High Dimensional Imputation for the Social Sciences: A Comparison of State-of-the-Art Methods

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Abstract

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Introduction

Today's social, behavioral and medical scientists have access to large multidimensional datasets that can be used to investigate the complex relationships between social, psychological and biological factors in shaping individual and societal outcomes. Large social science datasets, such as the World Values Survey, or the European Values Study (EVS), are easily available to researchers and initiatives have been undertaken to link and extend these datasets into a system of linked open data. Making use of the full potential of these data sets requires dealing with the crucial problem of multivariate missing data.

Rubin's Multiple Imputation (MI) approach (Rubin, 1987) was developed to specifically address the issue of missing responses in surveys. MI is a three-step process that entails an imputation, analysis, and pooling phase. The fundamental idea of the imputation phase is to replace each missing data point with m plausible values sampled from their posterior predictive distributions given the observed data. This procedure leads to the definition of m complete versions of the original data that can be analyzed separately using standard complete-data analysis models (analysis phase). Finally, the m estimates of any parameter of interest can be pooled following Rubin's rules (Rubin, 1987) (pooling phase).

Since Rubin's seminal work, two main strategies have become popular for multiple imputation of multivariate missing data: joint modelling (JM) (Schafer, 1997, ch. 4) and full conditional specification (FCS), also known as Multiple Imputation by Chained Equation (MICE). (van Buuren, Brand, Groothuis-Oudshoorn, & Rubin, 2006). The first one relies on defining a multivariate distribution for the missing data, deriving conditional distributions for each missing data pattern, and obtaining samples from it by means of a Markov Chain Monte Carlo algorithm. The second method defines conditional densities for each incomplete variable and performs iterative imputations on a variable-by-variable basis.

When applied to large multidimensional datasets, there are at least two reasons to prefer the FCS approach over the JM. First of all, the complexity of the FCS method increases with the number of variables with missing values, while the complexity of the JM approach increases with the number of missing data patterns that manifest in a dataset. Given a number of p variables, the FCS approach needs to specify at most p imputation models, while the JM approach requires an imputation model for each missing data pattern. Furthermore, the FCS approach allows a great level of flexibility to accommodate the peculiarities of surveys and other large multidimensional datasets. FCS can easily accommodate for the different distributions of variables and it can preserve unique features in the data, such as skip patterns or variables interactions.

Both the JM and the FCS approaches rely on the crucial *missing at random* (MAR) assumption. Meeting this assumption requires specifying imputation models for the MI procedure that include all observed variables that are correlates of missingness. Omitting from the imputation models an observed predictor related to both the missingness and the imputed variables creates a *missing not at random* (MNAR) problem. MI under MNAR leads to substantial bias in parameter estimation in the analysis and pooling phases, and invalidates hypothesis testing involving the imputed variables.

As a result, when it comes to defining the set of auxiliary variables for the imputation models within an MI procedure, an inclusive strategy (i.e. including numerous auxiliary variables) is generally preferred to restrictive approach (i.e. including few or no auxiliary variables). An inclusive approach reduces the chances of omitting important correlates of missingness, making the MAR assumption more plausible. Furthermore, the inclusive strategy has been shown to reduce estimation bias and increase efficiency (Collins, Schafer, & Kam, 2001), as well as reducing the chances of specifying uncongenial imputation and analysis models (Meng, 1994).

Specifying the imputation models for a FCS MI procedure remains one of the most challenging steps in dealing with missing values for large multidimensional data sets. In practice, the inclusive strategy faces identification and computational limitations. One serious risk of an inclusive strategy is the occurrence of singular matrices within the

imputation algorithm. When data is high-dimensional (i.e. the number of recorded units n is not substantially larger than the number of recorded variables p) or afflicted by high collinearity (i.e. one or more of the variables is equal to a linear combination of the others) the data covariance matrix is singular. Singular matrices are not invertible, an operation that is fundamental in the estimation of the imputation models in any parametric imputation procedure. As a result, the possible high dimensionality of the observed data matrix, resulting from an inclusive strategy, can prevent a straightforward application of MI algorithms or force researchers to make arbitrary choices regarding which variables to use.

Recent developments in high-dimensional data MI techniques represent interesting opportunities to embrace an inclusive strategy, without facing its downsides. Some statisticians and machine learning experts have focused on high-dimensional Single Imputation (SI) methods in an effort to improve the accuracy of individual imputations (e.g. D'Ambrosio, Aria, & Siciliano, 2012; Kim, Golub, & Park, 2005; Stekhoven & Bühlmann, 2011). However, the main task of social scientists is to make inference about a population based on a sample of observed data points, and SI is simply inadequate for this purpose: it does not provide statistically valid inference (Rubin, 1996). The concept of statistical validity as defined by (Rubin, 1996) is meant to capture two features of estimation. First, the point estimate of a parameter of interest must be unbiased, and second, the actual confidence interval coverage (CIC) must be equal or greater than nominal coverage. SI strategies might meet the first requirement, but cannot meet the second as they do not take into account the uncertainty regarding the imputed values. MI, on the other hand, was designed to provide statistically valid inference and therefore is more suitable for social scientific research.

The combination of MI with high-dimensional prediction models has been directly tackled by algorithms combining full conditional specification of imputation models with shrinkage methods (Deng, Chang, Ido, & Long, 2016; Zhao & Long, 2016), but their application has been studied only for biomedical sciences. Other researchers have proposed FCS strategies using dimensionality reduction to avoid the obstacles of an

inclusive strategy in high-dimensional data imputation. However, these solutions were either limited to the Joint Modeling approach (Song & Belin, 2004), or tested exclusively on particularly low-dimensional settings (Howard, Rhemtulla, & Little, 2015). Finally, tree-based FCS strategies also have the potential to overcome the limitations of inclusive strategies. The non-parametric nature of decision trees bypasses the identification issues most parametric methods face in high-dimensional contexts. However, these methods have been proposed to deal with other issues, such as imputation in the presence of interaction effects (Doove, Van Buuren, & Dusseldorp, 2014), or have been tested exclusively on biomedical datasets (A. D. Shah, Bartlett, Carpenter, Nicholas, & Hemingway, 2014).

Scope. The inclusion of shrinkage methods, principal component analysis and non-parametric decision trees within the FCS framework has the potential of simplifying the decisions social scientists need to make when dealing with missing values. The lack of comparative research on these methods performances makes it difficult for social scientiest working with large multidimensional data sets to decide which imputation method to adopt. With this article, we provide a comparison of these state-of-the-art high-dimensional imputation algorithms. We compared the imputation methods based on the statistical validity of the complete-data analyses they allow to perform. The comparison was based on three numerical experiments: two simulation studies and a resampling study using real survey data.

Outline. In what follows, we first present the general MICE framework, how the high-dimensional MI methods fit within it, and some single data missing data strategies considered for reference. Then we present the three experiments, their design and results. We then discus the implications of the results and provides recommendations for applied researchers. Finally, we provide a description of the limitations of the study, and possible future research directions.

Imputation methods and Algorithms

Consider a dataset $\boldsymbol{Z}$ of dimensionality $n \times p$, with n observations (rows) and p variables (columns). Assume that the first t ($t \leq p$) variables of $\boldsymbol{Z}$ have missing values. These t variables are part of some substantive model of scientific interest (e.g. a linear regression model), and are target of imputation. The subset of $\boldsymbol{Z}$ containing variables z_1 to z_t is referred to as the $n \times t$ matrix $\boldsymbol{T}$. The remaining $n \times (p-t)$ subset of $\boldsymbol{Z}$ contains variables that are not target of imputation. These variables constitute a pool of possible *auxiliary* variables that could be used to improve the imputation procedure. Let $\boldsymbol{A}$ denote this set of auxiliary variables so that $\boldsymbol{Z} = (T, A)$. For a given z_j variable, with $j = (1, ..., p)$, denote its observed and missing components by $z_{j,obs}$ and $z_{j,mis}$, respectively. Let $\boldsymbol{Z}_{-j} = (z_1, ..., z_{j-1}, z_{j+1}, ..., z_p)$ be the collection of $p-1$ variables in $\boldsymbol{Z}$ excluding z_j. Denote $\boldsymbol{Z}_{-j,obs}$ and $\boldsymbol{Z}_{-j,mis}$ the components of $\boldsymbol{Z}_{-j}$ corresponding to the data units in $z_{j,obs}$ and $z_{j,mis}$, respectively.

Multiple Imputation by Chained Equations

Assume that $\boldsymbol{Z}$ is the result of n random samples from a multivariate distribution defined by an unknown set of parameters $\boldsymbol{\theta}$. The chained equations approach obtains the posterior distribution of $\boldsymbol{\theta}$ by sampling iteratively from conditional distributions of the form $P(z_1|\boldsymbol{Z}_{-1}, \boldsymbol{\theta}_1)$ ... $P(z_t|\boldsymbol{Z}_{-t}, \boldsymbol{\theta}_t)$, where $\boldsymbol{\theta}_1$ ... $\boldsymbol{\theta}_t$ are imputation model parameters specific to the conditional densities of each variable with missing values.

More precisely, the MICE algorithm takes the form of a Gibbs sampler where the mth iteration ($m = 1, ..., M$) successively draws, for each jth target variable ($j = 1, ..., t$), from the following distributions:

$$\hat{\boldsymbol{\theta}}_j^{(m)} \sim p(\boldsymbol{\theta}_j|z_{j,obs}, \boldsymbol{Z}_{-j,obs}^{(m)}) \tag{1}$$

$$z_{j,mis}^{(m)} \sim p(z_{j,mis}|\boldsymbol{Z}_{j,mis}^{(m)}, \hat{\boldsymbol{\theta}}_j^{(m)}), \tag{2}$$

where $\hat{\boldsymbol{\theta}}_j^{(m)}$ and $z_{j,mis}^{(m)}$ are draws from the parameters full conditional posterior distribution (1) and the missing data posterior predictive distribution (2), respectively. After convergence, D different sets of values sampled from the predictive distribution are

kept as imputations and D differently imputed data sets are obtained. Any substantive model can then be fit to each dataset, and estimates can be pooled appropriately using Rubin's rules (Rubin, 1987).

Generally speaking, for each variable z_j target of imputation, a researcher needs to define a set of observed variables that will be included in $\boldsymbol{Z}_{-j}^{(m)}$. The high-dimensional imputation methods compared in this paper and described below follow the general MICE framework, but they differ in the elementary imputation methods they use to define equation (1) and (2). Each of them has a different way of processing the large number of auxiliary variables provided to the imputation algorithm to allow a maximal inclusive strategy while avoiding its usual obstacles.

MICE with fixed ridge penalty (bridge). This approach uses as elementary imputation method the Bayesian imputation under the normal linear model procedure as presented by van Buuren (2012) (p. 68, algorithm 3.1).

In this approach, the sampling of each $\hat{\boldsymbol{\theta}}_j^{(m)}$ in (1) relies on the inversion of the cross-product of the observed data matrix $\boldsymbol{Z}_{j,obs}^{(m)}$. By adding a biasing ridge penalty κ, singularity of the cross-product matrix is circumvented and the sampling scheme is possible even if $\boldsymbol{Z}_{j,obs}^{(m)}$ is afflicted by high collinearity and n is not substantially larger than p.

The value of κ is usually chosen close to zero (e.g. $\kappa = 0.0001$), as values larger than 0.1 may introduce systematic bias (Van Buuren, 2018, p. 68). However, larger values may be necessary to invert the observed data matrix cross-product in certain scenarios. In the present work, the value of κ was decided by means of a cross-validation procedure described below.

