



Imputation of Incomplete Multilevel Data with mice

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Abstract

This tutorial illustrates the imputation of incomplete multilevel data with the R package **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 abstract will look like: Lorem ipsum dolor sit amet, consectetur adipiscing elit, sed do eiusmod tempor incididunt ut labore 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.

1. 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-

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 observations 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, Ten Have, and Kimmel 2001). [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 observations. These models are also known as ‘multilevel models’, ‘hierarchical models’, ‘mixed effect models’ and ‘random effect models’. Table 1 provides an overview of some key concepts in multilevel modeling.

Missingness in multilevel data

```
<!-- Maybe besides CC and imputation name also likelihood based methods -->
```

Like any other dataset, clustered datasets are prone to missing data. Several strategies o

When clustered datasets are affected by missing values, we can distinguish between two typ

```
<!-- Systematic missingness implies that one or more variables are never observed in a cer
```

```
‘‘‘{=latex}
```

```
\begin{CodeChunk}
```

```
\begin{figure}
```

```
{\centering \includegraphics{Imputation_of_Incomplete_Multilevel_Data_files/figure-latex/p
```

```
}
```

```
\caption[Missingness in multilevel data]{Missingness in multilevel data}\label{fig:pattern
```

```
\end{figure}
```

```
\end{CodeChunk}
```

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 Table 2). For each of these three missingness generating mechanisms, different imputation strategies are warranted Yucel (2008) and Hox, van Buuren, and Jolani (2015). 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 2018). 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.]

1.1. Aim of this paper

This paper 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, including 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 familiarity with multilevel imputation (see e.g. Audigier, White, Jolani, Debray, Quartagno, Carpenter, van Buuren, and Resche-Rigon 2018, and Grund, Lüdtke, and Robitzsch (2018)) and the **lme4** notation for multilevel models (see Table 3).

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);
- **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);
- **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).

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 imputation. 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.

