

Comparison of Methods for Handling Covariate Missingness in Propensity Score Estimation with a Binary Exposure

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Research article

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Posted Date: June 12th, 2020

DOI: <https://doi.org/10.21203/rs.2.18726/v2>

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Version of Record: A version of this preprint was published on June 26th, 2020. See the published version at <https://doi.org/10.1186/s12874-020-01053-4>.

Comparison of Methods for Handling Covariate Missingness in Propensity Score Estimation
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Abstract

Background: Causal effect estimation with observational data is subject to bias due to confounding, which is often controlled for using propensity scores. One unresolved issue in propensity score estimation is how to handle missing values in covariates.

Method: Several approaches have been proposed for handling covariate missingness, including multiple imputation (MI), multiple imputation with missingness pattern (MIMP), and treatment mean imputation. However, there are other potentially useful approaches that have not been evaluated, including single imputation (SI) + prediction error (PE), SI+PE + parameter uncertainty (PU), and Generalized Boosted Modeling (GBM), which is a nonparametric approach for estimating propensity scores in which missing values are automatically handled in the estimation using a surrogate split method. To evaluate the performance of these approaches, a simulation study was conducted.

Results: Results suggested that SI+PE, SI+PE+PU, MI, and MIMP perform almost equally well and better than treatment mean imputation and GBM in terms of bias; however, MI and MIMP account for the additional uncertainty of imputing the missingness.

Conclusions: Applying GBM to the incomplete data and relying on the surrogate split approach resulted in substantial bias. Imputation prior to implementing GBM is recommended.

Keywords: propensity scores, missing data, causal inference, generalized boosted models

Background

Observational studies are common in epidemiology and medical studies when a randomized trial is not ethical or feasible. A major challenge facing observational studies is that the treatment or exposure is not randomized and the estimate of the effect of the exposure on an outcome may be due to confounders, variables associated with both the exposure and outcome. Propensity scores, the probability of receiving the observed exposure level given the covariates, are increasingly used to control for confounding. Propensity scores summarize many confounders into a single number[1] that can be used to reduce bias in the estimate of the effect of the exposure on an outcome. Using propensity scores to control for confounding assumes no unmeasured confounding and that all potential confounders are included in the propensity score model.[1] Thus, it is common to include many confounders in the propensity score model to satisfy the no unmeasured confounding assumption. However, there is often missingness in the confounders, which raises the question of how best to handle missingness when applying propensity score methods. There has been previous work around various imputation strategies (e.g., treatment mean imputation, multiple imputation [MI]) and how to combine results if multiple imputation is used. However, one approach that has not been examined in simulation studies when there is missingness on the confounders is Generalized Boosted Models (GBM).[2] GBM does not require complete data (as the commonly used logistic regression does) and has been shown to outperform logistic regression for propensity score estimation in complete data.[3] If GBM works well in the presence of missing data, using it would circumvent the issues that arise when using MI with propensity score analysis.[4-6] The goal of this paper is to examine the performance of GBM vs. other approaches through a simulation study in order to

provide guidance to analysts when implementing propensity score analysis in the presence of missingness on the covariates.

The paper is organized as follows. We briefly review the literature on missingness in the covariates when estimating propensity scores for binary exposures using logistic regression. We then briefly review previous work showing that GBM outperforms logistic regression, particularly in the presence of non-linear relationships, which leads to our choice of data generating scenarios for the simulation study. We then present the simulation study methods and the results in detail. We conclude with recommendations for researchers applying propensity score methods, specifically propensity score weighing, in the presence of missingness on the potential confounders.

Methods for Handling Covariate Missingness

Missingness on the propensity score model covariates poses a challenge in propensity score estimation. As propensity score estimation frequently involves a large number of covariates, a large proportion of observations may contain missingness on at least one covariate, and proper handling of covariate missingness is necessary for unbiased estimates of causal effects. Several approaches have been proposed for handling covariate missingness, including using only covariates with complete data, treatment mean imputation,[7] indicator variable,[8, 9] missingness pattern (MP),[10] the general location model,[11] MI, and multiple imputation missingness pattern (MIMP).[12] Several of these approaches will not be considered further. Specifically, using only covariates with complete data is not recommended,[7] the indicator variable approach is not recommended[13] as it ignores any relation between covariates and is inefficient,[12] and the MP approach is less efficient than MI or the MIMP approach discussed below.[7] The general location model,[11] which models the joint distribution of the exposure,

covariates, and missingness, is computationally intensive in practice. We review the remaining approaches in turn.

Treatment mean imputation. Treatment mean imputation has been suggested[7] as an alternative to MI when MI is not feasible because in a simulation study in which both the exposure and outcome were binary, treatment mean imputation performed reasonably well. Based on these results, we include the approach here in our simulation of a binary exposure and continuous outcome but speculate that if the missingness mechanism is anything other than missing completely at random (MCAR), this approach will not perform well.

Multiple Imputation (MI). A commonly used technique for handling missing data, MI could also be adopted for propensity score covariate missingness under the assumption of missing at random (MAR).[14] Multiple random draws from the posterior predictive distribution of the missing values conditional on the observed values are used to generate multiple complete datasets. Each complete dataset can be separately analyzed with standard methods and estimates are combined using Rubin's rules.[15, 16] The overall estimate ($\hat{\theta}$) is calculated as the average of point estimates ($\hat{\theta}_i$) over the m imputations:

$$\hat{\theta} = \frac{1}{m} \sum_{i=1}^m \hat{\theta}_i$$

and the overall variance (\widehat{var}) is estimated as the sum of within-imputation variance (W_i) and between-imputation variance (B):

$$\widehat{var} = \frac{1}{m} \sum_{i=1}^m W_i + \left(1 + \frac{1}{m}\right) B.$$

However, Rubin's rules for combining variance estimates may not be valid when MI is applied to propensity score model covariates due to the extra uncertainty of estimating propensity scores. Instead, a bootstrap or jackknife method could be applied for variance

estimation.[12] Using MI to handle missingness allows inclusion of auxiliary variables (i.e., variables associated with the missingness) in the imputation model. It has been suggested that both the exposure and outcome variables should be included in the imputation model to avoid biased estimates.[7] To implement MI, we used a fully conditional specification[17] using the MI via chained equations algorithm in the R package *mice*.[18, 19]

Several issues arise when using MI in propensity score analysis, including whether the causal effects estimated on each imputed data set should be combined or whether the propensity score for each individual should be combined across imputations[4, 5] prior to estimating the causal effect. Although this latter approach has been recommended,[5] it is not clear that Rubin's rules apply to this approach.[4] Other issues, which have not been addressed when using MI with propensity score analysis, include strategies for handling a situation in which balance is obtained in some imputations but not others.

Multiple Imputation Missingness Pattern (MIMP). Qu and Lipkovich[12] introduced a new approach to handling covariate missingness by combining MI and MP. As missingness on the covariates may be predictive of treatment assignment, incorporating the MP in the propensity score model has been suggested.[10] Observations are classified into groups based on the MP and assigned an indicator. Missing values are imputed with MI and the propensity scores are estimated using the covariates and an MP indicator for each imputed dataset. The estimated propensity score is thus conditional on both observed covariates and the MP. Including the MP indicator in the propensity score model balances MPs across exposure groups. This is important because in order for the strong ignorability assumption to hold balance must be obtained for the missing as well as the observed values of the potential confounders.[10, 20] Finally, the causal

effect is estimated for each imputed dataset and combined with Rubin's rules (point estimate) and the bootstrap (variance).

