Matching

EC 607, Set 8

Edward Rubin

Prologue

Schedule

Last time(s)

- DAGs
- The conditional independence assumption: $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$
- Omitted variable bias
- Good *vs.* bad controls

Today

- Matching estimators (*MHE* 3.2 and Cameron and Trivedi 25.4).
- Probably time for another problem set

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The gist

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If we really believe $(\mathbf{Y}_{1i}, \mathbf{Y}_{0i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$, then we can just calculate a bunch of treatment effects conditional on $\mathbf{X}_i$, *i.e.*,

$$\tau(x) = E[\mathbf{Y}_{1i} - \mathbf{Y}_{0i} \mid \mathbf{X}_i = x]$$

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The idea: Estimate a treatment effect only using observations with (nearly?) identical values of $\mathbf{X}_i$.

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$$\tau(x) = E[\mathbf{Y}_{1i} - \mathbf{Y}_{0i} \mid \mathbf{X}_i = x]$$

The idea: Estimate a treatment effect only using observations with (nearly?) identical values of $\mathbf{X}_i$. The CIA buys us causality within these groups.

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Matching

Goals

Let's return to **the fundamental problem of causal inference** for a moment.

1. We want/need to know $\tau_i = \mathbf{Y}_{1i} - \mathbf{Y}_{0i}$.
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Matching is no different.

We match untreated observations to treated observations using $\mathbf{X}_i$, *i.e.*, calculate a $\widehat{\mathbf{Y}_{0i}}$ for each $\mathbf{Y}_{1i}$, based upon "matched" untreated individuals.

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- N_T sets of weights
- with N_C weights in each set: $w_i(j)$ $(i = 1, \ldots, N_T;\ j = 1, \ldots, N_C)$

Assume $\sum_j w_i(j) = 1$. Our estimate for the counterfactual of treated i is

$$\widehat{\mathrm{Y}_{0i}} = \sum_{j \in (D=0)} w_i(j) \mathrm{Y}_j$$

Matching

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If our estimated counterfactual for treated individual i is

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then our estimated treatment effect (for individual i) is

$$\hat{\tau}_i = \mathrm{Y}_{1i} - \widehat{\mathrm{Y}_{0i}} = \mathrm{Y}_{1i} - \sum_j w_i(j)\mathrm{Y}_j$$

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$\therefore$ a generic matching estimator for the treatment effect on the treated is

$$\hat{\tau}_M = \frac{1}{N_T} \sum_{i \in (\mathrm{D}=1)} \left(\mathrm{Y}_{1i} - \widehat{\mathrm{Y}_{0i}} \right) = \frac{1}{N_T} \sum_{i \in (\mathrm{D}=1)} \left(\mathrm{Y}_{1i} - \sum_{j \in (D=0)} w_i(j)\mathrm{Y}_j \right)$$

Weight for it†

So all we need is those weights and we're done.††

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A You've got options, but you need to choose carefully/responsibly.

E.g., if $w_i(j) = \frac{1}{N_C}$ for all (i, j), then we're back to a difference in means.
This weighting doesn't abide by our conditional independence assumption.

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The plan Choose weights $w_i(j)$ that indicate ***how close*** $\mathbf{X}_j$ is to $\mathbf{X}_i$.

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If $\mathbf{X}$ is **discrete**, then we can consider equality, *i.e.*, $w_i(j) = \mathbb{I}(\mathbf{X}_i = \mathbf{X}_j)$, scaling as necessary to get $\sum_j w_i(j) = 1$.

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Nearest-neighbor matching chooses the single closest control observation using the Euclidean distance between $\mathbf{X}_i$ and $\mathbf{X}_j$, *i.e.*,

$$\mathrm{d}_{i,j} = \left(\mathbf{X}_i - \mathbf{X}_j\right)' \left(\mathbf{X}_i - \mathbf{X}_j\right)$$

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- $\hat{\tau}_i = \mathbf{Y}_{1i} - \mathbf{Y}_{0j}^i$, where $\mathbf{Y}_{0j}^i$ is i's nearest neighbor in the control group.
- **Estimator:** $\hat{\tau}_M = \frac{1}{N_T} \sum_i \hat{\tau}_i$
- Produces causal estimates if CIA is valid *and* we have sufficient overlap.
- Suffers from arbitrary choices of units.

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Nearest-neighbor matching with Mahalanobis distance chooses the single closest control using Mahalanobis distance between $\mathbf{X}_i$ and $\mathbf{X}_j$, *i.e.*,

$$\mathrm{d}_{i,j} = \left(\mathbf{X}_i - \mathbf{X}_j\right)' \Sigma_X^{-1} \left(\mathbf{X}_i - \mathbf{X}_j\right)$$

where Σ_X^{-1} is the covariance matrix of $\mathbf{X}$.

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- **Estimator:** $\hat{\tau}_M = \frac{1}{N_T} \sum_i \hat{\tau}_i$ where $\left(\hat{\tau}_i = \mathrm{Y}_{1i} - \mathrm{Y}_{0j}^i\right)$
- Produces causal estimates if CIA is valid *and* we have sufficient overlap.
- Does not suffer from arbitrary choices of units.

More neighbors?

Why limit ourselves to a **single** "best" match?

If we're going to let a function/algorithm choose the *nearest* match, can't we also let the function/algorithm choose *how many* matches?

Furthermore, if $N_C \gg N_T$, it we're throwing away *a lot* of information.

We could instead use this information and be more efficient.

More neighbors!

Kernel matching gives positive weight to all control observations within some **bandwidth** h, with higher weight for closer matches determined by some **kernel function** $K(\cdot)$,

$$w_i(j) = \frac{K\left(\frac{\mathrm{X}_j - \mathrm{X}_i}{h}\right)}{\sum_{j \in (D=0)} K\left(\frac{\mathrm{X}_j - \mathrm{X}_i}{h}\right)}$$

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Example The *Epanechnikov kernel* is defined as