1.2. Setup

[TODO: Add environment info, seed and version number(s) somewhere.] Set up the R environment 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
```

2. Case study I: popularity data

[TODO: explain case study]

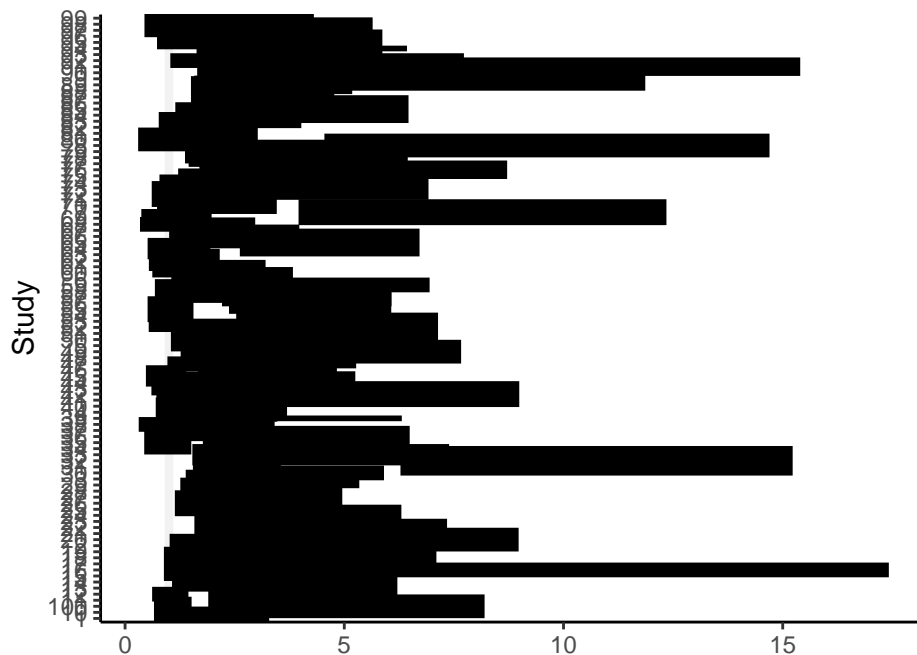
In this section we'll go over the different steps involved with imputing incomplete multilevel data with the R package *mice*. We consider the simulated `popmis` dataset, which included pupils ($n = 2000$) clustered within schools ($N = 100$). The following variables are of primary interest:

- `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:



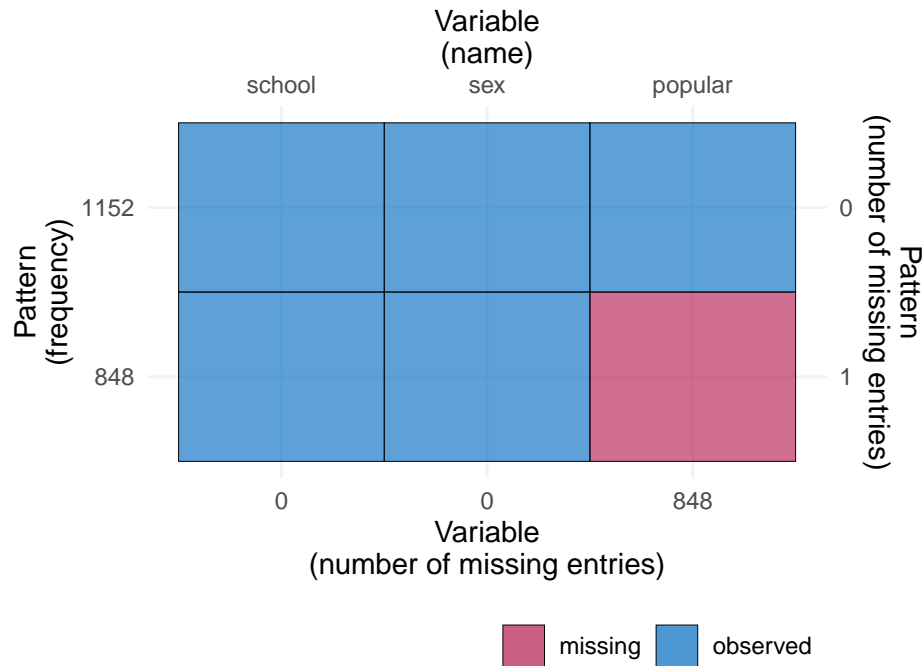


Figure 1: Missing data pattern in the popularity data

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

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

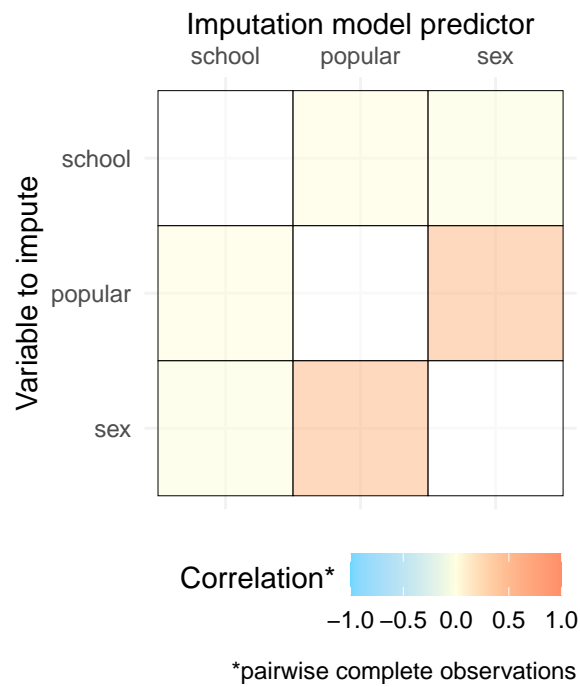
Plot the missing data pattern:

```
R> plot_pattern(popmis)
```

The missingness is univariate and sporadic, which is illustrated in the missing data pattern in Figure 1.

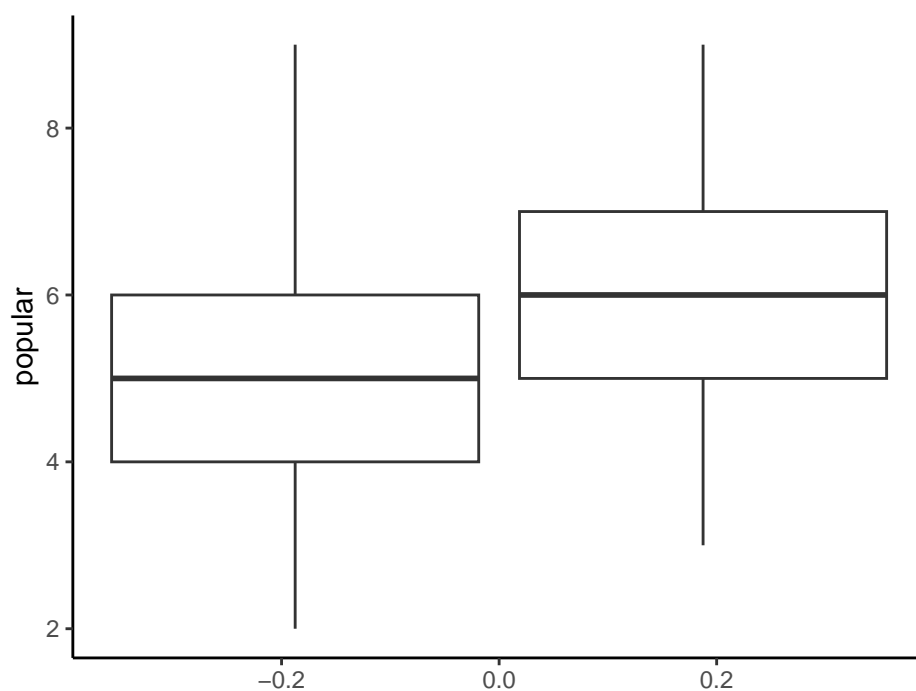
To develop the best imputation model for the incomplete variable **popular**, we need to know whether the observed values of **popular** are related to observed values of other variables. Plot the pair-wise complete correlations in the incomplete data:

```
R> plot_corr(popmis)
```



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

```
R> # ggmmice(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()
```

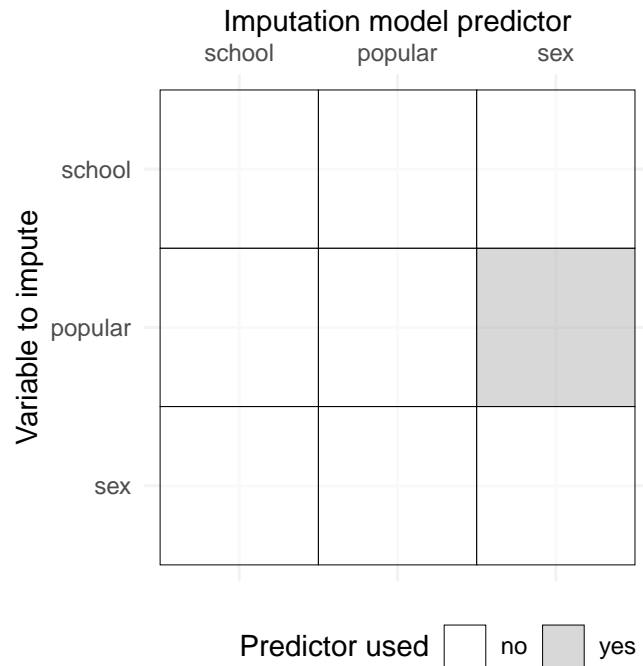


Imputation ignoring the cluster variable (not recommended)

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)
```



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)	5.012	0.295	16.994	4.362	0.000	22.587	0.969
sex	0.695	0.251	2.768	4.287	0.047	28.390	0.975

	Estimate
Intercept~~Intercept school	0.266


```
Residual~~Residual      1.035
ICC|school               0.208
```

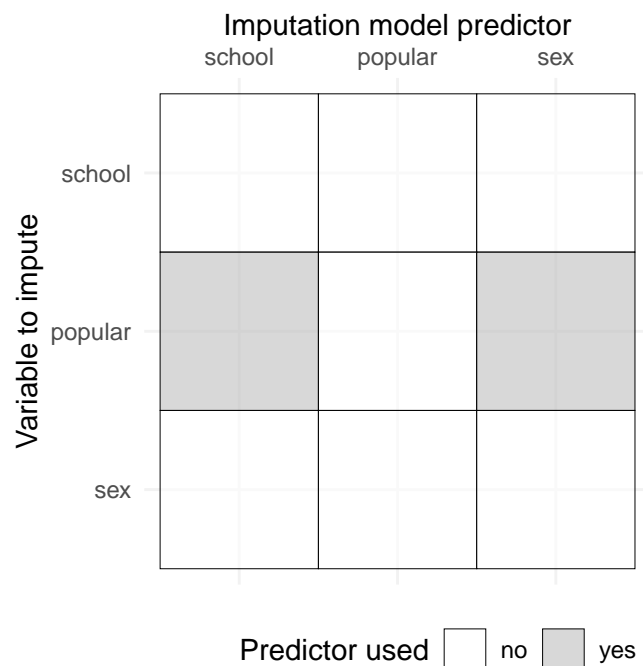
Unadjusted hypothesis test as appropriate in larger samples.

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 recommended practice, since it only works under certain circumstances and results may be biased (Drechsler 2015; Enders, Mistler, and Keller 2016). 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 Kinney 2006; Enders et al. 2016). 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)
```



```
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.