MICE with Bayesian lasso (blasso). A high-dimensional Bayesian lasso imputation algorithm was proposed by Zhao and Long (2016), but it was tested only in a univariate missing data context. The method relies on the Bayesian lasso model, a regular Bayesian multiple regression with prior specifications that allow to interpret the mode of the posterior distribution of the regression coefficients as lasso estimates (Hans, 2009; Park & Casella, 2008). Given data with sample size n, consider the dependent

variable y and a set of predictors X. The Bayesian Lasso linear regression specification we used within the blasso imputation algorithm is that specified by Hans (2010b):

$$p(y|\beta, \sigma^2, \tau) = \mathrm{N}(y|X\beta, \sigma^2 I_n) \tag{3}$$

$$p(\beta_j|\tau, \sigma^2, \rho) = (1-\rho)\delta_0\beta_j + \rho\left(\frac{\tau}{2\sigma}\right) \times \tag{4}$$

$$\exp\left(\frac{-\tau\left\|\beta\right\|_1}{\sigma}\right) \tag{5}$$

$$\sigma^2 \sim \text{Inverse-Gamma}(a, b) \tag{6}$$

$$\tau \sim \text{Gamma}(r, s) \tag{7}$$

$$\rho \sim \text{Beta}(g, h) \tag{8}$$

The expression in equation (3) represents the density function of a multivariate normal random variable with mean $X\beta$ and covariance matrix $\sigma^2 I_n$, evaluated at y. The prior expressed in equation (5) is the expansion on the Park and Casella (2008) double exponential prior developed by Hans (2010b) to accommodate for uncertainty regarding the value of the regression coefficients and the model sparsity. Finally, equations (6) to (8) represent hyper priors for the residual variance σ^2, the penalty parameter τ, and the sparsity parameter ρ. The blasso imputation algorithm used here is a standard MI MCMC sampler that replaces equation (1) with the full conditional posterior distributions derived by Hans (2010b), based of the prior specifications in equations (6) to (8), and uses posterior parameters draws to sample plausible values from the predictive distributions of the missing data for equation (2).

The R code to perform blasso imputation is based on the Bayesian Lasso R Package *blasso* (Hans, 2010a) and can be found on the author's GitHub page. `https://github.com/EdoardoCostantini/imputeHD-comp`. For a detailed description of the algorithm for Bayesian Lasso Multiple Imputation in a univariate missing data context we recommend reading Zhao and Long (2016).

Direct Use of Regularized Regression (DURR). As proposed by Zhao and Long (2016) and Deng et al. (2016), Frequentist Regularized Regression can be directly used in a MICE algorithm to perform multiple imputation of high dimensional data. At iteration m, for a target variable $\boldsymbol{z}_j$, the DURR algorithm uses as building blocks of the

MICE framework the following two steps:

- Generate a bootstrap sample $\boldsymbol{Z}^{*(m)}$ by sampling with replacement from $\boldsymbol{Z}$, and train a regularized linear regression model (such as Lasso regression) with $\boldsymbol{z}_{j,obs}^{*(m)}$ as outcome and $\boldsymbol{Z}_{-j,obs}^{*(m)}$ as predictors. This produces a set of parameter estimates (regression coefficients and error variance) $\hat{\boldsymbol{\theta}}_j^{(m)}$ that can be considered as a sample from equation (1).

- Predict $\boldsymbol{z}_{j,mis}$, based on $\boldsymbol{Z}_{-j,mis}$ and $\hat{\boldsymbol{\theta}}_j^{(m)}$, to obtain draws from the posterior predictive distribution of the missing data equation (2).

Indirect Use of Regularized Regression (IURR). While DURR performs simultaneously model trimming and parameter estimation in equation (1), another approach is to use regularized regression exclusively for model trimming, and to follow it with a standard multiple imputation procedure (Deng et al., 2016; Zhao & Long, 2016). At iteration m, the IURR algorithm performs the following steps for each target variable:

- Fit a multiple linear regression model using a regularized regression method with $\boldsymbol{z}_{j,obs}$ as dependent variable and $\boldsymbol{Z}_{-j,obs}^{(m)}$ as predictors (compared to DURR, the original data are used, not a bootstrap sample). In this model, the regression coefficients that are *not* shrunk to 0 identify the active set of variables that will be used as predictors in the actual imputation model.

- Obtain Maximum Likelihood Estimates of the regression parameters and error variance in the linear regression of $\boldsymbol{z}_{j,obs}$ on the active set of predictors in $\boldsymbol{Z}_{-j,obs}^{(m)}$ and draw a new value of these coefficients by sampling from a multivariate normal distribution centered around these MLEs

$$(\hat{\boldsymbol{\theta}}_j^{(m)}, \hat{\sigma}_j^{(m)}) \sim N(\hat{\boldsymbol{\theta}}_{MLE}^{(m)}, \hat{\boldsymbol{\Sigma}}_{MLE}^{(m)}) \tag{9}$$

  so that equation (9) corresponds to equation (1) in the general MICE framework.

- Impute $\boldsymbol{z}_{j,mis}$ by sampling from the posterior predictive distribution based on $\boldsymbol{Z}_{j,mis}^{(m)}$ and the parameters posterior draws $(\hat{\boldsymbol{\theta}}_j^{(m)}, \hat{\sigma}_j^{(m)})$.

MICE with PCA (MI-PCA). By extracting Principal Components from the auxiliary variables, it is possible to summarise the information contained in this set with just a few components, and then use them as predictors in a standard MICE algorithm in a low dimensional setting. The Multiple Imputation with Principal Component Analysis (MI-PCA) imputation procedure can be summarized as follows:

- Extract the first principal components that cumulative explain at most 50% of the variance in the auxiliary variables $\boldsymbol{A}$, and collect them in a new data matrix $\boldsymbol{A}'$;
- Create a new data matrix $\boldsymbol{Z}'$ by replacing the subset of auxiliary variables $\boldsymbol{A}$ with $\boldsymbol{A}'$
- Use the standard MICE algorithm with the Bayesian imputation under the normal linear model (van Buuren, 2012, p. 68, algorithm 3.1) as elementary imputation method to obtain multiply imputed datasets from the low dimensional $\boldsymbol{Z}'$.

Note that if missing values are present in the set of auxiliary variables, one can fill them in with a stochastic single imputation (SI) algorithm of choice. MI is preferred to SI because it accounts for the uncertainty regarding the missing values when producing standard errors. As the extraction of PCs does not require the estimation of standard errors, SI suffices. This method is inspired by Howard et al. (2015) and the *PcAux* R-package (Lang, Little, & PcAux Development Team, 2018) that implements and developed its ideas.

MICE with decision trees (MI-CART and MI-RANF). The MI-CART imputation method (Burgette & Reiter, 2010) is a MICE algorithm that uses classification and regression trees (CART) to define the conditional distributions used in the MI Gibbs sampler. Given an outcome variable y and a set of predictors X, CART is a nonparametric recursive partitioning technique that models the relationship between y and X by sequentially splitting observations in subsets of units with relatively homogeneous y values. At every splitting stage, a CART algorithm searches through all predictor variables in X to find the best binary partitioning rule to predict y/minimize a homogeneity criterion. The collection of binary splits can be visually represented by a

decision tree structure where each terminal node (or *leaf*) represents the conditional distribution of y for units that satisfy the splitting rules.

In MI-CART, at the m-th iteration for a target variable z_j, a CART model is trained to predict $z_{j,obs}$ based on $\boldsymbol{Z}^{(m)}_{-j,obs}$. Every observation with a missing value on z_j belongs to a terminal node of this CART model, depending on their values of $\boldsymbol{Z}^{(m)}_{-j,mis}$. Sampling from the $z_{j,obs}$ in a terminal node corresponds to sampling from the missing data posterior predictive distribution. The implementation of MI-CART used in this paper corresponds to the one presented by Doove et al. (2014) (p. 95, algorithm 1) and the *impute.mice.cart()* R function from the *mice* package.

In MI-RANF, at the m-th iteration for a target variable z_j, k bootstrap samples are drawn from the complete dataset and k single trees are fitted. In each sub-sample, only a small random group of input variables is used to find the best split at each node. All trees are used to compose the pool of candidates from which imputations are drawn. Bootstrapping and random input selection introduce the model and imputation uncertainty in the imputation procedure, as required by a proper MI procedure. For greater details on the algorithms, the reader may consult Doove et al. (2014) (algorithm A.1, p. 103). The programming of the algorithm was heavily inspired by the *impute.mice.rf()* function in the R package *mice*.

MICE optimal model (MI-OP). When dealing with a large set of possible predictors for the imputation models, a common recommendation in the MI literature is to decide which predictors to include by following three criteria (van Buuren, 2012, p. 168):

1. include all the variables that are part of the analysis models;
2. include all the variables that are related to the non-response;
3. include all the variables are correlated with the variables target of imputation.

In practice, researchers can never be sure that the second requirement is entirely met, as there is no way to know exactly which variables are responsible for missingness. However, if we knew which predictors were essential for the imputation models, we could

use this information to specify optimal imputation models. With simulated data, we have perfect knowledge over which variables are involved in the missing data mechanisms. MI-OP is an ideal specification of the MICE algorithm that uses as elementary imputation strategy a low dimensional univariate Bayesian imputation under the normal linear model and uses this knowledge to include only the relevant predictors in the imputation models.

Single data strategies

missForest. High dimensional imputation is often addressed with single imputation techniques. Most research on high-dimensional data imputation has focused on applications for DNA genetics data where the goal is to allow the use of large datasets for high-dimensional predictive algorithms, rather than inferential analysis. For this reason, a variety of single imputation machine learning algorithms have been proposed and compared (de Andrade Silva & Hruschka, 2009; Stekhoven & Bühlmann, 2011).

In this study, we consider the missForest imputation method proposed by Stekhoven and Bühlmann (2011), which is a popular non-parametric imputation approach (which does not suffer from the problem of unidentified imputation models) that can accommodate for mixed data type of the missing variables, and has been robustly implemented in a popular R-package (Stekhoven, 2013). The approach consists of an iterative imputation that first trains a random forest on observed values, and then uses it to impute the missing values by averaging the predictions from its different trees.

This is a single imputation method and we do not expect it will perform well for inferential tasks, at least compared to the other high dimensional MI methods discussed here.

Complete Case Analysis. Most data analysis software either ignore the presence of missing values or default to list wise deletion: only complete cases are used for the analysis (pandas development team, 2020; R Core Team, 2020). As a default behaviour of most analysis tools, Complete Cases Analysis remains a popular missing data treatments in the social sciences, despite its known flaws (Rubin, 1987, p. 8; van

Buuren, 2012, p. 9, Baraldi and Enders, 2010). Therefore, this method was included as a reference point.

Gold Standard. Finally, the substantive models were fitted to the fully observed data. Results obtained in this fashion are referred to here and in the results tables as the Gold Standard method. They represent the counterfactual analysis that would have been performed if there had been no missing data.

Experiment 1: Simulated Data from Multivariate Normal Distribution

In the first simulation experiment, we focused on an ideal setting where data come from a known multivariate normal distribution and imputation is required to estimate the mean, variance and, covariances of six items with missing values. We investigated the relative performance of the methods described in Section across a set of conditions defined by two experimental factors: the number of columns in the dataset p, taking values 50 or 500; and the proportion of *per* variable missing cases pm, taking values 0.1 or 0.3. Table 1 summarizes the four crossed conditions. Data with sample size $n = 200$ were independently generated $S = 1,000$ times for each condition. For each s-th replicate, missing values were imposed and then all the missing data treatment methods described above were used to obtain estimates for the parameters of a substantive analysis model of interest.

Simulation Study Procedure

Data Generation. At every replication, a data matrix $\boldsymbol{Z}_{n\times p}$ was generated according to a multivariate normal model centered around a mean of 0 with a covariance matrix $\boldsymbol{\Sigma}_0$, with diagonal elements (variances) equal to 1. The off-diagonal elements of $\boldsymbol{\Sigma}_0$ were used to define three blocks of variables: the first five variables were highly correlated among themselves ($\rho = .6$); variables 6 to 10 were weakly correlated with variables in block 1 and among themselves ($\rho = .3$), and all the remaining $p - 10$ variables were uncorrelated. Items were rescaled to have mean of 5.

