17C

Laboratory & Professional Skills: Data Analysis

Emma Rand Data Analysis in R

Chi-squared tests

Summary of this week

Analysing data that are counts falling into mutually exclusive categories'

Two types of chi-squared test and the difference between these two tests.

In the workshop we will discover how to apply chi-squares to data in both frequency tables and in a more raw state (i.e., tabulate the data yourself)

Learning objectives for the week

By the end of this week the successful student should be able to :

- Explain the principles of chi-squared Goodness of Fit and Contingency tests and know when each can be applied (MLO 2)
- Apply and interpret Goodness of fit and Contingency chi-squared tests R on data in frequency tables and in raw format (MLO 3 and 4)
- Summarise and illustrate with appropriate R figures test results scientifically (MLO 3 and 4)

Why chi-squared?

 When we count the number of things in categories and compare the numbers we observe to numbers we expect under a null hypothesis.

The null hypothesis might be:

Same number in each category

1:1

smooth	wrinkled
13	17

1:1:1:1

red	blue	green	yellow
8	11	12	9

1:1:1:1:1:1

Mon	Tues	Wed	Thurs	Fri	Sat	Sun
23	29	11	14	20	15	21

Goodness of fit

The null hypothesis might be:

Follow a particular pattern

1:3

smooth	wrinkled
13	58

1:3:3:9

Yellow	Yellow	Red plain	Red spot
plain	spot		
4	14	12	30

Goodness of fit

The null hypothesis might be:

match the pattern in another group

?

But same as

	blue	green	yellow
Group A	11	12	9
Group B	3	12	9

Contingency

Why chi-squared?

- When we count the number of things in categories and compare the numbers we observe to numbers we expect under a null hypothesis.
- H₀ might expect numbers to
 - be the same, or

Goodness of fit

- follow a particular pattern, or
- match the pattern in another group

Contingency

Chi-squared allows us to make the comparison statistically

Our two example scenarios

- The Candy-striped spider can be plain or striped
 - 2 alleles at one locus, striped dominant to plain
 - We perform: $Ss \times ss = Ss$, Ss, ss, ss, ss
 - We expect the ratio of striped : plain to be 1:1



Example scenarios

- Food choice by pig breeds
 - We don't know what proportions are expected but do expect it to be same for each breed

Welsh Tamworth Essex

cabbage sugarbeet swede

Two types of scenario thus two types of χ^2 test

 We know what the proportions should be (known as a priori expectations)

Goodness of fit (e.g., candy striped spiders)

 We don't know what the proportions should be (without a priori expectations) but we know they should be the same in each group Contingency (e.g., pigs and food)

The Chi-squared formula

$$\chi_{[d.f]}^2 = \sum \frac{(O-E)^2}{E}$$

O – observed number

E – expected numbers

 Σ – take the sum of

The Chi-squared formula

$$\chi^2_{[d.f]} = \sum \frac{(O-E)^2}{E}$$

The difference between what we see and what we expect to see if H_0 is true

...squared so positive

.....relative to expected value

Gets bigger as the difference increases.

Also as number of categories increase therefore d.f. matter

χ^2 Goodness of fit test

χ^2 Goodness of fit test

- The expected values (null hypothesis) are derived from some theory
- We test the fit of our data to the theory
- The 'theory' can be a uniform distribution
- In our first example the theory is Mendel's Law (and happens to be uniform too)

Our two example scenarios

- The Candy-striped spider can be plain or striped
 - 2 alleles at one locus, striped dominant to plain
 - We perform: $Ss \times ss = Ss$, Ss, ss, ss, ss
 - We expect the ratio of striped : plain to be 1:1



- The Candy-striped spider: Striped: plain is 1:1
 - 63 offspring



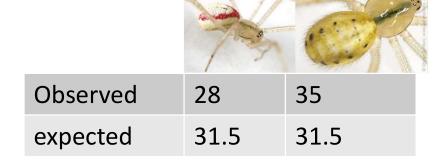
Observed	28	35
Expected	31.5	31.5

At least two ways to conduct in R.

