

Stat 515: Introduction to Statistics

Chapter 8

Confidence Intervals to Testing

- As we've seen in the past chapter we can come up with interesting observations from the confidence intervals we found
- Next we will learn how to formally test whether or not a population parameter is \neq , $<$, $>$ a particular value based off our sample statistics

Vocabulary of Testing

- The **null hypothesis** (H_0) is the hypothesis we conclude to be true unless we have data that is sufficient to suggest otherwise – think “innocent until proven guilty”
- The **alternative hypothesis** (H_a) is the hypothesis that we conclude to be true if we have data that is sufficient to suggest the null hypothesis is not true

Vocabulary of Testing

- The **test statistic** is a sample statistic that we will use to decide whether or not we have data that is sufficient to suggest the null hypothesis isn't true
 - If this is the case we say the test statistic is in the rejection region
- The **Rejection Region** of a statistical test is the set of values we will reject the null hypothesis

Errors Associated with Testing

- **Type I Error** occurs when H_0 is rejected but in reality H_0 is true
 - $P(\text{Type I Error}) = \text{significance level} = 1 - \text{confidence level}$
- **Type II Error** occurs when H_0 is not rejected but in reality H_0 is false

	<i>H_0 is true</i>	<i>H_a is true</i>
We failed to reject	No Error	Type II Error
We rejected	Type I Error	No Error

Errors Associated with Testing

Implication:

- **Type I Error** occurs when H_0 is rejected but in reality H_0 is true
 - $P(\text{Type I Error}) = \text{significance level} = 1 - \text{confidence level}$
- If we were to do 1000 hypothesis tests at 95% confidence or, at the .05 level of significance, we would make type one error 5% of the time.
 - THAT'S 50 TIMES!

Errors Associated with Testing

- This is actually my research area – trying to come up with better methods to do many hypothesis tests which is called multiple testing, or multiplicity.
- This is really important in comparing many different things – particularly the gene expression.
 - Yes, I model genes.

Controlling Error

- **We can control the probability of Type I Error** by our choice of the significance or confidence level
- Though we **can't control the probability of Type II Error** directly, when we decrease the probability of Type I Error the probability of Type II Error increases

Controlling Error

- **To increase Type I error:** decrease confidence
- **To decrease Type I error:** increase confidence

- **To increase Type II error:** decrease Type I error
→ increase confidence
- **To decrease Type II error:** increase Type I error
→ decrease confidence

Example

- Data is collected to see if there is evidence, at the .1 level of significance or 90% confidence, that the average contaminant concentration level exceeds the acceptable level for fishing, let's call this level μ_0 .
- H_0 : *Contaminant levels are low: $\mu \leq \mu_0$*
- H_a : *Contaminant levels are too high: $\mu > \mu_0$*

Example

- H_0 : *Contaminant levels are low: $\mu \leq \mu_0$*
- H_a : *Contaminant levels are too high: $\mu > \mu_0$*
- **Type I Error:** The committee determines that the contaminant level does exceed the acceptable level incorrectly
 - People can't fish when really it's safe

Example

- H_0 : *Contaminant levels are low: $\mu \leq \mu_0$*
- H_a : *Contaminant levels are too high: $\mu > \mu_0$*
- **Type II Error:** The committee determines that the contaminant level doesn't exceed the acceptable level incorrectly
 - People can eat contaminated fish leading to possible sickness or death

Example

- H_0 : *Safe to fish*
- H_a : *Not safe to fish*

- **Type I Error:** We say it's unsafe when really it is
- **Type II Error:** We say it's safe when really it isn't

Example

- Type I Error: People can't fish when really it's safe
- Type II Error: People can eat contaminated fish leading to possible sickness or death
- We see here that **Type II error would be worse** as they would be putting humans in danger. Clearly, it would be important here to **make the probability for Type II Error as small as possible**.
- We're happy that the **confidence is low** because that indicates a **higher P(Type I Error)** and subsequently a **lower P(Type II Error)**.

Example

- If it's such an important problem why don't we just shoot for the right answer?
- **We are shooting for the right answer, but in statistics we're never 100% sure – we only have evidence up to a point!**

Example

- The idea with confidence intervals and statistics is that we're coming up with an interval or statement about something so big we cannot measure it
- It's usually easy to get sample measurements, but a lot of times there are too many experimental objects in a population to make it feasible to take measurements for every one of them.

Example

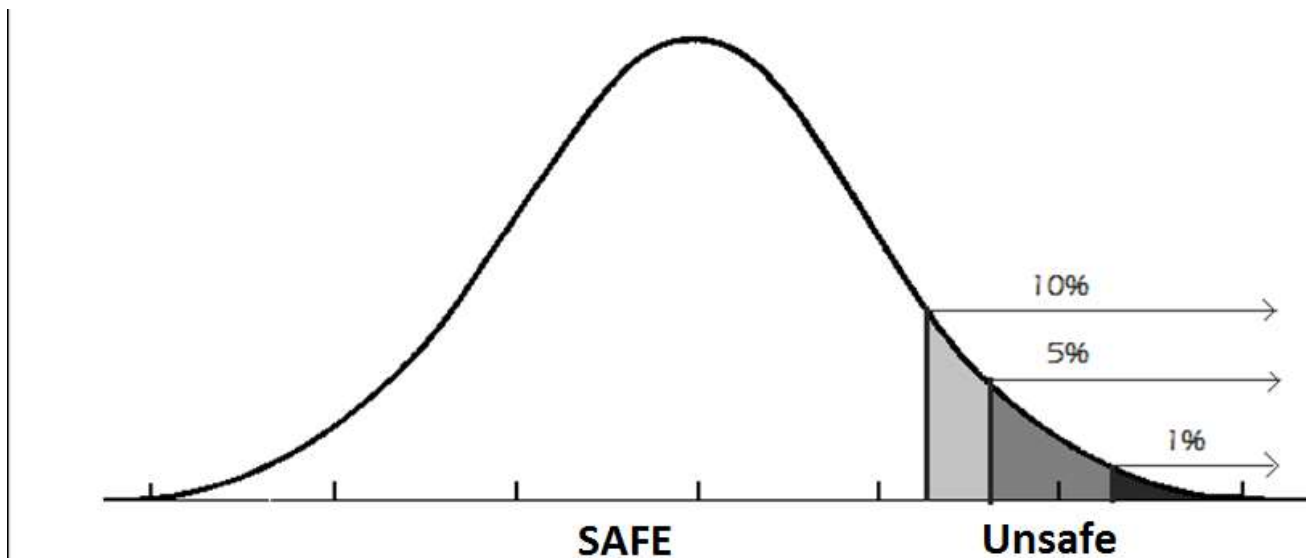
- For instance, according to , there are over 300 million cubic miles of water on earth!
 - That's enough to fill over 350 quintillion gallon containers!
- Now, think about taking each one of those gallons of water and testing them for contaminants
 - not bad if it's just a couple, but you'd be dead before you could check 350 quintillion

Example

- What scientists do is take measurements from random locations around a fishing area and they use statistics to come up with a decision.
- Yes, it would be better to drain all the water and test every molecule but that would be expensive and take an unreasonable amount of time

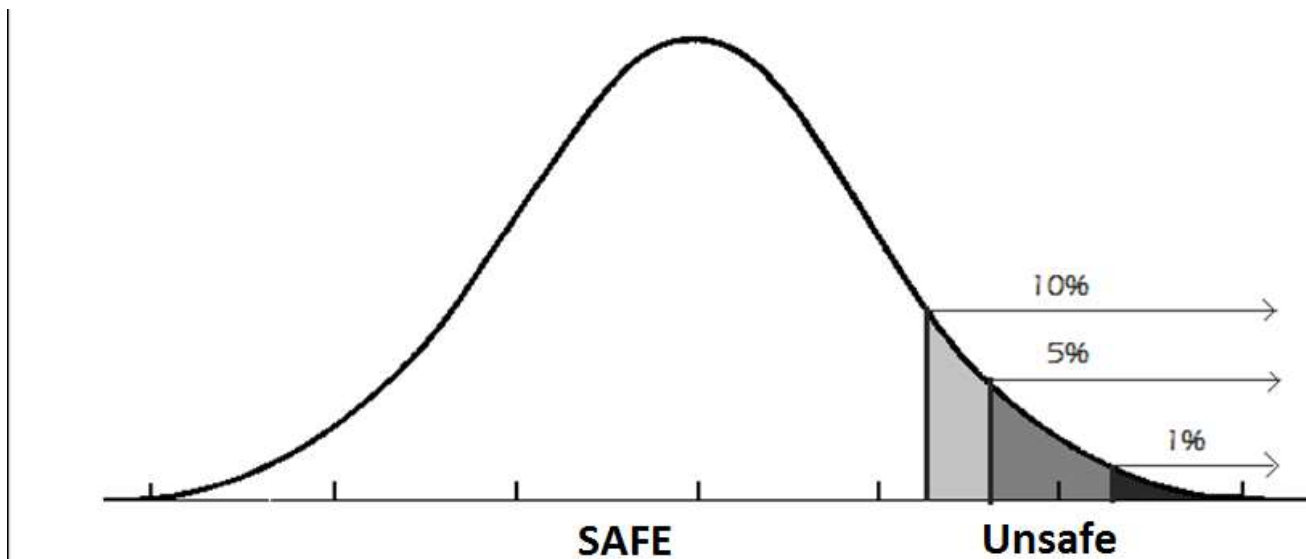
Example

- As we increase our confidence, we make our rejection region smaller which means we're less likely to reject.
 - We would need a more unusual sample to reject



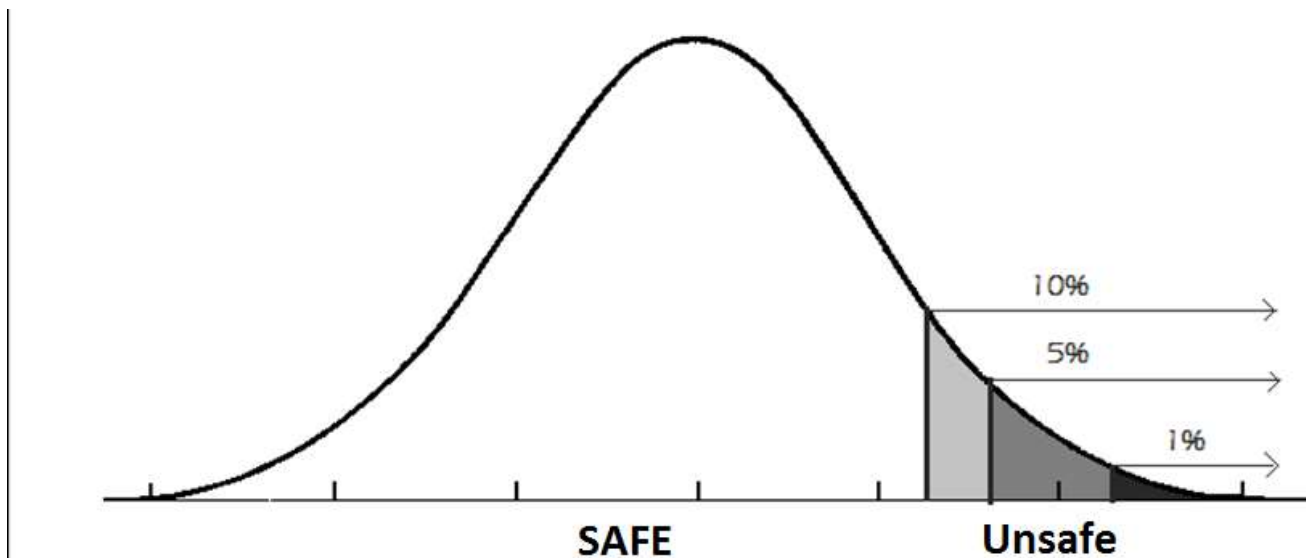
Example

- As we decrease our confidence, we make our rejection region larger which means we're more likely to reject.
 - We would need a less unusual sample to reject here



Example

- We're still going for the correct answer, but how we choose our confidence level allows us "sort of choose" what error we'll make if we are incorrect
 - I say sort of choose because it's still possible to make both mistakes – we can only make one mistake more likely than the other



Hypothesis Tests: Step 1

- State Hypotheses to some value we're interested in, c - it's usually easier to start with H_a
 - **Null hypothesis:**
 - $H_o: \text{parameter} \leq c$ (one sided test)
 - $H_o: \text{parameter} \geq c$ (one sided test)
 - $H_o: \text{parameter} = c$ (two sided test)
 - **Alternative hypothesis:**
 - $H_a: \text{parameter} > c$ (one sided test)
 - $H_a: \text{parameter} < c$ (one sided test)
 - $H_a: \text{parameter} \neq c$ (two sided test)

Hypothesis Tests: Step 2

- **Check Assumptions:**

- Each test has its own set of assumptions – we'll go through them as we cover each type of hypothesis test

Hypothesis Tests: Step 3

- **Calculate the Test Statistic:**
 - Each test has its own test statistic calculation – we'll go through them as we cover each type of hypothesis test
 - Recall: The **test statistic** is a sample statistic that we will use to decide whether or not we have data that is sufficient to suggest the null hypothesis isn't true - if this is the case we say the test statistic is in the rejection region

Hypothesis Tests: Step 4

- **Determine the P-value**

- The P-value describes how unusual the sample data would be if H_0 were true, which is what we're assuming.
- TS^* is the test statistic as calculated from the data

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \text{parameter} > c$	Right tail	$1 - P(\text{TestStat} < TS^*)$
$H_a: \text{parameter} < c$	Left tail	$P(\text{TestStat} < TS^*)$
$H_a: \text{parameter} \neq c$	Two-tail	$2 * P(\text{TestStat} < - TS^*)$