Missing Data Imposition. Missing values were imposed on six items in $\boldsymbol{Z}$: three variables in the block of highly correlated variables (z_j with $j = 1, 2, 3$), and three

in the block of lowly correlated variables (z_j with $j = 6, 7, 8$). Item non-response was imposed by sampling from a Bernoulli distribution with individual missing probabilities defined by

$$p_{miss} = p(z_{i,j} = miss|\tilde{Z}) = \frac{exp(\gamma_0 + \tilde{Z}_i\boldsymbol{\gamma})}{1 + exp(\gamma_0 + \tilde{Z}_i\boldsymbol{\gamma})} \tag{10}$$

where $z_{i,j}$ is the i-th subject's response on the j-th variable target of missing data imposition, $\tilde{Z}_i$ is a vector of responses for the i-th individual to the set of predictors involved in the missing data mechanism, γ_0 is an intercept parameter, and $\boldsymbol{\gamma}$ is a vector of slope parameters for the linear term. $\tilde{Z}$ was specified to include two fully observed variables from the highly correlated set, and two from the lowly correlated set (z_r with $r = 4, 5, 9, 10$). The probability of observing a response on a target variable did not depend on the variable itself, to avoid imputation under MNAR. Furthermore, when all the features in the data are provided to the MI procedures, the predictors in $\tilde{Z}$ are allowed to be part of the imputation models and the MAR assumption can be met. All slopes in $\boldsymbol{\gamma}$ were fixed to 1, while the value of γ_0 was chosen with an optimization algorithm that minimized the difference between the actual and desired proportion of missing values.

Imputation. Missing values were treated with all the methods described in Section 2. Convergence of the imputation models was assessed in a preprocessing step by observing trace plots. The imputation algorithms were considered to have converged after 50 iterations, after which 10 imputed data sets were store and used for the subsequent standard complete-data analysis and pooling. The only exception was blasso, which required approximately 2000 iterations for convergence.

The ridge penalty used in the bridge algorithm was fixed across iterations. The value used in the simulation was determined by means of cross-validation in a pre-processing phase. The ridge penalty values $10^{-1}, 10^{-2}, ..., 10^{-8}$ were used to impute data with bridge and we selected the value that resulted in the smallest average Fraction of Missing Information (FMI) across the analysis model parameters.

Both IURR and DURR could have been specified with a variety of penalty parameters. For example, one could use any of the following: ridge penalty (Hoerl & Kennard, 1970), lasso penalty (Tibshirani, 1996), elastic net penalty (Zou & Hastie,

2005), adaptive lasso (Zou, 2006). In this study we specified the regularization as a lasso penalty as it is computationally efficient, and it performed well for imputation in Zhao and Long (2016) and Deng et al. (2016). A 10-fold cross-validation procedure was used at every iteration of DURR and IURR to choose the penalty parameter.

For blasso, in order to maintain consistency with previous research, the hyper-parameters in equations (6), (7), and (8) were specified as in Zhao and Long (2016): $(a, b) = (0.1, 0.1)$, $(r, s) = (0.01, 0.01)$, and $(g, h) = (1, 1)$. In the MI-PCA algorithm, enough components were extracted to explain 50% of the total variance in the data. To impute data with the single imputation random forest approach we used the function *missForest* in the homonymous R package. This function implements algorithm 1 proposed by Stekhoven and Bühlmann (2011). The stopping criterion for the missForest algorithm was usually met within the first 10 iterations, but to make a conservative choice we fixed the maximum number of iterations to 20. Stekhoven and Bühlmann (2011) showed that increasing the number of trees grown in each forest has stagnating effects on the imputation error while linearly increasing the computation time. In their paper, the authors recommend growing 100 trees per forest, which offers a good compromise between imputation precision and computation time. Therefore, we used this value in our study.

Analysis. The substantive model of interest in Experiment 1 was a saturated model that estimated means, variances, and covariances of the six variables with missing values. This resulted in estimating six means, six variances, and 15 covariances.

Comparison Criteria

We compared methods in terms of bias an confidence interval coverage.

Bias. For a given parameter of interest θ (e.g., mean of item 1, variance of item 2), we used the Percent Relative Bias (PRB) to quantify the estimation bias introduced by the imputation procedures:

$$PRB = \frac{\bar{\hat{\theta}} - \dot{\theta}}{\dot{\theta}} \times 100 \tag{11}$$

where $\dot{\theta}$ is the *true* value of the focal parameter defined as $\sum_{s=1}^{S} \hat{\theta}_s^{GS}/S$, with $\hat{\theta}_s^{GS}$ being the Gold Standard parameter estimate for the s-th repetition. The averaged focal

parameter estimate under a given imputation method is computed as $\bar{\hat{\theta}} = \sum_{s=1}^{S} \hat{\theta}_s / S$, with $\hat{\theta}_s$ being the estimate obtained after using a given imputation approach in the s-th repetition. Following Muthén, Kaplan, and Hollis (1987), |PRB| > 10% was considered indicative of problematic estimation bias.

Confidence Intervals Coverage. To assess the correctness of hypothesis testing, the Confidence Interval Coverage (CIC) of the reference value was defined as

$$CIC = \frac{\sum_{s=1}^{S} I(\dot{\theta} \in \widehat{CI}_s)}{S} \tag{12}$$

where $\widehat{CI}_s$ is the confidence interval of the parameter estimate $\hat{\theta}_s$ in a given repetition, and $I(.)$ is the indicator function that returns 1 if the argument is true and 0 otherwise.

CICs below 0.9 are usually considered problematic for 95% confidence intervals (Van Buuren, 2018, p. 52) as they imply inflated Type I error rates. A high coverage (e.g., 0.99) may indicate confidence intervals that are too wide, implying inflated Type II error rates. Therefore, Confidence Intervals were considered to show severe under-coverage (over-coverage) if they were below 0.9 (above 0.99).

Following Burton, Altman, Royston, and Holder (2006), in simulation studies, a CIC can be considered as significantly different from the nominal coverage rate if it falls outside two Standard Errors of the nominal coverage probability ($SE(p)$) from the nominal coverage rate. The standard error of nominal coverage probability is defined as $SE(p) = \sqrt{p(1-p)/S}$, with p indicating the chosen nominal coverage probability. Therefore, for $S = 1000$, 95% CI coverages ($p = 0.95$) outside the range (0.94, 0.96) were considered as significantly different from the nominal coverage rate.

Results

Both PRB and CIC were computed for all the 27 parameters in the analysis model (6 means, 6 item variances, and 15 covariances). To summarize the results, we focus on the typical and extreme values of these measures. In Figures 1 and 2, we report the average, minimum, and maximum (absolute) PRB and CIC achieved by the missing data treatment methods for each parameter parameter type. In the supplementary material, we included figures reporting the PRB and CIC for every parameter estimate.

Means. Focusing first on the item means (top rows), the largest PRB is within 10 percentage points from 0 for all imputation methods. However, looking at relative performances, IURR and MI-PCA resulted in smaller bias than all other methods, except MI-OP. Furthermore, the tree-based MI methods, missForest, and CC lead to CICs significantly different from nominal coverage rates, resulting in extreme under-coverage of the true values in all conditions. In the conditions with high proportion of missing values (columns 3 and 4), all methods showed significant deviations from nominal of coverage, with all CICs outside of the interval $(0.94, 0.96)$. The only exceptions were MI-OP, and MI-PCA which showed non-significant deviations from nominal coverage for almost all estimates, with both the lowest and highest CIC falling within (0.94, 0.96) in all conditions.

Variances. Moving to the item variances (central rows), IURR, blasso, and the MI tree-based methods resulted in the lowest biases across all conditions, even in the high-dim-high-pm condition. These low biases were mostly paired with low deviations from nominal coverage, except for the high-dim-high-pm condition where IURR and the tree-based methods resulted in significant under-coverage of the true item variances (highest $CIC < 0.94$). Apart from MI-OP, blasso was the method with best coverage in this final condition.

DURR showed poor performance with regard to the item variances: in all conditions but the first, it led to large (negative) bias accompanied by significant CI under-coverage. Bridge was the only MI method showing larger bias than DURR in all the high-dimensional conditions (column 2 and 4), with even the minimum $|PRB|$ exceeding the 20% threshold. MI-PCA also showed poor performance with a noticeable positive bias in all conditions that became extreme in the high-dim-high-pm condition (column 4), where all PRBs exceeded 20%. This poor performance was reflected in extreme confidence interval under-coverage of the true item variances in the final experimental condition. Finally, missForest and complete case analysis led to substantial negative bias and CI under-coverage for all item variances, even in condition 1.

Covariances. IURR performed noticeably better than most other methods, with negligible negative bias and acceptable coverage for most covariances, but it struggled with a large negative covariance bias and extreme covariance under-coverage in the high-dim-high-pm condition (average $|PRB| > 10\%$). MI-PCA showed negligible negative bias for all the covariance estimates (with the maximum $|PRB| < 10\%$), and performed as well as MI-OP in all but the high-dim-high-pm condition. Furthermore, MI-PCA showed virtually no deviation from nominal coverage, with a CIC pattern similar to that of MI-OP, in all but the last condition. In the high-dim-high-pm condition, MI-PCA led to mild significant *over*-coverage of the items covariances: the average CIC was greater than 0.96, but smaller than 0.99.

All other methods, including DURR, showed absolute PRBs larger than the 10% threshold in all but the first condition, with persistently significant CI under-coverage of the true values. Bridge displayed acceptably low bias and coverage in the low dimensional conditions (columns 1 and 3), but extremely large biases and low CI coverage in all the high dimensional conditions (columns 2 and 4). MissForest and CC showed extreme bias and under-coverage for all the covariances (minimum $|PRB| > 10\%$), even in condition 1.

Experiment 2: Simulated Data with Latent Structure

In the second simulation experiment, we focused on data generated from a Factor Analysis model. The data social scientists analyse are often a collection of items measuring different latent constructs, a characteristic that is likely to impact imputation performances. For Experiment 2, we considered three experimental factors. First, the dimensionality of the data was controlled by the number of latent variables l (10, 100). 5 items were generated as measurements of each latent variable, resulting in either 50 or 500 items. Second, factor loadings were defined as a 2-level random experimental factor (high, low). High factor loadings were drawn from a uniform distribution between (0.9, 0.97), while low factor loadings were drawn from a uniform distribution between (0.5, 0.6). Third, the proportion of missing values was defined as a fixed experimental factor with two levels: 0.1 or 0.3. Table 2 summarizes the eight resulting conditions.

Data with sample size $n = 200$ were independently generated 1,000 times for each condition. On each replicate, missing values were imposed and then each missing data treatment described in Section was used to obtain estimates for the parameters of a substantive analysis model of interest. With a sample size fixed at 200, conditions with $l = 10$ resulted in a low-dimensional settings, while conditions with $l = 100$ resulted in a high-dimensional settings.

Simulation Study Procedure

For each replication, an observed data matrix $\boldsymbol{Z}_{n\times p}$ was created based on a Confirmatory Factor Analysis model. Each of l latent variables was assumed to be measured by 5 items, for a total of $p = 5 \times l$ columns. Values on the items for the i-th observation were obtained with the following measurement model:

$$\boldsymbol{z}_i = \boldsymbol{\Lambda}\boldsymbol{\xi}_{i.} + \boldsymbol{\delta}_{i.} \tag{13}$$

where $\boldsymbol{z}_i$ is a vector of $5 * l$ items scores for observations $i = 1, ..., n$; $\boldsymbol{\Lambda}$ is the $(5 * l) \times l$ matrix of factor loadings; $\boldsymbol{\xi}_{i.}$ is a vector of l latent scores for observation i; and $\boldsymbol{\delta}_{i.}$ is a vector of $5 * l$ uncorrelated measurement errors sampled from a multivariate normal distribution centered around a mean vector of 0s and with a diagonal covariance matrix $\boldsymbol{\Theta}$. All items are centered around a mean of 5. For notation and model specification the interested reader may refer to Bollen (1989).

