Confidence Intervals, based on the sample mean, σ known

There is a great deal of material to cover before we really get to **confidence intervals**. The background material is summarized in **Table 1**.

Table 1

Probability

1. We have discrete and continuous probability distributions.
2. For continuous probability distributions we can show a curve of the probability density function.
3. The area under the entire curve is 1.00.
4. The area under the curve and to the left of a value **v** is the probability that the random variable **X** is less than **v**. This is written as **P(X<v)**.
5. For a continuous probability, since there is no "area" under the curve at a value **v**, **P(X=v) = 0.** Therefore, **P(X < v) = P(X ≤ v)**.
6. For symmetric probability distributions we have **P(X < v) = P(X > -v)**.
7. For two values **a** and **b**, where **a < b**, we have **P(a < X < b) = 1 - P(X<a or X>b)**.

The Normal Distribution

8. The **normal** distribution is a continuous probability distribution.
9. The **normal** distribution is based on a mathematical formula.
10. The **standard normal distribution** has **mean=0** (**μ=0**) and **standard deviation=1** (**σ=1**).
11. We have a **table** to find the area under the **standard normal** distribution probability density function curve and to the left of a value **z**, i.e., **P(X<z)**.
12. We have a function in R called **pnorm()** to find the area under the **standard normal** density function to the left of a value **z**, **pnorm(z)**.
13. We know how to read the table "backwards" so that if we are given a probability **p** we can find the value **z** that makes **P(X<z)=p** true.
14. We have a function in R called **qnorm()** that finds the value **z** needed to make the **P(X<z)** be the value of a specified probability **p**, that is **qnorm(p)** produces the value **z** so that **P(X<z)=p**.
15. We use **N(μ, σ)** to symbolize a distribution that is **normal** with **mean=μ** and **standard deviation=σ**.
16. The standard normal distribution is **N(0,1)**.

17. We use $z = \frac{x - \mu}{\sigma}$ to map a non-standard normal distribution, **N(μ,σ)** to **N(0,1)**.
18. Both **pnorm()** and **qnorm()** have extended forms that allow us to use them directly with non-standard normal distributions.

The Sample Mean

19. For any original population if we take repeated samples of size **n**, with **n≥30**, with replacement, then the distribution of the mean of those samples will be approximately **N(μ,σ/sqrt(n))**, where **μ** is the mean of the original population and **σ** is the standard deviation of the original population.
20. If the original population is approximately **normal** then the value of **n** can be smaller than 30.

With all of this, consider the following situation. First, let us find the **z-score** in **N(0,1)** such that **P(X<z)=0.025**. We will do this with **qnorm(0.025)** as shown in Figure 1;

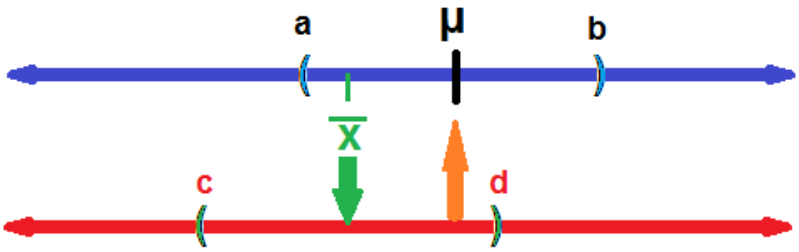
Figure 1

```
> qnorm(0.025)
[1] -1.959964
>
```

That value is so close to **-1.96** that we will use the rounded value for the rest of this discussion. The meaning of the **-1.96** is that for a **N(0,1)**, 2.5% of the area under the curve is to the left of **-1.96**. Since the **normal distribution is symmetric,** this means that **P(X>1.96)=0.025** also. Thus, 95% of the area is between **-1.96** and **1.96**. Remember that in our standard normal distribution the standard deviation is 1. Therefore, we really could have said that 95% of the area is within 1.96 standard deviations from the mean. This will be true of any normal distribution.

Now, we start with a population that has a known standard deviation, **σ**. It also has a known mean, **μ**. We plan to take a sample of size **36**. We know that the distribution of sample means from size 36 samples is **N(μ,σ/sqrt(36))**, or simplifying, **N(μ,σ/6).** If that is the distribution of the means of size 36 samples, then we know that 95% of the samples that we take will have a **sample mean** that is between **μ-1.96*σ/6** and **μ+1.96*σ/6**. This is shown at the top of Figure 2 where the point **a** is 1.96 standard deviations below the mean and point **b** is 1.96 standard deviations above the mean. Again, given the distribution of the sample means, if we take repeated samples of size 36, then 95% of those samples will have a sample mean that falls between **a** and **b**.

