Stat 515:
Introduction to Statistics

Chapter 9

Telling Which Parameter We’re After

- As statisticians, or data scientists, it’s our job to hear a problem and decide what we’re after
  - We call the parameter of interest the **target parameter**

Parameter	Point Estimate	Key Phrase	Type of Data
$\mu_1 - \mu_2$	$\overline{x_1} - \overline{x_2}$	Mean Difference	Quantitative
$\rho_1 - \rho_2$	$\widehat{p_1} - \widehat{p_2}$	Difference of Proportion, percentage, fraction, rate	Qualitative (Categorical)
σ_1^2/σ_2^2	s_1^2/s_2^2	Ratio of Variance, variability, spread	Quantitative

Sampling Distributions for the Difference of Sample Proportions

- The mean of the sampling distribution for the difference of sample proportions will always equal the difference of the population proportions: $\boldsymbol{\mu_{\widehat{p_1}-\widehat{p_2}} = \rho_1 - \rho_2}$
- The standard error, the standard deviation of the difference of sample proportion, is:

$$\boldsymbol{\sigma_{\widehat{p}} = \sqrt{\frac{\rho_1(1-\rho_1)}{n_1} + \frac{\rho_2(1-\rho_2)}{n_2}}}$$

Confidence Intervals: Step One

- **<u>Assumptions:</u>**
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. If all of the following are true
     - $n_1\widehat{p_1} \geq 15$
     - $n_1(1-\widehat{p_1}) \geq 15$
     - $n_2\widehat{p_2} \geq 15$
     - $n_2(1-\widehat{p_2}) \geq 15$

Confidence Intervals: Step Two

- $\widehat{p_1} - \widehat{p_2}$ is our **point-estimate** for the difference of the population proportions
- We consider $\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$ when we don't know ρ_1 and ρ_2 for the standard error as $\widehat{p_1}$ and $\widehat{p_2}$ can estimate the values of ρ_1 and ρ_2

Confidence Intervals: Step Two

- $\widehat{p_1} - \widehat{p_2}$ is our **point-estimate** for the difference of the population proportions
  - Our 'best' guess for the true difference of the population proportions, $\rho_1 - \rho_2$, is our difference of sample proportions, $\widehat{p_1} - \widehat{p_2}$.

Confidence Intervals: Step Two

- $z_{\left(1-\frac{\alpha}{2}\right)}\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1}+\frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$ is our **margin of error**
  - $z_{1-\frac{\alpha}{2}}$ is the **confidence coefficient** and is the z value such that $P\left(Z < z_{\left(1-\frac{\alpha}{2}\right)}\right) = 1 - \frac{\alpha}{2}$
  - $\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1}+\frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$ is the **estimated std. dev.**

Confidence Intervals – Step Two

- The most common values of Z are listed below
  - **Level of confidence** = (1-∝) * 100%
  - **Error Probability** = ∝ = 1- Level of confidence

Confidence	**Error Probability (∝)**	$z_{\left(1-\frac{\alpha}{2}\right)}$ **From Table**	$z_{\left(1-\frac{\alpha}{2}\right)}$ **From R**
.9	.1	1.645	1.644854
.95	.05	1.96	1.959964
.99	.01	2.58	2.57829

  - Our interval will get larger when the margin of error increases
    1) When we increase confidence → increase z → widen interval
    2) When we decrease confidence → decrease z → narrow interval

Confidence Intervals: Step Two

- $z_{\left(1-\frac{\alpha}{2}\right)}\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1}+\frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$ is our **margin of error**
  - **As n increases**, the margin of error decreases causing the width of the confidence interval to narrow
  - **As n decreases**, the margin of error increases causing the width of the confidence interval to grow wider

Confidence Intervals: Margin of Error

- $z_{\left(1-\frac{\alpha}{2}\right)}\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1}+\frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals Bounds

$$(\widehat{p_1} - \widehat{p_2}) \pm z_{\left(1-\frac{\alpha}{2}\right)} \sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$$

Lower Bound

$$=(\widehat{p_1} - \widehat{p_2}) - z_{\left(1-\frac{\alpha}{2}\right)} \sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$$

Upper Bound

$$=(\widehat{p_1} - \widehat{p_2}) + z_{\left(1-\frac{\alpha}{2}\right)} \sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$$

Confidence Intervals Bounds

$$(\widehat{p_1} - \widehat{p_2}) \pm z_{\left(1-\frac{\alpha}{2}\right)} \sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$$

“We are <u>--%</u> confident that the true difference of population proportions,$\boldsymbol{\rho_1 - \rho_2}$, is between the <u>lower bound</u> and <u>upper bound</u>.”

Confidence Intervals Bounds

- If all the values on the interval are negative then $\rho_1 < \rho_2$

- If all the values on the interval are positive then $\rho_1 > \rho_2$

- If 0 is on the interval then it's possible that $\rho_1 = \rho_2$

Example

- 6,450 transgender and gender non-conforming study participants were asked about whether or not they maintained their family bonds.
- 2773 maintained their family ties of which 887 had attempted suicide
- 3677 experienced rejection from their family of which 1,875 had attempted suicide

Example

- 2773 maintained their family ties of which 887 had attempted suicide

$$\widehat{p_1} = \frac{887}{2773} = .31987$$

- 3677 experienced rejection from their family of which 1,875 had attempted suicide

$$\widehat{p_2} = \frac{1875}{3677} = .50993$$

Example

- **Assumptions:**
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. If all of the following are true
     - $2773\widehat{p_1} = 887 \geq 15$
     - $2773(1-\widehat{p_1}) = 1886 \geq 15$
     - $3677\widehat{p_2} = 1875 \geq 15$
     - $3677(1-\widehat{p_2}) = 1802 \geq 15$

Example

Find a 95% for the true difference of population proportions:

$$(\widehat{p_1} - \widehat{p_2}) \pm z_{\left(1-\frac{\alpha}{2}\right)} \sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1} + \frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$$

$$(.31987 - .50993) \pm (1.959964) \sqrt{\frac{.31987(1-.31987)}{2773} + \frac{.50993(1-.50993)}{3677}}$$

$$(-.2137762 - .1663438)$$

Example

$$(-.2137762 - .1663438)$$

All the values on the interval are negative. This indicates $\rho_1 < \rho_2$ - that the population proportion of transgender and gender non-conforming people who are rejected by their family are more likely to attempt suicide than those that maintained their family ties

Example in R

Below is a function you can load into R:

```
diffprop.int<-function(conf.level, x1, n1,x2,n2){
  phat1=x1/n1
  phat2=x2/n2
  phatd = phat1-phat2
  z.crit = qnorm(1-(1-conf.level)/2);
  std.error = sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2);
  MOE=z.crit*std.error;
  c(phatd-MOE, phatd+MOE)
}
```

```
> diffprop.int(.95,887,2773,1875,3677)
[1] -0.2137726 -0.1663402
```

Hypothesis Test for Proportion Differences: Step 1

- State Hypotheses:
  - **Null hypothesis**: that the population proportion equals some p_o
    - H_o: $\rho_d = \rho_1 - \rho_2 \leq p_0$ (one sided test)
    - H_o: $\rho_d = \rho_1 - \rho_2 \geq p_0$ (one sided test)
    - H_o: $\rho_d = \rho_1 - \rho_2 = p_0$ (two sided test)
  - **Alternative hypothesis:** What we're interested in
    - H_a: $\rho_d = \rho_1 - \rho_2 > p_o$ (one sided test)
    - H_a: $\rho_d = \rho_1 - \rho_2 < p_o$ (one sided test)
    - Ha: $\rho_d = \rho_1 - \rho_2 \neq p_o$ (two sided test)

Hypothesis Test for Proportion Differences: Step 2

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. If all of the following are true
     - $n_1\widehat{p_1} \geq 15$
     - $n_1(1-\widehat{p_1}) \geq 15$
     - $n_2\widehat{p_2} \geq 15$
     - $n_2(1-\widehat{p_2}) \geq 15$

Hypothesis Test for Proportion Differences: Step 3

- **Calculate Test Statistic**
  - The test statistic measures how different the sample proportion we have is from the null hypothesis
  - We calculate the z-statistic by assuming that ${p_d}_0$ is the population proportion difference

$$z^* = \frac{((\hat{p}_1 - \hat{p}_2) - p_0)}{\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}}$$

Hypothesis Test for Proportion Differences: Step 4

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	**Probability**	**Formula for the P-value**
$H_a\!: \rho_1 - \rho_2 > p_o$	Right tail	1-P(Z<z*)
$H_a\!: \rho_1 - \rho_2 < p_o$	Left tail	P(Z<z*)
$H_a\!: \rho_1 - \rho_2 \neq p_o$	Two-tail	2*P(Z<-|z*|)