The latent scores in $\boldsymbol{\xi}_{i.}$ are sampled from a multivariate normal distribution centered around 0, and with a covariance matrix $\boldsymbol{\Psi}$, with diagonal elements equal to 1 and off-diagonal elements equal to correlation between latent factors. In particular, the first 4 latent variables are highly correlated ($\rho = .6$), the second block of 4 latent variables are weakly correlated ($\rho = .3$), while the remaining $l - 8$ latent variables are uncorrelated.

The matrix $\boldsymbol{\Lambda}$ defines a simple latent structure where each item loads on only 1 factor (5 items for each latent variable). Both the item and latent factor variances are set to 1 so that the measurement error variance is defined as $var(\delta) = 1 - \lambda^2$. This specification allows factor loadings λ_{ij}, with $i = 1, ..., n$ and $j = 1, ..., l$, to be defined as standardized values between 0 and 1. If all values in $\boldsymbol{\Lambda}$ are 0s, there is no latent structure

and items are simply drawn from a multivariate normal distribution centered around the item means with covariance matrix $\mathbf{\Theta}$. If all values in $\mathbf{\Lambda}$ are 1s, there is a *perfect* latent structure, meaning that items exactly measure the latent constructs. The exact values for the latent factors are drawn for each repetition from a uniform distribution between lower b_l and upper bound b_u, that are condition-specific (see below).

Item non-response was imposed on 10 items in $\boldsymbol{Z}$ using Equation 10 to define the probability of a value being missing. The items targeted by the missing data imposition measured the first two highly correlated latent variables ($l = 1, 2$). The predictors included in $\tilde{Z}$ were the latent scores for the other two highly correlated latent variables ($l = 3, 4$).

Missing values were treated according to all the methods described in Section . The imputation methods were parametrized as in Experiments 1. 50 iterations were sufficient for convergence of all MI methods except blasso, which required approximately 2000 iterations for convergence.

The substantive model of interest in Experiment 2 was a saturated model that estimates means, variances, and covariances of the raw items with missing values. Furthermore, the true Factor Analysis model for the same items was estimated to see how the factor loadings were recovered after imputation.

Results

We used the same comparison criteria described for Experiment 1 to assess the performances of the methods in Experiment 2. Figures 3 and 4 report the average, minimum, and maximum PRB and CIC obtained with each missing data treatment method for each parameter type (means, variances, and covariances) in the conditions with high factor loadings. Figures 5 and 6 report the same results for the conditions with low factor loadings. In the supplementary material you may find the figures reporting the PRBs and CICs for every parameter.

Means. All the imputation methods resulted in unbiased estimation of the item means with PRBs close to 0 for all items. Larger proportions of missing cases (columns 3

and 4 in the figures) resulted in a slight increase in PRB values for all methods except IURR, bridge, and MI-PCA. However, only Complete Case analysis led to unacceptable bias of the means. DURR, IURR and MI-PCA resulted in little to no deviations from nominal coverage in all conditions, while blasso, MI-CART, MI-RF, bridge, and missForest led to significant under-coverage of the true means when the proportion of missing cases was high (columns 3 and 4 in the figures).

Variances. All MI methods, except bridge, resulted in acceptable estimation bias for the item variances in all conditions with large factor loadings. The least biased estimates were obtained by MI-OP, IURR and MI-PCA. Keeping the data dimensionality constant, CIC decreased as the proportion of missing cases increased. For high-pm conditions (columns 3 and 4), only IURR and MI-PCA maintained CICs mostly within the range .94-.96, while blasso and the MI tree-based methods led to mild to extreme under-coverage (all CICs $< 90\%$). Single data approaches, missForest and CC, showed again extreme (negative) bias and large significant CI under-coverage in almost all conditions. The large positive bias (and low CIC) for the item variances that afflicted MI-PCA in the multivariate-normal set up (figures 1 and 2) was not present in figures 3 and 4. However, that pattern reappeared in the conditions with low factor loadings (see figures 5 and 6).

Covariances. For all the conditions with high factor loadings, IURR and DURR showed acceptable covariance biases ($|\text{PRB}| < 10\%$). However, they led to large negative bias in all the conditions with low factor loadings (see Figures 5 and 6). As in Experiment 1, MI-PCA resulted in the lowest bias and deviation from nominal coverage of the true item covariances. All other methods led to large negative biases and mild-to-extreme significant covariance under-coverage in all conditions.

Factor Loadings. Figure 7 shows the average, minimum, and maximum PRB values for all the factor loadings estimated by the Confirmatory Factor Analysis described above. Most MI-Methods provided acceptably low bias for these estimates in all conditions except the high-dim-high-pm ones (column 4). MI-OP, IURR, and MI-PCA outperformed all other methods and produced virtually unbiased estimates of the factor

loadings in all conditions. Furthermore, MI-PCA outperformed IURR when factor loadings were low (panel b), maintaining inconsequential biases even when data were high-dimensional and the proportion of missing values was high.

Experiment 3: EVS Resampling Study

In the third experiment, we performed a resampling study based on the EVS data to assess the how the result obtained for Experiments 1 and 2 carry over to real data applications. EVS is a large-scale, cross-national survey on human values administered in around 50 countries across Europe. It covers a wide range of human values regarding family, work, environment, perceptions of life, politics and society, religion, morality, and national identity. It is a high-quality survey widely used for comparative studies between European countries. Furthermore, it is accessible free of charge and it represents the type of data social scientist regularly analyse. Variables in the EVS data are discrete numerical and categorical items following a variety of distributions.

In Experiment 3, we considered the original EVS data as a population data for a resampling study. We investigated the performances of the methods by resampling $S = 1000$ datasets of n units from this population. For each replicate, we imposed missing values, treated them with the same methods used in experiments 1 and 2, and pooled the analysis model parameter estimates. This procedure was repeated for a low-dimensional and a high-dimensional condition. As the number of predictors in the data was fixed ($p = 243$), the dimensionality of the data was controlled by defining different sizes for the sample taken from the EVS population data ($n = (1000, 300)$).

Resampling Study Procedure

Data preparation and generation. We used the third pre-release of the 2017 wave of EVS data (EVS, 2020a) to define a population dataset with no missing values. The original dataset contained 55,000 observations from 34 countries. We selected only the four founding countries of the European Union included in the dataset (France, Germany, Italy, and the Netherlands) and excluded all columns of the data that were

either duplicated information (recoded versions of other variables), or meta data (e.g. time of interview, mode of data collection).

We run a single imputation predictive mean matching (PMM) algorithm to fill the originally missing values and obtain a pseudo fully-observed dataset. This imputation step was completed using the *mice*() imputation function in the mice R package. PMM was chosen for the task as it is a flexible imputation method that maintains the distributional characteristics of the original data. Predictors for the imputation models were selected based on the variable selection procedure described in Van Buuren, Boshuizen, and Knook (1999, pp. 687–688) by using the *quickpred()* R function and setting the minimum correlation threshold to 0.3. The number of iterations was set to 200. This imputation procedure is used to obtain a pseudo-population dataset, and therefore it does not require multiple imputation itself.

At the end of this data cleaning process, we obtained a fully-observed dataset ($\boldsymbol{Z}$) of 8,045 observations (n), across 4 countries, and 243 variables (p). For every s replicate in the resampling study, a bootstrap sample $\boldsymbol{Z}^*$ was generated by sampling with replacement n observations from $\boldsymbol{Z}$.

Analysis models. To define plausible analysis models, we searched for models that have been used in published articles testing social scientific theories on the EVS data. The search was performed by screening the repository of publications using EVS data available on the EVS website (EVS, 2020b).

As a result, we defined two linear regression models, models 1 and 2, of the same form:

$$y = \beta_0 + \beta_1 x + \boldsymbol{\beta C} \tag{14}$$

where a dependent variable y is regressed on a variable of interest x and a set of control variables $\boldsymbol{C}$. In this scenario, β_1 is a focal parameter that a researcher wants to use to test some hypothesis.

The first version of linear model (14), Model 1, was inspired by Köneke (2014): $y^{(1)}$, its dependent variable, was a 10-point EVS item measuring euthanasia acceptance ('Can [euthanasia] always be justified, never be justified, or something in between?'); the

predictor of interest $x^{(1)}$ was a 4-point item measuring the self-reported importance of religion in one's life; the matrix of covariates $\boldsymbol{C}^{(1)}$ included trust in the health care system, trust in the state, trust in the press, country, sex, age, education, and religious denomination. This model represents a plausible analysis a researcher would perform to test a hypothesis regarding the effect of religiosity on the acceptance of end-of-life treatments.

Model 2, the second version of the linear model in equation 14, was inspired by Immerzeel, Coffé, and Van der Lippe (2015). The dependent variable $y^{(2)}$ was an harmonized variable constructed by EVS to describe the respondents' tendency to vote left or right-wing parties, expressed on a 10-point left-to-right continuum. The predictor of interest $x^{(2)}$ was a scale measuring respondents' attitudes toward immigrants and immigration ('nativist attitudes scale'). The scale was obtained by taking the average of respondents' agreement, on a scale from 1 to 10, with three statements: 'immigrants take jobs away from natives', 'immigrants increase crime problems', and 'immigrants are a strain on welfare system'. The control variables used were: attitudes toward law and order, attitudes toward authoritarianism, interest in politics, level of political activity, country, sex, age, education, employment status, socio-economic status, importance of religion in life, religious denomination, and the size of town where interview was conducted. A researcher might fit this model and look at the estimate and standard error of $\beta_1^{(2)}$, the 'nativist attitude' regression coefficient, to test an hypothesis regarding the effect of xenophobia on voting tendencies.

Missing data imposition. Missing data were imposed on 6 variables according to the same strategy described in Subsection . The variables target of missing value imposition were the euthanasia acceptance item, and the left-to-right voting tendency, the two dependent variables in models 1 and 2; religiosity (the focal predictor and a control variable in models 1 and 2 respectively); and the three items making up the "nativist attitudes" scale (the focal predictor in the second model).

The response model form was the same as in Equation (10) and three variables were included in $\tilde{Z}$: age, education, and an item measuring trust in new people. Older

people tend to have higher item non-response rates than younger people, and lower educated people tend to have higher item non-response rates than higher educated people (De Leeuw, Hox, & Huisman, 2003; Guadagnoli & Cleary, 1992). We assumed that people with less trust in strangers have a higher item non-response tendency as they are likely to withhold more information from the interviewer (a stranger).

Imputation. Missing values were treated according to all the methods described in Section 2. The imputation methods were parametrized as in Experiments 1 and 2, and convergence checks were performed in the same way. The imputation models were considered to have converged after 60 iterations.

Results

When estimating multiple linear regressions, all partial regression coefficients are influenced by the imputation of the dependent variable and a handful predictors. Therefore, it is important to observe the estimation bias and CI coverage rates on all model parameters. Figure 8 reports the absolute values of the PRBs for the intercept and all the partial regression coefficients in Model 2, ordered by size, obtained under the different imputation methods. Figure 9 reports CIC results in the same way. Results for Model 1 are reported in the supplementary materials.

Focusing first on the focal parameter β_1, most of the MI methods resulted in negligible biases ($|PRB| < 10\%$) in both conditions. The two exceptions were bridge and MI-RF. The former was very competitive in the low dimensional condition but led to extreme bias and over-coverage in the high dimensional condition. The latter provided the largest focal PRB among the other MI methods, and it was consistently outperformed even by Complete Case analysis.

