Missing Data and Imputation

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Outline

- Types of missing data
- Simple methods for dealing with missing data
- Single and multiple imputation
- R example

Missing data is a complex problem

We must consider:

- The type of missingness present in our data

- How different methods yield biased and/or inefficient estimates

- No method perfectly “fixes” the problem of missing data

Missing Completely at Random (MCAR)

If Missing= missing indicator (1=missing, 0= not missing):
Pr (Missing | Xmiss, Xobs) = Pr (Missing)

- Being missing is independent of both observed and unobserved data

- Pr (missingness) is the same for all units

- R package: Little's MCAR test

- Example: participant flips coin to decide whether to answer survey question

Missing at Random (MAR)

If Missing= missing indicator (1=missing, 0= not missing):
Pr (Missing | Xmiss, Xobs) = Pr (Missing | Xobs)

- Pr (missingness) depends only on available information

- Example: In a survey, poor subjects were less likely to answer a survey question on drug use than wealthier subjects. The missingness of drug use is related to observed predictors (income) but not drug use itself.

- Problem with assuming MAR?

Missing Not at Random (MNAR)

If Missing= missing indicator (1=missing, 0= not missing):
Pr (Missing | Xmiss, Xobs) = Pr (Missing | Xmiss, Xobs)

-Pr (missingness) depends on unobserved information, biases the model

- Example 1: Suppose answering the question (from last slide) also depends on drug use itself; those who used drugs are less likely to report it.

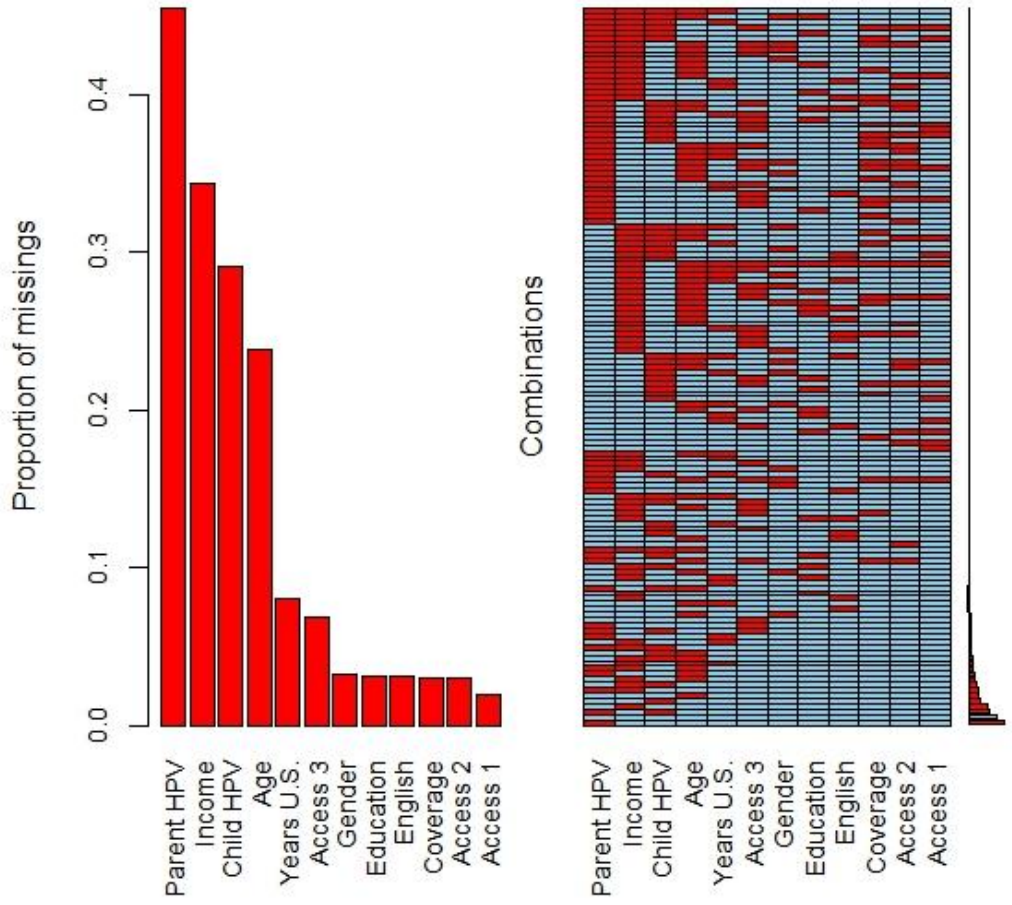
- Example 2: Those who are high earners are less likely to report their incomes.

