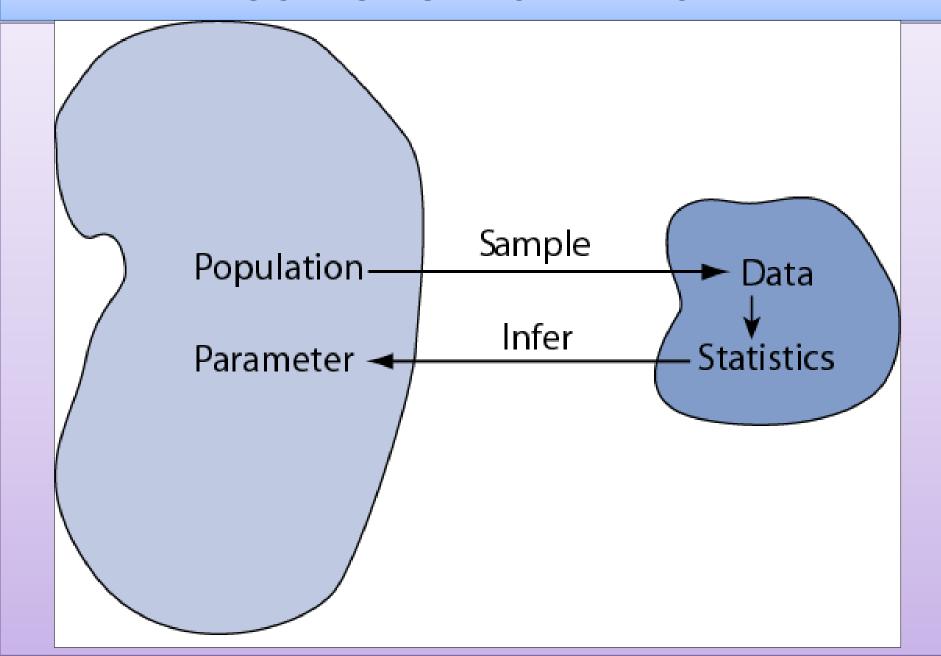
Hypothesis Testing

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- Population = all possible values
- Sample = a portion of the population
- Statistical inference = generalizing from a sample to a population with calculated degree of certainty
- Two forms of statistical inference
 - Hypothesis testing
 - Estimation
- Parameter = a characteristic of population, e.g., population mean µ
- Statistic = calculated from data in the sample, e.g., sample mean (\bar{x})



- Hypothesis
 - An educated guess
 - A claim or statement about a property of a Population

Goal: The goal in Hypothesis Testing is to analyze a sample in an attempt to distinguish between

population characteristics that are likely to occur and population characteristics that are *unlikely* to occur.

- Null hypothesis (H_0) is a claim of "no difference in the population"
- Alternative hypothesis (H_a) claims "H₀ is false"

We collect data and seek evidence against H_0 as a way of bolstering H_a

Null Hypothesis

- Statement about the value of a population parameter
- Represented by H₀
- Always stated as an Equality

Alternative Hypothesis

- Statement about the value of a population parameter that must be true if the null hypothesis is false
- Represented by H₁
- Stated in on of three forms
 - >
 - <
 - ≠

Example: Hypothesis

- The problem: In the 1970s, 20–29 year old men in the U.S. had a mean μ body weight of 170 pounds. Standard deviation σ was 40 pounds. We test whether mean body weight in the population now differs.
- Null hypothesis $H_{0:} \mu = 170$ ("no difference")
- The alternative hypothesis can be either

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H_{a:} \mu > 170 (one-sided test) or
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 $H_{a:} \mu \neq 170$ (two-sided test)

Example: Hypothesis

 In a trial a jury must decide between two hypotheses. The null hypothesis is
 H₀: The defendant is innocent

The alternative hypothesis or research hypothesis is
 H₁: The defendant is guilty

The jury does not know which hypothesis is true.
 They must make a decision on the basis of evidence presented.

