On Testability and Goodness of Fit Tests in Missing Data Models

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Abstract

Significant progress has been made in developing identification and estimation techniques for missing data problems where modeling assumptions can be described via a directed acyclic graph. The validity of results using such techniques rely on the assumptions encoded by the graph holding true; however, verification of these assumptions has not received sufficient attention in prior work. In this paper, we provide new insights on the testable implications of three broad classes of missing data graphical models, and design goodness-of-fit tests around them. The classes of models explored are: sequential missing-at-random and missing-not-atrandom models which can be used for modeling longitudinal studies with dropout/censoring, and a kind of no self-censoring model which can be applied to cross-sectional studies and surveys.

1 INTRODUCTION

Missing data is a common issue in applied problems. To infer a parameter of interest under missingness, often a statistical model is posed that encodes a set of assumptions on the missingness mechanisms. These assumptions are commonly divided into three main types: missing-completely-at-random (MCAR) where missingness does not have a cause and hence complete-case analysis is justifiable, missing-at-random (MAR) where all causes of missingness are assumed to be fully observed, and missing-not-at-random (MNAR) where causes of missingness are either only partially observed and/or fully unobserved [Little and Rubin, 2019].

MNAR models are perhaps the most common form of missingness in practice, and the most challenging since observations are systematically missing; yet such models are underused due to the complexity of the identification and estimation procedures needed to recover parameters of inter-

est as functions of observed data. A recent line of research has proposed to use causal graphical models as a representation of the statistical models for missing data [Glymour, 2006, Daniel et al., 2012, Martel García, 2013, Mohan et al., 2013, Thoemmes and Rose, 2014, Tian, 2015, Thoemmes and Mohan, 2015, Shpitser, 2016, Gain and Shpitser, 2018, Bhattacharya et al., 2019, Tu et al., 2019, Saadati and Tian, 2019, Nabi et al., 2020, Mohan and Pearl, 2021, Scharfstein et al., 2021]. A causal graph not only encodes conditional independence relations between variables but also depicts the causal mechanisms responsible for missingness, making it a useful tool for interpretation of the underlying assumptions. Further, just as in causal inference, graphical representations of missingness allow for the design of algorithms that automate certain steps of identification and estimation schemes.

While advances in graphical models of missing data have vielded useful insights into identifying and estimating parameters of interest, the validity of any result relies on the substantive assumptions encoded by the graph holding true. In order to confirm testability of a restriction in missing data models, we have to examine its implications on the observed data distribution; this enables the design of empirical testing procedures from finite (but partially unobserved) samples. Unfortunately, we may not always be able to test all the encoded restrictions. The permutation model, proposed by Robins [1997], is an example of a graphical MNAR model that is untestable. Mohan and Pearl [2014] provided examples of other impediments for testability in graphical missing data models. For instance, in many cases, the assumption that no variable influences its own missingness (a.k.a. lack of self-censoring causes) is untestable.

Nonetheless, there are MAR and MNAR models that entail empirically testable restrictions [Mohan and Pearl, 2014, Tian, 2015, Tu et al., 2019]. The contributions of this paper in this regard are two-fold: (i) We expand on testable implications of missing data models that resemble ordinary conditional independencies in the underlying full law, but manifest as generalized a.k.a. Verma independencies in the observed law; (ii) We design empirical tests for restrictions

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in three broad classes of missing data models that use ideas from weighted likelihood-ratio tests and odds-ratio parameterizations of joint distributions. The model classes are:

- Sequential MAR models where missingness at each time step depends only on past observed values,
- Sequential MNAR models where missingness at each time step may depend on past observed variables as well as future unmeasured/missing values, and
- MNAR models where missingness of each variable may depend on missing values of any other variable except itself.

The first two classes are useful for modeling missingness mechanisms in longitudinal studies with censoring, while the third class is better suited for survey studies and scenarios where there is no natural time ordering on the collection of data. Given our results, we can use partially observed data to reason about the underlying missingness mechanisms and verify the model specification of a missingness mechanism in our analyses. Our results are also relevant for discovery and model selection tasks where the objective is to learn not only the substantive relationships between variables of interest, but also the processes that drive their missingness.

All simulations and proofs are deferred to the appendix.

2 NOTATIONS AND PRELIMINARIES

Let $X=\{X_1,\ldots,X_K\}$ be a set of K random variables with probability distribution p(X). We denote the values of $X_k \in X$ by lower case letter $x_k \in \mathfrak{X}_k$, where \mathfrak{X}_k denotes the state space of X_k . We assume a sample of n i.i.d observations with missing values. To locate the missing cases, we consider a set of binary missingness indicators $R=\{R_1,\ldots,R_K\}$, where $R_k=0$ when x_k is missing and $R_k=1$ when x_k is observed. Let $X^*=\{X_1^*,\ldots,X_K^*\}$ denote the set of proxy random variables that represent the values of variables in X that we actually observe. Each $X_k^*\in X^*$ is deterministically defined in terms of $R_k\in R$ and $X_k\in X$ as follows: if $R_k=1,X_k^*=X_k$, otherwise $X_k^*=$ "?". We refer to p(X) as the target law, $p(R\mid X)$ as the missingness mechanism, p(X,R) as the full law, and $p(R,X^*)$ as the observed data law.

A missing data model is a set of distributions defined over variables in $\{X, R, X^*\}$. Following the conventions in Mohan et al. [2013], we represent the missing data model via a directed acyclic graph (DAG) $\mathcal{G}(V)$, where vertices V correspond to random variables in $\{X, R, X^*\}$. In addition to acyclicity, a missing data DAG (or m-DAG for short) imposes certain restrictions on the edges: variables in R cannot point to variables in X, and each $X_k^* \in X^*$ has only

two parents: X_k and R_k (due to the deterministic relationship.) Similar to Bhattacharya et al. [2019], we also allow for $X_i^* \to R_j$ edges. A few examples of m-DAGs are illustrated in Sections 3 and 4; we draw edges corresponding to the deterministic relations in gray. A full law $p(X, R, X^*)$ that is Markov relative to $\mathcal{G}(V)$ factorizes as follows:

$$\prod_{V_i \in X \cup R} p(V_i \mid \operatorname{pa}_{\mathcal{G}}(V_i)) \times \prod_{X_k^* \in X^*} p(X_k^* \mid R_k, X_k), \quad (1)$$

where $\operatorname{pa}_{\mathcal{G}}(V_i)$ denotes the parents of V_i in $\mathcal{G}(V)$. For convenience, we drop the deterministic terms, $p(X_k^*|R_k, X_k)$, when discussing the factorization of the full law.

The full law p(X,R) is identified (can be expressed as a function of the observed data) if and only if the missingness mechanism p(R|X) is identified; the target law p(X) is identified if and only if p(R=1|X) is identified. Thus, identification of the full law implies that the target law (and any function of the full law) is identified, but the reverse is not true. The missingness mechanism in an m-DAG factorizes as $\prod_k p(R_k|\operatorname{pa}_{\mathcal{G}}(R_k))$, where each conditional density $p(R_k|\operatorname{pa}_{\mathcal{G}}(R_k))$ is known as the *propensity score* of R_k . Many identification strategies in the graphical missing data literature focus on identifying each propensity score in some order (total or partial), e.g., Shpitser et al. [2015] and Bhattacharya et al. [2019]. We adopt similar strategies here.

Similar to regular DAGs, absence of an edge in a missing data DAG $\mathcal{G}(V)$ entails conditional independence restrictions between the endpoint variables in the underlying distribution p(V). These restrictions can be directly read off from the graph using Markov properties and d-separation rules [Pearl, 2009] – given disjoint sets $U, W, Z \subset V$, the global Markov property states that if $U \perp_{d\text{-sep}} W \mid Z$ in $\mathcal{G}(V)$, then $U \perp \!\!\! \perp W \mid Z$ in p(V). In this work, we focus on restrictions where all variables are at least partially observed, which allows us to narrow our focus to testability of ordinary conditional independence restrictions in the full law. However, as we will see, even ordinary restrictions in the full law may manifest as generalized equality restrictions in the observed law. Testability of generalized equality restrictions induced by latent variables in m-DAGs is a challenging problem left for future work; see Tian and Pearl [2002], Shpitser and Pearl [2006], Bhattacharya et al. [2020] for more details on such restrictions when there is no missingness.

Unlike regular DAGs where the independence constraints can be tested using observed samples from the joint distribution, a conditional independence restriction in a missing data DAG might be empirically untestable, or may manifest as more complex restrictions on the observed data law. If all the restrictions encoded in a missing data DAG are provably untestable (i.e., no restriction on the observed data law), the full law Markov relative to the DAG is said to be *non-parametric saturated* (as defined by Robins [1997]). Nonetheless, submodels of saturated missing data models may still be testable. In this paper, we discuss testability of

¹For simplicity of notations, we assume all variables have missing values. All discussions however, can be easily generalized to scenarios where a subset of variables are fully observed.

assumptions in the three aforementioned classes of missing data models as submodels of two known saturated models: the *permutation* model and the *no self-censoring* model.

Robins [1997] introduced the permutation model as follows: given an ordering on variables in X, indexed by $k \in \{1, \ldots, K\}$, each missingness indicator R_k is independent of the current and past variables in X given the past observed variables in R, X^* and future variables in X. Formally, the model is defined via the following set of conditional independence restrictions:

$$R_k \perp \!\!\! \perp X_{\prec k+1} \mid R_{\prec k}, X_{\prec k}^*, X_{\succ k}, \ \forall k \quad (permutation)$$
 (2)

where $V_{\prec k} = \{V_1, \dots, V_{k-1}\}, V_{\succ k} = \{V_{k+1}, \dots, V_K\}$. Robins [1997] showed that the full law in this model is identified and is non-parametrically saturated. A DAG representation of the permutation model with K = 2 variables is shown in Fig. 1(b).

The no self-censoring model was introduced by Shpitser [2016], Sadinle and Reiter [2017].² The central assumption in this model is that no variable directly causes its own missingness status. Formally, the model is defined by the following set of conditional independence restrictions:

$$R_k \perp \!\!\! \perp X_k \mid R_{-k}, X_{-k}, \forall k \quad (no self-censoring) \quad (3)$$

where $V_{-k} = V \setminus V_k$. Malinsky et al. [2021] showed that this model is non-parametrically saturated and identified via an odds-ratio parameterization of the missingness mechanism; a description of this parameterization, which was proposed by Chen [2007], is provided in Appendix A.1. The graphical representation of this model relies on a generalization of m-DAGs to allow for undirected edges between all pairs of R vertices – a graph with both directed and undirected edges is called a chain graph [Lauritzen, 1996, Shpitser, 2016]. An example of this model with K=2variables is shown in Fig. 4(b). The assumptions of the no self-censoring model are encoded in this chain graph by the following local Markov property: each missingness indicator R_i is independent of all other variables on the graph given its neighboring missingness indicators (joined via an undirected edge $R_i - R_j$) and its parents $(X_j \to R_i)$

3 NEW INSIGHTS INTO TESTABLE IMPLICATIONS

Although the restrictions we study in this paper can be phrased in terms of ordinary independence restrictions in the full law of a missing data DAG model, they may only manifest in the observed data law via relatively complex functionals. In this section, we show that a d-separation statement between missingness indicators and substantive

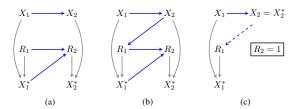


Figure 1: (a) Example of a MAR model; (b) Example of a saturated permutation model; (c) The absence of $X_2 \to R_1$ edge in (a) can be tested in the intervention distribution $p(V \setminus R_2 | \text{do}(R_2 = 1))$ where the dashed edge indicates whether p(V) is Markov equivalent to the MAR model in (a) or the permutation supermodel in (b).

variables may correspond to generalized equality constraints, a.k.a Verma constraints [Verma and Pearl, 1990], in the observed data distribution. This observation extends the current state of the art on testability in missing data models.

