The background of the slide features a photograph of several modern hospital buildings in New York City at dusk. The most prominent building on the left has a glass facade with the text "HELEN L. AND MARGARET KIMMEL PAVILION" visible. To its right is a large, dark grey rectangular building with a circular logo on top. Other buildings of various heights and architectural styles are visible in the background under a clear sky.

Overcoming positivity violations in observational studies with non-overlap bounds

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Emerging Leaders in Research Lecture Series

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arXiv > stat > arXiv:2509.20206

Statistics > Methodology

[Submitted on 24 Sep 2025]

Non-overlap Average Treatment Effect Bounds

Herbert P. Susmann, Alec McClean, Iván Díaz

The average treatment effect (ATE), the mean difference in potential outcomes under treatment and control, is a canonical causal effect. Overlap, which says that all subjects have non-zero probability of either treatment status, is necessary to identify and estimate the ATE. When overlap fails, the standard solution is to change the estimand, and target a trimmed effect in a subpopulation satisfying overlap; however, this no longer addresses the original goal of estimating the ATE. When the outcome is bounded, we demonstrate that this compromise is unnecessary. We derive non-overlap bounds: partial identification bounds on the ATE that do not require overlap. They are the sum of a trimmed effect within the overlap subpopulation and worst-case bounds on the ATE in the non-overlap subpopulation. Non-overlap bounds have width proportional to the size of the non-overlap subpopulation, making them informative when overlap violations are limited --- a common scenario in practice. Since the bounds are non-smooth functionals, we derive smooth approximations of them that contain the ATE but can be estimated using debiased estimators leveraging semiparametric efficiency theory. Specifically, we propose a Targeted Minimum Loss-Based estimator that is \sqrt{n} -consistent and asymptotically normal under nonparametric assumptions on the propensity score and outcome regression. We then show how to obtain a uniformly valid confidence set across all trimming and smoothing parameters with the multiplier bootstrap. This allows researchers to consider many parameters, choose the tightest confidence interval, and still attain valid coverage. We demonstrate via simulations that non-overlap bound estimators can detect non-zero ATEs with higher power than traditional doubly-robust point estimators. We illustrate our method by estimating the ATE of right heart catheterization on mortality.

Summary



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We propose **partial identification bounds** for the Average Treatment Effect and robust targeted estimators that can achieve **higher power** than traditional doubly-robust estimators when overlap fails.

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- What is the treatment effect of interest?
 - “*Estimand: A description of the exact treatment effect a study aims to quantify.*” (Kahan et al., 2024).
- What is the average treatment effect over the study population of critically ill patients?
- We can formalize the estimand using the concept of *counterfactual outcomes* from *causal inference*.

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- Interpretation: difference in mean 30-day survival if *every* patient had been given RHC versus if *no* patient had been given RHC.

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- We can't observe *both* Y^1 and Y^0 for the same patient.
- **Instead**, we can make an *educated guess*:

$$\text{ATE} = \mathbb{E}[\mathbb{E}[Y | A = 1, X]] - \mathbb{E}[\mathbb{E}[Y | A = 0, X]]$$

Identification Assumptions

Core assumptions:

- **No unmeasured confounding.**

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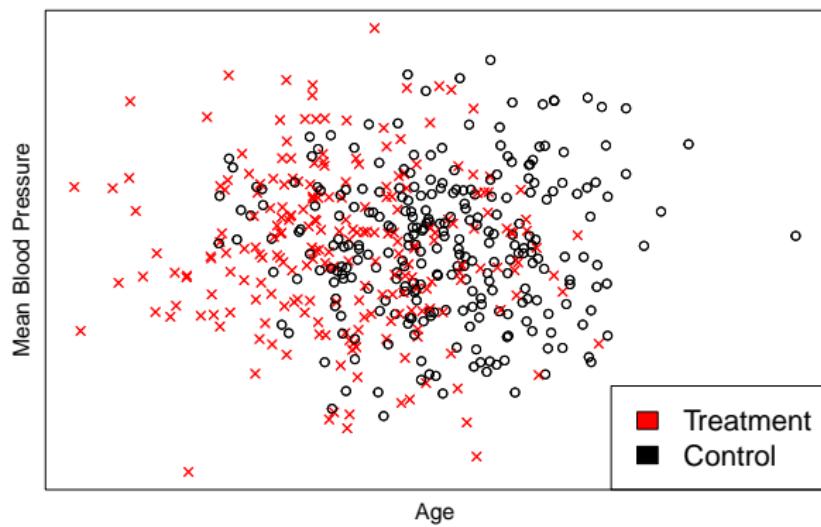
- **No unmeasured confounding.**

All common causes of RHC and 30-day survival are measured.

- **Overlap.**

Every type of patient had a positive probability of receiving RHC, or not receiving RHC.

Overlap is violated when some strata rarely receive either the treatment or the control



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- Practical implications of overlap violations:
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- Using a traditional approach, the estimated Average Treatment Effect of RHC on 30-day survival has the 95% confidence interval $(-1, 1)$
- The uncertainty is so high we learn **nothing** about the treatment effect.