-**Test statistic -** Quantity based on sample data and null hypothesis used to test between null and alternative hypotheses

 Rejection region - Values of the test statistic for which we reject the null in favor of the alternative hypothesis

Type I vs. Type II Error

Test Resul	t – H ₀ True	H ₀ False
True State		
H ₀ True	Correct	Type I Error
	Decision	
H ₀ False	Type II Error	Correct Decision

$$\alpha = P(Type\ I\ Error)$$
 $\beta = P(Type\ II\ Error)$

• Goal: Keep α , β reasonably small

Alpha vs. Beta

- a is the probability of Type I error
- b is the probability of Type II error
- The experimenters have the freedom to set the α -level for a particular hypothesis test. That level is called the level of significance for the test.
- Changing a can (and often does) affect the results of the test—whether you reject or fail to reject H₀.

Alpha vs. Beta

- It would be wonderful if we could force both α and β to equal zero.
- •Unfortunately, these quantities have an inverse relationship. As α increases, β decreases and vice versa.
- The only way to decrease both α and β is to increase the sample size.
- To make both quantities equal zero, the sample size would have to be infinite—you would have to sample the entire population.

- Every hypothesis test ends with the experimenters either
 - Rejecting the Null Hypothesis, or
 - Failing to Reject the Null Hypothesis
- If one never able to <u>accept</u> the Null Hypothesis, the best comment about the Null Hypothesis is that there not enough evidence, based on a sample, to reject it!

Brief Steps in Hypothesis Testing

The critical concepts are theses:

- 1. There are two hypotheses, the null and the alternative hypotheses.
- 2. The procedure begins with the assumption that the null hypothesis is true.
- 3. The goal is to determine whether there is enough evidence to infer that the alternative hypothesis is true, or the null is not likely to be true.
- 4. There are two possible decisions:
- Conclude that there is enough evidence to support the alternative hypothesis. Reject the null.
- Conclude that there is not enough evidence to support the alternative hypothesis. Fail to reject the null.

Hypothesis Testing Steps

- A. Null and alternative hypotheses
- B. Test statistic
- C. P-value and interpretation
- D. Significance level (optional)

Example: Hypothesis

- The problem: In the 1970s, 20–29 year old men in the U.S. had a mean μ body weight of 170 pounds. Standard deviation σ was 40 pounds. We test whether mean body weight in the population now differs.
- Null hypothesis $H_{0:} \mu = 170$ ("no difference")
- The alternative hypothesis can be either

```
H_{a:} \mu > 170 (one-sided test) or
```

 $H_{a:} \mu \neq 170$ (two-sided test)

Test Statistic

This is an example of a one-sample test of a mean when σ is known. Use this statistic to test the problem:

$$z_{\text{stat}} = \frac{\overline{x} - \mu_0}{SE_{\overline{x}}}$$

where μ_0 = population mean assuming H_0 is true

and
$$SE_{\bar{x}} = \frac{\sigma}{\sqrt{n}}$$

Example: z statistic

- For the illustrative example, $\mu_0 = 170$
- We know $\sigma = 40$
- Take an SRS of n = 64. Therefore

$$SE_{\overline{x}} = \frac{\sigma}{\sqrt{n}} = \frac{40}{\sqrt{64}} = 5$$

• If we found a sample mean of 173, then

$$z_{\text{stat}} = \frac{\overline{x} - \mu_0}{SE_{\overline{x}}} = \frac{173 - 170}{5} = 0.60$$