Figure 2



We take our sample. It turns out that our sample mean is $\overline{x}$ and, for this part of the discussion, we will assume that it is one of the 95% of the sample means that falls between **a** and **b**. We see this in Figure 2. Then, on a new line, the lower one in Figure 2, let us look at the interval that is just as wide as was the one from **a** to **b**. In Figure 2 that interval is from **c** to **d**.

Then, it must be true, if $\overline{x}$ is in the interval **(a,b)**, then the **mean, μ,** must be in the interval **(c,d)**. Try it again. Choose any point in **(a,b)**, drop down to the lower line, then construct a new interval around that value on the lower line (using the same width interval). The value of the true mean, **μ**, will have to be in that new interval.

Similarly, if you choose to put $\overline{x}$ outside of the interval from **a** to **b** (so it is one of the 5% of the sample means that fall outside of the interval), then it must be the case that the true mean, **μ** is not in that new interval.

This is a **spectacular** result! It tells us that if we take a sample of size 36 from a population with a known standard deviation, let us say it is 12, and if we find that the **sample mean** turns out to be **43**, then we can construct an interval around that value of **43** and make that interval go from **43-1.96*12/6 = 43-1.96*2 = 43-3.92 = 39.08** to **43+1.96*12/6 = 43+1.96*2 = 43+3.92 = 46.92**. We have no way of knowing **if** the true mean of the population is in that interval, but we can say that if we follow this same procedure over and over, 95% of the intervals that we would construct will contain the true mean. **This is a 95% confidence interval.**

The beauty of this is that we did not need to know the population mean to do this. In fact, if we know the population mean then there is no sense in finding a confidence interval for the population mean. This procedure is to be used when we do not know the population mean but we want to make a good guess as to the value of that mean.

Our best **point estimate** for the **population mean** is the **sample mean**. However, the **point estimate** is almost certainly wrong. It might be off by a little; it might be off by a lot, but it is almost always off. What we want is an **interval** of values where we can be relatively certain that our method of creating the interval tells us that some specified high percentage of the intervals created this way do in fact hold the population mean. The little twist to this is that to use our method we need to know the population standard deviation.

If we know **σ**, for a new case we say it is 3.41, then we can choose a **level of significance**, say 90%. We calculate the percent we are missing, 100%-90%=10%. We figure that we need half of that 10% below and half of that above our interval. In this case we would have 5% below and 5%

above. Since sample means form a **normal** distribution, we can find the **z-score** that has 5% to its left by using **qnorm(0.05)**. This turns out to be approximately **-1.645**. We set the size of the sample, in this case we will use a sample of size **30**. With the population standard deviation being 3.41, the standard deviation of the means of samples of size **30** will be **3.41/sqrt(30)≈3.41/5.4772≈0.62258**. We take the sample and find that $\overline{x}$ **=94.2**. Then we construct our 90% confidence interval by taking $\overline{x}$ **±-1.645*3.41/sqrt(30)** or **94.2±(-1.645*0.62258)** or **94.2±-1.02414** or from **93.175859** to **95.22414**, which we might express in rounded form as **(93.176,95.224)**. These computations are shown in Figure 3.

Figure 3

```
> z<-qnorm(0.05)
> z
[1] -1.644854
> x_bar <- 94.2
> samp_sd <- 3.41/sqrt(30)
> samp_sd
[1] 0.622578
> lower_side <- x_bar + z*samp_sd
> lower_side
[1] 93.17595
> upper_side <- x_bar - z*samp_sd
> upper_side
[1] 95.22405
>
```

A few notes on this before we state the general formula, look at numerous examples, and then look at automating the process. First, to do this we need to know four things: the population standard deviation, the sample size, the desired confidence interval, and finally the sample mean. Second, by looking at the left tail, asking as we did above for the **z-score** such that **P(X<z)=0.05**, the result stored in **x** will be a negative value. That is why the we use addition in `lower_side <- x_bar + z*samp_s`. There are many ways for us to have changed the value in **z** to be the positive side of the pair, and then we would have been able to use a more sensible subtraction to get the **lower_side** and an addition to get the **upper_side**. Third, and I wanted to sneak this in where few people will actually read it, this type of problem is at best an academic exercise. We are supposed to know the population standard deviation without knowing the population mean? To find the standard deviation we need to know either the mean for one formula or the sum of the values and the number of values for the other. Still we need to do this because it sets the stage for a more realistic problem, finding the confidence intervals when we know neither the mean nor the standard deviation of the population

The General Formula

In general, we start with a population and we know that the population standard deviation is **σ**.

