Analysis of Frequencies

Lecture 10

1 Outline

- Introduction to Categorical Data
- Goodness-of-Fit Tests
- Test of Homogeneity
- Test of Independence
- Fisher's Exact Test
- Symmetry Tests
- Measures of Association

2 Categorical Data

2.1 Associations between Categorical Data

Often, we are interested in testing for association between categorical data. These variables can be nominal or ordinal.

> **Note**
>
> Suppose we want to test whether there is an association between the type of hospital a patient is admitted to and their diagnosed conditions.

2.2 Contingency Tables

A contingency table is a table of frequencies or counts for each possible combination of the variables.

Example

The hair and eye color of male statistics students were measured. The findings were summarized in the following contingency table.

```
       Eye
Hair    Brown Blue Hazel Green
  Black    32   11    10     3
  Brown    53   50    25    15
  Red      10   10     7     7
  Blond     3   30     5     8
```

2.3 Contingency tables in R

You can use `xtabs()` to produce contingency tables in `R`. The data should be formatted such that the two variables are defined by two columns. If these columns are `x` and `y` from a data frame `df`, the sample code would look like:

```
xtabs(~x+y,data=df)
```

`x` will be assigned as the row variable, `y` will be assigned as the column variable.

2.4 Example

The data set `penguins` preloaded in `R` includes data from penguins at the Palmer Archipelago in Antarctica.

2.4.1 Question

Create a contingency table for this data that summarizes the number of penguins belonging to each species and sex.

2.4.2 Answer

```
xtabs(~species+sex,data=penguins)
```

```
           sex
species     female male
  Adelie        73   73
  Chinstrap     34   34
  Gentoo        58   61
```

2.5 Chi-Squared Distribution

Tests involving categorical data use the chi-squared distribution to approximate the distribution of the test statistics.

2.5.1 Support

The chi-squared distribution is defined for non-negative values $(0, \infty)$.

2.5.2 Parameter

The chi-squared distribution can be defined by the degrees of freedom ν or df.

Like the t-distribution, we only need one value for the degree of freedom.

2.5.3 Relation to Gaussian Distribution

Suppose Z follows the standard Gaussian distribution N(0,1). Then Z^2 follows a chi-square distribution with 1 degree of freedom.

2.5.4 Mean and Variance

The mean of the chi-squared distribution is k, and the variance of the chi-squared distribution is $2k$.

3 Goodness-of-Fit Tests

3.1 Goodness of Fit

Suppose we want to test if the data follows a specified distribution.

Example

Suppose we want to know if a six-sided die is fair. We would expect to roll the numbers uniformly after a large number of throws. However, there will be variability due to randomness. The goodness-of-fit test will provide information if we have evidence of deviating from the pre-specified uniform distribution.

3.2 Hypothesis Test

The null hypothesis of the goodness-of-fit test is that **the observed data follows the specified distribution**, while the alternative is that it does not follow the specified distribution.

3.3 Test Statistic

Suppose there are k bins separating the data and that the distribution provides an expected number/counts of events E_i for $i = 1, 2, ...k$. If the observed number/counts in the data is O_i, we define the test statistics Q such that

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

Important

Q approximately follows the chi-squared distribution with $k - 1$ degrees of freedom, denoted by χ^2_{k-1}.
For the chi-squared distribution assumption to be valid, the expected value of each bin should be greater than 5.

3.4 p-value calculation

The p-values can be calculated using the chi-squared distribution such that:

$$p - value = P(\chi^2_{k-1} \geq Q)$$

3.5 `R` implementation

There are two ways to check for goodness of fit: formal statistical analysis and exploratory data visualization.

3.5.1 Expected Values

For discrete distributions, the expected values can be calculated using the PDF functions (`dpois`, `dbinom`) for discrete distributions, and CDF functions (`pnorm`,`punif`, `pt`).

3.5.2 Formal Statistical Analysis

The `chisq.test` function performs the chi-squared test of goodness of fit. The function needs a vector of the observed variables, `x_observed` and a vector of probabilities `p`.

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

> **!** Important
>
> The `chisq.test()` function includes a continuity correction in calculating the test statistic and the corresponding p-value. If we want the uncorrected statistic and p-value, we need to specify `correct=FALSE`.

3.5.3 Visualization

Once the expected values are calculated, we can plot these values using `ggplot()`.

3.6 Example

Electronic integrated circuits are produced from thin wafers that are cut from some material. The wafers produced sometimes have tiny flaws on them that make part of the wafer unusable. Suppose we produce 1000 wafers and for each we determine the number of flaws.

