

Title in Progress

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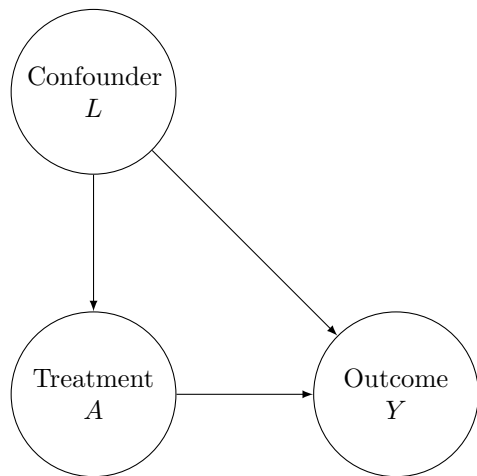
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- ▶ . . . but there is no consensus on the best way to estimate standard errors when using the PSM algorithm.
- ▶ How can we assess which procedures reliably estimate standard errors?

Motivation

A simulation study!

A Quick Foray into Confounding



Taking a Step Back, What is Propensity Score Matching?

- ▶ A *propensity score* is the probability that an individual receives a treatment A ; that is, $P(A = 1)$. In an RCT, treatments are randomized, and hence outcomes Y are independent of treatment A .

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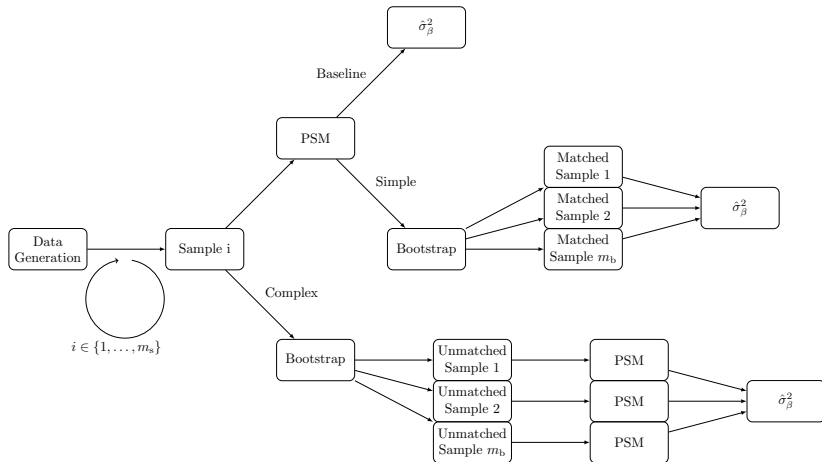
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- ▶ The PSM algorithm intakes an unmatched dataset and outputs a matched one.
- ▶ When do we execute the bootstrap - before the match or after it?
- ▶ Let's try both!

Roadmap of the Simulation Study

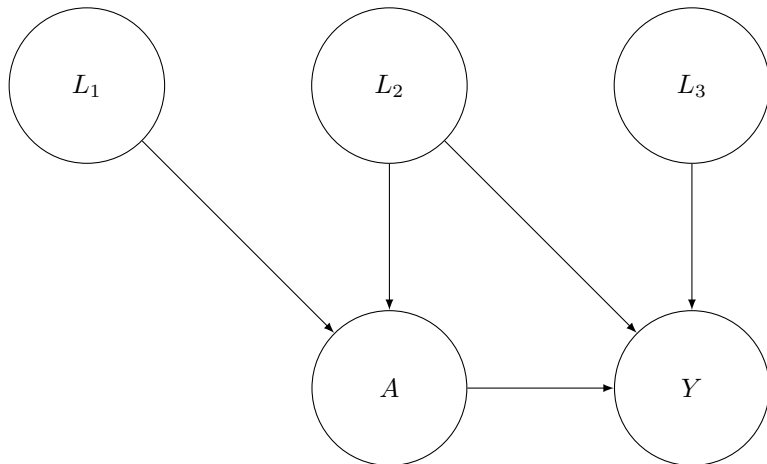


Data Generation

Let's generate some data.

