(1), R_{1j}(0), R_{2j}(1), R_{2j}(0)\}$ as well as the correlation between $\{Y_{1j}(1), Y_{1j}(0), Y_{2j}(1), Y_{2j}(0)\}$ and $\{R_{1j}(1), R_{1j}(0), R_{2j}(1), R_{2j}(0)\}$.

Assumption 4. (Pattern mixture model)

For each pair $j = 1, 2, \dots, J$, we assume the following conditional independence:

$$Y_{ij}(t) \perp\!\!\!\perp T_{ij} \mid \{R_{ij}(t), R_{i'j}(1-t)\}$$

for $i \neq i'$ and $t = 0, 1$.

In other words, we assume that the within-pair unconfoundedness of treatment assignment holds even after conditioning on the potential values of response indicator variables. We motivate Assumption 4 by pattern mixture models that are widely used in the missing data literature.²⁸ In the causal inference literature, for example, D'Agostino and Rubin²⁹ used a pattern mixture model to account for partially observed covariates in the estimation of propensity scores. In the current context, we consider the setting where we construct matched pairs based on a set of observed confounders X for the treatment-outcome relationship (such that Assumption 3 holds), but there exists another set of unobserved pretreatment covariates that confound the relationship between the treatment and missingness (such that $T_{ij} \not\perp\!\!\!\perp \{R_{1j}(0), R_{1j}(1), R_{2j}(0), R_{2j}(1)\}$). Then, the pattern mixture decomposition is given by

$$P(Y_{1j}, Y_{2j}, R_{1j}, R_{2j}, T_{1j}) = P(Y_{1j}, Y_{2j} \mid R_{1j}, R_{2j}, T_{1j})P(R_{1j}, R_{2j}, T_{1j}).$$

Assumption 4 implies that within each missingness pattern, the treatment assignment is independent of potential outcomes.

Under Assumptions 3 and 4, we develop a sensitivity analysis by operationalizing the possible existence of unobserved confounders for the treatment and missingness relationship as

$$\frac{\Pr(R_{ij}(t) = 1 \mid T_{ij} = 1)}{\Pr(R_{ij}(t) = 1 \mid T_{ij} = 0)} = \kappa_t \quad (7)$$

for $t = 0, 1$. It is clear that when $\kappa_1 = \kappa_0 = 1$, we have $\{R_{1j}(0), R_{1j}(1), R_{2j}(0), R_{2j}(1)\} \perp\!\!\!\perp T_{ij}$. Because of the relationships, $\Pr(R_{ij}(t) = 1 \mid T_{ij} = 0) = \alpha_t / \kappa_t$ for $t = 0, 1$, the observed data have some restrictions on the possible ranges of κ_1 and κ_0 , ie, $\kappa_1 \geq \alpha_1$ and $\kappa_0 \leq 1/\alpha_0$. Furthermore, we can write the proportion of missingness using these sensitivity parameters,

$$\Pr(R_{ij}(1) = 1) = \frac{\alpha_1(1 + \kappa_1)}{2\kappa_1}, \quad \Pr(R_{ij}(0) = 1) = \frac{\alpha_0(1 + \kappa_0)}{2} \tag{8}$$

for $t = 0, 1$. Using this relationship, the next theorem shows that under Assumptions 3 and 4, the sharp bounds for the ATOP can be expressed as a function of these sensitivity parameters, ie, κ_0 and κ_1 .

Theorem 4. (Sensitivity analysis for observational studies)

Suppose that the outcome variable is bounded such that $Y_{ij} \in [l, u]$ where $l < u$. Then, under Assumptions 3 and 4, the sharp bounds for the average treatment effect for always-observed pairs (ATOP) are

$$ATOP \in \begin{cases} [f^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*), g^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*)] & \text{if } \Delta^* > 0 \\ [l - u, \quad u - l] & \text{if } \Delta^* \leq 0 \end{cases}$$

where $\Delta^* = \max_{t \in \{0,1\}} \{2\pi - 2 + 2\gamma(1 - \alpha_t^*), \pi - 2(1 - \gamma)(\alpha_1^* + \alpha_0^*), 2\pi - 2(2 - \gamma)\alpha_t^*, \pi - 2(1 - \gamma)(2 - \alpha_1^* - \alpha_0^*), \pi - 2(1 - \gamma)(1 - |\alpha_1^* - \alpha_0^*|)\} / \pi$, and $\alpha_t^* = \Pr(R(t) = 1)$ defined in Equation 8.

