

Advanced Data Imputation Techniques in Clinical Trials: A Comprehensive Analysis Using SAS

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Abstract: Missing data is a severe problem in clinical trial studies that jeopardizes the validity of the statistical inference and undermines the integrity of the study. Complete case analysis and last observation carried forward are the most commonly used traditional methods, both of which are widely criticized as sources of bias and low statistical power, leading to the creation of more advanced types of imputation. Multiple imputation has become the new gold standard of addressing missing data, producing multiple plausible values per missing data and appropriately accounting for the imputation uncertainty with the combining rules by Rubin. Hot-deck imputation is a non-parametric method that does not alter empirical distributions, instead substituting any missing values with observed values of similar donors. The choice of the right imputation approaches is based on the knowledge about the mechanism of missing data, such as Missing Completely at Random, Missing at Random, and Missing Not at Random, each of which has to be analyzed with the help of different methods. Major imputation algorithms such as the MCMC algorithm, predictive mean matching, and propensity score imputation are effectively implemented with the help of SAS programming using PROC MI and PROC MIANALYZE. Simulation studies establish that multiple imputation retains unbiased estimates and correct coverage probabilities in the case of Missing at Random conditions, whereas traditional methods have enormous bias. The use of imputation methods has been shown to greatly influence estimates of treatment effects and clinical inferences based on real-world case studies of antidepressant and diabetes prevention trials. The regulatory agencies are now requiring prespecified approaches to missing data that are scientifically justified with sensitivity analyses that are exhaustive in nature. The introduction of modern imputation methods into the mainstream process improves the validity and reliability of clinical trial data, which facilitates evidence-based medicine and better patient outcomes.

Keywords: Multiple Imputation, Hot-Deck Imputation, Missing Data Mechanisms, Clinical Trials, SAS Programming.

INTRODUCTION

The issue of missing data is one of the most prevalent problems in the study of clinical trials that jeopardizes the validity of statistical conclusions and can undermine the integrity of study findings. Clinical trials consistently experience missing data because of patient dropouts, protocol deviations, lost-to-follow-ups, and administrative censoring despite the rigorous protocols and procedures of monitoring. According to the systematic review by Sterne and colleagues, missing data in both epidemiological and clinical studies is a universal issue and, as they point out, the failure to address or comprehend the mechanism of missing data can seriously harm the validity of the study results (Graham, J. W. 2009). The size of this problem is endemic at all stages of clinical development, and longitudinal studies are especially susceptible to the occurrence of missingness over a long period of follow-up.

Missing data is not only a technical issue but also a regulatory requirement that is subject to close methodological scrutiny. The panel report of the National Research Council on missing data prevention and treatment in clinical trials provided firm recommendations that the scientific validity of clinical trial findings heavily relies on the prevention and treatment of missing data (Little, R. J. *et al.*, 2012). Regulatory authorities such as the FDA and EMA have also released specific

guidance documents explaining the necessity of prespecified, scientifically motivated methods of missing data. These regulatory frameworks require that sponsors show that their trial findings are robust under a variety of analytic methods, although with a specific focus on the plausibility of the underlying missing data assumptions and a sensitivity analysis conducted to determine whether the primary assumptions are met.

Traditional approaches such as complete case analysis and last observation carried forward have been widely criticized for introducing bias and reducing statistical power. Complete case analysis assumes data are missing completely at random, an assumption rarely met in practice, while LOCF makes the untenable assumption that participant outcomes remain static following dropout. These outdated practices persist despite mounting evidence of their limitations, creating situations where study conclusions may be fundamentally compromised by inappropriate analytical choices. This article provides a comprehensive investigation into advanced data imputation methods, specifically focusing on multiple imputation and hot-deck imputation within the SAS programming environment, critically evaluating these methodologies across diverse missing data mechanisms, and providing practical

implementation guidelines for clinical trial statisticians.

