P8160 - Comparing Bootstrapping Methods Report

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Introduction

detail to be added

Simulation Planning

Aims

The primary goal of this simulation study is to assess the performance of two bootstrap methods (detailed below) in estimating the sampling variability of treatment effects obtained from a nearest-neighbor propensity-score matching (NNM). In this study, NNM will select a treated subject at random from simulated observational data. The untreated subject with the nearest propensity score is then selected to be paired with the treated subject, without replacement. Treatment effects can then be estimated by comparing outcomes (continuous or binary) between the treated and untreated subjects. The bootstrapping methods will be used to assess the variance of estimated treatment effects.

Data Generation

The data for this simulation study were generated from a parametric model. For each subject, three baseline covariates (L_1, L_2, L_3) were simulated from independent standard normal distributions, $N(0, 1)$. Two of these covariates (L_1 and L_2) affected treatment selection, while two (L_2 and L_3) affected the outcome. The probability of treatment for each subject was determined by the following model:

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

where $\alpha_0 = \log(\frac{\pi}{1-\pi})$ as close approximation of desired treatment prevalence. **Due to the nature of the logit normal there is no closed form solution to the mean of the logit normal distibution however, calculating α_0 in this fashion gives us a very close but always biased above approximation.**

For continuous outcomes, 100 sub-populations of 100 or 1,000 subjects will be generated using the following parametric model:

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

where Y_i indicates the outcome for each subject, A_i indicates the treatment status of each subject (0 or 1), L_{2i} and L_{3i} indicate observed covariate values for each subject, and ϵ_i denotes random error. Because L_{2i} affects both A_i and Y_i, it acts as a confounder in estimating the treatment effect.

Is there a β_0 value here? For binary outcomes, the same procedure will be performed using the following parametric model:

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

where $Y_i \sim \text{Bernoulli}(\tau_i)$. The binary outcome model does not feature an error term, as realizations of Y_i are innately subject to noise.

Here I am attempting to explain what the truth is but will need to be revised!

In the choice of parameter distributions and structure of our treatment assignment and outcome generation the true distribution can be calculated. This will allow the simulation estimates to be compared to a truth.

The treatment assignment for follows a logit normal with $\mu = \alpha_0$ and $\sigma^2 = \alpha_2^2 + \alpha_3^2$.

The outcome variable for the binary data follows at logit normal distribution with $\mu = \beta_1$ and $\sigma^2 = \beta_2^2 + \beta_3^2$.
Talk about the MCMC method that Jimmy created

The outcome variable for the continuous data data follows at normal distribution with $\mu = \beta_1$ and $\sigma^2 = \beta_2^2 + \beta_3^2$.

Thus the true treatment effect will depend on the assignment of β_1.

