

## Title in Progress

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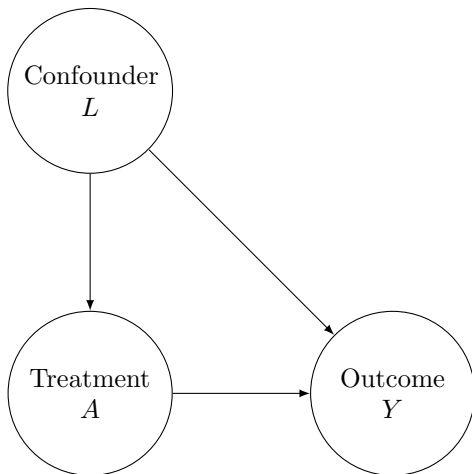
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- ▶ . . . but there is no consensus on the best way to estimate standard errors when using the PSM algorithm.
- ▶ How can we assess which procedures reliably estimate standard errors?

# Motivation

A simulation study!

## A Quick Foray into Confounding





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- (4) We end with a matched dataset.

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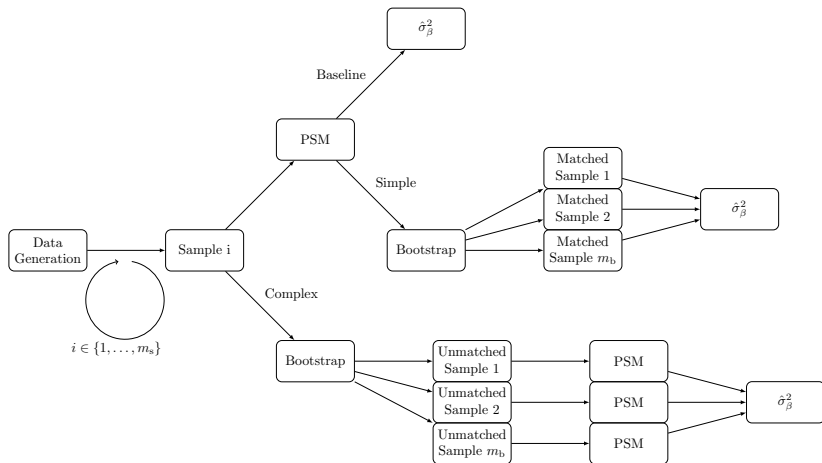
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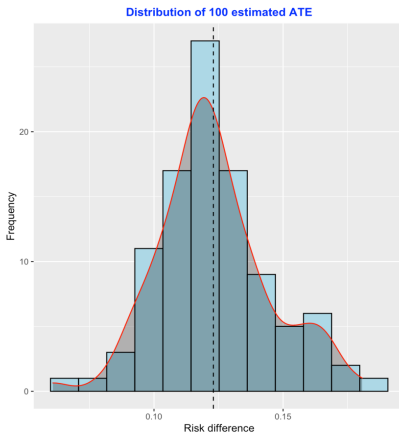
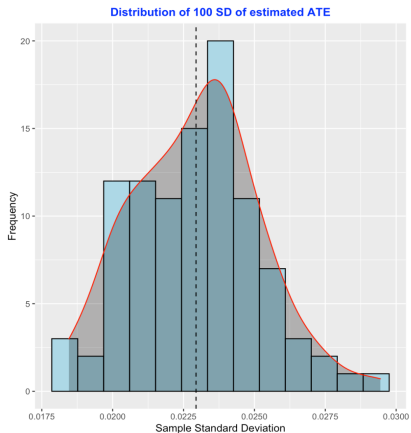
- ▶ Bootstrapping is one of the most common procedures for estimating standard errors.
- ▶ The PSM algorithm intakes an unmatched dataset and outputs a matched one.
- ▶ **Primary Research Question:** When do we execute the bootstrap - before the match or after it?
- ▶ Let's try both!



