Problem Set 1

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```
# Question 1

# 1.1: Formula for population mean

pop_mean <- function(x) {
    out_vector <- sum(x)/length(x)  # divide sum by total number of observations
    return(out_vector)
}
```

```
# 1.2: Formula to calculate variance

pop_var <- function(x) {
    var = sum((x - pop_mean(x))^2)/(length(x))  #(sum of each number - the mean)^2/sample size
    return(var)
}
```

```
# 1.3

gapminder <- read.csv("data/gapminder.csv")

pop_mean(gapminder$lifeExp)
```

```
## [1] 59.47444
```

```
pop_var(gapminder$lifeExp)
```

```
## [1] 166.7537
```

```
mean(gapminder$lifeExp)
```

```
## [1] 59.47444
```

```
var(gapminder$lifeExp)
```

```
## [1] 166.8517
```

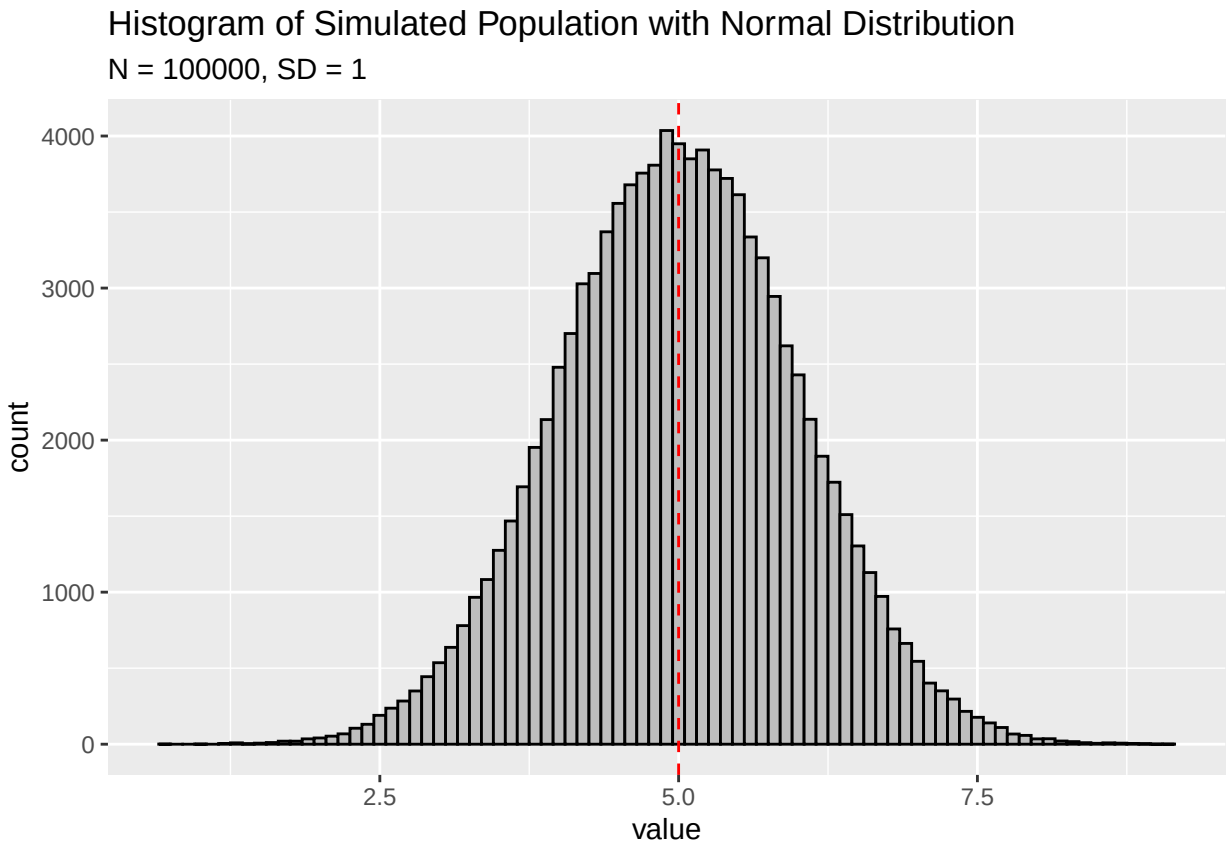
```r
# The mean value for both functions is 59.474. The variance for the
# function I wrote is 166.753. The variance for the R function is
# 166.852. They are different because my function calculcates
# population variance, while R's function calculates sample variance.
```

