

Contingency tables

Theory

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Contingency tables

We count cases and divide them into categories:

		Disease
treatment	yes	no
treated	4	96
untreated	10	90

Proportions:

$$4/100 = 0.04$$

$$10/100 = 0.1$$

Question:

Is there an association between disease and treatment?

Are the proportions of diseased persons different in the two treatment groups?

Contingency tables

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		yes	no
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Terminology:

cell counts	n_{11}	n_{12}	$n_{1\cdot}$	row totals
	n_{21}	n_{22}	$n_{2\cdot}$	
	$n_{\cdot 1}$	$n_{\cdot 2}$	$n_{\cdot \cdot}$	
column totals				total count

Contingency tables

... with frogs

	Colour	
sex	light	dark
female		
male		

To answer this question, we have to understand where the cell counts come from.

Question:

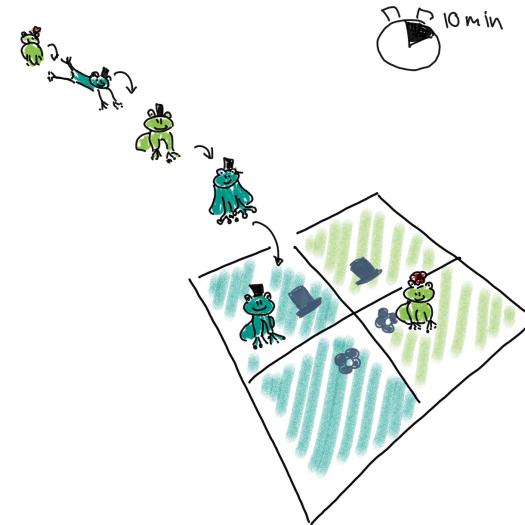
Is there an association between sex and colour?

Different study designs

Poisson sampling:

- Each category has its own Poisson rate:

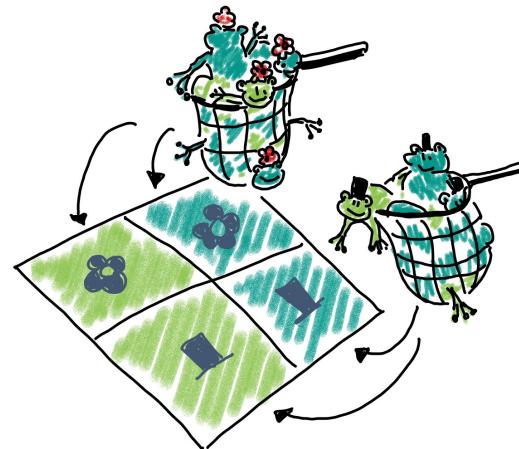
$$\lambda = n * p$$



Different study designs

Binomial sampling:

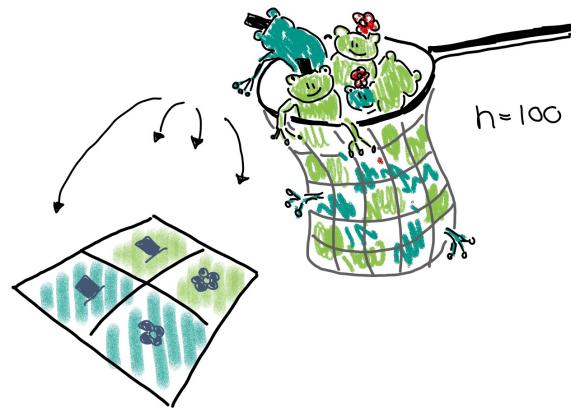
- Fixed number of n_f female frogs
- Fixed number of n_m male frogs
- For each sex, there is the probability of being light: p



Different study designs

Multinomial sampling:

- Fixed number of n frogs
- Each category has its own probability: p



Expected counts

The expected counts are the same for these study designs:

	Colour	
sex	light	dark
female	 $n * p_{11}$	 $n * p_{12}$
male	 $n * p_{21}$	 $n * p_{22}$

New question:

Are the probabilities dependent on each other?

