

Homework 1

Github link: https://github.com/xxou617/bios731_hw1_ou

$$Y_i = \beta_0 + \beta_{treatment}X_{i1} + \mathbf{Z}_i^T \boldsymbol{\gamma} + \epsilon_i$$

Notation is defined below:

- Y_i : continuous outcome
- X_{i1} : treatment group indicator; $X_{i1} = 1$ for treated
- \mathbf{Z}_i : vector of potential confounders
- $\beta_{treatment}$: average treatment effect, adjusting for \mathbf{Z}_i
- $\boldsymbol{\gamma}$: vector of regression coefficient values for confounders
- ϵ_i : errors, we will vary how these are defined

In our simulation, we want to

- Estimate $\beta_{treatment}$ and $se(\hat{\beta}_{treatment})$
 - Evaluate $\beta_{treatment}$ through bias and coverage
 - We will use 3 methods to compute $se(\hat{\beta}_{treatment})$ and coverage:
 1. Wald confidence intervals (the standard approach)
 2. Nonparametric bootstrap percentile intervals
 3. Nonparametric bootstrap t intervals
 - Evaluate computation times for each method to compute a confidence interval
- Evaluate these properties at:
 - Sample size $n \in \{10, 50, 500\}$
 - True values $\beta_{treatment} \in \{0, 0.5, 2\}$
 - True ϵ_i normally distributed with $\epsilon_i \sim N(0, 2)$
 - True ϵ_i coming from a right skewed distribution
 - * **Hint:** try $\epsilon_i \sim \text{logNormal}(0, \log(2))$
- Assume that there are no confounders ($\boldsymbol{\gamma} = 0$)
- Use a full factorial design

Problem 1.1 ADEMP Structure

Answer the following questions:

(1) How many simulation scenarios will you be running?

- 3 $\beta_{treatment}$
- 3 sample sizes
- 3 methods

- 2 error term distribution

$$3 * 3 * 2 * 3 = 54$$

Thus, we have 54 scenarios in total.

(2) What are the estimand(s)

- $\beta_{treatment}$

(3) What method(s) are being evaluated/compared?

- Wald confidence intervals (the standard approach), nonparametric bootstrap percentile intervals and nonparametric bootstrap t intervals for $se(\hat{\beta}_{treatment})$ in different scenario will be evaluated.

(4) What are the performance measure(s)?

- bias
- $se(\hat{\beta})$
- coverage
- computation time

Problem 1.2 nSim

Based on desired coverage of 95% with Monte Carlo error of no more than 1%, how many simulations (n_{sim}) should we perform for each simulation scenario? Implement this number of simulations throughout your simulation study.

$$n_{sim} = \frac{0.95(1 - 0.95)}{(0.01)^2} = 475$$

Problem 1.3 Implementation

We will execute this full simulation study. For full credit, make sure to implement the following:

- Well structured scripts and subfolders following guidance from `project_organization` lecture
- Use relative file paths to access intermediate scripts and data objects
- Use readable code practices
- Parallelize your simulation scenarios
- Save results from each simulation scenario in an intermediate `.Rda` or `.rds` dataset in a `data` subfolder
 - Ignore these data files in your `.gitignore` file so when pushing and committing to GitHub they don't get pushed to remote
- Make sure your folder contains a Readme explaining the workflow of your simulation study
 - should include how files are executed and in what order
- Ensure reproducibility! I should be able to clone your GitHub repo, open your `.Rproj` file, and run your simulation study

Problem 1.4 Results summary

Create a plot or table to summarize simulation results across scenarios and methods for each of the following.

- Bias of $\hat{\beta}$
- Coverage of $\hat{\beta}$
- Distribution of $se(\hat{\beta})$
- Computation time across methods

```
library(tidyverse)
library(gt)
```

```
load(here::here("data", "all_scenarios.Rdata"))
```

```
# summarise results grouped by the scenarios
```

```
final_results <- final_results |>
  mutate(
    beta_true = as.factor(beta_true),
    epsilon_distr = factor(epsilon_distr, levels = c("Normal", "logNormal")),
    CI_method = factor(CI_method, levels = c("Wald", "boot quantile", "boot t"))
  )
```

```
simu_evaluate <- final_results |>
  group_by(n, beta_true, epsilon_distr, CI_method) |>
  summarise(
    bias = mean(error),
    avg_se = mean(est_se),
    avg_time = mean(cal_CI_time),
    coverage_rate = mean(coverage),
    .groups = "drop"
  )
```

```
head(simu_evaluate)
```

```
## # A tibble: 6 x 8
##       n beta_true epsilon_distr CI_method      bias avg_se avg_time coverage_rate
##   <dbl> <fct>      <fct>      <fct>      <dbl> <dbl>   <dbl>      <dbl>
## 1    10 0        Normal      Wald      -0.0512  1.29    0.0190      0.909
## 2    10 0        Normal      boot qua~ -0.0512  1.15    0.351      0.857
## 3    10 0        Normal      boot t    -0.0512  1.29    61.8      0.981
## 4    10 0        logNormal    Wald      -0.00809  2.52    0.0194      0.987
## 5    10 0        logNormal    boot qua~ -0.00809  0.758    0.676      0.811
## 6    10 0        logNormal    boot t    -0.00809  2.52    118.      1
```

