Distribution-free methods

(Module 7)

Statistics (MAST20005) & Elements of Statistics (MAST90058)

Semester 2, 2018

Contents

Aims of this module

- Introduce inference methods that do not make strong distributional assumptions
- Explain the highly used Pearson's chi-squared test

1 Introduction

Distribution-free methods

- So far, have only considered tests that assume a specified form for the population distribution.
- We don't always want to make such assumptions.
- Instead, we can use *distribution-free* methods.
- Here, we will learn about various distribution-free hypothesis tests.

An aside: *distribution-free* versus *non-parametric*

- The term *non-parametric* is also often used to describe methods that do not assume a specific distributional form.
- It is usually a misnomer: the methods typically **do** make use of parameters, but there are usually a large number of them and they adapt to the data.
- Thus, a better term might be **super-parameteric**.
- (Note: we won't be covering any advanced methods of this form in this subject.)
- In any case, the convention has stuck, so you will see either of the labels 'distribution-free' or 'non-parameteric' being used.

Distribution-free tests

- Even without making distributional assumptions, it is possible to obtain exact or asymptotic sampling distributions for various statistics.
- Can use these as a basis for hypothesis tests.
- Often the distribution-free test statistic is approximately normally distributed
- ... the Central Limit Theorem strikes again!

2 Testing for a difference in location

Extracting information with fewer assumptions

- How can we assess the information in a sample without assuming a distribution?
- Specifying a distribution is somewhat analogous to specifying a scale of measurement, so...
- How do we compare numbers without a scale?
- Two strategies:
  1. **(Sign)** Only record whether a number is smaller or greater than a reference number, i.e. replace them by binary indicator variables.
  2. **(Rank)** Only retain information about the order of the numbers, i.e. replace them by their rank order.
- Each of these throws away some information, but hopefully retains enough to be useful.
- We now look at a few methods that use these strategies.

Aim: test for the median

- Let X have median m
- We have an iid sample of size n from X
- Can we test $H_0\colon m = m_0$ with very few assumptions?
- (Want to find distribution-free alternatives to tests about the mean, such as the t-test)
- (Typically consider medians rather than means when distribution-free)

2.1 Sign test

Sign test

- We assume X is continuous
- (No further assumptions!)
- Compute, Y, the number of positive numbers amongst $X_1 - m_0, \ldots, X_n - m_0$
- In other words, replace X_i with $\mathrm{sgn}(X_i - m_0)$
- Under H_0, we have $Y \sim \mathrm{Bi}(n, 0.5)$
- Tests proceed as usual...

Example (sign test)

The time between calls to a switchboard is represented by X.

$$H_0\colon m = 6.2 \quad \text{versus} \quad H_1\colon m < 6.2$$

i	x_i	$x_i - 6.2$	Sign	i	x_i	$x_i - 6.2$	Sign
1	6.80	0.60	+1	11	18.90	12.70	+1
2	5.70	−0.50	−1	12	16.90	10.70	+1
3	6.90	0.70	+1	13	10.40	4.20	+1
4	5.30	−0.90	−1	14	44.10	37.90	+1
5	4.10	−2.10	−1	15	2.90	−3.30	−1
6	9.80	3.60	+1	16	2.40	−3.80	−1
7	1.70	−4.50	−1	17	4.80	−1.40	−1
8	7.00	0.80	+1	18	18.90	12.70	+1
9	2.10	−4.10	−1	19	4.80	−1.40	−1
10	19.00	12.80	+1	20	7.90	1.70	+1

- Y is the number of positive signs. Reject H_0 if Y too small. (If median < 6.2 then expect fewer than 1/2 of the observations to be greater than 6.2.)
- Since $\Pr(Y \leqslant 6) = 0.0577 \approx 0.05$, an appropriate rejection rule is to reject H_0 if $Y \leqslant 6$. (In R: `pbinom(6, 20, 0.5)`)
- We observed $y = 11$, so cannot reject H_0.
- The p-value is $\Pr(Y \leqslant 11) = 0.75 > 0.05$ so cannot reject H_0. (In R: `pbinom(11, 20, 0.5)`)

R code

```
> binom.test(11, 20, alternative = "less")

    Exact binomial test

data:  11 and 20
number of successes = 11, number of trials = 20,
 p-value = 0.7483
alternative hypothesis: true probability of
                        success is less than 0.5
95 percent confidence interval:
 0.0000000 0.7413494
sample estimates:
probability of success
                  0.55
```

Sign test for paired samples

Can also use the sign test for paired samples: simply replace (x_i, y_i) with $\text{sgn}(x_i - y_i)$.

