Handling missing values: model-based approaches



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MSc Data Science

What are missing values?

A few examples Mathematical framework

Statistical models of incomplete data

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Example: heath records

		Center	Acciden	t Age	Sex	Weight	Height	BM1	E BP	SBP	
1		Beaujon	Fall	54	m	85	NR	NR	180	110	
2		Lille	Other	33	m	80	1.8	24.69	130	62	
3	Pitie	Salpetriere	Gun	26	m	NR	NR	NR	131	62	
4		Beaujon	AVP moto	63	m	80	1.8	24.69	145	89	
6	Pitie	Salpetriere	AVP bicycle	33	m	75	NR	NR	104	86	
7	Pitie	Salpetriere	AVP pedestria	n 30	W	NR	NR	NR	107	66	
9		HEGP	White weapon	n 16	m	98	1.92	26.58	118	54	
10		Toulon	White weapon	20	m	NR	NR	NR	124	73	
	Sp02	Temperature	Lactates Hb	Glas	gow 1	ransfu	sion				
1	97	35.6	<na> 12.7</na>		12		yes				
2	100	36.5	4.8 11.1		15		no				
3	100	36	3.9 11.4		3		no				
4	100	36.7	1.66 13		15		yes				
6	100	36	NM 14.4		15		no				
7	100	36.6	NM 14.3		15		yes				
9	100	37.5	13 15.9		15		yes				
10	100	36.9	NM 13.7		15		no				

Figure: Traumabase data set (figure from Julie Josse).

Example: heath records

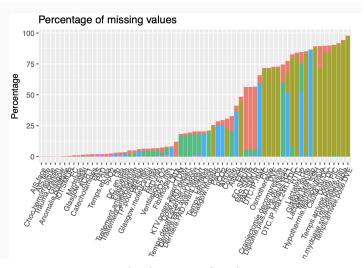


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Example: the Netflix prize

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Example: semi-supervised image classification

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Example: semi-supervised medical image segmentation

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Example 1 (bad thermometer): we have a thermometer that breaks when the temperature is above 39 degrees Celsius. Then, it is impossible to learn the distribution of temperatures above 39 degrees, even given a very large data set!

There is a peculiarity when learning with incomplete data. In usual machine learning without missing data, given a very large data set, we usually have guarantees that we will learn the data generating distribution. When there are missing data, things get trickier.

Example 2 (incomplete questionnaire): in a poll with multiple questions, there is a question about a sensitive issue in a questionnaire (e.g. on a US presidential election). Let's say that the people in favour of the Republican candidate are more likely to choose not to respond to the question. Then, just looking at the observed data, it will be very hard to predict the result of the election, without making additional assumption about the reasons for nonresponse.

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This explains why model-based approaches are a natural way to deal with missing values.

A mathematical framework for incomplete data

We assume that there exists a complete data matrix $\mathbf{X} \in \mathbb{R}^{n \times d}$. We do not observe \mathbf{X} , and only have access to an incomplete version $\mathbf{Z} \in \mathbb{R}^{n \times p}$ where some values have been replaced by NAs. The values of the observed data matrix \mathbf{Z} belong to $\mathbb{R} = \mathbb{R} \cup \{\text{NA}\}$.

We also define a binary matrix $\mathbf{M} \in \{0,1\}^{n \times d}$ whose nonzero entries correspond to missing values.

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 9 \\ 2 & 7 & 0 \end{pmatrix}, \mathbf{M} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 1 \end{pmatrix}, \mathbf{Z} = \begin{pmatrix} \mathtt{NA} & 3 & \mathtt{NA} \\ 2 & \mathtt{NA} & \mathtt{NA} \end{pmatrix}.$$

Keep in mind that X is hidden: we only have access to M and Z, and we will need to build our models and algorithms accordingly.

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Supervised vs unsupervised

To keep things simple, we are going to consider unsupervised learning of continuous data $\mathbf{X} \in \mathbb{R}^{n \times d}$.

If you want to look at the supervised case, pretty much everything we're going to see today is still valid if you replace \boldsymbol{X} by $(\boldsymbol{X},\boldsymbol{Y})$. Of course, a few things will need to be adapted.