Consider the m-DAG shown in Fig. 1(a): a MAR submodel of the permutation model in Fig. 1(b) where $X_2 \rightarrow R_1$ is removed. Though the permutation model itself is nonparametric saturated, it is natural to ask if this MAR submodel, which imposes an additional d-separation relation $R_1 \perp \!\!\! \perp X_2$, has a testable restriction on the observed data. We first try to apply the criterion proposed by Mohan and Pearl [2014] to determine testability: A d-separation condition displayed in an m-DAG \mathcal{G} is testable if the missingness indicators associated with all partially observed variables involved in the relation are either already present in the separating set, or can be added to the set without spoiling the separation. Applying this criterion we see that the relation $R_1 \perp \!\!\!\perp_{d\text{-sep}} X_2 | R_2 \text{ does } not \text{ hold in } \mathcal{G} \text{ due to the open col-}$ lider R_2 in the path $R_1 \to R_2 \leftarrow X_1^* \leftarrow X_1 \to X_2$, and so one might conclude that $R_1 \perp \!\!\! \perp X_2$ is not testable.

Assume for a moment that X in Fig. 1(a) consists of binary variables. Let us compare number of parameters in the full law using (1) against the saturated observed data law using pattern-mixture factorization Rubin [1976] given by the marginal distribution of R and conditional distribution of X^* given R. The full law in Fig. 1(a) requires 7 parameters (3 for p(X), 1 for $p(R_1)$, and 3 for $p(R_2|R_1, X_1^*)$) which is less than the number of parameters in the saturated observed law which is $R_1 = R_1 = R$

In Fig. 1(a), conditioning on R_2 opened up the collider $R_1 \to R_2 \leftarrow X_1^*$ on the path from R_1 to X_2 . From a causal perspective, removal of these edges corresponds to an intervention in which R_2 is set to a specific value, which results in the m-conditional DAG (m-CDAG), as

²In Sadinle and Reiter [2017], the model is referred to as *itemwise conditionally independent nonresponse* model.

³See Appendix A.2 for more on parameter counting arguments.

shown in Fig. 1(c). Due to determinism (alternatively consistency), once R_2 is set to 1, then $X_2 = X_2^*$ forming a single (observed) node. Following standard notation in Pearl [2009] we denote the intervention where we set R_2 to 1 as $do(R_2 = 1)$ and the corresponding intervention distribution as $p(X, R \setminus R_2, X^* | do(R_2 = 1))$, or $p(.| do(R_2 = 1))$ for short. This intervention distribution can be obtained via truncation of the full law factorization where the propensity score of R_2 , $p(R_2|\operatorname{pa}_G(R_2))$, is dropped. That is, $p(.|do(R_2=1)) = p(X, R, X^*)/p(R_2|R_1, X_1^*)|_{R_2=1}$ and it factorizes according to the m-CDAG shown in Fig. 1(c). The relation $R_1 \perp \!\!\! \perp_{d\text{-sep}} X_2$ holds in the resulting m-CDAG, and X_2 is now fully observed. Further, the propensity score of R_2 that takes us to the intervention distribution is a function of observed data. These facts combined imply that $R_1 \perp \!\!\! \perp X_2$ imposes a restriction on the observed data in the form of a Verma constraint; i.e., a d-separation statement in an identified intervention distribution.

The above example leads to extensions of the testability criterion in Mohan and Pearl [2014, 2021]: A d-separation condition displayed in an m-DAG is also testable if the missingness indicators associated with all partially observed variables involved in the relation can be intervened on (or, in other words, their corresponding propensity scores are identified) without spoiling the separation. We formalize this extension of testable restrictions in the next section, where we also consider testability of independence statements between proxy variables and missingness indicators, and among missingness indicators themselves.

4 TESTABLE IMPLICATIONS AND GOODNESS-OF-FIT TESTS

In this section, we investigate independence assumptions in the full law and their implications on the observed data law in three broad classes of missing data models, and provide ways of empirically evaluating these constraints. We formulate the testability criteria and goodness-of-fit tests for the general case of a missing data model with K variables and illustrate the steps via examples. We consider likelihood-ratio tests for evaluating the independence $A \perp \!\!\! \perp B \mid C$, which is typically performed by fitting $p(A \mid C)$ and $p(A \mid B, C)$ and comparing their goodness-of-fit. Under the null hypothesis of independence, both models should fit the data equally well. In addition to likelihood-ratio tests, we consider evaluating $A \perp \!\!\!\perp B \mid C$ by computing the odds ratio of A and B conditioned on C – the independence relation holds if and only if the odds ratio equals one for all values of A, B, C. Therefore, if under the alternative hypothesis of dependence, the odds ratio still equals one (with statistical significancelevel α), then the data agrees with the independence relation. In the following discussion, we let \mathcal{M}_o denote the statistical model where the independence relation holds (the null hypothesis), and let \mathcal{M}_a denote the statistical supermodel

where the independence relation does not hold (the *alternative* hypothesis).

4.1 SEQUENTIAL MAR MODELS

We call a missing data model a *sequential MAR* model if under an ordering \prec that indexes variables by k = 1, ..., K, the following set of independence restrictions hold:

$$R_k \perp \!\!\! \perp X \mid R_{\prec k}, X_{\prec k}^*, \forall k$$
 (sequential-MAR) (4)

Examples of this model are shown in Fig. 1(a) and Fig. 2(a) (without the dashed edges). In addition to restrictions of a permutation model described in (2), the sequential MAR model assumes $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*$, $\forall k$ (it is straightforward to see this using graphoid axioms; see e.g., [Lauritzen, 1996] for description of the axioms). Thus, we can view the sequential MAR model as a submodel of the permutation model. Since assumptions imposed by the permutation model alone are untestable, we focus on testable implications of these extra assumptions and propose ways to empirically evaluate them.

The independence $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*$ would be easily testable using observed data if we could add $R_{\succ k} = 1$ in the conditioning set and thus evaluate the restriction using only observed cases of $X_{\succ k}$. Unfortunately, the independence no longer holds if we condition on $R_{\succ k}$ (this is easily confirmed from discussion in the previous section and Fig. 2(a).) However, we can instead intervene on $R_{\succ k}$ and check if the independence holds in the intervention distribution. The following theorem formalizes that restrictions in sequential MAR models defined above can always be tested as Verma constraints, i.e., (i) the independence holds in the corresponding m-CDAG, and (ii) the required intervention distributions are identified from observed data.

Theorem 1. The independence $R_k \perp \!\!\! \perp X_{\succ k}|R_{\prec k}, X_{\prec k}^*$ has a testable implication on the observed data distribution in form of a Verma constraint: $R_k \perp \!\!\! \perp X_{\succ k}|R_{\prec k}, X_{\prec k}^*, do(R_{\succ k}=1)$, where the intervention distribution $p(X, R \setminus R_{\succ k}, X^*|do(R_{\succ k}=1))$ is identified.

The intuition for this result will become clear as we discuss testing such constraints using n (finite) i.i.d samples (denoted by \mathcal{D}_n). One possibility is to use a likelihood-ratio test and compare goodness-of-fits between $p(R_k|R_{\prec k}, X_{\prec k}^*)$ and $p(R_k|R_{\prec k}, X_{\prec k}^*, X_{\succ k})$ but with respect to a distribution where $R_{\succ k}$ are intervened on and set to 1. This intervention distribution is a truncated factorization of the full law where propensity scores of $R_{\succ k}$ are dropped, i.e.,

$$p(.\mid \operatorname{do}(R_{\succ k}=1)) = \frac{p(V)}{\prod_{j \succ k} \ p(R_j \mid \operatorname{pa}_{\mathcal{G}}(R_j))} \Big|_{R_{\succ k}=1}.$$

Let $W_k(\beta_k^o) := p(R_k|R_{\prec k}, X_{\prec k}^*; \beta_k^o)$ and $W_k(\beta_k^a) := p(R_k|R_{\prec k}, X_{\prec k}^*, X_{\succ k}; \beta_k^a)$ (the null and alternative respectively.) Estimating β_k^o is relatively straightforward as

 $W_k(\beta_k^o)$ is a direct function of observed data, but estimating β_k^a is more involved. We propose to estimate β_k^a , wrt the truncated/weighted distribution above. This entails using a weighted estimating equation where propensity scores of $R_{\succ k}$ are used as inverse weights to fit β_k^a . It is important to note however, that a propensity score $p(R_j \mid R_{\prec j}, X_{\prec j}^*, X_{\succ j})$ for any $R_j \in R_{\succ k}$, may itself need to be fitted via a weighted estimating equation, since $X_{\succ j}$ appears in the conditioning set and $R_j \not\perp R_{\succ j} \mid R_{\prec j}, X_{\prec j}^*, X_{\succ j}$.

As an example, consider the sequential MAR model in Fig. 2(a) (without the dashed edges). The null hypothesis \mathcal{M}_o is the statistical model of this DAG and the alternative \mathcal{M}_a is the permutation supermodel with the dashed edges. We are interested in evaluating the independencies $R_1 \perp \!\!\! \perp X_2, X_3$ and $R_2 \perp \!\!\! \perp X_3 | R_1, X_1^*$, which given Theorem 1 translates into independence restrictions in $p(.|do(R_2 = 1, R_3 = 1))$ and $p(.|do(R_3 = 1))$, respectively. Testing $R_1 \perp \!\!\! \perp X_2, X_3$ entails fitting $W_{r_1}(\beta_{r_1}^a) :=$ $p(R_1|X_2,X_3;\beta_{r_1}^a)$ wrt the truncated/weighted factorization Markov relative to Fig. 2(b) where R_2 and R_3 are intervened on and set to 1. Thus, we can use propensity scores of R_2 and R_3 as inverse weights to estimate $\beta_{r_1}^a$. Let $\mathbb{P}_n[U(\beta_{r_1}^a)] = 0$ be an unbiased estimating equation for $\beta_{r_1}^a$ wrt the full law $(\mathbb{P}_n[.] = \frac{1}{n} \sum_{i=1}^n (.))$. In other words, $\mathbb{P}_n[U(\beta_{r_1}^a)]$ is any estimating equation that is unbiased for $\beta_{r_1}^a$ had there been no missingness. The following weighted estimating equation then yields an unbiased estimator for $\beta_{r_1}^a$ wrt the observed data law:

$$\mathbb{P}_n \left[\frac{R_2 \times R_3}{p(R_2 \mid \mathrm{pa}_{\mathcal{G}}(R_2)) \times p(R_3 \mid \mathrm{pa}_{\mathcal{G}}(R_3))} \times U(\beta_{r_1}^a) \right] = 0,$$

where propensity score of R_3 , $p(R_3|R_1,R_2,X_1^*,X_2^*)$, can be fit using just observed data, denote it with $W_{r_3}(\widehat{\beta}_{r_3})$. However, fitting the propensity score of R_2 , $p(R_2|R_1,X_1^*,X_3)$, requires an intermediate step involving the intervention distribution where R_3 is intervened on and set to 1, i.e., $p(X,R,X^*)/p(R_3|\operatorname{pa}_{\mathcal{G}}(R_3))$ evaluated at $R_3=1$. Similar to the above logic, this entails a weighted estimating equation using $W_{r_3}(\widehat{\beta}_{r_3})$ as inverse weights to fit the propensity score of R_2 , denoted by $W_{r_2}(\widehat{\beta}_{r_2})$. Now that we have a way of estimating $\beta_{r_1}^a$, we can test $R_1 \perp \!\!\!\perp X_2, X_3$ using a weighted likelihood-ratio by computing

$$\rho = n \mathbb{P}_n \left[\frac{R_2 \times R_3}{W_{r_2}(\widehat{\beta}_{r_2}) \times W_{r_3}(\widehat{\beta}_{r_3})} \times \log \left(\frac{W_{r_1}(\widehat{\beta}_{r_1}^a)}{W_{r_1}(\widehat{\beta}_{r_1}^o)} \right) \right],$$

where $W_{r_1}(\beta_{r_1}^o) := p(R_1; \beta_{r_1}^o)$ and $\beta_{r_1}^o$ is simply the proportion of complete cases of X_1 , we can use likelihood chisquare or Wald tests to compare goodness-of-fits [Robins and Wasserman, 1997, Agostinelli and Markatou, 2001].

