

Multiple Imputation of Missing Data in Simple and More Complex Settings

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Outline

Part I: Multiple Imputation

How does multiple imputation work?

- The ideas behind MI
- Understanding sources of uncertainty
- Implementation of MI and MICE

Part II: Multiple Imputation Workflow

How to perform MI with the **mice** package in R, from getting to know the data to the final results.

Practicals: visualization & exploration of incomplete data, imputation with **mice**, checking imputed data, analysis of imputed data

Outline (cont.)

Part III: When MICE might fail

Introduction to

- settings where standard use of **mice** is problematic
- alternative imputation approaches
- alternative R packages

Practicals: Imputation with non-linear functional forms, longitudinal outcomes and survival outcomes

Part IV: Multiple Imputation Strategies

Some tips & tricks

Part I

Multiple Imputation

1. What is Multiple Imputation?

1.1. History & Ideas

- Developed by **Donald B. Rubin** in the 1970s
- to handle missing values in **public use databases** (e.g., census data provided by the government),
- motivated by the **increase in missing values**, and
- increased **availability of computers**.

1. What is Multiple Imputation?

1.1. History & Ideas

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Goal: data should be usable by [10]

- a **large number of analysts**, who commonly have to rely on
- standard **software that can only handle complete data**, and usually
- are **not experts in handling incomplete data**.

1. What is Multiple Imputation?

1.1. History & Ideas

Rubin's thoughts: [11]

One imputed value can not be correct in general.
→ We need to represent missing values by a **number of imputations**.

To find **sensible values** to fill in, we need some kind of **model**.

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This **distribution depends on assumptions** that have been made about the model.

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What we want is the '**predictive distribution**' of the missing values given the observed values.

1. What is Multiple Imputation?

1.1. History & Ideas

How to obtain that predictive distribution?

How to represent the multiple imputed values?

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1.1. History & Ideas

How to obtain that predictive distribution?

Idea: assume nonrespondents are just like respondents

- fit a model to the observed data
- obtain for each “nonrespondent” the conditional distribution of the missing data (given the observed data) as if he/she was a respondent

How to represent the multiple imputed values?

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How to represent the multiple imputed values?

- for each set of imputed values, create a dataset
(those datasets agree in the observed values but imputed values differ)
- analyse each dataset
- combine results from all analyses

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How to represent the multiple imputed values?

- for each set of imputed values, create a dataset
(those datasets agree in the observed values but imputed values differ)
 - analyse each dataset
 - combine results from all analyses
- We can describe
- the overall results
 - how (much) the **results vary between the imputed datasets**

1. What is Multiple Imputation?

1.2. Notation

- X : $n \times p$ data matrix with n rows and p variables x_1, \dots, x_p
- X_{obs} : observed data, X_{mis} : missing data
- R : $n \times p$ missing indicator matrix containing 0 (missing) or 1 (observed)

$$\mathbf{X} = \begin{array}{c|ccccc} & X_{-2} & X_2 & X_{-2} \\ \hline & x_{1,1} & x_{1,2} & \dots & x_{1,p} \\ & x_{2,1} & x_{2,2} & \dots & x_{2,p} \\ & \vdots & \vdots & \ddots & \vdots \\ & x_{n,1} & x_{n,2} & \dots & x_{n,p} \end{array} \quad \mathbf{R} = \begin{array}{c|cccc} & R_{1,1} & R_{1,2} & \dots & R_{1,p} \\ & R_{2,1} & R_{2,2} & \dots & R_{2,p} \\ & \vdots & \vdots & \ddots & \vdots \\ & R_{n,1} & R_{n,2} & \dots & R_{n,p} \end{array}$$

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For example:

$$\mathbf{X} = \begin{array}{cccc} X_1 & X_2 & X_3 & X_4 \\ \hline \checkmark & NA & \checkmark & \checkmark \\ \checkmark & \checkmark & NA & NA \\ \checkmark & NA & \checkmark & NA \end{array} \quad \Rightarrow \mathbf{R} = \begin{array}{cccc} 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \end{array}$$

1. What is Multiple Imputation?

1.3. Missing data mechanisms

Missing Completely At Random (MCAR)

Missing At Random (MAR)

Missing Not At Random (MNAR)

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1.3. Missing data mechanisms

Missing Completely At Random (MCAR)

$$p(R | X_{obs}, X_{mis}) = P(R)$$

Missingness is independent of all data

questionnaire got lost in mail

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Missingness depends only on observed data

overweight participants are less likely to report their chocolate consumption (and we know their weight)

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Missingness depends only on observed data

overweight participants are less likely to report their chocolate consumption (and we know their weight)

Missing Not At Random (MNAR)

$$p(R | X_{obs}, X_{mis}) \neq P(R | X_{obs})$$

Missingness depends (also) on unobserved data

overweight participants are less likely to report their weight

1. What is Multiple Imputation?

1.3. Missing data mechanisms

- **MCAR** is a special case of **MAR**
- not possible to distinguish **MNAR** from **MAR** with just the observed data
- **Ignorability:**
If **M(C)AR** and parameters in $p(R | X, \psi)$ are (a priori) independent of parameters in $p(X | \theta)$ \rightarrow missingness process does not need to be modelled
- Complete case analysis (mostly) only unbiased in **MCAR**

1. What is Multiple Imputation?

1.3. Missing data mechanisms

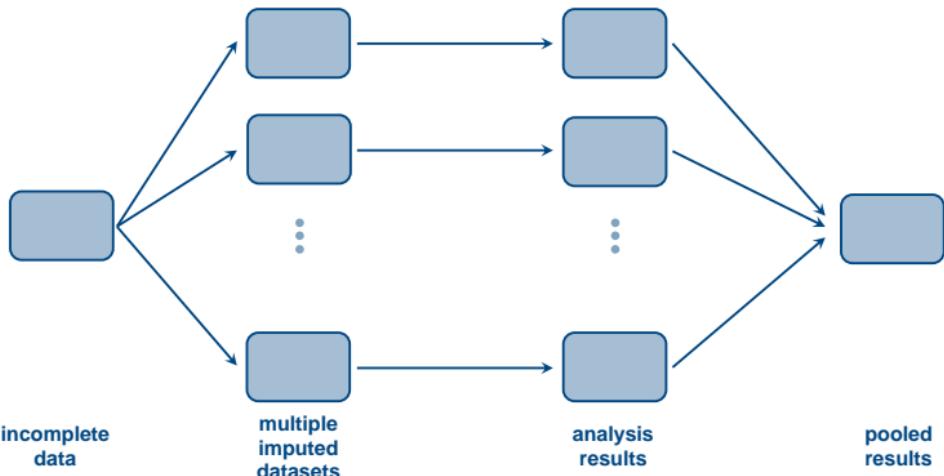
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- Complete case analysis (mostly) only unbiased in **MCAR**

Here:

- we assume **MAR**,
- focus on missing values in covariates, and
- cross-sectional data (for now)

1. What is Multiple Imputation?

1.4. Three steps



In summary:

1. **Imputation:** impute multiple times → multiple completed datasets
2. **Analysis:** analyse each of the datasets
3. **Pooling:** combine results, taking into account additional uncertainty

2. Imputation step

2.1. Univariate missing data

How can we actually get imputed values?

For now: assume only one continuous variable has missing values (**univariate missing data**).

X_1	X_2	X_3	X_4
✓	NA	✓	✓
✓	✓	✓	✓
✓	NA	✓	✓
:	:	:	:

2. Imputation step

2.1. Univariate missing data

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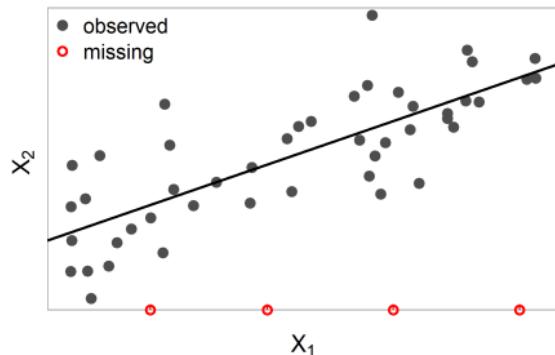
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✓	NA	✓	✓
⋮	⋮	⋮	⋮

Idea: Predict values

Model:

$$x_{i2} = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i3} + \beta_3 x_{i4} + \varepsilon_i$$



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Idea: Predict values

Model:

$$x_{i2} = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i3} + \beta_3 x_{i4} + \varepsilon_i$$

Imputed/predicted value:

$$\hat{x}_{i2} = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 x_{i3} + \hat{\beta}_3 x_{i4}$$

2. Imputation step

2.1. Univariate missing data

Problem:

- We can obtain **only one imputed value** per missing value, but we wanted a whole distribution.
- The predicted values do not take into account the added **uncertainty** due to the missing values.

2. Imputation step

2.1. Univariate missing data

Problem:

- We can obtain **only one imputed value** per missing value, but we wanted a whole distribution.
 - The predicted values do not take into account the added **uncertainty** due to the missing values.
- ➡ We need to take into account **two sources of uncertainty**:
- The **parameters** are estimated with **uncertainty** (represented by the std. error).
 - There is **random variation / prediction error** (variation of the residuals).

2. Imputation step

2.1. Univariate missing data

Taking into account uncertainty about the parameters β :

We assume that β has a distribution, and we can sample realizations of β from that distribution.

When plugging the different realizations of β into the predictive model, we obtain slightly different regression lines.

2. Imputation step

2.1. Univariate missing data

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When plugging the different realizations of β into the predictive model, we obtain slightly different regression lines.

With each set of coefficients, we also get slightly different predicted values.

2. Imputation step

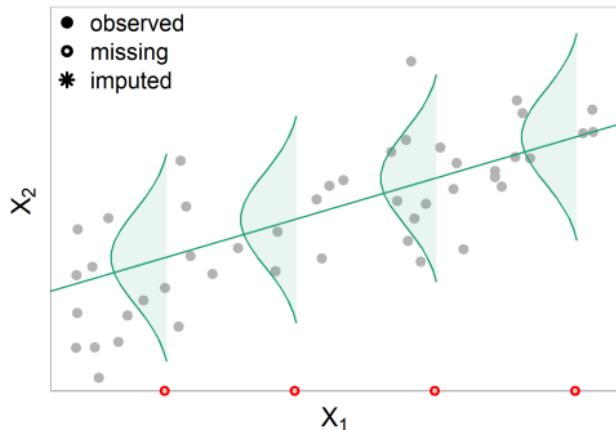
2.1. Univariate missing data

Taking into account the prediction error:

The model does not fit the data perfectly: observations are scattered around the regression lines.

We assume that the **data have a distribution**, where

- the **mean** for each value is given by the **predictive model**, and



2. Imputation step

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2. Imputation step

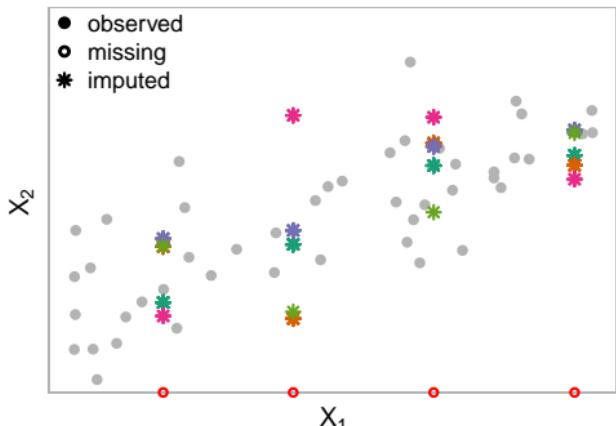
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The model does not fit the data perfectly: observations are scattered around the regression lines.

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- the **mean** for each value is given by the **predictive model**, and
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In the end, we obtain one imputed dataset for each color.

2. Imputation step

2.2. Semi-parametric imputation

Assumption of **distributions** for **parameters** and **missing values**:

Bayesian

Alternative to take into account **uncertainty in parameters**:

Bootstrap

2. Imputation step

2.2. Semi-parametric imputation

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Both require the assumption of a **distribution for the missing values**.

2. Imputation step

2.2. Semi-parametric imputation

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Bootstrap

Both require the assumption of a **distribution for the missing values**.

What if none of the standard distribution fits?

2. Imputation step

2.2. Semi-parametric imputation

Predictive Mean Matching (PMM)

- semi-parametric approach to imputation
- developed for settings where the normal distribution is not a good choice for the predictive distribution.[7, 8]

2. Imputation step

2.2. Semi-parametric imputation

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Idea:

- **find cases** in the observed data that are **similar** to the cases with missing values
- **fill in** the missing value with the **observed value** from one of those cases

To find similar cases, the **predicted values** of complete and incomplete cases are compared.

2. Imputation step

2.2. Semi-parametric imputation

The steps in PMM:

1. Obtain parameter estimates for $\hat{\beta}$ and $\hat{\sigma}$.
2. Calculate the predicted values for the observed cases

$$\hat{\mathbf{y}}_{obs} = \mathbf{X}_{obs}\hat{\beta}.$$

3. Calculate the predicted value for the missing cases

$$\hat{\mathbf{y}}_{mis} = \mathbf{X}_{mis}\hat{\beta}.$$

4. For each missing value, find d donor candidates that fulfill a given criterium.
5. Randomly select one of the donors.

2. Imputation step

2.2. Semi-parametric imputation

Several **criteria to select donors** have been proposed:

1. The donor is the **(one) case with the smallest absolute difference**

2. Imputation step

2.2. Semi-parametric imputation

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2. Imputation step

2.2. Semi-parametric imputation

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3. Donor candidates are those cases for which the **absolute difference is smaller than some limit η** . The donor is selected randomly from the candidates.
4. Select candidates like in 2. or 3., but select the donor from the candidates with probability that depends on the absolute difference.[14]

2. Imputation step

2.2. Semi-parametric imputation

Potential issues with donor selection

- If the same donor is chosen in many/all imputations (e.g., because only a few similar observed cases are available), the **uncertainty about the missing values will be underestimated.**

2. Imputation step

2.2. Semi-parametric imputation

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- Therefore, using one donor is not a good idea. On the other hand, using too many candidates can lead to bad matches.

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2.2. Semi-parametric imputation

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 - Therefore, using one donor is not a good idea. On the other hand, using too many candidates can lead to bad matches.
- PMM may be **problematic** when
- the **dataset is very small,**
 - the **proportion of missing values is large**, or
 - one/some **predictor variable(s) are strongly related to the missingness.**

2. Imputation step

2.2. Semi-parametric imputation

For the **sampling of the parameters** (step 1 on slide 17), different approaches have been introduced in the literature:

Type-0 $\hat{\beta}_{LS/ML}$ (least squares or maximum likelihood) are used in both prediction models

Type-I $\hat{\beta}_{LS/ML}$ to predict \hat{y}_{obs} ; $\tilde{\beta}_{B/BS}$ (Bayesian or bootstrap) to predict \hat{y}_{mis}

Type-II $\tilde{\beta}_{B/BS}$ to predict \hat{y}_{obs} as well as \hat{y}_{mis}

Type-III different draws $\tilde{\beta}_{B/BS}^{(1)}$ and $\tilde{\beta}_{B/BS}^{(2)}$ to predict \hat{y}_{obs} and \hat{y}_{mis} , respectively

The use of Type-0 and Type-I matching **underestimates the uncertainty** about the regression parameters.

2. Imputation step

2.2. Semi-parametric imputation

Another point to consider:

the **choice of the set of data used to train the prediction models.**

In the version presented on slide 17, the same set of data (all cases with observed y) is used to train the model and to produce predicted values of y_{obs} .

The predictive model will likely fit the observed cases better than the missing cases, and, hence, **variation will be underestimated.**

Alternatives:

- the **model could be trained on the whole data** (using previously imputed values)
- use a **leave-one-out approach** on the observed data

2. Imputation step

2.3. What is implemented in software?

mice (in R):

- **PMM** via `mice.impute.pmm()`
 - specification of number of donors d (same for all variables)
 - Type-0, Type-I, Type-II matching
- **PMM** via `mice.impute.midastouch()`
 - allows leave-one-out estimation of the parameters
 - distance based donor selection
 - Type-0, Type-I, Type-II matching
- **bootstrap** linear regression via `mice.impute.norm.boot()`
- **bootstrap** logistic regression via `mice.impute.logreg.boot()`
- **Bayesian** linear regression via `mice.impute.norm()`
- ...

2. Imputation step

2.4. Multivariate missing data

Multivariate missing data:

What if we have **missing values in more than one variable?**

2. Imputation step

2.4. Multivariate missing data

Multivariate missing data:

What if we have **missing values in more than one variable?**

In case of **monotone missing values** we can use
the technique for univariate missing data in a chain:

impute x_4 given x_1

impute x_3 given x_1 and x_4

impute x_2 given x_1 , x_4 and x_3

X_1	X_4	X_3	X_2
✓	✓	✓	NA
✓	✓	NA	NA
✓	NA	NA	NA
:	:	:	:

2. Imputation step

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X_1	X_4	X_3	X_2
✓	✓	✓	NA
✓	✓	NA	NA
✓	NA	NA	NA
⋮	⋮	⋮	⋮

When we have **non-monotone missing data** there is no sequence without conditioning on unobserved values.

X_1	X_2	X_3	X_4
✓	NA	✓	✓
NA	✓	NA	NA
✓	NA	✓	NA
⋮	⋮	⋮	⋮

2. Imputation step

2.4. Multivariate missing data

There are **two popular approaches** for the imputation step in **multivariate non-monotone** missing data:

Fully Conditional Specification

- Multiple Imputation using Chained Equations (**MICE**)
- sometimes also: sequential regression
- implemented in SPSS, R, Stata, SAS, ...
- our focus here

2. Imputation step

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Joint Model Imputation

(see for example Carpenter & Kenward [2])

2. Imputation step

2.5. FCS/MICE

Algorithm 1 MICE algorithm [15] for **one** imputed dataset

- 1: **for** j in $1, \dots, p$: ▷ Setup
- 2: Specify imputation model for variable X_j
 $p(X_j^{mis} | X_j^{obs}, X_{-j}, R)$
- 3: Fill in starting imputations \dot{X}_j^0 by random draws from X_j^{obs} .
- 4: **end for**

2. Imputation step

2.5. FCS/MICE

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4: end for

5: for  $t$  in  $1, \dots, T$ :                          ▷ loop through iterations
6:   for  $j$  in  $1, \dots, p$ :                      ▷ loop through variables
     ...
10:  end for
11: end for
```

2. Imputation step

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5: for  $t$  in  $1, \dots, T$ :                            ▷ loop through iterations
6:   for  $j$  in  $1, \dots, p$ :                      ▷ loop through variables
7:     Define currently complete data except  $X_j$ 
      $\dot{X}_{-j}^t = (\dot{X}_1^t, \dots, \dot{X}_{j-1}^t, \dot{X}_{j+1}^{t-1}, \dots, \dot{X}_p^{t-1})$ .
8:   end for
9: end for
10: end for
11: end for
```

