PS207 Quantitative Causal Inference

Selection on Observables

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Observational Studies

- Randomization allows unbiased estimation of $\mathbb{E}[Y_{0i}|D_i = 1]$ via $\mathbb{E}[Y_{0i}|D_i = 0]$ and $\mathbb{E}[Y_{1i}|D_i = 0]$ via $\mathbb{E}[Y_{1i}|D_i = 1]$.

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- What is your strategy for identifying the missing potential outcomes from observational data?
- What assumptions does it involve? Can we weaken these?
- Are they credible? Which of them can we test?

The Good, the Bad, and the Ugly

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  Can convincingly answer the following question: Why do two units who are identical on measured covariates receive different treatments?

- Poorer Observational Study: Hard to say when treatment began or what the treatment really is. Distinction between covariates and outcomes is blurred. No precise knowledge of assignment mechanism

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- Poorer Observational Study: No attention given to assignment process, units self-select into treatment based on potential outcomes

The Good, the Bad, and the Ugly

Were treated and controls comparable?

- Randomized Experiment: Balance table for observables.
- Better Observational Study: Balance table for observables. Ideally sensitivity analysis for unobservables.
- Poorer Observational Study: No direct assessment of comparability is presented.

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Eliminating plausible alternatives to treatment effects?

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- Better Observational Study: List plausible alternatives and study design includes features that shed light on these alternatives (e.g. multiple control groups, longitudinal covariate data, etc.). Rules out some alternatives, examines sensitivitiy. Requires more work than in experiment since there are usually many more alternatives.

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- Poorer Observational Study: Alternatives are mentioned in discussion section of the paper or not at all. Over-sells causal claim.

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- Multiple control groups that are know to differ on unobservables
- Sensitivity analysis and bounds

Outline

1. Identification under Conditional Ignorability
2. Estimation by Subclassification
3. Matching
   - Matching in X
   - Measuring Distance
   - Balance
   - Variance Estimation
   - Matching Functions
   - Example: Blattman and Annan (2009)

Pre-treatment Covariates

- Units: $i = 1, ..., n$
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  Question: Can we identify τ_{ATE} and τ_{ATT} when D_i is not randomized?

- Pre-treatment covariates: $X_i = [X_{i1}, ..., X_{iK}]^\top \in \mathcal{X}$
  - Predetermined and causally precedent with respect to D_i
  - Examples: Sex, race, age, etc.
  - X_i may be correlated with both D_i and $Y_i(d)$, thereby confounding the causal relationship
  - Excludes correlates that are potentially affected by D_i (post-treatment covariates)

Conditional Ignorability

Recall that randomized experiments work because:

$$\{Y_i(0), Y_i(1)\} \perp\!\!\!\perp D_i$$

Assumption: Conditional Ignorability

$$\{Y_i(0), Y_i(1)\} \perp\!\!\!\perp D_i \mid X_i = x \quad \text{for any} \quad x \in \mathcal{X}$$

(a.k.a. exogeneity, unconfoundedness, selection on observables, no omitted variables)

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Assumption: Common Support

$$0 < \Pr(D_i = 1 \mid X_i = x) < 1 \quad \text{for any} \quad x \in \mathcal{X}$$

Read: For any value of X_i, unit could have received treatment or control

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Part 1. Identifiability of $\tau(X)$:

$$\begin{aligned}\mathbb{E}[Y_{1i} - Y_{0i}|X_i = x] &= \mathbb{E}[Y_{1i}|X_i = x, D_i = 1] - \mathbb{E}[Y_{0i}|X_i = x, D_i = 0] \\ &= \mathbb{E}[Y_i|X_i = x, D_i = 1] - \mathbb{E}[Y_i|X_i = x, D_i = 0] \\ &= \mathbb{E}[\hat{\tau}|X_i]\end{aligned}$$

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Part 2. Common support gets you back to τ:

$$\begin{aligned}\tau_{ATE} &= \mathbb{E}[Y_{1i} - Y_{0i}] \\ &= \mathbb{E}\Big[\mathbb{E}[Y_{1i} - Y_{0i}|X_i]\Big] \quad \text{Why?} \\ &= \int \Big(\mathbb{E}[Y_i|D_i = 1, X_i = x] - \mathbb{E}[Y_i|D_i = 0, X_i = x]\Big)p(x)dX \\ &= \mathbb{E}\Big[\mathbb{E}[\hat{\tau}|X_i]\Big] = \mathbb{E}[\hat{\tau}]\end{aligned}$$

Identification of ATT

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&= \int \mathbb{E}[Y_i(1) - Y_i(0) \mid X_i = x, D_i = 1] p(x \mid D_i = 1) dx \\
&= \int \{\mathbb{E}[Y_i \mid X_i = x, D_i = 1] - \mathbb{E}[Y_i \mid X_i = x, D_i = 0]\} p(x \mid D_i = 1) dx \\
&= \mathbb{E}[\hat{\tau}(x) \mid D_i = 1].
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Is $\tau_{ATE} = \tau_{ATT}$ when CI holds?

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- Because M_i is potentially affected by the treatment, the *observed* post-treatment covariate only equals one of its *potential* value:

$$M_i = D_i M_i(1) + (1 - D_i) M_i(0)$$

Therefore, we have a mismatch problem:

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  - but then we would not be concerned with controlling for M_i!
- Better to think of post-treatment outcomes of potential mediators, a topic we will come back to.

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Two challenges remain:

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- matching: with and without propensity score
- re-weighting: with and without propensity score
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For now: the most natural, sub-classification

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1. Identification under Conditional Ignorability
2. Estimation by Subclassification
3. Matching
   - Matching in X
   - Measuring Distance
   - Balance
   - Variance Estimation
   - Matching Functions
   - Example: Blattman and Annan (2009)

Identification Results for Discrete Covariates

If X_i is discrete, the identification results can be rewritten as:

$$\tau_{ATE} = \sum_{x \in \mathcal{X}} \{\mathbb{E}[Y_i \mid D_i = 1, X_i = x] - \mathbb{E}[Y_i \mid D_i = 0, X_i = x]\} \Pr(X_i = x)$$

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So τ_{ATE} can be calculated by:

(1) Group units into strata (or cells) defined by the values of X_i.

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τ_{ATT} can be calculated similarly:

(1) $\cdot$ (2) Same as (1) $\cdot$ (2) for ATE.

(3) Calculate the weighted average of (2), with weights equal to the proportions of units in the strata within the treatment group.

Subclassification Estimators

This gives us the subclassification estimators:

$$\hat{\tau}_{ATE} = \sum_{j=1}^{M} \left\{ \overline{Y}_{1j} - \overline{Y}_{0j} \right\} \frac{n_j}{n}$$

$$\hat{\tau}_{ATT} = \sum_{j=1}^{M} \left\{ \overline{Y}_{1j} - \overline{Y}_{0j} \right\} \frac{n_{1j}}{n_1}$$

where
$$\begin{cases} M = \text{\# of strata} \\ n_j = \text{\# of units in cell } j \\ n_{1j} = \text{\# of treated units in cell } j \\ \overline{Y}_{dj} = \text{mean outcome for units with } D_i = d \text{ in cell } j \end{cases}$$

Example: Smoking and Mortality (Cochran 1968)

TABLE 1

DEATH RATES PER 1,000 PERSON-YEARS

Smoking group	Canada	U.K.	U.S.
Non-smokers	20.2	11.3	13.5
Cigarettes	20.5	14.1	13.5
Cigars/pipes	35.5	20.7	17.4

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TABLE 2

MEAN AGES, YEARS

Smoking group	Canada	U.K.	U.S.
Non-smokers	54.9	49.1	57.0
Cigarettes	50.5	49.8	53.2
Cigars/pipes	65.9	55.7	59.7

Subclassification: Example

	Death Rates Pipe Smokers	# Pipe-Smokers	# Non-Smokers
Age 20 - 50	15	11	29
Age 50 - 70	35	13	9
Age + 70	50	16	2
Total		40	40

What is the average death rate for Pipe Smokers?