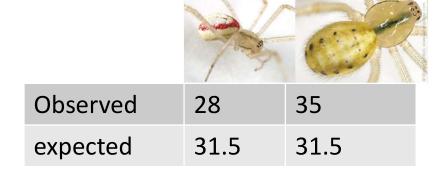
- 1. By coding the formula
- 2. By using the inbuilt function

We'll do both; you can use either.

- 1. By coding the formula
 - a) Observed values



- 1. By coding the formula
 - b) Expected values

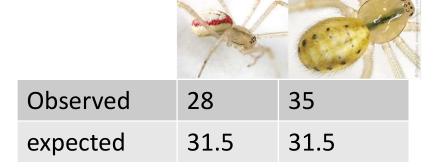


```
# calculate the expected values
# the H0 is for a 1:1 ratio
# i.e., half the total in each
exp <- c(total / length(obs), total / length(obs))</pre>
```

I used length(obs) rather than 2 because it makes the code more reusable

- 1. By coding the formula
 - c) Code the formula

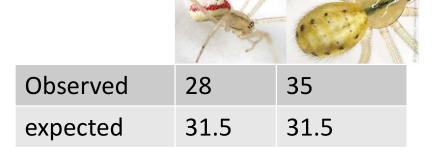
$$\chi_{[d.f]}^2 = \sum \frac{(O-E)^2}{E}$$



```
# code the formula
chi <- sum(((obs - exp)^2) / exp)
# [1] 0.7777778</pre>
```

1. By coding the formula

d) Find the probability of getting a χ^2 of 0.778 or more extreme (bigger)



```
# look up the probability of getting a chi squared
# of 0.778 or more extreme (bigger)
#
# the degrees of freedom are the number of
# categories minus 1
df <- length(obs) - 1
pchisq(chi, df = df, lower.tail = FALSE)
# [1] 0.3778216</pre>
```

Conclusion

- $\chi^2 = 0.78$; *d.f.* = 1; p = 0.38
 - -p > 0.05, therefore the test is not significant
 - Results are consistent with a 1:1 ratio

"There was no significant difference between the observed and the expected ratio."

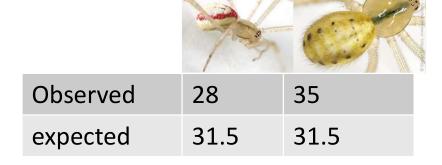
Conclusion

- IF you had $\chi^2 = 4.6$; *d.f.* = 1; p = 0.032
 - -p < 0.05 therefore the test is significant
 - Results are NOT consistent with a 1:1 ratio

"There was a significant difference between the observed and expected ratio ($\chi^2 = 4.6$; d.f. = 1; p = 0.032)."

"There were significantly more xxxx and fewer xxxx than expected ($\chi^2 = 4.6$; d.f. = 1; p = 0.032)."

1. By using the inbuilt function



But what to use?? What you prefer but....

1. By coding the formula

Useful when your expected are derived from a more complex theory/idea (e.g., poisson distribution, binomial distribution) or you need to alter the d.f.

2. By using the inbuilt function

Easy when the ratio is 1:1, 1:1:1, 1:1:1 etc

But take care – other H₀ must be specified

Summary

Goodness of fit

- We know what the proportions should be (known as a priori expectations)
 - fit to a theory or distribution
- Single row/column of observations
 - One explanatory
- Inbuilt chisq.test() function is good for 1:1:1 expectations, otherwise specify prob
- For complex cases, calculate expected values and code the test.

