Chapter 7: Categorical data

Previously we looked at comparing means and medians for quantitative variables from one or more groups.

We can think of these problems has having a quantitative response variable with a categorical predictor variable, which is the group or treatment variable (such as placebo vs. treatment A vs treatment B).

In this section, we consider when **all variables are categorical**.

- An example might be college major vs political affiliation.
- A typical null hypothesis for this type of data is that there is no association between the two variables.
  ——For this example, the null hypothesis might be that the proportions of students supporting the Democrat, Republican, Libertarian, and Green parties are the same for different majors: psychology, biology, statistics, history, etc.

Categorical data: a motivating example

An interesting historical example are the data of survivors from the Titanic shipwreck of 1912. Passengers from the event are classified as

- male or female, (sex)
- child or adult, (age)
- and 1st, 2nd, 3rd class, and crew members (class)
- survival (yes or no)

```
library(datasets)
data(Titanic)
Titanic
```

Categorical data

```
, , Age = Child, Survived = No
      Sex
Class  Male Female
  1st     0      0
  2nd     0      0
  3rd    35     17
  Crew    0      0

, , Age = Adult, Survived = No
     Sex
Class  Male Female
  1st   118      4
  2nd   154     13
  3rd   387     89
  Crew  670      3
```

Categorical data

```
, , Age = Child, Survived = Yes
       Sex
Class  Male Female
  1st     5      1
  2nd    11     13
  3rd    13     14
  Crew    0      0

, , Age = Adult, Survived = Yes
       Sex
Class  Male Female
  1st    57    140
  2nd    14     80
  3rd    75     76
  Crew  192     20
```

Categorical data

The data can be reshaped into a single narrow format for the three variables, plus a frequency for the number of times each combination occurs.

```
library(reshape2)
df.titanic <- melt(Titanic, value.name = "Freq")
df.titanic
## Class Sex Age Survived Freq
## 1 1st Male Child No 0
## 2 2nd Male Child No 0
## 3 3rd Male Child No 35
## 4 Crew Male Child No 0
## 5 1st Female Child No 0
## 6 2nd Female Child No 0
## 7 3rd Female Child No 17
## 8 Crew Female Child No 0
## 9 1st Male Adult No 118
## 10 2nd Male Adult No 154
## 11 3rd Male Adult No 387
```

Categorical data

We usually like to think of statistical inferences as being based on collecting data in order to test a certain scientific hypothesis. In this case, we have the data first. What kinds of questions can be asked about this data?

One question is whether survival probability depended on age (child or non-child), passenger status and/or class (crew member vs passenger, 1st class vs 3rd class, etc.) or on sex.

Categorical data: inference for a proportion

We'll return to the Titanic example later. We'll start with making inferences for a single proportion. That is, we have a single yes/no or 0-1 variable, and we wish to know what proportion of the population is a yes. Examples include

- survival for patients receiving a certain treatment, such as a transplant
- proportion of college students graduating within five years
- proportion of high school students going to college
- proportion of likely voters plannng to vote for candidate X
- proportion of registered voters who will actually vote
- proportion of products made a factory that are defective (or will be returned)
- proportion of free throws made successfully by a basketball player

Categorical data: inference for a proportion

For a sample with n items, the best guess for the population proportion is:

$$\widehat{p} = \frac{\#\text{ yes}}{n}$$

This is particularly convenient if you record "yes" as 1 and "no" as 0. Then the sample mean is also the sample proportion.

Categorical data: inference for a proportion

Note that the CI follows the usual approach:

$$\text{best guess} \pm \text{critical value} \times SE$$

where here

$$SE = \sqrt{\frac{\widehat{p}(1-\widehat{p})}{n}}$$

Categorical data: inference for a proportion

Often for proportions, we want a confidence interval (CI) for the proportion. The theory is based on the binomial distribution and the assumption that for large enough samples, the proportion is roughly normally distributed. Letting $\widehat{p}$ be the sample proportion and z_{crit} be the critical value for the standard normal distribution, the normal approximation CI is

$$\widehat{p} \pm z_{crit} \sqrt{\frac{\widehat{p}(1-\widehat{p})}{n}}$$

Categorical data: inference for a proportion

For a 95% interval, z_{crit} is chosen so that the area in the middle of the standard normal distribution is 95% of the entire distribution. This means we use the value corresponding to the 97.5% quantile. This can be obtained in R as

```
qnorm(.975)
#[1] 1.959964
```

which is often rounded to 1.96. Thus the 95% interval is usually computed as

$$\widehat{p} \pm 1.96\sqrt{\frac{\widehat{p}(1-\widehat{p})}{n}}$$

Categorical data: inference for a proportion

A rule of thumb is the margin of error is close to $1/\sqrt{n}$ when $p \approx 0.5$. Why is this?

The function $f(p) = p(1-p)$ is an upside-down parabola (like a frowny face) which has a maximum at $p = 0.5$. When $p = .5$, and using $z_{crit} \approx 2$, and $\widehat{p} \approx p$, we have

$$z_{crit}\sqrt{\frac{\widehat{p}(1-\widehat{p})}{n}} \approx 2\sqrt{(1/2)(1/2)/n} = 2(1/2)\sqrt{1/n} = \sqrt{1/n}$$

Some useful values of n to keep in mind are say, $n = 100, 400, 900$. Then the margin of error is about 10%, 5% and 3.3%, respectively.

Political opinion polls, or polls for election candidates often use sample sizes of around 900 to 1200 respondents. The margin of error (i.e., $z_{crit}SE$) of 3.5% or so is often reported for these polls, which corresponds to a bit more than 900 respondents. Margins of error can be a bit more complicated for more complex kinds of polling such as stratified polling, cluster samplng etc. See STAT572 for more on this topic...

Categorical data: inference for a proportion

The 1983 Tylenol poisoning episode highlighted the desirability of using tamper-resistant packaging. The article "Tamper Resistant Packaging: Is it Really?" (Packaging Engineering, June 1983) reported the results of a survey on consumer attitudes towards tamper-resistant packaging.

- A sample of 270 consumers was asked the question: "Would you be willing to pay extra for tamper resistant packaging?"
- The number of yes respondents was 189.

Construct a 95% CI for the proportion p of all consumers who were willing in 1983 to pay extra for such packaging.

- Here $n = 270$ and $\widehat{p} = 189/270 = 0.700$.
- The 95% CI is

$$0.7 \pm 1.96\sqrt{(0.7)(0.3)/270} = 0.7 \pm 0.055 = (0.645, 0.755)$$

- This means that you are 95% confident that between 64.5% and 75.5% of consumers would be willing to pay extra for the packaging. The population here is consumers in 1983, so this proportion might have changed over time.

Categorical data: inference for a proportion

Function `prop.test()`.

- The syntax is `prop.test(x,n,p)`. Here x is the number of "successes", n is the number of trials, and p is the probability of success under the null hypothesis.
- The default null hypothesis is $H_0 : p = 0.5$, you can change it.
- We are more interested in the confidence interval.

```
prop.test(189,270,correct=F)
# 1-sample proportions test without continuity correction
#data:  189 out of 270, null probability 0.5
#X-squared = 43.2, df = 1, p-value = 4.942e-11
#alternative hypothesis: true p is not equal to 0.5
#95 percent confidence interval:
# 0.6428459 0.7515429
#sample estimates:
 # p
#0.7
```

Categorical data: inference for a proportion

The function `prop.test()` actually uses a somewhat different formula than the usual one we presented, and it is supposed to have slightly better performance.

- The formula (without continuity correction) is method 3 from the Newcombe reference, also called the **Wilson score interval**:

$$CI = \frac{2n\widehat{p} + z^2}{2(n + z^2)} \pm \frac{z\sqrt{z^2 + 4n\widehat{p}(1 - \widehat{p})}}{2(n + z^2)}$$

  where z is the critical value, or 1.96 for a 95% interval. The interval is centered at 0.5 for $\widehat{p} = 0.5$ and otherwise is centered at a value in between 0.5 and $\widehat{p}$, and closer to $\widehat{p}$ for larger n.
- There are quite a few variations on formulas for confidence intervals for proportions, as referenced in
  Newcombe R.G. (1998) Two-Sided Confidence Intervals for the Single Proportion: Comparison of Seven Methods. *Statistics in Medicine* **17**, 857–872.

```
Package{Hmisc}
library{Hmisc}
binconf(x, n, alpha=0.05,
        method=c("wilson","exact","asymptotic","all"),
        include.x=FALSE, include.n=FALSE, return.df=FALSE)
 #method=‘‘exact’’ gives the usual confidence interval
        > binconf(189, 270, alpha=0.05,
+          method="exact")
 PointEst     Lower    Upper
      0.7   0.6415003 0.754047
#method=‘‘wilson’’ gives the wilson score interval ,
same as the one given by prop.test
  > binconf(189, 270, alpha=0.05,
+          method="wilson")
 PointEst     Lower     Upper
      0.7 0.6428459 0.7515429
```

Appropriateness of the CI

The standard CI is based on a **large-sample** standard normal approximation to

$$z = \frac{\hat{p} - p}{SE}.$$

- A simple rule of thumb requires $n\hat{p} \geq 5$ and $n(1 - \hat{p}) \geq 5$ for the method to be suitable.
- Given that $n\hat{p}$ and $n(1 - \hat{p})$ are the observed numbers of successes and failures, you should have at least 5 of each to apply the large-sample CI.
- In the packaging example, $n\hat{p} = 270 \times (0.700) = 189$ (the number who support the new packaging) and $n(1 - \hat{p}) = 270 \times (0.300) = 81$ (the number who oppose) both exceed 5. The normal approximation is appropriate here.