Subclassification: Example

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Age 20 - 50	15	11	29
Age 50 - 70	35	13	9
Age + 70	50	16	2
Total		40	40

What is the average death rate for Pipe Smokers?

$15 \cdot (11/40) + 35 \cdot (13/40) + 50 \cdot (16/40) = 35.5$

Subclassification: Example

	Death Rates Pipe Smokers	# Pipe-Smokers	# Non-Smokers
Age 20 - 50	15	11	29
Age 50 - 70	35	13	9
Age + 70	50	16	2
Total		40	40

What is the average death rate for Pipe Smokers if they had same age distribution as Non-Smokers?

Subclassification: Example

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Age 20 - 50	15	11	29
Age 50 - 70	35	13	9
Age + 70	50	16	2
Total		40	40

What is the average death rate for Pipe Smokers if they had same age distribution as Non-Smokers?

$15 \cdot (29/40) + 35 \cdot (9/40) + 50 \cdot (2/40) = 21.2$

Smoking and Mortality (Cochran (1968))

TABLE 3

ADJUSTED DEATH RATES USING 3 AGE GROUPS

Smoking group	Canada	U.K.	U.S.
Non-smokers	20.2	11.3	13.5
Cigarettes	28.3	12.8	17.7
Cigars/pipes	21.2	12.0	14.2

Subclassification by Age ($M = 2$)

X_j	Death Rate Smokers	Death Rate Non-Smokers	# Smokers	# Obs.
Old	28	24	3	10
Young	22	16	7	10
Total			10	20

Subclassification by Age ($M = 2$)

X_j	Death Rate Smokers	Death Rate Non-Smokers	# Smokers	# Obs.
Old	28	24	3	10
Young	22	16	7	10
Total			10	20

What would the (unadjusted) difference in mean death rates for smokers versus non-smokers be?

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What would the (unadjusted) difference in mean death rates for smokers versus non-smokers be? 6

What is the subclassification estimator for the ATE of smoking?

$$\hat{\tau}_{ATE} = (28 - 24) \cdot \frac{10}{20} + (22 - 16) \cdot \frac{10}{20} = 5$$

Subclassification by Age and Gender ($M = 4$)

X_j	Death Rate Smokers	Death Rate Non-Smokers	# Smokers	# Obs.
Old, Male	28	22	3	7
Old, Female		24	0	3
Young, Male	21	16	3	4
Young, Female	23	17	4	6
Total			10	20

What is the subclassification estimate for the ATE of smoking on death rate?

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X_j	Death Rate Smokers	Death Rate Non-Smokers	# Smokers	# Obs.
Old, Male	28	22	3	7
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Total			10	20

What is the subclassification estimate for the ATE of smoking on death rate?

Not identified! (because of the lack of common support)

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X_j	Death Rate Smokers	Death Rate Non-Smokers	# Smokers	# Obs.
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What is the subclassification estimate for the ATT of smoking on death rate?

$$\begin{aligned}\hat{\tau}_{ATT} &= (28-22)\cdot\frac{3}{10}+(21-16)\cdot\frac{3}{10}+(23-17)\cdot\frac{4}{10}\\ &= 5.1\end{aligned}$$

Food for thought

The primary difficulty with this approach is believing the assumptions.

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Why do you think sub-classification is of limited use in most real applications?

Summary

- Causal inference in observational studies often rests on this "SOO" (or CI) assumption

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Next up: more estimation strategies, same assumptions. Matching, weighting, regression.

Outline

1 Identification under Conditional Ignorability

2 Estimation by Subclassification

3 Matching
- Matching in X
- Measuring Distance
- Balance
- Variance Estimation
- Matching Functions
- Example: Blattman and Annan (2009)

SOO: Identification and Estimation

Recall the SOO identification assumption:

Assumption: Conditional Ignorability

$$\{Y_i(0), Y_i(1)\} \perp\!\!\!\perp D_i \mid X_i = x \quad \text{for any} \quad x \in \mathcal{X}$$

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Some methods do this quite literally:

- sub-classification
- matching

Matching is Not an Identification Strategy

ATT Estimation by Matching

- For each treated unit i with covariates X_i, you would like to estimate $\tau_i = Y_{1i} - Y_{0i}$.

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We can also use the average of M closest matches:

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Does SOO assumption guarantee that this gets you the *ATT*?

Matching: Example with a Single X

unit	Potential Outcome under Treatment	Potential Outcome under Control		
i	Y_{1i}	Y_{0i}	D_i	X_i
1	6	?	1	3
2	1	?	1	1
3	0	?	1	10
4		0	0	2
5		9	0	3
6		1	0	-2
7		1	0	-4

What is $\widehat{\tau}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left(Y_i - Y_{j(i)} \right)$?

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7		1	0	-4

What is $\widehat{\tau}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left(Y_i - Y_{j(i)} \right)$?

$\widehat{\tau}_{ATT} = 1/3 \cdot (6 - 9) + 1/3 \cdot (1 - 0) + 1/3 \cdot (0 - 9) = -3.7$

Common Distance Metrics

What do we mean by "closeness" in X when it is multi-dimensional?

Covariate vectors for i, j: $X_i = [X_i^{(1)}, X_i^{(2)}, ..., X_i^{(k)}]^\top$ and $X_j = [X_j^{(1)}, X_j^{(2)}, ..., X_j^{(k)}]^\top$

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Some common options:

1. Euclidean distance:

$$||X_i - X_j|| = \sqrt{(X_i - X_j)^\top (X_i - X_j)}$$
$$= [(X_i^{(1)} - X_j^{(1)})^2 + ... + (X_i^{(P)} - X_j^{(P)})^2]^{\frac{1}{2}}$$

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2. "StataD" (`nnmatch`)/default in `Match()` for `R`: rescaled Euclidean

$$StataD(X_i, X_j) = \sqrt{(X_i - X_j)^\top diag(\Sigma_X^{-1})(X_i - X_j)}$$

where Σ is the Variance-Covariance-Matrix. Invariant to rescaling of X

Common Distance Metrics

3. Mahalanobis distance:

$$MD(X_i, X_j) = \sqrt{(X_i - X_j)^\top \Sigma^{-1} (X_i - X_j)}$$

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4. GeneticD (`GenMatch`):

$$GeneticD(X_i, X_j) = \sqrt{(X_i - X_j)^\top (S^{-1/2})^\top \, W \, S^{-1/2} (X_i - X_j)}$$

where W is a $(P \times P)$ positive definite weight matrix with zeros in off-diagonals, controlling "variable importance"

Mahalanobis Distance: Example

	X_1	X_2
Treated	0	0
Control A	2	2
Control B	1.8	0

$$X_T = \begin{pmatrix} 0 & 0 \end{pmatrix}^\top \quad X_A = \begin{pmatrix} 2 & 2 \end{pmatrix}^\top \quad X_B = \begin{pmatrix} 1.8 & 0 \end{pmatrix}^\top$$

$$\Sigma = \begin{pmatrix} & X^{(1)} & X^{(2)} \\ X^{(1)} & 1 & .9 \\ X^{(2)} & .9 & 1 \end{pmatrix}$$

Which control is closer?