```r
# Question #2

# Import data

parent_inc <- read.csv("data/parent_inc.csv")

# Tidy data

parent_inc %>% rename(father_income = fincome, mother_income = mincome) %>%
    pivot_longer(cols = c(father_name, mother_name, father_income, mother_income),
        names_to = c("type", ".value"), names_sep = "_")
```

```
## # A tibble: 6 x 4
##   famid type   name   income
##   <int> <chr>  <chr>   <int>
## 1     1 father Arthur  42000
## 2     1 mother Jess    45000
## 3     2 father Harry   35000
## 4     2 mother Pam     24000
## 5     3 father Matt    78000
## 6     3 mother Mary    55000
```

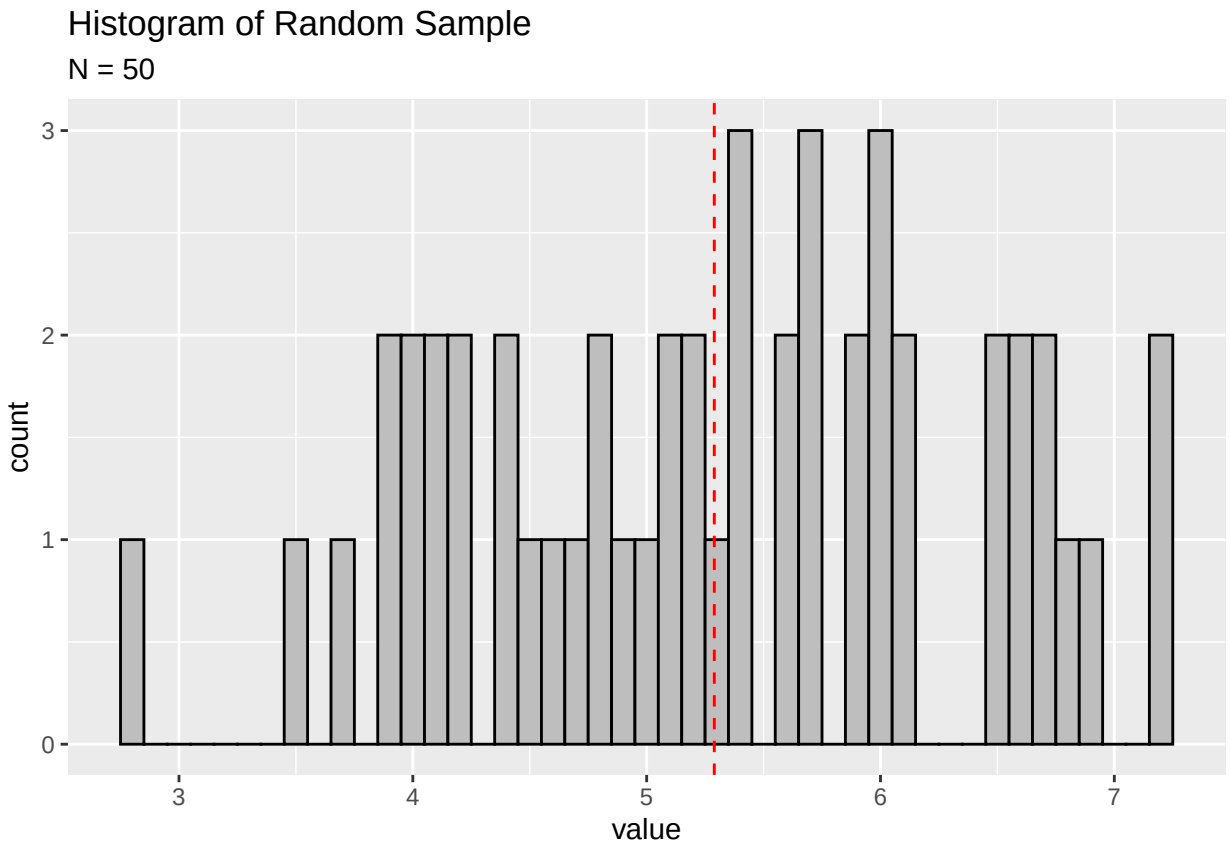
```r
# Question #3 3.1: Create a population data frame