Hypothesis testing for a proportion

To do hypothesis testing for a proportion, we can test

$$H_0 : p = p_0$$

against alternatives such as

$$H_A : p < p_0, \quad H_A : p \neq p_0, or \quad H_A : p > p_0$$

The test statistic in this case is a z-score

$$z_{obs} = \frac{\widehat{p} - p_0}{SE} \text{ with } SE = \sqrt{\frac{p_0(1-p_0)}{n}}$$

——-Note that SE here is different from the standard (Wald) CI because we use p_0 from the null hypothesis instead of using $\widehat{p}$.
Reject H_0 if $|z_{obs}|$ is greater than a critical value (two sided test)

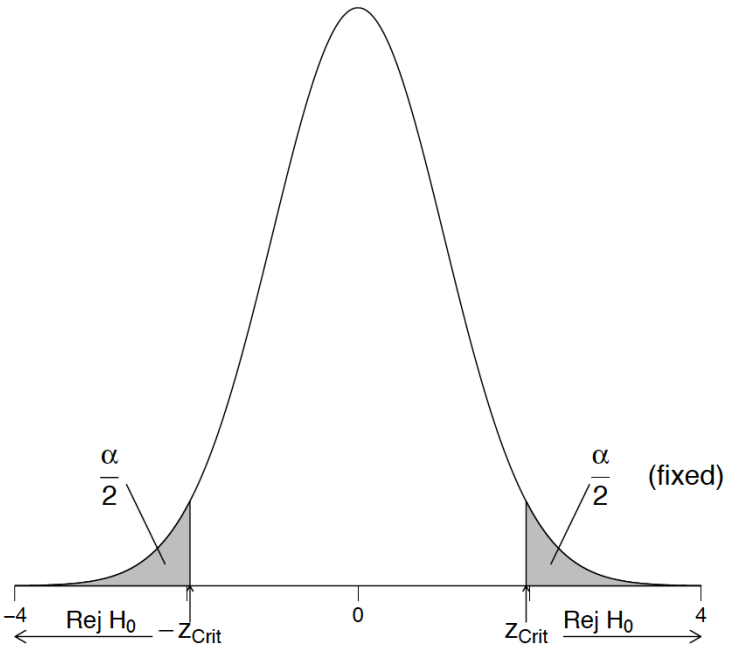
Hypothesis testing for a proportion

Hypothesis testing is then just based on comparing z_{obs} to a critical value, or comparing the p-value to α, as usual. As usual, you can just an R function such as `prop.test()` to do the hypothesis test.

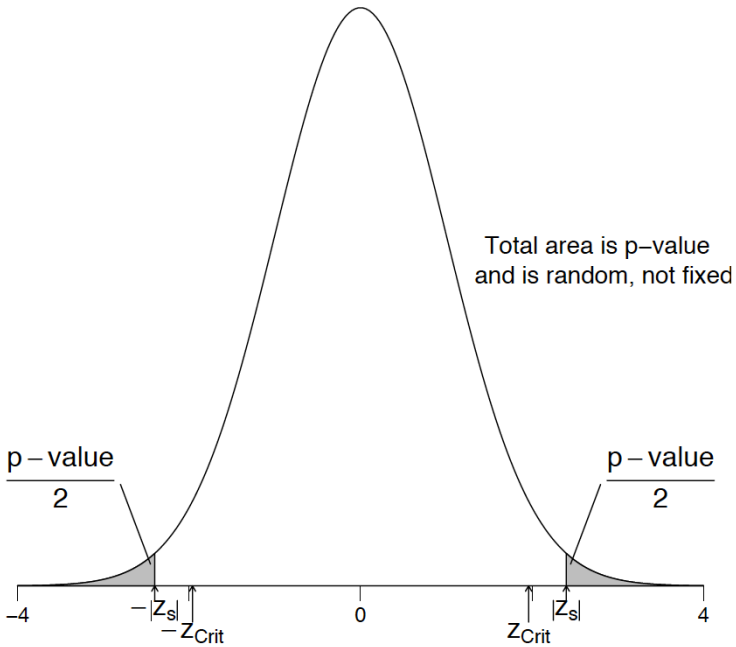
For small sample sizes, you might also consider using an exact binomial test, which uses probabilities from a binomial probability distribution instead of using a normal approximation. This is done using `binom.test()` in R, but works very similarly.

Hypothesis testing for a proportion

Z–distribution with two–sided size $\alpha = .05$ critical region



Z–distribution with two–sided p–value



Hypothesis testing for a proportion

Example: (brain hemispheres) An article in the April 6, 1983 edition of The Los Angeles Times reported on a study of 53 learning-impaired youngsters at the Massachusetts General Hospital. The right side of the brain was found to be larger than the left side in 22 of the children.

The proportion of the general population with brains having larger right sides is known to be 0.25. Does the data provide strong evidence for concluding, as the article claims, that the proportion of learning impaired youngsters with brains having larger right sides exceeds the proportion in the general population? Answer this question by computing a p-value for a one-sided test.

Hypothesis testing for a proportion

The null hypothesis is $H_0 : p = 0.25$ and the alternative is $H_A : p > 0.25$. In the formulas, $p_0 = 0.25$, the hypothesized value. We have $\widehat{p} = 22/53 = 0.415$ and

$$z_{obs} = \frac{0.415 - 0.25}{\sqrt{(0.25)(0.75)/53}} = 2.78$$

For this one-sided test, the p-value is the area to the right of 2.78 under a standard normal curve. In R, this is

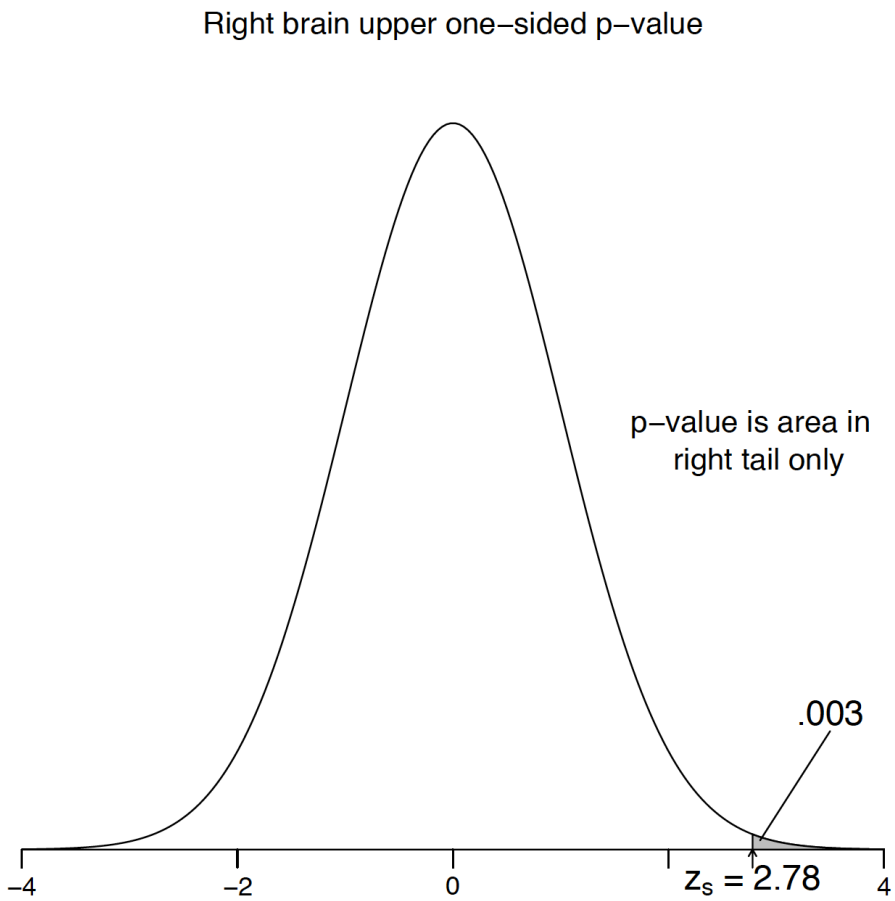
```
1-pnorm(2.78)
#[1] 0.002717945
```

A p-value of 0.0027 means that there is sufficient evidence to reject the hypothesis, conclude that learning-impaired youngsters at the Massachusetts General Hospital have higher proportion (greater than 25%) of right-side heavier brains.

