# Distribution-free methods

(Module 7)

Statistics (MAST20005) & Elements of Statistics (MAST90058)

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### 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 $X_1 - m_0, \dots, X_n - m_0$
- In other words, replace $X_i$ with $\operatorname{sgn}(X_i - m_0)$
- 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 (due to symmetry assumption)
- $W$ is the sum of the integers $1, \dots, n$, each with a positive or negative sign
- Under $H_0$, $W = \sum_{i=1}^{n} W_i$ where

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

- 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, $\mathrm{var}(W_i) = \mathbb{E}(W_i^2) = i^2$ and

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

- 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 $\mathrm{var}(V) = n(n+1)(2n+1)/24$. 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
```

$\Rightarrow$ 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):

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

- $W$ 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 $\operatorname{var}(U) = \operatorname{var}(W)$

### 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 ($\chi^2$)

## 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 $i$th 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: $p_1, p_2, \dots, p_k$
- 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 $\chi^2_{k-1}$.

**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 $\chi^2$

**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:

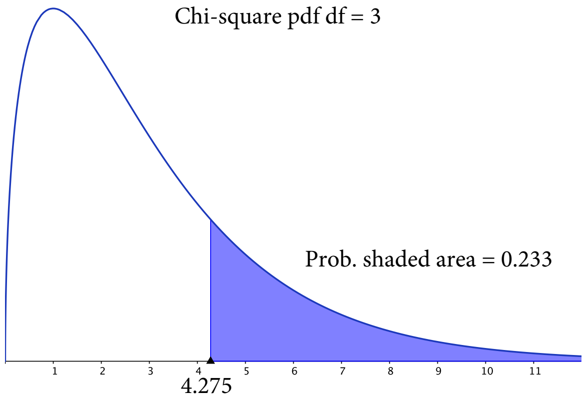
| Bus | Train | Car | Other |
|---|---|---|---|
| 20 | 12 | 40 | 8 |

- 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 $\chi^2_3$ 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 $\lambda$ 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, Inf))
> 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,Inf]
       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)
```

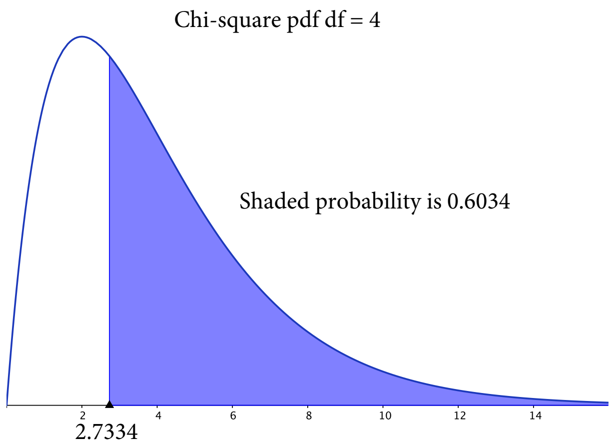


Then, run the test:

```
> 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 $\chi^2_4$, 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, $H_0: p_{ij} = p_{i\cdot}p_{\cdot j}$
- 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 $\chi^2$ 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
```

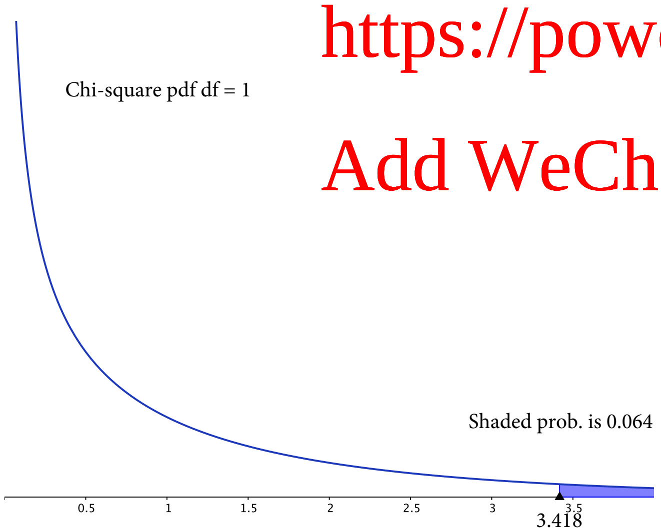
### Using R: run the test

```
> 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
```