

Foundations for statistical inference - Confidence intervals

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.

The data

In the previous lab, "Sampling Distributions", we looked at the population data of houses from Ames, Iowa. Let's start by loading that data set.

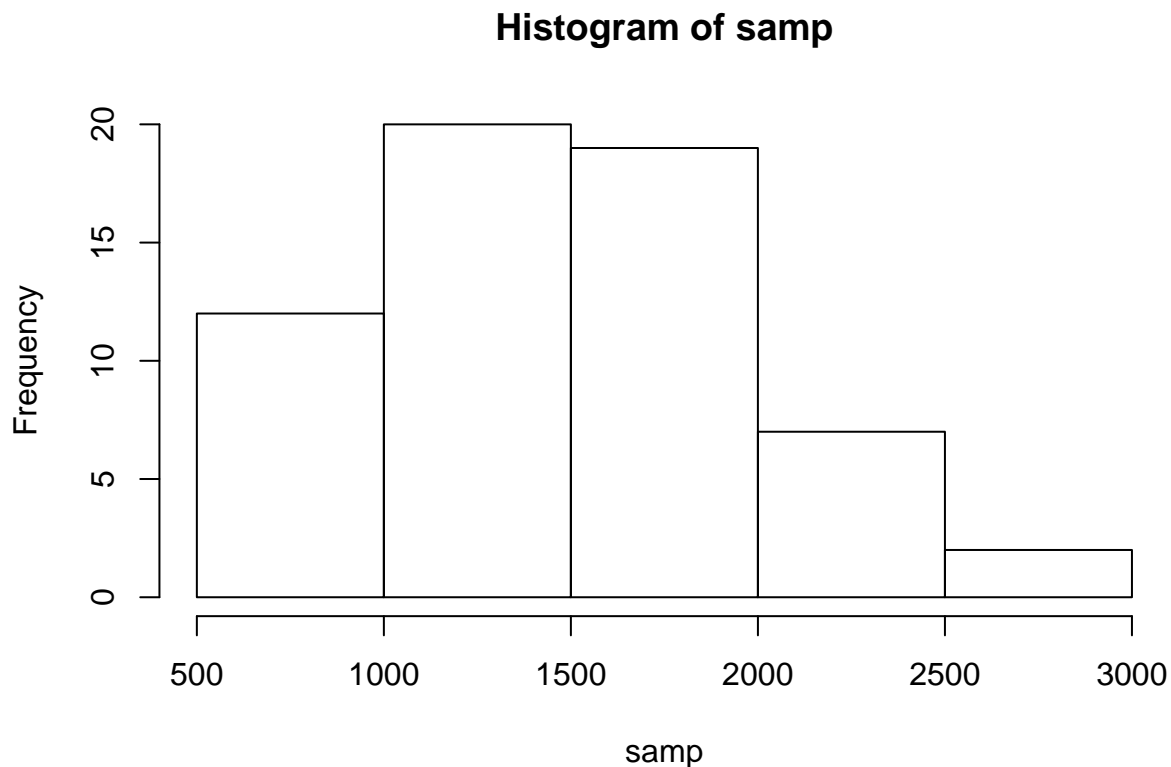
```
load("more/ames.RData")
```

In this lab we'll start with a simple random sample of size 60 from the population. Specifically, this is a simple random sample of size 60. Note that the data set has information on many housing variables, but for the first portion of the lab we'll focus on the size of the house, represented by the variable `Gr.Liv.Area`.

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

1. Describe the distribution of your sample. What would you say is the "typical" size within your sample? Also state precisely what you interpreted "typical" to mean.

```
hist(samp)
```



```
mean(samp)
```

```
## [1] 1480.117
```

The sample distribution looks it's skewed to the right. The typical size of the houses are from 1000 to 2000. How I interpret typical is by taking the two bars with greatest area, which seems to be between 1000 and 2000.

2. Would you expect another student's distribution to be identical to yours? Would you expect it to be similar? Why or why not?

Not identical since it's a sample. It may be similar since the sample size is 60, which is large enough to be a good representation of the population.

