# MY457/MY557: Causal Inference for Observational and Experimental Studies

## Week 2: Randomized Experiments

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1. The experimental ideal
2. The ‘magic’ of randomization
3. Estimation
4. Inference
5. Example: JTPA
6. Beyond simple randomized experiments

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# (Randomized) Experiments

Experiment:
A research design where the assignment mechanism is individualistic, probabilistic, uncounfounded, and controlled by the researcher.

Randomization:
Treatment values are assigned to $N$ units at random, with known and positive assignment probabilities for each treatment to each unit (often called a 'randomized controlled trial' or RCT).

We consider the 'completely randomized experiment': a random subset of $N_1$ units assigned to treatment ($D = 1$) and remaining $N_0 = N - N_1$ to control.

- Note the slight difference to simple randomization (Bernoulli trials).
- Extension to cases with more than two levels is reasonably straightforward.
- Other randomized designs are introduced briefly at the end of this lecture.

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"It's an illusion, Michael"

# The Problem

Recall our basic problem:

$$E[Y|D=1] - E[Y|D=0] = E[Y_1|D=1] - E[Y_0|D=0]$$
$$= \underbrace{E[Y_1|D=1] - E[Y_0|D=1]}_{\text{ATT}} + \underbrace{\{E[Y_0|D=1] - E[Y_0|D=0]\}}_{\text{Selection bias}}$$

# Randomization: Identification Assumption

Our goal is to find conditions under which we can identify our unobservable causal estimand with only observed data.

Randomization implies that assignment probabilities do not depend on potential outcomes (in expectation):

$$P(D|Y_0, Y_1) \quad = \quad P(D)$$

This is often called independence or unconfoundedness:

$$(Y_1, Y_0) \perp\!\!\!\perp D$$

(Note: $\perp\!\!\!\perp$ means "is independent of".)

To check understanding, does randomization imply $Y \perp\!\!\!\perp D$? No!

$(Y_1, Y_0) \perp\!\!\!\perp D$ means $Y_0$ is (in expectation) the same for those with $D = 1$ and $D = 0$ (similarly for $Y_1$). Says nothing about equivalence of $Y$ between groups.

# Randomization: Key Identification Result

Under independence from randomization:

$$E[Y_0|D=1] = E[Y_0|D=0] = E[Y_0]$$
$$\therefore E[Y_0|D=1] - E[Y_0|D=0] = 0$$

Read: Selection bias is, in expectation, equal to zero.

Returning to the problem at hand:

$$E[Y|D=1] - E[Y|D=0] = E[Y_1|D=1] - E[Y_0|D=0]$$
$$= \underbrace{E[Y_1|D=1] - E[Y_0|D=1]}_{\text{ATT}} + \underbrace{\{E[Y_0|D=1] - E[Y_0|D=0]\}}_{\text{Selection bias = 0}}$$
$$= \underbrace{E[Y_1|D=1] - E[Y_0|D=1]}_{\text{ATT}}$$

We can prove that our estimator equals our estimand → identification.

# Randomization: Equivalence of Estimands

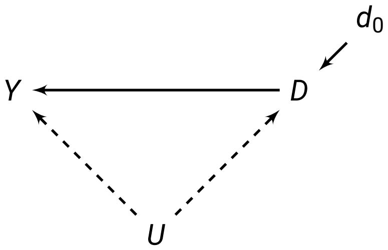
Independence tells us that $E[Y_1|D=1] = E[Y_1|D=0] = E[Y_1]$ (and for $Y_0$) , thus:

$$\begin{aligned}
\tau_{ATT} &= E[Y_1|D=1] - E[Y_0|D=1] = E[Y_1|D=0] - E[Y_0|D=0] \\
&= \tau_{ATU} = E[Y_1] - E[Y_0] \\
&= \tau_{ATE}
\end{aligned}$$

Read: Under independence, the ATE, ATT, and ATU are equal, and are thus simultaneously identified by the observed difference-in-means.

Note: We can also identify most other population-level causal effects, since they are comparisons of some features of the distributions of $Y_0$ and $Y_1$ and we can now estimate both of these distributions.

# Graphical Representation



Consider a setting in which $D \leftarrow U \rightarrow Y$ is a back-door path connecting $D$ and $Y$ through unobserved $U$.

This is canonical confounding with the unobserved $U$ confounding $D \rightarrow Y$

Randomization is equivalent to imposing $do(d_0)$ or $do(d_1)$, eliminating $U \rightarrow D$

There are now no back-door paths, so $D \rightarrow Y$ is identified.

