# Assignment 5

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4/28/2020

## Sampling from Ames, Iowa

Sampling from Ames, Iowa: If you have access to data on an entire population, say the size of every house in Ames, Iowa, it's straight forward to answer questions like, "How big is the typical house in Ames?" and "How much variation is there in sizes of houses?". If you have access to only a sample of the population, as is often the case, the task becomes more complicated. What is your best guess for the typical size if you only know the sizes of several dozen houses? This sort of situation requires that you use your sample to make inference on what your population looks like.

## Data

Load the ames.RData dataset (same as last homework).

```
load("ames.RData")
```

We'll start with a simple random sample of size 60 from the population. Note that the data set has information on many housing variables, but initially we'll focus on the size of the house, represented by the variable Gr.Liv.Area.

First, set the random seed. This will initialize the state of the random number generator so that it is the same for the whole class (631 is an arbitrary value):

```
set.seed(631)
population <- ames$Gr.Liv.Area
samp <- sample(population, 60)
```

## Confidence intervals

Confidence intervals: One of the most common ways to describe the typical or central value of a distribution is to use the mean. In this case we can calculate the mean of the sample using

```
sample_mean <- mean(samp)
```

Based only on this single sample, the best estimate of the average living area of houses sold in Ames would be the sample mean, usually denoted as $\bar{x}$ (in LaTeX embedded in RMarkdown this is written as `$\bar x$` and as an R variable we're calling it `sample_mean`). That serves as a good point estimate but it would be useful to also communicate how uncertain we are of that estimate. This can be captured by using a confidence interval.

We can calculate a 95% confidence interval for a sample mean by adding and subtracting 1.96 standard errors to the point estimate. Remember, ±1.96 comes from `qnorm(.025)` and `qnorm(.975)`.

```
se <- sd(samp)/sqrt(60)
lower <- sample_mean - 1.96 * se
upper <- sample_mean + 1.96 * se
c(lower, upper)
```

```
## [1] 1307.728 1509.672
```

This is an important inference that we've just made: even though we don't know what the full population looks like, we're 95% confident that the true average size of houses in Ames lies between the values lower and upper. There are a few conditions that must be met for this interval to be valid.

# Question 1

For the confidence interval to be valid, the sample mean must be normally distributed and have standard error s/sqrt(n). Which of the following is not a condition needed for this to be true?

- (a) The sample is random.
- (b) The sample size, 60, is less than 10% of all houses.
- (c) The sample distribution must be nearly normal.

C

# Question 2

What does "95% confidence" mean?

- (a) 95% of the time the true average area of houses in Ames, Iowa, will be in this interval.
- (b) 95% of random samples of size 60 will yield confidence intervals that contain the true average area of houses in Ames, Iowa.
- (c) 95% of the houses in Ames have an area in this interval.
- (d) 95% confident that the sample mean is in this interval.

B

# Question 3

Does your confidence interval capture the true average size of houses in Ames? I.e.,

```
mean(population)
```

```
## [1] 1499.69
```

Yes, Because it is in the range of 1307.728 and 1509.672.

## Testing the Theory

Using R, we're going to recreate many samples to learn more about how sample means and confidence intervals vary from one sample to another. Loops come in handy here. Here is the rough outline:

1) Obtain a random sample.
2) Calculate the sample's mean and standard deviation.
3) Use these statistics to calculate a confidence interval.
4) Repeat steps (1)-(3) 50 times.

But before we do all of this, we need to first create empty vectors where we can save the means and standard deviations that will be calculated from each sample. And while we're at it, let's also store the desired sample size as n.

```
samp_mean <- rep(NA, 50)
samp_sd <- rep(NA, 50)
n <- 60
```

Now we're ready for the loop where we calculate the means and standard deviations of 50 random samples.

```
set.seed(123) # initialize random number generator
for(i in 1:50){
   samp <- sample(population, n) # obtain a sample of size n = 60 from the population
   samp_mean[i] <- mean(samp)    # save sample mean in ith element of samp_mean
   samp_sd[i] <- sd(samp)        # save sample sd in ith element of samp_sd
}
```