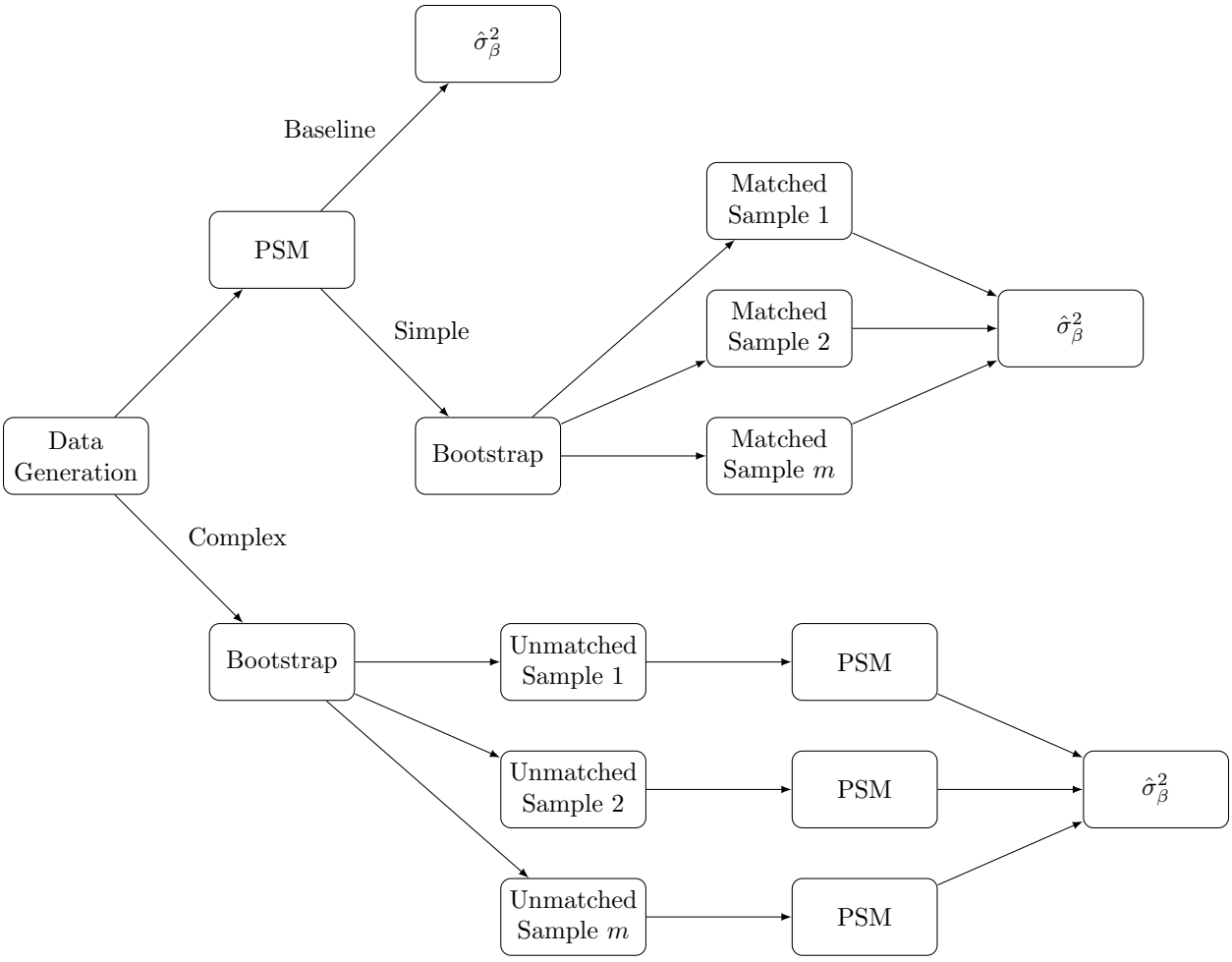
Methods for Evaluation

Two bootstrap methods will be assessed in this simulation: the simple bootstrap and the complex bootstrap.

In the simple bootstrap, one draws repeated samples from an original sample with replacement to imitate the process of drawing samples from a population. Here, 500 repeated samples (m_{boot}) of matched pairs ($n_{boot} = n_{sample} \cdot P(A = 1)$) will be drawn from the matched pairs of observations for each of the 100 initial samples (m_{sample}). The distribution of the estimated treatment effect ($\hat{\beta}_1$) across the 500 bootstraps is assessed for each of the 100 initial samples.

The complex bootstrap considers two additional sources of variability compared to the simple bootstrap. In this approach, a sample is drawn with replacement from the original, unmatched observational data. The propensity-score model is estimated using this bootstrap sample, and NNM proceeds as before. The treatment effect is estimated from the newly matched sample. This process is repeated 500 times (m_{boot}) for each of the 100 samples (m_{sample}).

The resulting standard error estimates, $\hat{\sigma}_\beta$, will be the primary targets of this analysis.



Parameters of Interest

In simulations, three parameters will vary to aid in the comparison of the two bootstrap techniques. These three parameters are dataset sample size (n_{sample}), population proportion of treated individuals (π) and the true average treatment effect (β_1). Varying the sample size and proportion of treated individuals will help make suggestions for studies that have varying amounts of participants and amount of treatment. The range the number of the sample size tried is $n_{\text{sample}} \in \{100, 1000\}$, one a low sample and one a larger sample. The range of population proportion of treated individuals $\pi \in \{0.113, 0.216, 0.313\}$. This is to approximate low, medium, and high treatment levels in a study. The true average treatment effect will take on $\beta_1 \in \{0.15, 0.30\}$ in a binary study and $\beta_1 \in \{-1, 1\}$ in a continuous study.