Hypothesis testing for a proportion

```
#### Example: brain hemispheres
# Approximate normal test for proportion, without Yates
 continuity correction
prop.test(22, 53, p = 0.25, alternative = "greater",
correct = FALSE)
##
## 1-sample proportions test without continuity correction
## data: 22 out of 53, null probability 0.25
## X-squared = 7.7044, df = 1, p-value = 0.002754
## alternative hypothesis: true p is greater than 0.25
## 95 percent confidence interval:
## 0.3105487 1.0000000
## sample estimates:
## p
## 0.4150943
```

Hypothesis testing for a proportion



Comparing two proportions

Just like we can test whether two populations have the same mean by comparing two independent samples, we can also test whether two populations have the same proportion by comparing two independent samples.

In addtion, we can form confidence intervals for the difference in two proportions.

Comparing two proportions

Example. (Vitamin C) Two hundred and seventy nine (279) French skiers were studied during two one-week periods in 1961. One group of 140 skiers receiving a placebo each day, and the other 139 receiving 1 gram of ascorbic acid (Vitamin C) per day. The study was double blind — neither the subjects nor the researchers knew who received which treatment. The skiers getting a cold or not is recorded.

Want to compare the proportion of getting cold between the two groups.

Comparing two proportions

- Use $\widehat{p}_1 - \widehat{p}_2$ to estimate the difference in proportions
- For a confidence interval, we follow the usual pattern of

$$\text{best estimate} \pm \text{critical value} \times \text{SE}$$

$$\widehat{p}_1 - \widehat{p}_2 \pm z_{crit} \times \text{SE}(\widehat{p}_1 - \widehat{p}_2)$$

where

$$SE(\widehat{p}_1 - \widehat{p}_2) = \sqrt{\frac{\widehat{p}_1(1-\widehat{p}_1)}{n_1} + \frac{\widehat{p}_2(1-\widehat{p}_2)}{n_2}}$$

Comparing two proportions

Hypothesis test, $H_0 : p_1 = p_2$

- Test statistic:

$$z_{obs} = \frac{\widehat{p}_1 - \widehat{p}_2}{SE_{test}}$$

where

$$SE_{test} = \sqrt{\frac{\overline{p}(1-\overline{p})}{n_1} + \frac{\overline{p}(1-\overline{p})}{n_2}} = \sqrt{\overline{p}(1-\overline{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$$

with

$$\overline{p} = \frac{n_1\widehat{p}_1 + n_2\widehat{p}_2}{n_1 + n_2}$$

——-$\overline{p}$ is a pooled estimate of the common proportion
——-i.e., assuming that both populations have the same proportion $p = p_1 = p_2$, you could pool all the data treating it as a single population to get a more precise estimate of the proportion p.

- Compare the test statistic to corresponding critical values to make decisions

Comparing two proportions

Comments:

Because the formulas for computing the SE of the CI and SE of the hypothesis tests are different, it is possible that the conclusions reached by hypothesis testing might not agree with whether or not the CI includes 0, but such cases would be unusual.

Comparing two proportions

To get back to the sample, we can perform both a CI and a hypothesis test. It is convenient to arrange the data in a 2×2 table.

Outcome	Ascorbic acid	Placebo
# with cold	17	31
# without cold	122	109
Totals	139	140

- Proportion of cold of the Ascorbic acid group is $\widehat{p}_1 = 17/139 = 0.122$
- Proportion of cold of the Placebo group is $\widehat{p}_2 = 31/140 = 0.221$
- Proportion of cold of the pooled sample is $\overline{p} = 48/279 = 0.172$

Comparing two proportions

Want to test

$$H_0 : p_1 = p_2 \text{ vs } p_1 \neq p_2$$

- $$\widehat{p}_1 - \widehat{p}_2 = 0.122 - 0.221 = -0.99$$
- The SE values are

$$SE_{CI} = \sqrt{\frac{0.221 \times (1 - 0.22)}{140} + \frac{0.122 \times (1 - 0.122)}{139}} = 0.04472$$

$$SE_{test} = \sqrt{0.172 \times (1 - 0.172)\left(\frac{1}{139} + \frac{1}{140}\right)} = 0.0452$$

- The CI is

$$-0.99 \pm 1.96(0.04472) = -0.99 \pm 0.088 = (-0.187, -0.011)$$

Comparing two proportions

- The z-test gives

$$z_{obs} = \frac{0.122 - 0.221}{0.0452} = -2.19$$

The p-value is

```
2*pnorm(-2.19)
#[1]  0.02852424
```

The area is multiplied by two because it is a two-sided test.

Comparing two proportions

Findings from the experiment:

- Both the CI and the hypothesis test suggest that there is evidence against the null hypothesis, conclude that the proportion of skiers getting colds was not the same for those on placebo versus those on Vitamin C.
- From the CI, a plausible effect for Vitamin C was that it made skiers between 1% and 18.7% less likely to develop a cold. At the time the study was controversial, as many studies since have not found an association between Vitamin C use and cold prevention.
- Consider this was a randomized study, if all the other factors that will affect the cold (exercises time/day, health condition, age etc) is the same, this suggests that Vitamin C had a causal role in preventing in colds.

Comparing two proportions

```
#### Example, vitamin C
# Approximate normal test for two-proportions, without Yates
 continuity correction
prop.test(c(17, 31), c(139, 140), correct = FALSE)
##
## 2-sample test for equality of proportions without continuity
## correction
##
## data: c(17, 31) out of c(139, 140)
## X-squared = 4.8114, df = 1, p-value = 0.02827
## alternative hypothesis: two.sided
## 95 percent confidence interval:
## -0.18685917 -0.01139366
## sample estimates:
## prop 1 prop 2
## 0.1223022 0.2214286
```

Comparing two proportions within the same sample

Many surveys might have more than two categories.

- For example, during the 2016 election, registered voters might have indicating favoring Clinton, Trump, or another candidate.
  ——A typical poll before the election might have had Clinton at 48% and Trump at 44%.
  —— These numbers add up to 92%, not 100%, and the remaining 8% might have been due to undecided voters or due to voters supporting Gary Johnson (Libertarian), Jill Stein (Green) or other less well known candidates.
- We might be interested in comparing whether 48% is "significantly" larger than 44%. The idea is whether Clinton could have felt reasonably confident that she had more support than Trump, or whether the sample was consistent with no difference in support in the population between the two candidates.
- This is not a two sample problem because we are trying to compare two proportions from within the same sample. The two proportions are not independent. In particular, it would be impossible for both percentages to be larger than 50%.

Comparing two proportions within the same sample

Example: suppose the poll had 1000 respondents
———with 480 supporting Clinton
——— 440 supporting Trump
———-50 supported Johnson
———- and 30 supported Stein.

How could we analyze the data to determine whether Clinton had a lead that was "statistically significant"?

Comparing two proportions within the same sample

Method 1: condition on respondents supporting either Clinton or Trump, and ignore everyone else.

- Clinton's proportion would be $\widehat{p}_1 = 480/920 = 0.522$.
  ——- In other words, 52% of people (supporting either Clinton or Trump) supported Clinton in this poll.
- Test whether this proportion was significantly larger than 50%.

```
prop.test(480,920)
#
# 1-sample proportions test with continuity correction
#
#data:  480 out of 920, null probability 0.5
#X-squared = 1.6533, df = 1, p-value = 0.1985
#alternative hypothesis: true p is not equal to 0.5
#95 percent confidence interval:
# 0.4888946 0.5543999
```

Comparing two proportions within the same sample

The margin of error in this case is approximately

$$1.96\sqrt{0.522(1-0.522)/920} = 0.032$$

meaning 3.2%, which is very typical in these types of polls.

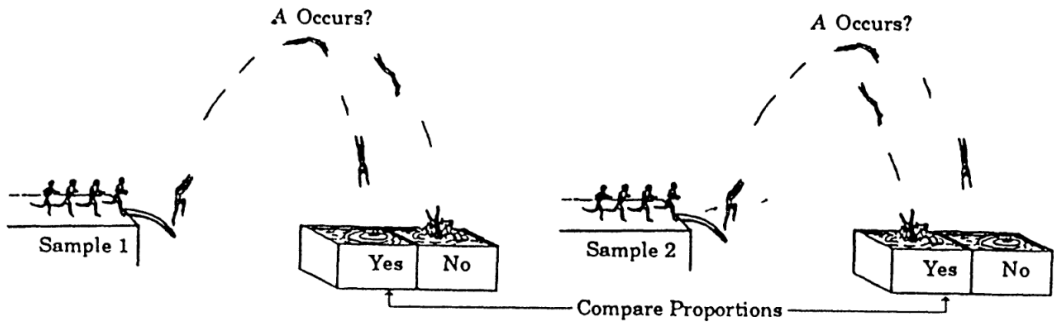
This margin of error is not for the 48%, but for the 52% conditional on only Trump or Clinton in the sample. It would also not apply to the other categories in the sample (Johnson and Stein).

