Bootstrap_Simulation

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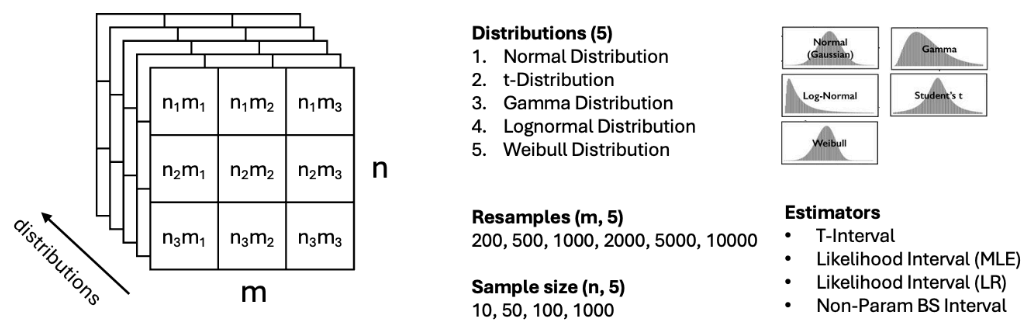
Aim

To find the smallest number of simulations (m) and sample size (n) needed to accurately calculate bootstrap parameters for different distributions with known parameters.



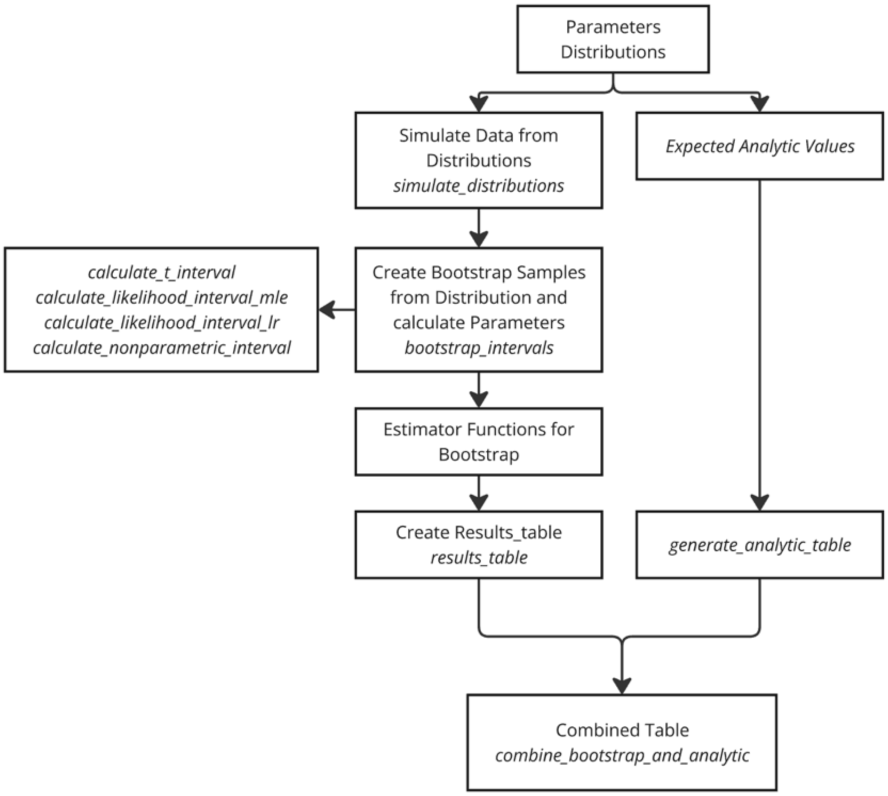
Unique combinations of $\boldsymbol{n \cdot m \cdot 5 = 120}$

Number of Bootstrap Resamples Required Per n per Distribution

$$\sum_{\substack{m=[200,500,1000,\\2000,5000,10000]}} m \cdot 4 \cdot 5$$

374,000 resamples

Methods



Parameters

```
set.seed(123)

m_list <- list(200, 500, 1000, 2000, 5000, 10000) # num
#m_list <- list(20, 50, 100, 200, 500, 1000) # number o
n_list <- list(10, 50, 100, 1000) # sample size
```

Distributions of Interest

1. **Normal Distribution**
   The probability density function (PDF) of a normal distribution is given by:

$$f(x; \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

   where ( ) is the mean and ( ) is the standard deviation.

2. **t-Distribution**

The PDF of the t-distribution is:

$$f(x;\nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sqrt{\nu\pi}\Gamma\left(\frac{\nu}{2}\right)}\left(1+\frac{x^2}{\nu}\right)^{-\frac{\nu+1}{2}}$$

where ( ) is the degrees of freedom and ( ) is the gamma function.

