```
# HW 6 - Due Tuesday October 18, 2016 in moodle and hardcopy in class.
# Upload R file to Moodle with name: HW6_490IDS_YourClassID.R
# Do not remove any of the comments. These are marked by #

# Please ensure that no identifying information (other than your class ID)
# is on your paper copy, including your name

# We will use the bootstrap technique to generate confidence intervals

# 1. Suppose we have a sample of data from an exponential distribution
# with parameter lambda. In this case use lambda.hat = 1/mean(X).

# As the number of observations increases, does the estimate for lambda
# become roughly normally distributed? We will answer this question in
# the following parts.

# 1a. (1) Generate 100 observations of test data, with lambda=3. Remember
# to set your seed before carrying out any computations.
set.seed(0)
test = rexp(100, rate = 3)

# 1b. (1) What is the mean of your test data? (give the code and the value)
mean(test)
# The mean is 0.344049.

# 1c. (1) What is your estimate lambda.hat? (give the code and the value)
lambda.hat = 1 / mean(test)
# My estimate of lambda.hat is 2.906563.

# 2. Now use the bootstrap to estimate the distribution of
# lambda.hat and create bootstrap confidence intervals for lambda,
# rather than the approach in 1).
```

2a. (1) Form a set of bootstrap estimates of our parameter by generating B

random samples as you did once in 1a but use lambda.hat since we do not

know the true lambda in this case (keep n=100). Set B=1000, and again set

your seed.

```
> set.seed(0)
> B = 1000
> boot.samples = matrix(nrow = B, ncol = 100)
> for (i in 1:B) {
+   boot.samples[i,] = rexp(100, rate = lambda.hat)
+ }
```

2b. (1) Get a new estimate for lambda.hat from each of the bootstrap samples

in 2a. You'll want to create a matrix to receive each value. You should

have 1000 estimates for lambda.hat now.

```
> boot.samples.estimates = matrix(nrow = 1, ncol = B)
> for (i in 1:B) {
+      boot.samples.estimates[i] = 1/mean(boot.samples[i,])
+ }
```

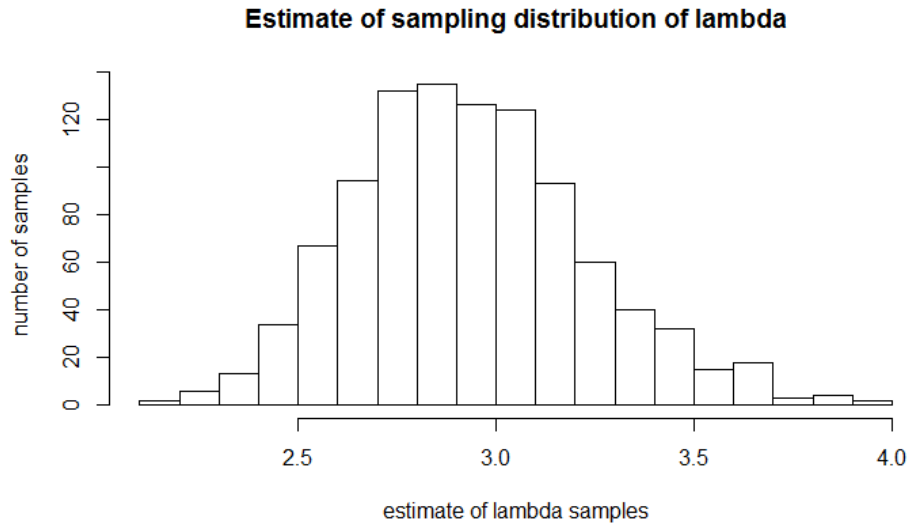
2c. (2) Now look at the sampling distribution for lambda.hat, using the hist

function. Remember the graphing techniques discussed in class and use them

to make the plot look professional. Does the distribution look normal?

hist(boot.samples.estimates, main="Estimate of sampling distribution of lambda", xlab = "estimate of lambda samples", ylab = "number of samples", breaks = 20)

The distribution looks normal.