Proof is given in Appendix A.6. Because $\Delta^* \leq \Delta$ always holds, the bounds in Theorem 4 are at least as wide as those in Theorem 3. In typical situations with $\alpha_i^* > 1/2$ for $i = 0, 1$, we can simplify the expression of Δ^* as $\Delta^* = \max_{i \in \{0,1\}} \{2\pi - 2 + 2\gamma(1 - \alpha_i^*), \pi - 2(1 - \gamma)(2 - \alpha_1^* - \alpha_0^*)\} / \pi$. From the expressions of the bounds, we have

$$f^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*) \geq \frac{\omega_1 - \omega_0}{\Delta^*} - \left(\frac{1}{\Delta^*} - 1\right)(u - l),$$

$$g^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*) \leq \frac{\omega_1 - \omega_0}{\Delta^*} + \left(\frac{1}{\Delta^*} - 1\right)(u - l).$$

Thus, similar to Theorems 1 and 3, the informativeness of these sensitivity bounds depends on the (expected) magnitude of the naive ATOP estimator $\hat{\tau}_{ATOP}$. In addition, the width of the bounds is less than or equal to

$$2(u - l) \left(\frac{1}{\Delta^*} - 1\right),$$

which is decreasing in Δ^* . When $\gamma = 1$, we have $\Delta^* = 1$, reducing the bounds to a point and identifying the ATOP as $\omega_1 - \omega_0$. When $\alpha_i^* > 1/2$ for $i = 0, 1$, the width of the bounds is decreasing in γ and is decreasing in α_i^* if the within-pair similarity is high.

3 | SIMULATION STUDIES

In this section, we conduct simulation studies to evaluate the finite sample performance of our approach under several different missing data mechanisms. To be consistent with Assumption 1, we consider randomized experiments where the treatment is independently and randomly assigned to one of the units within each pair, ie, $\Pr(T_{1j} = 1) = 0.5$ and $T_{2j} = 1 - T_{1j}$ for each j . Next, we generate the potential response indicator variables, ie, $\{R_1(1), R_1(0), R_2(1), R_2(0)\}$. Let us denote $\zeta_{ijkl} = \Pr\{R_1(1) = i, R_1(0) = j, R_2(1) = k, R_2(0) = l\}$. Because the labels are arbitrarily assigned within each pair, we have $\zeta_{1011} = \zeta_{1110}, \zeta_{1001} = \zeta_{0110}, \zeta_{1100} = \zeta_{0011}$, and $\zeta_{0001} = \zeta_{0100}$. We generate $\{R_1(1), R_1(0), R_2(1), R_2(0)\}$ from a multinomial distribution with probabilities $\zeta = (\zeta_{1111}, \zeta_{1101}, \zeta_{0111}, \zeta_{1011}, \zeta_{1110}, \zeta_{1001}, \zeta_{0110}, \zeta_{1010}, \zeta_{0101}, \zeta_{1100}, \zeta_{0011}, \zeta_{0001}, \zeta_{0100}, \zeta_{1000}, \zeta_{0010}, \zeta_{0000})$. Based on the values of ζ , we can calculate the proportions of missingness under the treatment and control conditions as follows:

$$\Pr\{R_{ij}(1) = 1\} = \sum_{j,k,l=0,1} \zeta_{1jkl} \quad \text{and} \quad \Pr\{R_{ij}(0) = 1\} = \sum_{i,k,l=0,1} \zeta_{i1kl}.$$

We consider the following 3 scenarios with different missing proportions under the treatment and control conditions:

1. **Low level of missingness:** $\Pr\{R_{ij}(1) = 1\} = 0.85$ and $\Pr\{R_{ij}(0) = 1\} = 0.9$ where $\zeta = (3/4, 1/40, 1/40, 1/80, 1/80, 1/80, 1/80, 1/80, 1/20, 1/80, 1/80, 1/80, 1/80, 1/80, 1/80, 1/80)$.
2. **Moderate level of missingness:** $\Pr\{R_{ij}(1) = 1\} = 0.7$ and $\Pr\{R_{ij}(0) = 1\} = 0.75$ where $\zeta = (39/80, 1/40, 1/40, 1/32, 1/32, 1/32, 1/32, 1/32, 7/80, 1/32, 1/32, 1/32, 1/32, 1/32, 1/32, 1/32)$.
3. **High level of missingness:** $\Pr\{R_{ij}(1) = 1\} = 0.55$ and $\Pr\{R_{ij}(0) = 1\} = 0.6$ where $\zeta = (9/40, 1/40, 1/40, 1/20, 1/20, 1/20, 1/20, 1/20, 1/8, 1/20, 1/20, 1/20, 1/20, 1/20, 1/20, 1/20)$.

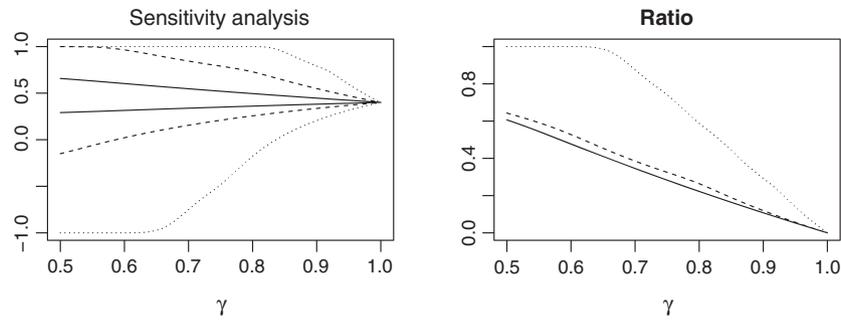


FIGURE 1 Sensitivity analysis with different levels of missing proportions. In the left plot, the solid, dashed, and dotted lines represent the bounds under the scenarios of the low, moderate, and high levels of missing proportions, respectively. The sensitivity parameter γ , which represents the within-pair similarity of missingness pattern, is shown on the horizontal axis. In the right plot, we plot the ratio of bound widths under different values of the sensitivity parameter relative to the widths of the no-assumption bounds. Again, the solid, dashed, and dotted lines denote the scenarios of the low, moderate, and high levels of missing proportions, respectively

