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Department of Mathematics and Statistics *high-dimensional data; missing value; variable selection; missForest; self-training selection; random lasso; stability selection; Meta-analysis, sun157@uwindsor.ca*

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ON VARIABLE SELECTIONS
IN HIGH-DIMENSIONAL INCOMPLETE DATA

by

TAO SUN

A Major Research Paper
Submitted to the Faculty of Graduate Studies
through the Department of Mathematics and Statistics
in Partial Fulfillment of the Requirements for
the Degree of Master of Science at the
University of Windsor

Windsor, Ontario, Canada

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ON VARIABLE SELECTIONS
IN HIGH-DIMENSIONAL INCOMPLETE DATA

by

TAO SUN

APPROVED BY:

A. Hussein

Department of Mathematics and Statistics

S. Nkurunziza, Advisor

Department of Mathematics and Statistics

April 23, 2020

Author's Declaration of Originality

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Abstract

Modern Statistics has entered the era of Big Data, wherein data sets are too large, high-dimensional, incomplete and complex for most classical statistical methods. This analysis of Big data firstly focuses on missing data. We compare different multiple imputation methods. Combining the characteristics of medical high-throughput experiments, we compared multivariate imputation by chained equations (MICE), missing forest (missForest), as well as self-training selection (STS) methods. A phenotypic data set of common lung disease was assessed. Moreover, in terms of improving the interpretability and predictability of the model, variable selection plays a pivotal role in the following analysis. Taking the Lasso-Poisson model as an example, we illustrate the robust random Lasso method in the Meta-analysis of multiple datasets for variable selection. Thus, the real data analysis clarifies that missForest and STS outperform MICE. Moreover, the simulation results show that although this method is as effective in selecting important variables as using the random Lasso method, meta-analysis based on the random Lasso is better in terms of coefficient estimation and elimination of unimportant variables. In conclusion, We firstly propose a missForest random lasso (MFRL) method to complete the multiple imputation of the high-dimensional data and robustly select important variables.

Key Words: high-dimensional data; missing value; variable selection; missForest; self-training selection; random lasso; stability selection; Meta-analysis

To my loving Family
My wife Yueing Yang and My daughters

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It is the dream of everyone to play an important role on the stage surrounded by loyal audiences. However, our sense of security, hopefulness, confidence, and self-worth are built by members of our family who can hold our hands tightly even in

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Chapter 1

Introduction

Recently, the research of variable selections in high-dimensional incomplete data has attracted a lot of attention. This kind of study includes two parts, missing data and variable selections.

Missing data are commonly encountered in many data analyses. High-dimensional data sets often lead to biased or less precise results under traditional statistical methods. Importantly, this problem has begun to be solved by the data mining methods, aided by the rapidly developing computational power of artificial intelligence (Lee and Siau (2001) [30]).

In addition, high-dimensional data present new challenges for variable selection in regression analysis. Variable selection plays a pivotal role in regression analysis as it identifies important variables that are associated with outcomes and have been shown to improve predictive accuracy and interpretability of the resulting models. Variable

selection methods have been widely investigated for complete data including classical model selection methods, penalization methods and Bayesian variable selection methods (Fan and Lv (2010) [15]).

1.1 Missing Data

In medicine, finance, transportation, telecommunications and a variety of other fields, missing data are commonly encountered (Lee and Siau (2001) [30]). Since all statistical analysis techniques strictly derive information from data sets, the quality of the information depends to a large extent on the deviation of the data set. As one of the important factors affecting the behavior of data, missing data may not only cause the deviation of the estimator but also lead to the distortion of the estimator variance, which reduces the efficiency of traditional statistical methods (Kang (2013) [26]). Therefore, statistical approaches coping with missing data have naturally become a crucial issue for researchers.

To introduce some notations, let X be a fully observable d -dimensional covariate. Further, let X_{obs} be the observed value, let X_{mis} be the missing value and let δ be the missing indicator function.

In term of missing data and data dependencies, Little and Rubin ((1989) [34]) classify the missing data mechanisms into three categories: (1) Missing not at random (MNAR): the reason of missing data depends on the true value of the missing vari-

able. That is, $P(\delta = 1|X_{obs}, X_{mis}) \neq P(\delta = 1|X_{obs})$. When $\delta = 0$, it means the data is observable. When $\delta = 1$, it means the data is missing. (2) Missing at random (MAR) (Rosenbaum and Rubin (1983) [49]): the missingness is not random, but the probability of missing data depends on the value of the observable variable in the sample. MAR provides asymptotically unbiased estimates. That is, $P(\delta = 1|X_{obs}, X_{mis}) = P(\delta = 1|X_{obs}) = \pi(X_{obs})$, where $\pi(z)$ is the selection probability function. (3) Missing completely at random (MCAR): Whether the data is missing or not does not depend on any observed or missing data. That is, $P(\delta = 1|X_{obs}, X_{mis}) = P(\delta = 1)$. MAR is the most commonly used in statistical research (Little and Rubin (1989) [34]). Therefore, the missing mechanism of this paper is based on this MAR assumption.

Historically, the approaches for dealing with missing data in the past can be classified into three categories: deleting cases with missing values, grouping cases with missing values as a new class of values and filling cases with missing values. Firstly, the simplest method of dealing with missing data is the complete data analysis method, which consists of deleting the missing data and solely using the fully observed data for statistical inference. Because the missing data information is ignored, this method will lead to the loss of statistical efficiency. Meanwhile, if the missing data is not completely at random, the estimates obtained by this method are usually biased. Secondly, when the structure of the observed values is not comprehensive enough, it is not reasonable to treat the missing values as a new class of values. Imputation provides a tool for maximizing the reception of information for analyzing data with complex missing data patterns. Therefore, scholars have been focusing on the study

of missing value imputation methods.

Imputation techniques can be classified into two types, single imputation and multiple imputation. The former is divided into mean imputation, random imputation, regression imputation and regression random imputation; the latter is based on Bayesian theory and on the expectation–maximization (EM) algorithm to achieve the processing of missing data. There are two main disadvantages of the single imputation method. First, some approaches fundamentally change the original distribution of data, resulting in sampling errors, such as mean imputation and regression imputation. Second, the single imputation method cannot accurately reflect the uncertainty of the missing values, which usually underestimates the variance of the imputed estimator. However, since multiple imputation theory is based on single imputation theory and overcomes the shortcomings of single imputation theory, this major paper focuses on the selection of multiple imputation methods for high-dimensional data.

There are three main types of approaches to handle multiple imputation. Firstly, inverse probability weighting corrections are usually available (Horvitz and Thompson (1952) [19]). However, inverse probability weighting approaches are always not applicable in the complicated missing data patterns. Secondly, some approaches rely on the improved models of missing data, such as using beta distribution to simulate the molecular rotation of genes and work well in some traditional situations. With the increasing trend of the number of variables (large p), variable analysis becomes cumbersome to ensure the success of multiple imputation or maximum likelihood imputation. Meanwhile, phenotypic data has been emerging in large numbers. Phenotypic data is

data obtained by repeatedly observing the same group of individuals at different times and in different spaces. It is hierarchical or multi-level data that is composed of time series data and cross-sectional data. The complexity of phenotypic data with mixed data types (multi-class classification, ordinal, and continuous) further exacerbates the difficulty of modeling the joint distribution of all variables. Although some algorithms are designed to analyze data sets with continuous variables and categorical variables, the implementation of these complex methods in high-dimensional phenotypic data is not straightforward. Estimation approaches through accurate statistical modeling often suffer from “dimensionality collapse” and overfitting, which means there are huge data values in every dimension and overfitting happens easily. Thirdly, the problems of stochastic error in complicated data must be fully considered (Wallace, et al. (2010) [60]). In recent years, the estimation of the missing values of high-throughput experimental data has attracted enormous attention. Mass spectrometry data and microarray data are two new major challenges. In addition, microarray data contain completely continuous intensity measurements, while phenotypic data has a mixed data type. This character invalidates most of the established microarray imputation approaches for phenotypic data. Moreover, gene microarray data monitors gene expression for thousands of genes, and most genes are thought to be co-regulated in a systemic sense with other genes, which results in a high degree of correlation of variables and makes imputation more complicated. In addition, phenotypic data is more likely to contain isolated variables that are “unattributable” to other observed variables.