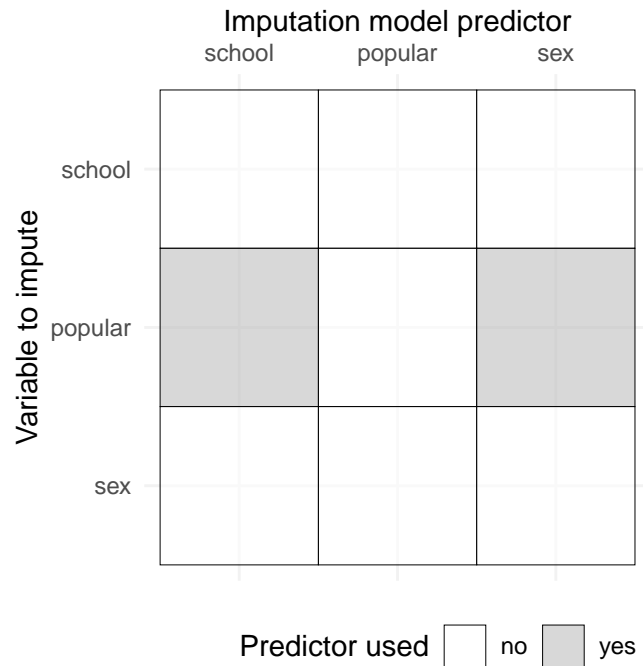
	Estimate	Std.Error	t.value	df	P(> t)	RIV	FMI
(Intercept)	4.915	0.217	22.642	4.926	0.000	9.110	0.926
sex	0.975	0.283	3.444	4.250	0.024	32.504	0.978

	Estimate
Intercept~~Intercept school	0.351
Residual~~Residual	1.153
ICC school	0.233

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)
```



```
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)	5.011	0.410	12.222	4.226	0.000	35.955	0.980
sex	0.928	0.381	2.434	4.168	0.069	48.221	0.985

	Estimate
Intercept~~Intercept school	0.313
Residual~~Residual	1.428

ICC|school 0.188

Unadjusted hypothesis test as appropriate in larger samples.

3. Case study II: IMPACT data (syst missingness, pred matrix)

[TODO: check if there is systematic missingness in this dataset, if not make Marshall Computerized 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](#)). [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)
```

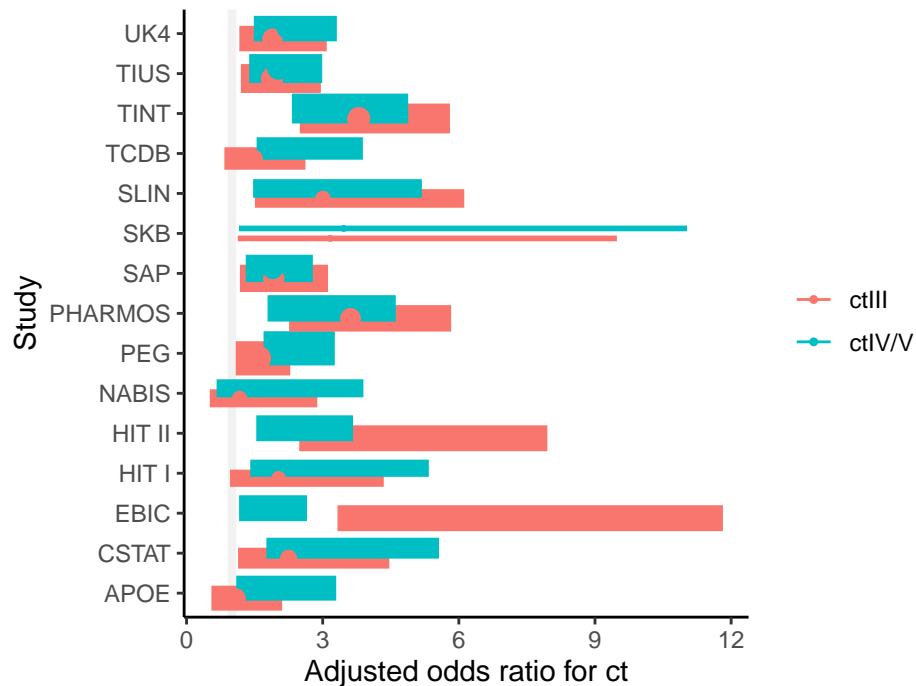
Note that variables `hypots`, `hypox`, `tsah` and `edh` are not part of the analysis model, and may thus serve as auxiliary variables for imputation.

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](#).

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 ??.