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- **a** joint model p(X, M) will imply a model p(Z), so we are still indirectly modelling Z.

Building a joint model p(X, M)

We will call p(X, M) a joint model, because it jointly models the features X and the missingness pattern M. Part of the features are not observed so this will be a latent-variable model (the latent variables being the missing values).

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Today, we will focus on models where the ordering of the observations does not matter, so we will assume that $(\mathbf{x}_1, \mathbf{m}_1), ..., (\mathbf{x}_n, \mathbf{m}_n)$ (the rows of \mathbf{X} and \mathbf{M}), are independent and identically distributed samples from a distribution $p(\mathbf{x}, \mathbf{m})$. This means that the model can be written

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In that context, what we "just" need to specify is $p(\mathbf{x}, \mathbf{m})$, a distribution over $\mathbb{R}^d \times \{0,1\}^d$. Now, we will look at the assumptions we mentioned in the beginning of the lecture.

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With these assumption, we saw that the likelihood can be written

$$\sum_{i=1}^n \log p_{\boldsymbol{\theta}}(y_i, \mathbf{x}_i) = \sum_{i=1}^n \log p_{\boldsymbol{\theta}}(y_i | \mathbf{x}_i) + \sum_{i=1}^n \log p(\mathbf{x}_i),$$

but, since we don't model $p(\mathbf{x})$, $\sum_{i=1}^{n} \log p(\mathbf{x}_i)$ is constant, and maximising the likelihood is equivalent to maximising $\sum_{i=1}^{n} \log p_{\theta}(y_i|\mathbf{x}_i)$.

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We will use similar tricks to build our joint model p(x, m).

Building a joint model p(x, m)

Using the product rule from probability theory, any model can be decomposed as

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Now, what's left is to specify $p(\mathbf{m}|\mathbf{x})$. In general, this is very hard, and we usually need to have strong knowledge about the problem at hand. Indeed, let us go back to the election example: we would need to know which voters are more likely not to respond to model $p(\mathbf{m}|\mathbf{x})$ properly (and knowing this is hard!). Suprisingly, under some suitable assumptions, it is actually possible to not model $p(\mathbf{m}|\mathbf{x})$ at all, similarly to when we did not model $p(\mathbf{x})$ in logistic regression.

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A convenient thing is to split a complete feature vector \mathbf{x} into observed features \mathbf{x}^{obs} and mission ones \mathbf{x}^{miss} , such that $\mathbf{x} = (\mathbf{x}^{obs}, \mathbf{x}^{miss})$. Using this in the equation gives

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$$p(\mathbf{x}^{obs}, \mathbf{m}) = \int p(\mathbf{m}|\mathbf{x}^{obs}, \mathbf{x}^{miss}) p(\mathbf{x}^{obs}, \mathbf{x}^{miss}) d\mathbf{x}^{miss}.$$

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in a way that avoids modelling explicitly $p(\mathbf{m}|\mathbf{x})$.

A first way to do this is to assume that m and x are actually independent. This is called the missing completely at random (MCAR) assumption. In that case,

$$p(\mathbf{m}|\mathbf{x}^{obs},\mathbf{x}^{miss})=p(\mathbf{m}),$$

and we can write

$$p(\mathbf{x}^{obs}, \mathbf{m}) = p(\mathbf{m}) \int p(\mathbf{x}^{obs}, \mathbf{x}^{miss}) d\mathbf{x}^{miss} = p(\mathbf{m})p(\mathbf{x}^{obs}).$$

Let's assume that we have chose a parametric model $p_{\theta}(\mathbf{x})$ for the features. Under the MCAR assumption, the likelihood of the data is

$$\ell(\theta) = \sum_{i=1}^{n} \log p_{\theta}(\mathbf{x}_{i}^{obs}, \mathbf{m}_{i}) = \sum_{i=1}^{n} \log p(\mathbf{m}_{i}) p_{\theta}(\mathbf{x}_{i}^{obs})$$
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and since the red term does not depend on θ , maximising $\ell(\theta)$ is equivalent to maximising

$$\sum_{i=1}^n \log p_{\theta}(\mathbf{x}_i^{obs}),$$

which is the likelihood of the observed features only.