



A Note on Convergence Diagnostics for Multiple Imputation using Chained Equations (MICE)

Research Report (Preparation for Research Master Thesis, Research Seminar)
Methodology and Statistics for the Behavioural, Biomedical and Social Sciences

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Abstract

The ubiquitous problem of missing information may be circumvented by implementing the framework of multiple imputation (MI). With MI, missing data points are ‘filled in’ (i.e. imputed) several times, and statistical inference is performed on each imputed data set. The validity of inferences may be threatened by non-convergence of this iterative algorithmic procedure, but diagnostics to evaluate algorithmic convergence have not been implemented in MI software. This note investigates the performance of two convergence diagnostics (\hat{R} (Gelman and Rubin 1992), auto-correlation (Schafer 1997)) through model-based simulation. To investigate convergence of the algorithm, the number of iterations is varied between one and one-hundred. Each of these 100 simulation conditions is replicated 1000 times. The convergence diagnostics are evaluated against three recommended simulation diagnostics (bias, confidence interval width, and coverage rate (Van Buuren 2018), since no benchmark diagnostic is available. This simulation study shows that three iterations may be sufficient to obtain ... **This Research Report contains a simulation study that serves as the basis of the technical paper that will be submitted for publication in *Journal of Statistical Software*. I aim to publish a pre-print of this research report on [arXiv](#). That way, I can refer to the simulation study described here, without ‘bulking up’ the technical paper that I want to submit for publication in JSS. Another option would be to attach this note as an online appendix to the technical paper on ShinyMICE.**

Keywords: multiple imputation, convergence, **mice**, R.

1. Introduction

At some point, any scientist conducting statistical analyses will run into a missing data problem (Allison 2001). Missingness is problematic because statistical inference cannot be performed on incomplete data without employing *ad hoc* solutions (e.g., list-wise deletion), which may yield wildly invalid results (Van Buuren 2018). A popular answer to the ubiquitous problem of missing information is to use the framework of multiple imputation (MI), proposed by Rubin (1987). MI is an iterative algorithmic procedure in which each missing data point is ‘imputed’ (i.e. filled in) several times. The variability between imputations is used to reflect how much uncertainty in the inference is introduced by the missingness. Therefore, MI can provide valid inferences despite missing information.

To obtain valid inferences with MI, the variability between imputations should be properly represented (Rubin 1987; Van Buuren 2018). If the variance between imputations is underestimated, confidence intervals around estimates will be too narrow, which can yield spurious results. On the other hand, over-estimation of the variance between imputations results in unnecessarily wide confidence intervals, which can be costly because it lowers the statistical power. Since both of these situations are undesirable, imputations and their variability should be evaluated. Evaluation measures, however, are currently missing or under-developed in MI software, like the world-leading **mice** package (Van Buuren and Groothuis-Oudshoorn 2011) in R (Core Team 2019).

The goal of this research project is to develop novel methodology and guidelines for evaluating MI methods. These evaluation measures and guidelines will subsequently be implemented in an interactive evaluation framework for multiple imputation to aid applied researchers in drawing valid inference from incomplete datasets. This note provides the theoretical foundation for one of these evaluation measures that is vital in evaluating MI procedures: a diagnostic to assess convergence of the MI algorithm. More specifically, this note focuses on the MI algorithm that is implemented in the R package **mice**: ‘Multiple Imputation using Chained Equations’ (MICE). The research question that will be addressed is: ‘*How to diagnose convergence of the multiple imputation algorithm MICE?*’. **REMOVE THE :’s HERE!**

The convergence properties of MICE are investigated through model-based simulation in R (Core Team 2019). The results of this simulation study are guidelines for assessing convergence of the MI algorithm. These guidelines will be implemented in an interactive evaluation tool for **mice**, ‘ShinyMICE’, which is currently under development. All programming code used in this note is available from github.com/gerkovink/ShinyMICE/simulation.

1.1. Terminology

The intended audience of this note consists of empirical researchers and statisticians who use multiple imputation to solve missing data problems. Basic familiarity with MI methodology is assumed. For the theoretical foundation of MI, see Rubin (1987). For an accessible and comprehensive introduction to MI from an applied perspective, see Van Buuren (2018).