```
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]

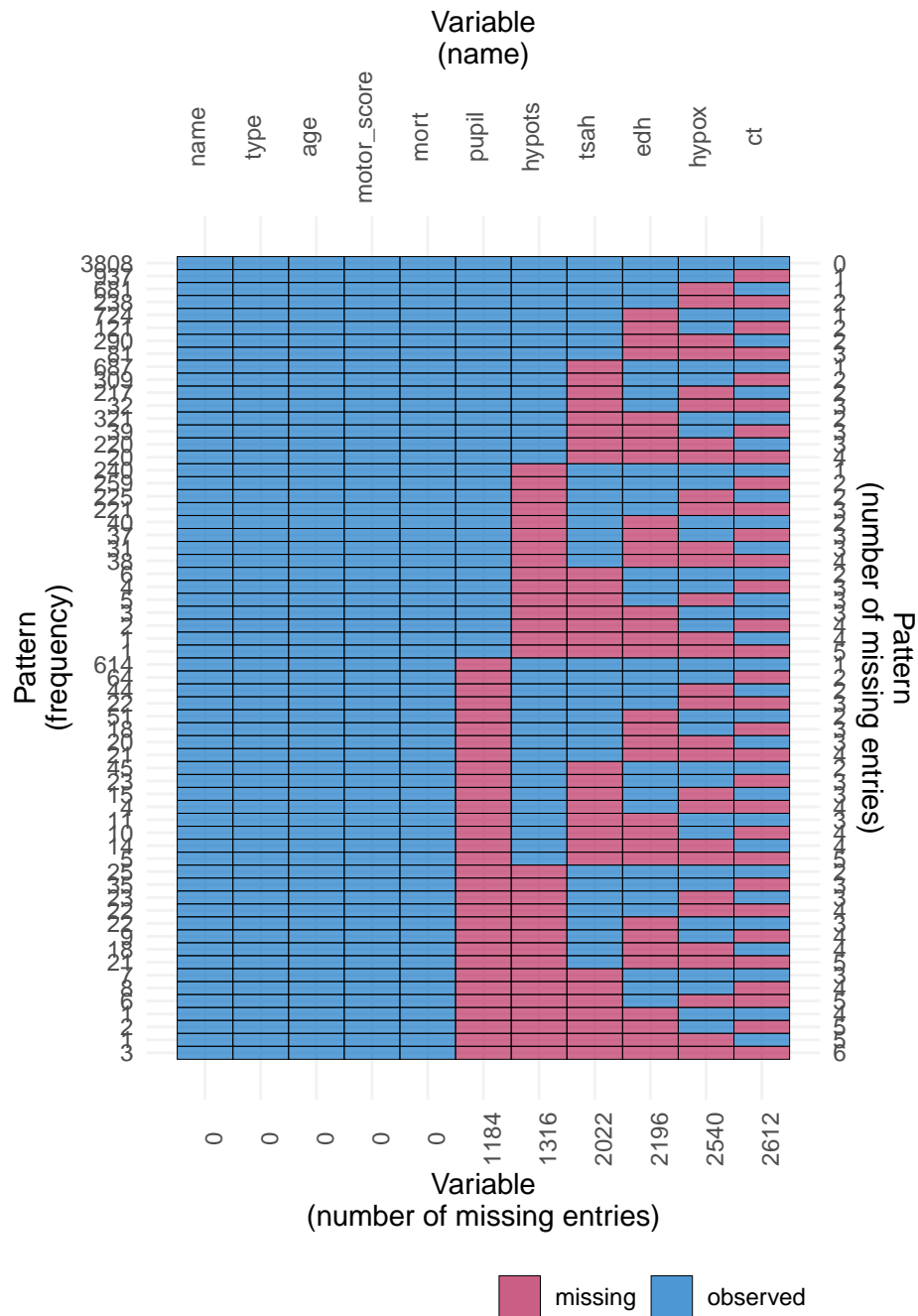
[TODO: add ICC before/after imputation and interpret: This tells us that the multilevel structure of the data should probably be taken into account. If we don't, we'll may end up with incorrect imputations, biasing the effect of the clusters towards zero.]

[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
```

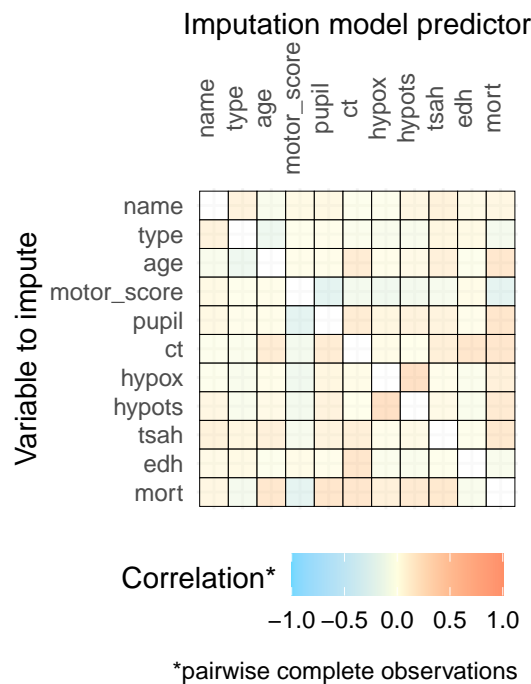


This shows... [TODO: fill in that we need to impute `ct` and `pupil`.]

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
```