For example:

i	x_i	y_i	Sign
1	8.9	10.3	−1
2	26.7	11.7	+1
3	12.4	5.2	+1
4	34.3	36.9	−1

Use of the sign test

- The sign test requires few assumptions
- But it doesn't use information on the size of the differences, so it can be insensitive to departures from H_0
- In other words, large type II error or small power
- Tends to only be used when the data are not numerical but for which comparisons between values are meaningful (e.g. ordinal data)

2.2 Wilcoxon signed-rank test (one-sample)

Wilcoxon one-sample test

- Now, assume the underlying distribution is also symmetrical (as well as continuous)
- Same null hypothesis ($H_0\colon m = m_0$) against a one-sided or two-sided alternative
- Determine the ranks of: $|X_1 - m_0|, \dots, |X_n - m_0|$
- Replace the data by signed ranks, X_i becomes $\operatorname{sgn}(X_i - m_0) \cdot \operatorname{rank}(|X_i - m_0|)$
- The *Wilcoxon signed-rank statistic*, W, is the sum of these signed ranks
- Using this as a basis for a test gives the *Wilcoxon signed-rank test*, also known as the *Wilcoxon one-sample test.*

Alternative definitions

- Textbooks and software packages vary in the statistic they use
- We just defined: W is the sum of the signed ranks
- A popular alternative: V is the sum of the positive ranks only
- V is a bit easier to calculate, esp. by hand
- R uses V
- V and W are deterministically related (can you derive the formula?)
- V and W have different (but related) sampling distributions
- Using either statistic leads to equivalent test procedures

Example (Wilcoxon one-sample test)

- The lengths of 10 fish are:

  5.0, 3.9, 5.2, 5.5, 2.8, 6.1, 6.4, 2.6, 1.7, 4.3
- Interested in testing: $H_0\colon m = 3.7$ versus $H_1\colon m > 3.7$

i	x_i	$x_i - 3.7$	$\lvert x_i - 3.7\rvert$	Rank	Signed rank
1	5.0	1.3	1.3	5	5
2	3.9	0.2	0.2	1	1
3	5.2	1.5	1.5	6	6
4	5.5	1.8	1.8	7	7
5	2.8	−0.9	0.9	3	−3
6	6.1	2.4	2.4	9	9
7	6.4	2.7	2.7	10	10
8	2.6	−1.1	1.1	4	−4
9	1.7	−2.0	2.0	8	−8
10	4.3	0.6	0.6	2	2

- The sum of signed ranks is:

$$W = 5 + 1 + 6 + 7 - 3 + 9 + 10 - 4 - 8 + 2 = 25$$

- Alternatively, the sum of positive ranks is:

$$V = 5 + 1 + 6 + 7 + 9 + 10 + 2 = 40$$

Decision rule

- What is an appropriate critical region?
- If $H_1\colon m > 3.7$ is true, we expect more positive signs. Then W should be large, so the critical region should be $W \geqslant c$ for a suitable c.
- (For other alternative hypotheses, e.g. two-sided, need to modify this accordingly.)

- If H_0 is true then $\Pr(X_i < m_0) = \Pr(X_i > m_0) = \frac{1}{2}$.
- Assignment of the n signs to the ranks are mutually independent
- W is the sum of the integers $1, \ldots, n$, each with a positive or negative sign
- Under H_0, $W = \sum_{i=1}^{n} W_i$ where

$$\Pr(W_i = i) = \Pr(W_i = -i) = \frac{1}{2}, \quad i = 1, \ldots, n$$

- The mean under H_0 is $\mathbb{E}(W_i) = -i \cdot \frac{1}{2} + i \cdot \frac{1}{2} = 0$, so $\mathbb{E}(W) = 0$
- Similarly, $\text{var}(W_i) = \mathbb{E}(W_i^2) = i^2$ and

$$\text{var}(W) = \sum_{i=1}^{n} \text{var}(W_i) = \sum_{i=1}^{n} i^2 = \frac{n(n+1)(2n+1)}{6}$$