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)
```

Return for a moment to the question that first motivated this lab: based on this sample, what can we infer about the population? 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} (here 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 (See Section 4.2.3 if you are unfamiliar with this formula).

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

```
## [1] 1354.598 1605.636
```

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.

3. For the confidence interval to be valid, the sample mean must be normally distributed and have standard error s/\sqrt{n} . What conditions must be met for this to be true?

Each observation must be independent of each other and the sample should be less than 10% of the population.

Confidence levels

4. What does "95% confidence" mean? If you're not sure, see Section 4.2.2.

It means that if we were to get a parameter range with 2 standard error X number of times, 95 percent of parameter ranges will contain the actual parameter.

In this case we have the luxury of knowing the true population mean since we have data on the entire population. This value can be calculated using the following command:

```
mean(population)
```

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

5. Does your confidence interval capture the true average size of houses in Ames? If you are working on this lab in a classroom, does your neighbor's interval capture this value?

Yes the confidence interval calculated above contains the mean of the population.

6. Each student in your class should have gotten a slightly different confidence interval. What proportion of those intervals would you expect to capture the true population mean? Why? If you are working in this lab in a classroom, collect data on the intervals created by other students in the class and calculate the proportion of intervals that capture the true population mean.

I would expect about 95% of the intervals to capture the true population mean. Because we are looking within $1.96*se$, which represents about 95%.

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 (If you are unfamiliar with loops, review the Sampling Distribution Lab).

Here is the rough outline:

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

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.

```
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_vector <- samp_mean - 1.96 * samp_sd / sqrt(n)
upper_vector <- samp_mean + 1.96 * samp_sd / sqrt(n)
```

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

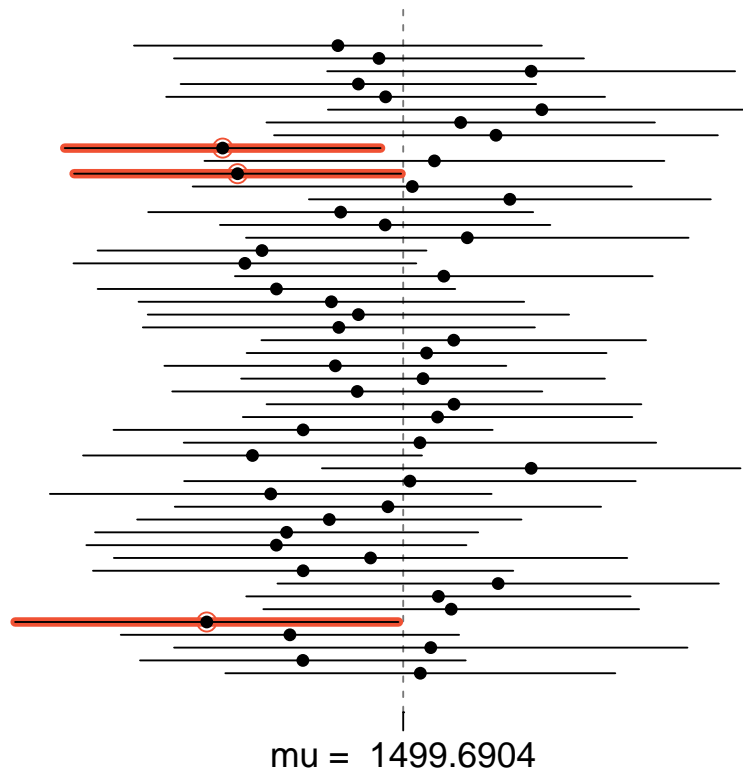
```
c(lower_vector[1], upper_vector[1])
```

```
## [1] 1390.160 1630.306
```

On your own

- Using the following function (which was downloaded with the data set), plot all intervals. What proportion of your confidence intervals include the true population mean? Is this proportion exactly equal to the confidence level? If not, explain why.