# Randomization and the Balancing Property

In expectation, complete randomization balances all observed and unobserved pre-treatment characteristics between treatment and control.

Why? For units with the same probability of treatment, $X_i$ is independent of treatment assignment $\rightsquigarrow$ the balancing property.

(Note: We will dive deeper into this next week, when we introduce propensity scores.)

In a given experimental sample, we can empirically check for balance in observed pre-treatment covariate $X$ using so called 'balance tests' (e.g., $t$-tests or equivalence tests) to see if the distributions $p(X|D=1)$ and $p(X|D=0)$ are not meaningfully different:

- In any one sample and treatment regime we might expect some chance imbalance.
- You could 'control' for imbalanced covariates, but don't 'have to' (more later).
- Stratified randomization can guarantee exact balance in some observed $X$.
- Even more aggressive randomization procedures exist (e.g. pair-matching).

# Complications and Limitations in Randomized Experiments

Randomization (and thus internal validity) can be complicated by:

- Missing data (e.g. dropout/attrition) – outcome is unobserved for some units in a way that is associated with $D$ or potential outcomes.
- Measurement problems – Hawthorne effects etc.
- Non-compliance – some units receive a different treatment than the one they were assigned to.

Randomization does not help with external validity: How well do causal effects for this sample apply to broader population, or other populations?

- Can differentiate Sample ATE (SATE) from Population ATE (PATE) – randomization identifies SATE, but PATE also requires random sampling.
- Moving to a different population entirely would require other (often heroic) assumptions.

Randomized experiments can be weak in construct validity: How well do treatment and outcome in the experiment match the concept we are substantively interested in?

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# Estimation vs. Inference

Estimation:

- Choosing the right function to apply to our observed data.
- We can use the distributions $p(Y|D = 1)$ and $p(Y|D = 0)$ in the observed data to estimate the distributions of $Y_1$ and $Y_0$ in the population, and thus population causal effects.
- Typically quite simple and familiar methods are sufficient for experiments.

Statistical inference:

- Characterizing uncertainty around our estimates and testing statistical hypotheses.
- Hypothesis tests and confidence intervals tend to be based on the source of identifying variation (i.e., what is 'random?')
- See the discussion in Chapters 5–8 of Imbens & Rubin for more on this, if you are interested.

# Estimating ATE

$$\tau_{ATE} = E[Y_1] - E[Y_0]$$

An obvious estimator we have already seen is the sample difference-in-means:

$$\widehat{\tau} = \bar{Y}_1 - \bar{Y}_0$$

where

$$\bar{Y}_1 = \frac{\sum Y_i \cdot D_i}{\sum D_i} = \frac{1}{N_1} \sum_{D_i=1} Y_i$$

$$\bar{Y}_0 = \frac{\sum Y_i \cdot (1 - D_i)}{\sum (1 - D_i)} = \frac{1}{N_0} \sum_{D_i=0} Y_i$$

with $N_1 = \sum_i D_i$
and $N_0 = \sum_i (1 - D_i) = N - N_1$

Have already proven that $\widehat{\tau}$ is an unbiased estimator of $\tau_{ATE}$ under randomization!

# Estimating ATE: Regression

The same $\tau_{ATE}$ can also be estimated using a linear regression model

$$Y_i = \hat{\gamma} + \hat{\tau} D_i + \hat{\varepsilon}_i$$

(Recall: $\hat{\tau}$ from a bivariate regression with a binary independent variable is equivalent to the diff-in-means.)

It is not necessary to include covariates $\boldsymbol{X}$ in this model. Why?

But pre-treatment covariates are sometimes included:

- Can increase precision (reduce standard error) by modeling residual variation in $Y$
- Control for observable imbalance (generated by random chance)
- Allow for estimation of heterogeneous treatment effects by $\boldsymbol{X}$ (by including interactions in the model)
- There is a risk of inducing small-sample bias (Freedman, 2008) – more in a few weeks when we introduce the 'fully-interacted estimator' (Lin, 2013)
- Note: do not include post-treatment covariates. (Montgomery et al., 2018; Cinelli et al., 2022)

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# Asymptotic Inference

When using either a simple difference-in-means or a linear regression, inference can be performed with a $t$-test:

1. Estimate the parameter of interest ($\tau_{ATE}$) and variance
2. State hypotheses of interest, typically: $H_0$: $\tau_{ATE} = 0$ and H$_1$: $\tau_{ATE} \neq 0$
3. Calculate the relevant $t$-statistic:
   a. For a difference-in-means, a two-sample $t$-test:

$$t = \frac{\widehat{\tau}}{\sqrt{\frac{\widehat{\sigma}_1^2}{N_1} + \frac{\widehat{\sigma}_0^2}{N_0}}} \xrightarrow{d} N(0,1),$$

$$\text{where} \quad \widehat{\sigma}_d^2 = \textstyle\sum_{D_i=d}(Y_i - \bar{Y}_d)^2/N_d \quad \text{for} \quad d \in \{0,1\}.$$

   b. For regression, estimate robust standard errors and calculate $t$-statistic
4. We reject the null hypothesis H$_0$: $\tau_{ATE} = 0$ at the asymptotic $\alpha = 5\%$ significance level if $|t| > 1.96$. (The choice of $\alpha$ is arbitrary.)

With more complex randomization schemes (e.g. cluster randomization), adjust standard error estimation ('analyze as you randomize').

# Randomization Inference

For our ***t***-tests, the null hypothesis was that the average treatment effect $\tau_{ATE}$ is zero, i.e.

$$H_0 : E[Y_1] = E[Y_0], \quad H_A : E[Y_1] \neq E[Y_0]$$

Consider now instead the sharp null hypothesis (and alternative)

$$H_0^s : Y_1 = Y_0, \quad H_A^s : Y_1 \neq Y_0$$

i.e. that all individual causal effects are zero.

Assuming $H_0^s$, then $Y_i = Y_{0i} = Y_{1i}$ for every unit. We can thus construct the full population distributions of $Y_{0i}$ and $Y_{1i}$, under the null hypothesis!

Why? Under the sharp null the observed data $Y_i$ for every unit would have been exactly the same, no matter the value of $D_i$

This is called randomization inference, permutation test, or Fisher's exact test

# Randomization Inference

Procedure for randomization inference with complete randomization:

1. Permute the values of $D_i$ ($N_1$ 1s and $N_0$ 0s) differently across the $N$ units, keeping $Y_i$ unchanged.
2. Calculate and store the value of $\widehat{\tau}_j$ (or any other appropriate statistic, such as the $t$-test statistic) for each of these permuted datasets $j$.
3. Calculate $p$-value as the proportion of $\widehat{\tau}_j$ that are as or more extreme than the actually observed $\widehat{\tau}$

With small $N$, we can consider *all* the permutations of $D_i$

- There are $\binom{N}{N_1} = N!/(N_1!N_0!)$ of them
- With larger $N$, use a random sample of all the permutations

# Randomization Inference Example

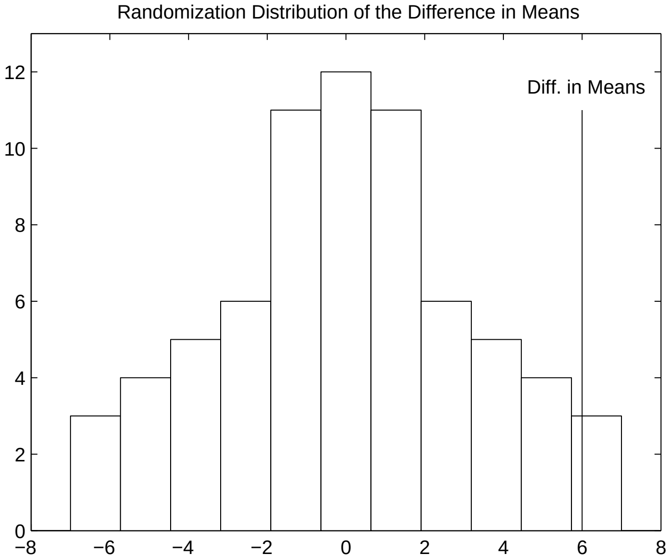
Consider an experiment with 8 units, 4 randomly assigned to treatment.

We can permute all $\binom{8}{4} = 70$ possible assignments.

We can then calculate the sample mean differences that would have been obtained for each of them if the sharp null hypothesis were true.

