# Model based clustering with Missing Not At Random data 

Maasai Seminar

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## Outline

(1) Introduction on missing data
(2) Missing data in model-based clustering
(3) Estimation of the parameters
(4) Numerical experiments
(5) Conclusion

## Missing values are everywhere

- Growing masses of data, multiplication of sources $\Rightarrow$ Not Available values (NA)
- Our public health application: the Traumabase ${ }^{\circledR}$ dataset.

250 clinical variables (heterogeneous)

1 patient; in total: $\mathbf{3 0 0 0 0}$ patients

## Missing values are everywhere

- Growing masses of data, multiplication of sources $\Rightarrow$ Not Available values (NA)
- Our public health application: the Traumabase ${ }^{\circledR}$ dataset.

| Trauma.center Heart <br> rate Death Anticoagulant. <br> therapy Glascow <br> score <br> Pitie-Salpêtrière 88 0 No 3 <br> Beaujon 103 0 NA 5 <br> Bicêtre NA 0 Yes 6 <br> Bicêtre NA 0 No NA <br> Lille 62 0 Yes 6 <br> Lille NA 0 No NA <br> $\vdots$ $\vdots$ $\vdots$ $\vdots$ $\vdots$23 different <br> hospitals |
| :---: |

## Missing values are everywhere

## Traumabase ${ }^{R}$ dataset

- now $\mathbf{3 0} 000$ patients.
- 250 heterogeneous variables: continuous, categorical, ordinal,...
- 23 different hospitals
- missing values everywhere ( $1 \%$ to $90 \%$ NA in each variable).
- Imputation: provide a complete dataset to the doctors.
- Estimation: explain the level of platelet with pre-hospital characteristics.
- Prediction: predict the administration or not of the tranexomic acid.
- Clustering: identify relevant groups of patients sharing similarities.

Q: How to deal with missing values?

## What we should not do

$\left(\begin{array}{ccccc}\text { Pitie-Salpêtrière } & 88 & 0 & \text { No } & 3 \\ \text { Beaujon } & 103 & 0 & \text { NA } & 5 \\ \text { Bicêtre } & \text { NA } & 0 & \text { Yes } & 6 \\ \text { Bicêtre } & \text { NA } & 0 & \text { No } & \text { NA } \\ \text { Lille } & 62 & 0 & \text { Yes } & 6 \\ \text { Lille } & \text { NA } & 0 & \text { No } & \text { NA }\end{array}\right) \quad\left(\begin{array}{cccccc}\text { Pitie-Salpêtrière } & 88 & 0 & \text { No } & 3 \\ \text { Beaujon } & 103 & 0 & \text { NA } & 5 \\ \text { Biêttre } & \text { NA } & 0 & \text { Yes } & 6 \\ \text { Bieêtre } & \text { NA } & 0 & \text { No } & \text { NA } \\ \text { Lille } & 62 & 0 & \text { Yes } & 6 \\ \text { Lille } & \text { NA } & 0 & \text { No } & \text { NA }\end{array}\right)$

Discarding individuals with missing values is not a solution

- Loss of information.

Traumabase ${ }^{\circledR}$ : only $5 \%$ of the rows are kept.

- Bias in the analysis.

Kept observations: sub-population not necessarily representative of the overall population.

What we should do: handling missing values

## The right method to choose

Q: How to choose the right method to handle missing values?


## Imputation? Estimation? Prediction?

- The goal is not necessarily to obtain a complete dataset.
- A solution can be to embed missing data management into the statistical paradigm.


## Missing-data notations

- $Y=\left\{y_{1}|\ldots| y_{n}\right\}^{T}$ : full dataset with $n$ individuals
- Continuous, categorical or mixed data.
- $C=\left\{c_{1}|\ldots| c_{n}\right\}^{T} \in\{0,1\}^{n \times d}$ : pattern of missing data for the full dataset

$$
c_{i j}=1 \Leftrightarrow y_{i j} \text { is missing }
$$

- $y_{i}^{\text {obs }}$ : the observed variables values for individual $i$
- $y_{i}^{\text {mis }}$ : the missing variables values for individual $i$


## Missing-data mechanism (Rubin, 1976)



$$
f(c \mid y ; \psi), \psi \in \Omega_{\psi}
$$

## Missing Completely At Random (MCAR)

$$
f(c \mid y ; \psi)=f(c ; \psi)
$$

## Missing At Random (MAR)

$y^{\text {obs }}$ : observed component of $y$.

$$
f(c \mid y ; \psi)=f\left(c \mid y^{\mathrm{obs}} ; \psi\right)
$$

## Missing Not At Random (MNAR)

The MAR assumption does not hold. The missingness can depend on the missing data value itself.