3. **Gamma Distribution**
   The PDF of the gamma distribution is:

$$f(x;\alpha,\beta) = \frac{\beta^\alpha x^{\alpha-1}e^{-\beta x}}{\Gamma(\alpha)}$$

   where ( ) is the shape parameter and ( ) is the rate parameter.

4. **Lognormal Distribution**
   The PDF of the lognormal distribution is:

$$f(x;\mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}}e^{-\frac{(\ln x-\mu)^2}{2\sigma^2}}$$

   where ( ) and ( ) are the mean and standard deviation of the variable's natural logarithm.

5. **Weibull Distribution**
   The PDF of the Weibull distribution is:

$$f(x;\lambda,k) = \frac{k}{\lambda}\left(\frac{x}{\lambda}\right)^{k-1}e^{-\left(\frac{x}{\lambda}\right)^k}$$

   where ( ) is the scale parameter and (k) is the shape parameter.

Simulate Distributions

```
library(MASS)

# Set params here
simulate_distributions <- function(distribution, n) {
```

```
    switch(distribution,
           "normal" = rnorm(n, mean = 0, sd = 1),
           "t" = rt(n, df = 10),
           "gamma" = rgamma(n, shape = 2, rate = 1),
           "lognormal" = rlnorm(n, meanlog = 0, sdlog = 1
           "weibull" = rweibull(n, shape = 2, scale = 1))
  }

  distributions <- c("normal", "t", "gamma", "lognormal",
```

Estimators of Interest

1) T-Interval

The t-interval is calculated as the 2.5th and 97.5th percentiles of the bootstrap sample means:

$$\text{T-Interval} = \text{Quantile}(\text{means}, \{0.025, 0.975\})$$

2) Likelihood Interval Based on MLE

The likelihood interval based on the maximum likelihood estimate (MLE) uses the sample mean (( )) and the standard error ((SE)):

$$\text{MLE} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

$$SE = \frac{\text{SD}(\text{data})}{\sqrt{n}}$$

The interval is then:

$$\text{Likelihood Interval (MLE)} = [\text{MLE} - 1.96 \times SE, \text{MLE} + 1.96 \times SE]$$

3) Likelihood Interval Based on Likelihood Ratio

The likelihood interval based on the likelihood ratio uses the negative log-likelihood function:

$$\ell(\mu) = -\sum_{i=1}^{n} \log\left(f(x_i; \mu, \sigma)\right)$$

Where (f(x_i; ,)) is the normal PDF:

$$f(x_i; \mu, \sigma) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{(x_i - \mu)^2}{2\sigma^2}\right)$$

The MLE for ( ) minimizes (()):

$$\hat{\mu} = \arg\min_{\mu} \ell(\mu)$$

The likelihood interval is calculated as:

$$\text{Likelihood Interval (Likelihood Ratio)} = \left[\hat{\mu} - 1.96 \times SE, \hat{\mu} + 1.96 \times SE\right]$$

4) Non-Parametric Bootstrap Interval

The non-parametric bootstrap interval is calculated as the 2.5th and 97.5th percentiles of the bootstrap sample means:

$$\text{Non-Parametric Bootstrap Interval} = \text{Quantile}(\text{means}, 0.025, 0.975)$$

Functions for Estimators

```
# 1) T-Interval
calculate_t_interval <- function(means) {
  quantile(means, c(0.025, 0.975))
}

# 2) Likelihood Interval Based on MLE
calculate_likelihood_interval_mle <- function(data) {
  mle <- mean(data)
  n <- length(data)
  se <- sd(data) / sqrt(n)
  c(mle - 1.96 * se, mle + 1.96 * se)
}

# 3) Likelihood Interval Based on Likelihood Ratio
calculate_likelihood_interval_lr <- function(data) {
  log_likelihood <- function(mean) {
    -sum(dnorm(data, mean = mean, sd = sd(data), log =
  }
  mle_mean <- optimize(log_likelihood, interval = range
  n <- length(data)
  se <- sd(data) / sqrt(n)
  c(mle_mean - 1.96 * se, mle_mean + 1.96 * se)
}
```

```
# 4) Non-Parametric Bootstrap Interval
calculate_nonparametric_interval <- function(means) {
  quantile(means, c(0.025, 0.975))
}
```