$$K(z) = \frac{3}{4}\left(1 - z^2\right) \times \mathbb{I}(|z| < 1)$$

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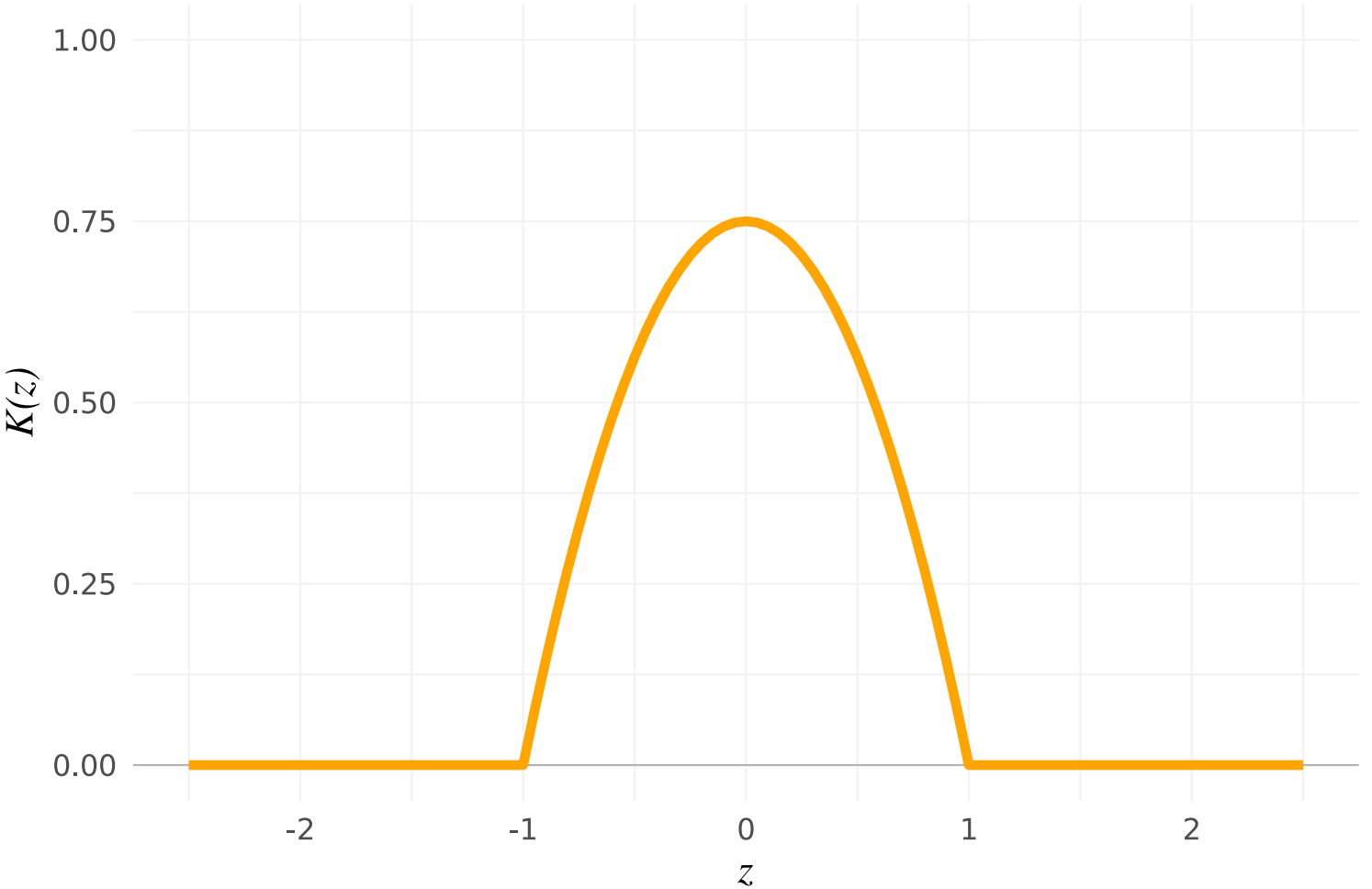
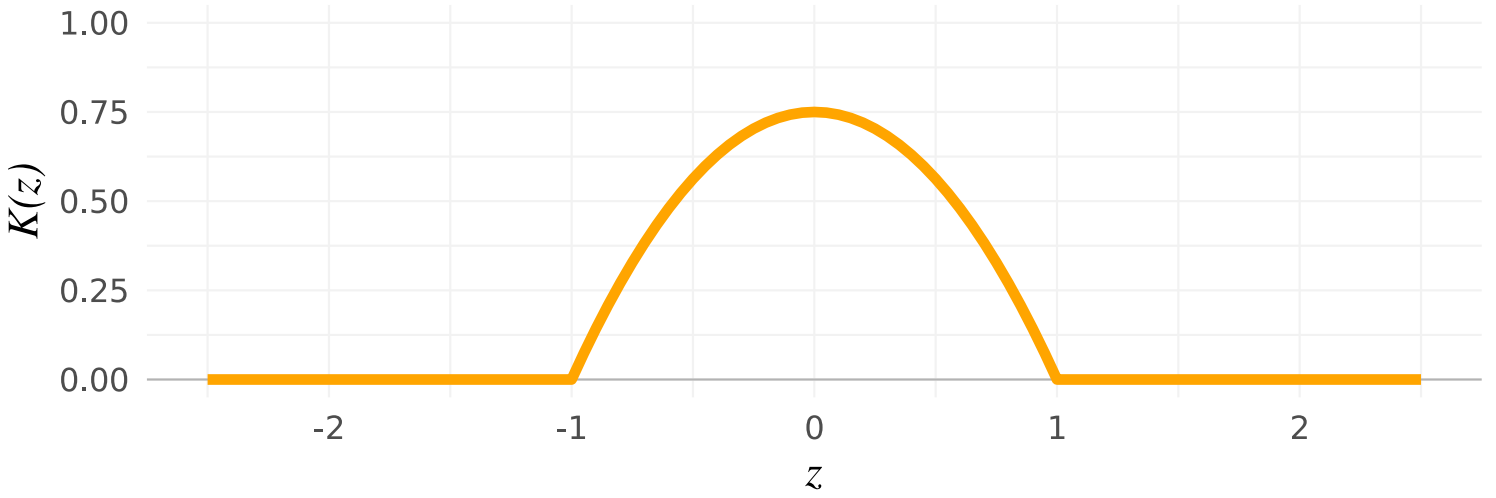
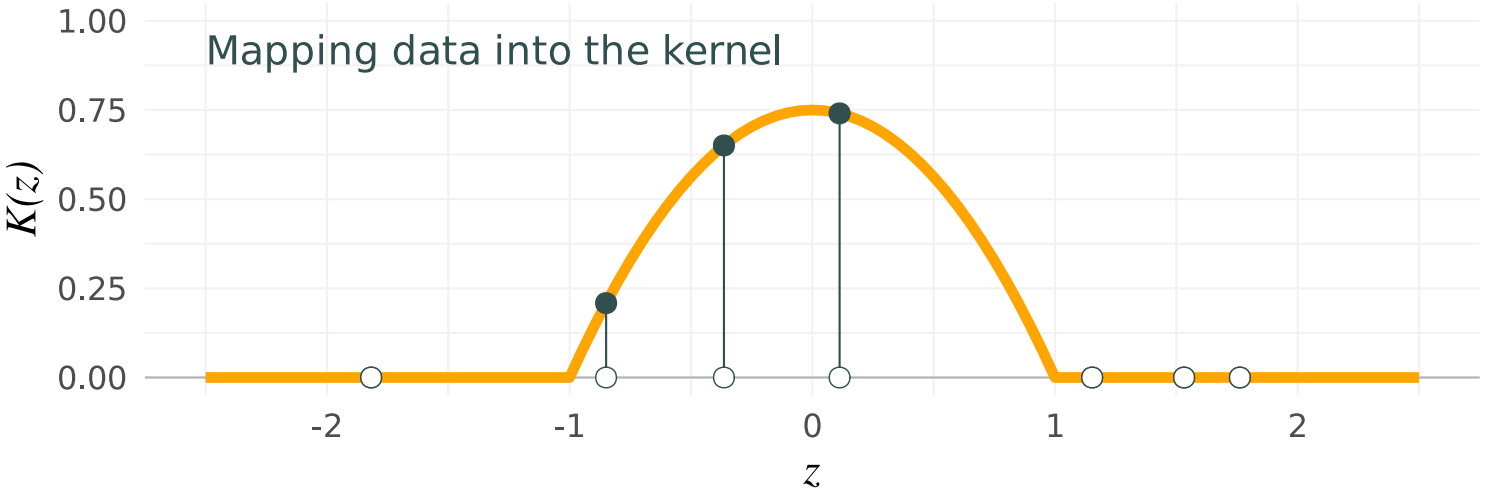