3.6.1 Data

Number of Flaws	Observed Frequency
0	10
1	220
2	130
3	80
4	60
5 or more	90

3.6.2 Question

Test whether these data follow a Poisson distribution with $\lambda = 1.44$. Visualize the observed and expected counts to support the results of the test.

3.6.3 Answer

We specify the observed variable.

```
observed <- c(10,220,130,80,60,90)
observed
```

```
[1]  10 220 130  80  60  90
```

```
total <- sum(observed)
total
```

```
[1] 590
```

The specified distribution is the Poisson distribution. We can then calculate the expected probabilities using `dpois` and `ppois`.

```
expected <- c(
dpois(0,lambda=1.44),
dpois(1,lambda=1.44),
dpois(2,lambda=1.44),
dpois(3,lambda=1.44),
dpois(4,lambda=1.44),
1-ppois(4,lambda=1.44)
)
expected
```

```
[1] 0.23692776 0.34117597 0.24564670 0.11791042 0.04244775 0.01589140
```

```
sum(expected) # must be 1
```

```
[1] 1
```

```
total*expected # there should not be more than 1.5 bins that have less than 5 expected counts
```

```
[1] 139.787378 201.293824 144.931553  69.567145  25.044172   9.375928
```

All expected counts are above 5. We can now use the chi-square approximation for the p-value.

```
chisqtest <- chisq.test(x=observed,p=expected)
chisqtest
```

```
    Chi-squared test for given probabilities

data:  observed
X-squared = 867.42, df = 5, p-value < 2.2e-16
```

The test statistic is 867.4246622 with a p-value $<$ 2.2e-16. We reject the null hypothesis. We have sufficient evidence to conclude that the observed data does not follow the Poisson distribution.

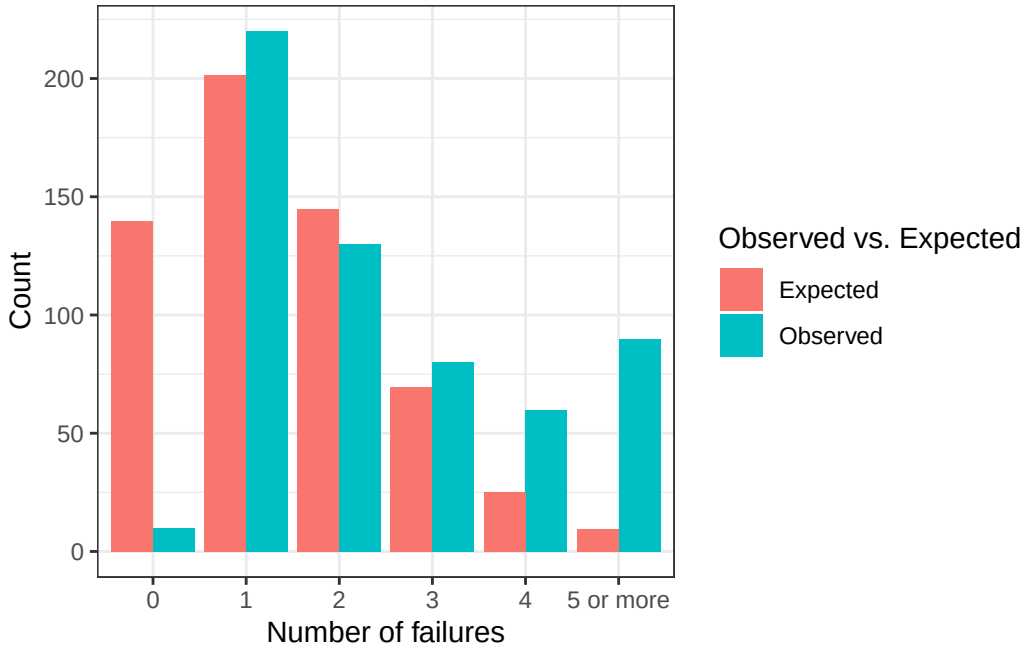
3.6.4 Plot

The function `bind_rows` appends the expected data frame to the observed data frame.

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.2
v ggplot2   4.0.0     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```r
df_observed <- data.frame(bin = c(0,1,2,3,4,"5 or more"),y=observed,type="Observed")
df_expected <- data.frame(bin = c(0,1,2,3,4,"5 or more"),y=total*expected,type="Expected")
df <- bind_rows(df_observed,df_expected)

ggplot(df,aes(x=bin,y=y,group=type,fill=type)) +
  geom_bar(position="dodge",stat="identity") +
  theme_bw() +
  labs(x="Number of failures", y="Count",fill="Observed vs. Expected")
```



3.7 Exercise

In the "nighttime" lottery run by the state of Texas, three numbers are selected from the digits 0 through 9. The frequencies of the first digit selected over a period of almost 30 years (from 1993 to 2023) are shown below for each of the 9,215 days.

3.7.1 Data Set

Digit	Frequency
0	918
1	905

Digit	Frequency
2	908
3	916
4	900
5	911
6	963
7	948
8	937
9	909

3.7.2 Question

Test whether each digit is equally likely to have been selected in the Texas "nighttime" lottery.

3.7.3 Answer

We specify the observed variable.