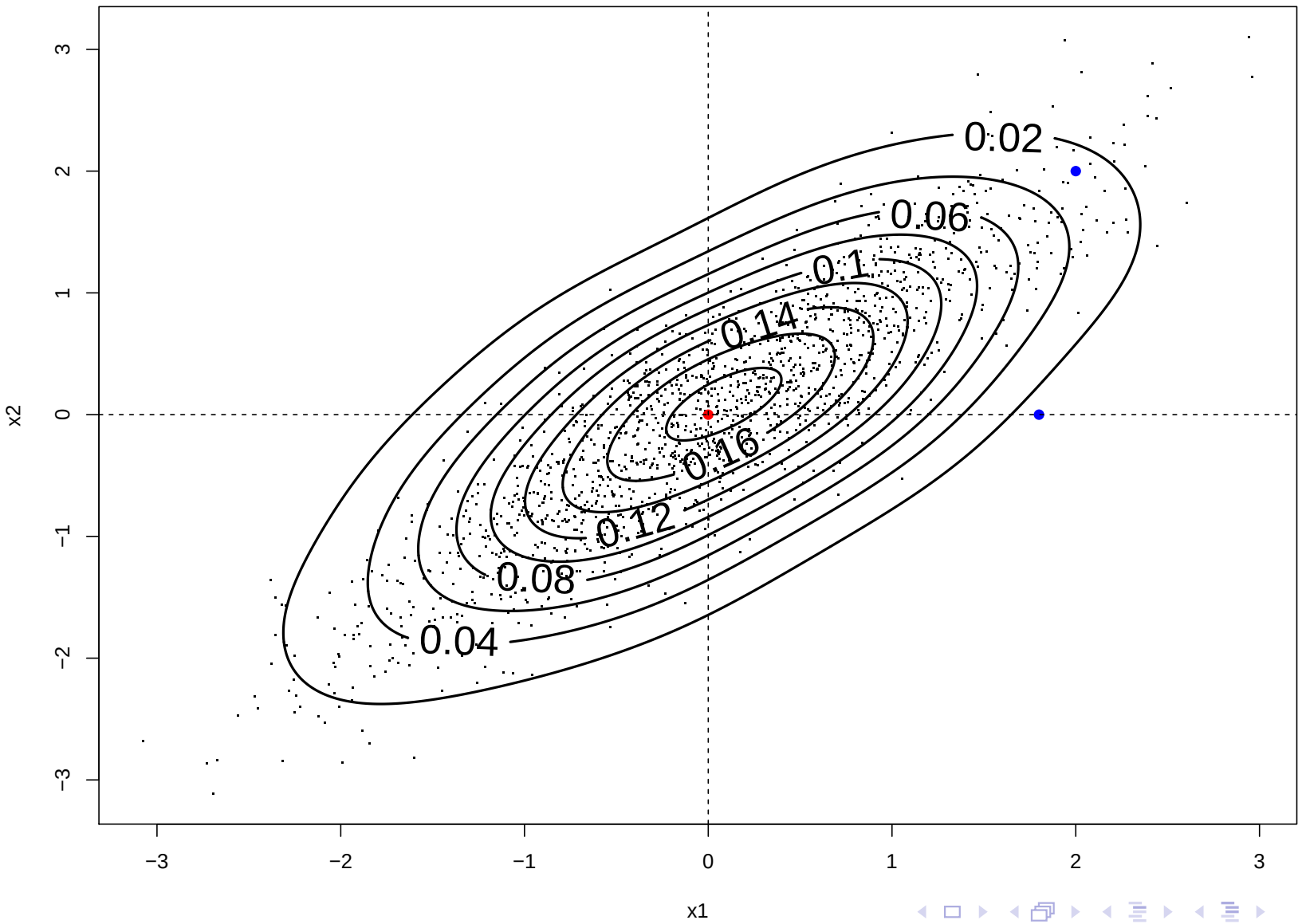
Mahalanobis Distance

$$X_T = \begin{pmatrix} 0 & 0 \end{pmatrix}^\top \quad X_A = \begin{pmatrix} 2 & 2 \end{pmatrix}^\top \quad X_B = \begin{pmatrix} 1.8 & 0 \end{pmatrix}^\top \quad \Sigma = \begin{pmatrix} & X^{(1)} & X^{(2)} \\ X^{(1)} & 1 & .9 \\ X^{(2)} & .9 & 1 \end{pmatrix}$$

$$\begin{aligned} MD(X_A, X_T) &= \sqrt{(X_A - X_T)^\top \Sigma^{-1} (X_A - X_T)} \\ &= \sqrt{[\begin{pmatrix} 2 & 2 \end{pmatrix} - \begin{pmatrix} 0 & 0 \end{pmatrix}] \begin{pmatrix} 1 & .9 \\ .9 & 1 \end{pmatrix}^{-1} [\begin{pmatrix} 2 & 2 \end{pmatrix} - \begin{pmatrix} 0 & 0 \end{pmatrix}]^\top} \\ &= \sqrt{\begin{bmatrix} 2 & 2 \end{bmatrix} \begin{pmatrix} 5.2 & -4.7 \\ -4.7 & 5.2 \end{pmatrix} \begin{bmatrix} 2 & 2 \end{bmatrix}^\top} \\ &= 4.2 \\ MD(X_B, X_T) &= \sqrt{\begin{bmatrix} 1.8 & 0 \end{bmatrix} \begin{pmatrix} 5.2 & -4.7 \\ -4.7 & 5.2 \end{pmatrix} \begin{bmatrix} 1.8 & 0 \end{bmatrix}^\top} \\ &= 17 \end{aligned}$$

With $StataD(X_A, X_T) = \sqrt{(X_i - X_T)^\top diag(\Sigma_X^{-1})(X_i - X_T)}$ we find $StataD(X_A, X_T) = 84$ and $StataD(X_B, X_T) = 17$ since correlation is ignored.

Mahalanobis Distance



Local Methods and the Curse of Dimensionality

Big Problem: the volume increases exponentially when adding extra dimensions

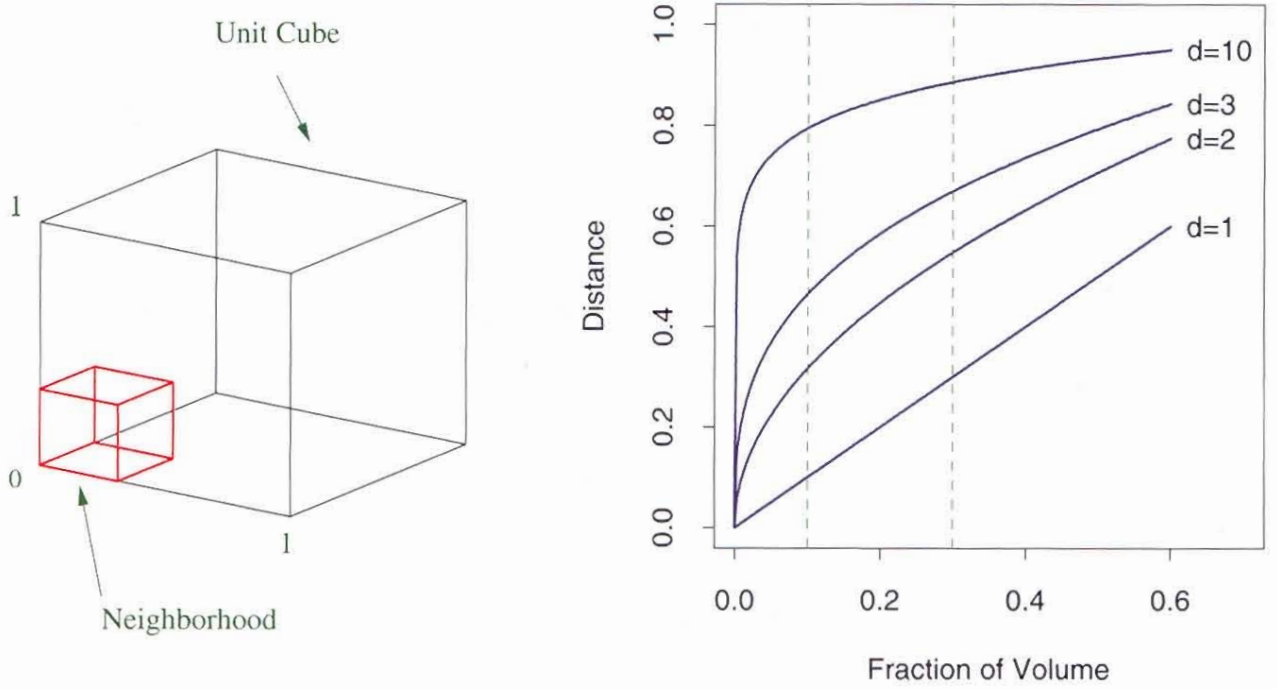


FIGURE 2.6. *The curse of dimensionality is well illustrated by a subcubical neighborhood for uniform data in a unit cube. The figure on the right shows the side-length of the subcube needed to capture a fraction r of the volume of the data, for different dimensions p. In ten dimensions we need to cover 80% of the range of each coordinate to capture 10% of the data.*