2. Imputation step

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8:     Draw parameters  $\dot{\theta}_j^t \sim p(\theta_j^t | X_j^{obs}, \dot{X}_{-j}^t, R)$ .
```

10: **end for**

11: **end for**

2. Imputation step

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 $\dot{X}_{-j}^t = (\dot{X}_1^t, \dots, \dot{X}_{j-1}^t, \dot{X}_{j+1}^{t-1}, \dots, \dot{X}_p^{t-1})$.
- 8: Draw parameters $\dot{\theta}_j^t \sim p(\theta_j^t | X_j^{obs}, \dot{X}_{-j}^t, R)$.
- 9: Draw imputations $\dot{X}_j^t \sim p(X_j^{mis} | \dot{X}_{-j}^t, R, \dot{\theta}_j^t)$.
- 10: **end for**
- 11: **end for**

2. Imputation step

2.5. FCS/MICE

The imputed values from the **last iteration**,

$$\left(\dot{X}_1^T, \dots, \dot{X}_p^T \right),$$

are then used to replace the missing values in the original data.

One run through the algorithm ➔ one imputed dataset.

2. Imputation step

2.5. FCS/MICE

The imputed values from the **last iteration**,

$$\left(\dot{X}_1^T, \dots, \dot{X}_p^T \right),$$

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One run through the algorithm ➔ one imputed dataset.

➔ To obtain m imputed datasets: **repeat m times**

2. Imputation step

2.5. FCS/MICE

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are then used to replace the missing values in the original data.

One run through the algorithm ➔ one imputed dataset.

➔ To obtain m imputed datasets: **repeat m times**

- The **sequence of imputations** for one missing value (from starting value to final iteration) is called a **chain**.
- Each run through the MICE algorithm produces one chain per missing value.

2. Imputation step

2.5. FCS/MICE

Why iterations?

- Imputed values in one variable depend on the imputed values of the other variables (Gibbs sampling).
- If the starting values (random draws) are far from the actual distribution, imputed values from the first few iterations are not draws from the distribution of interest.

2. Imputation step

2.5. FCS/MICE

Why iterations?

- Imputed values in one variable depend on the imputed values of the other variables (Gibbs sampling).
- If the starting values (random draws) are far from the actual distribution, imputed values from the first few iterations are not draws from the distribution of interest.

How many iterations?

Until **convergence**

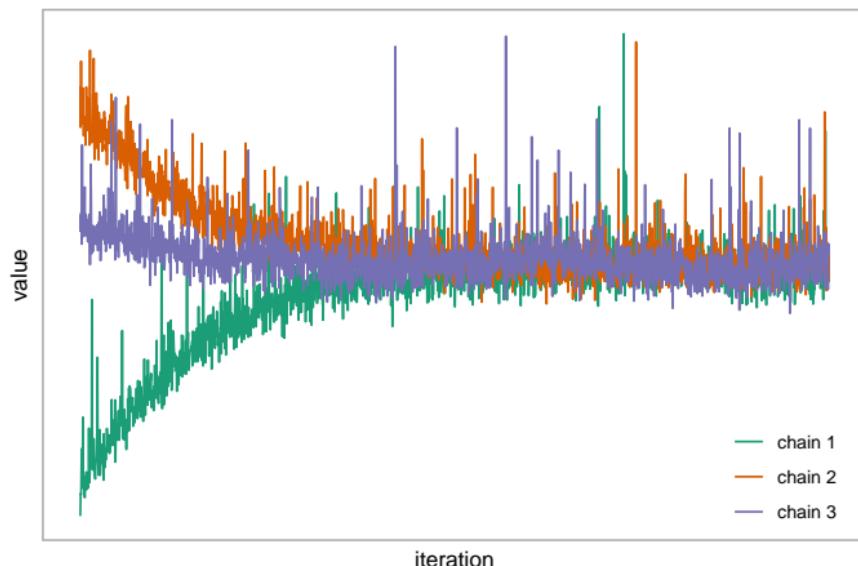
= when the sampling distribution does not change any more
(Note: the imputed value will still vary between iterations.)

How to evaluate convergence?

The **traceplot** (x-axis: iteration number, y-axis: imputed value) should show a horizontal band.

2. Imputation step

2.6. Checking convergence



Each chain is the sequence of imputed values (from starting value to final imputed value) for the same missing value.

3. Analysis step

Multiple imputed datasets:

X_1	X_2	X_3	X_4
1.4	9.2	1.8	2.0
0.5	12.4	2.3	0.1
-0.5	10.7	2.6	-1.6
:	:	:	:

X_1	X_2	X_3	X_4
1.4	13.3	1.8	2.0
0.5	12.4	2.1	0.6
-0.5	10.2	2.6	-1.7
:	:	:	:

X_1	X_2	X_3	X_4
1.4	10.0	1.8	2.0
0.5	12.4	2.2	-1.4
-0.5	8.6	2.6	-1.0
:	:	:	:

3. Analysis step

Multiple imputed datasets:

X_1	X_2	X_3	X_4
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-0.5	10.7	2.6	-1.6
:	:	:	:

X_1	X_2	X_3	X_4
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-0.5	10.2	2.6	-1.7
:	:	:	:

X_1	X_2	X_3	X_4
1.4	10.0	1.8	2.0
0.5	12.4	2.2	-1.4
-0.5	8.6	2.6	-1.0
:	:	:	:

Analysis model of interest, e.g.,

$$x_1 = \beta_0 + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4$$

3. Analysis step

Multiple imputed datasets:

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:	:	:	:

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-0.5	10.2	2.6	-1.7
:	:	:	:

X_1	X_2	X_3	X_4
1.4	10.0	1.8	2.0
0.5	12.4	2.2	-1.4
-0.5	8.6	2.6	-1.0
:	:	:	:

Analysis model of interest, e.g.,

$$x_1 = \beta_0 + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4$$

Multiple sets of results:

	est.	se
β_0	-0.15	0.22
β_1	0.16	0.02
β_2	-0.59	0.03
β_3	0.28	0.03

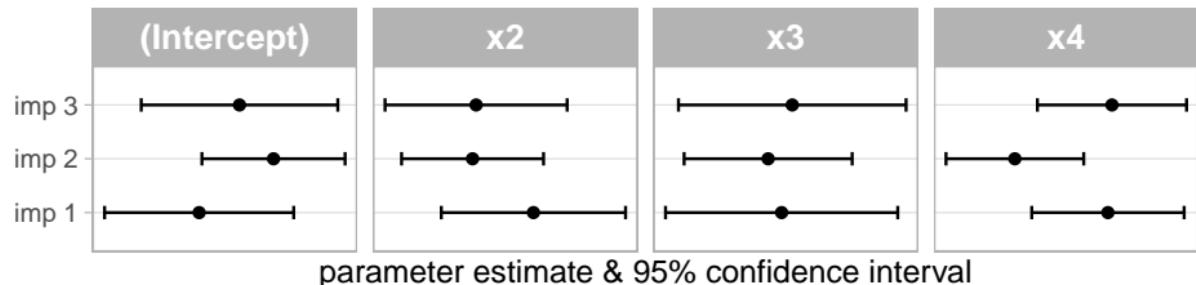
	est.	se
β_0	0.19	0.16
β_1	0.14	0.01
β_2	-0.59	0.03
β_3	0.2	0.03

	est.	se
β_0	0.04	0.22
β_1	0.14	0.01
β_2	-0.58	0.03
β_3	0.28	0.03

4. Pooling

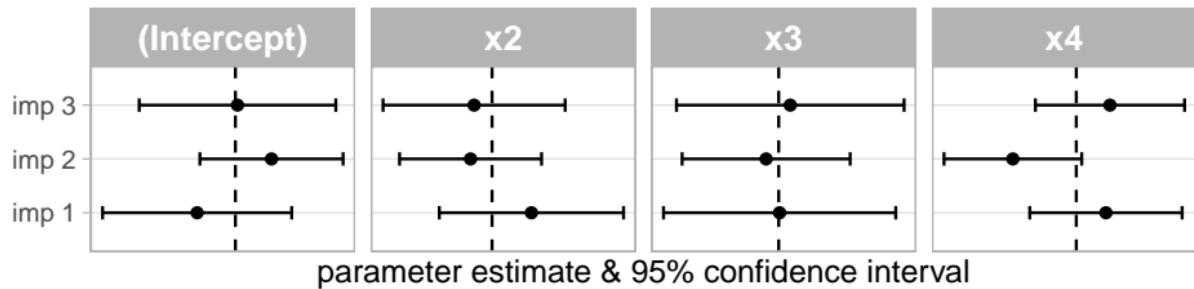
In the results from multiply imputed data there are **two types of variation/uncertainty**:

- **within** imputation (represented by the confidence intervals)
- **between** imputation (horizontal shift between imputations)



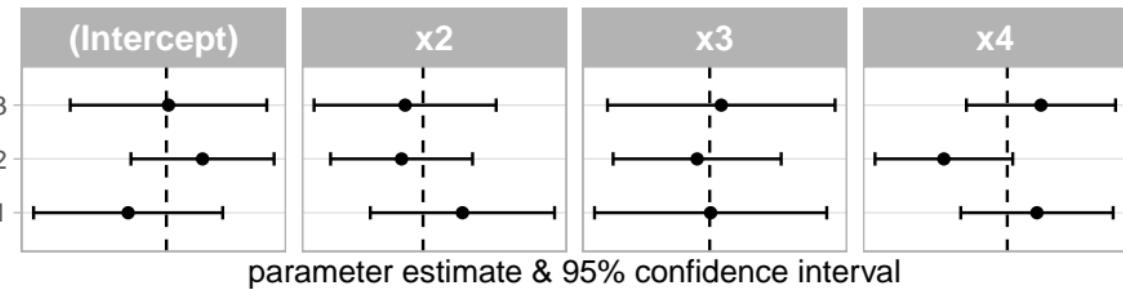
4. Pooling

To summarize the results, we can take the mean of the results from the separate analyses. This is the **pooled point estimate**.



4. Pooling

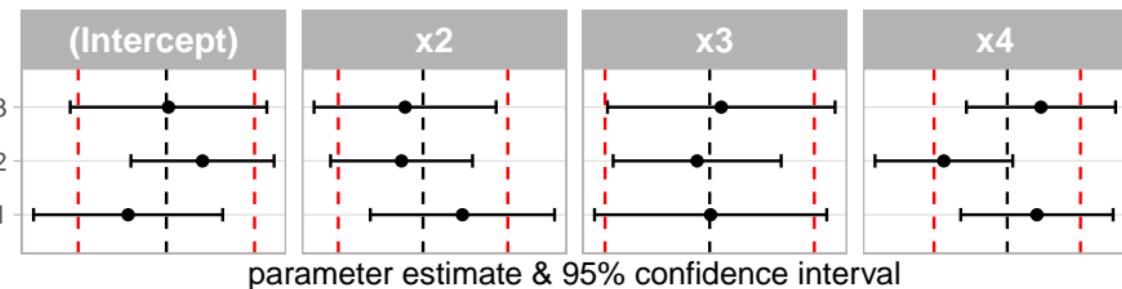
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But does the same work for the standard error (or bounds of the CIs)?

4. Pooling

To summarize the results, we can take the mean of the results from the separate analyses. This is the **pooled point estimate**.



But does the same work for the standard error (or bounds of the CIs)?

The averaged CI's (marked in red) underestimate the total variation (within + between).

4. Pooling

4.0.

The most commonly used method to pool results from analyses of multiply imputed data was introduced by Rubin [9], hence **Rubin's Rules**.

Notation:

m : number of imputed datasets

Q_ℓ : quantity of interest (e.g., regr. parameter β) from ℓ -th imputation

U_ℓ : variance of Q_ℓ (e.g., $\text{var}(\beta) = \text{se}(\beta)^2$)

Pooled parameter estimate:

$$\bar{Q} = \frac{1}{m} \sum_{\ell=1}^m \hat{Q}_\ell$$

4. Pooling

The **variance** of the pooled parameter estimate is calculated from the **within and between imputation variance**.

Average within imputation variance:

$$\bar{U} = \frac{1}{m} \sum_{\ell=1}^m \hat{U}_\ell$$

Between imputation variance:

$$B = \frac{1}{m-1} \sum_{\ell=1}^m (\hat{Q}_\ell - \bar{Q})^T (\hat{Q}_\ell - \bar{Q})$$

Total variance:

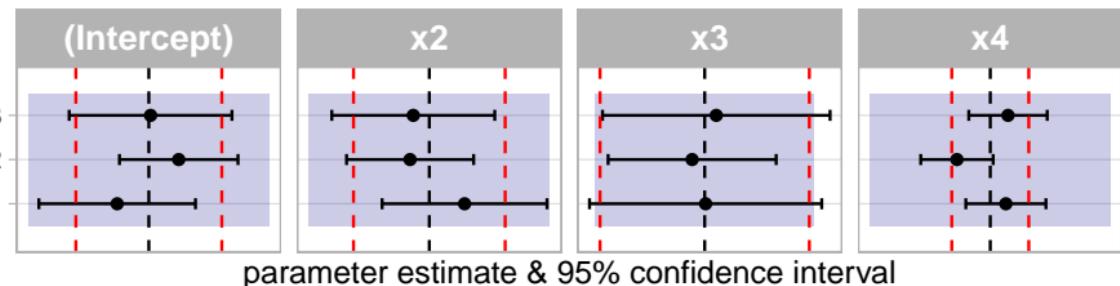
$$T = \bar{U} + B + B/m$$

4. Pooling

The $(1 - \alpha)$ 100% confidence interval is then

$$\bar{Q} \pm t_\nu(\alpha/2)\sqrt{T},$$

where t_ν is the $\alpha/2$ quantile of the t distribution with $\nu = (m - 1)(1 + r_m^{-1})^2$ degrees of freedom¹, where $r_m = \frac{(B+B/m)}{\bar{U}}$ is the relative increase in variance that is due to the missing values.



¹Barnard et al. [1] proposed an improvement to calculate the degrees of freedom. This improved version is implemented in the **mice** package.

Part II

Multiple Imputation Workflow

5. Know your data

5.1. Missing data patterns

To demonstrate the work flow when performing multiple imputation with the **mice** package, we use data from the National Health and Nutrition Examination Survey (NHANES).

There are several packages in R that provide functions to visualize incomplete data.

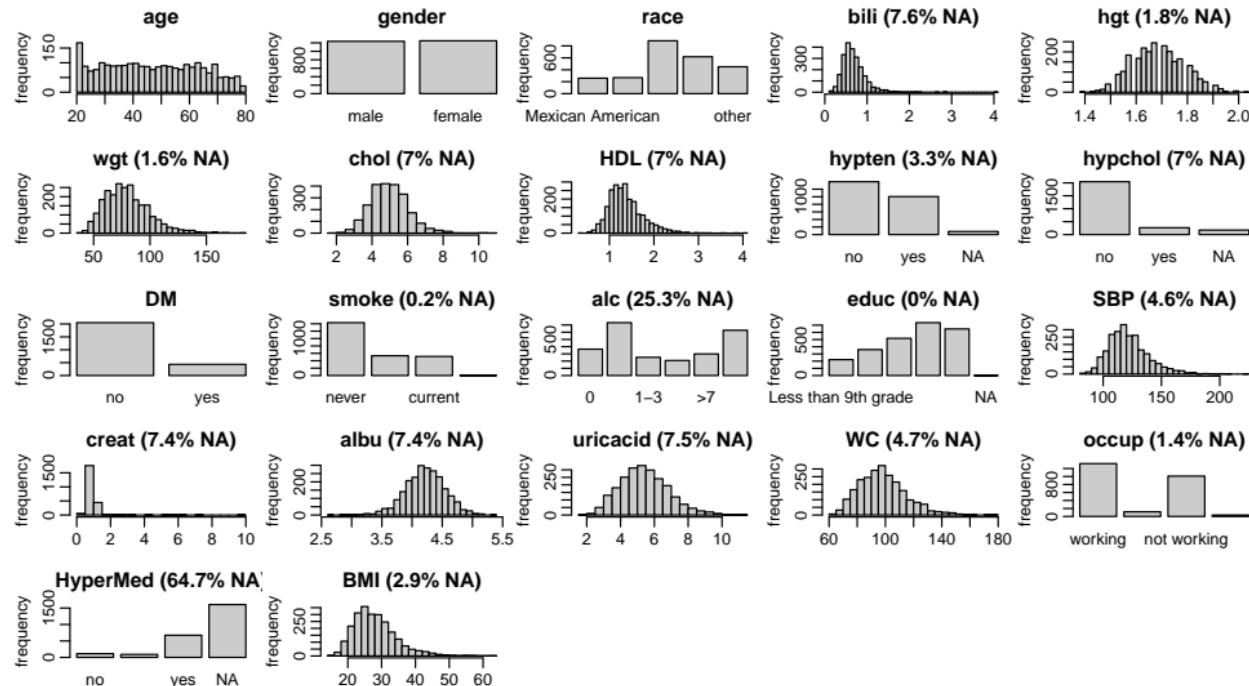
Examples are:

naniar, **VIM**, **visdat**, **mice**, **JointAI**, **Amelia**, ...

5. Know your data

5.2. Data distributions

```
JointAI::plot_all(NHANES, nclass = 30)
```



5. Know your data

5.2. Data distributions

```
mdp <- mice::md.pattern(NHANES, plot = FALSE)
head(mdp[, -c(8:14)]) # omit some columns to fit it on the slide

##      age gender race DM educ smoke occup HDL hypchol creat albu uricacid bili alc HyperMed
## 568    1       1   1  1     1     1     1   1       1     1     1     1     1     1     1     1
## 1040   1       1   1  1     1     1     1   1       1     1     1     1     1     1     1     1
## 141    1       1   1  1     1     1     1   1       1     1     1     1     1     1     1     0
## 300    1       1   1  1     1     1     1   1       1     1     1     1     1     1     1     0
## 2      1       1   1  1     1     1     1   1       1     1     1     1     1     0     1     0
## 1      1       1   1  1     1     1     1   1       1     1     1     1     1     1     0     0

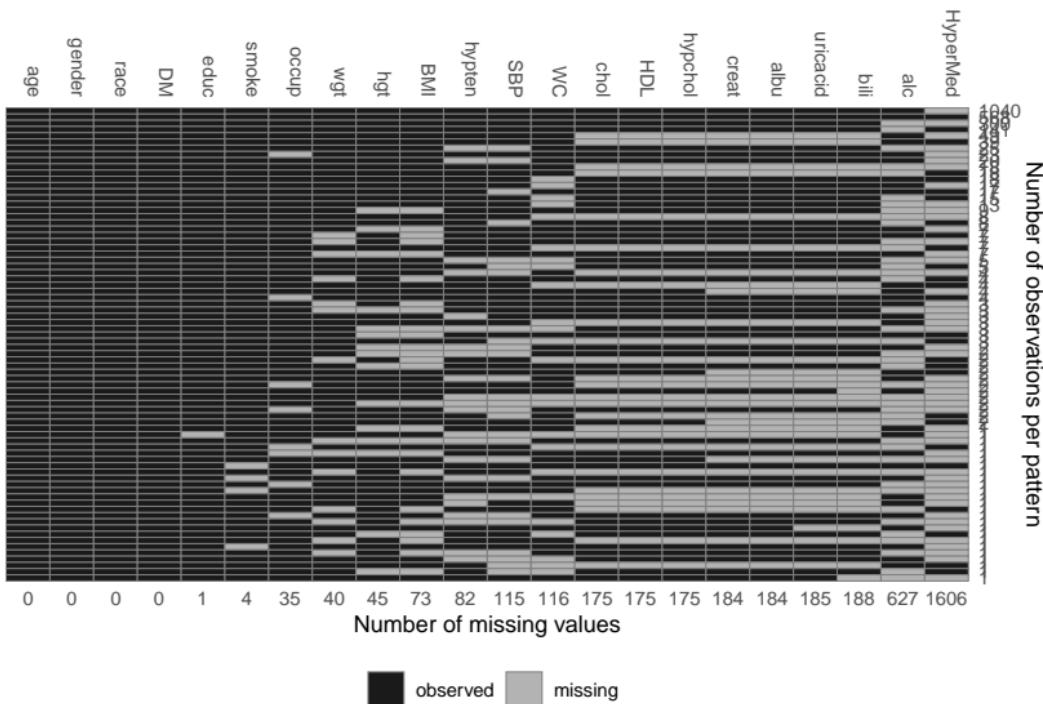
tail(mdp[, -c(8:14)])

