Leveraging Random Assignment in Multiple Imputation of Missing Covariates in Causal Studies

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Abstract

Baseline covariates in randomized experiments are often used in the estimation of treatment effects, for example, when estimating treatment effects within covariate-defined subgroups. In practice, however, covariate values may be missing for some data subjects. To handle missing values, analysts can use multiple imputation to create completed datasets, from which they can estimate the treatment effects. We investigate the performance of multiple imputation routines that utilize randomized treatment assignment, that is, make use of the fact that the true covariate distributions are the same across treatment arms. We do so for both ignorable and non-ignorable missing data, using simulation studies to compare the quality of inferences when we respect or disregard randomization. We consider this question for imputation routines

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estimated with covariates only, and imputation routines estimated conditional on the
outcome variable. In either case, accounting for randomization does not noticeably
improve inferences when sample sizes are in hundreds of units.

**Keywords:** causal; randomization; treatment effect; non-ignorable; identifying restriction.

1 **Introduction**

Randomized experiments are widely considered to be the gold standard for causal inference. Their appeal, in large part, is attributed to randomized treatment assignment, which ensures baseline comparability of all treatment groups. Alternatively stated, randomization balances all covariates on average (Rubin, 2008), facilitating simple causal comparisons. Randomized studies are also separated into two stages, namely (1) the design stage, where covariates are measured and treatments assigned, and (2) the outcome stage, where the outcome variable is measured and compared across treatment groups. Since the design stage is executed without any outcome data in view (Rubin, 2007), results do not systematically favor particular treatment groups (Rubin, 2008).

As with all studies, the data from randomized experiments can suffer from missing values, both in the outcomes and the covariates. While much research focuses on missing outcomes (e.g., Frangakis and Rubin, 1999; Chen et al., 2009; Imai, 2009), we focus on missing covariates here, assuming for didactic reasons that no outcome values are missing. In this situation, analysts who estimate average treatment effects with simple comparisons of outcome means can disregard the missingness in the covariates. However, analysts generally cannot do so when they estimate subgroup treatment effects or use regression adjustment. In such cases, a complete case (CC) analysis sacrifices information and can result in biased estimates. Moreover, a CC analysis violates the intention to treat (ITT) principle in randomized studies (White and Thompson, 2005).

An alternative is to use multiple imputation (MI) (Rubin, 1987, 1996; Little and Rubin,
2002). Here, the analyst fills in missing values with draws from predictive distributions estimated with the observed data. The analyst generates multiple completed datasets, performs complete-data causal inference on each completed dataset, and combines the results using the methods of Rubin (1987).

When implementing MI in randomized experiments, analysts can utilize the randomization in imputation modeling. In other words, they can require the imputed data to be samples from the same covariate distribution, regardless of treatment assignment. In this article, we examine the performance of such MI routines, that is, those that take the marginal independence of the covariates and the treatment into account. We present and illustrate methods for imputing multiple covariates under both ignorable and non-ignorable missingness. We consider MI methods that adhere to the tenets of Rubin (2007, 2008) by keeping the design and outcome stages separate; that is, we do not include the outcome in the covariate imputation model. We also consider MI methods that use the outcome in imputation modeling, as recommended by other authors (e.g., Vach, 1994; Moons et al., 2006). Using simulation studies, we find that respecting randomization in MI offers no appreciable gains over not respecting it, for studies with hundreds of units.

Our results contribute to previous work on using MI for missing covariates in randomized experiments. In particular, as part of broader simulation studies, Sullivan et al. (2018) compare properties of causal estimates when performing MI with a treatment indicator included in the imputation model, and separately within treatment arms. They use methods and run simulations for a single covariate, whereas we use more than one covariate. Additionally, they use MI methods that assume the covariate values to be missing at random, whereas we explicitly develop and use methodology for handling covariate values that are not missing at random. This methodology is presented in detail in the supplementary materials. Finally, they focus on constant treatment effects, whereas we examine scenarios where treatment effects are modified by covariate values.

The remainder of this article is organized as follows. In Section 2, we provide background
on randomized experiments and on our approach to specifying imputation models when multiple covariates may be non-ignorably missing. For the latter, we ensure non-parametric identification (Vansteelandt et al., 2006), which is described in Section 2.2. In Section 3, we show how to respect random assignment in the context of MI with non-parametric identification. In Section 4, we describe the simulation design and results. In Section 5, we implement the methodology using data from Foos and Gilardi (in press). Finally, in Section 6, we conclude with a discussion.

2 Background

We begin with notation and key assumptions in randomized experiments. Here and throughout, we assume a parallel design with an active treatment and a control.

2.1 Randomized experiments

We consider a randomized experiment with \( n \) units. For \( i = 1, \ldots, n \), let \( T_i = 1 \) when unit \( i \) is assigned to the treatment, and \( T_i = 0 \) when unit \( i \) is assigned to the control. For \( i = 1, \ldots, n \), let \( X_{ij} \) denote the value of covariate \( j \) measured for unit \( i \), and let \( X_i = (X_{i1}, \ldots, X_{ip}) \) represent measurements on \( p \) covariates of interest. Let \( Y_i(1) \) and \( Y_i(0) \) be the potential outcomes associated with the treatment and the control, respectively. We assume that all \( n \) units’ potential outcomes, \((Y_i(1), Y_i(0))\), are independent. For each unit, let \( Y_i \) be the outcome value observed at the end of the experiment. In what follows, we forgo the subscript \( i \) when convenient for notation.

We derive results under the stable unit treatment value assumption (SUTVA) (Rubin, 1978). Specifically, we assume that there is only one version of the treatment and no interference between units. With SUTVA, we can express \( Y \) as a deterministic function of \( Y(1) \), \( Y(0) \), and \( T \), namely \( Y = TY(1) + (1 - T)Y(0) \).

For a completely randomized experiment under SUTVA, the treatment status \( T \) is in-
dependent of the potential outcomes \((Y(1), Y(0))\) and the covariates \(X\). We write this as \(T \perp \perp \{Y(1), Y(0), X\}\).

### 2.2 Missing data modeling

If covariate values are non-ignorably missing (Rubin, 1976), the analyst needs to jointly model the covariates and their missingness indicators. This joint distribution cannot be identified without recourse to generally untestable assumptions (Imbens and Pizer, 2000; Ding and Geng, 2014), also known as identifying restrictions. In this section, we describe the approach that we use to make such assumptions, following extant work (e.g., Vansteelandt et al., 2006; Linero and Daniels, 2018).

For ease of exposition, we momentarily ignore \(T\) and \(Y\), and consider \(p\) generic variables, \(X = (X_1, \ldots, X_p)\), that are partly missing. Let \(D = (D_1, \ldots, D_p)\) denote their missingness indicators, such that \(D_j = 1\) when \(X_j\) is missing, and \(D_j = 0\) otherwise, for \(j = 1, \ldots, p\). Here, \(D\) represents a missingness pattern, according to which \(X\) can be divided into two components. We call these \(X_{obs}\), the observed part of \(X\), and \(X_{mis}\), the missing part of \(X\).

The full data distribution, \(f(X_{mis}, X_{obs}, D)\), can be factored into the product of the observed data distribution \(f(X_{obs}, D)\), and the extrapolation distribution \(f(X_{mis}|X_{obs}, D)\) (Daniels and Hogan, 2008). \(f(X_{obs}, D)\) is identifiable from the observed data, whereas \(f(X_{mis}|X_{obs}, D)\) is not. Thus, we need to construct \(f(X_{mis}|X_{obs}, D)\), and consequently \(f(X_{mis}, X_{obs}, D)\), by imposing identifying restrictions. Several restrictions proposed in the literature serve this purpose (see Linero and Daniels, 2018, and references therein). In this article, we confine our attention to two, namely the itemwise conditionally independent non-response (ICIN) assumption (Sadinle and Reiter, 2017), and the missing at random (MAR) assumption (Gill et al., 1997).