- A more advanced argument shows that for large n this statistic approximately follows a normal distribution when H_0 is true. In other words,

$$Z = \frac{W - 0}{\sqrt{n(n+1)(2n+1)/6}} \approx \mathrm{N}(0, 1)$$

- $\Pr(W \geqslant c \mid H_0) \approx \Pr(Z \geqslant z \mid H_0)$, which allows us to determine c.
- In this case, for $n = 10$ and $\alpha = 0.05$, we reject H_0 if

$$Z = \frac{W}{\sqrt{10 \cdot 11 \cdot 21/6}} \geqslant 1.645$$

(because $\Phi^{-1}(0.95) = 1.645$) which is equivalent to

$$W \geqslant 1.645 \times \sqrt{\frac{10 \cdot 11 \cdot 21}{6}} = 32.27$$

- For the example data we have $w = 25$, so we do not reject H_0

Using R

- R uses V rather than W
- For small sample sizes R will use the exact sampling distribution (which we haven't explored) rather than the normal approximation.
- To carry out the test, use: `wilcox.test`
- To work with the sampling distribution of V, use: `psignrank`
- Note: $\mathbb{E}(V) = n(n+1)/4$ and $\text{var}(V) = n(n+1)(2n+1)/24$. You can derive these in a similar way to W.

```
> wilcox.test(x, mu = 3.7, alternative = "greater",
              exact = TRUE)

Wilcoxon signed rank test

data:  x
V = 40, p-value = 0.1162
alternative hypothesis: true location is greater than 3.7

# Calculate exact p-value manually.
> 1 - psignrank(39, 10)
[1] 0.1162109

# Calculate approximate p-value, based on W.
> z <- 25 / sqrt(10 * 11 * 21 / 6)
> 1 - pnorm(z)
[1] 0.1013108
```

⇒ Close agreement between exact and approximate p-values

Paired samples

- Like other tests, we can use the Wilxcon signed-rank test for paired samples by first taking differences and treating these as a sample from a single distribution.
- The assumption of symmetry is quite reasonable in this setting, since under H_0 we would typically assume X and Y have the same distribution and therefore $X - Y \sim Y - X$.
- Indeed, this test is most often used in such a setting, due to the plausibility of this assumption.

Tied ranks

- We assumed a continuous population distribution
- Thus, all observations will differ (with probablity 1)
- In practice, the data are reported to finite precision (e.g. due to rounding), so we could have exactly equal values
- This will lead to ties when ranking our data
- If this happens, the 'rank' assigned for the tied values should be equal to the average of the ranks they span
- Example:

Value:	2.1	4.3	4.3	5.2	5.7	5.7	5.7	5.9
Rank:	1	2.5	2.5	4	6	6	6	8

- The presence of ties complicates the derivation of the sampling distribution, but R knows how to do the right thing

2.3 Wilcoxon rank-sum test (two-sample)

Wilcoxon two-sample test

- We can create a two-sample version of the Wilcoxon test.
- Independent random samples $X_1, \dots, X_{n_X}$ and $Y_1, \dots, Y_{n_Y}$ from two different populations with medians m_X and m_Y respectively.
- Want to test $H_0\colon m_X = m_Y$ against a one-sided or two-sided alternative
- Order the **combined** sample and let W be the sum of the ranks of $Y_1, \dots, Y_{n_Y}$. This is the *Wilcoxon rank-sum statistic*.
- Note: this captures information on X as well as Y! (Why?)
- The test based on this statistic is called the *Wilcoxon rank-sum test*, also known as the *Wilcoxon two-sample test* and the *Mann-Whitney U test*.

Rejection region

- Suppose our alternative hypothesis is $H_1\colon m_X > m_Y$
- If $m_X > m_Y$ then we expect W to be small, since the Y values will tend to be smaller than X and thus have smaller ranks
- Therefore, the critical region should be of the form $W \leqslant c$ for a suitable c.
- Properties of W (derivation not shown):

$$\mathbb{E}(W) = \frac{n_Y(n_X + n_Y + 1)}{2}$$
$$\mathrm{var}(W) = \frac{n_X n_Y(n_X + n_Y + 1)}{12}$$

- W is approximately normally distributed when n_X and n_Y are large

Alternative definitions

- Like for the one-sample version, the definition of the statistic varies
- We just defined: W is the sum of the ranks in the Y sample
- A popular alternative: U is the number of all pairs (X_i, Y_j) such that $Y_j \leqslant X_i$ (the number of 'wins' out of all possible pairwise 'contests')
- U and W are deterministically related (can you derive the formula?)
- U and W have different (but related) sampling distributions
- Using either statistic leads to equivalent test procedures
- Note: $\mathbb{E}(U) = n_X n_Y / 2$ and $\text{var}(U) = \text{var}(W)$