value <- rnorm(n = 1e+05, mean = 5, sd = 1) %>% as_tibble()
```

```r
# 3.2: Create a histogram
value %>% ggplot(aes(value)) + geom_histogram(binwidth = 0.1, color = "black",
    fill = "grey") + geom_vline(aes(xintercept = mean(value)), color = "red",
    linetype = "dashed") + labs(title = "Histogram of Simulated Population with Normal Distribution",
    subtitle = "N = 100000, SD = 1")
```




```
# 3.3: Draw random sample n=50

set.seed(110001)
sample <- value %>% sample_n(size = 50, replace = FALSE)
```

```
# 3.4: Plot a histogram of the sample

sample %>% ggplot(aes(value)) + geom_histogram(binwidth = 0.1, color = "black",
    fill = "grey") + geom_vline(aes_string(xintercept = paste0("mean(",
    sample, ")")), color = "red", linetype = "dashed") + labs(title = "Histogram of Random Sample",
    subtitle = "N = 50")
```




```
# 3.5:

# Calculate point estimate for population mean
point_est <- sum(sample)/count(sample)
print(point_est)
```

```
##          n
## 1 5.289375
```

```
# Calculate standard error of point estimate
standard_error <- sapply(sample, sd)/sqrt(length(sample))
print(standard_error)
```