**Definition 1** (Itemwise Conditionally Independent Non-response (ICIN)). \((X_1, \ldots, X_p)\) are missing according to the itemwise conditionally independent non-response assumption when \(X_j \perp \perp D_j|X_{-j}, D_{-j}\), for \(j = 1, \ldots, p\). Here, \(X_{-j} = (X_1, \ldots, X_{j-1}, X_{j+1}, \ldots, X_p)\), and \(D_{-j}\) is
defined likewise.

In other words, with ICIN we presume that controlling for all other variables and their missingness indicators, the missingness of $X_j$ does not predict its value and vice versa.

**Definition 2 (Missing at Random (MAR)).** If $(X_1, \ldots, X_p)$ are missing at random, then for each missingness pattern $D$, $f(D|X_{\text{mis}}, X_{\text{obs}}) = f(D|X_{\text{obs}})$. This can be re-expressed as $f(X_{\text{mis}}|X_{\text{obs}}, D) = f(X_{\text{mis}}|X_{\text{obs}})$.

With MAR, for every $D$, we assume that the missingness is independent of the missing data conditional on the observed data. In the supplementary materials, we illustrate how ICIN and MAR result in identifiable joint distributions for $p = 2$ variables.

For MI, we fill in missing values $M > 1$ times, by drawing independently from the extrapolation distribution $f(X_{\text{mis}}|X_{\text{obs}}, D)$. This creates $M$ complete data sets, each of which is analyzed separately. Point and variance estimates are then combined using the rules provided in Rubin (1987).

### 3 Methods for handling missing covariates

For purposes of illustration, we consider a randomized experiment with two binary covariates, $(X_1, X_2) \in \{0, 1\}^2$, having associated missingness indicators $(D_1, D_2) \in \{0, 1\}^2$. The treatment status $T \in \{0, 1\}$, and the binary outcome $Y \in \{0, 1\}$, are fully observed.

#### 3.1 Design stage modeling

Covariates are design stage quantities. To follow the principle that the design stage should remain free of any influence from the outcome, the imputation model for $(X_1, X_2)$ should only include quantities observable at the time of treatment assignment. Hence, in our example, the data used for imputation modeling will be $(X_1, X_2, D_1, D_2, T)$. This can be expressed as a $2^5$ contingency table.
In many contexts, covariates are measured before randomizing units to treatment or control. In such scenarios, it is unlikely that the reasons for missingness in the covariates depend on treatment group membership. As a result, it is reasonable to regard \((D_1, D_2)\) as pretreatment variables, implying that \((X_1, X_2) \perp\!\!\!\perp T\). Since we have \((X_1, X_2) \perp\!\!\!\perp T\), we can collapse the 2\(^5\) table over \(T\), forming a 2\(^4\) marginal table for \((X_1, X_2, D_1, D_2)\). Thus, in the design stage, respecting randomization is equivalent to treating \((X_1, X_2, D_1, D_2)\) as full data. MI then proceeds by identifying \(f(X_1, X_2, D_1, D_2)\), and drawing imputations from \(f(X_{mis}|X_{obs}, D_1, D_2)\). The ICIN and MAR assumptions used for identification will respectively be \(X_j \perp D_j|X_{-j}, D_{-j}\), and \(f(X_{mis}|X_{obs}, D_1, D_2) = f(X_{mis}|X_{obs})\).

On the contrary, not utilizing randomization means disregarding the independence of \((X_1, X_2)\) and \((D_1, D_2)\) with respect to \(T\). We hence use the full 2\(^5\) contingency table, and identify \(f(X_1, X_2, D_1, D_2, T)\). Imputations are then generated from \(f(X_{mis}|X_{obs}, D_1, D_2, T)\), analogous to separately imputing within the \(T = 0\) and \(T = 1\) groups. Thus, the ICIN and MAR assumptions are, respectively, \(X_j \perp D_j|X_{-j}, D_{-j}, T\) and \(f(X_{mis}|X_{obs}, D_1, D_2, T) = f(X_{mis}|X_{obs}, T)\).

Intuitively, accounting for randomization can offer the potential for improved accuracy in estimating treatment effects. By collapsing over treatment groups, we estimate imputation model parameters using the full study sample. In contrast, by imputing separately within treatment groups, we estimate imputation model parameters in each group, using a smaller sample size. This decreased sample size can result in larger parameter uncertainty, which in turn can result in greater variability in the imputations, and hence MI inferences.

We remark here that we interpret randomization to imply that \((X_1, X_2)\) and \((D_1, D_2)\) are both independent of \(T\). Yet, situations exist where this independence does not apply to the missingness indicators. For example, suppose covariate information is collected in surveys administered shortly after treatment assignment. This technically makes \((X_1, X_2)\) outcome variables, but analysts may still treat them as pre-treatment covariates. When missing values in the covariates occur after treatment assignment, the \((D_1, D_2)\) distribution...
could be dissimilar across treatment groups. We do not consider MI inferences under such scenarios, which we leave as a subject of future work.

3.2 Outcome stage modeling

For missing covariates in regression models, it has been generally recommended that the outcome $Y$ be used in MI (Rubin and Schenker, 1991; Vach and Blettner, 1991; Greenland and Finkle, 1995; Barnard and Meng, 1999; Little and Rubin, 2002; Moons et al., 2006; Sterne et al., 2009). In randomized experiments, this has the disadvantage of allowing $Y$ to directly influence the design stage, which can bring the face validity of the final conclusions into question. At the same time, not controlling for $Y$ in imputations can lead to distorted estimates, particularly when regression-adjusted estimators are of interest. Little (1992) elucidates this issue: if a partly missing covariate $X$ is highly predictive of $Y$, then $Y$ will carry information about $X$ that may not be captured by other variables in the imputation model. If $X$ is imputed without using $Y$, then the imputed part of $X$ will have no (conditional) association with $Y$. This could falsely attenuate the overall covariate-outcome association.

In our example, an imputation model in the outcome stage uses $(X_1, X_2, D_1, D_2, T, Y)$ as data. This forms a contingency table with $2^6$ cells. One way to allow randomization to play a role here is to collapse this $2^6$ table across $T$. However, this makes a strong assumption that $Y \perp T$, which ultimately could underestimate the treatment effect (see Lu and Ashmead, 2018, for an illustrative simulation). A more principled way is to factorize the joint distribution $f(X_{mis}, X_{obs}, D_1, D_2, T, Y)$ to naturally represent the design and outcome stages as

$$f(X_{mis}, X_{obs}, D_1, D_2, T, Y) = f(X_{mis}, X_{obs}, D_1, D_2, T) f(Y|X_{mis}, X_{obs}, D_1, D_2, T).$$

(1)

Here, $f(X_{mis}, X_{obs}, D_1, D_2, T)$ represents the joint distribution of the design stage quantities, and $f(Y|X_{mis}, X_{obs}, D_1, D_2, T)$ is the entire outcome response surface. Under random
assignment, we have \((X_{\text{mis}}, X_{\text{obs}}) \perp \perp T\), and assume \((D_1, D_2) \perp \perp T\), so that we have

\[
\begin{align*}
    f(X_{\text{mis}}|X_{\text{obs}}, D_1, D_2, T, Y) &\propto f(X_{\text{mis}}, X_{\text{obs}}, D_1, D_2, T, Y) \\
    &\propto f(X_{\text{mis}}, X_{\text{obs}}, D_1, D_2) f(Y|X_{\text{mis}}, X_{\text{obs}}, D_1, D_2, T).
\end{align*}
\]  

(2)

We can use (2) to generate imputations, as we explain in the ensuing section.