1.00
0.75
0.50
0.25
0.00
K(z)
-2
-1
0
1
2
z


Mapping data into the kernel
1.00
0.75
0.50
0.25
0.00
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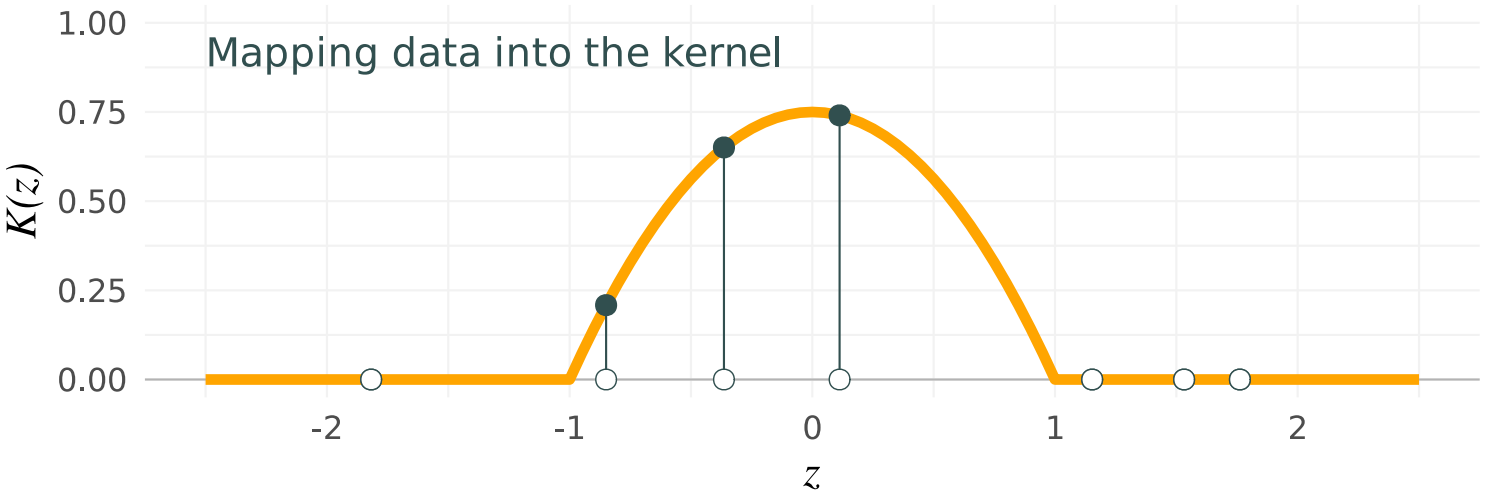
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1.00
0.75
0.50
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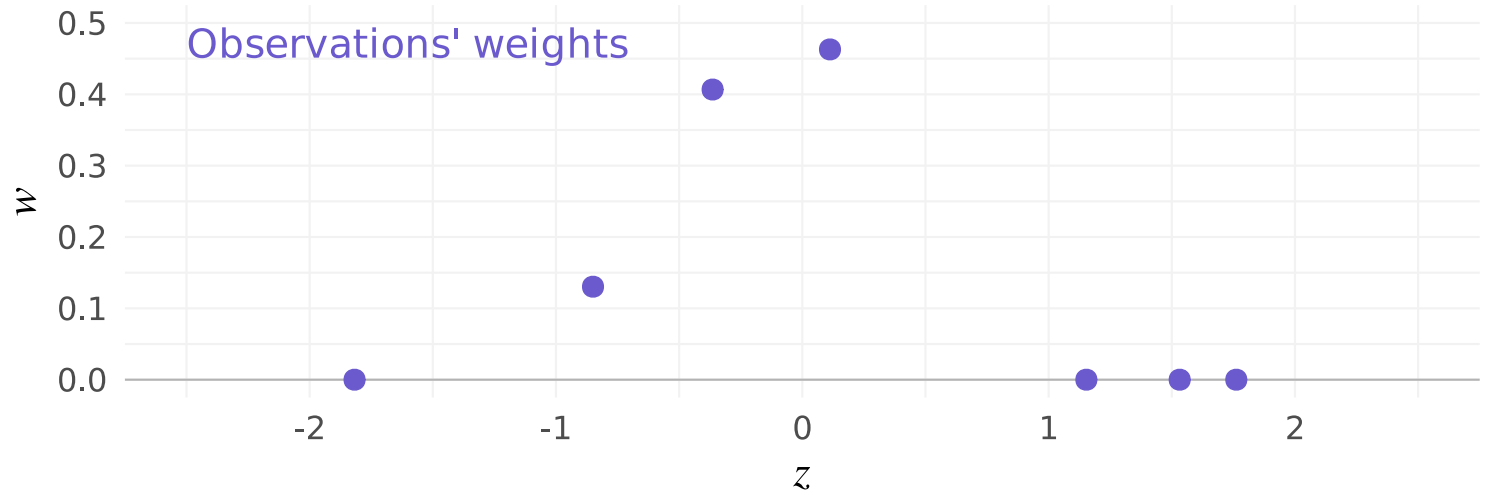
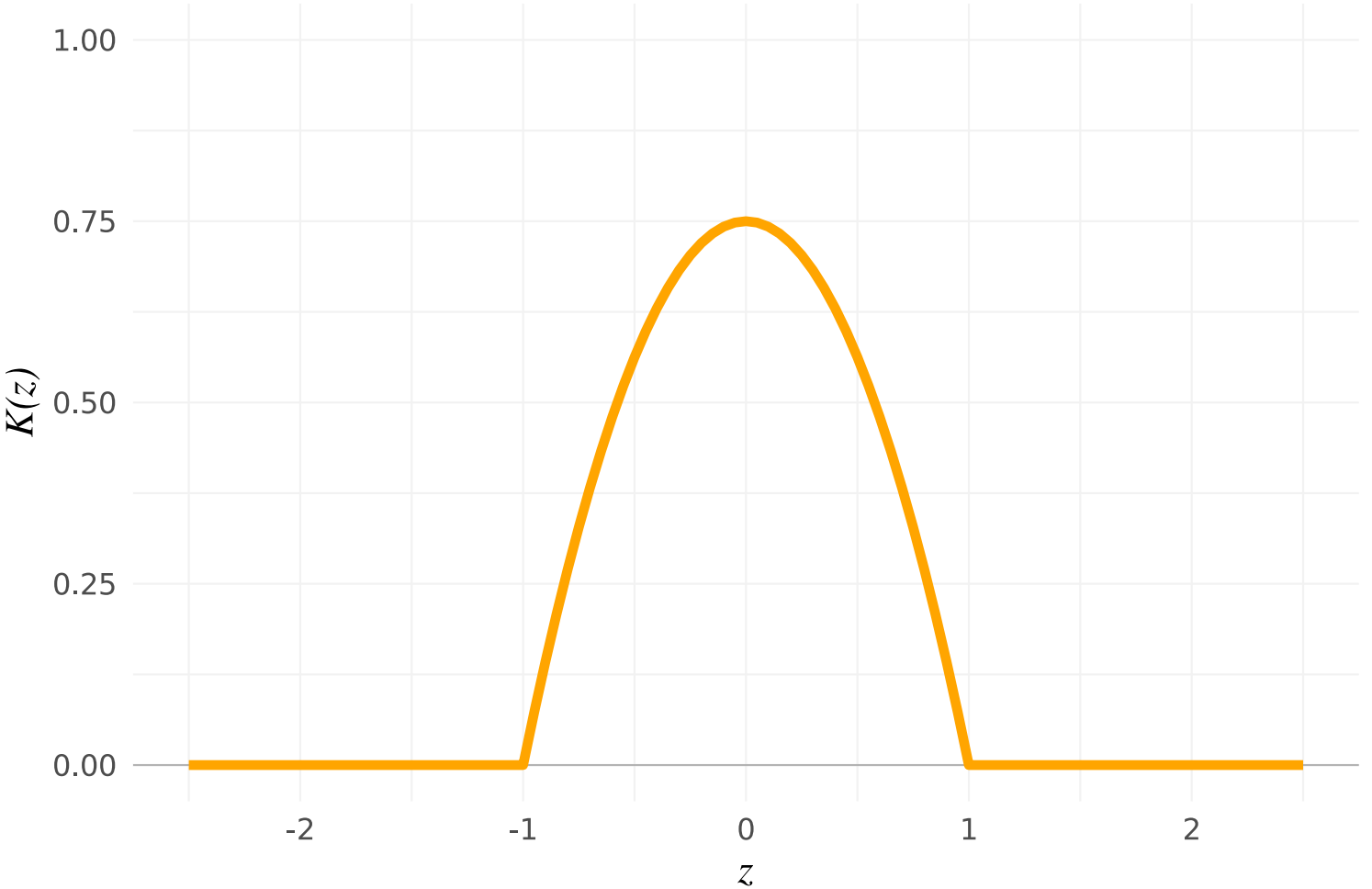
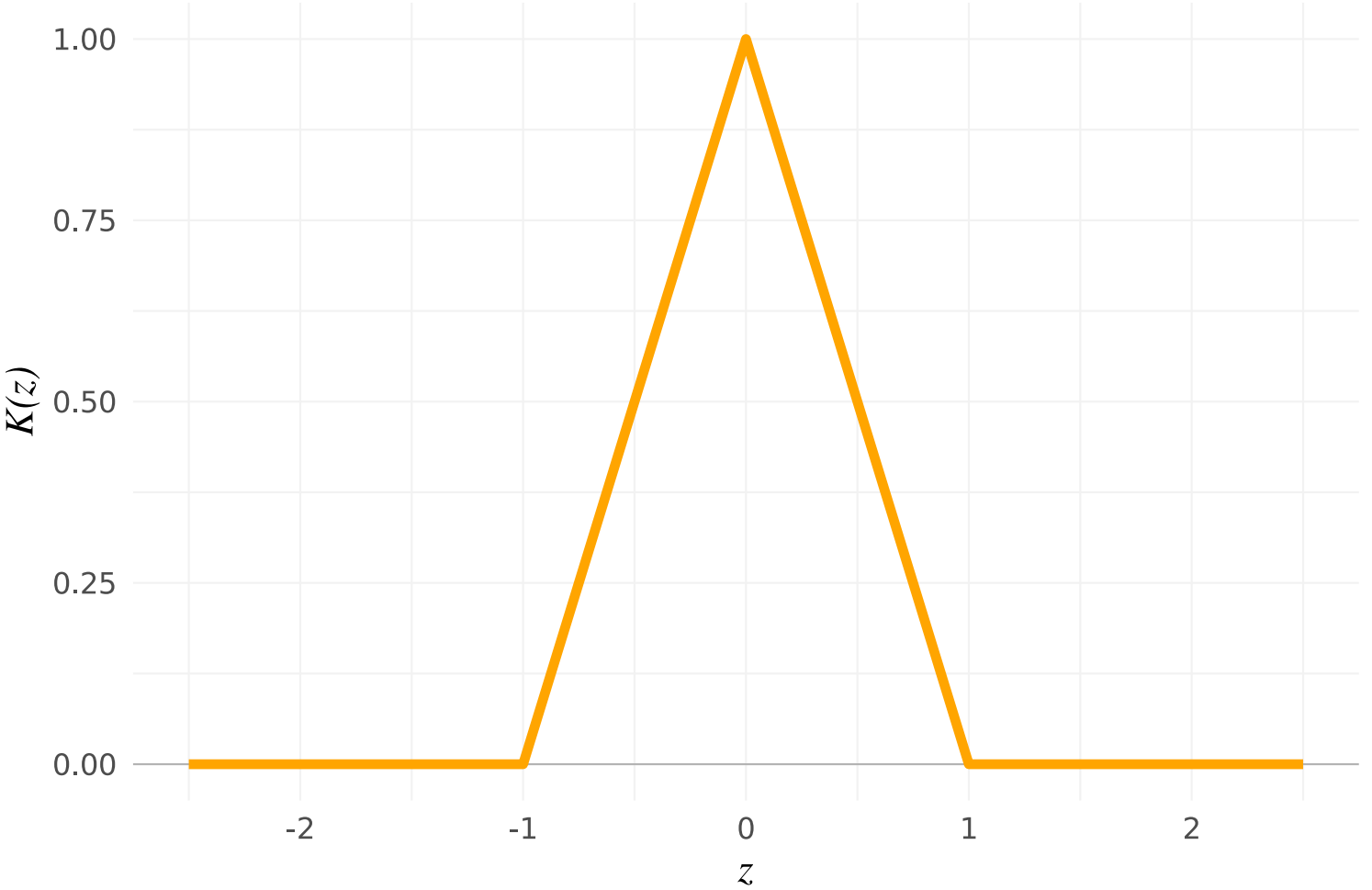

