Missing Data

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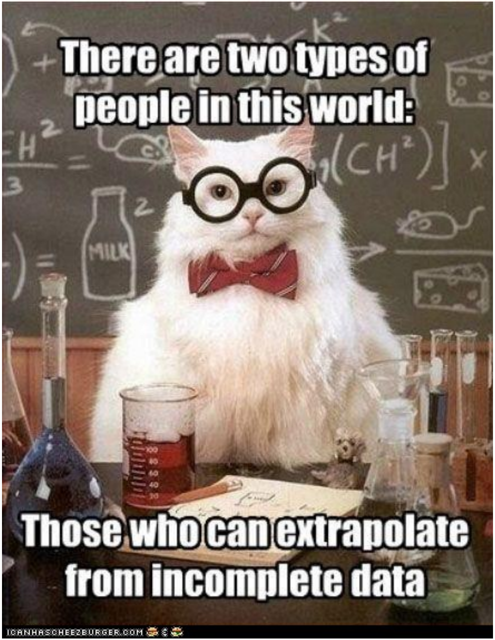
This material is part of the ***statsTeachR*** *project*

Today's Lecture

- Types of missing data
- Ways to describe missing data
- Multiple imputation


There are two types of people in this world:
MILK
Those who can extrapolate from incomplete data
ICANHASCHEEZBURGER.COM

Best practices

Hard to argue with an approach that does the following:

- quantify the completeness of covariate data
- present and discuss patterns of or reasons for missing data
- provide details about your approach for handling missing data in the analysis

Proposed guidelines for reporting missing covariate data (Burton and Altman 2004)

Quantifying missing data

```r
library(Hmisc)
getHdata(titanic)
colnames(titanic)
```

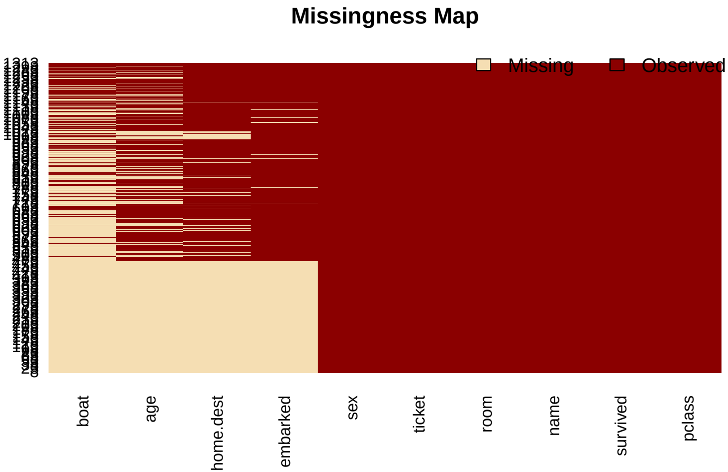
```
##  [1] "pclass"    "survived"  "name"      "age"       "embarked"
##  [6] "home.dest" "room"      "ticket"    "boat"      "sex"
```

```r
na.pattern(titanic)
```

```
## pattern
## 0000000000 0000000010 0000010000 0000010010 0000100000 0000100010
##        279        315          6         27          4          2
## 0001000000 0001000010 0001010000 0001010010 0001100010 0001110010
##         51         95          7         41          8        478
```

Quantifying missing data

```r
library(Amelia)
missmap(titanic)
```



Quantifying missing data

What percentage of each variable's observations are missing?

```
t(t(apply(titanic, MAR=2, FUN = function(x) round(sum(is.na(x))/length(x)*100))))
```

```
##           [,1]
## pclass       0
## survived     0
## name         0
## age         52
## embarked    37
## home.dest   43
## room         0
## ticket       0
## boat        74
## sex          0
```

Formal Missing Data Classifications

Missing Completely at Random (MCAR)

- No data, observed or unobserved, are related to missingness.

Missing at Random (MAR)

- No unobserved data are related to missingness, but missingness may depend on observed data.

Missing Not at Random (MNAR) or unignorable missingness

- Missingness relationship cannot be simplified: it depends on unobserved data!

What kind of missingness did the titanic dataset have?