##      age gender race DM educ smoke occup HDL hypchol creat albu uricacid bili alc HyperMed
## 1      1       1   1  1     1     0     1   1       1     1     1     1     1     1     1     1
## 1      1       1   1  1     1     0     1   1       1     1     1     1     1     1     1     0
## 1      1       1   1  1     1     0     1   0       0     0     0     0     0     0     0     0
## 1      1       1   1  1     1     0     1   1       1     1     1     1     1     1     1     0
## 1      1       1   1  1     0     1     1   0       0     0     0     0     0     0     1     0
## 0      0       0   0  0     1     4    35  175    175   184   184   185   188   627   1606  40
```

5. Know your data

5.2. Data distributions

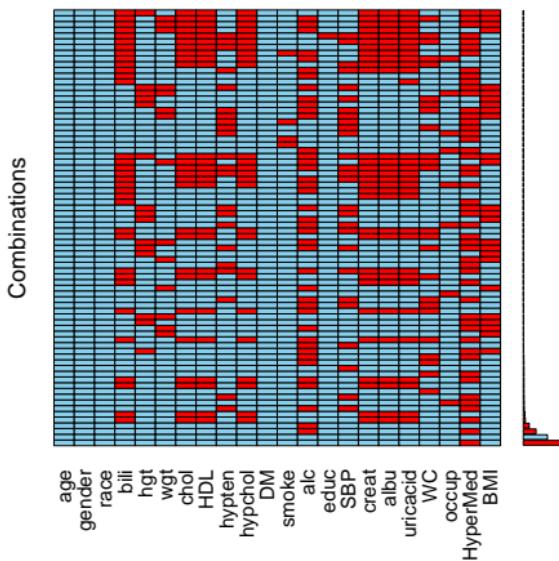
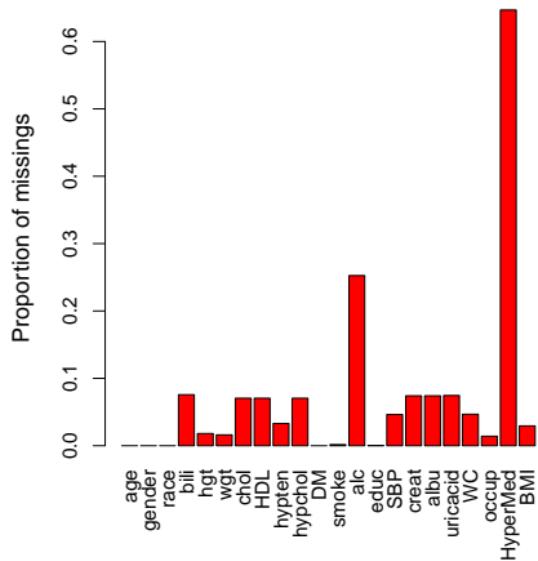
JointAI::md_pattern(NHANES)



5. Know your data

5.2. Data distributions

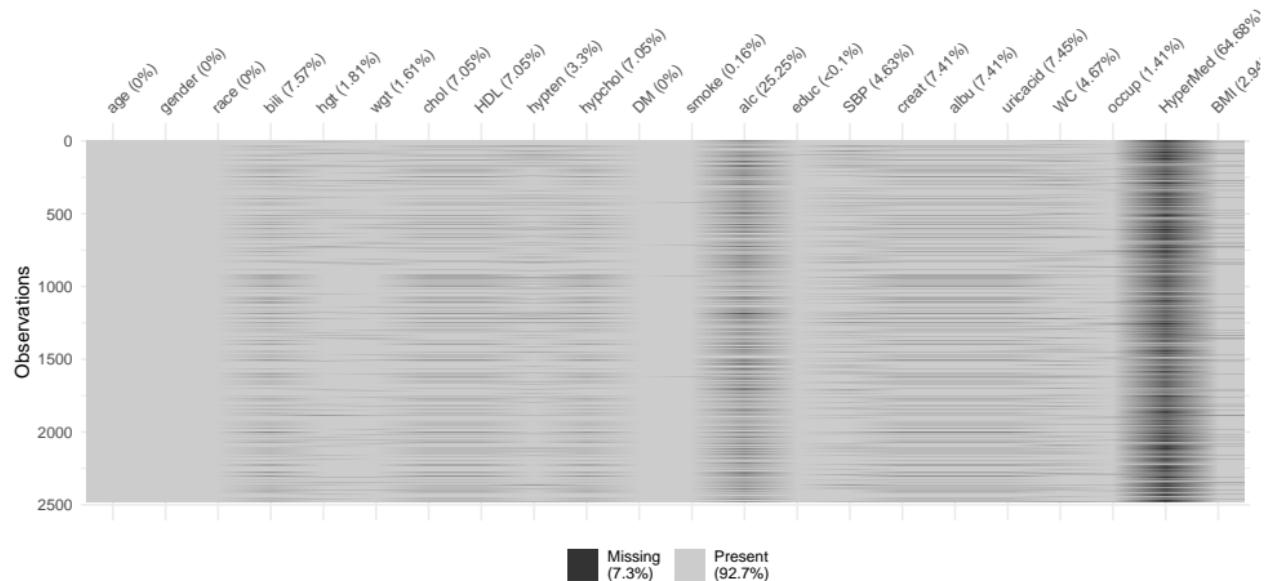
```
VIM:::aggr(NHANES, prop = TRUE, numbers = FALSE)
```



5. Know your data

5.2. Data distributions

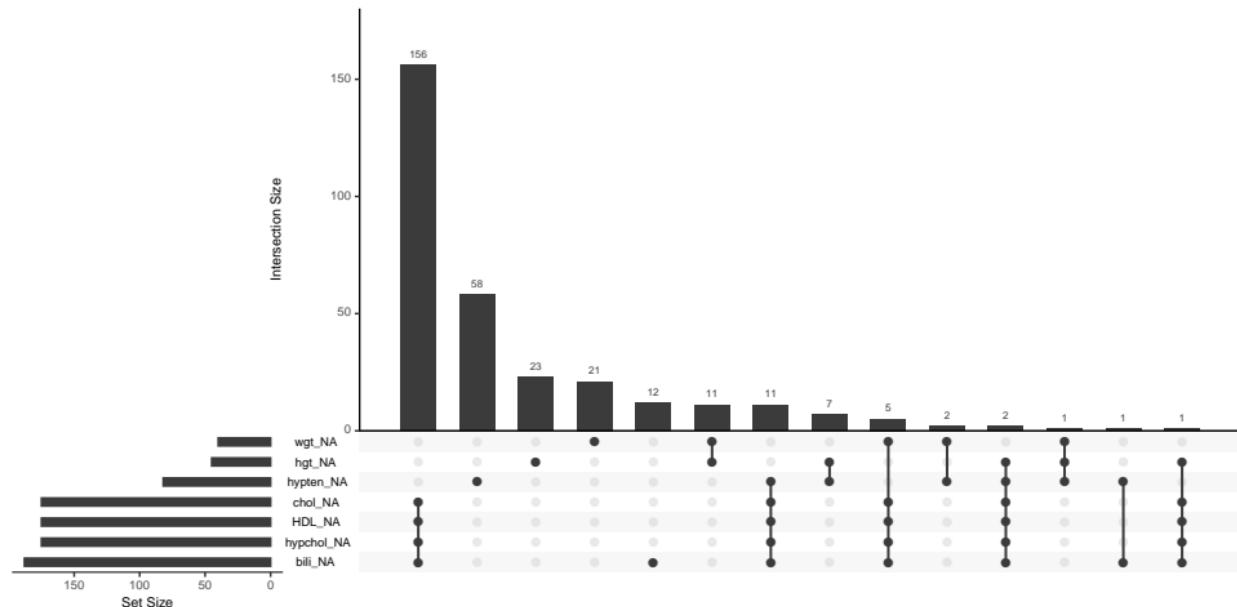
```
naniar::vis_miss(NHANES)
```



5. Know your data

5.2. Data distributions

```
naniar::gg_miss_upset(NHANES[, 1:10], nsets = 10)
```



5. Know your data

5.2. Data distributions

We are also interested in the number and proportion of (in)complete cases ...

```
cbind(  
  "#" = table(ifelse(complete.cases(NHANES), 'incompl.', 'complete')),  
  "%" = round(100 * table(complete.cases(NHANES))/nrow(NHANES), 2)  
)  
  
##           #      %  
## complete 1915 77.12  
## incompl.  568 22.88
```

5. Know your data

5.2. Data distributions

... and the proportion of missing values per variable:

```
cbind("# NA" = sort(colSums(is.na(NHANES))),  
      "% NA" = round(sort(colMeans(is.na(NHANES))) * 100, 2))  
# see also: naniar::miss_var_summary()
```

	# NA	% NA
## age	0	0.00
## gender	0	0.00
## race	0	0.00
## DM	0	0.00
## educ	1	0.04
## smoke	4	0.16
## occup	35	1.41
## wgt	40	1.61
## hgt	45	1.81
## BMI	73	2.94
## hypten	82	3.30

	# NA	% NA
## SBP	115	4.63
## WC	116	4.67
## chol	175	7.05
## HDL	175	7.05
## hypchol	175	7.05
## creat	184	7.41
## albu	184	7.41
## uricacid	185	7.45
## bili	188	7.57
## alc	627	25.25
## HyperMed	1606	64.68

5. Know your data

5.3. Correlations & patterns

A quick (and dirty) way to check for strong correlations between variables is:

```
# re-code all variables as numeric and calculate spearman correlation
Corr <- cor(sapply(NHANES, as.numeric),
             use = "pairwise.complete.obs", method = "spearman")
```

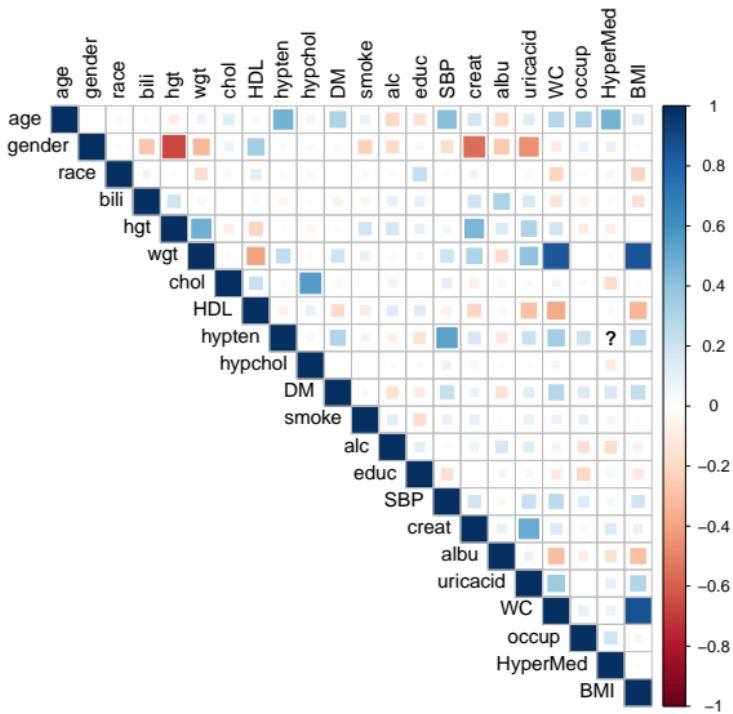
```
## Warning in cor(sapply(NHANES, as.numeric), use =
"pairwise.complete.obs", : the standard deviation is zero
```

```
corrplot::corrplot(Corr, method = "square", type = "upper",
                    tl.col = "black")
```

Note: We only use the correlation coefficient for categorical variables for visualization, not as a statistical result!

5. Know your data

5.3. Correlations & patterns



5. Know your data

5.3. Correlations & patterns

Check out what the problem is with `hypertension` and `HyperMed`:

```
table(hypertension = NHANES$hypten,
      HyperMed = NHANES$HyperMed, exclude = NULL)

##                      HyperMed
## hypertension   no previous yes <NA>
##           no      0        0     0 1397
##           yes     114       90    673 127
##           <NA>     0        0     0   82
```

5. Know your data

5.4. Why are values missing?

Knowing your data also means being able to answer these questions:

- Do missing values in multiple variables always **occur together**?
(e.g. blood measurements)
- Are there **structural missing values**? (e.g. pregnancy status in men)
- Are there **patterns** in the missing values?
(e.g. only patients with hypertension have observations of [HyperMed](#))
- Are values **missing by design**?
- Is the **assumption of ignorable missingness** (MAR or MCAR) justifiable?

5. Know your data

5.5. Auxiliary variables

Auxiliary variables are variables that are not part of the analysis but **can help during imputation.**

Good auxiliary variables [15]

- are **related to the probability of missingness** in a variable, or
- are **related to the incomplete variable** itself,
- do **not have many missing values** themselves and
- are (mostly) **observed** when the incomplete variable of interest is missing.

6. Imputation with `mice()`

6.1. Main function arguments

The main arguments needed to impute data with `mice()` are:

- `data`: the dataset
- `m`: number of imputed datasets (default is 5)
- `maxit`: number of iterations (default is 5)
- `method`: vector of imputation methods
- `defaultMethod`: vector of default imputation methods for numerical, binary, unordered and ordered factors with > 2 levels
(default is `c("pmm", "logreg", "polyreg", "polr")`)
- `predictorMatrix`: matrix specifying roles of variables

6. Imputation with mice()

6.2. Imputation methods

mice has implemented many **imputation methods**, the most commonly used ones are:

- `pmm`: predictive mean matching (any)
- `norm`: Bayesian linear regression (numeric)
- `logreg`: binary logistic regression (binary)
- `polr`: proportional odds model (ordered factors)
- `polyreg`: polytomous logistic regression (unordered factors)

6. Imputation with mice()

6.2. Imputation methods

Change the default imputation method:

Example: To use `norm` instead of `pmm` for all continuous incomplete variables, use:

```
mice(NHANES, defaultMethod = c("norm", "logreg", "polyreg", "polr"))
```

6. Imputation with mice()

6.2. Imputation methods

Change the default imputation method:

Example: To use `norm` instead of `pmm` for all continuous incomplete variables, use:

```
mice(NHANES, defaultMethod = c("norm", "logreg", "polyreg", "polr"))
```

Change imputation method for a single variable:

To change the imputation method for single variables (but also for changes in other arguments) it is convenient to **do a setup run** of `mice()` without iterations (`maxit = 0`) and to extract and modify the parameters from there.

6. Imputation with mice()

6.2. Imputation methods

Change the default imputation method:

Example: To use `norm` instead of `pmm` for all continuous incomplete variables, use:

```
mice(NHANES, defaultMethod = c("norm", "logreg", "polyreg", "polr"))
```

Change imputation method for a single variable:

To change the imputation method for single variables (but also for changes in other arguments) it is convenient to **do a setup run** of `mice()` without iterations (`maxit = 0`) and to extract and modify the parameters from there.

Exclude variable from imputation:

When a variable that has missing values should not be imputed, the method needs to be set to `""`.

6. Imputation with mice()

6.2. Imputation methods

```
library("mice")
imp0 <- mice(NHANES, maxit = 0)
meth <- imp0$method
meth

##      age    gender     race     bili     hgt     wgt
##      ""      ""      ""     "pmm"    "pmm"    "pmm"
##      chol      HDL    hypten   hypchol      DM     smoke
##      "pmm"    "pmm"  "logreg"  "logreg"      ""    "polr"
##      alc       educ     SBP     creat    albu uricacid
##      "polr"  "polyreg"  "pmm"    "pmm"    "pmm"    "pmm"
##      WC       occup HyperMed      BMI
##      "pmm"  "polyreg"  "polr"    "pmm"

meth["albu"] <- "norm"
meth["HyperMed"] <- ""
# imp <- mice(NHANES, method = meth)
```

6. Imputation with mice()

6.3. Predictor matrix

The `predictorMatrix` is a matrix that specifies **which variables are used as predictors** in which imputation model.

Each row represents the model for the variable given in the rowname.

```
head(imp0$predictorMatrix) [, 1:11]
```

```
##      age gender race bili hgt wgt chol HDL hypten hypchol DM
## age     0     1   1   1   1   1   1   1   1   1   1
## gender   1     0   1   1   1   1   1   1   1   1   1
## race     1     1   0   1   1   1   1   1   1   1   1
## bili     1     1   1   0   1   1   1   1   1   1   1
## hgt      1     1   1   1   0   1   1   1   1   1   1
## wgt      1     1   1   1   1   0   1   1   1   1   1
```

Variables **not used as predictor** are (or have to be set to) **zero**.

By **default, all variables** (except the variable itself) **are used** as predictors.

6. Imputation with mice()

6.3. Predictor matrix

Important:

A variable that has **missing values needs to be imputed** in order to be used as a predictor for other imputation models!!!

Note:

By default, **ALL** variables with missing values are imputed and **ALL** variables are used as predictor variables.

- ➡ Make sure to adjust the `predictorMatrix` and `method` to avoid using ID variables or other columns of the data that should not be part of the imputation.
- ➡ Make sure all **variables are coded correctly**, so that the automatically chosen imputation models are appropriate.

6. Imputation with mice()

6.3. Predictor matrix

```
library(mice)
# setup-run
imp0 <- mice(NHANES, maxit = 0,
              defaultMethod = c("norm", "logreg", "polyreg", "polr"))

# adjust imputation methods
meth <- imp0$method
meth["educ"] <- "polr"
meth["HyperMed"] <- ""

# adjust predictor matrix
pred <- imp0$predictorMatrix
pred[, "HyperMed"] <- 0

# run imputation with adjusted settings
imp <- mice(NHANES, method = meth, predictorMatrix = pred,
            printFlag = FALSE)
```

6. Imputation with mice()

6.4. Passive imputation

In some cases, variables are **functions of other variables**, e.g., $BMI = \frac{wgt}{hgt^2}$.

If we impute `BMI` directly, its values may be **inconsistent** with the (imputed) values of `hgt` and `wgt`.

```
DF1 <- complete(imp, 1) # select the first imputed dataset
round(cbind("wgt/hgt^2" = DF1$wgt/DF1$hgt^2,
            BMI = DF1$BMI)[is.na(NHANES$BMI), ], 2)[1:5, ]

##      wgt/hgt^2    BMI
## [1,]    23.87 25.91
## [2,]    28.75 27.95
## [3,]    23.73 21.67
## [4,]    25.25 24.95
## [5,]    27.43 26.58
```

The imputed values of `BMI` are impossible given the corresponding values of `hgt` and `wgt`.

6. Imputation with mice()

6.4. Passive imputation

Moreover, if some components of a variable are observed we want to use that **information to reduce uncertainty**.

```
table(wgt_missing = is.na(NHANES$wgt),  
      hgt_missing = is.na(NHANES$hgt))  
  
##           hgt_missing  
## wgt_missing FALSE  TRUE  
##          FALSE 2410   33  
##          TRUE   28    12
```

Here we have $33 + 28 = 61$ cases in which either `hgt` or `wgt` is observed.

We would like to impute `hgt` and `wgt` separately and calculate `BMI` from the (imputed) values of the two variables.

6. Imputation with mice()

6.4. Passive imputation

If `BMI` is not a relevant predictor in any of the other imputation models, we could just exclude BMI from the imputation and **re-calculate it afterwards.**

To use `BMI` as predictor in the imputation, it has to be **calculated in each iteration** of the algorithm. In `mice` this is possible with **passive imputation**.

6. Imputation with mice()

6.4. Passive imputation

If `BMI` is not a relevant predictor in any of the other imputation models, we could just exclude `BMI` from the imputation and **re-calculate it afterwards.**

To use `BMI` as predictor in the imputation, it has to be **calculated in each iteration** of the algorithm. In `mice` this is possible with **passive imputation**.

Instead of using a standard imputation `method`, we can specify a formula to calculate `BMI`:

```
meth["BMI"] <- "~I(wgt/hgt^2)"      # formula to impute BMI  
pred[c("wgt", "hgt"), "BMI"] <- 0  # prevent feedback
```

To **prevent feedback** from `BMI` in the imputation of `hgt` and `wgt` the `predictorMatrix` needs to be modified.

6. Imputation with mice()

6.4. Passive imputation

Since `BMI` depends on `wgt`, and the two variables are highly correlated ($\rho = 0.87$) it may be beneficial **not to use them simultaneously** as predictors in the other imputation models.

Which one to use may differ between imputation models.

Passive imputation can also be useful in settings where

- imputation models include **interaction terms** between incomplete variables (see [15, p. 133] for an example), or when
- a number of covariates is used to form a **sum score**. The sum score, instead of all single elements, can then be used as predictor in other imputation models.

6. Imputation with mice()

6.5. Post processing

`mice()` has an argument `post` that can be used to specify functions that modify imputed values.

Helpful functions are

- `squeeze()` to censor variables at given boundaries
- ~~`ifdo()` for conditional manipulation (not yet implemented)~~

6. Imputation with mice()

6.5. Post processing

`mice()` has an argument `post` that can be used to specify functions that modify imputed values.

Helpful functions are

- `squeeze()` to censor variables at given boundaries
- ~~`ifdo()` for conditional manipulation (not yet implemented)~~

Example:

When inspecting the imputed values from `imp`, we find that some imputed values in `creat` are negative.

```
# DF1 is the first imputed dataset we extracted earlier
summary(DF1$creat)
```

```
##      Min. 1st Qu. Median      Mean 3rd Qu.      Max.
## -0.2829  0.7000  0.8400  0.8882  0.9900  9.5100
```

6. Imputation with mice()

6.5. Post processing

With the following syntax all imputed values of `creat` that are outside the interval $c(0, 100)$ will be **set to those limiting values**.

```
post <- imp$post
post["creat"] <- "imp[[j]][,i] <- squeeze(imp[[j]][,i], c(0, 100))"
imp2 <- update(imp, post = post, maxit = 20, seed = 123)
```

Note:

When many observations are outside the limits it may be better to **change the imputation model** since the implied **assumption of the imputation model** apparently **does not fit the** (assumption about the) **complete data distribution**.

6. Imputation with mice()

6.5. Post processing

This **post-processing** of imputed values allows for many **more data manipulations** and is not restricted to `squeeze()` (and `ifdo()`).

Any strings of R commands provided will be evaluated after the corresponding variable is imputed, within each iteration.

For example, if subjects with SBP > 140 should be classified as hypertensive:

```
post["hypoten"] <- "imp[[j]][p$data[where[, j], 'SBP'] > 140, i] <- 'yes'"
```

This also allows for (some) **MNAR scenarios**, for example, by multiplying or adding a constant to the imputed values, or to re-impute values depending on their current value.

6. Imputation with mice()

6.6. Visit sequence

When the **post-processed or passively imputed values** of a variable depend on other variables, the **sequence in which the variables are imputed** may be important to obtain **consistent values**.

Example:

If `BMI` is passively imputed (calculated) before the new imputations for `hgt` and `wgt` are drawn, the resulting values of `BMI`, will match `hgt` and `wgt` from the **previous iteration**, but not the iteration given in the imputed dataset.

In `mice()` the argument `visitSequence` specifies in which order the columns of the data are imputed. By default `mice()` imputes in the order of the columns in `data`.

6. Imputation with mice()

6.6. Visit sequence

```
visitSeq <- imp2$visitSequence  
visitSeq  
  
## [1] "age"        "gender"      "race"       "bili"       "hgt"        "wgt"  
## [7] "chol"       "HDL"         "hypten"     "hypchol"    "DM"        "smoke"  
## [13] "alc"        "educ"        "SBP"        "creat"      "albu"      "uricacid"  
## [19] "WC"         "occup"       "HyperMed"   "BMI"
```

Currently, `hypten` is imputed before `SBP`, but the imputed values of `hypten` are post-processed depending on the current value of `SBP`. To get consistent values of these two variables, we need to change the `visitSequence`.

6. Imputation with mice()

6.6. Visit sequence

```
visitSeq <- c(visitSeq[-which(visitSeq == "hypten")],  
            "hypten")  
  
visitSeq  
  
## [1] "age"        "gender"      "race"       "bili"       "hgt"        "wgt"  
## [7] "chol"       "HDL"        "hypchol"    "DM"        "smoke"     "alc"  
## [13] "educ"       "SBP"        "creat"      "albu"       "uricacid"   "WC"  
## [19] "occup"      "HyperMed"   "BMI"        "hypten"
```

The `visitSequence` may specify that a column is visited multiple times during one iteration. All incomplete variables must be visited at least once.

6. Imputation with mice()

6.7. Good to know

`mice()` performs some **pre-processing** and **removes**

- incomplete variables that are not imputed but are specified as predictors,
- constant variables, and
- collinear variables.

In each iteration

- linearly dependent variables are removed and
- `polr` imputation models that do not converge are replaced by `polyreg`.

Why?

To avoid problems in the imputation models.

6. Imputation with mice()

6.7. Good to know

As a **consequence**

- imputation models may differ from what the user has specified or assumes is happening, or
- variables that should be imputed are not.

- ▶ Know your data
- ▶ Make sure `method` and `predictorMatrix` are specified appropriately
- ▶ Check the output and log of these automatic actions carefully

Practical

To practice the content of the previous section find the **html version** of the practical here:

[https://nerler.github.io/EP16_Multiple_Imputation/practical/
mimice/EP16_MImice.html](https://nerler.github.io/EP16_Multiple_Imputation/practical/mimice/EP16_MImice.html)

7. Convergence & diagnostics

7.1. Logged events

The log of the automatic changes is returned as part of the `mids` object:

```
demo <- NHANES[, 1:5]
demo$dupl <- demo[, 4]
demo$const <- 1
demo$age[demo$gender == 'male'] <- NA
```

```
demoimp <- mice(demo)
head(demoimp$loggedEvents)
```

Warning: Number of logged events: 8

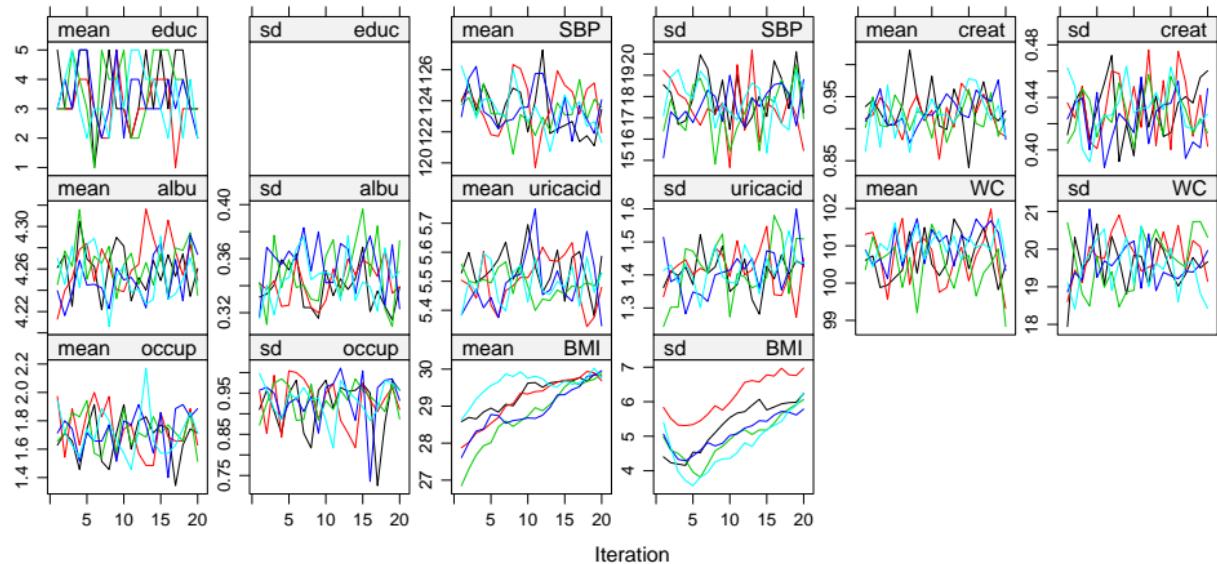
```
##   it im dep      meth          out
## 1  0  0 constant    const
## 2  0  0 collinear    dupl
## 3  1  1 age       pmm genderfemale
## 4  1  2 age       pmm genderfemale
## 5  1  3 age       pmm genderfemale
## 6  2  1 age       pmm genderfemale
```

With columns

<code>it</code>	iteration number
<code>im</code>	imputation number
<code>dep</code>	dependent variable
<code>meth</code>	imputation method used
<code>out</code>	names of altered or removed predictors

7. Convergence & diagnostics

7.2. Convergence



7. Convergence & diagnostics

7.2. Convergence

Strong trends and traces that show **correlation** between variables indicate **problems of feedback**. This needs to be investigated and resolved in the specification of the `predictorMatrix`.

Weak trends may be artefacts that often disappear when the imputation is performed with more iterations.

7. Convergence & diagnostics

7.3. Diagnostics

When MCMC chains have converged, the **distributions of the imputed and observed values** can be compared to investigate differences between observed and imputed data.

Note:

Plots usually show the **marginal** distributions of observed and imputed values, which do not have to be identical under MAR.

Recall:

The **conditional** distributions (given all the other variables in the imputation model) of the imputed values are assumed to be the same as the conditional distributions of the observed data.

7. Convergence & diagnostics

7.3. Diagnostics

mice provides several functions for visual diagnosis of imputed values:

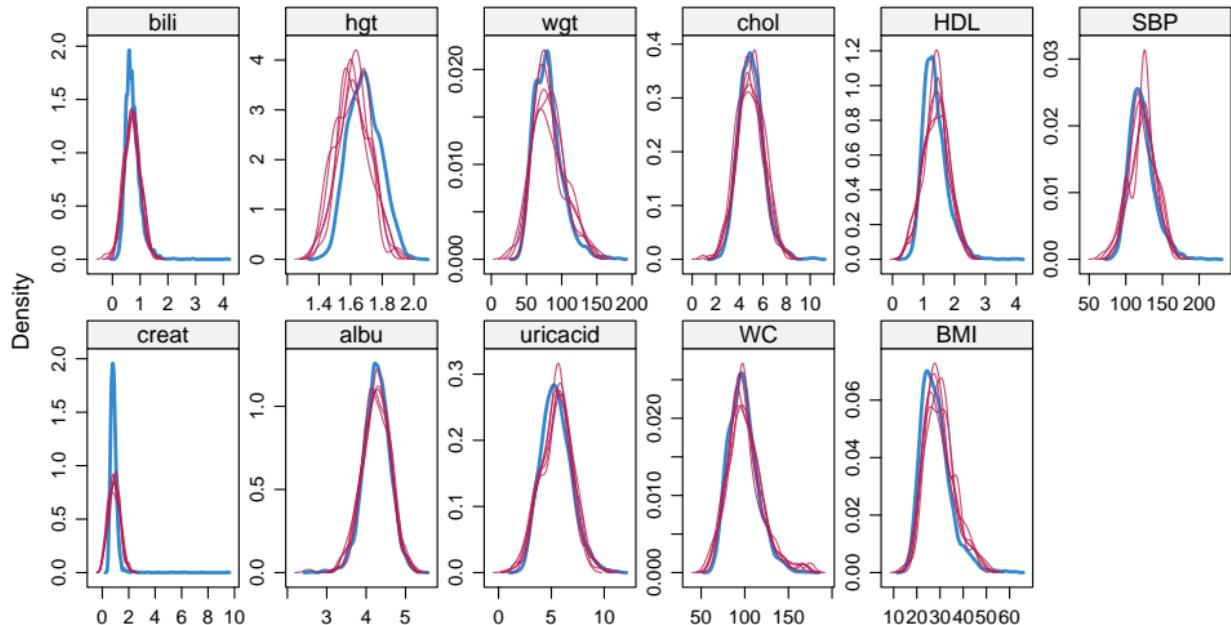
- `densityplot()` (for large datasets and variables with many NAs)
- `stripplot()` (for smaller datasets and/or variables with few NAs)
- `bwplot()`
- `xyplot()`

These functions create **lattice graphics**, which can be modified analogously to their parent functions from the **lattice** package.

7. Convergence & diagnostics

7.3. Diagnostics

```
densityplot(imp2)
```



7. Convergence & diagnostics

7.3. Diagnostics

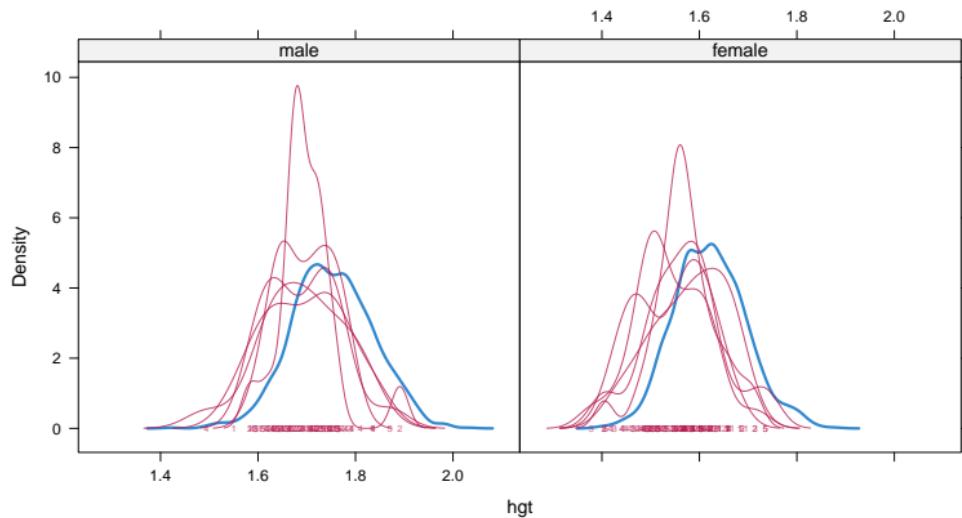
The `densityplot()` shows that the distribution of imputed values of `creat` is wider than the distribution of the observed values and that imputed values of `hgt` are smaller than the observed values.

7. Convergence & diagnostics

7.3. Diagnostics

In some cases, differences in distributions can be explained by strata in the data, however, here, `gender` does not explain the difference in observed and imputed values.

```
densityplot(imp2, ~hgt|gender, plot.points = TRUE)
```

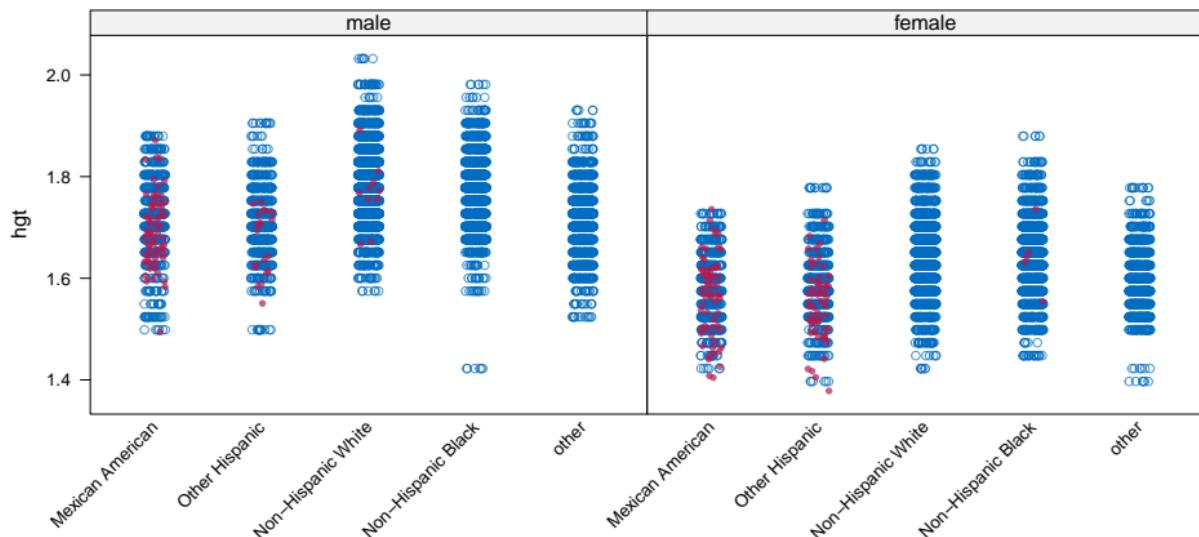


7. Convergence & diagnostics

7.3. Diagnostics

For (combinations of) variables with very few missing values a `stripplot()` may be better suited. Here we can also split the data for `gender` and `race`.

```
stripplot(imp2, hgt ~ race|gender, pch = c(1, 20),  
          scales = list(x = list(rot = 45)))
```

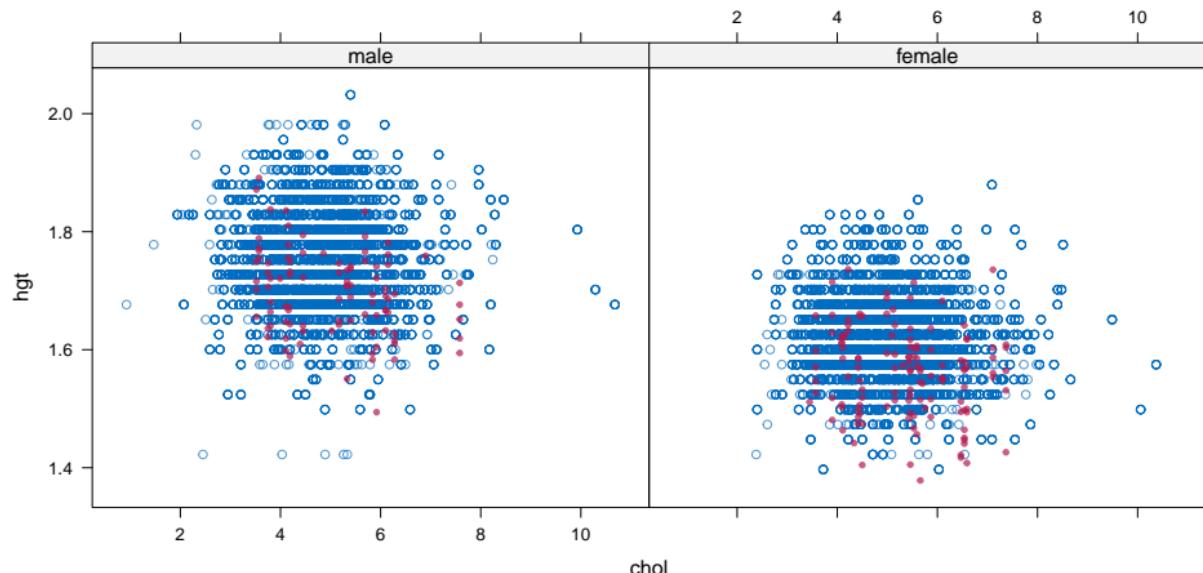


7. Convergence & diagnostics

7.3. Diagnostics

The function `xyplot()` allows multivariate investigation of the imputed versus observed values.

```
xyplot(imp2, hgt ~ chol | gender, pch = c(1, 20))
```



7. Convergence & diagnostics

7.3. Diagnostics

All of the above graphs displayed only continuous imputed variables.

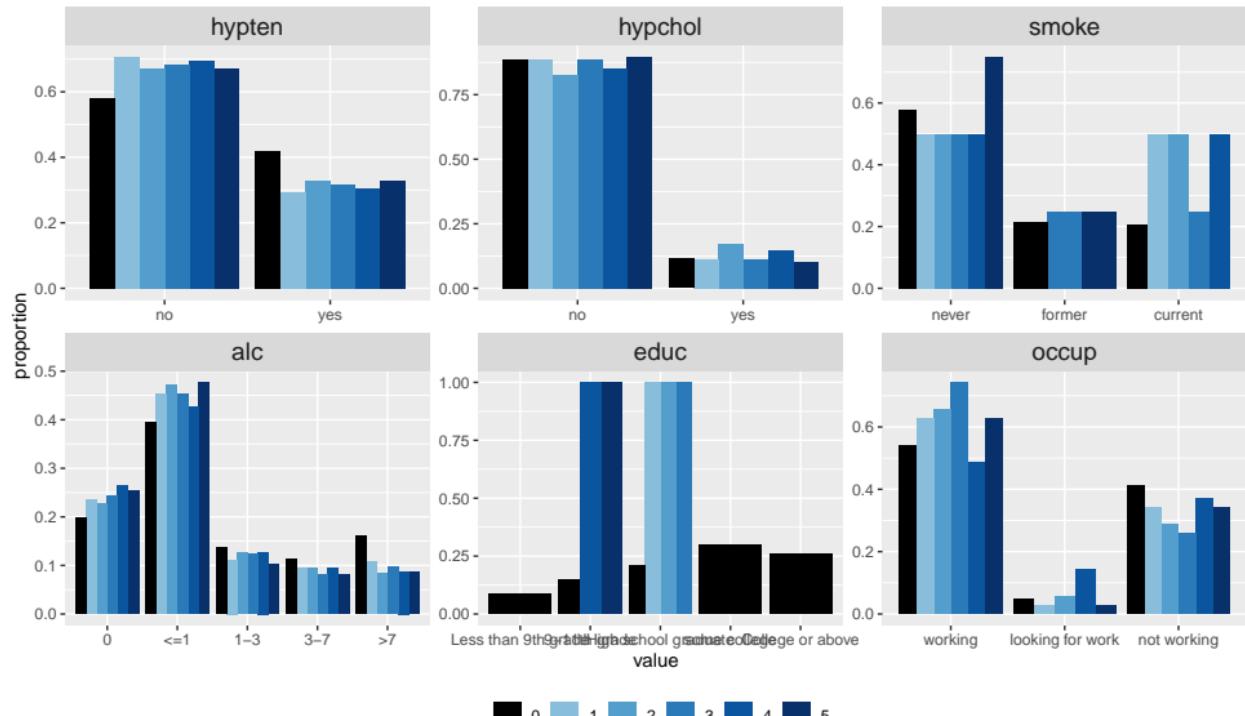
For categorical variables we can compare the proportion of values in each category.

mice does not provide a function to do this, but we can write one ourselves, as for instance the function `propplot()`, for which the syntax can be found here:
<https://gist.github.com/NErlr/0d00375da460dd33839b98faeee2fdab>

7. Convergence & diagnostics

7.3. Diagnostics

```
propplot(imp2, strip.text = element_text(size = 14))
```



7. Convergence & diagnostics

7.3. Diagnostics

`smoke` and `educ` have very few missing values (4 and 1, respectively), so we do not need to worry about differences between observed and imputed data for those variables.

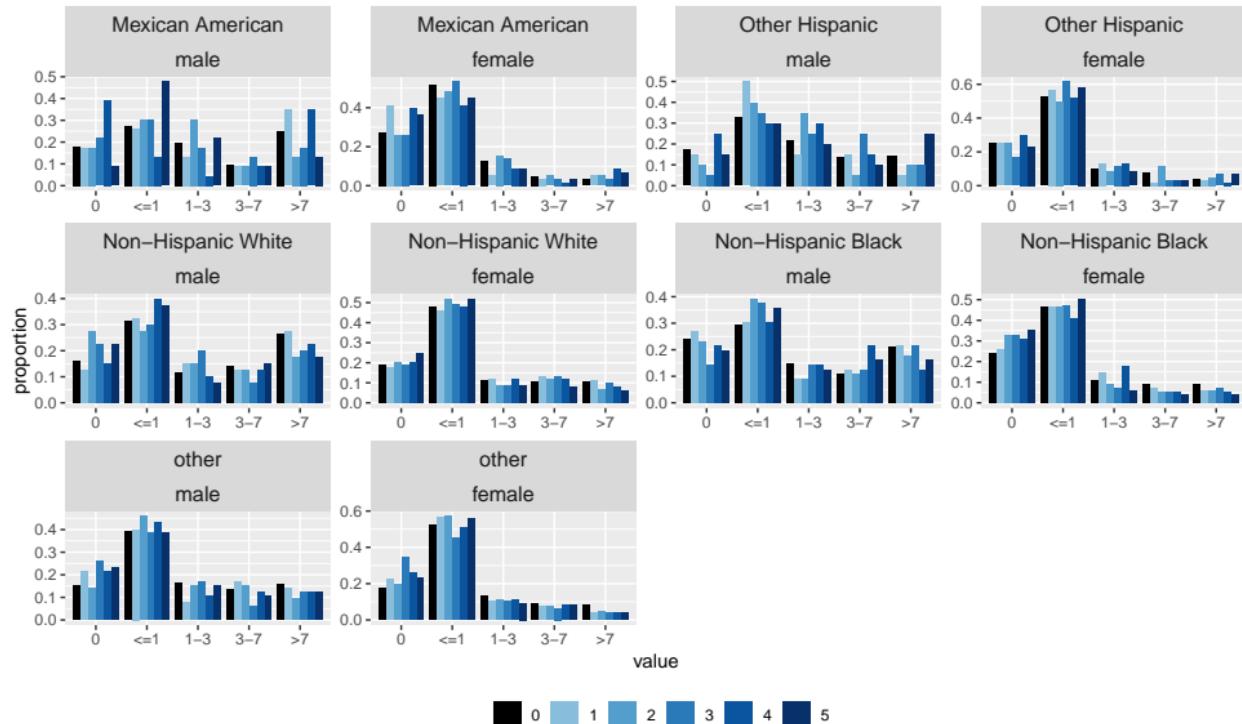
- `alc`: missing values are imputed in the lower consumption categories more often than we would expect from the observed data
- `hypnten` is less frequent and
- `hypchol` a bit more frequent, in the imputed data compared to the observed.

If we expect that `gender` and `race` might explain the differences for `alc`, we can include those factors into the plot.

7. Convergence & diagnostics

7.3. Diagnostics

```
propplot(imp2, formula = alc ~ race + gender)
```



7. Convergence & diagnostics

7.3. Diagnostics

Since hypertension is more common in older individuals, we may want to investigate if `age` can explain the differences in imputed values of `hypten`.