Lastly, we construct the confidence intervals.

```
lower <- samp_mean - 1.96 * samp_sd/sqrt(n)
upper <- samp_mean + 1.96 * samp_sd/sqrt(n)
```

Lower bounds of these 50 confidence intervals are stored in lower, and the upper bounds are in upper. Let's view the first interval.

```
c(lower[1], upper[1])
```

```
## [1] 1390.046 1677.388
```

Now, we'll use a function `plot_ci` which is stored in the 'ames.RDatafile, but we could also copy-and-paste the function from https://rdrr.io/github/andrewpbray/oilabs/src/R/plot_ci.R , e.g.,

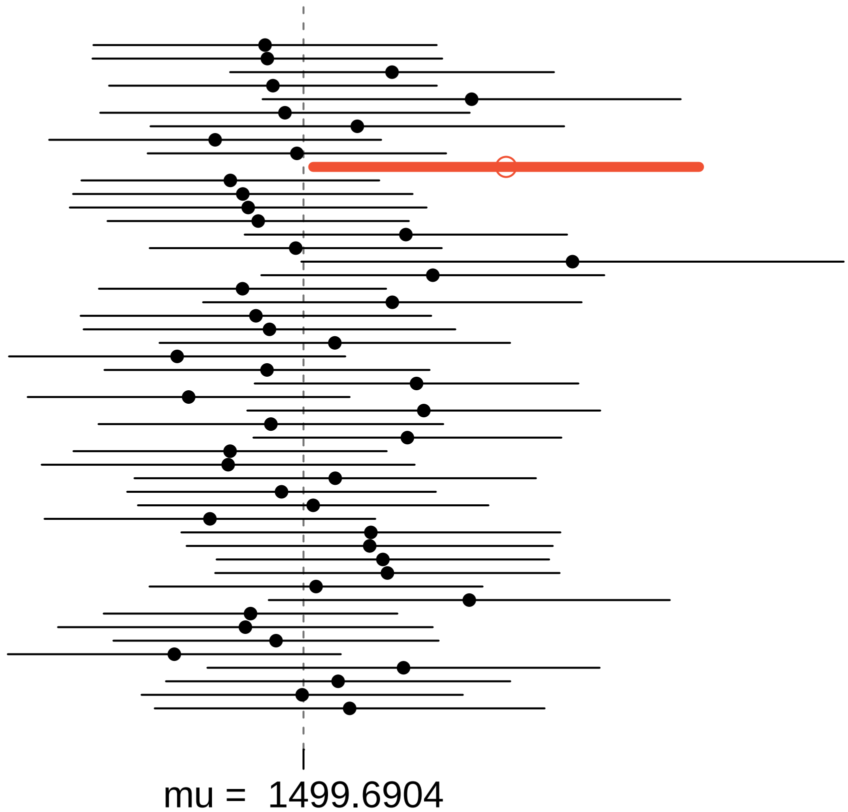
```r
plot_ci <- function(lo, hi, m) {
  par(mar=c(2, 1, 1, 1), mgp=c(2.7, 0.7, 0))
  k <- length(lo)
  ci.max <- max(rowSums(matrix(c(-1*lo,hi),ncol=2)))

  xR <- m + ci.max*c(-1, 1)
  yR <- c(0, 41*k/40)

  plot(xR, yR, type='n', xlab='', ylab='', axes=FALSE)
  abline(v=m, lty=2, col='#00000088')
  axis(1, at=m, paste("mu = ",round(m,4)), cex.axis=1.15)
  #axis(2)
  for(i in 1:k){
    x <- mean(c(hi[i],lo[i]))
    ci <- c(lo[i],hi[i])
    if((m < hi[i] & m > lo[i])==FALSE){
      col <- "#F05133"
      points(x, i, cex=1.4, col=col)
      #       points(x, i, pch=20, cex=1.2, col=col)
      lines(ci, rep(i, 2), col=col, lwd=5)
    } else{
      col <- 1
      points(x, i, pch=20, cex=1.2, col=col)
      lines(ci, rep(i, 2), col=col)
    }
  }
}
```

Then run `plot_ci` with our upper and lower bounds together with the population mean

```r
plot_ci(lower, upper, mean(population))
```




## Question 4

How many confidence intervals do not contain the true population mean?

```
1/50
```

```
## [1] 0.02
```

## Question 5

Question 5 [MULTIPLE CHOICE] What is the appropriate critical value for a 99% confidence level?