In practice, we specify \(f(Y|X_{\text{mis}}, X_{\text{obs}}, D_1, D_2, T)\) using the outcome model posited for analysis. Often, however, analysis models of interest do not adjust for the missingness indicators, in which case, the conditional independence assumption \(Y \perp \perp (D_1, D_2)|X_1, X_2, T\) is implicitly made.

If we ignore randomization, we essentially use the treatment as well as the outcome in the imputation model. This amounts to identifying \(f(X_1, X_2, D_1, D_2, T, Y)\), and generating imputations from \(f(X_{\text{mis}}|X_{\text{obs}}, D_1, D_2, T, Y)\). The ICIN and MAR assumptions used for identification will now be \(X_j \perp \perp D_j|X_{-j}, D_{-j}, T, Y\), and \(f(X_{\text{mis}}|X_{\text{obs}}, D_1, D_2, T, Y) = f(X_{\text{mis}}|X_{\text{obs}}, T, Y)\), respectively.

4 Simulation study

We now conduct repeated sampling studies to evaluate the performance of the methods discussed in Section 3. We use twelve simulation settings, comprising all combinations of three missingness scenarios, two identifying restrictions, and two covariate-outcome associations. We begin by describing the data generation process.

4.1 Data generation

We simulate the randomized experiment from our running example for \(n = 1000\) units. Each unit is randomized to the treatment or the control arm with equal probabilities, i.e., \(T\) is generated from a Bernoulli distribution with mean 0.5. We generate \((X_1, X_2)\) and \((D_1, D_2)\)
as per the MAR and ICIN assumptions, under three missingness scenarios.

4.1.1 Scenario 1

In scenario 1, we regard \((D_1, D_2)\) as pre-treatment variables, and generate them independently of \(T\).

To simulate an MAR situation under this scenario, we first draw \(X_1 \sim \text{Bernoulli}(0.7)\), followed by \(X_2|X_1 = 1 \sim \text{Bernoulli}(0.45)\) and \(X_2|X_1 = 0 \sim \text{Bernoulli}(0.6)\). Subsequently, we delete at random 35% of the observations from \(X_1\), and 40% of the observations from \(X_2\). The true missingness mechanism is thus missing completely at random (MCAR), which is a special case of MAR.

To create missingness as per ICIN, we make use of the relationship between the ICIN assumption and hierarchical loglinear models. A discussion of this relationship and the data generation approach that follows is deferred to the supplementary materials. We begin by generating \(D_1 \sim \text{Bernoulli}(0.35)\) and \(D_2 \sim \text{Bernoulli}(0.40)\). Next, we split the \(2^4\) contingency table for \((X_1, X_2, D_1, D_2)\) into four, partial \(2^2\) tables, controlling for \((D_1, D_2)\). Let \(m(x_1, x_2), (d_1, d_2)\) represent the expected count for \((X_1, X_2) = (x_1, x_2)\) in the partial table with \((D_1, D_2) = (d_1, d_2)\). We simulate \(m(x_1, x_2), (d_1, d_2)\) from the loglinear model

\[
\log m(x_1, x_2), (d_1, d_2) = 5 + 0.3x_1 - 0.5x_2 + 0.009d_1 + 0.05d_2 
+ 0.5x_1x_2 + 0.75x_1d_2 + 1x_2d_1 + 0.25d_1d_2. \tag{3}
\]

Further, we obtain multinomial probabilities \(\pi(x_1, x_2), (d_1, d_2)\) using (Agresti, 2012)

\[
\pi(x_1, x_2), (d_1, d_2) = \frac{m(x_1, x_2), (d_1, d_2)}{\sum_{x_1} \sum_{x_2} m(x_1, x_2), (d_1, d_2)}. \tag{4}
\]

For each missingness pattern \((D_1, D_2) = (d_1, d_2)\), we jointly draw \((X_1, X_2) = (x_1, x_2)\) with probability \(\pi(x_1, x_2), (d_1, d_2)\), and set \(X_j\) to missing wherever \(D_j = 1\), where \(j = 1, 2\). Similar to the MAR setting, this approach gives \(P(X_1 = 1) \approx 0.7\), \(P(X_2 = 1|X_1 = 0) \approx 0.6\), and
Table 1: Counts for the observed data generated as per ICIN using the loglinear model approach, for a fixed random seed. NA represents a missing value.

|             | $X_2 = 0$ | $X_2 = 1$ | $X_2 = NA$ |
|-------------|-----------|-----------|------------|
| $X_1 = 0$   | 103       | 55        | 65         |
| $X_1 = 1$   | 97        | 133       | 197        |
| $X_1 = NA$  | 68        | 155       | 127        |

$P(X_2 = 1|X_1 = 1) \approx 0.45$. To illustrate, we display counts for one random draw from the ICIN data generation procedure in Table 1.

We generate $Y$ from a Bernoulli distribution with probabilities defined by

$$\text{logit}(Pr(Y = 1|X_1, X_2, T)) = \alpha_1 X_1 + \alpha_2 X_2 + \alpha T + \alpha_{tx} TX.$$  \hspace{1cm} (5)

We set $\alpha_t = 0.3$. We vary the strength of the association between $(X_1, X_2)$ and $Y$ in two settings. In the high association setting, we set $\alpha_1 = 0.8, \alpha_2 = 0.9, \text{and} \alpha_{tx} = 0.5$. In the low association setting, we set $\alpha_1 = 0.02, \alpha_2 = 0.05, \text{and} \alpha_{tx} = 0.015$.

### 4.1.2 Scenario 2

In scenario 2, we regard $(D_1, D_2)$ to be post-treatment variables. Here, data are generated using the models for $(X_1, X_2, T, Y)$ from scenario 1, except that we draw $D_1$ and $D_2$ from the conditional distributions $D_1|T = 1 \sim \text{Bernoulli} (0.35), D_1|T = 0 \sim \text{Bernoulli} (0.1), \text{and} D_2|T = 1 \sim \text{Bernoulli} (0.40), D_2|T = 0 \sim \text{Bernoulli} (0.1)$. Thus, missingness rates differ by treatment arms, but do not depend on the covariate values.

### 4.1.3 Scenario 3

In scenario 3, we allow $(D_1, D_2)$ to be predictive of $Y$. We generate $(X_1, X_2)$ and $(D_1, D_2)$ as in scenario 1. We linearly adjust for $(D_1, D_2)$ in the outcome generation model, i.e., we
logit \( (Pr(Y = 1|X_1, X_2, D_1, D_2, T)) = \alpha_1 X_1 + \alpha_2 X_2 + \alpha_t T + \alpha_{tx2} TX_2 - 0.6D_1 - 0.4D_2, \) 

(6)

where \((\alpha_1, \alpha_2, \alpha_t, \alpha_{tx2})\) are defined as in scenario 1.

4.2 Methods

For analysis, we specify a working model that adjusts for \((X_1, X_2)\), and introduce effect modification with respect to \(X_2\). We use the logistic regression

\[
\text{logit} \ (Pr(Y = 1|X_1, X_2, T)) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_t T + \beta_{tx2} TX_2. \tag{7}
\]

For scenarios 1 and 2, this model has the same form as the outcome generation model, except that we estimate a non-zero intercept. For scenario 3, the analysis model is misspecified. In all scenarios, the adjusted treatment effect (on the log-odds scale), heterogeneous across categories of \(X_2\), is given by \(\beta_t + \beta_{tx2} x_2\). The parameters of interest are hence \(\beta_t\) and \(\beta_{tx2}\).

We create multiply imputed datasets as per four approaches, including respecting randomization in the design stage (R), not respecting randomization in the design stage (NR), respecting randomization in the outcome stage (RY), and not respecting randomization in the outcome stage (NRY). We first describe MI inference under methods R, NR, and NRY.