IURR, DURR and MI-PCA resulted in the lowest bias for the focal parameter. They also resulted in non-significant deviations from nominal coverage in both the low and high dimensional conditions. However, while IURR and DURR resulted in slightly smaller PRB than MI-PCA, the latter resulted in the smallest deviations from nominal coverage. Apart from bridge, MI-RF provided the worst CI (under) coverage for the focal

regression coefficient.

Looking at all the estimated regression coefficients and intercept, even making use of perfect information regarding the missing data mechanism and data structure in the imputation procedure (MI-OP) resulted in bias for some parameters. Around half of the estimates obtained with MI-OP had large bias ($|PRB| > 10\%$). The largest MI-OP bias was considerable: around 40%, in the low dimensional condition, and 20%, in the high-dimensional one. In both the high- and low-dimensional conditions, DURR, IURR, blasso, MI-CART, and missForest showed only slightly larger PRBs than MI-OP. MI-PCA and MI-RF showed similar trends but presented larger PRBs above the 10% threshold. For all of these methods, PRBs were smaller in the high-dimensional condition. Bridge demonstrated the same results described in the simulation studies. It was a competitive method in low dimensional scenarios, but it was inadequate to deal with high-dimensional data imputation (all but one PRB are larger than 100%).

DURR, IURR, and MI-CART maintained similar coverage patterns to MI-OP, with only a few significant CICs deviations from nominal coverage rates. MI-PCA, blasso, and MI-RF over-covered more than half of the parameters. All MI methods led to CIC closer to nominal rates in the high-dimensional condition.

As expected, imputation by missForest led to significant under-coverage of most regression coefficients, including the focal parameter. Despite showing poor performances in terms of bias, Complete Case analysis manifested good coverage of all true parameter values. However, this was a result of the smaller sample size used for estimating the analysis model, rather than a positive feature of the method. The smaller samples produced wider intervals which covered the true values even when the point-estimates were biased.

Imputation Time. Table 3 reports the average imputation time for the different methods. IURR and DURR were the most time-consuming methods with imputation times above the hour in our low-dimensional conditions. MI-PCA and blasso imputation had imputation times of a minute or less. In the high-dimensional condition, IURR and DURR were not as time-intensive due to the smaller sample size, but still required more

than ten times the time of MI-PCA and blasso imputation.

Discussion

The inclusion of State-of-the-art modern regression techniques within the MICE framework has the potential to simplify the use of MI for social scientist. We studied bias and coverage of parameter estimates after imputation with 7 high-dimensional data imputation methods. Although extensive simulation studies had already been carried out by the researchers proposing these methods, no comparison study had been developed to assess their relative performances. Our research fills this gap and provides initial insights into applying such methods in social scientific research. In this section, we discuss the overall performance of the methods and we give recommendations for social scientists facing high-dimensional data imputation problems.

Methods that do not work well. We found that bridge is inadequate to deal with high-dimensional data imputation problems. In both the simulation and resampling study the use of a fixed ridge penalty within the imputation algorithm manifested the same undesirable performance. The method worked well when many predictors were included in the imputation model, but the imputation task remained low dimensional. However, bridge led to extreme bias and unacceptable confidence interval coverage in all the high dimensional conditions.

MissForest, the high-dimensional data SI method, leads to low estimation bias. However, it results in severe confidence interval under-coverage of the true parameter values. Under-coverage coupled with unbiased estimates indicates that too little uncertainty is incorporated in the imputation procedure, which is to be expected from a single imputation approach. As a result, missForest should be avoided by a social scientist with the goal of drawing inferential conclusions from their data analysis.

Methods that work best. IURR and MI-PCA were the two strongest performers. IURR excelled with the smallest estimation bias for item means, variances and regression coefficients. The method also produced the small deviations from nominal coverage rates for these parameters. Furthermore, the negative covariance estimation bias

introduced by IURR in the high-dim-high-pm conditions only slightly exceeded the 10% threshold and the CI coverage was just around 0.9. Comparatively, most of the other MI methods resulted in covariance PRBs larger than 20%, and CICs well below 0.9.

IURR is easy to specify. Compared to regular low dimensional MI, IURR does not require the imputer to make choices regarding which variables are relevant for the imputation procedure, and the only additional decision required of the imputer is the number of folds for the cross-validation of lasso penalties. As a result, IURR is an extremely appealing method for large surveys imputation. However, IURR is a relatively computationally intensive. If the number of variables with missing values is large, IURR might result in prohibitive imputation time. In such a scenario, a researcher might prefer to address imputation with the MI-PCA method.

MI-PCA showed low bias and good coverage for both item means and covariances in experiments 1 and 2. Although it exhibited large bias of the item variances, the relationships between variables with missing values were always correctly estimated. It was the only method resulting in low bias and close-to-nominal CI coverage of the true covariance values, even in the high-dimensional conditions. Furthermore, it produced the lowest bias for the latent factor loadings. MI-PCA also resulted in low bias and CIC close to nominal rates for the focal regression coefficient in Experiment 3. Finally, when the CICs obtained with MI-PCA deviated significantly from nominal rates, they over-covered. This tendency is less worrisome than under-coverage as it leads to conservative, rather than liberal, inferential conclusions.

Compared to regular low dimensional MI, using MI-PCA requires to make decisions only on the number of principal components to extract. As a result, this method is excellent approach for data analysts interested in testing theories on large social scientific datasets with missing values.

Methods with mixed results. DURR produced low bias and good CI coverage for item means, variances and regression coefficients. However, compared to IURR, it suffered from greater performance deterioration when applied to high-dimensional data. As a result, DURR should not be preferred to IURR.

The tree-based MI methods, MI-CART and MI-RF, produced large covariance bias in experiments 1 and 2. Although, bias for means, variances, and regression coefficients was acceptable, it was usually larger than that obtained by all other MI methods. In terms of CI coverage, they showed significant large under-coverage of most parameters in the high-dim-high-pm conditions.

There was little difference in performances between the use of CART and Random Forests as building blocks of the imputation algorithm. When a difference was noticeable, it was in favor of the use of the simpler single CART, which is in line with what Doove et al. (2014) found. Although the non-parametric nature of these approaches elegantly avoids imputation model over-parametrization, these methods are outperformed by IURR and MI-PCA.

Blasso resulted in low item means and variances bias, even in the high-dimensional conditions. While the covariance bias was large in experiments 1 and 2, blasso performed well in the resampling study, where the overall biasing performance was similar to that of MI-OP. In terms of confidence interval coverage, blasso showed poor performances resulting in either CI under-coverage or CI over-coverage of true parameter values in almost all high-dimensional conditions, across the three different experimental set ups. Furthermore, blasso did not fair particularly well in the recovery of the latent structure in our second experiment. Its factor loading PRBs were the highest among the MI methods.

Theses mixed performances of blasso are also accompanied by a few obstacles to its application for social scientific research. Using Hans (2010b)'s Bayesian Lasso requires the specification of 6 hyper-parameters, which introduces more researcher degrees of freedom and demands a strong grasp of Bayesian statistics. Furthermore, the method has not currently been developed for multi-categorical data imputation, a common task in the social sciences. As a result, blasso is not recommended for imputation of large social scientific datasets.

Limitations and future directions

The present work was aimed at comparing current implementations of different existing methods. As a result, the scope of the simulation and resampling studies was limited by the current development state of the different methods. For example, both IURR, DURR, and MI-PCA allow imputation of any type of data: IURR and DURR have been developed for categorical data imputation (Deng et al., 2016), and MI-PCA can be performed with any standard imputation model for categorical data. However, blasso has not been formally developed for multi-categorical imputation target variables yet, which forced us to work with missing values on variables that are either continuous, or usually considered as such in practice. To maintain a fair comparison with blasso, they were implemented with the assumption that the imputed variables are continuous and normally distributed. However, IURR, DURR and MI-PCA could have performed differently in the resampling study had they been used in their ordered categorical data implementations.

Another limitation of this study is the assumption of a linear missing data mechanism. In real social scientific data the response mechanism might be non-linear, a condition that would require including interactions and polynomial terms in the imputation models. This factor was not part of the scope of this project. However, all of the high-dimensional imputation methods considered have great potential to account for more complex response mechanisms.

Finally, these results only apply to the specific implementations of the algorithms we used. Many of the methods discussed could have been implemented differently. Zhao and Long (2016) proposed versions of IURR and DURR using the elastic net penalty (Zou & Hastie, 2005) or the adaptive lasso (Zou, 2006), instead of the lasso penalty. Although no substantial performance differences between penalty specifications emerged from the joint work of Zhao and Long (2016) and Deng et al. (2016), the impact of different types of regularized regression was not investigated in the present study.

MI-PCA requires making a decision on the number of components to extract from the auxiliary variables. In this study, we decided to retain the first components that

explained 50% of the total variance in the auxiliary variables. However, this decision was arbitrary. We are currently working on assessing its effect on the imputation accuracy as part of a project to expand and improve the use of principal components within the FCS framework.

As for blasso, we have not investigated the sensibility of results to different hyper-parameters choices. Furthermore, alternative implementations of Bayesian Lasso could be used within a MICE framework. In particular, the well known Bayesian Lasso proposed by Park and Casella (2008) is a viable option.

The use of Random Forests within a MICE algorithm could have also been implemented differently. We decided to use Doove et al. (2014) version which is supported in the popular *mice* R package. However, A. D. Shah et al. (2014) independently developed another integration of Random Forests within the MICE algorithm, which was available in the now archived R package *CALIBERrfimpute* (A. Shah, 2018). We are not aware of any evidence or theoretical reason to expect differences between the two implementations, but we did not verify this empirically.

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condition	label	n	p	pm
1	low-dim-low-pm	200	50	.1
2	high-dim-low-pm	200	500	.1
3	low-dim-high-pm	200	50	.3
4	high-dim-high-pm	200	500	.3

Table 1

Summary of conditions for experiment 1.

condition	label	n	p	l	pm	λ range
1	low-dim-low-pm-high-λ	200	50	10	0.1	[.9, .97]
2	high-dim-low-pm-high-λ	200	500	100	0.1	[.9, .97]
3	low-dim-high-pm-high-λ	200	50	10	0.3	[.9, .97]
4	high-dim-high-pm-high-λ	200	500	100	0.3	[.9, .97]
5	low-dim-low-pm-low-λ	200	50	10	0.1	[.5, .6]
6	high-dim-low-pm-low-λ	200	500	100	0.1	[.5, .6]
7	low-dim-high-pm-low-λ	200	50	10	0.3	[.5, .6]
8	high-dim-high-pm-low-λ	200	500	100	0.3	[.5, .6]

Table 2

Summary of conditions for experiment 2.

condition	DURR	IURR	blasso	bridge	MI-PCA	MI-CART	MI-RF	MI-OP
1	73.20	75.90	1.40	8.10	0.60	4.00	11.30	2.20
2	6.10	9.70	0.50	3.20	0.40	1.40	4.70	1.90

Table 3

Average imputation time in minutes.