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
```

3.2. 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	2.98e-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	7.39e-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	8.19e-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.]

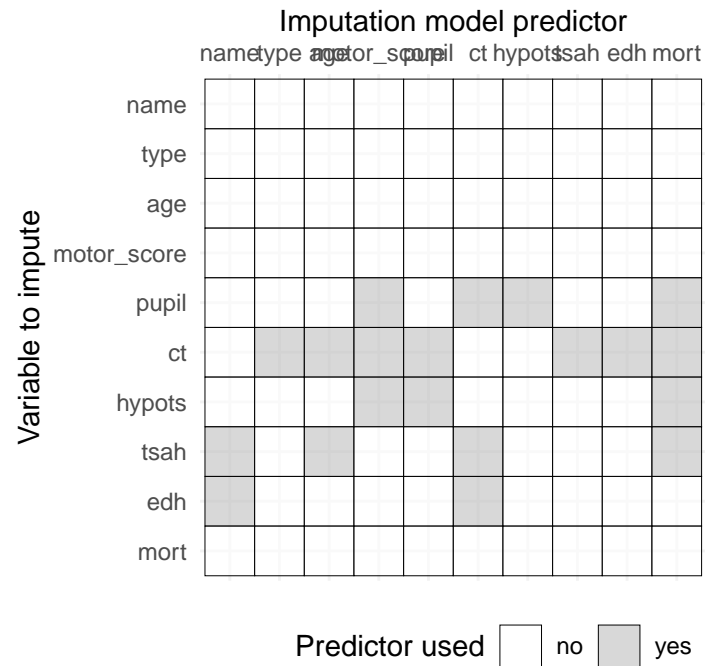
3.3. Imputation model

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 predictor, but as clustering variable:

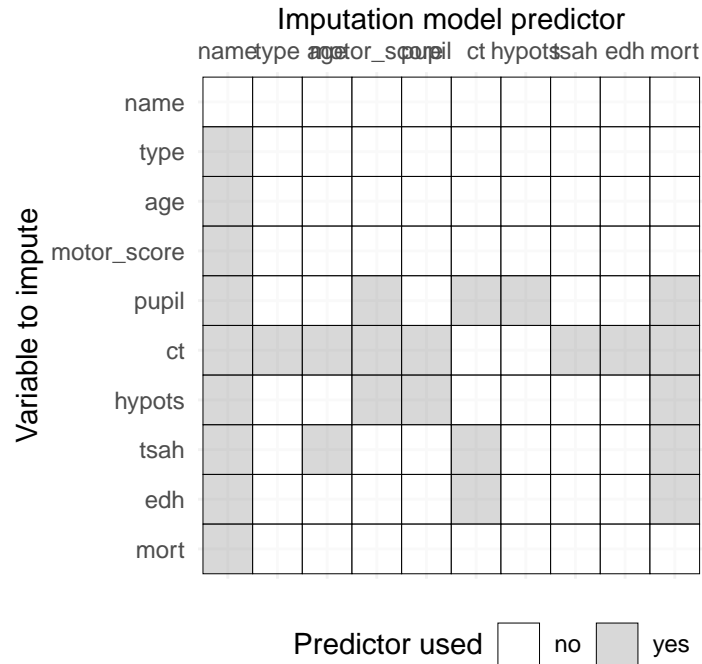
```
R> meth <- make.method(dat) # methods vector
R> pred <- quickpred(dat)   # predictor matrix
R> plot_pred(pred)
```

```

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)

```



```
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)	-2.35201485	0.340106796	-6.915519	4.943219e-12
2	type	-0.41266362	0.180240358	-2.289518	2.206828e-02
3	age	0.03049017	0.001570142	19.418732	1.231236e-81
4	as.factor(motor_score)2	-0.66765094	0.068736642	-9.713174	3.473396e-22
5	as.factor(motor_score)3	-1.05520421	0.070218236	-15.027495	2.532464e-50
6	as.factor(motor_score)4	-1.51238926	0.072304429	-20.916966	1.894925e-90
7	pupil	0.48421322	0.038983420	12.421004	6.807219e-17
8	ct	0.43474506	0.029967898	14.507025	2.318762e-36
	b	df	dfcom	fmi	lambda
				m	riv

```

1 5.283158e-04 10118.53147 11013 0.005677319 0.005480804 5 0.005511008
2 4.875905e-05 10894.06456 11013 0.001984282 0.001801077 5 0.001804327
3 3.333802e-08 6323.24413 11013 0.016538196 0.016227183 5 0.016494848
4 4.185462e-05 8330.19444 11013 0.010867814 0.010630361 5 0.010744580
5 5.135737e-05 7632.09368 11013 0.012757930 0.012499256 5 0.012657465
6 1.404727e-04 2826.80320 11013 0.032927570 0.032243595 5 0.033317884
7 3.572093e-04 49.95954 11013 0.309174397 0.282061687 5 0.392877330
8 8.584367e-05 294.82759 11013 0.120648604 0.114703577 5 0.129565165