One challenge with the MIMP approach is that with a large number of covariates, it is not uncommon to observe MPs containing very few observations, resulting in estimated propensity scores with large variability. This could be solved by pooling similar MPs to reach a pre-specified minimum number of observations.[12]

Single Imputation (SI). As only a point estimate of the propensity score is used in the outcome analysis model, one could argue that a SI that incorporates prediction error (SI+ prediction error, or SI+PE) or a SI that incorporates both prediction error and parameter uncertainty (SI+ prediction error + parameter uncertainty, or SI+PE+PU) may be sufficient to eliminate bias due to missingness in the propensity score model covariates. However, one could also argue that the uncertainty of the missing data imputation should be carried over to the outcome analysis. Performance of SI+PE and SI+PE+PU has not been evaluated or compared with the methods discussed above even though they have been used in applications of propensity score analysis.[21] We suspect that either of these approaches would perform better than treatment mean imputation and would avoid the potential issues with MI described above. Thus, we consider two SI methods: SI+PE and SI+PE+PU.

SI+PE involves fitting a regression model of the variable containing missing values on the auxiliary variables and imputing the missing values by adding random noise to the predicted value. Although the approach may result in incorrect standard errors due to its inability to account for uncertainty in the regression coefficients, and therefore underestimate variability of the imputed values,[16] this may be less of an issue for propensity score estimation where only

the point estimate of the propensity scores is used for later outcome analysis. SI+PE+PU is similar but uses Bayesian methods to draw the parameters from their posterior distributions.

Propensity Score Estimation

Logistic Regression. Logistic regression is most commonly used for propensity score estimation by regressing the binary treatment or exposure indicator variable on pre-treatment covariates (i.e., potential confounders). The propensity score model for a binary exposure variable is estimated as

$$\text{logit}(p_i(T = 1)) = \mathbf{X}'\boldsymbol{\beta}, \quad i = 1, 2, \dots, n,$$

where $\mathbf{X} = (1, X_1, X_2, \dots, X_k)$, $\boldsymbol{\beta} = (\beta_0, \beta_1, \beta_2, \dots, \beta_k)$, k is the number of covariates, and n is the number of observations. The propensity score for each individual is then estimated as

$$p_i = \frac{e^{\mathbf{X}'_i \boldsymbol{\beta}}}{1 + e^{\mathbf{X}'_i \boldsymbol{\beta}}}.$$

Although logistic regression is most commonly used to estimate propensity scores, it may not be the best choice in some situations. Using logistic regression to model the probability of exposure level assumes a linear relationship between the log-odds of the exposure and the covariates. However, this assumption is not always satisfied and including lower- (e.g., the square root) or higher-order terms of covariates in the logistic model is unlikely to accurately capture nonlinear relationships.[2] Also, the propensity score model usually involves a large number of covariates and variable selection is often required. This process could be tedious and may exclude important covariates. In addition, inclusion of two-way or higher-order interaction terms in a logistic regression requires users to manually specify all interaction terms.

Generalized Boosted Modeling (GBM). The limitations of estimating propensity scores using a parametric model, such as logistic regression, motivated development of more powerful and flexible nonparametric methods, including GBM.[2] GBM estimates propensity scores by

iteratively fitting many regression trees using the covariates and linearly combines all regression trees to form a smoothed function for the final estimate of the propensity scores. Similar to

logistic regression, GBM also models the log-odds of exposure level, $g(X) = \log \frac{p(T=1|X)}{1-p(T=1|X)}$.

The algorithm starts with the average log-odds of exposure level, $g(X) = \log \frac{\hat{p}(T=1)}{1-\hat{p}(T=1)}$, where $\hat{p}(T = 1)$ is the average probability of being exposed, and $g(X)$ is iteratively updated to $g(X) + \alpha \cdot h(X)$ to find the model that maximizes the log-likelihood of $g(X)$,

$$l(g) = \sum_{i=1}^n T_i g(X_i) - \log(1 + \exp(g(X_i))),$$

where $h(X)$ is estimated by fitting a regression tree that models the residuals from the current fit to the covariates, and α ($0 < \alpha \leq 1$) is a shrinkage parameter which allows a smaller adjustment between iterations to reduce variance without necessarily increasing bias. A small shrinkage parameter helps achieve better model fit. Another tuning parameter in GBM is the interaction depth. A maximum depth of four, which allows all four-way interactions between covariates, is recommended for best model estimation and prediction.[2] The process continues until the maximum number of iterations is reached; propensity scores are calculated from the iteration where the average absolute standardized mean (AASM) difference is minimized. AASM is estimated as the average of absolute differences between the exposed mean and weighted unexposed mean across the k covariates:

$$\frac{1}{k} \sum_k \left| \frac{\sum_{i=1}^{n_{T=1}} X_k (T = 1)_i - \frac{\sum_{j=1}^{n_{T=0}} w_j X_k (T = 0)_j}{\sum_{j=1}^{n_{T=0}} w_j}}{\widehat{s.d.}(X_k)_{T=1}} \right|$$

where $w_j = \frac{p_j}{1-p_j}$.

Using GBM for propensity score estimation has several advantages. First, GBM can adaptively include the covariates that improve prediction of exposure level, and therefore does not require covariate selection. Second, GBM automatically includes all higher-order and interaction terms of the covariates to the depth specified by the user. Thus, nonlinear relationships can be accounted for in propensity score estimation to yield more accurate estimates. Third, the iterative fitting nature of GBM can identify the propensity score model that minimizes the differences between exposure groups on the covariates. One disadvantage in comparison to logistic regression is that GBM does not provide parameter estimates, such as logistic regression coefficients, that allow interpretation of the association between a covariate and the probability of exposure. However, this is less of a concern as the main purpose of the propensity score model is to estimate the conditional probability of exposure.

One potentially important advantage of GBM over logistic regression for propensity score estimation is that GBM does not require complete data on the covariates. Missing values are handled using the surrogate split method. At each iteration, a regression tree, called a base learner, is built by splitting observations into left and right nodes. Suppose that a splitting variable and split point (for partitioning to the left and right nodes) have been chosen for the next split. This variable will be referred to as the primary variable. If there are missing values on the primary variable, these observations are sent to a separate third node, called the missing node. For this node, a surrogate variable is found by predicting the left and right nodes of the primary variable using the other predictor variables. If the values on both the primary variable and surrogate variable are missing, then a second-best surrogate split can be found that yields a splitting of the data most similar to the primary split. A simple rule of “go with the majority” is also evaluated, and surrogates that perform worse than this rule are not used for the surrogate

split. Ultimately, the goal of the surrogate is to split the data as similarly as possible to the primary variable, although there is no guarantee that it does so.

Propensity scores estimates, whether estimated by GBM or logistic regression, can then be used to match, stratify, or weight observations to balance the covariate distributions across exposure groups. In this study, we will focus on inverse probability weighting (IPW). To reduce the variance that may be incurred by extreme weights, the weight is multiplied by the expected value of being assigned to the observed group.[22] Thus, the exposed group is weighted by $\frac{\hat{p}}{p_i}$, and the unexposed group is weighted by $\frac{1-\hat{p}}{1-p_i}$, where $\hat{p} = \frac{\sum_i p_i}{n}$.

Methods

Although many methods have been proposed for handling covariate missingness and several have been shown to have good performance, SI+PE and SI+PE+PU have not been previously examined. Performance of GBM with incomplete covariates using the surrogate split has also not been evaluated in simulation studies, particularly in comparison to the other approaches described above. Cham and West examined the surrogate split approach with GBM in a single simulated data set but noted that more extensive simulation studies were needed.[20] To address these knowledge gaps, a simulation study was conducted.

Data Generation

The data generation model is illustrated in Figure 1. Complete data generation was similar to that of Setoguchi et al.[23] and Lee et al.[3] and included a binary exposure, denoted as T , a continuous outcome, denoted as Y , and 10 covariates, denoted as $x_1 - x_{10}$.

