

# PLSC 502 – Fall 2022

## Statistical Inference

October 20, 2022

- “Worth a possible 50 points” means:
  - $50 = 100$  percent (“perfect” – nope)
  - $47-49 \approx$  “A”
  - $45-46 \approx$  “A-”
  - $43-44 \approx$  “B+”
- Pointers:
  - *Label* figures and tables
  - Include informative *captions*
  - Don’t use *concepts incorrectly*
  - Cutting and pasting figures is usually bad
- Don’t sweat your code

- Confidence Intervals
- Hypothesis Testing

A range of values for  $\hat{\theta}$  (say,  $[\hat{\theta}_L, \hat{\theta}_H]$ ) for which:

- $\Pr(\hat{\theta}_L \leq \theta \leq \hat{\theta}_H)$  is high, and
- $\hat{\theta}_L - \hat{\theta}_H$  is small

Define:

$$\Pr(\hat{\theta}_L \leq \theta \leq \hat{\theta}_U) = 1 - \alpha,$$

# C.I.s: The “Pivotal” Method

“Pivotal method”:  $\hat{\theta}$

- is a function *only* of the sample data and the population parameter  $\theta$ , and
- whose sampling distribution *does not* depend on  $\theta$ .

This will then allow us to “invert” C.I.s to do hypothesis testing (and vice-versa...)

Recall that:

$$\bar{X} \sim \mathcal{N}(\mu, \sigma_{\bar{X}}^2)$$

Because  $E(\bar{X}) = \mu$ , we use  $\bar{X}$  as the “center” of our C.I.

Suppose  $\alpha = 0.05$ , so  $1 - \alpha = 0.95$ . Then

$$\Pr(\bar{X}_L \leq \mu \leq \bar{X}_U) = 0.95$$

Then choose:

$$\Pr(\mu < \bar{X}_L) = \int_{-\infty}^{\bar{X}_L} \phi_{\bar{X}}(u) du = 0.025$$

and

$$\Pr(\mu > \bar{X}_H) = \int_{\bar{X}_H}^{\infty} \phi_{\bar{X}}(u) du = 0.025.$$

For

$$Z = \frac{\hat{\theta} - \theta}{\sigma_{\hat{\theta}}} \sim \mathcal{N}(0, 1)$$

we have:

$$\begin{aligned} 1 - \alpha &= \Pr \left( -z_{\alpha/2} \leq \frac{\hat{\theta} - \theta}{\sigma_{\hat{\theta}}} \leq z_{\alpha/2} \right) \\ &= \Pr \left( -z_{\alpha/2} \sigma_{\hat{\theta}} \leq \hat{\theta} - \theta \leq z_{\alpha/2} \sigma_{\hat{\theta}} \right) \\ &= \Pr \left( -\hat{\theta} - z_{\alpha/2} \sigma_{\hat{\theta}} \leq -\theta \leq -\hat{\theta} + z_{\alpha/2} \sigma_{\hat{\theta}} \right) \\ &= \Pr \left( \hat{\theta} - z_{\alpha/2} \sigma_{\hat{\theta}} \leq \theta \leq \hat{\theta} + z_{\alpha/2} \sigma_{\hat{\theta}} \right) \end{aligned}$$

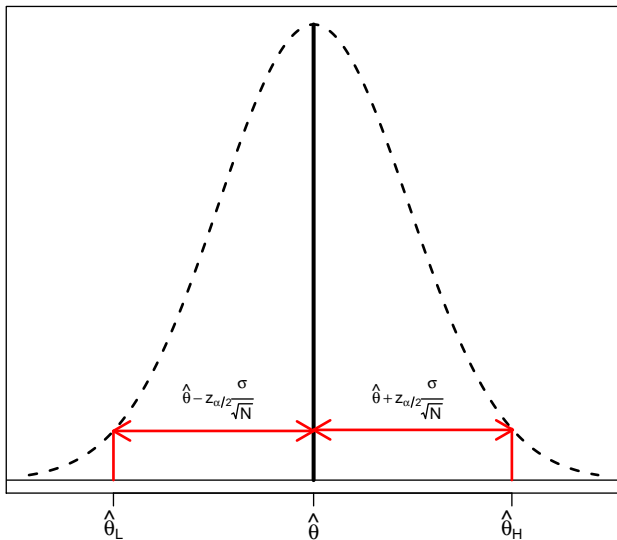
This means that

$$[\hat{\theta}_L, \hat{\theta}_U] = \left[ \hat{\theta} - z_{\alpha/2} \sigma_{\hat{\theta}}, \hat{\theta} + z_{\alpha/2} \sigma_{\hat{\theta}} \right]$$

Steps:

- Select your level of confidence  $1 - \alpha$ ,
- Calculate the sample statistic  $\hat{\theta}$ ,
- Calculate the z-value associated with the  $1 - \alpha$  level of confidence,
- Divide that z-value by  $\sigma_{\hat{\theta}}$ , the standard error of the sampling statistic, and
- Construct the confidence interval according to the above equation.