Let \(\theta\) denote the vector of probabilities offered by the observed data. Under method R,
we have $\theta = (\theta_1, \ldots, \theta_9)$, where,

\[
\begin{align*}
\theta_1 &= \Pr(X_1 = 0, X_2 = 0, D_1 = 0, D_2 = 0), \\
\theta_2 &= \Pr(X_1 = 0, X_2 = 1, D_1 = 0, D_2 = 0), \\
\theta_3 &= \Pr(X_1 = 1, X_2 = 0, D_1 = 0, D_2 = 0), \\
\theta_4 &= \Pr(X_1 = 1, X_2 = 1, D_1 = 0, D_2 = 0), \\
\theta_5 &= \Pr(X_1 = 1, D_1 = 0, D_2 = 1), \\
\theta_6 &= \Pr(X_1 = 0, D_1 = 0, D_2 = 1), \\
\theta_7 &= \Pr(X_2 = 1, D_1 = 1, D_2 = 0), \\
\theta_8 &= \Pr(X_2 = 0, D_1 = 1, D_2 = 0), \\
\theta_9 &= \Pr(D_1 = 1, D_2 = 1).
\end{align*}
\]

We treat the corresponding counts as a multinomial sample, and place a Dirichlet \((\frac{1}{9})\) prior on \(\theta\). For method NR, we have eighteen observed probabilities, given by (8) - (16) in each treatment arm. Here, we use a Dirichlet \((\frac{1}{18})\) prior for \(\theta\). Similarly, for NRY, \(\theta\) is a vector of thirty six observed probabilities, given by (8) - (16) in each category of \((Y, T)\). We use a Dirichlet \((\frac{1}{36})\) prior for \(\theta\) under NRY.

We carry out multiple imputation in three steps. We first sample a value for \(\theta\) from its posterior distribution, which is also Dirichlet. Using this value, we obtain extrapolation distributions for all missingness patterns, under the identifying restriction of choice. We derive these distributions for the ICIN and MAR assumptions in the supplementary materials. For each missing value, we then generate an imputation from the pattern-specific extrapolation distribution. We repeat these steps \(M = 100\) independent times, creating 100 completed datasets. For each of these, we obtain point and variance estimates for \(\beta_t\) and \(\beta_{tx_2}\), and combine them for MI inferences.

For MI under method RY, we use the data augmentation strategy introduced by Tanner
and Wong (1987). For a given draw of the parameter vector $\gamma = (\theta, \beta)$, where $\theta = (\theta_1, \ldots, \theta_9)$ and $\beta = (\beta_0, \beta_1, \beta_2, \beta_t, \beta_{tx^2})$, we generate an imputation using

$$f(X_{mis}|X_{obs}, D_1, D_2, T, Y, \gamma) \propto f(X_{mis}, X_{obs}, D_1, D_2, \theta) f(Y|X_{obs}, X_{mis}, D_1, D_2, T, \beta). \tag{17}$$

Given the imputed dataset, we update $\theta$ and $\beta$ from their full conditional posterior distributions. For $\theta$, this is a Dirichlet distribution. For sampling from the non-standard conditional posterior of $\beta$, we use the technique based on Polya-Gamma latent variables outlined in Polson et al. (2013).

We repeat all simulations 1000 times and compare the four methods based on the absolute bias, the multiple imputation standard error (MI-SE), the Monte Carlo standard deviation (MC-SD), and coverage of the 95% confidence intervals (95% credible intervals for method RY).

4.3 Results

Here, we present results under the ICIN assumption. Results under the MAR assumption are qualitatively similar, and are included in the supplementary materials.

4.3.1 Scenario 1: High association

Figure 1 displays the coefficient estimates for $\beta_t$ and $\beta_{tx^2}$ under scenario 1, when the covariate-outcome association is high. Table 2 displays the MC-SDs, MI-SEs, and coverage probabilities for the same scenario.

For both coefficients, R and NR produce almost equivalent distributions of MI point estimates. We also see little difference in the MI standard errors for the two approaches. We ascribe this finding to the relatively large sample size. With 500 units in each treatment arm, we are able to estimate the parameters of the MI model, i.e., the probabilities of generating each missing value, fairly accurately, regardless of whether we combine the data or impute
Figure 1: Results for scenario 1 under ICIN for the high association setting. The left panel represents the distribution of $\beta_t$ estimates over 1000 replications, where the true value of $\beta_t = 0.3$. The right panel represents the distribution of $\beta_{tx_2}$ estimates over 1000 replications, where the true value of $\beta_{tx_2} = 0.5$.

separately in each treatment arm. With binary covariate data, small differences in the precision of the probabilities do not substantially alter the posterior predictive distribution for the missing values. The accuracy gain is further diluted, since only a modest fraction of cases are missing. Finally, we note that the analysis model adjusts for both $X_1$ and $X_2$. This can dampen the effect of the accuracy gain even further, as adjustment for covariates is known to increase precision against any residual imbalances that exist in spite of randomization. Comparing RY and NRY, we see a similar pattern. The distributions of point estimates under both the methods are quite similar, although MI standard errors are slightly smaller under RY than under NRY.

For $\beta_t$, the outcome stage methods produce approximately unbiased estimates (simulated absolute bias $\leq 0.001$). The simulated absolute biases for their design stage counterparts are higher ($\approx 0.04$). Differences are more pronounced for the interaction coefficient $\beta_{tx_2}$, with biases for methods R and NR escalating to 0.2 in the negative direction. As $\beta_{tx_2}$ measures how the conditional association between $Y$ and $X_2$ is modified by $T$, this coefficient is attenuated
Table 2: MC standard deviations, MI standard errors and coverage probabilities for $\beta_t$ and $\beta_{tx^2}$, under the high association setting in scenario 1.

| Method | $\beta_t$ MC-SD | $\beta_t$ MI-SE | $\beta_t$ Coverage | $\beta_{tx^2}$ MC-SD | $\beta_{tx^2}$ MI-SE | $\beta_{tx^2}$ Coverage |
|--------|----------------|----------------|------------------|----------------------|-------------------|-------------------|
| R      | 0.192          | 0.225          | 0.974            | 0.255                | 0.370             | 0.978             |
| NR     | 0.192          | 0.225          | 0.975            | 0.255                | 0.371             | 0.983             |
| RY     | 0.232          | 0.228          | 0.950            | 0.433                | 0.427             | 0.946             |
| NRY    | 0.233          | 0.235          | 0.957            | 0.436                | 0.443             | 0.947             |

as a result of imputing $X_2$ without using $Y$, explaining the large negative bias. We note that the design stage methods do exhibit some efficiency gains over the outcome stage methods, with empirical standard errors for $\beta_{tx^2}$ about 14% smaller.

In the case of methods R and NR, MI-SEs for both coefficients are fairly large compared to the corresponding MC-SDs. Particularly for $\beta_{tx^2}$, we observe that MI-SEs are large even relative to the point estimates. It is well known that the MI variance estimator can be positively biased (Wang and Robins, 1998; Robins and Wang, 2000; Reiter and Raghunathan, 2007), and in this case, its mean value is almost 45% larger than the corresponding Monte Carlo variance. Given the diluted estimates for $\beta_{tx^2}$, such large standard errors often lead to wide confidence intervals containing 0; in fact, this happens almost 95% of the times in the simulations. This has clear implications for assessing the significance of the treatment effect. Both R and NR provide coverage rates around 97%, whereas RY and NRY exhibit close to nominal coverage.