If we start our tests for the sequential MAR model by testing the restriction $R_2 \perp \!\!\! \perp X_3 | R_1, X_1^*$, there are two possibilities: (i) The null might be rejected which immediately implies that the missing data model is not sequential MAR; (ii) The null is accepted which means R_2 does not have

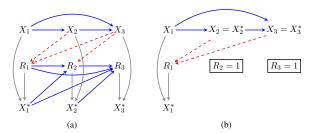


Figure 2: (a) Example of a sequential MAR model (without the dashed edges) along with its permutation supermodel (with the dashed edges); (b) The graph Markov equivalent to intervention distribution $p(.|do(R_2 = 1, R_3 = 1))$.

 X_3 as a cause. In future tests, say for $R_1 \perp \!\!\! \perp X_2, X_3$ in this case, this justifies fitting a simplified propensity score $p(R_2|R_1,X_1^*,X_3^*)$ that makes use of all the observed data. This simplified propensity score also corresponds to the same model we would have already fit for the previous null hypothesis $\beta_{r_2}^o$. This example reveals that there is a natural way to order the tests. For a model with K variables, we would proceed backwards by first testing restrictions involving R_{K-1} , moving to R_{K-2} , and so on. If the current test succeeds, the corresponding model for the null can be re-used to produce weights for future estimating equations; if the test fails, then the assumptions of sequential MAR does not hold. Following such a sequence may help improve the power of each test by using all of the observed samples to estimate the weights in each step. We formalize this sequence of goodness-of-fit tests based on weighted likelihood-ratios in Algorithm 1, which takes an ordering ≺ on the missingness indicators, null and alternative models as a tuple \mathcal{M} , and data samples \mathcal{D}_n as input. The k^{th} iteration of the for loop concerns testing the independence $R_k \perp \!\!\! \perp X_{\succ k} \mid R_{\prec k}, X_{\prec k}^*$. Note however, that as we proceed with the tests, we are restricted to fewer and fewer samples which impacts the power of our tests. Although weighting approaches are common in missing data models [Li et al., 2013], an interesting direction for future work is to develop semiparametric methods to use data more efficiently.

4.2 SEQUENTIAL MNAR MODELS

We call a missing data model a sequential MNAR model if under an ordering \prec that indexes variables by k = 1, ..., K, the following set of independence restrictions hold:

$$R_k \perp \!\!\! \perp X_{\prec k+1}, X_{\prec k}^* \mid R_{\prec k}, X_{\succ k}, \forall k \ (sequential-MNAR) (5)$$

An example of this model is shown in Fig. 3(a) (without the dashed edges.) We can view the sequential MNAR model as a submodel of the permutation model since in addition to the restrictions in (2), it assumes $R_k \perp \!\!\! \perp X_{\prec k}^* \mid R_{\prec k}, X_{\succ k}, \forall k$. Thus, we focus on testable implications of these extra assumptions and propose ways to empirically evaluate them.

Unlike sequential MAR models, the d-separation state-

Algorithm 1 TESTING SEQUENTIAL MAR $(\prec, \mathcal{M}, \mathcal{D}_n)$

- 1: Let \prec index variables by $k = 1, \dots, K$.
- 2: Let $W_K(\beta_K^o) := p(R_K | R_{\prec K}, X_{\prec K}^*; \beta_K^o)$.
- 3: Estimate β_K^o (denote it by $\widehat{\beta}_K^o$).
- 4: **for** $k \in \{K-1, ..., 1\}$ **do**
- 5: Let $W_k(\beta_k^o) \coloneqq p(R_k | R_{\prec k}, X_{\prec k}^*; \beta_k^o)$ and $W_k(\beta_k^a) \coloneqq p(R_k | R_{\prec k}, X_{\prec k}^*, X_{\succ k}; \beta_k^a).$
- 6: Estimate β_k^o (denote it by $\widehat{\beta}_k^o$).
- 7: Estimate β_k^a via the weighted estimating equation:

$$\mathbb{P}_n \left[\frac{\mathbb{I}(R_{\succ k} = 1)}{\prod_{i \succ k}^K W_j(\widehat{\beta}_i^o)} \times U(\beta_k^a) \right] = 0,$$

where $\mathbb{P}_n[U(\beta_k^a)] = 0$ is an unbiased estimating equation for β_k^a wrt the full law (denote it by $\widehat{\beta}_k^a$).

8: Compute a weighted likelihood-ratio as follows:

$$\rho = n \mathbb{P}_n \left[\frac{\mathbb{I}(R_{\succ k} = 1)}{\prod_{j \succ k}^K W_j(\widehat{\beta}_j^o)} \times \log \left(\frac{W_k(\widehat{\beta}_k^a)}{W_k(\widehat{\beta}_k^o)} \right) \right].$$

- 9: Test ρ with α significance level.
- 10: **if** \mathcal{M}_o is rejected (i.e., $R_k \not\perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*$) **then**
- 11: **return** not sequential MAR
- 12: return sequential MAR

ments being tested in sequential MNAR models are between missingness indicators and proxy variables, which can be viewed as context-specific restrictions. Due to determinism, when $R_j=0, X_j^*=$ "?" and thus an independence such as $R_k \perp \!\!\! \perp X_j^*|R_j=0$ becomes a statement of independence between a random variable R_k and some constant, which is trivially true. Hence, the set $R_k \perp \!\!\! \perp X_{\prec k}^* | R_{\prec k}, X_{\succ k}, \forall k$ is equivalent to context-specific restrictions $R_k \perp \!\!\! \perp X_{\prec k} | R_{\prec k} = 1, X_{\succ k}, \forall k$. This differs from restrictions $R_k \perp \!\!\! \perp X_{\prec k} | R_{\prec k}, X_{\succ k}, \forall k$, which refer to independencies involving partially observed variables rather than proxies. Even though, the independence $R_k \perp \!\!\! \perp X_{\prec k} | R_{\prec k} = 1, X_{\succ k}$ restricts us to rows where $X_{\prec k}$ is fully observed, we still need enough assumptions to plug in $R_{\succ k} = 1$ in the conditioning set, since $X_{\succ k}$ is in the conditioning set. Unfortunately, the independence between R_k and $X_{\prec k}^*$ no longer holds if we condition on $R_{\succ k}$. However, the following theorem formalizes that restrictions in sequential MNAR models defined above can also be tested as Verma constraints in identified intervention distributions where $R_{\succ k}$ are intervened and $X_{\succ k}$ are fully observed.

Theorem 2. The independence $R_k \perp \!\!\! \perp X_{\prec k}^*|R_{\prec k}, X_{\succ k}$ has a testable implication on the observed data distribution in form of a Verma constraint $R_k \perp \!\!\! \perp X_{\prec k}^*|R_{\prec k}, X_{\succ k}, do(R_{\succ k}=1)$, where the intervention distribution $p(X, R \setminus R_{\succ k}, X^*|do(R_{\succ k}=1))$ is identified.

To evaluate these Verma constraints, we use weighted

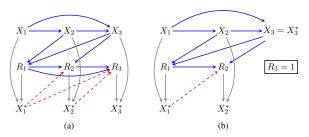


Figure 3: (a) Example of a sequential MNAR model (without the dashed edge) along with its permutation supermodel (with the dashed edge); (b) The graph Markov equivalent to intervention distribution $p(.|do(R_3 = 1))$.

likelihood-ratio tests again. We explain this via a sequential MNAR example in Fig. 3(a) (without the dashed edges.) \mathcal{M}_o is the statistical model of this DAG and \mathcal{M}_a is the permutation supermodel with the dashed edges. We are interested in testing absence of the dashed edges which imply $R_3 \perp \!\!\! \perp X_1^*, X_2^* \mid R_1, R_2 \text{ and } R_2 \perp \!\!\! \perp X_1^* \mid R_1, X_3.$ To empirically evaluate the first restriction, we need to compare $p(R_3 \mid R_1, R_2, X_1^*, X_2^*)$ and $p(R_3 \mid R_1, R_2)$, which is straightforward since these two models are direct functions of observed data. To evaluate the second restriction however, we need to compare $p(R_2|X_1^*, R_1, X_3)$ and $p(R_2|R_1, X_3)$ wrt the intervention distribution $p(.|do(R_3 =$ 1), which corresponds to the truncated factorization $p(X, R, X^*)/p(R_3|R_1, R_2, X_1^*, X_3^*)$ (evaluated at $R_3 =$ 1) and is Markov relative to the graph in Fig. 3(b). Thus, we can use $p(R_3|R_1, R_2, X_1^*, X_2^*)$ as inverse weights to fit models wrt this truncated distribution. Let $W_{r_2}(\beta_{r_2}^a) :=$ $p(R_2|R_1,X_1^*,X_3;\beta_{r_2}^a)$ and let $\mathbb{P}_n[U(\beta_{r_2}^a)]=0$ be an unbiased estimating equation for $\beta^a_{r_2}$ wrt the full law. We can estimate $\beta_{r_2}^a$ using observed data via this weighted estimating equation: $\mathbb{P}_n[\{R_3/p(R_3|R_1,R_2,X_1^*,X_2^*;\widehat{\eta})\} \times$ $U(\beta_{r_2}^a)$] = 0, where $\hat{\eta}$ is the estimated parameters for $p(R_3|R_1, R_2, X_1^*, X_2^*)$. Following the same logic, we can also estimate $\beta_{r_2}^o$ in $W_{r_2}(\beta_{r_2}^o) := p(R_2|R_1, X_3; \beta_{r_2}^o)$. Finally, we use the following statistic in a weighted likelihoodratio to test the restriction $R_2 \perp \!\!\! \perp X_1^* \mid R_1, X_3$:

$$\rho = n \mathbb{P}_n \bigg[\frac{R_3}{p(R_3 \mid R_1, R_2, X_1^*, X_2^*; \widehat{\eta})} \times \log \Big(\frac{W_{r_2}(\widehat{\beta}_{r_2}^a)}{W_{r_2}(\widehat{\beta}_{r_2}^o)} \Big) \bigg].$$

If we test the restriction $R_3 \perp \!\!\! \perp X_1^*, X_2^* | R_1, R_2$ first and conclude that the independence holds, we can use the R_3 fitted propensity score under the accepted null, that is $p(R_3 \mid R_1, R_2; \widehat{\beta}_{r_3}^o)$, in above (without conditioning on X_1^*, X_2^*). This implies that for testing $R_2 \perp \!\!\! \perp X_1^* \mid R_1, X_3$, we do not have to use the full permutation model as a supermodel. Instead, we can use the permutation model where $R_3 \rightarrow \{X_2^*, X_3^*\}$ edges are absent. A sequential goodness-of-fit tests based on weighted likelihood-ratios is provided in Algorithm 2.