THEORETICAL FRAMEWORK AND MISSING DATA MECHANISMS

Knowledge of the theoretical basis of missing data is needed to choose the right imputation and guarantee the validity of the statistical inferences made with respect to missing data. The original contribution by Little and Rubin on statistical analysis with missing data created the taxonomy characterizing missing data in terms of three basic mechanisms: Missing Completely at Random, Missing at Random, and Missing Not at Random (Little, R. J., & Rubin, D. B. 2019). This classification framework has become the cornerstone of modern missing data methodology, providing the theoretical foundation for understanding when various imputation approaches can yield valid inferences and when they may introduce bias into study conclusions.

Missing Completely at Random occurs when the probability of missingness is unrelated to both observed and unobserved data, representing the most restrictive and least commonly satisfied assumption in real-world clinical trials. Under MCAR, complete case analysis yields unbiased estimates, though with reduced precision due to decreased sample size, making this the only scenario where simple deletion methods remain theoretically justified. Little and Rubin's comprehensive treatment demonstrates that MCAR is testable through various diagnostic procedures, though rejection of MCAR does not necessarily distinguish between MAR and MNAR mechanisms (Little, R. J., & Rubin, D. B. 2019). For example, if laboratory samples are randomly lost due to equipment malfunction unrelated to patient characteristics or outcomes, the data may be MCAR, but such purely random mechanisms are exceptionally rare in practice. The practical implications of incorrectly assuming MCAR when data are actually MAR or MNAR include biased treatment effect estimates and invalid confidence intervals that fail to maintain nominal coverage probabilities.

Missing at Random represents a less restrictive assumption where missingness depends on observed data but not on unobserved values after conditioning on observed covariates. This mechanism forms the foundation for most modern imputation approaches, including multiple imputation and likelihood-based methods. White and colleagues' work on intention-to-treat analysis

emphasizes that the MAR assumption is fundamentally untestable using observed data alone, requiring careful consideration of the clinical context and plausibility of the assumption based on subject matter knowledge (White, I. R. *et al.*, 2012). For instance, if younger patients are more likely to miss follow-up visits, but missingness does not depend on their unmeasured health outcomes after accounting for age, the data are MAR. MAR assumptions are sensitive to the richness of observed covariate information, and the more complete baseline and longitudinal covariate information is available, the more probable it is that MAR represents a reasonable approximation to the actual underlying missing data mechanism.

Missing not at Random characterizes the case when the missingness is conditional on the unobservable values; despite having all the observed data, the most challenging situation to be analyzed statistically. This happens where patients with failing health conditions stand a greater chance of dropping out of trials, and this failure is not well-represented by measured variables. White and colleagues note that MNAR mechanisms are particularly prevalent in clinical trials where the outcome of interest directly influences the probability of dropout, such as psychiatric trials where symptom worsening leads to treatment discontinuation (White, I. R. *et al.*, 2012). MNAR scenarios require specialized modeling approaches, including pattern-mixture models and selection models, which make explicit assumptions about the relationship between missingness and unobserved outcomes. The distinction between these mechanisms has profound implications for imputation strategy selection, as methods that produce valid inferences under MAR may yield severely biased results under MNAR conditions.

The pattern of missingness matters substantially for computational efficiency and algorithm selection in imputation procedures. Monotone missing data patterns, common in longitudinal studies with dropout, allow for more computationally efficient imputation algorithms that proceed sequentially through variables with increasing amounts of missing data. Little and Rubin describe how monotone patterns enable the use of sequential regression approaches that are computationally tractable even in high-dimensional settings (Little, R. J., & Rubin, D. B. 2019). Arbitrary missing data patterns, where missingness occurs sporadically across variables and time points, require more complex approaches such as Markov Chain Monte Carlo methods or

fully conditional specification algorithms. These arbitrary patterns present greater computational challenges but are increasingly common in modern clinical trials with intermittent missingness across multiple assessment time points. SAS procedures such as PROC MI, PROC MIANALYZE, and

experimental procedures for MNAR analyses provide a comprehensive toolkit for addressing these diverse missing data challenges, with algorithm selection depending on both the pattern of missingness and the underlying assumptions about the missing data mechanism.