```
observed <- c(918,905,908,916,900,911,963,948,937,909)
observed
```

```
 [1] 918 905 908 916 900 911 963 948 937 909
```

```
total <- sum(observed)
total
```

```
[1] 9215
```

The specified distribution is the discrete uniform distribution. We can then calculate the uniform probabilities as 1/10 (10 bins).

```
expected <- c(1/10,1/10,1/10,1/10,1/10,1/10,1/10,1/10,1/10,1/10
)
expected
```

```
 [1] 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
```

```r
sum(expected) # must be 1
```

```
[1] 1
```

```r
total*expected # there should not be more than 1.5 bins that have less than 5 expected counts
```

```
 [1] 921.5 921.5 921.5 921.5 921.5 921.5 921.5 921.5 921.5 921.5
```

All expected counts are above 5. We can now use the chi-square approximation for the p-value.

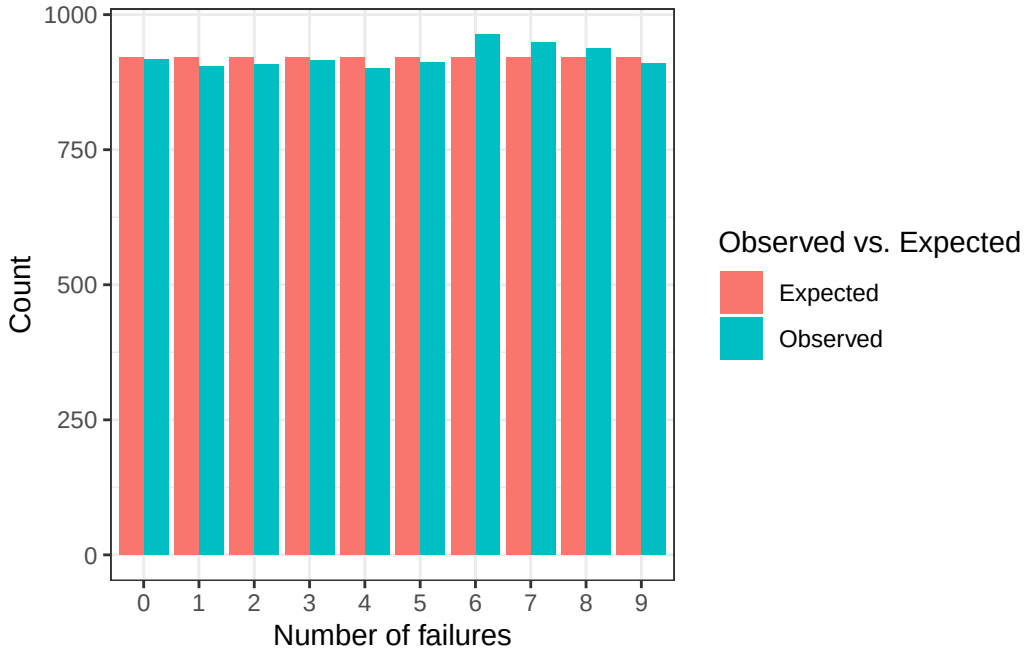
```r
chisqtest <- chisq.test(x=observed,p=expected)
chisqtest
```

```
    Chi-squared test for given probabilities

data:  observed
X-squared = 4.2219, df = 9, p-value = 0.8962
```

The test statistic is 4.2219208 with a p-value 0.8962084. We fail to reject the null hypothesis. We have insufficient evidence to conclude that the digits are not equally likely to be chosen for the "nighttime" lottery.

3.7.4 Plot

