smdi: An R package to perform structural missing data investigations on partially observed confounders in real-world databases

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# Abstract

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| --- |
| Highlights |
| * … |

# Background

Electronic health records (EHR) are increasingly used to conduct real-world evidence (RWE) studies to complement evidence coming from randomized controlled trials (RCTs) [1,2]. Due to their detailed capture of clinical parameters such as vital signs, lab measurements, physician assessments and lifestyle factors, EHRs can significantly improve the ability to control for confounding and imbalances in prognostic factors between treatment groups, especially when linked to administrative claims databases [3]. However, such prognostic factors are often just partially observed which challenges the statistical analysis of the data and can result in severe bias when predicting or estimating treatment effects if not handled appropriately [4–6].

In order to make an informed decision about the most appropriate analytic approach to arrive at unbiased estimates, it is crucial to investigate and understand the potential patterns and mechanisms that underlie the partially observed confounder data [7–9]. Usually these are not known for a given RWE study but general guidance papers and frameworks have suggested various routine diagnostics to investigate missing data patterns and mechanisms. These methods comprise standard procedures such as comparing distributions of baseline characteristics and outcomes between patients with and without the partially observed covariate(s) [10–13], checking the ability to predict missingness based on observed data [11] and assessing if causal relationships between variables and their missingness are recoverable based on available data [14] and guided by directed acyclic graphs [15,16] or M-graphs [17]. However, these methods have so far been only described and tested in isolation from each other and no principled approach exists. In addition, the practical implementation of all of these diagnostics is time-consuming, tedious and is consequently not often performed in both RWE and RCTs [18–20].

To overcome these shortcomings, we [21] have recently developed and evaluated a principled approach combining a range of missing data diagnostics in an US EHR-claims database linkage [22]. The results of this study revealed that the combination of these diagnostics characterized simulated missing data mechanisms well and provided helpful insights for the appropriate choice of analytic methods to handle the partially observed confounder data (e.g., missing data imputation).

To streamline and ease the implementation of these routine missing data diagnostics for confounder data in RWE studies, we here present and demonstrate the use of the smdi (structural missing data investigations) R package [23]. To that end, we first provide some brief background on the theoretical assumptions that underlie the diagnostic functions of this package. We then give an overview of the implemented functions and demonstrate an end-to-end workflow application of the package with a hypothetical RWE study using simulated oncology EHR dataset that comes bundled with the package.

# Methods

## Problem formalization

As opposed to clinical trials, which are designed to collect data for research purposes in a harmonized manner, real-world data (RWD) are typically generated for administrative purposes (e.g., health insurance claims for billing purposes) or clinical documentation (e.g., EHR). Hence, confounders and prognostic factors, which need to be balanced between treatment groups in RWE studies are usually not available for all patients at all neccessary time points [24]. If the underlying mechanism for the missingness of such covariates is informative towards the outcome under study, e.g., patients who have a certain biomarker measured have a significantly increased risk if experiencing the outcome, this can lead to bias in the resulting effect estimates for the studied treatments under common missing data approaches like complete case analysis or imputation [6]. Hence, it is of utmost importance to investigate the potential patterns and mechanisms to know if assumptions for specific missing data approaches hold [25,26].

## Theoretical background

In our previous work [22] and for the purpose of the smdi R package, we categorize the implemented principled missing data investigations into three groups of diagnostics, which will be discussed in this section **?@tbl-overview**

Functions overview

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Data generation for hypothetical study

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# Results

# Discussion

# References

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# Tables

Table 1: Overview of the main functions of the smdi package.

| Function | Description | Generic S3 print() output | Object output | Interpretation |
| --- | --- | --- | --- | --- |
| Group 1 Diagnostics - Comparing the distribution of observed covariates between patients with versus without a value for the partially observed covariate | | | | |
| **smdi\_asmd()** | Computes the absolute standardized mean differences (ASMD) of patient characteristics between patients with versus without a value for the partially observed covariate(s) | Aggregated summary table of the average/median and minimum/maximum ASMD range for all specified partially observed covariates | - Detailed *Table 1* illustrating distributions and individual ASMD for each compared patient characteristic  - ggplot2 graph illustrating the individual ASMD for each compared patient characteristic in descending order  - Aggregate summary of the average/median and minimum/maximum ASMD range for the selected partially observed covariate | - ASMD < 0.1: no imbalances in observed patient characteristics; missingness may be likely completely at random or not at random (~MCAR, ~MNAR)  - ASMD > 0.1: imbalances in observed patient characteristics; missingness may be likely at random (~MAR) |
| **smdi\_hotelling()** | Computes Hotelling's multivariate T^2^ t-test for each partially observed covariate, examining patient differences conditional on having an observed covariate value or not. | Aggregated summary table of the Hotelling's test p-values for all specified partially observed covariates | Detailed Hotelling test statistics | High test statistics and low p-values indicate differences in baseline covariate distributions and null hypothesis would be rejected (~MAR) |
| **smdi\_little()** | Computes a single global chi-square test statistic across all partially observed covariates with a null hypothesis that the data is missing completely at random. | Detailed Little's test statistics | Detailed Little's test statistics | High test statistics and low p-values indicate differences in baseline covariate distributions and null hypothesis would be rejected (~MAR) |
| Group 2 Diagnostics - Assessing the ability to predic missingness based on observed covariates | | | | |
| **smdi\_rf()** | Trains and fits a random forest classification model to assess the ability to predict missingness indicator for the partially observed covariate(s). | Aggregated summary table with the area under the receiver operating characteristic curve (AUC) value for each partially observed covariate | - Individual AUC value  - ggplot2 figure illustrating the variable importance for the prediction made expressed by the mean decrease in accuracy per predictor | - AUC values ~ 0.5 indicate completely random or not at random prediction (~MCAR, ~MNAR)  - Values meaningfully above 0.5 indicate stronger relationships between covariates and missingness (~MAR) |
| Group 3 Diagnostics - Evaluates whether missingness of a covariate is associated with the outcome | | | | |
| **smdi\_outcome()** | Fits outcome model (linear, logistic or proportional hazards depending on the outcome under study) with the missingness indicator of the partially observed covariate(s). The estimates are computed both as a univariate model (just considering the missingness indicator) and an adjusted model with all covariates in the dataset. | Aggregated summary table with the univariate and adjusted estimate for each partially observed covariate | Aggregated summary table with the univariate and adjusted estimate for each partially observed covariate | - No association in either univariate or adjusted model and no meaningful difference in the log HR after full adjustment (~MCAR).  - Association in univariate but not fully adjusted model (~MAR).  - Meaningful difference in the log HR also after full adjustment (~MNAR). |

**?(caption)**

# Figures