We determine a confidence level, **cl**. We determine a value we will call $\frac{\alpha}{2}$ read as "alpha over 2",

which is half the area not in the confidence interval. Thus, $\frac{\alpha}{2} = \frac{1 - cl}{2}$. Using $\frac{\alpha}{2}$ we find the **z-score** such that **P(X < z)=** $\frac{\alpha}{2}$. We refer to that **z-score** as $z_{\frac{\alpha}{2}}$. We determine a sample size **n** and take a sample of size **n** from which we compute the mean of the sample, $\overline{x}$. At that point we can compute the two ends of the **confidence interval** as being $= \overline{x} \pm z_{\frac{\alpha}{2}} \cdot \frac{\sigma}{\sqrt{n}}$.

Please note that $\left| z_{\frac{\alpha}{2}} \cdot \frac{\sigma}{\sqrt{n}} \right|$ is called the **margin of error**. The absolute value sign is there just so that we always get a positive value for the **margin of error**. The **width** of the **confidence interval** is always two times the **margin of error**.

We really have two ways that we can change the size of the **margin of error** and, thus, change the width of the **confidence interval**. The first is by changing the size of the sample. The larger we make the sample size, **n**, the larger is the denominator in the **margin of error**. The larger the denominator, the smaller the **margin of error**. Back in Figure 3 we never expressed the **margin of error** as a separate value. In Figure 4 we find and display that value. Then we recompute **samp_sd** using a sample size of 60. After that we can recompute and display a new **margin of error** based on that new sample size.

Figure 4

```
> moe <- abs(z*samp_sd)
> moe # based on a sample of size 30
[1] 1.02405
> samp_sd <- 3.41/sqrt(60)
> samp_sd
[1] 0.4402291
> moe <- abs(z*samp_sd)
> moe # based on a sample of size 60
[1] 0.7241124
> upper_side <- x_bar + moe
> lower_side <- x_bar - moe
> upper_side
[1] 94.92411
> lower_side
[1] 93.47589
>
```

By increasing the sample size from **30** to **60** we changed the standard deviation of the sample means from **0.622578** (in Figure 3) to **0.4402291** (in Figure 4). This changes the **margin of error** from **1.02405** to **0.7241124**. Clearly we can make the **margin of error** as small as we

want by increasing the sample size. But more on that later.

The other way that we can change the **margin of error** is to change the **desired confidence level**. Figure 3 starts with us finding the required **z-score** so that we have 90% of the area in the **interval.** If we were to change that so that we only wanted 80% of the area in the interval then the value of **|z|** will be smaller, that is, the **z-score** will be closer to 0. This, in turn would make the **margin of error** smaller. Figure 5 redoes the computations in our problem, still using sample size 60, but now with a **confidence level** set to **80%**.

Figure 5

```
> z<-qnorm(0.10)  # for a 80% confidence interval
> z
[1] -1.281552
> samp_sd <- 3.41/sqrt(60)
> samp_sd
[1] 0.4402291
> moe <- abs(z*samp_sd)
> moe # based on a sample of size 60 and 80% C.I.
[1] 0.5641763
> upper_side <- x_bar + moe
> lower_side <- x_bar - moe
> upper_side
[1] 94.76418
> lower_side
[1] 93.63582
>
```

Clearly, reducing the sample size or raising the **confidence level** will widen the **confidence interval.**

Automating the process

The process of computing a **confidence interval** in the case where we **know the population standard deviation** and where we have a sample of size **n** that yields a **sample mean** $\overline{x}$ is as follows:

1. From the **confidence level** compute the value of $\frac{\alpha}{2}$ using $\frac{\alpha}{2} = \frac{1 - cl}{2}$
2. Use **qnorm(** $\frac{\alpha}{2}$ **)** to find the associated **z-score**, $z_{\frac{\alpha}{2}}$
3. Find the **margin of error** as $\left| z_{\frac{\alpha}{2}} \cdot \frac{\sigma}{\sqrt{n}} \right|$