Observations' weights
0.5
0.4
0.3
0.2
0.1
0.0
w
-2
-1
0
1
2
z

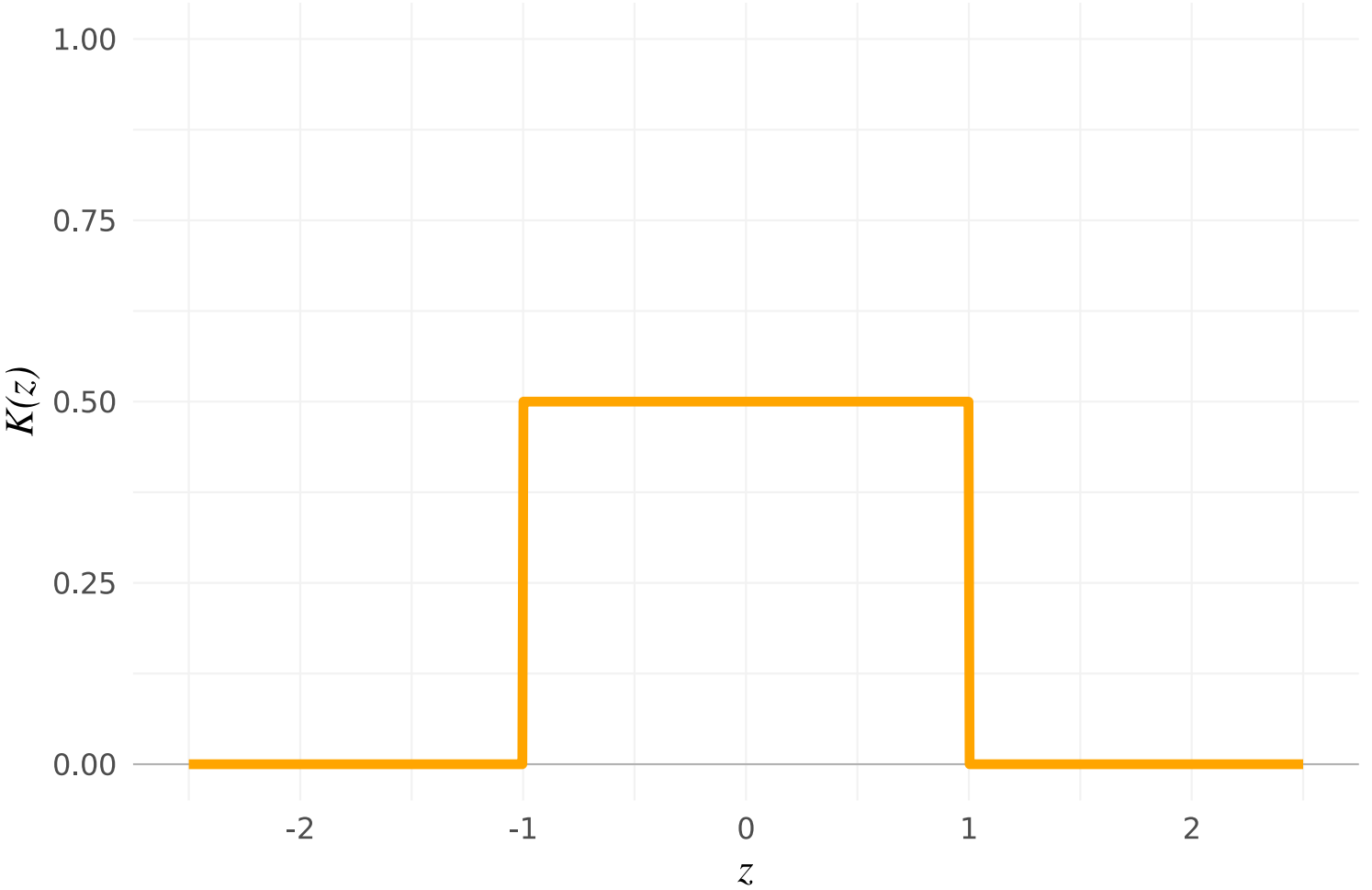
The Epanechnikov kernel $K(z) = \frac{3}{4}\left(1 - z^2\right) \times \mathbb{I}(|z| < 1)$



