Week 6: Bootstrapping Confidence Intervals

Two more kinds of Statistical Inference Tools

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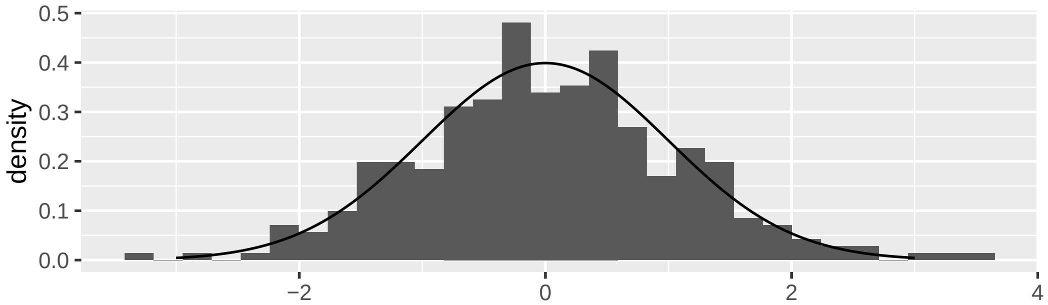
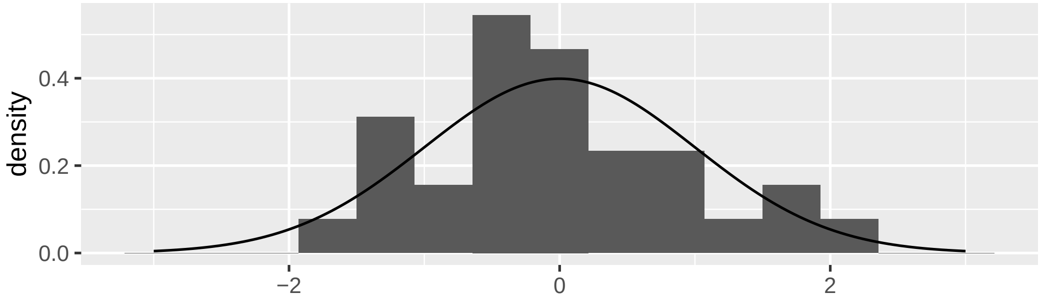
Samples Approximate Populations

```r
library(tidyverse); set.seed(130); n <- 300; support <- seq(-3,3,.01)
normal_pdf <- geom_line(data = tibble(`normal pdf`=dnorm(support), x=support),
                        aes(x=x, y=`normal pdf`))
normal_sample <- geom_histogram(data = tibble(x=rnorm(n=n)),
                                aes(x=x, y=..density..), bins=30)
# https://r-charts.com/distribution/histogram-density-ggplot2/
# https://stackoverflow.com/questions/16712800/overlay-lines-and-hist-with-ggplot2
ggplot() + normal_sample + normal_pdf # {r,fig.width=6, fig.height=2}
```



Samples Approximate Populations

```r
set.seed(130); n <- 30
normal_pdf <- geom_line(data = tibble(`normal pdf`=dnorm(support), x=support),
                        aes(x=x, y=`normal pdf`))
normal_sample <- geom_histogram(data = tibble(x=rnorm(n=n)),
                                aes(x=x, y=..density..), bins=15)
# https://r-charts.com/distribution/histogram-density-ggplot2/
# https://stackoverflow.com/questions/16712800/overlay-lines-and-hist-with-ggplot2
ggplot() + normal_sample + normal_pdf # {r,fig.width=6, fig.height=2}
```



How Well Do Samples Approximate Populations?

Clearly samples can't totally approximate populations

but if we're using them to learn population **parameters** they can be sufficient. . .

