The Chicken or the Egg: Bootstrapping in the Setting of Propensity Score Matching

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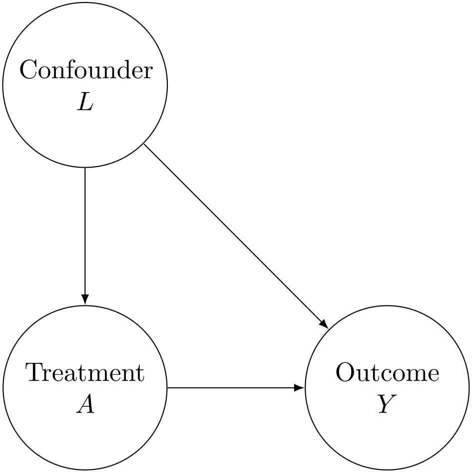
- Propensity score matching (PSM) is a tool that can help us mitigate the effects of confounders...
- ... but there is no consensus on the best way to estimate standard errors when using the PSM algorithm.
- How can we assess which procedures reliably estimate standard errors?

Motivation

A simulation study!

A Quick Foray into Confounding



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(4) We end with a matched dataset.

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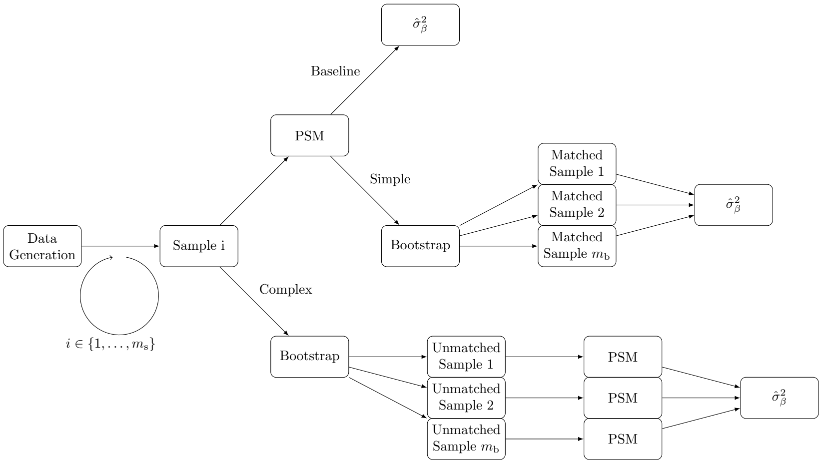
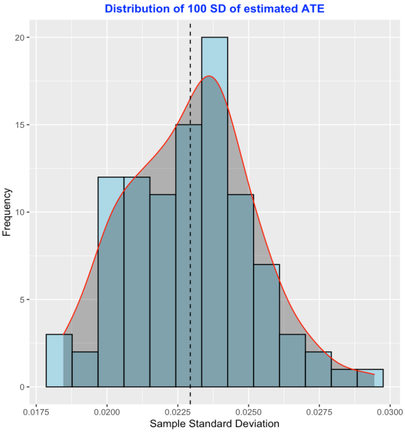
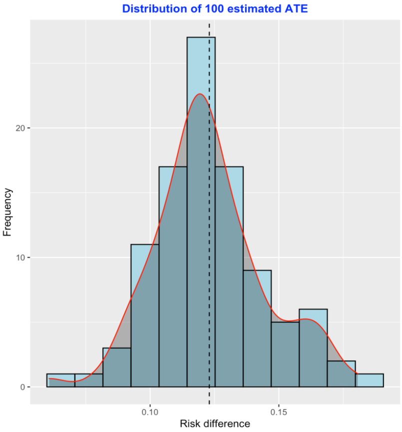
- The PSM algorithm intakes an unmatched dataset and outputs a matched one.
- **Primary Research Question:** When do we execute the bootstrap - before the match or after it?
- Let's try both!