Example (Wilcoxon two-sample test)

Two companies package cinnamon. Samples of size eight from each company yield the following weights:

X	117.1	121.3	127.8	121.9	117.4	124.5	119.5	115.1
Y	123.5	125.3	126.5	127.9	122.1	125.6	129.8	117.2

Want to test $H_0\colon m_X = m_Y$ versus $H_1\colon m_X \neq m_Y$

Use a significance level of 5%

Using R

- R uses U... but calls it W!
- For small sample sizes R will use the exact sampling distribution, otherwise it will use a normal approximation
- To carry out the test, use: `wilcox.test`
- To work with the sampling distribution of U, use: `pwilcox`

```
> wilcox.test(x, y)

    Wilcoxon rank sum test

data:  x and y
W = 13, p-value = 0.04988
alternative hypothesis:
    true location shift is not equal to 0

# Calculate exact p-value manually.
> 2 * pwilcox(13, 8, 8)
[1] 0.04988345
```

We reject H_0 and conclude that we have sufficient evidence to show that the median weights differ between the two companies.

3 Goodness-of-fit tests (χ^2)

3.1 Introduction

Goodness-of-fit tests

- How well does a given model fit a set of data?
- E.g. if we assume a Poisson model for a set of data, is it reasonable?
- We can assess this with a 'goodness-of-fit' test
- The most commonly used is *Pearson's chi-squared test*

- Unlike most of the other tests we've seen, this operates on categorical (discrete) data
- Can also apply it on continuous data by first partitioning the data into separate classes

3.2 Two classes

Binomial model

- Start with a binomial model $Y_1 \sim \mathrm{Bi}(n, p_1)$
- Our usual test statistic for this is
$$Z = \frac{Y_1 - np_1}{\sqrt{np_1(1-p_1)}} \approx \mathrm{N}(0,1)$$
- Therefore,
$$Q_1 = Z^2 \approx \chi_1^2$$
- To test $H_0\colon p = p_1$ versus $H_1\colon p \neq p_1$, we would reject H_0 if $|Z|$ (and, hence, Q_1) is too large.
- Next, notice that
$$Q_1 = \frac{(Y_1 - np_1)^2}{np_1(1-p_1)} = \frac{(Y_1 - np_1)^2}{np_1} + \frac{(Y_1 - np_1)^2}{n(1-p_1)}$$
- and
$$(Y_1 - np_1)^2 = (n - Y_1 - n(1-p_1))^2 = (Y_2 - np_2)^2$$
where $Y_2 = n - Y_1$ and $p_2 = 1 - p_1$.
- Therefore,
$$Q_1 = \frac{(Y_1 - np_1)^2}{np_1(1-p_1)} = \frac{(Y_1 - np_1)^2}{np_1} + \frac{(Y_2 - np_2)^2}{np_2}$$
- Y_1 is the observed number of successes, np_1 is the expected number of successes
- Y_2 is the observed number of failures, np_2 is the expected number of failures
- So
$$Q_1 = \sum_{i=1}^{2} \frac{(Y_i - np_i)^2}{np_i} = \sum_{i=1}^{2} \frac{(O_i - E_i)^2}{E_i} \approx \chi_1^2$$
where O_i is the observed number and E_i is the expected number.
- Even though there are two classes, we have only **one** degree of freedom. This is due to the constraint $Y_1 + Y_2 = n$.

3.3 More than two classes

Multinomial model

- Generalize to k possible outcomes (a multinomial model)
- p_i = probability of the ith class ($\sum_{i=1}^{k} p_i = 1$)
- Suppose we have n trials, with Y_i being the number of outcomes in class i
- $\mathbb{E}(Y_i) = np_i$
- Now we get,
$$Q_{k-1} = \sum_{i=1}^{k} \frac{(Y_i - np_i)^2}{np_i} = \sum_{i=1}^{k} \frac{(O_i - E_i)^2}{E_i} \approx \chi_{k-1}^2$$
- $k - 1$ degrees of freedom because $Y_1 + \cdots + Y_k = n$

Setting up the test

- Specify a categorical distribution: $p_1, p_2, \ldots, p_k$
- We use the Q_{k-1} statistic to test whether are data are consistent with this distribution
- The null hypothesis is that they do (i.e. the p_i define the distribution)
- The alternative is that they do not (i.e. a different set of probabilities define the distribution)
- Under the null, the test statistic will tend to be small (it measures 'badness-of-fit')
- Therefore, reject the null if $Q_{k-1} > c$ where c is the $1 - \alpha$ quantile from χ^2_{k-1}.