- (a) 0.01
- (b) 0.99
- (c) 1.96
- (d) 2.33
- (e) 2.58

```r
cl = 0.99
alpha = (1 - cl) / 2
qnorm(alpha, lower.tail=F)
```

```
## [1] 2.575829
```

E

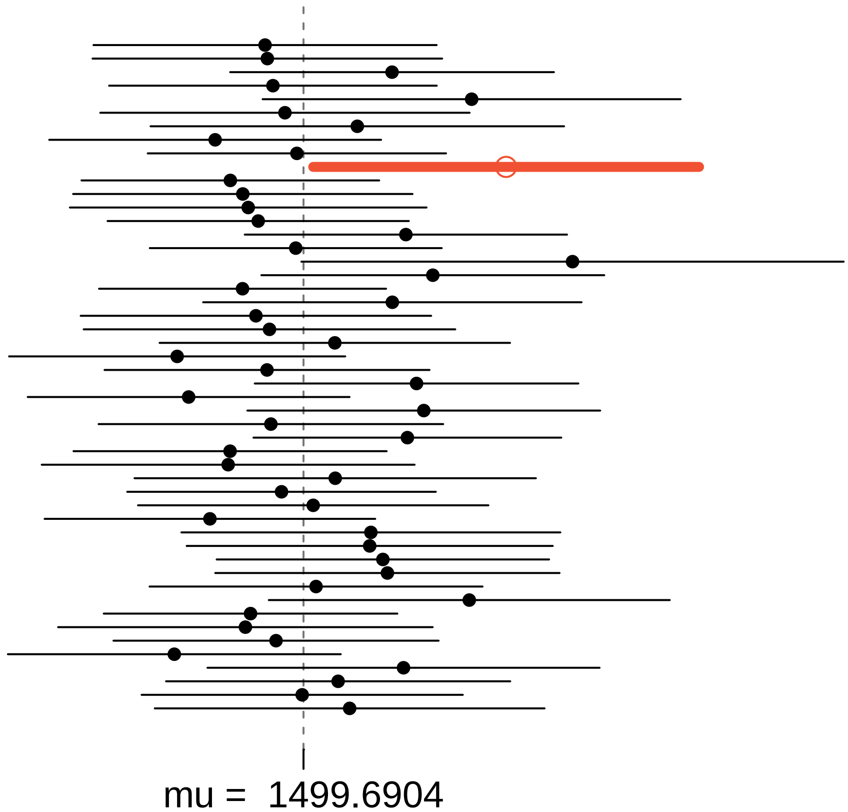
# Question 6

Calculate 50 confidence intervals at the 99% confidence level. Do not obtain new samples. Simply calculate new intervals based on the sample means and standard deviations you have already collected. Using the plot_ci function, plot all intervals and calculate the proportion of intervals that include the true population mean. What proportion do you get? Use a seed of 123.

```r
set.seed(123)
samp_mean <- rep(NA, 50)
samp_sd <- rep(NA, 50)
n <- 60
for(i in 1:50){
samp <- sample(population, n)
samp_mean[i] <- mean(samp)
samp_sd[i] <- sd(samp)
}
lower <- samp_mean - 1.96 * samp_sd / sqrt(n)
upper <- samp_mean + 1.96 * samp_sd / sqrt(n)
c(lower[1],upper[1])
```

```
## [1] 1390.046 1677.388
```

```r
plot_ci(lower, upper, mean(population))
```




```r
p <- 1-(1/50)
p
```

```
## [1] 0.98
```

98% proportion I got.

## Extra Question 1

Go through each line of `plot_ci` and briefly describe what it does. Use the line numbers from https://pastebin.com/GUDjgjWe to indicate which line you are describing.

