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**Imputation of Incomplete Multilevel Data with** mice

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**Abstract**

This tutorial illustrates the imputation of incomplete multilevel data with the R pack- ackage mice. Footnotes in the current version show work in progress/under construction. The last section is not part of the manuscript, but purely for reminders. See also all of the TODOs that need to be worked out. We aim to submit at JSS, so there is no word count limit (“There is no page limit, nor a limit on the number of figures or tables”). [Just adding some text to get a better guess of what the actura abstract will look like: Lorem ipsum dolor sit amet, consectetur adipiscing elit, sed do eiusmod tempor incididunt ut la- bore et dolore magna aliqua. Ut enim ad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat. Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum.]

*Keywords*: missing data, multilevel, clustering, mice, R.

# **Introduction**

Many datasets include individuals from multiple settings, geographic regions, or even different studies. In the simplest case, individuals (e.g., students) are nested within so-called clusters (e.g., school classes). More complex clustered structures may occur when there are multiple hierarchical levels (e.g., patients within hospitals within regions or countries), or when the clustering is non-nested (e.g., electronic health record data from diverse settings and popula-

Table 1: Concepts in multilevel methods

#### Concept Details

ICC The variability due to clustering is often measured by means of the intraclass coefficient (ICC). The ICC can be seen as the percentage of variance that can be attributed to the cluster-level, where a high ICC would indicate that a lot of variability is due to the cluster structure.

Random effect Multilevel models typically accommodate for variability by including a separate group mean for each cluster. In addition to random intercepts, multilevel models can also include random coefficients and heterogeneous residual error variances across clusters [see e.g.

@gelm06, @hox17 and @jong21]. [TODO: add stratification.]

tions within large databases). In general, individuals from the same cluster tend to be more similar than individuals from other clusters. In statistical terms, this implies that observa- tions from the same cluster are correlated. If this correlation is left unaddressed, estimates of p values, confidence intervals even model parameters are prone to bias ([Localio, Berlin,](#_bookmark11) [Ten Have, and Kimmel](#_bookmark11) [2001](#_bookmark11)). [TODO: make a link to imputation methods, which require adequate handling and propagation of variance; we are not recommending the adoption of multilevel models for data analysis here, but rather for imputation.] Statistical methods for clustered data typically adopt hierarchical models that explicitly describe the grouping of ob- servations. These models are also know as ‘multilevel models’, ‘hierarchical models’, ‘mixed effect models’ and ‘random effect models’. Table [1](#_bookmark0) provides an overview of some key concepts in multilevel modeling.

* 1. **Missingness in multilevel data**

Like any other dataset, clustered datasets are prone to missing data. Several strategies can be used to handle missing data, including complete case analysis and imputation. We focus on the latter approach and discuss statistical methods for replacing the missing data with one or more plausible values. Afterwards, the completed data can be analyzed as if they were completely observed. In contrast to single imputation (where missing data are only replaced once), multiple imputation allows to preserve uncertainty due to missingness and is therefore recommended (c.f. Rubin 1976).

When clustered datasets are affected by missing values, we can distinguish between two types of missing data: sporadic missingness and systematic missingness ([Resche-Rigon, White,](#_bookmark14) [Bartlett, Peters, and Thompson 2013](#_bookmark14)). Sporadic missingness arises when variables are missing for some but not all of the units in a cluster ([Van Buuren 2018](#_bookmark15); [Jolani 2018](#_bookmark10)). For example, it is possible that test results are missing for several students in one or more classes. [TODO: Provide an example for one of the case studies below.] When all observations are missing within one or more clusters, data are systematically missing. [TODO: Refer to Figure 1 and put interpretation in the figure caption.]

Imputation of missing data requires to consider the mechanism behind the missingness. Rubin proposed to distinguish between data that are missing completely at random (MCAR), data that are missing at random (MAR) and data that are missing not at random (MNAR; see

1

2

3

4

5

...

n

cluster X1 X2 X3 ... Xp

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 1 |  |  | **NA** |  |  |
| 1 |  |  |  |  |  |
| 2 |  | **NA** |  |  |  |
| 2 |  | **NA** | **NA** |  |  |
| 3 |  |  |  |  |  |
|  |  |  |  |  |  |
| N |  |  |  |  |  |

Figure 1: Missingness in multilevel data

Table 2: Concepts in missing data methods

#### Concept Details

MCAR Missing Completely At Random, where the probability to be missing is equal across all data entries

MAR Missing At Random, where the probability to be missing depends on observed information

MNAR Missing Not At Random (MNAR), where the probability to be missing depends on unrecorded information, making the missingness non-ignorable [@rubi76; @meng94].

[TODO: add congeniality, but maybe in-text?]

Table [2](#_bookmark1)). For each of these three missingness generating mechanisms, different imputation strategies are warranted [Yucel](#_bookmark17) ([2008](#_bookmark17)) and [Hox, van Buuren, and Jolani](#_bookmark9) ([2015](#_bookmark9)). We here consider the general case that data are MAR, and expand on special MNAR situations.