Comparing two proportions within the same sample

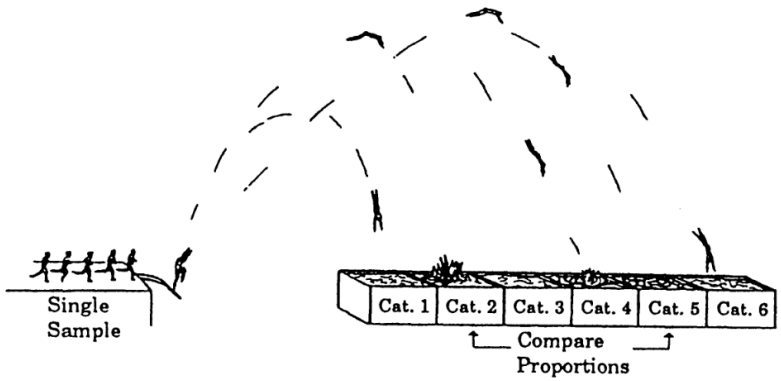
Method2: **multinomial distribution**.

- The multinomial distribution generalizes the binomial distribution to when there are more than two categories. In the binomial distribution, there are two categories: yes and no, or success and failure.
- The multinomial distribution allows any finite number of categories and counts how many observation are in each category.
  ——— each observation is assumed to be independent, and belongs to category i with probability p_i, where $p_1 + p_2 + \cdots + p_k = 1$, and k is the number of categories.

Comparing two proportions within the same sample



Situation (a) *Two independent samples.*



Situation (b) *Single sample, several response categories.*

Comparing two proportions within the same sample

An example of a multinomial sample would be a bag of M&M candy

- assuming that the pieces are independent.
- n pieces of candy, with n_1 brown, n_2 yellow, n_3 green, n_4 orange, and say n_5 blue (assuming there are only 5 colors.
- The sample proportions are

$$\widehat{p}_1 = \frac{n_1}{n}, \ \widehat{p}_2 = \frac{n_2}{n}, \ \widehat{p}_3 = \frac{n_3}{n}, \ \widehat{p}_4 = \frac{n_4}{n}, \ \widehat{p}_5 = \frac{n_5}{n}$$

Comparing two proportions within the same sample

To get a CI, trom the properties of the multionial distribution, the idea is to compute (as usual)

$$(\widehat{p}_1 - \widehat{p}_2) \pm z_{crit} SE(\widehat{p}_1 - \widehat{p}_2)$$

- need to take into account the lack of independence between the two samples.
- the formula is (for a 95% interval):

$$(\widehat{p}_1 - \widehat{p}_2) \pm 1.96 \sqrt{\frac{\widehat{p}_1 + \widehat{p}_2 - (\widehat{p}_1 - \widehat{p}_2)^2}{n}}$$

Comparing two proportions within the same sample

For the Clinton-Trump example. We get

$$(0.48-0.44)\pm 1.96\sqrt{\frac{.48+.44-(.48-.44)^2}{1000}} = 0.04\pm 0.059 \approx (-.02, .10)$$

Note that if this sample has a reported margin of error of 3.2%, you might be misled into thinking that 48% is significantly larger than 44%. Either the conditional analysis or the multinomial analysis lead to the conclusion that Clinton's lead was actually within the margin of error.

Goodness of fit tests

Another use of the multinomial distribution is to test whether proportions in several categories are significantly different from expectation.

Goodness of fit tests

Example: jury pool. The following data set was used as evidence in a court case.

- The data represent a sample of 1336 individuals from the jury pool of a large municipal court district for the years 1975–1977.
- The fairness of the representation of various age groups on juries was being contested.
  —— The strategy for doing this was to challenge the representativeness of the pool of individuals from which the juries are drawn.
  ——This was done by comparing the age group distribution within the jury pool against the age distribution in the district as a whole, which was available from census figures.

Goodness of fit tests

Are the observed proportions reasonable given the census proportions?

Age	Obs. Counts	Obs. Prop.	Census Prop.
18-19	23	0.017	0.061
20-24	96	0.072	0.150
25-29	134	0.100	0.135
30-39	293	0.219	0.217
40-49	297	0.222	0.153
50-64	380	0.284	0.182
65-99	113	0.085	0.102
Total:	1336	1.000	1.000

- Let p_{18} be the proportion in the jury pool population between ages 18 and 19. Define p_{20}, p_{25}, p_{30}, p_{40}, p_{50}, and p_{65} analogously.
- interested in testing that the true jury proportions equal the census proportions, $H_0 : p_{18} = 0.061$, $p_{20} = 0.150$, $p_{25} = 0.135$, $p_{30} = 0.217$, $p_{40} = 0.153$, $p_{50} = 0.182$, and $p_{65} = 0.102$ against H_A : not H_0

Goodness of fit tests

In a general case, the null hypothesis can be described as

$$H_0 : p_1 = p_{01}, p_2 = p_{02}, \ldots, p_k = p_{0k}$$

The alternative is that at least one of the proportions doesn't match the hypothesized proportion.

Goodness of fit tests

The idea for the test statistic is to compare the observed counts with the expected counts (observed versus expected number of individuals in each category): The test statistic for this problem is (with k categories):

$$\chi^2_{obs} = \sum_{i=1}^{k} \frac{(O_i - E_i)^2}{E_i}$$

where O_i is the observed count, E_i is the expected count with $E_i = np_{0i}$. In terms of proportions, this can be written as

$$\chi^2_{obs} = n \sum_{i=1}^{k} \frac{(\widehat{p}_i - p_{0i})^2}{p_{0i}}$$

Goodness of fit tests

The test statistic looks different from others you have seen so far, but if you think of it this way

$$\chi^2_{obs} = \sum_{i=1}^{k} \left(\frac{O_i - E_i}{\sqrt{E_i}} \right)^2$$

Then the terms

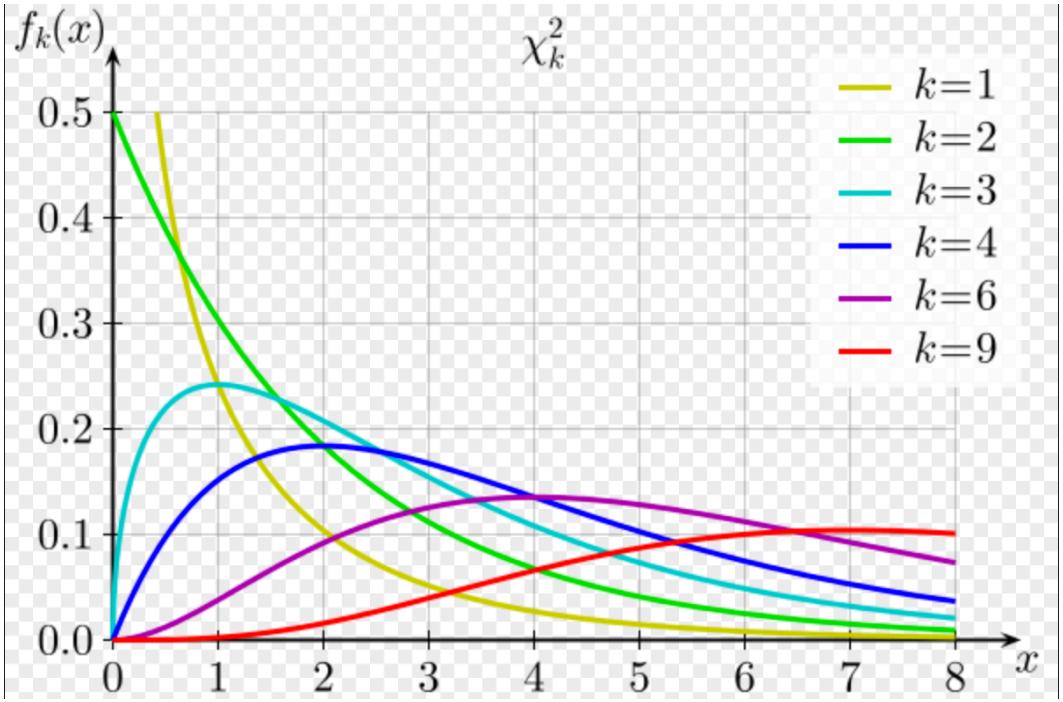
$$Z_i = \frac{O_i - E_i}{\sqrt{E_i}}$$

look like Z-scores and are also called category residuals:

$$Z = \frac{x - \mu}{\sqrt{\sigma^2}}$$

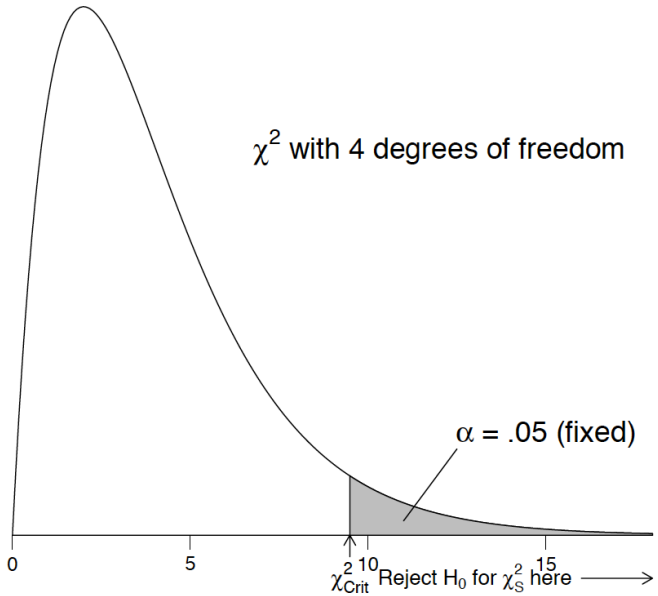
Goodness of fit tests

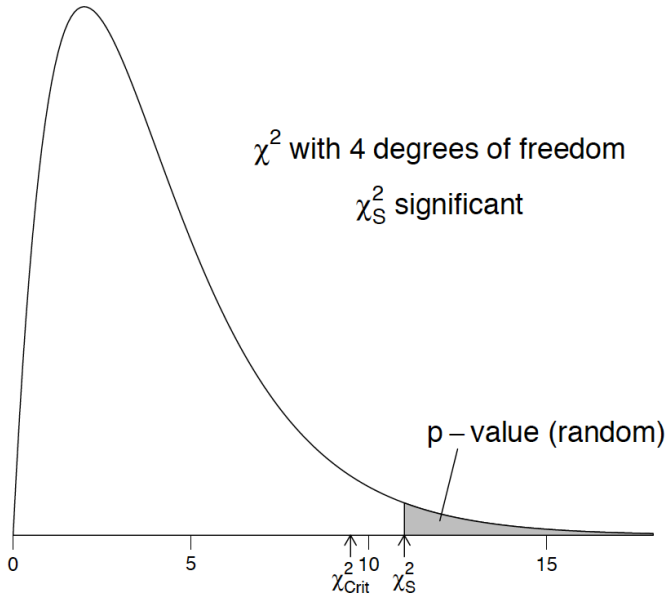
Under the null hypothesis, the statistic χ^2_{obs} has a chi-square distribution with with $k-1$ degrees of freedom.



Goodness of fit tests

Large values of χ^2_{obs} suggest that the proportions differ from expectation. We reject H_0 for sufficiently large values of χ^2_{obs}.





Goodness of fit tests

Example: jury pool

- Let p_{18} be the proportion in the jury pool population between ages 18 and 19.
- Define p_{20}, p_{25}, p_{30}, p_{40}, p_{50}, and p_{65} analogously.
- Interested in testing that the true jury proportions equal the census proportions, $H_0 : p_{18} = 0.061$, $p_{20} = 0.150$, $p_{25} = 0.135$, $p_{30} = 0.217$, $p_{40} = 0.153$, $p_{50} = 0.182$, and $p_{65} = 0.102$ against H_A : not H_0

Goodness of fit tests

As an example of how to compute the expected count, we have

$$E_{18} = 1336 \times 0.061 = 81.5$$

The observed number from this category is the observed proportion times the sample size of 1336:

$$O_{18} = 1336 \times 0.017 \approx 23$$

The contribution to the χ^2_{obs} statistic from this category is therefore

$$(23 - 81.5)^2/81.5 = 41.99.$$

The Pearson χ^2 statistic is

$$\chi^2_{obs} = (-6.48)^2 + (-7.37)^2 + (-3.45)^2 + 0.18^2 + 6.48^2 + 8.78^2 + (-1.99)^2 = 231.26$$

Goodness of fit tests

The critical value for the χ^2 test at the $\alpha = 0.05$ level can be obtained from R by

```
qchisq(1-.05,6)
#[1] 12.59159
```

- The expected value of a χ^2 random variable is it's degrees of freedom

$$E(\chi^2(v)) = v$$

- Reject H_0 if the χ^2_{obs} is much larger than the degrees of freedom.
- In this case, our observed test statistic is 231.26, which is much larger than the critical value of 12.59, so there is strong evidence that the ages in the jury pool have a different distribution than that of the general population.

Goodness of fit tests

To use the p-value approach instead of the critical value, you can use

```
1-pchisq(231.26,6)
#[1] 0
```

Here the p-value is so small that it is 0 to many decimal places.

Goodness of fit tests

Here is a way to implement this in R:

```
#### Example: jury pool
jury <- read.table(text="
Age Count CensusProp
18-19 23 0.061
20-24 96 0.150
25-29 134 0.135
30-39 293 0.217
40-49 297 0.153
50-64 380 0.182
65-99 113 0.102
", header=TRUE)
```

Goodness of fit tests

Here is a way to implement this in R:

```
x.summary <- chisq.test(jury$Count, correct = FALSE,
p = jury$CensusProp)
# print result of test
x.summary
##
## Chi-squared test for given probabilities
##
## data: jury$Count
## X-squared = 231.26, df = 6, p-value < 2.2e-16
```

Goodness of fit tests

To see how much individual categories deviate from the null hypothesis, it is helpful to look at the residuals. Here is a way to make a table:

```
x.table <- data.frame(age = jury$Age
, obs = x.summary$observed
, exp = x.summary$expected
, res = x.summary$residuals
, chisq = x.summary$residuals^2
, stdres = x.summary$stdres)
x.table
##     age obs  exp     res         chisq     stdres
## 1 18-19 23 81.496 -6.4797466 41.98711613 -6.6869061
## 2 20-24 96 200.400 -7.3748237 54.38802395 -7.9991194
## 3 25-29 134 180.360 -3.4520201 11.91644267 -3.7116350
## 4 30-39 293 289.912 0.1813611 0.03289186 0.2049573
## 5 40-49 297 204.408 6.4762636 41.94199084 7.0369233
## 6 50-64 380 243.152 8.7760589 77.01921063 9.7033764
## 7 65-99 113 136.272 -1.9935650 3.97430128 -2.1037408
```

Goodness of fit tests

Recall that the test statistic was $\chi^2_{obs} \approx 231$.

- The greatest contribution to this score was category 6, with a contribution of 77.
  —— This is for 50–64 year olds.
  ——-It's residual was 8.77 ($8.77^2 \approx 77$), which is positive, meaning that it had an excess of jury members.
  —— It's expected number of jurors (out of 1336) was 243, but 380 were in that age category
- 18-19 year olds had an expected representation of about 81 jurors, but only 23 jurors were of that age.
  —— This resulted in a negative residual of -6.48, and a contribution of 41.99 to the χ^2_{obs} statistic.
- The categories of 30–39 year olds and those aged 65 and over were the most consistent with the null hypothesis.
- In some cases, you might see that one category has much larger deviation from expectation than other categories. In this case, quite a few categories deviated quite strongly from expectation under the null hypothesis.

Goodness of fit tests

A follow up to the χ^2 test is to get confidence intervals for the proportions in each category. Here is an example of doing this for the age of jurors data. Here a confidence level of $1 - .05/7$ is used for Bonferroni adjustments.

```
b.sum1 <- prop.test(jury$Count[1], sum(jury$Count),
p = jury$CensusProp[1],conf.level=1-.05/7)
b.sum2 <- prop.test(jury$Count[2], sum(jury$Count),
p = jury$CensusProp[2],conf.level=1-.05/7)
b.sum3 <- prop.test(jury$Count[3], sum(jury$Count),
p = jury$CensusProp[3],conf.level=1-.05/7)
b.sum4 <- prop.test(jury$Count[4], sum(jury$Count),
p = jury$CensusProp[4],conf.level=1-.05/7)
b.sum5 <- prop.test(jury$Count[5], sum(jury$Count),
p = jury$CensusProp[5],conf.level=1-.05/7)
b.sum6 <- prop.test(jury$Count[6], sum(jury$Count),
p = jury$CensusProp[6],conf.level=1-.05/7)
b.sum7 <- prop.test(jury$Count[7], sum(jury$Count),
p = jury$CensusProp[7],conf.level=1-.05/7)
```

Goodness of fit tests

```
b.sum <- data.frame(
rbind( c(b.sum1$p.value, b.sum1$conf.int)
, c(b.sum2$p.value, b.sum2$conf.int)
, c(b.sum3$p.value, b.sum3$conf.int)
, c(b.sum4$p.value, b.sum4$conf.int)
, c(b.sum5$p.value, b.sum5$conf.int)
, c(b.sum6$p.value, b.sum6$conf.int)
, c(b.sum7$p.value, b.sum7$conf.int)
)
)
names(b.sum) <- c("p.value", "CI.lower", "CI.upper")
b.sum$Age <- jury$Age
b.sum$CensusProp <- jury$CensusProp
```

Goodness of fit tests

```
> b.sum
       p.value    CI.lower   CI.upper   Age CensusProp
1 3.362577e-11 0.009647384 0.03018145 18-19       0.061
2 1.709175e-15 0.054740455 0.09367530 20-24       0.150
3 2.410326e-04 0.079962727 0.12501521 25-29       0.135
4 8.636174e-01 0.190060970 0.25162323 30-39       0.217
5 2.579364e-12 0.192891624 0.25474777 40-49       0.153
6 4.126666e-22 0.252099261 0.31911186 50-64       0.182
7 3.953815e-02 0.065941074 0.10777784 65-99       0.102
```

Goodness of fit tests

Here is an example from genetics. In this case, a little bit of biology is needed to get the expected counts or proportions. (The example is from Falconer and Mackay, *Quantitative Genetics*).