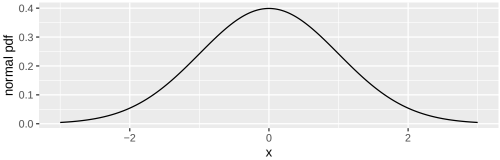
$$\text{(statistic) } \bar{x} \text{ approximates (parameter) } p$$

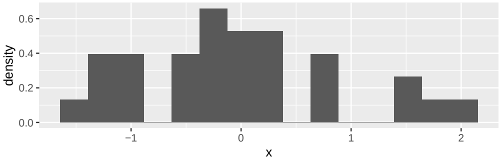
if x_i is only either 0 or 1 (and $p = Pr(x_i = 1)$)

$$\text{(statistic) } \bar{x} \text{ approximates (parameter) } \mu$$

otherwise (and $\mu = E[x_i]$)

How Well Do Samples Approximate Populations?






```r
set.seed(130); n <- 30; x <- rnorm(n=n); N <- 1000#0000000?
population_sample_means <- 1:N; bootstrap_sample_means <- 1:N
set.seed(130); for(i in 1:N){
  population_sample_means[i] <- mean(rnorm(n=n))
  bootstrap_sample_means[i] <- mean(sample(x, prob=rep(1/n,n), size=n, replace=TRUE))
} # Does Bootstrap Approximation Work?
```

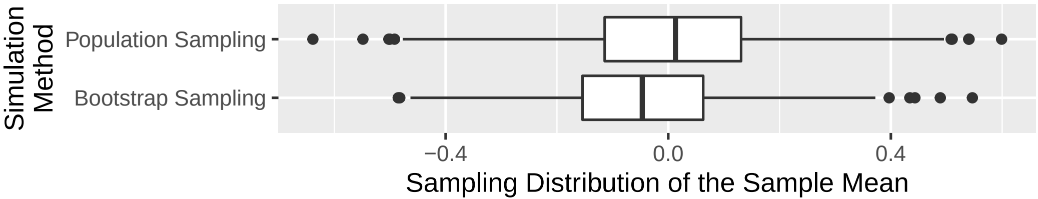
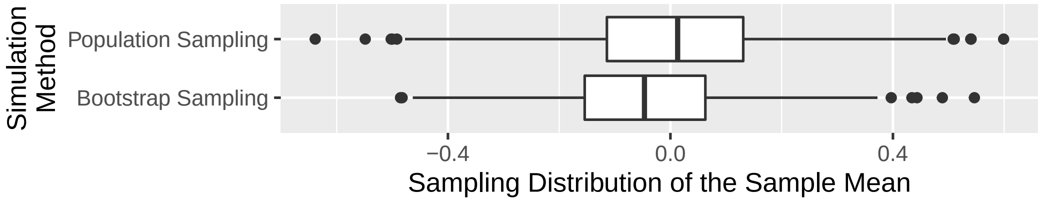
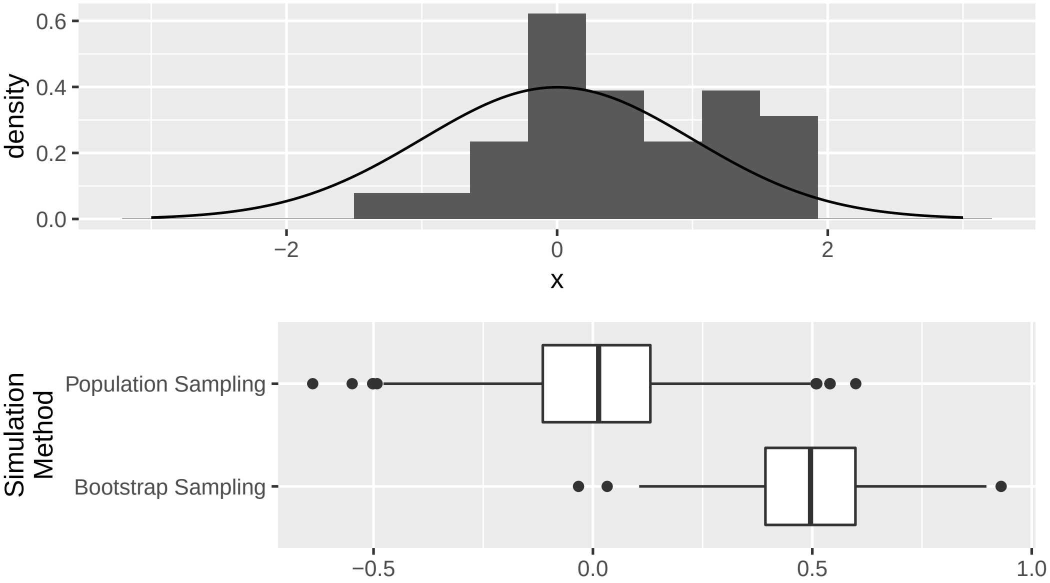


