



Imputation of Incomplete Multilevel Data with **mice**

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Abstract

Multilevel data is not spared the ubiquitous problem of missing information. This is a tutorial paper on imputing incomplete multilevel data with **mice**. Including methods for ignorable and non-ignorable missingness. Footnotes in the current version show work in progress/under construction. The last section is not part of the manuscript, but purely for reminders.

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

1. Introduction

1.1. Multilevel data

In many contemporary data analysis efforts, some form of hierarchical or clustered structure is recorded.¹ Ignoring such structures may be harmful to the inferences and can yield biased results. On the other hand, analyzing such multilevel data requires specialized techniques that take the clustered structure into account. Imagine a case where cross-level interactions between unit-level variables and cluster-level variables are present. The cluster to which a unit belongs may then influence the unit-level observations—and vice versa—for each of the

¹Add IPDMA back in: patient level data from multiple studies.

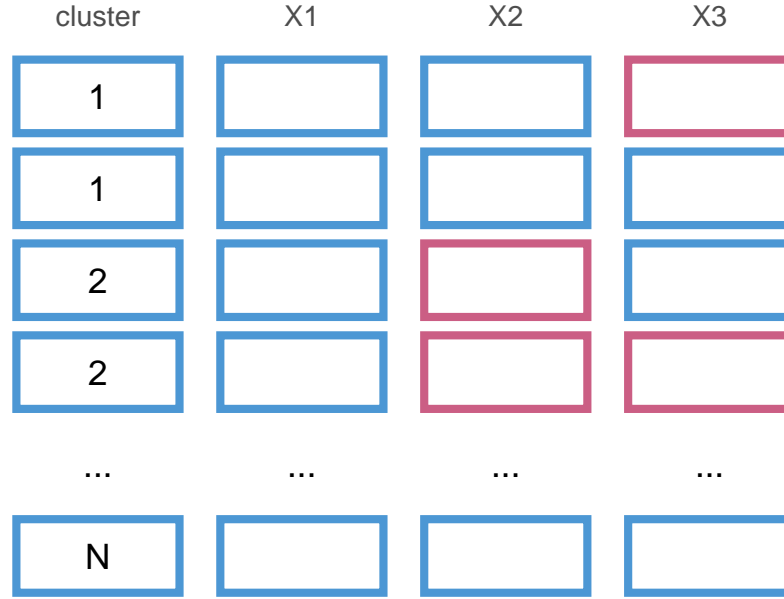


Figure 1: Missingness in multilevel data

units that make up the cluster (Hox, Moerbeek, and van de Schoot 2017). These relations can and should be taken into account when developing analysis models for multilevel data for the simple reason that groups of observations share some common variance.

The variability due to clustering is often measured by means of the intra-class 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. Multilevel models typically accommodate for this variability by including separate intercepts for each cluster. Such fixed effects relieve the restriction imposed by single-level models: equal group means across clusters. Additionally, there may be random predictor effects and/or random error terms (residual error variances), see e.g. Hox et al. (2017) and de Jong, Moons, Eijkemans, Riley, and Debray (2021).² There are many names for models that take clustering into account. Some popular examples are ‘multilevel models’, ‘hierarchical models’, ‘mixed effect models’ and ‘random effect models’.

1.2. Missing data

The process of analyzing multilevel data is further complicated when not all observations are observed. Just as with single level data, missingness may occur at the unit level. But with multiple levels of data comes the potential for clustered missingness. Missingness in multilevel data can therefore be categorized into two general patterns: systematic missingness and sporadic missingness, see Resche-Rigon, White, Bartlett, Peters, Thompson, and Group (2013). We have visualized the difference between these types of missingness in Figure 1. The figure shows an $n \times p$ set $\mathbf{X} = X_1, \dots, X_p$, with $n = 5$ units and $p = 3$ columns distributed

²Add that heterogeneity refers to variability within clusters.

over 3 clusters. Column **X1** is completely observed. Column **X2** is systematically missing and column **X3** is sporadically missing.³

Systematic missingness can be further subdivided into unobserved constants (i.e., the same value within clusters) and non-measured random variables (which may differ per unit within clusters). In Figure 1, the former would imply that the unobserved values for units 3 and 4 on column **X2** are identical. With the latter, the values would differ. The optimal strategy for dealing with the missingness may therefore depend on the observed missing data pattern.⁴