Covariates. Six covariates were binary ($x_1, x_3, x_5, x_6, x_8, x_9$) following a Bernoulli distribution with $x_1, x_6, x_8 \sim Bern(1, 0.3)$ and $x_3, x_5, x_9 \sim Bern(1, 0.5)$. Four covariates were continuous (x_2, x_4, x_7, x_{10}) following a normal distribution, $N(0,1)$. Four covariates ($x_1 - x_4$)

were correlated with both T and Y and were true confounders. Three covariates ($x_5 - x_7$) were correlated only with T and the other three covariates ($x_8 - x_{10}$) were correlated only with Y . Covariate x_1 was correlated with x_5 ($\rho = 0.2$), x_2 was correlated with x_6 ($\rho = 0.9$), x_3 was correlated with x_7 ($\rho = 0.2$), and x_4 was correlated with x_8 ($\rho = 0.9$).

Exposure. Generation of the exposure was similar to Setoguchi et al.[23] and Lee et al.'s[3] scenarios A and G with sample sizes $n = 500, 1000$, and 5000 . In scenario A (main effects only), linearity and additivity hold, so higher order terms and interactions among the confounders are not needed for the propensity score model. The true propensity model is given as:

$$\text{logit}(p(T = 1)) = 0.8x_1 - 0.25x_2 + 0.6x_3 - 0.4x_4 - 0.8x_5 - 0.5x_6 + 0.7x_7.$$

In scenario G (moderate non-additivity and non-linearity), neither linearity nor additivity hold, so both higher order terms and interactions among the confounders should be included in the propensity score model (10 two-way interactions and 3 quadratic terms). The true propensity score model is given as:

$$\begin{aligned} \text{logit}(p(T = 1)) = & 0.8x_1 - 0.25x_2 + 0.6x_3 - 0.4x_4 - 0.8x_5 - 0.5x_6 + 0.7x_7 - 0.25x_2^2 - \\ & 0.4x_4^2 + 0.7x_7^2 + 0.4x_1x_3 - 0.175x_2x_4 + 0.3x_3x_5 - 0.28x_4x_6 - 0.4x_5x_7 + \\ & 0.4x_1x_6 - 0.175x_2x_3 + 0.3x_3x_4 - 0.2x_4x_5 - 0.4x_5x_6. \end{aligned}$$

Outcome. The regression coefficient of Y on T , which is the true causal effect, was set to -0.4. The true outcome model is given as:

$$Y = -3.85 + 0.3x_1 - 0.36x_2 - 0.73x_3 - 0.2x_4 + 0.71x_8 - 0.19x_9 + 0.26x_{10} - 0.4T + \varepsilon_Y$$

where $\varepsilon_Y \sim N(0,1)$.

Missingness mechanisms

The design for the missingness mechanisms included four conditions where for each condition the overall rate of missingness was either 25% or 50%. The rationale for an overall rate of 50% missingness was that of a planned missingness design in which some individuals may receive subsets of questionnaire items.[24] The missingness mechanisms were based on the simulation design of Collins, Schafer, and Kam[25] but adapted, as described below, to our design for studying covariate missingness in the propensity score model. The rationale for the design of the missingness mechanisms is that in real empirical data, the missingness mechanism likely does not fall into discrete categories of MCAR, MAR, and MNAR. We do not include a condition in which the missingness is MNAR because all of the approaches we examine assume that the missingness is not MNAR and thus, all of the approaches would be expected to be biased under MNAR. We do, however, include different MAR conditions that are likely in real data.

MCAR. For MCAR, approximately 25% or 50% of observations were missing randomly (i.e., independently of any other covariate, the exposure, or the outcome) for each of the four true confounders, $x_1 - x_4$.

MAR-1. For MAR 1, missingness on x_1, x_2, x_3, x_4 is dependent on x_5, x_6, x_8, x_9 , respectively. Specifically, approximately 15% or 30% of observations are missing on x_1 when x_5 is equal to 0, and approximately 35% or 70% of observations are missing on x_1 when x_5 is equal to 1, yielding overall missingness percentages of 25% or 50%; x_2, x_3, x_4 follow the same pattern. Note that although $x_5 - x_7$ predict only the exposure, x_5 and x_6 are correlated with the true confounders (x_1 and x_2 respectively; see Figure 1). Similarly, although $x_8 - x_{10}$ predict only the outcome, x_8 and x_9 are correlated with the true confounders (x_3 and x_4 respectively). Thus, these variables (x_5, x_6, x_8, x_9) are important auxiliary variables that should be included in the

imputation model in order to satisfy the MAR assumption. If these variables are not included, then this mechanism is missingness not at random (MNAR).

MAR-2. For MAR 2, missingness on x_1, x_2, x_3, x_4 is dependent on x_5, x_6, x_8, x_9 , respectively, and Y . To generate missingness on x_1 , all observations were first divided into four groups based on the values of x_5 and Y (see Table 1). Each group was then assigned a specific missingness percentage and missing values were introduced within each group, yielding an overall missingness percentage of 25% or 50%. Missingness was generated on covariates x_2, x_3, x_4 using group specific missing percentages as shown in Tables 2, 3, and 4. For this condition, x_5, x_6, x_8, x_9 , and Y must be included in the imputation model in order to satisfy the MAR assumption. If these variables are not included, then this mechanism is MNAR.

MAR-sinister. For MAR sinister, missingness on x_1, x_2, x_3, x_4 is dependent on the correlation of two other variables. Specifically, missingness on x_1 is dependent on the correlation between x_5 and T . The observations were first randomly divided into 20 groups and the correlation between x_5 and T was calculated for each group. The 10 groups with lower correlation were assigned a missingness percentage of either 10% or 30% and the 10 groups with higher correlation were assigned a missingness percentage of either 40% or 70%, resulting in an overall missingness percentage of 25% or 50%. Missingness on x_2, x_3, x_4 was generated based on the correlation between x_6 and T , x_7 and Y , and x_8 and Y , respectively. For this condition, x_5, x_6, x_8, x_9, T , and Y must be included in the imputation model in order to satisfy the MAR assumption. If these variables are not included, then this mechanism is MNAR.

Analysis

Analysis began with imputation of missing data, followed by estimation of propensity scores, and finally estimation of the causal effect.

Imputation. Methods included treatment mean imputation, SI+PE, SI+PE+PU, MI, and MIMP using the R package *mice*. The imputation models include all variables except x_7 and x_{10} , which are not correlated with x_1, x_2, x_3, x_4 . To implement the SI+PE method, we used the *mice* function from the R *mice* package with ‘method=norm.nob’.[19] To implement the SI+PE+PU method, we used the *mice* function with ‘method=norm’ and $m = 1$.[19] For MI and MIMP, we used $m = 20$ imputations. For treatment mean imputation, missing values in binary variables x_1 and x_3 are replaced by the unrounded mean of observed values within each exposure group, as rounding has been suggested to increase bias.[26] For MIMP, missingness patterns with less than 100 observations were pooled using the algorithm proposed by Qu and Lipkovich.[12]

Propensity score estimation. To estimate propensity scores, we used logistic regression applied to the data imputed by treatment mean imputation, SI+PE, SI+PE+PU, MI, and MIMP; and GBM applied to the incomplete data and the data imputed by SI+PE. In practice, an analyst would not know the true propensity score model and would need to make decisions regarding which variables, as well as higher order terms and interactions, to include in the propensity score model. To examine how these decisions may affect the causal effect estimate, we considered four variable inclusion strategies for the logistic regression propensity score model:

- a) true confounders x_1, x_2, x_3, x_4 ,
- b) x_1 left out,
- c) nonconfounder x_5 included and
- d) x_1 left out and x_5 included.

When logistic regression was used for propensity score estimation, only main effects were considered and no higher order terms or interactions were included in the model. As GBM

is computationally time consuming, it was only implemented for strategy a) true confounders, using the *ps* function in the R package *twang*.[27] The shrinkage parameter was set to 0.05.