```r
library(tidyverse)
df_observed <- data.frame(bin = 0:9,y=observed,type="Observed")
df_expected <- data.frame(bin = 0:9,y=total*expected,type="Expected")
df <- bind_rows(df_observed,df_expected)

ggplot(df,aes(x=as.factor(bin),y=y,group=type,fill=type)) +
  geom_bar(position="dodge",stat="identity") +
  theme_bw() +
  labs(x="Number of failures", y="Count",fill="Observed vs. Expected")
```



4 Test of Independence

4.1 Test of Independence

Suppose we are interested in a contingency table made from two distinct categorical variables.

> **Assumptions**
>
> Suppose the row variables has r levels and the column variables has c levels. This implies that any unit/subject can fall in any of the rc categories.

4.2 Hypothesis Test

The null hypothesis for the test of independence is that **the row and column variables are independent of each other**, while the alternative hypothesis is that the row and column variables are not independent.

4.3 Null Hypothesis Assumption

Suppose we define p_{ij} as the probability of a unit to be found at row i and column j, denoted by (i, j). We also define $p_{i\cdot}$ and $p_{\cdot j}$ as the respective probabilities of finding the unit at row i and finding the unit at row j. The assumption of independence implies that for all i and j,

$$p_{ij} = p_{i\cdot} p_{\cdot j}$$

> **Note**
>
> Under the assumption that the null hypothesis is true, the expected counts for each cell can be calculated as:
>
> $$E_{ij} = r_i c_j / n$$
>
> where r_i is the row total for row i, c_j is the column total for column j, and n is the total sample size.

4.4 Test Statistic

The test statistic compares the deviation of the observed data to the expected data similar to the goodness-of-fit.

$$Q = \sum_{i=1}^{r} \sum_{j=1}^{c} \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

The test statistic approximately follows a chi-squared distribution with degrees of freedom $(r-1)(c-1)$, $\chi^2_{(r-1)(c-1)}$ where r and c are the total numbers of rows and columns, respectively.

> **Important**
>
> It is important to check the expected number of events for each cell. If the expected number of events is less than 5 for 25% of the cells, the chi-square distribution does not hold.

4.5 p-value

The p-value can be calculated using the probability $P(\chi^2_{(r-1)(c-1)} \geq Q)$.

4.6 R implementation

The `chisq.test()` can also be used to perform tests of independence.

> **Note**
>
> When dealing with data sets, it would be beneficial to create a contingency table with `xtabs()` first to check for data sparsity (low cell counts) before using it as an input in `chisq.test()`.

```
xtabs(~x+y, data=df)
chisq <-chisq.test(df$x,df$y)
chisq
```

> **Tip**
>
> `chisq.test()` calculates the expected values using the `chisq$expected` option.

4.7 Example

Consider the sleep health data, `SleepHealthData.csv`.

```
sleep <- read.csv("SleepHealthData.csv")
```

4.7.1 Question

Test whether gender (variable `gender`) is associated with reported sleep disorders (variable `sleep_disorder`. Use a significance level of 0.01.

4.7.2 Answer

Check for sparsity of data first.

```
xtabs(~gender+sleep_disorder,data=sleep)
```

```
        sleep_disorder
gender   Insomnia None Sleep Apnea
  Female       36   82          67
  Male         41  137          11
```

```r
chisqtest <- chisq.test(sleep$gender,sleep$sleep_disorder)
chisqtest
```

```
    Pearson's Chi-squared test

data:  sleep$gender and sleep$sleep_disorder
X-squared = 54.306, df = 2, p-value = 1.613e-12
```

```r
chisqtest$expected
```

```
            sleep$sleep_disorder
sleep$gender Insomnia     None Sleep Apnea
      Female 38.08824 108.3289    38.58289
      Male   38.91176 110.6711    39.41711
```

All expected values are above 5, which means the chi-squared assumption is valid. The p-value is $1.6128634 \times 10^{-12}$, the test statistic is 54.3060201 with 2 degrees of freedom. At a significance level of 0.01, we reject the null hypothesis. We have sufficient evidence to conclude that the gender and occurrence of sleep disorder are not independent.

4.8 Exercise

Consider the sleep health data, `SleepHealthData.csv`.

```r
sleep <- read.csv("SleepHealthData.csv")
```

4.8.1 Question

Test whether stress level (variable `stress_level`) is associated with reported sleep disorders (variable `sleep_disorder`). Treat stress level as an ordinal categorical variable. Use a significance level of 0.01.

4.8.2 Answer

Check for sparsity of data first.

