HW6_490IDS_17

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HW 6 - Due Tuesday October 18, 2016 in moodle and hardcopy in class.

Upload R file to Moodle with name: HW6_490IDS_YourClassID.R

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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(1)
obs = rexp(n = 100, rate = 3)
```

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

```
mean(obs)

## [1] 0.3435588
```

1c. (1) What is your estimate lambda.hat? (give the code and the value)

```
lambda.hat = 1/mean(obs)
print (lambda.hat)

## [1] 2.91071
```

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)
library(boot)
samplemean <- function(x,d) {
  return(1/mean(x[d]))
}
x = rexp(n = 100, rate = lambda.hat)
bootbet = boot(x,samplemean, 1000)
```

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.

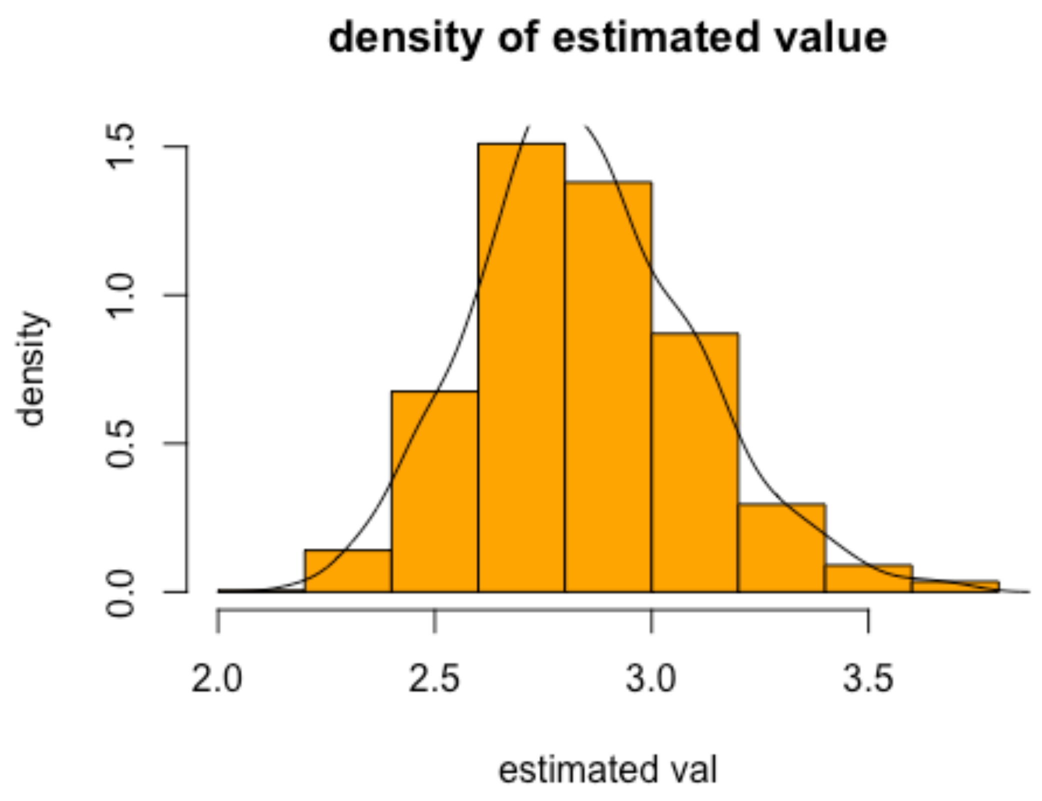
```
m=as.numeric(bootbet$t)
```

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(m,main="density of estimated value", prob = TRUE,xlab = "estimated
val",ylab= "density", col = "orange")
lines(density(m))
```



```
print("Yes,this distribution looks normal. It is bell shaped and most of the
values are around lambda.hat.")
```

```
## [1] "Yes,this distribution looks normal. It is bell shaped and most of the
values are around lambda.hat."
```

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?

```
std = sd(bootbet$t)
se = std/sqrt(1000)
mid = mean(bootbet$t)
low = mid-1.96*se
hi = mid+1.96*se
paste("The 95% ci is:", low,hi)

## [1] "The 95% ci is: 2.82736316185876 2.85909301483569"
```

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)
  library(boot)
  samplemean <- function(x,d) {
    return(1/mean(x[d]))
  }
  x = rexp(n = sample.size, rate = lambda.hat)
  bootbet = boot(x,samplemean, B)
  std = sd(bootbet$t)
  se = std/sqrt(B)
```

```r
  mid = mean(bootbet$t)
  low = mid-1.96*se
  hi = mid+1.96*se
  return (c(low,hi))
}
a = boot.sample(100,1000)
b = a[1]
c = a[2]
ssize = as.numeric(seq(from = 100, to = 1000, by = 100))
blist = as.numeric(seq(from = 1000, to = 10000, by = 1000))
resultl = list()
resulth = list()
print("use 100 as sample size")
```

```
## [1] "use 100 as sample size"
```

```r
for(bb in blist){
  a = boot.sample(100,bb)
  l = a[1]
  h = a[2]
  resultl = c(resultl,l)
  resulth = c(resulth,h)
}
print("use 5000 as b size")
```