Remark 1. The sequential MNAR model is an example of a DAG with no *colluders* that were studied in Nabi et al.

Algorithm 2 TESTING SEQUENTIAL MNAR $(\prec, \mathcal{M}, \mathcal{D}_n)$

- 1: Let \prec index variables by $k = 1, \dots, K$.
- 2: Let $\Omega_{K+1} = 1$.
- 3: **for** $k \in \{K, \dots, 2\}$ **do**
- 4: Let $W_k(\beta_k^o) := p(R_k | R_{\prec k}, X_{\succ k}; \beta_k^o)$ and $W_k(\beta_k^a) := p(R_k | R_{\prec k}, X_{\succ k}, X_{\prec k}^*; \beta_k^a).$
- 5: Estimate β_k^o and β_k^a via the following:

$$\mathbb{P}_n[\Omega_{k+1} \times U(\beta_k^o)] = 0, \quad \mathbb{P}_n[\Omega_{k+1} \times U(\beta_k^a)] = 0,$$

where $\mathbb{P}_n\big[U(\beta_k^o)\big]=0$ and $\mathbb{P}_n\big[U(\beta_k^a)\big]=0$ are estimating equations for β_k^o and β_k^a wrt the full law.

6: Compute a weighted likelihood-ratio as follows:

$$\rho = n \mathbb{P}_n \left[\Omega_{k+1} \times \log \left(\frac{W_k(\widehat{\beta}_k^a)}{W_k(\widehat{\beta}_k^o)} \right) \right].$$

- 7: Test ρ with α significance level.
- 8: **if** \mathcal{M}_o is rejected (i.e., $R_k \not\perp \!\!\! \perp X_{\prec k}^* | R_{\prec k}, X_{\succ k}$) **then**
- 9: **return** not sequential MNAR
- 10: **else** $\Omega_{k+1} = \frac{\mathbb{I}(R_{\succ k} = 1)}{\prod_{j \succ k}^{K} W_j(\widehat{\beta}_j^o)}$.
- 11: return sequential MNAR

[2020]. A colluder exists at R_i if there exists $X_i \in X \setminus X_i$ such that $X_i \to R_j \leftarrow R_i$. Nabi et al. [2020] considered a class of missing data DAG models with no outgoing edges from the proxies, and proved that under the absence of colluder structures and self-censoring edges $(X_k \to R_k)$, the full law Markov relative to such a DAG is identified and is a submodel of the saturated no self-censoring model defined in (3). Thus, it is possible to use the no self-censoring model as an alternative supermodel to test some of the restrictions in the sequential MNAR model. Namely, we can empirically evaluate this set of restrictions: $R_k \perp \!\!\! \perp X_{\prec k} \mid R_{-k}, X_{\succ k}$. As a simple example, consider the DAG in Fig. 4(a). We are interested in the absence of an edge between X_1 and R_2 which implies $R_2 \perp \!\!\! \perp X_1 | R_1$. The no self-censoring supermodel is drawn in Fig. 4(b) (with R_1, R_2 edge undirected). We can evaluate this independence by showing $p(R_2|R_1,X_1)$ is not a function of X_1 . For this, we use the following odds-ratio factorization of p(R|X) [Chen, 2007]:

$$p(R_1, R_2 \mid X_1, X_2) = \frac{1}{Z} \times$$

$$p(R_1 \mid R_2 = 1, X_2) \times p(R_2 \mid R_1 = 1, X_1) \times OR(R_1, R_2 \mid X),$$
(6)

where Z is a normalizing term and $\operatorname{OR}(R_1,R_2|X)$ is the conditional odds ratio between R_1 and R_2 . Since the no self-censoring model is identified, each piece above must be a function of observed data. This is trivial for the univariate conditionals, however, it can also be shown that $\operatorname{OR}(R_1,R_2|X)=f(R_1,R_2)$, i.e., is not a function of X (see Appendix A, Eq. 9.) By definition $p(R_2|R_1,X_1)=p(R|X)/\sum_{R_2}p(R|X)$; to show $p(R_2|R_1,X_1)$ is not a function of X_1 , it suffices to show $p(R_1|X)$ is not a func-

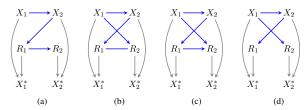


Figure 4: The sequential MNAR model in (a) can be tested as a submodel of the saturated no self-censoring model in (b); (c) A criss-cross supermodel of (a) where the restriction is not identified; (d) Example of a block-parallel MNAR model which can be tested as a submodel of (b).

tion of X_1 which using (6) only requires us to show $p(R_2|R_1=1,X_1)$ is not a function of X_1 which is easy to evaluate. This can be generalized to K>2, but it involves higher order interactions terms in the odds-ratio parameterization, which is why we prefer the permutation model as our supermodel choice; see Appendix B.1 for more details.

Remark 2. The DAG in Fig. 4(c) is also a supermodel of Fig. 4(a). However, we cannot use this model to evaluate the independence $R_2 \perp \!\!\! \perp X_1 \mid R_1$, because $p(R_2 \mid R_1, X_1)$ in this graph is not fully identified. Bhattacharya et al. [2019] showed that due to the colluder structure at R_2 , $p(R_2 \mid R_1 = 0, X_1)$ is not a function of observed data. We call the DAG in Fig. 4(c), the *criss-cross* structure. Unlike the permutation and no self-censoring models, neither the full law nor the target law is identified in the criss-cross model. The reason the full law is not identified is due to the colluder structure at R_2 . Bhattacharya et al. [2019] conjectured that the target law is also not identified but never formally proved it. We formalize and prove the statement in the following theorem.

Theorem 3. The target law p(X) is not identified in a missing data DAG model where there exists at least one crisscross structure between a pair of variables.

This result characterizes an additional graphical structure (besides self-censoring) that impedes target law identification; this may lead to further insights on sound and complete algorithms for target law identification (an open problem.)

Remark 3. As an alternative to the likelihood-ratio test, we can compute odds ratios to perform independence tests. For instance, in the MAR model of Fig. 1(a), $R_1 \perp \!\!\! \perp X_2$ translates into $\mathrm{OR}(R_1, X_2) = 1$. We can write down this odds ratio as a function of $p(R_1 = r_1|X_2 = x_2)$, and since we already know how to fit this model using a weighting estimating equation, we can easily compute the odds ratio and perform our test. As another example, in the MNAR model of Fig. 4(a), $R_2 \perp \!\!\! \perp X_1^*|R_1$ translates into $\mathrm{OR}(R_2, X_1|R_1 = 1) = 1$, which can be empirically evaluated using only complete cases on X_1 . We can generalize the idea of using odds ratio for goodness-of-fit tests to sequential MAR and MNAR models with K > 2 variables; see Appendix B.2 and B.3 for more details.

4.3 BLOCK PARALLEL MNAR MODELS

We call a missing data model a *block-parallel MNAR* model⁴ if it satisfies the following set of independence restrictions:

$$R_k \perp \!\!\!\perp R_{-k}, X_k \mid X_{-k}, \forall k \ (block-parallel MNAR)$$
 (7)

An example of this model is shown in Fig. 4(d). Using graphoid axioms, it is easy to show that the block-parallel model assumes $R_k \perp \!\!\! \perp R_j \mid X, \forall j \neq k$ on top of what the no self-censoring model already assumes. Thus, we view the block-parallel model (\mathcal{M}_o) as a submodel of the saturated no self-censoring model (\mathcal{M}_a) defined in (3), and focus on testable implications and empirical evaluations of these extra assumptions. Unlike the sequential models, the independence statements here are between missingness indicators and there is no predefined ordering.

If we were to follow ideas from the previous two subsections, we would need to intervene on R_k and R_j to test the independence $R_k \perp \!\!\! \perp R_j \mid X$ as X_k, X_j appear in the conditioning set. Interventions on R_k and R_j fix them to constants, which prevent us from evaluating independence. One might then conclude that such constraints are untestable. However, we use odds-ratio parameterization of the missingness mechanism to argue that these restrictions are indeed testable. We formalize the results in the following theorem.

Theorem 4. The independence $R_k \perp \!\!\! \perp R_j | X \forall j \neq k$ has a testable implication on observed data which can be stated via $OR(R_k, R_j | X_{-kj}, R_{-kj} = 1) = 1$.

We illustrate how to empirically evaluate the odds ratios via an example. Consider the block-parallel model in Fig. 4(d) along with its no self-censoring supermodel in (b). We are interested in the absence of R_1 and R_2 edge which implies $R_1 \perp \!\!\! \perp R_2 \mid X_1, X_2.$ This translates into showing that $\mathrm{OR}(R_1=0,R_2=0|X)=1$ (the OR is already one when either R_1 or R_2 is at its "reference" value of 1.) As discussed in Remark 1, the odds ratio is identified in the no self-censoring model. Let $\theta(r_1,r_2)=\mathrm{OR}(R_1=r_1,R_2=r_2\mid X_1,X_2).$ To estimate $\theta(r_1,r_2),$ we use the odds-ratio parameterization of p(R|X) in (6) in the following unbiased estimating equation proposed by Malinsky et al. [2021]:

$$\mathbb{P}_n \Big[R_1 R_2 \times \frac{p(R_1 = 0, R_2 = 0 \mid X)}{p(R_1 = 1, R_2 = 1 \mid X)} - (1 - R_1)(1 - R_2) \Big] = 0,$$

where the density ratio is equal to

$$\frac{p(R_1=0 \mid R_2=1, X_2) \times p(R_2=0 \mid R_1=1, X_1)}{p(R_1=1 \mid R_2=1, X_2) \times p(R_2=1 \mid R_1=1, X_1)} \times \theta(0,0).$$

Thus, we can find a closed form estimator for $\theta(R_1=0,R_2=0)$ using the above unbiased estimating equation. See Appendix A.1 for more details.

Algorithm 3 TESTING BLOCK-PARALLEL $(\mathcal{M}, \mathcal{D}_n)$

- 1: for $k \in \{1, \dots, K-1\}$ do
- 2: Let $W_k(\beta_k) := p(R_k = 1 \mid R_{-k} = 1, X_{-k}; \beta_k)$.
- 3: Estimate β_k (denoted by $\widehat{\beta}_k$).
- 4: for each pair $k, j \in \{1, \dots, K\}$ s.t. $k \neq j$ do
- 5: Let $\theta(r_k, r_j) = OR(R_k = R_j = 0 \mid R_{-kj} = 1, X)$
- 6: Compute $\theta(R_k = 0, R_j = 0)$ via the following:

$$\frac{\mathbb{P}_n\left[\prod_{i\neq\{k,j\}} R_i \times (1 - R_k) \times (1 - R_j)\right]}{\mathbb{P}_n\left[\prod_{i=1}^K R_i \times \frac{(1 - W_k(\widehat{\beta}_k)) \times (1 - W_j(\widehat{\beta}_j))}{W_k(\widehat{\beta}_k) \times W_j(\widehat{\beta}_j)}\right]}$$

- 7: Test $\theta(R_k = 0, R_j = 0) = 1$ at significance level α
- 8: **if** test fails (i.e., $R_k \not\perp \!\!\! \perp R_j | X$) **then**
- 9: **return** not block-parallel MNAR
- 10: return block-parallel MNAR

For block-parallel models with K>2 variables, we can test the absence of edges between any two pairs of missingness indicators by computing pairwise odds ratios. We formalize the goodness-of-fit tests based on these calculations in Algorithm 3. It is worth pointing out that the criss-cross model in Fig. 3(b) can also be a supermodel of the block-parallel MNAR model. However, it does not allow for identification of pairwise odds ratios. This motivates our use of the no self-censoring chain graph as the supermodel.