To compare these three parameters there are number of other parameters that will be held constant from simulation to simulations. Such as the number of datasets ($m_{\text{sample}} = 100$), the number of bootstrap re-sample ($m_{\text{boot}} = 500$), the strength of covariate correlation on treatment status (α_1, α_2), and strength of covariate correlation on outcome variable (β_2, β_3). Without loss of generality for the continuous data ($\alpha_1 = 1, \alpha_2 = 2, \beta_2 = 2, \beta_3 = 1$), and for the binary data ($\alpha_1 = \log(1.25), \alpha_2 = \log(1.75), \beta_2 = \log(1.75), \beta_3 = \log(1.25)$).

Performance Measures

The standard error estimates from each bootstrap method will be assessed in two ways. First, coverage rates of confidence intervals will be analyzed to assess how frequently the true average treatment effect (β_1) is

included in confidence intervals using the bootstrap-estimated treatment effect ($\bar{\hat{\beta}}_1$) and estimated standard errors ($\hat{\sigma}_\beta$). Second, standard error estimates from each bootstrap method will be compared to the sample standard deviation of treatment effects of the initial samples to determine how bootstrapping aligns with a simpler approach.

Bias is also calculated using the true treatment effect. This measure helps confirm that each method is able to accurately identify the treatment effect. A 95% percent confidence interval is also constructed around the bias using the standard error.