The convergence guidelines introduced in this paper are developed to be integrated into the **mice** environment (Van Buuren and Groothuis-Oudshoorn 2011) in R (Core Team 2019). This note, therefore, follows notation and conventions of Van Buuren and Groothuis-Oudshoorn (2011). Deviations from the ‘original’ notation by Rubin (1987) are described in (Van Buuren

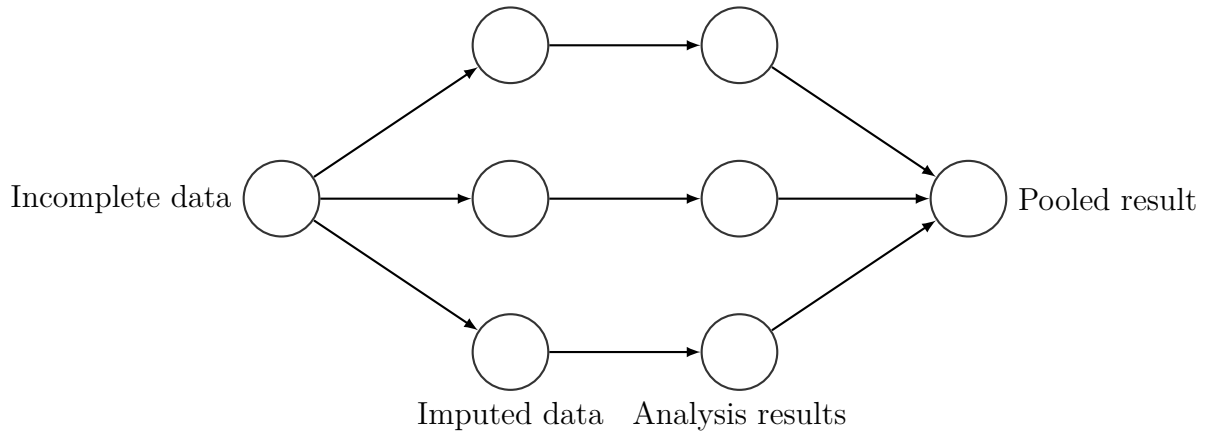


Figure 1: Scheme of the main steps in multiple imputation ($m = 3$). Adapted from (Van Buuren 2018, § 1.4.1).

2018, § 2.2.3).

Let Y denote an $n \times p$ matrix containing the data values on p variables for all n units in a sample. The collection of observed data values in Y is denoted as Y_{obs} ; the missing part of Y is referred to as Y_{mis} . Response indicator R shows whether a data value in Y is missing or observed. The relation between R , Y_{obs} , and Y_{mis} determines the missingness mechanism. This note only considers a ‘missing completely at random’ (MCAR) mechanism, where the probability of being missing is equal for all $n \times p$ cells in Y .

In this note, the terms ‘unobserved’ and ‘missing’ data are used interchangeably. Both refer to Y_{mis} , e.g. ‘NA’ values in R or ‘999’ in SPSS. The terms ‘incomplete’ or ‘observed’ data denote Y_{obs} . Incomplete data is the starting point of the multiple imputation procedure. Figure 1.1 provides a schematic overview of the steps involved with MI.

Missing data in Y is ‘imputed’ (i.e., filled in) m times. The imputed data is combined with observed data Y_{obs} to create m completed data sets. On each completed data set, the analysis of scientific interest (or ‘complete data model’) is performed. The quantity of scientific interest (e.g., a regression coefficient) is denoted with Q . Since Q is estimated on each completed data set, m separate \hat{Q} values are obtained. These m values are combined into a single pooled estimate \bar{Q} .

This note focuses on the algorithmic properties of the imputation step. The algorithm employed within this step has an iterative nature. That is, before drawing m imputed values for each missing data point in Y_{mis} , a ‘chain’ of potential values is sampled. Each of the m chains starts with an initial value, drawn randomly from Y_{obs} . The chains are terminated after a predefined number of iterations. Only the ultimate sample that a chain lands on is imputed and subsequently used in the analysis and pooling steps. The collection of samples across iterations (between the initial value and the imputed value) for each of the m imputations will be referred to as an ‘imputation chain’. The number of iterations will be denoted with t [NOG TOEPASSEN].