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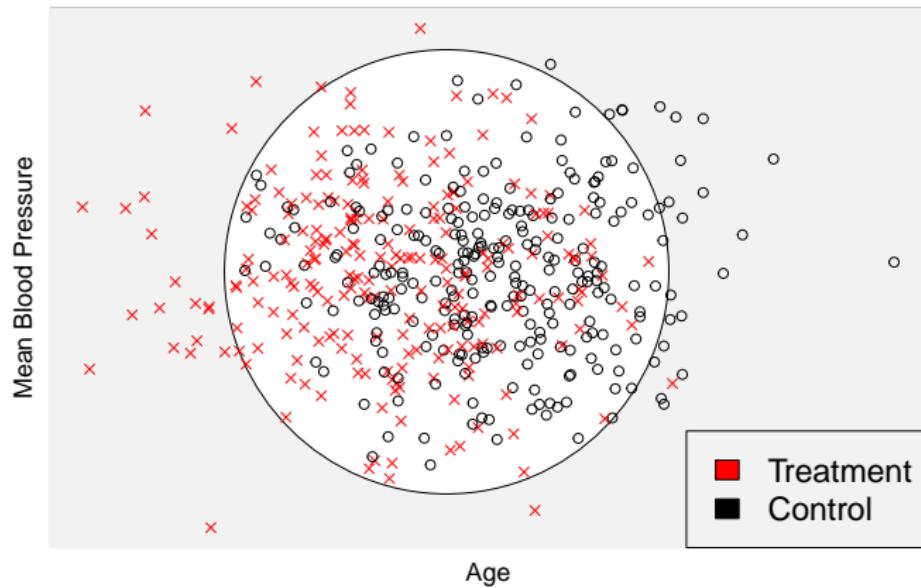
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 - Overlap weighting (Li et al., 2018)
 - Incremental propensity score interventions (Kennedy, 2019)

Overlap Treatment Effect



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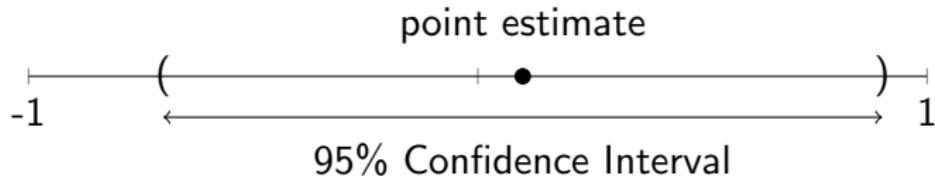
- The new estimand *might not answer the scientific question of interest* (Rizk 2025 Journal of Clinical Epidemiology).
- **Average Treatment Effect:** expected mean difference in survival *over population of critically ill adult patients*.
- **Overlap Treatment Effect:** expected mean difference in survival *over population of critically ill adult patients satisfying overlap*.

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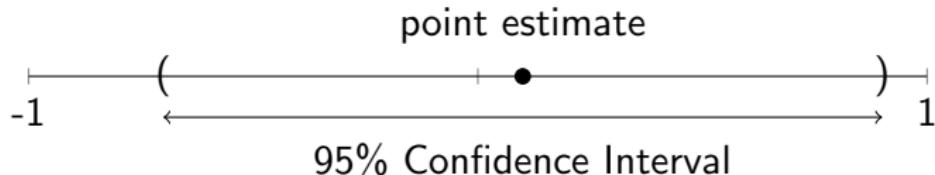
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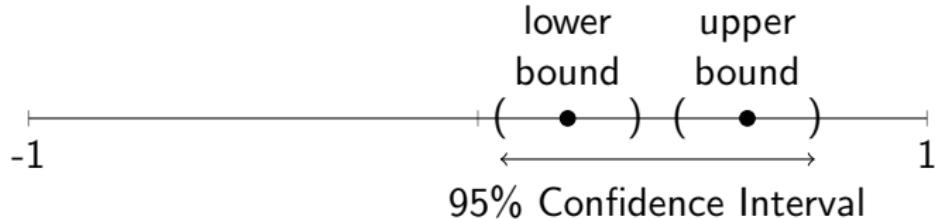


Our proposal: estimate *bounds* on the treatment effect

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- Our approach: estimate **lower** and **upper bounds** and combine to form a **95% confidence interval**:



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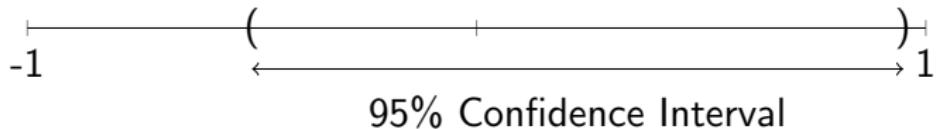
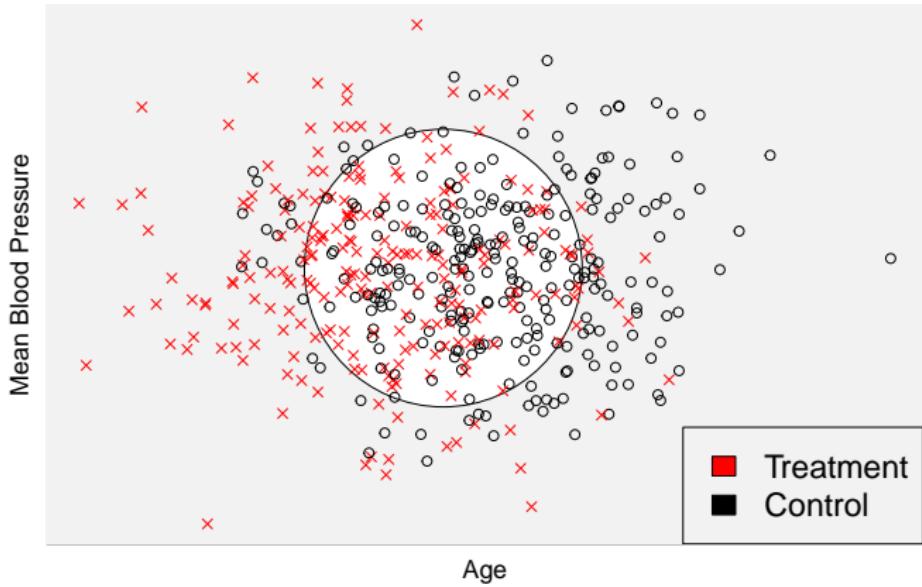
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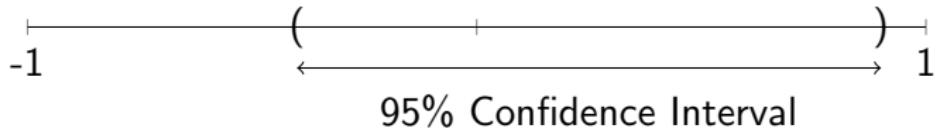
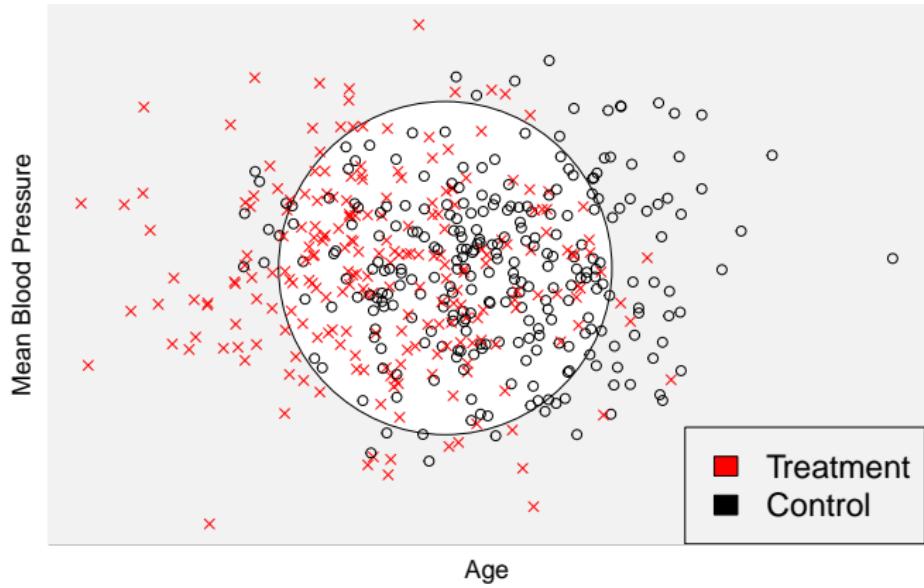
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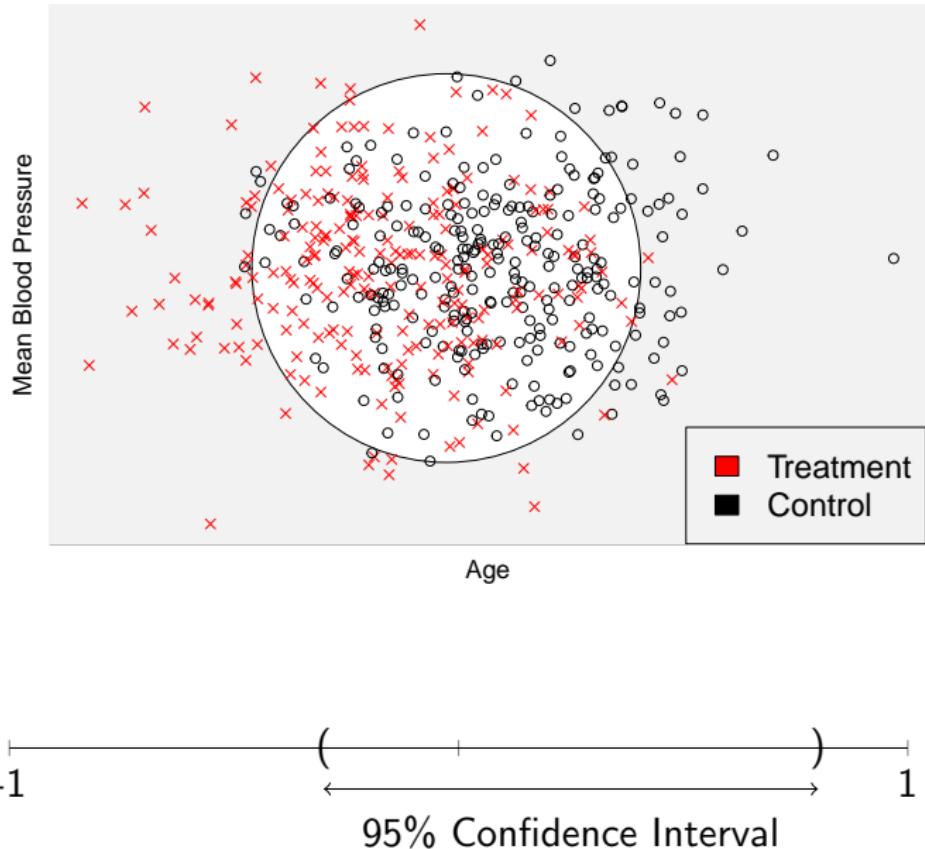
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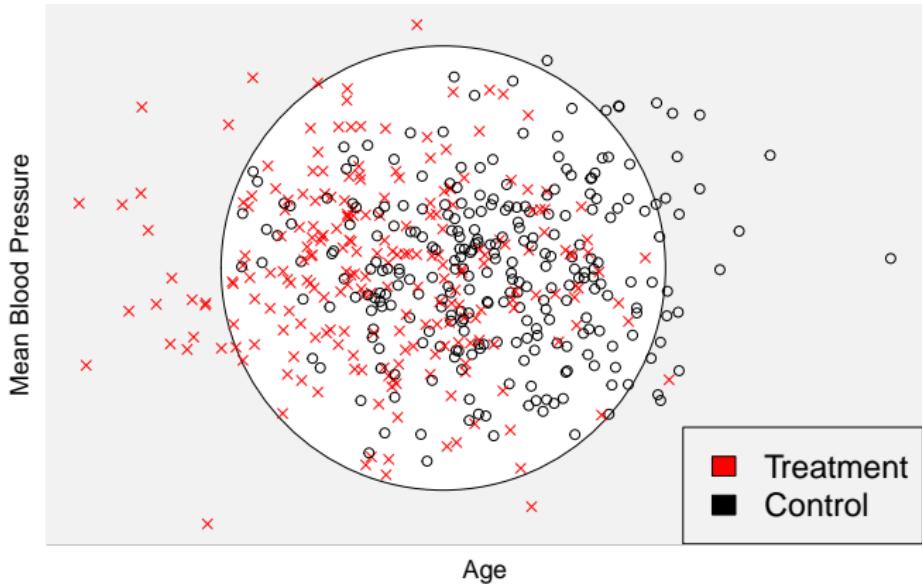
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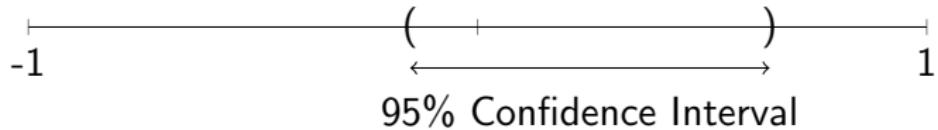
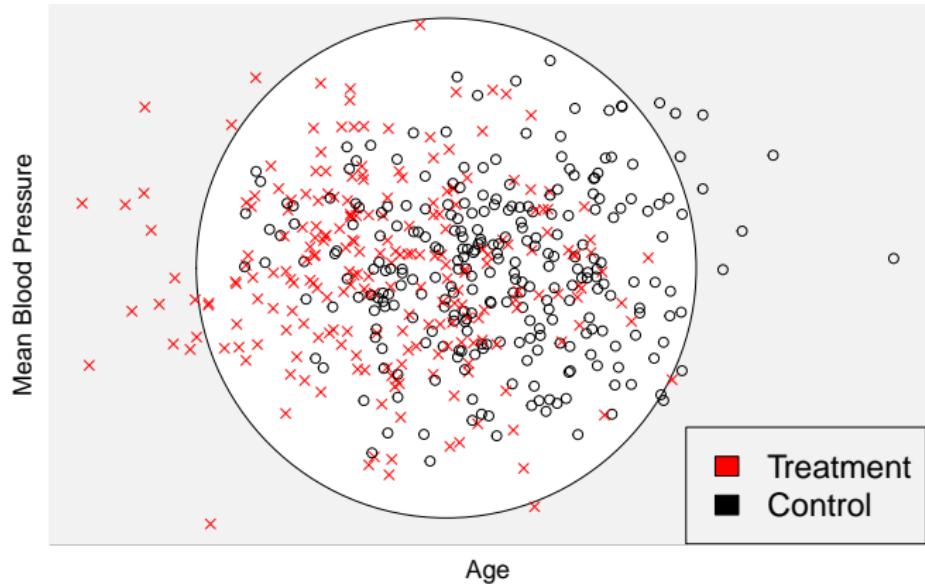
$$\text{ATE} \in \mathbb{E}(Y^1 - Y^0 \mid \text{overlap})\mathbb{P}(\text{overlap}) \pm \mathbb{P}(\text{non-overlap}).$$