Finally, we generate potential outcomes conditional on the potential response indicator so that missing data are not ignorable. Specifically, for each of the above missingness mechanism, we use

$$\begin{aligned} \Pr\{Y_{ij}(1) = 1 \mid R_{ij}(1) = 0, R_{1-i,j}(0) = 0\} &= 0.2, & \Pr\{Y_{ij}(1) = 1 \mid R_{ij}(1) = 0, R_{1-i,j}(0) = 1\} &= 0.7, \\ \Pr\{Y_{ij}(1) = 1 \mid R_{ij}(1) = 1, R_{1-i,j}(0) = 0\} &= 0.3, & \Pr\{Y_{ij}(1) = 1 \mid R_{ij}(1) = 1, R_{1-i,j}(0) = 1\} &= 0.6, \\ \Pr\{Y_{ij}(0) = 1 \mid R_{ij}(0) = 0, R_{1-i,j}(1) = 0\} &= 0.7, & \Pr\{Y_{ij}(0) = 1 \mid R_{ij}(0) = 0, R_{1-i,j}(1) = 1\} &= 0.6, \\ \Pr\{Y_{ij}(0) = 1 \mid R_{ij}(0) = 1, R_{1-i,j}(1) = 0\} &= 0.4, & \Pr\{Y_{ij}(0) = 1 \mid R_{ij}(0) = 1, R_{1-i,j}(1) = 1\} &= 0.2. \end{aligned}$$

According to this data generating process, all scenarios have an identical true value of 0.4 for the ATOP. For each scenario, we generate 1000 pairs of units and calculate the average bounds across 500 simulated datasets. Note that the bounds for the ATOU are (0.259, 0.594), (−0.105, 0.909), and (−0.998, 1) for the scenarios with low, moderate, and high levels of missingness, respectively. The bounds are particularly noninformative under moderate and high missing proportions.

We now report the simulation results concerning the bounds of the ATOP. The no-assumption bounds of the ATOP are (0.066, 0.667), (−0.772, 1), and (−1, 1) for the scenarios with the low, moderate, and high levels of missing data, respectively. As expected, these bounds are wider than those of the ATOU reported above. To narrow these bounds, we conduct sensitivity analysis by varying the sensitivity parameter γ . The left plot of Figure 1 shows the results of the sensitivity analysis with different values of γ , whereas the right plot shows the ratio of the bound widths under different values of the sensitivity parameter to the widths of the no-assumption bounds. Under the scenarios of the low (solid lines) and moderate (dashed lines) levels of missing proportions, the bounds become narrower as γ increases from 0.5 to 1. In contrast, the bounds under the scenario of the high level of missing proportion remain unchanged when γ is less than 0.65. Similarly, when the level of missing proportion is moderate, the bounds do not cover zero so long as $\gamma \geq 0.6$, whereas when the missing proportion is high, the bounds cover zero unless $\gamma \geq 0.85$. Thus, as expected, when the amount of missing data is great, informative bounds require the assumption of greater within-pair similarity.

4 | EMPIRICAL ILLUSTRATION

In this section, we apply the sensitivity analysis developed above to the data from a matched-pairs randomized experiment that was conducted to evaluate the efficacy of the Mexican universal health insurance program, Seguro Popular.¹⁷

4.1 | Data and quantities of interest

The evaluation study employed the cluster matched-pairs design where within each of 50 pairs of health clusters, the treatment was randomly assigned to one health cluster. Within a treatment cluster, households were encouraged to enroll in Seguro Popular. In contrast, the households of a control cluster did not receive such an encouragement. We analyze the household-level satisfaction of Seguro popular as an outcome. Unfortunately, this variable suffers from the truncation-by-death problem because the satisfaction variable is not well defined for those households who did not enroll in the program. Nevertheless, it is of interest to estimate the treatment effect on satisfaction among those households who

would have enrolled in the program anyway because the treatment here does more than encouraging people to enroll in the program. For example, the federal government provides funds to improve local health facilities.¹⁷ Hence, those who would have enrolled in the program anyway may still receive benefits of improved health care.

For the sake of empirical illustration, we create pairs at the individual household level. Specifically, we conduct one-to-one nearest neighbor propensity score matching without replacement by pairing each household of one treatment cluster with a similar household from its paired control cluster. We use R package MatchIt³⁰ for implementation. For some cluster pairs, the number of the households in a control cluster is different from that in a treated cluster of the same pair. In those cases, we simply remove unmatched households. As a result, we have a total of 14 902 matched household pairs. Although, unlike cluster-level pairs, these household pairs were created retrospectively, we emphasize that Assumption 1 still holds within each pair.