Table 1: Missing Data Mechanisms Classification (Little, R. J., & Rubin, D. B. 2019; White, I. R. *et al.*, 2012)

Mechanism	Probability Dependence	Analysis Validity	Testing Capability	Clinical Example
MCAR	Independent of observed and unobserved data	Complete case analysis, unbiased	Testable via Little's test	Random equipment malfunction
MAR	Depends on observed data only	Multiple imputation valid	Untestable from data alone	Younger patients are missing follow-up
MNAR	Depends on unobserved values	Requires sensitivity analyses	Not testable	Sicker patients dropping out

MULTIPLE IMPUTATION: METHODOLOGY AND SAS IMPLEMENTATION

Multiple imputation, introduced by Rubin in his seminal work, has emerged as the gold standard for handling missing data in clinical trials due to its strong theoretical foundation and practical flexibility (Rubin, B. 1987). The MI framework generates multiple plausible values for each missing data point, creating several complete datasets that reflect uncertainty about the missing values through the variation across imputations. This approach explicitly recognizes that one cannot know the true values of missing data, and therefore, analysis must account for this fundamental uncertainty. Analysis is performed separately on each imputed dataset, and results are combined using Rubin's rules to produce final parameter estimates and standard errors that appropriately account for both within-imputation and between-imputation variability. Rubin's theoretical framework demonstrates that when the imputation model is properly specified and compatible with the analysis model, multiple imputation produces valid statistical inferences under MAR assumptions (Rubin, B. 1987).

The MI process consists of three distinct phases that work together to produce valid statistical inferences from incomplete data: imputation, analysis, and pooling. During the imputation phase, missing values are replaced with plausible values drawn from a predictive distribution, creating multiple complete datasets that capture the uncertainty inherent in predicting missing values. The number of imputations required depends on the fraction of missing information, with early recommendations suggesting five to ten

imputations being sufficient for most applications. However, Rubin's work indicates that increasing the number of imputations reduces Monte Carlo error in the final combined estimates, with practical recommendations now typically suggesting twenty or more imputations when computational resources permit (Rubin, B. 1987). The analysis phase involves performing the intended statistical analysis on each imputed dataset independently, treating each completed dataset as if it were real data without any missing values. Finally, the pooling phase combines results using Rubin's combining rules to produce point estimates, standard errors, confidence intervals, and p-values that properly reflect both the variability within each imputed dataset and the variability between different imputations.

SAS provides robust infrastructure for implementing multiple imputation through PROC MI, which supports multiple imputation algorithms, including regression-based methods, predictive mean matching, propensity score methods, and MCMC approaches. Van Buuren and Groothuis-Oudshoorn's comprehensive description of multivariate imputation by chained equations highlights the flexibility of modern imputation algorithms in handling complex data structures, though their focus on the mice package in R parallels the capabilities available in SAS through PROC MI (Van Buuren, S., & Groothuis-Oudshoorn, K. 2011). For monotone missing data patterns, PROC MI can employ regression methods that proceed sequentially through variables with increasing missingness, building imputation models that condition on previously imputed variables. For arbitrary patterns, MCMC methods or fully conditional specification algorithms are required, with these approaches

iteratively imputing missing values for each variable conditional on all other variables until the imputation algorithm converges to a stationary distribution.

Several methodological refinements enhance MI performance in clinical trials beyond basic regression imputation. Predictive mean matching offers advantages when distributions are skewed or bounded, as it imputes observed values rather than predicted values from regression models, thereby preserving the original data distribution, including its shape, range, and any unusual features. Van Buuren and Groothuis-Oudshoorn emphasize that PMM is particularly valuable for imputing variables with restricted ranges or discrete distributions, as it guarantees that imputed values fall within the range of observed data (Van Buuren, S., & Groothuis-Oudshoorn, K. 2011). Auxiliary variables representing covariates correlated with missingness or the outcome variable but not included in the primary analysis model should be incorporated in the imputation model to improve MAR plausibility and increase efficiency. The inclusion of auxiliary variables can substantially reduce bias when data are MAR and improve the precision of treatment effect estimates by capturing additional information about the missing data mechanism. Treatment-by-covariate interactions may be necessary when treatment effects differ across subgroups, ensuring that imputation models properly capture heterogeneous

treatment effects. Proper model specification requires including all variables in the analysis model plus additional predictors of missingness and outcomes, creating what is sometimes called a congeniality requirement between imputation and analysis models.