```
##    value
## 1.053264
```

```
# Calculate 95% confidence interval of point estimate

# The formula is: population mean +/- t-critical value * standard error

# Calculate critical value
observed_t <- point_est/standard_error
print(observed_t)
```

```
##          n
## 1 5.021889
```

```
crit_val <- qt(p = 0.5 * 0.05, df = 49)
print(crit_val)
```

```
## [1] -2.009575
```

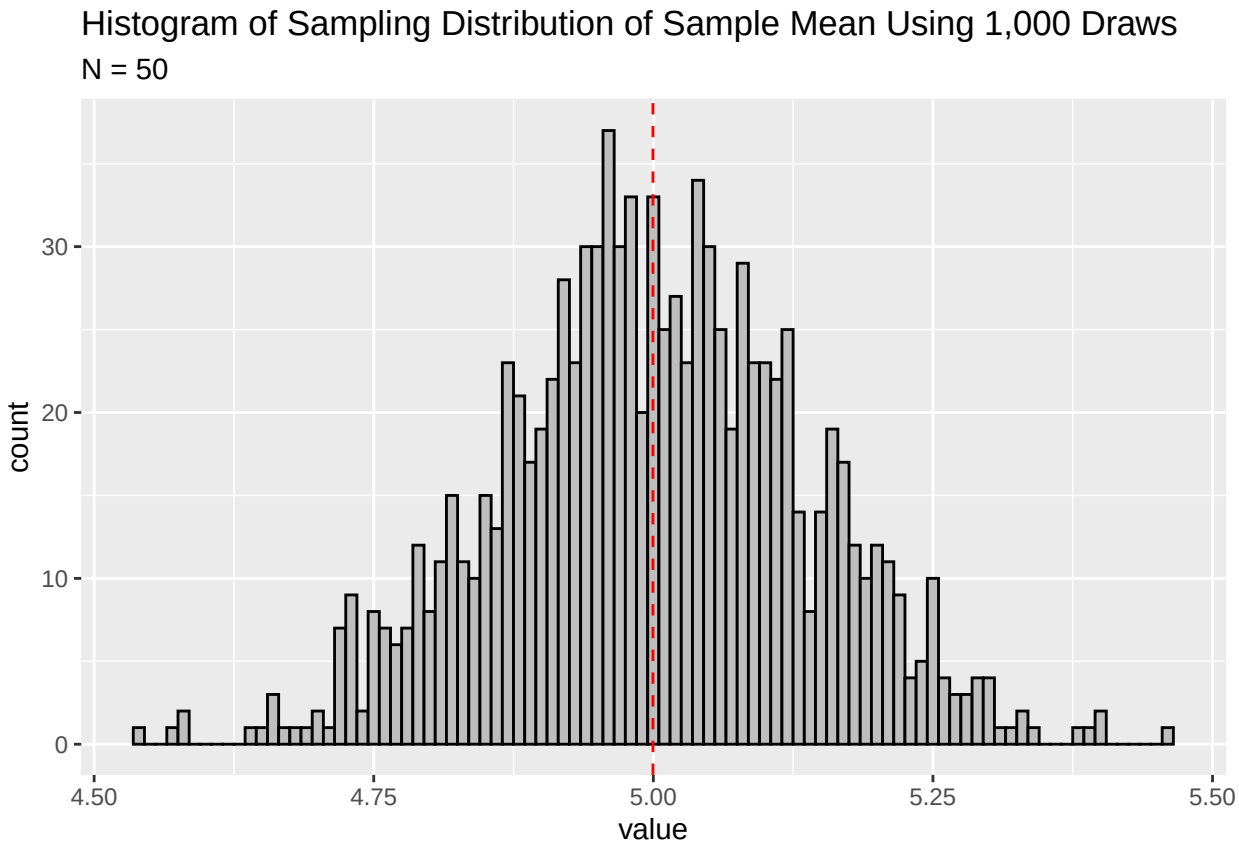
```
# Caclulate confidence interval

upper_bound <- as.numeric(point_est) - (as.numeric(crit_val) * as.numeric(standard_error))
lower_bound <- as.numeric(point_est) + (as.numeric(crit_val) * as.numeric(standard_error))
CI <- c(lower_bound, upper_bound)
print(CI)
```

```
## [1] 3.172762 7.405989
```

```
# 3.6 Simulate the sampling distribution of the sample mean (n = 50)
# using 1,000 draws

mean_container <- vector(mode = "numeric", length = 1000)

set.seed(110001)
for (i in 1:1000) {
    sample_two <- value %>% sample_n(size = 50, replace = FALSE)
    mean_container[i] <- mean(sample_two$value)
}

head(mean_container, n = 10)
```

```
##  [1] 5.289375 4.889904 5.094229 5.059246 4.829965 5.017235 4.917106 5.194634
##  [9] 5.021282 4.888220
```

```
# 3.7 Create a histogram of the sampling distribution of the sample
# mean

mean_container %>% as_tibble %>% ggplot(aes(value)) + geom_histogram(binwidth = 0.01,
    color = "black", fill = "grey") + geom_vline(aes_string(xintercept = mean(mean_container)),
    color = "red", linetype = "dashed") + labs(title = "Histogram of Sampling Distribution of Sample Mea
    subtitle = "N = 50")
```




```
# 3.8 Calculate point estimate for population mean

point_est_two <- sum(mean_container)/length(mean_container)
print(point_est_two)
```

```
## [1] 4.999681
```

```
# Calculate standard error of point estimate

# Sample standard deviation/square root of sample size

standard_error_two <- sd(mean_container)/sqrt(length(mean_container))
print(standard_error_two)
```