1.2 Variable Selection in High-dimensional Data

In the fields of Genetics, Financial Mathematics, etc., the data dimension is getting higher and higher with an abundance of irrelevant and redundant information. Since high-dimensional data is often sparse data in nature, variable selection becomes one of the core issues. Some variable selection methods in high-dimensional data have been recommended (Fan and Lv (2010) [15]; Candes and Tao (2007) [8]).

Variable selection was originally proposed by Blum and Langley ((1997) [5]), Kohavi and John ((1997) [28]). At that time, almost no data would fall into more than 40 features. The sample size was usually greater than the number of variables. In this context, many traditional variable selection criteria have been proposed, such as forward regression, the Akaike information criterion (AIC) (Akaike (1973) [1]), the Bayesian information criterion (BIC) (Schwarz (1978) [52]), Mallows' C_p criteria (Mallows (1973) [40]), and so on.

However, with the development of science and technology, research on a large number of variables and a small number of observations has increased dramatically. Using the traditional methods mentioned above can be a challenge, and the computational time grows exponentially with dimensions. Therefore, for the cases of large “ p ” and small “ n ”, if we follow the traditional variable selection method, the calculation becomes extremely heavy, and variable screening is also cumbersome to obtain. Thus, we need to find some new approaches.

First of all, we considered how to select variables in the case of a linear model.

The classical approaches are penalized least squares (PLS) and penalized likelihood methods, which select variables and predict coefficients simultaneously. According to the different penalty functions, we can also use bridge regression (Fu (1998) [16]), Lasso (Tibshirani (1996) [57]) or the smoothly clipped absolute deviation (SCAD) estimator (Fan and Li (2001) [14]). Although these methods are more robust than the traditional ones, the performance of the corresponding estimates is also different for distinct penalty functions. Statisticians continue to study and propose improved methods. Zhao and Yu ((2006) [65]) named “the irrepresentable condition,” which meant that when p grew with n and $p \gg n$, the Lasso model chose the almost sufficient and necessary condition for matching. However, Lin et al. ((2009) [32]) and Huang et al. ((2008) [20]) found that when the covariates were highly correlated, “the irrepresentable condition” was not satisfied, and the selection of the Lasso estimation model was inconsistent. Obtaining a consistent Lasso estimate of the model became an important research issue. The elastic network estimate proposed by Zou and Hastie ((2005) [67]) is a combination of the ridge estimate and Lasso. This method not only combines the advantages of both but also upgrades the consistency of model selection. Bach ((2008) [4]) proposed “*Bolasso*” based on resampling. This method guarantees a high probability of selecting important variables. Therefore, under certain conditions, combining Bootstrap and Lasso can be used to obtain consistent parameter estimates in the model.

In the second part of this research, for the complete high-dimensional data after multiple imputation, variable selection becomes fundamentally important. Meanwhile, when researchers need to carry out a large-scale experiment, like a lung disease ex-

periment, but with limited time, they can combine the results of previous studies on the same topic and analyze them. This is a meta-analysis. It plays a pivotal role in summarizing and synthesizing multidisciplinary scientific evidence. As the use of data increases, the accuracy and precision of estimators can be improved. When the dimensionality of the data set is high, variable selections need to be included in the meta-analysis to upgrade the interpretability and prediction ability of the model.

Thus, it is essential to address the variable selections in high-dimensional incomplete data. This problem can be solved in two parts. The first part focuses on missing data. In the first chapter of this major paper, we compare different multiple imputation methods. Combining the characteristics of medical high-throughput experiments, we compared MICE, missForest, as well as STS methods. A phenotypic data set of lung disease was assessed. In the second chapter, we review the corresponding rationale for MICE, missForest and STS. In the third chapter, the real data analysis clarifies that missForest and STS outperform MICE. The second part of the fourth chapter is about variable selections. In terms of improving the interpretability and predictability of the model, variable selection plays a pivotal role. Taking the Lasso-Poisson model as an example, we introduce the robust random Lasso method in the Meta-analysis of multiple datasets for variable selection. At last, we get the conclusion that MFRL is our recommendation for variable selections in high-dimensional incomplete data.

Chapter 2

Literature Review

In the previous chapter, we focused on understanding the basic concepts. In this chapter, we further study variable selections in high-dimensional incomplete data from the perspective of historical development.

Missing data refers to data that have not been completely observed in the resulting data set for some reason. In the past few decades, many scholars have conducted comprehensive research and proposed several approaches to analyzing the data with missing values. Although longitudinal data have their own characteristics, the method of dealing with missing values in longitudinal data is also derived from the existing methods. We can use the mean maximization imputation method, multiple imputation method, mixed regression model and external estimation data to be related. In particular, marginal models are more common methods (Troxel, et al. (1998) [59]).

2.1 Progress in Research

The research on missing data in statistical analysis can be divided into the following three periods (Kalton (2019) [23]).

The first period was the start-up period (1915 - 1950). The corresponding researchers began preliminary research on missing data. Bowley (1915) first proposed the missing data problem and made a great contribution to the sampling method. In a social condition survey, the uncertainty and error were classified into the non-sampling error category. In 1926, the control for various sources of error was further emphasized. Deming ((1944) [11]) conducted a good summary of the factors that should be considered when there were evaluating and controlling survey errors, including bias factors that resulted in missing data due to non-response.

The second period was the period of special research and method development (1950s - 1990s). A variety of classical approaches to dealing with the remedy of missing data have been developed during this period.

To reduce the missing data in the investigation, it was generally necessary to start with both prevention and ex post facto remedy. Early scholars also paid more attention to pre-existing prevention methods and measures to reduce missing data. Pre-existing prevention was also the easiest and most efficient way to deal with missing data. Kish (1965), Lininger (1975), and Mosteller (1979) have separately discussed measures to improve the response rate in the survey (Langer (2013) [29]). Politz and Deming ((1953) [44]), Orley and Peirce ((1966) [3]) and later Potthoff, et al. ((1993) [46])

used different methods to determine the number of ideal attempts in the household survey to reduce the lack of data due to the reasons, such that the respondent was not at home. However, the method of prevention in advance was not a complete method, and the problem has not been overcome. Therefore, many researchers have conducted theoretical research and empirical exploration of the after-the-fact remedy for missing data. Deming and Stephan ((1940) [12]) proposed a reciprocal weighting method based on sample extraction probability; Politz and Simmons ((1949) [45]) proposed a classic adjustment method for eliminating the need for call-backs. These approaches were based on the number of respondents who were at home and could be surveyed at the same time. The various weighting methods in the later stages were based on these early ideas.

Actually, the imputation method was briefly used for remediation of unanswered items in the project, while the weighting method was generally used for units that could not answer. Many researchers have proposed new approaches and conducted extensive discussions and improvements during this period. Methods, like mean imputation, cold-deck imputation, hot-deck imputation, regression imputation and model imputation, have been proposed. Nordbotten ((1963) [43]) and Schiffer, et al. ((1978) [50]) explored the role of the cold-deck method in periodic surveys. Sonquist, Chaqman, Ford (1983) and Sander (1983) separately discussed and improved the hot-deck imputation method (Andridge and Little (2010) [2]). Kalton and Kasprzyk (1986) (Kalton and Anderson (1986) [24]; Kalton and Kasprzyk (1986) [25]) proposed a distance function matching method (nearest neighbour imputation method) for tree branch classification based on the hot-deck method to avoid the defects of regression

imputation and hot-deck imputation.

In addition, Hansen and Hurwitz (1946) proposed a double-sampling method based on traditional inferences, which was extensively discussed by Zarkovich ((1966) [64]), Cochran ((1977) [9]) and Rao ((1973) [48]). Rao ((1972) [47]) and Singh ((1984) [54]) published a large number of papers on the application of Bayesian methods in the treatment of missing data. Importantly, Dempster, et al. ((1977) [13]) proposed a data algorithm that effectively evaluated the incompleteness, namely the EM algorithm. The EM algorithm was not only an effective calculation tool but also a theoretical basis for subsequent missing value estimate methods. Based on this algorithm, Rubin proposed multiple imputation methods in a series of papers in the early 1980s (Little and Rubin (1991) [35]). Currently, the improved approaches and applied research based on multiple imputation methods still have a long-lasting impact.