Figure Code

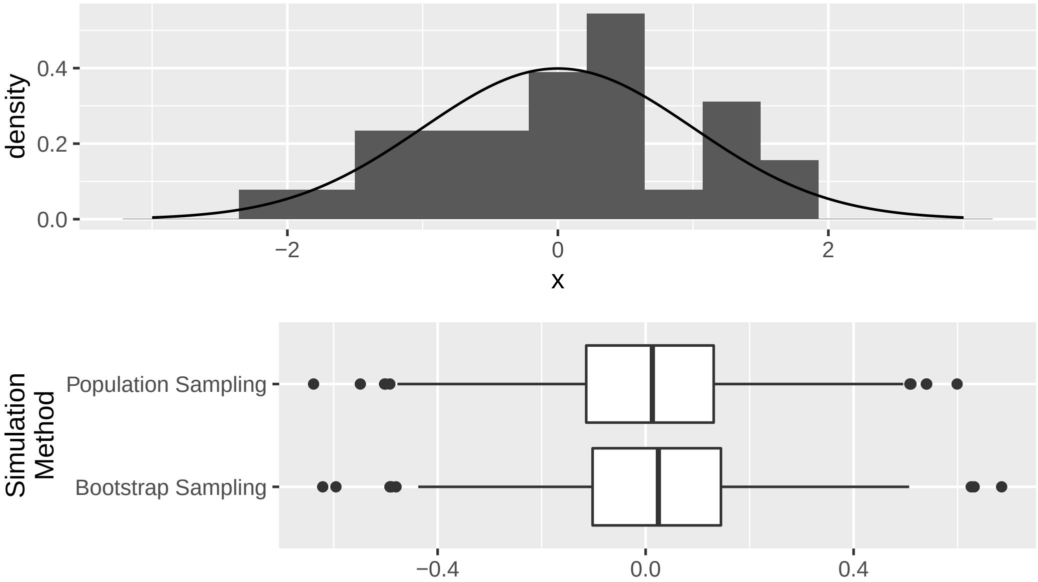
```r
# {r, include=TRUE, echo=TRUE, fig.width=6, fig.height=1.25}
sampling_distribution <- c(population_sample_means,
                           bootstrap_sample_means)
simulation_method <- c(rep("Population Sampling",N),
                       rep("Bootstrap Sampling",N))
tibble(`Sampling Distribution` = sampling_distribution,
       `Simulation\nMethod` = simulation_method) %>%
  ggplot(aes(x=`Sampling Distribution`, y=`Simulation\nMethod`)) +
  geom_boxplot() + xlab("Sampling Distribution of the Sample Mean")
# Does Bootstrap Approximation Work?
```