Estimation of the causal effect. To estimate the causal effect, we used a weighted regression model in which the IPWs were the weights and the exposure variable was the only predictor of the outcome (i.e., we did not incorporate the confounders in the outcome analysis model). Weights were trimmed at the 1st and 99th percentiles of their distribution. For MI and MIMP, estimates were combined using Rubin's rules by taking the average of the estimates over the $m = 20$ imputations.

Evaluation. To summarize, there are 8 data generating scenarios: 2 (exposure models) x 4 (missingness mechanisms); 7 propensity score estimation strategies; and 4 variable inclusion strategies. The procedure was replicated 1000 times in each of these conditions before summarizing results for the different approaches. Approaches are compared in terms of i) bias, calculated as the difference between the mean estimate across the 1000 replications in each condition and the true value; ii) standard deviation (SD) of the estimates from the 1000 replications, iii) standard error (SE), estimated from the weighted regression in each replication and averaged across the 1000 replications, and iv) root mean square error (RMSE), calculated as the mean square of the differences between each estimate ($\hat{\beta}_i$) and the true value (β):

$$RMSE = \sqrt{\frac{1}{r} \sum_{i=1}^r (\hat{\beta}_i - \beta)^2}$$

Results

Scenario A – Main Effects Only

Table 5 shows simulation results for scenario A with $n = 500$ and 25% missingness. When only true confounders were used as covariates for propensity score estimation, there was

no bias associated with SI+PE, SI+PE+PU, MI, and MIMP under all missingness mechanisms, and the bias was comparable to that obtained prior to introducing missing data (see first row of Table 5). Logistic regression with treatment mean imputation had a larger bias than other imputation approaches under all missingness mechanisms. Although not as large as treatment mean imputation, the bias obtained when applying GBM to incomplete data for propensity score estimation was substantially more than the SI or MI approaches. Imputing missing values by SI+PE before estimating propensity scores using GBM helped reduce the bias, but it was still larger than the bias obtained when applying GBM to complete data prior to introducing missingness (see second row of Table 5). GBM using incomplete data had slightly smaller SEs than the other approaches, whereas GBM with SI+PE had SEs in line with the other SI and MI approaches and with the analysis on the complete data prior to introducing missingness.

Treatment mean imputation had larger SEs than the other approaches.

The causal effect estimates were affected by the variable inclusion strategies (see Table 5). When true confounder x_1 was omitted from the propensity score model, an increase in bias was observed for all approaches under all missingness mechanisms; however, it was comparable to the bias obtained in the complete data prior to introducing missingness, with the exception of treatment mean imputation, which had much larger bias. The SEs did not differ in comparison to inclusion of only true confounders. When non-confounder x_5 was included in the propensity score estimation, there was no increase in bias for the SI and MI approaches under all missingness mechanisms but there was increased bias for treatment mean imputation. The SEs slightly increased for all approaches in comparison to inclusion of only true confounders. When true confounder x_1 was omitted and non-confounder x_5 was included in the propensity score model, an even larger bias was observed for all approaches and all missingness mechanisms than

when only true confounder x_1 was omitted although the SEs did not increase. However, as before the SI and MI approaches have bias that is similar to that obtained in the complete data prior to introducing missingness.

The same pattern of results was obtained with sample sizes of 1000 or 5000 (except that as expected the SEs decreased) and thus the results are not presented here but are available in the supplementary materials. When the missingness increased from 25% to 50%, the bias for GBM using incomplete data increased quite substantially and GBM with SI+PE had slightly larger bias (see supplementary materials). For the SI and MI approaches using logistic regression, the bias increased for the MAR sinister mechanism and 50% missingness, that is, as the missingness mechanism became more complex. The increase to 50% missingness did not have an effect on SEs in comparison to 25% missingness but within the 50% missingness condition, the SEs decreased as the sample size increased. Treatment mean imputation performed at least as poorly in the 50% missingness condition as it did in the 25% missingness condition.

Scenario G – Moderate non-additivity and non-linearity

Table 6 shows simulation results for scenario G with $n = 500$ and 25% missingness. Recall that the approaches using logistic regression included only main effects. Thus, bias was observed for logistic regression and GBM when applied to the complete data prior to introducing missingness; however, for GBM, the bias was the same magnitude as in Scenario A.

When only true confounders were included in the propensity score model, causal effect estimates based on propensity scores estimated from GBM were biased, with the largest bias observed when applying GBM directly to the incomplete data, and smaller bias when applying GBM to SI+PE data. Treatment mean imputation had the largest bias. SI+PE, SI+PE+PU, MI, and MIMP have little to no bias and actually have less bias than before the missingness was

introduced. This may be a result of the bias due to excluding interactions counteracting that due to missingness.

As in Scenario A, SEs were largest for treatment mean imputation. GBM using the incomplete data and GBM with SI+PE had smaller SEs than the other approaches; these SEs were similar to those of GBM using the complete data before missingness was introduced. SI+PE, SI+PE+PU, MI, and MIMP had larger SEs than either GBM approach; these SEs were similar to those obtained when logistic regression was used to estimate propensity scores on the complete data prior to introducing missingness.

Variable inclusion strategies for the propensity score model affected the estimates in a similar way as in Scenario A. When true confounder x_1 was omitted from the propensity score model, an increase in bias was observed for all approaches. When non-confounder x_5 was included, there was no increase in bias but the SEs increased slightly. When true confounder x_1 was omitted and non-confounder x_5 was included, an even larger bias was observed. All types of propensity model misspecification led to increased RMSE estimates, especially when a true confounder was excluded from the propensity score model.

As in Scenario A, the bias for GBM using either the incomplete data or with SI+PE decreased substantially as the sample size increased (see supplemental materials). However, the bias for the other approaches did not decrease as the sample size increased. As expected, the SE and RMSE estimates decreased as the sample size increased.

When missingness increased from 25% to 50%, a larger bias was observed for GBM with incomplete data (see supplemental materials). The bias of GBM with SI+PE also increased somewhat. Very little bias was observed for SI+PE, SI+PE+PU, MI, and MIMP when the data were missing under MCAR, MAR2, or MAR sinister, but the bias was larger when the

missingness mechanism was MAR1, with a larger magnitude than with 25% missingness.

SI+PE+PU had a larger bias than other approaches when the missingness was MAR sinister with 50% missingness.

The bias of approaches using logistic regression in scenario G was from two possible resources: missing data and propensity score model misspecification due to excluding interaction and higher order terms. Therefore, additional simulations were conducted for scenario G using the correct propensity score model. Table 7 shows the results for scenario G with a correct logistic model and 25% missingness under the three different sample sizes. Except for treatment mean imputation, very little bias was observed when the data were MCAR, MAR2, or MAR sinister. When the missingness mechanism was MAR1, all approaches were slightly biased, with treatment mean imputation having the largest bias. The results for 50% missingness using the correct logistic regression model, including interactions and higher order terms, were similar (see supplementary materials).

Discussion

The present study compared seven potentially useful approaches for missingness on the covariates used for estimating propensity scores. Results suggested that SI+PE, SI+PE+PU, MI, and MIMP have consistently good performance under Scenario A for all missingness mechanisms, sample sizes, and missing percentages. In contrast, treatment mean imputation was associated with a larger bias than the other approaches for all scenarios. This is inconsistent with other findings,[7] which suggested using treatment mean imputation when MI is not feasible. This discordance may be attributable to differences in the simulation study design: 1) the previous study had 12% missingness compared with 25% or 50% missingness in the present study; 2) the previous study imposed missing values on three covariates such that all were

missing or none were. Treatment mean imputation could be viewed as a single imputation procedure in which the only covariate is the exposure group and there is no prediction error or parameter uncertainty added to the imputed values. Thus, the imputation model would not include other variables related to the missingness, such as x_5, x_6, x_8, x_9, T , and Y for the *MAR-sinister* condition. It is likely for this reason that it does not perform as well as the other approaches. In any case, we strongly recommend against using treatment mean imputation.