Roadmap of the Simulation Study

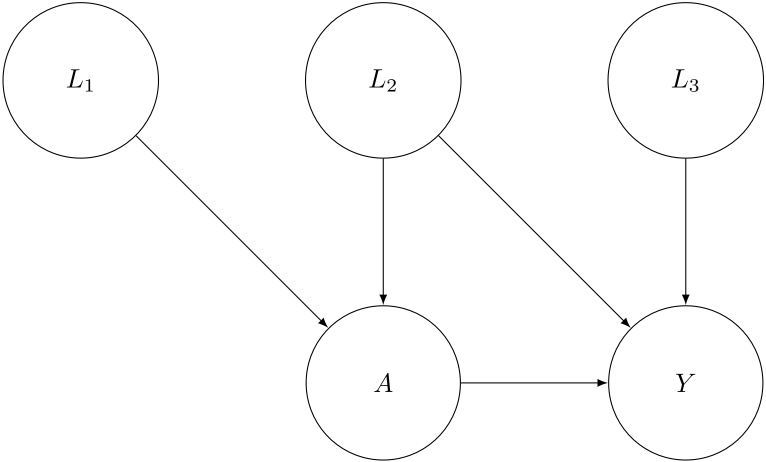


An Example of a Single Bootstrap Sample





Data Generation



Data Generation - Continuous Outcome

For each individual $i \in \{1, \ldots, n\}$, 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 $i \in \{1, \ldots, n\}$, 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

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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 $\beta_2 = \log(1.75), \beta_3 = \log(1.25)$

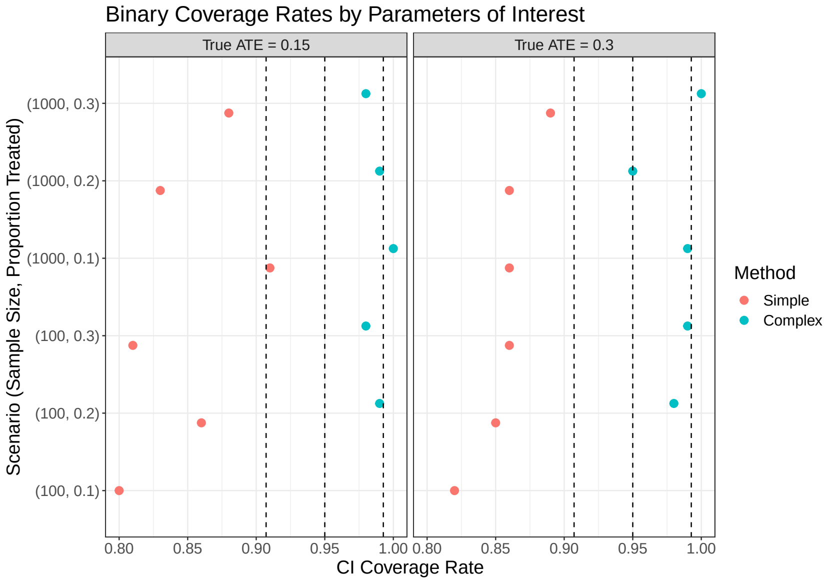
Measures of Interest

- **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 (β)