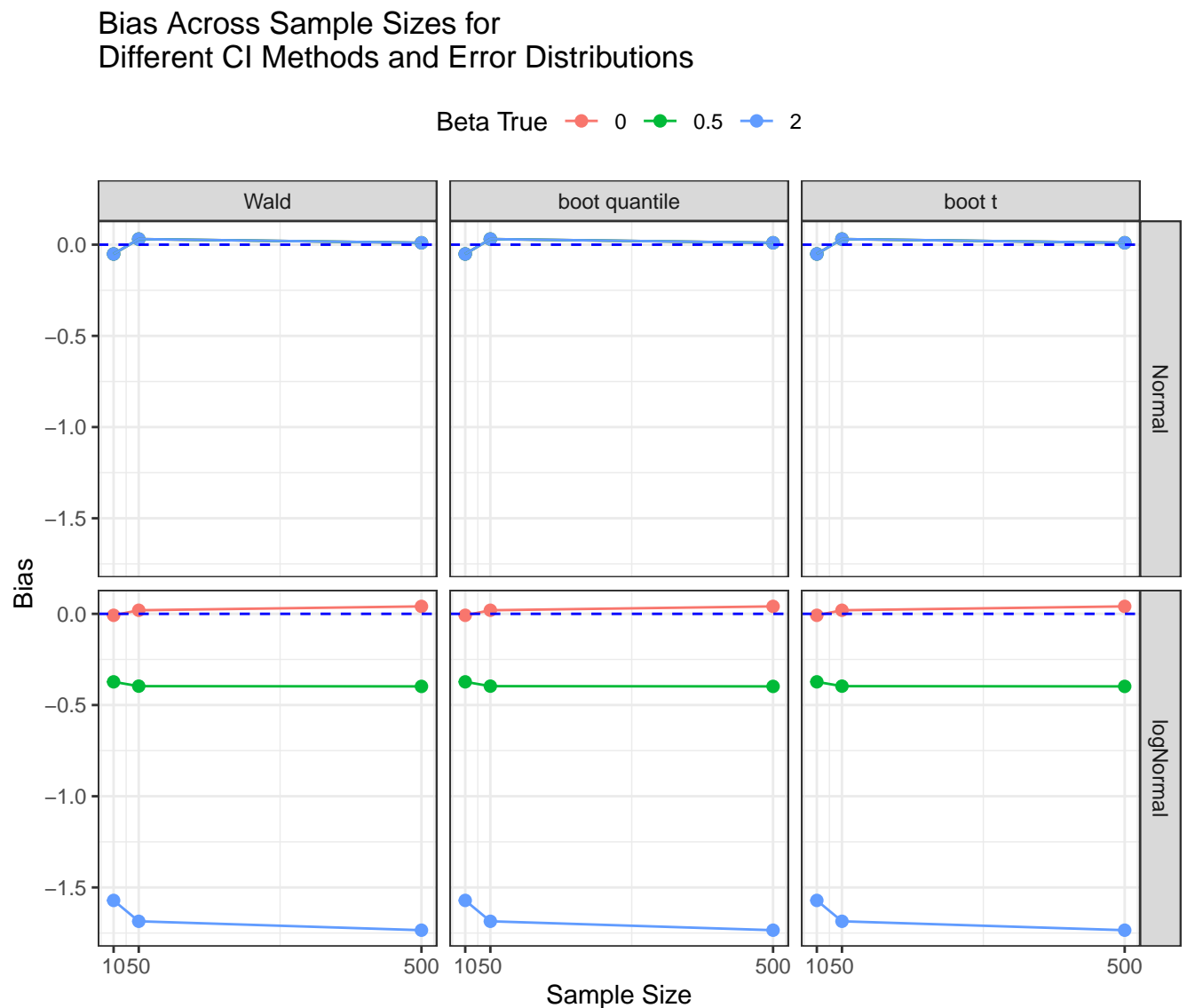
```
sample_size = unique(simu_evaluate$n)
```

```
# Plot for bias
```

```
ggplot(simu_evaluate,
  aes(x = n, y = bias, color = beta_true, group = beta_true)) +
  geom_point(size = 2) +
```

```
geom_line() +
geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
labs(x = "Sample Size", y = "Bias", color = "Beta True",
      title = "Bias Across Sample Sizes for \nDifferent CI Methods and Error Distributions") +
theme_bw() +
theme(legend.position = "top") +
facet_grid( cols = vars(CI_method), rows = vars(epsilon_distr)) +
scale_x_continuous(breaks = sample_size) -> plot_bias
```