The R package mice has become the de-facto standard for imputation by chained equations, which iteratively solves the missingness on a variable-by-variable basis. mice is known to yield valid inferences under many different missing data circumstances ([Van Buuren](#_bookmark15) [2018](#_bookmark15)). However, commonly used imputation methods were not designed for use in clustered data and usually generate observations that are independent. For this reason, we discuss how the R package mice can be used to impute multilevel data.

[TODO: clarify why clustering is relevant during imputation, and why this exposes the need for specialized imputation methods and more attention during their implementation (“thou shall not simply run mice() on any incomplete dataset”).] [TODO: Add that the more the random effects are of interest, the more you need multilevel imputation models.] [TODO: Add an overview of all possible predictor matrix values in manuscript or ggmice legend.]

## **Aim of this paper**

This papers serves as a tutorial for imputing incomplete multilevel data with mice in R. We provide practical guidelines and code snippets for different missing data situations, includ- ing non-ignorable mechanisms. For reasons of brevity, we focus on multilevel imputation by chained equations with mice exclusively; other imputation methods and packages (e.g., jomo and mdmb) are outside the scope of this tutorial. Assumed knowledge includes basic

Table 3: Notation

#### Concept Details

[TODO: explain lme4 notation here]

familiarity with multilevel imputation (see e.g. [Audigier, White, Jolani, Debray, Quartagno,](#_bookmark4) [Carpenter, van Buuren, and Resche-Rigon 2018](#_bookmark4), and [Grund, Lüdtke, and Robitzsch](#_bookmark8) ([2018](#_bookmark8))) and the lme4 notation for multilevel models (see Table [3](#_bookmark2)).

We illustrate imputation of incomplete multilevel data using three case studies:

* + - popmis from the mice package (simulated data on perceived popularity, *n* = 2*,* 000 pupils across *N* = 100 schools with data that are MAR, [van Buuren and Groothuis- Oudshoorn 2021](#_bookmark16));
    - impact from the metamisc package (empirical data on traumatic brain injuries, *n* = 11*,* 022 patients across *N* = 15 studies with data that are MAR, [Debray and de Jong 2021](#_bookmark5));
    - hiv from the GJRM package (simulated data on HIV diagnoses, *n* = 6*,* 416 patients across *N* = 9 regions with data that are MNAR, [Radice 2021](#_bookmark12)).

For each of these datasets, we discuss the nature of the missingness, choose one or more imputation models and evaluate the imputed data, but we will also highlight one specific aspect of the imputation workflow.

This tutorial is dedicated to readers who are unfamiliar with multiple imptuation. More experienced readers can skip the introduction (case study 1) and directly head to practical applications of multilevel imputation under MAR conditions (case study IMPACT) or under MNAR conditions (case study HIV).

TODO: explicit statement about not going into workings of the methods. Galimer 2l methods.

## **Setup**

[TODO: Add environment info, seed and version number(s) somewhere.] Set up the R envi- ronment and load the necessary packages:

*R> set.seed(2022)*

*R> library(mice) # for imputation R> library(miceadds) # for imputation*

*R> library(ggmice) # for visualization R> library(ggplot2) # for visualization R> library(dplyr) # for data wrangling*

*R> library(lme4) # for multilevel modeling R> library(mitml) # for multilevel pooling*

# **Case study I: popularity data**

[TODO: explain case study]

In this section we’ll go over the different steps involved with imputing incomplete multilevel data with the R package mice. We consider the simulated popmis dataset, which included pupils (*n* = 2000) clustered within schools (*N* = 100). The following variables are of primary interest:

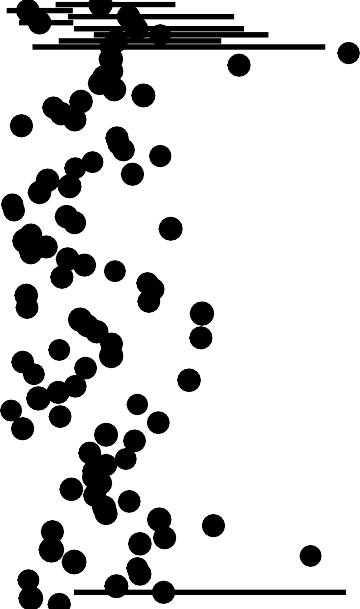
* + - school, school identification number (clustering variable);
    - popular, pupil popularity (self-rating between 0 and 10; unit-level);
    - sex, pupil sex (0=boy, 1=girl; unit-level);
    - texp, teacher experience (in years; cluster-level).

The research objective of the popmis dataset is to predict the pupils’ popularity based on their gender and the experience of the teacher. The analysis model corresponding to this dataset is multilevel regression with random intercepts, random slopes and a cross-level interaction. The outcome variable is popular, which is predicted from the unit-level variable sex and the cluster-level variable texp:

*R> mod <- popular ~ 1 + sex + (1 | school)*

The true effect is:

9987



9654

93

21

98089

8765

8432

10

798

7765

7432

7107

6987

6654

6321

650986

Study

5765

5432

10

495

48765

4432

4104

3987

3654

3321

320983

2765

2432

10

192

18765

1432

11001

1

0 5 10 15

Load the data into the environment and select the relevant variables:

*R> popmis <- popmis[, c("school", "popular", "sex")]*

Plot the missing data pattern:

Variable (name)

school sex popular

1152

Pattern (frequency)

848

0

1

Pattern

(number of missing entries)

|  |  |  |
| --- | --- | --- |
|  |  |  |
|  |  |  |

0 0 848

Variable

(number of missing entries)

observed missing

Figure 2: Missing data pattern in the popularity data

*R> plot\_pattern(popmis)*

The missingness is univariate and sporadic, which is illustrated in the missing data pattern in Figure [2](#_bookmark3).