```

ubar

```

1 1.150387e-01
2 3.242808e-02
3 2.425341e-06
4 4.674500e-03
5 4.868972e-03
6 5.059363e-03
7 1.091056e-03
8 7.950625e-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
	10495.423	10561.192	-5238.712	10477.423	11013

Random effects:

Groups Name	Std.Dev.
-------------	----------

name (Intercept)	0.2843
------------------	--------

Number of obs: 11022, groups: name, 15

Fixed Effects:

	(Intercept)	type	age
	-2.37193	-0.41015	0.03052
as.factor(motor_score)2	-0.65803	-1.04612	-1.51245
pupil	0.50405	0.42496	

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
10500.88 10566.65 -5241.44 10482.88    11013
Random effects:
  Groups Name      Std.Dev.
  name  (Intercept) 0.2917
Number of obs: 11022, groups:  name, 15
Fixed Effects:
              (Intercept)                  type                  age
              -2.37717                  -0.41511                  0.03067
as.factor(motor_score)2  as.factor(motor_score)3  as.factor(motor_score)4
              -0.66935                  -1.05210                  -1.49428
              pupil                      ct
              0.49013                  0.43835
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
10505.026 10570.795 -5243.513 10487.026    11013
Random effects:
  Groups Name      Std.Dev.
  name  (Intercept) 0.2908
Number of obs: 11022, groups:  name, 15
Fixed Effects:
              (Intercept)                  type                  age
              -2.32339                  -0.42359                  0.03023
as.factor(motor_score)2  as.factor(motor_score)3  as.factor(motor_score)4
              -0.67142                  -1.05776                  -1.51038
              pupil                      ct
              0.49756                  0.42474
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
10519.511 10585.280 -5250.755 10501.511    11013
Random effects:
  Groups Name      Std.Dev.
  name  (Intercept) 0.2961

```

```

Number of obs: 11022, groups:  name, 15
Fixed Effects:
              (Intercept)                  type                  age
              -2.33576                -0.40872                0.03039
as.factor(motor_score)2  as.factor(motor_score)3  as.factor(motor_score)4
              -0.66477                -1.05453                -1.51860
              pupil                      ct
              0.45928                  0.44419
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
10522.038 10587.807 -5252.019 10504.038    11013
Random effects:
Groups Name      Std.Dev.
name (Intercept) 0.2955
Number of obs: 11022, groups:  name, 15
Fixed Effects:
              (Intercept)                  type                  age
              -2.35182                -0.40575                0.03064
as.factor(motor_score)2  as.factor(motor_score)3  as.factor(motor_score)4
              -0.67468                -1.06551                -1.52623
              pupil                      ct
              0.47006                  0.44148
optimizer (Nelder_Mead) convergence code: 0 (OK) ; 0 optimizer warnings; 2 lme4 warnings

attr(,"class")
[1] "mitml.result" "list"

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