Possible Values of  $\bar{X}$

## Example: Proportions

We have

$$\hat{\theta} = \hat{\pi} = \frac{1}{N} \sum_{i=1}^N X_i$$

and

$$\sigma_{\hat{\pi}}^2 = \frac{\pi(1-\pi)}{N}$$

so that

$$\sigma_{\hat{\pi}} = \sqrt{\frac{\pi(1-\pi)}{N}}.$$

## Proportions (continued)

We know that:

$$\hat{\pi} \sim \mathcal{N}(\pi, \sigma_{\hat{\pi}}^2)$$

Implies:

$$\hat{\pi}_L = \hat{\pi} - z_{\alpha/2} \left[ \sqrt{\frac{\hat{\pi}(1 - \hat{\pi})}{N}} \right]$$

and

$$\hat{\pi}_U = \hat{\pi} + z_{\alpha/2} \left[ \sqrt{\frac{\hat{\pi}(1 - \hat{\pi})}{N}} \right].$$

## Proportions: Example

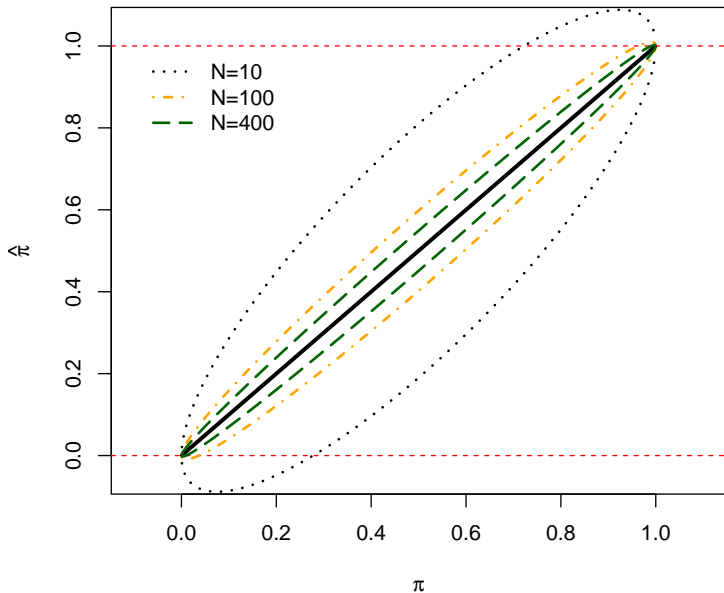
For  $N = 20$  and  $\hat{\pi} = 0.390$ , we have:

$$\begin{aligned}\hat{\pi}_L &= 0.390 - 1.96 \left[ \sqrt{\frac{0.39(0.61)}{20}} \right] \\ &= 0.390 - 0.214 \\ &= \mathbf{0.176}\end{aligned}$$

and

$$\begin{aligned}\hat{\pi}_U &= 0.390 + 1.96 \left[ \sqrt{\frac{0.39(0.61)}{20}} \right] \\ &= 0.390 + 0.214 \\ &= \mathbf{0.604}.\end{aligned}$$

## C.I.s for Proportions



# How Did That Happen?

Some code:

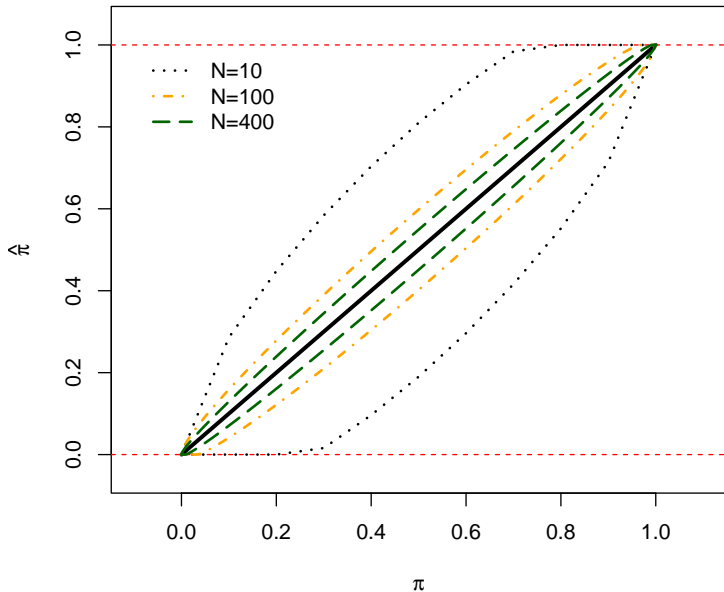
```
> Pi<-seq(0.001,0.999,by=0.001)      # Population value

> ub10 <- Pi + 1.96*(sqrt((Pi*(1-Pi))/(10))) # N=10
> lb10 <- Pi - 1.96*(sqrt((Pi*(1-Pi))/(10)))
> ub100 <- Pi + 1.96*(sqrt((Pi*(1-Pi))/(100))) # N=100
> lb100 <- Pi - 1.96*(sqrt((Pi*(1-Pi))/(100)))
> ub400 <- Pi + 1.96*(sqrt((Pi*(1-Pi))/(400))) # N=400
> lb400 <- Pi - 1.96*(sqrt((Pi*(1-Pi))/(400)))
```

Let's try something different:

```
CI10<-data.frame(BinomCI(c(0:10),10,method="wald"))    # N=10
CI100<-data.frame(BinomCI(c(0:100),100,method="wald")) # N=100
CI400<-data.frame(BinomCI(c(0:400),400,method="wald")) # N=400
```

## C.I.s for Proportions Redux



“Wilson” (1927):

$$\hat{\pi}_L = \frac{\hat{\pi} + \frac{z_{1-\alpha/2}^2}{2n} + z_{1-\alpha/2} \sqrt{\frac{\hat{\pi}(1-\hat{\pi})}{n} + \frac{z_{1-\alpha/2}^2}{4n^2}}}{1 + \frac{z_{1-\alpha/2}^2}{n}}$$

and:

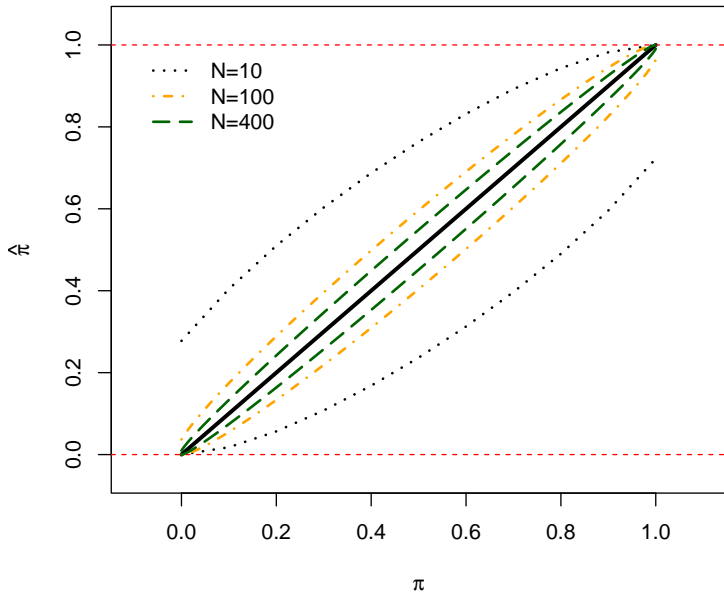
$$\hat{\pi}_U = \frac{\hat{\pi} + \frac{z_{\alpha/2}^2}{2n} + z_{\alpha/2} \sqrt{\frac{\hat{\pi}(1-\hat{\pi})}{n} + \frac{z_{\alpha/2}^2}{4n^2}}}{1 + \frac{z_{\alpha/2}^2}{n}}.$$

Other alternatives:

- “Exact” binomial methods
- Many, many others...



# C.I.s for Proportions Re-Redux



Consider:

$$T = \frac{\bar{X} - \mu}{\hat{\sigma}/\sqrt{N}}$$

As  $N \rightarrow \infty$ ,  $\hat{\sigma} \rightarrow \sigma$  and so  $T \rightarrow \mathcal{N}(0, 1)$ .