Remarks

- We are approximating a binomial with a normal
- Good approximation if n is large and the p_i are not too small
- Rule of thumb: need to have all $E_i = np_i \geqslant 5$
- The larger the k (i.e. more classes), the more powerful the test. However, we need the classes to be large enough
- If any of the E_i are too small, can combine some of the classes until they are large enough
- If Q_{k-1} is very small, this indicates that the fit is 'too good'. This can be used as a test for rigging of experiments / fake data. Typically need very large n to do this.
- Often refer to the test statistic as χ^2

Example (completely specified distribution)

- Proportions of commuters using various modes of transport, based on past records:

Bus	Train	Car	Other
0.25	0.15	0.50	0.1

- After a 3-month campaign, a random sample ($n = 80$) found:

Bus	Train	Car	Other
26	15	32	7

- Did the campaign alter commuters behaviour?
- The expected frequencies are:

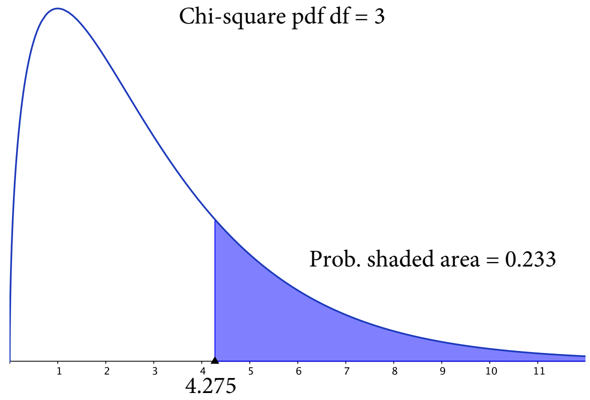
Bus	Train	Car	Other
20	12	40	8

- The value of the test statistic is:

$$\chi^2 = \frac{(26-20)^2}{20} + \frac{(15-12)^2}{12} + \frac{(32-40)^2}{40} + \frac{(7-8)^2}{8} = 4.275$$

- H_0: proportions have not changed, H_1: proportions have changed
- We have 4 classes, so the test statistic here has a χ^2_3 distribution.
- The 0.95 quantile is 7.81, which is greater than $\chi^2 = 4.275$
- Therefore, there is **insufficient** evidence that the proportions have changed
- The p-value is

$$p = \Pr(\chi^2_3 > 4.275) = 0.233 > 0.05$$



Using R

```
> x <- c(  26,   15,  32,   7)
> p <- c(0.25, 0.15, 0.5, 0.1)
> t1 <- chisq.test(x, p = p)
> t1

Chi-squared test for given probabilities

data:  x
X-squared = 4.275, df = 3, p-value = 0.2333

> rbind(t1$observed, t1$expected)
     [,1] [,2] [,3] [,4]
[1,]   26   15   32    7
[2,]   20   12   40    8

> t1$residuals
[1]  1.3416408  0.8660254 -1.2649111 -0.3535534

> sum(t1$residuals^2)
[1] 4.275

> 1 - pchisq(4.275, 3)
[1] 0.2332594
```

3.4 Estimating parameters

Fitting distributions

- We don't always have an exact model to compare against
- We might specify a family of distributions but still need to estimate some of the parameters
- For example, $\text{Pn}(\lambda)$ or $\text{N}(\mu, \sigma^2)$
- We would need to estimate the parameters using the sample, and use these to specify H_0
- We need to adjust the test to take into account that we've used the data to define H_0 (by design, it will be 'closer' to the data than if it we didn't need to do this)
- The 'cost' of this estimation is 1 degree of freedom for each parameter that is estimated
- The final degrees of freedom is $k - p - 1$, where p is the number of estimated parameters

Example (Poisson distribution)

- X is number of alpha particles emitted in 0.1 sec by a radioactive source
- Fifty observations:

  7, 4, 3, 6, 4, 4, 5, 3, 5, 3, 5, 5, 3, 2, 5, 4, 3, 3, 7, 6, 6, 4, 3, 9, 11, 6, 7, 4, 5, 4, 7, 3, 2, 8, 6, 7, 4, 1, 9, 8, 4, 8, 9, 3, 9, 7, 7, 9, 3, 10
- Is a Poisson distribution an adequate model for the data?
- H_0 : Poisson, H_1 : something else
- We have only specified the family of the distribution, not the parameters
- Estimate the Poisson rate parameter λ by the MLE, $\hat{\lambda} = \bar{x} = 5.4$
- Now we ask: does the Pn(5.4) model give a good fit?