Convergence diagnostics are crucial for MCMC-based imputation to ensure that the iterative algorithm has reached its stationary distribution before imputed values are drawn. PROC MI provides trace plots and autocorrelation diagnostics through the PLOTS option, allowing analysts to visually inspect whether the Markov chain has converged. Adequate burn-in iterations should precede data imputation to ensure the Markov chain has reached its stationary distribution, with the number of burn-in iterations depending on the complexity of the imputation model and the starting values used. Van Buuren and Groothuis-Oudshoorn note that convergence issues are more likely to arise with high-dimensional imputation models or when variables have complex relationships, necessitating careful diagnostic evaluation (Van Buuren, S., & Groothuis-Oudshoorn, K. 2011). The choice between different MCMC algorithms, such as data augmentation versus fully conditional specification, depends on the pattern of missingness and the types of variables being imputed, with each approach having distinct advantages in different contexts.

Table 2: Multiple Imputation Algorithm Comparison (Rubin, B. 1987; Van Buuren, S., & Groothuis-Oudshoorn, K. 2011)

Algorithm	Data Pattern	Computational Cost	Distribution Preservation	Key Advantage
Regression-based	Monotone	Low	Parametric assumptions	Efficiency with strong predictors
Predictive Mean Matching	Monotone/Arbitrary	Moderate	Excellent	Preserves original distribution
MCMC	Arbitrary	High	Good with convergence	Handles complex patterns
Fully Conditional Specification	Arbitrary	High	Variable-specific	Flexible variable types

HOT-DECK IMPUTATION: METHODOLOGY AND PRACTICAL APPLICATION

Hot-deck imputation represents a non-parametric alternative to model-based imputation methods, replacing missing values with observed values from similar donors in the dataset rather than relying on predicted values from regression models. Unlike multiple imputation's reliance on distributional assumptions, HDI imputes actual

observed values, making it attractive when model specification is uncertain or data distributions are complex. Schafer and Graham's comprehensive review of missing data methods describes hot-deck imputation as particularly valuable in survey research and other settings where preserving the empirical distribution of variables is paramount (Schafer, J. L., & Graham, J. W. 2002). The method preserves the marginal distribution of the imputed variable and maintains relationships

between variables evident in the observed data, avoiding some of the potential pitfalls of parametric imputation methods that may generate implausible values or distort distributional characteristics.

The term hot-deck originates from the era of punch-card computing, where data from recently processed cards, the hot deck, were used to fill in missing values, in contrast to cold-deck methods that used data from previous surveys or external sources. Contemporary HDI methods identify donor observations matching recipient observations on specified characteristics, then randomly select a donor value to impute each missing value. The complete analysis of hot-deck imputation on survey non-response by Andridge and Little shows that the underlying principle is that complete cases are identified as resembling the incomplete cases of observed characteristics, and the observed value of the complete case is then used to impute the missing value (Andridge, R. R., & Little, R. J. 2010). The use of this donor approach makes sure that the imputed values are realistic and are within the range of the observed values, which may be of particular importance with variables of limited range or with discrete values, with regression-based methods generating out-of-range predictions.

There are several ways of choosing donors in the hot-deck imputation process, each having its own pros and cons based on the data type and the logic of the research. Random hot-deck imputation randomly assigns donors to the entire cases, which is a relatively simple method with few assumptions to make, but it may not utilize available information on predictors of the missing values. Sequential hot-deck processes cases in order, using the most recent complete case as the donor, which can be efficient but may introduce bias if the ordering of cases is related to the variables being imputed. Distance-based hot-deck calculates similarity metrics such as Euclidean distance or Mahalanobis distance between recipients and potential donors, selecting the closest match based on observed characteristics. Andridge and Little note that distance-based approaches can be computationally intensive with large datasets but often provide superior performance by ensuring good matches between donors and recipients (Andridge, R. R., & Little, R. J. 2010). Propensity score hot-deck estimates the probability of missingness, then matches recipients to donors with similar propensity scores, effectively creating

matched pairs based on the likelihood of having complete data.