4.3.2 Scenario 1: Low association

Figure 2 displays the coefficient estimates under scenario 1 when the covariate-outcome association is low. Table 3 provides the corresponding empirical standard errors and coverage rates. Once again, we observe that methods R and NR produce similar distributions of point estimates and standard errors. MI-SEs for NRY are about 9% larger (for $\beta_t$) and
7% larger (for $\beta_{tx^2}$) than those under RY. Both the design and the outcome stage methods produce approximately unbiased coefficient estimates (simulated absolute bias $\leq 0.01$ for all). Owing to the low association, the outcome does not carry much information about the partly missing covariates, which reduces the omitted variable bias due to its exclusion in the covariate imputation model. The MI-SEs, particularly for $\beta_{tx^2}$, are largely inflated for all four imputation methods. This is not surprising, since adjustment for non-prognostic, “random-noise” covariates in logistic regression leads to a loss in precision when estimating treatment effects (Robinson and Jewell, 1991; Kahan et al., 2014). Although at the cost of wider confidence intervals, RY and NRY exhibit close to nominal coverage rates, and R and NR have larger than nominal coverage rates.

4.3.3 Scenarios 2 and 3

Under scenarios 2 and 3, conclusions about the four imputation methods do not fundamentally change. At $n = 1000$, methods respecting and not respecting randomization produce similar point estimates, standard errors, and coverage rates. When the association between the covariates and the outcome is high, the design stage methods continue to be biased—although biases are more marked than before—with lower MI standard errors, while the outcome stage methods are approximately unbiased, with higher MI standard errors. When this association is low, all four methods produce comparable point estimates. We present the related graphical and tabular displays in the supplementary materials.

5 Application

We now present an application of the four imputation methods to data from a randomized experiment analyzed in Foos and Gilardi (in press), available at https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/BSIFTF. The data comprise $n = 612$ women, randomized to receive ($T = 1$) or not to receive ($T = 0$) an invitation
Figure 2: Results for scenario 1 under ICIN for the low association setting. The left panel represents the distribution of $\beta_t$ estimates over 1000 replications, where the true value of $\beta_t = 0.3$. The right panel represents the distribution of $\beta_{tx_2}$ estimates over 1000 replications, where the true value of $\beta_{tx_2} = 0.015$.

to a career workshop in politics. Approximately two-thirds of the participants receive the treatment. The primary behavioral outcome $Y$ is binary, with $Y = 1$ if the participant applies to a political office mentoring program, and $Y = 0$ if she does not. Several pre-treatment covariates are measured in the original experiment. We consider two that are highly associated with the outcome, namely an indicator of whether the participant takes an active interest in planning her career ($X_1$), and an indicator of whether the participant wishes to have children in the future ($X_2$). $X_1$ is binary, and exhibits low levels of missingness (2.3%). $X_2$ contains a “perhaps/don’t know” category, which we regard as missing values, as in, for example, Rubin et al. (1995) and Sadinle and Reiter (2017). This results in 26% missingness in $X_2$.

We note that the distribution of the outcome variable is highly imbalanced, with only 1.5% of the participants applying to the mentoring program. This leads to analysis models with interaction terms exhibiting perfect prediction issues. We hence focus on estimating the regression-adjusted average treatment effect measured on the log-odds scale, and use the
Table 3: MC standard deviations, MI standard errors and coverage probabilities for $\beta_t$ and $\beta_{tx^2}$ under the low association setting in scenario 1.

| Method | $\beta_t$ MC-SD | $\beta_t$ MI-SE | $\beta_t$ Coverage | $\beta_{tx^2}$ MC-SD | $\beta_{tx^2}$ MI-SE | $\beta_{tx^2}$ Coverage |
|--------|-----------------|-----------------|-------------------|---------------------|---------------------|------------------------|
| R      | 0.168           | 0.208           | 0.989             | 0.208               | 0.302               | 0.995                  |
| NR     | 0.169           | 0.209           | 0.988             | 0.209               | 0.303               | 0.995                  |
| RY     | 0.222           | 0.220           | 0.988             | 0.334               | 0.327               | 0.948                  |
| NRY    | 0.225           | 0.240           | 0.948             | 0.340               | 0.351               | 0.944                  |

Model logit ($\pi$) = $\beta_0 + \beta_1X_1 + \beta_2X_2 + \beta_tT$, where $\pi = Pr(Y = 1|X_1, X_2, T)$. The coefficient of interest is $\beta_t$. We also note that there is non-compliance in the experiment, since not everyone in the treatment group attended the career workshop. Accordingly, we carry out an ITT analysis. Akin to the simulations, we use $M = 100$ imputations for methods R, NR, and NRY, and iterate to convergence for method RY. We also present results under a CC analysis as a standard against which to compare the MI methods.

Table 4 displays the resultant point estimates, MI standard errors and 95% confidence intervals (credible intervals for RY), obtained under the ICIN and MAR assumptions. In line with our simulation results for $\beta_t$, we see that estimates and standard errors are nearly identical for R and NR. There are slight differences between RY and NRY, with RY appearing to be marginally more efficient. The differences between design and outcome stage imputation are not remarkable, possibly due to the sparsity of $Y = 1$ cases in the sample and low missingness levels in the covariates. Results also seem fairly insensitive to the choice of the identifying assumption. We note, however, that CC analysis produces higher standard errors (due to the reduced sample size) and different point estimates in comparison to the four MI methods.
Table 4: Point estimates, MI standard errors and 95 % confidence (credible) intervals for log-odds scale average treatment effect under the ICIN and MAR assumptions.

| Method | Estimate | MI-SE | 95 % CI       | Estimate | MI-SE | 95 % CI       |
|--------|----------|-------|---------------|----------|-------|---------------|
| R      | -0.462   | 0.678 | (-1.790, 0.866) | -0.464   | 0.678 | (-1.792, 0.864) |
| NR     | -0.462   | 0.678 | (-1.791, 0.867) | -0.464   | 0.678 | (-1.792, 0.865) |
| RY     | -0.466   | 0.669 | (-1.810, 0.831) | -0.451   | 0.672 | (-1.812, 0.827) |
| NRY    | -0.469   | 0.678 | (-1.798, 0.860) | -0.470   | 0.679 | (-1.798, 0.859) |
| CC     | -0.692   | 0.715 | (-2.090, 0.709) | -0.692   | 0.715 | (-2.090, 0.709) |

6 Discussion

Our simulations show that, when units have been properly randomized in the design stage and sample sizes are modest, results are practically the same whether one respects or ignores randomization in multiple imputation of missing covariates. For not small \(n\), imputing using \(T\) can add unnecessary variance, but not enough to cause major inefficiencies. We consider samples of size 1000 in the simulations, but additional experiments with \(n = 500\) show similar conclusions. For randomized experiments where one treatment arm has a small sample size, say in the teens, we conjecture that the benefits of accounting for randomization may be more noticeable.

The results produced by the design and outcome stage methods notably differ, especially when the covariates are highly prognostic of the outcome and when one seeks to estimate heterogeneous treatment effects. We observe a trade-off between bias and efficiency. Estimates produced by methods R and NR can be biased, but have relatively low standard errors. The opposite is true for the outcome stage methods. When the covariate-outcome association is low, all four methods give approximately unbiased estimates, although R and NR continue to be more efficient. All in all, MI using the outcome manifests some advantages over MI in the design stage. Of course, this assumes that we use the right imputation model, which one cannot be sure of in practice. Additionally, as with any simulation study, these conclusions
may not generalize to all scenarios.

In practice, the outcome as well as the covariates contain missing values. In the framework of non-parametric identification, it is possible to separate the covariates and the outcome into blocks and place different identifying restrictions within these blocks. One such block-based method has been presented in Sadinle and Reiter (2018). Finally, we note that non-parametric identification and subsequent imputation entails breaking down a data set by the observed missingness patterns. For this procedure to work well, sufficient number of data points per pattern are required, which amounts to having a large enough sample size.