```
round(sapply(split(NHANES[, "age"], addNA(NHANES$hypten)), summary), 1)

##           no   yes <NA>
## Min.    20.0 20.0 20.0
## 1st Qu. 28.0 47.0 30.0
## Median  38.0 59.0 38.5
## Mean    40.7 56.9 41.5
## 3rd Qu. 51.0 68.0 50.8
## Max.    79.0 79.0 78.0
```

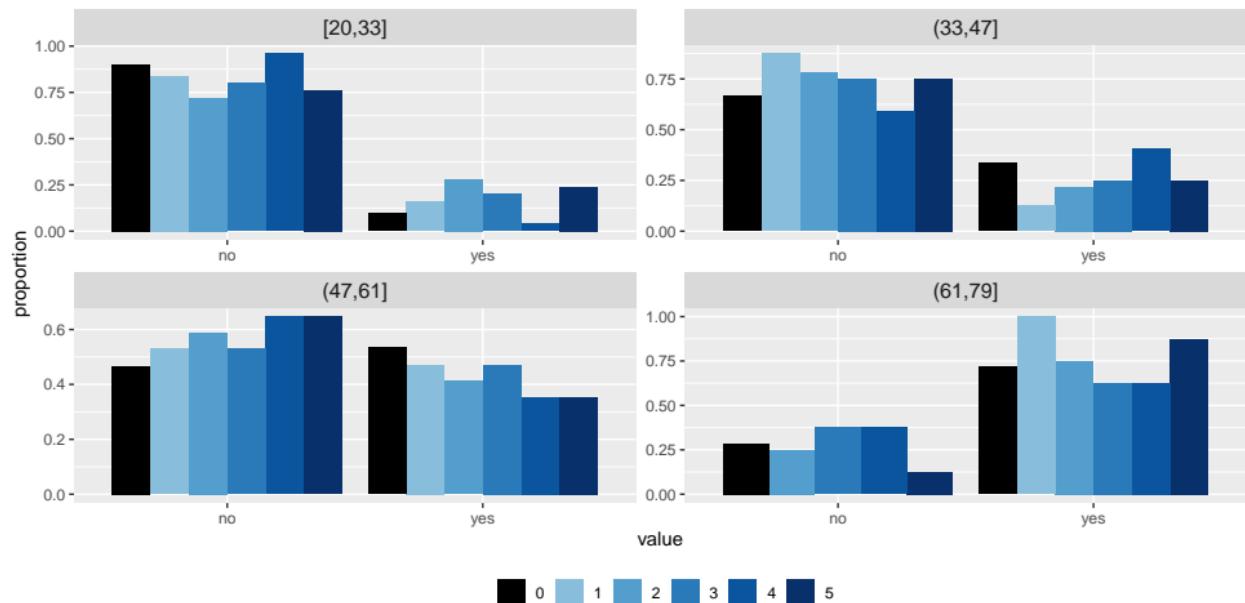
The table shows that the distribution of `age` in participants with missing `hypten` is very similar to the distribution of `age` in participants without `hypten`.

7. Convergence & diagnostics

7.3. Diagnostics

Plotting the proportions of observed and imputed `hypten` separately per quartile of `age`:

```
propplot(imp2, formula = hypten ~ cut(age, quantile(age), include.lowest = T))
```



Practical

To practice the content of the previous section you may find the **html version** of the practical here:

[https://nerler.github.io/EP16_Multiple_Imputation/practical/
micheck/EP16_MIcheck.html](https://nerler.github.io/EP16_Multiple_Imputation/practical/micheck/EP16_MIcheck.html)

8. Analyse & pool the imputed data

8.1. Analysing imputed data

Once we have confirmed that our imputation was successful, we can move on to the **analysis of the imputed data**.

For example, we might be interested in the following logistic regression model:

```
glm(DM ~ age + gender + hypchol + BMI + smoke + alc,  
family = "binomial")
```

8. Analyse & pool the imputed data

8.1. Analysing imputed data

Once we have confirmed that our imputation was successful, we can move on to the **analysis of the imputed data**.

For example, we might be interested in the following logistic regression model:

```
glm(DM ~ age + gender + hypchol + BMI + smoke + alc,  
family = "binomial")
```

To fit the model on each of the imputed datasets, we do not need to extract the data from the `mids` object, but can use `with()`.

```
mod1 <- with(imp2, glm(DM ~ age + gender + hypchol + BMI + smoke + alc,  
family = "binomial"))
```

`mod1` is an object of class `mira`.

8. Analyse & pool the imputed data

8.2. Pooling results

Pooled results can be obtained using `pool()` and its summary.

```
options(width = 90)
res1 <- summary(pool(mod1), conf.int = TRUE)
round(res1, 3)

##           estimate std.error statistic      df p.value   2.5 % 97.5 %
## (Intercept) -7.484     0.404   -18.520 2146.569  0.000 -8.277 -6.692
## age          0.056     0.004    12.698 1363.291  0.000  0.047  0.065
## genderfemale -0.424     0.127   -3.349 2333.764  0.001 -0.673 -0.176
## hypcholyes   0.009     0.201     0.043  87.509  0.966 -0.392  0.409
## BMI          0.105     0.009   11.509 2440.963  0.000  0.087  0.123
## smoke.L       0.063     0.116     0.545 2401.105  0.586 -0.165  0.291
## smoke.Q      -0.075     0.115   -0.650 2409.227  0.515 -0.300  0.151
## alc.L         -0.562     0.165   -3.402 197.275  0.001 -0.887 -0.236
## alc.Q         0.182     0.189     0.963  50.461  0.340 -0.197  0.560
## alc.C         0.017     0.188     0.089  49.989  0.930 -0.361  0.395
## alc^4        -0.045     0.206   -0.217  45.455  0.829 -0.460  0.371
```

8. Analyse & pool the imputed data

8.2. Pooling results

Pooling with `mice::pool()` is available for most types of models.

It extracts the model coefficients and variance-covariance matrices using `tidy()` from the package **broom**. Hence, pooling using the `pool()` function from **mice** only works for models of classes for which a method `tidy()` exists.

An alternative is offered by the package **mitools** and the function `MIcombine()`.

8. Analyse & pool the imputed data

8.3. Functions for pooled results

mice currently has two functions available for evaluating model fit / model comparison

For **linear** regression models the pooled R^2 can be calculated using `pool.r.squared()`.

```
mod2 <- with(imp2, lm(SBP ~ DM + age + hypten))
pool.r.squared(mod2, adjusted = TRUE)

##                  est      lo 95      hi 95 fmi
## adj R^2 0.3252735 0.2943749 0.3562265 NaN
```

The argument `adjusted` specifies whether the adjusted R^2 or the standard R^2 is returned.

8. Analyse & pool the imputed data

8.3. Functions for pooled results

The function `pool.compare()` allows comparison of **nested models** (i.e., models where one is a special case of the other, with some parameters fixed to zero) using a **Wald test**.

Example: To test if `smoke` has a relevant contribution to the model for `DM` from above we re-fit the model without `smoke` and compare the two models:

```
mod3 <- with(imp2, glm(DM ~ age + gender + hypchol + BMI + alc,  
                      family = "binomial"))  
# Wald test  
pool.compare(mod1, mod3)$pvalue  
  
## [,1]  
## [1,] 0.6978098
```

`anova()` allows comparison of multiple nested models

8. Analyse & pool the imputed data

8.3. Functions for pooled results

The package **miceadds** extends **mice**, for example with the following functionality:

Combine χ^2 or F statistics from multiply imputed data:

```
miceadds::micombine.chisquare(dk, df, ...)  
miceadds::micombine.F(values, df1, ...)
```

These functions take vectors of statistics computed on each imputed dataset and pool them.

8. Analyse & pool the imputed data

8.3. Functions for pooled results

The package **miceadds** extends **mice**, for example with the following functionality:

Combine χ^2 or F statistics from multiply imputed data:

```
miceadds::micombine.chisquare(dk, df, ...)  
miceadds::micombine.F(values, df1, ...)
```

These functions take vectors of statistics computed on each imputed dataset and pool them.

Calculate correlation or covariance of imputed data:

```
miceadds::micombine.cor(mi.res, ...)  
miceadds::micombine.cov(mi.res, ...)
```

These functions take `mids` objects as input.

9. Additional functions in mice()

9.1. Extract & export imputed data

The function `complete()` allows **extraction of the imputed data** from a `mids` object:

```
mice::complete(data, action = 1, include = FALSE, ...)
```

- `data`: the `mids` object
- `action`:
 - `1, ..., m` (single imputed dataset)
 - `"long"`: long format (imputed data stacked vertically)
 - `"broad"`: wide format (imputed data combined horizontally;
 ordered by imputation)
 - `"repeated"`: (like `"broad"`, but ordered by variable)
- `include`: include the original data?
(if `action` is `"long"`, `"broad"` or `"repeated"`)

9. Additional functions in mice()

9.1. Extract & export imputed data

The function `mids2spss()` allows the **export of imputed data** (mids objects) to SPSS.

```
mids2spss(imp2,
            filedat = "datafile.txt", # the file containing the data
            filesps = "importsyntax.sps", # syntax to get .sav from .txt
            silent = TRUE, ...
)
```

Data from mids objects can also be exported to MPLUS using `mids2mplus()`.

9. Additional functions in mice()

9.2. Combining mids objects

To **increase the number of imputed datasets** without re-doing the initial m imputations, a second set of imputations can be done and the two `mids` objects combined using `ibind()`.

```
# same syntax as before, but different seed
imp2b <- update(imp2, post = post, maxit = 20, seed = 456)
imp2combi <- ibind(imp2, imp2b)
```