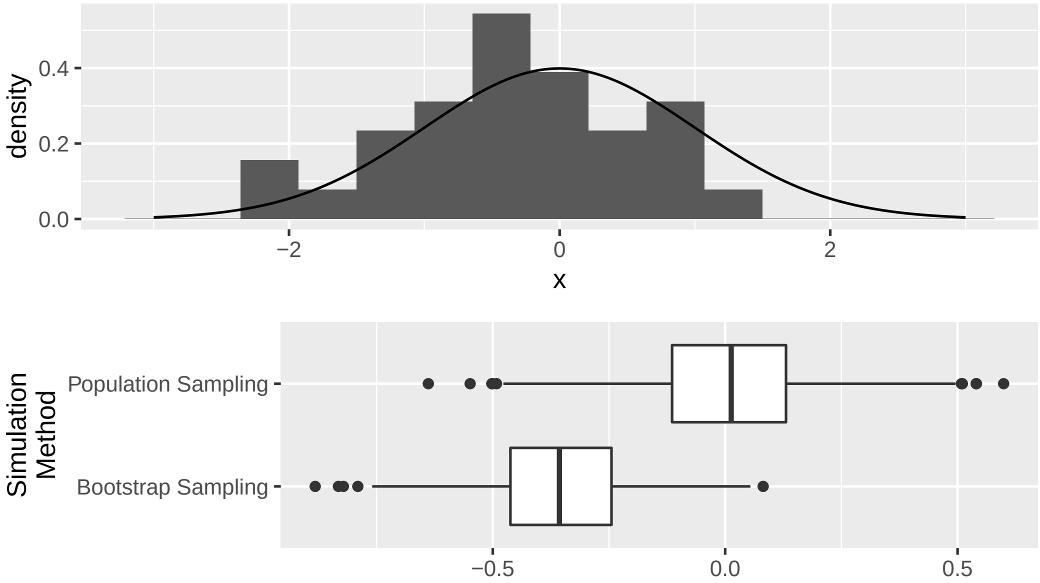
How Well Do Samples Approximate Populations?



How Well Do Samples Approximate Populations?



How Well Do Samples Approximate Populations?



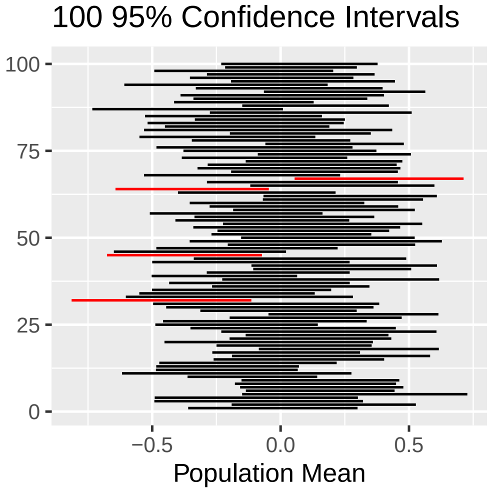
Sanity Check

1. What is x_i?
2. What is the **population** of x_i?
3. What is a parameter?
4. What is the sample `x = c(x_1,x_2,...x_n)`?
5. What makes the sample a better approximation of the population?
6. What happens if you get a "bad" sample?
7. What is a statistic?
8. What is $\bar{x}$?
9. What is the **sampling distribution** of $\bar{x}$?
10. How is the **sampling distribution** of $\bar{x}$ created?
11. What happens if you get a "bad" sample? What can be done about this?

How Well Do Samples Approximate Populations?

```
plot<-ggplot();mu<-0; n<-30;set.seed(130)
for(i in 1:R){
  x <- rnorm(mean=mu, n=n)
  bootstrap_xbar <- 1:N
  for(j in 1:N){
    tmp <- sample(x, replace=TRUE)
    bootstrap_xbars[j] <- mean(tmp)
  }
  ConfidenceInterval <-
    quantile(bootstrap_xbars, percentiles)
  if( all(ConfidenceInterval < mu) |
      all(ConfidenceInterval > mu) ){
      col="red"}else{col="black"}
  plot <- plot + geom_line(color = col,
    data = tibble(x=ConfidenceInterval,
      y=c(i,i)), aes(x=x, y=y))
}; plot+xlab("Population Mean")+labs(title=
  paste(R, " ", (1-2*half_alpha)*100,
        "% Confidence Intervals", sep=""))+
  theme(axis.title.y=element_blank())
```