Simulation Execution

discussion of coding will go here, perhaps even excerpts of code

Results

Figure 2: Binary Coverage Rates

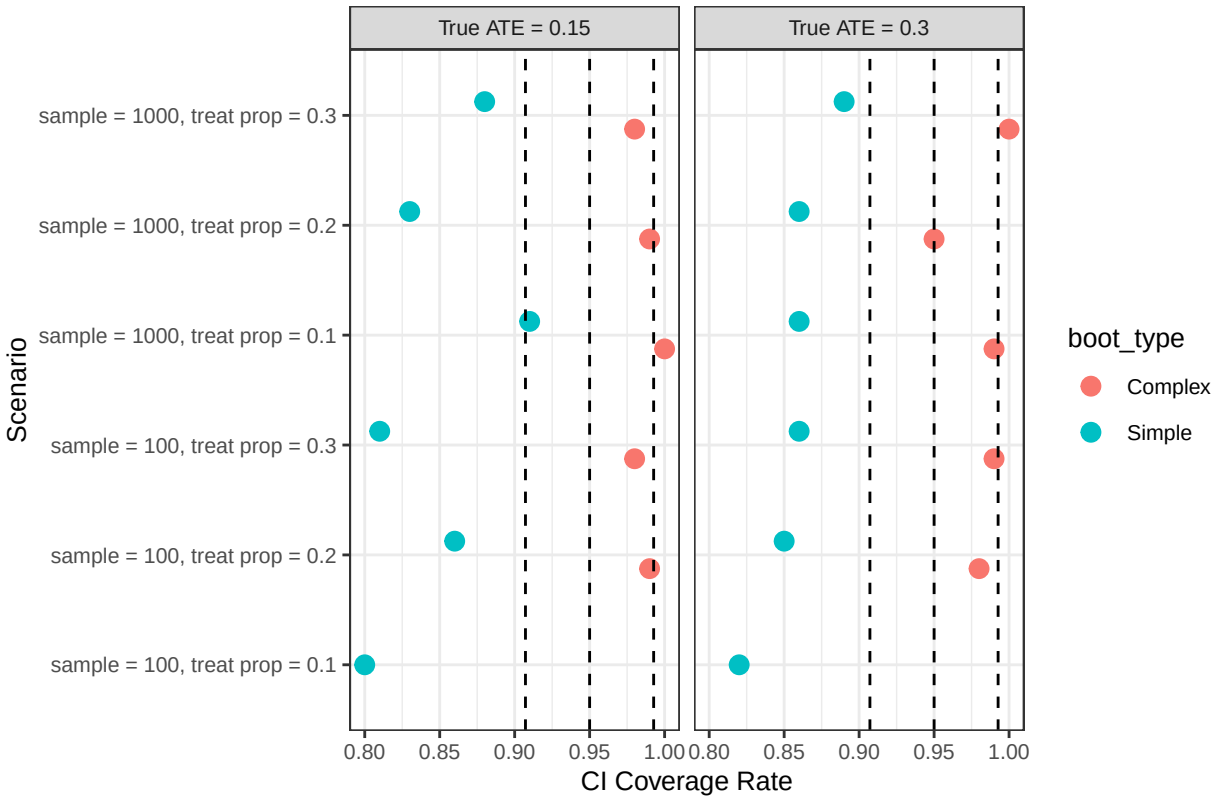
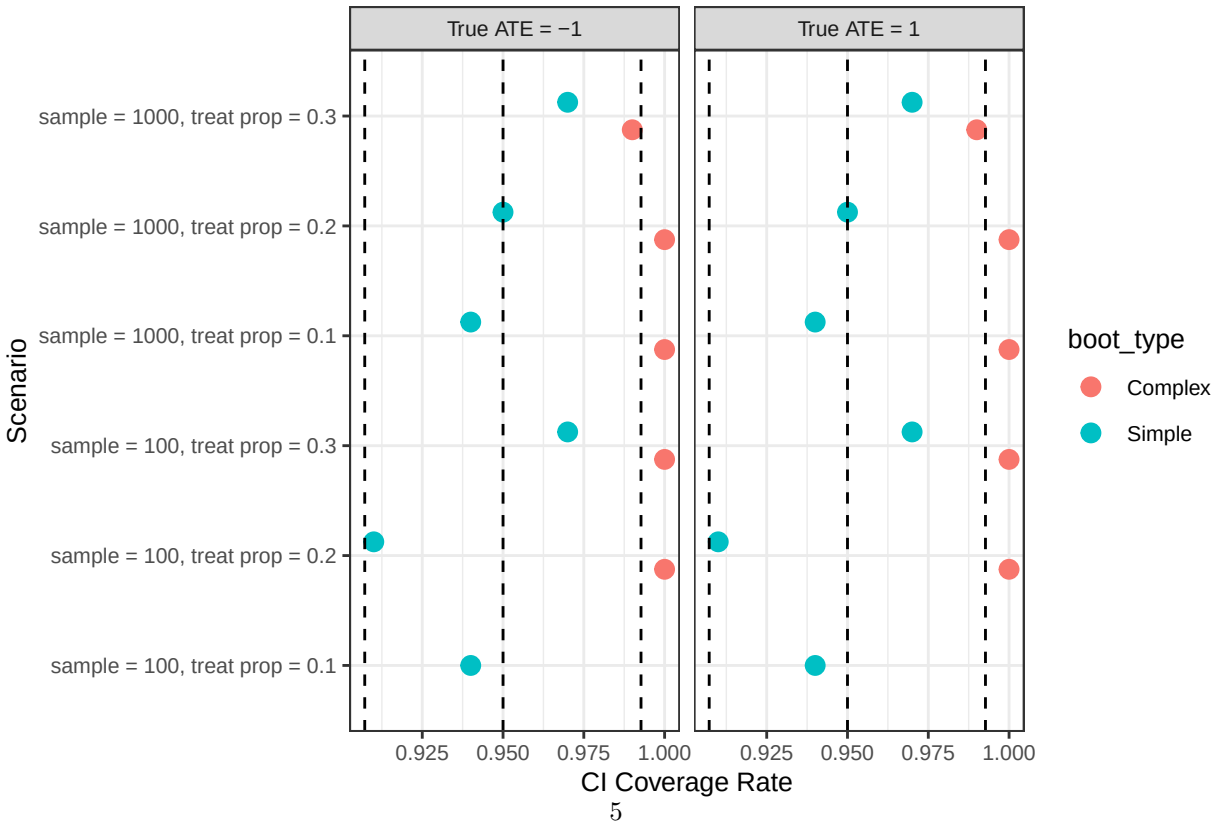


