POLI 273: Causal Inference Professor Umberto Mignozzetti

Lecture 07 | Experimental Political Science I



Experiments

- ► Randomization
- ► SUTVA
- ► Ignorability of the Treatment
- ► Good. Now what?

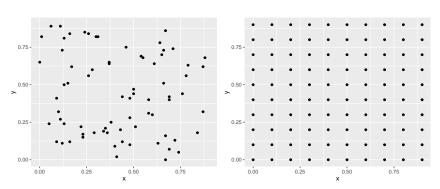
Simple Randomization

Randomization

- Randomization is complex.
- ► Computers: Produce pseudo-random numbers.
- Random: There are no observable patterns in the draws.
- Pseudo-random: There might be a pattern, even if hard to find, in the draw.

Randomization

▶ Which one do you think is *more random*?



Estimation and sampling distribution

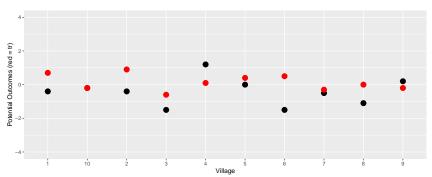
- Statistics: Quantification of uncertainty.
- ► We want to know **if** and **by how much** we can trust the result of the experiment.
- ► Population distribution: How do the values appear in the population?
- Let us see an example of a *cooked* experiment.

Population distribution

- ► Population: 10 villages
- ► Treatment: Effect of having a woman as a village representative on sanitation spending.
- ► Theory: Women invest more in sanitation than men.
 - ► Men tend to invest more in roads
- Let us say that this is true

Population distribution

```
dt <- data.frame(Village = as.character(1:10),
    Yi0 = round(rnorm(10), 1), Yi1 = 0.5+round(rnorm(10), 1))</pre>
```



Population distribution

► Studying the population, we would find the PATE: Population Average Treatment Effect

Village	Yi0	Yi1	tau
1	-0.4	0.7	1.1
2	-0.4	0.9	1.3
3	-1.5	-0.6	0.9
4	1.2	0.1	-1.1
5	0.0	0.4	0.4
6	-1.5	0.5	2.0
7	-0.5	-0.3	0.2
8	-1.1	0.0	1.1
9	0.2	-0.2	-0.4
10	-0.2	-0.2	0.0

Since the ATE is: $ATE = \frac{1}{N} \sum_{i=1}^{N} \tau_i$, the *theoretical* PATE for this case is 0.55.

Sampling distribution

But we only observe a few of these outcomes: fundamental problem of causal inference.

combn (10.5)

► For treatments with size 5, we have 252 possible options!

```
## [2.1
## [4,]
## [1,]
## [2,]
## [4,]
              10
## [5.1
## [1.]
## [4.1
```

Computing the ATE

▶ In the first assignment, we have: 1, 2, 3, 4, 5. And we would observe:

Yi0	Yi1
-0.4	NA
-0.4	NA
-1.5	NA
1.2	NA
0.0	NA
NA	0.5
NA	-0.3
NA	0.0
NA	-0.2
NA	-0.2
	-0.4 -0.4 -1.5 1.2 0.0 NA NA NA

- ► With $E(Y_i(0)) = -0.22$ and $E(Y_i(1)) = -0.04$.
- ▶ The ATE for this case is 0.18.

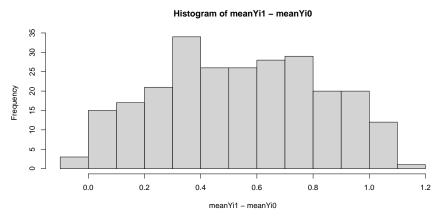
Uncertainty

- ▶ But we have 252 possible combinations. How do they behave?
- ► To find that out, we may compute the average for all combinations:

```
meanYi0 <- numeric()
meanYi1 <- numeric()
cbn <- combn(10,5)
for (i in 1:choose(10,5)) {
    meanYi0[i] <- mean(dt$Yi0[cbn[,i]])
    meanYi1[i] <- mean(dt$Yi1[11-cbn[,i]])
}
hist(meanYi1-meanYi0)</pre>
```

Uncertainty in ATE measurement

► The theoretical PATE is 0.55. The mean of the ATEs is 0.55.