Simulation studies are provided in Appendix D.

5 CONCLUSIONS

Independence restrictions in the full law of missing data models might be empirically untestable or might translate into more complex restrictions on the observed data law than ordinary d-separation statements. In this paper, we considered three broad classes of missing data models and investigated testable implications of the assumed statistical models on the observed data law. We have extended the notion of testability in missing data models by viewing ordinary conditional independence tests as Verma constraints in intervention distribution. We have proposed goodness-of-fit tests based on weighted likelihood-ratio tests. We also used an odds-ratio parameterization to analyze implications of independence between missingness indicators. Our results and discussions are useful in validating the statistical models of missing data in practice as well as discovering the mechanisms that drive the missingness of variables. A fruitful future direction is developing semiparametric methods that would complement our weighting procedures by allowing to use data more efficiently in estimating parameters and performing goodness-of-fit tests.

⁴Block-parallel model was introduced in Mohan et al. [2013].

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APPENDIX

The appendix is organized as follows. In Appendix A, we cover additional preliminaries: we provide the odds-ratio parameterization of a missing data process, illustrate how to estimate an odds ratio via a simple example, and elaborate more on parameter counting to argue whether the assumptions in a full law impose restrictions on observed data in discrete models. Appendix B contains additional discussions on the use of odds-ratio parameterization in the sequential MAR and sequential MNAR models. Appendix C contains the proofs. Appendix D contains simulation results.

A PRELIMINARIES

A.1 ODDS-RATIO PARAMETERIZATION

The odds-ratio parameterization of joint distributions p(R|X) was introduced in Chen [2007]. Assuming we have K missingness indicators, p(R|X) can be expressed as follows:

$$p(R \mid X) = \frac{1}{Z} \times \prod_{k=1}^{K} p(R_k \mid R_{-k} = 1, X) \times \prod_{k=2}^{K} OR(R_k, R_{\prec k} \mid R_{\succ k} = 1, X),$$
(8)

where $R_{-k} = R \setminus R_k, R_{\prec k} = \{R_1, \dots, R_{k-1}\}, R_{\succ k} = \{R_{k+1}, \dots, R_K\}$, and

$$OR(R_k, R_{\prec k} \mid R_{\succ k} = 1, X) = \frac{p(R_k \mid R_{\succ k} = 1, R_{\prec k}, X)}{p(R_k = 1 \mid R_{\succ k} = 1, R_{\prec k}, X)} \times \frac{p(R_k = 1 \mid R_{-k} = 1, X)}{p(R_k \mid R_{-k} = 1, X)}.$$

Z in Eq. (8) is the normalizing term and is equal to $\sum_{r} \Big\{ \prod_{k=1}^{K} \ p(r_k \mid R_{-k}=1,X) \times \prod_{k=2}^{K} \mathrm{OR}(r_k,r_{\prec k} \mid R_{\succ k}=1,X) \Big\}.$

A.1.1 Estimating equations for computing odds ratios

Consider the no self-censoring model with two variables, shown in Fig. 4(b). Let $\theta(r_1, r_2) = OR(R_1 = r_1, R_2 = r_2 \mid X_1, X_2)$. We can estimate $\theta(r_1 = 0, r_2 = 0)$ with the following unbiased estimating equation where an odds-ratio parameterization of p(R|X) is used in place. We have:

$$p(R_1 = r_1, R_2 = r_2 \mid X) = \frac{1}{Z} \times p(R_1 = r_1 \mid R_2 = 1, X_2) \times p(R_2 = r_2 \mid R_1 = 1, X_1) \times \theta(r_1, r_2).$$

Therefore,

$$\begin{split} \mathbb{P}_n \Big[R_1 R_2 \times \frac{p(R_1 = 0, R_2 = 0 \mid X)}{p(R_1 = 1, R_2 = 1 \mid X)} - (1 - R_1)(1 - R_2) \Big] \\ &= \mathbb{P}_n \Big[R_1 R_2 \times \frac{p(R_1 = 0 \mid R_2 = 1, X_2) \times p(R_2 = 0 \mid R_1 = 1, X_1) \times \theta(R_1 = 0, R_2 = 0)}{p(R_1 = 1 \mid R_2 = 1, X_2) \times p(R_2 = 1 \mid R_1 = 1, X_1) \times \theta(R_1 = 1, R_2 = 1)} - (1 - R_1)(1 - R_2) \Big] \\ &= \mathbb{P}_n \Big[R_1 R_2 \times \frac{p(R_1 = 0 \mid R_2 = 1, X_2) \times p(R_2 = 0 \mid R_1 = 1, X_1)}{p(R_1 = 1 \mid R_2 = 1, X_2) \times p(R_2 = 1 \mid R_1 = 1, X_1)} \times \theta(R_1 = 0, R_2 = 0) - (1 - R_1)(1 - R_2) \Big] \\ &= 0. \end{split}$$

The first equality holds by definition, the second equality holds because $OR(R_1 = 1, R_2 = 1) = 1$, and the third equality can be simply proved with tower laws of expectations. Given the above, we can find a closed form estimator for $\theta(R_1 = 0, R_2 = 0)$:

$$\theta(R_1 = 0, R_2 = 0) = \frac{\mathbb{P}_n \Big[(1 - R_1) \times (1 - R_2) \Big]}{\mathbb{P}_n \Big[R_1 \times R_2 \times \frac{p(R_1 = 0 | R_2 = 1, X_2) \times p(R_2 = 0 | R_1 = 1, X_1)}{p(R_1 = 1 | R_2 = 1, X_2) \times p(R_2 = 1 | R_1 = 1, X_1)} \Big]}.$$

For K>2, we need to compute odds ratio terms of the form $\theta(R_k=0,R_j=0)\coloneqq \mathrm{OR}(R_k=0,R_j=0|R_{-kj}=1,X)$. The following unbiased estimating equation that incorporates R_{-kj} can be used to estimate $\theta(R_k=0,R_j=0)$:

$$\mathbb{P}_n \left[\prod_{i=1}^K R_i \times \frac{p(R_k = 0 | R_{-k} = 1, X_{-k}) \times p(R_j = 0 | R_{-j} = 1, X_{-j})}{p(R_k = 1 | R_{-k} = 1, X_{-k}) \times p(R_j = 1 | R_{-j} = 1, X_{-j})} \times \theta(R_k = 0, R_j = 0) - \prod_{i \neq \{j, k\}} R_i (1 - R_k) (1 - R_j) \right] = 0.$$

Using the tower laws of expectations, it is easy to show why the above estimating equation holds.

A.2 PARAMETER COUNTING ARGUMENT

How does one know that a missing data DAG imposes restrictions that are testable from the observed data distribution? When all substantive variables take on values in a finite discrete state space, one simple check is to compare the number of parameters in the full law using the DAG factorization in (1) and the saturated observed data law using the *pattern-mixture* factorization [Rubin, 1976]. The pattern-mixture factorization is given by the marginal distribution of R and the conditional distribution of R are given R. If a missing data DAG with an identified full law can be described with fewer parameters than the saturated pattern-mixture model, we may conclude that the restrictions on full law impose constraints on the observed data distribution. Shpitser [2016] has used parameter counting to give an intuition for why the no self-censoring model is identified. Nabi et al. [2020] also have relied on a parameter counting argument to prove the completeness of their results for full law identification in missing data DAG models.

As an example, consider a missing data model with two substantive binary variables X_1 and X_2 . Assume the full law satisfies the assumptions of the permutation model in (2), which are $R_1 \perp \!\!\! \perp X_1 | X_2$ and $R_2 \perp \!\!\! \perp X_1, X_2 | R_1, X_1^*$. The full law then factorizes as $p(X_1, X_2) \times p(R_1 | X_2) \times p(R_2 | R_1, X_1^*)$. We need 3 parameters for parameterizing $p(X_1, X_2)$, 2 parameters for $p(R_1 \mid X_2)$, and 3 parameters for $p(R_2 \mid R_1, X_1^*)$; thus a total of 8 parameters. (We excluded the deterministic terms $p(X_1^* \mid R_1, X_1)$ and $p(X_2^* \mid R_2, X_2)$ as they do not add any parameters.) On the other hand, the pattern-mixture factorization of the observed data law $p(R, X^*)$ can be written as $p(R_1, R_2) \times p(X_1^*, X_2^* \mid R_1, R_2)$. Since R_1 and R_2 are binary, it requires at most 3 parameters to parameterize $p(R_1, R_2)$. Using chain rule factorization, we have $p(X^* \mid R) = p(X_1^* \mid R_1, R_2) \times p(X_2^* \mid R_1, R_2, X_1^*)$. Due to the deterministic relations, if $R_1 = 0$ then $X_1^* = "?"$, thus we need at most 2 parameters to parameterize $p(X_1^* \mid R_1, R_2)$. Similarly, we need at most 3 parameters to parameterize $p(X_2^* \mid R_1, R_2, X_1^*)$. In total, 8 parameters are required to encode a saturated observed data law. As expected, the number of parameters in the full law of the permutation model (which is proven to be identified as a function of observed data) and the saturated observed data law are the same, reaffirming the fact that permutation model is saturated and places no restrictions on the observed data distribution.