Figure 3: Continuous Coverage Rates



Analysis was performed on 24 different scenarios, 12 in a binary outcome setting and 12 in a continuous setting. To assess the standard error estimates produced by each bootstrapping method, confidence intervals were created and coverage rates calculated, see Figure 2. Each of our scenarios included 100 initial, base samples, which resulted in 100 confidence intervals. Based on the binomial distribution where n = 100, p = 0.95, and a confidence interval containing the true treatment effect is considered a success, we ascertained a statistically significant coverage rate range with which to assess our results. A coverage rate below 90% and above 99% indicates a statistically significant under- or over-estimation of the standard error. Based on this criteria, the simple bootstrap method underestimated the standard error in five out of the six binary outcome scenarios with a lesser true average treatment effect, and the standard bootstrap underestimated the standard error of the true average treatment effect in all six of the scenarios involving the larger treatment effect. Conversely, the complex bootstrap method overestimated the standard error in one of the five possible scenarios in each of the lesser and greater treatment effect cases. Note the complex bootstrapping method was not reliable in the scenario where $n_{sample} = 100$ and treated proportion was equal to 10%.

In the continuous setting (Figure 3), the coverage rate from the simple bootstrapping method fell within the statistically significant range for all 12 scenarios. However, the complex bootstrap seems to have over-estimated the standard error in eight of the 10 possible scenarios. Again, the complex bootstrap was not reliable in the two scenarios where $n_{sample} = 100$ and treated proportion was equal to 10%.