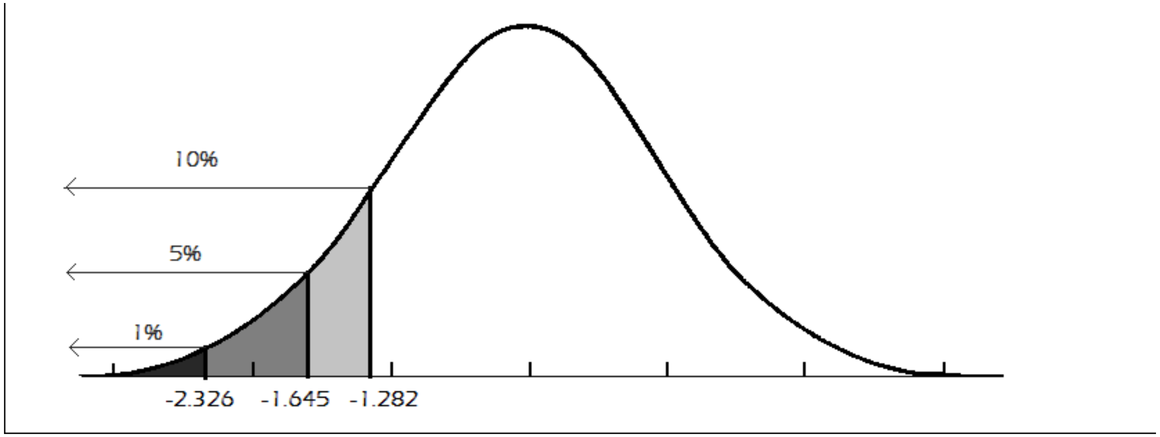
Hypothesis Test for Proportion Differences: Step 5

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

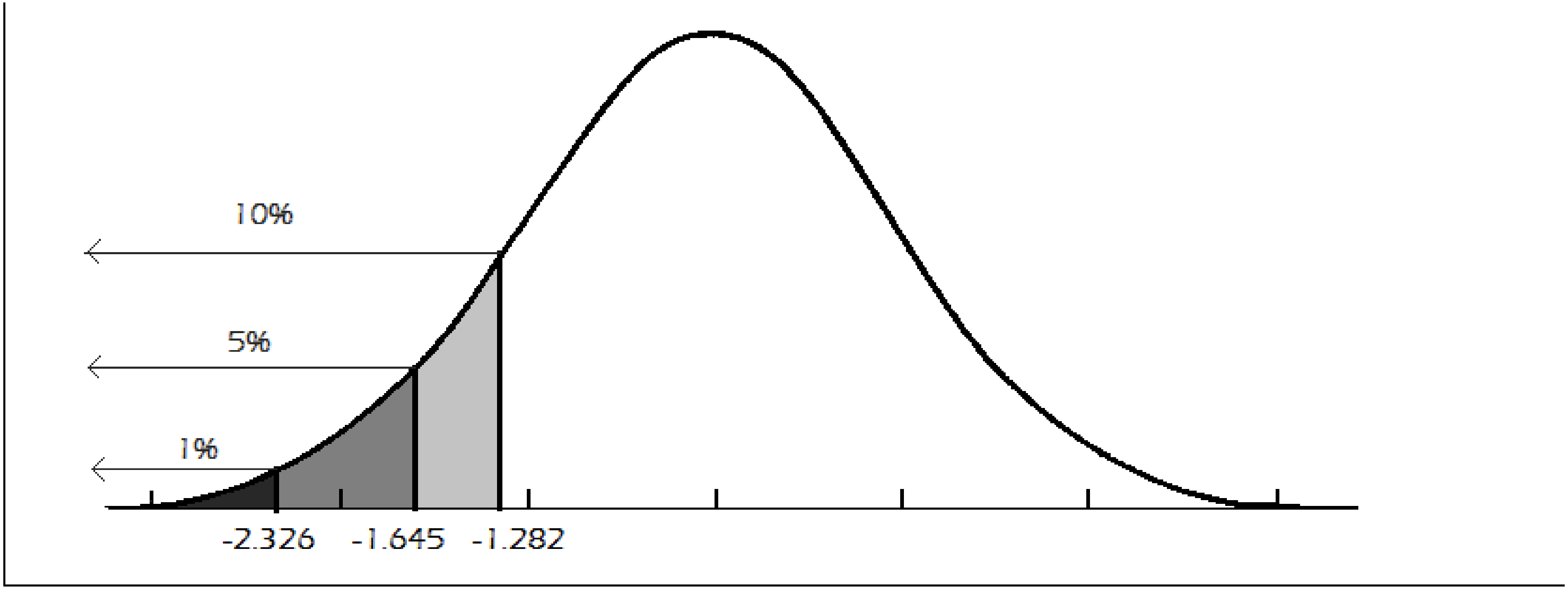
Hypothesis Test for Proportion Differences: Step 5 with Pictures

- For a left tailed test: $H_a: p_1 - p_2 < p_0$ → We have rejection regions for H_o are as follows
  - Note that we lose another degree of freedom

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



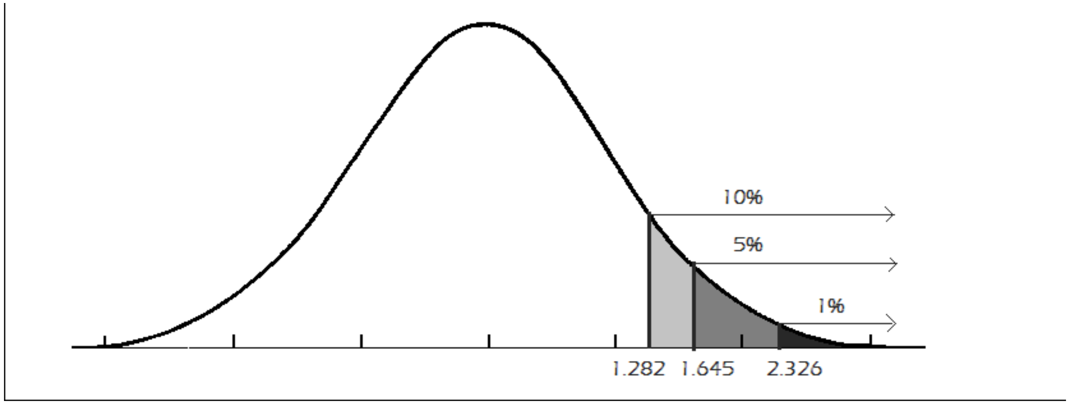
Zoom In



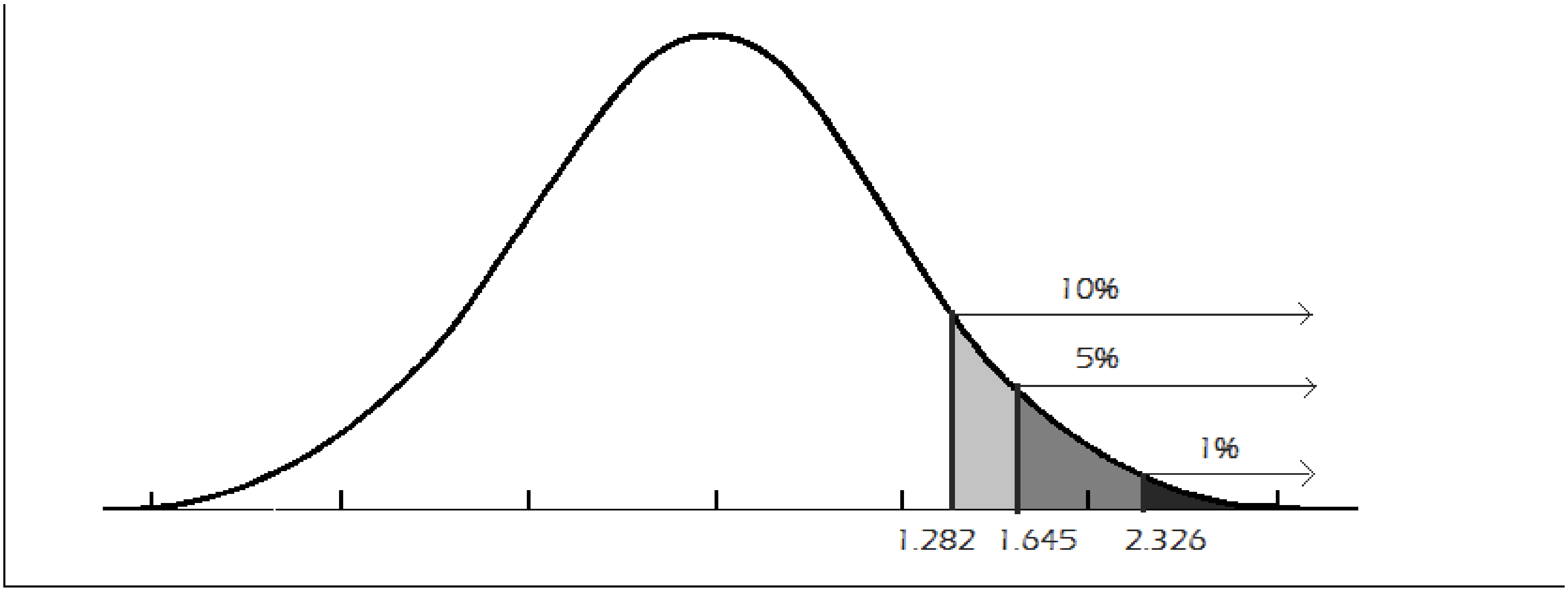
Hypothesis Test for Proportion Differences: Step 5 with Pictures

- For a right tailed test: $H_a: p_1 - p_2 > p_0$ → We have rejection regions for H_o are as follows
  - Note that we lose another degree of freedom