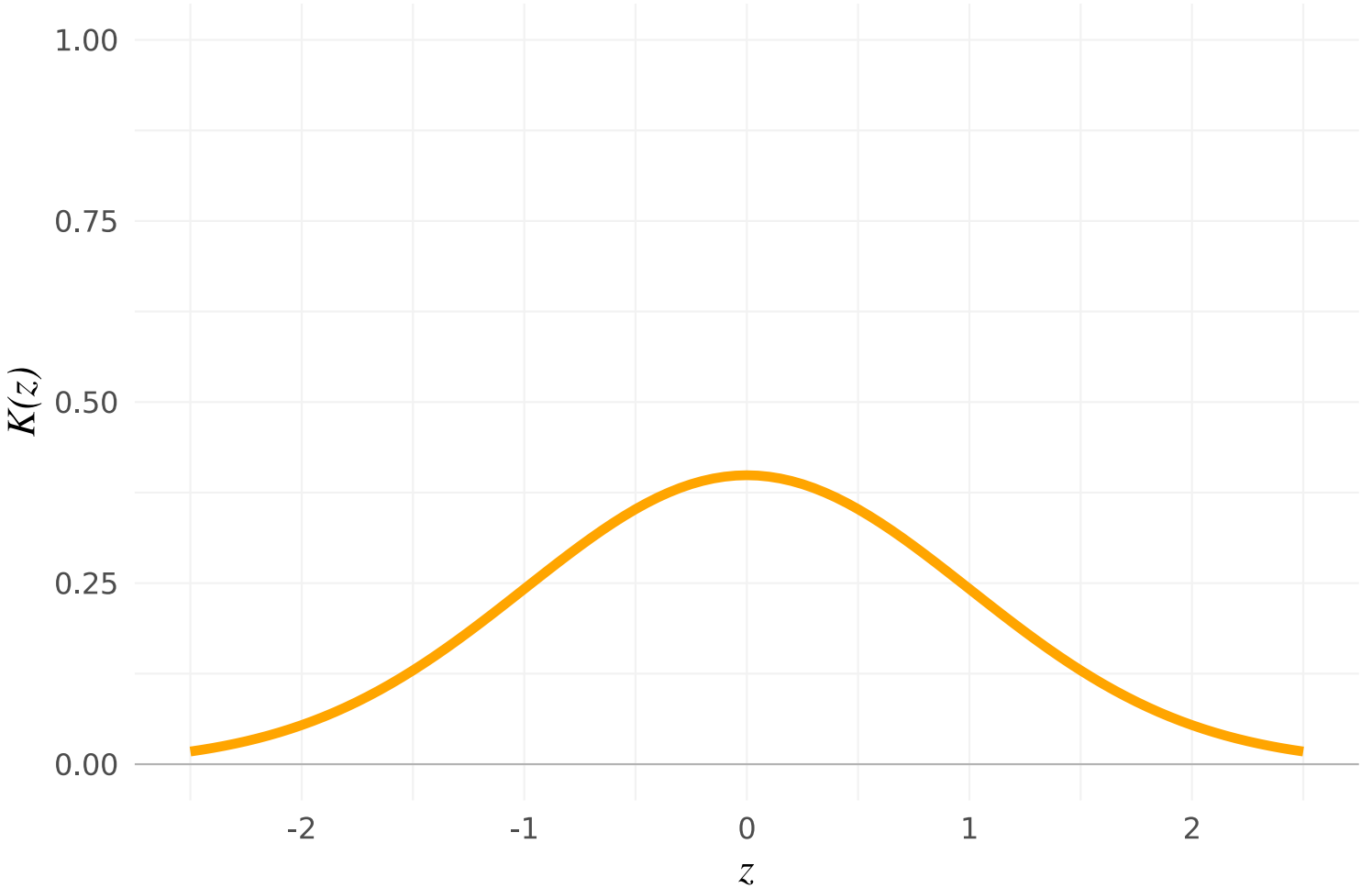
The Triangle kernel $K(z) = (1 - |z|) \times \mathbb{I}(|z| < 1)$



The Uniform kernel $K(z) = \frac{1}{2} \times \mathbb{I}(|z| < 1)$



The Gaussian kernel $K(z) = (2\pi)^{-1/2} \exp\left(-z^2/2\right)$



Kernels

Aside

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You will most commonly see/use them smoothing out densities—providing a smooth, moving-window average.

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E.g., R's (`ggplot2`'s) smooth, density-plotting function `geom_density()`.

`geom_density()` defaults to `kernel = "gaussian"`, but you can specify many other kernel functions (including `"epanechnikov"`).

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`geom_density()` defaults to `kernel = "gaussian"`, but you can specify many other kernel functions (including `"epanechnikov"`).

You can also change the `bandwidth` argument. The default is a bandwidth-choosing function called `bw.nrd0()`.

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As we add more neighbors—either moving from 1 to $n > 1$ or increasing our bandwidth—we potentially increase the efficiency of our estimator.

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CIA requires that we're actually conditioning on the observables—it does not allow us to take a simple average across all control observations.

The curse of dimensionality[†]

It turns out kernel- and bandwidth-selection are not our biggest enemies.

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We need a way to shrink the dimensionality of $\mathbf{X}$.

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Propensity-score methods

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Setup

Let's begin with two assumptions—one old and one new.

1. **Conditional independence:** $(\mathrm{Y}_{0i},\ \mathrm{Y}_{1i}) \perp\!\!\!\perp \mathrm{D}_i | \mathrm{X}_i$

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Propensity scores propose a solution to this mess.

Propensity-score methods

The magic

It turns out that if $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$, then we actually only need to match/condition on $p(\mathbf{X}_i) = E[\mathbf{D}_i | \mathbf{X}_i]$.

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Propensity-score theorem If $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$, then $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | p(\mathbf{X}_i)$.

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This theorem extends our CIA to a one-dimensional score, avoiding the curse of dimensionality.

Propensity-score methods

Theorem If $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$, then $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | p(\mathbf{X}_i)$.

Proof

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Theorem If $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | \mathbf{X}_i$, then $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i | p(\mathbf{X}_i)$.

Proof

To prove this theorem, we will show $\Pr(\mathbf{D}_i = 1 \mid \mathbf{Y}_{0i}, \mathbf{Y}_{1i}, p(\mathbf{X}_i)) = p(\mathbf{X}_i)$, *i.e.*, $\mathbf{D}_i$ is independent of $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i})$ after conditioning on $p(\mathbf{X}_i)$.

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Proof

$$\Pr\left[\mathbf{D}_i = 1 \middle| \mathbf{Y}_{0i},\ \mathbf{Y}_{1i},\ p(\mathbf{X}_i)\right]$$

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Theorem If $(\mathbf{Y}_{0i},\ \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i|\mathbf{X}_i$, then $(\mathbf{Y}_{0i},\ \mathbf{Y}_{1i}) \perp\!\!\!\perp \mathbf{D}_i|p(\mathbf{X}_i)$.