For the M-N blood group, a sample of individuals from Iceland is given with the following genotype counts, both observed and expected:

	Genotypes			
	MM	MN	NN	Total
Observed	233	385	129	747
Expected	242.36	366.26	138.38	747
$(O_i - E_i)^2/E_i$	0.362	0.959	0.634	1.956

Goodness of fit tests

To compute the expected values, we need a little bit of genetics here. The idea is that each person has two alleles, so there are 233 individuals with two copies of the M allele, 385 individuals with one M and one N, and 129 with two Ns. The total number of individuals is $233 + 385 + 129 = 747$, but the total number of allele copies is $747 * 2 = 1494$.

Goodness of fit tests

The total number of copies of M in the sample is $233 \times 2 + 385$, because each person with MM contributes two Ms to the sample, and each person with MN contributes one M. Thus the total number of Ms is $233 * 2 + 385 = 851$. The total number of N alleles in the sample is $385 + 2 \times 129 = 643$. The probability of a random allele being M or N is

$$P(M) = \frac{851}{851 + 643} = 0.5696, \quad P(N) = \frac{643}{851 + 643} = 0.4304$$

The expected proportion of individuals with genotype MM is $P(M) \times P(M) = 0.3245$ (assuming that alleles are random), with MN is $2P(M)P(N) = 0.4903$ and with NN is $P(N) \times P(N) = 0.1852$. The expected counts are these expected proportions multiplied by the sample size of 747 individuals. For example, $747 \times 0.3245 \approx 242.36$.

Goodness of fit tests

```
> o <- c(233, 385, 129)
m <- 233*2+385
n <- 385+2*129
pm <- m/(m+n)
pn <- n/(m+n)
eMM <- pm^2*sum(o)
e <- c(pm^2,2*pm*pn,pn^2)*sum(o)
chisq <- sum((o-e)^2/e)
#[1] 1.955521
 (o-e)^2/e
#[1] 0.3622291 0.9588085 0.6344837
```

Goodness of fit tests

To use R to conduct the test, we need to specify the expected proportions. Because the p-value is greater than 0.05, we conclude that that there is not sufficient evidence to reject the hypothesis that the proportions are consistent with their expected values.

```
a <- chisq.test(o,p=c(pm^2,2*pm*pn,pn^2))
a
#
# Chi-squared test for given probabilities
#
#data:  o
#X-squared = 1.9555, df = 2, p-value = 0.3762
```

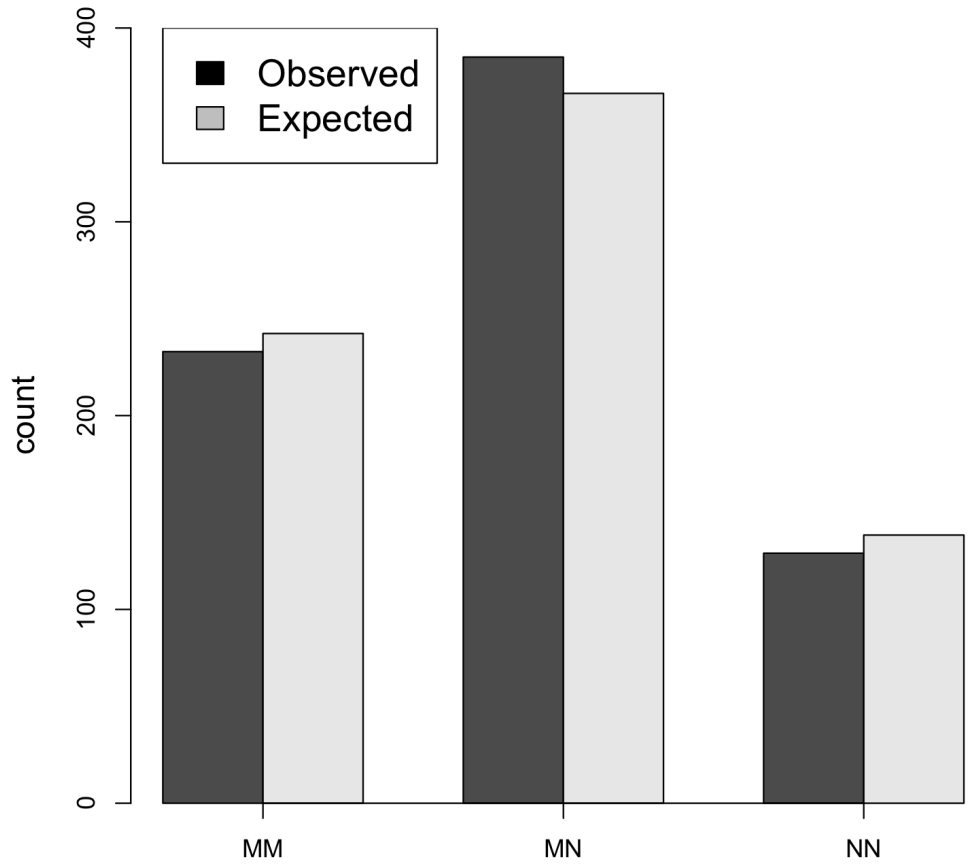
Goodness of fit tests

A nice way to visualize what is happening is to plot the observed versus expected counts. This can be done by making a matrix where each row is the frequency count. In this case, the rows are for observed and expected.

```
counts <- c(o,e)
counts <- matrix(counts,ncol=3,byrow=T)
barplot(counts,beside=TRUE,ylim=c(0,400),ylab="count",
cex.lab=1.3)
legend(1,400,legend=c("Observed","Expected"),
fill=c("black","grey"),cex=1.5)
axis(1,at=c(2,5,8),c("MM","MN","NN"),cex=1.5)
```

Goodness of fit tests

Comparison of observed versus expected counts.



2×2 tables and conditional probability

Contingency tables, particularly 2×2 tables, can be a good way to understand conditional probabilities.

Here is an example for a 2×2 table relating sex and migraine headaches, based on a survey of 50 women and 50 men:

	Migraines		
	Yes	No	Total
Women	12	38	50
Men	5	45	50
Total	17	83	100

Conditional probability

We can ask questions like:

- what is the probability that a person experienced a migraine given that they were a woman?
- What is the probability that someone was a man, given that they experienced a migraine?

From probability theory, we can use

$$P(A|B) = \frac{P(A \text{ and } B)}{P(B)}$$

when individuals are sampled randomly, we can think of this as

$$P(A|B) = \frac{\#\text{ in category A and category B}}{\#\text{ in category B}}$$

2×2 tables and conditional probability

	Migraines		
	Yes	No	Total
Women	12	38	50
Men	5	45	50
Total	17	83	100

- $P(\text{woman}|\text{migraine}) = \frac{12}{17} \approx 0.71$
- $P(\text{migraine}|\text{man}) = \frac{5}{50} = 0.1$

2×2 tables

- want to test whether the proportion of men versus women experiencing migraines was different for the population that was sampled
—-could use either a test of proportions or a χ^2 test.

```
prop.test(c(12,38),c(17,83),correct=FALSE)
prop.test(c(12,5),c(50,50),correct=FALSE)
```

- Both commands will result in the exact same p-value, but have different interpretations in terms of the CI.
- The first tests whether the proportion of women is the same among those experiencing migraines versus those not experiencing migraines.
—-uses the proportions $12/17$ and $38/83$
- The second tests whether the proportion experiencing migraines is different for women versus men. The second compares $12/50$ versus $5/50$
- Both are equivalent to the χ^2 test of whether there is an association between sex and migraines.

```
 prop.test(c(12,38),c(17,83),correct=FALSE)

        2-sample test for equality of proportions without
        continuity correction

data:  c(12, 38) out of c(17, 83)
X-squared = 3.4727, df = 1, p-value = 0.06239
alternative hypothesis: two.sided
95 percent confidence interval:
 0.006385628 0.489716428
sample estimates:
   prop 1    prop 2
0.7058824 0.4578313
```

```
prop.test(c(12,5),c(50,50),correct=FALSE)

2-sample test for equality of proportions without
continuity correction

data:  c(12, 5) out of c(50, 50)
X-squared = 3.4727, df = 1, p-value = 0.06239
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.004666056  0.284666056
sample estimates:
prop 1 prop 2
  0.24   0.10
```

```
> obsn <- c(12,38,5,45)
> data <- matrix(obsn,byrow=T,ncol=2)
> chisq.test(data,correct=FALSE)

        Pearson's Chi-squared test

data:  data
X-squared = 3.4727, df = 1, p-value = 0.06239
```

2×2 tables

Here hypothesis test shows weak evidence of a difference, with a p-value greater than 0.05.

