# Statistical Methods for Analysis with Missing Data 

Lecture 15: identifiability, nonignorability, pattern-mixture models

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## So Far

The approaches that we have covered for handling missing data:

- Ad-hoc approaches (imputation, complete cases)
- Frequentist likelihood-based inference
- Bayesian inference
- Multiple imputation
- Inverse-probability weighting

Something they have in common:

- We have assumed MAR (or MCAR), sometimes avoiding to handle the response mechanism $p(r \mid z)$


## Today's Lecture

- What if we want to move away from MAR?
- We will talk about some fundamental issues for handling missing data
- Identifiability
- Nonignorability
- This discussion naturally leads to pattern-mixture models
- Reading: Chapter 6 of the lecture notes of Davidian and Tsiatis


## Back to the Basics: Lecture 1

- $Y$ : study variable
- $R$ : response indicator


We cannot recover $p(y \mid R=0)$ nor $p(y)$ from observed data alone

The fundamental problem of inference with missing data: it is impossible without extra, usually untestable, assumptions on how missingness arises

## Sample Data

- The full-data sample are independent and identically distributed (i.i.d.) draws from some distribution $F$

$$
\left\{\left(Z_{i}, R_{i}\right)\right\}_{i=1}^{n} \stackrel{i . i . d .}{\sim} F
$$

- $R_{i}$ determines the part of $Z_{i}$ that we get to observe: $Z_{i\left(R_{i}\right)}$
- We can think of the generative process, for each $i$ :

$$
Z_{i} \Longrightarrow R_{i} \Longrightarrow\left(Z_{i\left(R_{i}\right)}, R_{i}\right)
$$

- In this lecture, we delete the subindex $i$ to talk about
- A generic draw from $F$
- What we could recover provided an infinite sample size
- Separate identifiability issues from estimation issues


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## Types of Data

- Full data: $(Z, R)$
- Observed data: $\quad\left(Z_{(R)}, R\right)$
- Missing data:

$$
Z_{(\bar{R})}
$$

Relationship:

$$
(Z, R)=\left(Z_{(\bar{R})}, Z_{(R)}, R\right)
$$

## Distributions of Interest

- Full-data distribution: joint distribution of $(Z, R)$ with density

$$
p(z, r) \equiv p\left(z_{(\bar{r})}, z_{(r)}, r\right), \text { for all } r
$$

- Observed-data distribution: joint distribution of $\left(Z_{(R)}, R\right)$ with density

$$
p\left(z_{(r)}, r\right)=\int p\left(z_{(F)}, z_{(r)}, r\right) d z_{(F)}, \text { for all } r
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- Missing-data distribution, or extrapolation distribution: conditional distribution of $Z_{(\bar{R})}$ given $\left(Z_{(R)}, R\right)$



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## The Full-Data Distribution

- Joint distribution of $(Z, R)$ with density

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p(z, r)
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- Quantities of interest $\theta$ (parameters) depend on the full-data distribution
$p(z, r) \longrightarrow p(z)=\sum_{r} p(z, r) \longrightarrow \theta=E[f(Z)]=\int f(z) p(z) d z$
- For example, say $f(Z)=Z_{j}$, then

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\theta_{j}=E\left(z_{j}\right)=\int z_{j p} p\left(z_{j}\right) d z_{j}=\int z_{j} p(z) d z
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## The Observed-Data Distribution

- Given $R=r$, we observe $Z_{(r)}$
- We can estimate $p\left(z_{(r)} \mid R=r\right)$ and $p(R=r)$ from observed data
- The observed-data distribution is all we can hope to recover from data alone

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p\left(z_{(r)}, r\right)=p\left(z_{(r)} \mid r\right) p(r)
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- For example, say you can sample indefinitely from the joint distribution of

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- If $R_{j}=0$ you don't see the value of $\bar{Z}_{j}$
$\Rightarrow$ What we can estimate from such data:
$\square$
- $p\left(z_{1} \mid R=10\right)$
$p^{\prime}\left(z_{2} \mid R=01\right)$
$\Rightarrow p\left(z_{1}, z_{2} \mid R=11\right)$