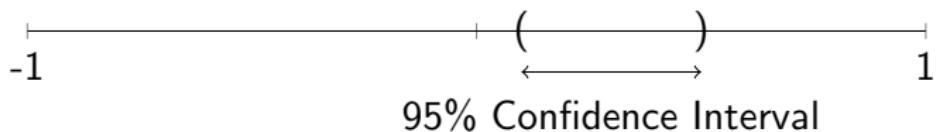
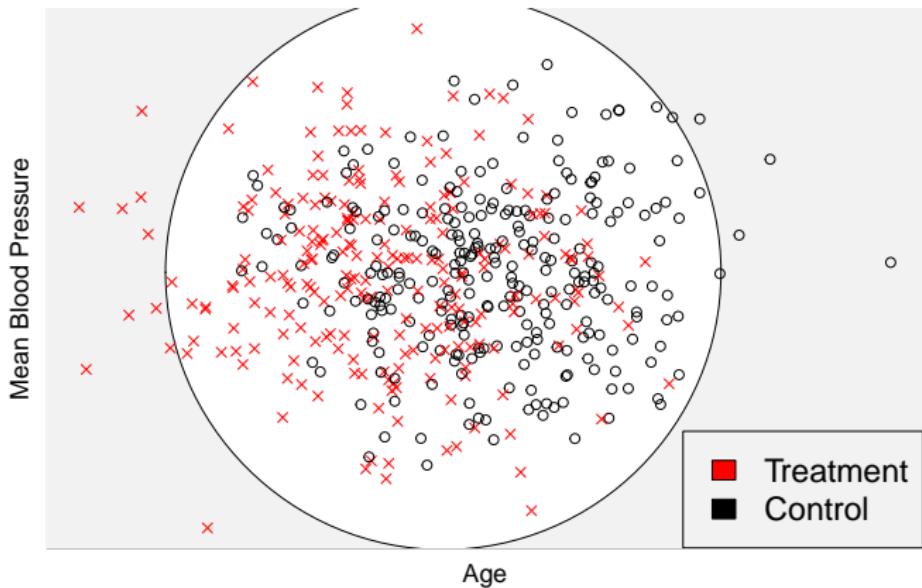