At the $\alpha = .05$ level, there is insufficient evidence to conclude that there is a difference in proportions experiencing migraines at the population level. —-However, the p-value is close to .05. The confidence barely included 0, with difference ranging from women experiencing between -0.5% to 28% more migraines than men.

Testing for Homogeneity of Proportions

- The "test of homogeneity" is a way of determining whether two or more DIFFERENT POPULATIONS (or GROUPS) share the same distribution of a SINGLE CATEGORICAL VARIABLE.
  ——– do people of different races have the same proportion of smokers to non-smokers
  ——– do different education levels have different proportions of Democrats, Republicans, and Independent.
- The data are collected by randomly sampling from each sub-group separately. (Say, 100 blacks, 100 whites, 100 American Indians, and so on.) The null hypothesis is that each sub-group shares the same distribution of another categorical variable. (Say, chain smoker, occasional smoker, non-smoker.)

- The test of homogeneity expands on the two-proportion z-test. The two proportion z-test is used when the response variable has only two categories as outcomes and we are comparing two groups.
- The homogeneity test is used if the response variable has several outcome categories, and we wish to compare two or more groups.

$$H_0 : p_{\text{level i, 1}} = p_{\text{level i, 2}} = \cdots = p_{\text{level i, c}}$$

where $i = 1, 2 \cdots, r$ are r categories of variable X and c is the number of different populations, i.e., the proportion of X is the same in all the c populations studied.
H_α: At least one proportion of X is not the same.

Testing for Homogeneity of Proportions

Example: compare numbers of voters for Clinton and Trump in two polls, one for ABC and one for Fox.

- The polls (only include Clinton and Trump) can be summarized as follows

Candidate	ABC	Fox	Total
Clinton	532	537	1069
Trump	488	501	989
Total	1020	1038	2058

Testing for Homogeneity of Proportions

The proportions can be summarized as follows

Candidate	ABC	Fox	Pooled
Clinton	0.5216	0.5173	0.5194
Trump	0.4784	0.4827	0.4806
Total	1	1	1

where the **pooled proportions** are the Row Totals divided by the total sample size of 2058.

- To formally compare the observed proportions, one might view the data as representative sample of voters collected by the two broadcasting companies. ——Assuming independent samples collected by the two companies (two populations)

Testing for Homogeneity of Proportions

The proportions can be summarized as follows

Candidate	ABC	Fox	Pooled
Clinton	0.5216	0.5173	0.5194
Trump	0.4784	0.4827	0.4806
Total	1	1	1

where the **pooled proportions** are the Row Totals divided by the total sample size of 2058.

- The null hypothesis states that the distribution of voters for Clinton and Trump is identical whether it is done by ABC or by Fox

$$H_0 : p_{\text{Clinton, ABC}} = p_{\text{Clinton, Fox}}$$

—-Column proportion sum to 1, therefore the null is the same as proportion of voters for Clinton is the same reported by ABC and Fox
—-This is the same as a two sample proportion test

- For a two-by-two table of counts, the chi-squared test of homogeneity of proportions is identical to the two-sample proportion test we discussed earlier.
- In general, we have one categorical variables that has r levels, and c different populations, then we can make an $r \times c$ contingency table (think r for rows and c for columns).
  —— The χ^2 test then tests whether the distribution of row levels are identical across the column levels.
- The degrees of freedom for this type of test is $(r-1) \times (c-1)$.

Testing for Homogeneity of Proportions

To implement the test:

1. Compute the (estimated) **expected** count for each cell in the table as follows:
$$\mathrm{E} = \frac{\text{Row Total} \times \text{Column Total}}{\text{Total Sample Size}}.$$
2. Compute the Pearson test statistic
$$X_{\mathrm{s}}^2 = \sum_{\text{all cells}} \frac{(O-E)^2}{E},$$
where O is the **observed** count.
3. For a size α test, reject the hypothesis of homogeneity if $X_{\mathrm{s}} \geq \chi^2_{\mathrm{crit}}$, where χ^2_{crit} is the upper α critical value from the chi-squared distribution with $df = (r-1)(c-1)$, r is the number of rows, and c is number of columns

Testing for Homogeneity of Proportions

For a chi-square test on a 2×2 table, you can enter the table as a matrix. For `prop.test()`, give a vector of counts for one category, and a vector of sample sizes for independent samples.

```
x <- c(532,537,488,501)
x <- matrix(x,ncol=2,byrow=T)
chisq.test(x,correct=FALSE)
# Pearson's Chi-squared test
#X-squared = 0.036834, df = 1, p-value = 0.8478
#
prop.test(c(532,537),c(1020,1038),correct=FALSE)
#
2-sample test for equality of proportions without continuity
#
#data:  c(532, 537) out of c(1020, 1038)
#X-squared = 0.036834, df = 1, p-value = 0.8478
```

Testing for Homogeneity of Proportions

Both the independent proportions test and χ^2 test lead to exactly same conclusion,
——namely that the ABC and Fox polls did not have signficantly different proportions of respondents supporting Clinton versus Trump conditional on respondents supporting either Clinton or Trump.

The fact that the two analyses lead to the same conclusion (and p-value) is related to the fact that the square of a standard normal random variable has a χ^2 distribution with one degree of freedom.

ABC and Fox example continued

Consider again the data for ABC versus Fox polls. This time, we can use all five categories: Clinton, Trump, Johnson, Stein, and Other. Our contingency table is then 5×2 (or you can arrange it to be 2×5).

Company	ABC	Fox	Total
Clinton	532	537	1069
Trump	488	501	989
Johnson	44	85	129
Stein	11	37	48
Other	34	61	95
Total	1109	1221	2330

- Expected counts can be obtained by taking the row total times the column total divided by the overall total.
  —-For example, the expected count for Clinton and ABC is $1069 \times 1109/2330 = 508.8073$.

Let's organize the contingency table in 2×5 to save space.

Company	Clinton	Trump	Johnson	Stein	Other	Total
ABC	532	488	44	11	34	1109
Fox	537	501	85	37	61	1221
Total	1069	989	129	48	95	2330

```
o <- c(532,488,44,11,34,537,501,85,37,61)
o <- matrix(o,byrow=T,ncol=5)
a <- chisq.test(o,correct=FALSE)
a
# Pearson's Chi-squared test
#X-squared = 29.667, df = 4, p-value = 5.721e-06
a$expected
#         [,1]   [,2]     [,3]     [,4]     [,5]
#[1,] 508.8073 470.73 61.39957 22.84635 45.21674
#[2,] 560.1927 518.27 67.60043 25.15365 49.78326
1109*1069/2330
#[1] 508.8073
```

- Based on the X^2 test, the distribution of voters for the different candidates are different from Fox and ABC.
- To get an idea of which categories deviate most from expectation, we can look at the contribution to the X^2 test. The X^2 test statistic is the sum of the squared residuals.

```
# also try (o-a$expected)^2/a$expected
a$residuals
#           [,1]       [,2]      [,3]      [,4]      [,5]
#[1,]  1.028193  0.7959858 -2.220526 -2.478427 -1.668080
#[2,] -0.979902 -0.7586007  2.116235  2.362023  1.589736
(a$residuals)^2
#          [,1]      [,2]     [,3]     [,4]     [,5]
#[1,] 1.057181 0.6335933 4.930736 6.142602 2.782492
#[2,] 0.960208 0.5754750 4.478449 5.579153 2.527259
```

- The biggest contributions to the χ^2 statistic come from columns 3 and 4 in the residuals or squared residuals.
  ——Here the contribution to the χ^2 statistic is greater than 4 for each category.
  —— These columns are for the support for Johnson and Stein.
- The critical value for the χ^2 test here is based on $(2-1) \times (5-1) = 4$ degrees of freedom, and is

```
qchisq(.95,4)
#[1] 9.487729
```

Testing for Independence

The "test of independence" is a way of determining whether **TWO CATEGORICAL VARIABLES** are associated with one another in **ONE SINGLE POPULATION**.

——For example, we draw a single group of 200 subjects and record their gender information, and their political affiliation. Trying to see if there is a relationship between the gender and political affiliation.

$$H_0 : X \text{and } Y \text{ are independent v.s.} H_\alpha : X \text{and } Y \text{ are not independent}$$

Recall: The "test of homogeneity" is a way of determining whether two or more **DIFFERENT POPULATIONS (or GROUPS)** share the same distribution of a **SINGLE CATEGORICAL VARIABLE.**

Testing for Independence

- The row and column classifications for a population where each individual is cross-classified by two categorical variables are said to be **independent** if each **population** cell proportion in the two-way table is the product of the proportion in a given row and the proportion in a given column.

$$H_0 : p_{ij} = p_{i+} \times p_{+j}$$

where p_{i+} is row total divided by total, and p_{+j} is column total divided by total.

