Title in Progress

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2022-02-21

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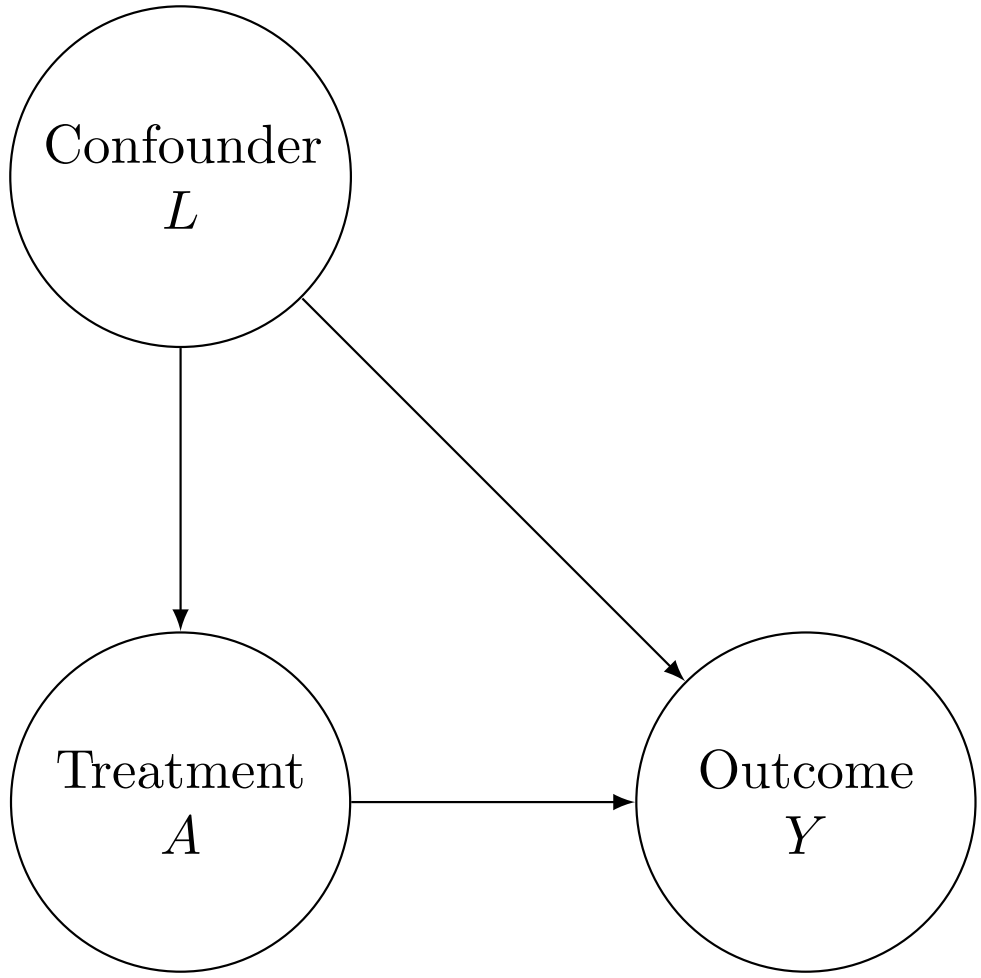
- Propensity score matching (PSM) is a tool that can help us mitigate the effects of confounders...
- ... but there is no consensus on the best way to estimate standard errors when using the PSM algorithm.
- How can we assess which procedures reliably estimate standard errors?

Motivation

A simulation study!

A Quick Foray into Confounding



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(4) We end with a matched dataset.