Taking Action On Missingness

- Not always necessary!

- If we have ~5% missingness in a variable, estimates will not change much, probably will not be biased

- If we have ~30% missingness in a variable, estimates will change a lot→ reason to consider imputation methods



Complete-Case Analysis

- “Listwise Deletion”

- Exclude all data for a case that has 1 or more missing values

- Done automatically in R for linear regression, other regressions

- Assumes MCAR, biased estimates, ignoring information

- Inverse Probability Weighting- used to correct for bias from this
→ Complete cases are weighted as the inverse of their probability of being a complete case; corrects for unequal sampling fractions

	Variables			
	A	B	C	D
1	1	2	3	4
2	1	2	3	4
3	4	3	2	1
4	4	3	2	1
5	1	2		1
6		2	2	1
7	1	2	2	
8	1		2	1

Available-Case Analysis

- “Pairwise Deletion”

- Can use ‘regtools’ package in R

- Involves computation of pairs of variables, can include in the calculation any observations for which the pair is intact
  Ex: predicting weight from height, age: can estimate covariance between height and weight using all records when height and weight are intact, even if age is missing

- Assumes MCAR, standard errors over or under estimated

Types of Imputation

A. Single Imputation
- Can take on many forms: impute the missing values based on values of other variable(s)

B. Multiple Imputation
- Introduced by Rubin in 1987
- Impute the missing values **multiple** times based on values of other variables

Single Imputation Methods

Mean Imputation
- Impute with the mean of the observed values of that variable. Underestimates SEs, pulls estimates of correlation toward 0

Random Imputation
- replace NA's with random sample of non-missing values from that variable

LOCF (Last Observation Carried Forward)
- in studies where we have "pre-treatment" and "post-treatment" measures. Conservative?