1.2. Theoretical Background

The multiple imputation algorithm ‘MICE’ is a special case of Markov chain Monte Carlo

(MCMC) methods—the general framework of iterative algorithmic procedures. While methodology for diagnosing convergence of multiple imputation algorithms has not been systematically studied (Van Buuren 2018), several convergence diagnostics have been proposed for other types of MCMC methods (e.g., Gibbs samplers), or the framework in general. This section provides a brief review of: 1) how convergence is defined in the general context of iterative algorithmic procedures; 2) what diagnostic tools are available; and 3) which of these may apply to MI algorithms.

Loosely speaking, the aim of MCMC algorithms (e.g., Gibbs samplers, or MICE) is to sample values from an unknown target distribution (e.g., the posterior distribution of a parameter in Bayesian inference, or a distribution of missing values, respectively). Convergence is reached once the algorithm samples exclusively from the target distribution (Cowles and Carlin 1996). Since this target distribution is unknown by definition, convergence can only be monitored by evaluating signs of non-convergence (Hoff 2009). Therefore, in practice, the definition of convergence consists of two components: ‘mixing’ of chains together, and ‘stationarity’ of individual chains (Gelman, Carlin, Stern, Dunson, Vehtari, and Rubin 2013, p. 284). The mixing component is satisfied when chains intermingle such that the only difference between the chains is caused by the randomness induced by the algorithm. Stationarity refers to the absence of trending within chains. **Figure XYZ shows a pathological case of non-convergence concerning both components.**

The two components of convergence may be evaluated with convergence diagnostics. Diagnostics that target the stationarity component are auto-correlation (Schafer 1997; Gelman *et al.* 2013), numeric standard error (Geweke 1992, which is commonly called ‘MC error’), and Raftery and Lewis’s 1991 procedure to determine the increase in the necessary number of iterations due to dependence within chains. The mixing component of convergence, on the other hand, is primarily assessed with the ‘Gelman-Rubin statistic’—potential scale reduction factor \hat{R} (Gelman and Rubin 1992). An adapted version of \hat{R} has been proposed by Vehtari, Gelman, Simpson, Carpenter, and Bürkner (2019), which may also assess the stationarity component of convergence. Therefore, the focus of this study is mainly on \hat{R} . Stationarity will also be evaluated with auto-correlation as diagnostic, as recommended by (Cowles and Carlin 1996, p. 898). Other convergence diagnostics are outside the scope of this study.¹

It is not known whether any convergence diagnostic is appropriate to diagnose convergence of the MICE algorithm. As recommended by (Van Buuren 2018, § 6.5.2), the current practice is to visually inspect imputation chains for signs of non-mixing and non-stationarity. Not only is visually assessing convergence challenging to the untrained eye—it might also be futile. That is, there is no scientific consensus on the convergence properties of multiple imputation algorithms (Takahashi 2017), and in some situations, the default techniques in `mice` might not converge to stable target distributions at all (Murray 2018). Therefore, the need for convergence diagnostics is extra pressing in the context of the MICE algorithm.

Explain the measures that I’m investigating here. R hat is ... Auto-correlation is... How are they computed? What do they say? How are they computed on MI data? Looking at imputation chains. Explain that there is no baseline to

¹All of these methods evaluate the convergence of univariate scalar summaries (e.g., chain means or variances). These convergence diagnostics cannot diagnose convergence of multivariable statistics (i.e., relations between scalar summaries). Van Buuren (2018) proposed to implement multivariable evaluation by means of eigenvalue decomposition MacKay and Mac Kay (2003). This method is outside of the scope of the current study.

compare the measures with. The only current convergence check is to visually inspect trace plots. (But in the trace-plots convergence seems immediate).

The potential scale reduction factor \hat{R} tells us by how much the variance of an estimate could be shrunk down if the chains were to be infinitely long [Gelman and Rubin \(1992\)](#). That then informs us about how dependent the chains are on the starting values. If there is no dependence on the initial values anymore, the chains have converged (in the mixing sense of the word). \hat{R} is then equal to one. The conventionally acceptable threshold was $\hat{R} < 1.2$. More recently, [Vehtari et al. \(2019\)](#) proposed a more stringent threshold: $\hat{R} < 1.01$.