Figure 4: Binary Standard Error Estimates

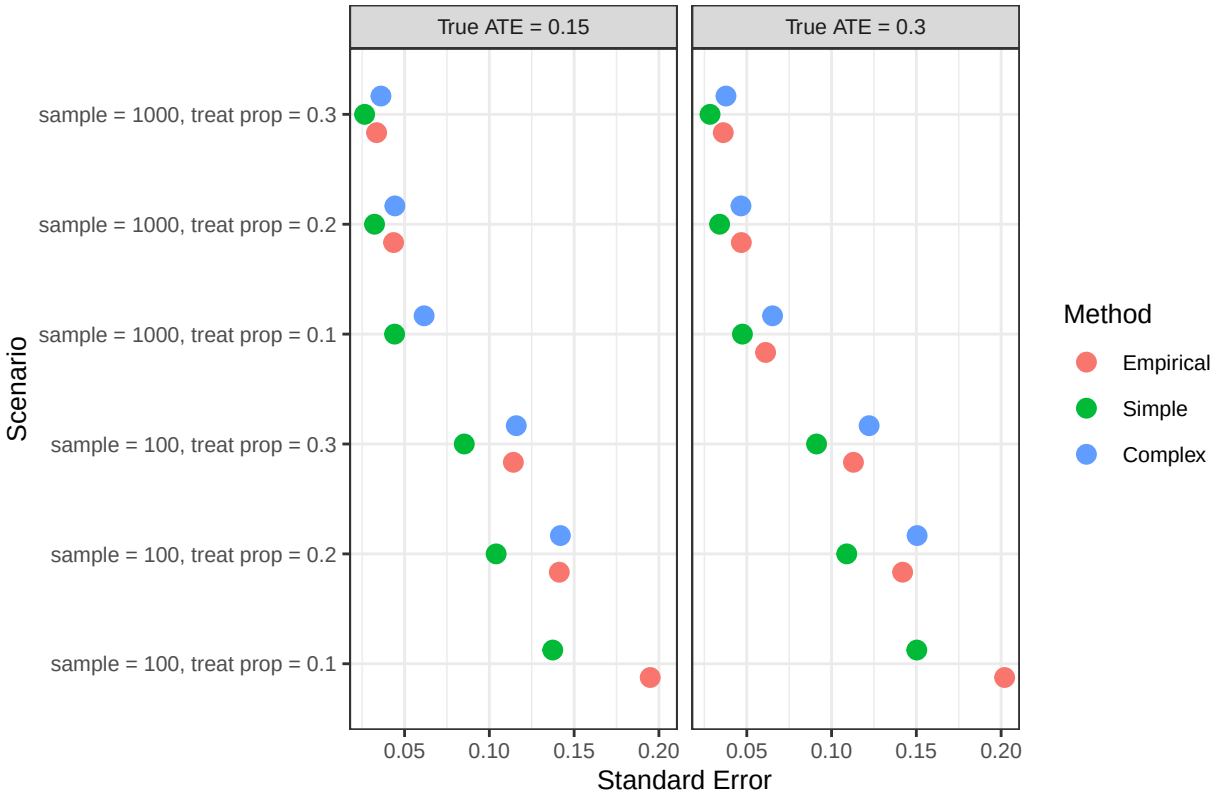
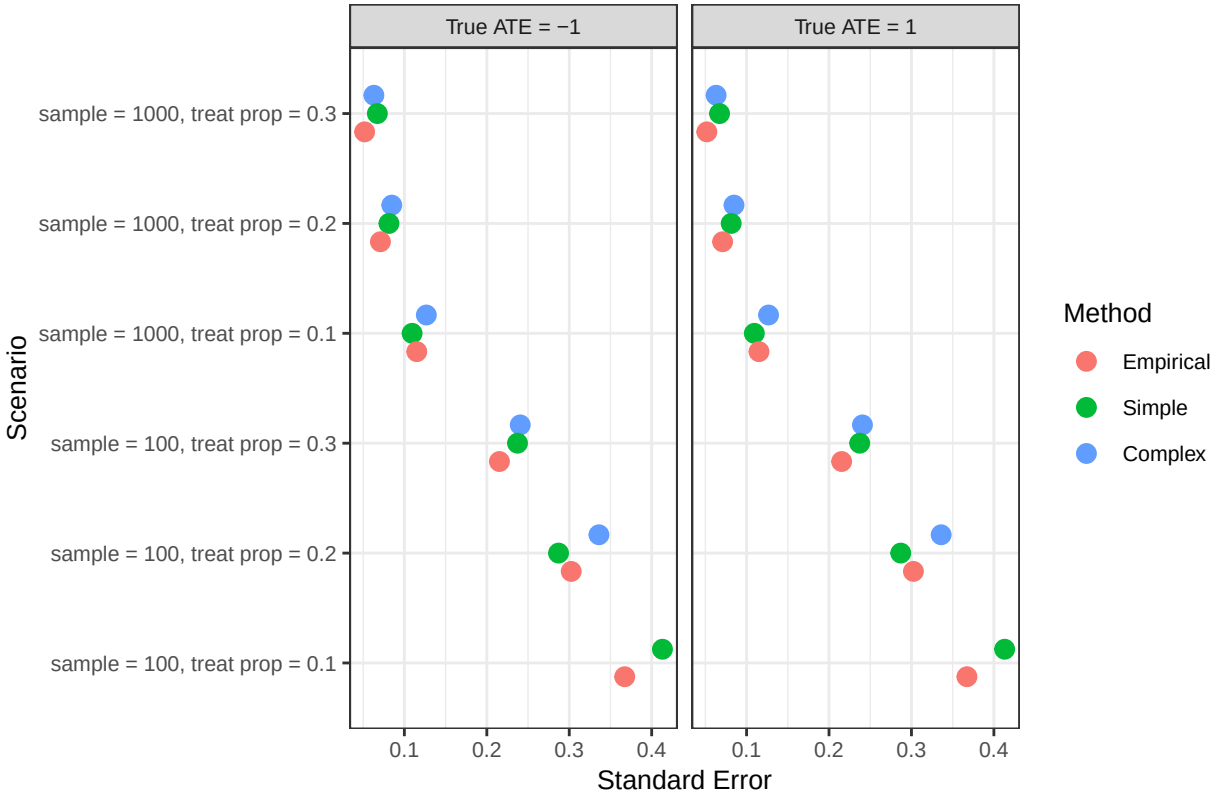