Matching with Bias Correction

Weakness of matching: discrepancy=$||X_i - X_{j(1)}||_d > 0$

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Compromise: adjust for discrepancy:

- On average, Y_{0j} differs from Y_{0i} by $\mathbb{E}[Y_0|X_i] - \mathbb{E}[Y_0|X_{j(i)}]$
- Consider population regression function $\mu_0(X) = \mathbb{E}[Y_0|X]$
- Let's estimate $\hat{\mu}_0$ by OLS regression of Y on X among controls

$$\hat{\mu}_0(X) = \beta_0 + \beta_1 X$$

Matching with Bias Correction

So subtract off estimated discrepancy on Y_0 from each pair (Abadie & Imbens, 2005)

$$\tilde{\tau}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} (Y_i - Y_{j(i)}) - (\widehat{\mu}_0(X_i) - \widehat{\mu}_0(X_{j(i)})),$$

- these "bias-corrected" matching estimators are an improvement even if $\hat{\mu}_0$ is misspecified
- the large sample distribution of this estimator (for the case of matching with replacement) is roughly normal.

In R: `Match(Y,Tr, X,BiasAdjust = TRUE)`

Bias Adjustment with Matched Data

unit	Potential Outcome under Treatment	Potential Outcome under Control		
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5		9	0	3
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What is $\tilde{\tau}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \Big((Y_i - Y_{j(i)}) - (\widehat{\mu}_0(X_i) - \widehat{\mu}_0(X_{j(i)})) \Big)$?

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Estimate $\widehat{\mu}_0(x) = \beta_0 + \beta_1 x = 5 - .4x$.

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Estimate $\widehat{\mu}_0(x) = \beta_0 + \beta_1 x = 5 - .4x$. Now plug in:

$$\begin{aligned} \widehat{\tau}_{ATT} &= 1/3\{((6-9) - (\widehat{\mu}_0(3) - \widehat{\mu}_0(3))) \\ &+ ((1-0) - (\widehat{\mu}_0(1) - \widehat{\mu}_0(2))) \\ &+ ((0-1) - (\widehat{\mu}_0(10) - \widehat{\mu}_0(8)))\} \\ &= -0.86 \end{aligned}$$

(Unadjusted: $1/3((6-9) + (1-0) + (0-1)) = -1$)

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- With or Without Replacement?

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- How many matches?
- Which Matching Algorithm?
  - genetic matching, kernel Matching, full matching
  - coarsened exact matching
  - matching as pre-processing
  - propensity score matching
- Good rule: use whatever gives you the best balance! Checking balance is important to get a sense for how much extrapolation is needed
  - should check balance on interactions and higher moments
- With insufficient overlap, all adjustment methods are problematic because we have rely on a model to impute missing potential outcomes.

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- Ideally, compare the joint distribution of all X_i between the treated and untreated in the matched sample

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Workflow:

- Estimate $\rightarrow$ Check Balance $\rightarrow$ Re-estimate $\rightarrow$ Check Balance $\rightarrow \cdots$ (ad infinitum until you get a good balance)
- Is this data snooping? No, because inference remains blind to Y

Kolmogorov-Smirnov (KS) Test

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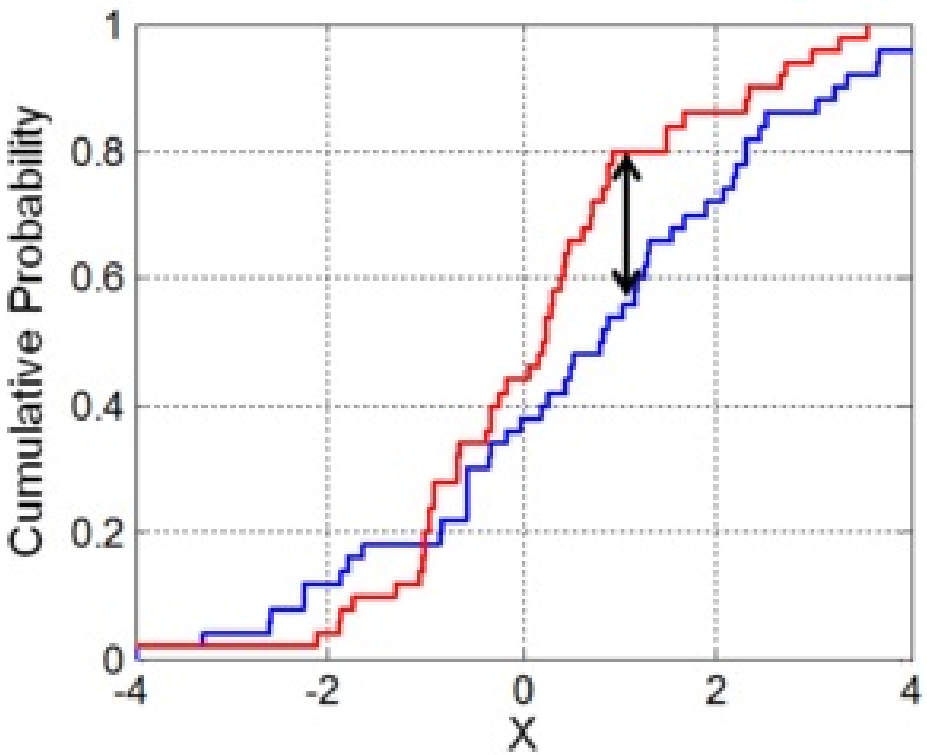

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Under the null, D has the Kolmogorov distribution as $n \to \infty$.