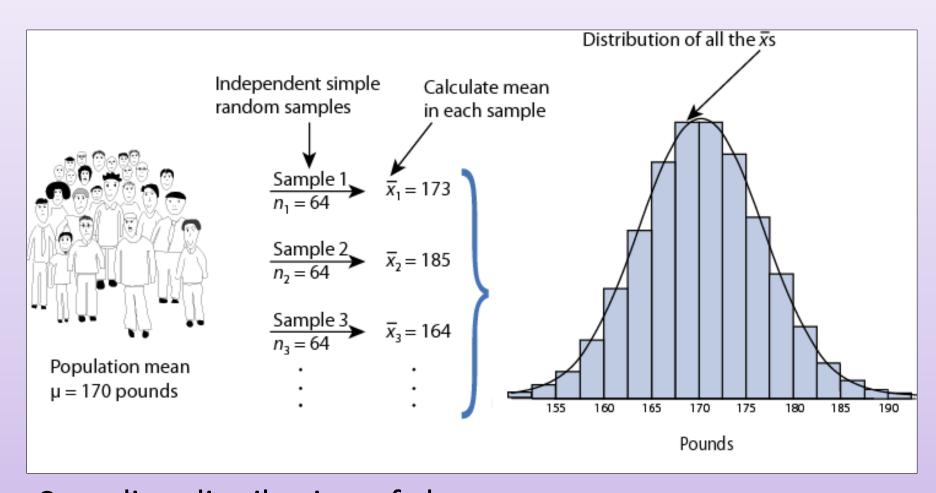
Example: z statistic

If we found a sample mean of 185, then

$$z_{\text{stat}} = \frac{\overline{x} - \mu_0}{SE_{\overline{x}}} = \frac{185 - 170}{5} = 3.00$$

- $\mu_{H0} + z \sigma_x = 8000 + 1.96(40) = 8078.4$
- 185 + 1.96 x 40 = 263.4
- μ_{H0} z $\sigma_x = 8000 + 1.96(40) = 8078.4$
- 185 1.96 x 40 = 106.6
- 106.4 <= pop mean <= 263.4

Reasoning Behind μ and z_{stat}



Sampling distribution of xbar under H_0 : $\mu = 170$ for $n = 64 \Rightarrow$

$$\bar{x} \sim N(170,5)$$

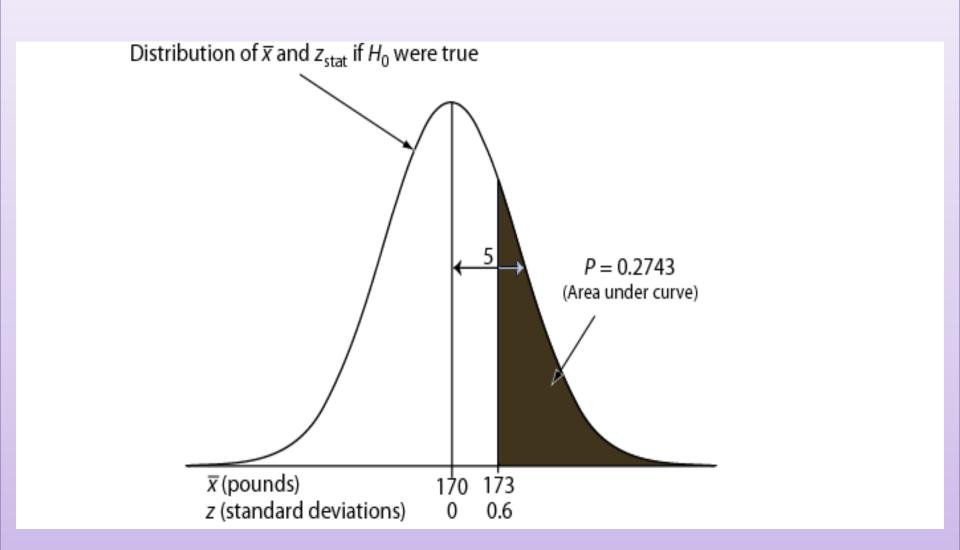
P-value

- The P-value answer the question: What is the probability of the observed test statistic or one more extreme when H_0 is true?
- This corresponds to the AUC in the tail of the Standard Normal distribution beyond the $z_{\text{stat.}}$
- Convert z statistics to P-value :