Expected Analytic Values

```
# Define expected analytic values for each distribution
expected_analytic_values <- function(dist_name, n) {
  switch(dist_name,
         "normal" = list(mean = 0, se = 1 / sqrt(n)),
         "t" = list(mean = 0, se = sqrt(10 / (10 - 2))
         "gamma" = list(mean = 2 / 1, se = sqrt(2 / (1^
         "lognormal" = list(mean = exp(0 + (1^2) / 2),
         "weibull" = list(mean = 2 * gamma(1 + 1 / 2),
  )
}

# Generate a table of analytic values
generate_analytic_table <- function(m_list, n_list, dis
  analytic_table <- do.call(rbind, lapply(n_list, funct
    do.call(rbind, lapply(distributions, function(dist_
      analytic_values <- expected_analytic_values(dist_
      analytic_mean <- analytic_values$mean
      analytic_se <- analytic_values$se
      analytic_t_interval <- c(analytic_mean - 1.96 * a

      data.frame(
        n = n_value,
        distribution = dist_name,
        analytic_mean = analytic_mean,
        analytic_se = analytic_se,
        analytic_t_interval_lower = analytic_t_interval
        analytic_t_interval_upper = analytic_t_interval
      )
    }))
  }))
  return(analytic_table)
}

analytic_table <- generate_analytic_table(m_list, n_lis

# Display the analytic table
```

```
print(head(analytic_table,5))
```

```
   n distribution analytic_mean analytic_se
analytic_t_interval_lower
1 10       normal      0.000000   0.3162278
-0.6198064
2 10            t      0.000000   0.3535534
-0.6929646
3 10        gamma      2.000000   0.4472136
1.1234614
4 10    lognormal      1.648721   0.6834306
0.3091972
5 10      weibull      1.772454   0.2929859
1.1982015
  analytic_t_interval_upper
1                 0.6198064
2                 0.6929646
3                 2.8765386
4                 2.9882453
5                 2.3467062
```

Bootstrap Function

```
# Usage within the bootstrap_intervals function
bootstrap_intervals <- function(data, m) {
  n <- length(data)
  means <- numeric(m)
  for (i in 1:m) {
    sample_data <- sample(data, size = n, replace = TRU
    means[i] <- mean(sample_data)
  }

  list(
    t_interval = calculate_t_interval(means),
    likelihood_interval_mle = calculate_likelihood_inte
    likelihood_interval_lr = calculate_likelihood_inter
    nonparametric_interval = calculate_nonparametric_in
  )



}
```

Iterate through all combinations of each distribution

```
results <- list()

for (m in m_list) {
  for (n in n_list) {
    for (dist_name in distributions) {
      set.seed(123)  # Ensure reproducibility
      data <- simulate_distributions(dist_name, n)
      intervals <- bootstrap_intervals(data, m)
      results[[paste("m", m, "n", n, dist_name, sep = "

    }
  }
}
```

Bootstrap Results

```
# Define expected parameter values for each distribu io
distribution_params <- list(
  normal = list(mean = 0, sd = 1),
  t = list(df = 10),
  gamma = list(shape = 2, rate = 1),
  lognormal = list(meanlog = 0, sdlog = 1),
  weibull = list(shape = 2, scale = 1)
)

# Convert results list to a data frame with parameter v
results_table <- do.call(rbind, lapply(names(results),
  # Extract m, n, and distribution from the name
  split_name <- strsplit(name, "_")[[1]]
  m_value <- as.numeric(split_name[2])
  n_value <- as.numeric(split_name[4])
  dist_name <- split_name[5]

  # Extract intervals
  intervals <- results[[name]]

  # Extract parameters for the distribution
  params <- distribution_params[[dist_name]]

  BS_mean <- mean(intervals$t_interval)
```

```
      # Create a row
      data.frame(
        m = m_value,
        n = n_value,
        distribution = dist_name,
        expected_params = paste(names(params), unlist(param
        bs_mean = BS_mean,
        t_interval_lower = intervals$t_interval[1],
        t_interval_upper = intervals$t_interval[2],
        likelihood_mle_lower = intervals$likelihood_interva
        likelihood_mle_upper = intervals$likelihood_interva
        likelihood_lr_lower = intervals$likelihood_interval
        likelihood_lr_upper = intervals$likelihood_interval
        nonparametric_lower = intervals$nonparametric_inter
        nonparametric_upper = intervals$nonparametric_inter
      )
    }))

    # Display the table
    print(head(results_table,5))
```

```
        m  n distribution    expected_params    bs_mean
t_interval_lower
2.5%  200 10       normal       mean=0, sd=1 0.08382257
-0.4757399
2.5%1 200 10            t              df=10 0.08037697
-0.5735814
2.5%2 200 10        gamma    shape=2, rate=1 1.77881286
0.9761261
2.5%3 200 10    lognormal meanlog=0, sdlog=1 1.76782387
0.6961665
2.5%4 200 10      weibull   shape=2, scale=1 0.79270562
0.5438618
      t_interval_upper likelihood_mle_lower
likelihood_mle_upper
2.5%         0.6433850           -0.5165358
0.6657871
2.5%1        0.7343354           -0.7777221
0.8275486
2.5%2        2.5814996            0.9101920
2.7482641
2.5%3        2.8394813            0.5287796
2.8507046
```

```
2.5%4        1.0415495           0.4887924
1.0513919
      likelihood_lr_lower likelihood_lr_upper
nonparametric_lower
2.5%          -0.5165358           0.6657871
-0.4757399
2.5%1         -0.7777221           0.8275486
-0.5735814
2.5%2          0.9101920           2.7482641
0.9761261
2.5%3          0.5287796           2.8507046
0.6961665
2.5%4          0.4887924           1.0513919
0.5438618
      nonparametric_upper
2.5%           0.6433850
2.5%1          0.7343354
2.5%2          2.5814996
2.5%3          2.8394813
2.5%4          1.0415495
```

```r
# Save the table as a CSV file
write.csv(results_table, "results_table_with_params.csv
```