As another example of a saturated model, consider the no self-censoring model in Fig. 4(b). The odds-ratio parameterization of the missingness mechanism p(R|X) is as follows:

$$p(R_{1} = r_{1}, R_{2} = r_{2} \mid X_{1}, X_{2})$$

$$= \frac{1}{Z} \times p(R_{1} = r_{1} \mid R_{2} = 1, X_{1}, X_{2}) \times p(R_{2} = r_{2} \mid R_{1} = 1, X_{1}, X_{2}) \times OR(R_{1} = r_{1}, R_{2} = r_{2} \mid X_{1}, X_{2})$$

$$= \frac{1}{Z} \times p(R_{1} = r_{1} \mid R_{2} = 1, X_{2}) \times p(R_{2} = r_{2} \mid R_{1} = 1, X_{1}) \times f(R_{1} = r_{1}, R_{2} = r_{2}),$$
(9)

where $Z = \sum_{r_1, r_2} p(R_1 = r_1 \mid R_2 = 1, X_2) \times p(R_2 = r_2 \mid R_1 = 1, X_1,) \times \text{OR}(R_1 = r_1, R_2 = r_2 \mid X_1, X_2)$. The second equality in (9) holds because $R_1 \perp \!\!\! \perp X_1 \mid R_2, X_2$ and $R_2 \perp \!\!\! \perp X_2 \mid R_1, X_1$. Further, $\text{OR}(R_1 = r_1, R_2 = r_2 \mid X_1, X_2)$ is just a function of R_1 and R_2 because:

$$\begin{split} \operatorname{OR}(R_1 = r_1, R_2 = r_2 \mid X_1, X_2) &= \frac{p(R_1 = r_1 \mid R_2 = r_2, X_2)}{p(R_1 = 1 \mid R_2 = r_2, X_2)} \times \frac{p(R_1 = 1 \mid R_2 = 1, X_2)}{p(R_1 = r_1 \mid R_2 = 1, X_2)} \\ &= \frac{p(R_2 = r_2 \mid R_1 = r_1, X_1)}{p(R_2 = 1 \mid R_1 = r_1, X_1)} \times \frac{p(R_2 = 1 \mid R_1 = 1, X_1)}{p(R_2 = r_2 \mid R_1 = 1, X_1)} \\ &= f(R_1, R_2). \end{split}$$

The first equality holds because $R_1 \perp \!\!\! \perp X_1 \mid R_2, X_2$, the second equality holds because $R_2 \perp \!\!\! \perp X_2 \mid R_1, X_1$, and together they imply the last equality which means $\operatorname{OR}(R_1,R_2\mid X_1,X_2)$ is a function of R_1,R_2 (all observed data). In the above argument, we have used the fact that odds ratios is symmetric (i.e., $\operatorname{OR}(A,B|Z) = \operatorname{OR}(B,A|Z)$). Assuming X_1 and X_2 are binary, the full law in a no self-censoring model would have 8 parameters (same number as in a saturated observed data law). Those parameters are as follows: 3 parameters for $p(X_1,X_2)$, 1 parameter for $\operatorname{OR}(R_1=0,R_2=0|X_1,X_2) = f(R_1,R_2)$ (since the OR evaluated at other levels of R_1 and R_2 , i.e., the reference values, is always one), 2 parameters for $p(R_1=1|R_2=1,X_2)$, and 2 parameters for $p(R_2=1|R_1=1,X_1)$.

Examples of the three class of missing data models that we are interested in are provided in Fig. 1(a), 4(a), and 4(d), where $X = \{X_1, X_2\}$. Here, we compare the full law parameterization of each example against the pattern-mixture parameterization as an illustrative step to show that the conditional independence restrictions on the full law impose restrictions on the observed data law. Given the MAR model in Fig. 1(a), the full law factorizes as $p(X_1, X_2) \times p(R_1) \times p(R_2 \mid R_1, X_1^*)$. Given the MNAR model in Fig. 4(a) (without the dashed edge), the full law factorizes as $p(X_1, X_2) \times p(R_1) \times p(R_1 \mid R_1, X_1^*)$.

 $X_2) \times p(R_2 \mid R_1)$. Given the MNAR model in Fig 4(d), the full law factorizes as $p(X_1, X_2) \times p(R_1 \mid X_2) \times p(R_2 \mid X_1)$. In all the three examples, the full law requires 7 parameters to encode the independencies (less than the number of parameters in the saturated observed data law). The above implies that there must be a testable implication, at least in the binary case, on the observed data laws of the three classes of missing data models that we consider. The parameter counting argument can be simply generalized to discrete data. Results in the main draft confirm that this generalizes to situations where no distributional assumptions are made.

B MORE ON GOODNESS-OF-FIT TESTS WITH ODDS RATIOS

B.1 SEQUENTIAL MNAR MODEL AS A SUBMODEL OF NO SELF-CENSORING MODEL

As mentioned in Remark 1, the sequential MNAR model can be viewed as a submodel of the no self-censoring model. This provides a way to test independence restrictions of the form $R_k \perp \!\!\! \perp X_{\prec k} \mid R_{-k}, X_{\succ k}$. We provided an example with two variables using the m-DAG in Fig. 4(a) and showed how to use odds-ratio parameterization of the missingness mechanism to test the absence of an edge between X_1 and R_2 which implied $R_2 \perp \!\!\! \perp X_1 \mid R_1$. Extending the idea to sequential MNAR models with K>2 involves higher order interaction terms in the odds-ratio parameterization. We use the sequential MNAR model with three variables, shown in Fig. 5(a), to illustrate this point. The no self-censoring supermodel is shown in Fig. 5(b). We are interested in testing the absence of $X_1 \rightarrow R_2, X_1 \rightarrow R_3, X_2 \rightarrow R_3$ edges which implies the independence restrictions: $R_3 \perp \!\!\!\!\!\!\perp X_1, X_2 \mid R_1, R_2$ and $R_2 \perp \!\!\!\!\perp X_1 \mid R_1, R_3, X_3$. Let us focus on the former independence, i.e, $R_3 \perp \!\!\!\!\perp X_1, X_2 \mid R_1, R_2$ which entails showing that $p(R_3 \mid R_1, R_2, X_1, X_2)$ is not a function of X_1 and X_2 . Note that $p(R_3 \mid R_1, R_2, X_1, X_2) = p(R \mid X) / \sum_{R_3} p(R \mid X)$. The odds-ratio parameterization of $p(R \mid X)$ is as follows:

$$\begin{split} p(R\mid X) &= \frac{1}{Z} \times p(R_1|R_2 = R_3 = 1, X) \times p(R_2|R_1 = R_3 = 1, X) \times p(R_3|R_1 = R_2 = 1, X) \\ &\times \mathrm{OR}(R_2, R_1|R_3 = 1, X_1, X_2, X_3) \times \mathrm{OR}(R_3, R_1, R_2|X) \\ &= p(R_1|R_2 = R_3 = 1, X_2, X_3) \times p(R_2|R_1 = R_3 = 1, X_1, X_2) \times p(R_3|R_1 = R_2 = 1, X_1, X_2) \\ &\times f(R_2, R_1, X_3) \times \mathrm{OR}(R_3, R_1, R_2|X). \end{split}$$

The equality uses assumptions in the no self-censoring supermodel: $R_k \perp \!\!\! \perp X_k | R_{-k}, X_{-k}, \forall k$ and the symmetry of the odds ratio to show $\operatorname{OR}(R_2, R_1 | R_3 = 1, X_1, X_2, X_3) = f(R_1, R_1, X_3)$. Thus, to show $p(R_3 | R_1, R_2, X_1, X_2)$ is not a function of X_1 and X_2 , it suffices to show that $p(R_3 | R_1 = 1, R_2 = 1, X_1, X_2) \times \operatorname{OR}(R_3, R_1, R_2 | X)$ is not a function of X_1, X_2 . Here, we see the higher order interaction term $\operatorname{OR}(R_3, R_1, R_2 | X)$ appearing. Even though estimating equations have been discussed in Malinsky et al. [2021] to estimate these higher order terms, they make the tests more challenging.

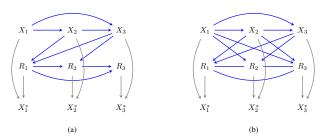


Figure 5: (a) Example of a sequential MNAR model; (b) The permutation supermodel.

The above representation becomes more complex as the number of variables increase. This makes it clear why using the saturated permutation model is relatively easier to test the sequential MNAR models.

B.2 SEQUENTIAL MAR MODEL AS A SUBMODEL OF PERMUTATION MODEL

Here, we discuss odds ratio independence test as an alternative to likelihood-ratio goodness-of-fit test in sequential MAR models (as submodels of permutation model). The independence restrictions we would like to test are: $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*, \forall k$. We break down the independencies involving R_k into K-k individual tests, i.e., we would like to test $R_k \perp \!\!\! \perp X_j | R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}, \forall X_j \in X_{\succ k}$, where $X_{\succ k, \prec j}$ denotes $\{X_{k+1}, \ldots, X_{j-1}\}$. As mentioned in the main draft, the conditional independence $A \perp \!\!\! \perp B | C$ holds if and only if $\mathrm{OR}(A, B | C) = 1$ for all values of A, B, C. Therefore, to show

the independence between R_k and X_j , we need to show that the following odds ratio is one for all levels of R_k, X_j with statistical significance-level α :

$$\begin{split} \text{OR}(R_k = r_k, X_j = x_j \mid R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}) \\ = \frac{p(R_k = r_k \mid X_j = x_j, R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}; \beta_k^a)}{p(R_k = 1 \mid X_j = x_j, R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}; \beta_k^a)} \times \frac{p(R_k = 1 \mid X_j = 1, R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}; \beta_k^a)}{p(R_k = r_k \mid X_j = 1, R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}; \beta_k^a)}. \end{split}$$

To estimate the odds ratio, we need an estimate of β_k^a parameters. We use weighted estimating equations to estimate β_k^a . The intuition is as follows. Given that we have the permutation model as the supermodel, the independence restriction involving R_k and X_j is equivalent to the following Verma constraint:

$$R_k \perp \!\!\!\perp X_j \mid R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}, \operatorname{do}(R_{\succ k, \prec j+1} = 1), \ \forall X_j \in X_{\succ k},$$

where the post intervention distribution is defined as follows:

$$p(. \mid do(R_{\succ k, \prec j+1} = 1)) = \frac{p(V)}{\prod_{i=k+1}^{j} p(R_i \mid pa_{\mathcal{G}}(R_i))} \bigg|_{R_i, t \in \mathcal{A}}.$$

Let $W_k(\beta_k) := p(R_k | R_{\prec k}, X_{\prec k}^*, X_{\succ k, \prec j}, X_j; \beta_k)$ and let $\mathbb{P}_n[U(\beta_k)] = 0$ be an unbiased estimating equation for β_k wrt the full law (i.e., had there been no missingness). We can estimate β_k via the following weighted estimating equation:

$$\mathbb{P}_n\left[\frac{\mathbb{I}(R_{\succ k, \prec j+1} = 1)}{\prod_{i=k+1}^j \omega_i(\widehat{\eta}_i)} \times U(\beta_k)\right] = 0,$$

where $\omega_i(\eta_i) := p(R_i \mid \text{pa}_{\mathcal{C}}(R_i); \eta)$, and $\widehat{\eta}_i$ denotes an estimate of η_i .

Since we have to evaluate the odds ratio for all values of X_j , the tests can become expensive in discrete cases and even more challenging in continuous cases, [Chen, 2021]. Hence, the likelihood-ratio test in Algorithm 1 might be preferred over odds ratio independence tests for larger graphs.

B.3 SEQUENTIAL MNAR MODEL AS A SUBMODEL OF PERMUTATION MODEL

The independence restrictions we would like to test are: $R_k \perp \!\!\! \perp X_{\prec k}^*|R_{\prec k},X_{\succ k}, \forall k$. We break down the independencies involving R_k into k-1 individual tests, i.e., $R_k \perp \!\!\! \perp X_j^*|R_{\prec k},X_{\succ k},X_{\prec j}^*, \forall X_j^* \in X_{\prec k}^*$. As mentioned in the main draft, this is a context-specific independence restriction and is equivalent to $R_k \perp \!\!\! \perp X_j|R_{\prec k}\setminus R_j,R_j=1,X_{\succ k},X_{\prec j}^*$. This independence holds if and only if the following odds ratio is one for all levels of X_j with statistical significance-level α :

$$\begin{aligned} & \text{OR}(R_k = r_k, X_j = x_j \mid R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*) \\ & = \frac{p(R_k = r_k \mid X_j = x_j, R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*; \beta_k^a)}{p(R_k = 1 \mid X_j = x_j, R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*; \beta_k^a)} \times \frac{p(R_k = 1 \mid X_j = 1, R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*; \beta_k^a)}{p(R_k = r_k \mid X_j = 1, R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*; \beta_k^a)} \end{aligned}$$

We can estimate the odds ratio by estimating the parameters β_k^a . We use weighted estimating equations to estimate the parameters and the intuition behind the choice of weights is that the restriction between R_k and X_j^* can be viewed as the following Verma constraint (under the permutation supermodel):

$$R_k \perp \!\!\! \perp X_j^* | R_{\prec k}, X_{\succ k}, X_{\prec j}^*, \operatorname{do}(R_{\succ k} = 1), \ \forall X_j^* \in X_{\prec k}^*.$$

Let $W_k(\beta_k^a) \coloneqq p(R_k|X_j, R_{\prec k} \setminus R_j, R_j = 1, X_{\succ k}, X_{\prec j}^*; \beta_k^a)$ and let $\mathbb{P}_n\big[U(\beta_k^a)\big] = 0$ is unbiased estimating equation for β_k^a wrt the full law (had there been no missingness). We can estimate β_k^a via the following weighted estimating equation:

$$\mathbb{P}_n \left[\frac{\mathbb{I}(R_{\succ k} = 1)}{\prod_{j=k+1}^K p(R_j | \operatorname{pa}_{\mathcal{G}}(R_j); \widehat{\eta}_j)} \times U(\beta_k^a) \right] = 0,$$

where $\hat{\eta}_i$ is an estimate of η_i that parameterize the conditional density of $p(R_i|\operatorname{pa}_{\mathcal{C}}(R_i))$.