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



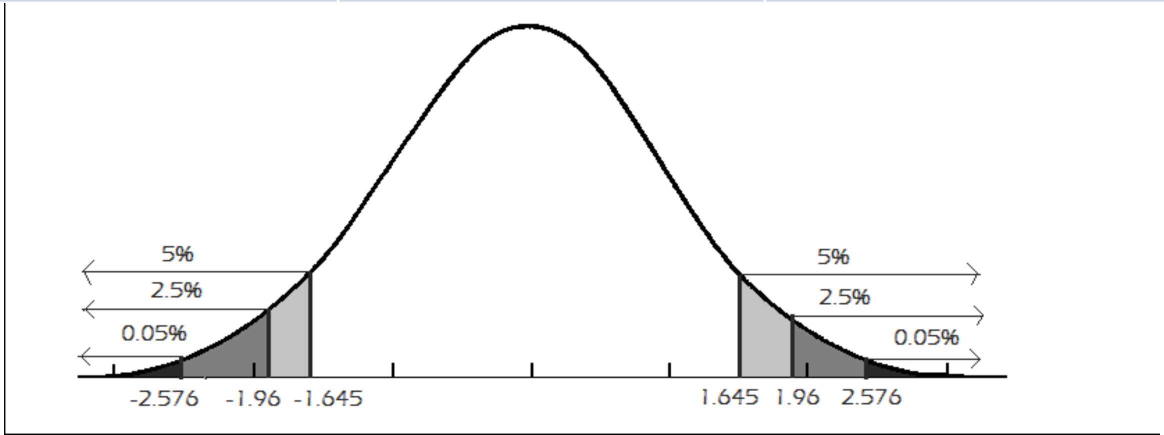
Zoom In



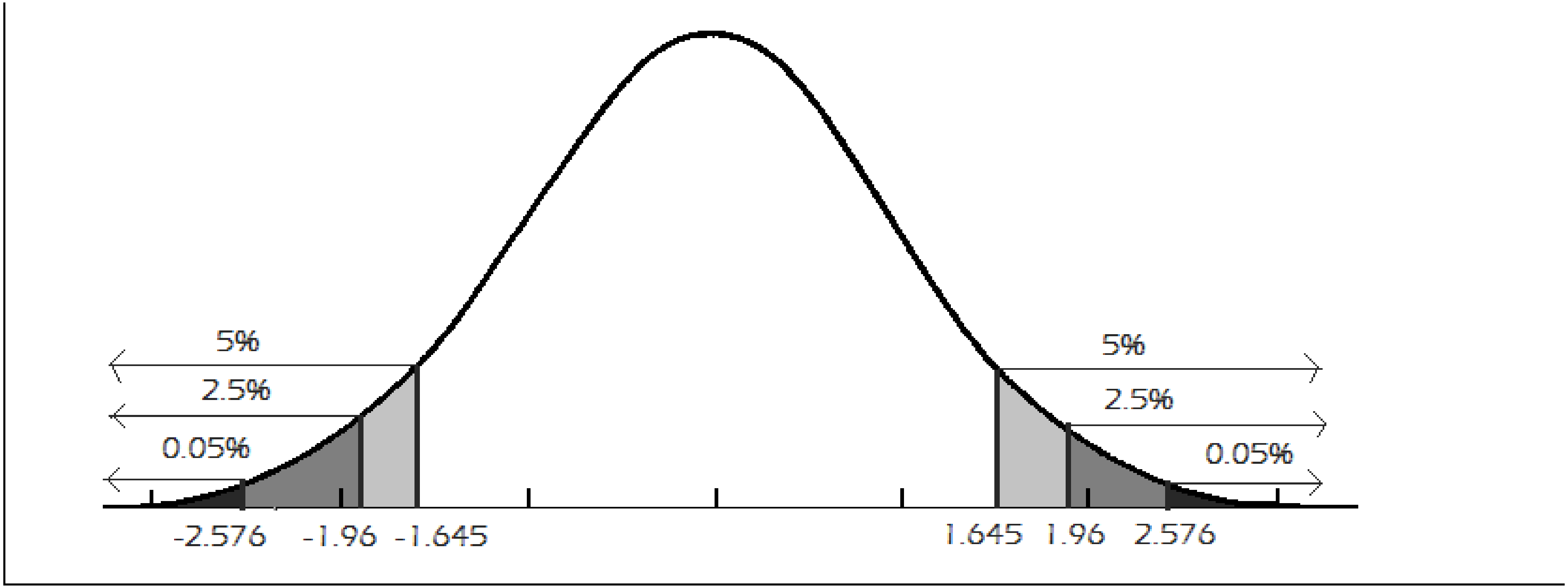
Hypothesis Test for Proportion Differences: Step 5 with Pictures

- For a two tailed test: $H_a: p_1 - p_2 \neq p_0 \rightarrow$ We have rejection regions for H_o are as follows
  - Note that we lose another degree of freedom

Confidence	Reject (test stat)	Reject (p-value)
0.90	|Test-stat|<1.645	P-value<.1
0.95	|Test-stat|<1.960	P-value<.05
0.99	|Test-stat|<2.576	P-value<.01



Zoom In



Example

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- 3677 experienced rejection from their family of which 1,875 had attempted suicide

$$\widehat{p_2} = \frac{1875}{3677} = .50993$$

Example

- Test, with 99% confidence, that the population proportion of transgender and gender non-conforming people who are rejected by their family and those that maintained their family ties are not equally likely to attempt suicide

$$H_o\colon \rho_d = \rho_1 - \rho_2 = 0$$
$$Ha\colon \rho_d = \rho_1 - \rho_2 \neq 0$$

Example

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. If all of the following are true
     - $2773\widehat{p_1} = 887 \geq 15$
     - $2773(1 - \widehat{p_1}) = 1886 \geq 15$
     - $3677\widehat{p_2} = 1875 \geq 15$
     - $3677(1 - \widehat{p_2}) = 1802 \geq 15$

Example

- **Calculate Test Statistic**

$$z^* = \frac{((\hat{p}_1 - \hat{p}_2) - p_0)}{\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}}$$

$$= \frac{((.31987 - .50993) - 0)}{\sqrt{\frac{.31987(1-.31987)}{2773} + \frac{.50993(1-.50993)}{3677}}}$$

$$= \frac{((.31987 - .50993) - 0)}{\sqrt{\frac{.31987(1-.31987)}{2773} + \frac{.50993(1-.50993)}{3677}}} = -15.70704$$

Example

- Determine the P-value:

$2P(Z < -|-15.70704|)$

$=2P(Z < -15.70704)$

$=2 * pnorm(-15.70704,0,1)$

≈ 0

Example

- Summarize the test by reporting and interpreting the P-value:

If $0 \leq (1 - .99) = .01$

  - Reject H_o, we have sufficient evidence that the alternative hypothesis might be true - the population proportion of transgender and gender non-conforming people who are rejected by their family and those that maintained their family ties are not equally likely to attempt suicide

Example in R

```
#TestType: 1 for <, 2 for >, 3 for not equal
diffp.test<-function(conf.level,x1,n1,x2,n2,p0,TestType){
 txt<-"";  phat1<-x1/n1;  phat2<-x2/n2;  phatd<-phat1-phat2;  TestStat<-((phat1-phat2)-p0)/sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2);
 xax<-seq(p0-5*max(sqrt(phat1*(1-phat1)/n1),sqrt(phat2*(1-phat2)/n2)),p0+5*max(sqrt(phat1*(1-phat1)/n1),sqrt(phat2*(1-phat2)/n2)),.001);
 P_x<-dnorm(xax,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));
 if(TestType==1){    txt<-paste("Test Alternative: parameter diff< ",p0,"\n",sep="");
  CritVal<-qnorm(1-conf.level,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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 diff>",p0,"\n",sep="");
   CritVal<-qnorm(conf.level,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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 diff !=",p0,"\n",sep="");
   CritVal1<-qnorm((1-conf.level)/2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));
   CritVal2<-qnorm(conf.level+(1-conf.level)/2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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(phatd<min(cord.x2)){   loc<-"topright"   }else{    loc<-"topleft"  } }
 if(n1*phat1<15|n1*(1-phat1)<15|n2*phat2<15|n2*(1-phat2)<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(phatd,2),c(0,max(P_x)),col="red");
 if(TestType==3){    y.shade<-c(0,dnorm(cord.x1,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0,0,dnorm(cord.x2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0) ;
 }else{    y.shade<-c(0,dnorm(cord.x,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0);  }
 polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));}
```

```
diffp.test(.99,887,2773,1875,3677,0,3){
```

Sampling Distributions for the Difference of Sample Means

- The mean of the sampling distribution for the difference of sample means

$$\mu_{\overline{x_1}-\overline{x_2}} = \mu_{x_1} - \mu_{x_2}$$

- The standard error of the sampling distribution for the difference of sample means

$$\sigma_{\overline{x_1}-\overline{x_2}} = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

Types of Two Sample Groupings

- **Independent Sample:** Data from a designed experiment in which the samples are independently drawn from the population
  - The two samples are unrelated
- **Dependent Sample:** Data from a designed experiment in which the samples are dependent. This often refers to paired data
  - When two samples are “naturally paired” or related
    - Ie: Before and after measurements on one subject
  - Here, the two samples must be the same size

Confidence Intervals
For the Population Difference of Means

- When we talk about confidence intervals for the population mean we have two approaches
- Independent Samples
  1. With known σ_1 & σ_2
  2. With unknown $\sigma_1 = \sigma_2$
  3. With unknown $\sigma_1 \neq \sigma_2$
- Dependent, or paired, Samples
  4. With known σ_1 & σ_2
  5. With unknown σ_1 & σ_2

Confidence Intervals
Case One With known σ_1 & σ_2

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - If $n_1 > 30$ & $n_2 > 30$

       OR
     - If both populations follow the normal distribution

Confidence Intervals
Case One With known σ_1 & σ_2

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean

- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$ is our **margin of error**

Confidence Intervals
Case One With known σ_1 & σ_2

- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$ is our **margin of error**
  - **As either n increases**, $\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$ decreases, causing the margin of error to decrease causing the width of the confidence interval to narrow
  - **As either n decreases**, $\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$ increases, causing the margin of error to increase causing the width of the confidence interval to widen

Confidence Intervals
Case One With known σ_1 & σ_2

- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals
Case One With known σ_1 & σ_2

Lower Bound = $(\overline{x_1} - \overline{x_2}) - z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$

Upper Bound =$(\overline{x_1} - \overline{x_2}) + z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$

We are --% confident that the true population difference of means is between the **lower** and **upper** bound.