As expected, none of the approaches using logistic regression for propensity score estimation performed well in Scenario G. When the propensity score model included the true confounders, including interaction and higher-order terms, SI+PE, SI+PE+PU, MI, and MIMP produced unbiased estimates.

Including a non-confounder in the propensity score model did not increase bias but the estimate was not as efficient. In practice, it may be difficult to identify true confounders from a set of baseline covariates. Including non-confounder covariates has the benefit of reducing bias with the chance of slightly reducing efficiency. Our results are similar to previous simulation studies on variable selection in propensity score models with complete data.[28]

The missingness mechanism played more of a role at smaller samples sizes, a larger missingness rate, and in Scenario G. The missingness mechanisms satisfied the assumptions of MI and MIMP, which assume MAR, but they differed in terms of the complexity of the MAR dependencies. However, the missingness mechanism did not play a large role, particularly in comparison with role of GBM vs. logistic regression.

We expected GBM, either with the incomplete data or SI+PE, to have similar performance to logistic regression in Scenario A and better performance than logistic regression in Scenario G. However, results suggested that applying GBM to the incomplete data for

propensity score estimation resulted in a larger bias than logistic regression with any imputation approach except for treatment mean imputation in both Scenarios A and G. We suspect that this may be due to the lack of inclusion of Y in the surrogate split approach used by GBM. GBM with SI+PE does include information on Y and the bias did decrease, though not entirely.

Even when there was no missing data involved, the estimate using GBM was more biased than the estimate with logistic regression. This finding contradicts a previous study comparing the performance of logistic regression and GBM using a similar study design[3] when the covariates do not contain missing values. That study's results showed that GBM was superior to logistic regression in both Scenarios A and G. This discrepancy could be explained by the weight trimming used in the present study. Lee et al.[3] did not trim weights although extreme weights were observed, with a higher percentage of extreme weights for logistic regression than GBM. Lee et al.[29] examined weight trimming with complete data using the same simulation design. They found that weight trimming decreased the bias in the case of logistic regression but that the bias for GBM did not decrease in any scenario when weights were trimmed. Future research should evaluate the effect of weight trimming on bias when there is missing data.

Limitations. The conclusions drawn from the current study may not generalize to a scenario where the exposure, outcome, and covariates are correlated differently. For example, if the outcome is strongly correlated with the missingness, then it is possible that the GBM surrogate split approach may be even more biased for the MAR-2 and MAR-sinister conditions because in these conditions the missingness mechanism depended on the outcome but the outcome is not included in the surrogate split approach. In addition, we did not examine balance because doing so would have required resolving the issue of the most appropriate strategy when

balance is obtained in some imputations but not others. We leave this assessment to future research.

The present simulation study did not include a condition for missingness on the outcome variable. If there is missingness on the outcome variable, then based on the missing data literature more generally, multiple imputation would be necessary to account for the uncertainty in the imputation of the outcome variable. We chose not to include a condition in the simulation study for missingness on the outcome because the real data we have worked with has often included planned missingness on some of the potential confounders or other intermittent missingness on the questionnaire items but the outcome data are present. Future simulations should examine whether MI or MIMP performs better when there is also missingness on the outcome.

A further direction for future research is a more comprehensive assessment of methods for including interaction terms in the imputation model. Recent research[30] has shown if the model is congenial, then multiple imputation via chained equations, and specifically the mice R package, using the just-another-variable approach is unbiased. The problem with some of the original simulations on the topic (e.g., [31]) is that the parametric models were not congenial with the analytic models. In other words, they used the defaults in the mice R package, which do not include interaction terms in the parametric models. These issues have not yet been sorted out either specifically to propensity score models or more generally, as van Buuren[32] describes a simulation study in which a newer approach, a rejection sampling method that creates congenial imputations,[33] appears to perform the best.

Conclusions

In summary, the results suggest that missing values in the covariates should be imputed before fitting the propensity score model to obtain unbiased causal effect estimates. We had expected the standard errors for MI and MIMP to be uniformly larger because these approaches take into account both the uncertainty due to imputation and that due to propensity score estimation. However, the single imputation approaches, which take into account only uncertainty due to propensity score estimation, had similar standard errors. This finding could be due to our choice of 20 imputations given that previous research has shown that as the number of imputations increases, the standard errors decrease.[34] Given that our results did not indicate differences in bias or SEs between the multiple and single imputation approaches, the single imputation approaches may be preferred due to their simplicity. Among the multiple imputation approaches, we recommend the use of MI over MIMP due to the implementation issues of needing to combine missingness patterns with too few observations. We do not recommend using GBM with incomplete data using the surrogate split method. Rather, imputation should be done prior to using GBM. We also do not recommend using treatment mean imputation.

Abbreviations

AASM: average absolute standardized mean

GBM: Generalized Boosted Modeling

IPW: inverse probability weighting

MCAR: missing completely at random

MAR: missing at random

MNAR: missing not at random

MI: multiple imputation

MP: missingness pattern

MIMP: multiple imputation with missingness pattern

RMSE: root mean squared error

SD: standard deviation

SE: standard error

SI: single imputation

SI+PE: SI + prediction error

SI+PE+PU: SI + PE + parameter uncertainty

Declarations

Ethics Approval and Consent to Participate: Not Applicable

Consent for Publication: Not Applicable

Availability of Data and Materials: The code used to generate the data and conduct the simulation is available from the corresponding author upon request.

Competing Interests: The authors declare that they have no competing interests.

Funding: Preparation of this article was supported by National Institutes of Health (NIH) grants K01 ES025437 and R01 DA045049. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institute of Environmental Health Sciences (NIEHS), the National Institute on Drug Abuse (NIDA), or the NIH.

Author's Contributions: DLC conceptualized the study and drafted the manuscript. JZ and XC performed the simulation and analyzed the results. All authors read and approved the final manuscript.

Acknowledgements: We thank Lucia Pattulo for editorial assistance with the manuscript, tables, and figure.

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Table 1. Percentages of missingness on x_1 based on x_5 and Y .

| Group | x_5 | $I\{Y > \text{mean}(Y)\}$ | % of observations | % missing on x_1 | % missing on x_1 |
|-------|-------|---------------------------|-------------------|--------------------|--------------------|
| 1 | 0 | 0 | 25 | 10 | 20 |
| 2 | 0 | 1 | 25 | 20 | 40 |
| 3 | 1 | 0 | 25 | 30 | 60 |
| 4 | 1 | 1 | 25 | 40 | 80 |
| Total | | | | 25 | 50 |

Table 2. Percentages of missingness on x_2 based on x_6 and Y .

| Group | x_6 | $I\{Y > \text{mean}(Y)\}$ | % of observations | % missing on x_2 | % missing on x_2 |
|-------|-------|---------------------------|-------------------|--------------------|--------------------|
| 1 | 0 | 0 | 30 | 25 | 50 |
| 2 | 0 | 1 | 40 | 30 | 60 |
| 3 | 1 | 0 | 20 | 20 | 40 |
| 4 | 1 | 1 | 10 | 15 | 30 |
| Total | | | | 25 | 50 |

Table 3. Percentages of missingness on x_3 based on x_8 and Y .

| Group | x_8 | $I\{Y > \text{mean}(Y)\}$ | % of observations | % missing on x_3 | % missing on x_3 |
|-------|-------|---------------------------|-------------------|--------------------|--------------------|
| 1 | 0 | 0 | 40 | 30 | 60 |
| 2 | 0 | 1 | 30 | 25 | 50 |
| 3 | 1 | 0 | 10 | 15 | 30 |
| 4 | 1 | 1 | 20 | 20 | 40 |
| Total | | | | 25 | 50 |

Table 4. Percentages of missingness on x_4 based on x_9 and Y .