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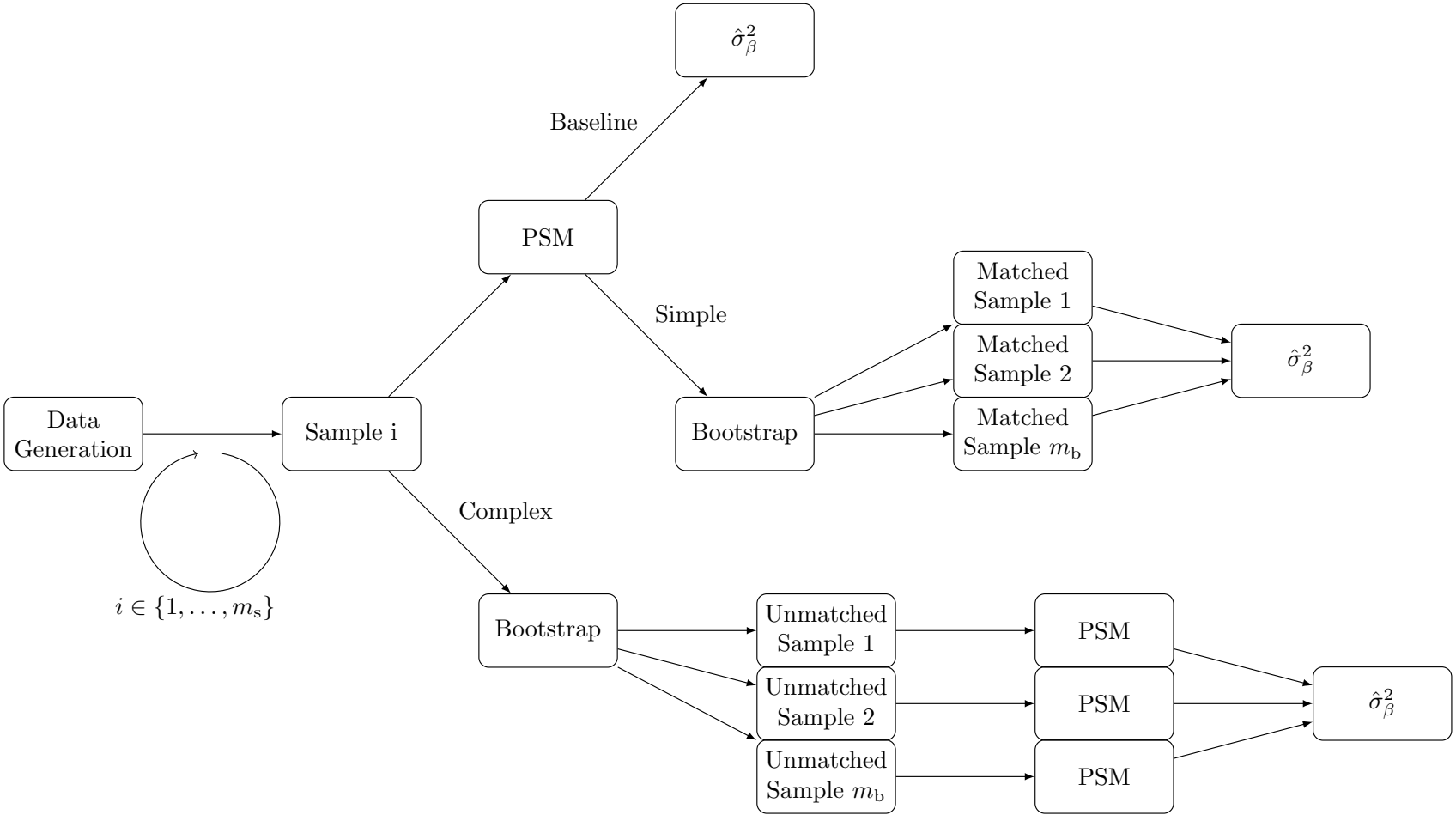
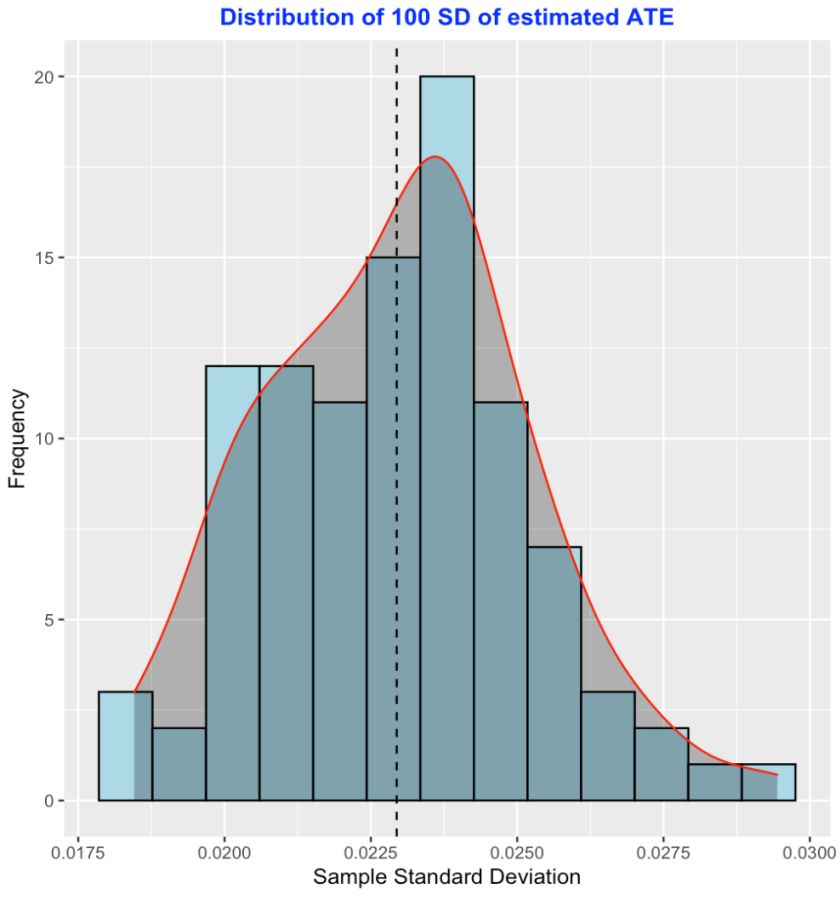
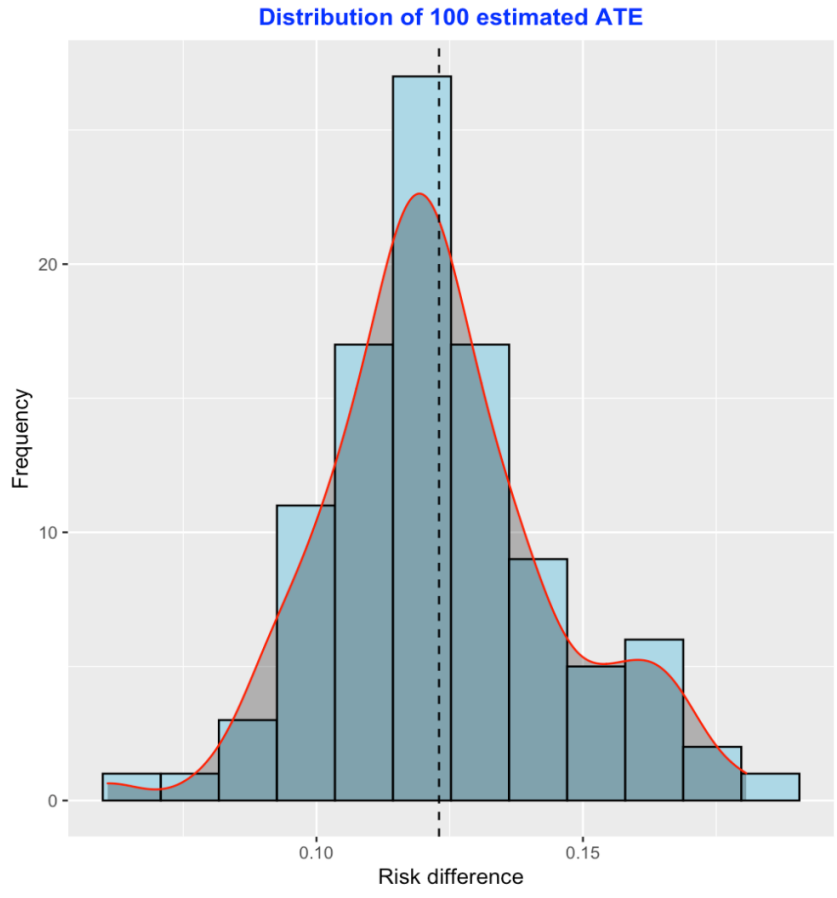
- The PSM algorithm intakes an unmatched dataset and outputs a matched one.
- When do we execute the bootstrap - before the match or after it?
- Let's try both!