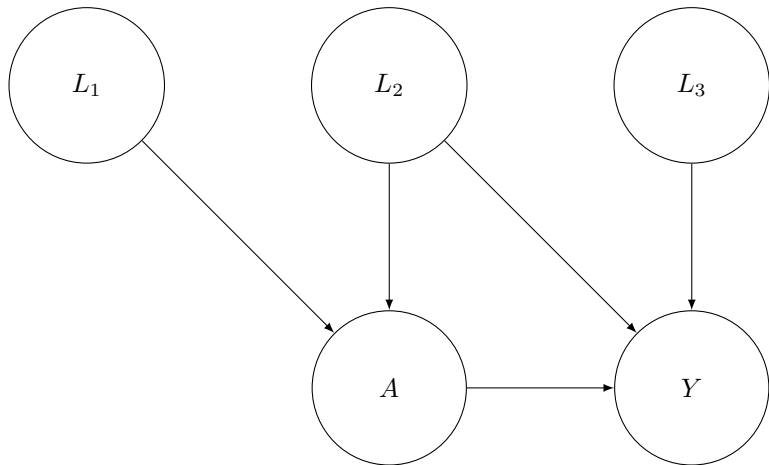
# Roadmap of the Simulation Study



# An Example of a Single Bootstrap Sample



## Data Generation



## Data Generation - Continuous Outcome

For each individual  $i \in \{1, \dots, n\}$ , we consider covariates  $L_{1i}, L_{2i}, L_{3i} \sim N(0, 1)$ . Treatments are distributed according to law  $A_i \sim B(\pi_i)$ , where  $\pi_i$  - the true propensity to be treated - is subject to the data-generating process

$$\log \left( \frac{\pi_i}{1 - \pi_i} \right) = \alpha_0 + \alpha_1 L_{1i} + \alpha_2 L_{2i}.$$

Given this, we further define the data-generating process of our continuous outcome via

$$Y_i = \beta_1 A_i + \beta_2 L_{2i} + \beta_3 L_{3i} + \varepsilon_i,$$

where  $\varepsilon_i$  denotes random error. Because  $L_{2i}$  effects both  $A_i$  and  $Y_i$ , it acts as a confounder in estimating the treatment effect.

## Data Generation - Binary Outcome

For each individual  $i \in \{1, \dots, n\}$ , we consider covariates  $L_{1i}, L_{2i}, L_{3i} \sim N(0, 1)$ . Treatments are distributed according to law  $A_i \sim B(\pi_i)$ , where  $\pi_i$  - the true propensity to be treated - is subject to the data-generating process

$$\log \left( \frac{\pi_i}{1 - \pi_i} \right) = \alpha_0 + \alpha_1 L_{1i} + \alpha_2 L_{2i}.$$

Given this, we further define the data-generating process of our binary outcome via  $Y_i \sim B(\tau_i)$  where

$$\log \left( \frac{\tau_i}{1 - \tau_i} \right) = \beta_0 + \beta_1 A_i + \beta_2 L_{2i} + \beta_3 L_{3i}.$$

Observe that we have omitted a random error term, as realizations of our binary  $Y_i$  are innately subject to noise.

# Parameters of Interest

- ▶ The sample size of each dataset  $n_{\text{sample}} \in \{100, 1000\}$
- ▶ The population proportion of treated individuals  $\pi \in \{0.113, 0.216, 0.313\}$
- ▶ The true average treatment effect  $\beta_1 \in \{0.15, 0.30\}$  for binary data;  $\beta_1 \in \{-1, 1\}$  for continuous data

## *Other Parameters*

- ▶ The number of datasets  $m_{\text{sample}} = 100$
- ▶ The number of bootstrap re-samples  $m_{\text{boot}} = 500$
- ▶ The sample size of bootstrap re-samples  $n_{\text{simple}} = n_{\text{complex}} = n_{\text{sample}} \times \pi$
- ▶ Strength of covariate effect on treatment  $\alpha_1 = \log(1.25), \alpha_2 = \log(1.75)$
- ▶ Strength of covariate effect on outcome  $\beta_2 = \log(1.75), \beta_3 = \log(1.25)$