Hypothesis Tests: Step 5

- Summarize the test by reporting and interpreting the P-value
 - Smaller p-values give stronger evidence against H_0
- If $p\text{-value} \leq (1 - \textit{confidence}) = \alpha$
 - Reject H_0 , with a p-value = _____, we have sufficient evidence that the alternative hypothesis might be true
- If $p\text{-value} > (1 - \textit{confidence}) = \alpha$
 - Fail to reject H_0 , with a p-value = _____, we do not have sufficient evidence that the alternative hypothesis might be true

[Note: We never prove or are sure of anything]

Hypothesis Test for Proportions: Step 1

- State Hypotheses to some value we're interested in, p_o - it's usually easier to start with H_a
 - **Null hypothesis:** we assume that the population proportion equals some p_o
 - $H_o: \rho \leq p_o$ (one sided test)
 - $H_o: \rho \geq p_o$ (one sided test)
 - $H_o: \rho = p_o$ (two sided test)
 - **Alternative hypothesis:** What we're interested in
 - $H_a: \rho > p_o$ (one sided test)
 - $H_a: \rho < p_o$ (one sided test)
 - $H_a: \rho \neq p_o$ (two sided test)

Hypothesis Test for Proportions: Step 2

- **Check the assumptions:**

1. The variable must be categorical
2. The data should be obtained using randomization
3. The sample size is sufficiently large where p_o is the testing value (note we use $\rho = p_o$)
 - $np_o \geq 15$ & $n(1 - p_o) \geq 15$
 - It is safe to assume the distribution of p_o has a bell shaped distribution if both are ≥ 15

Hypothesis Test for Proportions: Step 3

- **Calculate Test Statistic, z^***
 - The test statistic measures how different the sample proportion we have is from the null hypothesis
 - We calculate the z-score by assuming that p_o is the population proportion (we use $\rho = p_o$)

$$z^* = \frac{(\hat{p} - p_o)}{\sqrt{\frac{p_o(1 - p_o)}{n}}}$$

Hypothesis Test for Proportions: Step 4

- **Determine the P-value**

- The P-value describes how unusual the sample data would be if we use $\rho = p_0$
- z^* is the test statistic from step 3

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \rho > p_0$	Right tail	$1 - P(Z < z^*)$
$H_a: \rho < p_0$	Left tail	$P(Z < z^*)$
$H_a: \rho \neq p_0$	Two-tail	$2P(Z < - z^*)$

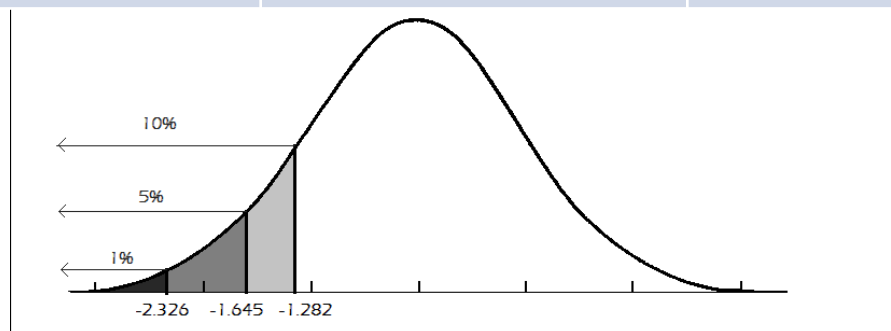
Hypothesis Test for Proportions: Step 5

- Summarize the test by reporting and interpreting the P-value
 - Smaller p-values give stronger evidence against H_0
- If $p\text{-value} \leq (1 - \textit{confidence}) = \alpha$
 - Reject H_0 , with a p-value = _____, we have sufficient evidence that the alternative hypothesis might be true
- If $p\text{-value} > (1 - \textit{confidence}) = \alpha$
 - Fail to reject H_0 , with a p-value = _____, we do not have sufficient evidence that the alternative hypothesis might be true

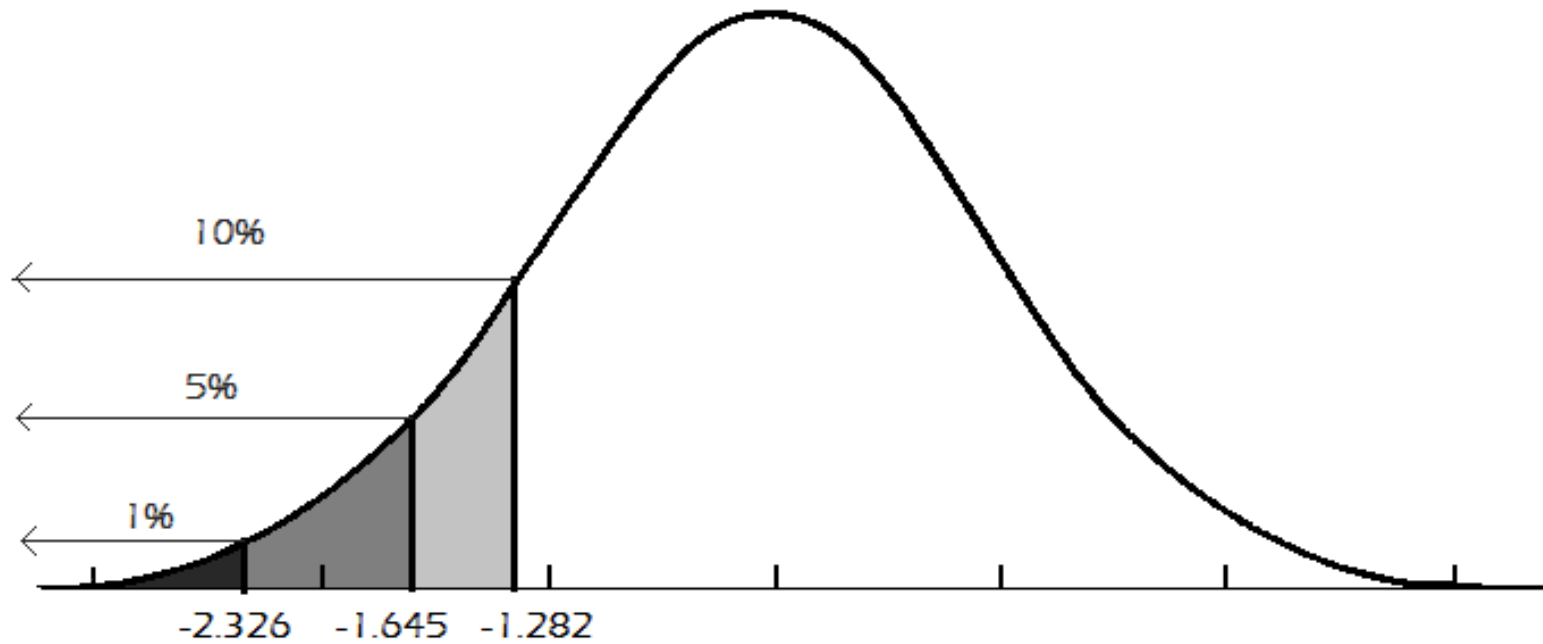
Hypothesis Test for Proportions: Step 5 with Pictures

- For a left tailed test: $H_a: \rho < p_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: all of the rejection region is in the left tail, where \hat{p} is much smaller than p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat < -1.282	P-value < .1
0.95	Test-stat < -1.645	P-value < .05
0.99	Test-stat < -2.326	P-value < .01



Zoom In

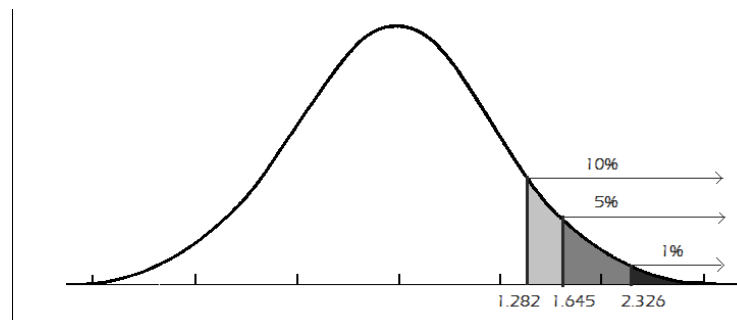


Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat < -1.282	P-value < .1
0.95	Test-stat < -1.645	P-value < .05
0.99	Test-stat < -2.326	P-value < .01

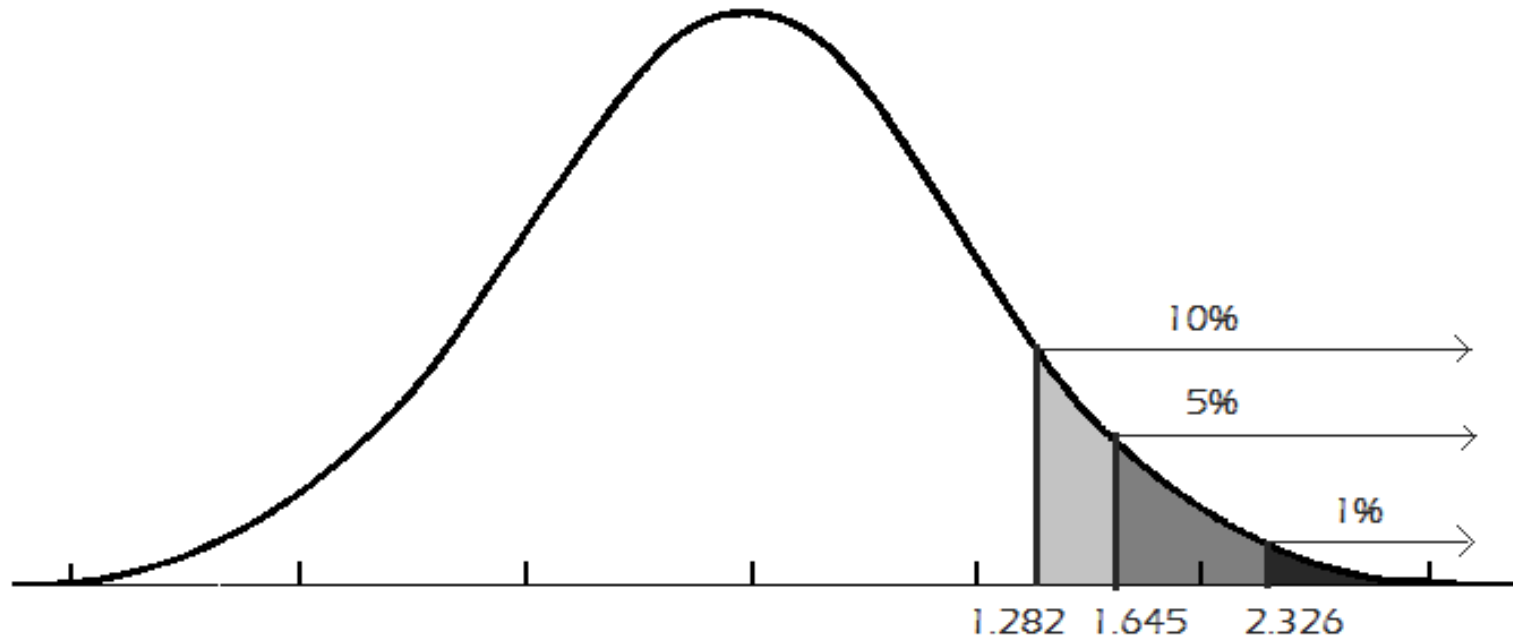
Hypothesis Test for Proportions: Step 5 with Pictures

- For a right tailed test: $H_a: \rho > p_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: all of the rejection region is in the right tail, where \hat{p} is much larger than p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat > 1.282	P-value < .1
0.95	Test-stat > 1.645	P-value < .05
0.99	Test-stat > 2.326	P-value < .01



Zoom In

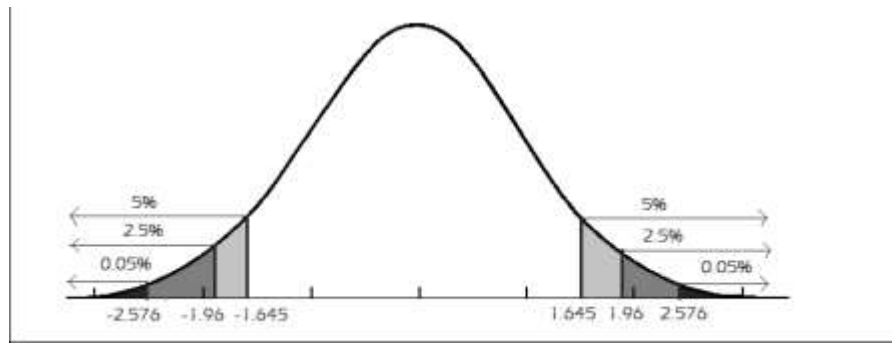


Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat > 1.282	P-value < .1
0.95	Test-stat > 1.645	P-value < .05
0.99	Test-stat > 2.326	P-value < .01