Data Generation

- ▶ Three covariates (L_1 , L_2 , L_3), one confounding covariate (L_2) related to both treatment (A) and outcome (Y).



Data Generation - Random Number Generation

```
set.seed(20220217)
```

```
seed_vec <-  
  runif(100000,  
        min = 100,  
        max = 99999999) %>%  
  round(0) %>%  
  unique()
```

```
simple_boot <-  
  function(df,  
            n = m_boot,  
            size = df %>% pull(A) %>% sum(),  
            seeds = seed_vec){  
    boots <- list()  
    for (i in 1:n) {  
      set.seed(seeds[i])  
      boots[[i]] <-  
        df %>%
```

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 π_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 ε_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 π_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 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 $\beta_1 \in \{0.15, 0.30\}$

Other Parameters

- ▶ The number of datasets $m_{\text{sample}} = 100$
- ▶ The number of bootstrap re-sample $m_{\text{boot}} = 500$
- ▶ The sample size of bootstrap re-samples
 $n_{\text{simple}} = n_{\text{complex}} = n_{\text{sample}} \times \pi$
- ▶ Strength of Covariate Correlation on Treatment Status α_1, α_2
(continuous data (1,2), binary data ($\log(1.25), \log(1.75)$)))
- ▶ Strength of Covariate Correlation on Outcome Variable β_2, β_3
(continuous data (2,1), binary data ($\log(1.75), \log(1.25)$)))

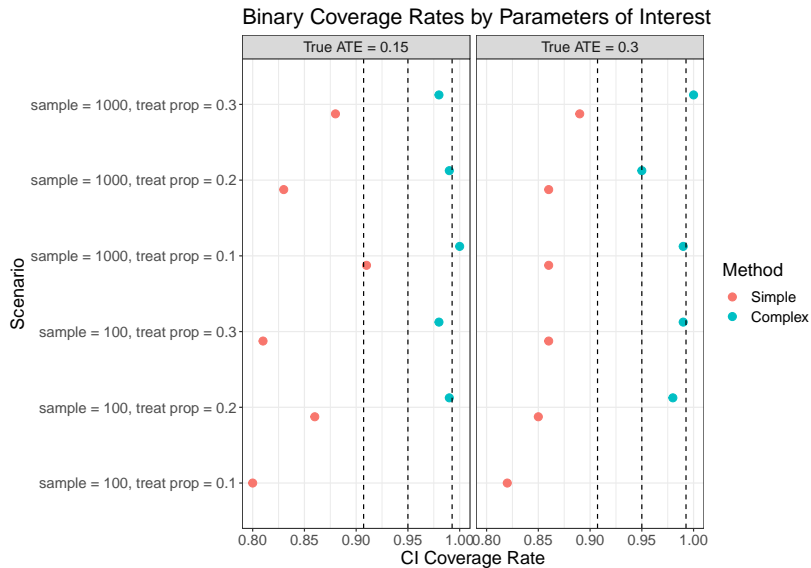
Measures of Interest

- ▶ **Coverage Rate:** Looks at the rate of the true average treatment effect falling in the 95% confidence intervals.
 $\hat{ATE} \pm 1.96 \times SE$
- ▶ **Standard Error:** the variability of the average estimate.