Ignoring the missingness in analyses can be extremely harmful to inferences. Complete case analysis (i.e., excluding all units with one or more missing entries) can introduce bias in statistical inference and lowers statistical power. Instead, the missingness should be accommodated before or within the analysis of scientific interest. Especially the former is very generic and popular and is widely known as imputation. Imputing (i.e., filling in) the missing values separates the missing data problem from the scientific problem: missing data are replaced by plausible values whereafter the completed data is analysed as if it were completely observed. 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). In this paper, we'll discuss how to use **mice** in the context of multilevel data, under varying missing data mechanisms.⁵

1.3. Aim of this paper

This paper serves as a tutorial for imputing incomplete multilevel data with **mice**. We provide practical guidelines and code snippets for different missing data situations. For reasons of brevity, we focus on imputation by chained equations⁶. Other useful packages for incomplete multilevel data include **mitml**, **miceadds**, and **mdmb**.⁷

We structure this tutorial around three case studies:

- `mice::popmis` (simulated data on school kids, $n = 199$ units, $N = 10$ clusters, with MNAR/MAR mixture);
- `metamisc::impact` (real IPD on traumatic brain injuries, without NAs);⁸
- `GJRM::hiv` (simulated patient data on HIV, without NAs)

For each case study we focus on a different aspect to illustrate how to impute incomplete multilevel data. In the `mice::popmis` data, we show the advantages of including the multilevel

³Explain why. GV: not necessary

⁴add missing data mechanisms here? GV: No, patterns are different from mechanisms

⁵Discuss missingness mechanisms before this point, add references Yucel (2008) and Hox, van Buuren, and Jolani (2015).

⁶add that JOMO is available in **mice** as well?

⁷Rephrase: Some level of knowledge on multilevel models is assumed. We're providing an overview of implementations. It's up-to the reader to decide which multilevel strategy suits their data. So we won't go into detail for the different methods (and equations). Refer to Meng (1994), Audigier, White, Jolani, Debray, Quartagno, Carpenter, van Buuren, and Resche-Rigon (2018), and Grund, Lüdtke, and Robitzsch (2018). This paper is just a software tutorial. We'll keep it practical.

⁸add cross-level interaction?

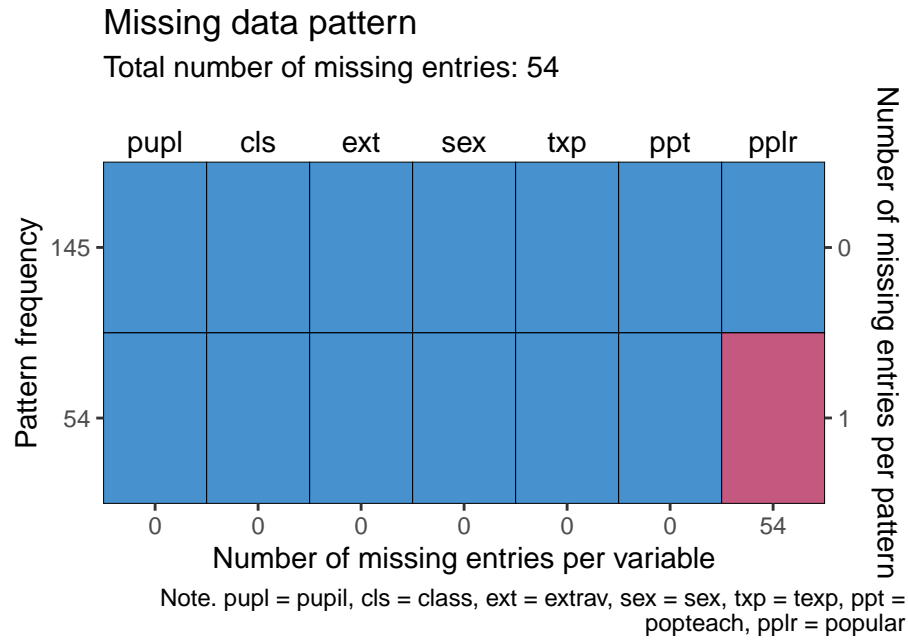


Figure 2: Missing data pattern in the popularity data

structure of the data into the imputation model. In the `metamisc::impact` data we'll show how to induce missingness and solve it in real-world data. In the `GJRM::hiv` we provide novel methodology⁹ for imputing MNAR missingness according to the Heckman model. For all case studies we discuss the nature of the incomplete data, the imputation model(s), and evaluation of the imputed data.