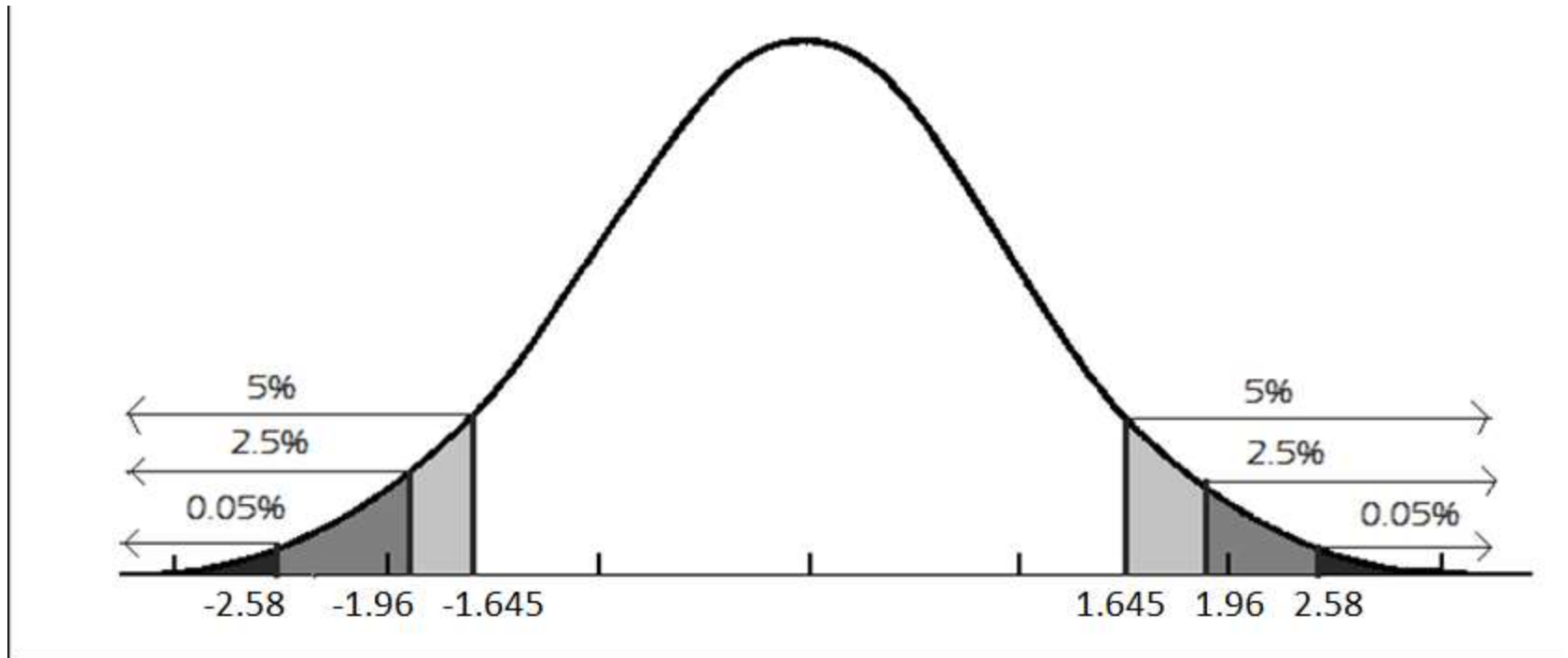
Hypothesis Test for Proportions: Step 5 with Pictures

- For a two tailed test: $H_a: \rho \neq p_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: here we split the rejection region into both tails, where \hat{p} is very different from p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	$ \text{Test-stat} < 1.645$	P-value < .1
0.95	$ \text{Test-stat} < 1.960$	P-value < .05
0.99	$ \text{Test-stat} < 2.576$	P-value < .01



Zoom In



Hypothesis Test for Proportions: Step 5 with Pictures

- The idea is – if our z^* is in the rejection region, our sample \hat{p} is too unusual for the null hypothesis to be true so the data shows sufficient evidence against the null suggesting the alternative might be true.

Example

- A random sample of MLB home games showed that the home teams won 1335 of 2429 games.
- At the .01 level of significance (99% confidence) is there evidence that there is a home field advantage?
- $\hat{p} = \frac{1335}{2429} = .5496$

Example – Step One

- State the Hypotheses: we are interested in whether or not there was a home field advantage, whether or not the population proportion of home games won by the home team is **greater than .50**

$$- H_o: \rho \leq .5$$

$$- H_a: \rho > .5$$

Example – Step Two

- Check Assumptions
 - The variable is categorical
 - Either the home team won or they didn't
 - The data was collected randomly
 - $np_o = 2429(.5) = 1214.5 \geq 15$
 - $n(1 - p_o) = 2429(.5) = 1214.5 \geq 15$
 - So, it is safe to assume the distribution of p_o has a bell shaped distribution

Example – Step Three

- Calculate the test statistic:

$$z^* = \frac{(\hat{p} - p_o)}{\sqrt{\frac{p_o(1 - p_o)}{n}}} = \frac{(.5496 - .5)}{\sqrt{\frac{.5(1 - .5)}{2429}}} = 4.89$$

Example – Step Four

- Determine P-value
 - From the table $pvalue = 1 - P(Z < z^*)$

$$\begin{aligned} pvalue &= 1 - P(Z < 4.89) \\ &= 1 - \text{pnorm}(4.89, 0, 1) \\ &= .0000005041799 \end{aligned}$$

Z-table:

$$pvalue = 1 - P(Z < 4.89) \approx 1 - 1 = 0$$

Example – Step Five

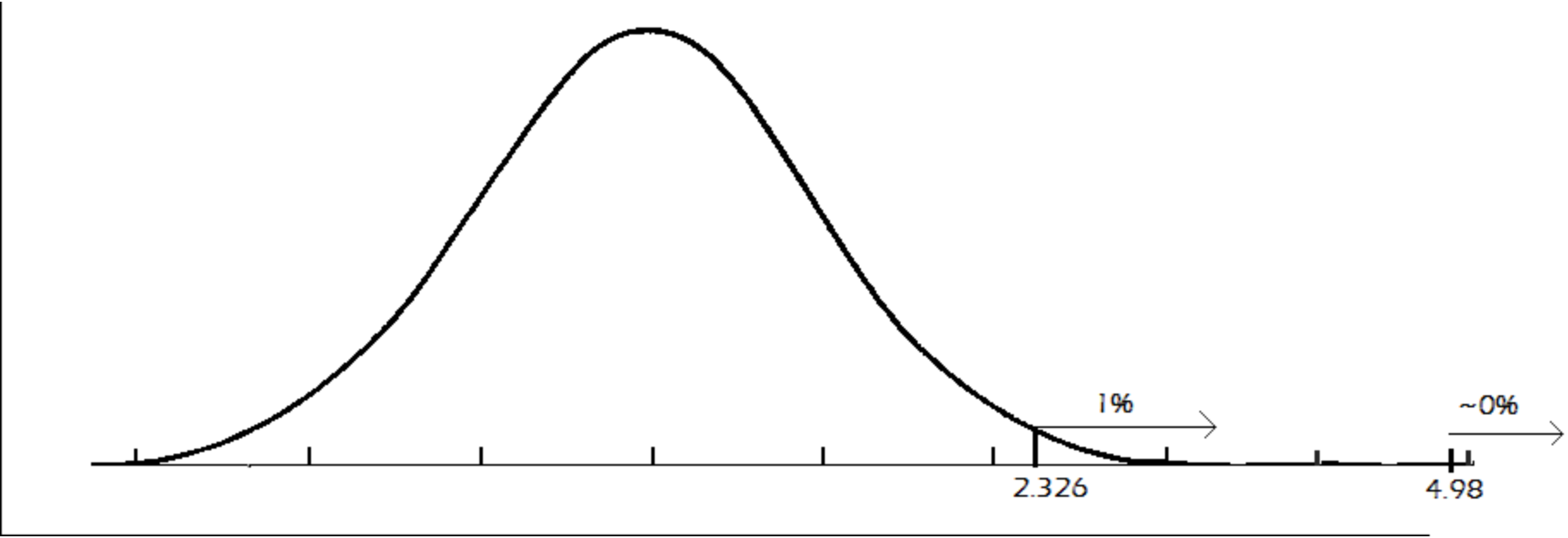
- State Conclusion
 - Since $.0000005041799 < .01$ we reject H_0

At the .01 level of significance, or 99% confidence level, there is sufficient evidence to suggest that there is a home field advantage (the alternative)

Example – Step Five

- State Conclusion: We reject H_0 for any of the following reasons
 - By P-value:
 - $.0000005041799 < .01$
 - By Z-statistic:
 - $|4.89| > 2.575829$
 - By \hat{p} :
 - $.5496 > x = z\sigma_{\hat{p}} + \mu_{\hat{p}} = 2.575829 \sqrt{\frac{.5(1-.5)}{2429}} + .5 = .526132$

Example – Step Five



Example

```
#TestType: 1 for <, 2 for >, 3 for not equal
p.test<-function(conf.level,x,n,p0,TestType){
  txt<-""; phat<-x/n; TestStat<-(phat-p0)/sqrt(p0*(1-p0)/n); xax<-seq(p0-5*sqrt(p0*(1-p0)/n),p0+5*sqrt(p0*(1-p0)/n),.001);
  P_x<-dnorm(xax,p0,sqrt(p0*(1-p0)/n));
  if(TestType==1){ txt<-paste("Test Alternative: parameter < ",p0,"\n",sep=""); CritVal<-qnorm(1-conf.level,p0,sqrt(p0*(1-p0)/n));
    pvalue<-pnorm(TestStat,0,1); cord.x <- seq(min(xax),CritVal,0.001); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright";}
  if(TestType==2){ txt<-paste("Test Alternative: parameter > ",p0,"\n",sep=""); CritVal<-qnorm(conf.level,p0,sqrt(p0*(1-p0)/n));
    pvalue<-1-pnorm(TestStat,0,1); cord.x <- seq(CritVal,max(xax),0.001); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft";}
  if(TestType==3){ txt<-paste("Test Alternative: parameter !=",p0,"\n",sep=""); CritVal1<-qnorm((1-conf.level)/2,p0,sqrt(p0*(1-p0)/n));
    CritVal2<-qnorm(conf.level+(1-conf.level)/2,p0,sqrt(p0*(1-p0)/n)); pvalue=2*pnorm(-abs(TestStat),0,1); cord.x1 <- seq(min(xax),CritVal1,0.001);
    cord.x2 <- seq(CritVal2,max(xax),0.001); x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax));
    if(phat<min(cord.x2)){ loc<-"topright" }else{ loc<-"topleft" } }
  if(n*phat<15|n*(1-phat)<15){ txt<-cat(txt,"Sample size assumptions not met.\n") }else{ txt<-cat(txt,"Sample size assumptions met.\n") }
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){ txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep="")); txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
  }else{ txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep="")); }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep=""));
  plot(xax,P_x,type='l');
  lines(rep(phat,2),c(0,max(P_x)),col="red");
  if(TestType==3){ y.shade<-c(0,dnorm(cord.x1,p0,sqrt(p0*(1-p0)/n)),0,0,dnorm(cord.x2,p0,sqrt(p0*(1-p0)/n)),0) }else{ y.shade<-c(0,dnorm(cord.x,p0,sqrt(p0*(1-
p0)/n)),0) }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Test Statistic"),fill=c("gray","red")) ;}

p.test(.95,1335,2429,.5,2)
```

Onto Hypothesis Testing for Means

Hypothesis Test for Means: Step 1

- **State Hypotheses:** it's usually easier to write the alternative hypothesis first
 - **Null hypothesis:** that the population mean equals some μ_0
 - $H_0: \mu \leq \mu_0$ (one sided test)
 - $H_0: \mu \geq \mu_0$ (one sided test)
 - $H_0: \mu = \mu_0$ (two sided test)
 - **Alternative hypothesis:** What we're interested in
 - $H_a: \mu > \mu_0$ (one sided test)
 - $H_a: \mu < \mu_0$ (one sided test)
 - $H_a: \mu \neq \mu_0$ (two sided test)

Hypothesis Test for Means: Step 2

- Check the assumptions
 - The variable must be quantitative
 - The data are obtained using randomization
 - We're dealing with data from the normal distribution
 - If $n > 30$
 - If a histogram of the data is approximately normal which indicates that the probability is normal

Hypothesis Test for Means: Step 3

- When we don't know σ_x
- Calculate Test Statistic, t^*
 - The test statistic measures how different the sample mean we have is from the null hypothesis
 - We calculate the t-statistic by assuming that μ_0 is the population mean

$$t^* = \frac{(\bar{x} - \mu_0)}{\frac{s_x}{\sqrt{n}}}$$

Hypothesis Test for Means: Step 3

- When we know σ_x
- Calculate Test Statistic, z^*
 - The test statistic measures how different the sample mean we have is from the null hypothesis
 - We calculate the t-statistic by assuming that μ_0 is the population mean

$$z^* = \frac{(\bar{x} - \mu_0)}{\frac{\sigma_x}{\sqrt{n}}}$$

Hypothesis Test for Means: Step 4

- When we don't know σ_x
- Determine the P-value
 - The P-value describes how unusual the sample data would be if H_0 were true.
 - t^* is the test statistic from step 3

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \mu > \mu_0$	Right tail	$P(T > t^*)$
$H_a: \mu < \mu_0$	Left tail	$P(T < t^*)$
$H_a: \mu \neq \mu_0$	Two-tail	$2 * P(T < - t^*)$

Hypothesis Test for Means: Step 4

- When we know σ_x
- Determine the P-value
 - The P-value describes how unusual the sample data would be if H_0 were true.
 - z^* is the test statistic from step 3

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \mu > \mu_0$	Right tail	$P(Z > z^*)$
$H_a: \mu < \mu_0$	Left tail	$P(Z < z^*)$
$H_a: \mu \neq \mu_0$	Two-tail	$2 * P(Z < - z^*)$