SUPPLEMENTARY MATERIAL

We provide two additional supplements as supporting materials for this article.

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Leveraging Random Assignment in Multiple Imputation of Missing Covariates in Causal Studies - Supplement 1

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1 Introduction

In this supplement, we derive the non-parametric identified distributions used in the multiple imputation (MI) approach in the main text. In Section 2 and Section 3, we obtain the full data and extrapolation distributions under the ICIN and MAR assumptions, respectively. In Section 4, we provide mathematical justification for the loglinear model used to simulate expected counts under ICIN. Throughout, we consider variables $X = (X_1, X_2) \in \{0, 1\}^2$, with missingness indicators $D = (D_1, D_2) \in \{0, 1\}^2$.

2 Identification under the ICIN assumption

Identification under ICIN follows from Theorem 1 in Sadinle and Reiter (2017). We begin by restating a key formula from the theorem. Define

$$\eta_D(X_{obs}) = \log f(X_{obs}, D) - \log \int_{X_{mis}} \exp \sum_{D^* < D} \eta_{D^*}(X_{obs})1(D^* < D) \, dX_{mis}. \quad (1)$$
Here, $D^* < D$ if $D$ has strictly greater number of missing elements than $D^*$. For each missingness pattern, the $\eta$ are obtained as follows.

\[
\eta_{00}(X_1, X_2) = \log f(X_1, X_2, D_1 = 0, D_2 = 0),
\]

\[
\eta_{01}(X_1) = \log f(X_1, D_1 = 0, D_2 = 1) - \log \int_{X_2} f(X_1, X_2, D_1 = 0, D_2 = 0) \, dX_2
\]

\[
= \log \frac{f(X_1, D_1 = 0, D_2 = 1)}{f(X_1, D_1 = 0, D_2 = 0)},
\]

\[
\eta_{10}(X_2) = \log f(X_2, D_1 = 1, D_2 = 0) - \log \int_{X_1} f(X_1, X_2, D_1 = 0, D_2 = 0) \, dX_1
\]

\[
= \log \frac{f(X_2, D_1 = 1, D_2 = 0)}{f(X_2, D_1 = 0, D_2 = 0)},
\]

\[
\eta_{11} = \log f(D_1 = 1, D_2 = 1)
\]

\[
- \log \int_{X_1} \int_{X_2} \exp \left[ \eta_{00}(X_1, X_2) + \eta_{01}(X_1) + \eta_{10}(X_2) \right] \, dX_2 \, dX_1
\]

\[
= \log \frac{f(D_1 = 1, D_2 = 1)}{C},
\]

where,

\[
C = \int_{X_1} \int_{X_2} \left( \frac{f(X_1, X_2, D_1 = 0, D_2 = 0)f(X_1, D_1 = 0, D_2 = 1)}{f(X_2, D_1 = 1, D_2 = 0)} \right. \\
\left. \quad \times \frac{f(X_1, D_1 = 0, D_2 = 0)}{f(X_2, D_1 = 0, D_2 = 0)} \right) \, dX_2 \, dX_1.
\]
Further, for each \((D_1, D_2)\) we have

\[
f(X_1, X_2, D_1, D_2) = \exp \sum_{D^* \leq D} \eta_{D^*}(X_{\text{obs}}). \tag{7}
\]

Hence,

\[
f(X_1, X_2, D_1 = 0, D_2 = 1) = \exp \left[ \eta_{00}(X_1, X_2) + \eta_{01}(X_1) \right]
\]

\[
= \frac{f(X_1, X_2, D_1 = 0, D_2 = 0) f(X_1, D_1 = 0, D_2 = 1)}{f(X_1, D_1 = 0, D_2 = 0)}, \tag{8}
\]

\[
f(X_1, X_2, D_1 = 1, D_2 = 0) = \exp \left[ \eta_{00}(X_1, X_2) + \eta_{10}(X_2) \right]
\]

\[
= \frac{f(X_1, X_2, D_1 = 0, D_2 = 0) f(X_2, D_1 = 1, D_2 = 0)}{f(X_2, D_1 = 0, D_2 = 0)}, \tag{9}
\]

\[
f(X_1, X_2, D_1 = 1, D_2 = 1) = \exp \left[ \eta_{00}(X_1, X_2) + \eta_{01}(X_1) + \eta_{10}(X_2) + \eta_{11} \right]
\]

\[
= \frac{f(X_1, X_2, D_1 = 0, D_2 = 0) f(X_1, D_1 = 0, D_2 = 1)}{f(X_1, D_1 = 0, D_2 = 0)} \times \frac{f(X_2, D_1 = 1, D_2 = 0) f(D_1 = 1, D_2 = 1)}{f(X_2, D_1 = 0, D_2 = 0)} \times \frac{1}{C}, \tag{10}
\]

where \(C\) is as defined in (6). It is straightforward to compute the extrapolation distribution for each \((D_1, D_2)\) using

\[
f(X_{\text{mis}}|X_{\text{obs}}, D_1, D_2) \propto f(X_{\text{mis}}, X_{\text{obs}}, D_1, D_2). \tag{11}
\]
3 Identification under the MAR assumption

Under MAR, the following condition holds:

\[
 f(X_{\text{mis}}|X_{\text{obs}}, D) = f(X_{\text{mis}}|X_{\text{obs}}) = \sum_{D^* \in \mathcal{D}} f(X_{\text{mis}}|X_{\text{obs}}, D^*) f(D^*|X_{\text{obs}}), \tag{12}
\]

where \( \mathcal{D} \) is the set of all missingness patterns that have been realized in the data. In other words, the extrapolation distribution for a particular missingness pattern is obtained by marginalizing across all observed missingness patterns. We note here that an MCAR distribution can also be obtained using (12), simply by replacing \( f(D^*|X_{\text{obs}}) \) with \( f(D^*) \).

When \( p = 2 \), we have \( \mathcal{D} = \{(0, 0), (0, 1), (1, 0), (1, 1)\} \). For purposes of illustration, we assume that all patterns in \( \mathcal{D} \) have been realized. For \((D_1, D_2) = (0, 1)\), we have

\[
 f(X_2|X_1, 0, 1) = f(X_2|X_1, 0, 0)f(0, 0|X_1) + f(X_2|X_1, 0, 1)f(0, 1|X_1) \\
+ f(X_2|X_1, 1, 0)f(1, 0|X_1) + f(X_2|X_1, 1, 1)f(1, 1|X_1). \tag{13}
\]

For each pattern in the RHS above, we equate the appropriate extrapolation distribution to the corresponding distribution under \((D_1, D_2) = (0, 0)\). That is, for \( D^* \in \mathcal{D} \), we equate \( f(X_{\text{mis}}|X_{\text{obs}}, D^*) = f(X_{\text{mis}}|X_{\text{obs}}, 0, 0) \). Thus, we have

\[
 f(X_2|X_1, 0, 1) = f(X_2|X_1, 0, 0), \tag{14}
\]
\[
 f(X_2|X_1, 1, 0) \propto f(X_1, X_2, 1, 0) \\
\propto f(X_1|X_2, 1, 0)f(X_2, 1, 0) = f(X_1|X_2, 0, 0)f(X_2, 1, 0), \tag{15}
\]
\[
 f(X_2|X_1, 1, 1) \propto f(X_1, X_2, 1, 1) \\
\propto f(X_1, X_2|1, 1)f(1, 1) = f(X_1, X_2|0, 0)f(1, 1). \tag{16}
\]
We similarly identify the extrapolation distribution for \((D_1, D_2) = (1, 0)\). We have

\[
f(X_1 | X_2, 1, 0) = f(X_1 | X_2, 0, 0) f(0, 0 | X_2) + f(X_1 | X_2, 0, 1) f(0, 1 | X_2) \\
+ f(X_1 | X_2, 1, 0) f(1, 0 | X_2) + f(X_1 | X_2, 1, 1) f(1, 1 | X_2),
\]

where,

\[
f(X_1 | X_2, 1, 0) = f(X_1 | X_2, 0, 0),
\]

\[
f(X_1 | X_2, 0, 1) \propto f(X_1, X_2, 0, 1) \\
\propto f(X_2 | X_1, 0, 1) f(X_1, 0, 1) = f(X_2 | X_1, 0, 0) f(X_1, 0, 1),
\]

\[
f(X_1 | X_2, 1, 1) \propto f(X_1, X_2, 1, 1) \\
\propto f(X_1, X_2 | 1, 1) f(1, 1) = f(X_1, X_2 | 0, 0) f(1, 1).
\]