2. Case Study I: Popularity

`popNCR2` is a simulated dataset with pupils clustered in classes, where the number of units $n = 2000$, and the number of clusters $N = 100$, on 7 variables:

- `pupil` Pupil number within class,
- `class` Class number,
- `extrav` Pupil extraversion,
- `sex` Pupil gender,
- `texp` Teacher experience (years),
- `popular` Pupil popularity,
- `popteach` Teacher popularity.

Incomplete data

⁹not really, the methods exist already, but how to show that this is something new and exciting?

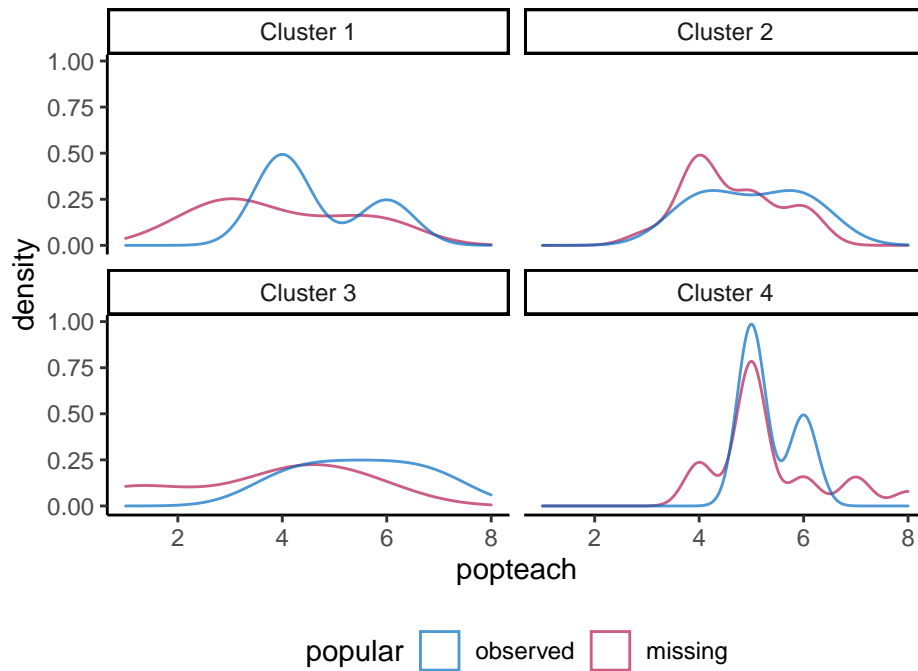


Figure 3: Conditional distributions in the popularity data

The popularity data is created such that there are strong relations between the incomplete variables and the clustering variable `class`. We can express this using the intra-class correlation (ICC). For `popular` the ICC is 0.4. For `popteach` it is 0.36. It would thus be wise to use multilevel modeling.

The missingness in this dataset is induced conform MAR and MNAR mechanisms. The missing data pattern, Figure 2, shows that just one variable is incomplete [**the next part is not yet updated to reflect this**].

To develop the best imputation model, we need to know whether the missingness in one variable depends on the observed values of other variables. Visual inspection usually suffices. We'll highlight only two variables to illustrate, but ideally one would inspect all relations. The questions we'll ask are: 'Does the missing data of `popular` depend on `popteach`?' and 'Does the missingness in teacher popularity depend on pupil popularity?' We'll evaluate this by making a histogram of `popteach` separately for the pupils with known popularity and missing popularity, and the other way around.

In Figure 3 we see that the distribution for the missing `popular` is further to the right than the distribution for observed `popular`. This would indicate a right-tailed MAR missingness. In fact, this is exactly what happens, because the missingness in these data was created manually. Now, we've made it observable by examining the relations between the missingness in `popular` and the observed data in `popteach`. There is also a dependency between the missingness in teacher popularity and pupil popularity. The relation seems to be right-tailed as well.