Reject the null at level α if

$$\frac{D}{\sqrt{(n_1 + n_0)/n_1 n_0}} > c_\alpha$$

level (α)	.1	.05	.01
critical value (c_α)	1.22	1.36	1.63

Balance Checks

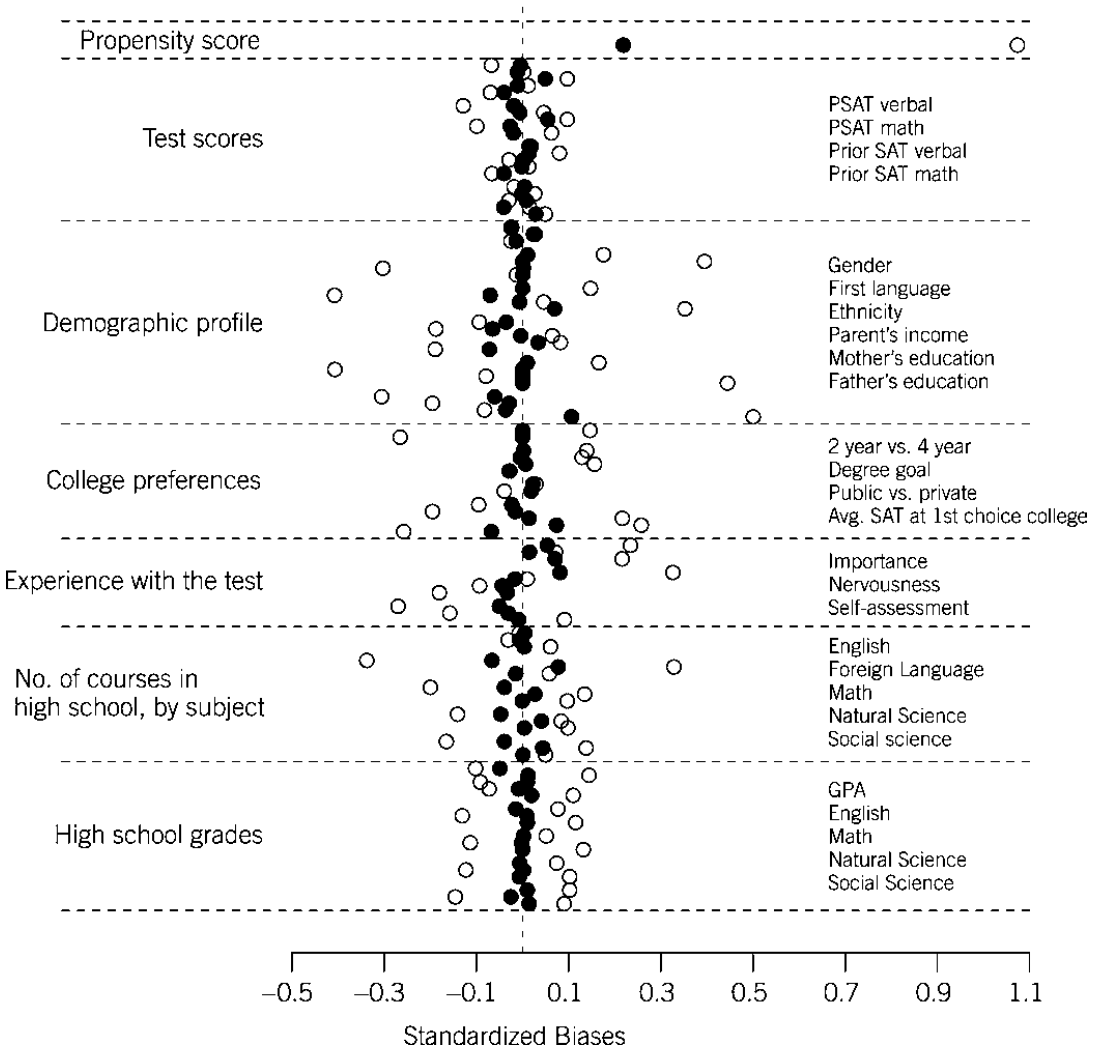

Figure 3. Standardized Biases Without Stratification or Matching, Open Circles, and Under the Optimal [.5, 2] Full Match, Shaded Circles.

Balance Checks

TABLE 2. Balance Summary Statistics and Tests: Russian and Chechen Sweeps

Pretreatment Covariates	Mean Treated	Mean Control	Mean Difference	Std. Bias	Rank Sum Test	K-S Test
Demographics						
Population	8.657	8.606	0.049	0.033	0.708	0.454
Tariqa	0.076	0.048	0.028	0.104	0.331	—
Poverty	1.917	1.931	−0.016	−0.024	0.792	1.000
Spatial						
Elevation	5.078	5.233	−0.155	−0.135	0.140	0.228
Isolation	1.007	1.070	−0.063	−0.096	0.343	0.851
Groznyy	0.131	0.138	−0.007	−0.018	0.864	—
War Dynamics						
TAC	0.241	0.282	−0.041	−0.095	0.424	—
Garrison	0.379	0.414	−0.035	−0.072	0.549	—
Rebel	0.510	0.441	0.070	0.139	0.240	—
Selection						
Presweep violence	3.083	3.117	−0.034	0.009	0.454	0.292
Large-scale theft	0.034	0.055	−0.021	−0.115	0.395	—
Killing	0.117	0.090	0.027	0.084	0.443	—
Violence Inflicted						
Total abuse	0.970	0.833	0.137	0.124	0.131	0.454
Prior sweeps	1.729	1.812	−0.090	−0.089	0.394	0.367
Other						
Month	7.428	6.986	0.442	0.130	0.260	0.292
Year	2004.159	2004.110	0.049	0.043	0.889	1.000

Note: 145 matched pairs. Matching with replacement.

Variance of the Matching Estimator

Option 1. Ignore the matching uncertainty and estimate the SEs from whatever model you run on the matched sample

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- NO. Not consistent
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Option 3. Abadie-Imbens asymptotic SEs

- uses matched pairs to estimate local variance in Y_0 and takes weighted sum that accounts for matching
- provided by `Match()` package.
- generally use these
- but still an open area of research

Useful Matching Functions

The workhorse model is the `Match()` function in the `Matching` package:

```
Match(Y = NULL, Tr, X, Z = X, V = rep(1, length(Y)),
    estimand = "ATT", M = 1, BiasAdjust = FALSE, exact = NULL,
    caliper = NULL,  replace = TRUE, ties = TRUE,
    CommonSupport = FALSE, Weight = 1, Weight.matrix = NULL,
    weights = NULL, Var.calc = 0,  sample = FALSE, restrict = NULL
    match.out = NULL, distance.tolerance = 1e-05,
    tolerance = sqrt(.Machine$double.eps), version = "standard")
```

Default distance metric (`Weight=1`) is normalized Euclidean distance

- `MatchBalance(formu)` for balance checking
- `GenMatch()` for genetic matching

Example: Blattman and Annan (2009)

The Consequences of Child Soldiering. The Review of Economics and Statistics.

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ID Strategy: SOO. According to the logic by which abduction occurred, we will assume that abduction is indiscriminate, conditional on age and location.

> *Abduction was large-scale and seemingly indiscriminate; 60,000 to 80,000 youth are estimated to have been abducted and more than a quarter of males currently aged 14 to 30 in our study region were abducted for at least two weeks...*
>
> *Youth were typically taken by roving groups of 10 to 20 rebels during night raids on rural homes. Adolescent males appear to have been the most pliable, reliable and effective forced recruits, and so were disproportionately targeted by the LRA. Youth under age 11 and over 24 tended to be avoided and had a high probability of immediate release.*

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Data: panel survey of male youth in war-afflicted regions of Uganda.

- `abd`: abducted by the LRA (the treatment)
- `c_ach - c_pal`: Location indicators
- `age`: age in years
- `fthr_ed`,`mthr_ed` : father's/mother's education (years)
- `orphan96`: indicator if parent's died before 1997
- `hh_fthr_frm`: indicator if father is a farmer
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Now, to `R`.

Roadmap

1. Theory: Potential outcomes, identification, key quantities
2. Randomization
   - difference in means, variance estimation
   - covariate adjustment
   - blocking
   - cluster randomization
3. Selection on Observables
   - sub-classification
   - matching (on X)
   - weighting (on X)
   - matching and weighting on $Pr(D = 1)$ (propensity scores)
   - regression
4. Instrumental Variables
5. Regression Discontinuity
6. Difference in Differences and Synthetic Control
7. Sensitivity and Bounds

We have to keep saying this...

Assumption: Conditional Ignorability

$$\{Y_i(0), Y_i(1)\} \perp\!\!\!\perp D_i \mid X_i = x \quad \text{for any} \quad x \in \mathcal{X}$$

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- This will allow us to estimate things as if we have done so conditionally on X then averaged over some density in X

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Suggests "moving" treated and control to same density in X, then diff. in means

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$$\begin{aligned}\mathbb{E}[\hat{\tau}_{IPW}] &= \int \mathbb{E}[Y_i|D_i = 1, X_i]\frac{p(X|D = 1)p(D_i)}{p(D_i|X_i)}dx - \int \mathbb{E}[Y_i|D_i = 0, X_i]\frac{p(X|D_i = 0)p(D_i)}{p(D_i|X_i)}d \\ &= \int \mathbb{E}[Y_i|D_i = 1, X_i]p(X_i)dx - \int \mathbb{E}[Y_i|D_i = 0, X_i]p(X_i)dx\end{aligned}$$

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How convenient! These are the (stabilized) Inverse Propensity Score (IPW) weights.

- these are great in theory: not matching discrepancy to worry about, $dim(X)$ doesn't matter
- but require a model to get $p(D_i|X_i)$, so vulnerable to misspecification
- This is one view of propensity scores, $p(D_i = 1|X_i)$. More on that soon.

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Entropy balancing (Hainmueller, 2011) is one option (`ebal` in `R`), as well as generalized method of moments (GMM), empirical likelihood (EL)

Weighting for (mean) balance

Entropy balancing (and similar) try to find weights on control units s.t. the mean of X (and possible higher-order transforms) for controls matches that of treated.