```
plot_ci(lower_vector, upper_vector, mean(population))
```



Here, 3 intervals does not capture the population mean. This is 85% so it does not match to the 95% confidence level. Probably increasing the number of samples taken will make it closer to 95% every single time.

- Pick a confidence level of your choosing, provided it is not 95%. What is the appropriate critical value?

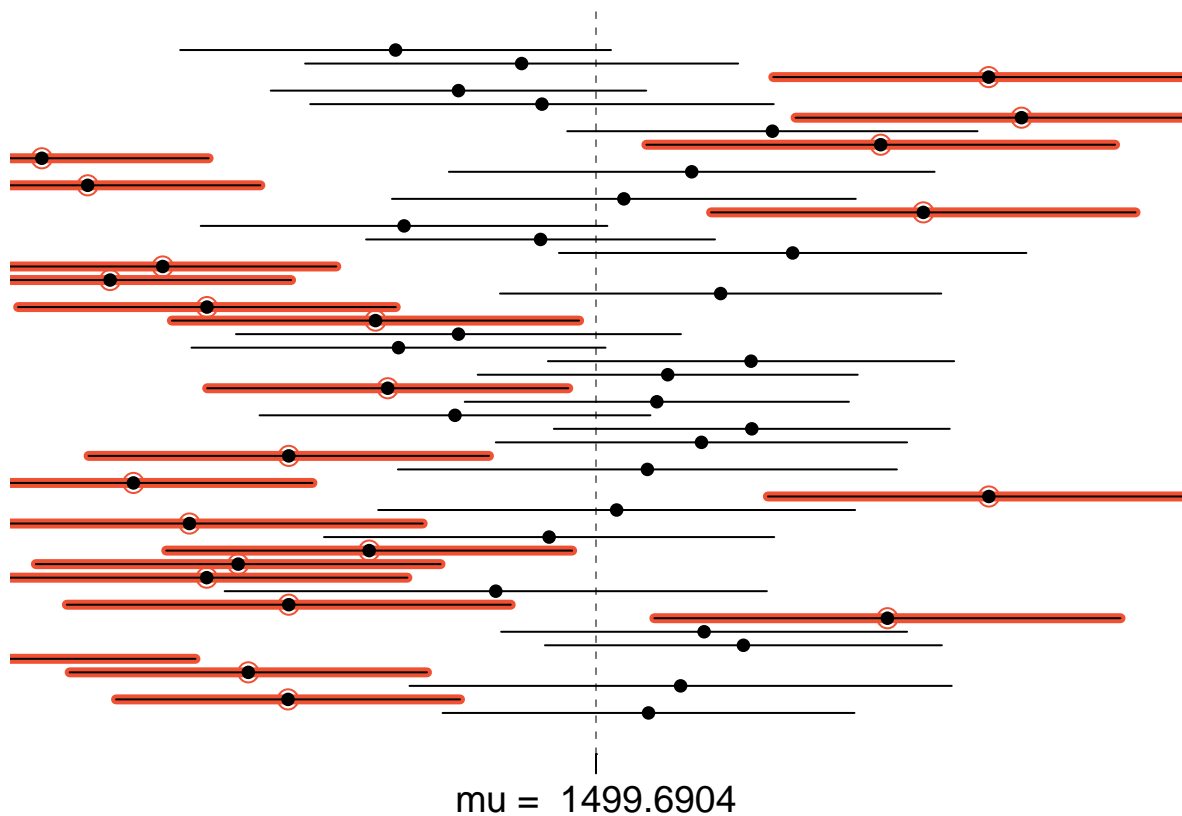
I choose 50%. Just for fun.

```
z<-qnorm(0.75)
z
```

```
## [1] 0.6744898
```

- Calculate 50 confidence intervals at the confidence level you chose in the previous question. You do not need to 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. How does this percentage compare to the confidence level selected for the intervals?

```
lower_vector_z <- samp_mean - z * samp_sd / sqrt(n)
upper_vector_z <- samp_mean + z * samp_sd / sqrt(n)
plot_ci(lower_vector_z, upper_vector_z, mean(population))
```



There are 27 intervals that has population mean. This turns out to be 54%. This is slightly higher than 50% c.i.

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