During this period, classical theories on the study of missing data have also emerged in large numbers. For example, Little and Rubin ((1991) [35]) systematically summarized the theoretical framework of missing data mechanisms and some classical approaches. These methods dealt with missing data in “Statistical Analysis with Missing Data”, such as the likelihood function method and the EM algorithm. In the topic of “Survey Errors and Survey Costs”, Groves ((1989) [18]) introduced the non-response rate and proposed the corresponding statistical model. It was important to emphasize that the “Incomplete Data Research Group” made a serious theoretical study of missing data problems (Lessler (1992) [31]). These theories can be studied in detail from Madow, et al. ((1983) [39]), Cox and Cohen ((1985) [10]), Kalton ((1988)

[22]), and Little ((1988) [33]).

The third period was the time of the method perfection (from 1990s to the present). During this period, there were fewer new ideas on non-response analysis, but more researchers extended and improved the approaches. For example, many extended EM algorithms, such as GEM algorithm (Dempster, et al. (1977) [13]), ECM algorithm (Meng and Rubin (1993) [42]), ECME algorithm (Liu and Rubin (1994) [36]) and parameter extended EM (PX-EM) algorithm (Liu, et al. (1998) [37]). Finally, with the emergence of modern statistical methods, like support vector machines, neural networks and the rapid development of computer technology and the application of missing data research, this field has flourished (Goh and Lee (2019) [17]). We can study them from non-parametric multiple imputation methods based on the concept of “Generalized Regression Neural Networks” (GRNN) (Shalabi, et al. (2006) [53]) and the Random Forest algorithm (Tang and Ishwaran (2017) [56]).

2.2 Trends in Research Development

From the history of missing value research, we can learn how to gradually reveal deeper statistical problems. On the theoretical method route, from the beginning of the use of more traditional single-mean imputation to the recent statistical learning methods, the method is gradually complex, more and more accurate.

In the past, because the cost of collecting data was too high, people often made deci-

sions based on limited information. With the advent of the information age, technology for discovering and searching for useful information grows rapidly. Data mining technology has been rapidly developing and playing an essential role in business decision support, economics, management, medical research and so on. It includes mass statistical learning methods such as decision trees, artificial neural networks, support vector machines and random forests. For traditional statistical methods, a classical model usually relies on a number of strong assumptions. The ideal assumptions of the model are often difficult to be verified in the real data set. Therefore, the accuracy of traditional statistical methods may not be as good as that of statistical learning methods. The statistical learning method does not require a large number of assumptions. It has strong accuracy for the model, and its effect on the large sample high-dimensional data is often better than that of a traditional statistical method. However, its model is equivalent to a black box, which is less explanatory than that of a traditional statistical method. Statistical learning methods also rely on the development of Computer Science. Many algorithms combined with their models produce better results. These approaches can be used for data prediction. However, there are few studies on the use of predictive models for high-dimensional phenotypic dataset as well as for missing remedies and remedial effects. Therefore, in this major paper, we use the existing computer technology to make use of multiple imputation, missForest and STS scheme prediction. These approaches are used to simulate the filling of high-dimensional phenotypic datasets with random missing values at different missing rates. The advantages and disadvantages of the datasets are compared by comparing the root mean square deviation (RMSD) of the datasets before and after imputation. The concept of RMSD is defined at Section 2.3.

2.3 Existing Work on Multiple Imputation

2.3.1 Multiple Imputation Algorithm

Multiple Imputation (MI) was first proposed by Dempster, et al. ((1977) [13]). The main idea is to construct m different imputation values for each missing value in the data set, subsequently generate m complete data sets, and then treat the m complete data sets into one set to get the final result for the estimation of missing data. The reason for constructing m imputation values for one missing is to simulate the distribution corresponding to the estimated values under the assumptions, so researchers can use these conditions to predict the actual posterior distribution of the target variables. The difference from the previous simple imputation method is that MI fills each missing value with an imputation method to reflect the uncertainty of missing values. Multiple imputation has the following advantages:

1. By simulating the distribution of missing data, multiple imputation can better preserve the intrinsic relationship between variables;
2. Compared to the simple estimation results given by single-value imputation, multiple imputation provides a large amount of information to measure the uncertainty of the estimation results;
3. The filling values are generated from multiple imputation. The variation between them can indicate the randomness of the missing data.

Commonly used approaches based on multiple imputation:

1. Predictive Mean Matching (PMM): the residual term to the linear regression is added to represent the randomness of the predicted value. The missing value is filled with the closest one. The PMM method guarantees that the data used for imputation is random, and the specific values for imputation are also based on the actual observed values, so that the imputation value is close to the actual value, which has accuracy and reliability.
2. Propensity Score (PS) method: a conditional probability that is first randomly assigned to an observed variable. For each variable with a missing value, a trend score is generated to indicate the probability of the sample missing, and then the samples are grouped and each group is filled using the approximate Bayesian method.
3. Markov Chain Monte Carlo (MCMC) is a commonly used method for posterior distribution in Bayesian inference. It calculates the filling and posterior parts by repeated loops, so as to extract the imputation values to fill the missing data. In general, MCMC method is more advantageous in comparison to fully parametric linear regression imputation. It is used in this major paper to impute missing data.

In our study, three types of covariables are involved: continuous, ordinal, and nominal. Since there are many clustering structures involved, we select the MCMC method in MI. The philosophy behind the MICE methodology is below.

Notation

Let $Y = (Y_1, \dots, Y_p)$. For $j = 1, \dots, p$, let Y_j be one of p incomplete variables. Y_j^{obs} and Y_j^{mis} stand for the observed and missing parts of Y_j respectively. The number of imputation is equal to m with $m \geq 1$. The h^{th} imputed data set is denoted by $Y^{(h)}$ where $h = 1, \dots, m$. Let $Y_{-j} = (Y_1, \dots, Y_{j-1}, Y_{j+1}, \dots, Y_p)$, which denotes the collection of the $p - 1$ components in Y except Y_j . Let Q represent the quantity of scientific interest. In practice, Q often stands for a multivariate vector. More precisely, Q encompasses any interesting model.

We assume that the completed data Y is a random sample of partial observations from the p -variable multivariate distribution $P(y|\theta)$. Let the multivariate distribution of Y be completely specified by θ (vector of unknown parameters). The question is how to obtain the multivariate distribution of θ explicitly or implicitly. The MICE algorithm obtains the posterior distribution of θ by iteratively sampling from the conditional distribution of the form

$$P(y_1|y_{-1}, \theta_1)$$

$$\vdots$$

$$P(y_p|y_{-p}, \theta_p)$$

$\theta_1, \dots, \theta_p$ as parameters are specific to the respective conditional densities and are not necessarily the product of a factorization of the ‘true’ joint distribution $P(y|\theta)$. A

simple draw is triggered from observed marginal distributions, the h^{th} iteration of chained equations is a Gibbs sampler that successively draws

$$\begin{aligned}\theta_1^{*(h)} &\sim P(\theta_1|y_1^{obs}, y_2^{h-1}, \dots, y_p^{h-1}) \\ Y_1^{*(h)} &\sim P(y_1|y_1^{obs}, y_2^{h-1}, \dots, y_p^{h-1}, \theta_1^{*(h)}) \\ &\vdots \\ \theta_p^{*(h)} &\sim P(\theta_p|y_p^{obs}, y_1^h, \dots, y_{(p-1)}^h) \\ Y_1^{*(h)} &\sim P(y_1|y_p^{obs}, y_1^h, \dots, y_p^h, \theta_p^{*(h)}),\end{aligned}$$

where $y_j^h = (y_j^{obs}, y_j^{*(h)})$ is the j^{th} estimated variable at the h^{th} iteration. It is observed that the previous imputation $Y_j^{*(h-1)}$ enters $Y_j^{*(h)}$ merely by the relationship with other variables. Therefore, unlike many other MCMC methods, this method converges quickly. In addition, monitoring convergence is important. Usually, the number of iterations is a small number, such as 10 - 20 times. In fact, the chain equation refers to a series of missing data that the MICE algorithm can easily implement as a single variable process. m streams are executed by the MICE function in parallel. Each stream generates an imputed data set.

The method has been found to be effective in many cases, important in practice and easy to apply. Note that we can specify a model which does not follow a known joint distribution. For example, two linear regressions specify a joint multivariate normal given specific regularity condition. However, the coefficients of the joint normal distribution are unknown, but can be easily specified using the MICE framework. The conditionally specified models can be incompatible in that the effects of incompati-

bility on the quality of the imputation are unknown.