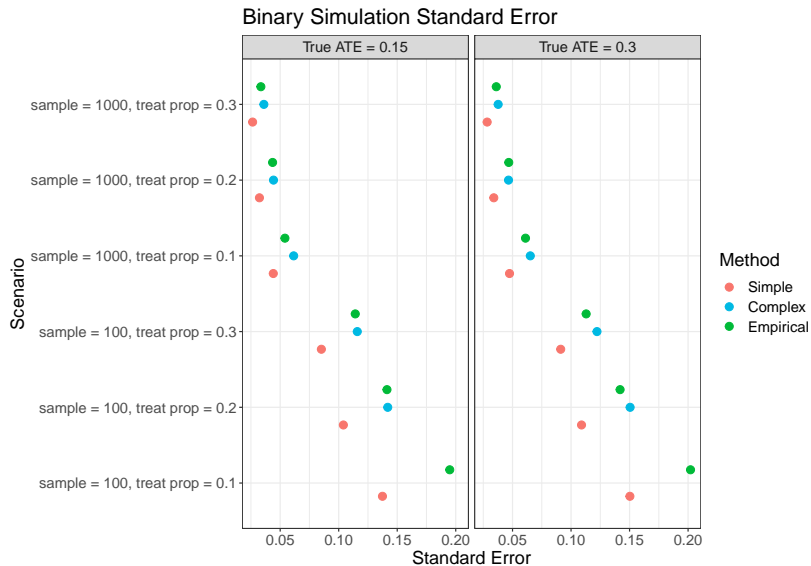
Other Measures

- ▶ **Bias:** This is mean of the average estimate subtract the true ATE
- ▶ **95% Confidence Intervals:**

Results

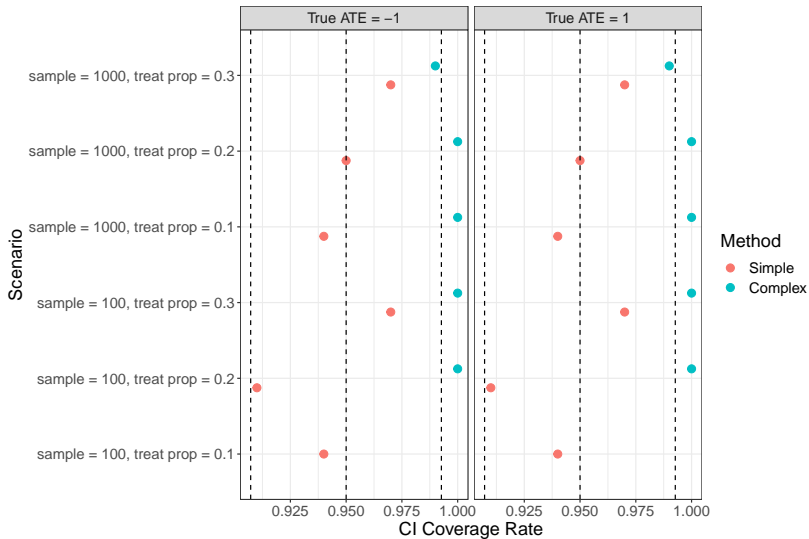


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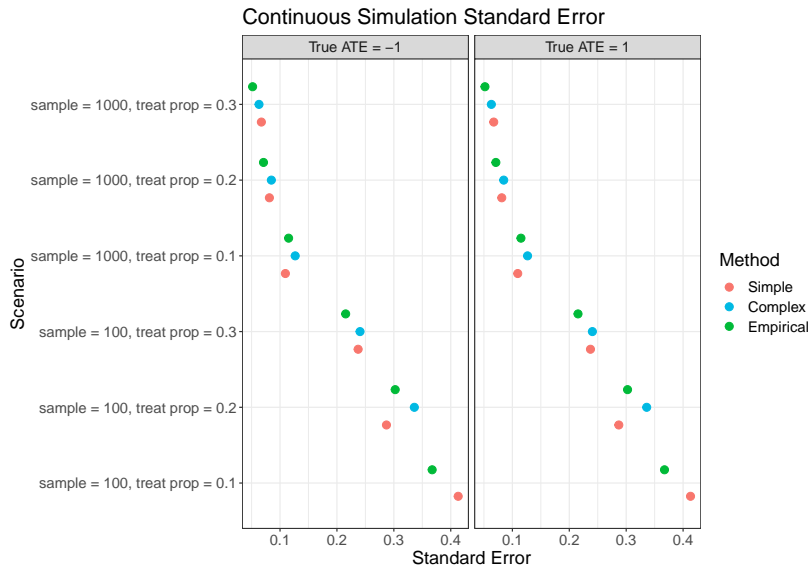


Results

Continuous Coverage Rates by Parameters of Interest



Results



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