Confidence Intervals
Case One With known σ_1 & σ_2

- If all the values on the interval are negative then $\mu_1 < \mu_2$

- If all the values on the interval are positive then $\mu_1 > \mu_2$

- If 0 is on the interval then it's possible that $\mu_1 = \mu_2$

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - If $n_1 > 30$ & $n_2 > 30$

       <u>OR</u>

     - If both populations follow the normal distribution

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2}, n_1+n_2-1} \sqrt{s_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$$

Where: $s_p^2 = \frac{(\mathrm{n}_1-1)\mathrm{s}_1^2+(\mathrm{n}_2-1)\mathrm{s}_2^2}{n_1+n_2-2}$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $t_{1-\frac{\alpha}{2}, n_1+n_2-1} \sqrt{s_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$ is our **margin of error**

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

- $t_{1-\frac{\alpha}{2}, n_1+n_2-1}\sqrt{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$ is our **margin of error**
  - **As either n increases,** $\sqrt{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$ decreases, causing the margin of error to decrease causing the width of the confidence interval to narrow
  - **As either n decreases**, $\sqrt{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$ increases, causing the margin of error to increase causing the width of the confidence interval to widen

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

- $t_{1-\frac{\alpha}{2},n_1+n_2-1}\sqrt{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

Lower Bound

$$(\overline{x_1} - \overline{x_2}) - t_{1-\frac{\alpha}{2}, n_1+n_2-1}\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$$

Upper Bound

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2}, n_1+n_2-1}\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$$

We are --% confident that the true population difference of means is between the **lower** and **upper** bound.

Confidence Intervals
Case Two With unknown $\sigma_1 = \sigma_2$

- If all the values on the interval are negative then $\mu_1 < \mu_2$
- If all the values on the interval are positive then $\mu_1 > \mu_2$
- If 0 is on the interval then it’s possible that $\mu_1 = \mu_2$

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

$$v = \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\frac{\left(\frac{s_1^2}{n_1}\right)^2}{n_1 - 1} + \frac{\left(\frac{s_2^2}{n_2}\right)^2}{n_2 - 1}}$$

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$ is our **margin of error**

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$ is our **margin of error**

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- $t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1}+\frac{s_2^2}{n_2}}$ is our **margin of error**
  - **As either n increases**, $\sqrt{\frac{s_1^2}{n_1}+\frac{s_2^2}{n_2}}$ decreases, causing the margin of error to decrease causing the width of the confidence interval to narrow
  - **As either n decreases**, $\sqrt{\frac{s_1^2}{n_1}+\frac{s_2^2}{n_2}}$ increases, causing the margin of error to increase causing the width of the confidence interval to widen

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- $t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1}+\frac{s_2^2}{n_2}}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

Lower Bound

$$(\overline{x_1} - \overline{x_2}) - t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

Upper Bound

$$(\overline{x_1} - \overline{x_2}) + t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

We are --% confident that the true population difference of means is between the **lower** and **upper** bound.

Confidence Intervals
Case Three With unknown $\sigma_1 \neq \sigma_2$

- If all the values on the interval are negative then $\mu_1 < \mu_2$

- If all the values on the interval are positive then $\mu_1 > \mu_2$

- If 0 is on the interval then it's possible that $\mu_1 = \mu_2$

Example

- According to a NY Times article a survey conducted showed that 22 men averaged about 3 hours of housework per day with a standard deviation of .85 and 49 women averaged about 6 hours of housework per day with a standard deviation of 1.3
- Find a 90% confidence interval for the true population difference of means.

Example

First we solve for v:

$$v = \frac{\left(\frac{.85^2}{22} + \frac{1.3^2}{49}\right)^2}{\frac{\left(\frac{.85^2}{22}\right)^2}{22-1} + \frac{\left(\frac{1.3^2}{49}\right)^2}{49-1}} = 59.5402 \approx 59$$

Example

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

$$(3 - 6) \pm t_{1-\frac{.1}{2},59}\sqrt{\frac{.85^2}{22} + \frac{1.3^2}{49}}$$

$$(-3) \pm (1.671093)\sqrt{\frac{.85^2}{22} + \frac{1.3^2}{49}}$$

$$= (-3.433618, -2.566382)$$

Example

$$(-3.433618, -2.566382)$$

All the values on the interval are negative. This indicates $\mu_1 < \mu_2 -$ that the population mean of hours spent doing housework per day for women is higher than it is for males.

Confidence Intervals unknown $\sigma_1 \neq \sigma_2$ - R code

Below is a function you can load into R:

```
t.diffint.neqvar<-function(conf.level, xbar1, sx1, n1, xbar2, sx2, n2){
  xbard=xbar1-xbar2
  v=((sx1^2/n1 + sx2^2/n2)^2)/((sx1^2/n1)^2/(n1-1)+ (sx2^2/n2)^2/(n2-1))
  t.crit = qt(1-(1-conf.level)/2,v);
  std.error = sqrt(sx1^2/n1+sx2^2/n2);
  MOE=t.crit*std.error;
  c(xbard-MOE, xbard+MOE)
}
```

```
> t.diffint.neqvar(.90, 3, .85, 22, 6, 1.3, 49)
[1] -3.433555 -2.566445
```

Confidence Intervals
Case Four With known σ_1 & σ_2

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm z_{1-\frac{\alpha}{2}} \sqrt{\frac{s_d^2}{n}}$$

Confidence Intervals
Case Four With known σ_1 & σ_2

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**

Confidence Intervals
Case Four With known σ_1 & σ_2

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**

Confidence Intervals
Case Four With known σ_1 & σ_2

- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**
  - **As either n increases,** $\sqrt{\frac{s_d^2}{n}}$ decreases, causing the margin of error to decrease causing the width of the confidence interval to narrow
  - **As either n decreases,** $\sqrt{\frac{s_d^2}{n}}$ increases, causing the margin of error to increase causing the width of the confidence interval to widen

Confidence Intervals
Case Four With known σ_1 & σ_2

- $z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals
Case Four With known σ_1 & σ_2

Lower Bound

$$(\overline{x_1} - \overline{x_2}) - z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$$

Upper Bound

$$(\overline{x_1} - \overline{x_2}) + z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$$

We are --% confident that the true population difference of means is between the **lower** and **upper** bound.

Confidence Intervals
Case Four With known σ_1 & σ_2

- If all the values on the interval are negative then $\mu_1 < \mu_2$
- If all the values on the interval are positive then $\mu_1 > \mu_2$
- If 0 is on the interval then it's possible that $\mu_1 = \mu_2$

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$$

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean

- $t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- We use our sample means to make inference on the population mean

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$$

- $\overline{x_1} - \overline{x_2}$ is our **point-estimate** for the population mean
- $t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- $t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**
  - **As either n increases**, $\sqrt{\frac{s_d^2}{n}}$ decreases, causing the margin of error to decrease causing the width of the confidence interval to narrow
  - **As either n decreases**, $\sqrt{\frac{s_d^2}{n}}$ increases, causing the margin of error to increase causing the width of the confidence interval to widen

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- $t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$ is our **margin of error**
  - **As the confidence level decreases**, z decreases causing the margin of error to decrease, causing the width of the confidence interval to narrow
  - **As the confidence level increases**, z increases causing the margin of error to increase, causing the width of the confidence interval to grow wider

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

Lower Bound

$$(\overline{x_1} - \overline{x_2}) - t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$$

Upper Bound

$$(\overline{x_1} - \overline{x_2}) + t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$$

We are --% confident that the true population difference of means is between the **lower** and **upper** bound.

Confidence Intervals
Case Five With Unknown σ_1 & σ_2

- If all the values on the interval are negative then $\mu_1 < \mu_2$

- If all the values on the interval are positive then $\mu_1 > \mu_2$

- If 0 is on the interval then it's possible that $\mu_1 = \mu_2$

Example

- I had a random sample of forty students rate their attractiveness on a scale of 1 to 10, ten being most attractive and then I had them rate the rest of the group on the same scale
- The sample difference, self score – group score, was .475 with a standard deviation of 1.7095134.

Example

- Find a 90% confidence interval for the population difference of means – the difference of the self rating and group rating

Example

$$(\overline{x_1} - \overline{x_2}) \pm t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$$

$$(.475) \pm t_{1-\frac{.1}{2},40-1}\sqrt{\frac{1.7095134^2}{40}}$$

$$(.475) \pm (1.684875)\sqrt{\frac{1.7095134^2}{40}}$$

$$(.01958199, .930418)$$

Example

$$(.01958199, .930418)$$

We are 90% confident the true population mean difference is between .01958199 and .930418. All of the values on the interval are positive. This indicates $\mu_1 > \mu_2$, that the mean self rating is larger than the mean group rating.