```
# check the new number of impute datasets:
imp2combi$m

## [1] 10
```

Part III

When MICE might fail

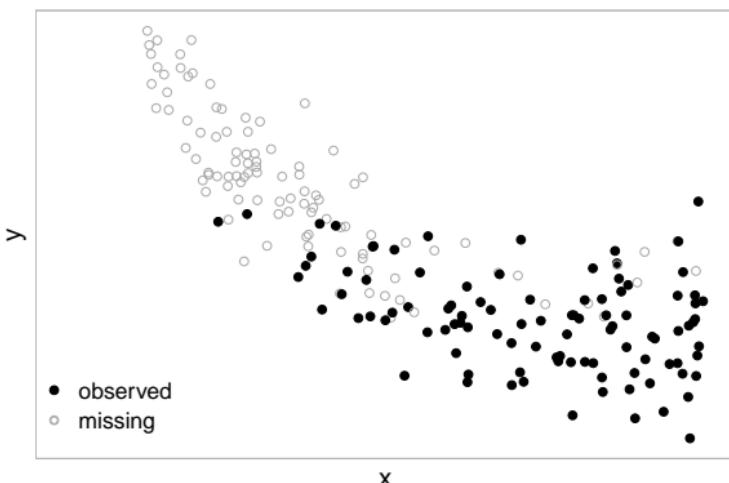
10. Settings where MICE may have problems

10.1. Quadratic effect

Consider the case where the **analysis model** (which we assume to be true) is

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + \dots,$$

i.e., y has a **quadratic relationship** with x , and x is incomplete.



The original data show a curved pattern.

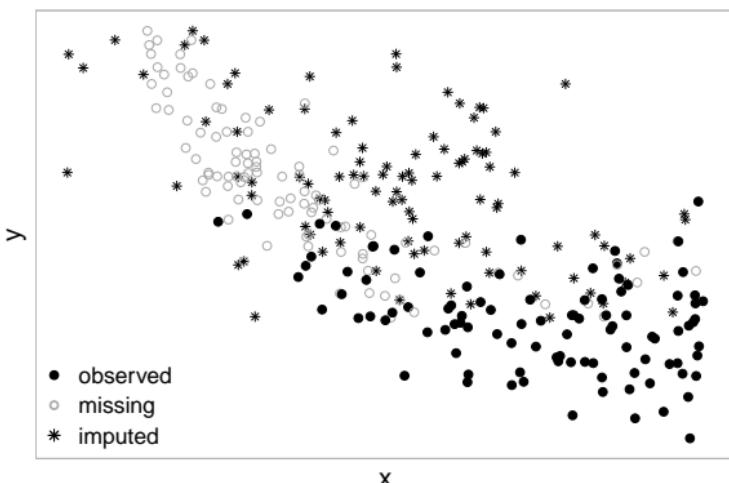
10. Settings where MICE may have problems

10.1. Quadratic effect

The model used to **impute** x when using MICE (naively) is

$$x = \theta_{10} + \theta_{11}y + \dots,$$

i.e., a **linear relation** between x and y is assumed.

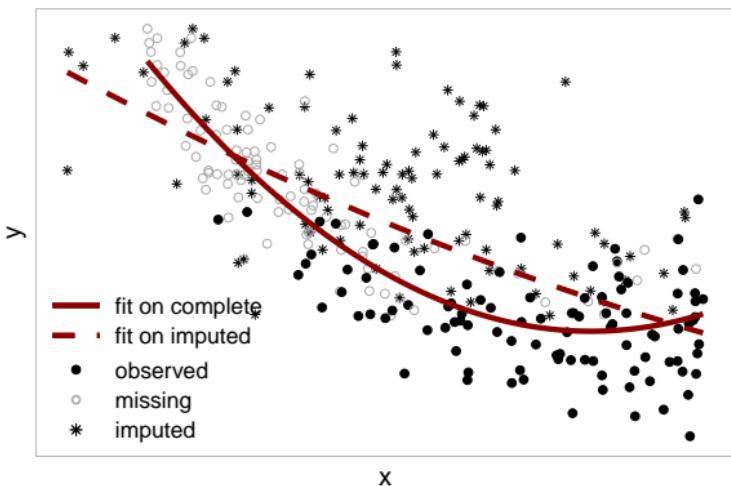


The imputed values **distort the curved pattern** of the original data.

10. Settings where MICE may have problems

10.1. Quadratic effect

The model fitted on the imputed data gives **severely biased results**; the non-linear shape of the curve has almost completely disappeared.



	β	95% CI
Original		
Intercept	-0.99	[-1.04, -0.95]
x	-0.61	[-0.66, -0.56]
x^2	0.52	[0.43, 0.62]
Imputed		
Intercept	-0.73	[-0.79, -0.66]
x	-0.53	[-0.62, -0.44]
x^2	0.07	[-0.07, 0.22]

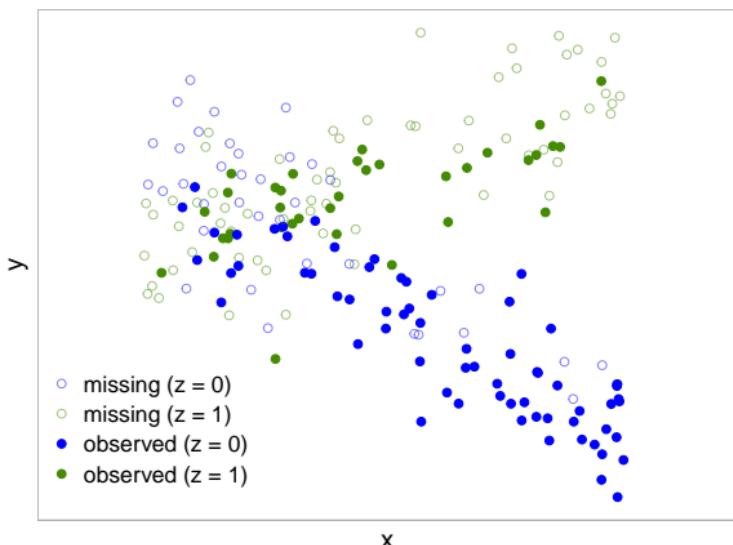
10. Settings where MICE may have problems

10.2. Interaction effect

Another example occurs when the analysis model (again, assumed to be true) is

$$y = \beta_0 + \beta_x x + \beta_z z + \beta_{xz} xz + \dots,$$

i.e., y has a **non-linear relationship** with x due to the **interaction term**.



The original data shows a “<” shaped pattern.

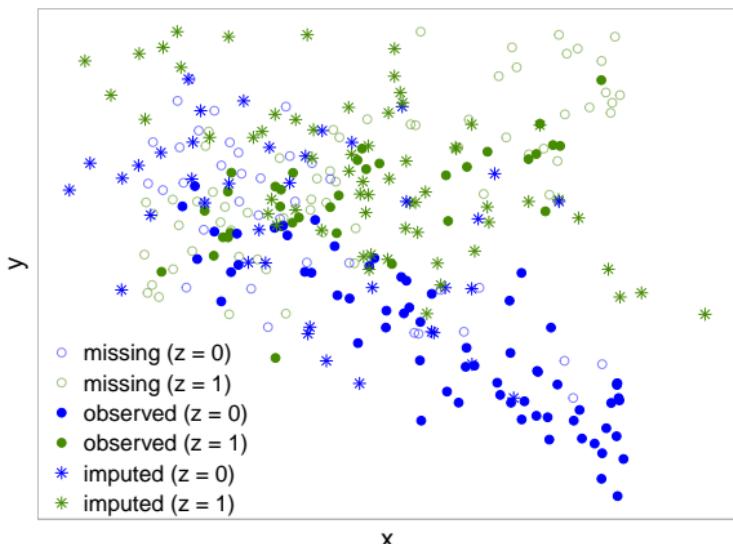
10. Settings where MICE may have problems

10.2. Interaction effect

The model used to impute x when using MICE (naively) is

$$x = \theta_{10} + \theta_{11}y + \theta_{12}z + \dots,$$

i.e., a linear relation between x and y is assumed.

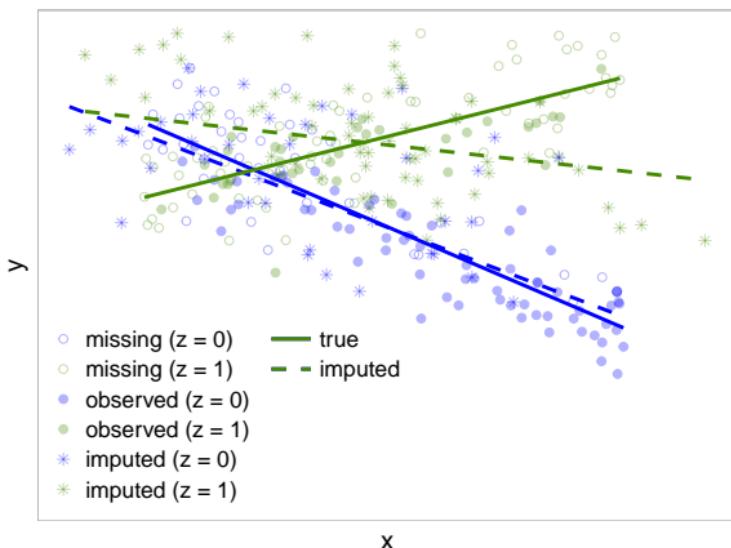


The “<” shaped pattern of the true data is **distorted by the imputed values**.

10. Settings where MICE may have problems

10.2. Interaction effect

And the analysis on these naively imputed values leads to **severely biased estimates**.

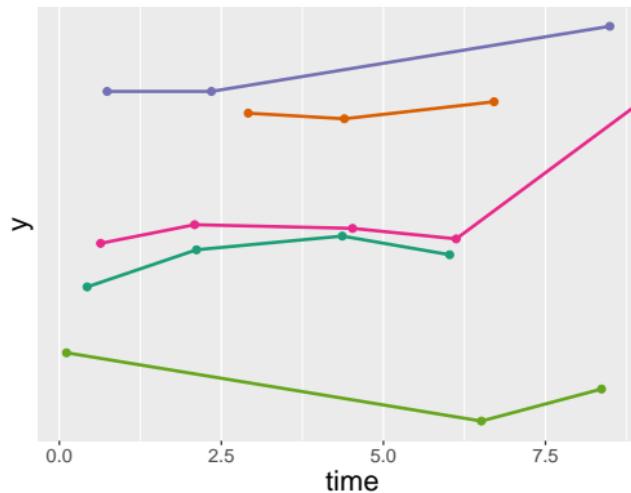


	β	95% CI
Original		
Intercept	-0.96	[-1.00, -0.92]
x	-0.59	[-0.65, -0.53]
z	0.5	[0.45, 0.56]
x:z	0.94	[0.85, 1.03]
Imputed		
Intercept	-0.96	[-1.01, -0.91]
x	-0.52	[-0.61, -0.44]
z	0.46	[0.39, 0.54]
x:z	0.37	[0.24, 0.51]

10. Settings where MICE may have problems

10.3. Longitudinal outcome

Another setting where imputation with MICE is not straightforward is when the **outcome variable is longitudinal**.



ID	y	x ₁	x ₂	x ₃	x ₄	time	
5	✓	✓	✓	NA	✓	0.43	
5	✓	✓	✓	NA	✓	2.12	
5	✓	✓	✓	NA	✓	4.37	
5	✓	✓	✓	NA	✓	6.02	
6	✓	✓	✓	NA	NA	✓	2.91
6	✓	✓	NA	NA	✓	4.40	
6	✓	✓	NA	NA	✓	6.71	
8	✓	✓	✓	✓	NA	0.64	
8	✓	✓	✓	✓	NA	2.09	
8	✓	✓	✓	✓	NA	4.52	
8	✓	✓	✓	✓	NA	6.12	
8	✓	✓	✓	✓	NA	8.93	
18	✓	✓	✓	NA	✓	✓	0.11
18	✓	✓	NA	✓	✓	6.51	
18	✓	✓	NA	✓	✓	8.37	
⋮	⋮	⋮	⋮	⋮	⋮	⋮	

Here, x_1, \dots, x_4 are baseline covariates, i.e., not measured repeatedly (e.g. age at baseline, gender, education level, ...)

10. Settings where MICE may have problems

10.3. Longitudinal outcome

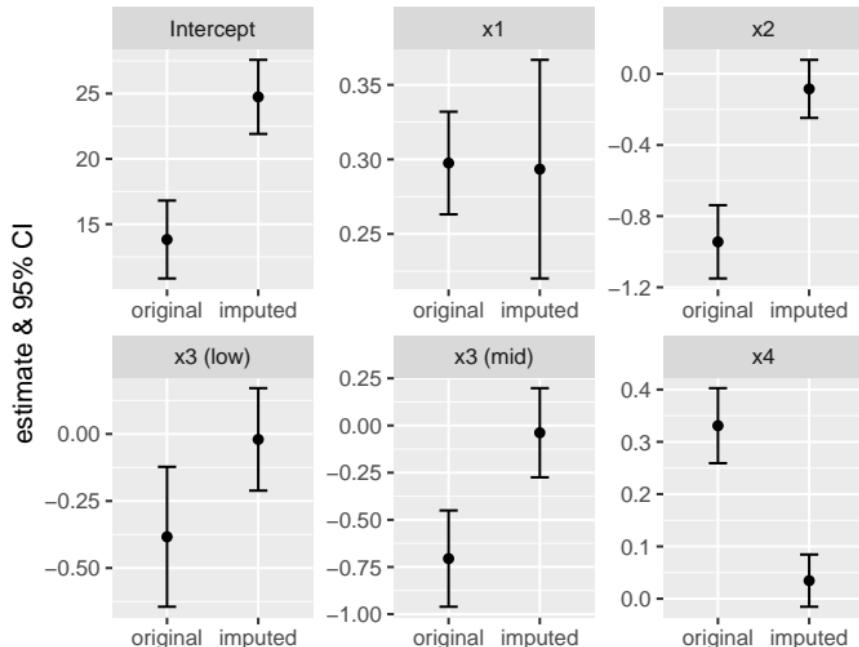
If we use MICE in the data in this (long) format, each row would be regarded as independent, which may cause bias and **inconsistent imputations**.

ID	y	x ₁	x ₂	x ₃	x ₄	time
5	✓	✓	✓	low mid high low	✓	0.43
	✓	✓	✓		✓	2.12
	✓	✓	✓		✓	4.37
	✓	✓	✓		✓	6.02
6	✓	✓	boy boy boy	low high low	✓	2.91
	✓	✓			✓	4.40
	✓	✓			✓	6.71
8	✓	✓	✓	✓	✓	39.75
	✓	✓	✓	✓	✓	39.64
	✓	✓	✓	✓	✓	41.41
	✓	✓	✓	✓	✓	39.58
	✓	✓	✓	✓	✓	40.37
18	✓	✓	boy girl girl	✓ ✓ ✓	✓	0.11
	✓	✓			✓	6.51
	✓	✓			✓	8.37
⋮	⋮	⋮	⋮	⋮	⋮	⋮

Imputed values of baseline covariates are imputed with different values, creating data that could not have been observed.

10. Settings where MICE may have problems

10.3. Longitudinal outcome

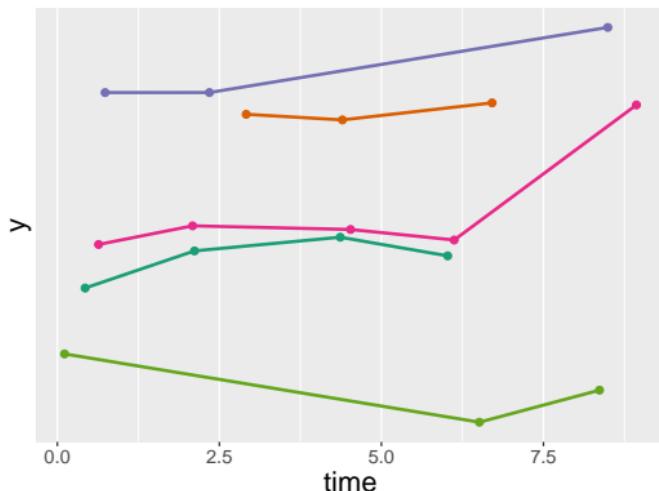


Estimates can be severely biased.

10. Settings where MICE may have problems

10.3. Longitudinal outcome

In some settings **imputation in wide format** may be possible.

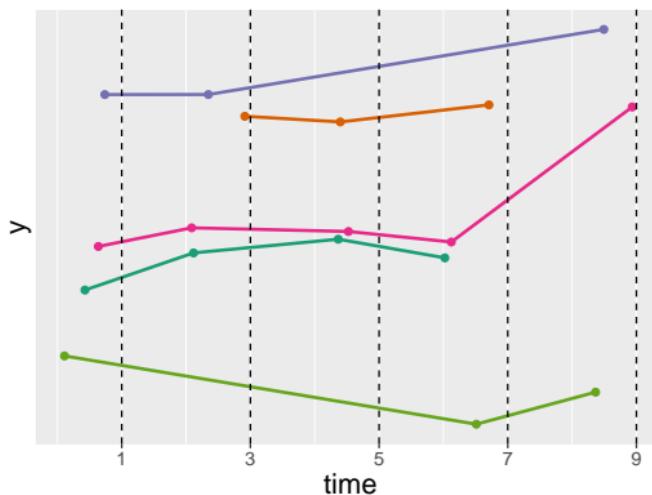


ID	y	x ₁	x ₂	x ₃	x ₄	time
5	✓	✓	✓	NA	✓	0.43
5	✓	✓	✓	NA	✓	2.12
5	✓	✓	✓	NA	✓	4.37
5	✓	✓	✓	NA	✓	6.02
6	✓	✓	NA	NA	✓	2.91
6	✓	✓	NA	NA	✓	4.40
6	✓	✓	NA	NA	✓	6.71
8	✓	✓	✓	✓	NA	0.64
8	✓	✓	✓	✓	NA	2.09
8	✓	✓	✓	✓	NA	4.52
8	✓	✓	✓	✓	NA	6.12
8	✓	✓	✓	✓	NA	8.93
18	✓	✓	NA	✓	✓	0.11
18	✓	✓	NA	✓	✓	6.51
18	✓	✓	NA	✓	✓	8.37
⋮	⋮	⋮	⋮	⋮	⋮	⋮

10. Settings where MICE may have problems

10.3. Longitudinal outcome

In some settings **imputation in wide format** may be possible.



ID	y	x ₁	x ₂	x ₃	x ₄	time
5	✓	✓	✓	NA	✓	0.43
5	✓	✓	✓	NA	✓	2.12
5	✓	✓	✓	NA	✓	4.37
5	✓	✓	✓	NA	✓	6.02
6	✓	✓	NA	NA	✓	2.91
6	✓	✓	NA	NA	✓	4.40
6	✓	✓	NA	NA	✓	6.71
8	✓	✓	✓	✓	NA	0.64
8	✓	✓	✓	✓	NA	2.09
8	✓	✓	✓	✓	NA	4.52
8	✓	✓	✓	✓	NA	6.12
8	✓	✓	✓	✓	NA	8.93
18	✓	✓	NA	✓	✓	0.11
18	✓	✓	NA	✓	✓	6.51
18	✓	✓	NA	✓	✓	8.37
⋮	⋮	⋮	⋮	⋮	⋮	⋮

10. Settings where MICE may have problems

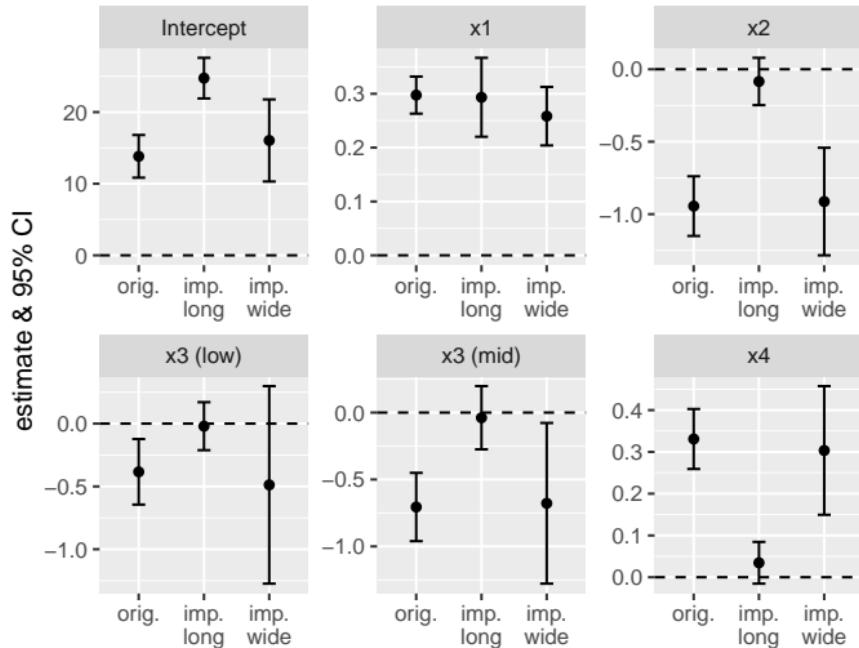
10.3. Longitudinal outcome

id	y.1	y.3	y.5	y.7	y.9	time.1	time.3	time.5	time.7	time.9	...
5	33.57	33.87	33.98	33.83	NA	0.43	2.12	4.37	6.02	NA	...
6	NA	34.96	34.92	35.05	NA	NA	2.91	4.4	6.71	NA	...
8	33.92	34.07	34.04	33.96	35.04	0.64	2.09	4.52	6.12	8.93	...
18	33.05	NA	NA	32.5	32.76	0.11	NA	NA	6.51	8.37	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮

In this **wide format data** frame, missing values in the outcome and measurement times need to be imputed (to be able to use them as predictors to impute covariates), even though we would not need to impute them for the analysis (mixed model is valid when outcome measurements are M(C)AR).

10. Settings where MICE may have problems

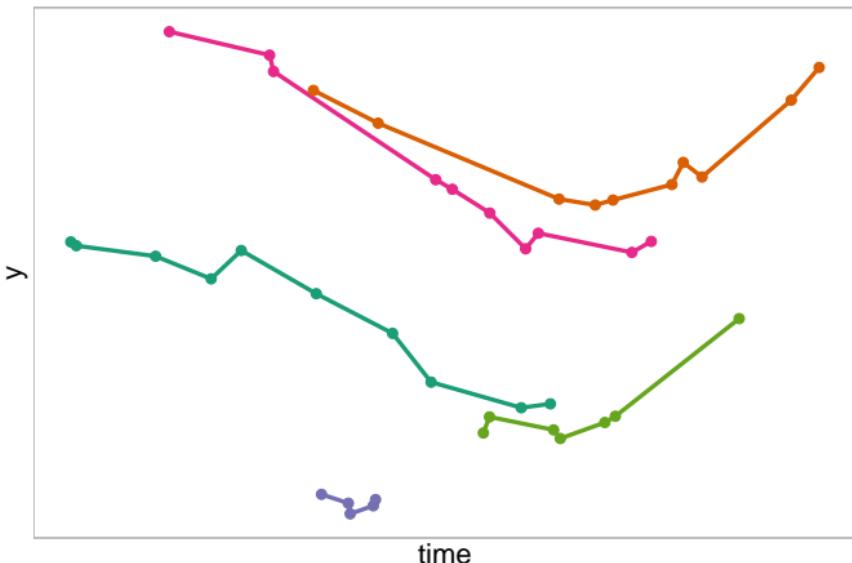
10.3. Longitudinal outcome



Better, but large
confidence intervals.

10. Settings where MICE may have problems

10.3. Longitudinal outcome

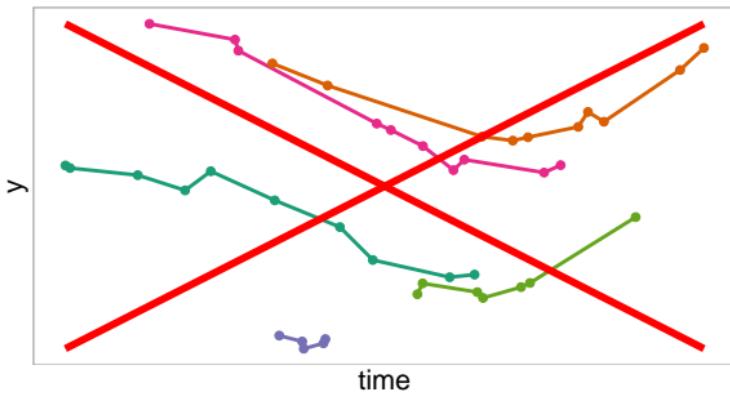


When the data is very **unbalanced**, transformation to wide format is not possible.

(Or at least transformation to wide format leads to variables with high proportions of missing values.)

10. Settings where MICE may have problems

10.3. Longitudinal outcome

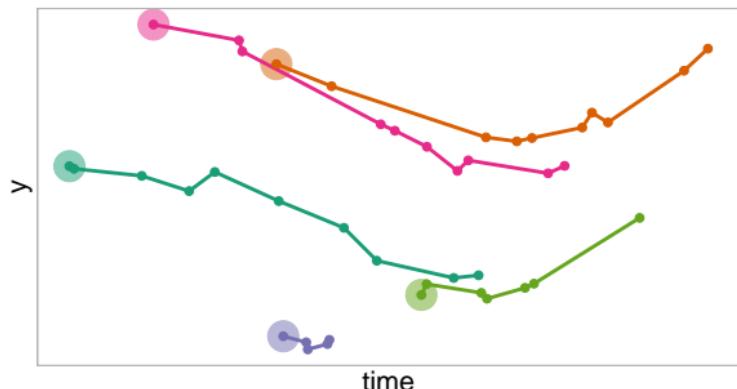
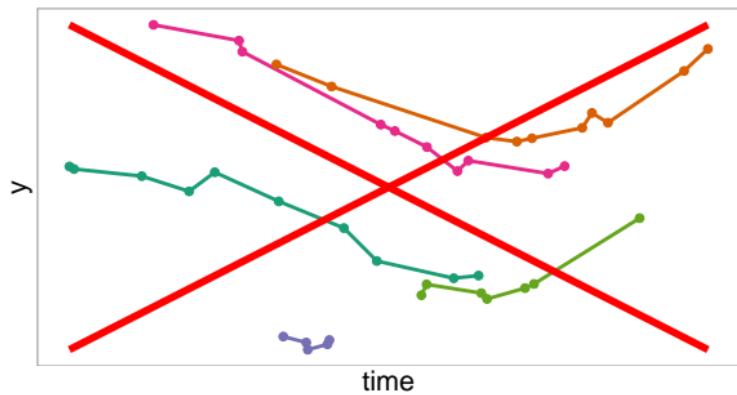


Naive approaches that are sometimes used are to

- **ignore the outcome** in the imputation

10. Settings where MICE may have problems

10.3. Longitudinal outcome

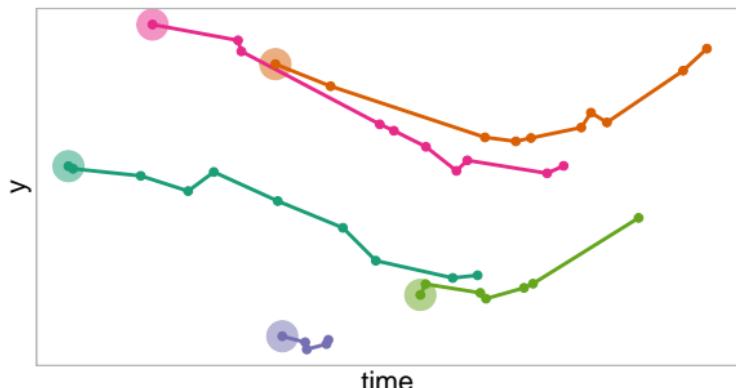
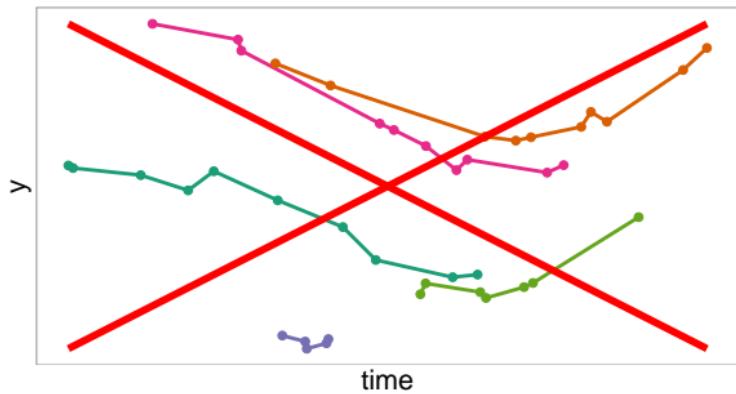


Naive approaches that are sometimes used are to

- ignore the outcome in the imputation, or to
- use only the **first/baseline outcome**

10. Settings where MICE may have problems

10.3. Longitudinal outcome



Naive approaches that are sometimes used are to

- ignore the outcome in the imputation, or to
- use only the **first/baseline outcome**

However, **important information may be lost**, resulting in invalid imputations and biased results.

10. Settings where MICE may have problems

10.4. Survival data

In **survival analysis**, the aim is to estimate the effect of covariates on the **time until an event** of interest happens.

10. Settings where MICE may have problems

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In **survival analysis**, the aim is to estimate the effect of covariates on the **time until an event** of interest happens.

Commonly used method: **Cox proportional hazards model**

$$h(t) = h_0(t) \exp(x\beta_x + z\beta_z),$$

- $h(t)$: hazard = the instantaneous risk of an event at time t , given that the event has not occurred until time t
- $h_0(t)$: unspecified baseline hazard
- x and z : **incomplete** and **complete** covariates, respectively

10. Settings where MICE may have problems

10.4. Survival data

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- $h_0(t)$: unspecified baseline hazard
- x and z : **incomplete** and **complete** covariates, respectively

Survival outcomes are usually represented by the **observed event time T** and the **event indicator D** ($D = 1$: event, $D = 0$: censored).

10. Settings where MICE may have problems

10.4. Survival data

Naive use of MICE

- T and D are treated just like any other variable.
- The resulting imputation model for X would have the form

$$p(x \mid T, D, \mathbf{z}) = \theta_0 + \theta_1 T + \theta_2 D + \theta_3 z + \dots$$

10. Settings where MICE may have problems

10.4. Survival data

Naive use of MICE

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$$p(x \mid T, D, z) = \theta_0 + \theta_1 T + \theta_2 D + \theta_3 z + \dots$$

The **correct conditional distribution** of x given the other variables is, however,

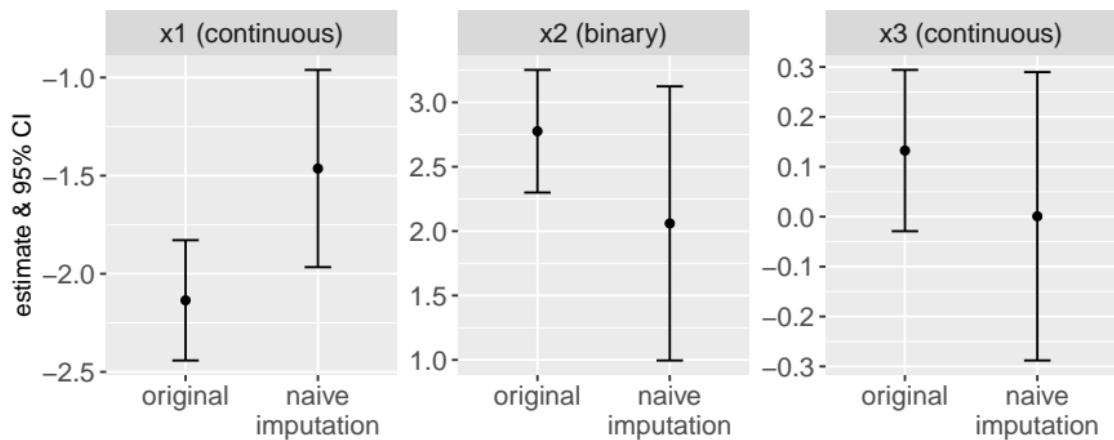
$$\begin{aligned} \log p(x \mid T, D, z) &= \log p(x \mid z) + D(\beta_x x + \beta_z z) - \\ &\quad H_0(T) \exp(\beta_x x + \beta_z z) + \text{const.}, \end{aligned}$$

where $H_0(T)$ is the cumulative baseline hazard. [17]

10. Settings where MICE may have problems

10.4. Survival data

Using the naively assumed imputation model can lead to **severe bias**:



(Results from MICE imputation with two incomplete normal and one incomplete binary covariate.)

11. Requirements for MICE to work (well)

11.1. Joint and conditional distributions

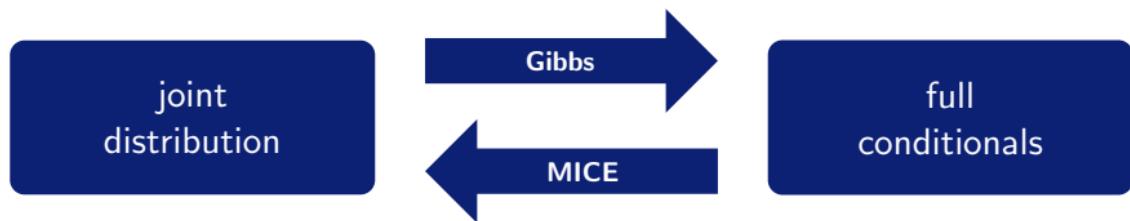
The MICE algorithm is based on the idea of Gibbs sampling.

11. Requirements for MICE to work (well)

11.1. Joint and conditional distributions

The MICE algorithm is based on the idea of Gibbs sampling.

Gibbs sampling exploits the fact that a joint distribution is fully determined by its full conditional distributions.



In MICE, the full conditionals are not derived from the joint distribution: we directly specify the full conditionals and hope a joint distribution exists.

11. Requirements for MICE to work (well)

11.2. Some conditions and definitions

Two important definitions:

Compatibility:

A joint distribution exists, that has the full conditionals (imputation models) as its conditional distributions.

Congeniality:

The imputation model is compatible with the analysis model.

11. Requirements for MICE to work (well)

11.2. Some conditions and definitions

Important requirements for MICE to work well include:

- Compatibility
- Congeniality
- MAR or MCAR (in the standard implementations)
- **All relevant variables** need to be included. (Omission might result in MNAR.)
- **The outcome needs to be included** as predictor variable (but we usually do not impute missing outcome values).
- The imputation models (and analysis model) need to be **correctly specified** (which is a requirement in any standard analysis).

12. Alternatives to MICE

12.1. Joint model imputation

To **avoid incompatible** and **uncongenial** imputation models, we need to

- specify the joint distribution
- and derive full conditionals / imputation models from this joint distribution

instead of specifying them directly.

12. Alternatives to MICE

12.1. Joint model imputation

To **avoid incompatible** and **uncongenial** imputation models, we need to

- specify the joint distribution
- and derive full conditionals / imputation models from this joint distribution

instead of specifying them directly.

Problem:

The joint distribution may not be of any known form:

$$x_1 \sim N(\mu_1, \sigma_1^2) \quad \Rightarrow \quad \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} \sim N\left(\begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix}, \begin{bmatrix} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_2^2 \end{bmatrix}\right)$$

but $x_1 \sim N(\mu_1, \sigma_1^2)$ \Rightarrow $\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} \sim ???$

$$x_2 \sim Bin(\mu_2)$$

12. Alternatives to MICE

12.1. Joint model imputation

Possible approaches:

Approach 1: **Multivariate Normal Model**

Approximate the joint distribution by a known multivariate distribution (usually the normal distribution; this is the joint model MI mentioned before).

Approach 2: **Sequential Factorization**

Factorize the joint distribution into a (sequence of) conditional and a marginal distributions.

12. Alternatives to MICE

12.2. Sequential Factorization

The **joint distribution** of two variables y and x can be written as the product of conditional distributions:

$$p(y, x) = p(y | x) p(x)$$

(or alternatively $p(y, x) = p(x | y) p(y)$)

12. Alternatives to MICE

12.2. Sequential Factorization

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$$p(y, x) = p(y | x) p(x)$$

(or alternatively $p(y, x) = p(x | y) p(y)$)

This can easily be **extended for more variables**:

$$p(y, x_1, \dots, x_p, X_c) = \underbrace{p(y | x_1, \dots, x_p, X_c)}_{\text{analysis model}} p(x_1 | x_2, \dots, x_p, X_c) \dots p(x_p | X_c)$$

where x_1, \dots, x_p denote incomplete covariates and X_c contains all completely observed covariates.

12. Alternatives to MICE

12.2. Sequential Factorization

The analysis model is part of the specification of the joint distribution.

➡ Advantages:

- The outcome is **automatically included in the imputation** procedure.
- The outcome does not appear in any of the predictors of the imputation models:
 - **no need to approximate** complex outcomes,
 - **no need to summarize** complex outcomes.

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 - imputation and analysis in one step

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- The parameters of interest are obtained directly
 - imputation and analysis in one step
- **Non-linear associations** or interactions involving incomplete covariates are specified in the analysis model and thereby **automatically taken into account**

Since the joint distribution usually does not have a known form, Gibbs sampling is used to estimate parameters and sample imputed values.

12. Alternatives to MICE

12.3. R package JointAI

Joint Analysis and Imputation,

uses the **sequential factorization approach** to perform simultaneous analysis and imputation in the Bayesian framework [4, 5, 3].

JointAI (version 0.6.0) can analyse incomplete data using

- linear regression
- generalized linear regression
- linear mixed models
- generalized linear mixed models
- (ordinal) cumulative logit regression
- (ordinal) cumulative logit mixed models
- parametric (Weibull) survival models
- Cox proportional hazards models

while assuring compatibility between analysis model and imputation models when non-linear functions or interactions are included.

12. Alternatives to MICE

12.3. R package JointAI

The necessary **Gibbs sampling** is performed using **JAGS** (an external program), which is free, but needs to be installed from

<https://sourceforge.net/projects/mcmc-jags/files/.>

JointAI can be installed from CRAN or **GitHub** (development version containing bug fixes and other improvements)