plot_bias



```
# plot for coverage

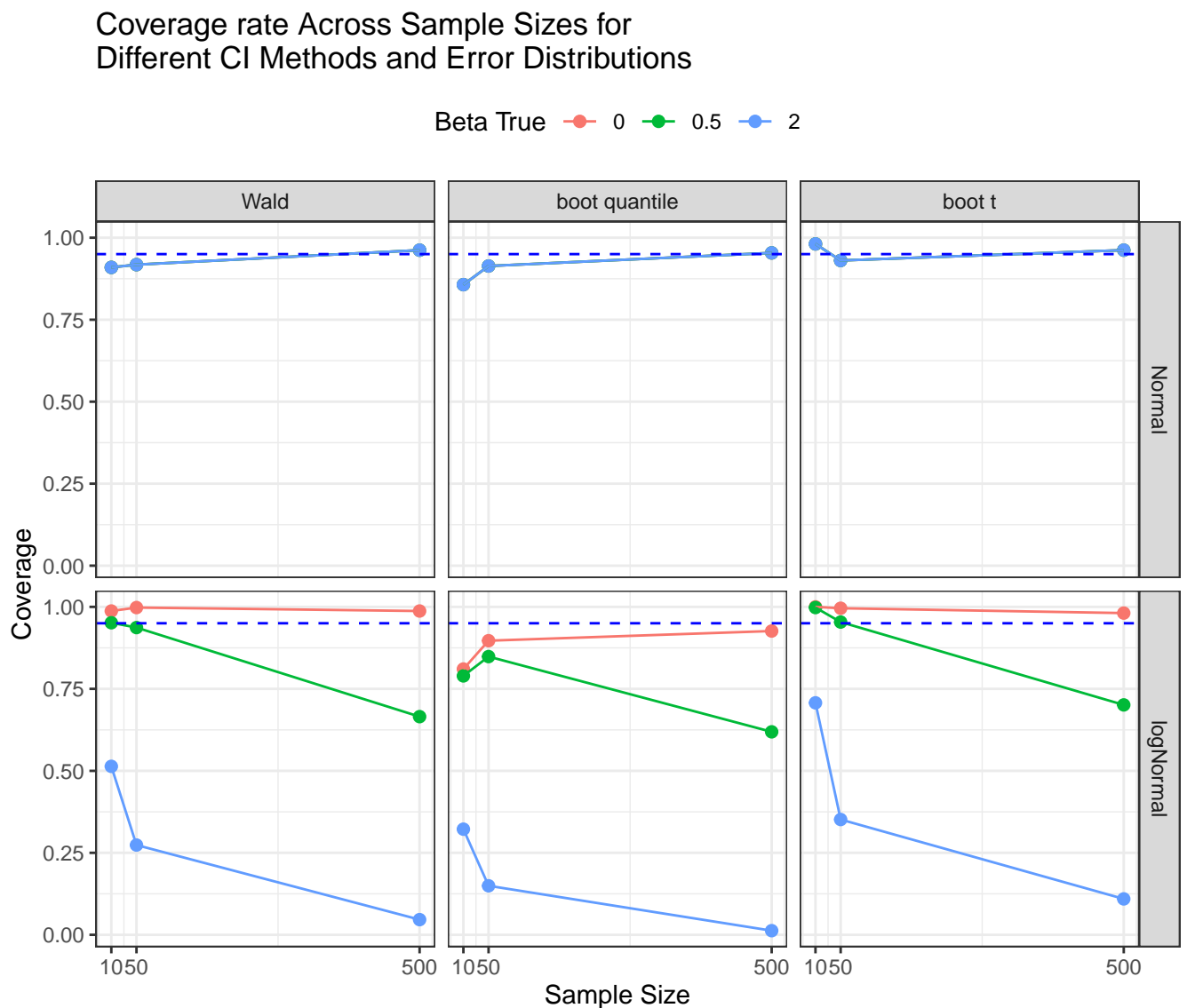
ggplot(simu_evaluate,
      aes(x = n, y = coverage_rate, color = beta_true, group = beta_true)) +
geom_point(size = 2) +
```

```

geom_line() +
geom_hline(yintercept = 0.95, linetype = "dashed", color = "blue") +
labs(x = "Sample Size", y = "Coverage", color = "Beta True",
      title = "Coverage rate Across Sample Sizes for \nDifferent CI Methods and Error Distributions") +
theme_bw() +
theme(legend.position = "top") +
facet_grid( cols = vars(CI_method), rows = vars(epsilon_distr)) +
scale_x_continuous(breaks = sample_size) -> plot_coverage

```

plot_coverage



```

# distribution of se(beta_hat)
ggplot(final_results,
      aes(x = as.factor(n), y = est_se, color = beta_true)) +
geom_boxplot() +
labs(x = "Sample Size",