## MCAR

Machines fail, Doctors forget to fill the form

## MAR

Aggregation of datasets

|  | HR | Death | A. therapy | GCS |
| :---: | :---: | :---: | :---: | :---: |
| Lille | 65 | 0 | Yes | 6 |
| Lille | 59 | 0 | No | 4 |
| Pitié | 62 | 0 | NA | 6 |
| Pitié | 84 | 0 | NA | 5 |

## MNAR

Emergency situations

| HR |  | HR |
| :---: | :---: | :---: |
| 65 |  | 65 |
| 59 | "underlying" values: | 59 |
| 62 |  | 62 |
| NA |  | 84 |

## Ignorable vs. non ignorable mechanism

- Parametric estimation: model the joint distribution $(Y, C)$ parametrized by $\gamma, \psi \in \Omega_{\gamma, \psi}$.
- Likelihood-approach: maximizing the full observed likelihood.

$$
\begin{aligned}
L_{\text {full,obs }}\left(\gamma, \psi ; y^{\mathrm{obs}}, c\right) & =\int L_{\text {full }}(\gamma, \psi ; y, c) d y^{\text {mis }} \\
& =\int f(y ; \gamma) f(c \mid y ; \psi) d y^{\text {mis }} \\
& =f\left(c \mid y^{\mathrm{obs}} ; \psi\right) \int f(y ; \gamma) d y^{\text {mis }} \quad \text { M(C)AR mecha. } \\
& \propto L_{\text {ign }}\left(\gamma ; y^{\mathrm{obs}}\right)=\int f(y ; \gamma) d y^{\text {mis }}
\end{aligned}
$$

M(C)AR: one can ignore the mechanism.

MNAR: one should consider the mechanism.

## Focus on MNAR mechanism

```
We should consider (Y,C) (not-ignorable mechanism).
```

The main MNAR specifications

- selection model [Heckman, 1979]:

$$
f(y, c ; \gamma, \psi)=f(y ; \gamma) f(c \mid y ; \psi)
$$

- pattern-mixture model [Little, 1993]:

$$
f(y, c ; \xi, \varphi)=f(c ; \xi) f(y \mid c ; \varphi)
$$

Q: How to choose the MNAR specification ?

- Estimate the parameters of the data distribution: selection models.
- Distribution is not the same for the observed data and the missing data: pattern-mixture models.


## Focus on MNAR mechanism

## We should prove the identifiability of the parameters.

Identifiability issue in the MNAR case Credit: llya Shpitser

$$
Y^{\mathrm{NA}}=[1, \mathrm{NA}, 0,1, \mathrm{NA}, 0] .
$$

- Case 1: $Y$ missing only if $Y=1$.

$$
Y=[1,1,0,1,1,0], \mathbb{P}(Y=1)=2 / 3
$$

- Case 2: $Y$ missing only if $Y=0$.

$$
Y=[1,0,0,1,0,0], \mathbb{P}(Y=1)=1 / 3 .
$$

$\Rightarrow$ We start from 2 equal observed distribution. It leads to different parameters of the data distribution $\mathbb{P}(Y=1)$.

Identifiability: the parameters of $(Y, C)$ are uniquely determined from available information $(Y, C=0)$.

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## Our goals

- MNAR mechanism.
- Selection model: $f(y, c ; \gamma, \psi)=f(y ; \gamma) f(c \mid y ; \psi)$.

Embed missing data management into the analysis to:

- Perform clustering: identify relevant groups of individuals.
- Estimate the parameters of the data distribution.
- (Impute missing values.)


## Clustering: model-based approach

- Partition with $K$ clusters: $Z=\left(z_{1}|\ldots| z_{n}\right)^{T} \in\{0,1\}^{n \times K}$, with $z_{i k}=1$ if $y_{i}$ belongs to cluster $k$.

Mixture model

$$
f\left(y_{i} ; \gamma\right)=\sum_{k=1}^{K} \overbrace{\pi_{k}}^{=\mathbb{P}\left(z_{i k}=1\right)} \underbrace{f_{k}\left(y_{i} ; \lambda_{k}\right)}_{\text {pdf in the cluster } k}
$$

## Clustering: model-based approach

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$$

- Missing data in $Y$.