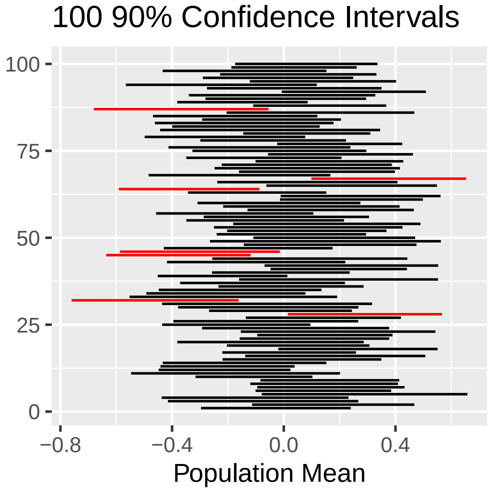
```
half_alpha <- 0.025; R <- 100; N <- 1000#00?
percentiles <- c(half_alpha, 1-half_alpha)
```



How Well Do Samples Approximate Populations?

```r
plot<-ggplot();mu<-0; n<-30;set.seed(130)
for(i in 1:R){
  x <- rnorm(mean=mu, n=n)
  bootstrap_xbar <- 1:N
  for(j in 1:N){
    tmp <- sample(x, replace=TRUE)
    bootstrap_xbars[j] <- mean(tmp)
  }
  ConfidenceInterval <-
    quantile(bootstrap_xbars, percentiles)
  if( all(ConfidenceInterval < mu) |
      all(ConfidenceInterval > mu) ){
      col="red"}else{col="black"}
  plot <- plot + geom_line(color = col,
    data = tibble(x=ConfidenceInterval,
      y=c(i,i)), aes(x=x, y=y))
}; plot+xlab("Population Mean")+labs(title=
  paste(R, " ", (1-2*half_alpha)*100,
        "% Confidence Intervals", sep=""))+
  theme(axis.title.y=element_blank())
```

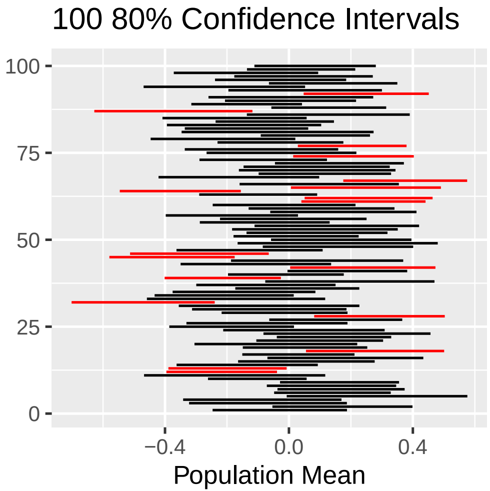
```r
half_alpha <- 0.05; R <- 100; N <- 1000#00?
percentiles <- c(half_alpha, 1-half_alpha)
```



How Well Do Samples Approximate Populations?

```
plot<-ggplot();mu<-0; n<-30;set.seed(130)
for(i in 1:R){
  x <- rnorm(mean=mu, n=n)
  bootstrap_xbar <- 1:N
  for(j in 1:N){
    tmp <- sample(x, replace=TRUE)
    bootstrap_xbars[j] <- mean(tmp)
  }
  ConfidenceInterval <-
    quantile(bootstrap_xbars, percentiles)
  if( all(ConfidenceInterval < mu) |
      all(ConfidenceInterval > mu) ){
      col="red"}else{col="black"}
  plot <- plot + geom_line(color = col,
    data = tibble(x=ConfidenceInterval,
      y=c(i,i)), aes(x=x, y=y))
}; plot+xlab("Population Mean")+labs(title=
  paste(R, " ", (1-2*half_alpha)*100,
        "% Confidence Intervals", sep=""))+
  theme(axis.title.y=element_blank())
```

```
half_alpha <- 0.1; R <- 100; N <- 1000#00?
percentiles <- c(half_alpha, 1-half_alpha)
```



Sanity Check

1. What is the “population” when bootstrapping a sampling distribution?
2. Should `replace=TRUE` or `replace=FALSE` when bootstrapping with `sample()`?
3. Why would we use the `quantile()` function in the bootstrapping context?
4. What value of the `probs` parameter gives a 90% confidence intervals?
5. How does the confidence level relate to the width of the Confidence Intervals?
6. Are there one or two `for` loops when we’re bootstrapping a confidence interval?