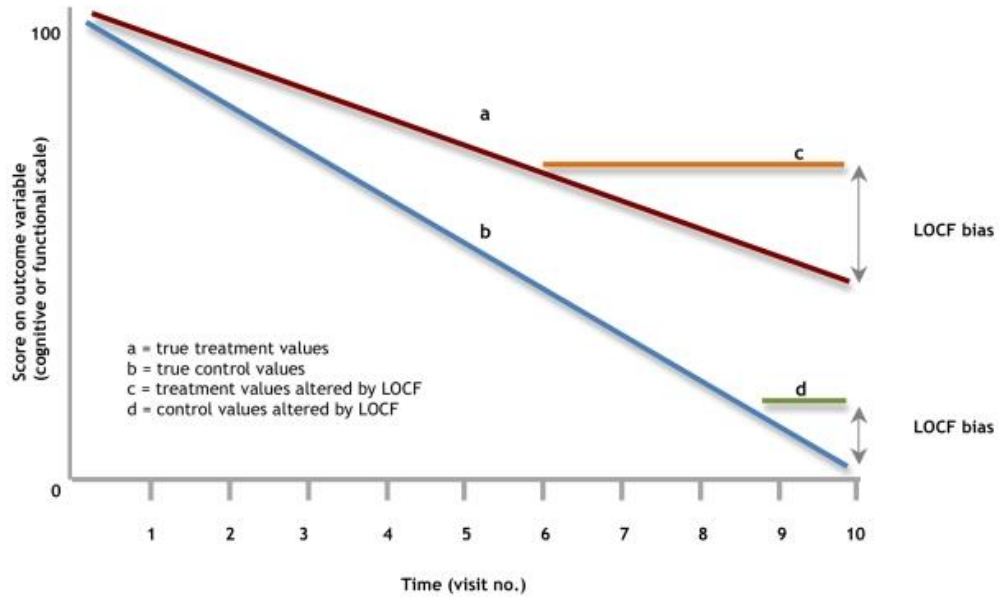


Figure 1: Differential last observation carried forward (LOCF) bias when there are more or earlier dropouts in the *treatment group* than in the control group. (Effect measured by LOCF [c–d] > true effect [a–b], resulting in an exaggerated positive effect, biased in favour of treatment.)

Single Imputation Methods (II)

Indicator Variables for Missingness in Categorical Predictors
- add an extra category that indicates missingness (if unordered categories)

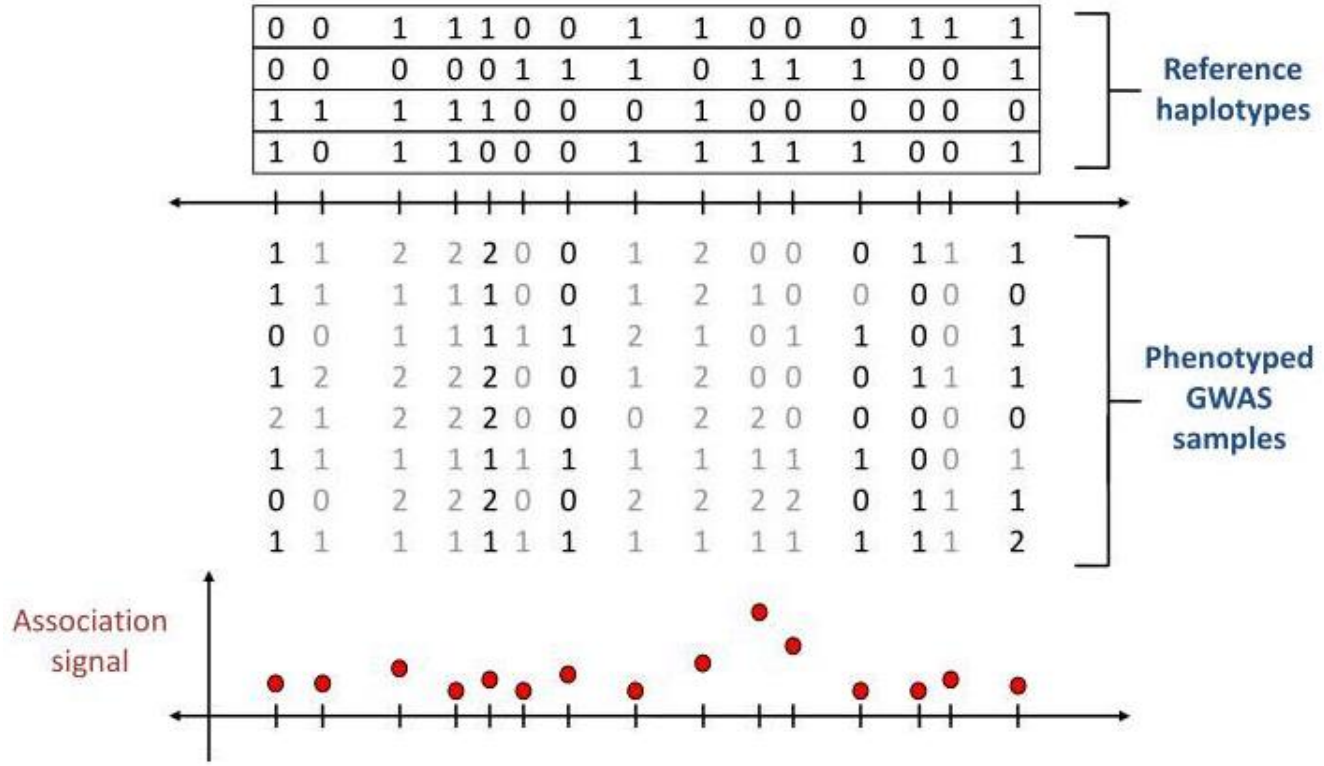
Regression Imputation
- use models of the non-missing data to predict values of the missing data, may inflate correlation, produced biased estimates/SEs