Mixture model with missing data

$$
f\left(y_{i}, c_{i} ; \theta\right)=\sum_{k=1}^{K} \pi_{k} f_{k}\left(y_{i} ; \lambda_{k}\right) f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)
$$

## A zoology of MNAR models in clustering

Q: Which distribution $\frac{f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)}{\text { context? }}$ to propose in this clustering

$$
f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)=\prod_{j=1}^{d}\left(\rho\left(\alpha_{k j}+\beta_{k j} y_{i j}\right)\right)^{c_{i j}}\left(1-\rho\left(\alpha_{k j}+\beta_{k j} y_{i j}\right)\right)^{1-c_{i j}},
$$

where $\psi_{k}=\left(\alpha_{k 1}, \beta_{k 1}, \ldots, \alpha_{k K}, \beta_{k K}\right)$ and $\rho$ is a link function.

## How to understand this distribution?

- $\alpha_{k j}$ : the missingness depends on the class membership $k$, not the same effect for every variable.
- $\beta_{k j}$ : the missingness depends on the value itself $\left(y_{i j}\right)$, not the same effect for each cluster.
- Simplest model:

$$
\text { MCAR: } \quad \beta_{k j}=0, \forall(k, j) \text { and } \alpha_{1 j}=\ldots=\alpha_{K j}, \forall j .
$$

## A zoology of MNAR models in clustering

Parcimonious models: the probability of being missing depend

- on both the variable and the class membership:

$$
\begin{aligned}
\operatorname{MNARyz}^{j}: & \beta_{1 j}=\ldots=\beta_{K j}, \forall j \\
\text { MNARy }^{k} z: & \alpha_{k j}=\ldots=\alpha_{k 1}, \forall k \\
\text { MNARyz: } & \beta_{1 j}=\ldots=\beta_{K j}, \forall j \text { and } \alpha_{k j}=\ldots=\alpha_{k 1}, \forall k
\end{aligned}
$$

- only on the variable itself:

$$
\text { MNARy: } \quad \alpha_{11}=\ldots=\alpha_{1 d}=\alpha_{21}=\ldots=\alpha_{K d} \text { and } \beta_{1 j}=\ldots=\beta_{K j}, \forall j
$$

$$
\text { MNARy }{ }^{k}: \quad \alpha_{11}=\ldots=\alpha_{1 d}=\alpha_{21}=\ldots=\alpha_{K d}
$$

- only on the class membership:

$$
\begin{aligned}
\text { MNARz: } & \beta_{k j}=0, \forall(k, j) \text { and } \alpha_{k j}=\ldots=\alpha_{k d}, \forall k \\
\text { MNARz }^{j}: & \beta_{k j}=0, \forall(k, j) .
\end{aligned}
$$

Proposed zoology of MNAR models in clustering


## MNARz from every angle

## (1) $C$ gives information on partition $Z$

- MNARz model, Bivariate Gaussian model
- cluster overlap: $\Delta_{\mu}=\left|\mu_{1}-\mu_{2}\right|$ varies.
- difference of percentage of NA between the 2 clusters: $\Delta_{\text {perc }}$ varies.



## MNARz from every angle

(2) MNARz (and MNARz ${ }^{j}$ ) models interpreted as MAR

$$
\begin{gathered}
Y^{\text {obs }}=\left(\begin{array}{ccc}
? & 2.6 & 5 \\
\text { blue } & 1.9 & 4 \\
\text { red } & 2.3 & ?
\end{array}\right), \quad C=\left(\begin{array}{lll}
1 & 0 & 0 \\
0 & 0 & 0 \\
0 & 0 & 1
\end{array}\right) \\
\tilde{Y}^{\text {obs }}=\left(\begin{array}{cccccc}
? & 2.6 & 5 & 1 & 0 & 0 \\
\text { blue } & 1.9 & 4 & 0 & 0 & 0 \\
\text { red } & 2.3 & ? & 0 & 0 & 1
\end{array}\right) .
\end{gathered}
$$

Proposition 1: in terms of maximum likelihood
MLE associated to $\tilde{Y}^{\text {obs }}$ under MAR model
$\Leftrightarrow$ MLE associated to $Y^{\text {obs }}$ under MNARz/MNARz ${ }^{j}$ models.

## Identifiability results

Previous works: [Teicher, 1963], [Allman et al., 2009] (without NA),
[Miao et al., 2016] (for MNAR data).
Proposition 2: identifiability for continuous and count data Assume
(1) The marginal mixture $\sum_{k=1}^{K} \pi_{k} f_{k}\left(y_{i} ; \theta_{k}\right)$ is identifiable
(2) There exists a total ordering $\preceq$ of $\mathcal{F}_{j} \times \mathcal{R}$, for $j \in\{1, \ldots, d\}$ fixed, where $\mathcal{F}_{j}=\left\{f_{1 j}, \ldots, f_{k j}\right\}$ and $\mathcal{R}=\left\{\rho_{1}, \ldots, \rho_{K}\right\}$.
The mixture model with any MNAR* is identifiable.
Proposition 3: identifiability for categorical data Assume $d_{\text {cat }} \geq 2\left\lceil\log _{2} K\right\rceil+1$ and $f_{k}\left(\cdot ; \theta_{k}\right)=\prod_{j=1}^{d} f_{k j}\left(\cdot ; \theta_{k j}\right)$ $\checkmark$ The mixture model with MNARz or MNARz ${ }^{j}$ is identifiable.
$X$ The mixture model with any MNARy* is not identifiable.