For \((D_1, D_2) = (1, 1)\), we have

\[
f(X_1, X_2 | 1, 1) = f(X_1, X_2 | 0, 0) f(0, 0) + f(X_1, X_2 | 0, 1) f(0, 1) \\
+ f(X_1, X_2 | 1, 0) f(1, 0) + f(X_1, X_2 | 1, 1) f(1, 1),
\]

where,

\[
f(X_1, X_2 | 1, 1) = f(X_1, X_2 | 0, 0),
\]

\[
f(X_1, X_2 | 0, 1) \propto f(X_1, X_2, 0, 1) \\
\propto f(X_2 | X_1, 0, 1) f(X_1, 0, 1) = f(X_2 | X_1, 0, 0) f(X_1, 0, 1),
\]

\[
f(X_1, X_2 | 1, 0) \propto f(X_1, X_2, 1, 0) \\
\propto f(X_1 | X_2, 1, 0) f(X_2, 1, 0) = f(X_1 | X_2, 0, 0) f(X_2, 1).\]
The full data distribution for each \((D_1, D_2)\) can be obtained using
\[
f(X_{mis}, X_{obs}, D_1, D_2) = f(X_{mis}|X_{obs}, D_1, D_2) f(X_{obs}, D_1, D_2).
\] (25)

4 Data generation under ICIN

We let \((x_1, x_2)\) and \((d_1, d_2)\) denote the values taken by \((X_1, X_2)\) and \((D_1, D_2)\) respectively. For loglinear models, we use the notation established in Agresti (2012).

Following Sadinle and Reiter (2017), we regard each term in \(\eta\) (defined in Section 2) to be a hierarchical loglinear model, where the highest order term is a two-way interaction between the observed component of \((X_1, X_2)\) and the indicator of the missing component. Thus, we have

\[
\eta_{00}(x_1, x_2) = \log f(X_1, X_2, D_1 = 0, D_2 = 0)
= \lambda_{x_1 x_2} + \lambda_{x_1} + \lambda_{x_2} + \lambda,
\] (26)

\[
\eta_{01}(x_1) = \log f(X_1, D_1 = 0, D_2 = 1) - \log f(X_1, D_1 = 0, D_2 = 0)
= \lambda_{x_1 D_2} + \lambda_{x_1} + \lambda_{D_2} + \lambda - \left[ \lambda_{x_1} + \lambda \right]
= \lambda_{x_1 D_2} + \lambda_{D_2},
\] (27)

\[
\eta_{10}(x_2) = \log f(X_2, D_1 = 1, D_2 = 0) - \log f(X_2, D_1 = 0, D_2 = 0)
= \lambda_{x_2 D_1} + \lambda_{x_2} + \lambda_{D_1} + \lambda - \left[ \lambda_{x_2} + \lambda \right]
= \lambda_{x_2 D_1} + \lambda_{D_1},
\] (28)
\[ \eta_{11} = \log f(D_1 = 1, D_2 = 1) \]
\[ = \lambda_{11}^{D_1D_2}. \]  

We now use (26) - (29) to express the joint distribution of \((X_1, X_2, D_1, D_2)\) in terms of hierarchical loglinear models. We have

\[
\begin{align*}
\log f(X_1, X_2, D_1 = 0, D_2 = 0) &= \eta_{00}(x_1, x_2) \\
&= \lambda + \lambda_{x_1}^{X_1} + \lambda_{x_2}^{X_2} + \lambda_{x_1x_2}^{X_1X_2}, \quad (30) \\
\log f(X_1, X_2, D_1 = 0, D_2 = 1) &= \eta_{00}(x_1, x_2) + \eta_{01}(x_1) \\
&= \lambda + \lambda_{x_1}^{D_2} + \lambda_{x_1}^{X_1} + \lambda_{x_2}^{X_2} + \lambda_{x_1D_1}^{X_1D_2} + \lambda_{x_1x_2}^{X_1X_2}, \quad (31) \\
\log f(X_1, X_2, D_1 = 1, D_2 = 0) &= \eta_{00}(x_1, x_2) + \eta_{10}(x_2) \\
&= \lambda + \lambda_{x_1}^{D_1} + \lambda_{x_1}^{X_1} + \lambda_{x_2}^{X_2} + \lambda_{x_1D_1}^{X_1D_2} + \lambda_{x_1x_2}^{X_1X_2}, \quad (32) \\
\log f(X_1, X_2, D_1 = 1, D_2 = 1) &= \eta_{00}(x_1, x_2) + \eta_{01}(x_1) + \eta_{10}(x_2) + \eta_{11} \\
&= \lambda + \lambda_{x_1}^{D_1} + \lambda_{x_1}^{D_2} + \lambda_{x_1}^{X_1} + \lambda_{x_2}^{X_2} + \lambda_{x_1D_1}^{X_1D_2} + \lambda_{x_1x_2}^{X_1X_2} \\
&\quad + \lambda_{x_1x_2}^{X_1X_2} + \lambda_{11}^{D_1D_2}. \quad (33)
\end{align*}
\]

(30) - (33) can be combined into a single loglinear model as

\[
\begin{align*}
\log f(X_1, X_2, D_1, D_2) &= \lambda + \lambda_{x_1}^{X_1} + \lambda_{x_2}^{X_2} + \lambda_{d_1}^{D_1} + \lambda_{d_2}^{D_2} + \lambda_{x_2d_1}^{X_2D_1} + \lambda_{x_1d_2}^{X_1D_2} \\
&\quad + \lambda_{x_1x_2}^{X_1X_2} + \lambda_{d_1d_2}^{D_1D_2}. \quad (34)
\end{align*}
\]

**References**

Agresti, A. (2012), *Categorical Data Analysis*, Hoboken, NJ: John Wiley & Sons.
Sadinle, M. and Reiter, J. P. (2017), “Itemwise conditionally independent nonresponse modeling for incomplete multivariate data,” *Biometrika*, 104(1), 207–220.
1 Introduction

In this supplement, we present additional simulation results. In Section 2, we outline all results under MAR. In Section 3, we display additional results under ICIN that are described in the main text.