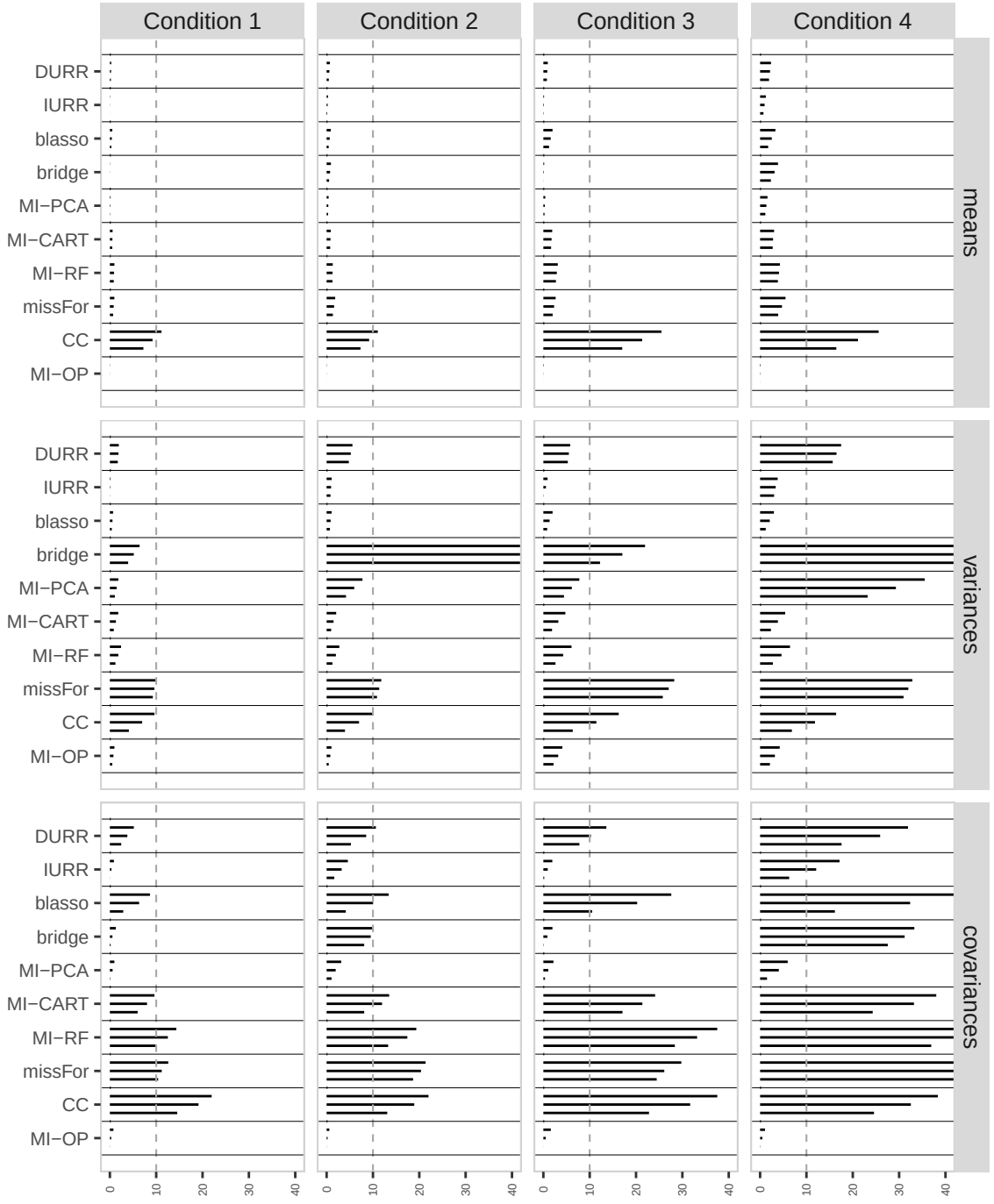

Figure 1. Percent Relative Bias (PRB) for item means, variances, and covariances. Conditions 1 to 4 correspond to the labels low-dim-low-pm, high-dim-low-pm, low-dim-high-pm, and high-dim-low-pm in Table 1.

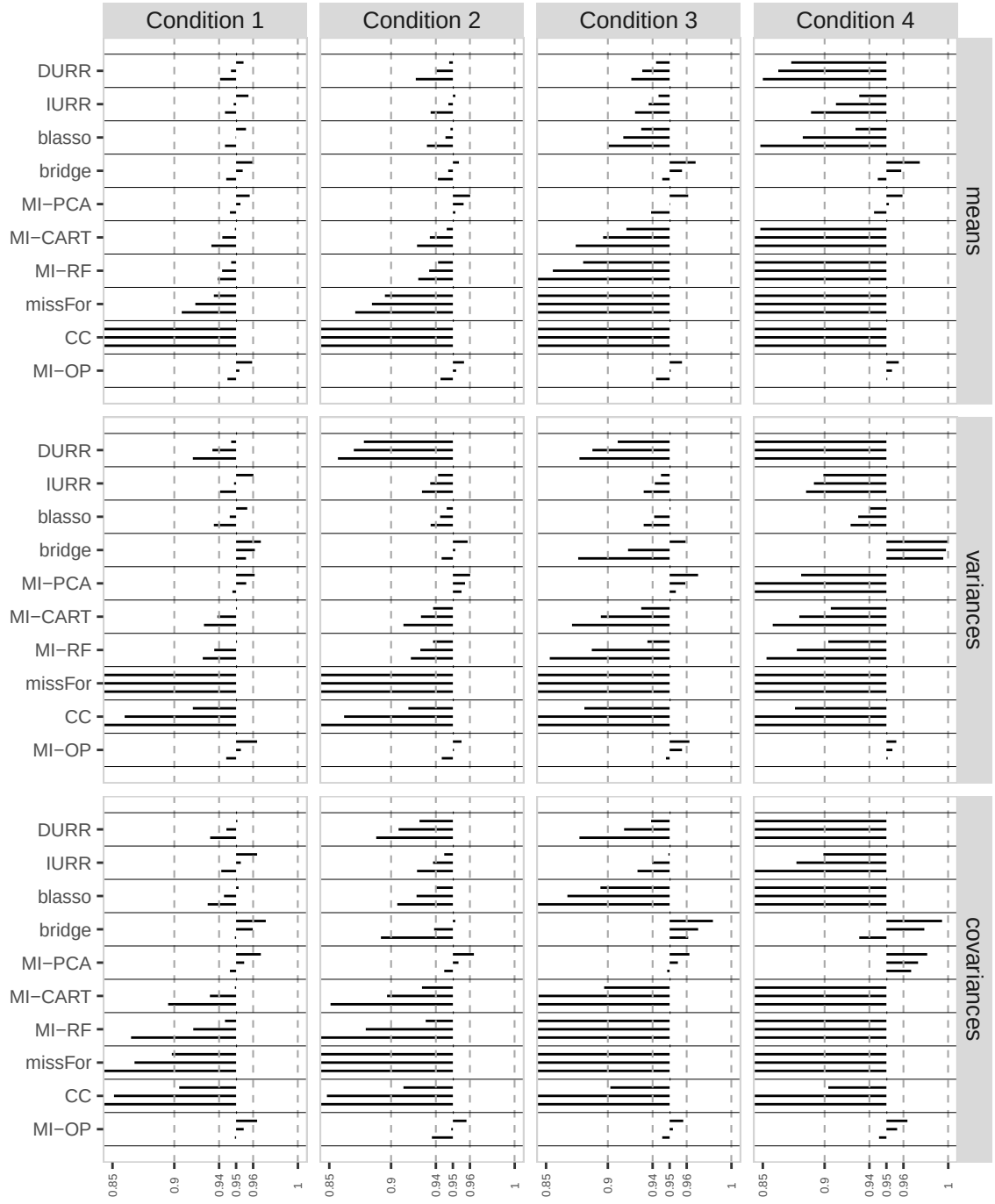

Figure 2. Confidence Interval Coverage (CIC) for item means, variances, and covariances. Conditions 1 to 4 correspond to the labels low-dim-low-pm, high-dim-low-pm, low-dim-high-pm, and high-dim-low-pm in Table 1.

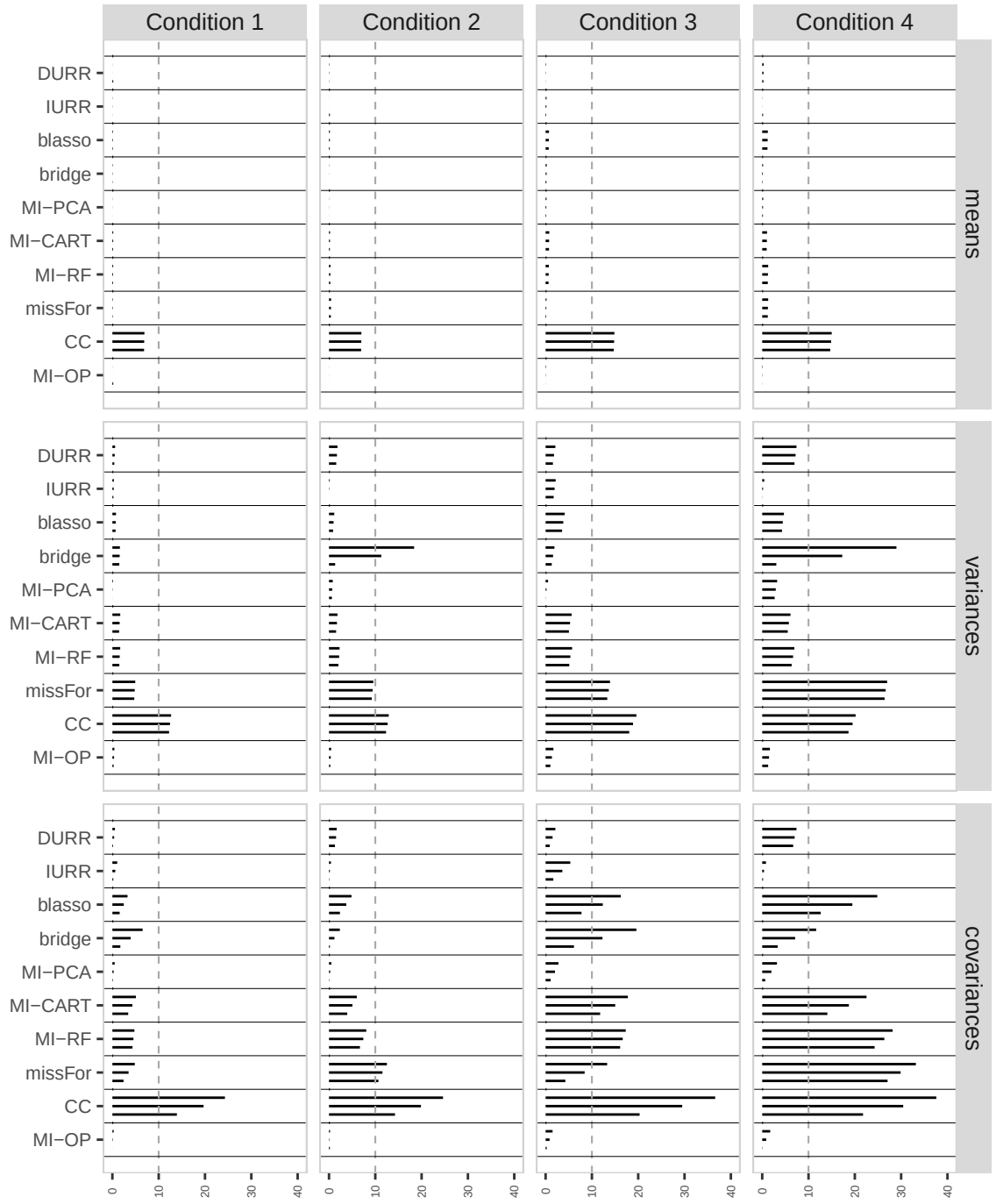

Figure 3. PRBs for the means, variances and covariances (PRB) for condition 1 to 4. Conditions 1 to 4 correspond to the labels low-dim-low-pm-high-λ, high-dim-low-pm-high-λ, low-dim-high-pm-high-λ, and high-dim-low-high-low-λ in Table 2.