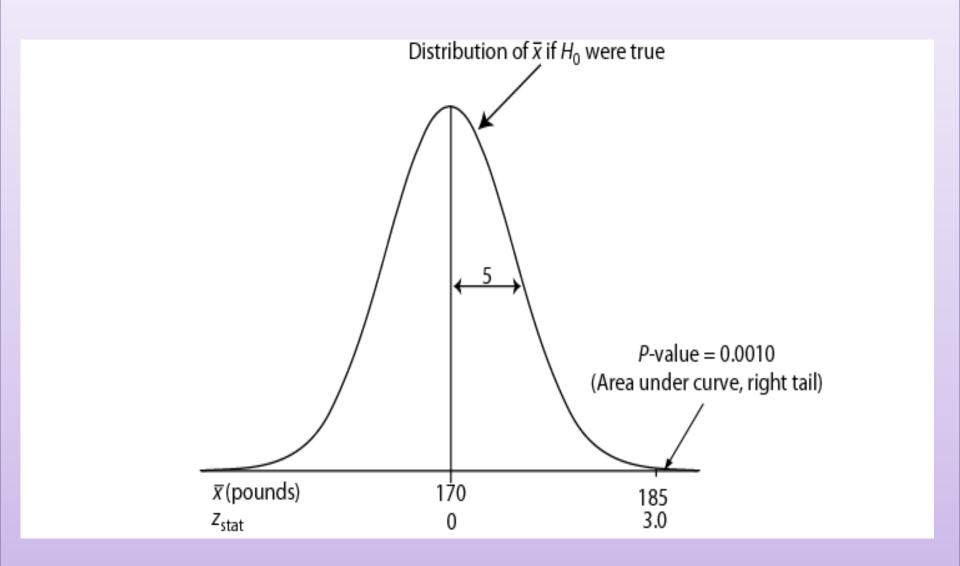
For
$$H_a$$
: $\mu > \mu_0 \Rightarrow P = \Pr(Z > z_{\text{stat}}) = \text{right-tail beyond } z_{\text{stat}}$
For H_a : $\mu < \mu_0 \Rightarrow P = \Pr(Z < z_{\text{stat}}) = \text{left tail beyond } z_{\text{stat}}$
For H_a : $\mu \neq \mu_0 \Rightarrow P = 2 \times \text{one-tailed } P\text{-value}$

Use Table B or software to find these probabilities

One-sided P-value for z_{stat} of 0.6

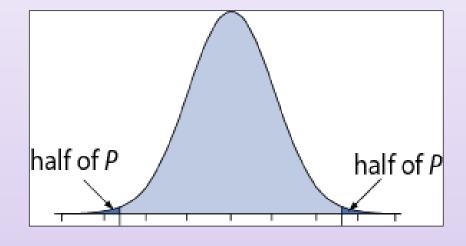


One-sided P-value for z_{stat} of 3.0



Two-Sided P-Value

- One-sided $H_a \Rightarrow$ AUC in tail beyond z_{stat}
- Two-sided $H_a \Rightarrow$ consider potential deviations in both directions \Rightarrow double the onesided P-value



Examples: If one-sided P = 0.0010, then two-sided $P = 2 \times 0.0010 = 0.0020$. If one-sided P = 0.2743, then two-sided $P = 2 \times 0.2743 = 0.5486$.

Interpretation

- P-value answer the question: What is the probability of the observed test statistic ... when H_0 is true?
- Thus, smaller and smaller P-values provide stronger and stronger evidence against H_0
- Small P-value ⇒ strong evidence

Interpretation

Conventions*

 $P > 0.10 \Rightarrow$ non-significant evidence against H_0 $0.05 < P \le 0.10 \Rightarrow$ marginally significant evidence $0.01 < P \le 0.05 \Rightarrow$ significant evidence against H_0 $P \le 0.01 \Rightarrow$ highly significant evidence against H_0

Examples

 $P = .27 \Rightarrow$ non-significant evidence against H_0 $P = .01 \Rightarrow$ highly significant evidence against H_0

* It is unwise to draw firm borders for "significance"