However, in small samples,

$$\hat{\sigma}/\sqrt{N} \sim \chi_N^2$$

which means

$$[\bar{X}_L, \bar{X}_U] = \bar{X} \pm t_{\alpha/2} \left( \frac{\hat{\sigma}}{\sqrt{N}} \right).$$

“ $[(1 - \alpha) \times 100]\%$  of all confidence intervals constructed from independent simple random samples will contain the population parameter  $\theta$ , and  $(\alpha \times 100)\%$  of them will not.”

*Never* “There is a 95% chance that our confidence interval contains the true population value  $\theta$ .”

# Example: SCOTUS Cases, 1946-2020

Data from the [Supreme Court Judicial Database](#):

- All SCOTUS decisions, OT1946-2020 ( $N \approx 10500$ )
- 50+ variables about each decision
- `Constitutional` = 1 if the decision is a constitutional one, 0 otherwise

```
> summary(df$Constitutional)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0000	0.0000	0.0000	0.3109	1.0000	1.0000

Code:

```
> set.seed(7222009)
> DFsample <- with(df, sample(Constitutional,20,replace=F))

> summary(DFsample)

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.0    0.0    0.0    0.4    1.0    1.0

> BinomCI(sum(DFsample),length(DFsample))

      est      lwr.ci      upr.ci
[1,] 0.4 0.2188065 0.6134185
```

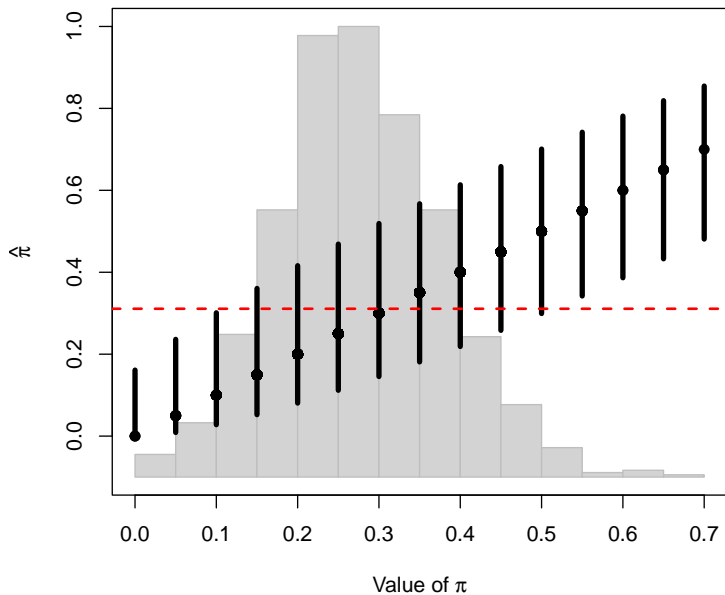
So for this sample:

- $\pi = 0.311$
- $\hat{\pi} = 0.4$
- $\widehat{\text{C.I.}} = [0.219, 0.613]$

How many times (out of 1000) does a C.I. created from a random sample with  $N = 20$  contain the population value  $\mu = 0.311$ ?