First, find an appropriate partition of the value (collapse the data):

```
> X1 <- cut(X, breaks = c(0, 3.5, 4.5, 5.5, 6.5, 7.5, 100))
> T1 <- table(X1)
> T1
X1
  (0,3.5] (3.5,4.5] (4.5,5.5] (5.5,6.5] (6.5,7.5] (7.5,100]
       13         9         6         5         7        10
```

Then, prepare the data for the test:

```
> x <- as.numeric(T1)
> x
[1] 13  9  6  5  7 10

> n <- sum(x)
> p1 <- sum(dpois(0:3, 5.4));
> p2 <- dpois(4, 5.4)
> p3 <- dpois(5, 5.4)
> p4 <- dpois(6, 5.4)
> p5 <- dpois(7, 5.4)
> p6 <- 1 - (p1 + p2 + p3 + p4 + p5)
> p <- c(p1, p2, p3, p4, p5, p6)
```

Then, run the test:

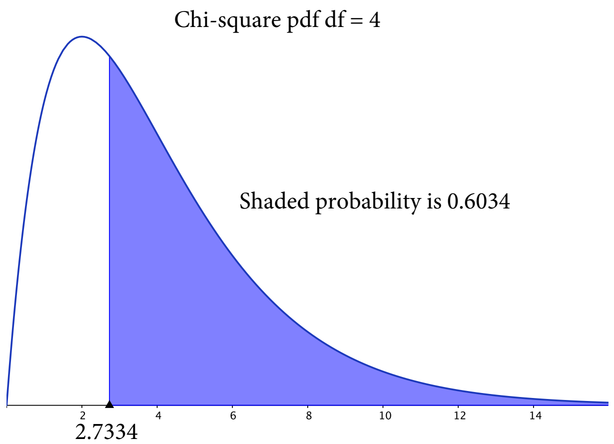
```
> chisq.test(x, p = p)

Chi-squared test for given probabilities

data:  x
X-squared = 2.7334, df = 5, p-value = 0.741
```

But this is the wrong df! Need to adjust manually:

```
> 1 - pchisq(2.7334, 4)
[1] 0.6033828
```



- Needed to adjust p-values as we have estimated the mean
- The critical value is the 0.95 quantile from χ^2_4, which is 9.488, so we cannot reject H_0
- Not enough evidence against the Poisson model
- Therefore, this is an adequate fit (at least, until further data proves otherwise)

	0–3	4	5	6	7	8+
Observed	13.0	9.0	6.0	5.0	7.0	10.0
Expected	10.7	8.0	8.6	7.8	6.0	8.9

4 Tests of independence (contingency tables)

Contingency tables

- Suppose we have multiple categorical variables (which could be continuous variables partitioned into classes)
- A *contingency table* records the number of observations for each possible cross-classification of these variables
- We are often interested in whether two categorical variables are related to each other
- For example, height and weight
- Define height classes $A_1, \dots, A_r$, and weight classes $B_1, \dots, B_c$
- Each person is assigned to a single combination (A_i, B_j)
- A sample of people can be summarised with a $r \times c$ table of counts (a contingency table)

Independence model

- A general model for these data is:

$$p_{ij} = \Pr(A_i \cap B_j), \quad i = 1, \dots, r, \quad j = 1, \dots, c$$

- Are the two variables independent?
- We can set this up as a hypothesis test:

$$H_0\colon p_{ij} = \Pr(A_i)\Pr(B_j) \quad \text{versus} \quad H_1\colon p_{ij} \neq \Pr(A_i)\Pr(B_j)$$

- This has the same structure as a goodness-of-fit test, can use Pearson's chi-squared statistic
- Show how this works through an example...