```
## [1] 0.004349864
```

```
# Calculate 95% confidence interval of point estimate

# The formula is: population mean +/- t-critical value * standard error

# Calculate critical value

observed_t_two <- point_est_two/standard_error_two
print(observed_t_two)
```

```
## [1] 1149.388
```

```
crit_val_two <- qt(p = 0.5 * 0.05, df = 49)
print(crit_val_two)
```

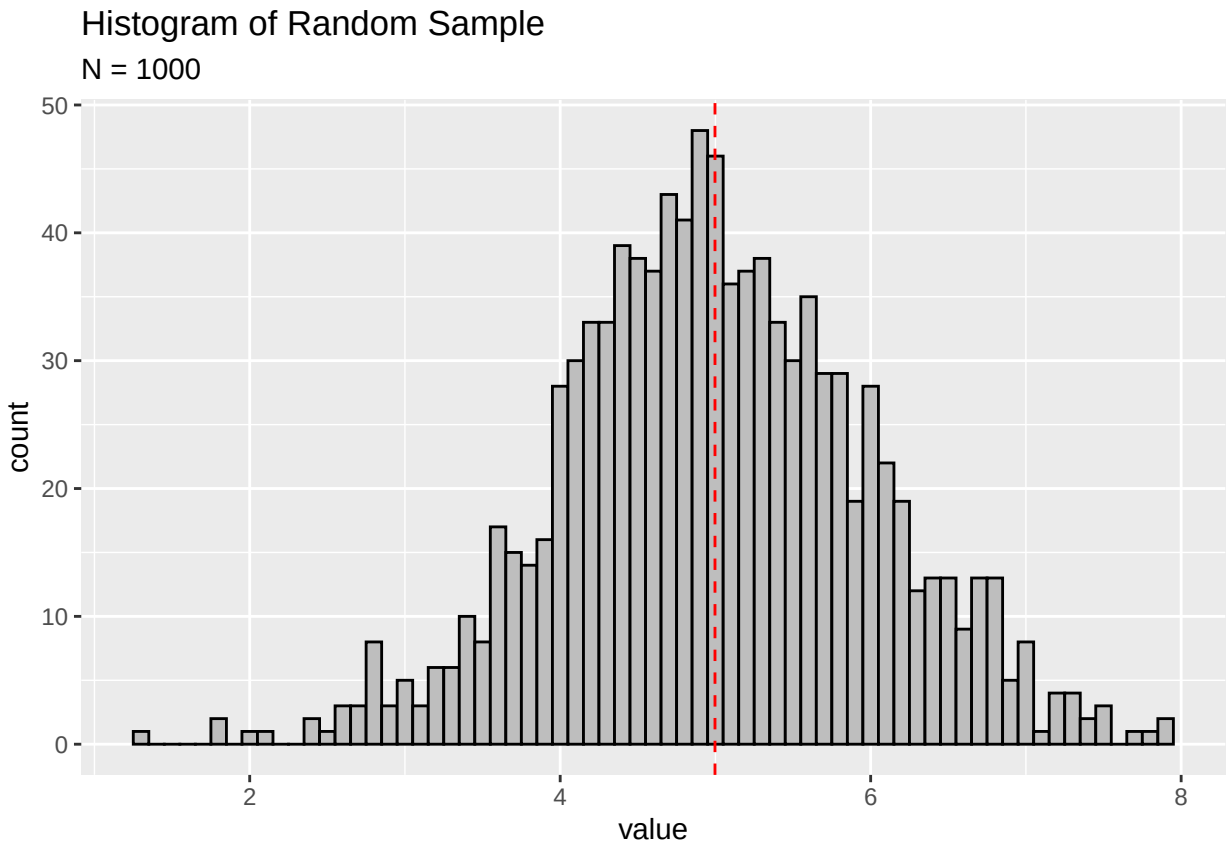
```
## [1] -2.009575
```

```
# Caclulate confidence interval

upper_bound_two <- as.numeric(point_est_two) - (as.numeric(crit_val_two) *
    as.numeric(standard_error_two))
lower_bound_two <- as.numeric(point_est_two) + (as.numeric(crit_val_two) *
    as.numeric(standard_error_two))
CI_two <- c(lower_bound_two, upper_bound_two)
print(CI_two)
```