While SAS does not provide a dedicated procedure specifically designed for hot-deck imputation, HDI can be implemented through creative use of existing procedures and data step programming. PROC SURVEYIMPUTE offers hot-deck functionality with various sampling options for donor selection, allowing analysts to specify the variables that define donor classes and the method for selecting donors within classes. Alternative implementations using PROC SQL and DATA steps provide greater control over donor selection criteria, enabling analysts to define custom matching algorithms based on multiple characteristics simultaneously. Schafer and Graham emphasize that the flexibility to define custom matching criteria represents both an advantage and a challenge, as analysts must make thoughtful decisions about which characteristics should define donor classes and how to handle situations where no perfect matches exist (Schafer, J. L., & Graham, J. W. 2002). The implementation involves creating separate datasets for cases with complete and incomplete data, defining matching strata or donor classes based on observed characteristics, and then randomly selecting donors from appropriate strata to fill in missing values for recipients.

Hot-deck imputation offers several advantages that make it attractive in certain contexts. It requires no distributional assumptions, making it robust to violations of normality or other parametric assumptions that underlie regression-based methods. It preserves the marginal distribution of imputed variables, ensuring that features like skewness, outliers, and multimodality in the observed data are reflected in the imputed values. It naturally handles both categorical and continuous variables without requiring separate imputation models for different variable types. Andridge and Little note that HDI is computationally efficient compared to iterative algorithms like MCMC, making it practical even with very large datasets (Andridge, R. R., & Little, R. J. 2010). These characteristics make HDI particularly attractive for complex datasets with mixed variable types or unknown distributions where specifying appropriate parametric models would be challenging.

However, HDI has notable limitations that must be considered when choosing an imputation approach. Standard implementations produce a single imputed dataset, failing to account for

imputation uncertainty and potentially underestimating standard errors in subsequent analyses. This limitation can be addressed by performing HDI multiple times with different random seeds to create multiple imputed datasets, though this requires additional programming and is not automatically supported by standard procedures. Donor availability can be problematic with small samples or many matching criteria, potentially leading to poor matches or bias when suitable donors cannot be found. Schafer and Graham caution that when donor pools become too small within matching strata, the quality of matches deteriorates, potentially introducing bias

that may be worse than simpler imputation approaches (Schafer, J. L., & Graham, J. W. 2002). HDI does not directly model associations between variables, unlike model-based methods, and thus can be less efficient than MI where there exist strong predictive associations between variables that might be exploited to enhance the accuracy of imputation. The selection of hot-deck and multiple imputation finally varies on the peculiarities of the data set, the likelihood of the modeling assumption, and the significance of the computational efficiency compared to the statistical efficiency.

Table 3: Hot-Deck Imputation Donor Selection Strategies (Schafer, J. L., & Graham, J. W. 2002; Andridge, R. R., & Little, R. J. 2010)

Strategy	Matching Approach	Computational Demand	Best Application	Potential Limitation
Random	No matching criteria	Very low	Large homogeneous samples	Ignores available information
Sequential	Most recent complete case	Low	Ordered data	Sensitive to case ordering
Distance-based	Similarity metrics	High	Continuous covariates	Computationally intensive
Propensity Score	Missingness probability	Moderate	Known predictors of dropout	Requires model specification

**COMPARATIVE ANALYSIS:
PERFORMANCE EVALUATION AND
CASE STUDIES**

To rigorously evaluate MI and HDI performance, comprehensive simulation studies and real-world case analyses provide essential evidence about the relative merits of different imputation approaches under various conditions. Morris and colleagues' guidance on using simulation studies to evaluate statistical methods emphasizes that well-designed simulations must span realistic scenarios that capture the complexity of real-world data while maintaining sufficient control to identify the specific factors driving performance differences (Morris, T. P. *et al.*, 2019; Gollapudi, 2024). The evaluation framework examined bias, variance, mean squared error, coverage probability, and statistical power under various missing data scenarios, providing a multidimensional assessment of imputation method performance that considers both point estimation and interval estimation properties (Benneh, 2024).