```
xtabs(~stress_level+sleep_disorder,data=sleep)
```

```
            sleep_disorder
stress_level Insomnia None Sleep Apnea
           3        1   40          30
           4       24   43           3
           5        6   57           4
           6        2   43           1
           7       41    3           6
           8        3   33          34
```

```
chisqtest <- chisq.test(sleep$stress_level,sleep$sleep_disorder)
chisqtest
```

```
    Pearson's Chi-squared test

data:  sleep$stress_level and sleep$sleep_disorder
X-squared = 240.2, df = 10, p-value < 2.2e-16
```

```
chisqtest$expected
```

```
                  sleep$sleep_disorder
sleep$stress_level  Insomnia     None Sleep Apnea
                 3 14.617647 41.57487   14.807487
                 4 14.411765 40.98930   14.598930
                 5 13.794118 39.23262   13.973262
                 6  9.470588 26.93583    9.593583
                 7 10.294118 29.27807   10.427807
                 8 14.411765 40.98930   14.598930
```

All expected values are above 5, which means the chi-squared assumption is valid. The p-value is $6.2217174 \times 10^{-46}$, the test statistic is 240.1993685 with 10 degrees of freedom. At a significance level of 0.01, we reject the null hypothesis. We have sufficient evidence to conclude that the stress level and occurrence of sleep disorder are not independent.

5 Test of Homogeneity

5.1 Test of Homogeneity

Suppose the sampling strategy was to select a fixed sample size per group, and measure the response for each unit/individual.

> **Note**
>
> If the samples are stratified per group, the groups are not random. The response remains random. The margins for the grouping variable, typically assigned in the rows, are fixed in advance.

5.2 Homogeneity vs. Independence

> **Important**
>
> Because people assigned to/sampled from groups are no longer random, there is no sense to test for independence. Instead, we test whether the probability of being in each of the outcome groups is the same across all treatments.
> Hence, the test is referred to as the **test of homogeneity**.

5.3 Hypothesis Test

The null hypothesis is that the marginal probability of the outcome variable is the same across all the groups/populations/treatments considered in the study.

The alternative hypothesis is that at least one marginal probability is not equal to the others.

> **Note**
>
> This test is similar to comparing the difference of two proportions for a 2x2 contingency table.

5.4 Null Hypothesis Assumption

Suppose we define p_{ij} as the probability of a unit to be found at row i and column j, denoted by (i, j). The assumption of homogeneity assumes that the marginal probability across the columns are the same. Hence,

$$p_{ij} = c_j/n$$

> **Note**
>
> Under the assumption that the null hypothesis is true, the expected counts for each cell can be calculated as:
>
> $$E_{ij} = r_i p_{ij} = r_i(c_j/n)$$
>
> where r_i is the row total for row i, c_j is the column total for column j, and n is the total sample size.

5.5 Test Statistic

The test statistic compares the deviation of the observed data to the expected data similar to the goodness-of-fit.

$$Q = \sum_{i=1}^{r} \sum_{j=1}^{c} \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

The test statistic approximately follows a chi-squared distribution with degrees of freedom $(r-1)(c-1)$, $\chi^2_{(r-1)(c-1)}$ where r and c are the total numbers of rows and columns, respectively.

> **Important**
>
> Note that the test statistic is the same for independence and homogeneity tests, but the assumptions and hypotheses are different.
> It is important to check the expected number of events for each cell. If the expected number of events is less than 5 for 25% of the cells, the chi-square distribution does not hold.

5.6 p-value Calculation

The p-value can be calculated using the probability $P(\chi^2_{(r-1)(c-1)} \geq Q)$.

5.7 `R` Implementation

The `R` implementation of the homogeneity test is similar to that of the independence test.

5.8 Example

The data set `covid.csv` includes data from a clinical trial for treatments of COVID-19. Suppose that subjects are randomly assigned to one of two treatments: an experimental drug and a placebo (best available treatment).

```
library(tidyverse)
covid <- read.csv("datasets/covid.csv")
glimpse(covid)
```

```
Rows: 1,297
Columns: 3
$ ID        <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 1~
$ Treatment <chr> "Experimental", "Experimental", "Experimental", "Experimenta~
$ Outcome   <chr> "Not Hospitalized", "Not Hospitalized", "Not Hospitalized", ~
```

5.8.1 Question

We want to test whether the marginal probabilities of each outcome (not hospitalized, hospitalized, and died) are the same across each treatment. Use a significance level of 0.05.

5.8.2 Answer

Create a contingency table first to test whether there are sparse counts.

```
contingency <- xtabs(~Treatment+Outcome,data=covid)
contingency
```

```
              Outcome
Treatment      Died Hospitalized Not Hospitalized
  Experimental   11           67              572
  Placebo        23           81              543
```

We implement the chi-squared test using `chisq.test()`.