(Summary) One-Sample z Test

A. Hypothesis statements

$$H_0$$
: $\mu = \mu_0$ vs.

$$H_a$$
: $\mu \neq \mu_0$ (two-sided) or

$$H_a$$
: $\mu < \mu_0$ (left-sided) or

$$H_a$$
: $\mu > \mu_0$ (right-sided)

B. Test statistic

$$z_{\text{stat}} = \frac{\overline{x} - \mu_0}{SE_{\overline{x}}} \text{ where } SE_{\overline{x}} = \frac{\sigma}{\sqrt{n}}$$

- C. P-value: convert z_{stat} to P value
- D. Significance statement (usually not necessary)

Two-Sample t-tests

Clearly, we are often faced with making judgments for circumstances that involve more than one population and sample. For the moment, we will focus on the so-called *two sample situation*. That is, we consider two populations.

	City A	City B
Mean	μ_{A}	μ_{B}
SD	σ_{A}	σ_{B}

Question:

Do you believe the two populations have the same mean?

Two Sample Hypotheses

$$H_0$$
: $\mu_A = \mu_B$ versus H_1 : $\mu_A \neq \mu_B$

or equivalently

$$H_0$$
: $\Delta = \mu_A - \mu_B = 0$ versus H_1 : $\Delta = \mu_A - \mu_B \neq 0$.

Parameters vs. Estimates

Popula	ation
--------	-------

Population 2

Parameter

Estimate

Parameter

Estimate

Populations of individual values

$$\mu_{\scriptscriptstyle 1}$$

 x_1

 μ_2

 \mathcal{X}_{2}

$$\sigma_{\scriptscriptstyle 1}^{\;2}$$

 S_1^2

 σ_2^2

 S_2^2

$$\sigma_1$$

 S_1

 σ_2

 S_2

Populations of means, samples of size n₁ and n₂

$$\mu_{\scriptscriptstyle 1}$$

 \overline{x}_2

$$\sigma_1^2/n_1$$

 s_1^2/n_1

 σ_2^2/n_2

 s_2^2/n_2

$$\sigma_1/\sqrt{n_1}$$

 $s_1/\sqrt{n_1}$

 $\sigma_2/\sqrt{n_2}$

 $s_2/\sqrt{n_2}$

Parameters vs. Estimates

We are interested in

$$d = \overline{x}_1 - \overline{x}_2$$

$$\Delta = \mu_1 - \mu_2$$

If the samples are independent, then

$$Var(\overline{x}_1 - \overline{x}_2) = Var(\overline{x}_1) + Var(\overline{x}_2)$$

$$Var(\overline{x}_1 - \overline{x}_2) = \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}$$

When

$$\sigma_1^2 = \sigma_2^2$$
, $Var(\overline{x}_1 - \overline{x}_2) = \sigma^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)$

Pooled Average

Hence, we use the weighted average of the two sample variances, with the weighting done according to sample size. This weighted average is called the pooled estimate:

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

To estimate $Var(\overline{x}_1 - \overline{x}_2)$, we can use

$$S_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)$$

Example 1: Blood Pressures of Children

To investigate the question of whether the children of city A and city B have the same systolic blood pressure, a random sample of n = 10 children was selected from each city and their blood pressures measured. These samples provided the following data:

Statistic	City A	City B
N	10	10
\overline{x} (mmHg)	105.8	97.2
s^2 (mmHg) 2	78.62	22.40
s (mmHg)	8.87	4.73

Blood Pressures of Children

We are interested in the difference:

$$\Delta = \mu_A - \mu_B$$

and we have \overline{X}_A as an estimate of μ_A and \overline{X}_B as an estimate of μ_B ; hence it is reasonable to use:

d =
$$\overline{x}_{\overline{A}} \overline{x}_{B}$$
 = 105.8 - 97.2 = 8.6 (mm Hg)

as an estimate of $\Delta = \mu_A - \mu_B$.