Imputation in Genomics

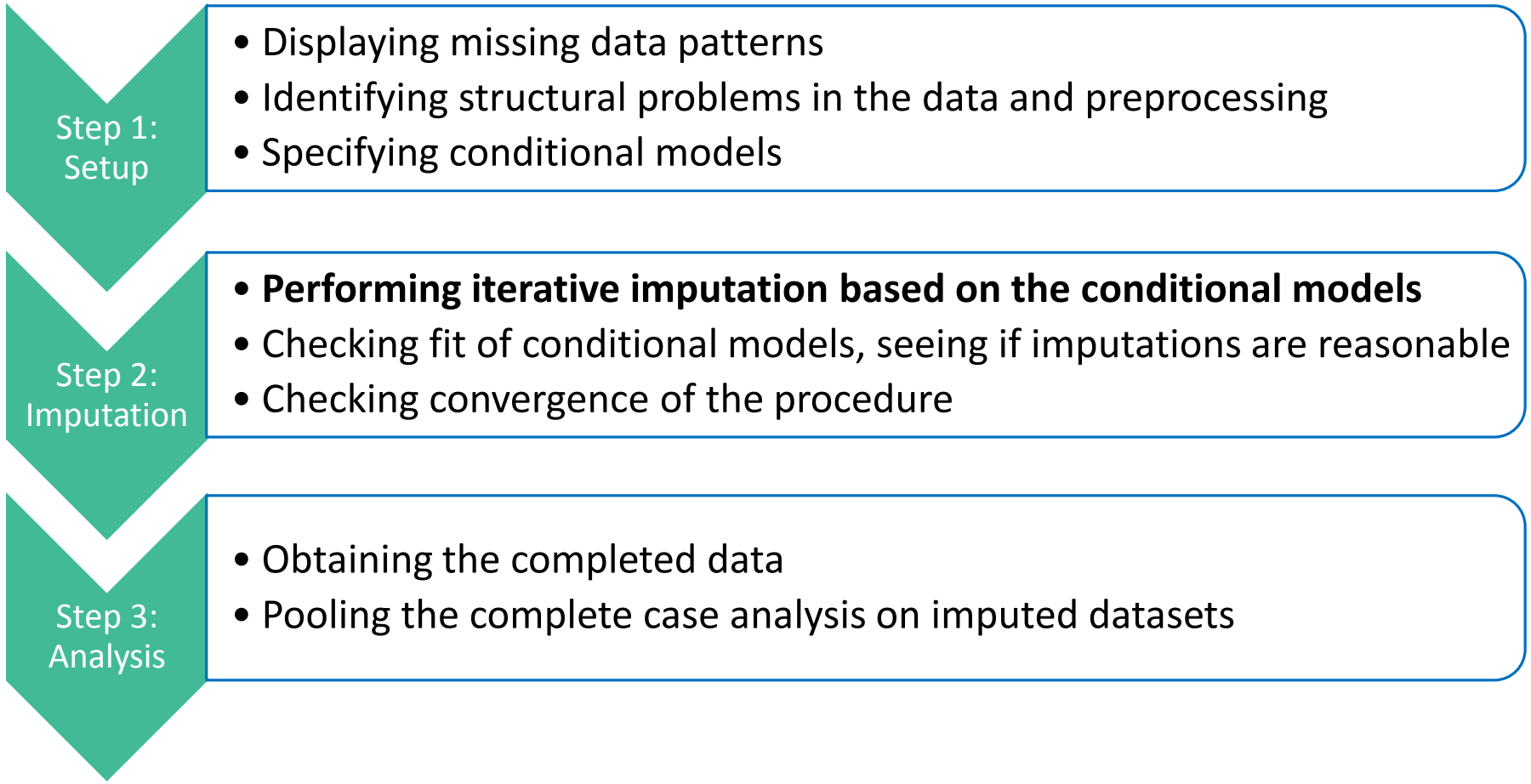
- Inference of unobserved genotypes done by using known haplotypes in the population