Probability rules for independence

Independence:

$$P(A, B) = P(A) * P(B)$$

Example: Flip two coins

$$P(\text{head, head}) = P(\text{head}) * P(\text{head}) = 1/4$$



The outcomes of the two coins are independent.

Association:

$$P(A, B) \neq P(A) * P(B)$$

Example: hair and eye colour

$$P(\text{blond, blue}) = P(\text{blond}) * \underline{P(\text{blue}|\text{blond})}$$



conditional probability: blonds are more likely to have blue eyes than dark-haired

Hair and eye colour are associated.

Expected counts under H_0

Observed counts:

		disease	
		yes	no
treatment	yes	n_{11}	n_{12}
	no	n_{21}	n_{22}

$$P(disease) = \frac{n_{11} + n_{21}}{n_{..}}$$

marginal probabilities

$$P(treat) = \frac{n_{11} + n_{12}}{n_{..}}$$

Null hypothesis: disease and treatment are independent.

→ We expect that the product of the marginal probabilities is a good estimate for the cell count:

Expected counts:

$$\mu_{11} = P(disease) * P(treat) * n_{..}$$

...

Expected counts

		Disease		
treatment	yes	no	total	
treated	4	96	100	
untreated	10	90	100	
total	14	186	n = 200	

{

$$P(D) = \frac{14}{200} = 0.07$$

}

$$P(\text{treated}) = \frac{100}{200} = 0.5$$

Expected counts
assuming independence:

$$\begin{aligned}
 E(n_{\text{treated}, \text{disease}}) &= P(\text{treated}) * P(\text{disease}) * n.. \\
 &= 0.5 * 0.07 * 200 \\
 &= 7
 \end{aligned}$$

Chi-Square test

Statistic:

$$\chi^2 = \sum_{ij} \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

O : observed count

E : expected count under H_0

i, j : row and column index

r : number of rows

c : number of columns

χ^2 quantifies the deviation from independence.

χ^2 follows a chi-squared distribution with $(r - 1) * (c - 1)$ degrees of freedom.

Question: How can we use this information to perform a test?

In our example

Disease			
treatment	yes	no	total
treated	4	96	100
untreated	10	90	100
total	14	186	n = 200

Question: What else should we report?

Output from R:

```
chisq.test(array(c(4,96,10,90), dim=c(2,2)), correct=FALSE)
```

Pearson's Chi-squared test

```
data: array(c(4, 96, 10, 90), dim = c(2, 2))
X-squared = 2.765, df = 1, p-value = 0.09635
```

Quantifying association

Difference in proportions

$$D = P(\text{disease} | N) - P(\text{disease} | T)$$

The absolute difference between the proportions of disease cases in the two groups is **6%**.

Relative risk

$$RR = \frac{P(\text{disease} | T)}{P(\text{disease} | N)}$$

The proportion of disease cases in the treated group is **0.4** times the proportion of disease cases in the no treatment group.

Odds ratio

$$OR = \frac{P(\text{disease}|T)/(1 - P(\text{disease}|T))}{P(\text{disease}|N)/(1 - P(\text{disease}|N))}$$