\hat{R} is defined by [Vehtari et al. \(2019\)](#) as follows:

REPHRASE: In the equations below, N is the number of draws per chain, M is the number of chains, and $S = MN$ is the total number of draws from all chains. For each scalar summary of interest θ , we compute B and W , the between- and within-chain variances:

$$B = \frac{N}{M-1} \sum_{m=1}^M \left(\bar{\theta}^{(\cdot m)} - \bar{\theta}^{(\cdot \cdot)} \right)^2, \text{ where } \bar{\theta}^{(\cdot m)} = \frac{1}{N} \sum_{n=1}^N \theta^{(nm)}, \quad \bar{\theta}^{(\cdot \cdot)} = \frac{1}{M} \sum_{m=1}^M \bar{\theta}^{(\cdot m)}$$

$$W = \frac{1}{M} \sum_{m=1}^M s_m^2, \text{ where } s_m^2 = \frac{1}{N-1} \sum_{n=1}^N \left(\theta^{(nm)} - \bar{\theta}^{(\cdot m)} \right)^2. \text{ (Vehtari et al. 2019, p. 5)}$$

The proportion of within chain variance W against the weighted average of B and W , $\widehat{\text{var}}^+$ tells us how much variance of θ could be shrunk down if $N \rightarrow \infty$. $\widehat{\text{var}}^+$ is computed as follows:

$$\widehat{\text{var}}^+(\theta|y) = \frac{N-1}{N} W + \frac{1}{N} B.$$

The potential scale reduction factor \hat{R} is obtained as:

$$\hat{R} = \sqrt{\frac{\widehat{\text{var}}^+(\theta|y)}{W}}.$$

High \hat{R} would indicate low \hat{R} values indicate

The second component of convergence stationarity requires chains to be stable across iterations, or non-recurring. Non-recurrence can be evaluated with auto-correlation. Auto-correlation shows how dependent subsequent draws of an imputation chain are on the previous value. If there is a lot of dependence, draws at e.g. iteration five are significantly correlated with the value of the first draw. A high auto-correlation indicates dependence within chains. The magnitude of the AC can be interpreted qualitatively or quantitatively. Quantitative evaluation of the AC entails comparing the observed ACs to the critical values of a two-tailed 95% confidence interval, divided by the square root of the number of iterations.

Convergence diagnostics applied to MI

\hat{R} may not be an appropriate diagnostic to evaluate MI data because it assumes over-dispersed initial values. This means that the initial values of the m imputation chains are ‘far away’ from the distribution that the chains are converging to. In the **mice** algorithm, initial values

are chosen randomly from the observed data. Therefore, we cannot be certain that the initial values are over-dispersed.

Without over-dispersed initial states, \hat{R} may falsely diagnose convergence (Brooks and Gelman 1998). This suggests that \hat{R} would not be sensitive enough to flag non-convergence of MI algorithms. An empirical finding, however, shows that the opposite may be true: Lacerda, Ardington, and Leibbrandt (2007) report \hat{R} values above the threshold of $\hat{R} < 1.1$ after fifty iterations.

1.3. Simulation Hypothesis

The aim is to evaluate whether the imputation procedure has converged. The primary research interest is in determining whether \hat{R} is an appropriate convergence diagnostic, and if so, which level of stringency suits MI data. **Or if there is a discrepancy between the visual and numeric inspection.**

This simulation study hypothesizes that \hat{R} will over-estimate non-convergence. [Or use:] **Hypothesis based on Lacerda *et al.* (2007) is that the conventional acceptable level of \hat{R} is too strict for MI data. We expect that the simulation diagnostics will indicate valid inference before \hat{R} will.**

2. Methods

To investigate the convergence properties of the `mice` algorithm, different lengths of imputation chains are considered. This simulation study considers 100 simulation conditions. Each condition has a different maximum number of iterations, varying between one and one-hundred iterations. In this study, 1000 simulation runs are performed for each of the 100 simulation conditions. **Estimands are convergence diagnostics. Performance measures are simulation diagnostics. where for one through one hundred the Rhat and ... are calculated.** The simulation set-up consists of several steps, summarized in the pseudo-code below. The complete R script of the simulation study is available on Github.

```
# pseudo-code of simulation
simulate data
for (number of simulation runs from 1 to 1000)
  for (number of iterations from 1 to 100)
    create missingness
    impute the missingness
    compute convergence diagnostics
    perform analysis
    pool results
    compute simulation diagnostics
aggregate convergence and simulation diagnostics
```