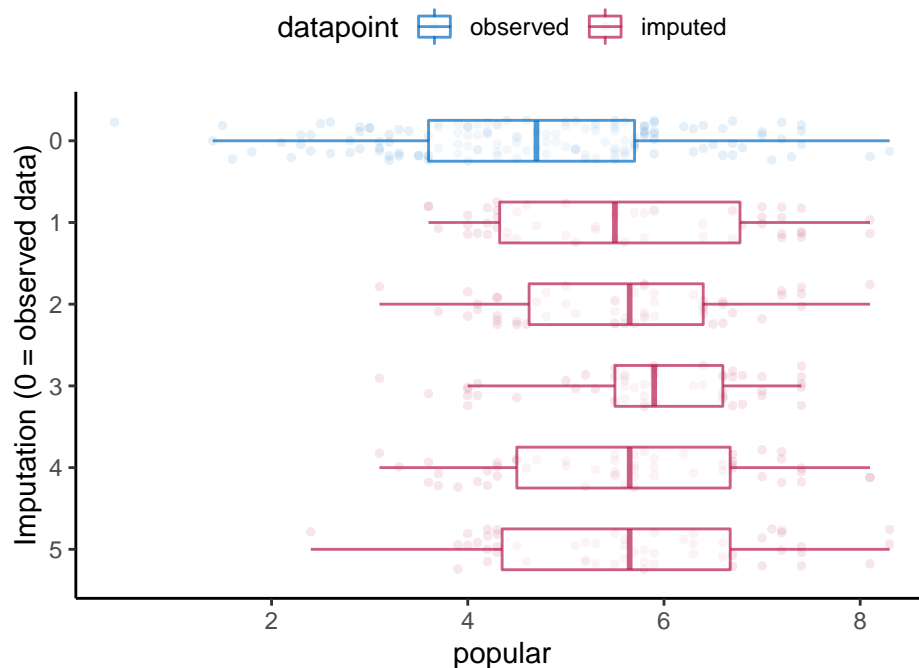
Imputation model

The first imputation model that we'll use is likely to be invalid. In this model, we ignore the multilevel structure of the data, despite the high ICCs. This is purely to illustrate the effects of ignoring the clustering in our imputation effort.

We'll use predictive mean matching to impute the continuous variables and logistic regression to impute the binary variable `sex`. We do not use the observation identifier `pupil` or cluster identifier `class` as predictors to impute other variables.

```
R> # dry run to get imputation parameters
R> ini <- mice(pop, maxit = 0)
R>
R> # extract predictor matrix and adjust
R> pred <- ini$pred
R> pred[, c("class", "pupil")] <- 0
R>
R> # impute the data, ignoring the cluster structure
R> imp_ignored <- mice(pop, maxit = 1, pred = pred, print = FALSE)
```

Imputed data



	vars	CCA	ignored
1	popular	0.3989463	0.4235643
2	popteach	0.3605902	0.3605902
3	texp	1.0000000	1.0000000

As the original ICCs show, 100% of the variance in `texp` can be attributed to the clustering variable `class`. This tells us that the multilevel structure of the data should be taken into

account. If we don't, we'll end up with incorrect imputations, biasing the effect of the clusters towards zero.