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$$\Pr\left[\mathbf{D}_i = 1 \middle| \mathbf{Y}_{0i},\ \mathbf{Y}_{1i},\ p(\mathbf{X}_i)\right]$$

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Propensity-score methods

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$$\therefore\ (\mathrm{Y}_{0i},\ \mathrm{Y}_{1i}) \perp\!\!\!\perp \mathrm{D}_i | \mathrm{X}_i \implies (\mathrm{Y}_{0i},\ \mathrm{Y}_{1i}) \perp\!\!\!\perp \mathrm{D}_i | p(\mathrm{X}_i) \quad ✔$$

Propensity-score methods

Intuition

Q What's going on here?

$\mathbf{X}_i$ carries way more information than $p(\mathbf{X}_i)$, so how can we still get conditional independence of treatment by only conditioning on $p(\mathbf{X}_i)$?

Propensity-score methods

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$\mathbf{A}_1$ Conditional independence of treatment isn't about extracting all of the information possible from $\mathbf{X}_i$. We actually only care about creating a situation in which $\mathbf{D}_i$|something is independent of $(\mathbf{Y}_{0i}, \mathbf{Y}_{1i})$.

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$\mathbf{A}_2$ Back to our main concern: **selection bias**. People select into treatment. If $\mathbf{X}$ says two people were equally likely to be treated, and if $\mathbf{X}_i$ explains all of selection (CIA), then there cannot be selection between these two people.

Propensity-score methods

Estimation

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We estimate them—and there are a lot of ways to do that.

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2. Kernel regression (remember kernel functions?)
3. Many others—machine learning, series-logit estimator, *etc.*

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Propensity-score methods

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A Sort of. Think about FWL. This route is going to be the same as a regression conditioning on $\mathbf{X}_i$.

Propensity-score methods

Estimation

From *MHE* (p. 83)

Question

> A big question here is how to best model and estimate $p(\mathbf{X}_i)$...

Answer

> The answer to this is inherently application-specific. A growing empirical literature suggests that a logit model for the propensity score with a few polynomial terms in continuous covariates works well in practice...

Propensity-score methods

Application

So you have some estimated propensity scores $\hat{p}(\mathbf{X}_i)$. What next?

Propensity-score methods

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Option 1 Conditioning via regression

Option 1a Use a **regression to condition** on $p(\mathbf{X}_i)$, *i.e.*,

$$\mathbf{Y}_i = \alpha + \delta \mathbf{D}_i + \beta p(\mathbf{X}_i) + u_i \tag{1a}$$

Propensity-score methods

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$$\mathbf{Y}_i = \alpha + \delta \mathbf{D}_i + \beta p(\mathbf{X}_i) + u_i \tag{1a}$$

Option 1b If we think treatment effects are heterogeneous and may covary with $\mathbf{X}$, then we might want to also **interact** treatment with $p(\mathbf{X}_i)$, *i.e.*,

$$\mathbf{Y}_i = \alpha + \delta_1 \mathbf{D}_i + \delta_2 \mathbf{D}_i p(\mathbf{X}_i) + \beta p(\mathbf{X}_i) + u_i \tag{1b}$$

Heterogeneity with regression

Let's think a bit more about heterogeneous treatment effects in this setting.

$$\mathrm{Y}_{0i} = \alpha + \beta \mathrm{X}_i + u_i$$
$$\mathrm{Y}_{1i} = \mathrm{Y}_{0i} + \delta_1 + \delta_2 \mathrm{X}_i$$

i.e., the treatment effect depends upon X_i.

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Let's think a bit more about heterogeneous treatment effects in this setting.

$$\begin{aligned}\mathrm{Y}_{0i} &= \alpha + \beta \mathrm{X}_i + u_i \\ \mathrm{Y}_{1i} &= \mathrm{Y}_{0i} + \delta_1 + \delta_2 \mathrm{X}_i\end{aligned}$$

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$$\mathrm{Y}_i = \mathrm{D}_i \mathrm{Y}_{1i} + (1 - \mathrm{D}_i)\, \mathrm{Y}_{0i}$$

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Heterogeneity

This final equation

$$\mathbf{Y}_i = \alpha + \delta_1 \mathbf{D}_i + \delta_2 \mathbf{D}_i \mathbf{X}_i + \beta \mathbf{X}_i + u_i$$

Propensity-score methods

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This final equation

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suggests that we want $p(\mathrm{X}_i)$ *and* $\mathrm{D}_i p(\mathrm{X}_i)$, *i.e.*,

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which yields

1. a **group-specific treatment effect** $\delta_1 + \delta_2 p(\mathrm{X}_i)$ for each X_i
2. an **average treatment effect** $\delta_1 + \delta_2 \overline{p}(\mathrm{X}_i)$

Propensity-score methods

More flexibility

We motivated propensity scores with a desire to reduce dimensionality and estimate/choose/assume fewer parameters.

Adding $p(\mathbf{X}_i)$ and $\mathbf{D}_i p(\mathbf{X}_i)$ as covariates in a linear regression doesn't quite exhaust our potential for flexible/nonparametric estimation.

Propensity-score methods

Blocking

Option 2 Block (stratify) on propensity scores.

Propensity-score methods

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1. Divide the range of $\hat{p}(\mathbf{X}_i)$ into K blocks (*e.g.*, 0.05-wide blocks).
2. Place each observation into a block via its $\hat{p}(\mathbf{X}_i)$.
3. Calculate $\hat{\tau}_k$ for each block via difference in means.
4. Average the $\hat{\tau}_k$ using their shares of the sample, *i.e.*,

$$\hat{\tau}_{\text{Block}} = \sum_{k=1}^{K} \hat{\tau}_k \frac{N_{1k} + N_{0k}}{N}$$

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Note Blocking is similar to NN/kernel matching using $p(\mathbf{X}_i)$ as distance.

Propensity-score methods

Choosing blocks

Blocking on propensity scores requires defining defining blocks.

One common route involves some iteration.

1. **Choose blocks**.
2. Check the **balance of the covariates** within each block.[†]
    - If covariates are not balanced, then split your blocks and repeat.
    - If covariates are balanced, then stop.

† Keep multiple-hypothesis testing in mind. With many covariates and many blocks, you are bound to find statistically significant relationships—even if you are balanced in truth.

Propensity-score methods

Overlap

Blocking emphasizes our overlap assumption, *i.e.*, $0 < \mathbf{Pr}(\mathbf{D}_i|\mathbf{X}_i) < 1$.

If a block contains zero treated/control units, we cannot calculate $\hat{\tau}_k$.

Propensity-score methods

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Common practice Empirically enforce overlap:

- Drop control units with $\hat{p}(\mathbf{X}_i)$ below the minimum propensity score in the treatment group.
- Drop treated units with $\hat{p}(\mathbf{X}_i)$ above the maximum propensity score in the control group.

Propensity-score methods

Weighting

Option 3 Weight observations by the inverse propensity score.