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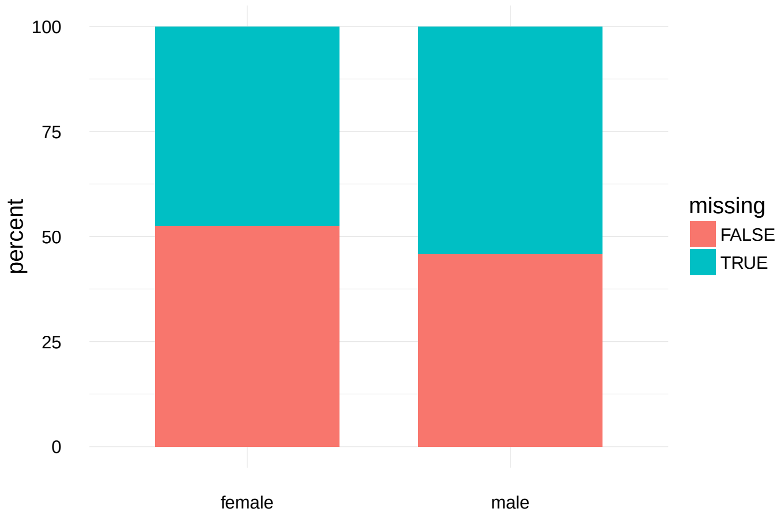

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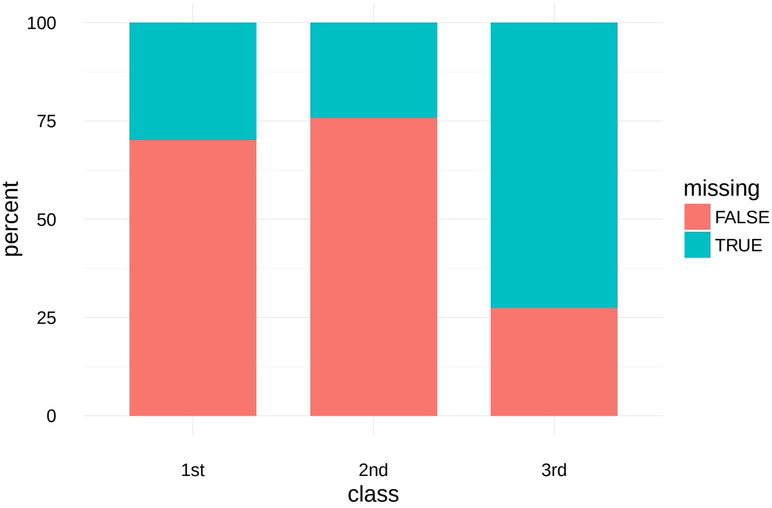


Example code used to create the last graphic

Harder than it should be, it felt like... Code adapted from this page.

```
t3 <- titanic %>%
  group_by(pclass, age_mis) %>%
  summarise(count=n()) %>%
  mutate(perc=count/sum(count))

ggplot(t3, aes(x = pclass, y = perc*100, fill = age_mis)) +
  geom_bar(stat="identity", width = 0.7) +
  labs(x = "class", y = "percent", fill = "missing") +
  theme_minimal(base_size = 14)
```

Testing for the different types of data

Tests about the type of data you have

- MAR vs. MNAR: Not a definitive test here. Best option is to use your domain-specific knowledge about the data.
- MCAR vs. MAR: Little's test can weigh evidence for/against these two settings.

Little's H_0: The data is MCAR

Low p-values suggest that the data are MAR; high p-values suggest they are MCAR.

```
test <- BaylorEdPsych::LittleMCAR(titanic[,c("pclass", "survived", "age", "sex"

## this could take a while

test$p.value

## [1] 0
```

Types of analyses for missing data

Analysis strategies (in rough order of desirability, low to high)

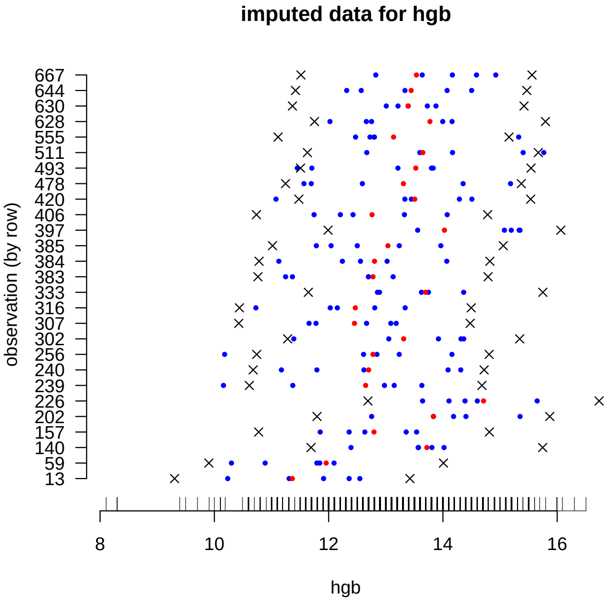
- MCAR only: Complete case a.k.a. "listwise deletion"
- Ad-hoc methods (e.g. mean imputation)
- Weighting methods
- MAR: Likelihood-based approaches (e.g. EM algorithm)
- MAR: Multiple Imputation (many flavors)
- MAR: Bayesian methods