We use the logistic regression model for estimating the propensity score and include assets, age, sex, education, household assets, household average age, household sex, and household education as predictors. To deal with the missing values of the covariates, we include a response indicator, which is equal to 1 if all the covariates are observed and 0 otherwise, as well as the original variable where the missing values are replaced with zero. The latter variable represents the value of the corresponding variable conditional on being observed. The outcome of interest is the satisfaction with Seguro Popular, which ranges from 1 (very good) to 5 (very bad). For the purpose of illustration, we dichotomize the outcome, ie, we denote $Y_{ij} = 1$ if the score is less than or equal to 3 and $Y_{ij} = 0$ otherwise. For those who did not enroll in the program, we do not observe their satisfaction level. As a result, we have a high missing proportion of 79.4%.

4.2 | Sensitivity analysis

We begin by computing the no-assumption bounds for the ATOU and ATOP. To account for sample variability, we construct confidence intervals for each set of bounds. Because the lower and upper bounds correspond to the minimum and maximum values for some parameters, we cannot directly use traditional techniques.³¹⁻³⁴ Instead, we use the method proposed by Jiang and Ding,³⁵ which gives the confidence intervals for a partial identification parameter π of the form,

$$\max\{L(1), \dots, L(Q)\} \leq \pi \leq \min\{U(1), \dots, U(R)\},$$

where $L(\cdot)$ and $U(\cdot)$ are functions of observed probabilities. To apply this procedure, we transform the bounds in Theorem 3 as

$$\max_k \{f^{[l,u]}(\omega_1, \Delta_k, \omega_0, \Delta_k)\} \leq \text{ATOP} \leq \min_k \{g^{[l,u]}(\omega_1, \Delta_k, \omega_0, \Delta_k)\},$$

where Δ_k is the k th term in the expression of Δ . A similar transformation can be applied to the other bounds as well.

Table 1 presents the naive estimates using available units and available pairs ($\hat{\tau}_{\text{ATOP}}$) as well as the no-assumption bounds for the ATOU and ATOP. For each estimate, we also report its corresponding 95% confidence interval. Although

TABLE 1 The naive estimates using available units and pairs for the average treatment effect on the satisfaction with Seguro Popular^a

Satisfaction with Seguro popular	
Naive estimates using available units	
Estimates	-0.023
95% confidence intervals	(-0.038, -0.010)
Naive estimates using available pairs ($\hat{\tau}_{\text{ATOP}}$)	
Estimates	-0.075
95% confidence intervals	(-0.118, -0.039)
Average treatment effect for always-observed units (ATOUs)	
Bounds	(-1, 1)
95% confidence intervals	(-1, 1)
Average treatment effect for always-observed pairs (ATOPs)	
Bounds	(-1, 1)
95% confidence intervals	(-1, 1)

^aThe no-assumption bounds for the average treatment effect for always-observed units (ATOUs) and for always-observed pairs (ATOPs) are also shown. Given a high proportion of missing values, these bounds are not informative.

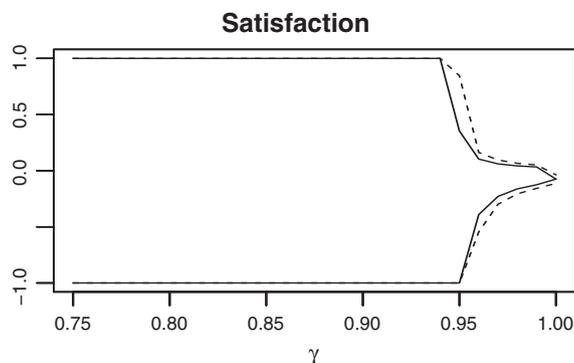


FIGURE 2 Sensitivity analysis for the ATOP. The solid lines are the bounds and the dashed lines are the confidence intervals

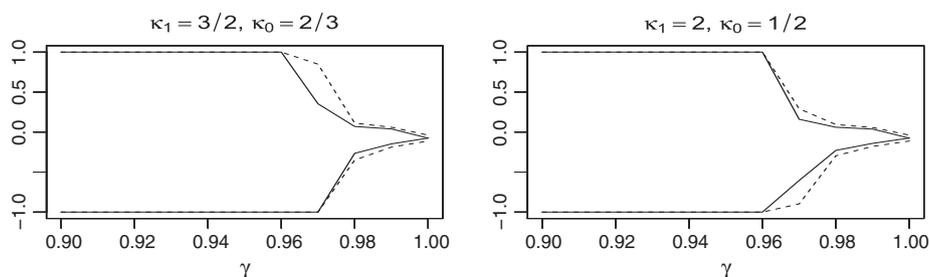


FIGURE 3 Sensitivity analysis for the ATOP in observational studies. The solid lines are the bounds, and the dashed lines are the confidence intervals. When $\kappa_1 = 3/2$ and $\kappa_0 = 2/3$, $\Pr\{R_{ij}(1) = 1\} = 0.297$ and $\Pr\{R_{ij}(0) = 1\} = 0.046$, and when $\kappa_1 = 2$ and $\kappa_0 = 1/2$, $\Pr\{R_{ij}(1) = 1\} = 0.268$ and $\Pr\{R_{ij}(0) = 1\} = 0.042$

the naive estimates are statistically significantly negative, the no-assumption bounds are not informative at all due to the high missing proportion.

Next, we conduct the proposed sensitivity analysis for the ATOP's with different values of γ . Figure 2 shows the results. The 95% confidence interval for the bounds do not cover zero unless γ is very close to 1. Therefore, unless pairing is done near perfectly, we cannot conclude that the ATOP is statistically significantly negative. However, when pairing is done well, the bounds become much narrower than the no-assumption bounds, giving us some information about the ATOP.