Simulation studies mimicking realistic clinical trial scenarios demonstrate substantial performance differences between imputation methods depending on the underlying missing data mechanism. Under MCAR conditions, where

missingness is completely independent of both observed and unobserved data, all principled imputation methods produce unbiased treatment effect estimates, though they differ in efficiency. Multiple imputation methods typically show smaller variance than complete case analysis due to the efficiency gain from using all available information rather than discarding incomplete cases. Morris and colleagues emphasize that even under MCAR, the choice of imputation method affects statistical power and precision, with implications for sample size requirements and the ability to detect true treatment effects (Morris, T. P. *et al.*, 2019). Hot-deck imputation typically shows slightly larger variance than regression-based multiple imputation under MCAR, reflecting its non-parametric nature and the additional variability introduced by the donor selection process. Coverage probabilities for confidence intervals generally remain near nominal levels across all methods under MCAR, as the absence of systematic bias allows standard error estimation procedures to function appropriately. (Suthari & Manam, 2025)

When missingness depends on observed data, representing MAR scenarios, performance differences become substantially more pronounced

and methodologically critical. Multiple imputation methods leveraging the relationship between observed covariates and the outcome variable maintain unbiased estimates, while methods that ignore this relationship exhibit systematic bias. Sterne and colleagues' examination of multiple imputation in epidemiological research demonstrates that properly specified MI models can effectively remove bias under MAR by incorporating the information contained in observed covariates about missing values (Sterne, J. A. *et al.*, 2009). Complete case analysis shows moderate bias under MAR when missingness is related to observed covariates, as the subsample with complete data is no longer representative of the original study population. Last observation carried forward exhibits substantial bias under MAR, particularly in settings where outcomes are expected to change over time, as it assumes no change after dropout regardless of observed trajectories before missingness. The magnitude of bias with LOCF can lead to severely distorted conclusions, potentially resulting in false negative findings where efficacious treatments appear ineffective or false positive findings where ineffective treatments appear beneficial (Rubinstein, 2024).

Variance and coverage probability patterns change dramatically under MAR compared to MCAR. Multiple imputation methods maintain appropriate variance estimation through Rubin's combining rules, which account for both within-imputation and between-imputation uncertainty. Coverage probabilities for MI remain near nominal levels when imputation models are properly specified, demonstrating the method's ability to produce valid statistical inference under MAR. In contrast, LOCF shows severely degraded coverage probability due to its systematic bias, with confidence intervals that exclude the true parameter value far more often than the nominal error rate would suggest. Sterne and colleagues emphasize that poor coverage probability represents a fundamental failure of statistical inference, as it indicates that reported uncertainty intervals do not accurately reflect the true uncertainty about parameter estimates (Sterne, J. A. *et al.*, 2009). Hot-deck imputation with appropriate donor selection maintains relatively good properties under MAR, though typically with slightly wider confidence intervals than optimally specified MI, reflecting its efficiency loss relative to model-based approaches (Diaz Munoz, 2025).

Real-world case studies from clinical trials provide complementary evidence about imputation method performance in authentic research contexts. Analysis of antidepressant trial data demonstrates how different imputation approaches can yield substantially different treatment effect estimates and conclusions, with implications for regulatory decision-making and clinical practice. The choice between imputation methods affects not only point estimates but also measures of uncertainty, with MI methods typically producing wider confidence intervals that appropriately reflect imputation uncertainty compared to single imputation approaches. Morris and colleagues note that case studies reveal practical implementation challenges not captured in idealized simulation settings, including issues related to model specification, convergence diagnosis, and sensitivity analysis (Morris, T. P. *et al.*, 2019). A diabetes prevention trial case study illustrates the value of auxiliary variables in improving imputation quality, with substantial gains in precision when rich longitudinal covariate data are incorporated into imputation models. The importance of sensitivity analyses becomes apparent in real data applications, where the true missing data mechanism remains unknown and conclusions must be evaluated for robustness across plausible alternative assumptions (A-Clottey, 2025).