To develop the best imputation model for the incomplete variable popular, we need to know whether the observed values of popular are related to observed values of other variables. Plot the pair-wise complete correlations in the incomplete data:

*R> plot\_corr(popmis)*

school

Variable to impute

popular

sex

school popular sex

|  |  |  |
| --- | --- | --- |
|  |  |  |
|  |  |  |
|  |  |  |

Correlation\*



−1.0 −0.5 0.0 0.5 1.0

\*pairwise complete observations

This shows us that sex may be a useful imputation model predictor. Moreover, the missing- ness in popular may depend on the observed values of other variables.

*R> # ggmice(popmis, aes(sex)) +*

*R> # geom\_histogram(fill = "white") +*

*R> # facet\_grid(. ~ is.na(popular), scales = "free", labeller = label\_both) R>*

*R> ggplot(popmis, aes(y = popular, group = sex)) +*

*+ geom\_boxplot() +*

*+ theme\_classic()*

8

6

popular

4

2

−0.2 0.0 0.2

### *Imputation ignoring the cluster variable (not recommended)*

The first imputation model that we’ll use is likely to be invalid. We do not use the cluster identifier school as imputation model predictor. With this model, we ignore the multilevel structure of the data, despite the high ICC. This assumes exchangeability between units. We include it purely to illustrate the effects of ignoring the clustering in our imputation effort.

Create a methods vector and predictor matrix for popular, and make sure school is not included as predictor:

*R> meth <- make.method(popmis) # methods vector R> pred <- quickpred(popmis) # predictor matrix R> plot\_pred(pred)*

school popular sex

|  |  |  |
| --- | --- | --- |
| 0 | 0 | 0 |
| 0 | 0 | 1 |
| 0 | 0 | 0 |

school

Variable to impute

popular

sex

predictor random effect inclusion−restriction variable

Impute the data, ignoring the cluster structure:

*R> imp <- mice(popmis, pred = pred, print = FALSE)*

Analyze the imputations:

*R> fit <- with(imp,*

*+ lmer(popular ~ 1 + sex + (1 | school)))*

Print the estimates:

*R> testEstimates(as.mitml.result(fit), extra.pars = TRUE)*

Call:

testEstimates(model = as.mitml.result(fit), extra.pars = TRUE)

Final parameter estimates and inferences obtained from 5 imputed data sets.

Estimate Std.Error t.value df P(>|t|) RIV FMI

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| (Intercept) | 4.932 | 0.274 | 18.012 | 4.420 | 0.000 | 19.514 | 0.964 |
| sex | 0.859 | 0.284 | 3.026 | 4.216 | 0.036 | 37.601 | 0.981 |

Estimate Intercept~~Intercept|school 0.265

Residual~~Residual 1.007

ICC|school 0.213

Unadjusted hypothesis test as appropriate in larger samples.

### *Imputation with the cluster variable as predictor (not recommended)*

We’ll now use school as a predictor to impute all other variables. This is still not recom- mended practice, since it only works under certain circumstances and results may be biased ([Drechsler 2015](#_bookmark6); [Enders, Mistler, and Keller 2016](#_bookmark7)). But at least, it includes some multilevel aspect. This method is also called ‘fixed cluster imputation’, and uses N-1 indicator variables representing allocation of N clusters as a fixed factor in the model ([Reiter, Raghunathan, and](#_bookmark13) [Kinney 2006](#_bookmark13); [Enders et al. 2016](#_bookmark7)). Colloquially, this is ‘multilevel imputation for dummies’.

[TODO: Add that it doesn’t work with systematic missingness (only with sporadic). There’s some pros and cons, and it may not even differ much if the number of clusters is low.]

*R> # adjust the predictor matrix R> pred["popular", "school"] <- 1 R> plot\_pred(pred)*

Imputation model predictor

school popular sex

|  |  |  |
| --- | --- | --- |
| 0 | 0 | 0 |
| 1 | 0 | 1 |
| 0 | 0 | 0 |

school

Variable to impute

popular

sex

predictor random effect inclusion−restriction variable

*R> # impute the data, cluster as predictor*

*R> imp <- mice(popmis, pred = pred, print = FALSE)*

Analyze the imputations:

*R> fit <- with(imp,*

*+ lmer(popular ~ 1 + sex + (1 | school)))*

Print the estimates:

*R> testEstimates(as.mitml.result(fit), extra.pars = TRUE)*

Call:

testEstimates(model = as.mitml.result(fit), extra.pars = TRUE)

Final parameter estimates and inferences obtained from 5 imputed data sets.

Estimate Std.Error t.value df P(>|t|) RIV FMI

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| (Intercept) | 5.054 | 0.266 | 19.029 | 4.554 | 0.000 | 14.936 | 0.954 |
| sex | 0.732 | 0.306 | 2.393 | 4.233 | 0.071 | 34.886 | 0.980 |

Estimate Intercept~~Intercept|school 0.318

Residual~~Residual 1.257

ICC|school 0.208

Unadjusted hypothesis test as appropriate in larger samples.