## T-Distribution

Depending on your data collection, it may be hard to get a sample of size 60. One issue we will have if we have smaller sample is that we will need to use the Student's t-distribution. The sample standard deviation in particular is the calculation that will require the t-distribution because the t-distribution has "fatter tails" when the degrees-of-freedom parameter is low. Let's say we have a sample of size 15. If we want to find the critical values for 95% confidence level using a 14 degrees-of-freedom t-distribution ($df = n - 1$), we would use $t^* = 2.14$ instead of $z^* = 1.96$

```r
qt(.025, 19)
```

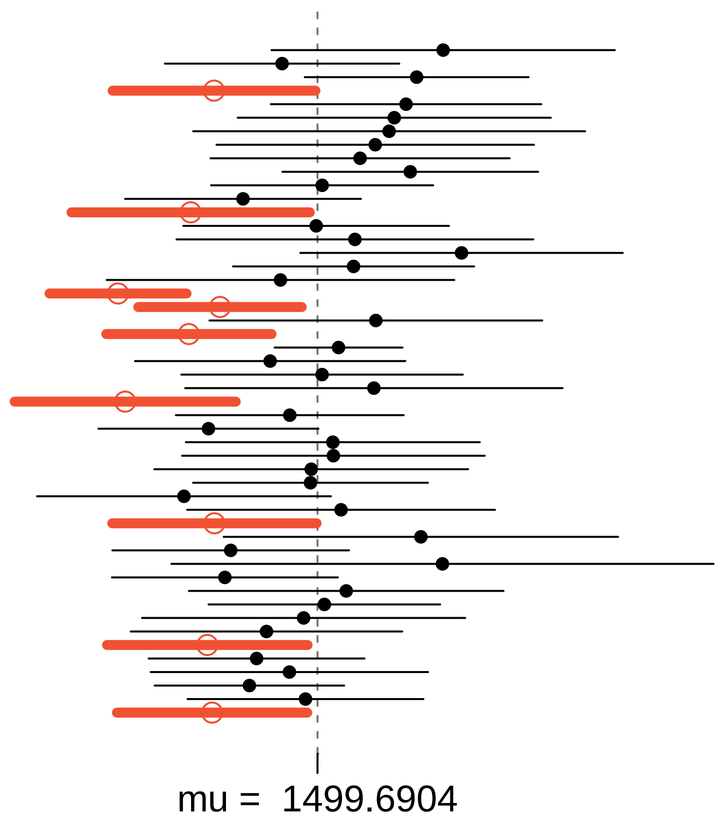
```
## [1] -2.093024
```

```r
qt(.975, 19)
```

```
## [1] 2.093024
```

To show this, let's rerun our earlier simulation with $n = 15$ instead of 60:

```r
samp_mean <- rep(NA, 50)
samp_sd <- rep(NA, 50)
n <- 15
set.seed(123)
for(i in 1:50){
   samp <- sample(population, n)  # obtain a sample of size n = 60 from the population
   samp_mean[i] <- mean(samp)     # save sample mean in ith element of samp_mean
   samp_sd[i] <- sd(samp)         # save sample sd in ith element of samp_sd
}
lower <- samp_mean - 1.96 * samp_sd/sqrt(n)
upper <- samp_mean + 1.96 * samp_sd/sqrt(n)
plot_ci(lower, upper, mean(population))
```



# Question 7

How many confidence intervals do not contain the true population mean now?

```
9/50
```

```
## [1] 0.18
```

# Question 8

We can see that the small sample size statistically led to more intervals that did not contain the population mean. Use the t-distribution to find critical values and then re-run the simulation and see if it fixes the problem, i.e. fewer intervals that do not contain the population mean.

To decrese the population mean which are not contained, we can simply increase the critical value into our calculation.

# Submission

Discussion Link: https://stthomas.instructure.com/courses/30116/discussion_topics/243126 hw5 <I bascially talked about my understanding of set.seed() function>

Discussion Link: https://stthomas.instructure.com/courses/30116/discussion_topics/242953 hw5 <I answered the problems on question 8>