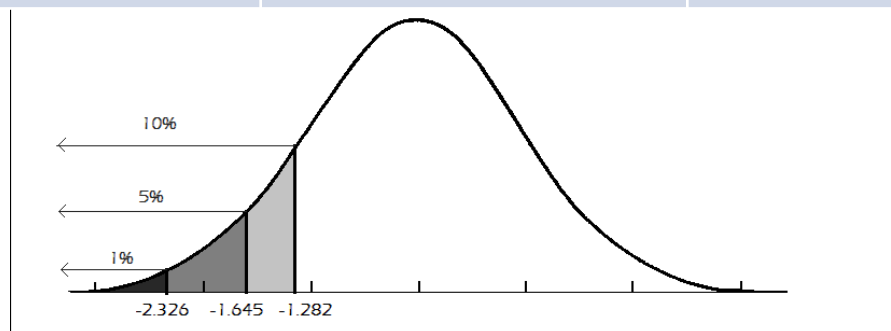
Hypothesis Test for Means: Step 5

- Summarize the test by reporting and interpreting the P-value
 - Smaller p-values give stronger evidence against H_0
- If $p\text{-value} \leq (1 - \textit{confidence}) = \alpha$
 - Reject H_0 , with a p-value = _____, we have sufficient evidence that the alternative hypothesis might be true
- If $p\text{-value} > (1 - \textit{confidence}) = \alpha$
 - Fail to reject H_0 , with a p-value = _____, we do not have sufficient evidence that the alternative hypothesis might be true

Hypothesis Test for Proportions: Step 5 with Pictures when we know σ_x

- For a left tailed test: $H_a: \mu < \mu_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: all of the rejection region is in the left tail, where \hat{p} is much smaller than p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat < -1.282	P-value < .1
0.95	Test-stat < -1.645	P-value < .05
0.99	Test-stat < -2.326	P-value < .01



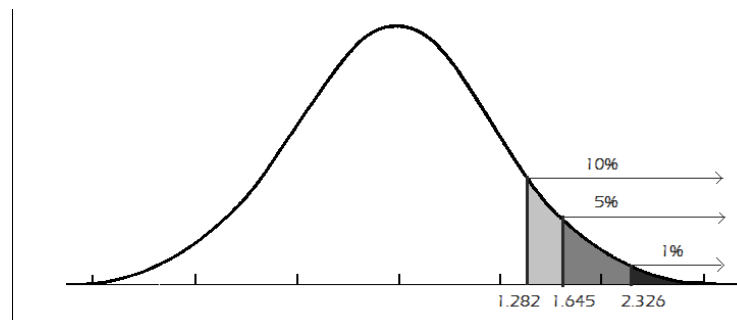
Zoom In



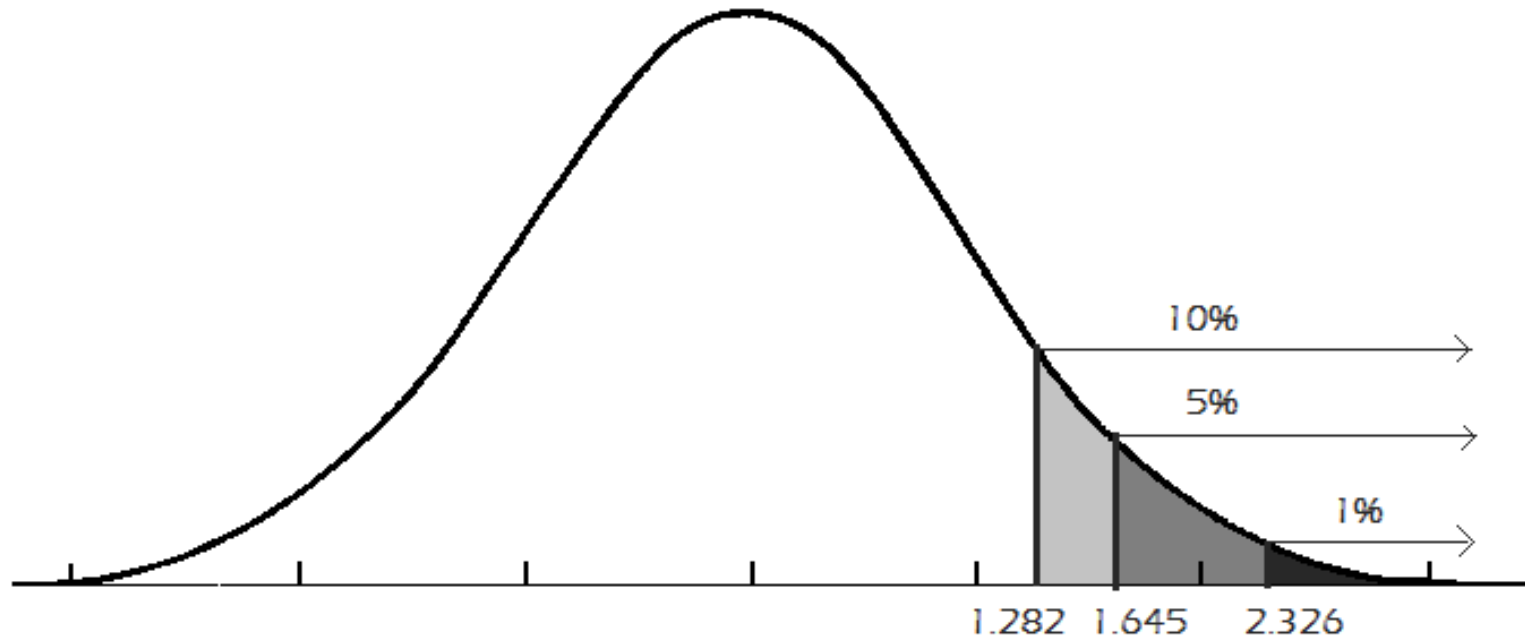
Hypothesis Test for Proportions: Step 5 with Pictures when we know σ_x

- For a right tailed test: $H_a: \mu > \mu_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: all of the rejection region is in the right tail, where \hat{p} is much larger than p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat > 1.282	P-value < .1
0.95	Test-stat > 1.645	P-value < .05
0.99	Test-stat > 2.326	P-value < .01



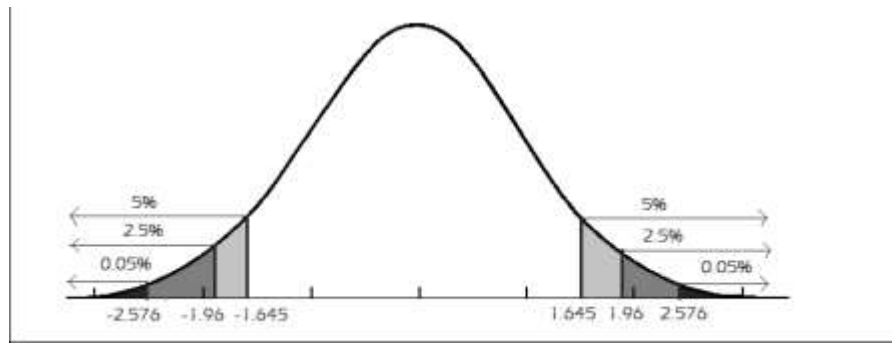
Zoom In



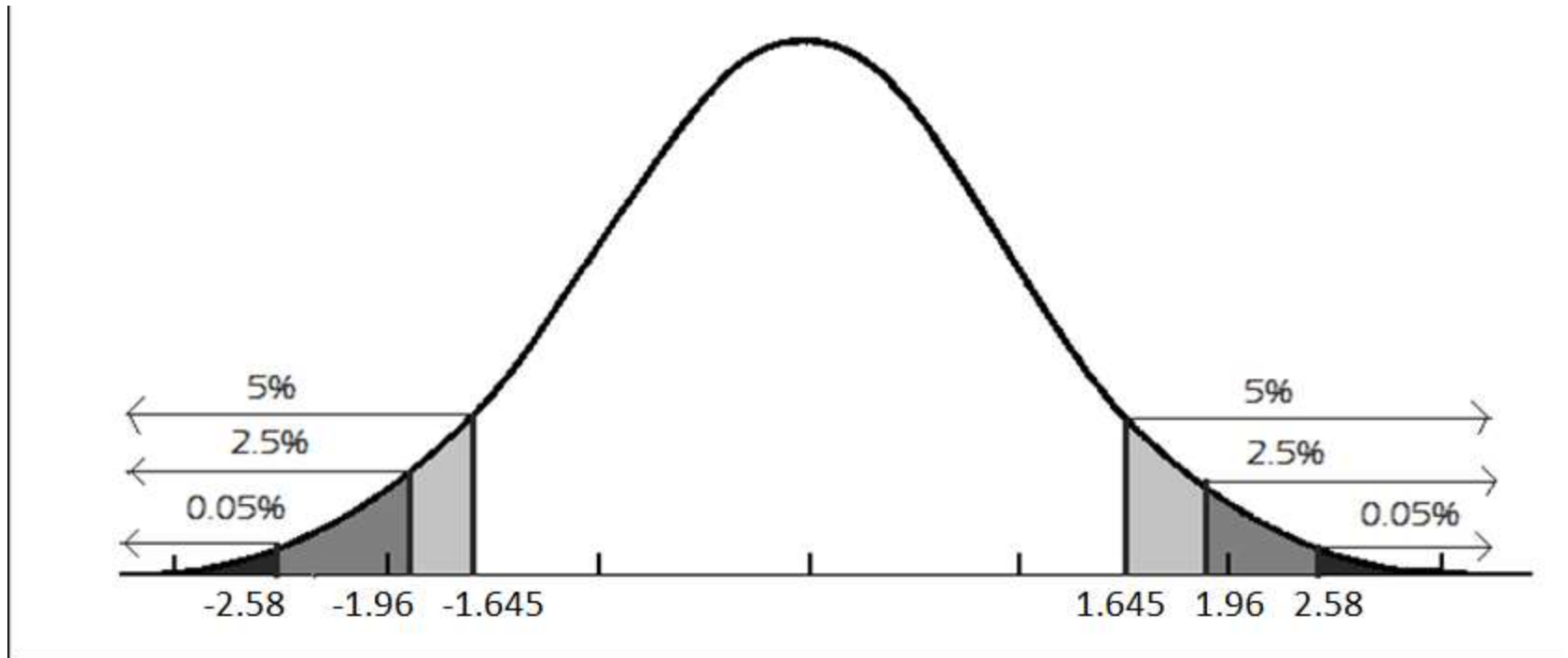
Hypothesis Test for Proportions: Step 5 with Pictures when we know σ_x

- For a two tailed test: $H_a: \mu \neq \mu_0 \rightarrow$ We have rejection regions for H_0 are as follows
 - Note: here we split the rejection region into both tails, where \hat{p} is very different from p_0

Confidence	Reject (test stat)	Reject (p-value)
0.90	$ \text{Test-stat} < 1.645$	P-value < .1
0.95	$ \text{Test-stat} < 1.960$	P-value < .05
0.99	$ \text{Test-stat} < 2.576$	P-value < .01