- For mixed data: result follows from Proposition 2 and 3.


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## EM algorithm

Initialized at the point $\theta^{[0]}=\left(\pi^{[0]}, \lambda^{[0]}, \psi^{[0]}\right)$, the iteration $[r]$ of the EM algorithm consists in performing two steps:

- E-step : compute the expectation of the complete-data $\log$-likelihood $Q\left(\theta ; \theta^{[r-1]}\right)=\mathbb{E}_{\theta^{[r-1]}}\left[\ell_{\text {comp }}(\theta ; Y, Z, C) \mid Y^{\text {obs }}, C\right]$, $\ell_{\text {comp }}(\theta ; Y, Z, C)=\sum_{i=1}^{n} \log \left(\sum_{k=1}^{K} \pi_{k} f_{k}\left(y_{i} ; \lambda_{k}\right) f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)\right)$.
- M-step: update the parameters by maximizing this function $\theta^{[r]}=\operatorname{argmax}_{\theta} Q\left(\theta ; \theta^{[r-1]}\right)$.


## EM algorithm: feasible computations?

One has: $Q\left(\theta ; \theta^{[r-1]}\right)=$
$\sum_{i} \sum_{k} t_{i k}\left(\theta^{[r-1]}\right)[\log \left(\pi_{k}\right)+\underbrace{\tau_{y}\left(\lambda_{k} y_{i}^{\text {obs }}, c_{i}, \theta^{[r-1]}\right.}_{=\mathbb{E}_{\theta[r-1]}\left[\ln f_{k}\left(y_{i} ; \lambda_{k}\right) \mid y_{i}^{\text {obs }}, c_{i}, z_{i k}=1\right]})+\overbrace{\tau_{c}\left(\psi_{k} ; y_{i}^{\text {obs }}, c_{i}, \theta^{[r-1]}\right)}^{\mathbb{E}_{\theta}[r-1]}\left[\ln f_{k}\left(c_{i} \mid y_{i} ; \phi_{k}\right) \mid y_{i}^{\text {obs }}, c_{i}, z_{i}=1\right]]$.
with $t_{i k}\left(\theta \theta^{[r-1]}\right)=\mathbb{P}\left(z_{i k}=1 \mid y_{i}^{\text {obs }}, c_{i}\right)$.

- Law of $y_{i}^{\text {mis }}$ given $\left(y_{i}^{\text {obs }}, z_{i k}=1, c_{i}\right)$ ?
- Computation of the expectation over this law of $f_{k}\left(c_{i} \mid y_{i} ; \phi_{k}\right)$ ?


## EM algorithm: feasible computations?

MNARz, MNARzj : needs some computations but still simple.

$$
f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)=\rho\left(\alpha_{k j}\right) \quad(\Perp Y)
$$

- $\Rightarrow \mathcal{L}\left(y_{i}^{\text {mis }} \mid y_{i}^{\text {obs }}, z_{i k}=1, c_{i}\right)=\mathcal{L}\left(y_{i}^{\text {mis }} \mid y_{i}^{\text {obs }}, z_{i k}=1\right)$
- EM algorithm for Gaussian data,
- EM for categorical data.

MNARy*: needs approximations

$$
f_{k}\left(c_{i} \mid y_{i} ; \psi_{k}\right)=\rho\left(\alpha_{k j}+\beta_{k j} y_{i j}\right) \quad(\text { not } \Perp Y)
$$

- $\left(y_{i}^{\text {mis }} \mid y_{i}^{\text {obs }}, z_{i k}=1, c_{i}\right)$ not classical if Logit link.
- No closed forms.