Example (contingency table)

150 executives were classified by sex, A, and whether or not they were firstborn, B:

	Firstborn	Not firstborn	Total
Male	34	74	108
Female	20	22	42
Total	54	96	150

Let's test whether these two variables are independent.

Estimating the marginals

- Recall discrete bivariate distributions:

	Firstborn	Not firstborn	Total
Male	p_{11}	p_{12}	$p_{1\cdot}$
Female	p_{21}	p_{22}	$p_{2\cdot}$
Total	$p_{\cdot 1}$	$p_{\cdot 2}$	1

- The marginals are:

$$p_{i\cdot} = \sum_{j=1}^{c} p_{ij} = \Pr(A_i)$$
$$p_{\cdot j} = \sum_{i=1}^{r} p_{ij} = \Pr(B_j)$$

- The null hypothesis of independence is just, $H_0 \colon p_{ij} = p_{i\cdot} p_{\cdot j}$
- Data:

	Firstborn	Not firstborn	Total
Male	y_{11}	y_{12}	$y_{1\cdot}$
Female	y_{21}	y_{22}	$y_{2\cdot}$
Total	$y_{\cdot 1}$	$y_{\cdot 2}$	n

- Estimates:

$$\hat{p}_{i\cdot} = \frac{y_{i\cdot}}{n}$$
$$\hat{p}_{\cdot j} = \frac{y_{\cdot j}}{n}$$

  where

$$y_{i\cdot} = \sum_{j=1}^{c} y_{ij}$$
$$y_{\cdot j} = \sum_{i=1}^{r} y_{ij}$$

- Pearson's χ^2 statistic for given p_{ij} is

$$Q = \sum_i \sum_j \frac{(Y_{ij} - np_{ij})^2}{np_{ij}}$$

- Under H_0, an estimator of p_{ij} is

$$\hat{p}_{ij} = \hat{p}_{i\cdot} \hat{p}_{\cdot j} = \frac{Y_{i\cdot} Y_{\cdot j}}{n^2}$$

- This gives the following,

$$Q = \sum_i \sum_j \frac{(Y_{ij} - Y_{i\cdot} Y_{\cdot j}/n)^2}{Y_{i\cdot} Y_{\cdot j}/n} \approx \chi^2_{(r-1)(c-1)}$$

Explanation for degrees of freedom

- Recall that we should have $k - p - 1$ degrees of freedom
- Here, $k = rc$, the total number of cells in the table
- We estimated $r-1$ marginal probabilities for the rows and $c-1$ for the columns, which makes $p = (r-1)+(c-1)$
- Therefore, the number of degrees of freedom remaining is:

$$\text{df} = rc - (r-1) - (c-1) - 1 = (r-1)(c-1)$$

Using R: set up the data

```
> x <- rbind(  male = c(first = 34, later = 74),
+            female = c(first = 20, later = 22))
> x
       first later
male      34    74
female    20    22
```

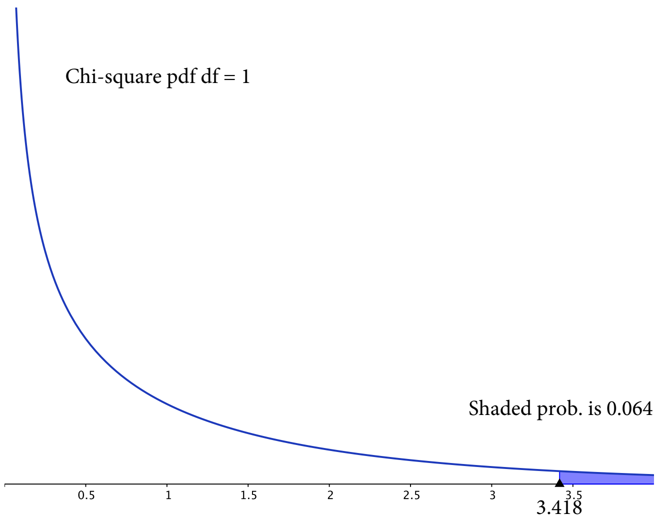
Using R: run the test

```
> c1 <- chisq.test(x, correct = FALSE)
> c1

Pearson's Chi-squared test

data:  x
X-squared = 3.418, df = 1, p-value = 0.06449
```

We do not have enough evidence to reject H_0 at a 5% significance level.



Using R: more output

```
> c1$observed
       first later
male      34    74
female    20    22

> c1$expected
       first later
male   38.88 69.12
female 15.12 26.88
```