2.3.2 missForest

Missing forests (`missForest`) is a new nonparametric imputation method in recent years. The principle of the algorithm is based on Random Forest, which is a relatively common nonlinear modeling algorithm. Its advantages include at least two points. First, it allows for special interactions and nonlinear features in data variables. Second, it can adapt to various structural forms of data, that is, it can process mixed types of data with numerical classifications. The algorithm trains a Random Forest model with the complete observations in the first step, then predicts the missing values, and finally repeats the iterations to address such missing value filling problems. The more prominent feature of random forests is the ability to process mixed-type data in both low- and high-dimensional structure, even in the complex case of data interactions and nonlinear structure. Due to the accuracy and robustness of its predictions, Random Forest has been being fully applied in various fields and complex issues. Stekhoven and Bühlmann ((2012) [55]) improved on this basis and proposed the `missForest` algorithm. `MissForest` can use the partially observed complete data set as a training set to train the random forest model to predict the missing values. The random forest algorithm and the missing forest filling process are detailed below.

- (1) Random Forest Algorithm. As a member of the cluster model, the algorithm, first published by Breiman ((2001) [6]), is an effective extension of the classic Bagging integrated learning approach. The basic learning device of the random

forest is the decision tree, which is used to construct the Bagging-type integrated learning. A modified tree is applied to learn algorithm that selects a random subset of the features at each candidate split in the learning process. The algorithm can be applied to handle classification problems and regression problems. In addition, the algorithm utilizes Bootstrap sampling.

The random forest algorithm has some characteristics. Firstly, there is the Out of Bag (OOB) estimate. Bootstrap is used in the Random Forest model to extract a small number of samples from the dataset. The probability of choosing any one item (say x_1) on the first draw is $\frac{1}{n}$. Therefore, the probability of not choosing that item is $(1 - \frac{1}{n})$. That's just for the first draw; there are a total of n draws, all of which are independent, so the probability of never choosing this item on any of the draws is $(1 - \frac{1}{n})^n$. If n is large, the probability converges to $\frac{1}{e} \approx 0.368$ because $\lim_{n \rightarrow \infty} (1 - \frac{1}{n})^n = \frac{1}{e}$. That means nearly 36.8% of the samples will not appear in the Bootstrap sample. These sample data can be used to test the prediction error of the training model, which is called out-of-bag. Secondly, there is random features. At the split node under each decision tree, only some features enter the segmentation as candidates. This process is equivalent to de-correlating the tree, so that the average value of the obtained tree has a smaller variance. Finally, there is importance measure in variables. The principle of the importance measure is to add random interference to the variable and compare whether the OOB error estimate changes significantly. If a large change occurs, the variable can be marked as an important variable.

(2) missForest filling process. Let us assume the data $X = (X_1, X_2, \dots, X_p)$ is a $n \times p$

matrix. If a missing value in a variable is filled, the data set can be divided into the following four parts (Stekhoven and Buhlmann (2012) [55]).

- 1) $y_{obs}^{(s)}$ represents the observed values of X_s .
- 2) $y_{mis}^{(s)}$ represents the missing values of X_s .
- 3) $x_{obs}^{(s)}$ represents the observed values other than X_s .
- 4) $x_{mis}^{(s)}$ represents the missing values other than X_s .

Due to the randomness of missing data, $x_{obs}^{(s)}$ is not completely known, and $x_{mis}^{(s)}$ is not completely missing. The filling process is as follows:

- a) Initial filling of X using mean padding or other simple filling methods;
- b) The missing columns in X are rearranged from small to large according to the size of the missing rate. The index set of the missing column is recorded as M ;
- c) When the stop criterion γ is not met:
 - * Store the existing padding matrix, labeled as X_{old}^{imp} ;
 - * For $s \in M$, putting the training sets $y_{obs}^{(s)}$ and $x_{obs}^{(s)}$ into a random forest model for training; putting the testing set $x_{mis}^{(s)}$ into the model and predict $y_{mis}^{(s)}$; using the obtained predicted value $y_{mis}^{(s)}$ to update the padding matrix, denoted as X_{new}^{imp} ; filling in the remaining missing variables in M in turn; until the criteria for iteration termination is met or the maximum number of iterations has been reached;
- d) Get the final filling matrix, denoted as X^{imp} .

The criteria for iteration termination γ is: if the difference between the new padding matrix and the previous padding matrix becomes larger, the loop is stopped.

The difference for the set of continuous variables N is defined below (Stekhoven and Buhlmann (2012) [55]).

$$\Delta_N = \frac{\sum_{j=1}^p \sum_{i=1}^n (x_{i,j}^{new} - x_{i,j}^{old})^2}{\sum_{j \in N} \sum_{i=1}^n (x_{i,j}^{new})^2}.$$

For the set of categorical variables F , the difference is

$$\Delta_F = \frac{\sum_{j=1}^p \sum_{i=1}^n I_{x_{i,j}^{new} \neq x_{i,j}^{old}}}{NA},$$

where NA is the number of missing values in the categorical variables.

2.3.3 The Self-training Selection (STS) Scheme

The STS scheme learns the structure of the expression data. It selects the optimal imputation algorithm by self-training. This is achieved by generating a small percentage of missing values among the data with complete expression profiles to simulate the missing pattern in the original data, assuming that expression values are missing at random. Results from the simulations indicate that this scheme picks the optimal or near-optimal imputation algorithm in each case but at an increased computational cost.

The STS procedure explicitly determines the optimal imputation algorithm for a par-

ticular data set. This procedure is implemented by simulating missing values in the subset of the expression matrix, filling these simulated missing values, and comparing these imputed values to the known expression values. Although for different purposes, this strategy has also been employed by others. Jornsten, et al. ((2005) [21]) used this idea to find a convex combination of the imputation methods. Kim, et al. ((2005) [27]) found the optimal number of nearest neighbors for the local least squares imputation. The rank of each imputation method, in terms of RMSE, is recorded in each simulation. The method with the smallest rank-sum statistic over multiple simulated data sets is selected.

More specifically, we randomly remove another 5% of expression values from each expression, and perform n iterations to generate data sets $D_j^{(k)(l)}$, $l = 1, \dots, n$. For each method M_i , the rank-sum statistic (Brock, et al. (2008) [7]) below are calculated

$$R(M_i, D_j^{(k)}) = \sum_{l=1}^n \text{Rank}_{M_i}(\text{RMSE}(D_{j;M_i}^{(k)(l)}, D_j^{(k)})).$$

The STS scheme is formally defined as

$$S_{STS}(D_j^{(k)}) = \text{argmin}_{M_i} R(M_i, D_j^{(k)}).$$

As mentioned in some papers (Brock, et al. (2008) [7]), the $n = 10$ replicates are

sufficient to determine the preferred imputation method. The null hypothesis that all methods are equally effective (i.e., the rank-sum statistics are all identical) was tested using Friedman's test.

Overall, the STS selection schemes can in principle be used with any imputation algorithms.

2.4 Assessment of Imputation Performance

2.4.1 Evaluating the Methods

We compared some typical imputation methods for different missing values in the situations of lung disease datasets. Imputation performance is evaluated by calculating the root mean square error (RMSE) of continuous and ordinal variables as well as the proportion of false classification (PFC) for nominal variables (Schmitt, et al. (2015) [51]). In raw data, missing values are few and all missing values are unimportant in the analysis of lung diseases. Thus, deleting the variables with missing values is similar with treating the variables with the related coefficients to be zero. We have a complete dataset from the original raw data set after deleting the variables with missing values. In analysis of the real dataset, we simulated missing values at some special rates to obtain the dataset with missing values. We imputed the missing values on the dataset and calculated the RMSE between the imputed value and the real value for evaluating the performance. For continuous variables, the squared errors are denoted as $e^2 = \frac{(\widehat{y}_{ij} - y_{ij})^2}{\text{var}(y_j)}$, where y_{ij} is the real value for subject i and variable j .

For ordinal variables, $e^2 = \left(\frac{\widehat{y}_{ij} - y_{ij}}{p-1}\right)^2$, where p is the number of possible levels of y_j . For the nominal variable, $e^2 = \chi(\widehat{y}_{ij} \neq y_{ij})$, where $\chi(\cdot)$ is an indicator function. The RMSE for continuous and ordinary variables is denoted as $\sqrt{\text{ave}(e^2)}$. The PFC for nominal variables is represented as $\text{ave}(e)$. The RMSE and PFC are estimated from 20 randomly generated missing value dataset.

2.5 A Variable Selection Method - Random Lasso

Wang, et al. ((2014) [62]) proposed the Meta-Lasso method, which uses random Lasso to select variables in some multiple high-dimensional data sets. It is necessary to review Random Lasso.