```

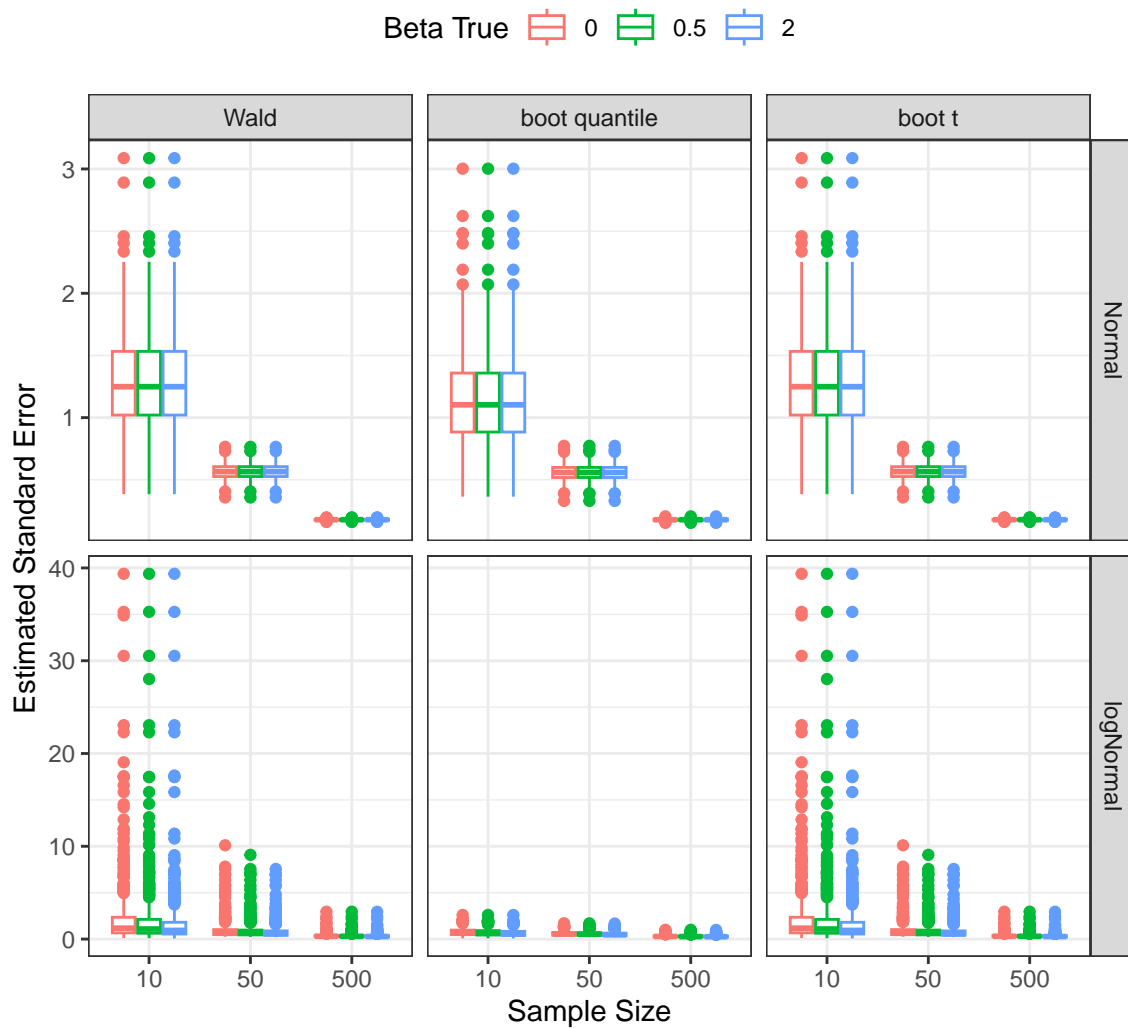
```

y = "Estimated Standard Error",
color = "Beta True",
title = "Distribution of Estimated Standard Errors Across \nSample Sizes, CI Methods, and Error Distributions",
theme_bw() +
theme(legend.position = "top") +
facet_grid(cols = vars(CI_method), rows = vars(epsilon_distr), scales = "free_y") +
scale_x_discrete(labels = sample_size) -> plot_se

```

plot_se

Distribution of Estimated Standard Errors Across
Sample Sizes, CI Methods, and Error Distributions