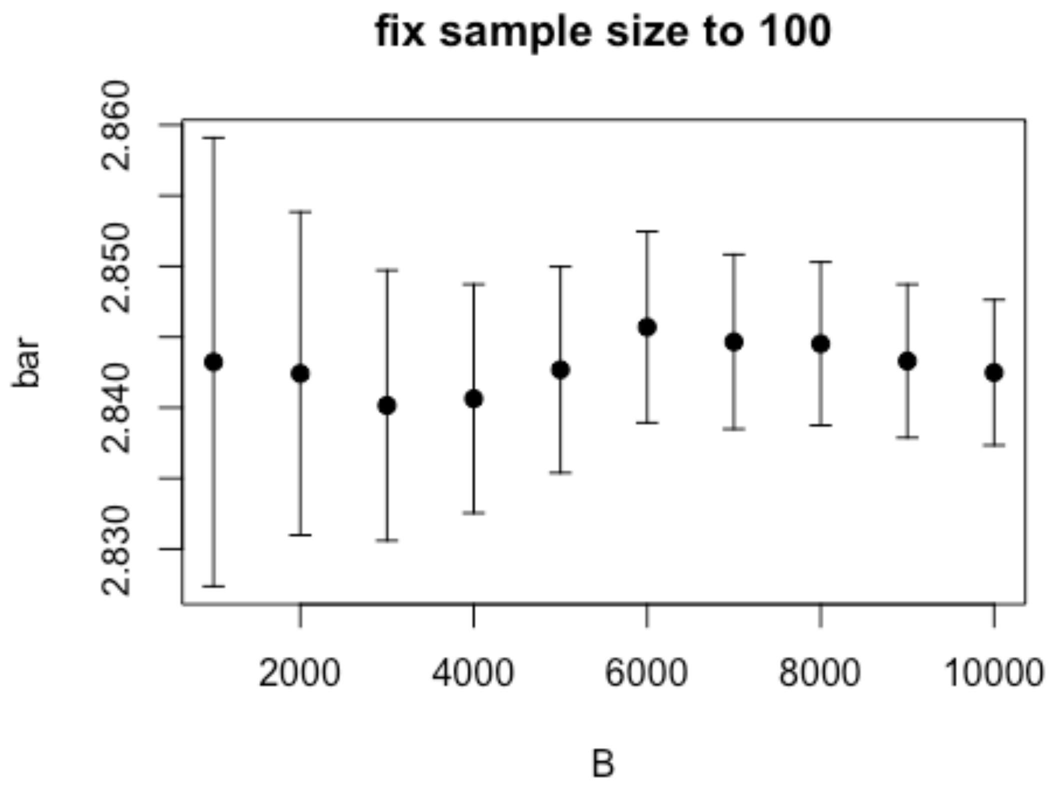
```
## [1] "use 5000 as b size"
```

```r
result2l = list()
result2h = list()
for(ss in ssize){
    a = boot.sample(ss,5000)
    l = a[1]
    h = a[2]
    result2l = c(result2l,l)
    result2h = c(result2h,h)
}
```

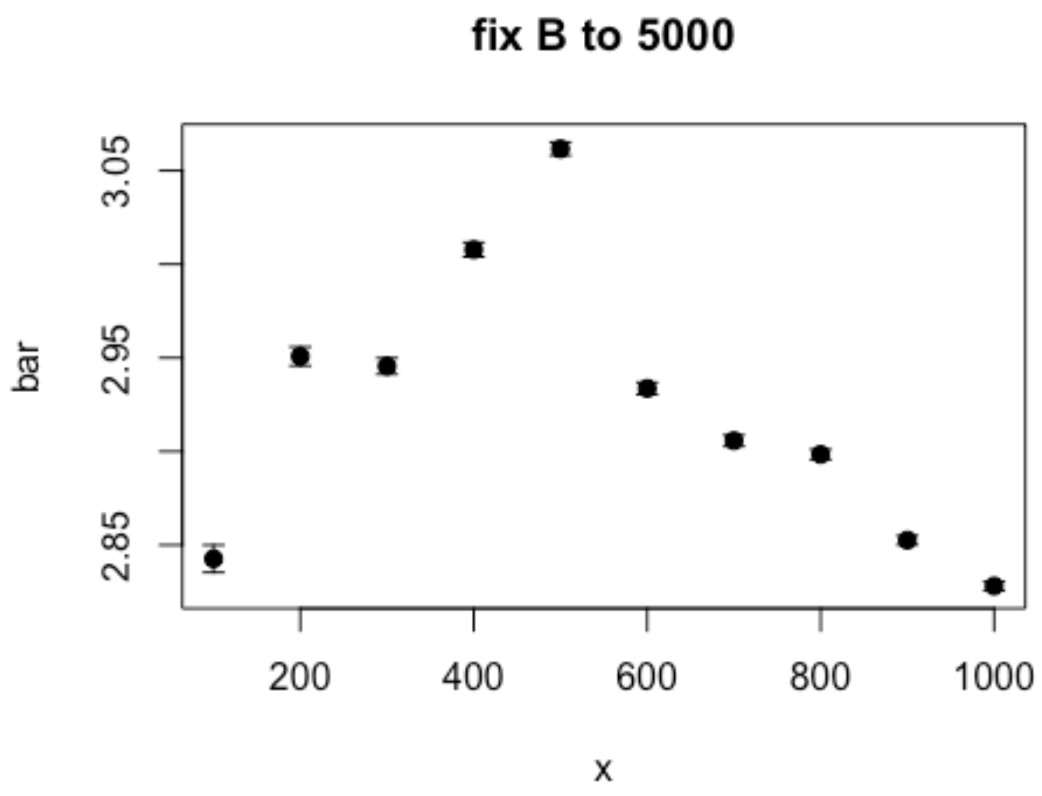
3b. (2) Plot your CI limits to show the effect of changing the sample size and