```
chisqtest <- chisq.test(covid$Treatment,covid$Outcome)
chisqtest
```

```
    Pearson's Chi-squared test

data:  covid$Treatment and covid$Outcome
X-squared = 6.307, df = 2, p-value = 0.0427
```

```
chisqtest$expected
```

```
               covid$Outcome
covid$Treatment     Died Hospitalized Not Hospitalized
   Experimental 17.03932     74.17116         558.7895
   Placebo      16.96068     73.82884         556.2105
```

```
# OR

chisqtest <- chisq.test(contingency)
chisqtest
```

```
    Pearson's Chi-squared test

data:  contingency
X-squared = 6.307, df = 2, p-value = 0.0427
```

All expected values are above 5, which means the chi-squared assumption is valid. The p-value is 0.042703, the test statistic is 6.3069732 with 2 degrees of freedom. At a significance level of 0.05, we reject the null hypothesis. We have sufficient evidence to conclude that the marginal probabilities of the outcome variable differ across treatments.

5.9 Exercise

The following data is from a study investigating the sources of health information from 200 urban young adults and 150 rural young adults.

5.9.1 Data

This is how to input aggregated data in R.

```r
source_data <- data.frame(
  Location = c("Urban", "Urban","Urban", "Rural", "Rural","Rural"),
  Source = c("Social Media", "Medical Professionals", "Others", "Social Media", "Medical Pro
  Count = c(84,96,20,17,31,53)
)

# Create a cross-table using xtabs
cross_table_xtabs <- xtabs(Count ~ Location + Source, data = source_data)
cross_table_xtabs
```

```
        Source
Location Medical Professionals Others Social Media
   Rural                    31     53           17
   Urban                    96     20           84
```

5.9.2 Question

Test whether the marginal probabilities are homogeneous across the urban and rural participants.

5.9.3 Answer

We can use the contingency table `cross_table_xtabs` in the function `chisq.test()`.

```r
chisqtest<- chisq.test(cross_table_xtabs)
chisqtest
```

```
    Pearson's Chi-squared test

data:  cross_table_xtabs
X-squared = 67.356, df = 2, p-value = 2.365e-15
```

```r
chisqtest$expected
```

```
        Source
Location Medical Professionals   Others Social Media
   Rural              42.61462 24.49502     33.89037
   Urban              84.38538 48.50498     67.10963
```

All expected counts are above 5, hence we can use the chi-squared assumption. All expected values are above 5, which means the chi-squared assumption is valid. The p-value is $2.3649711 \times 10^{-15}$, the test statistic is 67.3560212 with 2 degrees of freedom. At a significance level of 0.05, we reject the null hypothesis. We have sufficient evidence to conclude that the marginal probabilities are not homogeneous across the rurality of residence of the participants.

6 Fisher Exact Test

6.1 Chi-Squared Tests: Small Sample Size

For small sample sizes, the expected values for the cells might be less than 5 for most cells. The chi-squared assumption might not be valid for these cases.

6.2 Fisher Exact Test

The Fisher Exact Test calculates an *exact* p-value using the hypergeometric distribution.

> **!** Important
>
> Because the Fisher Exact Test does not rely on any asymptotic (long-run) behavior of the random variables, there is no requirement for a minimum sample size.
> The Fisher Exact Test is used primarily for 2x2 tables with small cell counts.

6.3 Hypothesis Test

The hypothesis tests for the test of independence and homogeneity still hold.

> **i** Note
>
> Unlike the chi-squared tests, the alternative hypothesis can be one-sided.
>
> - One sided H_a: There is a positive/negative association between the row and column variables. OR One combination of the row and column variable levels is more favored compared to the others.
> - Two-sided H_a: there is an association between the row and column variables.

6.4 Test statistic and p-value

The p-value is calculated based on the probability of the configuration of the contingency table. The test assumes that the row and column totals are fixed.

> **Note**
>
> The test statistic used is the upper left cell of the contingency table, X.
> The hypergeometric distribution is used to determine which numbers are more extreme than what was observed.
> Once the values are established, we sum the probabilities of all the values that are as extreme or more extreme than what was observed.

6.5 `R` implementation

The function `fisher.test()` can be used to perform the Fisher Exact Test. It can use the data frame or a cross table to calculate the exact p-values.

6.5.1 Sample Code

```r
fisher.test(df,alternative="greater")

# OR

fisher.test(contingency,alternative="two.sided")
```

6.6 Example

The table shown shows data from a study on treatments for healing severe infections.

6.6.1 Data

```r
aggregated_data <- data.frame(
  Treatment = c("A_Test", "A_Test", "B_Control", "B_Control"),
  Outcome = c("Favorable", "Unfavorable", "Favorable", "Unfavorable"),
  Count = c(10,2,2, 4)
)
```

```r
# Create a cross-table using xtabs
cross_table_xtabs <- xtabs(Count ~ Treatment + Outcome, data = aggregated_data)
cross_table_xtabs
```

```
           Outcome
Treatment   Favorable Unfavorable
  A_Test           10           2
  B_Control         2           4
```

6.6.2 Question

Use the Fisher's Exact Test to see if there is a positive association between the presence of the test treatment and the outcome. Use a significance level of 0.10.

6.6.3 Answer

```r
fisher<- fisher.test(cross_table_xtabs,alternative="greater")
fisher
```

```
    Fisher's Exact Test for Count Data

data:  cross_table_xtabs
p-value = 0.05726
alternative hypothesis: true odds ratio is greater than 1
95 percent confidence interval:
 0.9374086       Inf
sample estimates:
odds ratio
  8.457238
```

Compare the result to asymptotic chi-squared tests.

