Practice Session 5

In this practice section we will introduce the bootstrap distribution, bootstrap confidence interval, and hypothesis testing. You may use the functions: `sample()`, `do_it` to create the bootstrap distribution.

Part 1: Confidence interval concept

Practice 1.a: True or False/ Confidence interval interpretation

A catalog sales company promises to deliver orders placed on the Internet within 3 days. Follow-up calls to a few randomly selected customers show that a 95% confidence interval for the proportion of all orders that arrive on time is $85\% \pm 5\%$.

1.) Between 80% and 90% of all orders arrive on time.

2.) Ninety five percent of all random samples of customers will show that 85% of orders arrive on time.

3.) The interval between 80% and 90% gives a plausible range of values for where the true population parameter lies since 95% of intervals created will contain the population proportion.

Answers:

1.) Not correct. This statement implies certainty. There is no level of confidence in the statement.

2.) Not correct. Different samples will give different results. Many fewer than 95% of samples are expected to have exactly 88% on-time orders.

3.) Correct.

Practice 1.b: True or False/ confidence level, Sample size, and confidence interval

Several factors are involved in the creation of a confidence interval. Among them are the sample size, the level of confidence, and the margin of error.

1.) For a given sample size, higher confidence means a larger margin of error.

2.) For a specified confidence level, smaller samples provide smaller margins of error.

3.) For a fixed margin of error, larger samples provide greater confidence.

Answers:

1.) True. For a given sample size, higher confidence means a larger margin of error.

2.) False. Smaller samples lead to larger standard errors, which lead to larger margins of error.

3.) True. Larger samples are less variable, which makes us more confident that a given confidence interval succeeds in catching the population proportion.

Part 2: Construct Bootstrap Distribution

Here's the clever idea: We don't have the population, but we have a sample. Probably the sample is similar to the population in many ways.So let's sample from our sample. We'll call it `bootstrapping`. We want samples **the same size** as our original sample, so we will need to **sample with replacement**.This means that we may pick some members of the population more than once and others not at all. We'll replicate this many times.

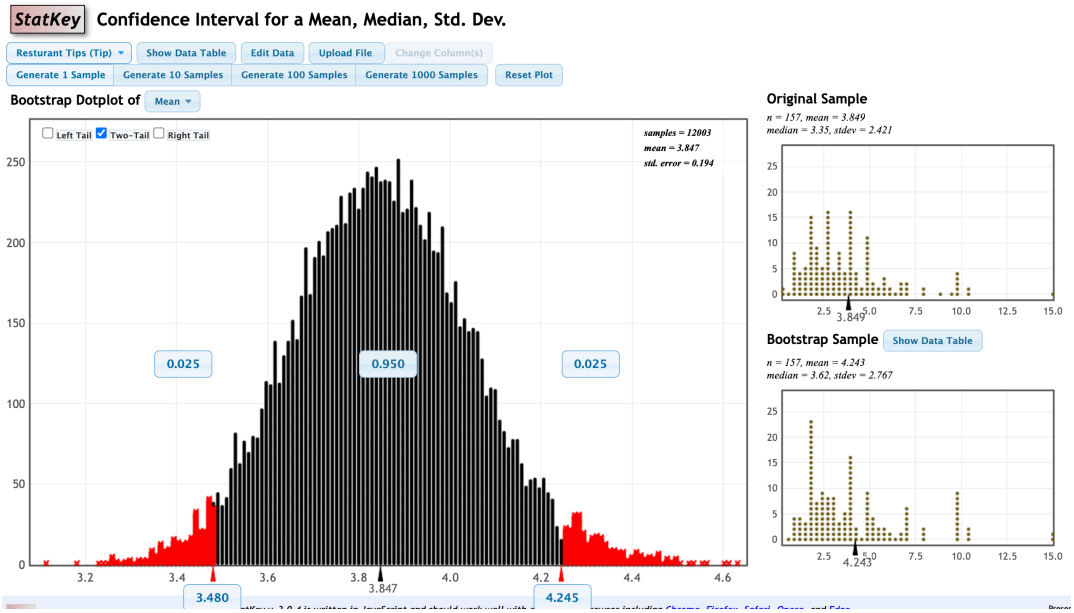
Generating a Bootstrap Distribution:

- Generate bootstrap samples by **sampling with replacement** from the original sample, using the **same sample size**.
- Compute the **statistic of interest** (called a bootstrap statistic), for each of the bootstrap samples.
- Collect the **samples statistics** for many bootstrap samples to create a **bootstrap distribution**.