Roadmap of the Simulation Study

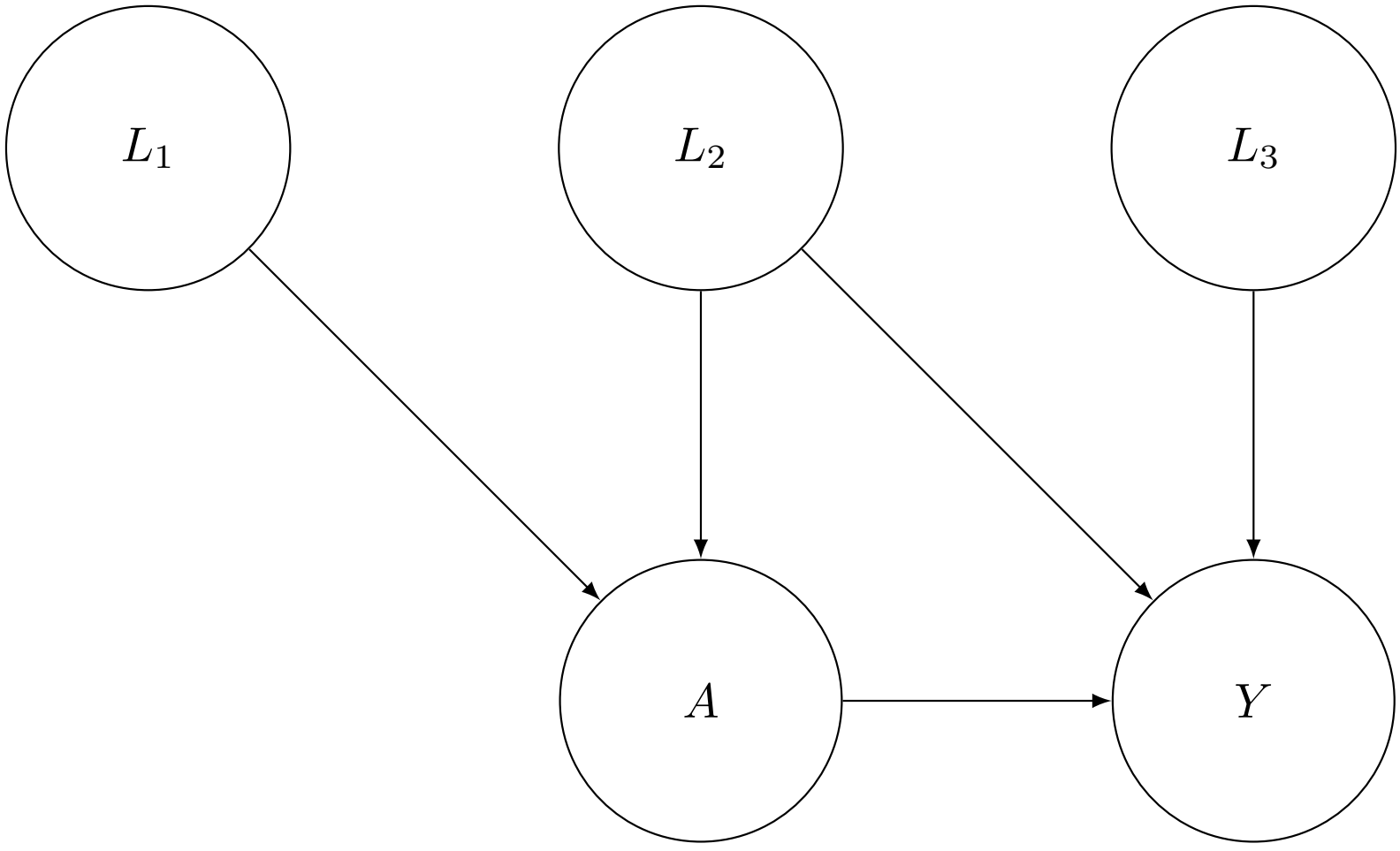


An Example of Bootstrap Result Image.