Narcissists!

Confidence Intervals with Paired Data unknown $\sigma_1 \& \sigma_2$ - R code

Below is a function you can load into R:

```
t.pairedint<-function(conf.level, xbard, sd, n){
  t.crit = qt(1-(1-conf.level)/2,n-1);
  std.error = sqrt(sd^2/n);
  MOE=t.crit*std.error;
  c(xbard-MOE, xbard+MOE)
}
```

```
> t.pairedint(.9,.475,1.7095134,40)
[1] 0.01958196 0.93041804
```

Hypothesis Test for Mean Difference: Step 1

- State Hypotheses:
  - **Null hypothesis**: that the population mean equals some μ_o
    - $H_o: \mu_d = \mu_1 - \mu_2 \leq \mu_o$ (one sided test)
    - $H_o: \mu_d = \mu_1 - \mu_2 \geq \mu_o$ (one sided test)
    - $H_o: \mu_d = \mu_1 - \mu_2 = \mu_o$ (two sided test)
  - **Alternative hypothesis:** What we're interested in
    - $H_a: \mu_1 - \mu_2 > \mu_o$ (one sided test)
    - $H_a: \mu_1 - \mu_2 < \mu_o$ (one sided test)
    - $Ha: \mu_1 - \mu_2 \neq \mu_o$ (two sided test)

Hypothesis Test for Mean Difference: Step 2

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - If $n_1 > 30$ & $n_2 > 30$

       OR

     - If both populations follow the normal distribution

Hypothesis Test for Mean Difference: Step 3: Case One With known σ_1 & σ_2

- Calculate Test Statistic
  - The test statistic measures how different the sample proportion we have is from the null hypothesis
  - We calculate the z-statistic by assuming that $\mu_{d\,0}$ is the population mean difference

$$z^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$$

Hypothesis Test for Mean Differences: Step 4: Case One With known σ_1 & σ_2

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \mu_1 - \mu_2 > \mu_o$	Right tail	P(Z>z*)
	Left tail	P(Z<z*)
$H_a: \mu_1 - \mu_2 \neq \mu_o$	Two-tail	2*P(Z<-|z*|)

Hypothesis Test for Mean Difference: Step 3: Case Two With unknown $\sigma_1 = \sigma_2$

- Calculate Test Statistic
  - The test statistic measures how different the sample proportion we have is from the null hypothesis
  - We calculate the t-statistic by assuming that μ_{d_0} is the population mean difference

$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}} \text{ where } s_p^2 = \frac{(\mathrm{n}_1 - 1)\mathrm{s}_1^2 + (\mathrm{n}_2 - 1)\mathrm{s}_2^2}{n_1 + n_2 - 2}$$

Hypothesis Test for Mean Difference: Step 4: Case Two With unknown $\sigma_1 = \sigma_2$

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \mu_1 - \mu_2 > \mu_o$	Right tail	P(T>t*)
	Left tail	P(T<t*)
$H_a: \mu_1 - \mu_2 \neq \mu_o$	Two-tail	2*P(T<-|t*|)

Hypothesis Test for Mean Difference: Step 3: Case Three With unknown $\sigma_1 \neq \sigma_2$

- Calculate Test Statistic
  - The test statistic measures how different the sample proportion we have is from the null hypothesis
  - We calculate the t-statistic by assuming that μ_{d_0} is the population mean difference

$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

Hypothesis Test for Mean Difference: Step 4: Case Three With unknown $\sigma_1 \neq \sigma_2$

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	**Probability**	**Formula for the P-value**
$H_a: \mu_1 - \mu_2 > \mu_o$	Right tail	P(T>t*)
	Left tail	P(T<t*)
$H_a: \mu_1 - \mu_2 \neq \mu_o$	Two-tail	2*P(T<-|t*|)

Hypothesis Test for Mean Difference: Step 5

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

Example

- According to a NY Times article a survey conducted showed that 22 men averaged 3 hours of housework per day with a standard deviation of .85 and 49 women averaged 6 hours of housework per day with a standard deviation of 1.3
- Test with 90% confidence interval that the true population difference of means is more males than females

Example

- State Hypotheses:
  - $H_o: \mu_d = \mu_1 - \mu_2 \leq 0$
  - $H_a: \mu_1 - \mu_2 > 0$

Example

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - If $n_1 < 30$ & $n_2 > 30$

       AND

     - We don’t know the populations follow the normal distribution

     Proceed with caution*

Example

- Calculate Test Statistic

$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

$$= \frac{((3 - 6) - 0)}{\sqrt{\frac{.85^2}{22} + \frac{1.3^2}{49}}}$$

$$= -11.56151$$

Example

First we solve for v:

$$v = \frac{\left(\frac{.85^2}{22} + \frac{1.3^2}{49}\right)^2}{\frac{\left(\frac{.85^2}{22}\right)^2}{22-1} + \frac{\left(\frac{1.3^2}{49}\right)^2}{49-1}} = 59.5402 \approx 59$$

Example

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

$$1 - P(T < t^*)$$
$$= 1 - P(T < -11.56151\ )$$
$$= 1 - \mathrm{qt}(-11.56151{,}59)$$
$$\approx 1 - 0 = 1$$

Example

- Summarize the test by reporting and interpreting the P-value

$1 > (1 - .9) = .1$

We fail to reject H_o, we do not have sufficient evidence to suggest that males do more housework than females

Example in R

```
#TestType: 1 for <, 2 for >, 3 for not equal
Mdiff.Ttest.neqvar<-function(conf.level,xbar1,sx1,n1,xbar2,sx2,n2,m0,TestType){
  txt<-"";  xbard<-xbar1-xbar2;  v<-floor((sx1^2/n1+sx2^2/n2)^2/((sx1^2/n1)^2/(n1-1)+(sx2^2/n2)^2/(n2-1)));
  TestStat<-(xbard-m0)/sqrt(sx1^2/n1+sx2^2/n2); xax<-seq(m0-5*sqrt(sx1^2/n1+sx2^2/n2),m0+5*sqrt(sx1^2/n1+sx2^2/n2),.01);
  P_x<-dt((xax-m0)/sqrt(sx1^2/n1+sx2^2/n2),v);
  if(TestType==1){    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep=""); CritVal<-qt(1-conf.level,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    pvalue<-pt(TestStat,v);  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,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    pvalue<-1-pt(TestStat,v); 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,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    CritVal2<-qt(conf.level+(1-conf.level)/2,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;  pvalue=2*pt(-abs(TestStat),v);
    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(n1<30|n2<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(xbard,2),c(0,max(P_x)),col="red");
  if(TestType==3){y.shade<- c(0,dt((cord.x1-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0,0,dt((cord.x2-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0) ;
  }else{y.shade<- c(0,dt((cord.x-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0) ;}
  polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red")) ;}
```

```
Mdiff.Ttest.neqvar(.90,3,.85,22,6,1.3,49,0,2)
```

Hypothesis Test for Mean Paired Difference: Step 1

- State Hypotheses:
  - **Null hypothesis**: that the population mean equals some μ_o
    - $H_o\colon \mu_d = \mu_1 - \mu_2 \leq \mu_o$ (one sided test)
    - $H_o\colon \mu_d = \mu_1 - \mu_2 \geq \mu_o$ (one sided test)
    - $H_o\colon \mu_d = \mu_1 - \mu_2 = \mu_o$ (two sided test)
  - **Alternative hypothesis:** What we're interested in
    - $H_a\colon \mu_1 - \mu_2 > \mu_o$ (one sided test)
    - $H_a\colon \mu_1 - \mu_2 < \mu_o$ (one sided test)
    - $Ha\colon \mu_1 - \mu_2 \neq \mu_o$ (two sided test)

Hypothesis Test for Mean Paired Difference: Step 2

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - If $n_1 > 30$ & $n_2 > 30$ such that $n_1 = n_2$

       OR
     - If both populations follow the normal distribution

Hypothesis Test for Mean Difference: Step 3: Case Four with known σ_d

- Calculate Test Statistic
  - The test statistic measures how different the sample mean we have is from the null hypothesis
  - We calculate the z-statistic by assuming that μ_{d_0} is the population mean difference

$$z^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{\sigma_d^2}{n}}}$$

Hypothesis Test for Mean Difference: Step 3: Case Four with known σ_d

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	Probability	Formula for the P-value
$H_a: \mu_1 - \mu_2 > \mu_o$	Right tail	P(Z>z*)
	Left tail	P(Z<z*)
$H_a: \mu_1 - \mu_2 \neq \mu_o$	Two-tail	2*P(Z<-|z*|)

Hypothesis Test for Mean Difference: Step 3: Case Five with unknown σ_d

- Calculate Test Statistic
  - 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 difference

$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_d^2}{n}}}$$

Hypothesis Test for Mean Difference: Step 4: Case Five with unknown σ_d

- Determine the P-value
  - The P-value describes how unusual the sample data would be if H_o were true.