2.5.1 Limitations and Improvements of Lasso

Before the introduction of Random Lasso, we have to discuss the limitations of Lasso. Suppose there are n sets of observations $(x_1, y_1), \dots, (x_i, y_i), \dots, (x_n, y_n)$, $i = 1, \dots, n$, of which the observations of the i^{th} group $x_i = (x_{i1}, \dots, x_{ip})$ and the observations y_i of the response variable Y_i have undergone mean correction processing, so there is no need to consider the intercept value. Let us consider the following linear model:

$$y_i = \sum_{j=1}^p \beta_j x_{ij} + \epsilon_i, \epsilon_i \sim N(0, \sigma^2) \quad (2.1)$$

When using the Lasso method to predict the coefficient $\beta = (\beta_1, \beta_2, \dots, \beta_p)$, the following term (2-2) is minimized.

$$\sum_{i=1}^n (y_i - \sum_{j=1}^p \beta_j x_{ij})^2 + \lambda \sum_{j=1}^p |\beta_j|, \quad (2.2)$$

where λ is a non-negative adjustment parameter. When λ is sufficiently large, some estimation coefficients will be accurately contracted to 0. However, there are still two drawbacks in this Lasso method. First, when the number of variables p is larger than the sample size n , Lasso can solely select at most n variables. Second, when highly related explanatory variables are used, this method cannot select all of these highly related explanatory variables. Only one or a part of them can be selected, and the other coefficients are compressed to zero.

In order to eliminate these two limitations of Lasso, Zou and Hastie ((2005) [67]) proposed the Elastic-Net method. When using this method to predict the coefficient β , one minimizes the following optimization function.

$$\sum_{i=1}^n (y_i - \sum_{j=1}^p \beta_j x_{ij})^2 + \lambda_1 \sum_{j=1}^p |\beta_j| + \lambda_2 \sum_{j=1}^p \beta_j^2, \quad (2.3)$$

where both λ_1 and λ_2 are non-negative adjustment parameters. Since there is a penalty term of L_2 norm in function (2.3), the number of variable selection is not limited by the sample size, which eliminates a limitation in the Lasso method. However, because of the penalty term of the L_2 norm, the new limitations arise. The L_2 norm is a penalty term for ridge regression, and this addition will make the coefficient estimates of highly correlated variables close to each other. This method can select

or not select all highly correlated variables with similar true coefficients. Meanwhile, it does not have the ability to predict the coefficients of corresponding variables at different degrees. It is even more difficult to accurately estimate the variable coefficients of different symbols.

Zou ((2006) [66]) proposed another Lasso method, adaptive Lasso, to overcome the limitations. This method is based on optimization function.

$$\sum_{i=1}^n (y_i - \sum_{j=1}^p \beta_j x_{ij})^2 + \lambda \sum_{j=1}^p \omega_j |\beta_j| \quad (2.4)$$

In the above term, $\omega_j = |\hat{\beta}_j^{ols}|^{-r}$, where r is a constant and $r > 0$. Meanwhile, $\hat{\beta}_j^{ols}$ is the ordinary least squares estimate of β_j . Adaptive Lasso has a good performance-asymptotic property that Lasso does not have. In adaptive lasso, when the number of variables p is constant, the sample size n tends to infinity, and the adjustment parameter λ tends to 0 at a certain rate. It is proved that the probability of choosing the true model is 1. If the true model is provided in advance, the estimated coefficient has the same asymptotic normal distribution as the true model provided in advance. This property was defined by Fan and Li ((2001) [14]) and it was named as "Oracle" property. Although adaptive Lasso has good asymptotic properties, its estimation depends on ordinary least squares. Thus, when ordinary least squares estimation is uncertain, adaptive Lasso is definitely worse than Lasso in terms of prediction performance.

In recent years, many scholars have proposed several improvements to Lasso. For

example, the SCAD (Smoothly Clipped Absolute Deviation) method proposed by Fan and Li ((2001) [14]) slows down two limitations of Lasso; Fused lasso method proposed by Tibshirani ((2005) [58]) selects variables for ordinal variables; the Group Lasso method proposed by Yuan and Lin ((2006) [63]) selects variables for grouped variables; the Relaxed Lasso method proposed by Meinshausen ((2007) [41]) addresses the shortcomings of Lasso over-compressing variables.

In 2011, Wang, et al., who proposed the random Lasso method (Wang, et al.(2011) [61]), broke through the limitations of Lasso. Compared with adaptive Lasso, Relaxed Lasso and Fused Lasso, this method can select all or highly unselected highly relevant variables into the model. The selection is also not limited by the sample size, especially when the degree of influence of the variables and the signs are different. The flexibility of coefficient estimation is more obvious.

2.5.2 The Principle of Random Lasso

In practice, we often have merely one data set. However, dividing the available data set directly into parts is not an effective way to use the data. The Bootstrap method produces distinct data sets by repeatedly sampling observations from the original data set, rather than repeatedly obtaining independent data sets from the population. Each bootstrap sample may include only a subset of highly correlated variables. Thus, the bootstrap method has a decomposed correlation ability. For each bootstrap sample, if $q \leq p$ and p is the total number of variables, q candidate variables can be randomly selected. This is the basic idea of random Lasso. The procedure of extract-

ing feature attributes and sample sets is similar with the random forest method.

Random Lasso in principle is a two-step method. In each step, the bootstrap sample generated by the Bootstrap method produces similar expected perturbations to multiple data sets. To maintain the maximum flexibility of the method, the number of randomly selected candidate variables in each step of the model can be different. q_1 candidate variables are randomly selected in each bootstrap sample in the first step, and q_2 candidate variables are randomly selected in each bootstrap sample in the second step. q_1 and q_2 are two adjustment parameters, where $q_1 \leq p$, $q_2 \leq p$, and p is the total number of variables.

2.5.3 The Algorithm of Random Lasso

The algorithm of the random Lasso method is divided into two parts, the importance measure and the variable selection for generating all coefficients. The specific algorithm is as follows:

Step1. Generate importance measure for all coefficients:

- 1a. B bootstrap samples with sample size n are drawn from the original training set;
- 1b. For the i^{th} bootstrap sample b_i ($i = 1, \dots, B$), randomly select q_1 candidate variables, and apply the Lasso method to obtain the estimated β_j . The coefficient of the unselected variable is estimated to be 0;
- 1c. Calculate the importance measure I_1, \dots, I_p of p variables X_1, \dots, X_p . The

importance measure of X_j is

$$I_j = \left| A_j^{-1} \sum_{i=1}^B \hat{\beta}_j^{(bi)} \right|,$$

where A_j is the number of times that the j^{th} variable X_j is selected in the B bootstrap samples;

Step2. Variable selection:

2a. Re-extract B bootstrap samples with sample size n from the original training set;

2b. For the i^{th} bootstrap sample b_i ($i = 1, \dots, B$), randomly select q_2 candidate variables. At this time, q_2 candidate variables are selected with a certain probability. The probability that each variable is selected is proportional to the importance measure calculated in 1c. After selection, we apply the Lasso method to obtain the estimated β_j , and the coefficient of the unselected variable is estimated to be 0;

2c. Calculate the final estimates of β_j ,

$$\hat{\beta}_j = A_j'^{-1} \sum_{i=1}^B \hat{\beta}_j^{(bi)},$$

where A_j' is the number of times the j^{th} variable X_j is selected in the B bootstrap samples.

In step 1c, in all bootstrap samples, the average coefficient value of each explanatory variable is used to generate an importance measure for the explanatory variable, which is beneficial for variable selection and coefficient estimation in the second step. It is done because, intuitively, for an important variable, the estimated coefficients in

different bootstrap samples may always be large, so the average value of the coefficient estimates will be large. However, for an unimportant variable, even if the signs are different, the estimated coefficients in different bootstrap samples may still be small, and the average value of the coefficient estimates is close to zero. Therefore, we choose the absolute value of the mean of the estimates to be a measure of importance for each explanatory variable. In step 2c, the average of the estimated coefficients of each variable from the B bootstrap samples is used as the predicted value of the coefficients corresponding to the final explanatory variable.

Chapter 3

Numerical Results

In this chapter, some typical imputation methods and variable selection methods are implemented by using real data and simulated datasets.