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

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

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

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

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 $\beta_1 \in \{0.15, 0.30\}$ 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-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 and 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

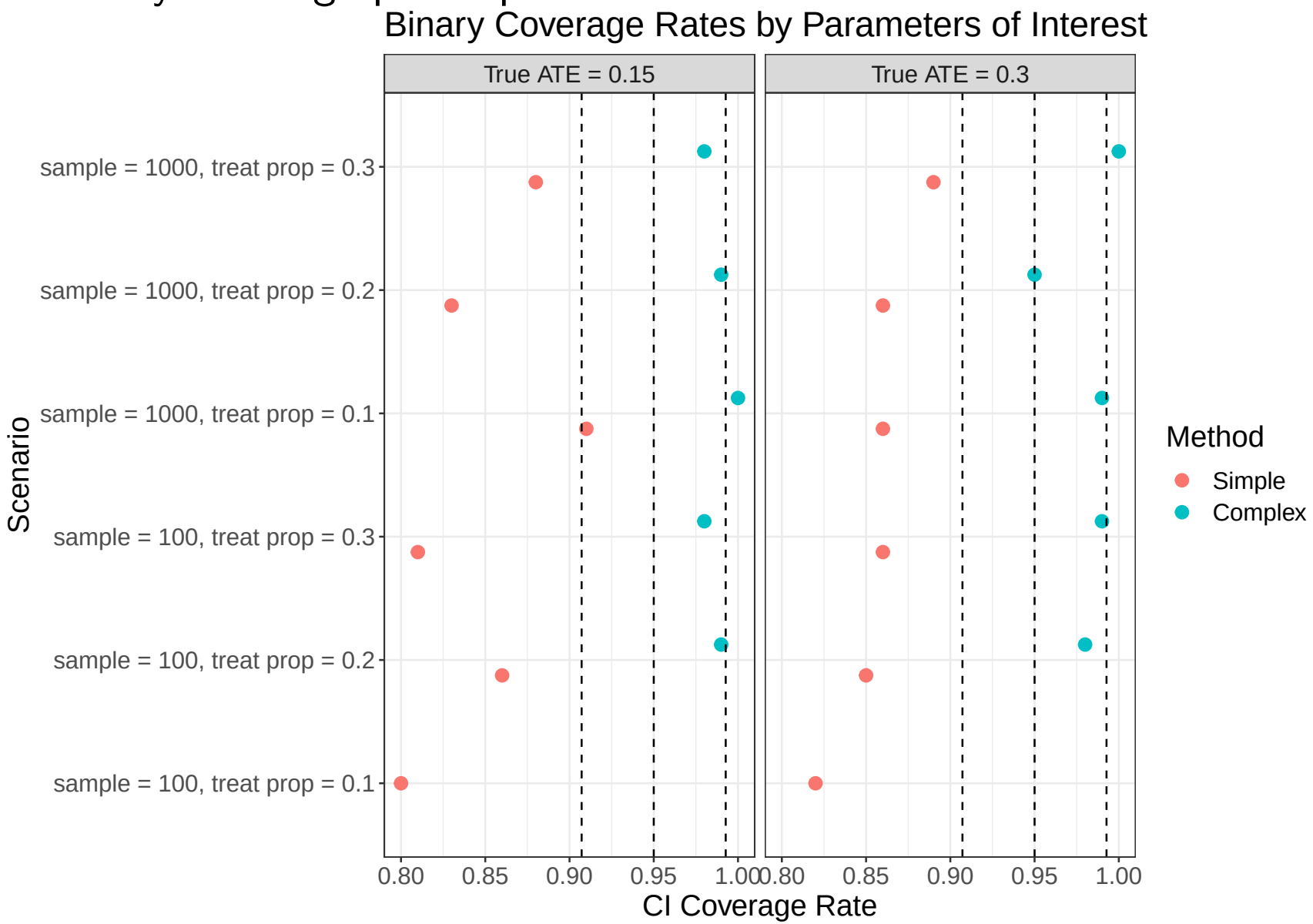
- **Coverage Rate:** Looks at the rate of the true avergae treatment effect falling in the 95% confidence intervals. $\hat{\text{ATE}} \pm 1.96 \times \text{SE}$
- **Standard Error:** the variability of the average estimate.