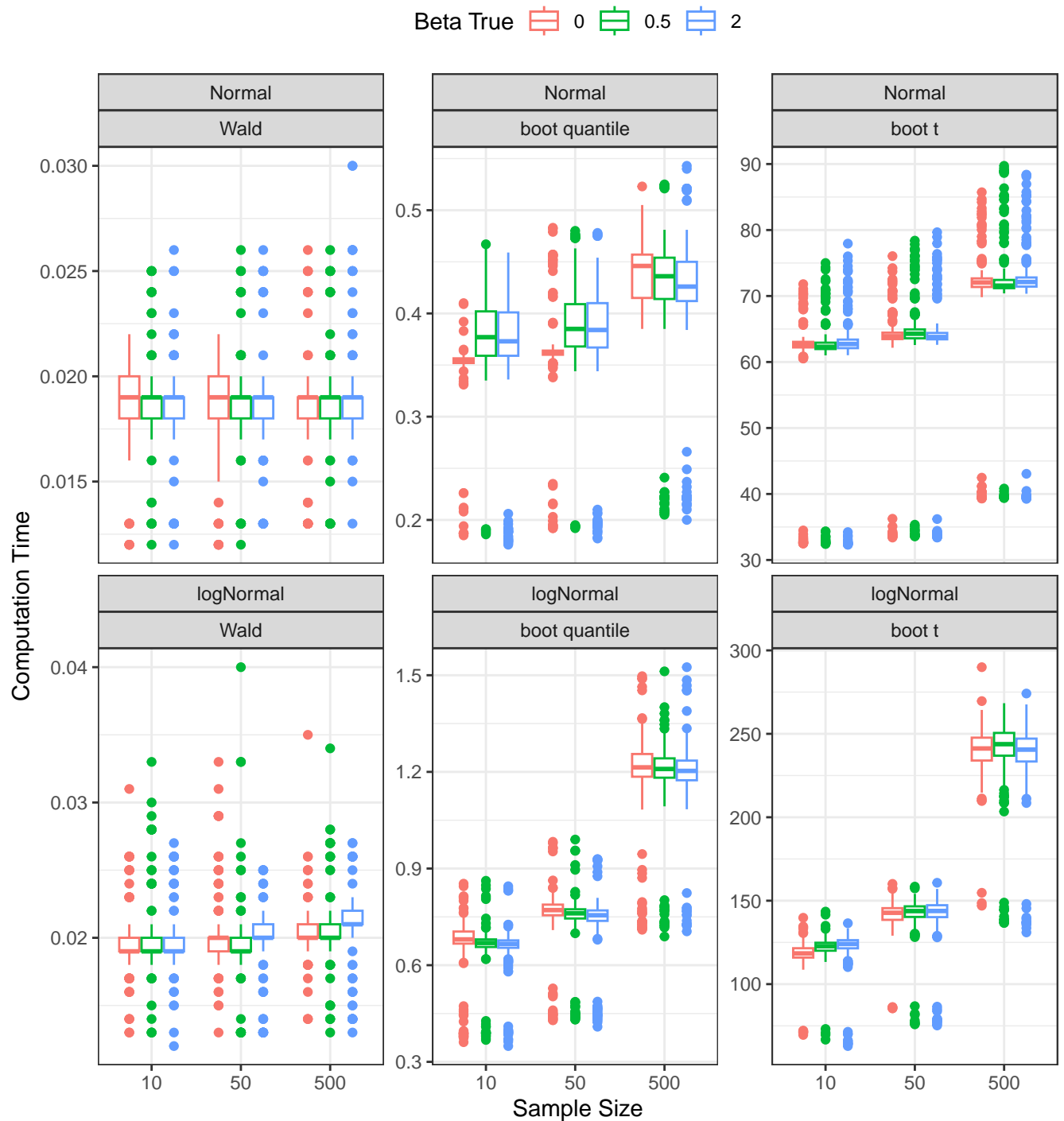
```

# plot for calculation time
ggplot(final_results, aes(x = as.factor(n), y = cal_CI_time, color = beta_true)) +
geom_boxplot() +
labs(x = "Sample Size",
y = "Computation Time",
color = "Beta True",
title = "Distribution of Time for CI Calculation Across \nSample Sizes, CI Methods, and Error Distributions")

```

```
theme_bw() +  
theme(legend.position = "top") +  
facet_wrap(~epsilon_distr+CI_method, scales = "free_y") +  
scale_x_discrete(labels = sample_size) -> plot_time  
  
plot_time
```

Distribution of Time for CI Calculation Across Sample Sizes, CI Methods, and Error Distributions



```
# save plots in results folder
ggsave(plot_bias, file = here::here("results", "plot_bias.jpg"),
       width = 7, height = 6)
ggsave(plot_coverage, file = here::here("results", "plot_coverage.jpg"),
       width = 7, height = 6)
```



```
ggsave(plot_se, file = here::here("results", "plot_se.jpg"),
       width = 6, height = 6)
ggsave(plot_time, file = here::here("results", "plot_time.jpg"),
       width = 7, height = 8)
```

Problem 1.5 Discussion

Interpret the results summarized in Problem 1.4. First, write a **paragraph** summarizing the main findings of your simulation study. Then, answer the specific questions below.

The simulation study evaluated three confidence interval (CI) methods—Wald intervals, bootstrapped quantile intervals, and bootstrapped t intervals—across varying sample sizes, treatment effects, and error distributions. Wald CI was the fastest but performed poorly under skewed errors. Boot quantile CI had moderate computation time, while Boot t CI improved coverage in skewed data but required the most computational resources. As sample size increased, bias decreased under the normal distribution but increased in the log-normal distribution when the treatment effect was nonzero, suggesting that GLM with a log link may not be ideal for estimating $\beta_{treatment}$ in this setting. The estimated standard error decreased as sample size grew, with Boot quantile CI producing the smallest standard errors.

- How do the different methods for constructing confidence intervals compare in terms of computation time?

Wald CI is the fastest, boot quantile CI requires Moderate computation time, and boot t CI is the slowest and requires significantly more computation time than the other two methods.

- Which method(s) for constructing confidence intervals provide the best coverage when $\epsilon_i \sim N(0, 2)$?