- Bayesian PCA, KNN Impute, SVD Impute useful for -omics data

- Some useful software packages: MaCH, Minimac, IMPUTE2, Beagle



Multiple Imputation Overview



Multiple Imputation Background

- Iteratively draw imputed values from the conditional distribution for each variable given the observed and imputed values of the other variables in the dataset

-Markov Chain Monte Carlo Method (MCMC) assuming multivariate normality is used by default in 'mi' package in R

→Markov Chain: sequence of R.V.s, each element's distribution depends on value of previous element, has transitional probability, converges to stationary distribution

→Monte Carlo: sampling techniques that draw pseudo-random numbers from probability distributions

- Some useful R packages: MI, MICE

MCMC Method Step-By-Step

1) Replace all missing data values (X_{un}) with starting values

2) Estimate parameters θ from $f(\theta \mid X_{obs}, X_{un})$ now that we have X_{un} from (1).

3) The next sample of X_{un} can be drawn from Bayesian predictive distribution $f(X_{un} \mid X_{obs}, \theta^t)$ where θ^t is current estimated parameter values
- known as Imputation-Step (I-Step)

4) Simulate next iteration of θ from the complete data posterior distribution-
-known as Prediction Step (P-Step)

5) Repeat Steps 3) and 4) iteratively until θ converges.

*We can choose how many iterations we want to run in R.

Last Steps of Multiple Imputation

- For each variable in the order specified, a univariate (single dependent variable) model is fit against all the predictors, and for each variable the MCMC method continues for the maximum number of iterations which allows distribution to stabilize

- Check convergence of the procedure
  - Can increase maximum number of iterations if does not converge

- Combine inferences across datasets using Rubin's Rule

Combining Results for Inference

- After imputing M datasets, final Beta estimate is mean of all of the Beta estimates from each dataset=

$$\widehat{\boldsymbol{\beta}} = \frac{\mathbf{1}}{\boldsymbol{M}} \sum_{\boldsymbol{j=1}}^{\boldsymbol{M}} \widehat{\boldsymbol{\beta}}^{(\boldsymbol{j})}$$

- Total variance= variance within imputations (**A**) + variance between imputations (**B**)

$$V_{\beta} = \frac{1}{M} \sum_{j=1}^{M} \hat{\sigma}^{2(j)} + \left(1 + \frac{1}{M}\right) \left(\frac{1}{M-1} \sum_{j=1}^{M} (\hat{\beta}^{(j)} - \hat{\beta})^2\right) = \mathbf{A + (1+ \frac{1}{M})B}$$

where $A = \frac{1}{M} \sum_{j=1}^{M} \hat{\sigma}^{2(j)}$ and $B = \left(\frac{1}{M-1} \sum_{j=1}^{M} (\hat{\beta}^{(j)} - \hat{\beta})^2\right)$

R Example

NlsyV data- Subset of data on children and their families in the U.S.

Outcome of interest:
pprvt.36- Peabody Picture Vocabulary test score administered at 36 months

Predictors:
first- indicator of child being first-born or not; b.marr- indicator of mother being married when child was born; income- family income in year after child was born; momage- age of mother when child was born; momed- educational status of mother when child was born; momrace- race of mother

Drawbacks of Multiple Imputation

1. Not a perfect method- making guesses about potentially many values

2. Operates under the **big** assumption that all missing data is MAR

3. How many variables to include?
   - Too few variables increases risk of separation→ when outcome is perfectly predicted by a predictor/linear combination of predictors

4. How many chains to run? Literature varies, but probably at least 5
   - Can calculate based on largest proportion of missingness in a variable

Final Thoughts

- There are many ways to go about imputation beyond those discussed today; increase in -omics data demands new missing data methods

- Important to remember that no imputation method is perfect

References

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