2.1. Data simulation

The simulated dataset is a finite population of $N = 1000$. The data are simulated to solve a multiple linear regression complete data problem. The quantity of scientific interest is the

estimated regression coefficient of predictor X on outcome variable Y . The linear regression model is $Y \sim \beta_1 X + \beta_2 Z_1 + \beta_3 Z_2$, where Y is the dependent variable, X is an independent variable, and Z_1 and Z_2 are covariates. The data generating model of the predictors is a multivariate normal distribution with means structure μ , and variance-covariance matrix Σ .

$$\begin{pmatrix} X \\ Z_1 \\ Z_2 \\ \epsilon \end{pmatrix} \sim N \left[\begin{pmatrix} 12 \\ 3 \\ 0.5 \\ 0 \end{pmatrix}, \begin{pmatrix} 4 & 4 & 1.8 & 0 \\ 4 & 16 & 4.8 & 0 \\ 1.8 & 4.8 & 9 & 0 \\ 0 & 0 & 0 & 100 \end{pmatrix} \right]$$

Outcome variable Y is subsequently calculated as $Y = 2X + .5Z_1 - Z_2 + \epsilon$.

2.2. Amputation

The complete data is the point of origin for all simulations. In each repetition of the simulation study, the complete data is ‘amputed’ once. That is, the **mice** function `ampute()` in R is used to impose an MCAR missingness mechanism upon the data. The missingness is univariate, and the probability to be missing is the same for all variables, namely 20%. This leaves 20% of the rows completely observed. The resulting amputed data is equal for all simulation conditions in the same repetition.

2.3. Imputation

Missing data points are imputed with **mice** in R. All simulations are performed with imputation method ‘norm’ (Bayesian linear regression imputation), and five imputation chains ($m = 5$). The number of iterations is varied over simulations (`maxit` argument between 1 and 100). Each simulation condition (i.e., each number of iterations) is simulated 1000 times. Simulation and convergence diagnostics are aggregated over the 1000 MCMC simulations.

2.4. Convergence Diagnostics

\hat{R} is computed within imputation chains: for each variable, each simulation condition, and each simulation. The maximum value across variables within the same simulation is reported. Maximum \hat{R} values per simulation condition are aggregated across simulations.

Auto-correlation (AC) is computed within imputation chains, as the correlation between θ at the i^{th} iteration and θ at the $i + 1^{th}$ iteration [**CHECK VARIABLE IN NOTATION**], where θ is a scalar summary of interest (i.e., chain means and chain variances). The AC of the variable with the highest absolute AC value is reported per simulation. These values are then averaged per simulation condition.

2.5. Analysis

Linear regression is performed using the R function `lm()`. The quantity of scientific interest Q is the regression coefficient of X on Y . Q is estimated in each imputation, in each simulation condition, in each repetition. The $m = 5$ estimated regression coefficients \hat{Q} are pooled according to Rubin’s 1987 rules with **mice** function `pool()`.

2.6. Simulation diagnostics

The simulation diagnostics are as recommended by (Van Buuren 2018, § 2.5.2). These evaluation criteria comprise of average bias, average confidence interval width, and empirical coverage rate across simulations. We could also look at distributional characteristics, and plausibility of imputed values, see Vink (n.d.). For now, this is outside of the scope of this study.

Bias is computed as the estimated regression coefficient after MI minus the true regression coefficient. Bias is averaged over all simulations with the same simulation condition.

Confidence interval width (CIW) is computed as the difference between the lower and upper bound of the 95% confidence interval (CI95%). The CI95% bounds are computed as the estimated regression coefficient plus or minus (respectively) the pooled SE across imputations times 2.66 (the quantile of a t distribution with $m-1$ degrees of freedom). CIW is averaged over all simulations with the same simulation condition.

Coverage rate is computed as the proportion of simulations (with the same simulation condition) in which the true regression coefficient is between the bounds of the CI95%.

3. Results

Figures 2 and 3 display results of the simulation study aggregated over 1000 repetitions. A subset of simulation conditions is presented in Table 1. This section describes convergence diagnostics (\hat{R} and auto-correlation) and simulation diagnostics (bias, confidence interval width and coverage rate) first separately, and then together.