Wald CI

- Which method(s) for constructing confidence intervals provide the best coverage when $\epsilon_i \sim \logNormal(0, \log(2))$?

boot t CI

Additional discussion

Below are the outcomes when the model is fitted using `lm()` for both the normal and log-normal distributions. In this case, the Wald CI provides the best coverage for both $\epsilon_i \sim N(0, 2)$ and $\epsilon_i \sim \logNormal(0, \log(2))$

```
load(here::here("data", "all_scenarios0.Rdata"))

# summarise results grouped by the scenarios

final_results <- final_results |>
  mutate(
    beta_true = as.factor(beta_true),
    epsilon_distr = factor(epsilon_distr, levels = c("Normal", "logNormal")),
    CI_method = factor(CI_method, levels = c("Wald", "boot quantile", "boot t"))
  )
```

```

simu_evaluate <- final_results |>
  group_by(n, beta_true, epsilon_distr, CI_method) |>
  summarise(
    bias = mean(error),
    avg_se = mean(est_se),
    avg_time = mean(cal_CI_time),
    coverage_rate = mean(coverage),
    .groups = "drop"
  )

head(simu_evaluate)

```

```

## # A tibble: 6 x 8
##       n beta_true epsilon_distr CI_method      bias avg_se avg_time coverage_rate
##   <dbl> <fct>      <fct>      <fct>      <dbl> <dbl>   <dbl>      <dbl>
## 1    10 0        Normal      Wald      -0.0512  1.29   0.0314      0.945
## 2    10 0        Normal    boot quan~ -0.0512  1.15   0.358       0.857
## 3    10 0        Normal    boot t      -0.0512  1.29   61.5       0.981
## 4    10 0      logNormal      Wald      -0.364   9.09   0.0312      0.977
## 5    10 0      logNormal    boot quan~ -0.364   8.15   0.349       0.811
## 6    10 0      logNormal    boot t      -0.364   9.09   63.3       0.992

```

```

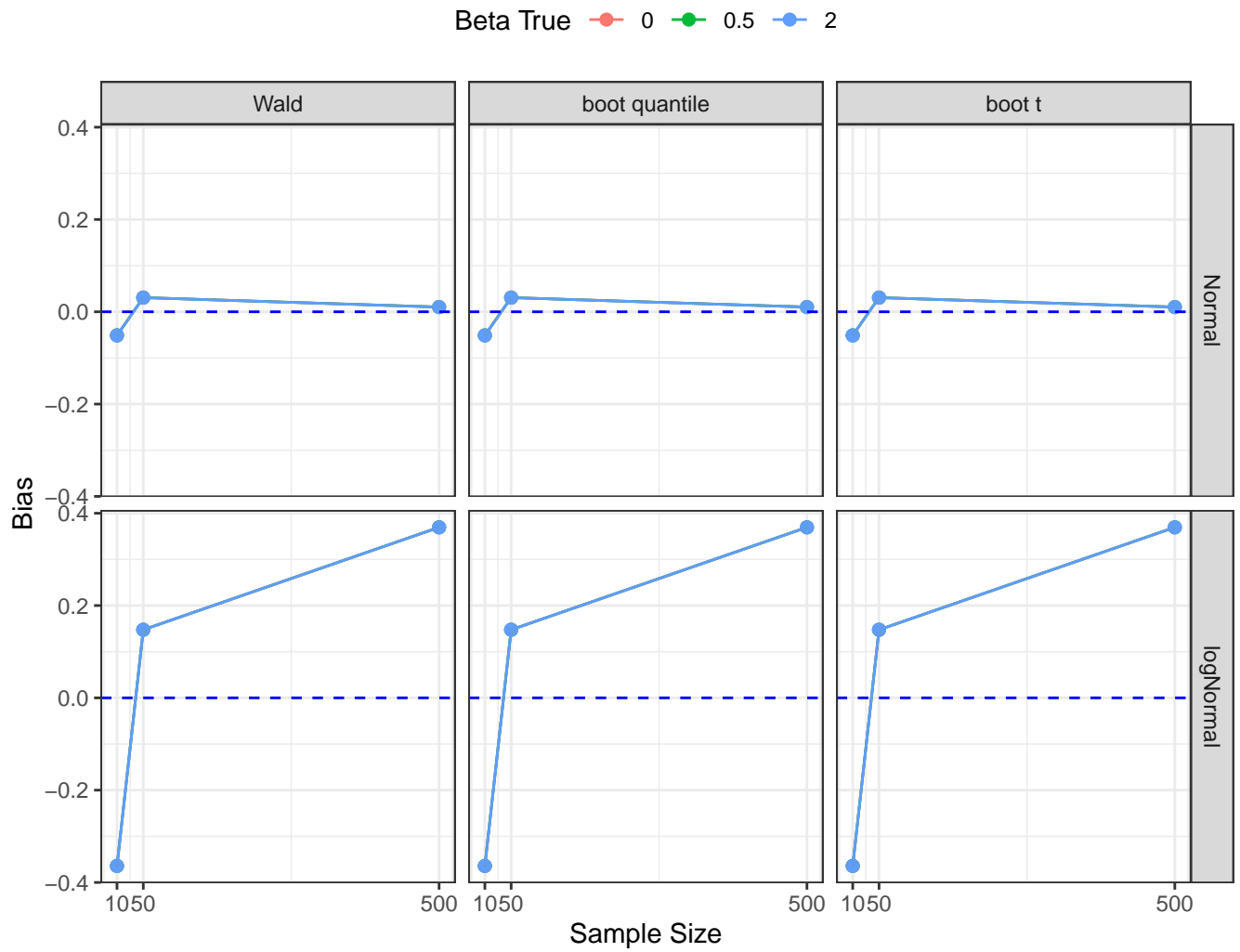
sample_size = unique(simu_evaluate$n)

# Plot for bias
ggplot(simu_evaluate,
  aes(x = n, y = bias, color = beta_true, group = beta_true)) +
  geom_point(size = 2) +
  geom_line() +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  labs(x = "Sample Size", y = "Bias", color = "Beta True",
    title = "Bias Across Sample Sizes for \nDifferent CI Methods and Error Distributions") +
  theme_bw() +
  theme(legend.position = "top") +
  facet_grid( cols = vars(CI_method), rows = vars(epsilon_distr)) +
  scale_x_continuous(breaks = sample_size) -> plot_bias

plot_bias