4. Find the two parts to the **confidence interval** by evaluating $= \overline{x} \pm z_{\frac{\alpha}{2}} \cdot \frac{\sigma}{\sqrt{n}}$

We should be able to describe these same actions using R statements inside an R function. Consider the following function definition:

```
ci_known <- function( sigma=1, n=30, x_bar=0, cl=0.95)
  {
    # try to avoid some common errors
    if( cl <=0 | cl>=1)
      {return("Confidence interval must be strictly between 0.0 and 1")
      }
    if( sigma < 0 )
      {return("Population standard deviation must be positive")}
    if( n <= 1 )
      {return("Sample size needs to be more than 1")}
    if( as.integer(n) != n )
      {return("Sample size must be a whole number")}
    # to get here we have some "reasonable" values
    samp_sd <- sigma/sqrt(n)
    z <- abs( qnorm( (1-cl)/2))
    moe <- z*samp_sd
    low_end <- x_bar - moe
    high_end <- x_bar + moe
    result <- c(low_end, high_end, moe, samp_sd)
    names(result)<-c("CI Low","CI High","MOE", "Std Error")
    return( result )
  }
```

This does all of our tasks, including returning the confidence interval as well as some other values. The function is available in the file ci_known.R. Figure 18 shows the console screen after the function has been entered into an R session.

Figure 18

```
> ci_known <- function( sigma=1, n=30, x_bar=0, cl=0.95)
+   {
+     # try to avoid some common errors
+     if( cl <=0 | cl>=1)
+       {return("Confidence interval must be strictly between 0.0 and 1")
+       }
+     if( sigma < 0 )
+       {return("Population standard deviation must be positive")}
+     if( n <= 1 )
+       {return("Sample size needs to be more than 1")}
+     if( as.integer(n) != n )
+       {return("Sample size must be a whole number")}
+     # to get here we have some "reasonable" values
+     samp_sd <- sigma/sqrt(n)
+     z <- abs( qnorm( (1-cl)/2))
+     moe <- z*samp_sd
+     low_end <- x_bar - moe
+     high_end <- x_bar + moe
+     result <- c(low_end, high_end, moe, samp_sd)
+     names(result)<-c("CI Low","CI High","MOE", "Std Error")
+     return( result )
+   }
> |
```

Figure 19 shows a use of the **ci_known()** function to do the problem that we did back in Figure 3. Fortunately, we get the same results.

Figure 19

```
> ci_known(3.41, 30, 94.2, .90 )
   CI Low   CI High       MOE Std Error
93.175950 95.224050  1.024050  0.622578
>
```

Figure 20 uses the information needed to find the **90% confidence intervals** for samples #65 and #66 in Figure 16. Again, the function produces the same values that had been on that web page.

Figure 20

```
> ci_known(100,  40, 473.205, 0.9)
   CI Low   CI High       MOE Std Error
447.19758 499.21242  26.00742  15.81139
> ci_known(100,  40, 507.004, 0.9)
   CI Low   CI High       MOE Std Error
480.99658 533.01142  26.00742  15.81139
>
```

If you read the text of the function you know that it tries to trap any obvious errors. Figure 21 shows a number of commands designed to test out those traps. It is interesting to note that the final example, specifying the sample size as 4.0, did not cause an error. Apparently, R has no problem if we use a decimal point in a whole number as long as the value of the number is still an integer.

Figure 21

```
> ci_known(100, 40, 507, 90)
[1] "Confidence interval must be strictly between 0.0 and 1"
> ci_known(-100, 40, 507, .90)
[1] "Population standard deviation must be positive"
> ci_known(100, -40, 507, .90)
[1] "Sample size needs to be more than 1"
> ci_known(100, 4.10, 507, .90)
[1] "Sample size must be a whole number"
> ci_known(100, 4.0, 507, .90)
   CI Low   CI High       MOE Std Error
424.75732 589.24268  82.24268  50.00000
>
```

It can be difficult to remember the correct order of the arguments in a call to the function. Figure 22 illustrates that we can name the arguments, and, if we do so, we do not have to give them in order. Again, this is the problem first done in Figure 3.