```

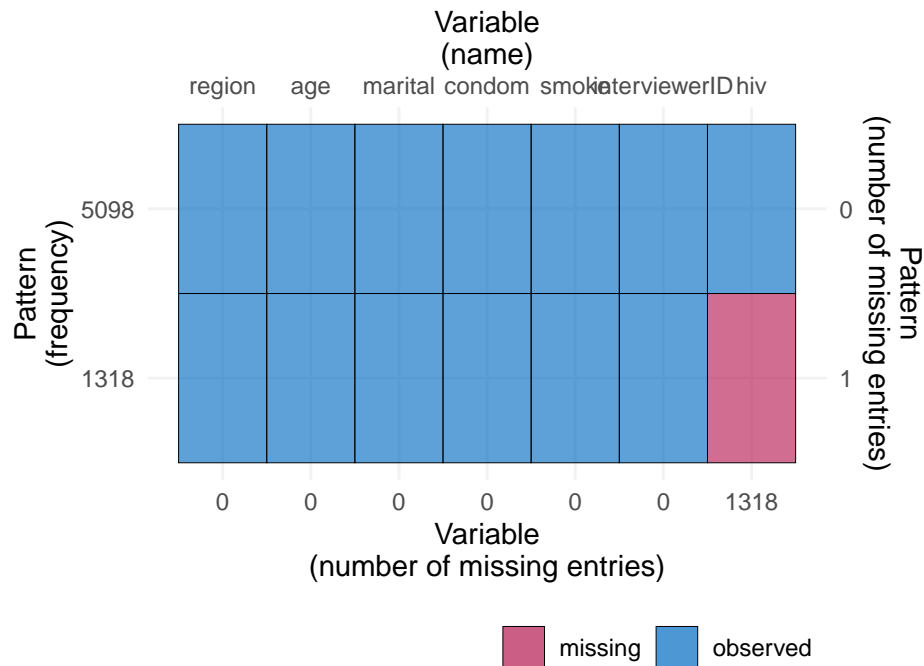
4. Case study III: HIV data

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 data is based on the toy example from [IPDMA Heckman Github repo](#).



$R = \text{region} + \text{language} + (1 | \text{InterviewID})$ model 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] "aids scare"      "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 not contain spaces
R>
R> hivdata$hiv <- as.factor(hivdata$hiv) #to use the 2l.heckman method, it is required that the level names should not contain spaces
R> #the missing variable is stored as a factor in the dataset, otherwise the method will not work
R> #apply the imputation correction for a missing continuous variable instead for 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 = hivdata)
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"

```

5. Discussion

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

6. Think about

- Adding evaluations of the imputations such as convergence checks
- 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
- I don't know if in your article you cover something about model complexity, for example sometimes I have to switch from 2l. methods to 1l. methods just because the model didn't converge.. this is due to the considered imputation model is very complex regarding the amount of information counted... I know that a solution for an imputation model with many predictors is to check correlation plots as you did or use `quickpred()`.. (maybe you can add this somewhere after the correlation plots)....But as for cluster specification, I don't know if besides plots of distribution per cluster there is something else can be done to see if i have to use 1l. or 2l. for a given variable, also I have no idea.. how to test which is better between 2l.norm or 2l.2stage.norm.

Translated with www.DeepL.com/Translator (free version)

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Table 1: Concepts in multilevel methods

Concept	Details
Sample unit	Units of the population from which measurements are taken in a sample. These should be distinct and not overlapping, e.g., patients, students.
Hierarchical levels	Data are grouped into clusters at different levels. A three-level hierarchical model could occur by collecting observations of math scores (lower level) which can be measured over the whole school year for each student, and then grouped by student (middle level) and these in turn can be aggregated into classrooms (high level).
Fixed effect	Here we assume that the values of an independent variable are fixed, i.e., the values observed in the study are representative of all values in the population we are interested in. In the case of a fixed factor variable, for example treatment type, we are only concerned with assessing the difference in the dependent variable y e.g., blood pressure between treatments A and B. There may be additional treatments, but based on the objective of the study, which in this case is the equivalence effect of A and B, the other treatment types are irrelevant and therefore the treatment type is included as a fixed effect with only the A and B levels in the hierarchical model.
Random effect	The values of an independent variable are assumed to be randomly drawn from a population with more values. In a random factor, the levels observed in the study represent a sample of all possible levels, e.g., hospitals, classrooms. For example, in a study to predict the blood pressure of patients on admission we might select only certain hospitals that are representative of the entire population of hospitals. Here we are not interested in measuring the difference of y between individual hospitals, but rather the variation of y between hospitals, to create a model that can be generalized to the entire population of hospitals.
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.]

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 3: Notation

Formula lme4	Details
$y \sim x1 + (1 g1)$	Fixed x1 predictor with random intercept varying among g
$y \sim x1*x2 + (1 g1)$	Interactions of x1 and x2 only in fixed effect
$y \sim x1*x2 + (x2 g1)$	Interactions of x1 and x2 only in fixed effect with slope of x2 randomly varying among g1
$y \sim x1*x2 + (x1*x2 g1)$	variance-covariance matrix estimated only with the variance terms of intercept, slope of x1, slope of x2 and interaction x1*x2
$y \sim x1*x2 + (x1 g1) + (x2 g1)$	variance-covariance matrix estimated separately, i.e, one for intercept and x1 and another for intercept and x2
$y \sim x1 + (x1 g1)$ or $1 + x1 + (1 + x1 g1)$	Fixed x1 with correlated random intercept and random slope of x
$y \sim x1 + (x1 g1)$ or $1 + x1 + (1 g1) + (0 + x1 g1)$	Fixed x1 with uncorrelated random intercept and random slope of x1
$y \sim (1 g1) + (1 g2)$	Random intercept varying among g1 and among g2
$y \sim (1 g1/g2)$ or $(1 g1)+(1 g1:g2)$	Random intercept varying among g1 and g2 [TODO: explain lme4 notation here https://data]