Alternative Hypothesis	**Probability**	**Formula for the P-value**
$H_a: \mu_1 - \mu_2 > \mu_o$	Right tail	P(T>t*)
	Left tail	P(T<t*)
$H_a: \mu_1 - \mu_2 \neq \mu_o$	Two-tail	2*P(T<-|t*|)

Hypothesis Test for Mean Difference: Step 5

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

Example

- I had a random of forty students rate their attractiveness on a scale of 1 to 10, ten being most attractive and then I had them rate the rest of the group on the same scale

- The sample difference, self score – group score, was .047 with a standard deviation of 1.7095134.

Example

- Test at the 90% that the difference of the self rating and group rating are different

Hypothesis Test for Mean Paired Difference: Step 1

- State Hypotheses:

$$H_o: \mu_d = \mu_1 - \mu_2 = 0$$
$$Ha: \mu_d = \mu_1 - \mu_2 \neq 0$$

Hypothesis Test for Mean Paired Difference: Step 2

- Check the assumptions
  1. Each sample must be obtained through randomization
  2. Samples are independent
  3. The differences are from the normal distribution
     - $n_1 = n_2 > \mathbf{30}$

Hypothesis Test for Mean Difference: Step 3: Case Five with unknown σ_d

- Calculate Test Statistic

$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_d^2}{n}}}$$

$$= \frac{((.475) - 0)}{\sqrt{\frac{1.7095134^2}{40}}}$$

$$= \frac{((.475) - 0)}{\sqrt{\frac{1.7095134^2}{40}}}$$

$$= 1.757321$$

Hypothesis Test for Mean Difference: Step 4: Case Five with unknown σ_d

- Determine the P-value

$$
\begin{gathered}
2P(T < -|t^*|) \\
= 2P(T < -|1.757321|) \\
= 2P(T < -1.757321) \\
= 2 * pt(-1.757321, 40 - 1) \\
= .08671139
\end{gathered}
$$

Hypothesis Test for Mean Difference: Step 5

- Summarize the test by reporting and interpreting the P-value:
- If .08671139$\leq (1-.90)=.10$
  - Reject H_o, we have sufficient evidence that the alternative hypothesis might be true – that students rate themselves higher than they rate the group

Example in R

```
#TestType: 1 for <, 2 for >, 3 for not equal
Mdiff.pairedTtest<-function(conf.level,xbar1,xbar2,sigmad,n,m0,TestType){
  txt<-"";  xbard<-xbar1-xbar2;  TestStat<-(xbard-m0)/sqrt(sigmad^2/n);  xax<-seq(m0-5*sqrt(sigmad^2/n),m0+5*sqrt(sigmad^2/n),.01);  P_x<-dt((xax-
m0)/sqrt(sigmad^2/n),n-1);
  if(TestType==1){txt<-paste("Test Alternative: parameter < ",m0,"\n",sep="");    CritVal<-qt(1-conf.level,n-1)*sqrt(sigmad^2/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)*sqrt(sigmad^2/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)*sqrt(sigmad^2/n)+m0;
    CritVal2<-qt(conf.level+(1-conf.level)/2,n-1)*sqrt(sigmad^2/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(xbard<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(xbard,2),c(0,max(P_x)),col="red");
  if(TestType==3){y.shade<- c(0,dt((cord.x1-m0)/sqrt(sigmad^2/n),n-1),0,0,dt((cord.x2-m0)/sqrt(sigmad^2/n),n-1),0);}else{y.shade<- c(0,dt((cord.x-
m0)/sqrt(sigmad^2/n),n-1),0)}
  polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));
}
```

```
Mdiff.pairedTtest(.95,7,6.525,1.7095134,40,0,3)
```

Skipping Stuff

- Sections 9.5 and 9.6 aren’t part of the requirements for this class but 9.6 is important. It provides a methodology for testing whether or not the variances across groups are equal.

Summaries

Confidence Intervals

Assumptions	Point Estimate	Margin of Error
1. Random Sample *2.* $n_1\widehat{p_1} \geq 15$ $n_1(1-\widehat{p_1}) \geq 15$ $n_2\widehat{p_2} \geq 15$ $n_2(1-\widehat{p_2}) \geq 15$	$\widehat{p_1} - \widehat{p_2}$	$z_{\left(1-\frac{\alpha}{2}\right)}\sqrt{\frac{\widehat{p_1}(1-\widehat{p_1})}{n_1}+\frac{\widehat{p_2}(1-\widehat{p_2})}{n_2}}$

- We are --% confident that the true difference of population proportions lays on the confidence interval.

Example in R

Below is a function you can load into R:

```
diffprop.int<-function(conf.level, x1, n1,x2,n2){
  phat1=x1/n1
  phat2=x2/n2
  phatd = phat1-phat2
  z.crit = qnorm(1-(1-conf.level)/2);
  std.error = sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2);
  MOE=z.crit*std.error;
  c(phatd-MOE, phatd+MOE)
}
```

Confidence Intervals known σ_1 and σ_2

Assumptions	**Point Estimate**	**Margin of Error**
1. Random Sample *2.* $n > 30$ OR the population is bell shaped	$\overline{x_1} - \overline{x_2}$	$z_{1-\frac{\alpha}{2}}\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$

- We are --% confident that the true difference of population means lays on the confidence interval.

Confidence Intervals known σ_1 and σ_2 - R code

Below is a function you can load into R:

```
z.diffint<-function(conf.level, xbar1, sigma1 , xbar2,
sigma2, n){
  xbard<-xbar1-xbar2
  z.crit = qnorm(1-(1-conf.level)/2);
  std.error = sqrt(sigma1^2/n1 +sigma2^2/n2) ;
  MOE=z.crit*std.error;
  c(xbar-MOE, xbar+MOE)
}
```

Confidence Intervals unknown $\sigma_1 = \sigma_2$

Assumptions	Point Estimate	Margin of Error
1. *Random Sample* 2. $n > 30$ OR the population is bell shaped	$\bar{x}$	$t_{1-\frac{\alpha}{2}, n_1+n_2-1}\sqrt{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$ Where: $s_p^2 = \frac{(\mathrm{n}_1-1)\mathrm{s}_1^2+(\mathrm{n}_2-1)\mathrm{s}_2^2}{n_1+n_2-2}$

- We are --% confident that the true difference of population means lays on the confidence interval.

Confidence Intervals unknown $\sigma_1 = \sigma_2$ - R code

Below is a function you can load into R:

```
t.diffint.eqvar<-function(conf.level, xbar1, sx1, n1, xbar2, sx2, n2){
  xbard=xbar1-xbar2
  sp=((n1-1)*sx1^2 + (n2-1)*sx2^2)/(n1+n2-2)
  t.crit = qt(1-(1-conf.level)/2,n1+n2-1);
  std.error = sp*(1/n1+1/n2);
  MOE=t.crit*std.error;
  c(xbard-MOE, xbard+MOE)
}
```

Confidence Intervals unknown $\sigma_1 \neq \sigma_2$

Assumptions	**Point Estimate**	**Margin of Error**
1. Random Sample 2. $n > 30$ OR the population is bell shaped	$\bar{x}_1 - \bar{x}_2$	$t_{1-\frac{\alpha}{2},v}\sqrt{\frac{s_1^2}{n_1}+\frac{s_2^2}{n_2}}$

- We are --% confident that the true difference of population means lays on the confidence interval.

Confidence Intervals unknown $\sigma_1 \neq \sigma_2$ - R code

Below is a function you can load into R:

```
t.diffint.neqvar<-function(conf.level, xbar1, sx1, n1, xbar2, sx2,
n2){
  xbard=xbar1-xbar2
  v=((s1^2/n1 + s2^2/n2)^2)/((s1^2/n1)^2/(n1-1)+
(s2^2/n2)^2/(n2-1))
  t.crit = qt(1-(1-conf.level)/2,v);
  std.error = sqrt(sx1^2/n1+sx2^2/n2);
  MOE=t.crit*std.error;
  c(xbard-MOE, xbard+MOE)
}
```

Confidence Intervals with Paired Data known $\sigma_1 \& \sigma_2$

Assumptions	**Point Estimate**	**Margin of Error**
1. *Random Sample* 2. $n > 30$ OR the population is bell shaped	$\bar{x}_1 - \bar{x}_2$	$z_{1-\frac{\alpha}{2}}\sqrt{\frac{s_d^2}{n}}$

- We are --% confident that the true difference of population means lays on the confidence interval.

Confidence Intervals with Paired Data known $\sigma_1 \& \sigma_2$ - R code

Below is a function you can load into R:

```
z.pairedint<-function(conf.level, xbard, sd, n){
  t.crit = qt(1-(1-conf.level)/2,n-1);
  std.error = sqrt(sd/n)^2;
  MOE=t.crit*std.error;
  c(xbard-MOE, xbard+MOE)
}
```

Confidence Intervals with Paired Data unknown $\sigma_1 \& \sigma_2$

Assumptions	**Point Estimate**	**Margin of Error**
1. Random Sample *2.* $n > 30$ OR the population is bell shaped	$\bar{x}_1 - \bar{x}_2$	$t_{1-\frac{\alpha}{2},n-1}\sqrt{\frac{s_d^2}{n}}$

- We are --% confident that the true difference of population means lays on the confidence interval.