### *Imputation with multilevel model*

*R> # adjust the predictor matrix R> pred["popular", "school"] < 2*

*R> plot\_pred(pred)*

Imputation model predictor

school popular sex

|  |  |  |
| --- | --- | --- |
| 0 | 0 | 0 |
| −2 | 0 | 1 |
| 0 | 0 | 0 |

school

Variable to impute

popular

sex

predictor random effect inclusion−restriction variable

*R> # impute the data, cluster as predictor*

*R> imp <- mice(popmis, pred = pred, print = FALSE)*

Analyze the imputations:

*R> fit <- with(imp,*

*+ lmer(popular ~ 1 + sex + (1 | school)))*

Print the estimates:

*R> testEstimates(as.mitml.result(fit), extra.pars = TRUE)*

Call:

testEstimates(model = as.mitml.result(fit), extra.pars = TRUE)

Final parameter estimates and inferences obtained from 5 imputed data sets.

Estimate Std.Error t.value df P(>|t|) RIV FMI

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| (Intercept) | 4.714 | 0.193 | 24.432 | 5.032 | 0.000 | 8.224 | 0.919 |
| sex | 1.286 | 0.288 | 4.460 | 4.218 | 0.010 | 37.215 | 0.981 |

Estimate Intercept~~Intercept|school 0.299

Residual~~Residual 1.050

ICC|school 0.228

Unadjusted hypothesis test as appropriate in larger samples.

# **Case study II: IMPACT data (syst missingness, pred matrix)**

[TODO: check if there is systematic missingness in this dataset, if not make Marshall Com- puterized Tomography classification (ct) systematically missing.]

We illustrate how to impute incomplete multilevel data by means of a case study: impact from the metamisc package (empirical data on traumatic brain injuries, *n* = 11*,* 022 units across *N* = 15 clusters, [Debray and de Jong 2021](#_bookmark5)). [TODO: add more info about the complete data.] The impact data set contains traumatic brain injury data on *n* = 11022 patients clustered in *N* = 15 studies with the following 11 variables:

* + name Name of the study,
  + type Type of study (RCT: randomized controlled trial, OBS: observational cohort),
  + age Age of the patient,
  + motor\_score Glasgow Coma Scale motor score,
  + pupil Pupillary reactivity,
  + ct Marshall Computerized Tomography classification, [TODO: make this one var? also shows that you don’t always need random effects everywhere?]
  + hypox Hypoxia (0=no, 1=yes),
  + hypots Hypotension (0=no, 1=yes),
  + tsah Traumatic subarachnoid hemorrhage (0=no, 1=yes),
  + edh Epidural hematoma (0=no, 1=yes),
  + mort 6-month mortality (0=alive, 1=dead).

The analysis model for this dataset is a prediction model with mort as the outcome. In this tutorial we’ll estimate the adjusted prognostic effect of ct on unfortunate outcomes. The estimand is the adjusted odds ratio for ct, after including type, age motor\_score and pupil into the analysis model:

*R> mod <- mort ~ 1 + type + age + motor\_score + pupil + ct + (1 | name)*

Note that variables hypots, hypox, tsah and edh are not part of the analysis model, and may thus serve as auxiliary variables for imputation.

The impact data included in the metamisc package is a complete data set. The original data has already been imputed once (Steyerberg et al, 2008). For the purpose of this tutorial we have induced missingness (mimicking the missing data in the original data set before imputation). The resulting incomplete data can be accessed from [zenodo link to be created](https://zenodo.com/).

Load the complete and incomplete data into the R workspace:

*R> data("impact", package = "metamisc") # complete data R> dat <- read.table("link/to/the/data.txt") # incomplete data*

The estimated effects in the complete data are visualized in Figure **??**.

UK4 TIUS TINT TCDB SLIN SKB SAP

Study

PHARMOS

PEG NABIS HIT II HIT I EBIC CSTAT APOE

0 3 6 9 12



Adjusted odds ratio for ct

ctIII ctIV/V

*R> # fit <- glmer(mod, family = "binomial", data = impact) # fit the model R> # tidy(fit, conf.int = TRUE, exponentiate = TRUE) # print estimates*

[TODO: show how much variance there is after different methods]

[TODO: add ICC before/after imputation and interpret: This tells us that the multilevel structure of the data should probably be taken into account. If we don’t, we’ll may end up with incorrect imputations, biasing the effect of the clusters towards zero.]

[TODO: add descriptive statistics of the complete and incomplete data.]