Propensity-score methods

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Propensity-score methods

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A Consider our old (likely biased) friend the difference in means, *i.e.*,

$$\hat{\tau}_{\text{Diff}} = \overline{\mathbf{Y}}_{\text{T}} - \overline{\mathbf{Y}}_{\text{C}} = \frac{\sum_i \mathbf{D}_i \mathbf{Y}_i}{\sum_i \mathbf{D}_i} - \frac{\sum_i (1 - \mathbf{D}_i) \mathbf{Y}_i}{\sum_i (1 - \mathbf{D}_i)}$$

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which we've discussed is biased due to selection into treatment, *i.e.*,

$$E[\mathbf{Y}_{0i} | \mathbf{D}_i = 1] \neq E[\mathbf{Y}_{0i}]$$

Weighting, justified

Suppose we know $p(\mathbf{X}_i)$ and we weight each **treated** individual by $1/p(\mathbf{X}_i)$

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Propensity-score methods

Weighting, justified

Suppose we know $p(\mathrm{X}_i)$ and we weight each **treated** individual by $1/p(\mathrm{X}_i)$

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Similarly, weighting **control** individuals by $1/(1-p(\mathrm{X}_i))$ yields

$$E\left[\frac{(1-\mathrm{D}_i)\mathrm{Y}_i}{1-p(\mathrm{X}_i)}\right] = E[\mathrm{Y}_{0i}]$$

Weighting: The estimator

Thus, we can estimate an unbiased treatment effect via

$$\hat{\tau}_{p\text{Weight}} = \frac{1}{N} \sum_{i=1}^{N} \left[\frac{\mathrm{D}_i \mathrm{Y}_i}{p(\mathrm{X}_i)} - \frac{(1 - \mathrm{D}_i)\mathrm{Y}_i}{1 - p(\mathrm{X}_i)} \right]$$

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We want to get back to *as-good-as random* variation in treatment.

So we upweight (**1**) **treated** individuals with low $p(\mathrm{X}_i)$ and (**2**) **control** observations with high $p(\mathrm{X}_i)$.

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Practical issue Nothing guarantees $\sum_i \hat{p}(\mathbf{X}_i) = 1$.

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Applying the normalized (and estimated) propensity scores

$$\hat{\tau}_{p\mathrm{Weight}} = \sum_{i=1}^{N} \frac{\frac{\mathrm{D}_i \mathrm{Y}_i}{\hat{p}(\mathrm{X}_i)}}{\sum_i \frac{\mathrm{D}_i}{\hat{p}(\mathrm{X}_i)}} - \sum_{i=1}^{N} \frac{\frac{(1-\mathrm{D}_i)\mathrm{Y}_i}{1-\hat{p}(\mathrm{X}_i)}}{\sum_i \frac{(1-\mathrm{D}_i)}{1-\hat{p}(\mathrm{X}_i)}}$$

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Hirano, Imbens, and Ridder (2003) suggests this estimator is efficient.

Propensity-score methods

Why choose one?

There's nothing special about weighted averages—regression can weight.

Thus, a **regression-based estimate**

$$\mathrm{Y}_i = \alpha + \mathrm{X}_i\beta + \tau\mathrm{D}_i + u_i$$

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offers a *doubly robust* property—you have two chances to be right: $p(\mathrm{X}_i)$ or the regression specification.

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Step 1 For each block k, we run the regression

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Step 2 Aggregate block-level treatment-effect estimates

$$\hat{\tau} = \sum_{k=1}^{K} \hat{\tau}_k \frac{N_{1k} + N_{0k}}{N}$$

Major requirements

Don't get (too) caught up in the bells and whistles.

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1. Is the **conditional-independence assumption** true?

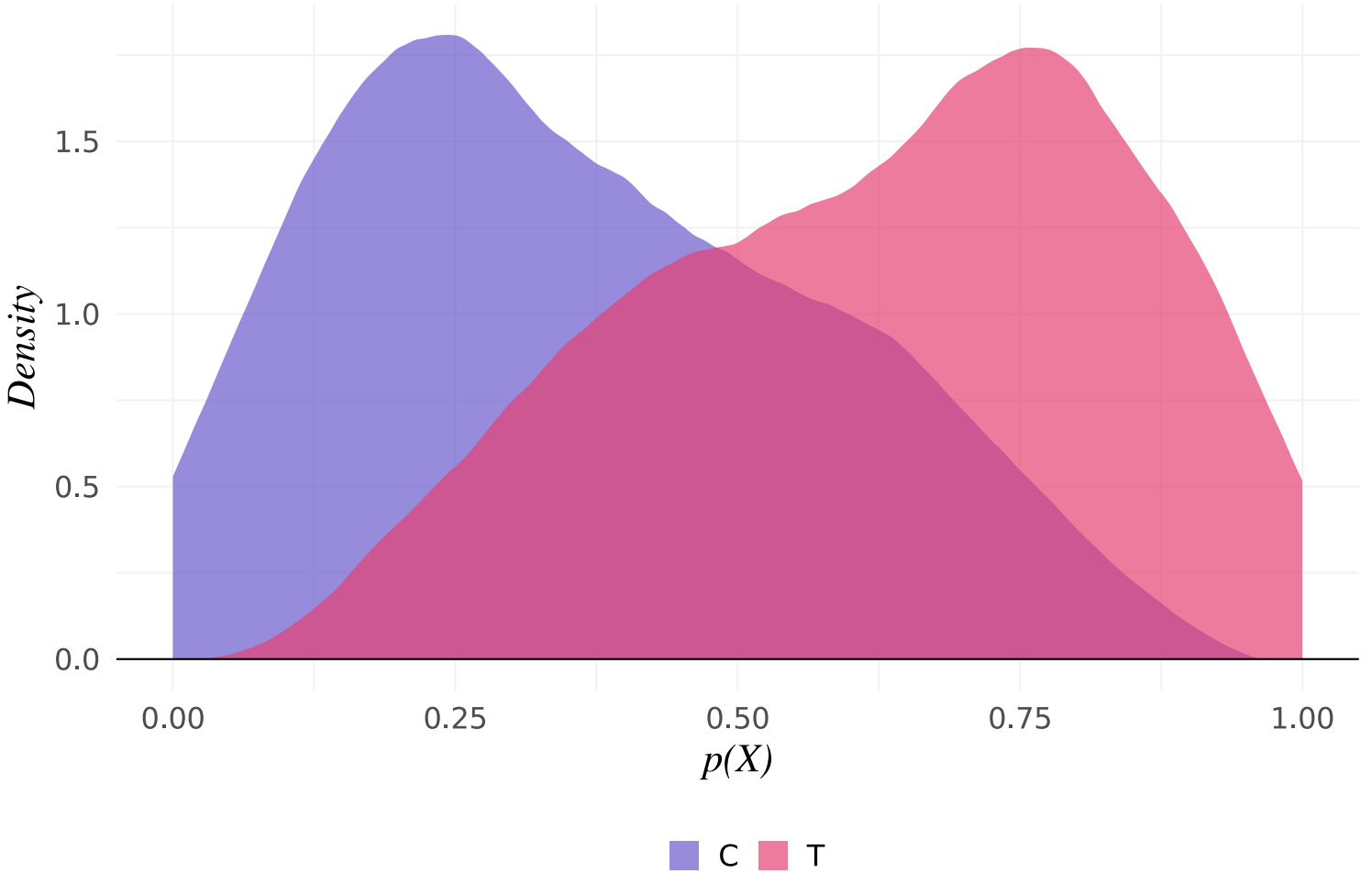
2. Do we have **overlap** between treatment and control units.