Confidence Interval for μ_A - μ_B , using s_p

$$C\left[(\overline{x}_{A} - \overline{x}_{B}) - t_{0.975}s_{p}\sqrt{\frac{1}{n_{A}} + \frac{1}{n_{B}}} \le \mu_{A} - \mu_{B} \le (\overline{x}_{A} - \overline{x}_{B}) + t_{0.975}s_{p}\sqrt{\frac{1}{n_{A}} + \frac{1}{n_{B}}}\right] = 0.95$$

$$df = (n_A - 1) + (n_B - 1)$$

$$\overline{x}_A - \overline{x}_B = 8.6$$
 $t_{0.975} = 2.1009$ $df = 18$

$$s_p^2 = \frac{(n_A - 1)s_A^2 + (n_B - 1)s_B^2}{(n_A - 1) + (n_B - 1)} = \frac{9(78.62) + 9(22.4)}{18} = 50.51$$

Confidence Interval for μ_A - μ_B , using s_p

$$S_p = \sqrt{50.51} = 7.11$$

$$C \left[8.6 - 2.1009(7.11) \sqrt{\frac{1}{10} + \frac{1}{10}} \le \mu_A - \mu_B \le 8.6 + 2.1009(7.11) \sqrt{\frac{1}{10} + \frac{1}{10}} \right] = 0.95$$

$$C[1.92 \le \mu_A - \mu_B \le 15.27] = 0.95$$

TABLE 2-Nurse Practitioners'	Responses to	10 Clinical C	ase Scenarios on
Occupational Health	Test	·	

Case Scenario Type	Occupational Program Graduates' No. of Correct Responses, Mean ± SD $n=31$	Nonoccupational Program Graduates' No. of Correct Responses, Mean ± SD n = 223
Occupational disease identification* Occupational case management* Both case scenario types*	3.9 ± 1.0 4.1 ± 1.2 8.0 ± 1.7	2.2 ± 1.2 3.4 ± 1.5 5.6 ± 2.4

Note. Five clinical case scenarios were included in each category.

 $^{^{\}star}P < .05$ (occupational as compared with nonoccupational program graduates).

	1	2
	OCCP Prog	Non OCCP Prog
n	31	223
mean	4.1	3.4
SD	1.2	1.5
S^2	1.44	2.25

- **1. The hypothesis:** $H_0: \mu_1 = \mu_2 \ vs. \ H_1: \mu_1 \neq \mu_2$
- 2. The assumptions: Independent random samples from normal distributions,

- 3. The α level: $\alpha = 0.05$
- 4. The test statistic:

5. The critical region: Reject H_0 if t is not between

6. Test result:

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

$$s_p^2 = \frac{30(1.44) + 222(2.25)}{30 + 222}$$

 $s_p = \sqrt{2.154} = 1.47$

$$s_p^2 = \frac{542.7}{252} = 2.154$$

$$s_p = \sqrt{2.15}$$

$$\sqrt{\frac{1}{n_1} + \frac{1}{n_2}} = \sqrt{\frac{1}{31} + \frac{1}{223}} = 0.19$$

$$t = \frac{4.1 - 3.4}{1.47(0.19)} = 2.5$$

7. The Conclusion: Reject H_0 since t = 2.5 is not between ± 1.97 ; 0.01

Independent Random Samples from Two Populations of Serum Uric Acid Values

	San	Sample	
	1	2	
	1.2	1.7	
	0.8	1.5	
	1.1	2.0	
	0.7	2.1	
	0.9	1.1	
	1.1	0.9	
	1.5	2.2	
	0.8	1.8	
	1.6	1.3	
	0.9	1.5	
Sum	10.6	16.1	
Mean	1.06	1.61	

Independent Random Samples from Two Populations of Serum Uric Acid Values

1. The hypothesis:
$$H_0$$
: $\mu_1 = \mu_2$ vs. H_1 : $\mu_1 \neq \mu_2$

2. The
$$\alpha$$
-level: $\alpha = 0.05$

3. The assumptions: Independent Random Samples Normal Distribution,
$$\sigma_1^2 = \sigma_2^2$$

4. The test statistic:
$$t = \frac{\overline{x}_1 - \overline{x}_2}{s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