```
install.packages("devtools")
devtools::install_github("NERler/JointAI")
```

JointAI has its own web page (<https://nerler.github.io/JointAI/>) with several vignettes on **Visualization of Incomplete Data**, a **Minimal Example**, details on **Model Specification**, etc.

13. Imputation with non-linear functional forms

13.1. With mice

There is no strategy for MICE that can guarantee valid imputations when non-linear functional forms and/or interactions are involved, but some settings in **mice** may help to reduce bias in the resulting estimates.

For imputation of variables that have non-linear associations

- PMM often works better than imputation with a normal model,
- the **Just Another Variable** approach can reduce bias in interactions,
- **quadratic** can help to impute variables with quadratic association.

13. Imputation with non-linear functional forms

13.1. With mice

Just Another Variable (JAV) approach:

- pre-calculate the non-linear form (or interaction term) in the incomplete data,
- add it as a column to the dataset, and
- impute it as if it was just another variable.

13. Imputation with non-linear functional forms

13.1. With mice

Just Another Variable (JAV) approach:

- pre-calculate the non-linear form (or interaction term) in the incomplete data,
- add it as a column to the dataset, and
- impute it as if it was just another variable.

`quadratic` uses the “polynomial combination” method to impute covariates that have a quadratic association with the outcome [15, pp. 139–141], [16].

This is to ensure the imputed values for x and x^2 are consistent, and to reduce bias in the subsequent analysis that uses x and x^2 .

In my experience, using `quadratic` can lead to numerical problems.

13. Imputation with non-linear functional forms

13.1. With mice

To demonstrate the approaches, we use a simulated example dataset DFnonlin, with

- continuous outcome y
- continuous (normal) covariate x (50% missing values MCAR)
- quadratic effect of x on y
- binary covariate z (complete)
- interaction between x and z

13. Imputation with non-linear functional forms

13.1. With mice

To demonstrate the approaches, we use a simulated example dataset DFnonlin, with

- continuous outcome y
- continuous (normal) covariate x (50% missing values MCAR)
- quadratic effect of x on y
- binary covariate z (complete)
- interaction between x and z

In the naive approach, we leave all settings to the defaults.

```
# naive imputation, using only y, x, z
impnaive <- mice(DF_nonlin, printFlag = F)
```

13. Imputation with non-linear functional forms

13.1. With mice

We use two different JAV approaches:

JAV: calculating the **quadratic and interaction term** before imputation

```
# add quadratic term and interaction to data
DF2 <- DF_nonlin
DF2$xx <- DF2$x^2
DF2$xz <- DF2$x * DF2$z

# JAV imputation
impJAV <- mice(DF2, printFlag = F, maxit = 20)
```

13. Imputation with non-linear functional forms

13.1. With mice

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# add quadratic term and interaction to data
DF2 <- DF_nonlin
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# JAV imputation
impJAV <- mice(DF2, printFlag = F, maxit = 20)
```

JAV2: additionally using an interaction between z and y

```
# add interaction between y and z to data
DF3 <- DF2
DF3$yz <- DF3$y * DF3$z

# JAV imputation with additional interaction
impJAV2 <- mice(DF3, printFlag = F, maxit = 20)
```

13. Imputation with non-linear functional forms

13.1. With mice

We also try using imputation method `quadratic`.

```
# adapt the imputation method for quadratic imputation
methqdr <- impJAV$meth
methqdr[c("x", "xx", "xz")] <- c("quadratic", "~I(x^2)", "~I(x*z)")

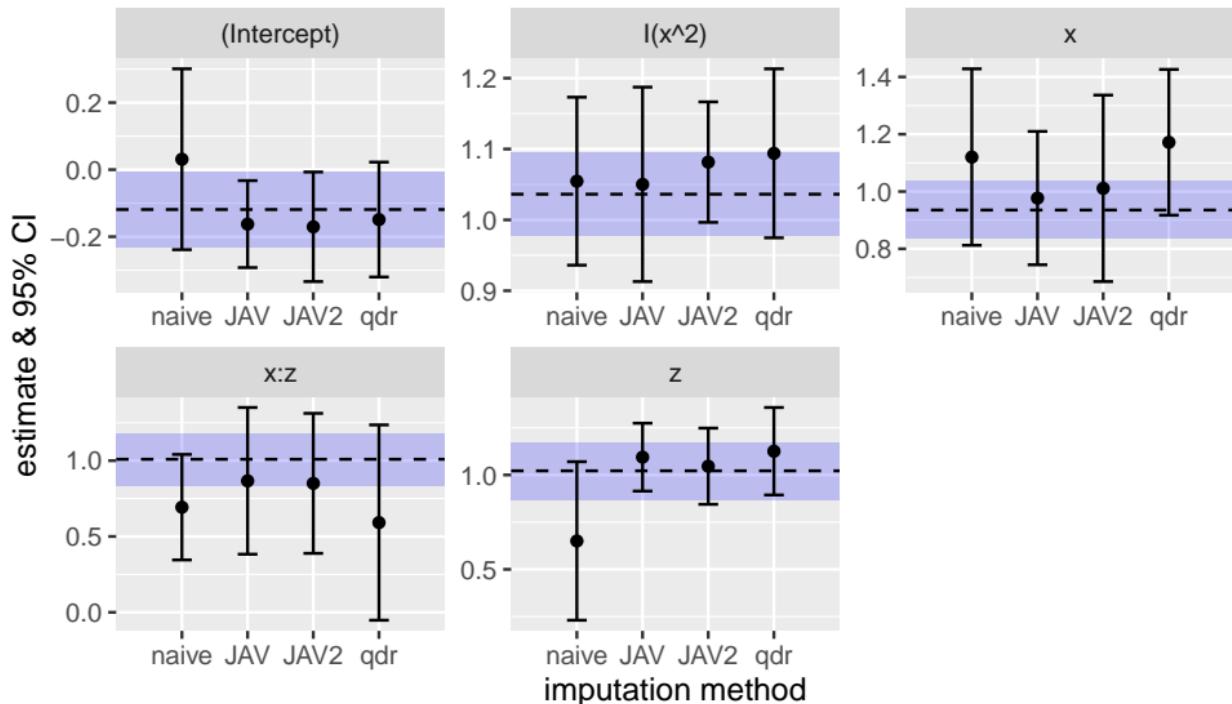
# adapt the predictor matrix
predqdr <- impJAV$pred
predqdr[, "xx"] <- 0

impqdr <- mice(DF2, meth = methqdr, pred = predqdr,
                 printFlag = F, maxit = 10)
```

Note: there were warning messages about numerical issues for this approach
(`glm.fit: fitted probabilities numerically 0 or 1 occurred`).

13. Imputation with non-linear functional forms

13.1. With mice



For this example, **none of the approaches provided satisfying results.**

13. Imputation with non-linear functional forms

13.2. With JointAI

The syntax we use to analyse and impute the current example using **JointAI** is similar to the specification of a standard linear model using `lm()`.

```
library(JointAI)
JointAI_nonlin <- lm_imp(y ~ x*z + I(x^2), data = DF_nonlin,
                           n.iter = 2500)
```

13. Imputation with non-linear functional forms

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Convergence of the Gibbs sampler can be checked using a traceplot.

```
traceplot(JointAI_nonlin, ncol = 3)
```

13. Imputation with non-linear functional forms

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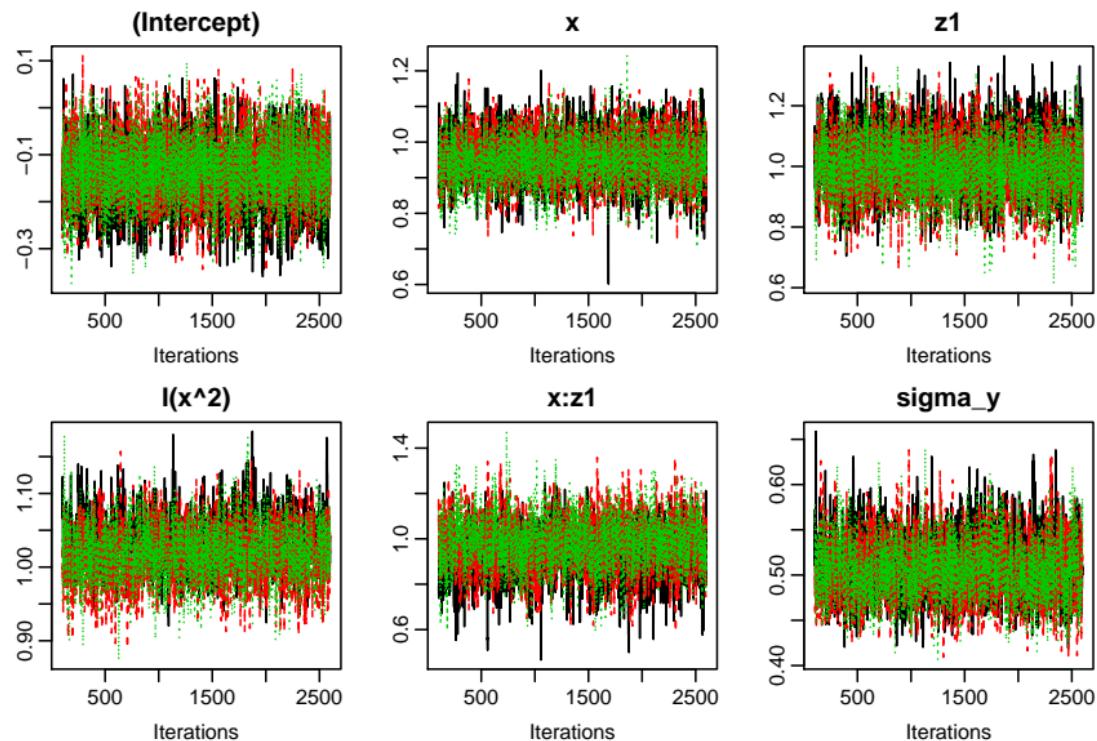
```
traceplot(JointAI_nonlin, ncol = 3)
```

Results (no separate analysis & pooling is necessary) can be obtained with the `summary()` function:

```
summary(JointAI_nonlin)
```

13. Imputation with non-linear functional forms

13.2. With JointAI



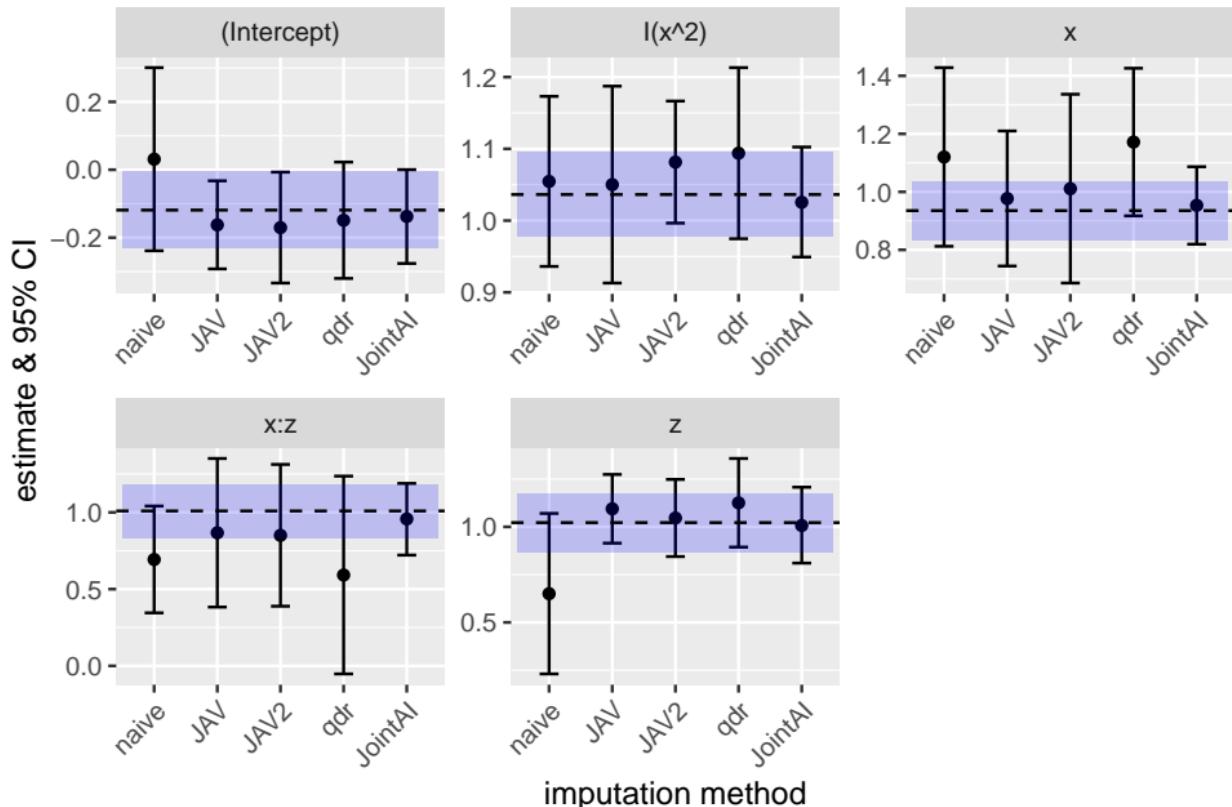
13. Imputation with non-linear functional forms

13.2. With JointAI

```
##  
##  Linear model fitted with JointAI  
##  
## Call:  
## lm_imp(formula = y ~ x * z + I(x^2), data = DF_nonlin, n.iter = 2500)  
##  
## Posterior summary:  
##          Mean      SD  2.5%   97.5% tail-prob. GR-crit  
## (Intercept) -0.138 0.0697 -0.276 0.000259     0.0512    1.09  
## x           0.954 0.0683  0.820 1.086675     0.0000    1.02  
## z1          1.007 0.1005  0.810 1.207309     0.0000    1.10  
## I(x^2)      1.026 0.0393  0.949 1.102465     0.0000    1.32  
## x:z1        0.957 0.1189  0.722 1.188642     0.0000    1.28  
##  
## Posterior summary of residual std. deviation:  
##          Mean      SD  2.5%   97.5% GR-crit  
## sigma_y 0.507 0.0334 0.447 0.576     1.01  
##  
##  
## MCMC settings:  
## Iterations = 101:2600  
## Sample size per chain = 2500  
## Thinning interval = 1  
## Number of chains = 3  
##  
## Number of observations: 200
```

13. Imputation with non-linear functional forms

13.2. With JointAI



Practical

To practice imputation with non-linear forms or interaction terms find the **html version** of the practical here:

[https://nerler.github.io/EP16_Multiple_Imputation/practical/
minonlin/EP16_MInonlin.html](https://nerler.github.io/EP16_Multiple_Imputation/practical/minonlin/EP16_MInonlin.html)

14. Imputation of longitudinal data

14.1. R package mice

mice has functions to allow imputation of longitudinal (2-level) data:

- **Level 1:**

repeated measurements within subjects or subjects within classes

- **Level 2:**

time-constant/baseline covariates, between subjects effects, variables on the group level

Imputation methods for **level-1** variables:

- `2l.pan`
- `2l.norm`
- `2l.lmer`
- `2l.bin`

Imputation methods for **level-2** variables:

- `2lonly.norm`
- `2lonly.pmm`
- `2lonly.mean`

14. Imputation of longitudinal data

14.1. R package mice

`21.pan` uses a linear two-level model with **homogeneous within group variances** using Gibbs sampling [13]. It needs the package **pan** to be installed.

`21.pan` allows for different roles of predictor variables, that can be specified as different values in the `predictorMatrix`:

- grouping/ID variable: -2
- random effects (also included as fixed effects): 2
- fixed effects of group means: 3
- fixed effects of group means & random effects: 4

```
# random effects of x in model for y
pred["y", "x"] <- 2
# fixed effects of x and group mean of x
pred["y", "x"] <- 3
# random effects of x and group mean of x
pred["y", "x"] <- 4
```

14. Imputation of longitudinal data

14.1. R package mice

`2l.norm` implements a (Bayesian) linear two-level model with **heterogenous** group variances.

In the current implementation all predictors should be specified as random effects (set to 2 in the `predictorMatrix`, because the algorithm does not handle predictors that are specified as fixed effects).

14. Imputation of longitudinal data

14.1. R package mice

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`2l.lmer/2l.bin` imputes univariate systematically and sporadically missing data using a two-level normal/logistic model using `lmer()`/`glmer()` from package **lme4**.

14. Imputation of longitudinal data

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`2l.lmer/2l.bin` imputes univariate systematically and sporadically missing data using a two-level normal/logistic model using `lmer()`/`glmer()` from package **lme4**.