## **3.1. Missingness**

To explore the missingness, it is wise to look at the missing data pattern:

*R> plot\_pattern(dat, rotate = TRUE) # plot missingness pattern*

Variable (name)

motor\_score

3808

937

681

238

724

121

290

81

687

309

217

32

321

39

220

20

240

259

225

221

40

37

31

38

6

4

Pattern (frequency)

5

3

2

1

1

614

64

44

22

51

18

20

21

45

23

15

4

11

10

14

5

25

35

23

22

22

9

18

21

7

8

6

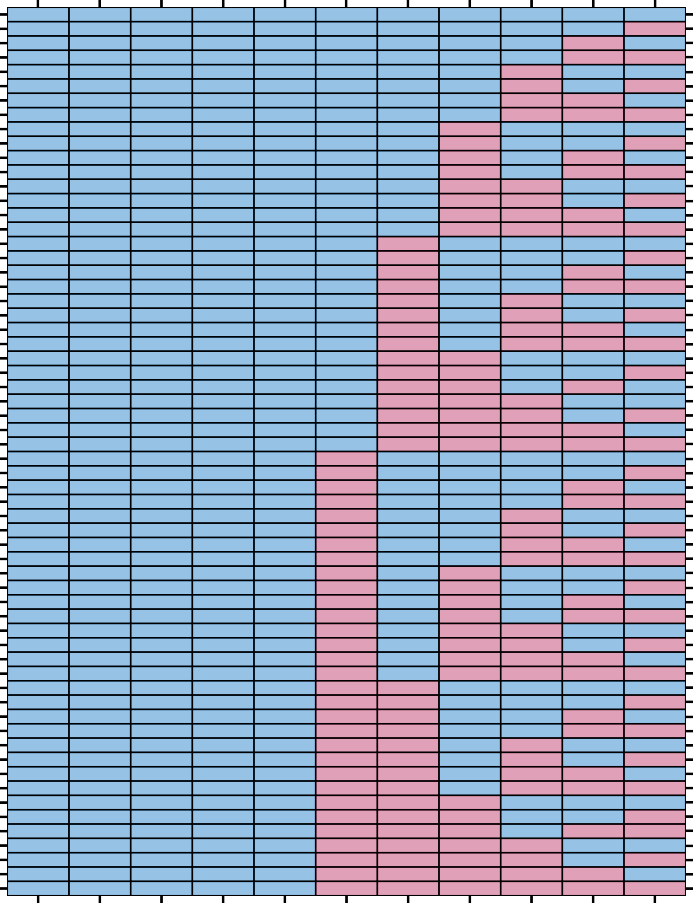
1

2

1

3

0

1

name

type

age

mort

pupil

hypots

tsah

edh

hypox

ct

1

2

1

2

2

3

1

2

2

3

2

3

3

4

1

2

2

Pattern

(number of missing entries)

3

2

3

3

4

2

3

3

3

4

4

5

1

2

2

3

2

3

3

4

2

3

3

4

3

4

4

5

2

3

3

4

3

4

4

5

3

4

5

4

5

5

6

0

0

0

0

0

1184

1316

2022

2196

2540

2612

Variable

(number of missing entries)

observed missing

This shows. . . [TODO: fill in that we need to impute ct and pupil.]

To develop the best imputation model, we need to investigate the relations between the observed values of the incomplete variables and the observed values of other variables, and the relation between the missingness indicators of the incomplete variables and the observed values of the other variables. To see whether the missingness depends on the observed values of other variables, we. . . [TODO: fill in that we can test this statistically or use visual inspection (e.g. a histogram faceted by the missingness indicator).]

We should impute the variables ct and pupil and any auxiliary variables we might want to use to impute these incomplete analysis model variables. We can evaluate which variables may be useful auxiliaries by plotting the pairwise complete correlations:

*R> plot\_corr(dat, rotate = TRUE) # plot correlations*

Imputation model predictor

name type age

motor\_score pupil

ct hypox hypots tsah edh mort

name type age

Variable to impute

motor\_score

pupil

ct hypox hypots tsah edh mort

Correlation\*



−1.0 −0.5 0.0 0.5 1.0

\*pairwise complete observations

This shows us that hypox and hypot would not be useful auxiliary variables for imputing ct. Depending on the minimum required correlation, tsah could be useful, while edh has the strongest correlation with ct out of all the variables in the data and should definitely be included in the imputation model. For the imputation of pupil, none of the potential auxiliary variables has a very strong relation, but hypots could be used. We conclude that we can exclude hypox from the data, since this is neither an analysis model variable nor an auxiliary variable for imputation:

*R> dat <- select(dat, !hypox) # remove variable*

## **Complete case analysis [TODO: remove this?]**

As previously stated, complete case analysis lowers statistical power and may bias results. The complete case analysis estimates are:

*R> fit <- glmer(mod, family = "binomial", data = na.omit(dat)) # fit the model R> tidy(fit, conf.int = TRUE, exponentiate = TRUE) # print estimates*