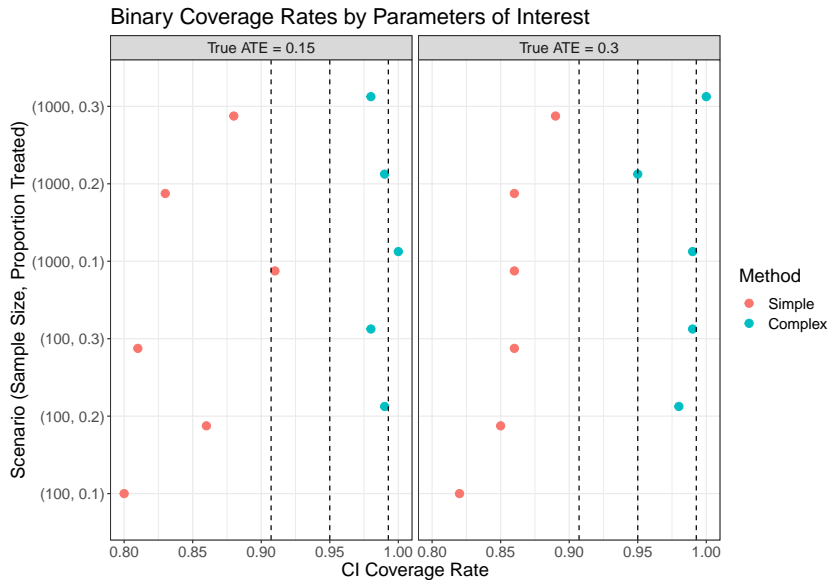
## Measures of Interest

- ▶ **Standard Error:** The variability of the average estimate of the treatment effect ( $SE(\hat{\beta}_1)$ ).
- ▶ **Coverage Rate:** The fraction of alleged 95% confidence intervals ( $\hat{\beta}_1 \pm 1.96 \times SE(\hat{\beta}_1)$ ) that contain the true treatment effect

### *Other Measures*

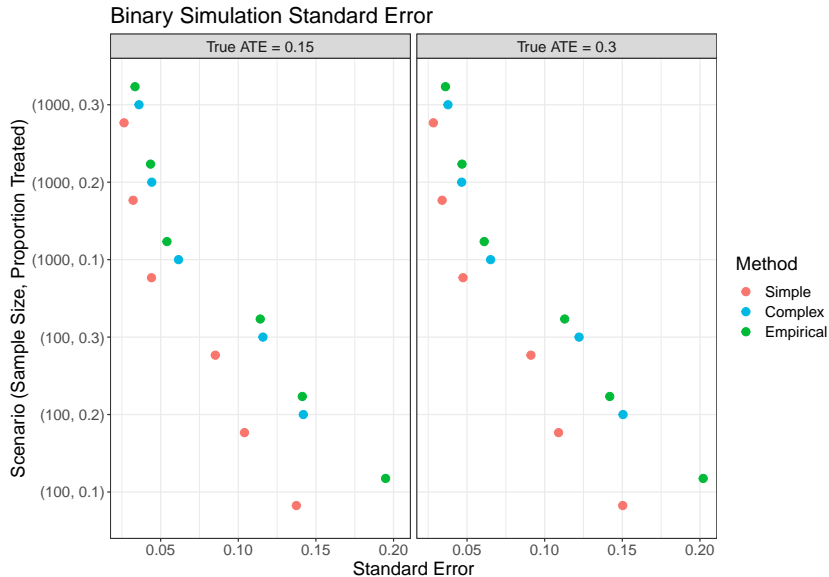
- ▶ **Bias:** The mean of the average estimate ( $\hat{\beta}_1$ ) less the true treatment effect ( $\beta$ )

