The Chi-square test for differences among more than 2 proportions

We are interested in the independent samples case.

Example:

- A study investigated the accuracy of death certificates by comparing the results of 575 autopies to the causes of death listed on the certificates.
- Two hospitals participated in the study.
  - community hospital, labeled A
  - university hospital, labeled B
- Three possible cases
  - death certificate confirmed accurate
  - death certificate contained inaccuracies but did not require correction of underlying cause of death

Another multiple comparisons problem!

\[ H_0 : p_c = p_i = p_r \]
\[ H_a : p_c \neq p_i \text{ or } p_c \neq p_r \text{ or } p_i \neq p_r \]

- We will first test whether there are any significant differences.
- Only if we reject \( H_0 \) in the overall test will we do pairwise tests to find out which population proportions are different.
Results

<table>
<thead>
<tr>
<th></th>
<th>Hospital A</th>
<th>Hospital B</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Confirmed accurate</td>
<td>157</td>
<td>268</td>
<td>425</td>
</tr>
<tr>
<td>Inacc, no recoding</td>
<td>18</td>
<td>44</td>
<td>62</td>
</tr>
<tr>
<td>Incorrect, recoding</td>
<td>54</td>
<td>34</td>
<td>88</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>229</td>
<td>346</td>
<td>575</td>
</tr>
</tbody>
</table>

The overall sample proportion of death certificates from hospital A is

\[
\frac{229}{575} = 0.398
\]

If \( H_0 \) is true, we would expect this same proportion of hospital A certificates in all three categories.

Observed and expected counts

<table>
<thead>
<tr>
<th></th>
<th>Hospital A</th>
<th>Hospital B</th>
<th>Hospital A</th>
<th>Hospital B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accurate</td>
<td>157</td>
<td>268</td>
<td>169.3</td>
<td>255.7</td>
</tr>
<tr>
<td>Incorrect</td>
<td>18</td>
<td>44</td>
<td>24.7</td>
<td>37.3</td>
</tr>
<tr>
<td>Recode</td>
<td>54</td>
<td>34</td>
<td>35.0</td>
<td>53.0</td>
</tr>
</tbody>
</table>

The Chi-square statistic is

\[
X^2 = 21.62
\]

- \( r = 3 \) rows
- \( c = 2 \) columns
- So the degrees of freedom is \((r - 1)(c - 1) = 2(1) = 2\)

According to Table E, the .05 cutoff under a Chi-square distribution with 2 d.f. is 5.99.

We can reject \( H_0 \) because 21.62 > 5.99. The \( p \)-value < 0.001.

We conclude that the proportions of death certificates from Hospital A are not the same for the three different categories of certificate status.

This Chi-square test in SAS

```sas
options linesize = 72 ;
data dthcert ;
input hosp $ status $ count ;
datalines ;
A C 157
A I 18
A R 54
B C 268
B I 44
B R 34 ;
proc freq data = dthcert ;
tables status * hosp / expected ;
weight count ;
run ;
proc freq data = dthcert ;
tables status * hosp / chisq ;
weight count ;
run ;
```
### Table of Status by Hosp

<table>
<thead>
<tr>
<th>STATUS</th>
<th>HOSP</th>
<th>Frequency</th>
<th>Expected</th>
<th>Percent</th>
<th>Row Pct</th>
<th>Col Pct</th>
<th>A</th>
<th>B</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td></td>
<td>157</td>
<td>268</td>
<td>425</td>
<td>27.30</td>
<td>46.61</td>
<td>73.91</td>
<td>36.94</td>
<td>63.06</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>169.26</td>
<td>255.74</td>
<td></td>
<td>68.56</td>
<td>77.46</td>
</tr>
<tr>
<td>I</td>
<td></td>
<td>18</td>
<td>44</td>
<td>62</td>
<td>3.13</td>
<td>7.65</td>
<td>10.78</td>
<td>29.03</td>
<td>70.97</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>24.692</td>
<td>37.308</td>
<td></td>
<td>7.86</td>
<td>12.72</td>
</tr>
<tr>
<td>R</td>
<td></td>
<td>54</td>
<td>34</td>
<td>88</td>
<td>9.39</td>
<td>5.91</td>
<td>15.30</td>
<td>61.36</td>
<td>38.64</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>35.047</td>
<td>52.953</td>
<td></td>
<td>23.58</td>
<td>9.83</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>229</td>
<td>346</td>
<td>575</td>
<td>39.83</td>
<td>60.17</td>
<td>100.00</td>
<td>39.83</td>
<td>60.17</td>
</tr>
</tbody>
</table>