- Food choice by pig breeds
 - We don't know what proportions are expected but do expect it to be same for each breed



 Null hypothesis: proportion of foods taken by each breed is the same, i.e., no association between breed and food type

The Data

	Welsh	Tamworth	Essex	
cabbage 📗	11	19	22	52
sugarbeet 🔯	21	16	8	44
swede 🍑	7	12	11	30
	39	47	41	127

Expected values are derived from the data

Overall pref for cabbage = 52/127We expect (the H_0)same for each breed

Where do the expected values come from?

	Welsh	Tamworth	Essex	
cabbage	11	19	22	52
sugarbeet	21	16	8	44
swede	7	12	11	30
	38	47	41	127

Overall preference for cabbage = 45/127

Thus: Exp no. of welsh preferring cabbage = 52/127 * 38 = 15.97

Exp no. of tamworth preferring cabbage 52/127 * 47 = 19.24

Exp no. of essex preferring cabbage 52/127 * 41 = 16.79

RULE: Expected number for each cell: Row total * Column total / Overall total

Where do the expected values come from?

Wow, that's a pain!

R to the rescue!

@allison_horst



R's inbuilt function will do that!

First, add the data

Note: this is the only time we'll use a matrix datatype – we normally use dataframes.

It's helpful to name the rows and columns

```
# make a list object to hold two vectors
# in a list the vectors can be of different lengths
vars <- list(breed = c("welsh",</pre>
                        "tamworth",
                        "essex"),
             food = c("cabbage",
                       "sugarbeet",
                       "swede"))
food pref <- matrix(c(11, 21, 7,
                       19, 16, 12,
                       22, 8, 11),
                     nrow = 3,
                     byrow = TRUE,
                     dimnames = vars)
```

χ² Contingency test example

Now we have...

```
food
breed cabbage sugarbeet swede
welsh 11 21 7
tamworth 19 16 12
essex 22 8 11
```

Run the inbuilt test

```
chisq.test(food_pref)

          Pearson's Chi-squared test

data: food_pref
X-squared = 10.64, df = 4, p-value = 0.03092
```

degrees of freedom

 Degrees of freedom are not number of categories – 1 but

$$(rows - 1)(cols - 1) = 2 * 2 = 4$$

•
$$\chi^2_{[4]} = 10.64$$

Conclusion

- Thus the test is significant (we reject the null hypothesis)
- Conclude: evidence of a preference for particular foods by different breeds

But in what way? ("direction of effect")
 Who likes what?

Conclusion

In what way – examine the observed and expected values. Observed:

```
# food
# breed cabbage sugarbeet swede
# welsh 11 21 7
# tamworth 19 16 12
# essex 22 8 11
```

Expected:

```
chisq.test(food_pref)$expected
# food

# breed cabbage sugarbeet swede
# welsh 15.96850 13.81890 9.212598
# tamworth 19.24409 16.65354 11.102362
# essex 16.78740 14.52756 9.685039
```

Conclusion

Direction of deviations; size of deviation Observed:

Higher than expected Less than 1 different Lower than expected

```
# food
# breed cabbage sugarbeet swede
# welsh 11 21 7
# tamworth 19 16 12
# essex 22 8 11
```

Expected:

```
chisq.test(food_pref)$expected
# food
# breed cabbage sugarbeet swede
# welsh 15.96850 13.81890 9.212598
# tamworth 19.24409 16.65354 11.102362
# essex 16.78740 14.52756 9.685039
```

Conclusion

Different pig breeds showed a significant preference for the different food types ($\chi^2 = 10.64$; d.f. = 4; p = 0.031) with Essex much preferring cabbage and disliking sugarbeet, Welsh showing a strong preferencing for sugarbeet and a dislike of cabbage and Tamworth showing no clear preference.

```
# food
# breed cabbage sugarbeet swede
# welsh 11 21 7
# tamworth 19 16 12
# essex 22 8 11
```

Summary

Contingency

- We don't know what the proportions should be (without a priori expectations) but we know they should be the same in each case
- At least 2 x 2 table
 - Two explanatory
- Inbuilt chisq.test() function is good