3.1 Analysis in Real Data (COPD Dataset)

Phenotypic data are high-dimensional, which have a mixture of continuous, ordinal and nominal covariates. In particular, the chronic obstructive pulmonary disease (COPD) is one of the major sequelae of Wuhan Novel Coronavirus Pneumonia from young people to the elderly. The COPD data set with missing values is an example of large phenotypic data sets. It was derived from the COPD study of the database of Genotypes and Phenotypes (dbGaP) (www.ncbi.nlm.nih.gov). There are a few missing values in the COPD data set. The variables with missing values in the raw COPD data are not important for the data analysis mainly because the related medical follow-up research support is lacking. As same as treating the variables with the

related coefficients to be zero, we deleted these few variables with missing values. Thus, we can analyze the complete real data. Then, hypothetical missing can be performed in the complete real data.

With the trend of small number of subjects and large number of variables in the complex phenotypic data, it becomes cumbersome to ensure success of modeling the joint distribution of all variables or using common multiple imputation. It also brings challenges that there are highly correlated structure of the data. According to the progression recent years, which are described in Chapter 2, some traditional statistical methods are not analyzed in this paper, such as group lasso. We typically and meaningfully compare the MICE, missForest, and STS methods in this study.

For implementing MICE in the comparative analysis, we have to remove variables with sparse (i.e. having less than 10% of the total observations). Even with the filtering treatment in MICE, missForest and STS methods outperformed MICE method in the COPD data.

In figure 3.1, 3.2 and 3.3, we use “con” to represent continuous data, “nom” to represent nominal data and “ord” to represent ordinal data.

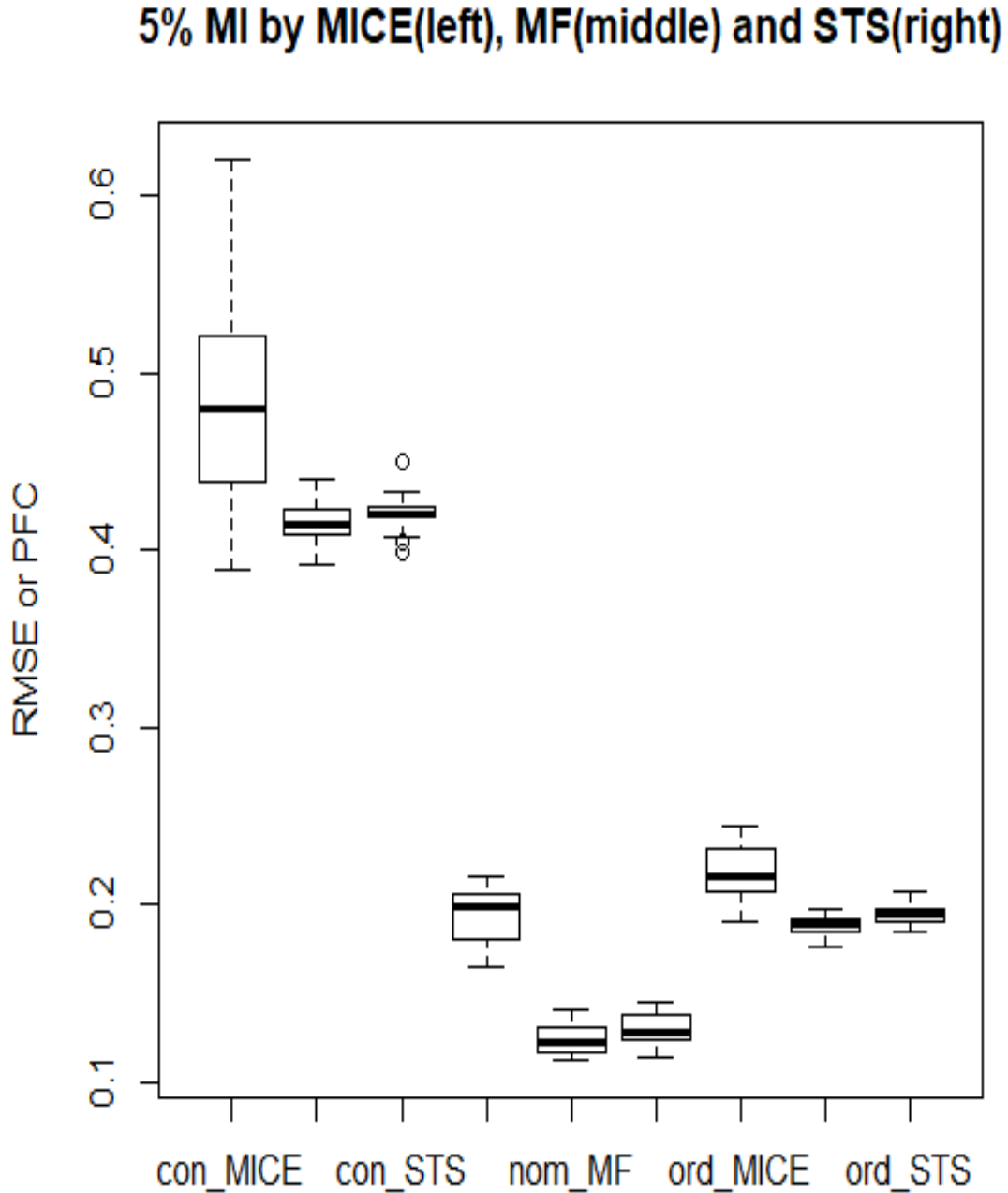


Figure 3.1: 5% MI by MICE (left), MF (middle) and STS (right) in COPD data. In continuous data and ordinal data, RMSE is lower in MF method and STS method than that in MICE. In nominal data, PFC is lower in MF method and STS method than that in MICE.

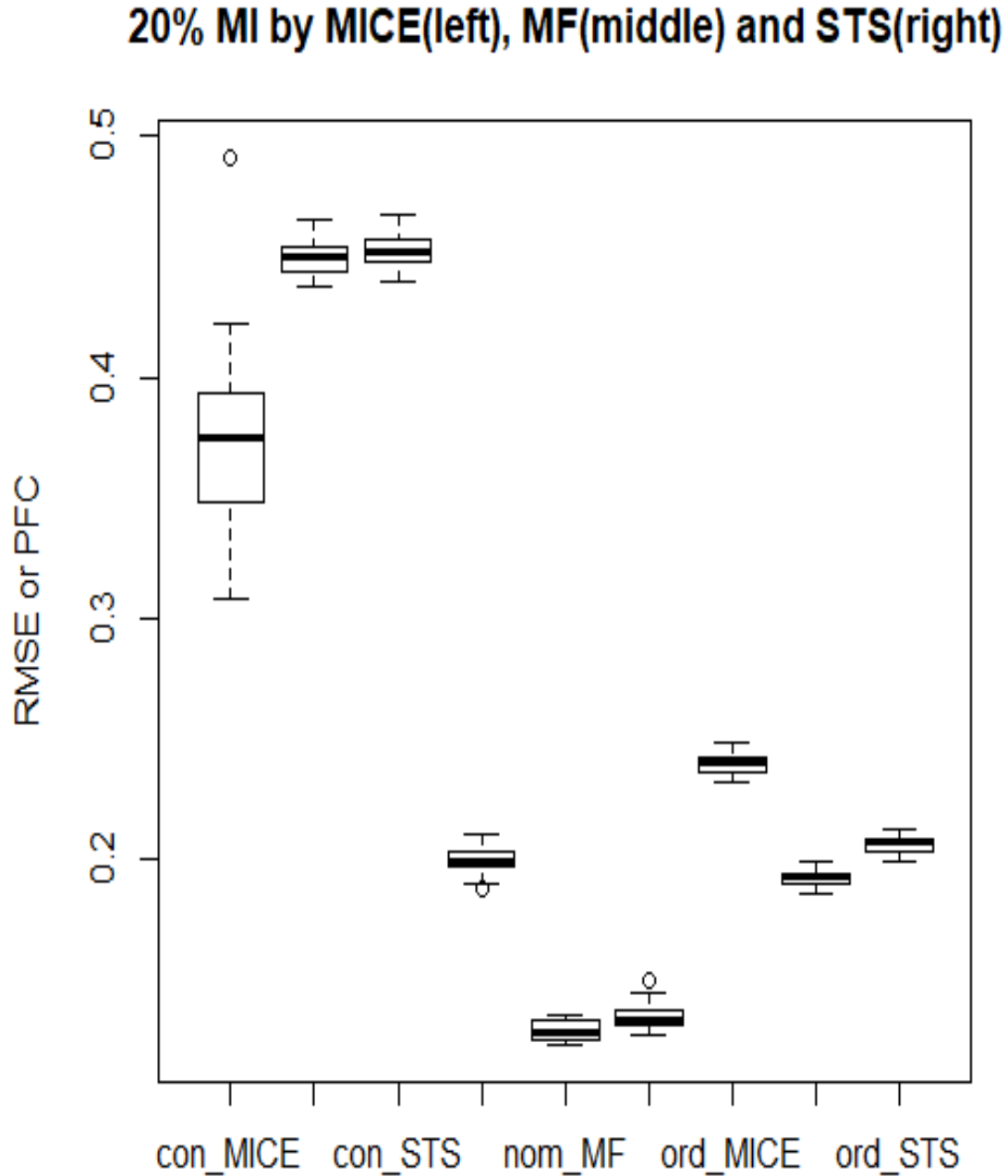


Figure 3.2: 20% MI by MICE (left), MF (middle) and STS (right) in COPD data. In continuous data, RMSE is higher in MF method and STS method than that in MICE. In nominal data, PFC is lower in MF method and STS method than that in MICE. In ordinal data, RMSE is lower in MF method and STS method than that in MICE.