2 Simulation results under the MAR assumption

The top panels of Figure 1 and Table 1 summarize estimates under missingness scenario 1, when the covariate-outcome association is high. Overall, we see that results closely mirror those under ICIN. Methods respecting and not respecting randomization produce analogous point estimates, standard errors, and coverage rates. The design stage methods continue to exhibit high biases, while the outcome stage methods remain approximately unbiased. Turning to the low association setting, all four methods produce nearly unbiased estimates. (see bottom panels of Figure 1 and Table 1). Figure 2 and Table 2 summarize results under missingness scenario 2. Figure 3 and Table 3 do so for scenario 3.
Figure 1: Results for scenario 1 under MAR. The top panel represents the distribution of $\beta_t$ (left) and $\beta_{tx_2}$ (right) estimates for the high association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx_2} = 0.5$. The bottom panel represents the distribution of $\beta_t$ (left) and $\beta_{tx_2}$ (right) estimates for the low association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx_2} = 0.015$. 
Figure 2: Results for scenario 2 under MAR. The top panel represents the distribution of \( \beta_t \) (left) and \( \beta_{tx2} \) (right) estimates for the high association setting, where the true values are \( \beta_t = 0.3 \) and \( \beta_{tx2} = 0.5 \). The bottom panel represents the distribution of \( \beta_t \) (left) and \( \beta_{tx2} \) (right) estimates for the low association setting, where the true values are \( \beta_t = 0.3 \) and \( \beta_{tx2} = 0.015 \).
Figure 3: Results for scenario 3 under MAR. The top panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the high association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.5$. The bottom panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the low association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.015$. 
Table 1: MC standard deviations, MI standard errors, and coverage probabilities for $\beta_t$ and $\beta_{tx^2}$ in scenario 1.

| Method | $\beta_t$ MC-SD | MI-SE | Coverage | $\beta_{tx^2}$ MC-SD | MI-SE | Coverage |
|--------|-----------------|-------|----------|--------------------|-------|----------|
| High Association |
| R      | 0.182           | 0.218 | 0.984    | 0.239              | 0.373 | 0.984    |
| NR     | 0.182           | 0.218 | 0.981    | 0.240              | 0.373 | 0.987    |
| RY     | 0.221           | 0.220 | 0.950    | 0.441              | 0.434 | 0.954    |
| NRY    | 0.223           | 0.223 | 0.953    | 0.441              | 0.435 | 0.954    |
| Low Association |
| R      | 0.166           | 0.197 | 0.985    | 0.202              | 0.303 | 0.996    |
| NR     | 0.167           | 0.198 | 0.984    | 0.203              | 0.304 | 0.997    |
| RY     | 0.214           | 0.208 | 0.942    | 0.338              | 0.332 | 0.947    |
| NRY    | 0.216           | 0.209 | 0.950    | 0.343              | 0.334 | 0.947    |

Table 2: MC standard deviations, MI standard errors, and coverage probabilities for $\beta_t$ and $\beta_{tx^2}$ in scenario 2.

| Method | $\beta_t$ MC-SD | MI-SE | Coverage | $\beta_{tx^2}$ MC-SD | MI-SE | Coverage |
|--------|-----------------|-------|----------|--------------------|-------|----------|
| High Association |
| R      | 0.188           | 0.210 | 0.984    | 0.259              | 0.357 | 0.978    |
| NR     | 0.188           | 0.211 | 0.987    | 0.257              | 0.358 | 0.979    |
| RY     | 0.213           | 0.209 | 0.949    | 0.412              | 0.404 | 0.940    |
| NRY    | 0.213           | 0.211 | 0.950    | 0.413              | 0.402 | 0.944    |
| Low Association |
| R      | 0.173           | 0.191 | 0.967    | 0.224              | 0.287 | 0.986    |
| NR     | 0.173           | 0.191 | 0.967    | 0.225              | 0.287 | 0.985    |
| RY     | 0.196           | 0.197 | 0.954    | 0.306              | 0.303 | 0.941    |
| NRY    | 0.196           | 0.198 | 0.958    | 0.308              | 0.305 | 0.944    |
Table 3: MC standard deviations, MI standard errors, and coverage probabilities for \( \beta_t \) and \( \beta_{tx} \) in scenario 3.

| Method | \( \beta_t \) | \( \beta_{tx} \) |
|--------|----------------|----------------|
|        | MC-SD          | MI-SE          | Coverage | MC-SD | MI-SE | Coverage |
| High Association | | | | | | |
| R      | 0.172          | 0.206          | 0.977    | 0.214 | 0.342 | 0.966    |
| NR     | 0.173          | 0.206          | 0.978    | 0.213 | 0.343 | 0.972    |
| RY     | 0.219          | 0.212          | 0.942    | 0.406 | 0.402 | 0.947    |
| NRY    | 0.222          | 0.213          | 0.944    | 0.421 | 0.411 | 0.942    |
| Low Association | | | | | | |
| R      | 0.164          | 0.197          | 0.981    | 0.203 | 0.303 | 0.996    |
| NR     | 0.164          | 0.197          | 0.981    | 0.202 | 0.303 | 0.996    |
| RY     | 0.211          | 0.208          | 0.940    | 0.335 | 0.329 | 0.945    |
| NRY    | 0.213          | 0.209          | 0.949    | 0.336 | 0.333 | 0.952    |

3 Simulation results under the ICIN assumption

Here, we provide graphical and tabular summaries for results under missingness scenarios 2 and 3. Figure 4 and Table 4 summarize estimates under missingness scenario 2. Figure 5 and Table 5 do so for missingness scenario 3.
Figure 4: Results for scenario 2 under ICIN. The top panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the high association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.5$. The bottom panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the low association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.015$. 
Figure 5: Results for scenario 3 under ICIN. The top panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the high association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.5$. The bottom panel represents the distribution of $\beta_t$ (left) and $\beta_{tx2}$ (right) estimates for the low association setting, where the true values are $\beta_t = 0.3$ and $\beta_{tx2} = 0.015$. 
Table 4: MC standard deviations, MI standard errors, and coverage probabilities for $\beta_t$ and $\beta_{tx_2}$ in scenario 2.

| Method | $\beta_t$ MC-SD | MI-SE | Coverage | $\beta_{tx_2}$ MC-SD | MI-SE | Coverage |
|--------|----------------|-------|----------|----------------------|-------|----------|
| High Association | | | | | | |
| R | 0.193 | 0.211 | 0.985 | 0.272 | 0.357 | 0.983 |
| NR | 0.194 | 0.212 | 0.986 | 0.274 | 0.358 | 0.979 |
| RY | 0.219 | 0.211 | 0.942 | 0.409 | 0.401 | 0.942 |
| NRY | 0.221 | 0.212 | 0.940 | 0.416 | 0.402 | 0.952 |
| Low Association | | | | | | |
| R | 0.178 | 0.196 | 0.970 | 0.219 | 0.286 | 0.991 |
| NR | 0.178 | 0.196 | 0.968 | 0.219 | 0.287 | 0.992 |
| RY | 0.209 | 0.202 | 0.944 | 0.297 | 0.301 | 0.954 |
| NRY | 0.210 | 0.204 | 0.944 | 0.297 | 0.304 | 0.948 |

Table 5: MC standard deviations, MI standard errors, and coverage probabilities for $\beta_t$ and $\beta_{tx_2}$ in scenario 3.

| Method | $\beta_t$ MC-SD | MI-SE | Coverage | $\beta_{tx_2}$ MC-SD | MI-SE | Coverage |
|--------|----------------|-------|----------|----------------------|-------|----------|
| High Association | | | | | | |
| R | 0.178 | 0.217 | 0.984 | 0.222 | 0.339 | 0.970 |
| NR | 0.179 | 0.217 | 0.984 | 0.224 | 0.340 | 0.970 |
| RY | 0.227 | 0.224 | 0.947 | 0.395 | 0.391 | 0.948 |
| NRY | 0.226 | 0.226 | 0.951 | 0.407 | 0.408 | 0.947 |
| Low Association | | | | | | |
| R | 0.165 | 0.208 | 0.984 | 0.203 | 0.301 | 0.998 |
| NR | 0.168 | 0.208 | 0.983 | 0.207 | 0.302 | 0.997 |
| RY | 0.216 | 0.219 | 0.959 | 0.325 | 0.325 | 0.952 |
| NRY | 0.220 | 0.222 | 0.959 | 0.335 | 0.333 | 0.948 |