Figure 5: Continuous Standard Error Estimates



In Figure 4, the standard error estimates from the binary setting can be seen in more detail. In general, the simple bootstrap seemed to produce lower estimates of standard error compared to an empirical estimate based on the initial sample distribution before any bootstrapping, while the complex bootstrap seems to produce larger estimates of the standard error. This aligns with the observation that the complex bootstrap confidence intervals tended to have higher coverage rates compared to the simple bootstrap method.

In Figure 5, a similar figure features the standard error estimates from the continuous setting. Again, the estimates from the two bootstrapping methods and the empirical measurement seem to produce similar values. In general, the complex bootstrap seems to produce larger estimates of standard error compared to the simple bootstrap, but the scenario in which $n_{sample} = 1000$ and treated proportion is 30% has a smaller simple bootstrap estimate compared to the complex bootstrap. These results are summarized in detail in Table ## and Table ##.

Figure 6: Binary Bias Distributi

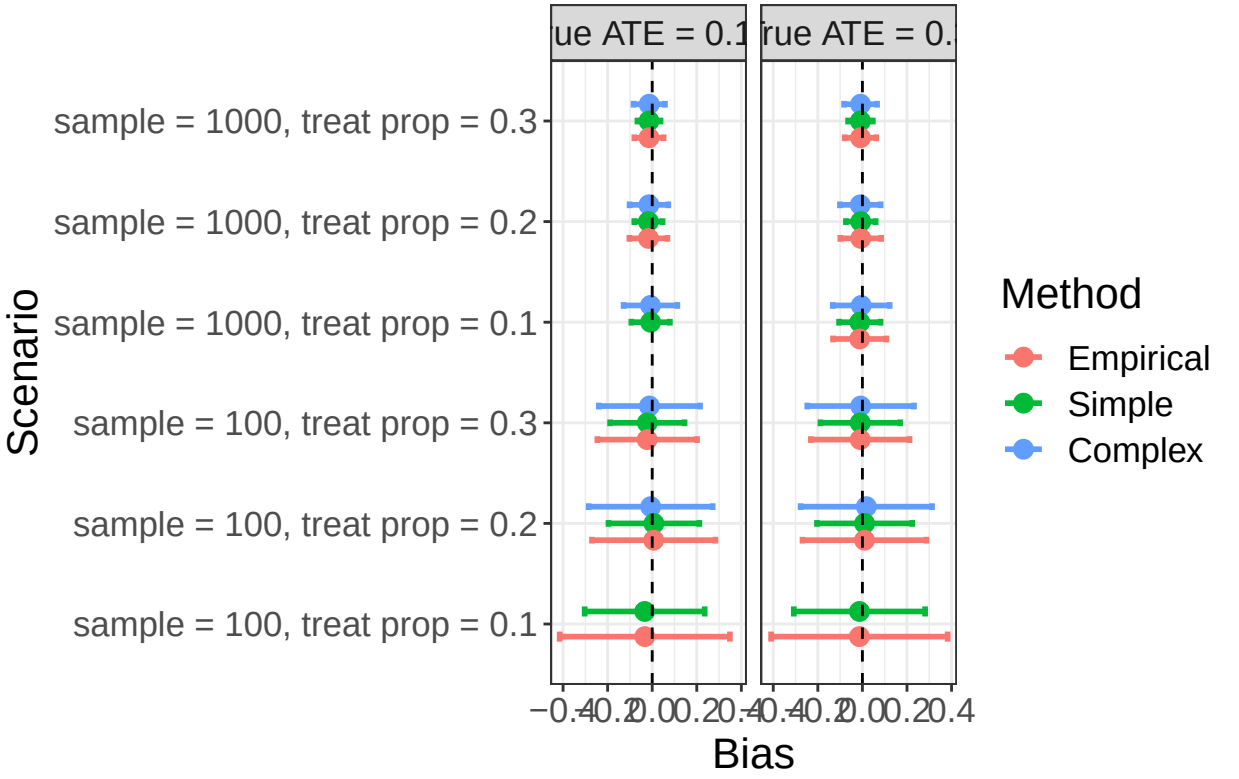
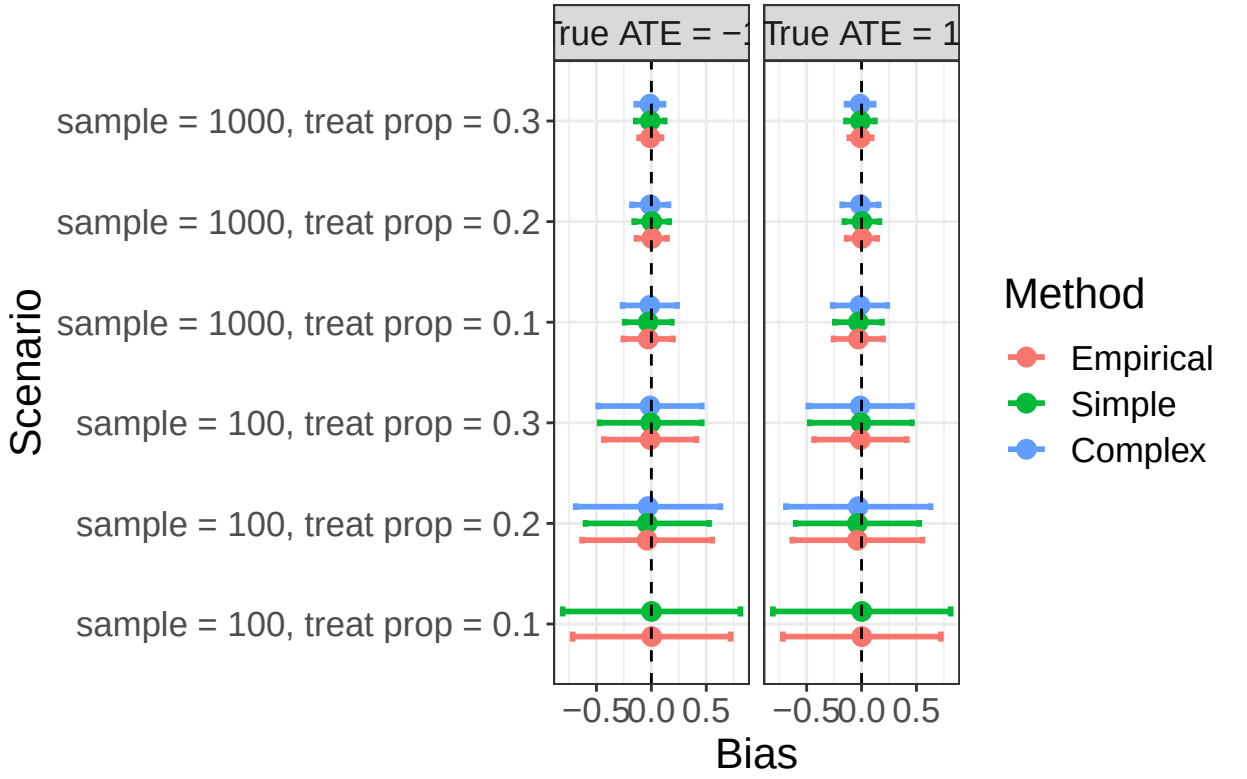


Figure 7: Continuous Bias Distr



Additional analysis was performed on the bias demonstrated in each of the bootstrap methods and the empirical calculation. In Figures 6 and 7, the mean and standard deviation of the bias (the difference between the estimated and true average treatment effect) are shown for all three methods in the binary and continuous settings, respectively. The standard deviation of bias increases as the number of initial samples (n_{sample}) decreases. These results are summarized in detail in Tables ## and ##.

Discussion

conclusions to be added