```

Bias Across Sample Sizes for Different CI Methods and Error Distributions

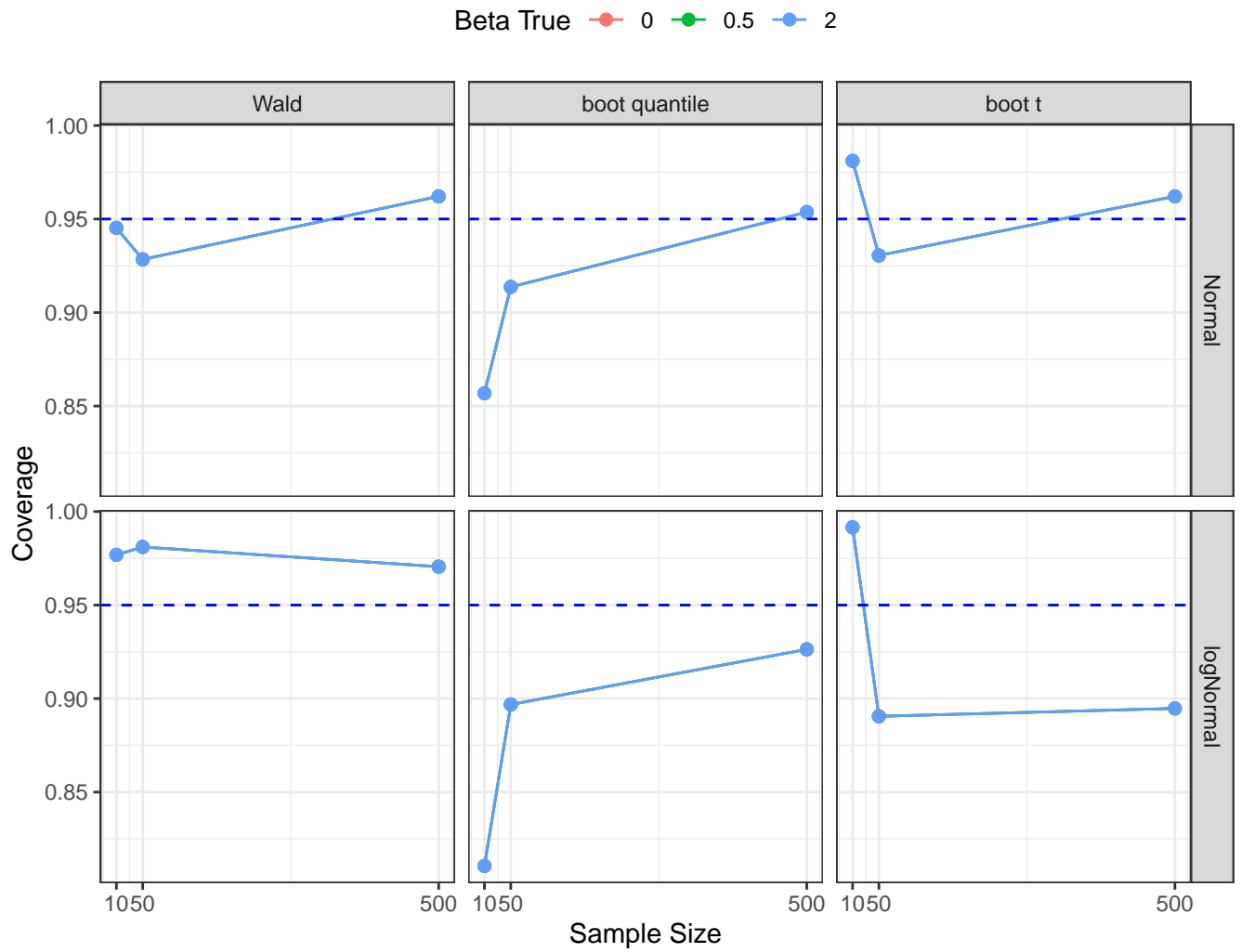


plot for coverage

```
ggplot(simu_evaluate,
  aes(x = n, y = coverage_rate, color = beta_true, group = beta_true)) +
  geom_point(size = 2) +
  geom_line() +
  geom_hline(yintercept = 0.95, linetype = "dashed", color = "blue") +
  labs(x = "Sample Size", y = "Coverage", color = "Beta True",
    title = "Coverage rate Across Sample Sizes for \nDifferent CI Methods and Error Distributions") +
  theme_bw() +
  theme(legend.position = "top") +
  facet_grid( cols = vars(CI_method), rows = vars(epsilon_distr)) +
  scale_x_continuous(breaks = sample_size) -> plot_coverage
```