| Group | x_9 | $I\{Y > \text{mean}(Y)\}$ | % of observations | % missing on x_4 | % missing on x_4 |
|-------|-------|---------------------------|-------------------|--------------------|--------------------|
| 1 | 0 | 0 | 20 | 15 | 30 |
| 2 | 0 | 1 | 30 | 25 | 50 |
| 3 | 1 | 0 | 30 | 35 | 70 |
| 4 | 1 | 1 | 20 | 20 | 40 |
| Total | | | | 25 | 50 |

Table 5. Simulation results for scenario A, n = 500, 25% missing.

| Missingness Mechanism | Method | True confounders | | | Leave x1 out | | | Add x5 | | | Leave x1 out + Add x5 | | |
|-----------------------|---------------|------------------|-------|-------|---------------|-------|-------|----------------|-------|-------|-----------------------|-------|-------|
| | | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE |
| | complete | -0.001 (0.041) | 0.068 | 0.041 | 0.036 (0.043) | 0.067 | 0.056 | -0.001 (0.043) | 0.070 | 0.043 | 0.042 (0.043) | 0.068 | 0.060 |
| | comGBM | 0.029 (0.042) | 0.067 | 0.050 | - | - | - | - | - | - | - | - | - |
| MCAR | SI + pe + pu | 0.000 (0.049) | 0.068 | 0.041 | 0.036 (0.049) | 0.067 | 0.061 | 0.000 (0.051) | 0.070 | 0.051 | 0.042 (0.050) | 0.068 | 0.065 |
| | SI + pe | -0.003 (0.049) | 0.068 | 0.041 | 0.035 (0.048) | 0.067 | 0.059 | -0.002 (0.050) | 0.070 | 0.050 | 0.041 (0.049) | 0.068 | 0.064 |
| | TMI | 0.105 (0.065) | 0.072 | 0.113 | 0.131 (0.064) | 0.071 | 0.146 | 0.109 (0.066) | 0.074 | 0.127 | 0.138 (0.066) | 0.072 | 0.153 |
| | MI | -0.001 (0.045) | 0.068 | 0.041 | 0.036 (0.046) | 0.067 | 0.058 | -0.001 (0.047) | 0.070 | 0.047 | 0.042 (0.047) | 0.068 | 0.063 |
| | MIMP | -0.001 (0.045) | 0.069 | 0.041 | 0.035 (0.046) | 0.067 | 0.058 | -0.001 (0.047) | 0.070 | 0.047 | 0.042 (0.047) | 0.068 | 0.063 |
| | GBM | 0.067 (0.050) | 0.066 | 0.079 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.035 (0.047) | 0.067 | 0.054 | - | - | - | - | - | - | - | - | - |
| MAR1 | SI + pe + pu | 0.000 (0.048) | 0.068 | 0.041 | 0.036 (0.048) | 0.067 | 0.060 | 0.000 (0.050) | 0.070 | 0.050 | 0.042 (0.049) | 0.068 | 0.065 |
| | SI + pe | 0.000 (0.048) | 0.068 | 0.041 | 0.036 (0.047) | 0.067 | 0.059 | 0.000 (0.050) | 0.070 | 0.050 | 0.042 (0.048) | 0.068 | 0.064 |
| | TMI | 0.102 (0.060) | 0.070 | 0.110 | 0.129 (0.060) | 0.069 | 0.142 | 0.109 (0.062) | 0.071 | 0.125 | 0.136 (0.062) | 0.070 | 0.149 |
| | MI | 0.000 (0.044) | 0.068 | 0.041 | 0.036 (0.045) | 0.067 | 0.058 | 0.000 (0.046) | 0.070 | 0.046 | 0.042 (0.046) | 0.068 | 0.062 |
| | MIMP | 0.000 (0.045) | 0.069 | 0.041 | 0.037 (0.045) | 0.067 | 0.058 | 0.000 (0.046) | 0.070 | 0.046 | 0.043 (0.046) | 0.068 | 0.063 |
| | GBM | 0.066 (0.048) | 0.066 | 0.078 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.036 (0.046) | 0.067 | 0.055 | - | - | - | - | - | - | - | - | - |
| MAR2 | SI + pe + pu | 0.000 (0.049) | 0.068 | 0.041 | 0.036 (0.049) | 0.067 | 0.061 | 0.001 (0.051) | 0.070 | 0.051 | 0.043 (0.049) | 0.068 | 0.065 |
| | SI + pe | -0.001 (0.048) | 0.068 | 0.041 | 0.035 (0.048) | 0.067 | 0.059 | -0.001 (0.050) | 0.070 | 0.050 | 0.042 (0.049) | 0.068 | 0.065 |
| | TMI | 0.104 (0.068) | 0.073 | 0.112 | 0.129 (0.068) | 0.072 | 0.146 | 0.111 (0.071) | 0.075 | 0.132 | 0.137 (0.069) | 0.073 | 0.153 |
| | MI | 0.000 (0.045) | 0.068 | 0.041 | 0.037 (0.046) | 0.067 | 0.059 | 0.001 (0.047) | 0.070 | 0.047 | 0.043 (0.047) | 0.068 | 0.064 |
| | MIMP | 0.002 (0.045) | 0.069 | 0.041 | 0.038 (0.045) | 0.067 | 0.059 | 0.001 (0.047) | 0.070 | 0.047 | 0.043 (0.046) | 0.068 | 0.063 |
| | GBM | 0.069 (0.050) | 0.067 | 0.080 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.037 (0.046) | 0.067 | 0.055 | - | - | - | - | - | - | - | - | - |
| MAR Sinister | SI + pe + pu | 0.003 (0.048) | 0.068 | 0.041 | 0.037 (0.048) | 0.066 | 0.061 | 0.004 (0.049) | 0.069 | 0.049 | 0.043 (0.048) | 0.067 | 0.064 |
| | SI + pe | -0.002 (0.049) | 0.068 | 0.041 | 0.035 (0.049) | 0.067 | 0.060 | -0.002 (0.050) | 0.070 | 0.050 | 0.041 (0.050) | 0.068 | 0.065 |
| | TMI | 0.118 (0.062) | 0.071 | 0.125 | 0.144 (0.062) | 0.070 | 0.157 | 0.122 (0.064) | 0.073 | 0.138 | 0.151 (0.064) | 0.071 | 0.164 |
| | MI | 0.003 (0.045) | 0.068 | 0.041 | 0.040 (0.045) | 0.067 | 0.060 | 0.003 (0.046) | 0.070 | 0.046 | 0.046 (0.046) | 0.068 | 0.065 |
| | MIMP | 0.003 (0.045) | 0.068 | 0.041 | 0.040 (0.046) | 0.067 | 0.061 | 0.003 (0.046) | 0.070 | 0.046 | 0.046 (0.046) | 0.068 | 0.065 |
| | GBM | 0.074 (0.049) | 0.066 | 0.085 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.036 (0.047) | 0.067 | 0.055 | - | - | - | - | - | - | - | - | - |

Note. **Complete:** logistic regression with complete data before introducing missingness; **comGBM:** GBM with complete data before introducing missingness; **SI + pe + pu:** single imputation + prediction error + parameter uncertainty; **SI + pe:** single imputation + prediction error; **TMI:** treatment mean imputation; **MI:** multiple imputation ($m = 20$); **MIMP:** multiple imputation missingness pattern ($m = 20$); **GBM:** GBM with incomplete data; **GBM + SI + pe:** GBM after single imputation + prediction error; **SD:** standard deviation; **SE:** standard error; **RMSE:** root mean squared error.