Table 1: Simulation and convergence diagnostics over 1000 MCMC simulations.

It.	Bias	CI width	Cov. rate	\hat{R}_{mean}	\hat{R}_{var}	AC_{mean}	AC_{var}
1	-0.137	0.954	0.932	NA	NA	NA	NA
2	-0.006	0.932	0.953	1.650	1.632	-0.500	-0.500
3	0.002	0.929	0.944	1.314	1.306	-0.660	-0.659
4	0.003	0.933	0.957	1.461	1.457	-0.733	-0.735
5	0.004	0.935	0.954	1.475	1.472	-0.705	-0.706
6	0.001	0.934	0.956	1.258	1.256	-0.656	-0.646
7	0.002	0.930	0.948	1.265	1.269	-0.591	-0.585
8	0.004	0.930	0.954	1.181	1.178	-0.495	-0.516
9	0.003	0.931	0.956	1.187	1.187	-0.442	-0.459
10	0.003	0.952	0.943	1.141	1.140	-0.403	-0.423
15	0.002	0.942	0.965	1.100	1.100	-0.276	-0.289
25	0.005	0.934	0.955	1.057	1.057	-0.143	-0.159
50	-0.002	0.929	0.959	1.027	1.026	-0.053	-0.075
100	0.000	0.920	0.946	1.013	1.013	0.022	-0.017

3.1. Convergence diagnostics

\hat{R} . The \hat{R} values for chain means and chain variances show equivalent trends, neither is there a clear difference between the four variables. Roughly speaking, we see that \hat{R} is higher for

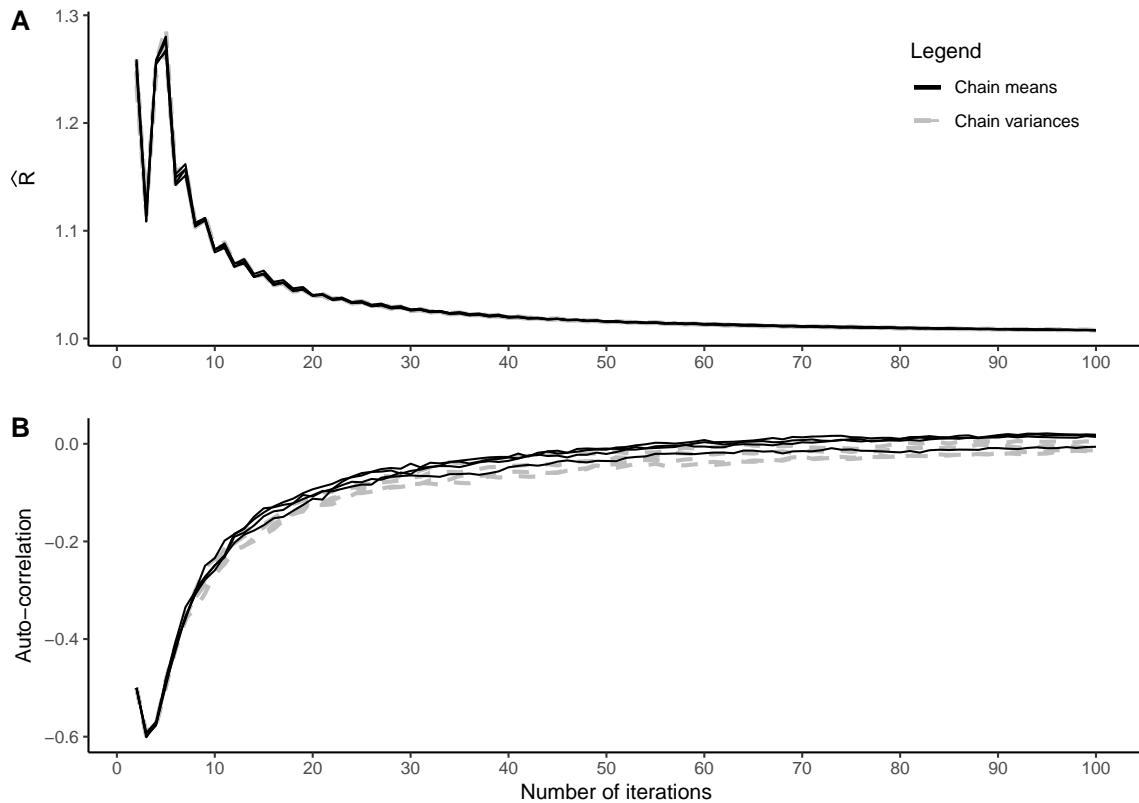


Figure 2: Convergence diagnostics over 1000 MCMC simulations.