Finally, even though this is an experimental study, for the sake of illustration, we conduct the proposed sensitivity analysis for observational studies using Theorem 4. We fix the values of the 2 sensitivity parameters, κ_1 and κ_0 , and vary the remaining sensitivity parameter γ . We choose 2 levels for both κ_1 and κ_0 : $(\kappa_1, \kappa_0) = (3/2, 2/3)$ and $(\kappa_1, \kappa_0) = (2, 1/2)$. Figure 3 shows the results. As expected, compared with Figure 2, the bounds in Figure 3 are wider. However, as in the case of randomized experiments, the bound widths become substantially narrower as we increase the value of γ . This implies that the within-pair similarity can help narrow the bounds in observational studies as well.

5 | CONCLUDING REMARKS

In this paper, we propose a sensitivity analysis for the matched-pairs design in the presence of missing outcome due to the truncation-by-death problem. We begin with the development of such methodology for randomized experiments and extend it to observational studies. Design considerations are essential for valid and efficient causal inference, and we believe that sensitivity analyses should also be based on the features of study designs. The current paper illustrates this new direction of methodological research by exploiting the fact that under the matched-pairs design similar units are used to form pairs: If matching is successful, the missingness pattern of one unit should be informative about that of the other unit within the same pair. Future research might explore a similar approach to more general randomized block designs in randomized experiments as well as stratification in observational studies.

The sensitivity analysis including the one developed in this paper is a general tool for assessing the robustness of empirical findings to the violation of key identification assumptions. In our empirical application, we find that the results are quite sensitive to the quality of matches. Our analysis also emphasizes the importance of high-quality matches in obtaining robust empirical findings. For this reason, we believe that a sensitivity analysis should play an essential role in empirical research.

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APPENDIX A: MATHEMATICAL APPENDIX

A.1 | Preliminaries

We need the following lemma to simplify the derivation of the bounds.

Lemma 1. (Cheng and Small³⁶)

Let X_0 be a mixture of two variables X_1 and X_2 with $X_0 \sim qX_1 + (1 - q)X_2, X_i \in [l, u]$, and a known mixing proportion q . Then we have

$$\begin{aligned} \max \left(l, u - \frac{u - \mathbb{E}(X_0)}{q} \right) &\leq \mathbb{E}(X_1) \leq \min \left(u, \frac{\mathbb{E}(X_0) - l}{q} + l \right), \\ \max \left(l, u - \frac{u - \mathbb{E}(X_0)}{1 - q} \right) &\leq \mathbb{E}(X_2) \leq \min \left(u, \frac{\mathbb{E}(X_0) - l}{1 - q} + l \right). \end{aligned}$$

We also introduce a general linear programming problem:

$$\begin{aligned} &\text{Minimize } \mathbf{c}^\top \mathbf{q}, \\ &\text{Subject to } \mathbf{A}\mathbf{q} = \mathbf{b}, \quad \mathbf{q} \geq \mathbf{0}. \end{aligned} \tag{A1}$$

The dual problem is

$$\begin{aligned} &\text{Maximize } \mathbf{b}^\top \mathbf{p}, \\ &\text{Subject to } \mathbf{A}^\top \mathbf{p} \leq \mathbf{c}. \end{aligned}$$

The set $\{\mathbf{p} | \mathbf{A}^\top \mathbf{p} \leq \mathbf{c}\}$ is a polyhedron and $\mathbf{b}^\top \mathbf{p}$ reaches its maximum at the vertexes of the polyhedron. According to Danzig and Thapa,³⁷ an optimal solution to the dual problem corresponds to an optimal solution to the original problem. Therefore, the solution to the original is

$$L = \max(\mathbf{b}^\top \mathbf{p}_1^*, \dots, \mathbf{b}^\top \mathbf{p}_K^*), \tag{A2}$$

where \mathbf{p}_k^* is the vertex of the polyhedron $\{\mathbf{p} | \mathbf{A}^\top \mathbf{p} \leq \mathbf{c}\}$ and K is the number of the vertexes.

To derive the bounds, we recall some notation in the main text and introduce some new notation. Denote

$$\begin{aligned} \pi &= P(R_{1j} = R_{2j} = 1) \\ \alpha_t &= P(R_{1j} = 1 | T_{1j} = t) = P(R_{2j} = 1 | T_{2j} = t) \\ \psi_t &= \mathbb{E}(Y_{1j} | R_{1j} = 1, T_{1j} = t) = \mathbb{E}(Y_{2j} | R_{2j} = 1, T_{2j} = t) \\ \omega_t &= \mathbb{E}(Y_{1j} | T_{1j} = t, R_{1j} = R_{2j} = 1) = \mathbb{E}(Y_{2j} | T_{2j} = t, R_{1j} = R_{2j} = 1), \\ \phi &= P\{R_1(1) = R_2(0) = 1 | R_1(0) = R_2(1) = 1\} \\ &= P\{R_1(0) = R_2(1) = 1 | R_1(1) = R_2(0) = 1\}, \\ \theta_t &= E\{Y(t) | R_1(1) = R_2(0) = R_2(1) = R_1(0) = 1\}, \\ \lambda_1 &= P\{R(0) = 1 | R(1) = 1\}, \quad \lambda_0 = P\{R(1) = 1 | R(0) = 1\}. \end{aligned}$$