Other Measures

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

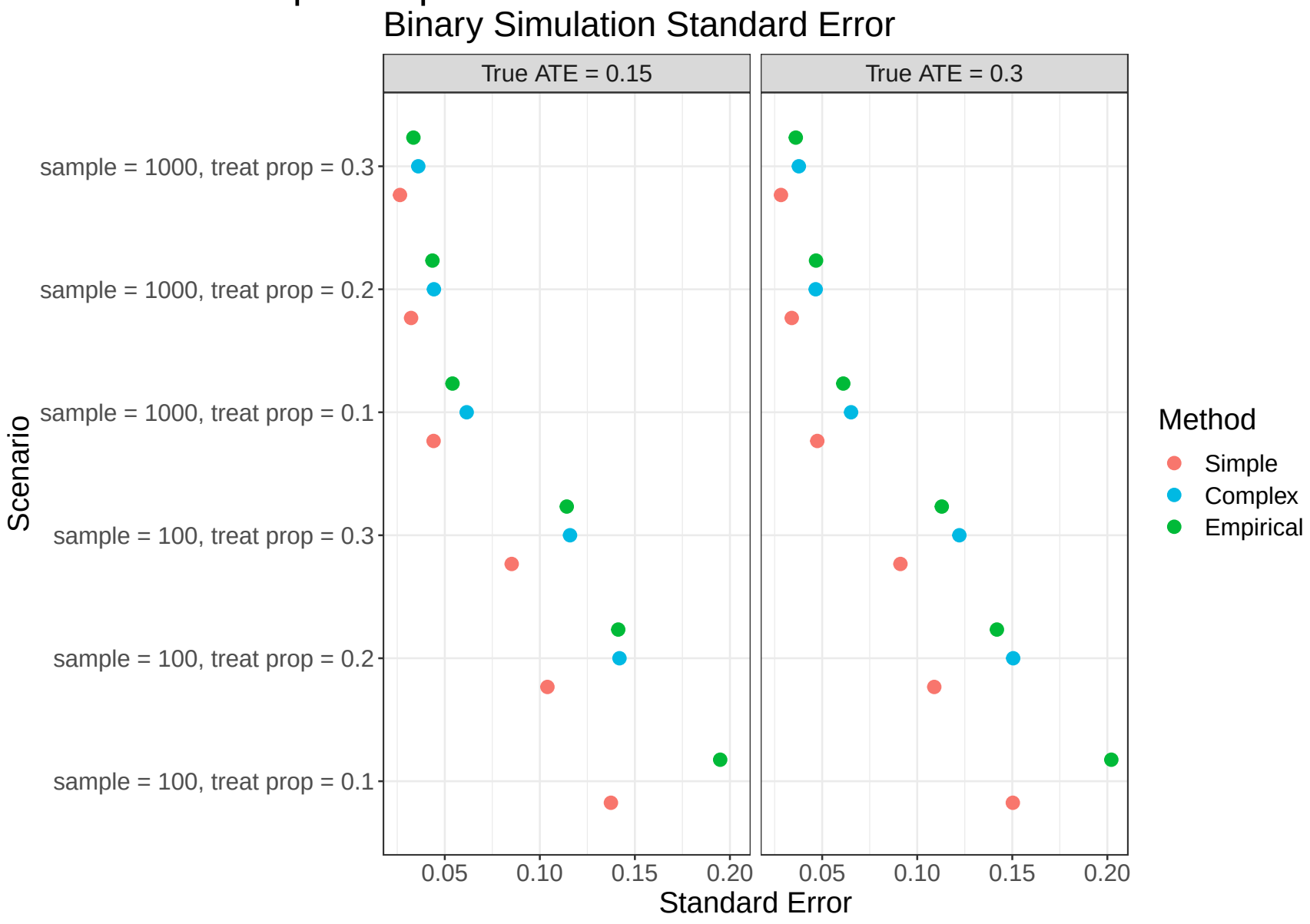
Results

in binary coverage plot-1.pdf