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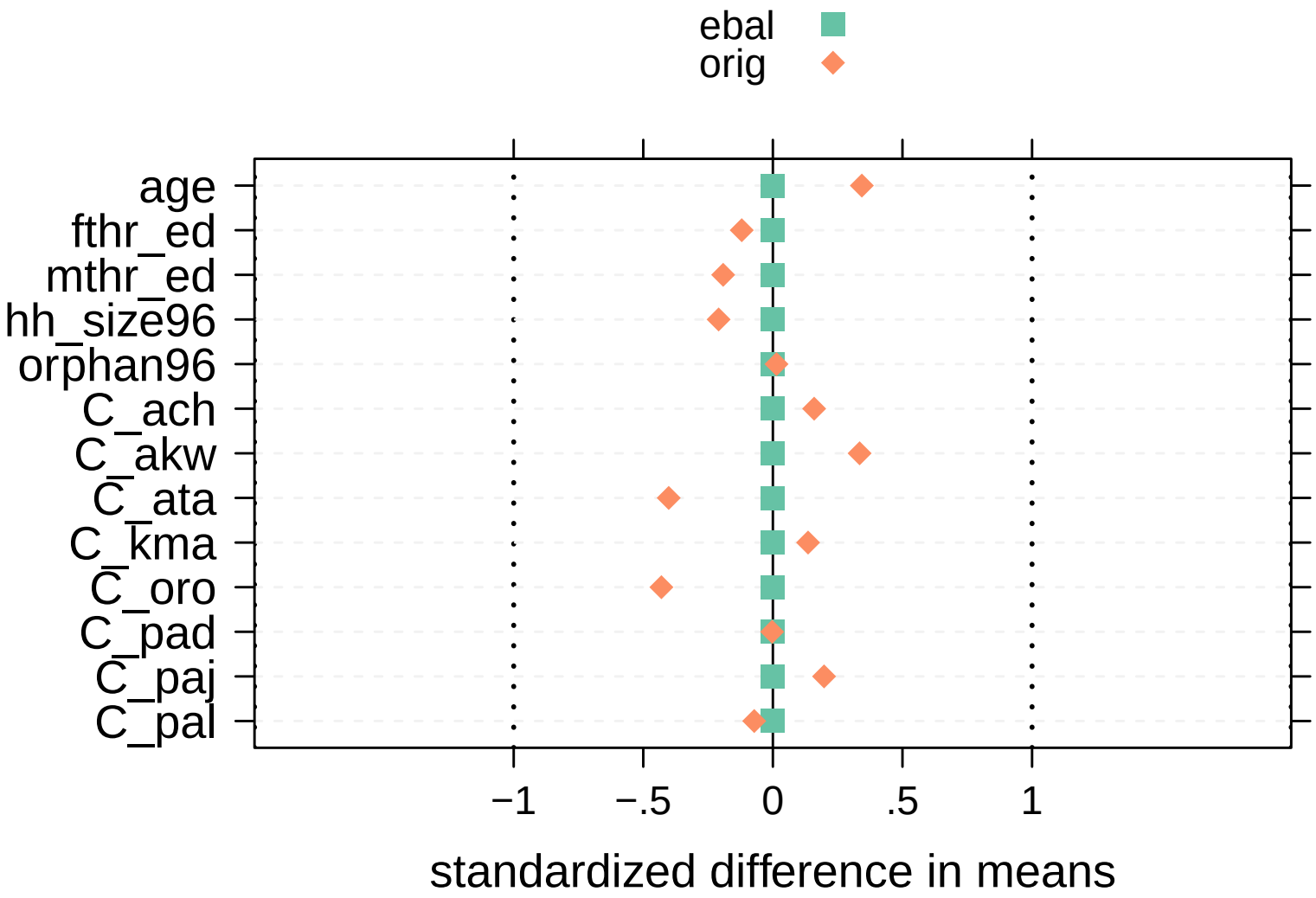
Resulting weights can be use to get weighted difference in means, or applied to any model (e.g. regression)

- Could also move treated to controls, or move both to common means
- Fast, often finds perfect mean balance, no iteration
- Can include higher order terms if you like
- Main downside: only getting balance on means or other included functions
- Standard errors are still an open question, but bootstrap has not been ruled out.

Now let's try it in `R`...

Balance on Blattman data with Ebal



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More commonly, we arrive at this idea through the propensity score:

Propensity Score

$$\text{Propensity Score} = \pi_i = p(D_i = 1|X_i)$$

Propensity Scores: Standard Motivation

- It can be hard to get close matches on X_i if X_i is multi-dimensional
- What if you could just match on a one-dimensional summary?

Conditioning on the Propensity Score

Under SOO and common support,

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The intuition:

- consider units with equal probabilities of getting the treatment as far as X can predict ($\pi(X_i)$ constant)
- recall SOO: conditionally on X, treatment is random
- now, conditionally on $\pi(X_i)$, $Pr(D = 1)$ does not depend on X.
- thus conditioning on $\pi(X)$ gets us random assignment (if SOO is true and $\pi(X)$ correct)
- See next slide for proof along these lines

Identification with Propensity Scores

Proof.

Show that $\Pr(D = 1 | Y_0, Y_1, \pi(X)) = \Pr(D = 1 | \pi(X)) = \pi(X)$, implying independence of (Y_0, Y_1) and D conditional on $\pi(X)$.

$$\Pr(D = 1 | Y_1, Y_0, \pi(X)) \quad = \quad \mathbb{E}[D | Y_1, Y_0, \pi(X)]$$

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Identification with Propensity Scores

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Using a similar argument

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therefore $\Pr(D = 1|Y_1, Y_0, \pi(X)) = \Pr(D = 1|\pi(X))$ □

Using Propensity Scores

Once estimated, you can match or weight on $\hat{\pi}_i$.

- Matching:
  - may need a *caliper* to trim cases without common support
  - or, some trim cases with extreme pscores by hand to improve common support
  - but beware, this changes your estimand
- Weighting
  - Simple IPW weights: $\frac{1}{p(D_i|X_i)} = \frac{1}{D_i\pi_i+(1-D_i)(1-\pi_i)}$
  - Stabilized IPW weights: $\frac{p(D_i)}{p(D_i|X_i)} = \frac{(D_i)Pr(D_i=1)+(1-D_i)(1-Pr(D_i0))}{(D_i)\pi_i+(1-D_i)(1-\pi_i)}$
  - But if using weights, check how extreme they get and how few units are doing most of the work

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Pros:

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Both at once:

Covariate balancing propensity scores (Imai, Ratkovic 2014)

Using Propensity Scores: Blattman & Annan

```
pi.out = glm(abd~age+fthr_ed+mthr_ed+hh_size96+orphan96+C_ach+C_akw+C_ata+
C_kma+C_oro+C_pad+C_paj+C_pal,data=dat,family="binomial"(link=logit))

matchout.pi=Match(Y=dat$educ,Tr=dat$abd,X=pi.out$fit,M=1,estimand="ATT")
summary(matchout.pi)

#Check balance
mb.out.pi =MatchBalance(match.out=matchout.pi,abd~age+fthr_ed+mthr_ed+
  hh_size96+orphan96+C_ach+C_akw+C_ata+C_kma+C_oro+C_pad+C_paj+C_pal,data=

btest_after_pi=baltest.collect(mb.out.pi,var.names=varnames,after=TRUE)

balancecompare.pi=cbind(round(btest[,c("mean.Tr","mean.Co","T pval","KS pv
                    round(btest_after_pi[,c("mean.Tr","mean.Co","T pval",
```