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- Given $R=r$, we observe $Z_{(r)}$, but we don't observe $Z_{(\bar{r})}$
- There is no way of estimating $p\left(z_{(\bar{r})} \mid z_{(r)}, r\right)$ without assumptions

- We say that $p\left(z_{(F)} \mid z_{(r)}, r\right)$, and therefore $p(z, r)$, are not identifiable
- Identifying assumptions explicitly or implicitly amount to constructing $p\left(z_{(\bar{r})} \mid z_{(r)}, r\right)$ from $p\left(z_{(r)}, r\right)$


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## General Identification Strategy



- Note that MAR (ignorability) gives you a shortcut to go from $p\left(z_{(r)}, r\right)$ to $p_{M A R}(z)$


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## Factorizations of the Full-Data Distribution

Selection model factorization:

$$
p(z, r)=p(r \mid z) p(z)
$$

- The response mechanism $p(r \mid z)$ represents the way in which values of study variables get selected into the sample
- Natural factorization when we initially had a model $\{p(z \mid \theta)\}_{\theta}$ in mind, say had we not had missing data
- Allows us to continue using model $\{p(z \mid \theta)\}_{\theta}$
- Identifying assumptions are expressed as restriction on response mechanism $p(r \mid z)$
- We have focused on this approach so far under MAR:

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Pattern-mixture model factorization:

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p^{\prime}(z)=\sum_{r} p(z \mid r) p(r)
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- This gives an alternative approach for handling missing data


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## Pattern-Mixture Models

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needs identifying assumption


- Explicitly shows what needs identifying assumptions and what can be obtained from data alone


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$$
\begin{aligned}
p(z) & =\sum_{r} p(z \mid r) p(r) \\
& =\sum_{r} p\left(z_{(\bar{r})} \mid z_{(r)}, r\right) p\left(z_{(r)} \mid r\right) p(r)
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## Identifying Assumptions for Pattern-Mixture Models

- Identifying assumptions in the framework of pattern mixture models amount to specifying how to construct

$$
\left\{p\left(z_{(\bar{r})} \mid z_{(r)}, r\right)\right\}_{r}
$$

from

$$
\left\{p\left(z_{(r)}, r\right)\right\}_{r}
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- Once $p_{A}\left(z_{(\bar{r})} \mid z_{(r)}, r\right)$ is specified, according to an assumption $A$, this defines a full-data density

$$
p_{A}\left(z_{(\bar{r})}, z_{(r)}, r\right)=p_{A}\left(z_{(\bar{r})} \mid z_{(r)}, r\right) p\left(z_{(r)}, r\right)
$$

- Note that this in turn implies a response mechanism

$$
p_{A}\left(r \mid z_{(F)}, z_{(r)}\right)=\frac{p_{A}\left(z_{(T)}, z_{(r)}, r\right)}{\sum_{r^{\prime}} p_{A}\left(z_{\left(F^{\prime}\right)}, z_{\left(r^{\prime}\right)}, r^{\prime}\right)}
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- Assumptions that lead to response mechanisms that are not particular cases of MAR are nonignorable


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## Identifying Assumptions for Pattern-Mixture Models

- Identifying assumptions in the framework of pattern mixture models amount to specifying how to construct

$$
\left\{p\left(z_{(\bar{r})} \mid z_{(r)}, r\right)\right\}_{r}
$$

from

$$
\left\{p\left(z_{(r)}, r\right)\right\}_{r}
$$

- Once $p_{A}\left(z_{(\bar{r})} \mid z_{(r)}, r\right)$ is specified, according to an assumption $A$, this defines a full-data density

$$
p_{A}\left(z_{(\bar{r})}, z_{(r)}, r\right)=p_{A}\left(z_{(\bar{r})} \mid z_{(r)}, r\right) p\left(z_{(r)}, r\right)
$$

- Note that this in turn implies a response mechanism

$$
p_{A}\left(r \mid z_{(\bar{r})}, z_{(r)}\right)=\frac{p_{A}\left(z_{(\bar{r})}, z_{(r)}, r\right)}{\sum_{r^{\prime}} p_{A}\left(z_{\left(\bar{r}^{\prime}\right)}, z_{\left(r^{\prime}\right)}, r^{\prime}\right)}
$$

- Assumptions that lead to response mechanisms that are not particular cases of MAR are nonignorable