```
N <- 20
reps <- 1000
PI20 <- numeric(reps)
UB20<-numeric(reps)
LB20<-numeric(reps)
set.seed(7222009)
for (i in 1:reps) {
  foo <- with(df, sample(Constitutional,N,replace=F))
  bar <- data.frame(BinomCI(sum(foo),length(foo)))
  PI20[i] <- bar$est
  LB20[i] <- bar$lwr.ci
  UB20[i] <- bar$upr.ci
}
```

Coverage,  $N = 20$

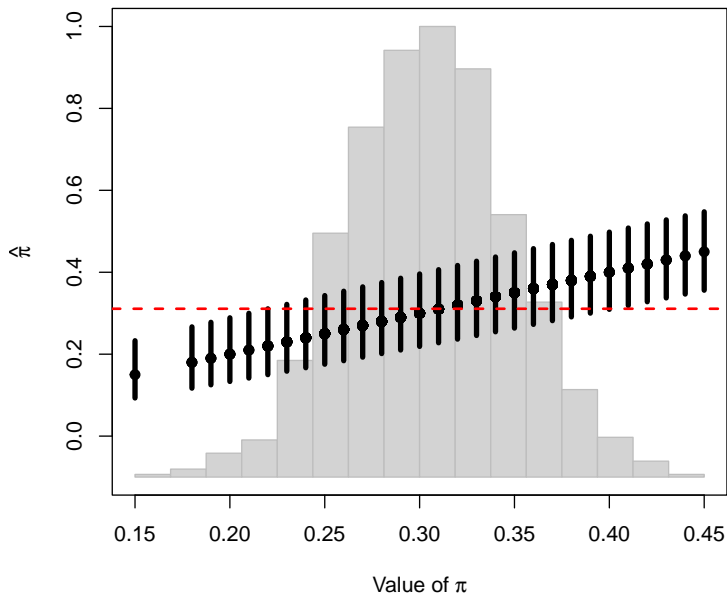


How about for  $N = 100$ ?

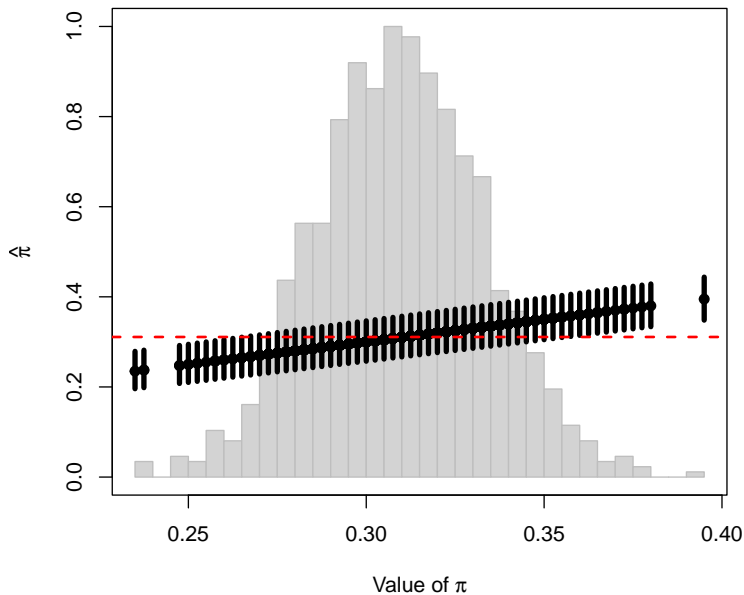
```
N <- 100
reps <- 1000
PI100 <- numeric(reps)
UB100<-numeric(reps)
LB100<-numeric(reps)
set.seed(7222009)
for (i in 1:reps) {
  foo <- with(df, sample(Constitutional,N,replace=F))
  bar <- data.frame(BinomCI(sum(foo),length(foo)))
  PI100[i] <- bar$est
  LB100[i] <- bar$lwr.ci
  UB100[i] <- bar$upr.ci
}
```



Coverage,  $N = 100$



Coverage,  $N = 400$



What proportion of our 95% C.I.s contain the population mean of Constitutional?

```
> popmean<-mean(df$Constitutional)
> prop.table(table(ifelse(UB20>popmean & LB20<popmean,1,0)))
```

```
      0      1
0.053 0.947
```

```
> # N = 100:
>
> prop.table(table(ifelse(UB100>popmean & LB100<popmean,1,0)))
```

```
      0      1
0.049 0.951
```

```
> # N = 400:
>
> prop.table(table(ifelse(UB400>popmean & LB400<popmean,1,0)))
```