changing the number of bootstrap replications. What do you conclude?

```r
mid1 = as.numeric(mapply("+",resulth,resultl)/2)
plot(blist, mid1,ylim=range(resultl, resulth),pch=19, xlab="B",
ylab="bar",main="fix sample size to 100")
arrows(blist,as.numeric(resultl), blist, as.numeric(resulth), length=0.05,
angle=90, code=3)
```



```r
mid2 = as.numeric(mapply("+",result2h,result2l)/2)
plot(ssize, mid2,ylim=range(result2l, result2h),pch=19, xlab="x",
ylab="bar",main="fix B to 5000")
arrows(ssize,as.numeric(result2l), ssize, as.numeric(result2h), length=0.05,
angle=90, code=3)
```



```r
print("change bootstrap replications makes more sense because the error bound
goes smaller when increasing the bootstrap rep size. When fixing B and
changing samplesize, it doesn't maek a difference")
```

```
## [1] "change bootstrap replications makes more sense because the error
bound goes smaller when increasing the bootstrap rep size. When fixing B and
changing samplesize, it doesn't maek a difference"
```

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

field of Data Science today. Do you agree or disagee? Why or why not? (Please

keep your answer less than 500 words).

```
## [1] "This paper has some impressive insights into the study of data
science. The author suggest that data science will be prosper in the future.
And it is true. He also suggests that the spread of computer will be useful
in data science; this is also true. He correctly anticipated that computer
will be very useful when the data set is huge. \nToday, most big firms has
high expectation on making use of data, and computer calculation just makes
everything convinient. I agree to him most that empirical sampling is
important. Although mathematicians may look forward to a ideal case or
establishing some sort of theory. Data science is more practical and models
must fit the empirical expirience.\nAbstract theory might be good to be
treated as a reference, but the model derived must be able to used to real
world applications. For example when we are trying to do classification, we
might want to be practical about the result, instead of what technique we are
using. And in order to make the application work, pure theoratical model
might fail.\nLots of experiments needed for optimize the answer and adapt to
real world situations.\nI think for some technical detailed he didn't make
the prediction very correctly, since there are just so many new technology
developped and people are viewing data science in a new angle thanks to these
new theories. For example, Bayesian theory is quite useful nowadays, but it
is underrated in Tukey's paper.\n      "
```

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).

```
## [1] "I will briefly discuss the Data processing and analysis part in the
Life Cycle of Data. In class we have discussed “every meaningful performance
goal which had classically been addressed by mathematical assumptions and
theoretical derivations, would in the future be addressed using empirical
data and heavy computation.” I will briefly express my thinking toward
this.\n      In general I think this is very true. 20 years ago if we are
looking a question, for example, what are the cause of diabetes. We might
select a few parameters that have been reported to cause a higher possibility
of diabetes; take them as hypothesis and collect some statistic datas like
mean, median, variance to determine if they are really related to diabetes or
not.\n      Now, thanks to the computing power we have, we can expand our
search to more aspects. Before we probably rely on datas from hospital, but
now we have hundreds times more dimensions to look into. \n      For example,
BBC used to publish an article that having fat friend will lead people to
become fat. I won't discuss the academic correctness of this article, but it
actually gives a new perspective to look into the cause of obesity. The
combination of social science, biology and statistics brings the health
analysis to a whole new level.\n      Back to the question of filtering the
cause of diabetes. Classical theory would fail on such tasks because its lack
of practical value. There are so many aspects to look into and each will take
years to accomplish. How to make it automatic? Can we simply appy theory to
every possible field and wait for a hundred years for the solution?\n
The answer is no. And that's why empirical data and heavy computation can
save us from manually looking for solutions. We can just assume that every
cause is possible and have indefinite data input. Design a system that can
train itself and calculate the weight to every cause. This whole process will
be automatic, which also provides generality.\n      If we can grant
generality to all type of datas and simply apply computations on them, the
analysis of data will be so much easier than make mathematical assumptions
and derivations. This is how I think modern day's hypothesis making and
evaluation should be."
```