# A tibble: 11 x 9

effect group term estim~1 std.er~2 stati~3 p.value conf.~4 conf.~5

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | <chr> | <chr> | <chr> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> |
| 1 | fixed | <NA> | (Intercept) | 0.0863 | 0.0182 | -11.6 | 2.99e-31 | 0.0571 | 0.130 |
| 2 | fixed | <NA> | typeRCT | 0.757 | 0.137 | -1.54 | 1.22e- 1 | 0.531 | 1.08 |
| 3 | fixed | <NA> | age | 1.03 | 0.00265 | 12.9 | 7.40e-38 | 1.03 | 1.04 |
| 4 | fixed | <NA> | motor\_scor~ | 0.651 | 0.0732 | -3.82 | 1.34e- 4 | 0.522 | 0.811 |
| 5 | fixed | <NA> | motor\_scor~ | 0.489 | 0.0555 | -6.30 | 2.97e-10 | 0.391 | 0.611 |
| 6 | fixed | <NA> | motor\_scor~ | 0.274 | 0.0321 | -11.0 | 2.28e-28 | 0.218 | 0.345 |
| 7 | fixed | <NA> | pupilNone | 3.20 | 0.317 | 11.7 | 8.18e-32 | 2.63 | 3.88 |
| 8 | fixed | <NA> | pupilOne | 1.75 | 0.195 | 5.06 | 4.27e- 7 | 1.41 | 2.18 |
| 9 | fixed | <NA> | ctIII | 2.41 | 0.268 | 7.89 | 3.05e-15 | 1.94 | 2.99 |
| 10 | fixed | <NA> | ctIV/V | 2.30 | 0.214 | 8.95 | 3.55e-19 | 1.92 | 2.76 |
| 11 | ran\_pars | name | sd (Inter~ | 0.230 | NA | NA | NA | NA | NA |

# ... with abbreviated variable names 1: estimate, 2: std.error, 3: statistic, # 4: conf.low, 5: conf.high

As we can see. . . [TODO: fill in.]

## **Imputation model**

Mutate data to get the right data types for imputation (e.g. integer for clustering variable).

*R> dat <- dat %>% mutate(across(everything(), as.integer))*

Create a methods vector and predictor matrix, and make sure name is not included as pre- dictor, but as clustering variable:

*R> meth <- make.method(dat) # methods vector R> pred <- quickpred(dat) # predictor matrix R> plot\_pred(pred)*

Imputation model predictor

nametype amgoetor\_scpourpeil ct hypotstsah edh mort

0 0 0 0 0 0 0 0 0 0

0 0 0 0 0 0 0 0 0 0

0 0 0 0 0 0 0 0 0 0

0 0 0 0 0 0 0 0 0 0

0 0 0 1 0 1 1 0 0 1

0 1 1 1 1 0 0 1 1 1

0 0 0 1 1 0 0 0 0 1

1 0 1 0 0 1 0 0 0 1

1 0 0 0 0 1 0 0 0 0

0 0 0 0 0 0 0 0 0 0

name type age

Variable to impute

motor\_score

pupil

ct hypots tsah edh mort

d predictor random effect inclusion−restriction variable

*R> pred[pred == 1] <- 2 R> pred["mort", ] <- 2*

*R> pred[, "mort"] <- 2*

*R> pred[c("name", "type", "age", "motor\_score", "mort"), ] <- 0 R> pred[, "name"] <- -2*

*R> diag(pred) <- 0 R> plot\_pred(pred)*

name type age

Variable to impute

motor\_score

pupil

ct hypots tsah edh mort

Imputation model predictor

nametype amgoetor\_scpourpeil ct hypotstsah edh mort

0 0 0 0 0 0 0 0 0 0

−2 0 0 0 0 0 0 0 0 0

−2 0 0 0 0 0 0 0 0 0

−2 0 0 0 0 0 0 0 0 0

−2 0 0 2 0 2 2 0 0 2

−2 2 2 2 2 0 0 2 2 2

−2 0 0 2 2 0 0 0 0 2

−2 0 2 0 0 2 0 0 0 2

−2 0 0 0 0 2 0 0 0 2

−2 0 0 0 0 0 0 0 0 0

d predictor random effect inclusion−restriction variable

*R> meth <- make.method(dat) R> meth*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| name | type | age | motor\_score | pupil | ct |
| "" | "" | "" | "" | "pmm" | "pmm" |
| hypots | tsah | edh | mort |  |  |
| "pmm" | "pmm" | "pmm" | "" |  |  |

Impute the incomplete data

*R> imp <- mice(dat, method = meth, predictorMatrix = pred, printFlag = FALSE) R> fit <- imp %>%*

*+ with(glmer(mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name), famil R> tidy(pool(fit))*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | term estimate | std.error | statistic | p.value |
| 1 | (Intercept) -2.33813790 | 0.340459131 | -6.867602 | 6.978862e-12 |
| 2 | type -0.41509929 | 0.179936773 | -2.306918 | 2.107792e-02 |
| 3 | age 0.03034813 | 0.001561834 | 19.431086 | 0.000000e+00 |
| 4 | as.factor(motor\_score)2 -0.66052409 | 0.068846376 | -9.594174 | 0.000000e+00 |
| 5 | as.factor(motor\_score)3 -1.05030912 | 0.070059114 | -14.991756 | 0.000000e+00 |
| 6 | as.factor(motor\_score)4 -1.49637069 | 0.071492961 | -20.930322 | 0.000000e+00 |
| 7 | pupil 0.48922641 | 0.038536483 | 12.695149 | 0.000000e+00 |
| 8 | ct 0.42634415 | 0.028388807 | 15.018037 | 0.000000e+00 |
|  | b df dfcom | fmi | lambda m | riv |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | 9.395965e-04 | 8668.10341 | 11013 | 0.0099557149 | 0.0097273074 | 5 | 0.0098228573 |
| 2 | 1.729929e-05 | 10991.51028 | 11013 | 0.0008229571 | 0.0006411648 | 5 | 0.0006415761 |
| 3 | 8.332782e-09 | 10482.95010 | 11013 | 0.0042891736 | 0.0040992241 | 5 | 0.0041160969 |
| 4 | 5.649577e-05 | 6979.24803 | 11013 | 0.0145856016 | 0.0143032580 | 5 | 0.0145108098 |
| 5 | 3.003051e-05 | 9526.87220 | 11013 | 0.0075503299 | 0.0073420043 | 5 | 0.0073963080 |
| 6 | 3.329522e-05 | 9362.42789 | 11013 | 0.0080288174 | 0.0078169354 | 5 | 0.0078785213 |
| 7 | 3.337070e-04 | 54.63795 | 11013 | 0.2949938851 | 0.2696512493 | 5 | 0.3692088868 |
| 8 | 1.180517e-05 | 5893.23780 | 11013 | 0.0179108151 | 0.0175775781 | 5 | 0.0178920775 |
|  | ubar |  | | | | | |
| 1 | 1.147849e-01 |
| 2 | 3.235648e-02 |
| 3 | 2.429325e-06 |
| 4 | 4.672029e-03 |
| 5 | 4.872243e-03 |
| 6 | 5.071289e-03 |
| 7 | 1.084612e-03 |
| 8 | 7.917581e-04 |