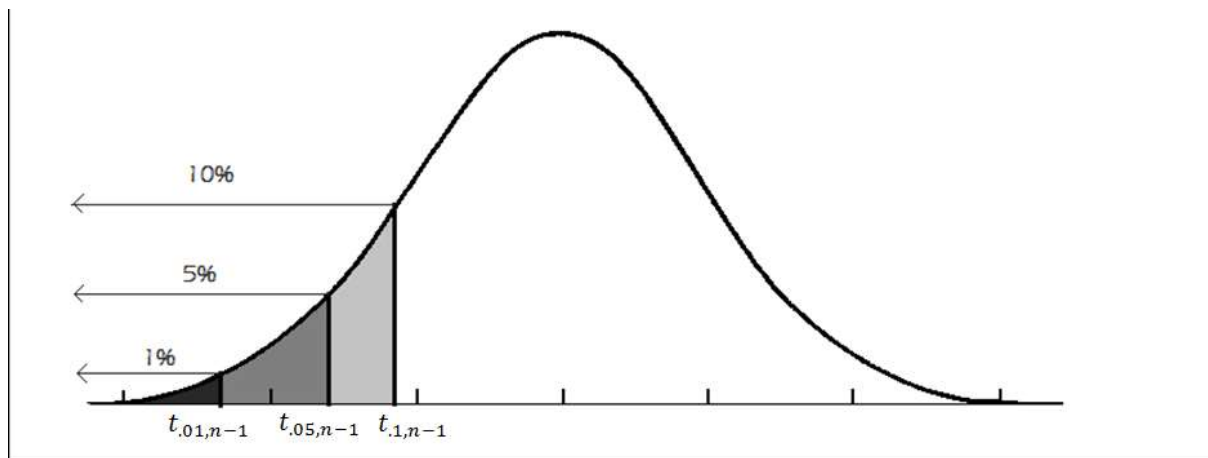
Zoom In



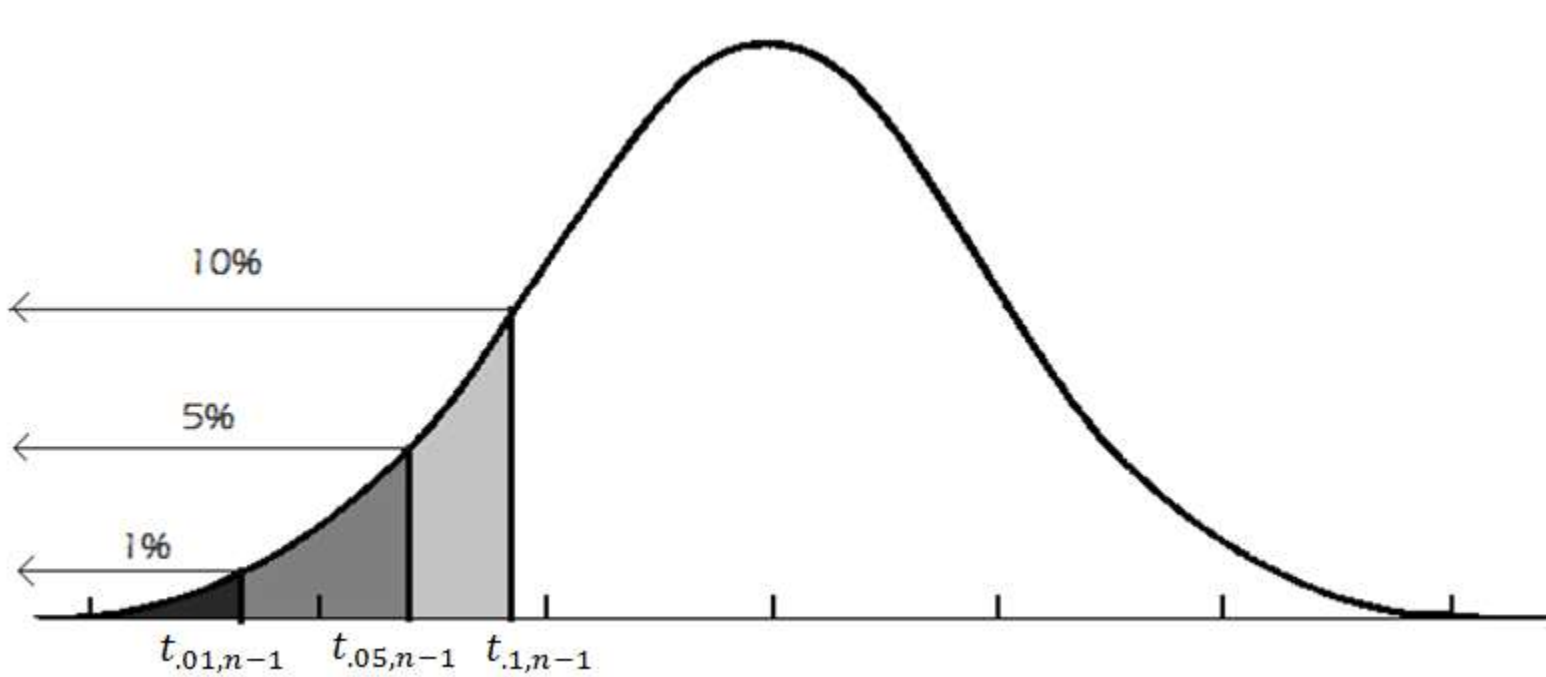
Hypothesis Test for Means– Step Five with Pictures when we don't know σ_x

- For a left tailed test: $H_a: \mu < \mu_o \rightarrow$ We have rejection regions for H_o are as follows

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat $< -t_{.10, n-1}$	P-value $< .1$
0.95	Test-stat $< -t_{.05, n-1}$	P-value $< .05$
0.99	Test-stat $< -t_{.01, n-1}$	P-value $< .01$



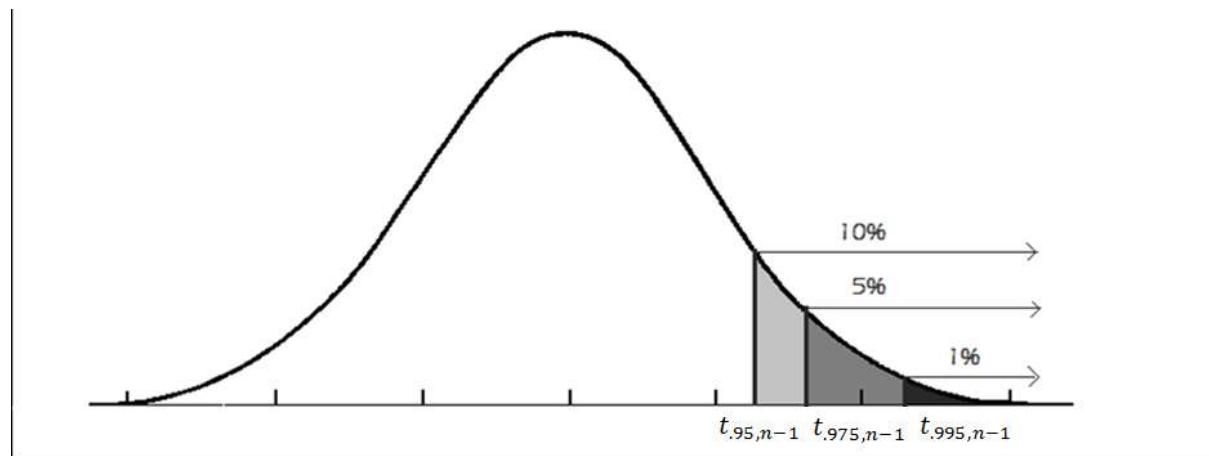
Zoom In



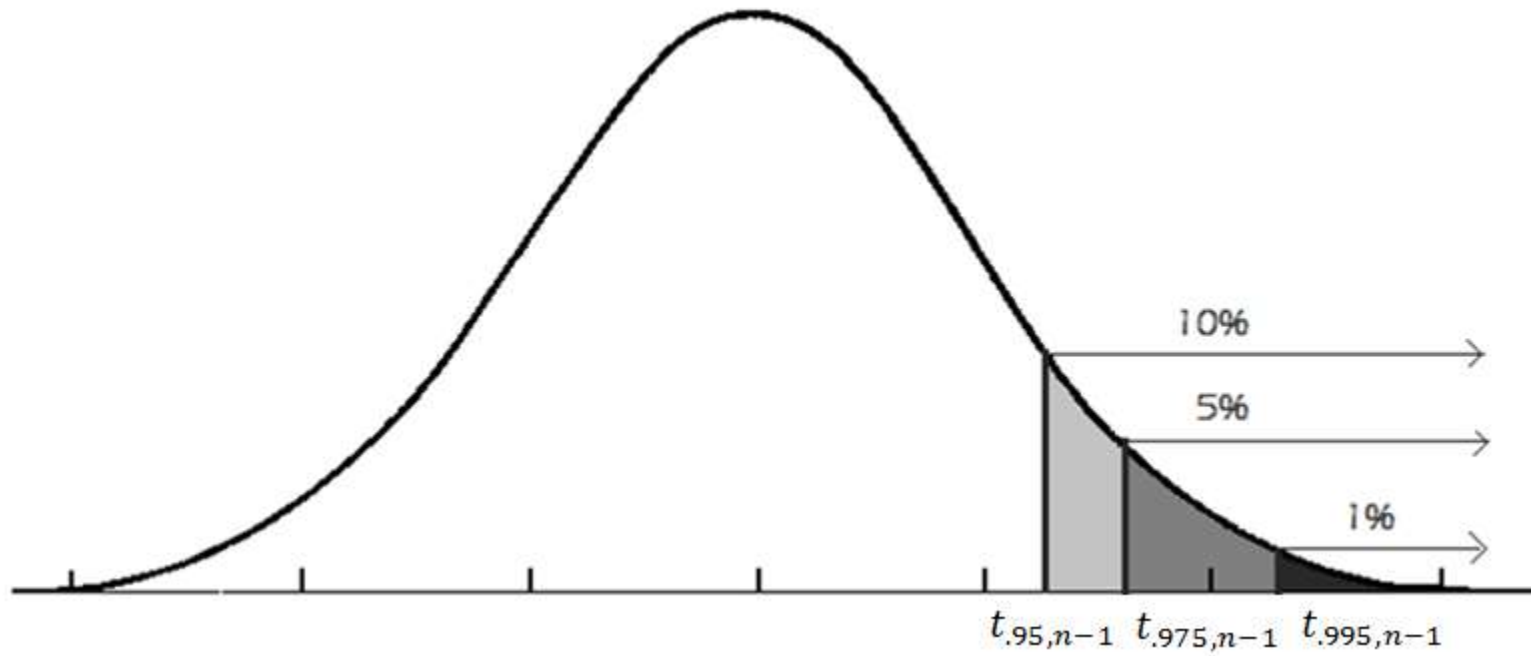
Hypothesis Test for Means– Step Five with Pictures when we don't know σ_x

- For a left tailed test: $H_a: \mu > \mu_0 \rightarrow$ We have rejection regions for H_0 are as follows

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat $< -t_{.90, n-1}$	P-value $< .1$
0.95	Test-stat $< -t_{.95, n-1}$	P-value $< .05$
0.99	Test-stat $< -t_{.99, n-1}$	P-value $< .01$



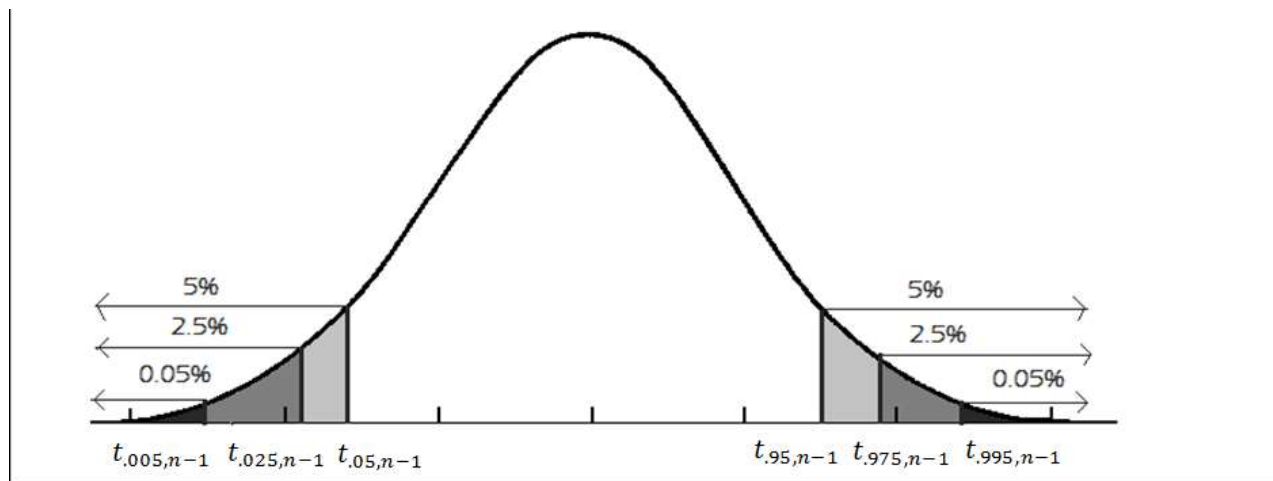
Zoom In



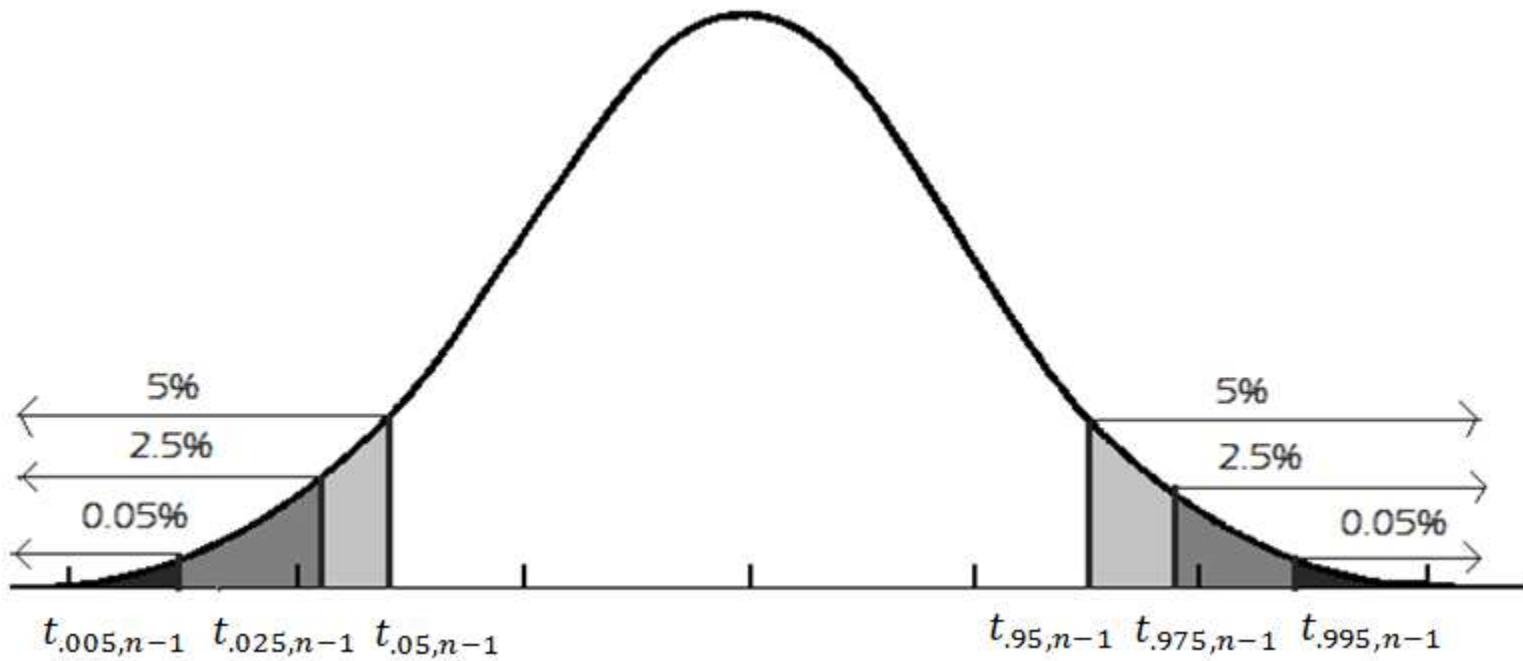
Hypothesis Test for Means– Step Five with Pictures when we don't know σ_x

- For a two tailed test: $H_a: \mu \neq \mu_o \rightarrow$ We have rejection regions for H_o are as follows

Confidence	Reject (test stat)	Reject (p-value)
0.90	$ \text{Test-stat} < -t_{.90, n-1}$	P-value < .1
0.95	$ \text{Test-stat} < -t_{.95, n-1}$	P-value < .05
0.99	$ \text{Test-stat} < -t_{.99, n-1}$	P-value < .01



Zoom In



Example

- Suppose a random sample of 38 yearly average temperature measures in New Haven, CT. Among the sampled years the **sample mean temperature was 51.0474** degrees Fahrenheit with a **sample standard deviation of 1.3112**.
- Test whether or not the population mean differs from 50 degrees at a .05 significance level, or 95% confidence.

