Title in Progress

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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!

Enter the Bootstrap

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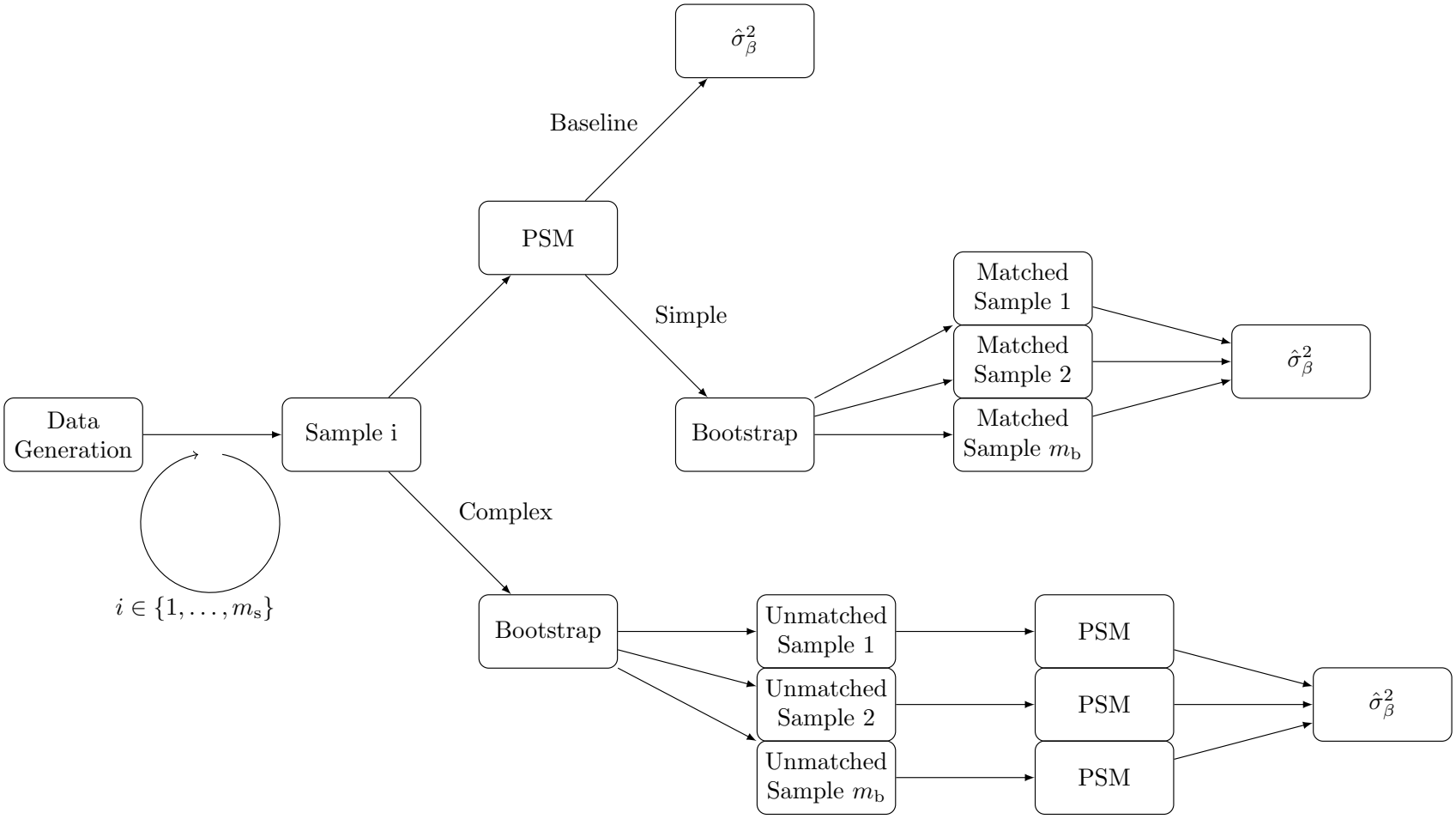
- The PSM algorithm intakes an unmatched dataset and outputs a matched one.
- When do we execute the bootstrap - before the match or after it?
- Let's try both!