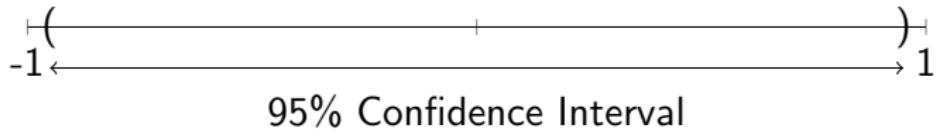
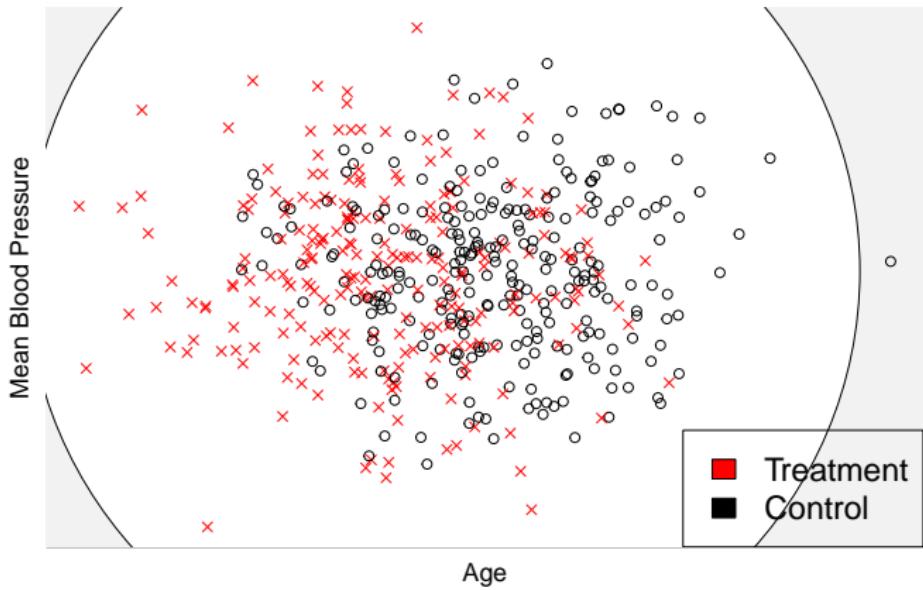