Uncertainty in ATE measurement

- But note some interesting things:
 - 1. The values have a large variance!
 - 2. Some values give treatment greater than one.
 - We would conclude that the treatment is super effective.
 - 3. Some give treatment effects are negative.
 - ► Having women decreases the chance of investments in sanitation?
- ▶ We need to think seriously about the uncertainty here.

Standard Error

- ► Standard error is the measure of how much uncertainty we have.
- Standard error in the ATE world is defined as:

$$SE(\widehat{ATE}) = \sqrt{\frac{1}{N-1} \sum_{i} (ATE_i - \overline{ATE})^2}$$

► An alternative formula, that you will derive in PS02, is:

$$\sqrt{\frac{1}{\mathit{N}-1}\left(\frac{\mathit{mVar}(Y_i(0))}{\mathit{N}-\mathit{m}} + \frac{(\mathit{N}-\mathit{m})\mathit{Var}(Y_i(1))}{\mathit{m}} + 2\mathit{Cov}(Y_i(0),Y_i(1))\right)}$$

Standard Error

$$\sqrt{\frac{1}{\mathit{N}-1}\left(\frac{\mathit{mVar}(Y_i(0))}{\mathit{N}-\mathit{m}} + \frac{(\mathit{N}-\mathit{m})\mathit{Var}(Y_i(1))}{\mathit{m}} + 2\mathit{Cov}(Y_i(0),Y_i(1))\right)}$$

- 1. Increasing *N* decreases the standard-error.
 - Practical advice: Increases your sample size whenever possible.
- 2. Decreasing the Variances decrease the standard-errors.
 - Practical advice: Try to measure things precisely.
- 3. If the variances are similar, half-half is the best strategy.
 - Practical advice: You need a good reason to deviate from this benchmark.

- ► Sharp null: No differences in treatment and control for all units.
- ► Null ATE: Treatment and control averages differ from zero.
- p-values: We use p-values in here (sorry, Bayesian folks).
- (now for Bayesian folks): Confidence Intervals:
 - Easy to compute from this standard error formulation
 - Quick note (from Sammi e Aronow, 2011): If you have a small sample, correct the SE by the factor

Block Randomization

Efficiency Gains

- Suppose now that our five cases are in two different blocks
- ► A way to randomize there would be to use this information to our advantage.

Block randomization

- ► What could be considered *blocks*?
 - 1. Gender
 - 2. Test scores
 - 3. Ages
 - 4. Other variables

Block randomization

- ► If we have two blocks, then we can randomize within these blocks.
- Assume we have blocks of size four and six.
- With simple randomization we have $\binom{10}{5}$ options, or 252 options.
- With block randomization, we would have $\binom{6}{3}\binom{4}{2}$, which is equal to 120 possible blocks.

Block randomization

And our ATE changes slightly:

$$ATE = \sum_{i=1}^{J} \frac{N_j}{N} ATE_j$$

► The standard error also changes:

$$SE(\widehat{ATE}) = \sqrt{\sum_{1}^{J} (\frac{N_{j}}{N})^{2} SE^{2} (ATE_{j})}$$

Weighted average/variance within blocks

Block Randomization

- Why to use block randomization?
- ► In some (most, really) situations, it may increase the efficiency of our estimates.
- ► Next class, I will bring some simulations for you to check this happening!
- Now, to fix the content, let us go to the R code for the class.

Next Class

- ► Matched pair design
- ► Population x Sample ATEs
- ► Block Randomization (how to do it)
- Cluster Randomization
- ► Block + Cluster Randomization
- Diseases that affect Experiments
- Declare Design

Questions?

See you next class!