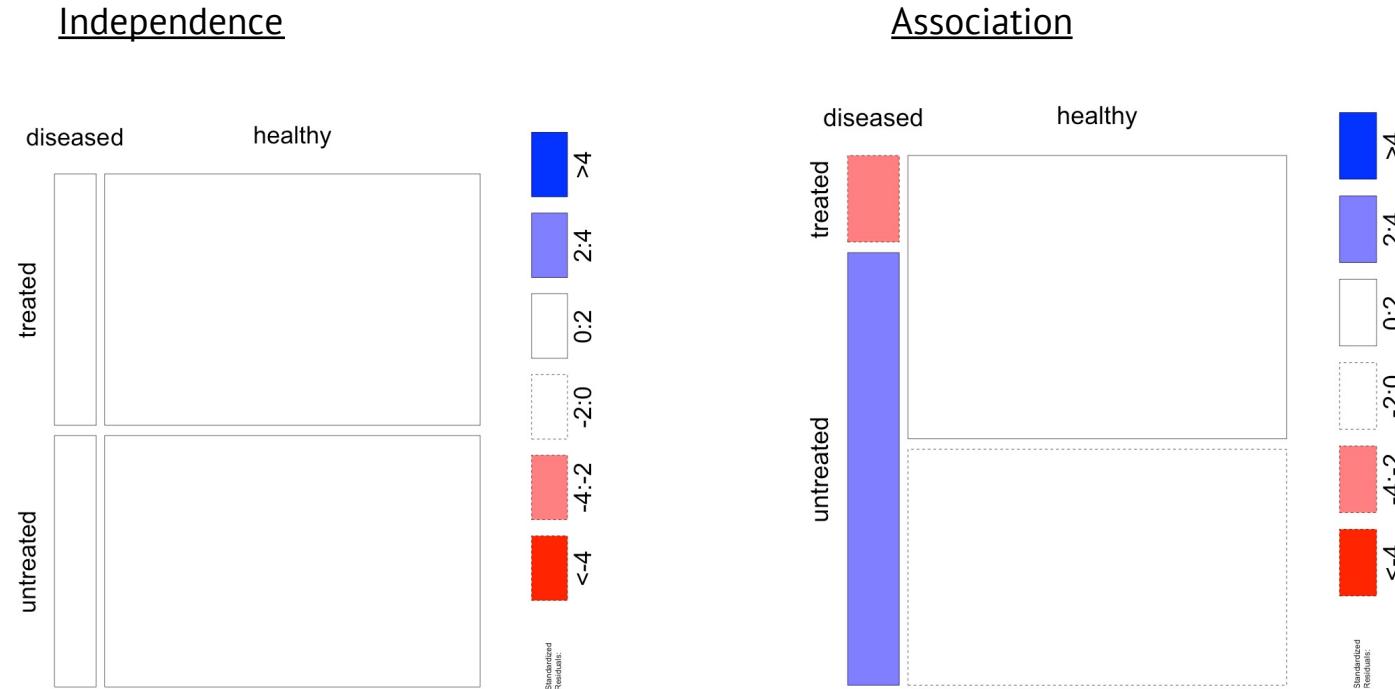
The odds for having the disease when treated is **0.38** times the odds when being untreated.

Log odds ratio

$$\log(OR)$$

... a useful parameter for models (**-0.97**)
 $\log(OR) > 0$: disease more likely when untreated
 $\log(OR) < 0$: disease more likely when treated

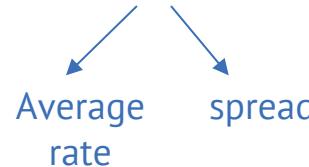
Visualizing association



Overdispersed data

Overdispersion: For each measurement, the rate lambda is slightly different (it's drawn from a gamma-poisson distribution).

For each cell: $\lambda \sim \text{GammaPois}(\mu, \theta)$



Question: How can we estimate the spread from a contingency table?

Example: Expression counts

	Cell type	
treatment	control	cancer
treated	0	5
untreated	10	28

Research question: is there a cell-type specific response to the treatment?

Known sources of variation: individual cell-to-cell differences in expression.

Overdispersed data

- We need more counts for each combination of variables.
- Represent data in a data frame:

treatment	Cell type	count
untreated	control	0
untreated	control	28
untreated	control	5
untreated	cancer	37
untreated	cancer	20
...

Several
measurements per
combination

Gamma-poisson regression fits:

- Overdispersion
- Individual effects of cell type and treatment
- Interaction between cell type and treatment

Summary

- **Contingency table:**
 - Row and column = two different variables
 - Each cell is a count from 1 combination of the two variables (Poisson or binomial counts)
- We are interested in the association between the two variables:
 - A **chi-square test** gives a significance of the association
 - The effect size is a **measure of association**, e.g. relative risk
- **Limitations** of contingency tables:
 - Can only deal with one count per combination of variables
 - Does not allow to estimate overdispersion
 - Use regression in these cases
- Contingency tables can be **extended** to more dimensions.