Multiple imputation

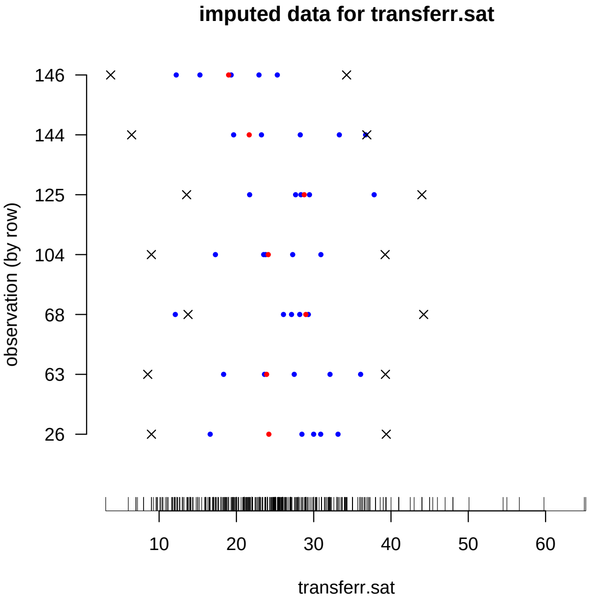
General approach

- For each missingness pattern, a model is built to use the available covariates to estimate the missing covariates.
- Random samples are taken from the predictive distribution to create multiple "complete" datasets.
- Typically, 10-15 datasets is seen as being sufficient.
- Coefficient and SE estimates are combined across datasets.

Multiple imputation: example



Multiple imputation: example



Multiple imputation results

Regression coefficients from five imputed data sets

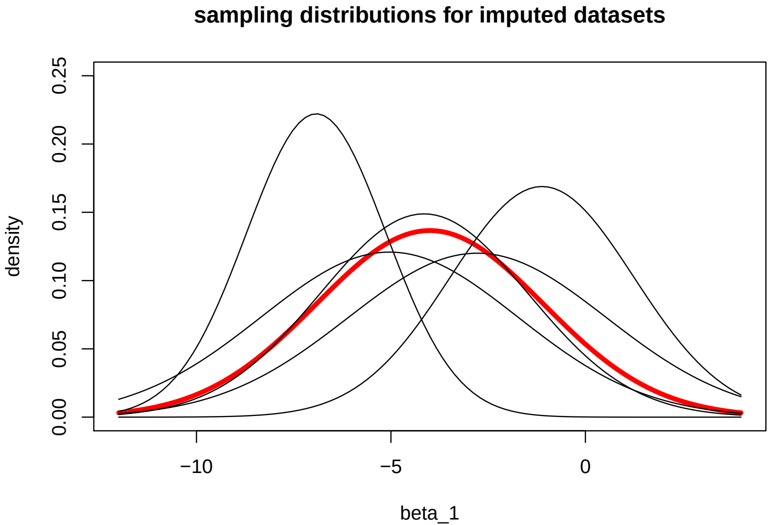
Data set	Estimated parameter	b_0	b_1	b_2	b_3	b_4	b_5
1	Coefficient	-11.535	-2.780	1.029	-.031	-0.359	0.572
	Variance	43.204	3.323	0.013	0.013	0.013	0.012
2	Coefficient	-11.501	-4.149	1.040	-0.093	-0.583	0.876
	Variance	40.488	2.680	0.010	0.009	0.009	0.007
3	Coefficient	-10.141	-5.038	0.766	0.123	-0.252	0.625
	Variance.	42.055	3.301	0.010	0.010	0.010	0.009
4	Coefficient	-11.533	-6.920	0.870	0.084	-0.458	0.815
	Variance	28.751	1.796	0.081	0.007	0.007	0.007
5	Coefficient	-14.586	-1.115	0.718	0.050	-0.373	0.814
	Variance	32.856	2.362	0.009	0.009	0.009	0.008
	Mean b_i	-11.859	-4.000	0.885	0.027	-0.405	0.740
	Mean Var.($\bar{W}$)	37.471	2.692	0.025	0.010	0.010	0.009
	Var. of b_i (B)	2.682	4.859	0.022	0.008	0.015	0.018
	T	40.69	8.523	0.051	0.020	0.028	0.031
	$\sqrt{T}$	6.379	2.919	0.226	0.141	0.167	0.176
	t	-1.859	-1.370	3.916*	0.191	2.425*	4.204*

* $p < .05$ "Var." refers to the squared standard error of the coefficient.

DC Howell, Treatment of Missing Data – Part II.

Multiple imputation results

The final estimated sampling distribution for each β is an average of the sampling distributions from each imputed dataset.