2d. (1) Calculate an estimate of the standard error of lambda.hat using your

collection of bootstrap estimated parameters. What is your 95% confidence interval?

I use Z=2 here because it is not perfectly normal distribution.

If we only keep two digits after the decimal point, there will hardly be any difference between Z=2 and Z=1.96.

```
> SE = sd(boot.samples.estimates)
> CI = c(mean(boot.samples.estimates)-2*SE, mean(boot.samples.estimates)+2
*SE)
```

The 95% confidence interval is (2.34,3.53).

3a. (5) We made some decisions when we used the bootstrap above that we can now question.

Repeat the above creation of a confidence interval for a range of values of data

(we had our sample size fixed at 100) and a range of bootstrap values (we had B

fixed at 1000). Suppose the sample size varies (100, 200, 300, ... , 1000) and

B varies (1000, 2000, ... , 10000). You will likely find it useful to write

functions to carry out these calculations. Your final output should be

upper and lower pairs for the confidence intervals produced using the bootstrap

method for each value of sample size and B.

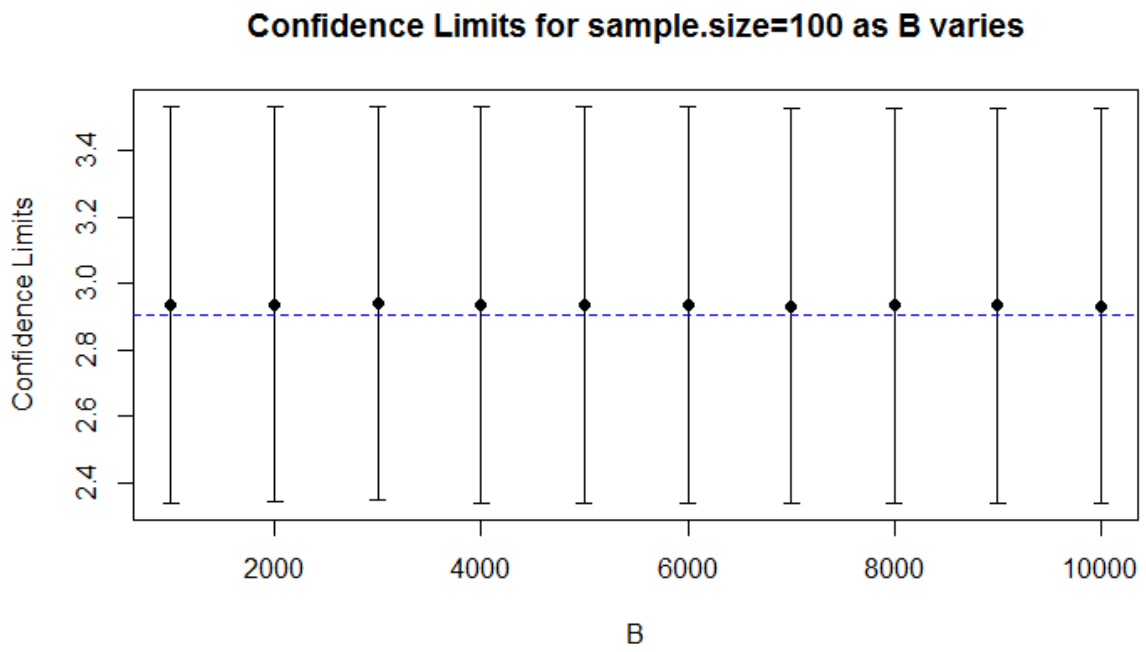
generalize 2b into a function, and vary inputs of sample size and B as we did above.

```
boot.sample <- function(sample.size, B){


 #code here
 set.seed(0)
 test = rexp(100, rate = 3)
 lambda.hat = 1 / mean(test)
 boot.estimates = matrix(nrow = 1, ncol = B)
 for (i in 1:B) {
  boot.estimates[,i] = 1/mean(rexp(sample.size,lambda.hat))
 }
 SE = sd(boot.estimates)
 upperCI = mean(boot.estimates)+2*SE
 lowerCI = mean(boot.estimates)-2*SE
 return(c(lowerCI,mean(boot.estimates),upperCI))
```

```
}

CI100sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI100sample[1,i] = boot.sample(sample.size = 100, B = i*1000)[1]