Confidence Intervals VS Hypothesis Testing

Confidence Intervals $[\hat{\mu}_{lower}, \hat{\mu}_{upper}]$

1. **Approximate** population as sample
2. Bootstrap **sampling distribution**
3. Define Confidence Interval with sampling distribution percentiles

$[(1-\alpha)\times 100]$**% Confidence Interval**

- α chance the confidence interval does not contain the true parameter value
- This is not $Pr(\mu \in [\hat{\mu}_{lower}, \hat{\mu}_{upper}])$, it is $Pr([\hat{\mu}_{lower}, \hat{\mu}_{upper}]$ bounds $\mu)$
- *True μ isn't a random thing, but $[\hat{\mu}_{lower}, \hat{\mu}_{upper}]$ based on the sample is

Hypothesis Testing $H_0 : \mu = \mu_0$

1. **Assume** a population through H_0
2. Get **sampling distribution** under H_0
3. Compute the sample p-value and either Reject or Fail to Reject H_0

α**-level significance testing**

- α chance of a Type I Error if H_0 rejected for a p-value smaller than α
- p-values are neither $Pr(H_0$ is `TRUE`$)$ nor $Pr(\mu = \mu_0)$
- *True μ and hence H_0 aren't random things, but sample based p-values are

Sanity Check

For a 95% Confidence Interval and α-level significance test

1. What is the probability $\mu \in [\hat{\mu}_{lower}, \hat{\mu}_{upper}]$
2. What is the probability that $[\hat{\mu}_{lower}, \hat{\mu}_{upper}]$ bounds μ)?
3. What is $Pr(H_0$ is $\texttt{TRUE})$?
4. What is $Pr(\mu = \mu_0)$?
5. What is the p-value?
6. What is the role of the test statistic, parameter, population, and sampling distribution relative to the p-value?

The p-value ConTROVersy/ContraVersy

- Why are p-values controversial?
- What a nerdy debate about p-values shows about science and how to fix it
- The reign of the p-value is over: what alternative analyses could we employ to fill the power vacuum?
- Scientists rise up against statistical significance
- Statistics experts urge scientists to rethink the p-value

The main problem is wrongly interpreting p-values as $Pr(H_0 \text{ is } \texttt{TRUE})$ and $Pr(\mu = \mu_0)$

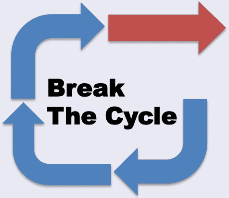
but the deeper problems with p-values are

- introduced here and presented here
- and rely upon understanding the simulation here

The p-value ConTROVersy/ContraVersy

George Cobb, Professor Emeritus, Mount Holyoke College

Q: Why do colleges/grad schools use $\alpha = 0.05$ thresholds for statistical significance?
A: Because that's still what the scientific community and journal editors use.
Q: Why do so many people use $\alpha = 0.05$ thresholds for statistical significance?
A: Because that's what they were taught in college or grad school.
$\alpha = 0.05$ *is arbitrary: better to either simply comment on the strength of the evidence against* H_0 *by reporting the p-value (or at least choose* α *before calculating the p-value)*



p-value	evidence against H_0
above 0.1	None
0.05 to 0.1	Weak
0.01 to 0.05	Moderate
0.0001 to 0.01	Strong
below 0.0001	Very Strong

FIX The p-value ConTROVersy/ContraVersy

0. Don't interpret p-values as $Pr(H_0 \text{ is } \texttt{TRUE})$ or $Pr(\mu = \mu_0)$:

   p-values are the probability of observing a test statistic that is *as or more extreme* than the one we got **if the NULL Hypothesis is actually `TRUE`**