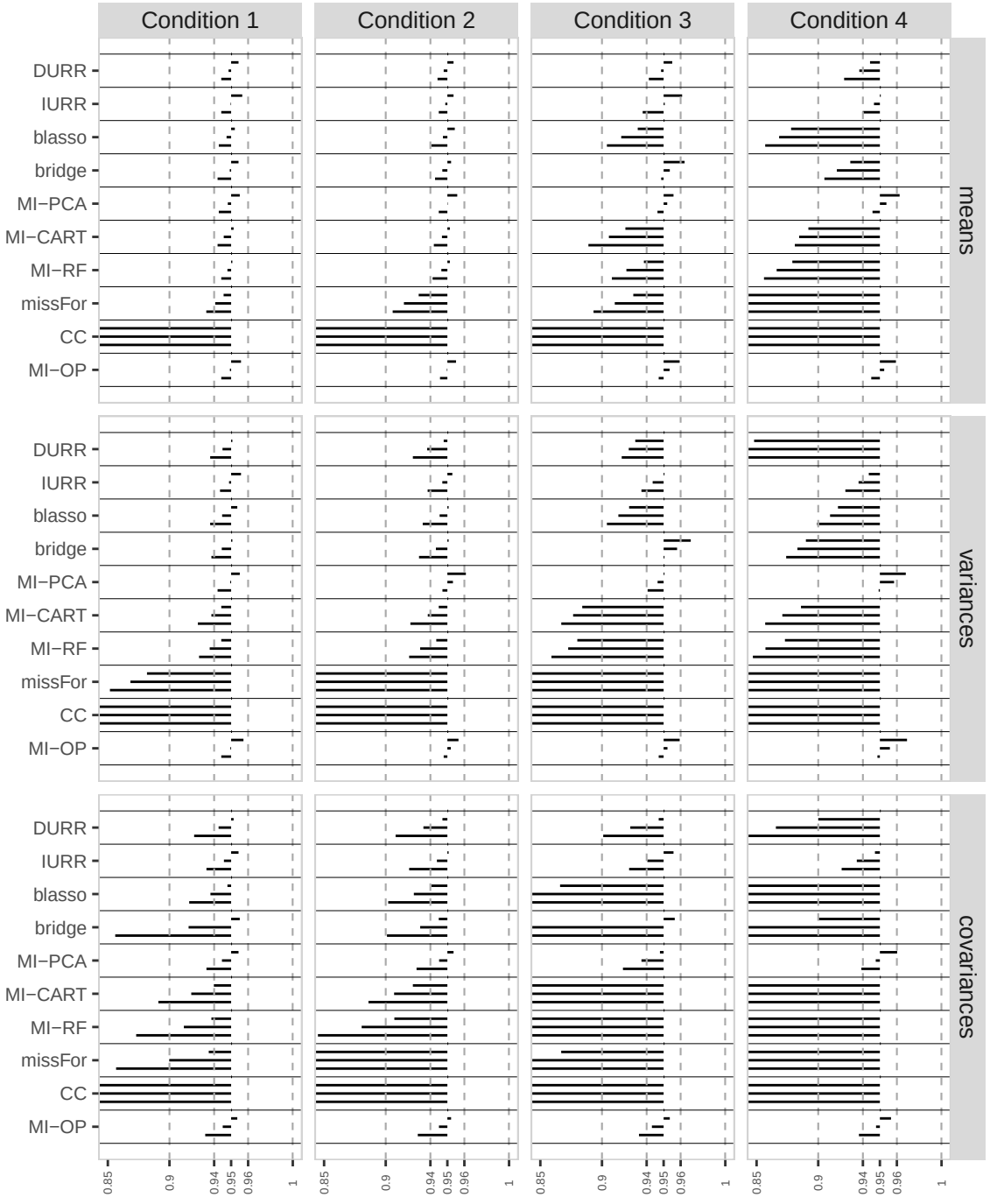

Figure 4. CIC for the means, variances, and covariances for condition 1 to 4. Conditions 1 to 4 correspond to the labels low-dim-low-pm-high-λ, high-dim-low-pm-high-λ, low-dim-high-pm-high-λ, and high-dim-low-high-low-λ in Table 2.

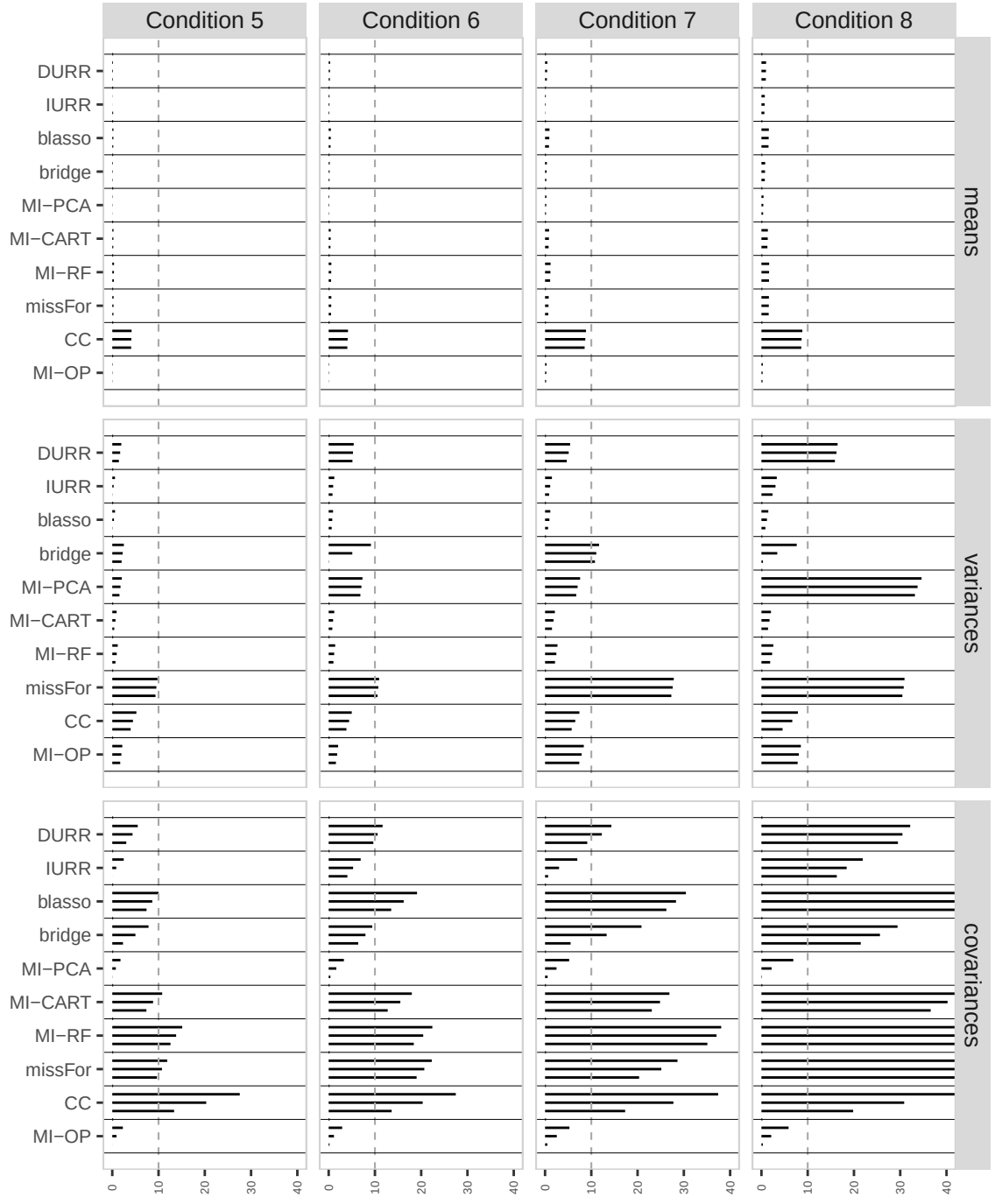

Figure 5. PRBs for the means, variances and covariances (PRB) for condition 1 to 4. Conditions 5 to 8 correspond to the labels low-dim-low-pm-low-λ, high-dim-low-pm-low-λ, low-dim-high-pm-low-λ, and high-dim-low-pm-low-λ in Table 2.

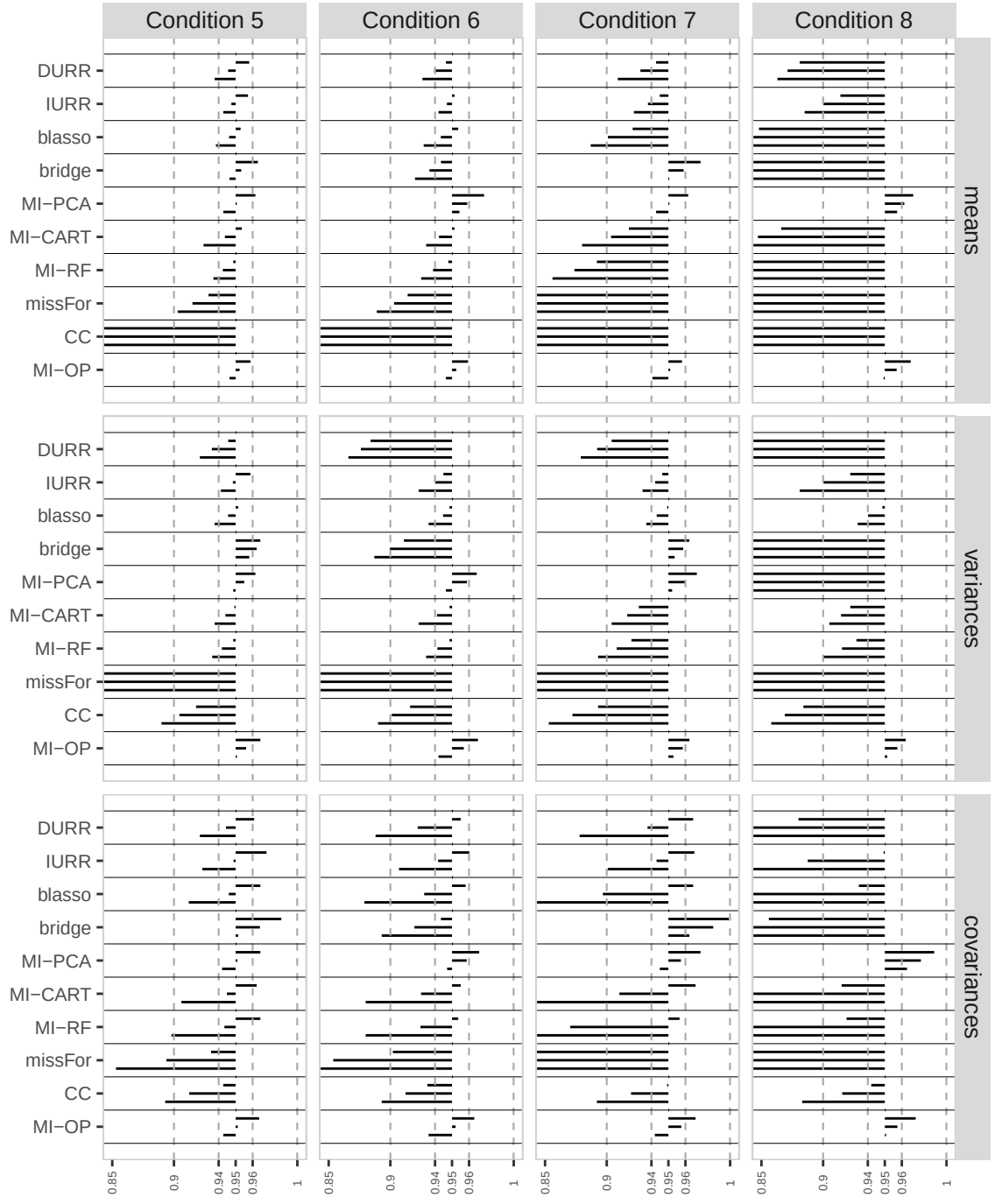

Figure 6. CIC for the means, variances, and covariances for condition 1 to 4. Conditions 5 to 8 correspond to the labels low-dim-low-pm-low-λ, high-dim-low-pm-low-λ, low-dim-high-pm-low-λ, and high-dim-low-pm-low-λ in Table 2.