40% MI by MICE(left), MF(middle) and STS(right)

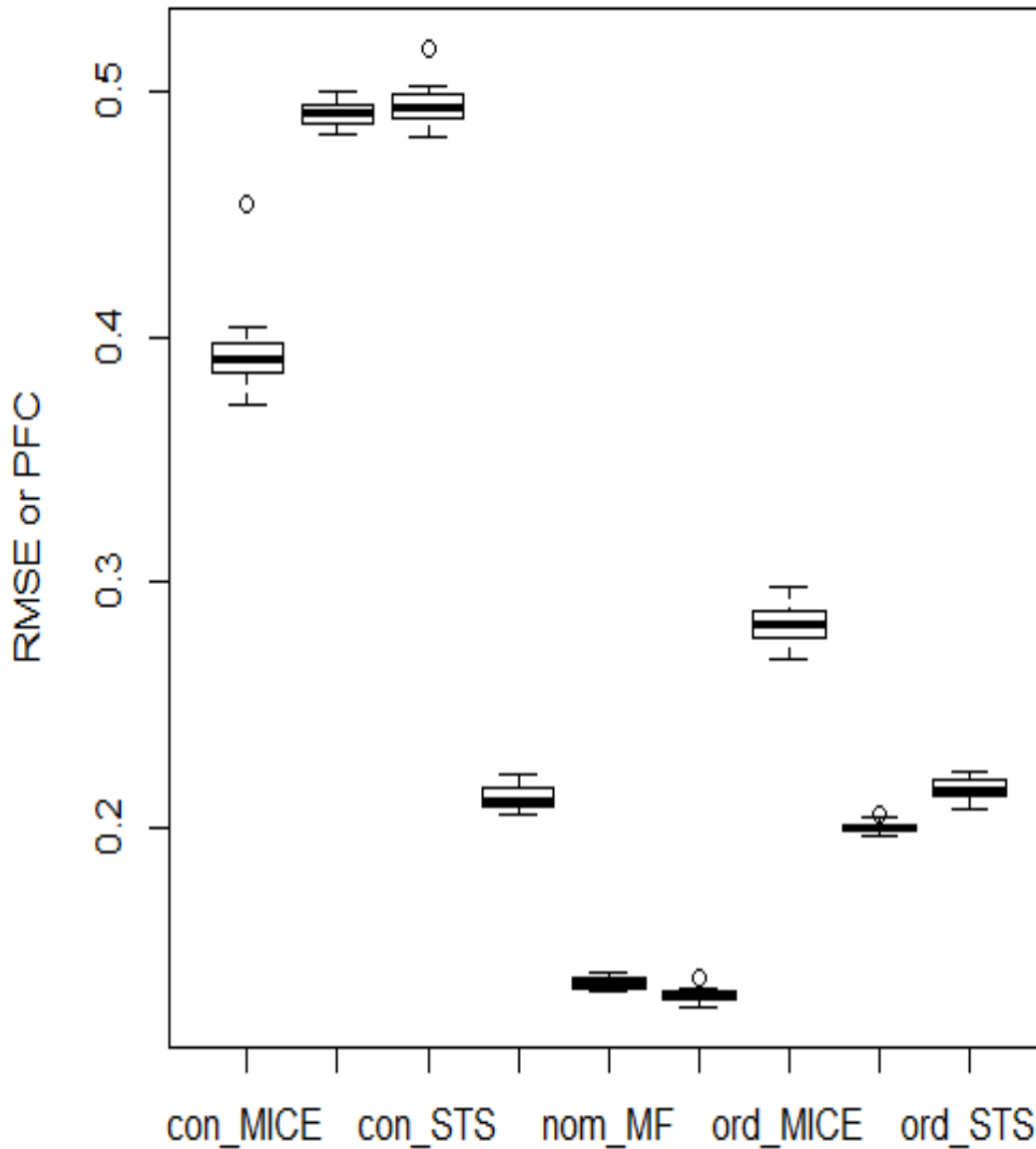


Figure 3.3: 40% MI by MICE (left), MF (middle) and STS (right) in COPD data. In continuous data, RMSE is higher in MF method and STS method than that in MICE. In nominal data, PFC is lower in MF method and STS method than that in MICE. In ordinal data, RMSE is lower in MF method and STS method than that in MICE.

In the comparative study of the imputation methods available for the large phenotypic data of COPD, missForest method outperforms MICE method in nominal and ordinal data types in all missing levels. Merely in the 20% and 40% missing continuous data part of COPD data, MICE does not encounter difficulty in comparison with missForest. The large variances in MICE limited its application to some real data. This is consistent with other reports (Stekhoven and Buhlmann (2012) [55]; Jornsten, et al. (2005) [21]; Kim, et al. (2005) [27]), which illustrate unstable performance of MICE. In addition, missForest usually was among the state-of-the-art imputation methods, especially in terms of stability and accuracy. STS method is identified to be in the top level for imputation in the COPD phenotypic data, if we do not consider the implementing time.

3.2 Simulation Results

Before simulation research, we discuss why do we use Poisson distribution in our simulation?

This study focuses on pneumonia. Some pneumonias, such as the Wuhan novel coronavirus pneumonia, are diffuse in lung. They have long-term disease characteristics. For each uninfected or infected individual, we only consider 0 and 1, without considering any decimals, such as 0.5. Thus, Poisson distribution can be modeled to this kind of count data.

In this subsection, we perform a simulation study of the proposed meta-analysis method based on random Lasso in the Lasso-Poisson regression model, and compare it with the random Lasso method based on the Lasso-Poisson regression model in a separate data set. Consider the equation in a Poisson regression model:

$$E(Y|X) = e^{X\beta}, \quad (3.1)$$

The simulation data is generated from the model (3.1), where Y has Poisson distribution. In the m^{th} data set, let $x_{mi} = (x_{mi,1}, \dots, x_{mi,p})'$ be the observed value of the i^{th} sample. Let y_{mi} be the observed value of the response variable $Y_{mi} \sim \text{Poisson}(\alpha_m)$ of the i^{th} sample in the m^{th} data set.

The number of explanatory variables is $p = 8$, the eight explanatory variables are pairwise related, and the correlation coefficients of x_{j_1} and x_{j_2} are $\rho(x_{j_1}, x_{j_2})$, which satisfies $\rho(x_{j_1}, x_{j_2}) = 0.5^{|j_1 - j_2|}$. The true values of the explanatory variable coefficients of the M data sets are all the same, $\beta_m = (3, 1.5, 0, 0, 2, 0, 0, 0)$.

To simplify the calculation procedure, in the simulation, the sample size of $M = 10$ data sets is the same, which is $n_m = 50$. The number of bootstrap samples drawn in each data set is also the same, which is $B_m = 200$.

The relative model error (RME) is depicted below to evaluate the prediction performance of each predictive model. Suppose that the fitted coefficient vector is $\hat{\beta}$ and

the true coefficient vector is β^0 , then the relative model error is defined below:

$$RME = \frac{(\hat{\beta} - \beta^0)' \Sigma (\hat{\beta} - \beta^0)}{\sigma^2}, \quad (3.2)$$

where Σ is the covariance matrix of the predictor X , that is $\Sigma = Cov(X)$, that is, $cov(x_{j_1}, x_{j_2}) = 0.5^{|j_1 - j_2|}$, and σ in the equation (3.2) is the standard deviation of the error term in the linear model (3.1) (Fan and Li (2001) [14]).