We can look for evidence of (**2**) in the data—particularly if we're using propensity-score methods.[†]

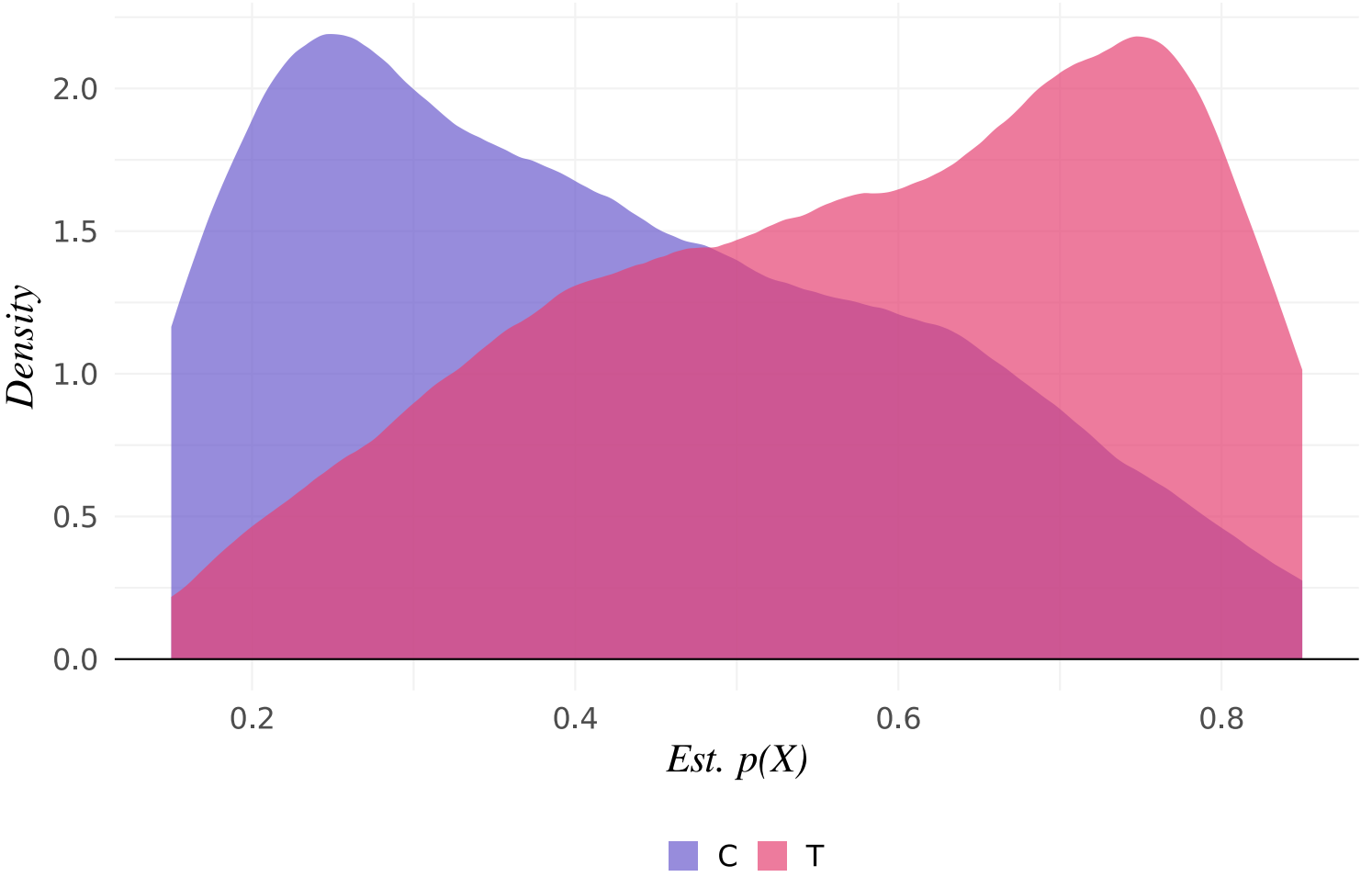
How? Plot the distributions of $p(\mathbf{X}_i)$ for **T** and **C**.

† Checking for overlap in $\mathbf{X}$-space, can be tough as the dimensions of $\mathbf{X}$ expand.

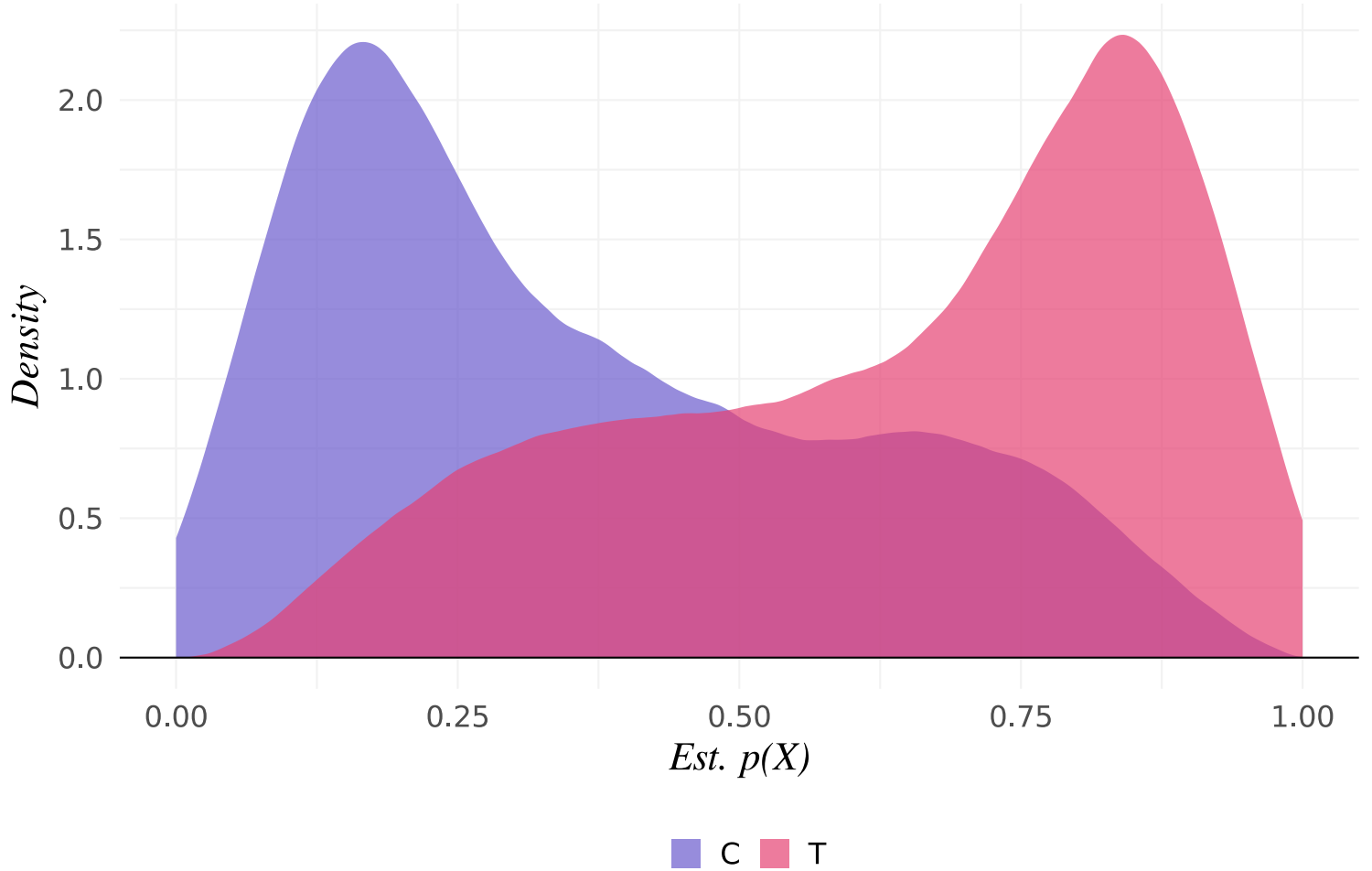
Missing overlap in $p(\mathbf{X}_i)$



Authentic (enforced) overlap in $p(\mathbf{X}_i)$



Logit-based $\hat{p}(\mathbf{X}_i)$ hiding some of the missing overlap in $p(\mathbf{X}_i)$



Overlap in one dimension does not guarantee in two dimensions.

Note Shading denotes **share of treatment:** white =0% and **pink**=100%.

Table of contents