# Results - Binary Outcome

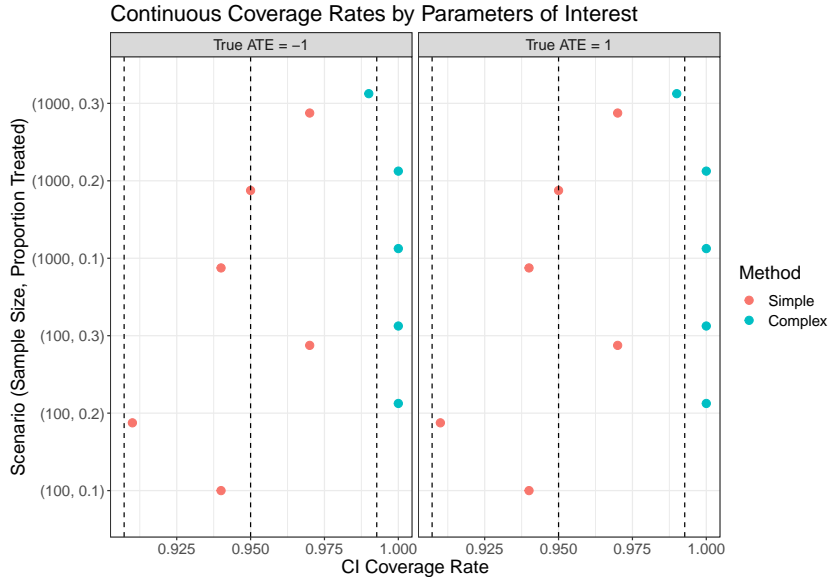




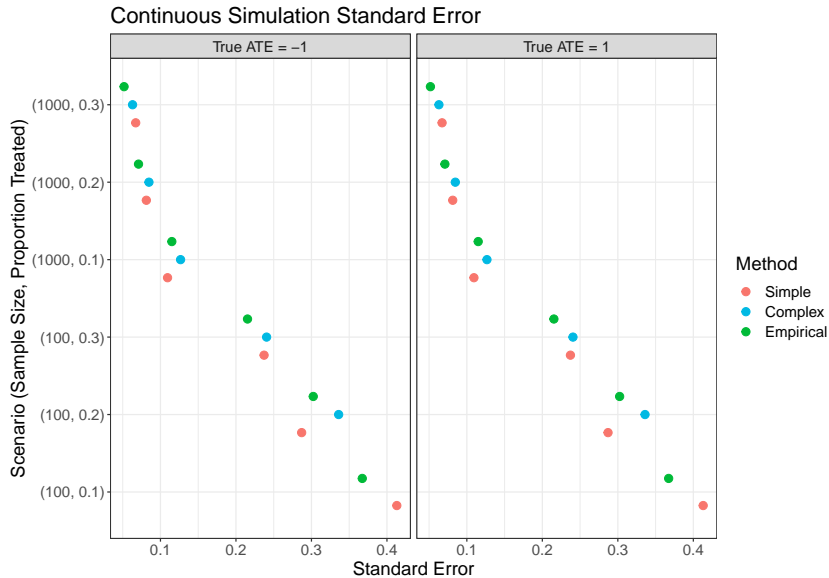
# Results - Binary Outcome



# Results - Continuous Outcome



# Results - Continuous Outcome



## Summary of Results

- ▶ For binary outcomes, the simple bootstrap tended to underestimate the standard error
- ▶ Larger standard error estimates from complex bootstrap in binary and continuous settings
- ▶ Differences between simple and complex bootstrap were smaller for larger sample sizes
- ▶ Complex bootstrap not as reliable in small sample sizes

# Limitations

- ▶ Sample size / treatment (or exposure) prevalence
- ▶ Small number of initial samples, limited in detecting significant differences in coverage rate

## Future Work

- ▶ Larger number of initial samples, narrower coverage window
- ▶ Increased sample size, changes in bootstrap performance?
- ▶ Changes in treatment propensity model
- ▶ Non-normal distributions of covariates