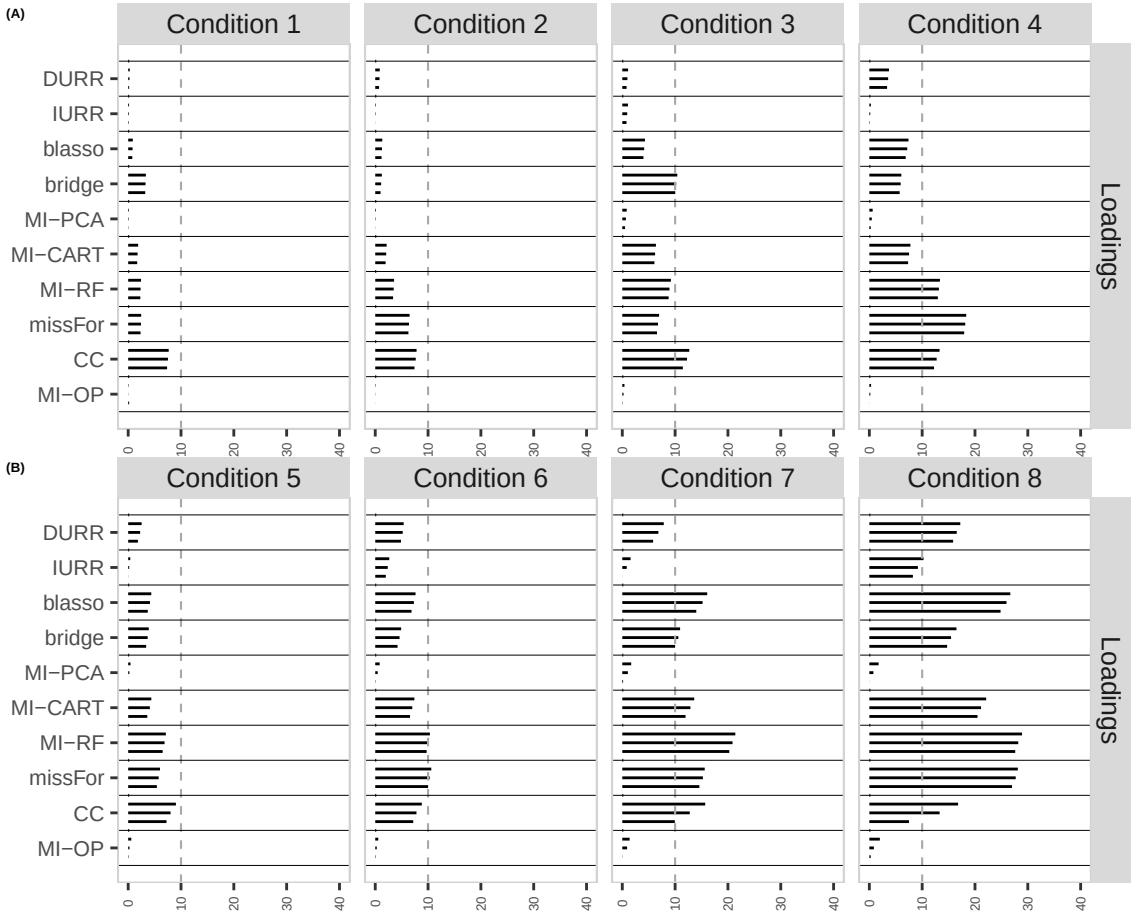

Figure 7. Percent Relative Bias (PRB) for the factor loadings in conditions 1 to 4 (panel A) and conditions 5 to 8 (panel B). Conditions 1 to 8 correspond to the labels in Table 2.

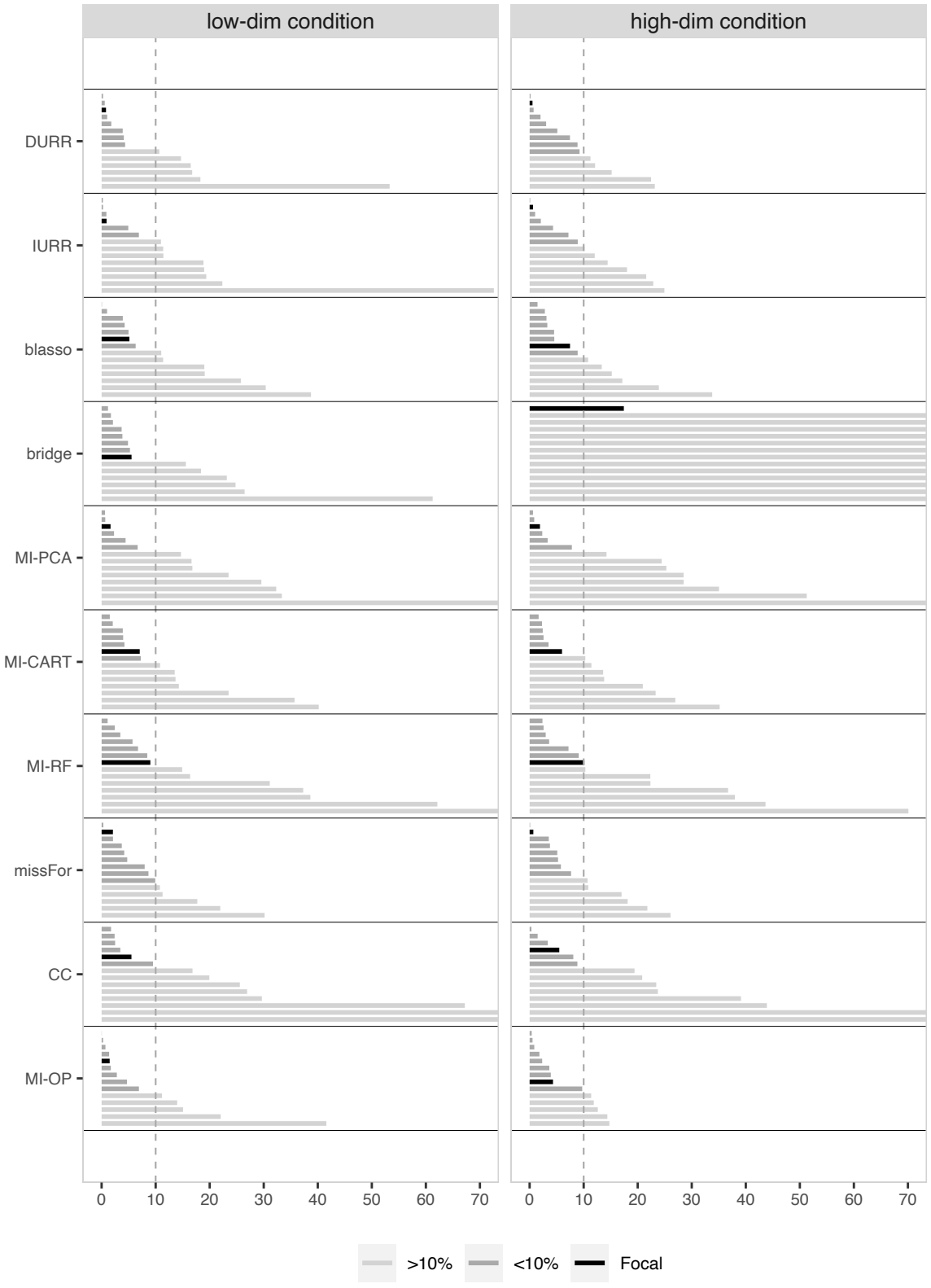

Figure 8. PRBs for all the model parameters in model 2. The order of the bars is based on the absolute value of the PRBs. The values for the intercept, the focal regression coefficient, and the regression coefficient with which most methods struggle (Largest Bias) are highlighted

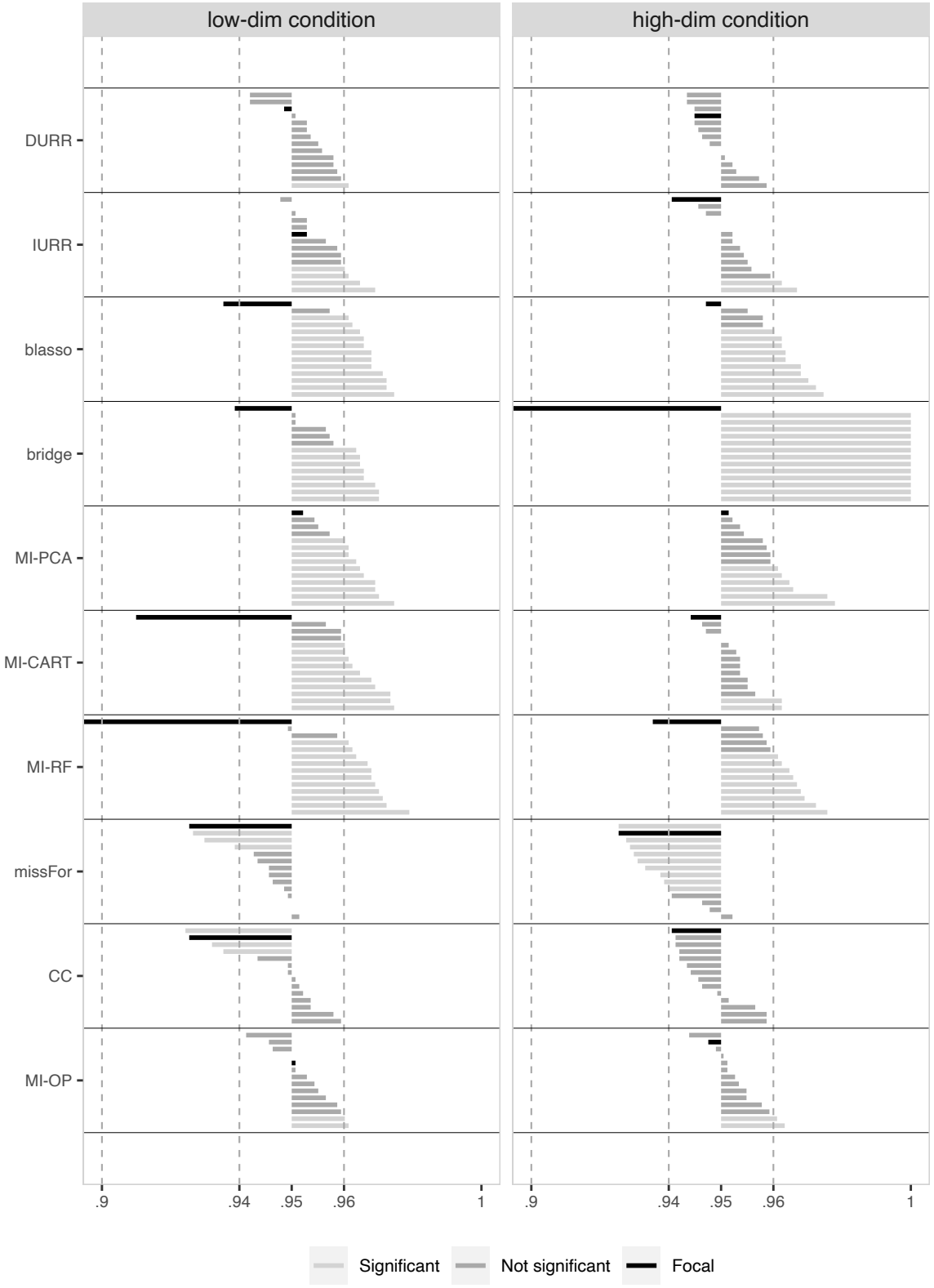

Figure 9. CIC for all model parameter in model 2. Bars are sorted in by ascending value. The values for the intercept, the focal regression coefficient, and the regression coefficient with which most methods struggle (Largest Bias) are highlighted