```r
chisq.test(cross_table_xtabs)
```

```
Warning in chisq.test(cross_table_xtabs): Chi-squared approximation may be
incorrect
```

```
    Pearson's Chi-squared test with Yates' continuity correction

data:  cross_table_xtabs
X-squared = 2.5312, df = 1, p-value = 0.1116
```

The resulting p-value from the Fisher exact test is 0.0572614. At a significance level of 0.10, we reject the null hypothesis. We have sufficient evidence to claim that there is a positive association between the treatment and the outcome.

> **Important**
>
> Note that the chi-squared assumption will yield a different decision for the hypothesis test, but this should be discarded because the chi-squared assumption does not hold (expected value less than 5).

7 Symmetry Tests

7.1 McNemar's Test

McNemar's test is a nonparametric test for homogeneity between two paired dichotomous variables.

> **Note**
>
> The usual test of homogeneity assumes each cell count is independent, which would not be the case when the column and row variables are paired.
> The McNemar's test is designed for a 2x2 contingency table. For larger nxn tables, we use the McNemar-Bowker Test.

> **Example**
>
> Suppose we are interested in the racial identity concordance of provider and patients at a certain region. The column variable could be assigned to describe the provider identity, while the row column could be assigned to describe the patient identity. The counts will not be independent of each other.

7.2 R implementation

The McNemar's test can be performed using `mcnemar.test()` in R. Like `chisq.test()` and `fisher.test()`, it can take individual columns or a contingency table as input.

> **Note**
>
> The chi-squared distribution is used as the distribution of the test-statistic.

7.3 Example

Consider the data in this table where patients were observed at Time 1 for the presence of a rash and then were observed at Time 2 for the presence of the rash. Each patient with a rash was provided a homeopathic treatment between Time 1 and Time 2.

7.3.1 Data

```r
source_data<- data.frame(
  T1_Presence= c("T1_Presence", "T1_Presence", "T1_Absence", "T1_Absence"),
  T2_Presence = c("T2_Presence", "T2_Absence", "T2_Presence", "T2_Absence"),
  Count = c(38, 12, 5, 45)
)

# Create a cross-table using xtabs
cross_table_xtabs <- xtabs(Count ~ T1_Presence+T2_Presence, data = source_data)
cross_table_xtabs
```

```
             T2_Presence
T1_Presence   T2_Absence T2_Presence
  T1_Absence          45           5
  T1_Presence         12          38
```

7.3.2 Question

Use McNemar's test to see if there is a difference in proportion for those with the rash and without the rash before and after treatment. Use a significance level of 0.05.

7.3.3 Answer

```
mcn <- mcnemar.test(cross_table_xtabs)
mcn
```

```
    McNemar's Chi-squared test with continuity correction

data:  cross_table_xtabs
McNemar's chi-squared = 2.1176, df = 1, p-value = 0.1456
```

The resulting p-value is 0.1456101. At a significance level of 0.05, we fail to reject the null hypothesis. We have insufficient evidence to claim that there is a difference in proportion for those with the rash and without the rash before and after treatment.

8 Measures of Association

8.1 Epidemiological Concepts

Observational Study

A research method where researchers observe and collect information without manipulation.

Risk Factor

A variable that is thought to be related to some outcome variable.

8.2 Prospective vs. Retrospective Study

Prospective Study

In a prospective study, two samples of subjects are selected: a group with the risk factor, and a group without the risk factor. These subjects are followed prospectively and outcomes are observed in the future.

Retrospective Study

In a retrospective study, two samples of subjects are selected: a group with the outcome of interest(cases), and a group without (control). These subjects are examined retrospectively to check if they have the risk factor.

8.3 Measures of Association

For prospective studies, the measure of association between the risk factor and outcome is the **relative risk**.

For retrospective studies, the measure of association between the risk factor and outcome is the **odds ratio**.

8.4 Relative Risk

	Disease Status		
Risk Factor	Present	Absent	Total at Risk
Present	a	b	$a+b$
Absent	c	d	$c+d$
Total	$a+c$	$b+d$	n

The relative risk (RR) is the ratio of the risk of being a case among subjects with the risk factor to the risk of developing the disease among subjects without the risk factor. The RR can be calculated using the following equation:

$$RR = \frac{a/(a+b)}{c/(c+d)}$$

8.5 Odds Ratio

Recall: Logistic Regression. The odds ratio is the ratio of the odds of developing into a case between those with and without the risk factor.

$$OR = \frac{a/b}{c/d} = ad/bc$$

8.6 R implementation

While the best estimate of the odds ratios and relative risk can easily be calculated using the values in the contingency table, the package `epitools` contains the `epitab()` function that calculates both relative risk/odds ratio and their corresponding intervals.

8.6.1 Sample Code