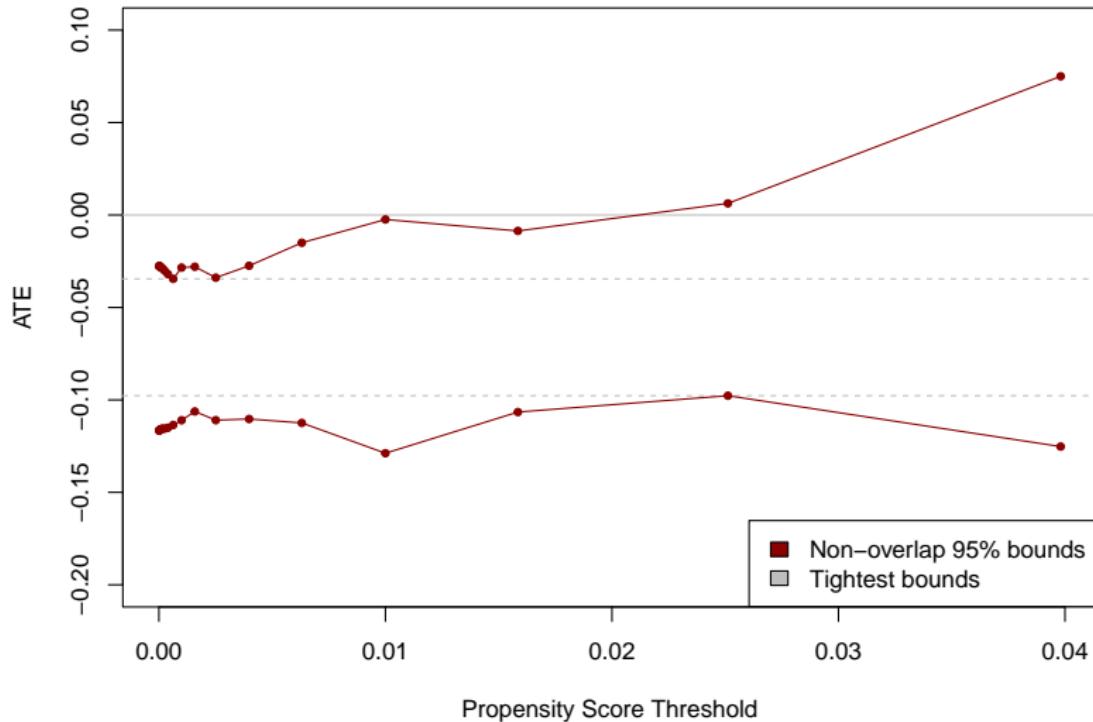








Population Average Treatment Effect of Right Heart Catheterization on 30-day Survival



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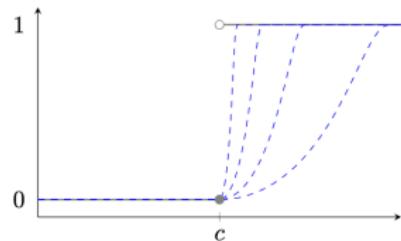
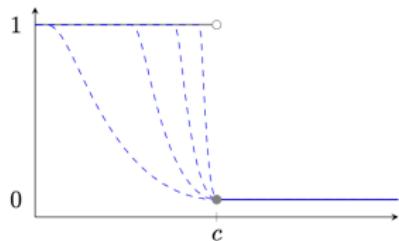
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 - Allows for the use of flexible machine-learning and AI to estimate propensity score and outcome regression models.
- When there are no overlap violations, bounds reduce to traditional confidence intervals around a doubly-robust point estimate.
- Uniform confidence sets via multiplier bootstrap allow for testing a range of thresholds without multiple testing problems.

$$s_l(x, c, \gamma) = \begin{cases} 1, & x \leq c - \gamma, \\ 0, & x \geq c, \\ 1 - \exp \left[1 + \frac{1}{\{(x-c)/\gamma\}^2 - 1} \right], & \text{otherwise, and} \end{cases}$$

$$s_g(x, c, \gamma) = \begin{cases} 1, & x \geq c + \gamma, \\ 0, & x \leq c, \\ 1 - \exp \left[1 + \frac{1}{\{(x-c)/\gamma\}^2 - 1} \right], & \text{otherwise.} \end{cases}$$

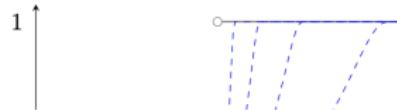
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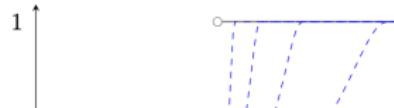


Theorem 1 (Efficient influence functions). *Under the setup of Proposition 2, suppose the maps $x \mapsto s_l(x, c, \gamma)$ and $x \mapsto s_g(x, c, \gamma)$ are twice-differentiable with bounded first and second derivatives. Let \dot{s} denote the first derivative. Then, the parameters $\psi_s(c, \gamma)$, $L_s(c, \gamma)$, and $U_s(c, \gamma)$ admit von-Mises expansions of the form (6), with, respectively, the following uncentered efficient influence functions:*

$$\begin{aligned} \varphi_\psi(Z, \eta, c, \gamma) &= \mu_1 s_g(\pi, c, \gamma) - \mu_0 s_l(\pi, 1 - c, \gamma) \\ &\quad + \frac{A}{\pi} s_g(\pi, c, \gamma) (Y - \mu_1) - \frac{1 - A}{1 - \pi} s_l(\pi, 1 - c, \gamma) (Y - \mu_0) \\ &\quad + \{\mu_1 \dot{s}_g(\pi, c, \gamma) - \mu_0 \dot{s}_l(\pi, 1 - c, \gamma)\} (A - \pi), \\ \varphi_L(Z, \eta, c, \gamma) &= \varphi_{\psi_s}(Z, \eta, c, \gamma) - 1 + s_l(\pi, 1 - c, \gamma) + \dot{s}_l(\pi, 1 - c, \gamma) (A - \pi), \\ \varphi_U(Z, \eta, c, \gamma) &= \varphi_{\psi_s}(Z, \eta, c, \gamma) + 1 - s_g(\pi, c, \gamma) - \dot{s}_g(\pi, c, \gamma) (A - \pi). \end{aligned}$$

$$s_l(x, c, \gamma) = \begin{cases} 1, & x \leq c - \gamma, \\ 0, & x \geq c, \\ 1 - \exp \left[1 + \frac{1}{\{(x-c)/\gamma\}^2 - 1} \right], & \text{otherwise, and} \end{cases}$$

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$$\varphi_\psi(Z, \eta, c, \gamma) = \mu_1 s_g(\pi, c, \gamma) - \mu_0 s_l(\pi, 1 - c, \gamma)$$