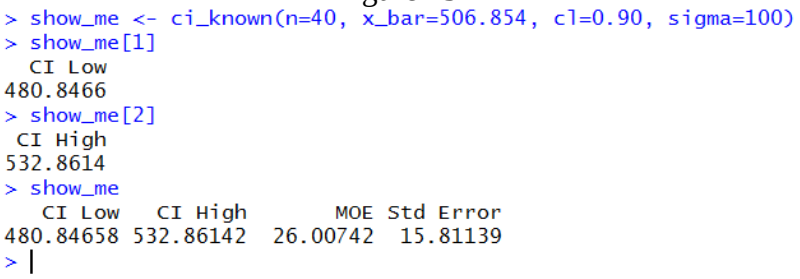
Figure 22

```
> ci_known( n=30, cl=0.9, sigma=3.41, x_bar=94.2)
   CI Low   CI High       MOE Std Error
93.175950 95.224050  1.024050  0.622578
>
```

The working examples above show the function used by itself. We could assign the results of the

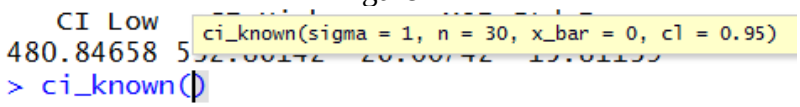
function to a variable and then just examine parts or all of that variable. This is done in Figure 23.

Figure 23



And, if we start typing the function (after it has been defined, of course) into an R session then R provides a little note to remind us of the needed arguments. This also shows the default value of each argument. It is true that if we wanted to take the default value then we need not specify it, but that practice should be discouraged.

Figure 24



Interpreting A Confidence Interval

Let us say that we have a population where we know the population standard deviation. We choose a confidence level, perhaps 90%. We take a sample and find the sample mean. From all of that we can compute a 90% confidence interval. **It would be wrong to say** "There is a 90% chance that the true population mean is within the confidence interval." The true population mean is either in the confidence interval or it is not! It is not a question of probability! What we can and should say is "If I follow the same procedure time and again, then 90% of the confidence intervals that I generate will contain the true mean." That says nothing about the one confidence interval that we did compute. It says a lot about the method of computing it.

Worksheet for a Confidence Interval

Here is a link to a worksheet with randomly generated problems related to finding confidence intervals when the standard deviation of the population is known.

Listing of all R commands used on this page

```
qnorm(0.025)
z<-qnorm(0.05)
z
x_bar <- 94.2
samp_sd <- 3.41/sqrt(30)
```

```
samp_sd
lower_side <- x_bar + z*samp_sd
lower_side
upper_side <- x_bar - z*samp_sd
upper_side

moe <- abs(z*samp_sd)
moe # based on a sample of size 30
samp_sd <- 3.41/sqrt(60)
samp_sd
moe <- abs(z*samp_sd)
moe # based on a sample of size 60
upper_side <- x_bar + moe
lower_side <- x_bar - moe
upper_side
lower_side

z<-qnorm(0.10)  # for a 80% confidence interval
z
samp_sd <- 3.41/sqrt(60)
samp_sd
moe <- abs(z*samp_sd)
moe # based on a sample of size 60 and 80% C.I.
upper_side <- x_bar + moe
lower_side <- x_bar - moe
upper_side
lower_side

ci_known <- function( sigma=1, n=30, x_bar=0, cl=0.95)
  {
    # try to avoid some common errors
    if( cl <=0 | cl>=1)
      {return("Confidence interval must be strictly between 0.0 and 1")
      }
    if( sigma < 0 )
      {return("Population standard deviation must be positive")}
    if( n <= 1 )
      {return("Sample size needs to be more than 1")}
    if( as.integer(n) != n )
      {return("Sample size must be a whole number")}
    # to get here we have some "reasonable" values
    samp_sd <- sigma/sqrt(n)
    z <- abs( qnorm( (1-cl)/2))
    moe <- z*samp_sd
    low_end <- x_bar - moe
    high_end <- x_bar + moe
    result <- c(low_end, high_end, moe, samp_sd)
    names(result)<-c("CI Low","CI High","MOE", "Std Error")
    return( result )
  }

ci_known(3.41, 30, 94.2, .90 )
ci_known(100,  40, 473.205, 0.9)
ci_known(100,  40, 507.004, 0.9)
ci_known(100, 40, 507, 90)
ci_known(-100, 40, 507, .90)
ci_known(100, -40, 507, .90)
```

```
ci_known(100, 4.10, 507, .90)
ci_known(100, 4.0, 507, .90)

ci_known( n=30, cl=0.9, sigma=3.41, x_bar=94.2)
show_me <- ci_known(n=40, x_bar=506.854, cl=0.90, sigma=100)
show_me[1]
show_me[2]
show_me
```