Practical guidance emerging from comprehensive comparative analyses emphasizes several key recommendations for clinical trial applications. Multiple imputation with appropriate algorithms provides the most reliable inference across diverse scenarios, particularly under MAR, where it leverages observed covariate information to reduce bias. Hot-deck imputation offers a viable alternative when model specification is uncertain or computational simplicity is valued, serving as an effective sensitivity analysis to complement primary MI analyses. Complete case analysis should be avoided except under verified MCAR conditions, which are rare in practice and difficult to confirm definitively. LOCF should never be used as a primary analysis method due to its substantial bias under realistic missing data mechanisms. Sterne and colleagues emphasize that the choice of imputation method should be prespecified in the study protocol based on thoughtful consideration of the likely missing data mechanism and the characteristics of the study design (Sterne, J. A. *et al.*, 2009). Regulatory submissions require the full sensitivity analysis of MNAR scenarios to consider the uncertainty inherent in the mechanisms of missing data and

whether the conclusions can still be strong in case of breaking the assumptions of MAR. The cost of advanced missing data techniques is an effort to

adhere to science that improves the validity and quality of clinical trial results (Ratnayake, 2025).

Table 4: Simulation Performance Metrics Under Different Missing Data Scenarios (Morris, T. P. *et al.*, 2019; Sterne, J. A. *et al.*, 2009)

Method	MCAR Bias	MCAR Power	MAR Bias	MAR Power	MAR Coverage	Efficiency Ranking
Multiple Imputation - Regression	Minimal	Highest	Minimal	Highest	Nominal	First
Multiple Imputation - PMM	Minimal	High	Minimal	High	Nominal	Second
Hot-Deck - Propensity Score	Minimal	Moderate	Low	Moderate	Near-nominal	Third
Complete Case Analysis	None	Low	Moderate	Low	Below-nominal	Fourth
Last Observation Carried Forward	Minimal	Moderate	Substantial	Lowest	Poor	Fifth

CONCLUSION

Data loss is an inevitable problem in clinical trial scenarios with far-reaching consequences on the inference of statistics, regulatory decision-making, and finally, the development of patient care. The selection of methodological decisions that should be used to address the incomplete data is essentially the source of treatment effect estimations, conclusions regarding the efficacy of therapies, and the credibility of evidence concerning clinical practice guidelines. In most clinical trial scenarios, multiple imputation is the most appropriate approach to dealing with missing data, which is both theoretically well grounded by Rubin and practically adaptable to deal with a variety of data structures and shapes of missing data. The SAS ecosystem provides complete implementation tools in the form of PROC MI and PROC MIANALYZE, which make it possible to offer complex imputation strategies with MCMC algorithms applied on any missing pattern, predictive mean matching to maintain distributional properties, and the addition of auxiliary variables to improve the quality of imputation and reduce bias. Hot-deck imputation offers a very useful complementary information, especially beneficial when the distributional assumptions upon which parametric models are based are doubtful, or when rapid sensitivity computation is needed because of computational simplicity. The fact that hot-deck methods are non-parametric and maintain their distribution properties is what makes them a great tool to determine that the conclusions will be robust, no matter the methodological framework one uses. Some of the critical success factors of an effective implementation of imputation include proper

model specification to capture appropriate relationships between variables, strategic inclusion of auxiliary variables that predict both missingness and outcomes, proper choice of algorithm to use based on characteristics of the data and patterns of missingness, enough imputations to reduce the effect of Monte Carlo error, rigorous convergence diagnostics of iterative algorithms, and comprehensive sensitivity analysis to test violations of Missing at random assumptions. The current regulatory environment is becoming more and more strict on the requirements of missing data management strategies, where there are clear expectations on the prespecified methodological strategies outlined in protocols and detailed sensitivity analyses that would prove the strength of inferences. The strategies discussed are consistent with the recommendations of regulatory bodies and modern-day best practices as illustrated in modern clinical trials literature, which gives biostatisticians and clinical investigators evidence-based frameworks to use in solving the problems of missing data. With the trend towards more pragmatic design, real-world evidence generation, and decentralized implementation models, which raise susceptibility to missing data, an increasingly complex imputation methodology is needed to preserve scientific integrity. These tools, in turn, are the added value of the high imputation methods adopted using the SAS programming capability, which is vital in maintaining the credibility and reliability of the clinical trial results, finally leading to the evolution of evidence-based medicine by using reliable research evidence that reasonably considers and handles the inherent uncertainty posed by missing data collection.

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