We perform 500 replicates for each example and calculate the average values of RME and $\hat{\beta}$. To simplify the calculation, we introduce the threshold $t_n = \frac{1}{n}$. When the absolute value of the coefficient estimate of the explanatory variable X_j is greater than the threshold t_n , the explanatory variable is selected.

We have a meta-analysis method based on the random Lasso in the Lasso-Poisson regression model and a random Lasso method in the Lasso-Poisson regression model on a separated dataset. In terms of prediction accuracy and the number of times of the explanatory variables to be selected, the performance of these two methods is compared. Besides, the number of selected unimportant explanatory variables is compared in the simulation. In the cells of the table, the numbers above are from the meta-analysis, and the numbers in parentheses are from the analysis of the separated data sets.

Table 3.1: Coefficient estimate of the important explanatory variables

	$\hat{\beta}_1$	$\hat{\beta}_2$	$\hat{\beta}_5$
M_1	2.84840 (2.83816)	1.45589 (1.39140)	1.86907 (1.83228)
M_2	2.88814 (2.88282)	1.42026 (1.37989)	1.86756 (1.85117)
M_3	2.87732 (2.83076)	1.40564 (1.36609)	1.90109 (1.89337)
M_4	2.87861 (2.82295)	1.44834 (1.37708)	1.84709 (1.82158)
M_5	2.87357 (2.84734)	1.37415 (1.35640)	1.91652 (1.85213)
M_6	2.91475 (2.89460)	1.43756 (1.40661)	1.92419 (1.87455)
M_7	2.90875 (2.87308)	1.39048 (1.34687)	1.87854 (1.80311)
M_8	2.90965 (2.89453)	1.41928 (1.38135)	1.87012 (1.80409)
M_9	2.88199 (2.81149)	1.42789 (1.41138)	2.02593 (1.91989)
M_{10}	2.92532 (2.88283)	1.37689 (1.26099)	1.87189 (1.80681)

Table 3.2: Coefficient estimate of the unimportant explanatory variables

	$\hat{\beta}_3$	$\hat{\beta}_4$	$\hat{\beta}_6$	$\hat{\beta}_7$	$\hat{\beta}_8$
M_1	0.02467 (0.05131)	0.01493 (0.01839)	0.08327 (0.09455)	0.01449 (-0.0489)	0.02017 (-0.0385)
M_2	0.00404 (0.00877)	0.01534 (0.05789)	0.00941 (0.03165)	0.00515 (0.02440)	-0.00132 (0.00201)
M_3	0.01266 (0.01882)	0.00865 (0.04185)	0.01182 (0.02513)	-0.00110 (0.00112)	-0.00206 (0.00796)
M_4	0.00903 (0.02483)	-0.00611 (0.01851)	-0.01227 (-0.0268)	0.002448 (-0.0245)	-0.00357 (-0.0155)
M_5	0.00420 (0.02749)	0.004679 (-0.00526)	0.01459 (0.02129)	-0.00162 (0.00787)	0.00180 (-0.0623)
M_6	0.01852 (0.02540)	0.01970 (0.02367)	-0.01112 (0.01312)	-0.00846 (0.03938)	0.01849 (0.05445)
M_7	-0.01223 (0.01327)	0.0201 (0.03069)	0.00646 (-0.0155)	0.01463 (-0.0152)	0.00387 (0.01047)
M_8	-0.00559 (0.01679)	-0.00064 (-0.00922)	0.01804 (0.03708)	0.00196 (-0.0121)	-0.01394 (-0.0145)
M_9	0.00180 (-0.00212)	0.01094 (0.04778)	0.01845 (0.02576)	-0.00255 (0.01231)	-0.03232 (0.04227)
M_{10}	0.01484 (0.01858)	0.01547 (0.01863)	-0.00841 (0.01866)	-0.00604 (0.01681)	0.00370 (-0.0186)

Table 3.3: Average RME times 100

	M_1	M_2	M_3	M_4	M_5	M_6	M_7	M_8	M_9	M_{10}
RME	57 (104)	56 (95)	65 (119)	60 (107)	59 (128)	63 (101)	67 (121)	66 (114)	62 (99)	60 (122)

Table 3.4: Numbers of unimportant variables to be selected

	X_3	X_4	X_6	X_7	X_8
M_1	4 (11)	6 (7)	4 (10)	7 (14)	8 (10)
M_2	6 (19)	8 (9)	5 (13)	6 (11)	7 (10)
M_3	3 (12)	6 (18)	5 (10)	7 (12)	5 (11)
M_4	2 (14)	3 (10)	4 (8)	4 (12)	4 (12)
M_5	6 (15)	3 (13)	3 (17)	3 (10)	3 (13)
M_6	6 (14)	3 (8)	5 (12)	3 (14)	4 (16)
M_7	6 (8)	6 (8)	6 (11)	2 (12)	1 (10)
M_8	5 (13)	4 (8)	3 (8)	4 (15)	6 (10)
M_9	3 (5)	6 (7)	3 (11)	4 (9)	5 (14)
M_{10}	5 (11)	6 (11)	7 (12)	6 (9)	1 (7)

In Table 3.1 and Table 3.2, we present the estimated value of the important explanatory variables and the estimated value of the unimportant explanatory variable coefficients. The estimated value obtained by the coefficients based on the meta-analysis method of random Lasso in multiple data sets is closer to the true coefficient value than the coefficient estimated value obtained by using the random Lasso method for multiple data sets respectively. From the average RME in Table 3.3, it is pointed out that the average RME obtained by the meta analysis method is smaller. In Table 3.4, the number of occurrences are summarized when unimportant explanatory variables are studied in 500 simulations by using these two methods. As can be seen from the table, the number of occurrences that a meta-analysis method selects unimportant

variables is smaller than that of other method. In summary, the performance of the meta-analysis method of random Lasso has a significant advantage over the predictive performance of using random Lasso method in the 10 respective data sets.

Chapter 4

Concluding Remarks

This major paper explores how to handle variable selection in high-dimensional missing data from two aspects. First, we compared and studied the imputation effects based on panel data under MICE, missForest, and STS methods. The results show that MICE, as a non-parametric model, has extremely high time efficiency, and has a good imputation effect on high missing rate phenotypic data. Although the missForest and STS based on modern statistical learning methods are inferior to MICE in time efficiency, they usually have better imputation effects. An imputation method can reduce the bias of the estimated amount caused by missing data. It should be noted that the method is not a panacea, and different imputation methods are suitable for different occasions. Therefore, before performing missing value imputation, studying the structure of the data can upgrade the effect of the imputation method.

Second, we studied the application of random Lasso in variable selection and combines it with meta-analysis. In the count data sets of the Lasso-Poisson regression model,

the estimated coefficients of the explanatory variables based on the meta-analysis method of random Lasso in multiple data sets are better than those of separated data sets. The coefficient estimate based on the meta-analysis method should be closer to the true coefficient value, and the effect of removing unimportant variables is significant. Even when multiple explanatory variables are highly correlated, the meta-analysis method based on random Lasso in multiple data sets still has good predictions.

There are at least five aspects of novelty in this study. First, this is a systematic comparative study of approaches for estimating missing values for large-scale phenotypic data. We compare the three existing methods (missForest, multivariate imputation by chained equations (MICE) and self-training selection (STS)). Second, we indicate missForest and STS significantly impute the correct missing values for each data type in a given data set, though STS selection method is time-consuming. Third, we illustrate the importance of variable selection by using random lasso method in a discrete model simulation. Fourth, we use meta-analysis to further analyze high-dimensional data sets. Fifth, MFRL approach is firstly illustrated as a principled method of addressing variable selections in high-dimensional incomplete data.

In conclusion, we suggest missForest for imputation and random Lasso for variable selection in high-dimensional incomplete data (Liu, et al. (2016)[38]). We name this method as MFRL. However, further investigations are needed. This work should contribute to data mining methods.

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Vita Auctoris

Mr. Tao Sun was born in 1972 in Zhengzhou, China. He had a medical degree from Peking University and obtained an undergraduate degree in Statistics from the Western University. He is currently a candidate for the Master of Science degree in Statistics at the University of Windsor. He hopes to graduate in 2020.