Similar to the sequential MAR model, the goodness-of-fit test based on odds ratio independence test can be rather challenging with continuous variables. Hence, the weighted likelihood-ratio tests might still be preferred.

C PROOF

Theorem 1. The independence $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*$ has a testable implication on the observed data distribution in form of a Verma constraint: $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X_{\prec k}^*, do(R_{\succ k} = 1)$, where the intervention distribution $p(X, R \setminus R_{\succ k}, X^* | do(R_{\succ k} = 1))$ is identified.

Proof. The intervention distribution $p(X, R \setminus R_{\succ k}, X^* | \text{do}(R_{\succ k} = 1))$ factorizes wrt a CDAG \mathcal{G}^* where edges into $R_{\succ k}$ have been removed from the sequential MAR graph \mathcal{G} . Factorization of this intervention distribution wrt a CDAG preserves the global Markov property, i.e., d-separation can be used to read dormant independencies in the intervention distribution. In \mathcal{G}^* we have $R_k \perp \!\!\! \perp X_{\succ k} | R_{\prec k}, X^*_{\prec k}$ by d-separation implying the same independence holds in the intervention distribution. Finally, testability of this dormant independence from observed data follows from the fact that the propensity scores $p(R_j | \operatorname{pa}_{\mathcal{G}}(R_j))$ for each $R_j \in R_{\succ k}$ is identified under the restrictions implied by the graph \mathcal{G} (identification is trivial since the sequential MAR model is a submodel of a permutation model that is fully identified), and upon intervention to $R_{\succ k} = 1$, each previously partially observed variable $X_j \in X_{\succ k}$ is now observed via a consistency argument $X_j = X_j^*$.

Theorem 2. The independence $R_k \perp \!\!\! \perp X_{\prec k}^* | R_{\prec k}, X_{\succ k}$ has a testable implication on the observed data distribution in form of a Verma constraint $R_k \perp \!\!\! \perp X_{\prec k}^* | R_{\prec k}, X_{\succ k}, do(R_{\succ k} = 1)$, where the intervention distribution $p(X, R \setminus R_{\succ k}, X^* | do(R_{\succ k} = 1))$ is identified.

Proof. The proof is very similar to the proof of Theorem 1. Interventions on $R_{\succ k}$ preserve the global Markov property and propensity scores of $R_{\succ k}$ are all identified as functions of observed data (since sequential MNAR is a submodel of fully identified permutation model). The m-CDAG we obtain after intervening on $R_{\succ k}$ and setting them to 1 is a graph where all incoming edges into $R_{\succ k}$ are removed and all $X_{\succ k}$ are observed random variables. Thus the dormant independence are direct functions of observed data.

Theorem 4. The independence $R_k \perp \!\!\! \perp R_j | X \forall j \neq k$ has a testable implication on observed data which can be stated via $OR(R_k, R_j | X_{-kj}, R_{-kj} = 1) = 1$.

Proof. Given the restrictions of a block-parallel model, we note that including R_{-kj} in the conditioning set of independence $R_k \perp \!\!\! \perp R_j | X$ does not spoil the independence. Hence, we can equivalently look at $R_k \perp \!\!\! \perp R_j | X, R_{-kj} = 1$. Further, we know this independence holds if and only if $\operatorname{OR}(R_k, R_j | X, R_{-kj} = 1) = 1$. All we need to show now is that $\operatorname{OR}(R_k, R_j | X, R_{-kj} = 1) = \operatorname{OR}(R_k, R_j | X_{-kj}, R_{-kj} = 1)$. Using an odds-ratio parameterization of $p(R_k, R_j | X, R_{-kj} = 1)$ we have:

$$\begin{split} \operatorname{OR}(R_k = r_k, R_j = r_j \mid X, R_{-kj} = 1) &= \frac{p(R_k = r_k \mid R_j = r_j, X, R_{-kj} = 1)}{p(R_k = 1 \mid R_j = r_j, X, R_{-kj} = 1)} \times \frac{p(R_k = 1 \mid R_j = 1, X, R_{-kj} = 1)}{p(R_k = r_k \mid R_j = r_j, X_{-k}, R_{-kj} = 1)} \\ &= \frac{p(R_k = r_k \mid R_j = r_j, X_{-k}, R_{-kj} = 1)}{p(R_k = 1 \mid R_j = r_j, X_{-k}, R_{-kj} = 1)} \times \frac{p(R_k = 1 \mid R_j = 1, X, R_{-kj} = 1)}{p(R_k = r_k \mid R_j = 1, X_{-k}, R_{-kj} = 1)} \\ &= f_1(R_k, R_j, X_{-k}, R_{-kj} = 1). \end{split}$$

The second equality holds because $R_k \perp \!\!\! \perp X_k | R_{-k}, X_{-k}$, and

$$\begin{split} \operatorname{OR}(R_{j} = r_{j}, R_{k} = r_{k} \mid X, R_{-kj} = 1) &= \frac{p(R_{j} = r_{j} \mid R_{k} = r_{k}, X, R_{-kj} = 1)}{p(R_{j} = 1 \mid R_{k} = r_{k}, X, R_{-kj} = 1)} \times \frac{p(R_{j} = 1 \mid R_{k} = 1, X, R_{-kj} = 1)}{p(R_{j} = r_{j} \mid R_{k} = r_{k}, X_{-j}, R_{-kj} = 1)} \times \frac{p(R_{j} = 1 \mid R_{k} = 1, X, R_{-kj} = 1)}{p(R_{j} = 1 \mid R_{k} = r_{k}, X_{-j}, R_{-kj} = 1)} \times \frac{p(R_{j} = 1 \mid R_{k} = 1, X_{-j}, R_{-kj} = 1)}{p(R_{j} = r_{j} \mid R_{k} = 1, X_{-j}, R_{-kj} = 1)} \\ &= f_{2}(R_{k}, R_{j}, X_{-j}, R_{-kj} = 1). \end{split}$$

The second equality holds because $R_j \perp \!\!\! \perp X_j | R_{-j}, X_{-j}$. Due to symmetry of odds ratio, $f_1(R_k, R_j, X_{-k}, R_{-kj} = 1)$ and $f_2(R_k, R_j, X_{-j}, R_{-kj} = 1)$ must be equal. This implies $\mathrm{OR}(R_k, R_j | X, R_{-kj} = 1) = \mathrm{OR}(R_k, R_j | X_{-kj}, R_{-kj} = 1)$ (all a function of observed data).

Even though the odds ratio is a function of observed data, estimation of odds ratio is not straightforward. We rely on the estimating equations discussed in Appendix A.1.1 and Malinsky et al. [2021] to estimate the odds ratios. \Box

Theorem 3. To prove this result, it suffices to show that the target law in the criss-cross structure on two variables (drawn on the right hand side) is not non-parametrically identified. For this purpose, we provide an example of two different full laws that factorize according to the criss-cross model, but map into the same observed data law.

R_1	R_2	X_1	X_2	p(FULL LAW)	X_1^*	X_2^*	p(OBSERVED LAW)			
	0	0	0	abdf		?				
0		1	0	(1-a)cdg	?		$\begin{bmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 $			
0		0	1	a(1-b)ef			d[abf + (1-a)cg] + e[a(1-b)f + (1-a)(1-c)g]			
		1	1	(1-a)(1-c)eg						
		0	0	abd(1-f)	?	0	J J (1 8) + (1 1) - (1 1)			
0	1	1	0	(1-a)cd(1-g)			$d \left[ab(1-f) + (1-a)c(1-g) \right]$			
0		0	1	a(1-b)e(1-f)		1	$\begin{bmatrix} \cdot \cdot (1 & k) \cdot (1 & k) + (1 & k) \cdot (1 & k) \end{bmatrix}$			
		1	1	(1-a)(1-c)e(1-g)			$e\left[a(1-b)(1-f)+(1-a)(1-c)(1-g)\right]$			
	0	0	0	ab(1-d)h	0	?	$I_{\lambda} \begin{bmatrix} 1/1 & 1/$			
1		1	0	(1-a)c(1-d)i			$ah \left[b(1-d) + (1-b)(1-e) \right]$			
1		0	1	a(1-b)(1-e)h			(1):[(1 1) + (1)(1)]			
		1	1	(1-a)(1-c)(1-e)i	1		(1-a)i[c(1-d)+(1-c)(1-e)]			
		0	0	ab(1-d)(1-h)	0	0	ab(1-d)(1-h)			
1	1	1	0	(1-a)c(1-d)(1-i)	1	0	(1-a)c(1-d)(1-i)			
1		0	1	a(1-b)(1-e)(1-h)	0	1	a(1-b)(1-e)(1-h)			
		1	1	(1-a)(1-c)(1-e)(1-i)	1	1	(1-a)(1-c)(1-e)(1-i)			

A concrete example is as follows:

				$X_2 \mid X_1 \mid p(X_2 \mid X_1) \mid M_1 \mid M_2$			P.		X_2	$p(R_1 \mid X_2)$		
X_1	p(Z)			212	1 211	M_1	M_2		161	212	M_1	M_2
Λ_1	M_1	M_2		0	0	6/7	4/5		0	0	19/20	189/200
0	7/15	5/11		1	0	1/7	1/5		1	0	1/20	11/200
1	7/15 8/15	6/11		0	1	3/4	2/3		0	1	85/100	89/100
				1	1	1/4	1/3		1	1	15/100	11/100

R_2	R.	X_1	$p(R_2 R_1, X_1)$					
102	111	АΙ	M_1	M_2				
0	0	0	268/323	7636/16821				
1	0	0	55/323	9185/16821				
0	0	1	208/323	16216/16821				
1	0	1	115/323	605/16821				
0	1	0	1/2	1/2				
1	1	0	1/2	1/2				
0	1	1	1/2	1/2				
1	1	1	1/2	1/2				

R_1 R_2		X_1	X_2	p(1)	X_1^*	X_2^*	$p(R, X^*)$	
	-2	1		M_1	M_2	1	2	$M_1 = M_2$
	0	0	0	134/425	3818/24475		?	
0		1	0	104/425	8108/24475	?		69/100
0		0	1	67/1425	1118/30439			68/100
		1	1	104/1425	8108/51975			
	1	0	0	11/170	167/890	?	0	9/10
0		1	0	23/170	11/890			2/10
0		0	1	11/1140	167/3780		1	1/20
		1	1	23/570	11/1890			
	0	0	0	1/100	1/100	0	?	3/200
1		1	0	1/100	1/100	U		3/200
1		0	1	1/200	1/200	1		2/100
		1	1	1/100	1/100	1		
	1	0	0	1/100	1/100	0	0	1/100
1		1	0	1/100	1/100	1	0	1/100
1		0	1	1/200	1/200	0	1	1/200
		1	1	1/100	1/100	1	1	1/100

From the above example, we see that none of the parameters in red are identified.