## Comments on Pattern-Mixture Models

## Advantages:

- Identifiability requirements are more explicit than with selection models: easier to understand what is it that you are assuming
- Provides a natural framework for sensitivity analyses


## Limitations:

- We cannot continue using model $\{p(z \mid \theta)\}_{\theta}$
- Parameters of scientific interest do not explicitly appear in the model
- Requires per-pattern model, say $\left\{p\left(z_{(r)} \mid r, \theta_{r}\right)\right\}_{\theta_{r}}$
- For general pattern of nonresponse we would need $2^{K}-1$ models, one for each pattern in $\{0,1\}^{K}$ ( minus $\left.\mathbf{0}_{K}\right)$
- Most developments under this approach assume monotone nonresponse (e.g., dropout)


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## Dropout in Longitudinal Study

If missingness comes only from subjects dropping out

- Missingness patterns are uniquely summarized by the dropout time

$$
D=1+\sum_{j=1}^{T} R_{j}
$$

- The observed data are obtained as realizations of

$$
\left(Z_{(D)}, D\right)
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where, if $D=d, Z_{(d)}=\left(Z_{1}, \ldots, Z_{d-1}\right)$ and $Z_{(\bar{d})}=\left(Z_{d}, \ldots, Z_{T}\right)$
> Pattern-mixture model requires modeling

- $p(D=d)$ : simply take empirical frequency
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## A Simple Pattern-Mixture Model Under Dropout

In some situations, the following simple implementation of pattern-mixture models (PMMs) might be reasonable

- Idea: for each dropout group, model observed data and extrapolate to missing data
- For each d, fit
using data from $j<d$, and predict for $j \geq d$
- This implies

- All parameters $p(d), \beta_{0 d}, \beta_{1 d}, d=1, \ldots, T$, can be directly estimated from the observed data (provided dropout starts at time $D=3$ )
- Note that this approach imposes parametric assumptions on the evolution of means over time, and assumes that this trend can be extrapolated


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## Identifying Assumptions for PMMs Under Dropout

- In general, how to obtain $p\left(z_{(\bar{d})} \mid z_{(d)}, d\right)$ from $p\left(z_{(d)}, d\right)$ ?
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p\left(z_{(\bar{d})} \mid z_{(d)}, d\right)=p\left(z_{d}, \ldots, z_{T} \mid z_{1}, \ldots, z_{d-1}, d\right)
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## The Complete-Case Identifying Assumption

Little (JASA 1993) proposed to tie the extrapolation distributions to the distribution of complete cases:

$$
p_{C C}\left(z_{\ell} \mid z_{(\ell)}, D=d\right) \equiv p\left(z_{\ell} \mid z_{(\ell)}, D=T+1\right)
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for all $\ell \geq d, d=1, \ldots, T$.

- The distributions for $D=T+1$ are identifiable from the complete cases
- This strategy could also be used with nonmonotone missingness

D 'HW/ say $T=3$, write down this restriction for $\ell \geq d^{\prime}, d=1,2,3$.

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## The Neighboring-Case Identifying Assumption

The extrapolation distributions could also be obtained from the closest dropout pattern where $\ell$ is available:

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- Among observations with $D=\ell+1$ we get to observe $z_{\ell}$ and $z_{(\ell)}$
> We could think that observations with $D=\ell+1$ are the best for basing extrapolation of the values of $Z_{\ell}$
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## Observational Equivalence

- Two full-data distributions are said to be observationally equivalent if their implied observed-data distributions are the same
- This is, say I have two full-data distributions $p_{A}\left(z_{(\vec{r})}, z_{(r)}, r\right)$
and

$$
p_{B}\left(z_{(F)}, z_{(r)}, r\right)
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$$
\begin{equation*}
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for all $\left(z_{(r)}, r\right)$, then they are observationally equivalent
= HW/4: the full-data distributions obtained under the CC, NC, and AC restrictions are observationally equivalent

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## Summary

Main take-aways from today's lecture:

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- Pattern-mixture models provide an alternative way of thinking about missing data
- Remember the universe of missing-data assumptions:


Next lecture:

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Next lecture:

- More on nonignorable missing data (MNAR), and sensitivity analysis