  CI100sample[2,i] = boot.sample(sample.size = 100, B = i*1000)[2]
  CI100sample[3,i] = boot.sample(sample.size = 100, B = i*1000)[3]
}

CI200sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI200sample[1,i] = boot.sample(sample.size = 200, B = i*1000)[1]
  CI200sample[2,i] = boot.sample(sample.size = 200, B = i*1000)[2]
  CI200sample[3,i] = boot.sample(sample.size = 200, B = i*1000)[3]
}

CI300sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI300sample[1,i] = boot.sample(sample.size = 300, B = i*1000)[1]
  CI300sample[2,i] = boot.sample(sample.size = 300, B = i*1000)[2]
  CI300sample[3,i] = boot.sample(sample.size = 300, B = i*1000)[3]
}

CI400sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI400sample[1,i] = boot.sample(sample.size = 400, B = i*1000)[1]
  CI400sample[2,i] = boot.sample(sample.size = 400, B = i*1000)[2]
  CI400sample[3,i] = boot.sample(sample.size = 400, B = i*1000)[3]
}

CI500sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
```

```
  CI500sample[1,i] = boot.sample(sample.size = 500, B = i*1000)[1]
  CI500sample[2,i] = boot.sample(sample.size = 500, B = i*1000)[2]
  CI500sample[3,i] = boot.sample(sample.size = 500, B = i*1000)[3]
}

CI600sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI600sample[1,i] = boot.sample(sample.size = 600, B = i*1000)[1]
  CI600sample[2,i] = boot.sample(sample.size = 600, B = i*1000)[2]
  CI600sample[3,i] = boot.sample(sample.size = 600, B = i*1000)[3]
}

CI700sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI700sample[1,i] = boot.sample(sample.size = 700, B = i*1000)[1]
  CI700sample[2,i] = boot.sample(sample.size = 700, B = i*1000)[2]
  CI700sample[3,i] = boot.sample(sample.size = 700, B = i*1000)[3]
}

CI800sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI800sample[1,i] = boot.sample(sample.size = 800, B = i*1000)[1]