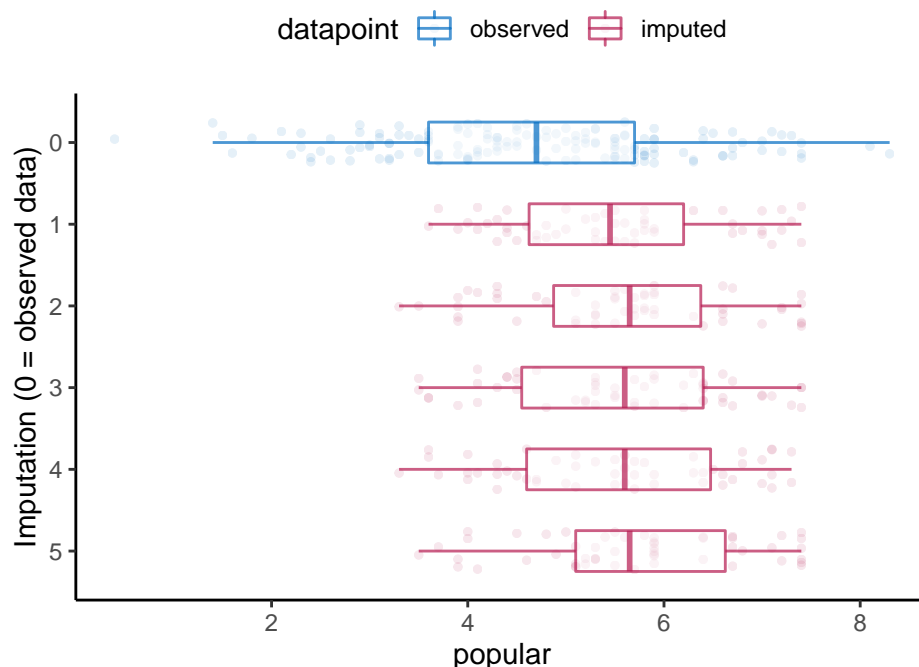
We can also observe that the teacher experience increases slightly after imputation. This is due to the MNAR missingness in `texp`. Higher values for `texp` have a larger probability to be missing. This may not be a problem, however, if at least one pupil in each class has teacher experience recorded, we can deductively impute the correct (i.e. true) value for every pupil in the class.

Imputation model

We'll now use `class` 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. But at least, it includes some multilevel aspect. Colloquially, this is 'multilevel imputation for dummies'.

```
R> # adjust the predictor matrix
R> pred <- ini$pred
R> pred[, "pupil"] <- 0
R>
R> # impute the data, cluster as predictor
R> imp_predictor <- mice(pop, maxit = 1, pred = pred, print = FALSE)
```

Imputed data



	vars	CCA	ignored	predictor
1	popular	0.3989463	0.4235643	0.3904372

```
2 popteach 0.3605902 0.3605902 0.3605902
3      texp 1.0000000 1.0000000 1.0000000
```

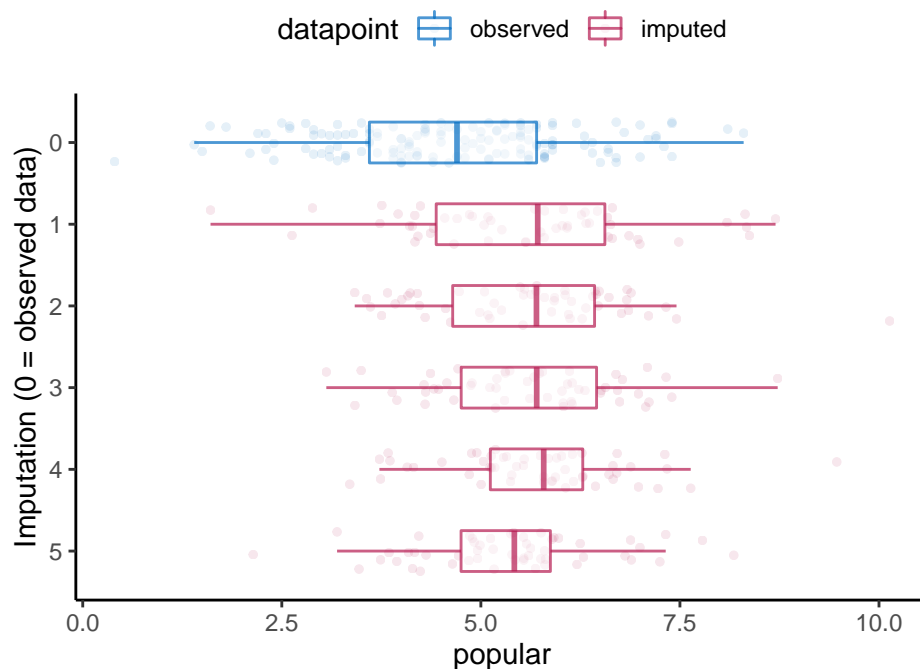
Now, we can clearly see that the imputed values of `texp` are higher than the observed values, which is in line with right-tailed MNAR.