*R> as.mitml.result(fit)*

[[1]]

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: binomial ( logit )

Formula: mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name)

AIC BIC logLik deviance df.resid 10522.944 10588.713 -5252.472 10504.944 11013

Random effects:

Groups Name Std.Dev. name (Intercept) 0.2913

Number of obs: 11022, groups: name, 15 Fixed Effects:

(Intercept) type age

-2.32713 -0.41953 0.03031

as.factor(motor\_score)2 as.factor(motor\_score)3 as.factor(motor\_score)4

-0.65651 -1.04719 -1.49327

pupil ct

0.48990 0.42335

optimizer (Nelder\_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings

[[2]]

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: binomial ( logit )

Formula: mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name)

AIC BIC logLik deviance df.resid 10525.723 10591.492 -5253.861 10507.723 11013

Random effects:

Groups Name Std.Dev. name (Intercept) 0.2937

Number of obs: 11022, groups: name, 15 Fixed Effects:

(Intercept) type age

-2.30150 -0.41940 0.03024

as.factor(motor\_score)2 as.factor(motor\_score)3 as.factor(motor\_score)4

-0.65497 -1.04451 -1.49454

pupil ct

0.47281 0.42888

optimizer (Nelder\_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings

[[3]]

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: binomial ( logit )

Formula: mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name)

AIC BIC logLik deviance df.resid 10512.28 10578.05 -5247.14 10494.28 11013

Random effects:

Groups Name Std.Dev. name (Intercept) 0.2852

Number of obs: 11022, groups: name, 15 Fixed Effects:

(Intercept) type age

-2.35320 -0.41028 0.03034

as.factor(motor\_score)2 as.factor(motor\_score)3 as.factor(motor\_score)4

-0.66933 -1.05474 -1.50379

pupil ct

0.49491 0.42442

optimizer (Nelder\_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings

[[4]]

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: binomial ( logit )

Formula: mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name)

AIC BIC logLik deviance df.resid 10530.02 10595.79 -5256.01 10512.02 11013

Random effects:

Groups Name Std.Dev. name (Intercept) 0.2923

Number of obs: 11022, groups: name, 15 Fixed Effects:

(Intercept) type age

-2.32670 -0.41286 0.03037

as.factor(motor\_score)2 as.factor(motor\_score)3 as.factor(motor\_score)4

-0.66801 -1.04770 -1.50070

pupil ct

0.47210 0.43109

optimizer (Nelder\_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings

[[5]]

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: binomial ( logit )

Formula: mort ~ type + age + as.factor(motor\_score) + pupil + ct + (1 | name)

AIC BIC logLik deviance df.resid 10488.615 10554.383 -5235.307 10470.615 11013

Random effects:

Groups Name Std.Dev. name (Intercept) 0.2939

Number of obs: 11022, groups: name, 15 Fixed Effects:

(Intercept) type age

-2.38215 -0.41343 0.03049

as.factor(motor\_score)2 as.factor(motor\_score)3 as.factor(motor\_score)4

-0.65379 -1.05740 -1.48956

pupil ct

0.51641 0.42397

optimizer (Nelder\_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings

attr(,"class")

1. "mitml.result" "list"

*R> # testEstimates(as.mitml.result(fit))*

# **Case study III: HIV data**

Data are simulated and included in the GJRM package. We will use the following variables:

* + region Cluster variable,
  + hiv HIV diagnosis (0=no, 1=yes),
  + age Age of the patient,
  + marital Marital status,
  + condom Condom use during last intercourse,
  + smoke Smoker (levels; inclusion restriction variable).

The imputation of these date is based on the toy example from [IPDMA Heckman Github](https://github.com/johamunoz/Heckman-IPDMA/blob/main/Toy_example.R) [repo](https://github.com/johamunoz/Heckman-IPDMA/blob/main/Toy_example.R).