Example – Step One

- State the Hypotheses: we are interested in whether or not the mean is **not equal to 50 degrees**
 - $H_o: \mu = 50$
 - $H_a: \mu \neq 50$

Example – Step Two

- Check Assumptions:
 - The data is quantitative
 - The sample is randomly selected
 - $n > 30$ so it is safe to assume the sampling distribution for the sample mean is normal

Example – Step Three

- Calculate Test Statistic

Variable	Sample Mean (\bar{x})	Standard Deviation (s_x)	Standard Error ($s_{\bar{x}}$)
Yearly Temperature	51.0474	1.3112	.2127047

$$t = \frac{(\bar{x} - \mu_o)}{\frac{s}{\sqrt{n}}} = \frac{51.0474 - 50}{\frac{1.3112}{\sqrt{38}}} = \frac{1.0474}{.2127047} = 4.924198$$

Example – Step Four

- Determine P-value

$$\begin{aligned} P \text{ value} &= 2 * P(T < -|t^*|) \\ &= 2 * P(T < -|4.924198|) \\ &= 2 * P(T < -4.924198) \\ &= 2 * pt(-4.924198, 38 - 1) \\ &= .00001782519 \end{aligned}$$

Example – Step Five

- State Conclusion

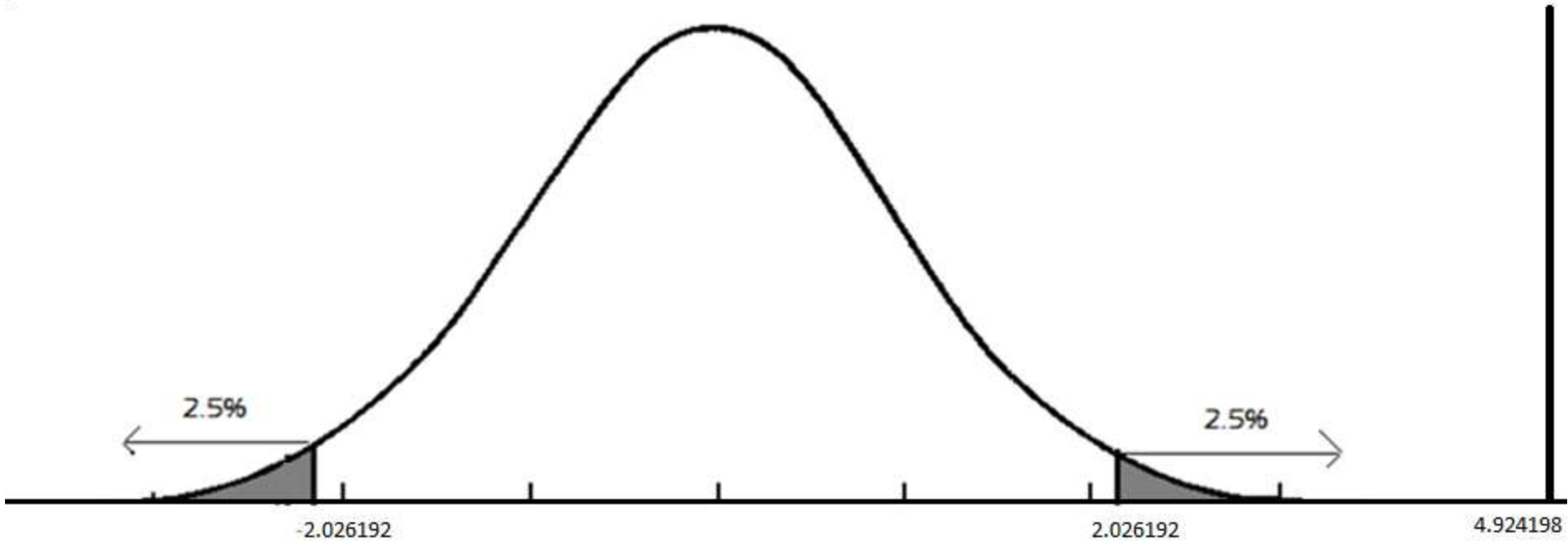
- Since $.00001782519 < .05$ we reject H_0

- At the .05 level of significance, or 95% confidence level, there is sufficient evidence that the mean yearly temperature is different than 50 degrees.

Example – Step Five with pictures

- State Conclusion
 - Anything with a p-value < .05 or a $|t\text{-value}| > t_{1-\frac{\alpha}{2}, n-1} = t_{.975, 37} = 2.026192$ will be in the rejection region
 - By P-value:
 - Since .00001782519 > .05 we reject H_0
 - By T-statistic:
 - Since $|4.924198| > 2.026192$ we reject H_0

Zoom In



Example

```
#TestType: 1 for <, 2 for >, 3 for not equal
M.Ttest<-function(conf.level,xbar,sx, n,m0,TestType){
  txt<-""; TestStat<-(xbar-m0)/(sx/sqrt(n)); xax<-seq(m0-5*(sx/sqrt(n)),m0+5*(sx/sqrt(n)),.01); P_x<-dt((xax-m0)/(sx/sqrt(n)),n-1);
  if(TestType==1){
    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep=""); CritVal<-qt(1-conf.level,n-1)*(sx/sqrt(n))+m0;
    pvalue<-pt(TestStat,n-1); cord.x <- seq(min(xax),CritVal,0.01); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright";
  }
  if(TestType==2){
    txt<-paste("Test Alternative: parameter > ",m0,"\n",sep=""); CritVal<-qt(conf.level,n-1)*(sx/sqrt(n))+m0;
    pvalue<-1-pt(TestStat,n-1); cord.x <- seq(CritVal,max(xax),0.01); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft";
  }
  if(TestType==3){
    txt<-paste("Test Alternative: parameter != ",m0,"\n",sep=""); CritVal1<-qt((1-conf.level)/2,n-1)*(sx/sqrt(n))+m0;
    CritVal2<-qt(conf.level+(1-conf.level)/2,n-1)*(sx/sqrt(n))+m0; pvalue=2*pt(-abs(TestStat),n-1); cord.x1 <- seq(min(xax),CritVal1,0.01);
    cord.x2 <- seq(CritVal2,max(xax),0.01); if(xbar<min(cord.x2)){loc<-"topright"}else{loc<-"topleft"}
    x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax));
  }
  if(n<30){ txt<-cat(txt,"Sample size assumptions not met; check if the population is normal.\n")}else{ txt<-cat(txt,"Sample size assumptions met.\n")}
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){
    txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep=""));txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
  }else{
    txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep=""));
  }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep="")); plot(xax,P_x,type='l'); lines(rep(xbar,2),c(0,max(P_x)),col="red");
  if(TestType==3){
    y.shade<- c(0,dt((cord.x1-m0)/(sx/sqrt(n)),n-1),0,0,dt((cord.x2-m0)/(sx/sqrt(n)),n-1),0);
  }else{
    y.shade<- c(0,dt((cord.x-m0)/(sx/sqrt(n)),n-1),0);
  }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Test Statistic"),fill=c("gray","red"));}
M.Ttest(.95,51.0474,1.3112,38,50,3);
```

Onto Hypothesis Testing for Variances

Hypothesis Test for Variance: Step 1

- **State Hypotheses:** it's usually easier to write the alternative hypothesis first
 - **Null hypothesis:** that the population variance equals some σ_0^2
 - $H_0: \sigma^2 \leq \sigma_0^2$ (one sided test)
 - $H_0: \sigma^2 \geq \sigma_0^2$ (one sided test)
 - $H_0: \sigma^2 = \sigma_0^2$ (two sided test)
 - **Alternative hypothesis:** What we're interested in
 - $H_a: \sigma^2 > \sigma_0^2$ (one sided test)
 - $H_a: \sigma^2 < \sigma_0^2$ (one sided test)
 - $H_a: \sigma^2 \neq \sigma_0^2$ (two sided test)

Hypothesis Test for Variance: Step 2

- Check the assumptions
 - The data are obtained using randomization
 - We're dealing with data from the normal distribution

Hypothesis Test for Variance: Step 3

- Calculate Test Statistic, χ^{2*}
 - The test statistic measures how different the sample variance we have is from the null hypothesis
 - We calculate the χ^2 -statistic by assuming that σ_0^2 is the population variance

$$\chi^{2*} = \frac{((n - 1)s^2)}{\sigma_0^2}$$

Hypothesis Test for Variance: Step 4

- Determine the P-value
 - The P-value describes how unusual the sample data would be if H_0 were true.
 - χ^{2*} is the test statistic from step 3

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \sigma^2 > \sigma_0^2$	Right tail	$1 - P(\chi^2 < \chi^{2*})$
$H_a: \sigma^2 < \sigma_0^2$	Left tail	$P(\chi^2 > \chi^{2*})$
$H_a: \sigma^2 \neq \sigma_0^2$	Two-tail	$2 * P(\chi^2 < - \chi^{2*})$

Hypothesis Test for Means: Step 5

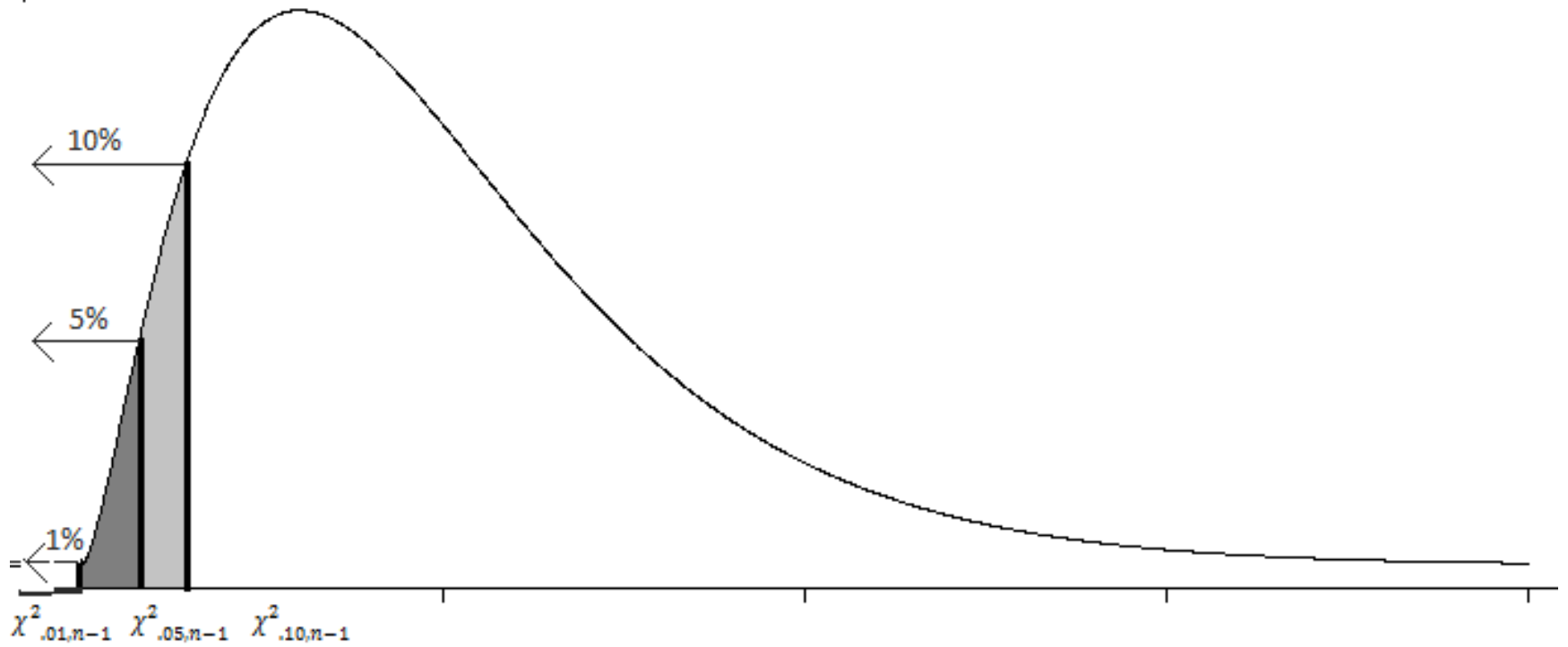
- Summarize the test by reporting and interpreting the P-value
 - Smaller p-values give stronger evidence against H_0
- If $p\text{-value} \leq (1 - \textit{confidence}) = \alpha$
 - Reject H_0 , with a p-value = _____, we have sufficient evidence that the alternative hypothesis might be true
- If $p\text{-value} > (1 - \textit{confidence}) = \alpha$
 - Fail to reject H_0 , with a p-value = _____, we do not have sufficient evidence that the alternative hypothesis might be true

Hypothesis Test for Variance– Step Five with Pictures when we don't know σ_x

- For a left tailed test: $H_a: \sigma^2 < \sigma_o^2 \rightarrow$ We have rejection regions for H_o are as follows

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat $< -\chi^2_{.10, n-1}$	P-value $< .1$
0.95	Test-stat $< -\chi^2_{.05, n-1}$	P-value $< .05$
0.99	Test-stat $< -\chi^2_{.01, n-1}$	P-value $< .01$