plot_coverage

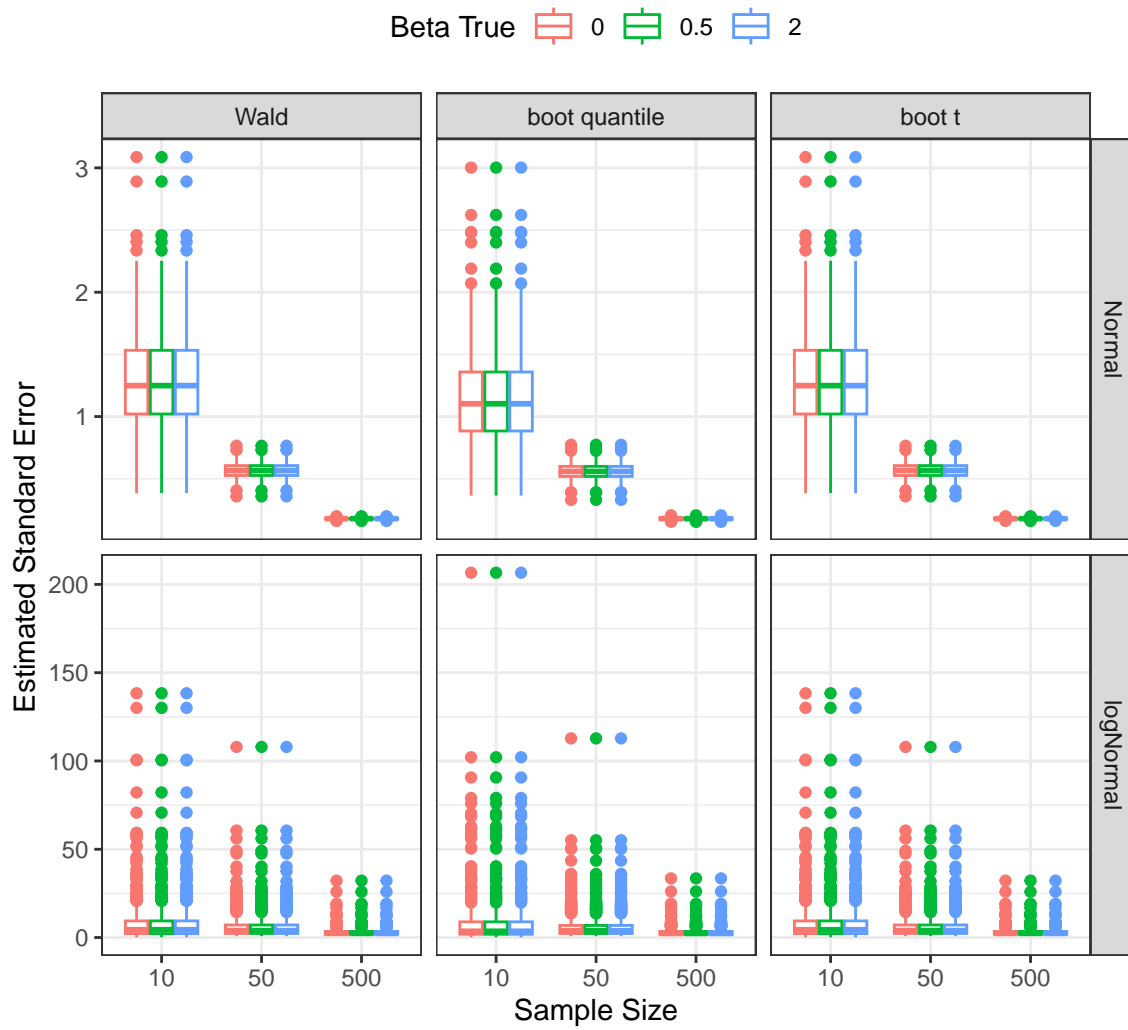
Coverage rate Across Sample Sizes for Different CI Methods and Error Distributions



```
# distribution of se(beta_hat)
ggplot(final_results,
  aes(x = as.factor(n), y = est_se, color = beta_true)) +
  geom_boxplot() +
  labs(x = "Sample Size",
    y = "Estimated Standard Error",
    color = "Beta True",
    title = "Distribution of Estimated Standard Errors Across \nSample Sizes, CI Methods, and Error I
  theme_bw() +
  theme(legend.position = "top") +
  facet_grid(cols = vars(CI_method), rows = vars(epsilon_distr), scales = "free_y") +
  scale_x_discrete(labels = sample_size) -> plot_se

plot_se
```

Distribution of Estimated Standard Errors Across Sample Sizes, CI Methods, and Error Distributions



```
# plot for calculation time
ggplot(final_results, aes(x = as.factor(n), y = cal_CI_time, color = beta_true)) +
  geom_boxplot() +
  labs(x = "Sample Size",
       y = "Computation Time",
       color = "Beta True",
       title = "Distribution of Time for CI Calculation Across \nSample Sizes, CI Methods, and Error Di
  theme_bw() +
  theme(legend.position = "top") +
  facet_wrap(~epsilon_distr+CI_method, scales = "free_y") +
  scale_x_discrete(labels = sample_size) -> plot_time

plot_time
```

Distribution of Time for CI Calculation Across Sample Sizes, CI Methods, and Error Distributions