`2lonly.norm` and `2lonly.pmm` can be used to impute level-2 variables (in combination with `2l.pan` for level-1 variables).

In all cases, the group identifier ("id" variable) needs to be set to -2 in the `predictorMatrix`.

14. Imputation of longitudinal data

14.1. R package mice

`2lonly.mean` imputes values with the mean of the observed values per class. This method should only be used to fill in values that are known to be constant per class and have some values observed in each class.

Example: In a multi-center trial the type of some medical equipment is known to be the same for all patients treated in the same hospital, but not filled in for some patients.

14. Imputation of longitudinal data

14.1. R package mice

As an example, we will impute the second (unbalanced) longitudinal data example from above. The data contain

- x_1 (complete)
- x_2 (binary, 30% missing values)
- x_3 (3 categories, 30% missing values)
- x_4 (continuous/normal, 30% missing values)
- y (longitudinal outcome)
- $time$ (time variable with quadratic effect)
- id (id variable)

Since there is no 2-level method for categorical data, we use `2lonly.pmm` to impute x_2 and x_3 .

14. Imputation of longitudinal data

14.1. R package mice

As usual, we start with the setup run of `mice()`

```
imp0 <- mice(DFexlong2, maxit = 0)
meth <- imp0$method
pred <- imp0$predictorMatrix
```

and adjust the imputation `method` and `predictorMatrix`

```
meth[c("x2", "x3")] <- "2lonly.pmm"
meth[c("x4")] <- "2lonly.norm"

pred[, "id"] <- -2 # identify id variable
pred[, "ti"] <- 0 # don't use time-point indicator
```

We can then perform the imputation.

```
imp <- mice(DFexlong2, maxit = 10, method = meth,
            predictorMatrix = pred, printFlag = FALSE)
```

14. Imputation of longitudinal data

14.1. R package mice

The imputed data can be analysed using either `lmer()` from the package **lme4**, or `lme()` from **nlme**. Here we use the former.

```
library(lme4)
models <- with(imp, lmer(y ~ x1 + x2 + x3 + x4 + time + I(time^2) +
                           (time|id),
                           control = lmerControl(optimizer = "Nelder_Mead"))
))
mice_longimp <- summary(pool(models), conf.int = TRUE)
```

14. Imputation of longitudinal data

14.2. R package JointAI

Linear mixed models with incomplete covariates can also be analysed using the package **JointAI**.

The syntax is analogous the syntax used in `lme()` of the package **nlme**.

```
library(JointAI)
JointAI_long <- lme_imp(y ~ x1 + x2 + x3 + x4 + time + I(time^2),
                        random = ~time|id, data = DFExlong2,
                        n.iter = 5000)
```

14. Imputation of longitudinal data

14.2. R package JointAI

Linear mixed models with incomplete covariates can also be analysed using the package **JointAI**.

The syntax is analogous the syntax used in `lme()` of the package **nlme**.

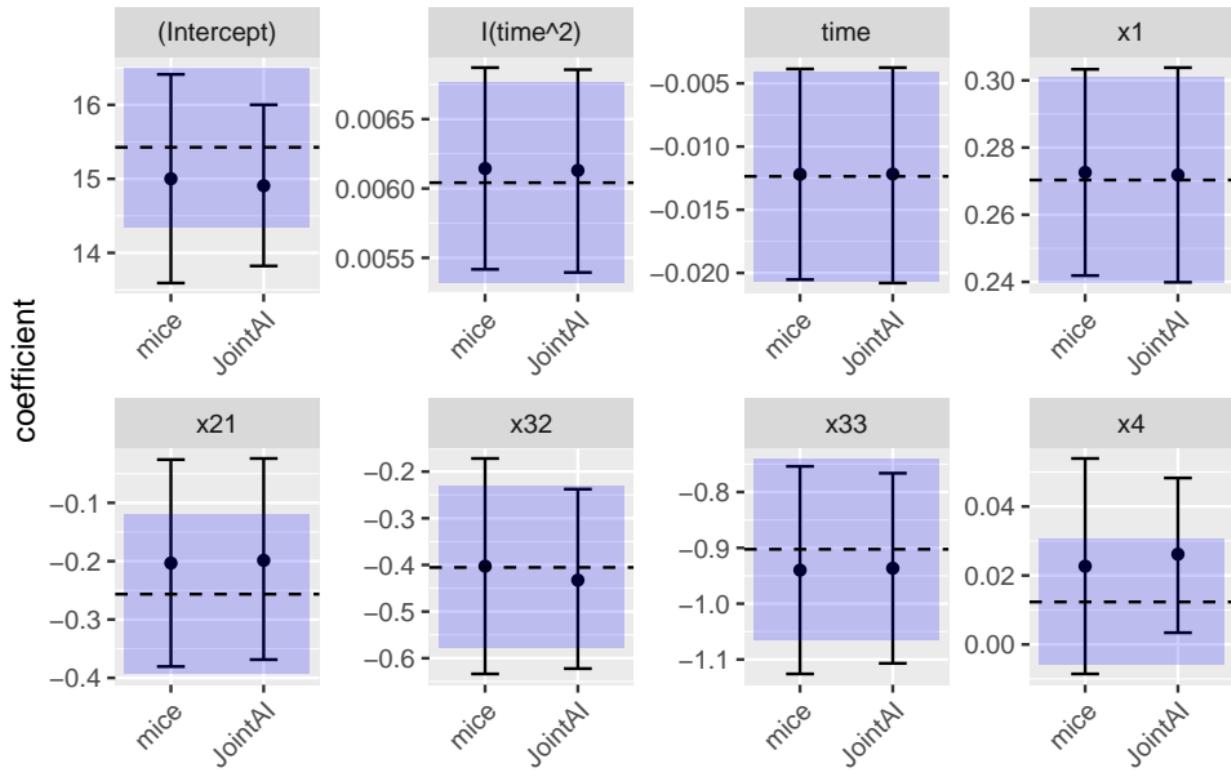
```
library(JointAI)
JointAI_long <- lme_imp(y ~ x1 + x2 + x3 + x4 + time + I(time^2),
                        random = ~time|id, data = DFExlong2,
                        n.iter = 5000)
```

Again, convergence of the Gibbs sampler should be checked, e.g., using `traceplot()` before obtaining the results.

Contrary to the two-level imputation of **mice**, non-linear associations are appropriately handled.

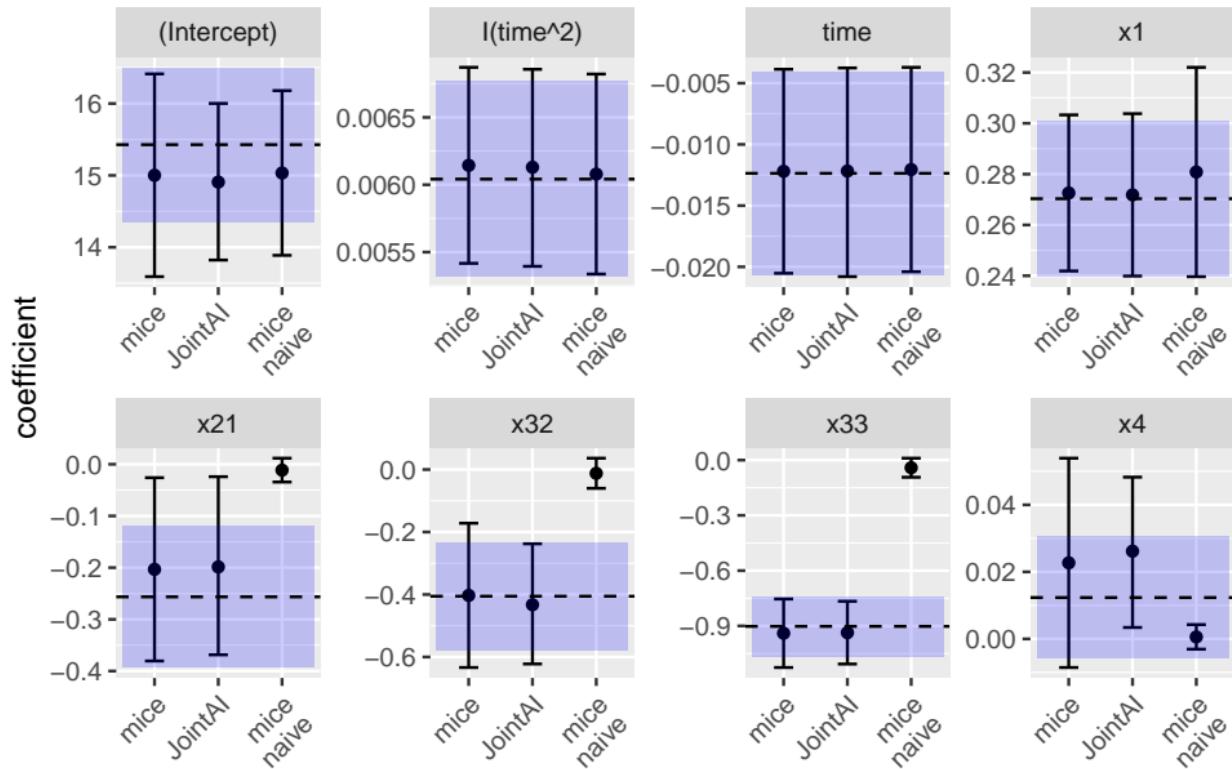
14. Imputation of longitudinal data

14.3. Comparison of results



14. Imputation of longitudinal data

14.3. Comparison of results



Practical

To practice imputation with longitudinal data find the **html version** of the practical here:

[https://nerler.github.io/EP16_Multiple_Imputation/practical/
milong/EP16_Milong.html](https://nerler.github.io/EP16_Multiple_Imputation/practical/milong/EP16_Milong.html)

Summary & Conclusion of Part III

- MICE requires **congenial & compatible imputation models** to work well.
- When this is not the case, (naive) use of MICE can lead to **biased results**.
- Common settings that require special attention are
 - non-linear functional forms & interaction terms
 - longitudinal data
 - survival data

Summary & Conclusion of Part III (cont.)

- When using the package **mice**, there are choices that can **reduce bias**
 - **pmm** tends to be less biased than **norm** for interactions or non-linear associations
 - JAV approach reduces bias in settings with interactions or non-linear associations
 - **special 2-level imputation methods** are available for longitudinal data
 - The **Nelson-Aalen estimator** can be used instead of the time variable for imputing survival data when effects are not too large.
- Generally, **problems** are more severe when
 - **proportions of missing values are large**,
 - effect sizes are large,
 - little other **covariate information** is available.

(Note that in the examples we had all of the above.)

Summary & Conclusion of Part III (cont.)

- In settings where MICE may not provide valid imputations, **alternative approaches** are available and should be considered.
- R packages that provide such alternative approaches are for example:
 - **JointAI** (non-linear, longitudinal & survival)
 - **smcfcs** (non-linear & survival)
 - **jomo** (non-linear, longitudinal & survival)
- These packages are very young.
 - Hence, they may still have some problems.
 - ➡ **Use them carefully!** (and email the maintainer about problems)
 - They are under **active development**, so resolutions of bugs and features are frequently added.

Part IV Multiple Imputation Strategies

15. Strategies for using MICE

15.1. Tips & Tricks

In complex settings, variables may need to be **re-calculated** or **re-coded** after imputation:

- Use `complete()` to convert the imputed data from a `mids` object to a `data.frame`.
- Perform the necessary calculations.
- Convert the changed `data.frame` back to a `mids` object using the functions such as `as.mids()`, `miceadds::datalist2mids()`, `mitools::imputationList()`, ...

15. Strategies for using MICE

15.1. Tips & Tricks

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Not just in imputation: Set a **seed value** to create reproducible results.

- in R: `set.seed()`
- in `mice()`: argument `seed`

15. Strategies for using MICE

15.2. Number of imputed datasets

Early publications on multiple imputation suggested that 3 – 5 imputations are sufficient and this is still a common assumption in practice.[11]

The reasoning behind using a small number of imputed datasets was that **storage of imputed data was “expensive”** (which is no longer the case) and a larger number of imputations would only have little advantage.[12]

More **recent work** from various authors [18, 15, 6] considers the efficiency of the pooled estimates, reproducibility of the results, statistical power of tests or the width of the resulting confidence intervals compared to the width of the true confidence intervals.

15. Strategies for using MICE

15.2. Number of imputed datasets

A **suggested rule of thumb** is that the **number of imputed datasets** should be similar to the **percentage of incomplete cases**.[18] Since this percentage depends on the size of the dataset, the **average percentage of missing values** per variable could be used as an alternative.[15]

Generally, using **more imputed datasets should be preferred**, especially in settings where the computational burden allows for it. Even though results are unlikely to change with a larger number of imputations, it can increase the efficiency and reproducibility of the results.

15. Strategies for using MICE

15.3. What to do with large datasets?

In imputation, generally the **advice is to include as much information as possible** in the imputation models.

Using a large number of predictor variables

- makes the **MAR assumption more plausible** (and, hence, reduces bias due to MNAR missingness)
- can **reduce uncertainty** about the missing values

15. Strategies for using MICE

15.3. What to do with large datasets?

In imputation, generally the **advice is to include as much information as possible** in the imputation models.

Using a large number of predictor variables

- makes the **MAR assumption more plausible** (and, hence, reduces bias due to MNAR missingness)
- can **reduce uncertainty** about the missing values

This can **work well in small or medium sized datasets** (20 – 30 separate variables, i.e. without interactions, variables derived from others, . . .)

However, **in large datasets** (contain hundreds or thousands of variables) this is **not feasible**.[15]

15. Strategies for using MICE

15.3. What to do with large datasets?

For large datasets a possible strategy is to

- Include all **variables used in the analysis model(s)** (including the outcome!).
- Include auxiliary variables if they are **strong predictors of missingness**.
- Include auxiliary variables if they have **strong associations with the incomplete variables**.
- Use **auxiliary variables only if they do not have too many missing values** themselves (and are observed for most of the incomplete cases of the variable of interest).
- Use **auxiliary variables** only in those imputation models for which they are **relevant** (and exclude them for others using the predictor matrix).
- Calculate **summary scores** from multiple items referring to the same concept and use the summary score as predictor variable.

15. Strategies for using MICE

15.4. How much missing is too much?

There is **no clear cut-off** for the proportion of missing values that can be handled adequately using MICE (or any other imputation method).

The amount of missingness that can be handled **depends on the information that is available** to impute it.

- Are there **strong predictor variables** available & observed?
- Are there **sufficient observed cases** to get reliable estimates for the predictive distribution?

15. Strategies for using MICE

15.4. How much missing is too much?

There is **no clear cut-off** for the proportion of missing values that can be handled adequately using MICE (or any other imputation method).

The amount of missingness that can be handled **depends on the information that is available** to impute it.

- Are there **strong predictor variables** available & observed?
- Are there **sufficient observed cases** to get reliable estimates for the predictive distribution?

Example:

- In a set of $N = 50$ cases, 50% missing values leaves 25 cases to estimate the parameters of the predictive distribution.
- In a large set of $N = 5000$ subjects, 50% missing cases leaves 2500 observed cases to estimate parameters.

15. Strategies for using MICE

15.5. Imputation of outcomes

Usually, **missing outcome values are not imputed.**

Why?

When there are no auxiliary variables, imputation and analysis model are equal.

- Parameters of the imputation model are estimated on observed cases of the outcome.
- Imputed values will fit the assumed model perfectly.
- Including imputed cases in the analysis does not add any information.

15. Strategies for using MICE

15.5. Imputation of outcomes

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Why?

When there are no auxiliary variables, imputation and analysis model are equal.

- Parameters of the imputation model are estimated on observed cases of the outcome.
- Imputed values will fit the assumed model perfectly.
- Including imputed cases in the analysis does not add any information.

Exception:

- When very strong auxiliary variables are available.
- Outcomes may be imputed when one imputation is performed for several analysis models, because not imputing the outcome(s) would mean
 - excluding cases with missing outcome(s) from the imputation, or
 - excluding the outcome variable(s) as predictor(s).

15. Strategies for using MICE

15.6. Notes of caution & things to keep in mind

Multiple imputation is **not a quick and easy solution for missing data**. It requires **care and knowledge** about

- the **data** to be imputed (and the context of the data),
- the statistical **method** used for imputation, and
- the **software** implementation used.

Moreover

- **Never accept default settings of software blindly.**
- **Question the plausibility of the MAR assumption.** If it is doubtful, use sensitivity analysis.

15. Strategies for using MICE

15.6. Notes of caution & things to keep in mind

Remember:

- **Use as much information as possible**
 - include all covariates **and the outcome**
 - use auxiliary information
 - use the most detailed version of variables if possible
- **Avoid feedback** from derived variables to their originals.
- **Imputation models must fit the data**
(correct assumption of error distribution and functional forms and possible interactions of predictor variables).
- Think carefully how to handle variables that are derived from other variables.
- Consider the impact the **visit sequence** may have.
- Choose an appropriate **number of imputations**.
- Make sure the imputation algorithm has **converged**.
- Use **common sense** when evaluating if the imputed values are plausible.

16. Imputation Software

16.1. R packages dealing with incomplete data

Currently, there are **288 packages** available on CRAN that use the word “**missing**” in either the title or description of the package, **162** that use either “**impute**” or “**imputation**” and **65** that use the word “**incomplete**”.

→ The mice package is often a good option, but certainly not the only option to perform imputation!

CRAN Task View on Missing Data:

<https://cran.r-project.org/web/views/MissingData.html>

- overview on the available R packages for missing data
- good starting point when searching for a package with a particular functionality

16. Imputation Software

16.2. Imputation methods

We have focussed on a few imputation methods that cover the most common types of data but there are many more methods implemented.

Imputation methods implemented in the **mice** package:

<code>mice.impute.2l.bin</code>	<code>mice.impute.lda</code>	<code>mice.impute.panImpute</code>
<code>mice.impute.2l.lmer</code>	<code>mice.impute.logreg</code>	<code>mice.impute.passive</code>
<code>mice.impute.2l.norm</code>	<code>mice.impute.logreg.boot</code>	<code>mice.impute.pmm</code>
<code>mice.impute.2l.pan</code>	<code>mice.impute.mean</code>	<code>mice.impute.polr</code>
<code>mice.impute.2lonly.mean</code>	<code>mice.impute.midastouch</code>	<code>mice.impute.polyreg</code>
<code>mice.impute.2lonly.norm</code>	<code>mice.impute.norm</code>	<code>mice.impute.quadratic</code>
<code>mice.impute.2lonly.pmm</code>	<code>mice.impute.norm.boot</code>	<code>mice.impute.rf</code>
<code>mice.impute.cart</code>	<code>mice.impute.norm.nob</code>	<code>mice.impute.ri</code>
<code>mice.impute.jomoImpute</code>	<code>mice.impute.norm.predict</code>	<code>mice.impute.sample</code>

Note: Just because a method is implemented does not mean you need to / should use it.

16. Imputation Software

16.2. Imputation methods

Imputation methods implemented in the **miceadds** package:

<code>mice.impute.2l.binary</code>	<code>mice.impute.hotDeck</code>
<code>mice.impute.2l.contextual.norm</code>	<code>mice.impute.lm</code>
<code>mice.impute.2l.contextual.pmm</code>	<code>mice.impute.lm_fun</code>
<code>mice.impute.2l.continuous</code>	<code>mice.impute.lqs</code>
<code>mice.impute.2l.groupmean</code>	<code>mice.impute.ml.lmer</code>
<code>mice.impute.2l.groupmean.elim</code>	<code>mice.impute.plausible.values</code>
<code>mice.impute.2l.latentgroupmean.mcmc</code>	<code>mice.impute.pls</code>
<code>mice.impute.2l.latentgroupmean.ml</code>	<code>mice.impute.pmm3</code>
<code>mice.impute.2l.plausible.values</code>	<code>mice.impute.pmm4</code>
<code>mice.impute.2l.pls</code>	<code>mice.impute.pmm5</code>
<code>mice.impute.2l.pls2</code>	<code>mice.impute.pmm6</code>
<code>mice.impute.2l.pmm</code>	<code>mice.impute.rlm</code>
<code>mice.impute.2lonly.function</code>	<code>mice.impute.smcfcs</code>
<code>mice.impute.2lonly.norm2</code>	<code>mice.impute.tricube.pmm</code>
<code>mice.impute.2lonly.pmm2</code>	<code>mice.impute.tricube.pmm2</code>
<code>mice.impute.bygroup</code>	<code>mice.impute.weighted.norm</code>
<code>mice.impute.grouped</code>	<code>mice.impute.weighted.pmm</code>

16. Imputation Software

16.2. Imputation methods

Imputation methods implemented in the **miceMD** package:

<code>mice.impute.2l.2stage.bin</code>	<code>mice.impute.2l.glm.bin</code>
<code>mice.impute.2l.2stage.norm</code>	<code>mice.impute.2l.glm.norm</code>
<code>mice.impute.2l.2stage.pmm</code>	<code>mice.impute.2l.glm.pois</code>
<code>mice.impute.2l.2stage.pois</code>	<code>mice.impute.2l.jomo</code>

16. Imputation Software

16.3. Packages worth mentioning

Besides **JointAI**, there are more alternatives for imputation in complex settings:

- **smcfcs**: substantive model compatible fully conditional specification (in GLMs & survival models)
- **jomo**: Joint model MI (GLMs, GLMMs, Cox, ordinal mixed model)
- **mdmb**: model based missing data models (linear, logistic, multi-level)

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