```
## [1] 4.990939 5.008422
```

```
# 3.9 Repeat questions 3 to 8 increasing sample size to n=1000

# a) Draw a random sample n=1,000

set.seed(110001)
final_sample <- value %>% sample_n(size = 1000, replace = FALSE) %>% as_tibble()
```

```
# b) Plot a histogram of the sample with appropriate title and labels

final_sample %>% ggplot(aes(value)) + geom_histogram(binwidth = 0.1, color = "black",
    fill = "grey") + geom_vline(aes_string(xintercept = paste0("mean(",
    final_sample, ")")), color = "red", linetype = "dashed") + labs(title = "Histogram of Random Sample
    subtitle = "N = 1000")
```




```
# c) Calculate point estimate

point_est_three <- sum(final_sample)/count(final_sample)
print(point_est_three)
```

```
##          n
## 1 4.997173
```

```
# Calculate standard error of point estimate

standard_error_three <- sapply(final_sample, sd)/sqrt(length(final_sample))
print(standard_error_three)
```

```
##     value
## 0.9931817
```

```
# Calculate 95% confidence interval of point estimate The formula is:
# population mean +/- t-critical value * standard error

# Calculate critical value

observed_t_three <- point_est_three/standard_error_three
print(observed_t_three)
```

```
##          n
## 1 5.031479
```

```
crit_val_three <- qt(p = 0.5 * 0.05, df = 999)
print(crit_val_three)
```

```
## [1] -1.962341
```

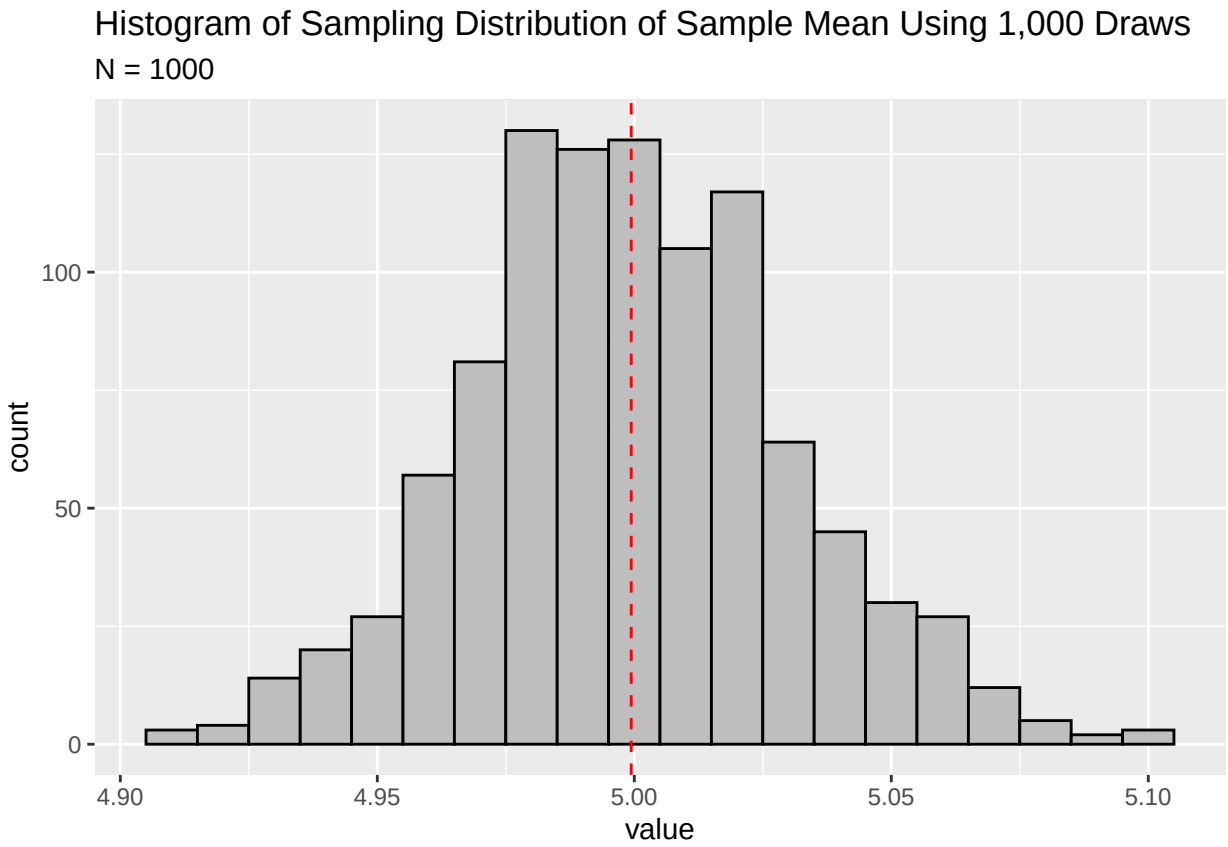
```
# Caclulate confidence interval