1. Want to control Type I error? Set α and do a α-significance test

2. Want to use a "measure of evidence" perspective without controlling Type I error?

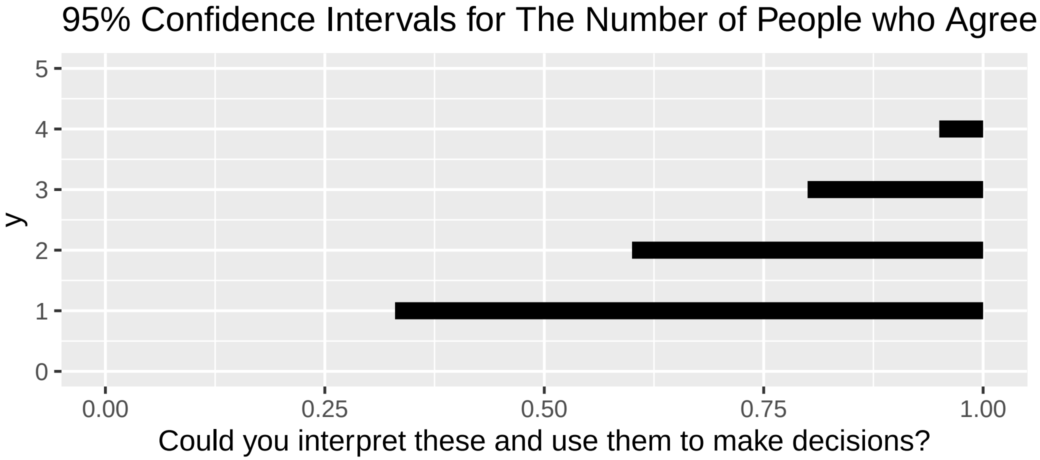
   Don't retroactively interpret p-value in terms of Type I error...

p-value	above 0.1	0.05 to 0.1	0.01 to 0.05	0.0001 to 0.01	below 0.0001
evidence against H_0	None	Weak	Moderate	Strong	Very Strong

3. Instead just use a **Confidence Interval**: get BOTH the estimate *AND* its strength

FIX The p-value ConTROVersy/ContraVersy

Do we need formal Hypotheses? Interpret and make decisions about these. . .



Confidence Intervals VS Hypothesis Testing

STATISTICAL INFERENCE*: Parameter *ESTIMATION

α-significance level **Hypothesis Testing** formally rejects implausible parameter values

- *What if we'd instead like to provide a range of plausible parameter values?*

At a fixed confidence level,
narrower intervals are more meaningful and therefore more likely actionable.

- "We have '95% Confidence' that anywhere between 1% to 99% of people agree!"

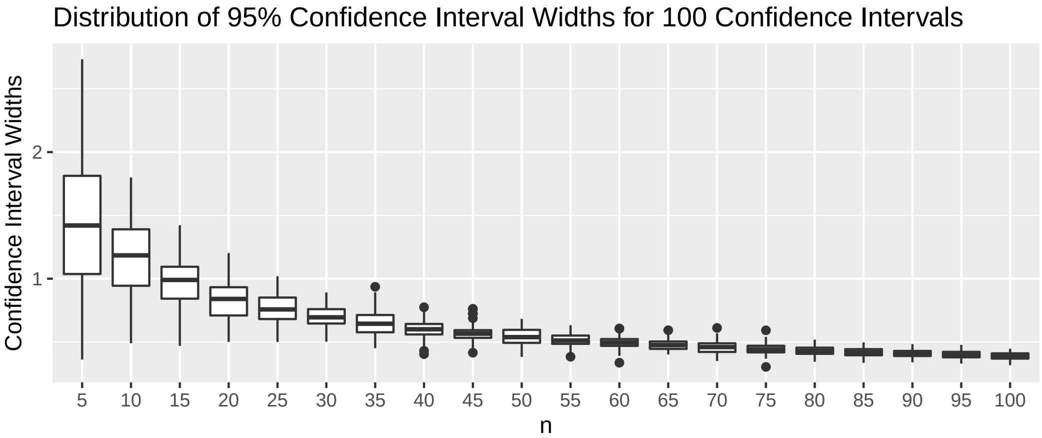
How Do We Get Tighter Confidence Intervals: ?