Roadmap of the Simulation Study



Data Generation - 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

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

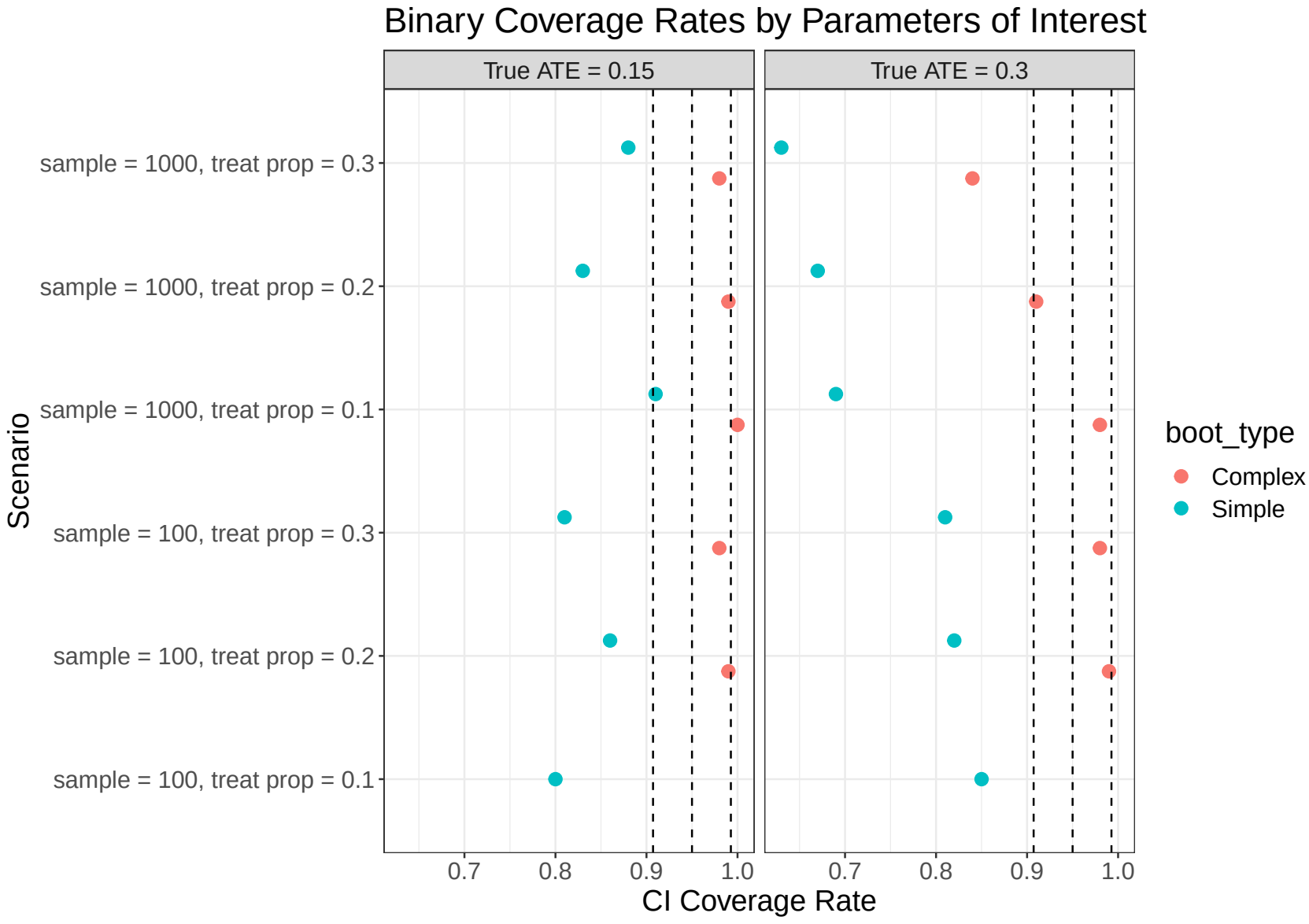
Given this, we further define the data-generating process of our binary outcome via $Y_i \sim B(\tau_i)$ where