D SIMULATIONS

In this section, we describe three sets of simulations to illustrate the key results and the utility of our proposed methods – each set focuses on a class of missing data models that we considered in the main draft. For each simulation, we generate four random variables from either a multivariate normal distribution or binomial distribution. We induce missing values in all four variables according to a missingness mechanism that follows restrictions of either sequential MAR, sequential MNAR, block-parallel, or supermodels of them.

Generating X: For Gaussian data, we generate four random variables from multivariate normal distribution with mean zero and covariance matrix σ where the ij-th entry is $\sigma_{ij} = 1 - |i-j| \times 0.25$. For binary data, variable X_k is generated from a binomial distribution with the probability of observing $X_k = 1$ given $X_{\prec k}$ equals to $\exp it(a_{x_k}^0 + \sum_{j \prec k} a_{x_k}^j \times X_j)$, where $\exp it(x) = 1/(1 + \exp(-x))$ and parameters $a_{x_k}^j$ (for all $k = 1, \ldots, K$ and $j \prec k$) are generated uniformly from the (-1,1) interval.

Generating R: In each class of missing data model, we consider generating R according to two scenarios: one where the restrictions in the missing data model we would like to test hold true (the null hypothesis should be accepted) and one where the restrictions are violated (the null hypothesis should be rejected in favor of accepting the corresponding supermodel). All missingness indicators are generated from binomial distributions. The details on missing data parameters are as follows.

$$p(R_{k} = 1 \mid R_{\prec k}, X_{\prec k}^{*}, X_{\succ k}) = \text{expit} \left(a_{k}^{0} + \sum_{j \prec k} b_{k}^{j} \times R_{j} + c_{k}^{j} \times R_{j} X_{j}^{*} + \sum_{i \succ k} d_{k}^{i} \times X_{i}\right), \ k = 1, \dots, 4 \quad \text{(Simulation 1)}$$

$$p(R_{k} = 1 \mid R_{\prec k}, X_{\succ k}, X_{\prec k}^{*}) = \text{expit} \left(a_{k}^{0} + \sum_{i \succ k} d_{k}^{i} \times X_{i} + \sum_{j \prec k} b_{k}^{j} \times R_{j} + c_{k}^{j} \times R_{j} X_{j}^{*}\right), \ k = 1, \dots, 4 \quad \text{(Simulation 2)}$$

$$p(R_{k} = 1 \mid X_{-k}) = \text{expit} \left(a_{k}^{0} + \sum_{j \neq k} b_{k}^{j} \times X_{j}\right), \ k = 1, \dots, 4 \quad \text{(Simulation 3)}. \tag{10}$$

Addition of the blue terms simulate scenarios where the independence assumptions we would like to test are violated. All the parameters are randomly generated from a uniform distribution. In order to control the proportion of missing values, we run the experiments with three different ranges for the uniform distribution: (-1, 1), (-0.5, 1.5), and (0, 2).

Generating X^* : For each given sample, if $R_k = 1$ then $X_k^* = X$, otherwise $X^* = NA$.

Our objective is to test the missing data restrictions by relying only on observed data, i.e., (R, X^*) samples.

Simulation 1. In the first set of simulations we focus on testing the sequential MAR model defined via the set of restrictions in (4). We follow Algorithm 1 to test the independence restrictions, which entails running a total of K-1 tests. Our test statistic is $2 \times \rho$ and we use a chi-square distribution with K-k degrees of freedom to evaluate the goodness-of-fits – the degree of freedom is chosen as the difference between number of parameters in $W_k(\beta_k^a)$ and $W_k(\beta_k^0)$, as defined in the algorithm. If the p-values are all greater than 0.05, we accept the sequential MAR model.

For a fixed sample size, we simulate 100 different datasets and calculate the acceptance rate of a sequential MAR model. The acceptance rate is plotted as a function of sample size in Fig. 6. The sample size ranges from 1,000 to 15,000 with 500 increments. In each panel, there are three plots that vary in terms of the proportion of complete cases in the dataset, i.e., 6%,35%,80% which is achieved by changing the range in the uniform distribution where the parameters are sampled from (the proportion of complete cases is taken as an average of complete cases over 100 iterations). The top row of Fig. 6 illustrates the results when the true underlying missingness mechanism satisfies the assumptions of the sequential MAR model (missingness indicators are generated from (10) without the blue terms) and the bottom row illustrates results for when the restrictions are no longer valid (missingness indicators are generated from (10) with the blue terms). As seen in the figure, the acceptance rate is quite high when the sequential MAR model holds true and it is low when the sequential MAR model does not hold, even if we have only 6% complete cases which is impressive performance with little data. The plots at the bottom row also illustrate that the tests would perform better in terms of rejecting the sequential MAR model when the truth is not MAR when the missingness rate decreases; with 80% complete cases the acceptance rate vanishes.

Simulation 2. In the second set of simulations we focus on testing the sequential MNAR model defined via the set of restrictions in (5). We follow Algorithm 2 to test the independence restrictions, which entails running a total of K-1 tests. Our test statistic is $2 \times \rho$ and we use a chi-square distribution with k-1 degrees of freedom to evaluate the goodness-of-fits – the degree of freedom is chosen as the difference between number of parameters in $W_k(\beta_k^a)$ and $W_k(\beta_k^0)$, as defined in the

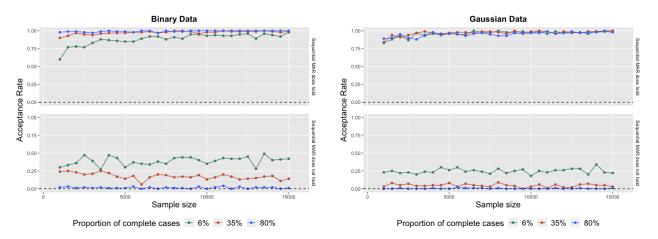


Figure 6: Results on testing **sequential MAR** models. In the top row, the sequential MAR model captures the true underlying missingness mechanism. The assumptions of sequential MAR model are violated in the bottom row.

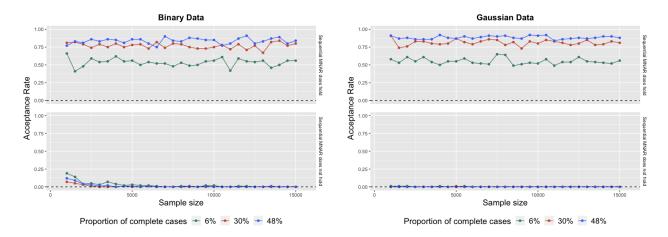


Figure 7: Results on testing **sequential MNAR** models. In the top row, the sequential MNAR model captures the true underlying missingness mechanism. The assumptions of sequential MNAR model are violated in the bottom row.

algorithm. If the p-values are all greater than 0.05, we accept the sequential MNAR model.

For a fixed sample size, we simulate 100 different datasets and calculate the acceptance rate of a sequential MNAR model. The acceptance rate is plotted as a function of sample size in Fig. 7. The sample size ranges from 1,000 to 15,000 with 500 increments. In each panel, there are three plots that vary in terms of the proportion of complete cases in the dataset, i.e, 6%,30%,48%. The top row illustrates the results when the true underlying missingness mechanism satisfies the assumptions of the sequential MNAR model (missingness indicators are generated from (10) without the blue terms) and the bottom row illustrates results for when the restrictions are no longer valid (missingness indicators are generated from (10) with the blue terms). As it is shown, the acceptance rate is quite low when the independence restrictions of a sequential MNAR model are not valid; even when we only have 6% of complete cases the tests perform well. When the sequential MNAR model assumptions are true, the acceptance rate increases as missing rate decreases and reaches very close to 1 when we have only 48% complete cases.

Simulation 3. In the third set of simulations we focus on testing independencies between missingness indicators in a block-parallel MNAR model defined via the set of restrictions in (7). Testing the full model requires following Algorithm 3 which entails running a total of $\binom{K}{2}$ tests (between all distinct pairs of missingness indicators.) For illustration purposes, we focus on testing only one pair of missingness indicator in two different scenarios: one where the true underlying missingness mechanism follows the restrictions of a block-parallel model – thus $R_k \in R$ is generated using (10), and one where the missingness mechanism factorizes as $\prod_{k=1}^K p(R_k|R_{\succ k},X_{\prec k})$ which is still a submodel of the no-self censoring model but violates the assumptions of the block-parallel model. We focus on testing the independence $R_1 \perp \!\!\!\perp R_2 | X$ by calculating the

Block-parallel model holds

Block-parallel model does not hold

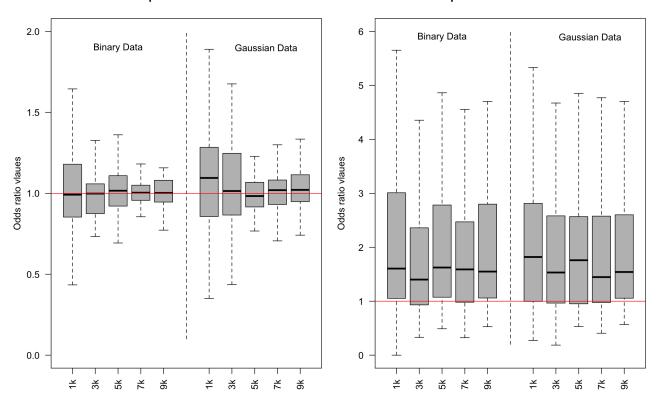


Figure 8: Results on computing (conditional) odds ratio between a pair of missingness indicators to test an independence restriction between them. On the left panel, the block-parallel MNAR model captures the true underlying missingness mechanism. The assumptions of block-parallel MNAR model are violated on the right panel.

odds ratio $\theta := OR(R_1 = 0, R_2 = 0|X)$ via the following estimating equation and showing that the value is one.

$$\mathbb{P}_n \Big[R_1 \times R_2 \times R_3 \times \frac{p(R_1 = 0 \mid R_2 = 1, R_3 = 1, X_2, X_3) \times p(R_2 = 0 \mid R_1 = 1, R_3 = 1, X_1, X_3)}{p(R_1 = 1 \mid R_2 = 1, R_3 = 1, X_2, X_3) \times p(R_2 = 1 \mid R_1 = 1, R_3 = 1, X_1, X_3)} \times \theta - R_3 \times (1 - R_1) \times (1 - R_2) \Big] = 0.$$

For a fixed sample size, we simulate 100 different datasets and calculate the odds ratio via the above estimating equation. We provide the boxplots in Fig. 8. The x-axis is sample size that ranges from 1,000 to 10,000 with 2,000 increments. The left panel illustrates the boxplots for binary and Gaussian data when the true missingness mechanism follows the restrictions of the block-parallel model, and in the right panel it does not. As it is shown, the boxplots are centered around 1 in the left panel as expected, but move away from 1 when the independence does not hold. To perform a formal test, we can construct confidence intervals for each sample size via bootstrapping the data generations and odds ratio calculations.