We previously saw that for the same data

- 80% Confidence Intervals are narrower than
  - 90% Confidence Intervals, which are narrower than
    - 95% Confidence Intervals, which are narrower than...

This won't really help us though...

How Do We Get Tighter Confidence Intervals: n



https://www.zoology.ubc.ca/~whitlock/Kingfisher/CLT.htm

Statistical Grammar Police

For a 95% Confidence Interval we say

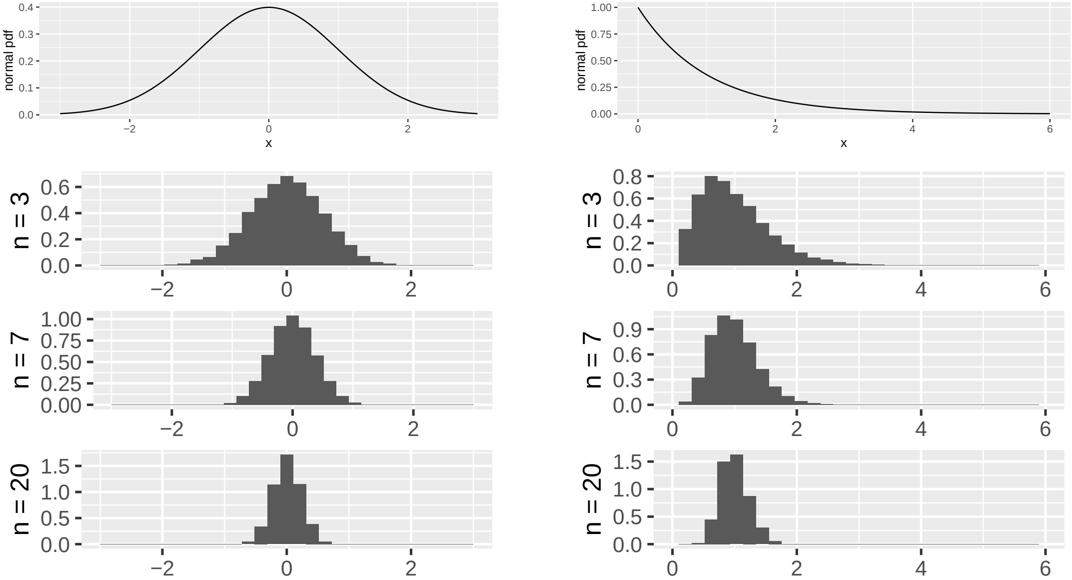
we have 95% **Confidence** the true parameter value is contained in the Interval

- We use the term **Confidence** (as opposed to *probability* or *chance*) to intentionally signal that this is a **Confidence Interval** formulation.
- We **DO NOT** want to say there's a 95% probability (or chance) that the true parameter value will be contained in some some interval.
  - This **might** be misinterpreted as saying that the true parameter is usually in the interval but sometimes not; but parameters are only just in the interval or not*

Are we just splitting hairs here?

The chance the constructed confidence interval bounds the true parameter value is 95%

The Sampling Distribution of $\bar{x}$ VS Skewness



Sanity Check

- True/False: If you have relevant data for each individual in the population, you can calculate the true value of parameters.
- True/False: In general, we know the true value of parameters.
- True/False: We only know the true value of parameters when we're doing Hypothesis Testing, not when we're estimating them with Confidence Intervals.
- True/False: A statistic is calculated from observed data and is an estimate of a true parameter value.
- True/False: Every random sample drawn from the population will yield the same values for statistics.