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| $Y_i$ | 12 | 4 | 6 | 10 | 6 | 0 | 1 | 1 | |
| $D_i$ | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | $\hat{\tau} = 6$ |
| | | | | | | | | | $\hat{\tau}_j$ |
| $j = 1$ | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 6 |
| $j = 2$ | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 4 |
| $j = 3$ | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 |
| $j = 4$ | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1.5 |
| | | | | $\dots$ | | | | | |
| $j = 70$ | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | -6 |

# Randomization Inference Example



$$p = \Pr(|\hat{\tau}_j| \geq 6) = 0.0857$$

# The Bootstrap

Another common method for uncertainty estimation is bootstrapping

The basic idea: Simulate the sampling distribution of a statistic via resampling with replacement

Useful when:

- Statistic is so complicated that analytically deriving its sampling variance is too difficult or cumbersome
- Data are so skewed that inference based on asymptotic normality is unlikely to perform well
- Statistic is of a form that makes CLT kick in only slowly, so normal approximation does not work well

Weakness: Computationally costly, sometimes prohibitively so.

Not a general solution for small samples (a common misunderstanding!)

# Nonparametric Bootstrap and Parametric Bootstrap

Nonparametric bootstrap:

1. Draw $B$ resamples of size $n$ from $X$ with replacement
2. For each $X_b^*$, compute $\hat{\theta}_b^*$, where $b = 1, ..., B$

3a. To estimate s.e. of $\hat{\theta}$, use the sample standard deviation of $\hat{\theta}^* = \{\hat{\theta}_1^*, ..., \hat{\theta}_B^*\}$ (bootstrap standard errors)

3b. To compute 95% CI, use 2.5/97.5 percentiles of $\hat{\theta}^* = \{\hat{\theta}_1^*, ..., \hat{\theta}_B^*\}$ as the lower/upper bounds (bootstrap percentile CI)

3c. If you know that $\hat{\theta} \overset{\text{approx.}}{\sim}$ N, you can use 3a. and compute the bootstrap normal CI

Not only can you do this without any assumption about $P$, you can use this for any function of data $\hat{\theta} = f(X)$

Block bootstrap: When observations are clustered, resample clusters with replacement instead of individual units

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"But it ain't how hard you hit; it's about how hard you can get hit, and keep moving forward."

# Example: Job Training Partnership Act (JTPA)

Largest randomized training evaluation ever undertaken in the U.S.; started in 1983 at 649 sites throughout the country

Sample: “Underskilled” and “economically disadvantaged” persons in the labor market (previously unemployed or low earnings)

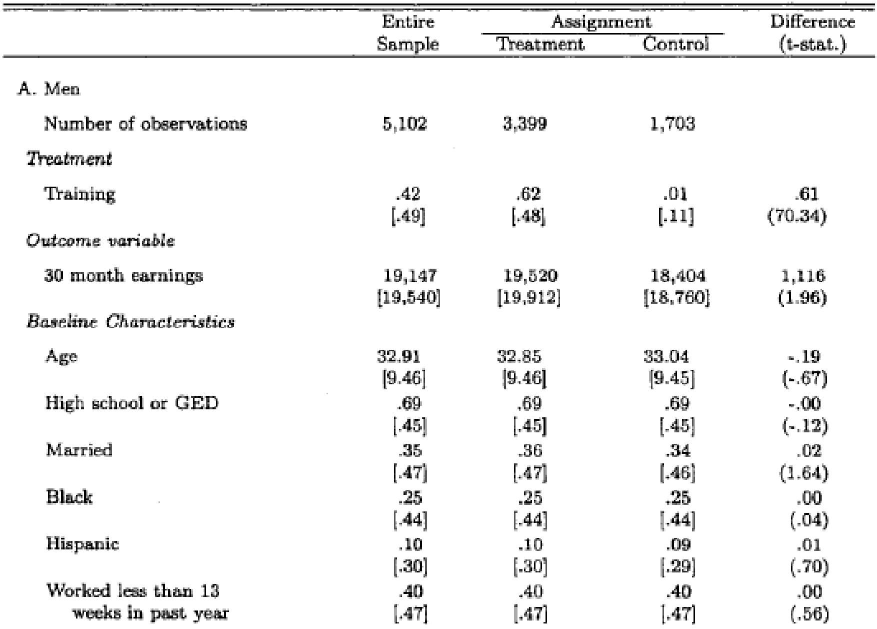
$D$: (Invitation) to one of three general service strategies:

- classroom training in occupational skills
- on-the-job training and/or job search assistance
- other services (eg. probationary employment)

$Y$: earnings 30 month following assignment

$X$: Characteristics measured before assignment (age, gender, previous earnings, race, etc.)