Results

standard error plot-1.pdf



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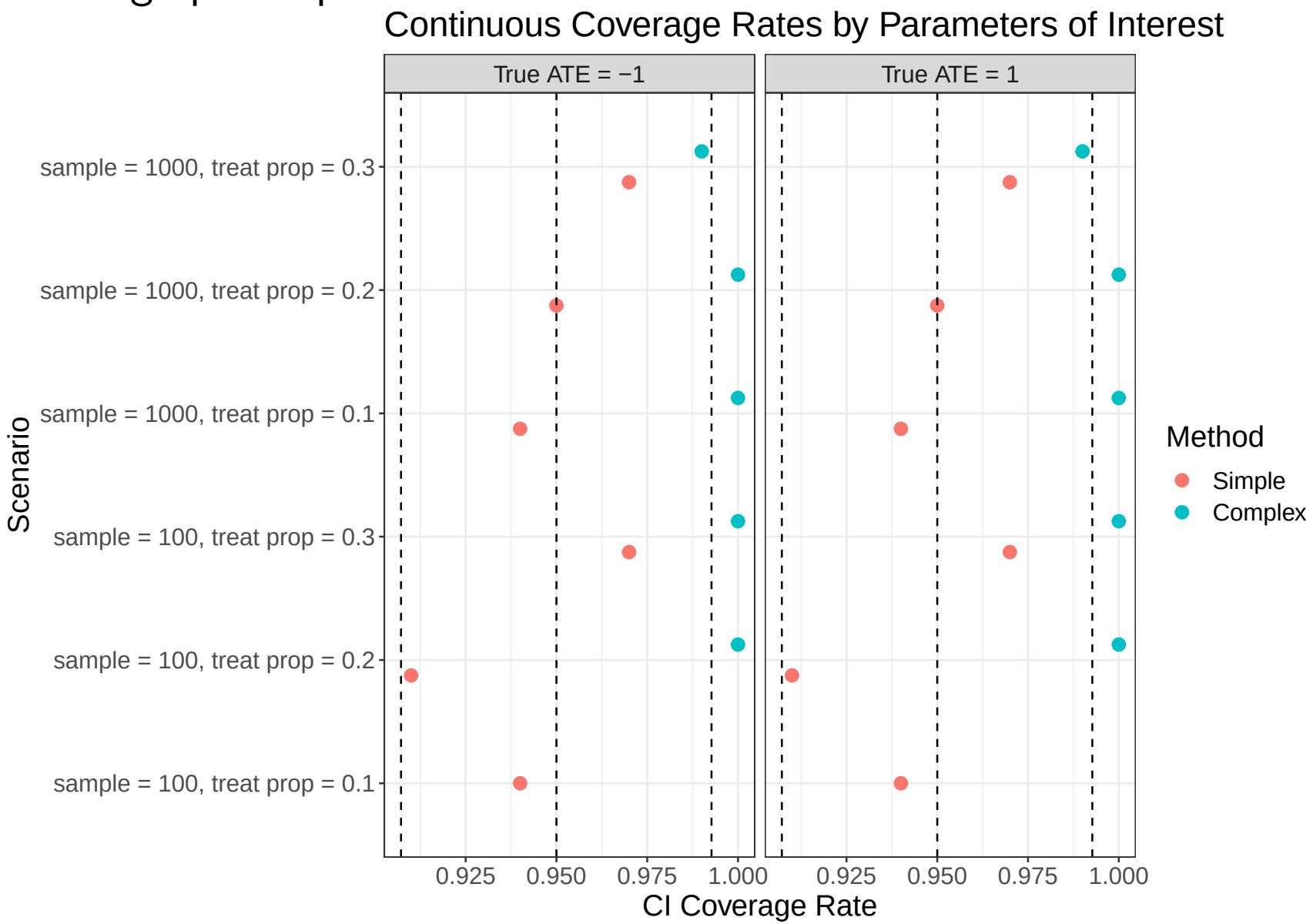