```
      0      1
0.053 0.947
```

# Hypothesis Testing

# Hypothesis Testing: Concepts

Conventional *hypothesis testing* requires:

- A *null hypothesis*,  $H_0$
- an *alternative hypothesis*  $H_a$
- a *test statistic*  $\theta = f(\mathbf{X})$
- a *rejection region* in the range of  $\theta$ .

October 18, 2016 [Quinnipiac poll](#) in PA:

- Clinton = 47 percent
- Trump = 41 percent
- $N = 660$  likely voters.

Hypothesis:

$$H_a : \pi > 0.5$$

Corresponding null:

$$H_0 : \pi = 0.5$$

Test statistic:  $\hat{\pi} = 0.47$

- **Type I error** = “false positive.”
- **Type II error** = “false negative.”

Test Statistic / Sample	Reality / Population	
	$H_a$	$H_0$
$H_a$	Correct	Type I error
$H_0$	Type II Error	Correct

# Alphas and Significance

By convention:

$$\Pr(\text{Type I Error}) = \alpha \text{ ( "significance level" )}$$

and

$$1 - \alpha = \text{"specificity"}$$

While

$$\Pr(\text{Type II Error}) = \beta$$

and

$$1 - \beta = \text{"sensitivity."}$$



# A New Table

Sample Result	Reality / Population		Frequency
	Positive	Negative	
Positive	True Positive ( $N_{TP}$ )	Type I error (False Positive) ( $N_{FP}$ )	$N_P = N_{TP} + N_{FP}$
Negative	Type II Error (False Negative) ( $N_{FN}$ )	True Negative ( $N_{TN}$ )	$N_N = N_{TN} + N_{FN}$
Frequency	$N_{(+)} = N_{TP} + N_{FN}$	$N_{(-)} = N_{TN} + N_{FP}$	$N$

- *False positive / significance rate*  $\alpha = N_{FP}/N_{(-)}$ ,
- *False negative rate*  $\beta = N_{FN}/N_{(+)}$ ,
- *False discovery rate*  $= N_{FP}/N_P$ ,
- *False omission rate*  $= N_{FN}/N_N$ ,
- *Accuracy*  $= (N_{TP} + N_{FP})/N$

In the Clinton / PA example, we know:

$$\hat{\pi} \sim \mathcal{N}(\pi, \sigma_{\hat{\pi}}^2).$$

and

$$\begin{aligned}\hat{\sigma}^2 &= 0.470(1 - 0.470) \\ &= 0.249\end{aligned}$$

and

$$\begin{aligned}\hat{\sigma}_{\hat{\pi}}^2 &= \frac{0.249}{660} \\ &= 0.00038.\end{aligned}$$

That means:

$$\hat{\pi} \sim \mathcal{N}(0.5, 0.00038).$$

# More Hypothesis Testing

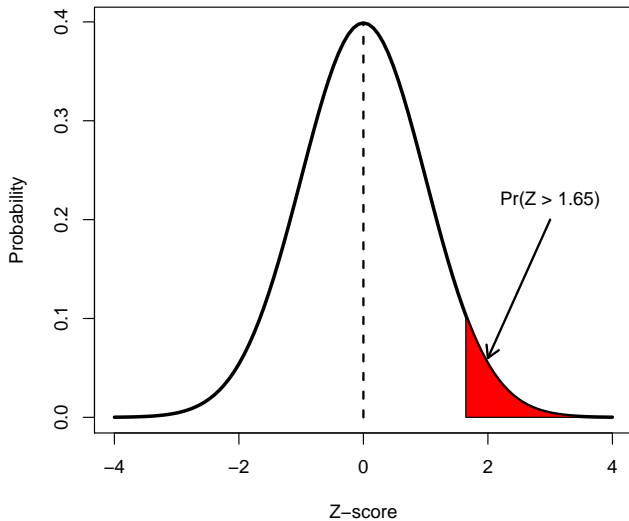
Converting  $\hat{\pi}$  to  $z$ :

$$\frac{\hat{\pi} - \pi}{\sigma_{\hat{\pi}}} = Z \sim \mathcal{N}(0, 1).$$

Decision rule:

Reject  $H_0$  if  $Z \geq z_{\alpha}$ .

$$\alpha = 0.05 \rightarrow Z \geq 1.65$$



Here,

$$Z = \frac{0.470 - 0.50}{0.0195} = -1.54$$

so we fail to reject the null.

Another alternative  $H_0 : \pi = 0.40$  yields

$$\begin{aligned} Z &= \frac{0.47 - 0.40}{0.0195} \\ &= 3.59 \end{aligned}$$

meaning we would reject that null.

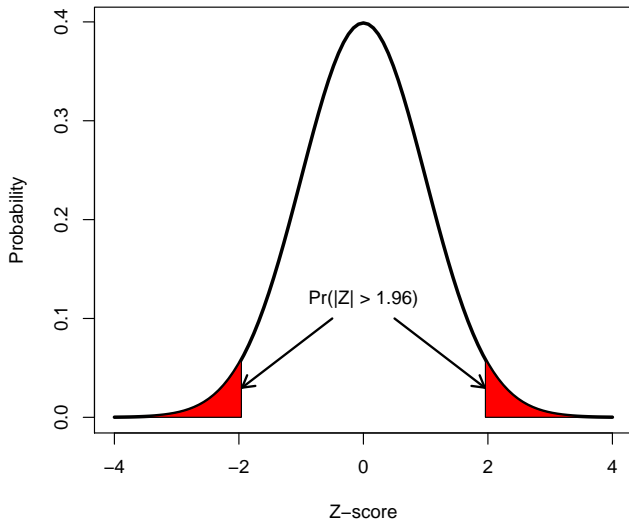
An alternative formulation:

$$H_a : \pi \neq 0.5.$$

Alternative decision rule:

$$\text{Reject } H_0 \text{ if } |Z| \geq z_{\alpha/2}$$

$$\alpha = 0.05 \rightarrow |Z| \geq 1.96$$





# P-Values Versus Significance Tests

*P-value (or “attained significance level”): The smallest level of significance  $\alpha$  for which the observed data indicate that the null hypothesis should be rejected.*

Why we like them:

- **Avoid arbitrary “cutoffs.”**
- **Provide more information.**

# Significance Tests and Confidence Intervals

C.I.:

$$\text{c.i.}_\alpha = \hat{\theta} \pm z_{\alpha/2} \sigma_{\hat{\theta}}$$

vs. test:

$$|Z| \equiv \left| \frac{\hat{\theta} - \theta}{\sigma_{\hat{\theta}}} \right| \geq z_{\alpha/2}.$$

# Significance Tests and Confidence Intervals

“Acceptance region”:

$$-z_{\alpha/2} \leq \frac{\hat{\theta} - \theta}{\sigma_{\hat{\theta}}} \leq z_{\alpha/2} = \hat{\theta} - z_{\alpha/2}\sigma_{\hat{\theta}} \leq \theta \leq \hat{\theta} + z_{\alpha/2}\sigma_{\hat{\theta}},$$

i.e., “Do not reject  $H_0$  at  $P = \alpha$  if  $\theta$  lies within a  $(1 - \alpha) \times 100$ -percent confidence interval around  $\hat{\theta}$ , and reject  $H_0$  if it does not.”

1.  **$P$ -values are not “the probability that the null hypothesis is false.”**

**BAD:**

*“The test statistic allows us to reject the null hypothesis at  $P < 0.01$ , indicating that there is a less than one in 100 chance that the null hypothesis is true.”*

**GOOD:**

*“The test statistic allows us to reject the null hypothesis at  $P < 0.01$ , which is strong evidence that the observed result is not due to chance.”*

## 2. One does not, in general, “accept” the null hypothesis.

### BAD:

*“The  $P$ -value for the regression coefficient on Female is 0.56, indicating that there is no relationship between gender and support for immigrants’ rights.”*

### GOOD:

*“The  $P$ -value for the regression coefficient on Female is 0.56, indicating the data do not support the hypothesized relationship between gender and support for immigrants’ rights.”*

3.  **$P$ -values are not the long-run frequency of a “statistically significant” test statistic.**

**BAD:**

*“The  $P$ -value of 0.01 means that 99 out of 100 hypothetical replications would reject the null hypothesis.”*

## 4. Statistical significance does not equate to substantive significance.