Example:

Using StatKey link, try to play with the creation of the bootstrap distribution from different data. The following picture shows the website and an example of bootstrap CI for the variable`tip` from the data `Resturant tips`.

`https://www.lock5stat.com/StatKey/bootstrap_1_quant/bootstrap_1_quant.html`



Practice 2:

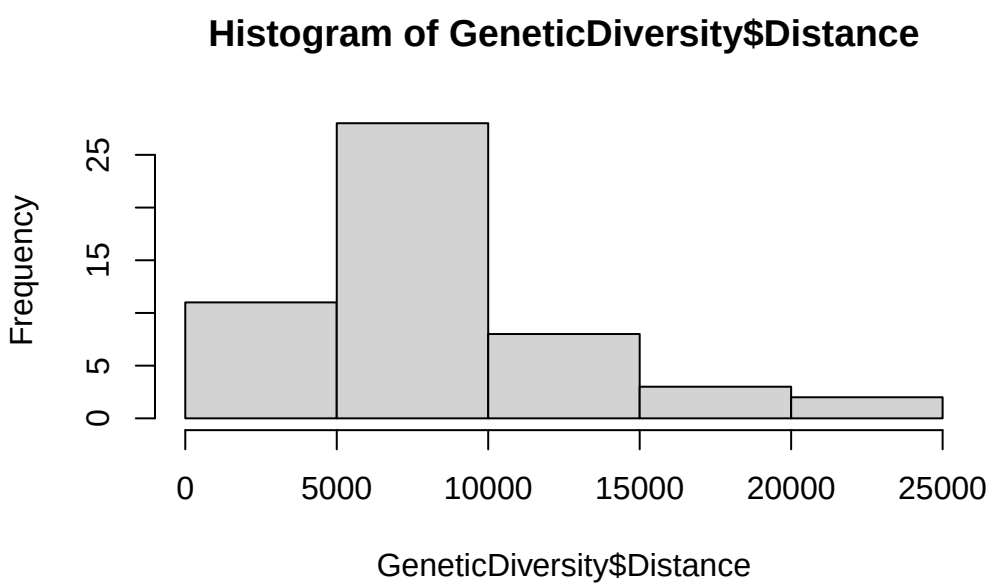
The `GeneticDiversity` data give a measure of genetic diversity for different populations and the geographic distance of each population from East Africa (Addis Ababa, Ethiopia), as one would travel over the surface of the earth by land (migration long ago is thought to have happened by land).

The variables in this study were : Population, Country, Continent,Genetic Diversity (a measure of genetic diversity in the population), Distance (distance by land to East Africa in km).

1) First, create `histogram` of `Distance`. What is the `sample size` of the data ?

```
library(Lock5Data)
library(SDS1000)
data(GeneticDiversity)

n <- length(GeneticDiversity$Distance)
hist(GeneticDiversity$Distance)
```



2) Second, create a one bootstrap sample from `Distance` . You might use the functions `sample`.

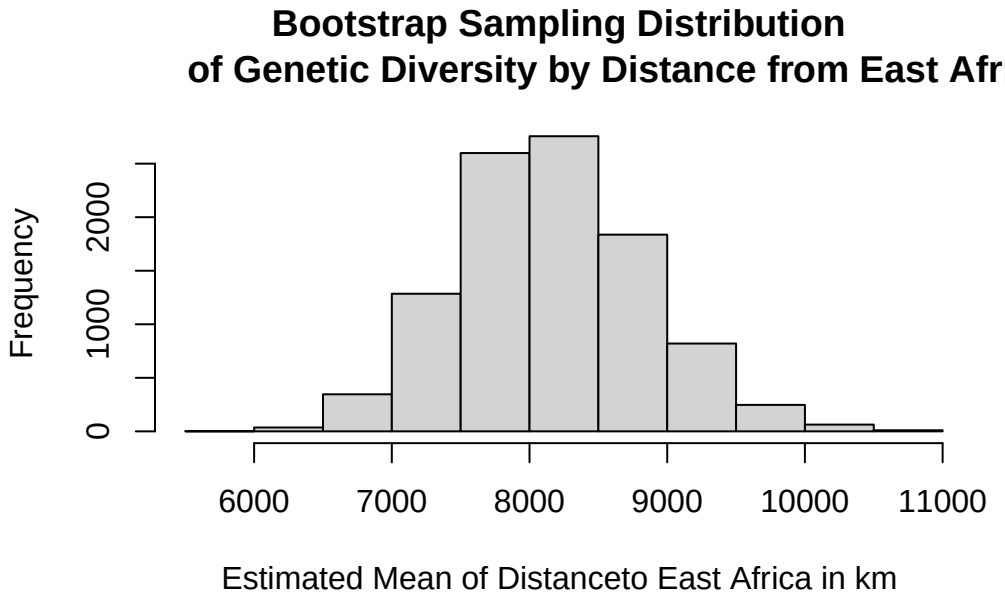
```
one_sample <- sample(GeneticDiversity$Distance,
                     size = n, replace = T)
```