The ICCs are way more in line with the ICCs in the incomplete data. But this is a quick and dirty way of imputing multilevel data. We should be using a multilevel model.

Imputation model

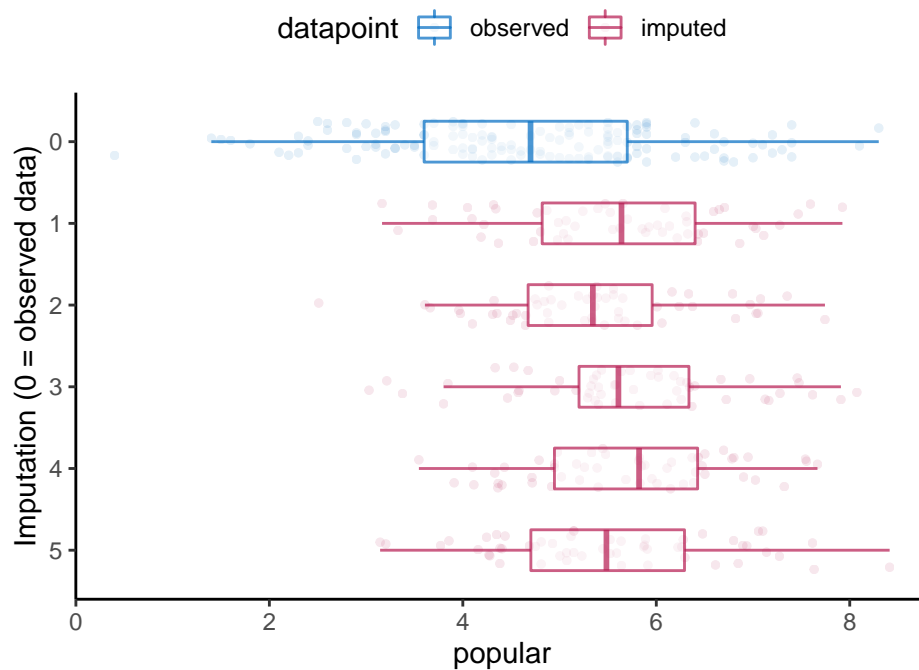
To include...

```
R> pred <- ini$pred
R> pred["popular", ] <- c(0, -2, 2, 2, 2, 0, 2)
R> #-2 for the cluster variable, 2 for random effects
R> meth <- ini$meth
R> meth <- c("", "", "", "", "", "2l.norm", "")
R> imp_norm_2l <-
+   mice(
+     pop %>% mutate(class = as.integer(class)),
+     pred = pred,
+     meth = meth,
+     maxit = 1,
+     print = FALSE
+   )
```



	vars	CCA	ignored	predictor	norm
1	popular	0.3989463	0.4235643	0.3904372	0.4165006
2	popteach	0.3605902	0.3605902	0.3605902	0.3605902
3	texp	1.0000000	1.0000000	1.0000000	1.0000000

```
R> pred["popular", ] <- c(0, -2, 2, 2, 1, 0, 2)
R> meth <- c("", "", "", "", "", "2l.pan", "")
R> imp_pan_2l <-
+ mice(
+   pop %>% mutate(class = as.integer(class)),
+   pred = pred,
+   meth = meth,
+   maxit = 1,
+   print = FALSE
+ )
```



	vars	CCA	ignored	predictor	norm	pan
1	popular	0.3989463	0.4235643	0.3904372	0.4165006	0.3827595
2	popteach	0.3605902	0.3605902	0.3605902	0.3605902	0.3605902
3	texp	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000

3. Case study II: IMPACT

`impact` is traumatic brain injury data with patients, $n = 11022$, clustered in studies, $N = 15$. 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,
- **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 data is already imputed (Steyerberg et al, 2008), so we'll induce missingness ourselves. For example, MAR missingness varying by cluster.¹⁰

4. Case study III: HIV

Toy example from [Heckman Github repo](#). We will use the following variables:

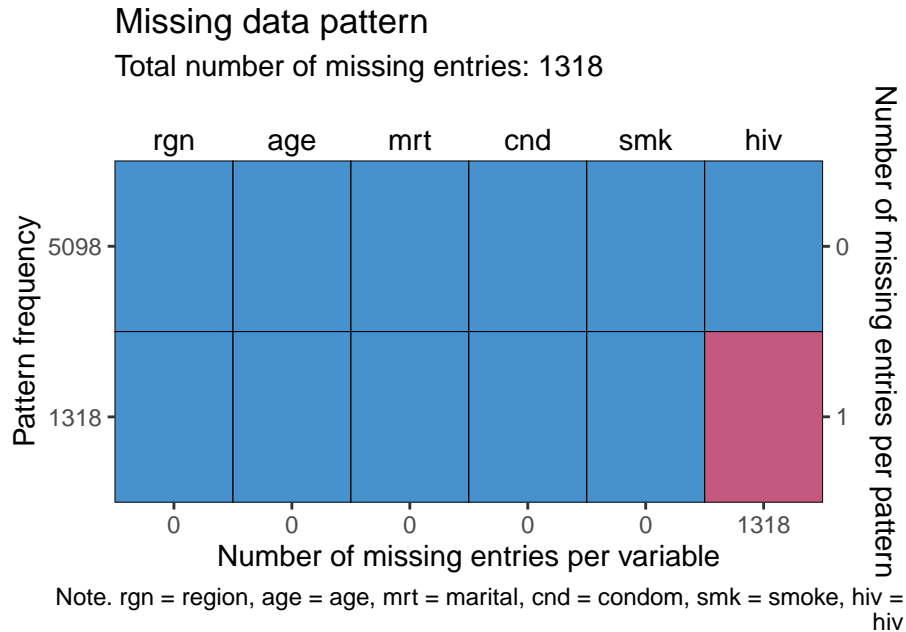
- **region** Cluster variable,
- **hiv** HIV diagnosis (0=no, 1=yes),
- **age** Age of the patient,
- **marital** Marital status,
- **condom** Condom use during last intercourse,
- **smoke** Smoker (levels; inclusion restriction variable).

There is a specific MNAR mechanism.

- main model = analysis model = predicting the prevalence of hiv
- people who have hiv are more reluctant to taking the test, not to reveal their status
- solution: take variables from analysis model like condom use, marital status, age, etc. that relate to hiv prevalence
- exclusion restriction variable = instrumental variable (from economics) = e.g. how kind the nurse was = smoke in this dataset = should be correlated to the missingness indicator, but not the variable itself
- include these variables in the selection equation
- take the missingness indicator of the variable of interest for the selection equation as DV
- heckman models estimate BOTH selection and mean models simultaneously, because linked through the error term
- if the errors are not correlated, the models are not linked at all -> not MNAR, but just MAR
- if the rho is significantly different from zero, the errors are correlated and the models are related so we have MNAR

¹⁰Observed data pattern should differ per cluster. So, in cluster 1, the missingness would depend on age, but not in cluster two. Split the dataframe and run `ampute()` on each cluster.

- now, we add clustering
- copulas = estimate 2 equations separately and use another equation to link them
- for each of the clusters, est the copula separately, so we have all coeffs for each cluster, incl the rho and sigma (the errors)
- put together all of the estimates through a meta-analysis model to get population distribution of the estimates
- use the population parameter estimates to draw marginal parameters from the distribution to get a cluster/study parameter
- with systematical miss we can est the values of the imputed values based on the marginal distribution
- optional to add shrinkage: the marginal in account as well
- the hiv data was simulated by the copula function/model developer
- we could add a systematically missing variable in the data, because these are all sporadically



From the missing data pattern we see that we can set `maxit` to 1, since there is only one variable with missingness.

The inclusion restriction variable should be a predictor of the missingness indicator for the variable of interest, but not of the actual value of the variable of interest. In this case, the data were simulated to adhere to this requirement. Namely, $\beta_{smoke} = -0.064$, 95% CI [-0.256, 0.126] for the analysis model (`formula = hiv ~ .`), and $\beta_{smoke} = -0.265$, 95% CI [-0.422, -0.11] for the selection model (`formula = is.na(hiv) ~ .`). This means the assumptions for the Heckman model are met.

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 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.

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