Algorithm 2. *Given K threshold and smooth parameter combinations $\{(c_k, \gamma_k)\}_{k=1}^K$:*

1. *For each $k \in [K]$, construct efficient influence function estimates as in the prior section: $\{\varphi_{L,k}(Z_i, \hat{\eta}), \varphi_{U,k}(Z_i, \hat{\eta})\}_{i=1}^n$. Also construct point estimates and standard error estimators for the upper and lower bounds: $\{\hat{L}_k, \hat{U}_k\}$ and $\{\hat{\sigma}_{L,k}, \hat{\sigma}_{U,k}\}$.*
2. *For B bootstrap samples, draw i.i.d. multipliers $\{\xi_i^{(b)}\}_{i=1}^n$ with $\mathbb{E}(\xi) = 0$, $\mathbb{E}(\xi^2) = 1$, and form the studentized residuals for each index k :*

$$\text{err}^{(b)} = 1 - \sum_{i=1}^n \text{err}^{(b)} \left\{ \varphi_{L,k}(Z_i, \hat{\eta}) - \hat{L}_k \right\} \quad \text{err}^{(b)} = 1 - \sum_{i=1}^n \text{err}^{(b)} \left\{ \varphi_{U,k}(Z_i, \hat{\eta}) - \hat{U}_k \right\}$$

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Non-overlap Average Treatment Effect Bounds

Herbert P. Susmann, Alec McClean, Iván Díaz

The average treatment effect (ATE), the mean difference in potential outcomes under treatment and control, is a canonical causal effect. Overlap, which says that all subjects have non-zero probability of either treatment status, is necessary to identify and estimate the ATE. When overlap fails, the standard solution is to change the estimand, and target a trimmed effect in a subpopulation satisfying overlap; however, this no longer addresses the original goal of estimating the ATE. When the outcome is bounded, we demonstrate that this compromise is unnecessary. We derive non-overlap bounds: partial identification bounds on the ATE that do not require overlap. They are the sum of a trimmed effect within the overlap subpopulation and worst-case bounds on the ATE in the non-overlap subpopulation. Non-overlap bounds have width proportional to the size of the non-overlap subpopulation, making them informative when overlap violations are limited -- a common scenario in practice. Since the bounds are non-smooth functionals, we derive smooth approximations of them that contain the ATE but can be estimated using debiased estimators leveraging semiparametric efficiency theory. Specifically, we propose a Targeted Minimum Loss-Based estimator that is \sqrt{n} -consistent and asymptotically normal under nonparametric assumptions on the propensity score and outcome regression. We then show how to obtain a uniformly valid confidence set across all trimming and smoothing parameters with the multiplier bootstrap. This allows researchers to consider many parameters, choose the tightest confidence interval, and obtain valid coverage. We demonstrate via simulations that non-overlap bound estimators can detect more outliers than traditional doubly-robust point estimators. We illustrate our method in a study of heart catheterization on mortality.



2. For B bootstrap samples, draw i : the studentized residuals for each

$n_{i=1}^n$ with $\mathbb{E}(\xi) = 0$, $\mathbb{E}(\xi^2) = 1$, and form

$$1 \leftarrow \frac{n}{B} \sum_{b=1}^B \int \varphi_{U,k}(Z_i, \hat{\eta}) - \hat{U}_k \right)$$

Practical benefits: higher precision, higher power

N	Mean Width		Power	
	Traditional	Bounds	Traditional	Bounds
<i>(A) Simulations conditional on non-overlap</i>				
100				
250				
500				
1000				

Practical benefits: higher precision, higher power

N	Mean Width		Power	
	Traditional	Bounds	Traditional	Bounds
<i>(A) Simulations conditional on non-overlap</i>				
100		1.91		
250		1.83		
500		1.65		
1000		1.35		

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N	Mean Width		Power	
	Traditional	Bounds	Traditional	Bounds
<i>(A) Simulations conditional on non-overlap</i>				
100	1.91	0.46		
250	1.83	0.29		
500	1.65	0.22		
1000	1.35	0.17		

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N	Mean Width		Power	
	Traditional	Bounds	Traditional	Bounds
<i>(A) Simulations conditional on non-overlap</i>				
100	1.91	0.46	0.02	
250	1.83	0.29	0.07	
500	1.65	0.22	0.16	
1000	1.35	0.17	0.31	

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N	Mean Width		Power	
	Traditional	Bounds	Traditional	Bounds
<i>(A) Simulations conditional on non-overlap</i>				
100	1.91	0.46	0.02	0.49
250	1.83	0.29	0.07	0.88
500	1.65	0.22	0.16	1.00
1000	1.35	0.17	0.31	1.00

No free lunch: tradeoffs

- No need for overlap to hold, but your outcome must be *bounded*.

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- Trade point identification for bounds.
- Only performs better than traditional approaches when the size of the non-overlap subpopulation is small relative to the effect size.