3) Third, you might replicate this one sample `10000` times `with replacement` using the function `do_it()` to create a `bootstrap sampling ditribution`

```
boot_dist <- do_it(10000) * {
  one_sample = sample(GeneticDiversity$Distance, size = n, replace = T)
  mean( one_sample)
  }
```

4) Fourth, create a `histogram` for the bootstrap distribution of the variable `Distance`

```
hist(boot_dist, main ="Bootstrap Sampling Distribution
            of Genetic Diversity by Distance from East Africa ",
                xlab = "Estimated Mean of Distanceto East Africa in km ")
```



5) congrats!, you created bootstrap sampling distribution from one sample !

Part 3: Construct Bootstrap Confidence Interval

The steps to Construct Bootstrap Confidence Interval are:

1. Compute the statistic from the original sample.
2. Create a bootstrap distribution by resampling from the sample.

- same size samples as the original sample
- with replacement
- compute the statistic for each sample. The distribution of these statistics is the bootstrap distribution.

3. Estimate the standard error SE by computing the standard deviation of the bootstrap distribution.
4. 95% CI is: $statistic \pm 2 * SE$

Practice 3:

From the `GeneticDiversity` bootstrap sampling distribution you have created in the previous question, create a 95% CI for the the sample mean of `Distance`.

1.) Calculate the mean of `Distance` from your original sample

```
x_bar <- mean(GeneticDiversity$Distance )

x_bar
```

```
[1] 8164.429
```

2.) Calculate the standard error of our bootstrap sampling distribution of the `Distance`

```
boot_se <- sd(boot_dist )

boot_se
```

```
[1] 688.4544
```

3.) Calculate the 95% CI, which is based on the formula:$statistic \pm 2 * SE$

```
#CI_lower <- x_bar - 2*boot_se
#CI_upper <- x_bar + 2*boot_se

CI95_lower_upper <- x_bar+2*boot_se*c(-1,1)

CI95_lower_upper
```

```
[1] 6787.521 9541.338
```

4) Calculate the confidence interval of 99% using the formula

```
# 99\% has different critical value than 95%

cv_99 <- qnorm(0.995)

CI99_lower_upper <- x_bar+(cv_99)*boot_se*c(-1,1)

CI99_lower_upper
```

```
[1] 6391.088 9937.770
```

Part 4:Create Bootstrap Confidence Interval with Percentiles

Practice 4:

1) Let create a 95% , 90% CI of the mean `Distance` in `R`, using **the percentiles** which they can be calculated using `quantile` function.

```
CI_95_lower_upper <- quantile(boot_dist, c(0.025, 0.975))
CI_95_lower_upper
```

```
    2.5%    97.5%
6903.643 9579.303
```

```
CI_90_lower_upper<-  quantile(boot_dist, c(0.05, 0.95))
CI_90_lower_upper
```

```
      5%      95%
7084.069 9341.457
```

```
CI_99_lower_upper <- quantile(boot_dist, c(0.005, 0.995))
CI_99_lower_upper
```

```
     0.5%     99.5%
 6545.244 10141.962
```

Part 5: Hypothesis testing

Statistical Tests:

A statistical test is used to determine whether results from a sample are convincing enough to allow us to conclude something about the population.

We have two competing claims about the population, the **null hypothesis**, denoted by `H0`, and the **alternative hypothesis**, denoted by `Ha`.

Practice 5:

State the null and alternative hypotheses for the statistical test described:

1.) Testing to see if there is evidence that a mean is less than 50.

2.) Testing to see if there is evidence that a proportion is greater than 0.3.

3.) Testing to see if there is evidence that the mean of group A is not the same as the mean of group B.

4.) Testing to see if there is evidence that the correlation between two variables is positive.

Answers:

1. $H_0 : \mu = 50$ vs $H_a : \mu < 50$
2. $H_0 : p = 0.3$ vs $H_a : p > 0.3$
3. $H_0 : \mu_A = \mu_B$ vs $H_a : \mu_A \neq \mu_B$
4. $H_0 : \rho = 0$ vs $H_a : \rho > 0$