Results - Binary Outcome



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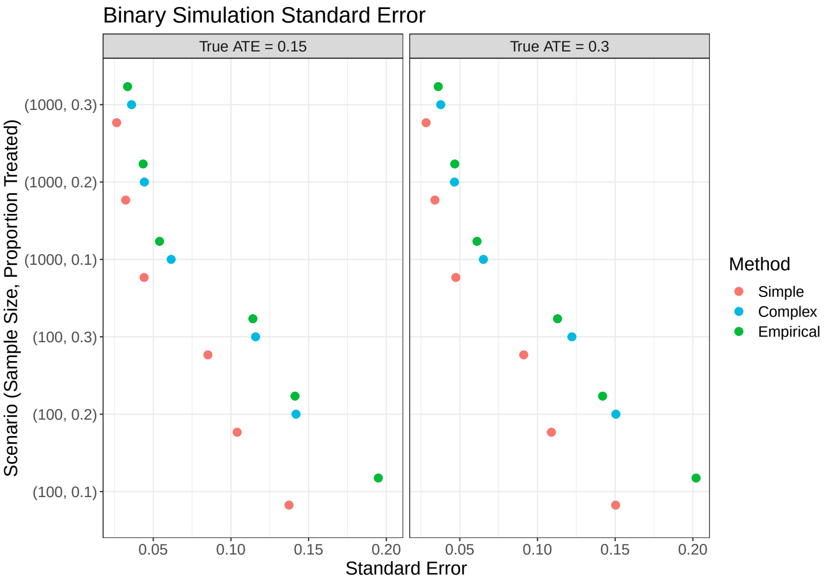
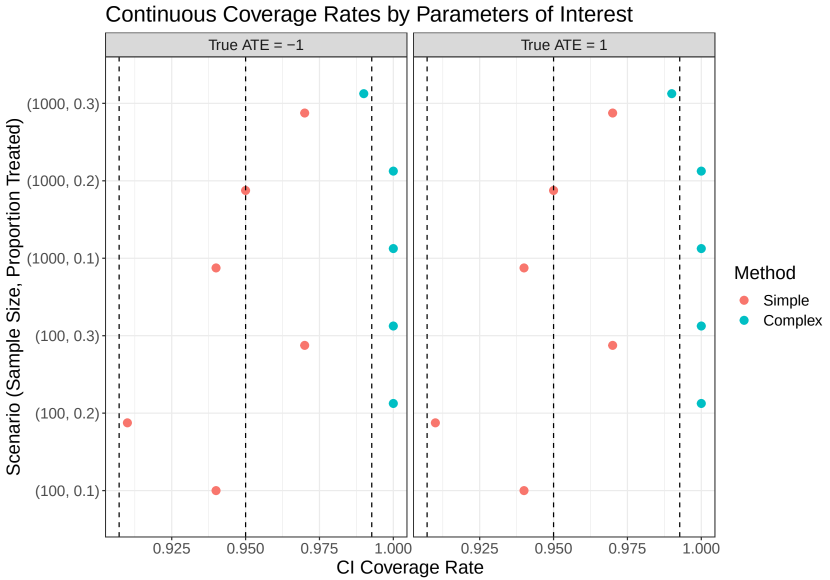


Results - Continuous Outcome



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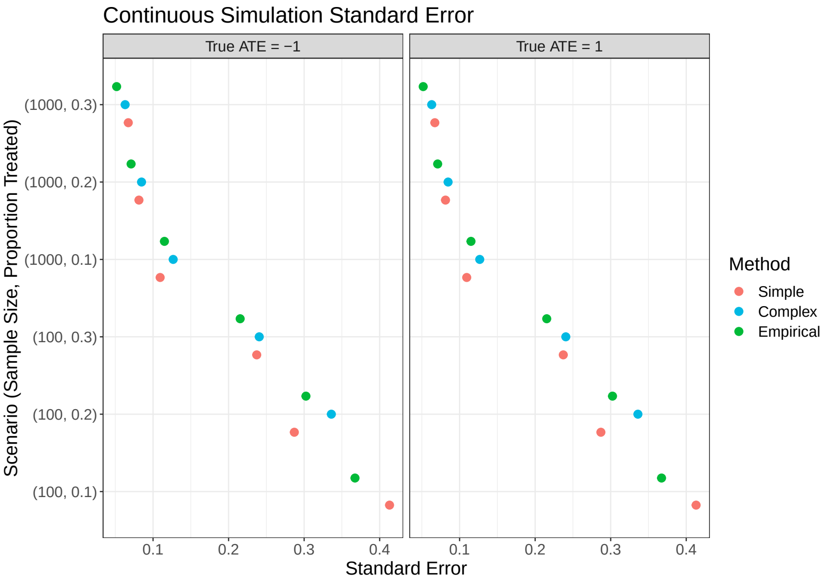

Summary of Results

- 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