Table 6. Simulation results for scenario G, n = 500, 25% missing.

| Missingness Mechanism | Method | True confounders | | | Leave x1 out | | | Add x5 | | | Leave x1 out + Add x5 | | |
|-----------------------|---------------|------------------|-------|-------|---------------|-------|-------|----------------|-------|-------|-----------------------|-------|-------|
| | | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE |
| | complete | -0.014 (0.044) | 0.071 | 0.046 | 0.037 (0.043) | 0.068 | 0.057 | -0.016 (0.045) | 0.073 | 0.048 | 0.040 (0.043) | 0.069 | 0.059 |
| | comGBM | 0.029 (0.044) | 0.067 | 0.053 | - | - | - | - | - | - | - | - | - |
| MCAR | SI + pe + pu | -0.011 (0.052) | 0.071 | 0.053 | 0.040 (0.049) | 0.068 | 0.063 | -0.012 (0.054) | 0.072 | 0.055 | 0.043 (0.050) | 0.068 | 0.066 |
| | SI + pe | -0.013 (0.051) | 0.071 | 0.053 | 0.039 (0.049) | 0.068 | 0.063 | -0.014 (0.053) | 0.072 | 0.055 | 0.042 (0.049) | 0.068 | 0.065 |
| | TMI | 0.096 (0.064) | 0.076 | 0.115 | 0.131 (0.061) | 0.073 | 0.145 | 0.096 (0.067) | 0.078 | 0.117 | 0.134 (0.063) | 0.074 | 0.148 |
| | MI | -0.011 (0.048) | 0.071 | 0.049 | 0.039 (0.046) | 0.068 | 0.060 | -0.013 (0.050) | 0.073 | 0.052 | 0.042 (0.047) | 0.069 | 0.063 |
| | MIMP | -0.011 (0.048) | 0.072 | 0.049 | 0.039 (0.046) | 0.068 | 0.060 | -0.013 (0.050) | 0.073 | 0.052 | 0.042 (0.047) | 0.069 | 0.063 |
| | GBM | 0.060 (0.051) | 0.067 | 0.079 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.033 (0.049) | 0.067 | 0.059 | - | - | - | - | - | - | - | - | - |
| MAR1 | SI + pe + pu | 0.000 (0.051) | 0.070 | 0.051 | 0.048 (0.048) | 0.067 | 0.068 | -0.002 (0.053) | 0.072 | 0.053 | 0.052 (0.049) | 0.068 | 0.071 |
| | SI + pe | -0.001 (0.050) | 0.070 | 0.050 | 0.048 (0.047) | 0.067 | 0.067 | -0.003 (0.052) | 0.072 | 0.052 | 0.051 (0.048) | 0.068 | 0.070 |
| | TMI | 0.113 (0.057) | 0.073 | 0.127 | 0.148 (0.055) | 0.070 | 0.158 | 0.116 (0.059) | 0.074 | 0.130 | 0.152 (0.056) | 0.071 | 0.162 |
| | MI | -0.001 (0.047) | 0.071 | 0.047 | 0.048 (0.045) | 0.068 | 0.066 | -0.002 (0.048) | 0.072 | 0.048 | 0.051 (0.046) | 0.068 | 0.069 |
| | MIMP | -0.001 (0.047) | 0.071 | 0.047 | 0.048 (0.045) | 0.068 | 0.066 | -0.002 (0.048) | 0.072 | 0.048 | 0.052 (0.046) | 0.069 | 0.069 |
| | GBM | 0.066 (0.050) | 0.067 | 0.083 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.039 (0.047) | 0.067 | 0.061 | - | - | - | - | - | - | - | - | - |
| MAR2 | SI + pe + pu | -0.009 (0.051) | 0.070 | 0.052 | 0.040 (0.050) | 0.068 | 0.064 | -0.011 (0.053) | 0.072 | 0.054 | 0.043 (0.050) | 0.068 | 0.066 |
| | SI + pe | -0.009 (0.051) | 0.070 | 0.052 | 0.041 (0.049) | 0.068 | 0.064 | -0.010 (0.053) | 0.072 | 0.054 | 0.045 (0.050) | 0.068 | 0.067 |
| | TMI | 0.090 (0.069) | 0.078 | 0.113 | 0.125 (0.066) | 0.074 | 0.141 | 0.093 (0.071) | 0.080 | 0.117 | 0.128 (0.067) | 0.076 | 0.144 |
| | MI | -0.008 (0.046) | 0.071 | 0.047 | 0.041 (0.046) | 0.068 | 0.062 | -0.010 (0.048) | 0.073 | 0.049 | 0.044 (0.046) | 0.069 | 0.064 |
| | MIMP | -0.008 (0.047) | 0.072 | 0.048 | 0.042 (0.046) | 0.068 | 0.062 | -0.010 (0.049) | 0.073 | 0.050 | 0.045 (0.047) | 0.069 | 0.065 |
| | GBM | 0.058 (0.051) | 0.067 | 0.077 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.036 (0.048) | 0.067 | 0.060 | - | - | - | - | - | - | - | - | - |
| MAR Sinister | SI + pe + pu | -0.006 (0.050) | 0.070 | 0.050 | 0.040 (0.048) | 0.067 | 0.062 | -0.007 (0.052) | 0.071 | 0.052 | 0.042 (0.048) | 0.068 | 0.064 |
| | SI + pe | -0.012 (0.051) | 0.071 | 0.052 | 0.039 (0.049) | 0.068 | 0.063 | -0.014 (0.053) | 0.072 | 0.055 | 0.042 (0.050) | 0.069 | 0.065 |
| | TMI | 0.113 (0.060) | 0.075 | 0.128 | 0.147 (0.057) | 0.072 | 0.158 | 0.113 (0.062) | 0.077 | 0.129 | 0.151 (0.059) | 0.073 | 0.162 |
| | MI | -0.007 (0.047) | 0.071 | 0.048 | 0.043 (0.045) | 0.068 | 0.062 | -0.009 (0.048) | 0.072 | 0.049 | 0.046 (0.046) | 0.069 | 0.065 |
| | MIMP | -0.007 (0.047) | 0.071 | 0.048 | 0.043 (0.046) | 0.068 | 0.063 | -0.009 (0.049) | 0.073 | 0.050 | 0.046 (0.046) | 0.069 | 0.065 |
| | GBM | 0.068 (0.050) | 0.067 | 0.084 | - | - | - | - | - | - | - | - | - |
| | GBM + SI + pe | 0.035 (0.048) | 0.067 | 0.059 | - | - | - | - | - | - | - | - | - |

Note. **Complete:** logistic regression with complete data before introducing missingness; **comGBM:** GBM with complete data before introducing missingness; **SI + pe + pu:** single imputation + prediction error + parameter uncertainty; **SI + pe:** single imputation + prediction error; **TMI:** treatment mean imputation; **MI:** multiple imputation ($m = 20$); **MIMP:** multiple imputation missingness pattern ($m = 20$); **GBM:** GBM with incomplete data; **GBM + SI + pe:** GBM after single imputation + prediction error; **SD:** standard deviation; **SE:** standard error; **RMSE:** root mean squared error.