Confidence Intervals with Paired Data unknown $\sigma_1 \& \sigma_2$ - R code

Below is a function you can load into R:

```
t.pairedint<-function(conf.level, xbard, sd, n){
  t.crit = qt(1-(1-conf.level)/2,n-1);
  std.error = sqrt(sd/n);
  MOE=t.crit*std.error;
  c(xbar-MOE, xbar+MOE)
}
```

Hypothesis Testing for ρ

Step One:	(i) $H_0: p_1 - p_2 = p_0$ & $H_a: p_1 - p_2 \neq \mathrm{p}_0$ (ii) $H_0: p_1 - p_2 \geq p_0$ & $H_a: p_1 - p_2 < \mathrm{p}_0$ (iii) $H_0: p_1 - p_2 \leq p_0$ & $H_a: p_1 - p_2 > \mathrm{p}_0$
Step Two:	1. Categorical 2. Random *3.* $n_1\widehat{p_1} \geq 15$ & $n_1(1-\widehat{p_1}) \geq 15$ $n_2\widehat{p_2} \geq 15$ & $n_2(1-\widehat{p_2}) \geq 15$
Step Three:	$z^* = \dfrac{((\hat{p}_1 - \hat{p}_2) - p_0)}{\sqrt{\dfrac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \dfrac{\hat{p}_2(1-\hat{p}_2)}{n_2}}}$
Step Four:	(i) $H_a: p_1 - p_2 \neq \mathrm{p}_0$→ p-value = $2*P(Z<-\lvert z^*\rvert)$ (ii) $H_a: p_1 - p_2 < \mathrm{p}_0$→ p-value = $P(Z<z^*)$ (iii) $H_a: p_1 - p_2 > \mathrm{p}_0$→ p-value = $P(Z>z^*) = 1-P(Z<z^*)$
Step Five:	If p-value$\leq (1 - confidene) = \alpha$ → Reject H_0 If p-value$> (1 - confidence) = \alpha$ → Fail to Reject H_0

Hypothesis Testing for ρ

```
#TestType: 1 for <, 2 for >, 3 for not equal
diffp.test<-function(conf.level,x1,n1,x2,n2,p0,TestType){
  txt<-"";  phat1<-x1/n1;  phat2<-x2/n2;  phatd<-phat1-phat2;  TestStat<-((phat1-phat2)-p0)/sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2);
  xax<-seq(p0-5*max(sqrt(phat1*(1-phat1)/n1),sqrt(phat2*(1-phat2)/n2)),p0+5*max(sqrt(phat1*(1-phat1)/n1),sqrt(phat2*(1-phat2)/n2)),.001);
  P_x<-dnorm(xax,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));
  if(TestType==1){    txt<-paste("Test Alternative: parameter diff< ",p0,"\n",sep="");
   CritVal<-qnorm(1-conf.level,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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 diff>",p0,"\n",sep="");
    CritVal<-qnorm(conf.level,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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 diff !=",p0,"\n",sep="");
    CritVal1<-qnorm((1-conf.level)/2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));
    CritVal2<-qnorm(conf.level+(1-conf.level)/2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2));    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(phatd<min(cord.x2)){   loc<-"topright"   }else{    loc<-"topleft"  } }
  if(n1*phat1<15|n1*(1-phat1)<15|n2*phat2<15|n2*(1-phat2)<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(phatd,2),c(0,max(P_x)),col="red");
  if(TestType==3){    y.shade<-c(0,dnorm(cord.x1,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0,0,dnorm(cord.x2,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0) ;
  }else{    y.shade<-c(0,dnorm(cord.x,p0,sqrt(phat1*(1-phat1)/n1+phat2*(1-phat2)/n2)),0);  }
  polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));}
```

Hypothesis Testing for μ known σ_1 and σ_2

Step One:	(i) $H_0: \mu_1 - \mu_2 = \mu_0$ & $H_a: \mu_1 - \mu_2 \neq \mu_0$ (ii) $H_0: \mu_1 - \mu_2 \geq \mu_0$ & $H_a: \mu_1 - \mu_2 < \mu_0$ (iii) $H_0: \mu_1 - \mu_2 \leq \mu_0$ & $H_a: \mu_1 - \mu_2 > \mu_0$
Step Two:	1. Quantitative *2. Random Sample* *3.* $n > 30$ OR the population is bell shaped
Step Three:	$z^* = \dfrac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\dfrac{\sigma_1^2}{n_1} + \dfrac{\sigma_2^2}{n_2}}}$
Step Four:	(i) $H_a: \mu_1 - \mu_2 \neq \mu_0$→ p-value = $2*P(Z<-\lvert z^*\rvert)$ (ii) $H_a: \mu_1 - \mu_2 < \mu_0$→ p-value = P(Z<z*) (iii) $H_a: \mu_1 - \mu_2 > \mu_0$→ p-value = P(Z>z*) = 1-P(Z<z*)
Step Five:	If p-value$\leq (1 - confidene) = \alpha$ → Reject H_0 If p-value$> (1 - confidence) = \alpha$ → Fail to Reject H_0

Hypothesis Testing for μ known σ_1 and σ_2

```
#TestType: 1 for <, 2 for >, 3 for not equal
mdiff.Ztest<-function(conf.level,xbar1,sigma1,n1,xbar2,sigma2,n2,m0,TestType){
 xbard<-xbar1-xbar2;txt<-"";  TestStat<-((xbar1-xbar2)-m0)/sqrt(sigma1^2/n1 + sigma2^2/n2);
 xax<-seq(m0-5*max(sigma1/sqrt(n1),sigma2/sqrt(n2)),m0+5*max(sigma1/sqrt(n1),sigma2/sqrt(n2)),.01);  P_x<-
dnorm(xax,m0,sqrt(sigma1^2/n1 + sigma2^2/n2));
 if(TestType==1){    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep="");
   CritVal<-qnorm(1-conf.level,m0,sqrt(sigma1^2/n1 + sigma2^2/n2));    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,sqrt(sigma1^2/n1 +
sigma2^2/n2));
   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,sqrt(sigma1^2/n1 +
sigma2^2/n2));
   CritVal2<-qnorm(conf.level+(1-conf.level)/2,m0,sqrt(sigma1^2/n1 + sigma2^2/n2));    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(xbard<min(cord.x2)){      loc<-"topright";    }else{      loc<-"topleft";    }  }
 if(n1<30|n2<30){    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(xbard,2),c(0,max(P_x)),col="red");
 if(TestType==3){    y.shade<-c(0,dnorm(cord.x1,m0,sqrt(sigma1^2/n1 + sigma2^2/n2)),0,0,dnorm(cord.x2,m0,sqrt(sigma1^2/n1 +
sigma2^2/n2)),0);
 }else{    y.shade<-c(0,dnorm(cord.x,m0,sqrt(sigma1^2/n1 + sigma2^2/n2)),0) ;  }
 polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));}
```

Hypothesis Testing for μ unknown $\sigma_1 = \sigma_2$

Step One:	(i) $H_0: \mu_1 - \mu_2 = \mu_0$ & $H_a: \mu_1 - \mu_2 \neq \mu_0$ (ii) $H_0: \mu_1 - \mu_2 \geq \mu_0$ & $H_a: \mu_1 - \mu_2 < \mu_0$ (iii) $H_0: \mu_1 - \mu_2 \leq \mu_0$ & $H_a: \mu_1 - \mu_2 > \mu_0$
Step Two:	1. Quantitative *2. Random Sample* *3.* $n > 30$ OR the population is bell shaped
Step Three:	$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$ where $s_p^2 = \frac{(\mathrm{n}_1 - 1)\mathrm{s}_1^2 + (\mathrm{n}_2 - 1)\mathrm{s}_2^2}{n_1 + n_2 - 2}$
Step Four:	(i) $H_a: \mu_1 - \mu_2 \neq \mu_0$ → p-value = $2*P(T<-\lvert t^* \rvert)$ (ii) $H_a: \mu_1 - \mu_2 < \mu_0$ → p-value = P(T<t*) (iii) $H_a: \mu_1 - \mu_2 > \mu_0$ → p-value = P(T>t*) = 1-P(T<t*)
Step Five:	If p-value$\leq (1 - confidene) = \alpha$ → Reject H_0 If p-value$> (1 - confidence) = \alpha$ → Fail to Reject H_0

Hypothesis Testing for μ unknown $\sigma_1 = \sigma_2$

```
#TestType: 1 for <, 2 for >, 3 for not equal
Mdiff.Ttest.eqvar<-function(conf.level,xbar1,n1,xbar2,n2,sp,m0,TestType){
  txt<-"";  xbard<-xbar1-xbar2;  TestStat<-(xbard-m0)/sqrt(sp^2*(1/n1+1/n2));  xax<-seq(m0-
5*sqrt(sp^2*(1/n1+1/n2)),m0+5*sqrt(sp^2*(1/n1+1/n2)),.01);
  P_x<-dt((xax-m0)/sqrt(sp^2*(1/n1+1/n2)),n1+n2-2);
  if(TestType==1){    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep="");    CritVal<-qt(1-conf.level,n1+n2-2)*sqrt(sp^2*(1/n1+1/n2))+m0;
    pvalue<-pt(TestStat,n1+n2-2);    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,n1+n2-2)*sqrt(sp^2*(1/n1+1/n2))+m0;
    pvalue<-1-pt(TestStat,n1+n2-2);    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,n1+n2-2)*sqrt(sp^2*(1/n1+1/n2))+m0;
    CritVal2<-qt(conf.level+(1-conf.level)/2,n1+n2-2)*sqrt(sp^2*(1/n1+1/n2))+m0;   pvalue=2*pt(-abs(TestStat),n1+n2-2);
    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(n1<30|n2<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(xbard,2),c(0,max(P_x)),col="red");
  if(TestType==3){    y.shade<- c(0,dt((cord.x1-m0)/sqrt(sp^2*(1/n1+1/n2)),n1+n2-2),0,0,dt((cord.x2-m0)/sqrt(sp^2*(1/n1+1/n2)),n1+n2-2),0);
  }else{    y.shade<- c(0,dt((cord.x-m0)/sqrt(sp^2*(1/n1+1/n2)),n1+n2-2),0);}
  polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));
}
Mdiff.Ttest.eqvar(.99,100,22,97,29,5.5,0,2)
```