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

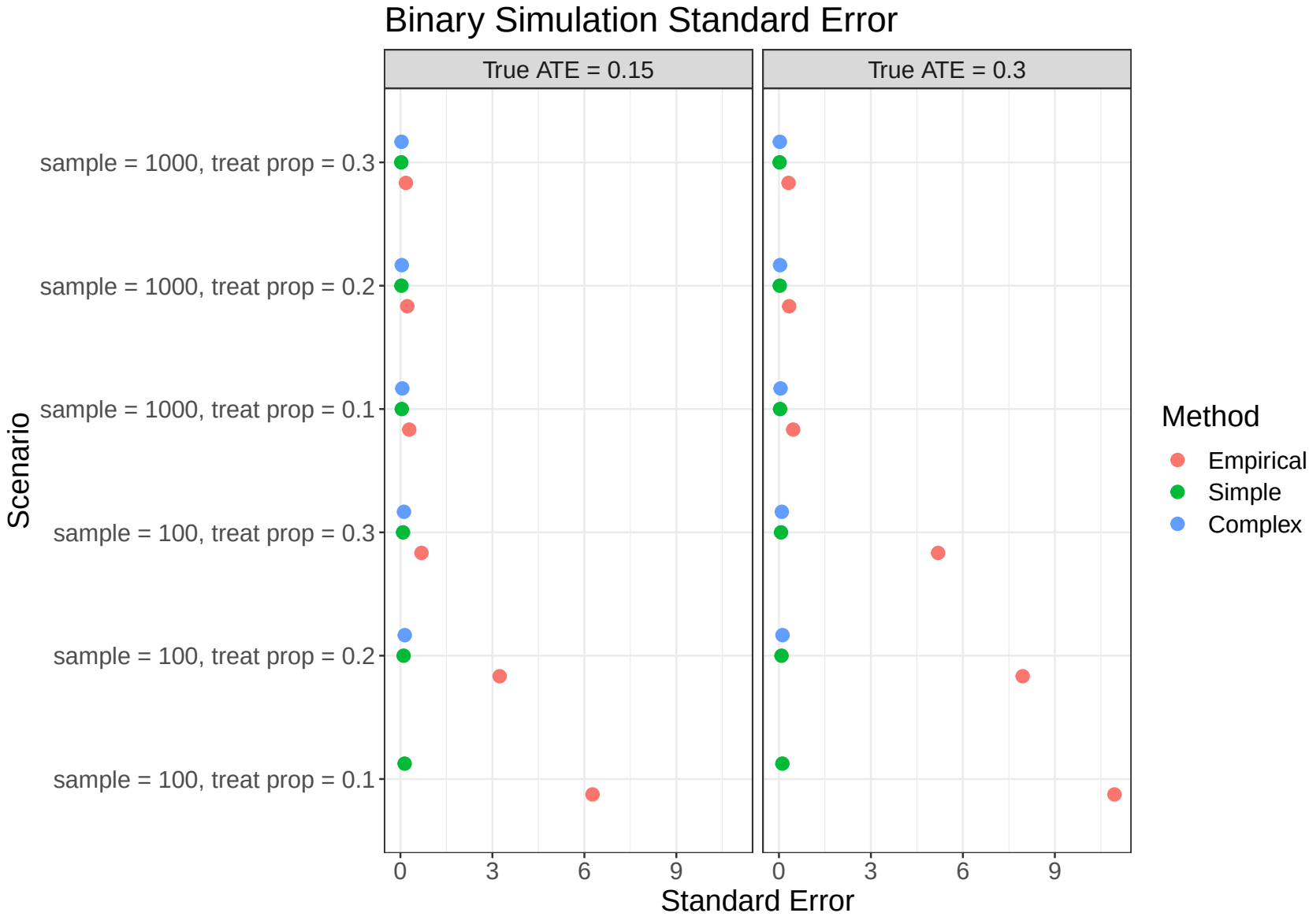
Observe that we have omitted a random error term, as realizations of Y_i are innately subject to noise.

Measures

Results


Binary Coverage Rates by Parameters of Interest
True ATE = 0.15
True ATE = 0.3
sample = 1000, treat prop = 0.3
sample = 1000, treat prop = 0.2
sample = 1000, treat prop = 0.1
sample = 100, treat prop = 0.3
sample = 100, treat prop = 0.2
sample = 100, treat prop = 0.1
Scenario
0.7
0.8
0.9
1.0
CI Coverage Rate
boot_type
Complex
Simple