A.2 | Proof of Theorem 1

By the law of total probability, we have

$$\theta_t \phi + E\{Y(t) \mid R_1(1)R_2(0) = 1, R_2(1)R_1(0) = 0\}(1 - \phi) = \omega_t.$$

Then according to Lemma 1, we have

$$\max\left(l, u - \frac{u - \omega_t}{\phi}\right) \leq \theta_t \leq \min\left(u, \frac{\omega_t - l}{\phi} + l\right).$$

Because $ATOP = \theta_1 - \theta_0$, we can express the bounds for $ATOP$ in terms of ϕ :

$$OPLB^{[l,u]}(\phi) = \max\left(l, u - \frac{u - \omega_1}{\phi}\right) - \min\left(u, \frac{\omega_0 - l}{\phi} + l\right), \tag{A3}$$

$$OPUB^{[l,u]}(\phi) = \min\left(u, \frac{\omega_1 - l}{\phi} + l\right) - \max\left(l, u - \frac{u - \omega_0}{\phi}\right). \tag{A4}$$

From the law of total probability, we have

$$\phi\pi + (1 - \pi)P(R_2(1)R_1(0) = 1 \mid R_1(1)R_2(0) = 0) = \pi.$$

According to Lemma 1, we have

$$\max\left(0, \frac{2\pi - 1}{\pi}\right) \leq \phi \leq 1.$$

From (A3) and (A4), $OPLB^{[l,u]}(\phi)$ is nondecreasing and $OPUB^{[l,u]}(\phi)$ is nonincreasing in ϕ , respectively. Thus, we can obtain the bounds for $ATOP$ by setting ϕ to its lower bound:

$$ATOP \in \begin{cases} \left[f^{[l,u]}(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi}), g^{[l,u]}(\omega_1, 2 - \frac{1}{\pi}, \omega_0, 2 - \frac{1}{\pi}) \right] & \text{if } \pi > \frac{1}{2}, \\ [l - u, u - l] & \text{if } \pi \leq \frac{1}{2}, \end{cases}$$

where

$$f^{[l,u]}(x_1, y_1, x_0, y_0) = \max\left\{l, u - \frac{u - x_1}{y_1}\right\} - \min\left\{u, \frac{x_0 - l}{y_0} + l\right\},$$

$$g^{[l,u]}(x_1, y_1, x_0, y_0) = \min\left\{u, \frac{x_1 - l}{y_1} + l\right\} - \max\left\{l, u - \frac{u - x_0}{y_0}\right\}.$$

A.3 | Proof of Theorem 2

Under Assumption 1, we have $P\{R(t) = 1\} = \alpha_1$. Thus, $\lambda_1\alpha_1 = \lambda_0\alpha_0$. By the law of total probability, we can obtain

$$\Delta\lambda_1 + E\{Y(1) \mid R(1) = 1, R(0) = 0\}(1 - \lambda_1) = E\{Y(1) \mid R(1) = 1\} = \psi_1.$$

Then according to Lemma 1, we have

$$\max\left(l, u - \frac{u - \psi_1}{\lambda_1}\right) \leq \Delta \leq \min\left(u, \frac{\psi_1 - l}{\lambda_1} + l\right).$$

Similarly, we have

$$\max\left(l, u - \frac{u - \psi_0}{\lambda_0}\right) \leq \delta_0 \leq \min\left(u, \frac{\psi_0 - l}{\lambda_0} + l\right).$$

Thus, we can write the bounds in terms of λ_1 .

$$\begin{aligned} \text{OUUB}^{[l,u]}(\lambda_1) &= \min\left(u, \frac{\psi_1 - l}{\lambda_1} + l\right) - \max\left(l, u - \frac{\alpha_0(u - \psi_0)}{\alpha_1 \lambda_1}\right), \\ \text{OULB}^{[l,u]}(\lambda_1) &= \max\left(l, u - \frac{u - \psi_1}{\lambda_1}\right) - \min\left(u, \frac{\alpha_0(\psi_0 - l)}{\alpha_1 \lambda_1} + l\right). \end{aligned}$$

By the law of total probability, $\lambda_1 \alpha_1 + P\{R(0) = 1 | R(1) = 0\}(1 - \alpha_1) = \alpha_0$. According to Lemma 1,

$$\lambda_1 \geq \max\left(0, \frac{\alpha_1 + \alpha_0 - 1}{\alpha_1}\right).$$

We can obtain the bounds by maximizing $\text{OUUB}^{[l,u]}(\lambda_1)$ and minimizing $\text{OULB}^{[l,u]}(\lambda_1)$ over γ . Because $\text{OUUB}^{[l,u]}(\lambda_1)$ is decreasing in λ_1 and $\text{OULB}^{[l,u]}(\lambda_1)$ is increasing in λ_1 , we can obtain the bounds for **ATOP** by setting λ_1 to its lower bound:

$$\text{ATOU} \in \begin{cases} \left[f^{[l,u]}(\psi_1, \frac{\Gamma}{\alpha_1}, \psi_0, \frac{\Gamma}{\alpha_0}), g^{[l,u]}(\psi_1, \frac{\Gamma}{\alpha_1}, \psi_0, \frac{\Gamma}{\alpha_0}) \right] & \text{if } \Gamma > 0 \\ [l - u, u - l] & \text{if } \Gamma \leq 0 \end{cases},$$

where $\Gamma = \alpha_1 + \alpha_0 - 1$.