Hypothesis Testing for μ unknown $\sigma_1 \neq \sigma_2$

<table>
<tr><td>Step One:</td><td>(i) $H_0: \mu_1 - \mu_2 = \mu_0$ & $H_a: \mu_1 - \mu_2 \neq \mu_0$
(ii) $H_0: \mu_1 - \mu_2 \geq \mu_0$ & $H_a: \mu_1 - \mu_2 < \mu_0$
(iii) $H_0: \mu_1 - \mu_2 \leq \mu_0$ & $H_a: \mu_1 - \mu_2 > \mu_0$</td></tr>
<tr><td>Step Two:</td><td>1. Quantitative
2. Random Sample
3. $n > 30$ OR the population is bell shaped</td></tr>
<tr><td>Step Three:</td><td>$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$</td></tr>
<tr><td>Step Four:</td><td>(i) $H_a: \mu_1 - \mu_2 \neq \mu_0$→ p-value = 2*P(T<-|t*|)
(ii) $H_a: \mu_1 - \mu_2 < \mu_0$→ p-value = P(T<t*)
(iii) $H_a: \mu_1 - \mu_2 > \mu_0$→ p-value = P(T>t*) = 1-P(T<t*)</td></tr>
<tr><td>Step Five:</td><td>If p-value$\leq (1 - confidene) = \alpha$
→ Reject H_0
If p-value$> (1 - confidence) = \alpha$
→ Fail to Reject H_0</td></tr>
</table>

Hypothesis Testing for μ unknown $\sigma_1 \neq \sigma_2$

```
#TestType: 1 for <, 2 for >, 3 for not equal
Mdiff.Ttest.neqvar<-function(conf.level,xbar1,sx1,n1,xbar2,sx2,n2,m0,TestType){
  txt<-"";  xbard<-xbar1-xbar2;  v<-floor((sx1^2/n1+sx2^2/n2)^2/((sx1^2/n1)^2/(n1-1)+(sx2^2/n2)^2/(n2-1)));
  TestStat<-(xbard-m0)/sqrt(sx1^2/n1+sx2^2/n2); xax<-seq(m0-5*sqrt(sx1^2/n1+sx2^2/n2),m0+5*sqrt(sx1^2/n1+sx2^2/n2),.01);
  P_x<-dt((xax-m0)/sqrt(sx1^2/n1+sx2^2/n2),v);
  if(TestType==1){    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep=""); CritVal<-qt(1-conf.level,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    pvalue<-pt(TestStat,v);  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,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    pvalue<-1-pt(TestStat,v); 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,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;
    CritVal2<-qt(conf.level+(1-conf.level)/2,v)*sqrt(sx1^2/n1+sx2^2/n2)+m0;  pvalue=2*pt(-abs(TestStat),v);
    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(n1<30|n2<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(xbard,2),c(0,max(P_x)),col="red");
  if(TestType==3){y.shade<- c(0,dt((cord.x1-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0,0,dt((cord.x2-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0) ;
  }else{y.shade<- c(0,dt((cord.x-m0)/sqrt(sx1^2/n1+sx2^2/n2),v),0) ;}
  polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red")) ;}
```

Hypothesis Testing for paired data μ known σ_d

Step One:	(i) $H_0: \mu_1 - \mu_2 = \mu_0$ & $H_a: \mu_1 - \mu_2 \neq \mu_0$ (ii) $H_0: \mu_1 - \mu_2 \geq \mu_0$ & $H_a: \mu_1 - \mu_2 < \mu_0$ (iii) $H_0: \mu_1 - \mu_2 \leq \mu_0$ & $H_a: \mu_1 - \mu_2 > \mu_0$
Step Two:	1. Quantitative *2. Random Sample* *3.* $n > 30$ OR the population is bell shaped
Step Three:	$z^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{\sigma_d^2}{n}}}$
Step Four:	(i) $H_a: \mu_1 - \mu_2 \neq \mu_0$ → p-value = 2*P(T<-|t*|) (ii) $H_a: \mu_1 - \mu_2 < \mu_0$ → p-value = P(T<t*) (iii) $H_a: \mu_1 - \mu_2 > \mu_0$ → p-value = P(T>t*) = 1-P(T<t*)
Step Five:	If p-value$\leq (1 - confidene) = \alpha$ → Reject H_0 If p-value$> (1 - confidence) = \alpha$ → Fail to Reject H_0

Hypothesis Testing for paired data μ known σ_d

```
#TestType: 1 for <, 2 for >, 3 for not equal
mdiff.pairedZtest<-function(conf.level,xbar1,xbar2,sigmad,n,m0,TestType){
 xbard<-xbar1-xbar2;  txt<-"";  TestStat<-((xbar1-xbar2)-m0)/sqrt(sigmad^2/n);  xax<-seq(m0-5*sqrt(sigmad^2/n),m0+5*sqrt(sigmad^2/n),.01);
 P_x<-dnorm(xax,m0,sqrt(sigmad^2/n));
 if(TestType==1){    txt<-paste("Test Alternative: parameter < ",m0,"\n",sep="");    CritVal<-qnorm(1-conf.level,m0,sqrt(sigmad^2/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,sqrt(sigmad^2/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,sqrt(sigmad^2/n));
   CritVal2<-qnorm(conf.level+(1-conf.level)/2,m0,sqrt(sigmad^2/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(xbard<min(cord.x2)){  loc<-"topright"; }else{ loc<-"topleft"; }  }
 if(n<30){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(xbard,2),c(0,max(P_x)),col="red");
 if(TestType==3){y.shade<-c(0,dnorm(cord.x1,m0,sqrt(sigmad^2/n)),0,0,dnorm(cord.x2,m0,sqrt(sigmad^2/n)),0);
 }else{ y.shade<-c(0,dnorm(cord.x,m0,sqrt(sigmad^2/n)),0);}
 polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));}
mdiff.pairedZtest(.95,100,97,4.2,21,0,3)
```

Hypothesis Testing for paired data μ unknown σ_d

Step One:	(i) $H_0: \mu_1 - \mu_2 = \mu_0$ & $H_a: \mu_1 - \mu_2 \neq \mu_0$ (ii) $H_0: \mu_1 - \mu_2 \geq \mu_0$ & $H_a: \mu_1 - \mu_2 < \mu_0$ (iii) $H_0: \mu_1 - \mu_2 \leq \mu_0$ & $H_a: \mu_1 - \mu_2 > \mu_0$
Step Two:	1. Quantitative *2. Random Sample* *3.* $n > 30$ OR the population is bell shaped
Step Three:	$$t^* = \frac{((\overline{x_1} - \overline{x_2}) - \mu_0)}{\sqrt{\frac{s_d^2}{n}}}$$
Step Four:	(i) $H_a: \mu_1 - \mu_2 \neq \mu_0$ → p-value = $2 * P(T < -\lvert t^* \rvert)$ (ii) $H_a: \mu_1 - \mu_2 < \mu_0$ → p-value = P(T<t*) (iii) $H_a: \mu_1 - \mu_2 > \mu_0$ → p-value = P(T>t*) = 1-P(T<t*)
Step Five:	If p-value$\leq (1 - \mathit{confidene}) = \alpha$ → Reject H_0 If p-value$> (1 - \mathit{confidence}) = \alpha$ → Fail to Reject H_0

Hypothesis Testing for paired data μ unknown σ_d

```
#TestType: 1 for <, 2 for >, 3 for not equal
Mdiff.pairedTtest<-function(conf.level,xbar1,xbar2,sigmad,n,m0,TestType){
 txt<-"";  xbard<-xbar1-xbar2;  TestStat<-(xbard-m0)/sqrt(sigmad^2/n);  xax<-seq(m0-5*sqrt(sigmad^2/n),m0+5*sqrt(sigmad^2/n),.01);  P_x<-dt((xax-m0)/sqrt(sigmad^2/n),n-1);
 if(TestType==1){txt<-paste("Test Alternative: parameter < ",m0,"\n",sep="");    CritVal<-qt(1-conf.level,n-1)*sqrt(sigmad^2/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)*sqrt(sigmad^2/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)*sqrt(sigmad^2/n)+m0;
   CritVal2<-qt(conf.level+(1-conf.level)/2,n-1)*sqrt(sigmad^2/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(xbard<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(xbard,2),c(0,max(P_x)),col="red");
 if(TestType==3){y.shade<- c(0,dt((cord.x1-m0)/sqrt(sigmad^2/n),n-1),0,0,dt((cord.x2-m0)/sqrt(sigmad^2/n),n-1),0);}else{y.shade<- c(0,dt((cord.x-m0)/sqrt(sigmad^2/n),n-1),0)}
 polygon(x.shade,y.shade,col='gray');  legend(loc,c("Rejection Region","Observation"),fill=c("gray","red"));
}
```