Results


Binary Simulation Standard Error
True ATE = 0.15
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sample = 1000, treat prop = 0.3
sample = 1000, treat prop = 0.2
sample = 1000, treat prop = 0.1
sample = 100, treat prop = 0.3
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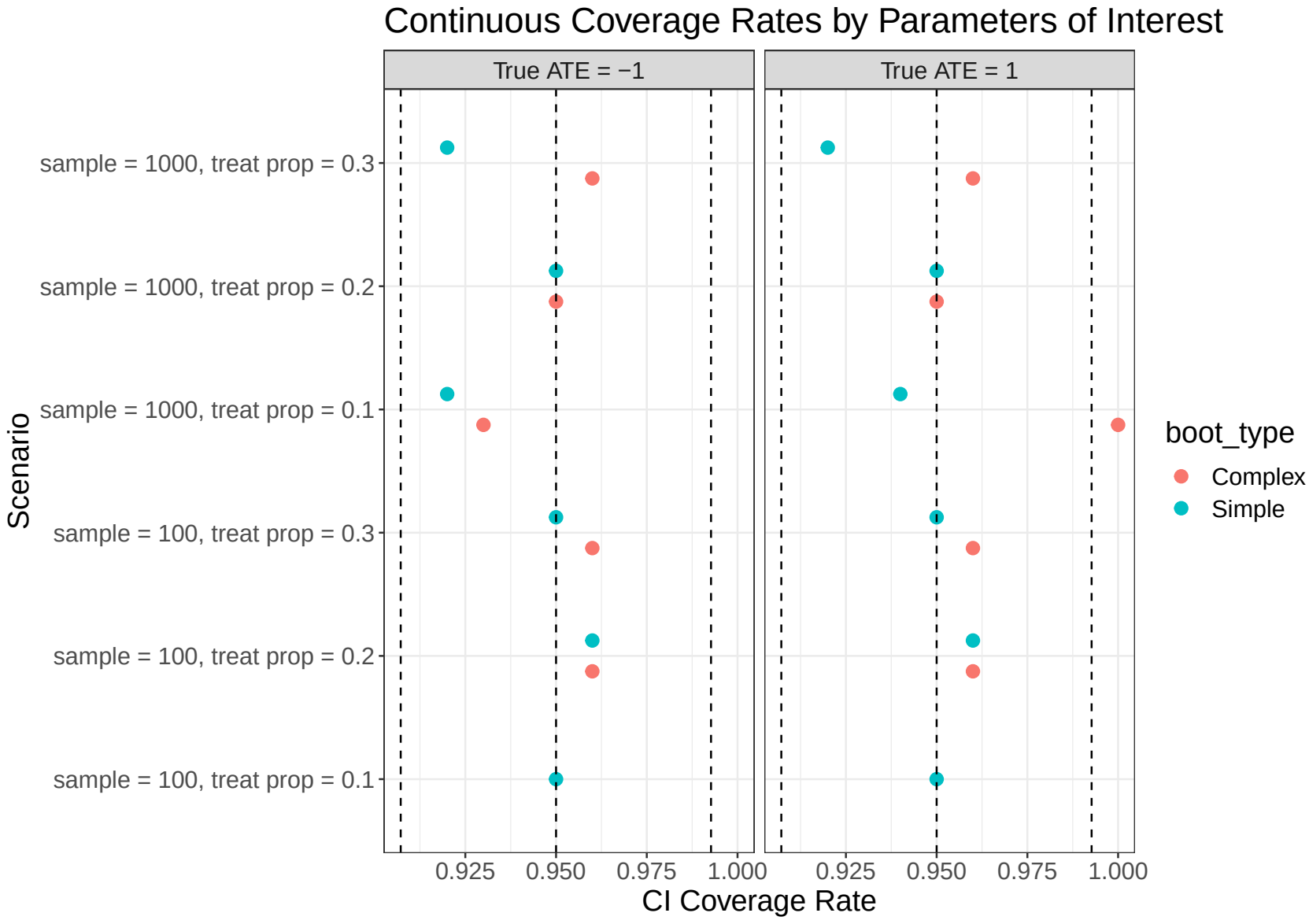
sample = 100, treat prop = 0.1
Scenario
0
3
6
9
Standard Error
Method
Empirical
Simple
Complex