Zoom In

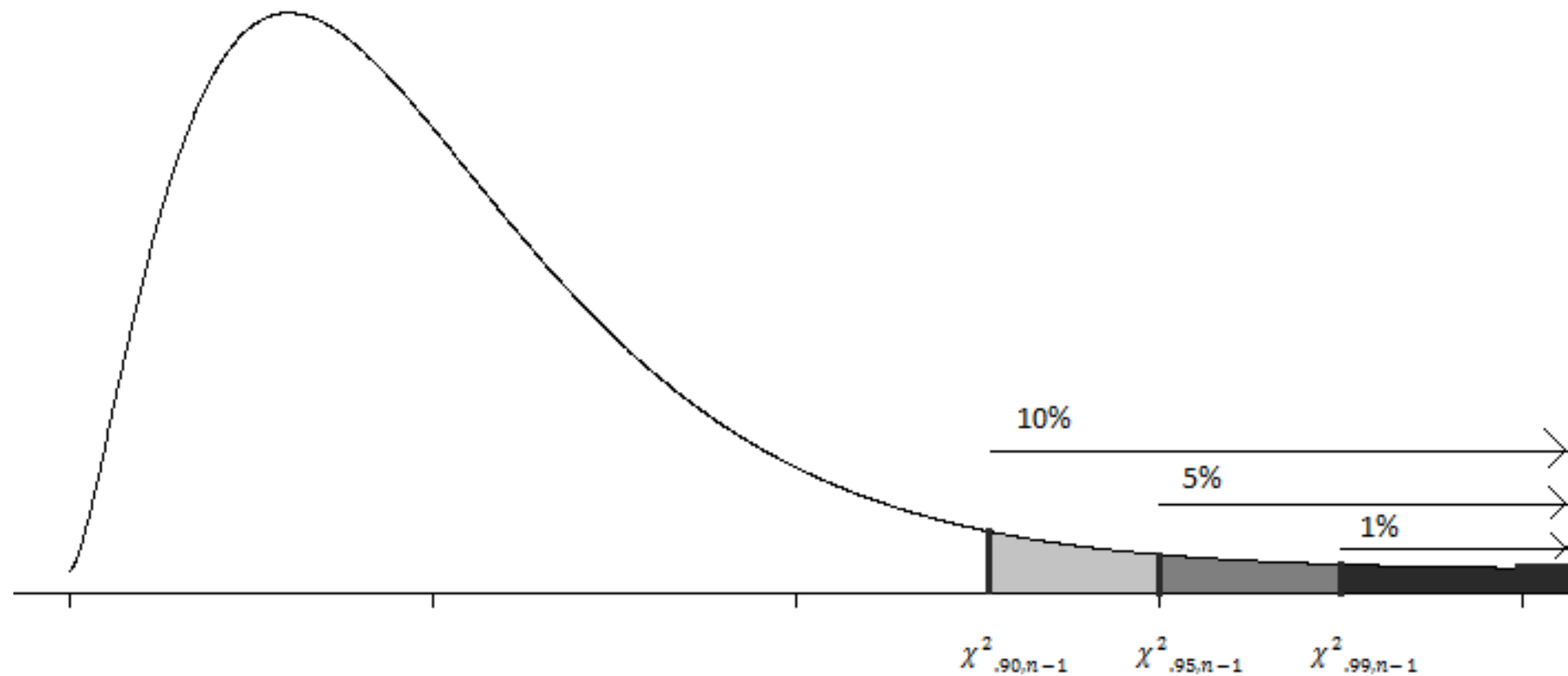


Hypothesis Test for Variance– Step Five with Pictures when we don't know σ_x

- For a left tailed test: $H_a: \sigma^2 > \sigma_o^2 \rightarrow$ We have rejection regions for H_o are as follows

Confidence	Reject (test stat)	Reject (p-value)
0.90	Test-stat $< \chi^2_{.90, n-1}$	P-value $< .1$
0.95	Test-stat $< \chi^2_{.95, n-1}$	P-value $< .05$
0.99	Test-stat $< \chi^2_{.99, n-1}$	P-value $< .01$

Zoom In



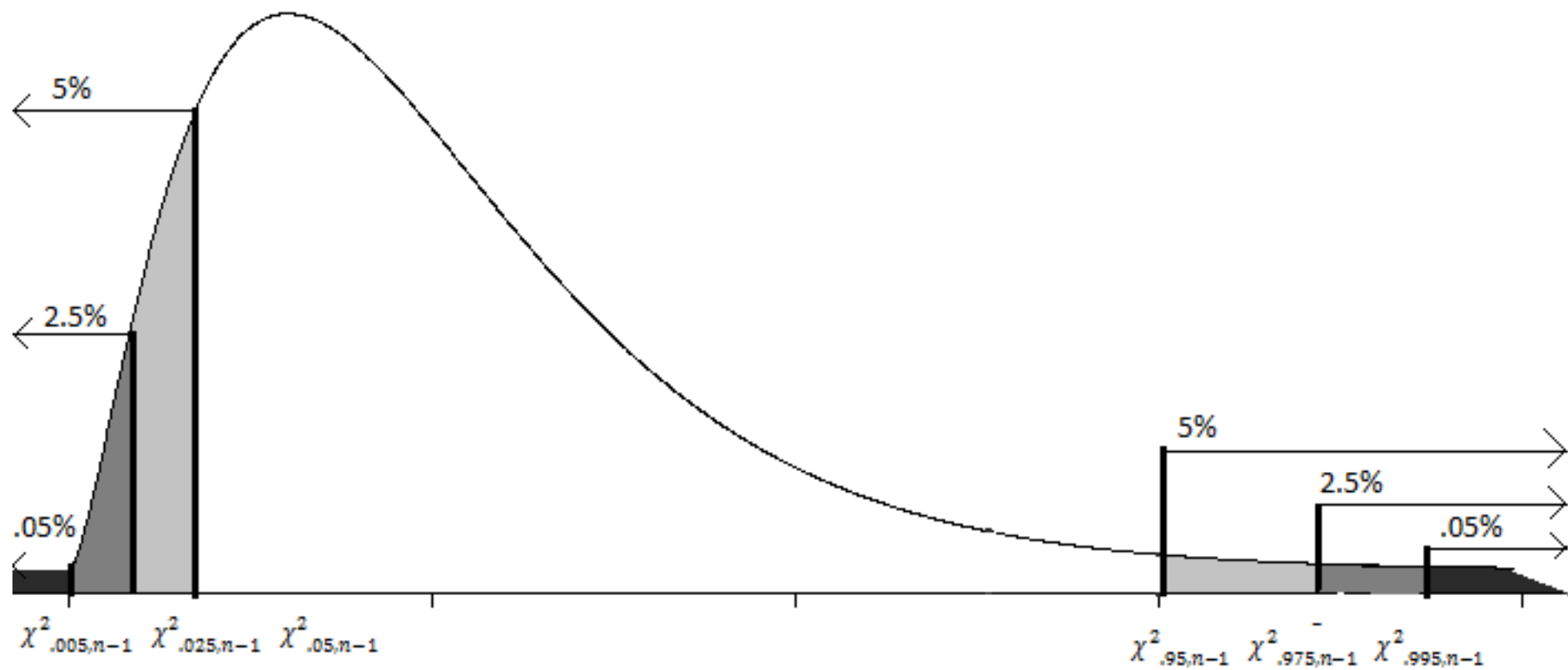
Hypothesis Test for Variance– Step Five with Pictures when we don't know σ_x

- For a two tailed test: $H_a: \sigma^2 \neq \sigma_o^2 \rightarrow$ We have rejection regions for H_o are as follows

$$\chi^2_{.005, n-1} \quad \chi^2_{.025, n-1} \quad \chi^2_{.05, n-1}$$

Confidence	Reject (test stat)	Reject (p-value)
0.90	$ \text{Test-stat} < \chi^2_{.95, n-1}$	P-value < .1
0.95	$ \text{Test-stat} < \chi^2_{.975, n-1}$	P-value < .05
0.99	$ \text{Test-stat} < \chi^2_{.995, n-1}$	P-value < .01

Zoom In



Example

- Suppose a random sample of 38 yearly average temperature measures in New Haven, CT. Among the sampled years the sample mean temperature was 51.0474 degrees Fahrenheit with a sample standard deviation of 1.3112.
- Test at the .05 significance level that σ_x^2 is **greater than 1.5**

Example: Step 1

- **State Hypotheses:**

- $H_o: \sigma^2 \leq \sigma_o^2$

- $H_a: \sigma^2 > \sigma_o^2$

Example: Step 2

- Check the assumptions
 - The data are obtained using randomization
 - We're dealing with data from the normal distribution

Example: Step 3

- Calculate Test Statistic, χ^{2*}

$$\chi^{2*} = \frac{\left((38 - 1) 1.3112^2 \right)}{1.5^2} = 28.27204$$

Example: Step 4

- Determine the P-value

$$\begin{aligned} 1-P(\chi^2 < \chi^{2*}) &= 1 - \text{pchisq}(28.27204, 38 - 1) \\ &= .8481018 \end{aligned}$$

Example: Step 5

- Summarize the test by reporting and interpreting the P-value
- $.8481018 > (1 - .95) = .05$
 - Fail to reject H_0 , with a p-value = $.8481018$, we do not have sufficient evidence that the alternative hypothesis might be true

Example

```
#TestType: 1 for <, 2 for >, 3 for not equal
var.test<-function(conf.level,sampleVar,n,var0,TestType){
  txt<-""; TestStat<-((n-1)*sampleVar)/var0; chisq.critL = qchisq(.9995,n-1); chisq.critU = qchisq(.0005,n-1);
  lower=(n-1)*(sampleVar)/chisq.critL; upper=(n-1)*(sampleVar)/chisq.critU; xax<-seq(lower,upper,.01);
  P_x<-dchisq(((n-1)*xax)/var0,n-1);
  if(TestType==1){ txt<-paste("Test Alternative: parameter < ",var0,"\n",sep=""); CritVal<-(n-
1)*(sampleVar)/qchisq(conf.level,n-1);
  pvalue<-pchisq(TestStat,n-1); cord.x <- seq(min(xax),CritVal,0.01); x.shade <- c(min(xax),cord.x,CritVal); loc<-
"topright"; }
  if(TestType==2){ txt<-paste("Test Alternative: parameter > ",var0,"\n",sep=""); CritVal<-(n-
1)*(sampleVar)/qchisq(1-conf.level,n-1);
  pvalue<-1-pchisq(TestStat,n-1); cord.x <- seq(CritVal,max(xax),0.01); x.shade <- c(CritVal,cord.x,max(xax));
loc<-"topleft"; }
  if(TestType==3){ txt<-paste("Test Alternative: parameter !=",var0,"\n",sep=""); CritVal1<-(n-
1)*(sampleVar)/qchisq((1-conf.level)/2,n-1);
  CritVal2<-(n-1)*(sampleVar)/qchisq(conf.level+(1-conf.level)/2,n-1); pvalue=min(2*(1-pchisq(TestStat,n-1)),2*(1-
pchisq(TestStat,n-1)));
  cord.x1 <- seq(min(xax),CritVal1,0.01); cord.x2 <- seq(CritVal2,max(xax),0.01); loc<-"topright";
  x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax)); }
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){ txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep="")); txt<-cat(txt,paste("Upper
Critical Value: ",CritVal2,"\n",sep=""));
  }else{ txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep="")); }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep=""));
  plot(xax,P_x,type='l'); lines(rep(sampleVar,2),c(0,max(P_x)),col="red");
  if(TestType==3){ y.shade<- c(0,dchisq(((n-1)*cord.x1)/var0,n-1),0,0,dchisq(((n-1)*cord.x2)/var0,n-1),0);
  }else{ y.shade<- c(0,dchisq(((n-1)*cord.x)/var0,n-1),0) }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));
  #####
}
var.test(.95,1.3112,38,1.3,2)
```

Summaries

Hypothesis Testing for ρ

Step One:	(i) $H_0: p = p_0$ & $H_a: p \neq p_0$ (ii) $H_0: p \geq p_0$ & $H_a: p < p_0$ (iii) $H_0: p \leq p_0$ & $H_a: p > p_0$
Step Two:	1. Categorical 2. Random 3. $np_0 \geq 15$ & $n(1 - p_0) \geq 15$
Step Three:	$z^* = \frac{(\hat{p} - p_0)}{\sqrt{\frac{p_0(1 - p_0)}{n}}}$
Step Four:	(i) $H_a: p \neq p_0 \rightarrow$ p-value = $2 * P(Z < - z^*)$ (ii) $H_a: p < p_0 \rightarrow$ p-value = $P(Z < z^*)$ (iii) $H_a: p > p_0 \rightarrow$ p-value = $P(Z > z^*) = 1 - P(Z < z^*)$
Step Five:	If p-value $\leq (1 - \text{confidence}) = \alpha$ \rightarrow Reject H_0 If p-value $> (1 - \text{confidence}) = \alpha$ \rightarrow Fail to Reject H_0