upper_bound_three <- as.numeric(point_est_three) - (as.numeric(crit_val_three) *
    as.numeric(standard_error_three))
lower_bound_three <- as.numeric(point_est_three) + (as.numeric(crit_val_three) *
    as.numeric(standard_error_three))
CI_three <- c(lower_bound_three, upper_bound_three)
print(CI_three)
```

```
## [1] 3.048211 6.946135
```

```
# d)

final_mean_container <- vector(mode = "numeric", length = 1000)

set.seed(110001)
for (i in 1:1000) {
    sample_three <- value %>% sample_n(size = 1000, replace = FALSE)
    final_mean_container[i] <- mean(sample_three$value)
}

head(final_mean_container, n = 10)
```

```
##  [1] 4.997173 4.984034 4.958647 5.031017 4.990072 4.976581 4.993773 5.004962
##  [9] 5.005620 4.996527
```

```
# e) Create a histogram of the sampling distribution of the sample mean
# you simulated

final_mean_container %>% as_tibble %>% ggplot(aes(value)) + geom_histogram(binwidth = 0.01,
    color = "black", fill = "grey") + geom_vline(aes_string(xintercept = mean(final_mean_container)),
    color = "red", linetype = "dashed") + labs(title = "Histogram of Sampling Distribution of Sample Mea
    subtitle = "N = 1000")
```




```
# f.1) Calculate point estimate for population mean

point_est_four <- sum(final_mean_container)/length(final_mean_container)
print(point_est_four)
```

```
## [1] 4.999397
```

```
# f.2) Calculate standard error of point estimate

# Sample standard deviation/square root of sample size

standard_error_four <- sd(final_mean_container)/sqrt(length(final_mean_container))
print(standard_error_four)
```

```
## [1] 0.0009872101
```

```
# f.3) Calculate 95% confidence interval of point estimate

# The formula is: population mean +/- t-critical value * standard error

# Calculate critical value

observed_t_four <- point_est_four/standard_error_four
print(observed_t_four)
```

```
## [1] 5064.167
```

```
crit_val_four <- qt(p = 0.5 * 0.05, df = 999)
print(crit_val_four)
```

```
## [1] -1.962341
```

```
# Caclulate confidence interval

upper_bound_four <- as.numeric(point_est_four) - (as.numeric(crit_val_four) *
    as.numeric(standard_error_four))
lower_bound_four <- as.numeric(point_est_four) + (as.numeric(crit_val_four) *
    as.numeric(standard_error_four))
CI_four <- c(lower_bound_four, upper_bound_four)
print(CI_four)
```

```
## [1] 4.997460 5.001334
```

```
# The concept being demonstrated here is the (Weak) Law of Large
# Numbers. As the sample size increases, and the number of samples
# draws increases, the sample mean more nearly equals the population
# mean. This is evidenced by the smaller standard errors and smaller
# confidence intervals, showing that the estimator became more precise.
```