# Means and Standard Deviations for JTPA Experiment



| | Entire Sample | Assignment | | Difference (t-stat.) |
|---|---|---|---|---|
| | | Treatment | Control | |
| A. Men | | | | |
| Number of observations | 5,102 | 3,399 | 1,703 | |
| *Treatment* | | | | |
| Training | .42<br>[.49] | .62<br>[.48] | .01<br>[.11] | .61<br>(70.34) |
| *Outcome variable* | | | | |
| 30 month earnings | 19,147<br>[19,540] | 19,520<br>[19,912] | 18,404<br>[18,760] | 1,116<br>(1.96) |
| *Baseline Characteristics* | | | | |
| Age | 32.91<br>[9.46] | 32.85<br>[9.46] | 33.04<br>[9.45] | -.19<br>(-.67) |
| High school or GED | .69<br>[.45] | .69<br>[.45] | .69<br>[.45] | -.00<br>(-.12) |
| Married | .35<br>[.47] | .36<br>[.47] | .34<br>[.46] | .02<br>(1.64) |
| Black | .25<br>[.44] | .25<br>[.44] | .25<br>[.44] | .00<br>(.04) |
| Hispanic | .10<br>[.30] | .10<br>[.30] | .09<br>[.29] | .01<br>(.70) |
| Worked less than 13 weeks in past year | .40<br>[.47] | .40<br>[.47] | .40<br>[.47] | .00<br>(.56) |

# JTPA Experiment: Estimated effects separately by group

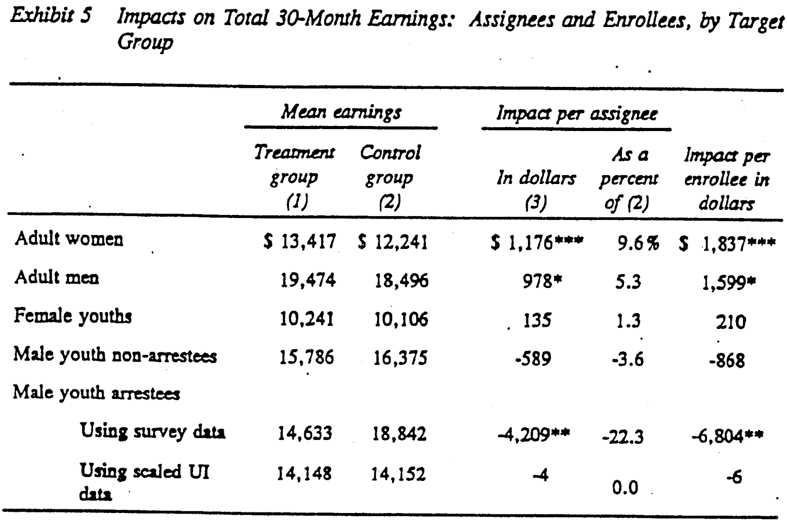


*Exhibit 5* *Impacts on Total 30-Month Earnings: Assignees and Enrollees, by Target Group*

| | *Mean earnings* | | *Impact per assignee* | | |
|---|---|---|---|---|---|
| | *Treatment group (1)* | *Control group (2)* | *In dollars (3)* | *As a percent of (2)* | *Impact per enrollee in dollars* |
| Adult women | $ 13,417 | $ 12,241 | $ 1,176*** | 9.6% | $ 1,837*** |
| Adult men | 19,474 | 18,496 | 978* | 5.3 | 1,599* |
| Female youths | 10,241 | 10,106 | 135 | 1.3 | 210 |
| Male youth non-arrestees | 15,786 | 16,375 | -589 | -3.6 | -868 |
| Male youth arrestees | | | | | |
| Using survey data | 14,633 | 18,842 | -4,209** | -22.3 | -6,804** |
| Using scaled UI data | 14,148 | 14,152 | -4 | 0.0 | -6 |

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# Some Other Randomization Schemes

The completely randomized design is only one option:

- Stratified (conditional, blocked) randomized experiment are randomized separately within levels of some covariate(s) $X$
  - e.g. separately for men and women
  - An extreme version is a pairwise randomized experiment: Each stratum (block) contains 2 units, one assigned to treatment, the other to control.
  - Stratification will be an important concept when we move on to observational assignment mechanisms.
- Cluster randomized experiments randomize units in groups. Every unit within a group (called a cluster) gets the same treatment level.
  - e.g. randomizing whole villages of people or whole classrooms of pupils.
- Cross-over experiments have units switch treatment status over time.
  - e.g. varying treatments for sick patients over time.