## SEM algorithm for MNARy*

SEM easier? random drawing instead of expectation

- SE-step: draw the missing data

$$
\left(\left(y_{i}^{\mathrm{mis}}\right)^{[r]}, z_{i}^{[r]}\right) \sim\left(. \mid y_{i}^{\mathrm{obs}}, c_{i} ; \pi^{[r-1]}, \lambda^{[r-1]}, \psi^{[r-1]}\right)
$$

- $\left(y_{i}^{\text {mis }}\right)^{[r]} \sim\left(\cdot \mid y_{i}^{\text {obs }}, z_{i}^{[r-1]}, c_{i} ; \lambda^{[r-1]}, \psi^{[r-1]}\right)$ :
- $z_{i}^{[r]} \sim\left(\cdot \mid y_{i}^{[r]}, c_{i} ; \pi^{[r-1]}, \lambda^{[r-1]}, \psi^{[r]}\right)$ : draw the membership $k$ of $z_{i}^{[r]}$ from the multinomial distribution
Let $Y^{[r]}=\left(y_{1}^{[r]}|\ldots| y_{n}^{[r]}\right), Z^{[r]}=\left(z_{1}^{[r]}|\ldots| z_{n}^{[r]}\right)$ be the imputed matrix and the partition.
- M-step: for $k=1, \ldots, K$, compute $\pi_{k}^{[r]}, \lambda_{k}^{[r]}, \psi_{k}^{[r]}$.
$\left(\cdot \mid y_{i}^{\text {obs }}, z_{i}^{[r-1]}, c_{i} ; \lambda^{[r-1]}, \psi^{[r-1]}\right)$ ?
- not classical if $\rho$ is Logit
- truncated Gaussian distribution if $\rho$ is Probit


## Summary of the algorithms

|  | EM |  | SEM |  |
| :--- | :---: | :---: | :---: | :---: |
|  | Gaussian | Categorical | Gaussian | Categorical |
| MNARz $^{j}$ | $\checkmark$ | $\checkmark$ | $\checkmark$ | $\checkmark$ |
| MNARz $^{j}$ |  |  | $\checkmark$ |  |
| MNARy* | no closed form | not ident. | $\checkmark$ <br> $($ Probit $)$ | not ident. |

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## Setting

- Gaussian mixture with three components having unequal proportions $(1=0.5,2=3=0.25)$, independent variables.
- Control the rates of misclassification ( $10 \%$ ) and missingness ( $30 \%$ ): we fix them equal for each scenario.


## Computation time



## MNARz vs other MNAR model



## MNARz: robustness to the misspecification of the data distribution

- Three-components Gaussian mixture with non-diagonal covariance matrices: $\Sigma_{i j}=\ell, i \neq j$, with $\ell \in\{0,0.1,0.25,0.5\}$
- Algorithm assumes $\ell=0$.



## Results on real data

41 mixed variables containing missing values assumed to be MNARz The variables related to the patient death are not taken into account.

Can the MNAR mechanism improve the classification ? Is there an influence of the mechanism ?

- Same number of clusters selected by the ICL criterion;
- For $K=3$, ARI between the classifications obtained assuming MNARz and MCAR $=0.9$;



## Results on rela data

$$
\sqrt{\sum_{i=1}^{n}\left(\mathbb{P}\left(z_{i k}=1 \mid y_{i s}^{\mathrm{obs}} ; \theta^{\mathrm{MCAR}}\right)-\mathbb{P}\left(z_{i \tilde{k}}=1 \mid y_{i s}^{\mathrm{obs}} ; \theta^{\mathrm{MNAR}}\right)\right)^{2}}, \forall k, \tilde{k} \in\{1,2,3\}
$$

|  | MNARz |  |  |
| :---: | :---: | :---: | :---: |
| MCAR |  | Class 1 | Class 2 |
| Class 3 |  |  |  |
| Class 1 | $\mathbf{2 . 4 3}$ | 26.5 | 37.6 |
| Class 2 | 26.2 | $\mathbf{3 . 4 0}$ | 20.1 |
| Class 3 | 39.3 | 19.2 | $\mathbf{2 . 0 5}$ |

Table: Euclidean distance between the conditional probabilities of the cluster memberships given the observed values of the variable Shock.index.ph in the Traumabase dataset, obtained using the algorithm considering MNARz data, and the ones obtained with the algorithm considering MCAR data.

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## Conclusion

## Summary

- Interest to put a model on c
- Interest of the simple but meaningful model MNARz
- Trade-off between biased mixture model and biased missingness mechanism.


## Ongoing works

- Implement the proposed models/algo. in the Mixmod software ${ }^{\text {a }}$

[^0]
# MNARz: robustness to the NA\% and choice of $K$ 



|  | MCAR | MNARz |
| :--- | :--- | :--- |
| $10 \%$ NA | $94 \%$ | $94 \%$ |
| $30 \%$ NA | $8 \%$ | $56 \%$ |
| $50 \%$ NA | $0 \%$ | $20 \%$ |

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[^0]:    ${ }^{a}$ http://www.mixmod.org