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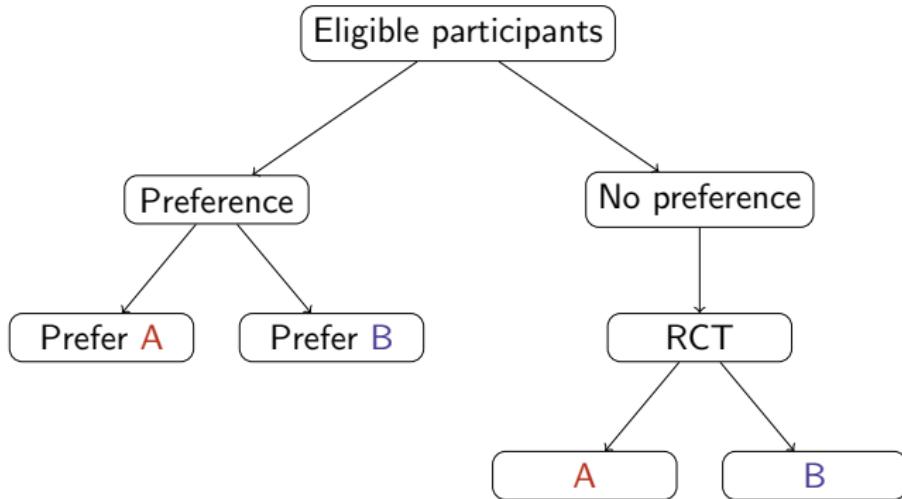
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- If there are overlap violations that make estimating a point estimate difficult, *non-overlap bounds may nevertheless yield useful information.*

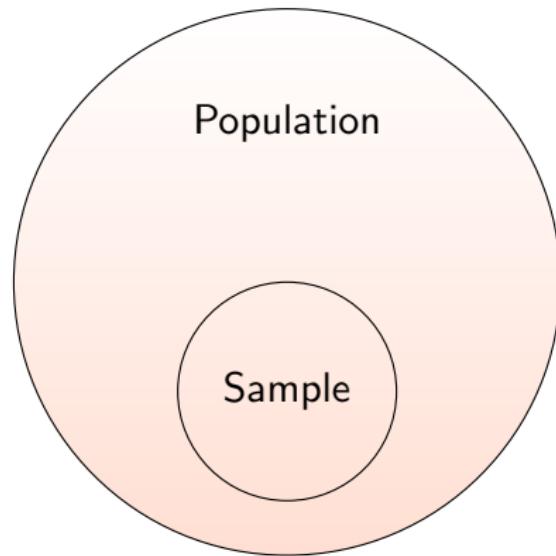
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- If the scientific estimand is the Average Treatment Effect, *then target the Average Treatment Effect.*
- If there are overlap violations that make estimating a point estimate difficult, *non-overlap bounds may nevertheless yield useful information.*
- As a *secondary* analysis, an alternative estimand can be estimated and reported.

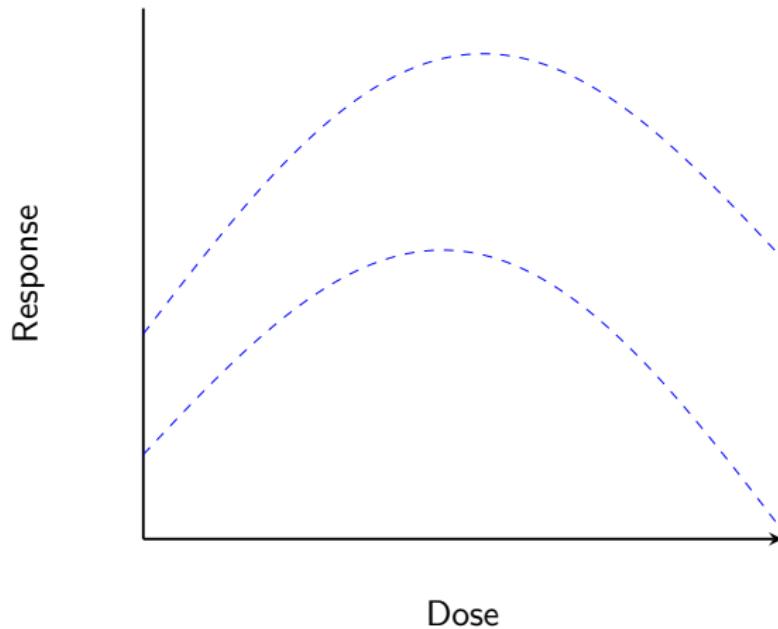
Next steps: partially randomized patient preference trials



Next steps: generalizing trial results



Next steps: dose-response curves



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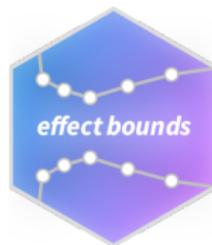


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Summary

effectbounds R package github.com/herbps10/effectbounds

□ README Apache-2.0 license

effectbounds

R-CMD-check.yaml passing



Overview

The `effectbounds` package provides tools for estimating non-overlap bounds for causal effects.

The identification of causal effects typically relies on the *overlap assumption* (also known as *positivity*), which requires that all units have a positive probability of being in either the treatment or control group.

When overlap fails in finite-samples, with some units having very small estimated probability of receiving the treatment (or control), then estimators of the causal effect can perform poorly.

Non-overlap bounds are an approach for estimating causal effects even when non-overlap is violated, by focusing on estimating *bounds* on the effect.

Installation

You can install the development version of `effectbounds` from [GitHub](#):

```
# install.packages("devtools")
devtools::install_github("herbps10/effectbounds")
```

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