Confidence Interval for μ_A - μ_B , using s_p

5. The reject region: Reject H_0 : $\mu_1 = \mu_2$ if t is not between $\pm t_{0.975}(18) = 2.1009$

6. The result:

$$t = \frac{1.06 - 1.61}{0.37\sqrt{\frac{1}{10} + \frac{1}{10}}} = \frac{-0.55}{0.37(0.45)} = -3.3$$

7. The conclusion: Reject H_0 : $\mu_1 = \mu_2$, since t is not between \pm 2.1009

	Before	After
	1.2	1.7
	0.8	1.5
	1.1	2.0
	0.7	2.1
	0.9	1.1
	1.1	0.9
	1.5	2.2
	0.8	1.8
	1.6	1.3
	0.9	1.5
Sum	10.6	6.1
Mean	1.06	1.61

Serum Uric Acid Values Before And After A Special Meal

***	1	1 4
W	orks	heet

Person	Before	After	d ^a	d^2
1	1.2	1.7	0.5	0.25
2	0.8	1.5	0.7	0.49
3	1.1	2.0	0.9	0.81
4	0.7	2.1	1.4	1.96
5	0.9	1.1	0.2	0.04
6	1.1	0.9	-0.2	0.04
7	1.5	2.2	0.7	0.49
8	0.8	1.8	1.0	1.00
9	1.6	1.3	-0.3	0.09
10	0.9	1.5	0.6	0.36
Sum	10.6	16.1	5.5	5.53
Mean	1.06	1.61	0.55	
Sum²/n			3.025	
SS			2.505	
Variance			0.278	
SD			0.528	

 $d^a = After - Before$

1. The hypothesis:
$$H_0$$
: $\Delta = 0$ vs. H_1 : $\Delta \neq 0$, where $\Delta = \mu_{After} - \mu_{Before}$

2. The
$$\alpha$$
-level: $\alpha = 0.05$

3. The assumptions: Random Sample of Differences, Normal Distribution

4. The test statistic:

$$t = \frac{\overline{d}}{s_{\overline{d}}} = \frac{\overline{x}_{After} - \overline{x}_{Before}}{s_d / \sqrt{n}}$$

5. The rejection region: Reject H_0 : $\Delta = 0$, if t is not between $\pm t_{0.975}(9) = 2.26$

6. The result:

$$t = \frac{0.55}{0.528/\sqrt{10}} = \frac{0.55}{0.528/(3.16)} = 3.29$$

7. The conclusion: Reject H_0 : $\Delta = 0$ since t is not between ± 2.26

- Chi-square test: an inferential statistics technique designed to test for significant relationships between two variables organized in a bivariate table.
- Chi-square requires no assumptions about the shape of the population distribution from which a sample is drawn.

- A statistical method used to determine goodness of fit
 - Goodness of fit refers to how close the observed data are to those predicted from a hypothesis

Note:

- The chi square test does not prove that a hypothesis is correct
 - It evaluates to what extent the data and the hypothesis have a good fit

Limitations of the Chi-Square Test

- The chi-square test does <u>not</u> give us much information about the *strength* of the relationship or its *substantive* significance in the population.
- The chi-square test is **sensitive** to **sample size**. The size of the calculated chi-square is **directly proportional** to the size of the sample, independent of the strength of the relationship between the variables.
- The chi-square test is also sensitive to small expected frequencies in one or more of the cells in the table.

Statistical Independence

- *Independence* (*statistical*): the **absence** of association between two cross-tabulated variables. The percentage distributions of the dependent variable within each category of the independent variable are **identical**.
 - The research hypothesis (H_1) proposes that the two variables are related in the population.

• The null hypothesis (H_o) states that no association exists between the two cross-tabulated variables in the population, and therefore the variables are statistically independent.

 H_1 : The two variables are **related** in the population.