A.4 | Proof of the relation between the bound widths in Theorems 1 and 2

We will show that $\Gamma/\alpha_i \geq 2 - 1/\pi$ for $i = 0, 1$. Without loss of generality, we assume $\alpha_1 \geq \alpha_0$. First, by definition, we have $\alpha_i \geq \pi$ for $i = 0, 1$. Then, for $i = 0$, we have

$$\Gamma/\alpha_0 = \frac{\alpha_1 + \alpha_0 - 1}{\alpha_0} \geq 2 - \frac{1}{\alpha_0} \geq 2 - \frac{1}{\pi}.$$

For $i = 1$, we have

$$\begin{aligned} \Gamma/\alpha_1 - 2 + \frac{1}{\pi} &= \frac{1}{\alpha_1} \left(\frac{\alpha_1}{\pi} + \alpha_0 - \alpha_1 - 1 \right) = \frac{1}{\alpha_1} \left(\frac{\alpha_1 - \alpha_0}{\pi} + \alpha_0 - \alpha_1 + \frac{\alpha_0}{\pi} - 1 \right) \\ &= \frac{1}{\alpha_1} \left\{ (\alpha_1 - \alpha_0) \left(\frac{1}{\pi} - 1 \right) + \frac{\alpha_0}{\pi} - 1 \right\} \geq 0, \end{aligned}$$

which implies $\Gamma/\alpha_1 \geq 2 - 1/\pi$.

For the proof of Theorem 3, we use linear programming. Denote $\zeta_{ijkl} = P\{R_1(1) = i, R_1(0) = j, R_2(1) = k, R_2(0) = l\}$. Because the labels are randomly assigned, some of ζ_{ijkl} are equal. To make it clear for linear programming, we denote

$$\begin{aligned} x_1 &= \zeta_{1111}, x_2 = \zeta_{1101} = \zeta_{0111}, x_3 = \zeta_{1011} = \zeta_{1110}, x_4 = \zeta_{1001} = \zeta_{0110}, x_5 = \zeta_{1010}, \\ x_6 &= \zeta_{0101}, x_7 = \zeta_{1100} = \zeta_{0011}, x_8 = \zeta_{0001} = \zeta_{0100}, x_9 = \zeta_{1000} = \zeta_{0010}, x_{10} = \zeta_{0000}. \end{aligned}$$

We specify the constraint imposed by Assumptions 1 and 2. By the law of total probability, we have the following constraints.

$$\begin{aligned} x_1 + x_2 + x_3 + x_4 &= \pi, \\ x_1 + 2x_3 + x_5 &= P\{R_2(1)R_1(1) = 1\} \geq \gamma\alpha_1, \\ x_1 + 2x_2 + x_6 &= P\{R_2(0)R_1(0) = 1\} \geq \gamma\alpha_0, \\ x_6 + 2x_8 + x_{10} &= P\{R_2(1) = R_1(1) = 0\} \geq \gamma(1 - \alpha_1), \\ x_5 + 2x_9 + x_{10} &= P\{R_2(0) = R_1(0) = 0\} \geq \gamma(1 - \alpha_0), \\ x_3 + x_5 + x_7 + x_9 &= P\{R_1(1) = 1, R_2(0) = 0\} = \alpha_1 - \pi, \\ x_2 + x_6 + x_7 + x_8 &= P\{R_1(1) = 0, R_2(0) = 1\} = \alpha_0 - \pi, \\ x_4 + x_8 + x_9 + x_{10} &= P\{R_1(1) = 0, R_2(0) = 1\} = 1 + \pi - \alpha_1 - \alpha_0, \\ x_i &\geq 0 \quad \text{for } i = 1, \dots, 10. \end{aligned} \tag{A5}$$

We can introduce additional parameter to transform the constraints from inequalities in (A5) to equalities:

$$\begin{aligned}
 x_1 + x_2 + x_3 + x_4 &= \pi, \\
 x_1 + 2x_3 + x_5 - x_{11} &= \gamma\alpha_1, \\
 x_1 + 2x_2 + x_6 - x_{12} &= \gamma\alpha_0, \\
 x_6 + 2x_8 + x_{10} - x_{13} &= \gamma(1 - \alpha_1), \\
 x_5 + 2x_9 + x_{10} - x_{14} &= \gamma(1 - \alpha_0), \\
 x_3 + x_5 + x_7 + x_9 &= \alpha_1 - \pi, \\
 x_2 + x_6 + x_7 + x_8 &= \alpha_0 - \pi, \\
 x_4 + x_8 + x_9 + x_{10} &= 1 + \pi - \alpha_1 - \alpha_0, \\
 x_i &\geq 0 \quad \text{for } i = 1, \dots, 14.
 \end{aligned} \tag{A6}$$

We will use these constraints to derive the bounds for ATOP.