simulation conditions with a lower number of iterations, and approaches one for conditions with more iterations. Figure 2 shows an initial dip, a small bump upwards, and then a steep decline. This decline holds up to iteration twenty, after which a more gradual decrease can be observed up to iteration forty. The \hat{R} values are more or less stable after that. The conventionally acceptable threshold for convergence, maximum $\hat{R} < 1.2$, [CHECK IN INTRO] is reached in the simulation condition with three iterations, and conditions with six iterations or more. The widely used threshold $\hat{R} < 1.1$ is met in conditions with ten or more iterations. The most recent recommended threshold is not reached within the 100 iterations considered in this simulation study. $\hat{R} > 1.01$ for all simulation conditions (see online appendix for the full table of results). Check is computing r ht is still correct! Also say something about Rh below 1.

Auto-correlation. All observed auto-correlations (aggregated over the 1000 repetitions) are negative or close to zero. There are some differences between variables, and the ACs of chain variances seem lower than the ACs of chain means. The general trend in figure 2 is that ACs decrease steeply as the number of iterations increases. The lowest AC observed is at four iterations. Simulation conditions with a higher number of iterations show a slow increase towards zero. Auto-correlations do not plateau completely within the range of simulation conditions considered in this study. It seems that ACs might become positive if more iterations would be allowed. The average absolute maximum ACs are negative up to 77 iterations for chain means, and for chain