```
> data<-read_csv("https://raw.githubusercontent.com/PrisonRodeo/PLSC502-2022-git/
  master/Exercises/PLSC502-2022-ExerciseFour.csv")
>
> data$DOB <- with(data, as.Date(DateOfBirth,format = "%d%b%Y"))
> data$Sign <- with(data, Zodiac(DOB))

> popmean <- with(data, prop.table(table(Active))) [2]
> popmean
  1
0.8956

> with(data[data$Sign=="Scorpio",],
+       prop.test(sum(Active),
+                 nrow(data[data$Sign=="Scorpio",]),
+                 p=popmean,correct=FALSE))
```

1-sample proportions test without continuity correction

```
data: sum(Active) out of nrow(data[data$Sign == "Scorpio", ]), null probability popmean
X-squared = 2.8, df = 1, p-value = 0.1
alternative hypothesis: true p is not equal to 0.8956
95 percent confidence interval:
 0.8823 0.8967
sample estimates:
  p
0.8897
```

**5. A statistic can never be “significant in the wrong direction.”**

**BAD:**

*“Our estimate of the effect of trade liberalization on the probability of a civil war – which we expected to be negative – is in fact positive, and statistically significant at  $P = 0.02$ .”*



- 6. Identical  $P$ -values are not “better” or “more reliable” if they are based on a larger sample.**
- 7. Failing to reject the null hypothesis in a larger sample is a bigger deal than failing to do so in a small one.**