Using Propensity Scores: Blattman & Annan

balancecompare.pi

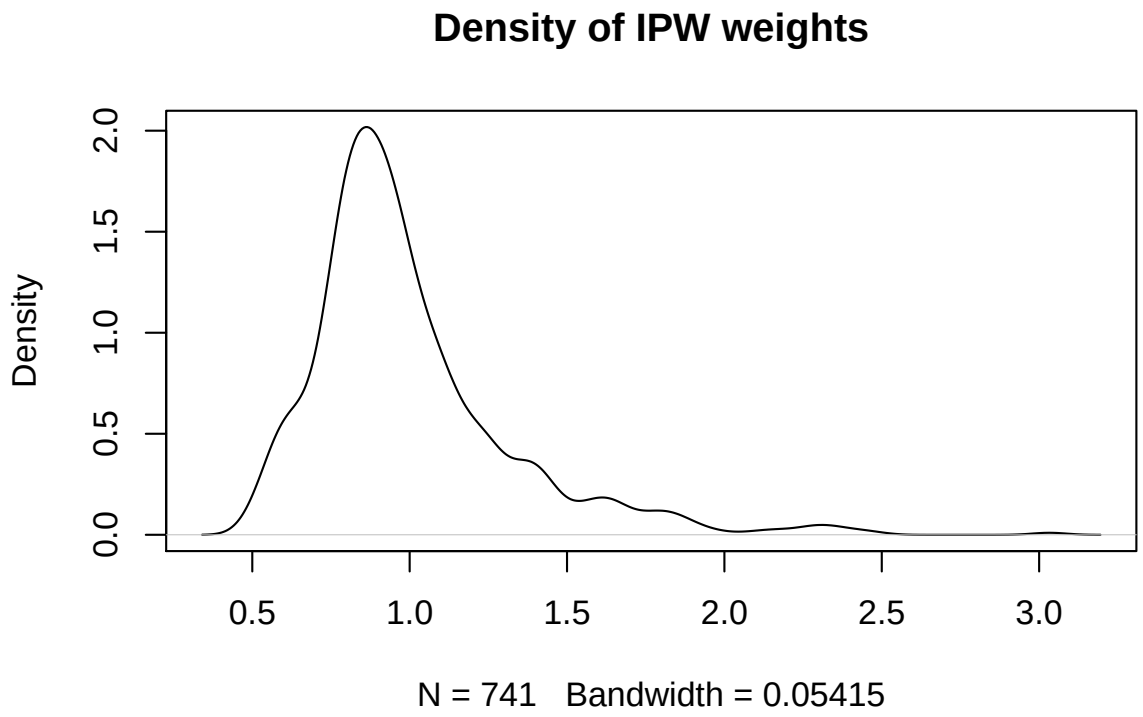
	mean.Tr	mean.Co	T pval	KS pval	mean.Tr	mean.Co	T pval	KS pval
age	21.37	20.15	0.00	0.00	21.37	21.04	0.27	0.17
fthr_ed	5.76	6.07	0.27	0.87	5.76	5.60	0.48	0.09
mthr_ed	2.09	2.49	0.09	0.35	2.09	2.40	0.11	0.20
hh_size96	8.09	8.70	0.06	0.04	8.09	8.02	0.79	0.03
orphan96	0.08	0.08	0.90	NA	0.08	0.11	0.07	NA
C_ach	0.15	0.11	0.13	NA	0.15	0.17	0.60	NA
C_akw	0.16	0.08	0.00	NA	0.16	0.17	0.62	NA
C_ata	0.10	0.20	0.00	NA	0.10	0.09	0.55	NA
C_kma	0.15	0.12	0.19	NA	0.15	0.16	0.87	NA
C_oro	0.05	0.14	0.00	NA	0.05	0.05	0.95	NA
C_pad	0.12	0.12	0.98	NA	0.12	0.09	0.10	NA
C_paj	0.15	0.10	0.06	NA	0.15	0.15	0.91	NA
C_pal	0.11	0.13	0.51	NA	0.11	0.13	0.45	NA

Using Propensity Scores: Blattman & Annan

Weighting on the propensity scores (stabilized IPW):

```
ps=pi.out$fit
D=dat$abd
PrD=mean(D)
IPW= (D*PrD+(1-D)*(1-PrD))/(D*ps+(1-D)*(1-ps))

#Good to check how crazy the weights are:
plot(density(IPW))
```



How does $p(\pi_i)$ look before/after weighting?

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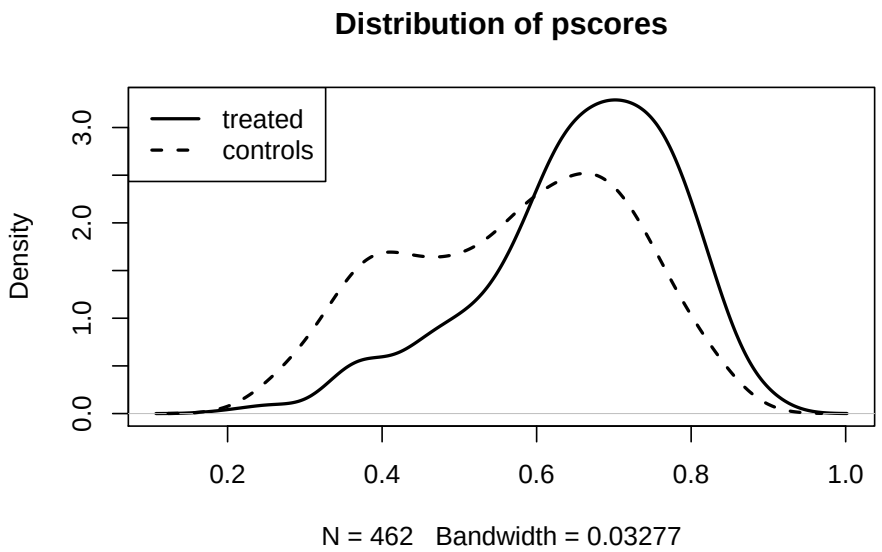
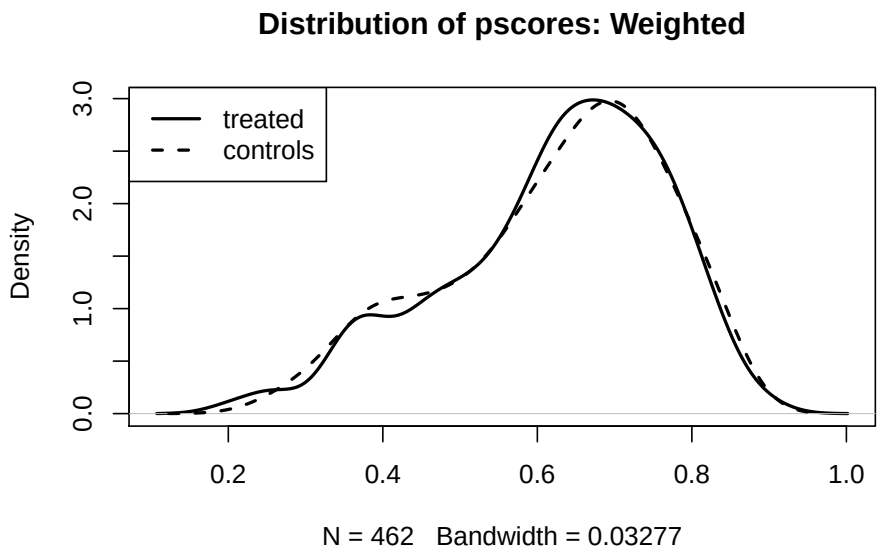
```
plot(density(pi.out$fit[D==1], weight=IPW[D==1]/sum(IPW[D==1])), lwd=2, ma
lines(density(pi.out$fit[D==0], weight=IPW[D==0]/sum(IPW[D==0])),lwd=2, lt
legend("topleft", legend=c("treated","controls"), lty=c(1,2), lwd=2)
```





Check Omnibus Balance

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```
omnibus.bal = lm(abd~age+fthr_ed+mthr_ed+hh_size96+orphan96+
                   C_ach+C_akw+C_ata+C_kma+C_oro+C_pad+C_paj+C_pal, data=dat)
summary(omnibus.bal)
#R2=0.08, F-statistic: 5.585 on 12 and 728 DF,  p-value: 3.303e-09
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                   C_ach+C_akw+C_ata+C_kma+C_oro+C_pad+C_paj+C_pal,
                   weight=IPW, data=dat)
summary(omnibus.bal.ipw)

Coefficients: (1 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  6.138e-01  1.058e-01   5.804 9.69e-09 ***
age          5.474e-04  3.691e-03   0.148    0.882
fthr_ed     -4.053e-04  5.352e-03  -0.076    0.940
mthr_ed     -2.116e-04  6.628e-03  -0.032    0.975
hh_size96    4.875e-04  4.689e-03   0.104    0.917
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...
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