```
#install.packages("epitools")
library(epitools)
epitab(contingency,method="oddsratio")

# OR

epitab(contingency,method="riskratio",pvalue="chi2")
```

> **!** Important
>
> The contingency table should be given in this particular format:
>
> ```
>                  Disease
>   Exposure       No (ref)  Yes
>    Level 1 (ref)  a         b
>    Level 2        c         d
>    Level 3        e         f
> ```

8.7 Example

The data below includes data from a prospective study on low-risk pregnant women. A group of 217 women did no voluntary or mandatory exercise during the pregnancy while 238 exercised extensively. One outcome variable of interest was experiencing preterm labor.

8.7.1 Data

```
source_data<- data.frame(
  Risk= c("Treatment","Treatment","Control","Control"),
  Outcome = c("Case", "Control", "Case", "Control"),
  Count = c(22,216,18,199)
```

```
)

# Create a cross-table using xtabs
cross_table_xtabs <- xtabs(Count ~ Risk+Outcome, data = source_data)
cross_table_xtabs
```

```
           Outcome
Risk        Case Control
  Control     18     199
  Treatment   22     216
```

8.7.2 Question

Calculate the relevant measure of association and provide a 95% confidence interval.

8.7.3 Answer

```
library(epitools)
```

```
Warning: package 'epitools' was built under R version 4.5.2
```

```
epitab(cross_table_xtabs,method="riskratio",pvalue="chi2",rev="columns")
```

```
$tab
           Outcome
Risk        Control        p0 Case         p1 riskratio     lower    upper
  Control       199 0.9170507   18 0.08294931  1.000000        NA       NA
  Treatment     216 0.9075630   22 0.09243697  1.114379 0.6145682 2.020672
           Outcome
Risk          p.value
  Control          NA
  Treatment 0.7211157

$measure
[1] "wald"

$conf.level
[1] 0.95
```

```
$pvalue
[1] "chi2"
```

The relative risk is 1.114 with a 95% confidence interval: (0.615,2.021). The resulting p-value from the chi-squared approximation is 0.72. At a significance level of 0.05, we fail to reject the null hypothesis. We have insufficient evidence to conclude that there is a difference in risk of experiencing preterm labor between those who exercise extensively and those who did not.

8.8 Exercise

The table shows 3970 subjects classified as cases or noncases of obesity and also classified according to smoking status of the mother during pregnancy (the risk factor).

```
source_data<- data.frame(
  Risk= c("Present","Present","Absent","Absent"),
  Outcome = c("Case", "Control", "Case", "Control"),
  Count = c(64,342,68,3496)
)

# Create a cross-table using xtabs
cross_table_xtabs <- xtabs(Count ~ Risk+Outcome, data = source_data)
cross_table_xtabs
```

```
         Outcome
Risk      Case Control
  Absent    68    3496
  Present   64     342
```

8.8.1 Question

- Is this study a prospective or a retrospective study?
- Calculate the appropriate measure of association to report for this study. Provide a 95% confidence interval.

8.8.2 Answer

```
epitab(cross_table_xtabs,method="oddsratio",rev="columns")
```

```
$tab
         Outcome
Risk      Control         p0 Case        p1 oddsratio    lower    upper
  Absent     3496 0.91089109   68 0.5151515  1.000000       NA       NA
  Present     342 0.08910891   64 0.4848485  9.620915 6.719328 13.77549
         Outcome
Risk           p.value
  Absent            NA
  Present 2.709464e-30

$measure
[1] "wald"

$conf.level
[1] 0.95

$pvalue
[1] "fisher.exact"
```

This is a retrospective study. The appropriate measure of association is the odds ratio. The estimated odds ratio is 9.62, with a 95% confidence interval: (6.72,13.78). The confidence interval shows that children with obesity are more likely to have had mothers who smoked than those without obesity.