Gender and fear of walking alone at night are *statistically dependent*.

Afraid	Men	Women	Total
No	83.3%	57.2%	71.1%
Yes	16.7%	42.8%	28.9%
Total	100%	100%	100%

 H_0 : There is **no association** between the two variables.

Gender and fear of walking alone at night are *statistically independent*.

Afraid	Men	Women	Total
No	71.1%	71.1%	71.1%
Yes	28.9%	28.9%	28.9%
Total	100%	100%	100%

Concept of Expected Frequencies

Expected frequencies f_e : the cell frequencies that would be expected in a bivariate table if the two tables were statistically independent.

Observed frequencies f_o : the cell frequencies <u>actually observed</u> in a bivariate table.

$$f_e =$$
(column marginal)(row marginal)

To obtain the expected frequencies for any cell in any cross-tabulation in which the two variables are assumed independent, **multiply** the row and column totals for that cell and **divide** the product by the total number of cases in the table.

Calculating the Obtained Chi-Square

• The test statistic that **summarizes** the differences between the **observed** (*fo*) and the **expected** (*fe*) frequencies in a bivariate table.

$$\chi^2 = \sum \frac{(f_e - f_o)^2}{f_e}$$

$$f_e$$
 = expected frequencies f_o = observed frequencies

$$df = (r-1)(c-1)$$

where

r = the number of rows

c = the number of columns

- The outcome
 - F₁ generation
 - All offspring have straight wings and gray bodies
 - F₂ generation
 - 193 straight wings, gray bodies
 - 69 straight wings, ebony bodies
 - 64 curved wings, gray bodies
 - 26 curved wings, ebony bodies
 - 352 total flies
- Applying the chi square test
 - Step 1: Propose a null hypothesis (Ho) that allows us to calculate the expected values based on Mendel's laws
 - The two traits are independently assorting

- Step 2: Calculate the expected values of the four phenotypes, based on the hypothesis
 - According to our hypothesis, there should be a 9:3:3:1 ratio on the F₂ generation

Phenotype	Expected probability	Expected number	Observed number
straight wings, gray bodies	9/16	9/16 X 352 = 198	193
straight wings, ebony bodies	3/16	3/16 X 352 = 66	64
curved wings, gray bodies	3/16	3/16 X 352 = 66	62
curved wings, ebony bodies	1/16	1/16 X 352 = 22	24

Step 3: Apply the chi square formula

$$\chi^2 = \frac{(O_1 - E_1)^2}{E_1} + \frac{(O_2 - E_2)^2}{E_2} + \frac{(O_3 - E_3)^2}{E_3} + \frac{(O_4 - E_4)^2}{E_4}$$

$$\chi^2 = \frac{(193 - 198)^2}{198} + \frac{(69 - 66)^2}{66} + \frac{(64 - 66)^2}{66} + \frac{}{}$$

$$\chi^2$$
 = 0.13 + 0.14 + 0.06 + 0.73

$$\chi^2 = 1.06$$

Expected number	Observed number
198	193
66	64
66	62
22	24

- Step 4: Interpret the chi square value
 - The calculated chi square value can be used to obtain probabilities, or P values, from a chi square table
 - These probabilities allow us to determine the likelihood that the observed deviations are due to random chance alone
 - Low chi square values indicate a high probability that the observed deviations could be due to random chance alone
 - High chi square values indicate a low probability that the observed deviations are due to random chance alone
 - If the chi square value results in a probability that is less than 0.05 (ie: less than 5%) it is considered statistically significant
 - The hypothesis is rejected

- Step 4: Interpret the chi square value
 - Before we can use the chi square table, we have to determine the degrees of freedom (df)
 - The df is a measure of the number of categories that are independent of each other
 - If you know the 3 of the 4 categories you can deduce the 4th (total number of progeny categories 1-3)
 - df = n 1
 - where n = total number of categories
 - In our experiment, there are four phenotypes/categories
 - Therefore, df = 4 1 = 3
 - Refer to Table