Table 7. Simulation results for scenario G with the correct logistic model (25% missing).

| Missingness Mechanism | Method | n = 500 | | | n = 1000 | | | n = 5000 | | |
|-----------------------|--------------|----------------|-------|-------|----------------|-------|-------|----------------|-------|-------|
| | | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE | Bias (SD) | SE | RMSE |
| | complete | -0.002 (0.045) | 0.070 | 0.045 | 0.000 (0.030) | 0.049 | 0.030 | 0.001 (0.014) | 0.022 | 0.014 |
| MCAR | SI + pe + pu | -0.002 (0.053) | 0.070 | 0.053 | -0.001 (0.035) | 0.049 | 0.035 | 0.000 (0.016) | 0.022 | 0.016 |
| | SI + pe | -0.003 (0.052) | 0.070 | 0.052 | 0.000 (0.035) | 0.049 | 0.035 | 0.000 (0.016) | 0.022 | 0.016 |
| | TMI | -0.013 (0.062) | 0.076 | 0.063 | -0.009 (0.041) | 0.053 | 0.042 | -0.008 (0.018) | 0.023 | 0.020 |
| | MI | -0.002 (0.048) | 0.071 | 0.048 | -0.001 (0.033) | 0.049 | 0.033 | 0.000 (0.015) | 0.022 | 0.014 |
| | MIMP | -0.002 (0.048) | 0.071 | 0.049 | -0.001 (0.033) | 0.050 | 0.033 | 0.000 (0.015) | 0.022 | 0.014 |
| MAR1 | SI + pe + pu | 0.009 (0.052) | 0.070 | 0.053 | 0.009 (0.035) | 0.049 | 0.036 | 0.010 (0.016) | 0.022 | 0.019 |
| | SI + pe | 0.008 (0.051) | 0.070 | 0.052 | 0.010 (0.034) | 0.049 | 0.035 | 0.011 (0.016) | 0.022 | 0.019 |
| | TMI | 0.019 (0.057) | 0.073 | 0.060 | 0.021 (0.039) | 0.051 | 0.044 | 0.023 (0.018) | 0.023 | 0.029 |
| | MI | 0.008 (0.047) | 0.070 | 0.048 | 0.009 (0.031) | 0.049 | 0.033 | 0.010 (0.015) | 0.022 | 0.017 |
| | MIMP | 0.008 (0.048) | 0.071 | 0.048 | 0.009 (0.032) | 0.049 | 0.034 | 0.009 (0.015) | 0.022 | 0.017 |
| MAR2 | SI + pe + pu | -0.001 (0.052) | 0.070 | 0.052 | 0.003 (0.036) | 0.049 | 0.036 | 0.002 (0.016) | 0.022 | 0.016 |
| | SI + pe | 0.000 (0.052) | 0.070 | 0.052 | 0.003 (0.035) | 0.049 | 0.035 | 0.002 (0.016) | 0.022 | 0.016 |
| | TMI | -0.019 (0.064) | 0.077 | 0.067 | -0.015 (0.043) | 0.054 | 0.046 | -0.015 (0.019) | 0.024 | 0.024 |
| | MI | 0.000 (0.047) | 0.071 | 0.048 | 0.003 (0.032) | 0.049 | 0.033 | 0.002 (0.015) | 0.022 | 0.014 |
| | MIMP | 0.001 (0.047) | 0.071 | 0.046 | 0.004 (0.033) | 0.050 | 0.033 | 0.005 (0.015) | 0.022 | 0.015 |
| MAR sinister | SI + pe + pu | 0.003 (0.050) | 0.070 | 0.050 | 0.002 (0.035) | 0.049 | 0.035 | 0.000 (0.016) | 0.022 | 0.016 |
| | SI + pe | -0.003 (0.052) | 0.070 | 0.052 | 0.002 (0.035) | 0.049 | 0.035 | 0.000 (0.016) | 0.022 | 0.016 |
| | TMI | 0.002 (0.061) | 0.076 | 0.061 | 0.003 (0.042) | 0.052 | 0.042 | -0.004 (0.018) | 0.023 | 0.018 |
| | MI | 0.001 (0.047) | 0.071 | 0.048 | 0.002 (0.033) | 0.049 | 0.032 | 0.000 (0.015) | 0.022 | 0.015 |
| | MIMP | 0.001 (0.047) | 0.071 | 0.047 | 0.002 (0.033) | 0.049 | 0.033 | 0.000 (0.015) | 0.022 | 0.014 |

Note. **Complete:** logistic regression with complete data before introducing missingness; **SI + pe + pu:** single imputation + prediction error + parameter uncertainty; **SI + pe:** single imputation + prediction error; **TMI:** treatment mean imputation; **MI:** multiple imputation (m = 20); **MIMP:** multiple imputation missingness pattern (m = 20); **SD:** standard deviation; **SE:** standard error; **RMSE:** root mean squared error.

Figures

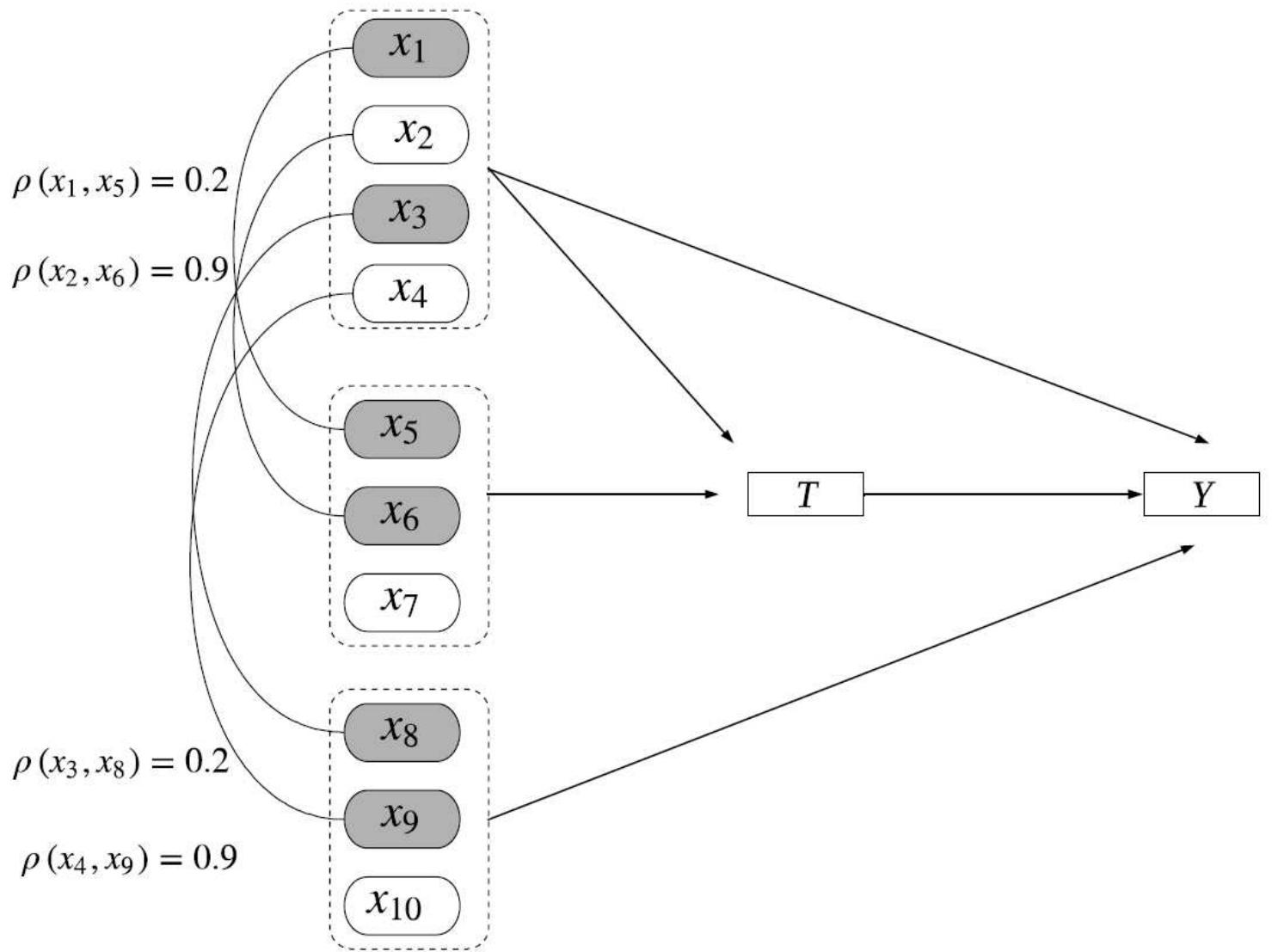


Figure 1

The data generation model

Supplementary Files

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- [supplement1.docx](#)