### Statistics for Table of Status by Hosp

<table>
<thead>
<tr>
<th>Statistic</th>
<th>DF</th>
<th>Value</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chi-Square</td>
<td>2</td>
<td>21.523</td>
<td>0.001</td>
</tr>
<tr>
<td>Likelihood Ratio Chi-Square</td>
<td>2</td>
<td>21.189</td>
<td>0.001</td>
</tr>
<tr>
<td>Mantel-Haenszel Chi-Square</td>
<td>1</td>
<td>12.864</td>
<td>0.001</td>
</tr>
<tr>
<td>Phi Coefficient</td>
<td></td>
<td>0.193</td>
<td></td>
</tr>
<tr>
<td>Contingency Coefficient</td>
<td></td>
<td>0.190</td>
<td></td>
</tr>
<tr>
<td>Cramer's V</td>
<td></td>
<td>0.193</td>
<td></td>
</tr>
</tbody>
</table>

Sample Size = 575
The sample proportions are

<table>
<thead>
<tr>
<th></th>
<th>Hospital A</th>
<th>Hospital B</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Confirmed accurate</td>
<td>157</td>
<td>268</td>
<td>0.369</td>
</tr>
<tr>
<td>Inacc, no recoding</td>
<td>18</td>
<td>44</td>
<td>0.409</td>
</tr>
<tr>
<td>Incorrect, recoding</td>
<td>54</td>
<td>34</td>
<td>0.614</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>229</strong></td>
<td><strong>346</strong></td>
<td><strong>0.575</strong></td>
</tr>
</tbody>
</table>

More advanced methods provide tests and confidence intervals to formalize analysis of which population proportions are significantly different.

**Comparing more than two population means**

Example: Does the presence of pets or friends affect responses to stress?

- subjects: 45 women who described themselves as dog lovers
- randomly assigned to three groups: to do a stressful task
  1. alone
  2. with a good friend present
  3. with their dog present
- Subjects' mean heart rate during the task was one measure of the effect of stress.

**Goal: to compare population means under three different “treatments”**

- a three-independent-sample problem
- Call the population mean heart rates $\mu_1$ for when pets are present, $\mu_2$ for when friends are present, and $\mu_3$ for when women perform task alone: then
  
  $- H_0 : \mu_1 = \mu_2 = \mu_3$

  $- H_a : \mu_1 \neq \mu_2$ or $\mu_1 \neq \mu_3$ or $\mu_2 \neq \mu_3$

  * not one-sided or 2-sided

**SAS descriptive statistics:**

```
                        Analysis Variable : BEATS
                        -----------------------------
                        -----------------------------
                        GROUP=C                       
                        -----------------------------
                        N    Mean    Std Dev   Minimum   Maximum
                        -----------------------------
                        15  82.524067 9.241574   62.646000  99.046000
                        -----------------------------
                        GROUP=F                       
                        -----------------------------
                        N    Mean    Std Dev   Minimum   Maximum
                        -----------------------------
                        15  91.325133 8.341134   76.908000 102.154000
                        -----------------------------
                        GROUP=P                       
                        -----------------------------
                        N    Mean    Std Dev   Minimum   Maximum
                        -----------------------------
                        15  73.483067 9.969820   58.692000  97.538000
```
To infer about the three population means, we might use the two-independent-sample \( t \) test 3 times:

- Test \( H_0 : \mu_1 = \mu_2 \) to see if mean heart rate when pet is present differs from mean when friend is present.
- Test \( H_0 : \mu_1 = \mu_3 \) to see if mean heart rate when pet is present differs from mean when alone.
- Test \( H_0 : \mu_2 = \mu_3 \) to see if mean heart rate when friend is present differs from mean when alone.

Problem with this approach:

- 3 \( p \)-values for 3 different tests don’t tell us how likely it is that three sample means are spread apart as far as these are.
- might be that \( \bar{x}_1 = 73.48 \) and \( \bar{x}_2 = 91.32 \) are significantly different if we look at just 2 groups but not significantly different if we know they are the smallest and largest means in 3 groups
  - As more and more groups are considered, we expect gap between smallest and largest sample mean to get larger.
  - (Imagine comparing heights of shortest and tallest person in larger and larger groups of people.)
- the probability of Type I error for the whole set of \( t \)-tests will be much bigger than the \( \alpha \) level set for each one

Multiple comparisons procedures in statistics

- issue: how to do many comparisons at once with some overall measure of confidence in all our conclusions
- two steps
  - overall test of whether there is good evidence of any differences among parameters we wish to compare
  - follow-up analysis to decide which of parameters differ and to estimate size of differences

Step one: One-Way Analysis of Variance (ANOVA)

- step one (overall test) for some difference among 3 or more population means
- uses an \( F \) test to compute a \( p \)-value
Dogs, friends, and stress example:

Analysis of Variance Procedure

Class Levels Values
GROUP 3 C F P

Number of observations in data set = 45

Analysis of Variance Procedure

Dependent Variable: BEATS

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>2</td>
<td>2387.688920</td>
<td>1193.844960</td>
<td>14.08</td>
<td>0.0001</td>
</tr>
<tr>
<td>Error</td>
<td>42</td>
<td>3561.2994916</td>
<td>84.7928450</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>44</td>
<td>5948.9884836</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square 0.401360  C.V. 11.16915  Root MSE 9.208303  BEATS Mean 82.444089

Source    | DF | Anova SS | Mean Square | F Value | Pr > F |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GROUP</td>
<td>2</td>
<td>2387.688920</td>
<td>1193.844960</td>
<td>14.08</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

Main idea of ANOVA

What matters is how far apart sample means are relative to variability of individual observations.

- F statistic
  \[ F = \frac{\text{variation among the sample means}}{\text{variation among individuals in the same sample}} \]
  - compare to a cutoff value in an F distribution

Notation:

- \( I \) = number of different populations whose means we are studying
- \( n_i \) = number of observations in sample from \( i \)th population
- \( N \) = total number of observations in all samples combined

F distributions

- many different F distributions, identified by two parameters
  - numerator degrees of freedom = \( I - 1 \)
  - denominator degrees of freedom = \( N - I \)

Example

Do four varieties of tomato plant differ in mean yield? Agronomists grew 10 plants of each variety and recorded the yield of each plant in pounds of tomatoes.

What are

- the populations of interest
- the variable of interest
- \( I \)
- each \( n_i \)
- the degrees of freedom for the ANOVA F statistic
Assumptions for One-Way ANOVA

- We have I independent simple random samples, one from each of I populations.
- Each population $i$ has a normal distribution with unknown mean $\mu_i$.
  - As with $t$-tests, if sample sizes are large enough in each sample, Central Limit Theorem says inference based on sample means is OK even if population distributions are not exactly normal.

- All of the populations have the same standard deviation $\sigma$ (unknown)
  - unlike $t$-tests, there is no general procedure when population standard deviations are not assumed to be equal
  - rough rule of thumb: if largest sample standard deviation is no more than twice the smallest sample standard deviation, then population standard deviations probably are close enough to equal that ANOVA procedure is OK

Step two: individual t-tests with correction for multiple comparisons

This is the follow-up test.

- should be carried out only if the F test from one-way ANOVA is significant at the chosen significance level.

Goal: to set the overall probability of committing a type I error at $\alpha$ when doing pairwise comparisons of $k$ different means

- we will perform $\binom{k}{2}$ two-independent-sample $t$-tests
- we will conduct each one at the significance level
  \[ \alpha^* = \frac{\alpha}{\binom{k}{2}} \]
- This is called the Bonferroni correction
Dogs, friends, and stress example

- There are \( k = 3 \) samples, so there are \( \binom{k}{2} \) = 3 different pairs to compare.
- To get an overall significance level \( \alpha = .05 \) on all 3 tests considered together, we conduct each one at
  \[
  \alpha^* = \frac{.05}{3} = .0167
  \]
  - That is, we would consider the difference between two population means to be significantly different from zero at the .05 level only if the p-value for the the t-test for that pair was less than .0167.

SAS does the adjusting and prints a grouped list of the classes. Means with the same letter are not significantly different at the specified alpha level.

Analysis of Variance Procedure

Bonferroni (Dunn) T tests for variable: BEATS

NOTE: This test controls the type I experimentwise error rate generally has a higher type II error rate than REGWQ.

Alpha= 0.05  df= 42  MSE= 84.79285
Critical Value of T= 2.49
Minimum Significant Difference= 8.3847

Means with the same letter are not significantly different.

<table>
<thead>
<tr>
<th>Bon Grouping</th>
<th>Mean</th>
<th>N</th>
<th>GROUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>91.325</td>
<td>15</td>
<td>F</td>
</tr>
<tr>
<td>B</td>
<td>82.524</td>
<td>15</td>
<td>C</td>
</tr>
<tr>
<td>C</td>
<td>73.483</td>
<td>15</td>
<td>P</td>
</tr>
</tbody>
</table>

- Equivalently, we could multiply the p-value from each t-test by 3.
  * If the result was less than .05, we would consider the difference between two population means to be significantly different from zero at the .05 level.

One-way ANOVA in SAS

```sas
options linesize = 79 ;
data pet ;
  infile '/temp/pet.dat' ;
  input group $ beats ;
run ;
proc sort data = pet ;
  by group ;
run ;
proc means data = pet ;
  by group ;
  var beats ;
run ;
proc anova data = pet ;
  class group ;
  model beats = group ;
run ;
proc anova data = pet ;
  class group ;
  model beats = group ;
  means group / bon alpha = .05 ;
run ;
```