Combine Expected and Analytic Values

```r
# Function to combine bootstrap and analytic tables
combine_bootstrap_and_analytic <- function(bootstrap_re
  # Iterate through bootstrap results and match with an
  combined_table <- do.call(rbind, lapply(names(bootstr
    # Extract m, n, and distribution from the name
    split_name <- strsplit(name, "_")[[1]]
    m_value <- as.numeric(split_name[2])
    n_value <- as.numeric(split_name[4])
    dist_name <- split_name[5]

    # Extract bootstrap intervals
    intervals <- bootstrap_results[[name]]

    BS_mean <- mean(intervals$t_interval)

    # Match with analytic values
    analytic_row <- analytic_table[
```

```
      analytic_table$n == n_value & analytic_table$dist

    # Create a combined row
    data.frame(
      m = m_value,
      n = n_value,
      distribution = dist_name,
      analytic_mean = analytic_row$analytic_mean,
      analytic_se = analytic_row$analytic_se,
      analytic_t_interval_lower = analytic_row$analytic
      analytic_t_interval_upper = analytic_row$analytic
      bs_mean = BS_mean,
      t_interval_lower = intervals$t_interval[1],
      t_interval_upper = intervals$t_interval[2],
      likelihood_mle_lower = intervals$likelihood_inter
      likelihood_mle_upper = intervals$likelihood_inter
      likelihood_lr_lower = intervals$likelihood_interv
      likelihood_lr_upper = intervals$likelihood_interv
      nonparametric_lower = intervals$nonparametric_int
      nonparametric_upper = intervals$nonparametric_int
    )
  }))

  return(combined_table)
}

# combine tables
combined_table <- combine_bootstrap_and_analytic(result

# Rearrange columns for better comparison
combined_table <- combined_table[, c(
  "m", "n", "distribution",
  "analytic_mean", "bs_mean",
  "t_interval_lower", "analytic_t_interval_lower", "t_i
  "analytic_se",
  "likelihood_mle_lower", "likelihood_lr_lower", "nonpa
  "likelihood_mle_upper", "likelihood_lr_upper", "nonpa
)]

# Re-name columns with BS results to include 'BS' prefi
colnames(combined_table) <- sub("^(t_interval|likelihoo

# Save the rearranged table as a CSV file
write.csv(combined_table, "rearranged_combined_bootstra
```

```
# Display the combined table
print(head(combined_table,5))
```

```
        m  n distribution analytic_mean    bs_mean
BS_t_interval_lower
2.5%  200 10       normal      0.000000 0.08382257
-0.4757399
2.5%1 200 10            t      0.000000 0.08037697
-0.5735814
2.5%2 200 10        gamma      2.000000 1.77881286
0.9761261
2.5%3 200 10    lognormal      1.648721 1.76782387
0.6961665
2.5%4 200 10      weibull      1.772454 0.79270562
0.5438618
      analytic_t_interval_lower BS_t_interval_upper
analytic_t_interval_upper
2.5%                 -0.6198064           0.6433850
0.6198064
2.5%1                -0.6929646           0.7343354
0.6929646
2.5%2                 1.1234614           2.5814996
2.8765386
2.5%3                 0.3091972           2.8394813
2.9882453
2.5%4                 1.1982015           1.0415495
2.3467062
      analytic_se BS_likelihood_mle_lower
BS_likelihood_lr_lower
2.5%    0.3162278              -0.5165358
-0.5165358
2.5%1   0.3535534              -0.7777221
-0.7777221
2.5%2   0.4472136               0.9101920
0.9101920
2.5%3   0.6834306               0.5287796
0.5287796
2.5%4   0.2929859               0.4887924
0.4887924
      BS_nonparametric_lower BS_likelihood_mle_upper
BS_likelihood_lr_upper
2.5%              -0.4757399               0.6657871
0.6657871
2.5%1             -0.5735814               0.8275486
```

```
0.8275486
2.5%2              0.9761261           2.7482641
2.7482641
2.5%3              0.6961665           2.8507046
2.8507046
2.5%4              0.5438618           1.0513919
1.0513919
      BS_nonparametric_upper
2.5%               0.6433850
2.5%1              0.7343354
2.5%2              2.5814996
2.5%3              2.8394813
2.5%4              1.0415495
```