Results


Continuous Coverage Rates by Parameters of Interest
True ATE = −1
True ATE = 1
Scenario
sample = 1000, treat prop = 0.3
sample = 1000, treat prop = 0.2
sample = 1000, treat prop = 0.1
sample = 100, treat prop = 0.3
sample = 100, treat prop = 0.2
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0.925
0.950
0.975
1.000
CI Coverage Rate
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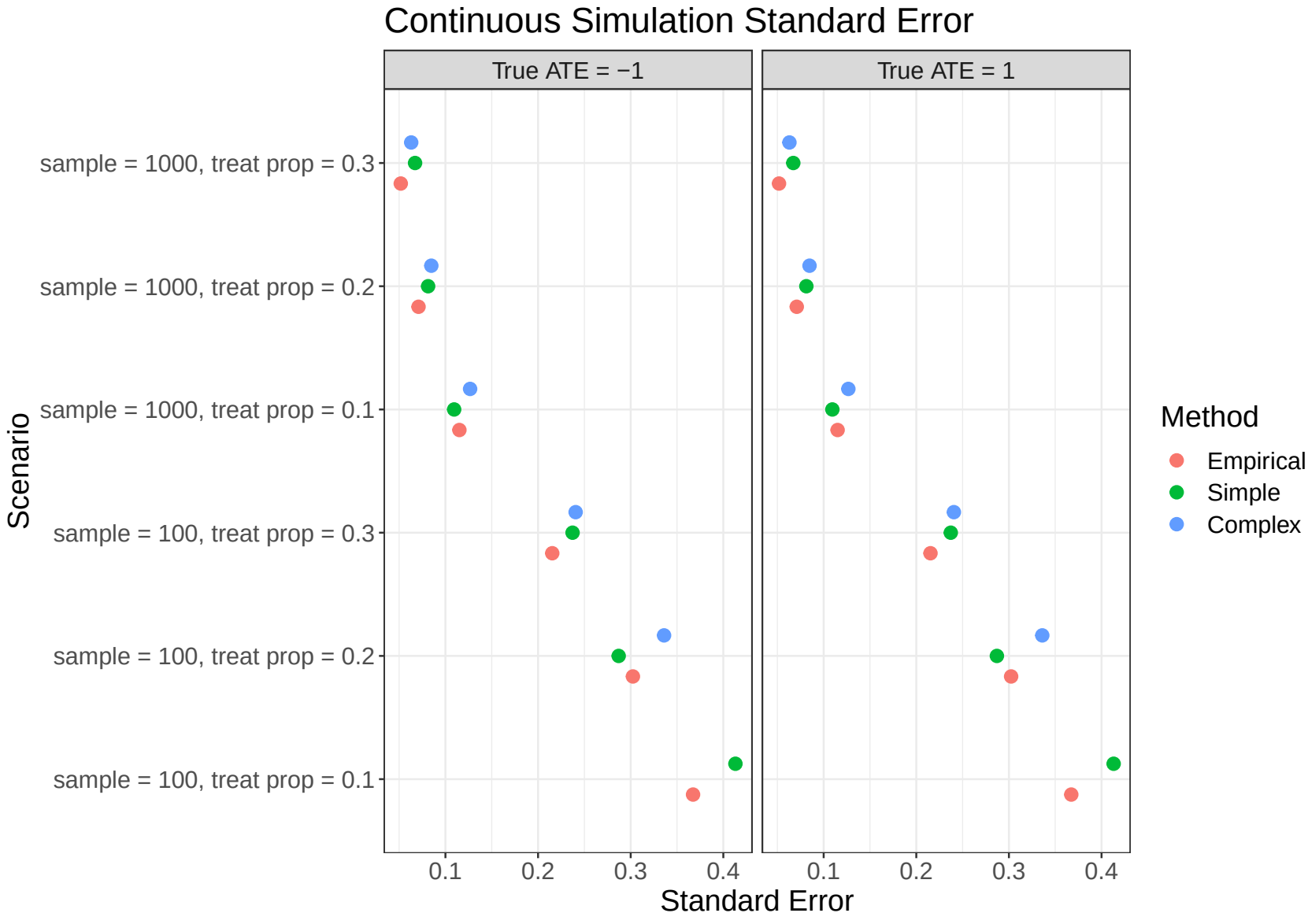
Results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sample = 100, treat prop = 0.2
sample = 100, treat prop = 0.1
Scenario
0.1
0.2
0.3
0.4
Standard Error
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Empirical
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Complex

Limitations

- Sample size / treatment (or exposure) prevalence

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- Small number of initial samples, limited in detecting differences in coverage rate

Future Work

- Larger number of initial samples, narrower coverage window

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- Increased sample size, changes in bootstrap performance?

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- 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