  CI800sample[2,i] = boot.sample(sample.size = 800, B = i*1000)[2]
  CI800sample[3,i] = boot.sample(sample.size = 800, B = i*1000)[3]
}

CI900sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI900sample[1,i] = boot.sample(sample.size = 900, B = i*1000)[1]
  CI900sample[2,i] = boot.sample(sample.size = 900, B = i*1000)[2]
  CI900sample[3,i] = boot.sample(sample.size = 900, B = i*1000)[3]
}
```

```
CI1000sample = matrix(nrow = 3, ncol = 10)
for (i in 1:10) {
  CI1000sample[1,i] = boot.sample(sample.size = 1000, B = i*1000)[1]
  CI1000sample[2,i] = boot.sample(sample.size = 1000, B = i*1000)[2]
  CI1000sample[3,i] = boot.sample(sample.size = 1000, B = i*1000)[3]
}

# 3b. (2) Plot your CI limits to show the effect of changing the sample size and
# changing the number of bootstrap replications. What do you conclude?
install.packages("Hmisc")
library("Hmisc", lib.loc="C:/Program Files for operation/R-3.3.1/library")

errbar(x=seq(1000,10000,by=1000),y=CI100sample[2,],yplus=CI100sample[3,],yminus=CI100sample[1,],main = "Confidence Limits for sample.size=100 as B varies",xlab = "B",ylab = "Confidence Limits")
title(main = "Confidence Limits for sample.size=100 as B varies")
abline(h=lambda.hat,col="blue",lty=2)
```




```
errbar(x=seq(100,1000,by=100),y=c(CI100sample[2,1],CI200sample[2,1],CI300sample[2,1],CI400sample[2,1],CI500sample[2,1],CI600sample[2,1],CI700sample[2,1],CI800sample[2,1],CI900sample[2,1],CI1000sample[2,1]),
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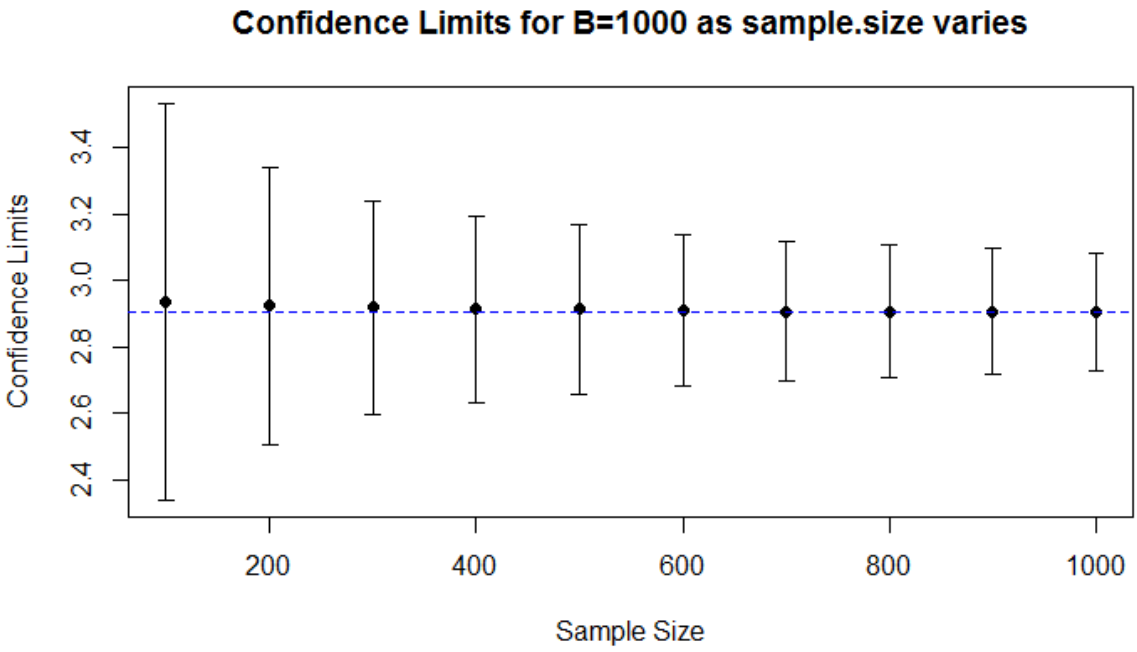
```
yplus=c(CI100sample[3,1],CI200sample[3,1],CI300sample[3,1],CI400sample[3,1],CI500sample[3,1],
CI600sample[3,1],CI700sample[3,1],CI800sample[3,1],CI900sample[3,1],CI1000sample[3,1]),