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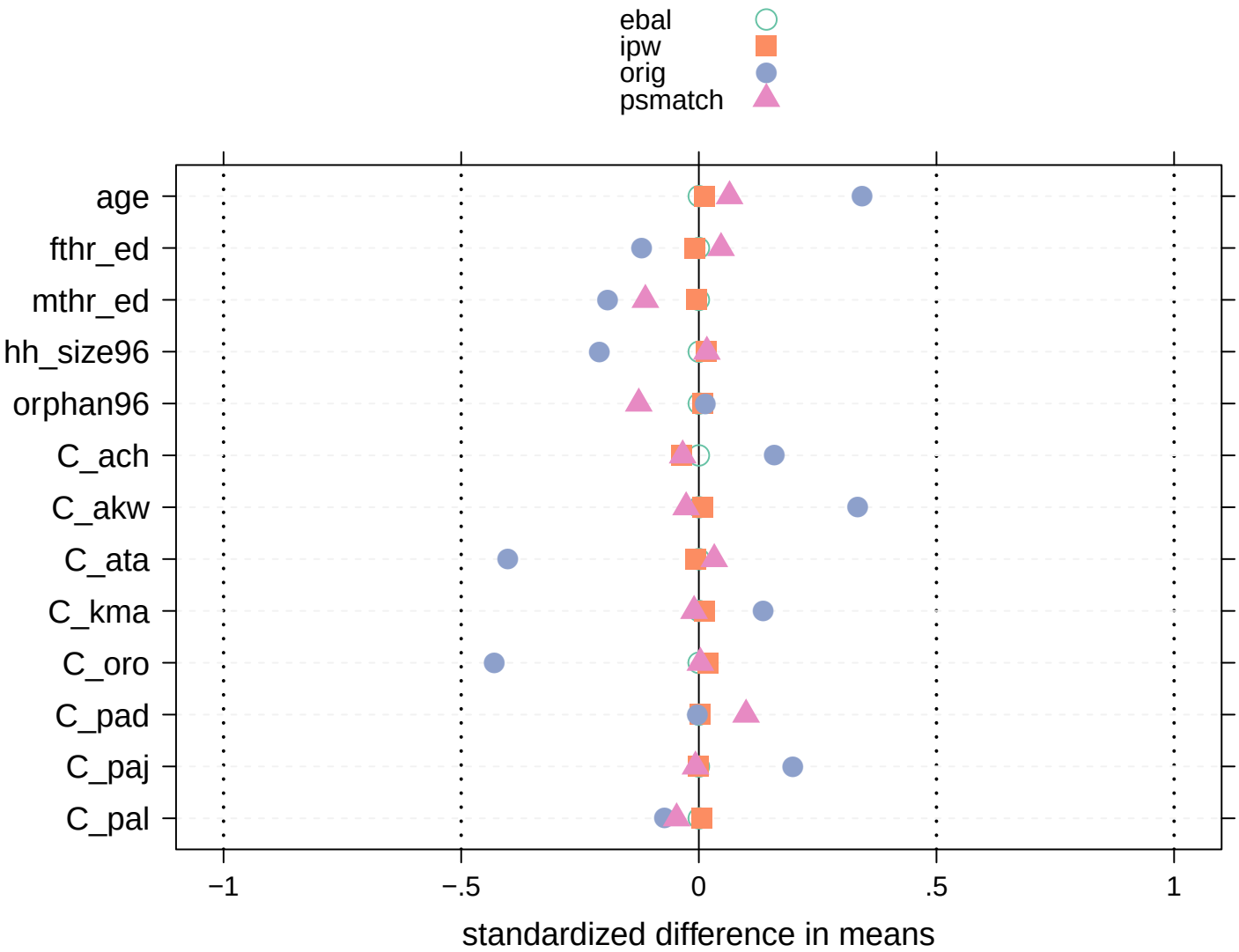
Yay!

Estimating the ATE with IPW weights

```
lm.out.naive = lm(educ~abd, data=dat)
lm.out.ipw = lm(educ~abd, weight=IPW, data=dat)
lm.out.ipw2=lm(educ~abd+age+fthr_ed+mthr_ed+hh_size96+orphan96+
    C_ach+C_akw+C_ata+C_kma+C_oro+C_pad+C_paj+C_pal,weight=IPW,data=dat)
```

	Dependent variable:		
	educ		
	(1)	(2)	(3)
abd	−0.595***	−0.726***	−0.735***
	(0.218)	(0.220)	(0.210)
Constant	7.416***	7.499***	6.113***
	(0.172)	(0.174)	(0.610)
Observations	741	741	741
R^2	0.010	0.014	0.128
Adjusted R^2	0.009	0.013	0.112
Residual Std. Error (df = 739)	2.876	2.904	2.754
Note:			*p<0.1; **p<0.05; ***p<0.01

Balance Plot after IPW



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- Which gives $\hat{\tau}(X) = \beta_1$. This implies the single model:

$$\mathbb{E}[Y_i \mid D_i, X_i] = \beta_0 + \beta_1 D_i + \gamma^\top X_i,$$

OLS as an Estimator of Causal Effects

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$$\mathbb{E}[Y_{id}|X_i] = \beta_0 + \beta_1 d_i + \gamma^\top X_i \quad \text{for} \quad d = 0, 1$$

Equivalently,

$$Y_{id} = \beta_0 + \beta_1 d_i + \gamma^\top X_i + \varepsilon \quad \text{for} \quad d = 0, 1$$

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Noting that (2) implies (1) (such that $\beta_1 = \tau$), there are 3 possible scenarios:

1. Both (1) and (2) are true.
2. Only (1) is true.
3. Neither (1) nor (2) is true.

Case 1: Constant Effect w/ Linear Potential Outcomes

Result: If treatment effect is constant across units and potential outcomes are linear in X_i, then the OLS estimate of β_1 in the following regression model

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Proof (just how we got here):

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\mathbb{E}[\beta_1] &= \mathbb{E}[Y_i|D_i = 1, X_i] - \mathbb{E}[Y_i|D_i = 0, X_i] \quad \text{(correct specification)} \\
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&= \tau(X) \\
\mathbb{E}[\beta_1] &= \tau \quad \text{(constant effect assumption)}
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&= \mathbb{E}[Y_{1i}|X_i] - \mathbb{E}[Y_{0i}|X_i] \quad \text{(SOO)} \\
&= \tau(X) \\
\mathbb{E}[\beta_1] &= \tau \quad \text{(constant effect assumption)}
\end{aligned}$$

Note that if CI and linearity hold, ε cannot be related to D: traditional CIA assumption

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- More flexible models (nonlinear, semi-/non-parametric, etc.) are a good idea

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- Intuition: OLS is minimizing MSE and learns more from strata of X where π_X closer to 0.50.
- think about what this means for your estimate, especially with lack of overlap
- (See Angrist and Pishke for derivation)

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  - largest weights for strata π_i close to 0.5,
- This result assumes discrete Xs, but intuition holds for continuous Xs.
- Another option: use regression to impute missing potential outcomes. E.g. Estimate $\mathbb{E}[Y_{0i}|X_i]$ and use as counterfactuals for observed Y_{1i}. Can weight each pairwise difference as you like.

Combining Regression, Matching and Weighting

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- Matching as nonparametric data preprocessing (Ho et al. 2007):
  - model-based estimation of causal effect is most likely to go wrong when it involves extrapolation due to poor overlap in covariates
  - use matching to make treatment and control groups similar
  - then run regression models to estimate causal effects

Summary: Estimation under Conditional Ignorability

- Matching, weighting and regression are main methods to estimate average causal effects when one can assume conditional ignorability
- These are estimation strategies; the validity of the identification strategy (SOO) remains a first-order concern
- No single method is dominant
- Key considerations
  - does it get you good balance?
  - is there risk of extrapolation due to non-overlap?
  - is there risk you are not doing the conditioning you mean to do? Ask yourself:
  - "what assumptions of the estimation procedure might be invalid?" (e.g. close matches, common support/overlap linearity, constant treatment effects...)