- Mathematically, one can show that independence is equivalent to homogeneity of proportions.
—- In particular, the two-way table of population cell proportions satisfies independence if and only if the population column proportions are homogeneous. If the population column proportions are homogeneous then so are the population row proportions.
—-This suggests that a test for independence or **no association** between two variables based on a cross-sectional study can be implemented using the chi-squared test for homogeneity of proportions.

Testing for Independence

Homogeneity and independence sound the same. The difference is a matter of design.

- In the test of independence, observational units are collected at random from ONE POPULATION and TWO CATEGORICAL VARIABLES are observed for each observational unit. We are trying to see if there is an association between the two variables or if the two variables are independent.
- In the test of homogeneity, the data are collected by randomly sampling from each sub-group (SEVERAL POPULATIONS) separately. (Say, 100 blacks, 100 whites, 100 American Indians, and so on.) The null hypothesis is that each sub-group shares the same distribution of A SINGLE CATEGORICAL VARIABLE. (Say, chain smoker, occasional smoker, non-smoker).

Chi-square type tests

- The default for the X^2 test in R is to use the continuity correction, sometimes called Yates' continuity correction. Here the formula is slightly different:

$$X^2_{Yates} = \sum_{i=1}^{k} \frac{(|O_i - E_i| - 0.5)^2}{E_i}$$

  This formula is intended to make the X^2 test more conservative when sample sizes are low.
- Based on simulations, it seems that the X^2 test without continuity correction already tends to be conservative when sample sizes are low, meaning that it is difficult to reject the null hypothesis for small sample sizes.
- Consequently, we tend not to use the continuity correction option.

Chi-square type tests

A common rule of thumb is to say that the X^2 test is reasonable when all expected cell counts are at least 5. Here is more specific advice:

"No more than 20% of the expected counts are less than 5 and all individual expected counts are 1 or greater" (Yates, Moore, & McCabe, *The Practice of Statistics*,1999, p. 734).

If your sample sizes are small for certain categories, R is likely to print out warnings, but will still compute results.

2×2 tables with correlated observations

Sometimes 2×2 tables are presented with correlated observations.

For example, if a sample of people is first given treatment A, asked to record whether or not symptoms occur, and then later the same group is given treatment B, again asked to record whether the symptoms occur, then you have two sets of proportions but they are correlated rather than independent samples.

For a nonmedical example, you could track a sample of individual's response, for example to who they plan to vote for, over time to see if same individuals change their opinion. This is different from taking a second sample of an independent set of individuals.

2×2 tables with correlated observations

Here an example looks at presidential approval (example from Agresti, 1990, *Categorical Data Analysis*).

- The data is from a sample of 1600 voter-aged people who were asked whether they approved or disapproved of the president two times separated by one month.
- someone who approves is likely to continue to approve one month later, and someone who disapproves is likely to disapprove one month later. What is interesting is how many people change their minds.
- Here is the data:

	Second survey		
First Survey	approve	disapprove	total
approve	794	150	944
disapprove	86	570	656
total	880	720	1600

2×2 tables with correlated observations

First Survey	Second survey: approve	Second survey: disapprove	total
approve	794	150	944
disapprove	86	570	656
total	880	720	1600

- The diagonals on the table represent people who's opinion of the president didn't change.
- The off-diagonals represent those who changed their mind.
  —-We see that 150 people changed from approval to disapproval, while 86 people changed from disapproval to approval.
  —- This means that the approval rating went down for this sample.
  —- The approval ratings started at $944/1600 = 59\%$ from the first survey to $880/1600 = 55\%$ in the second survey.

First Survey	Second survey approve	disapprove	total
approve	794	150	944
disapprove	86	570	656
total	880	720	1600

From independent samples each with a sample size of 1600, we would check whether 59% is significantly different from 55%. (This would give a p-value of .022).

—— we can instead check, among those who changed their mind, are the 150 who went from approval to disapproval significantly larger than the 86.

2×2 tables with correlated observations

In McNemar's test, let

- $\widehat{p}_{AA}$ be the proportion that approved both times
- $\widehat{p}_{DD}$ be the proportion that disapproved both times
- $\widehat{p}_{AD}$ be the proportion that approved only the first time
- $\widehat{p}_{DA}$ be the proportion that approved only the second time
- $\widehat{p}_{A+}$ be the proportion that approved the first month (i.e., $944/1600 = 59\%$)
- $\widehat{p}_{+A}$ be the proportion that approved the second month (i.e., $880/1600 = 55\%$)

2×2 tables with correlated observations

A **Confidence Interval** for the difference is

$$\widehat{p}_{A+} - \widehat{p}_{+A} \pm z_{crit} SE$$

where

$$SE = \sqrt{\frac{\widehat{p}_{A+}(1-\widehat{p}_{A+}) + \widehat{p}_{+A}(1-\widehat{p}_{+A}) - 2(\widehat{p}_{AA}\widehat{p}_{DD} - \widehat{p}_{AD}\widehat{p}_{DA})}{n}}$$

Plugging in the numbers, we get for the SE

$$\sqrt{\frac{(.59)(.41) + (.55)(.45) - 2((.496)(.356) - (.094)(.054))}{1600}} = .0095$$

The 95% CI is

$$(0.59 - 0.55) \pm 0.019 = (0.021, 0.059)$$

Thus an estimate of the change in approval rating is that it decreased by between 2 and 6% for the population represented by this sample.

2×2 tables with correlated observations

Hypothesis test

$$z_{obs} = \frac{\widehat{p}_{A+} - \widehat{p}_{+A}}{SE} = \frac{n_{AD} - n_{DA}}{\sqrt{n_{AD} + n_{DA}}}$$

where

$$SE = \sqrt{\frac{\widehat{p}_{A+}\widehat{p}_{+A} - 2\widehat{p}_{AA}}{n}}$$

- The numerator is the difference in the off-diagonals, and the denominator is the square root of the sum of the off-diagonals.
- The numbers on the diagonals make no difference to the test. We are only interested in those people who changed their minds, and whether among those who changed their minds, the direction of the change was larger in one direction than the other.

correlated 2×2 tables

The hypothesis test is implemented in R

```
x <- c(794,150,86,570)
# try x <- c(1,150,86,10000) results are the same
x <- matrix(x,byrow=T,ncol=2)
mcnemar.test(x)
# McNemar's Chi-squared test with continuity correction
#
#data:  x
#McNemar's chi-squared = 16.818, df = 1, p-value = 4.115e-05
```

correlated 2×2 tables

It is interesting to compare the results if the data had been two independent samples, each of size 1600, with the observed proportions of 59% and 55%.

```
o <- c(944,656,880,720)
o <- matrix(o,ncol=2,byrow=T)
prop.test(o,correct=FALSE)
#X-squared = 5.2224, df = 1, p-value = 0.0223
#alternative hypothesis: two.sided
#95 percent confidence interval:
# 0.005721636 0.074278364
#sample estimates:
#prop 1 prop 2
#  0.59   0.55
```

correlated 2×2 tables

You can also use the following to get the same results

```
 prop.test(c(944,880),c(1600,1600),correct=FALSE)

   2-sample test for equality of proportions without
   continuity correction

data:  c(944, 880) out of c(1600, 1600)
X-squared = 5.2224, df = 1, p-value = 0.0223
alternative hypothesis: two.sided
95 percent confidence interval:
 0.005721636 0.074278364
sample estimates:
prop 1 prop 2
  0.59   0.55
```

Relative risk and odds ratio

In medical examples, we often interpret the relative risk and odds ratio.

Outcome	Exposed population	non-exposed population
Diseased	p_1	p_2
Non-diseased	$1-p_1$	$1-p_2$

- Relative ratio

$$RR = p_1/p_2$$

  is the probability of disease in the exposed population divided by the probability in the non-exposed population.
- The odds of having the disease for the exposed population is $p_1/(1-p_1)$.
- The odds of having the disease for the non-exposed populatin is $p_2/(1-p_2)$.
- The odds ratio is

$$OR = \frac{p_1/(1-p_1)}{p_2/(1-p_2)}$$

Interpreting odds ratios

- Let's say that the probability of success is 0.8, thus

$$p = 0.8, q = 1 - p = 0.2$$

- The odds of success are defined as
  $\text{odds}(\text{success}) = p/q = 0.8/0.2 = 4$,
  —- that is, the odds of success are 4 to 1.
- The odds of failure would be
  $\text{odds}(\text{failure}) = q/p = 0.2/0.8 = 0.25$,
  —-that is, the odds of failure are 1 to 4.
- Odds ratio 1
  $\text{OR1} = \text{odds}(\text{success})/\text{odds}(\text{failure}) = 4/0.25 = 16$
  the odds of success are 16 times greater than for failure.
- Odds ratio 2
  $\text{OR2} = \text{odds}(\text{failure})/\text{odds}(\text{success}) = 0.25/4 = 0.0625$
  the odds of failure are one-sixteenth the odds of success.