Hypothesis Testing for ρ

```
#TestType: 1 for <, 2 for >, 3 for not equal
p.test<-function(conf.level,x,n,p0,TestType){
  txt<-""; phat<-x/n; TestStat<-(phat-p0)/sqrt(p0*(1-p0)/n); xax<-seq(p0-5*sqrt(p0*(1-p0)/n),p0+5*sqrt(p0*(1-p0)/n),.001);
  P_x<-dnorm(xax,p0,sqrt(p0*(1-p0)/n));
  if(TestType==1){ txt<-paste("Test Alternative: parameter < ",p0,"\n",sep=""); CritVal<-qnorm(1-conf.level,p0,sqrt(p0*(1-p0)/n));
    pvalue<-pnorm(TestStat,0,1); cord.x <- seq(min(xax),CritVal,0.001); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright";}
  if(TestType==2){ txt<-paste("Test Alternative: parameter > ",p0,"\n",sep=""); CritVal<-qnorm(conf.level,p0,sqrt(p0*(1-p0)/n));
    pvalue<-1-pnorm(TestStat,0,1); cord.x <- seq(CritVal,max(xax),0.001); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft";}
  if(TestType==3){ txt<-paste("Test Alternative: parameter !=",p0,"\n",sep=""); CritVal1<-qnorm((1-conf.level)/2,p0,sqrt(p0*(1-p0)/n));
    CritVal2<-qnorm(conf.level+(1-conf.level)/2,p0,sqrt(p0*(1-p0)/n)); pvalue=2*pnorm(-abs(TestStat),0,1); cord.x1 <- seq(min(xax),CritVal1,0.001);
    cord.x2 <- seq(CritVal2,max(xax),0.001); x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax));
    if(phat<min(cord.x2)){ loc<-"topright" }else{ loc<-"topleft" } }
  if(n*phat<15|n*(1-phat)<15){ txt<-cat(txt,"Sample size assumptions not met.\n") }else{ txt<-cat(txt,"Sample size assumptions met.\n") }
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){ txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep="")); txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
  }else{ txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep="")); }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep=""));
  plot(xax,P_x,type='l');
  lines(rep(phat,2),c(0,max(P_x)),col="red");
  if(TestType==3){ y.shade<-c(0,dnorm(cord.x1,p0,sqrt(p0*(1-p0)/n)),0,0,dnorm(cord.x2,p0,sqrt(p0*(1-p0)/n)),0) }else{ y.shade<-c(0,dnorm(cord.x,p0,sqrt(p0*(1-
p0)/n)),0) }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Test Statistic"),fill=c("gray","red")) ;}
```

Hypothesis Testing for μ known σ_x

Step One:	<p>(i) $H_0: \mu = \mu_0$ & $H_a: \mu \neq \mu_0$</p> <p>(ii) $H_0: \mu \geq \mu_0$ & $H_a: \mu < \mu_0$</p> <p>(iii) $H_0: \mu \leq \mu_0$ & $H_a: \mu > \mu_0$</p>
Step Two:	<ol style="list-style-type: none"> 1. Quantitative 2. <i>Random Sample</i> 3. $n > 30$ OR the population is bell shaped
Step Three:	$z^* = \frac{(\bar{x} - \mu_0)}{\frac{\sigma_x}{\sqrt{n}}}$
Step Four:	<p>(i) $H_a: \mu \neq \mu_0 \rightarrow$ p-value = $2 * P(Z < - z^*)$</p> <p>(ii) $H_a: \mu < \mu_0 \rightarrow$ p-value = $P(Z < z^*)$</p> <p>(iii) $H_a: \mu > \mu_0 \rightarrow$ p-value = $P(Z > z^*) = 1 - P(Z < z^*)$</p>
Step Five:	<p>If p-value $\leq (1 - \text{confidence}) = \alpha$ \rightarrow Reject H_0</p> <p>If p-value $> (1 - \text{confidence}) = \alpha$ \rightarrow Fail to Reject H_0</p>

Hypothesis Testing for μ known σ_x

```
#TestType: 1 for <, 2 for >, 3 for not equal
m.Ztest<-function(conf.level,xbar,sigma,n,m0,TestType){
  txt<-""; TestStat<-(xbar-m0)/(sigma/sqrt(n)); xax<-seq(m0-5*(sigma/sqrt(n)),m0+5*(sigma/sqrt(n)),.01); P_x<-dnorm(xax,m0,(sigma/sqrt(n)));
  if(TestType==1){ txt<-paste("Test Alternative: parameter < ",m0,"\n",sep=""); CritVal<-qnorm(1-conf.level,m0,(sigma/sqrt(n)));
    pvalue<-pnorm(TestStat,0,1); cord.x <- seq(min(xax),CritVal,0.01); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright"; }
  if(TestType==2){ txt<-paste("Test Alternative: parameter > ",m0,"\n",sep=""); CritVal<-qnorm(conf.level,m0,(sigma/sqrt(n)));
    pvalue<-1-pnorm(TestStat,0,1); cord.x <- seq(CritVal,max(xax),0.01); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft"; }
  if(TestType==3){ txt<-paste("Test Alternative: parameter != ",m0,"\n",sep=""); CritVal1<-qnorm((1-conf.level)/2,m0,(sigma/sqrt(n)));
    CritVal2<-qnorm(conf.level+(1-conf.level)/2,m0,(sigma/sqrt(n))); pvalue=2*pnorm(-abs(TestStat),0,1);
    cord.x1 <- seq(min(xax),CritVal1,0.01); cord.x2 <- seq(CritVal2,max(xax),0.01); x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax));
    if(xbar<min(cord.x2)){ loc<-"topright"; }else{ loc<-"topleft"; } }
  if(n*xbar<15|n*(1-xbar)<15){ txt<-cat(txt,"Sample size assumptions not met.\n"); }else{ txt<-cat(txt,"Sample size assumptions met.\n"); }
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){ txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep="")); txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
  }else{ txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep="")); }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep="")); plot(xax,P_x,type='l'); lines(rep(xbar,2),c(0,max(P_x)),col="red");
  if(TestType==3){ y.shade<-c(0,dnorm(cord.x1,m0,(sigma/sqrt(n))),0,0,dnorm(cord.x2,m0,(sigma/sqrt(n))),0) ;
  }else{ y.shade<-c(0,dnorm(cord.x,m0,(sigma/sqrt(n))),0); }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Test Statistic"),fill=c("gray","red")) ;}
m.Ztest(.95,51.0474,1.3112,38,50,2);
```

Hypothesis Testing for μ unknown σ_x

Step One:	<p>(i) $H_0: \mu = \mu_0$ & $H_a: \mu \neq \mu_0$</p> <p>(ii) $H_0: \mu \geq \mu_0$ & $H_a: \mu < \mu_0$</p> <p>(iii) $H_0: \mu \leq \mu_0$ & $H_a: \mu > \mu_0$</p>
Step Two:	<ol style="list-style-type: none"> 1. Quantitative 2. <i>Random Sample</i> 3. $n > 30$ OR the population is bell shaped
Step Three:	$t^* = \frac{(\bar{x} - \mu_0)}{\frac{s_x}{\sqrt{n}}}$
Step Four:	<p>(i) $H_a: \mu \neq \mu_0 \rightarrow$ p-value = $2 * P(T < - t^*)$</p> <p>(ii) $H_a: \mu < \mu_0 \rightarrow$ p-value = $P(T < t^*)$</p> <p>(iii) $H_a: \mu > \mu_0 \rightarrow$ p-value = $P(T > t^*) = 1 - P(T < t^*)$</p>
Step Five:	<p>If p-value $\leq (1 - \text{confidence}) = \alpha$ \rightarrow Reject H_0</p> <p>If p-value $> (1 - \text{confidence}) = \alpha$ \rightarrow Fail to Reject H_0</p>

Hypothesis Testing for μ unknown σ_x

```
#TestType: 1 for <, 2 for >, 3 for not equal
M.Ttest<-function(conf.level,xbar,sx, n,m0,TestType){
txt<-""; TestStat<-(xbar-m0)/(sx/sqrt(n)); xax<-seq(m0-5*(sx/sqrt(n)),m0+5*(sx/sqrt(n)),.001); P_x<-dt((xax-m0)/(sx/sqrt(n)),n-1);
if(TestType==1){
  txt<-paste("Test Alternative: parameter < ",m0,"\n",sep=""); CritVal<-qt(1-conf.level,n-1)*(sx/sqrt(n))+m0;
  pvalue<-pt(TestStat,n-1); cord.x <- seq(min(xax),CritVal,0.001); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright";
}
if(TestType==2){
  txt<-paste("Test Alternative: parameter > ",m0,"\n",sep=""); CritVal<-qt(conf.level,n-1)*(sx/sqrt(n))+m0;
  pvalue<-1-pt(TestStat,n-1); cord.x <- seq(CritVal,max(xax),0.001); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft";
}
if(TestType==3){
  txt<-paste("Test Alternative: parameter !=",m0,"\n",sep=""); CritVal1<-qt((1-conf.level)/2,n-1)*(sx/sqrt(n))+m0;
  CritVal2<-qt(conf.level+(1-conf.level)/2,n-1)*(sx/sqrt(n))+m0; pvalue=2*pt(-abs(TestStat),n-1); cord.x1 <- seq(min(xax),CritVal1,0.001);
  cord.x2 <- seq(CritVal2,max(xax),0.001); if(xbar<min(cord.x2)){loc<-"topright"}else{loc<-"topleft"}
  x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax));
}
if(n<30){ txt<-cat(txt,"Sample size assumptions not met; check if the population is normal.\n")}else{ txt<-cat(txt,"Sample size assumptions met.\n")}
txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
if(TestType==3){
  txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep=""));txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
}else{
  txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep=""));
}
txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep="")); plot(xax,P_x,type='l'); lines(rep(xbar,2),c(0,max(P_x)),col="red");
if(TestType==3){
  y.shade<- c(0,dt((cord.x1-m0)/(sx/sqrt(n)),n-1),0,0,dt((cord.x2-m0)/(sx/sqrt(n)),n-1),0);
}else{
  y.shade<- c(0,dt((cord.x-m0)/(sx/sqrt(n)),n-1),0);
}
polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Test Statistic"),fill=c("gray","red"));
```

Hypothesis Testing For σ_x

Step One:	<p>(i) $H_0: \sigma^2 = \sigma_0^2$ & $H_a: \sigma^2 \neq \sigma_0^2$</p> <p>(ii) $H_0: \sigma^2 \geq \sigma_0^2$ & $H_a: \sigma^2 < \sigma_0^2$</p> <p>(iii) $H_0: \sigma^2 \leq \sigma_0^2$ & $H_a: \sigma^2 > \sigma_0^2$</p>
Step Two:	<ol style="list-style-type: none"> 1. Random Sample 2. We're dealing with data from the normal distribution
Step Three:	$\chi^{2*} = \frac{((n - 1)s^2)}{\sigma_0^2}$
Step Four:	<p>(i) $H_a: \sigma^2 \neq \sigma_0^2 \rightarrow$ p-value = $2 * P(\chi^2 < - \chi^{2*})$</p> <p>(ii) $H_a: \sigma^2 < \sigma_0^2 \rightarrow$ p-value = $P(\chi^2 < \chi^{2*})$</p> <p>(iii) $H_a: \sigma^2 > \sigma_0^2 \rightarrow$ p-value = $1 - P(\chi^2 < \chi^{2*})$</p>
Step Five:	<p>If p-value $\leq (1 - \text{confidence}) = \alpha$ \rightarrow Reject H_0</p> <p>If p-value $> (1 - \text{confidence}) = \alpha$ \rightarrow Fail to Reject H_0</p>

Hypothesis Testing For σ_x

```
#TestType: 1 for <, 2 for >, 3 for not equal
var.test<-function(conf.level,sampleVar,n,var0,TestType){
  txt<-""; TestStat<-((n-1)*sampleVar)/var0; chisq.critL = qchisq(.995,n-1); chisq.critU = qchisq(.005,n-1);
  lower=(n-1)*(sampleVar)/chisq.critL; upper=(n-1)*(sampleVar)/chisq.critU; xax<-seq(lower,upper,.01);
  P_x<-dchisq(((n-1)*xax)/var0,n-1);
  if(TestType==1){ txt<-paste("Test Alternative: parameter < ",var0,"\n",sep=""); CritVal<-(n-1)*(sampleVar)/qchisq(conf.level,n-1);
    pvalue<-pchisq(TestStat,n-1); cord.x <- seq(min(xax),CritVal,0.01); x.shade <- c(min(xax),cord.x,CritVal); loc<-"topright"; }
  if(TestType==2){ txt<-paste("Test Alternative: parameter > ",var0,"\n",sep=""); CritVal<-(n-1)*(sampleVar)/qchisq(1-conf.level,n-1);
    pvalue<-1-pchisq(TestStat,n-1); cord.x <- seq(CritVal,max(xax),0.01); x.shade <- c(CritVal,cord.x,max(xax)); loc<-"topleft"; }
  if(TestType==3){ txt<-paste("Test Alternative: parameter !=",var0,"\n",sep=""); CritVal1<-(n-1)*(sampleVar)/qchisq((1-conf.level)/2,n-1);
    CritVal2<-(n-1)*(sampleVar)/qchisq(conf.level+(1-conf.level)/2,n-1); pvalue=min(2*(1-pchisq(TestStat,n-1)),2*(1-pchisq(TestStat,n-1)));
    cord.x1 <- seq(min(xax),CritVal1,0.01); cord.x2 <- seq(CritVal2,max(xax),0.01); loc<-"topright";
    x.shade <- c(min(xax),cord.x1,CritVal1,CritVal2,cord.x2,max(xax)); }
  txt<-cat(txt,paste("Test Statistic: ",TestStat,"\n",sep=""));
  if(TestType==3){ txt<-cat(txt,paste("Lower Critical Value: ",CritVal1,"\n",sep="")); txt<-cat(txt,paste("Upper Critical Value: ",CritVal2,"\n",sep=""));
  }else{ txt<-cat(txt,paste("Critical Value: ",CritVal,"\n",sep="")); }
  txt<-cat(txt,paste("P Value: ",pvalue,"\n",sep=""));
  plot(xax,P_x,type='l'); lines(rep(sampleVar,2),c(0,max(P_x)),col="red");
  if(TestType==3){ y.shade<- c(0,dchisq(((n-1)*cord.x1)/var0,n-1),0,0,dchisq(((n-1)*cord.x2)/var0,n-1),0);
  }else{ y.shade<- c(0,dchisq(((n-1)*cord.x)/var0,n-1),0) }
  polygon(x.shade,y.shade,col='gray'); legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));
  #####
}
```