A.5 | Proof of Theorem 3

From Equations A3 and A4, $OPLB^{[l,u]}(\phi)$ is nondecreasing and $OPUB^{[l,u]}(\phi)$ is nonincreasing in ϕ , respectively. Thus, we need only to obtain the sharp lower bound of ϕ . By definition, $\phi = x_1/\pi$. Therefore, we need only to minimize x_1 subject to Equation A6. By solving the dual problem, we have

$$\begin{aligned}
 x_1 \geq \max_{i=0,1} \{ &2\pi - 1 + \gamma(1 - \alpha_i), \pi - (1 - \gamma)(\alpha_1 + \alpha_0), 2\pi - (2 - \gamma)\alpha_i, \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0), \\
 &\pi - (1 - \gamma)(1 - |\alpha_1 - \alpha_0|) \}.
 \end{aligned}$$

Thus, we can obtain the bounds for ATOP:

$$\text{ATOP} \in \begin{cases} [f^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta), g^{[l,u]}(\omega_1, \Delta, \omega_0, \Delta)] & \text{if } \Delta > 0 \\ [l - u, u - l] & \text{if } \Delta \leq 0 \end{cases},$$

where $\Delta = \max_{i=0,1} \{2\pi - 1 + \gamma(1 - \alpha_i), \pi - (1 - \gamma)(\alpha_1 + \alpha_0), 2\pi - (2 - \gamma)\alpha_i, \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0), \pi - (1 - \gamma)(1 - |\alpha_1 - \alpha_0|)\} / \pi$.
 If $\alpha_1 \geq 1/2$ and $\alpha_0 \geq 1/2$, then

$$\begin{aligned}
 2\pi - 1 + \gamma(1 - \alpha_i) - \{2\pi - (2 - \gamma)\alpha_i\} &= (1 - \gamma)(2\alpha_i - 1) \geq 0, \\
 \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0) - \{\pi - (1 - \gamma)(1 - |\alpha_1 - \alpha_0|)\} &= (1 - \gamma)(\alpha_1 + \alpha_0 - 1 - |\alpha_1 - \alpha_0|) \geq 0.
 \end{aligned}$$

Therefore, in this case, we can simplify the expression of Δ as $\Delta = \max_{i=0,1} \{2\pi - 1 + \gamma(1 - \alpha_i), \pi - (1 - \gamma)(2 - \alpha_1 - \alpha_0)\} / \pi$.

A.6 | Proof of Theorem 4

Denote $\alpha_i^* = \Pr\{R(t) = 1\}$. According to Assumption 4, we have $\omega_t = E\{Y_1(t)|R_1(t) = 1, R_2(1 - t) = 1\}$ and

$$\alpha_1^* = \frac{\alpha_1(1 + \kappa_1)}{2\kappa_1}, \quad \alpha_0^* = \frac{\alpha_0(1 + \kappa_0)}{2}.$$

If we view π^* and α_i^* as known, then following the proof of Theorem 3, we have

$$\text{ATOP} \in \begin{cases} [f^{[l,u]}(\omega_1, \Delta(\pi^*), \omega_0, \Delta(\pi^*)), g^{[l,u]}(\omega_1, \Delta(\pi^*), \omega_0, \Delta(\pi^*))] & \text{if } \Delta(\pi^*) > 0 \\ [l - u, u - l] & \text{if } \Delta(\pi^*) \leq 0 \end{cases},$$

where $\Delta(\pi^*) = \max_{i \in \{0,1\}} \{2\pi^* - 1 + \gamma(1 - \alpha_i^*), \pi^* - (1 - \gamma)(\alpha_1^* + \alpha_0^*), 2\pi^* - (2 - \gamma)\alpha_i^*, \pi^* - (1 - \gamma)(2 - \alpha_1^* - \alpha_0^*), \pi^* - (1 - \gamma)(1 - |\alpha_1^* - \alpha_0^*|)\} / \pi$. Because $f^{[l,u]}(\omega_1, \Delta(\pi^*), \omega_0, \Delta(\pi^*))$ is decreasing in $\Delta(\pi^*)$, $g^{[l,u]}(\omega_1, \Delta(\pi^*), \omega_0, \Delta(\pi^*))$ is increasing in $\Delta(\pi^*)$, and $\Delta(\pi^*)$ is decreasing in π^* , we can obtain the bounds for ATOP by taking π^* to its lower bound, $\pi/2$:

$$\text{ATOP} \in \begin{cases} [f^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*), g^{[l,u]}(\omega_1, \Delta^*, \omega_0, \Delta^*)] & \text{if } \Delta^* > 0 \\ [l - u, u - l] & \text{if } \Delta^* \leq 0 \end{cases},$$

where $\Delta^* = \max_{i \in \{0,1\}} \{2\pi - 2 + 2\gamma(1 - \alpha_i^*), \pi - 2(1 - \gamma)(\alpha_1^* + \alpha_0^*), 2\pi - 2(2 - \gamma)\alpha_i^*, \pi - 2(1 - \gamma)(2 - \alpha_1^* - \alpha_0^*), \pi - 2(1 - \gamma)(1 - |\alpha_1^* - \alpha_0^*|)\} / \pi$.