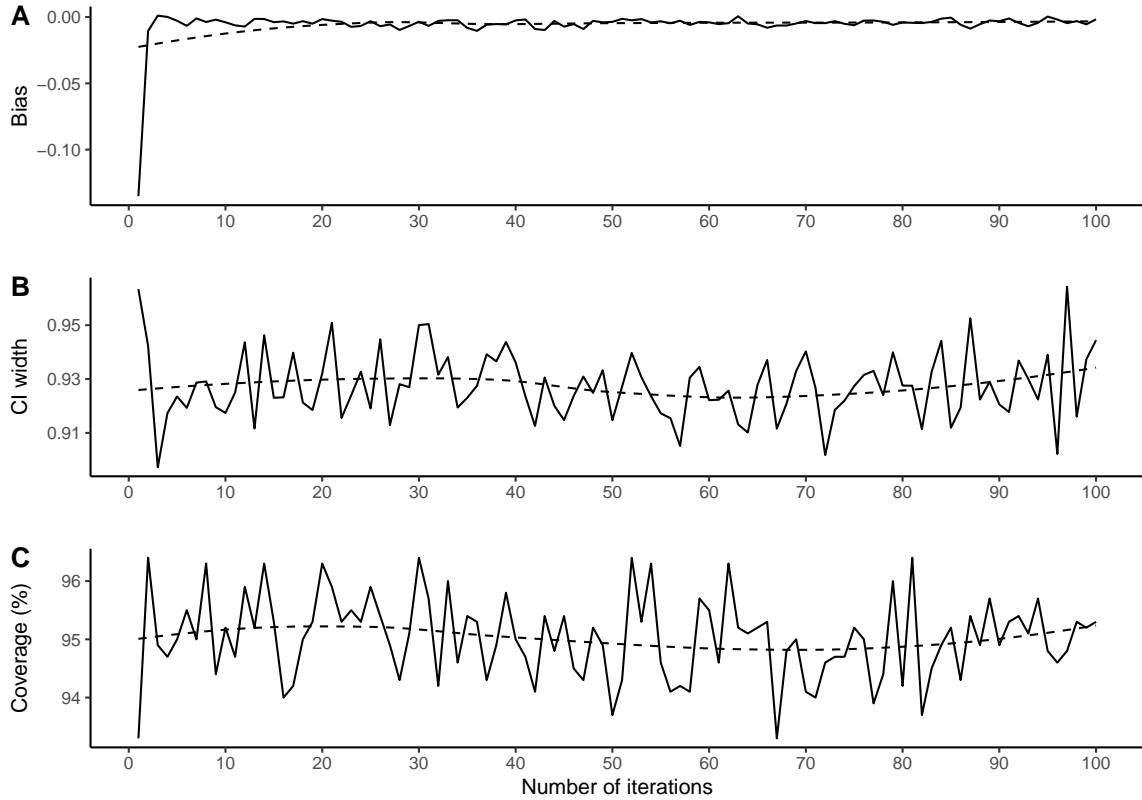


Figure 3: Simulation diagnostics over 1000 MCMC simulations.

variances all iterations considered here have negative ACs.

3.2. Simulation diagnostics

Bias. Figure 3 shows the average bias between the regression coefficient of X on Y in the complete dataset, and \bar{Q} , the pooled estimated regression coefficient and the ... Average bias is close to zero for simulation conditions with two iterations or more. The simulation condition with one iteration has a negative bias. From two iterations upwards, the average bias across repetitions is stable. Across iterations two to one hundred, bias fluctuates within a narrow range around zero. Loess line is flat around it = 20.

Confidence interval width. CIW is only clearly divergent for the simulation condition with one iteration. Conditions with two or more iterations have similar CIWs. The magnitude of differences from the loess line is somewhat larger up-to the condition with four iterations. From four iterations on, CIW seems to be stable across iterations. Loess line is never flat.

Coverage rate. The coverage rate is more or less stable from two iterations upwards. On average, the coverage rate is somewhat higher than the expected nominal coverage of 95% [Neyman \(1934\)](#), namely 95.3%. Loess line is never flat. give some implications for these measures. connect convergence and simulation diagnostics.

4. Summary and discussion

Answer RQ. How to diagnose non-convergence? It's complicated.

Summary. This note illustrates that conventional convergence diagnostics behave differently on MI data than other MCMC methods like Gibbs samplers in Bayesian analyses. The most recent recommended threshold for \hat{R} ($\hat{R} < 1.01$) may be too stringent for MI data. **However, using the 1.2 threshold may be too lenient because this was observed at three iterations and then again after six. If we would use 1.2, we might miss this increase after three iterations. The 1.1 threshold seems ok. Also, ten iterations are computationally not terrible. With increased performance and storage capacities, doubling the default is fine I guess.**

From the simulation diagnostics, it appears that as little as three iterations might be sufficient to obtain unbiased, confidence valid estimates. Convergence diagnostics \hat{R} and auto-correlation, however, indicate that convergence may only be reached after twenty or even forty iterations.

R hat below 1. \hat{R} could theoretically not be smaller than one, yet it occurred several times in this study (see online appendix XYZ). This can happen when the number of simulations is smaller than in 'regular' MCMC processes [explain that fewer iterations is an advantage of MI, not a disadvantage compared to MCMC]. Therefore, the ' $(n - 1/n)$ ' [add equation number] correction factor can influence the estimated potential scale reduction factor. This downwards bias is in the opposite direction than expected: "The mixture-of-sequences variance, V , should stabilize as a function of n . (Before convergence, we expect σ^2 to decrease with n , only increasing if the sequences explore a new area of parameter space, which would imply that the original sequences were not overdispersed for the particular scalar summary being monitored.)" (Brooks and Gelman 1998, p 438).

Negative ACs. Auto-correlation is dangerous when positive. These auto-correlations are negative. Still, we want the iterations to be stable and independent. Default maxit is five iterations now, should this be different? Are the 'waves' most pronounced at iteration 5? But why the dip??

An implication of the observed dip in AC is that default maxit value of five iterations is the worst possible number of iterations.

Future research. This study considered only a MCAR missingness mechanism. Necessary but not sufficient to demonstrate the performance of convergence diagnostics. This is just a proof of concept. Further research is needed to investigate the performance under violation of convergence, e.g. dependency between predictors (very high correlations).

Computational details

The results in this paper were obtained using R 3.6.1 Core Team (2019) with the **mice** 3.6.0.9000 package Van Buuren and Groothuis-Oudshoorn (2011). R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at <https://CRAN.R-project.org/>.

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