Variable (name)

region age marital condom smokeinterviewerID hiv

5098 0

Pattern

(number of missing entries)

Pattern (frequency)

1318 1

0 0 0 0 0 0 1318

Variable

(number of missing entries)

observed missing

R=region+language+(1|InterviewID) model with with interviewer as random effects, because the observations are not independent. Interviews are not allocated randomly. In theory we expect the inclusion-restriction variable to be randomly assigned, that’s why we’re adding region and language to compensate for non-random allocation.

Load the data:

*R> data("hiv", package = "GJRM")*

*R> # We select 5 predictor variables over 9 regions R> colnames(hiv)*

|  |  |  |  |
| --- | --- | --- | --- |
| [1] "hivconsent" | "hiv" | "age" | "education" |
| [5] "wealth" | "region" | "marital" | "std" |
| [9] "age1sex\_cat" | "highhiv" | "partner" | "condom" |
| [13] "aidscare" | "knowsdiedofaids" | "evertestedHIV" | "smoke" |
| [17] "religion" | "ethnicity" | "language" | "interviewerID" |
| [21] "sw" |  |  |  |

*R> hivdata <- hiv[,c("hiv","hivconsent","age","marital","condom","highhiv","interviewerID"*

Recode variables:

*R> # Study/group variable has to be recoded as integer R> hivdata$region<-as.integer(hivdata$region)*

*R>*

*R> # Categorical variables have to be recoded as factor*

*R> # to use the 2l.binary imputation method, it is required that the level names should no R>*

*R> hivdata$hiv <- as.factor(hivdata$hiv) #to use the 2l.heckman method, it is required tha R> #the missing variable is stored as a factor in the dataset, otherwise the method will R> #apply the imputation correction for a missing continuous variable instead for*

*R> #a missing binary variable,which is in this case the binary response of the hiv test. R>*

*R> hivdata$marital <- as.factor(hivdata$marital)*

*R> levels(hivdata$marital)<-c("never\_married","currently\_married","formerly\_married") R> hivdata$condom <- as.factor(hivdata$condom)*

*R> levels(hivdata$condom)<-c("No\_Condom\_Last\_Intercourse","Condom\_Last\_Intercourse") R> hivdata$highhiv <- as.factor(hivdata$highhiv)*

*R> levels(hivdata$highhiv)<-c("Not\_High\_Risk\_of\_HIV","High\_Risk\_of\_HIV") R> hivdata$interviewerID <- as.factor(hivdata$interviewerID)*

*R>*

*R> hivdata$interviewerID <- as.factor(as.character(hivdata$interviewerID)) R> interv<-as.data.frame(table(hivdata$interviewerID,hivdata$region))*

We obtain here the random effects for each interviewer, this is an approximation of the interviewer’s skill which will be used as an exclusion constraint. Here, since the location of the interviewer was not randomly assigned to the subjects, the assignment was corrected for region and language.

*R> hivdata$hivconsent <- as.factor(hivdata$hivconsent)*

*R> ID\_mixed <- lme4::glmer(hivconsent ~ region + language+(1 | interviewerID), data = hivd R> reffect <- ranef(ID\_mixed)$interviewerID*

*R> reffect$interviewerID <- levels(hivdata$interviewerID) R> colnames(reffect) <- c("IDreffect","interviewerID")*

*R> hivdata <- merge(hivdata, reffect, by="interviewerID", all.x=TRUE) R>*

*R> hivdata$interviewerID<-NULL R> hivdata$hivconsent<-NULL*

*R> hivdata$language<-NULL*

Set the Heckman model as imputation method

*R> #Set prediction matrix and methods R> ini <- mice(hivdata, maxit = 0)*

*R> meth<-ini$method*

*R> meth["hiv"]<-"2l.binary" R> pred <- ini$pred*

*R> pred[,"region"] <- 0 R> pred["region",] <- 0*

*R> pred["hiv","region"]<- -2*

*R> pred["hiv","IDreffect"]<- 0 R>*

*R> # Heckman model*

*R> pred["hiv","IDreffect"] <- -3 R> meth<-ini$method*

*R> meth["hiv"]<-"2l.heckman"*

Impute the data:

*R> imp <- mice( hivdata, # dataset with missing values*

*+ m = 10, # number of imputations*

*+ maxit = 1,*

*+ seed = 1234, #seed attached to the dataID*

*+ meth = meth, #imputation method vector*

*+ pred = pred, #imputation predictors matrix*

*+ print = T,*

*+ meta\_method="reml",*

*+ pmm=FALSE)*

iter imp variable

1 1 hiv

1 2 hiv

1 3 hiv

1 4 hiv

1 5 hiv

1 6 hiv

1 7 hiv

1 8 hiv

1 9 hiv

1 10 hiv

# **Discussion**

* + JOMO in mice -> on the side for now
  + Additional levels of clustering
  + More complex data types: timeseries and polynomial relationship in the clustering.

# **Think about**

* + Adding some kind of help function to mice that suggests a suitable predictor matrix to the user, given a certain analysis model.
  + Adding a multilevel\_ampute() wrapper function in mice.
  + Exporting mids objects to other packages like lme4 or coxme?
  + Adding a ICC=0 dataset to show that even if there is no clustering it doesn’t hurt.
  + Show use case for deductive imputation for cluster level variables?
  + env dump in repo

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