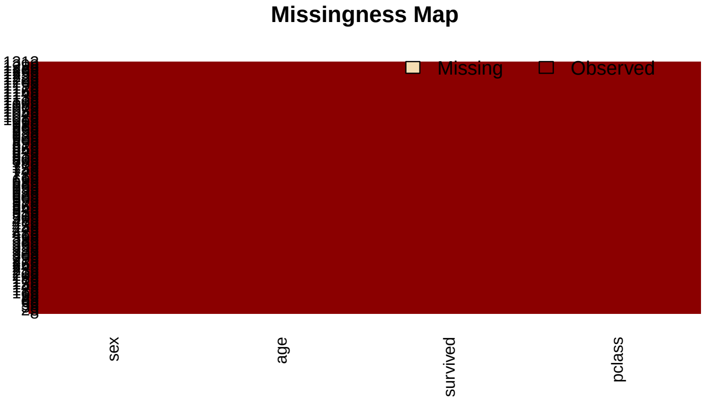
Multiple imputation software

There are two commonly used implementations of multiple imputation in R:

- MICE: http://www.stefvanbuuren.nl/mi/
- To be used together: Amelia (runs the MI) and Zelig (fits models to, among other things, MI datasets): http://gking.harvard.edu/amelia and http://zeligproject.org/

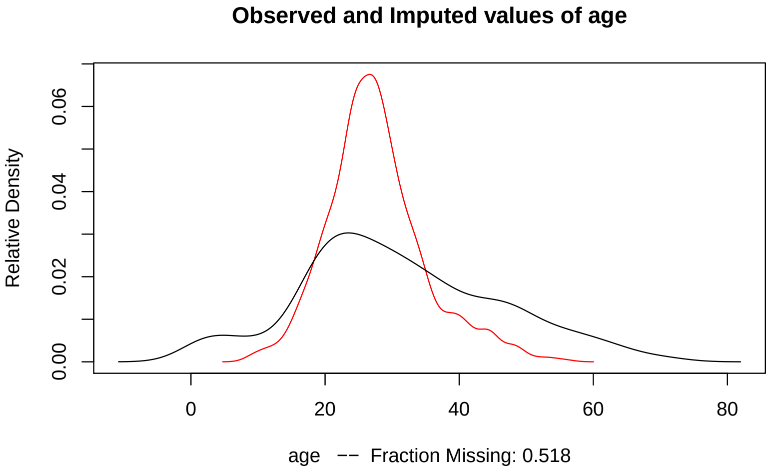
Multiple imputation for titanic data

```
t2 <- titanic[,c("pclass", "survived", "age", "sex")]
imp_titanic <- amelia(x = t2, m = 10, noms=c("sex", "pclass"))
missmap(imp_titanic$imputations$imp1)
```



Multiple imputation for titanic data

```
plot(imp_titanic, which.vars = "age")
```



Multiple imputation for titanic data

```
t2 <- t2[complete.cases(t2),] ## only include complete cases
m_full <- glm(survived~sex+age+pclass, data=t2, family=binomial)
summary(m_full)$coef
```

```
##                Estimate  Std. Error    z value     Pr(>|z|)
## (Intercept)  4.52216290 0.471007573   9.601041 7.914121e-22
## sexmale     -3.08670894 0.241062738 -12.804588 1.545447e-37
## age         -0.04930858 0.008732002  -5.646882 1.633840e-08
## pclass2nd   -1.49522913 0.281986441  -5.302486 1.142363e-07
## pclass3rd   -2.84127142 0.338897350  -8.383870 5.121522e-17
```

```
library(Zelig)
m_imp <- zelig(survived~sex+age+pclass, model="logit", data=imp_titanic)
```

```
summary(m_imp)
```

```
## Model: Combined Imputations
##             Estimate Std.Error z value  Pr(>|z|)
## (Intercept)  4.09799  0.456939   8.968 0.000e+00 ***
## sexmale     -2.53298  0.174426 -14.522 0.000e+00 ***
## age         -0.05106  0.008842  -5.775 7.687e-09 ***
## pclass2nd   -1.46677  0.247084  -5.936 2.915e-09 ***
## pclass3rd   -2.97530  0.252526 -11.782 0.000e+00 ***
## ---
```

Best practices

Hard to argue with an approach that does the following:

- quantify the completeness of covariate data
- present and discuss patterns of or reasons for missing data
- provide details about your approach for handling missing data

Proposed guidelines for reporting missing covariate data (Burton and Altman 2004)

Bonus: ROC for Titanic data

```
library(ROCR)
pred <- prediction(predict(m_full, type="response"), t2$survived)
perf <- performance(pred, measure = "tpr", x.measure = "fpr")
plot(perf)
```