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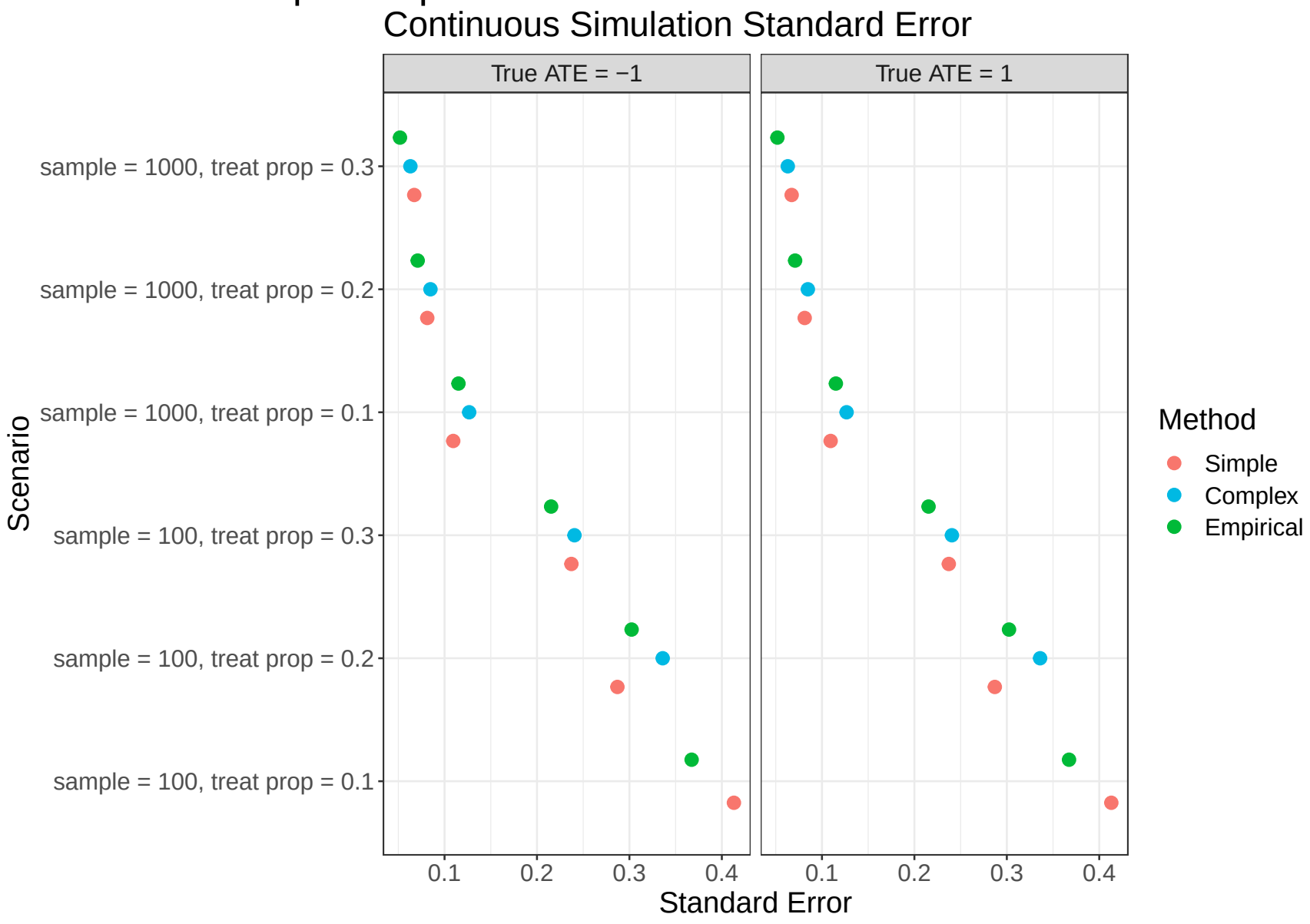

Summary of Results

- 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