yminus=c(CI100sample[1,1],CI200sample[1,1],CI300sample[1,1],CI400sample[1,1],CI500sample[1,
1],CI600sample[1,1],CI700sample[1,1],CI800sample[1,1],CI900sample[1,1],CI1000sample[1,1]),
    main = "Confidence Limits for B=1000 as sample.size varies",xlab = "Sample Size",ylab =
"Confidence Limits")
title( main = "Confidence Limits for B=1000 as sample.size varies")
abline(h=lambda.hat,col="blue",lty=2)
```




```
# From the graph of confidence limits for sample size = 100 as B varies, we can conclude that
# the confidence intervals almost remain the same regardless of how B varies. There is only slightly
# change for different B. And for each B, the estimate of lambda.hat (mean) is very close to
# the true value of lambda.hat.


# From the graph of confidence limits for B = 1000 as sample size varies, we can conclude that
# the confidence intervals become narrower as sample size increases. And as sample size increases,
# the estimate of lambda.hat (mean) also gets closer to the true value of lamda.hat.


# 4a. (5) In 1961 John Tukey wrote an article called The Future of Data Analysis
# (it is uploaded in moodle). Some people say it is prophetic regarding the
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field of Data Science today. Do you agree or disagree? Why or why not? (Please
keep your answer less than 500 words).

John Tukey's article titled The Future of Data Analysis is prophetic in some aspects regarding
the field of Data Science. But there exist some limitations as well.

For instance, his emphasis on judgement is critical to establish directions for any field.
In this case, in Data Science field, he argued that evaluation of data analysis should be based on
(1) experience of particular field of subject from which the data come from;
(2) broad experience with how particular techniques can be utilized in various fields of application;
(3) abstract results whether can be obtained by mathematical proofs.

Those judgements are practical in today's data analysis because different kinds of data analysis
can be made towards heterogeneous data (qualitative and quantitative data) from multiple subjects.
For history, maybe we are more interested in the trend, special events and causal relationships
in the data; but for chemistry, we may more curious about structures of materials and reaction principles
based on the data. The principal purposes for data analysis and the knowledge that we hope to discover
are various among distinct subjects. Effective data analysis should be good at satisfying the needs of
researchers in different subjects. This judgement is being considered in today's data science
so John Tukey made a good prediction. In addition, some common mathematical techniques are widely used
in today's data analysis such as regression model, hypothesis testing and correlation analysis.
The trend prediction is a common analysis among many subjects and it also requires mathematical proofs.
In general, the judgements that John proposed are prophetic in today's data science.

However, there are some limitations in John's article. Nowadays as the development of data mining,
machine learning, and natural language processing, even in digital humanities, text classification
and word trend can be easily applied during the data analysis. But John did not mention the
interdisciplinary cross and combination in computer science techniques towards multiple fields
and internet of things.

4b. (5) Relate the article to the Life Cycle of Data discussion from class.

You may wish to choose an example or idea from the article and clearly explore how it

relates to the Life Cycle of Data. (Please keep your answer less than 500 words).

John Tukey wrote in his paper that regression was one of the critical parts in factor

analysis since regression techniques always offer hopes of learning more from less data

than do variance-component techniques.

One of the major challenges in data life cycle assessment is the availability and quality

of data used to develop models and to make appropriate recommendations. The establishment

# of model based on original data can lead to further analysis and knowledge discovery procedure

during the Life Cycle of Data.

Approximations and assumptions are often made if appropriate data are not readily available.

However, these proxies may introduce uncertainty into the results. A regression model

framework may be employed to assess missing data in data life cycle assessment. (Steinmann et al., 2014)

The regression model during the data analysis section performs like a bridge between raw data

and reusable information. The coefficients, standard errors and outliers of the regression

model can help to evaluate our initial hypothesis and draw empirical conclusions. The information

about the regression effectiveness can be compared among different datasets, and we can discover

new knowledge based on them. And this new knowledge can be transmitted into next section during

the data life cycle such as data transformation and presentation. So regression analysis is

a critical tache in the Life Cycle of Data.

Steinmann, Z. J. N., Venkatesh, A., Hauck, M., Schipper, A. M., Karuppiah, R., Laurenzi, I. J., & Huijbregts, M. A. J. (2014).

How to address data gaps in life cycle inventories: a case study on estimating CO2 emissions from coal-fired electricity plants on a global scale.

Environmental Science & Technology, 48(9), 5282–5289. https://doi.org/10.1021/es500757p