

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.

Hair	Eye			
	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 $i = 1, 2, \dots, k$. 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_{k-1}^2 .

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:

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

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)
```

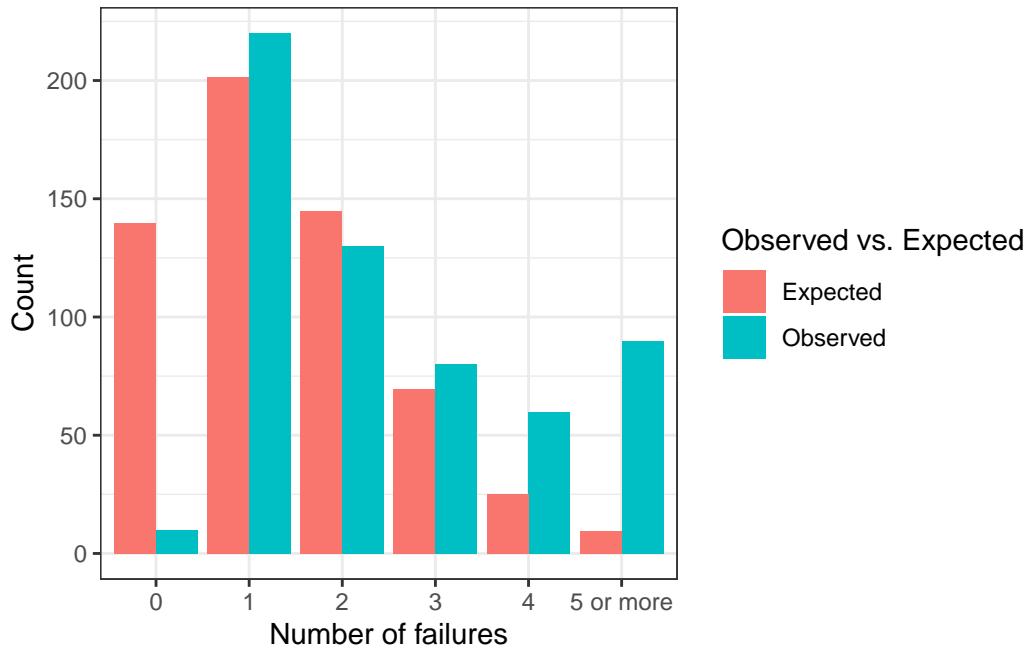
```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
vforcats    1.0.0     v stringr   1.5.2
v ggplot2   4.0.0     v tibble    3.3.0
v lubridate 1.9.4     v tidyrr    1.3.1
v purrr     1.1.0
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() 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
```

```

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
```

```

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] 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.

```

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.

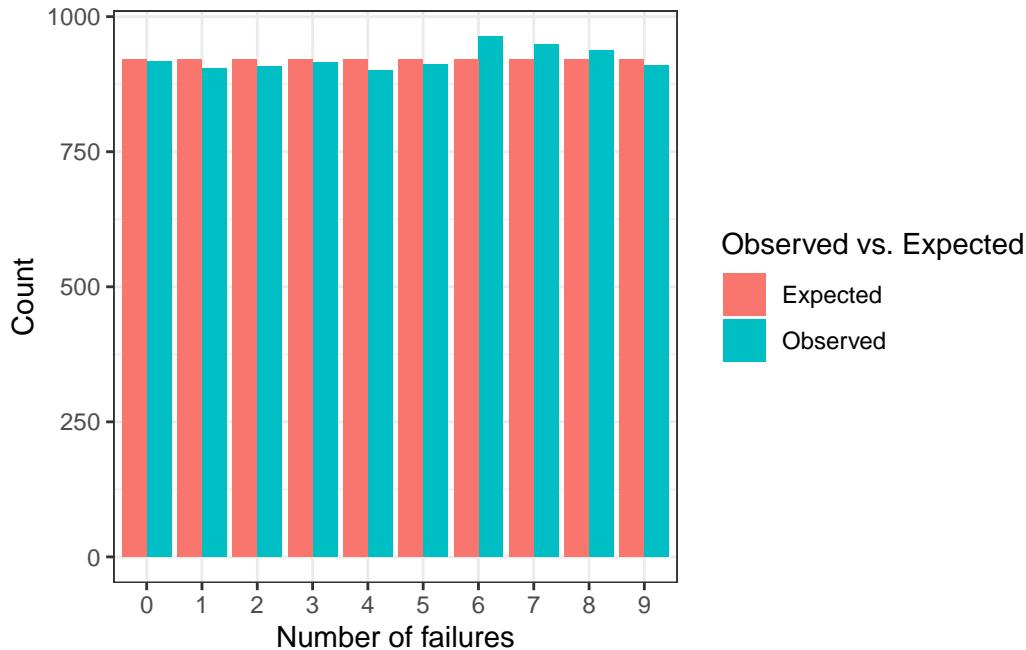
3.7.4 Plot

```

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.

i 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 $p_{\cdot i}$ 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 ,

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

i 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

```
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
```

```
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`.

```
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,

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

i 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		
		Died	Hospitalized	Not Hospitalized
Treatment	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.

```

source_data <- data.frame(
  Location = c("Urban", "Urban", "Urban", "Rural", "Rural", "Rural"),
  Source = c("Social Media", "Medical Professionals", "Others", "Social Media", "Medical Professionals", "Others"),
  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		
		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()`.

```

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

```

```

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

```
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

```
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)  
)
```

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

		Outcome	
		Favorable	Unfavorable
Treatment	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

```
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.

```
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.

i 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

```
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

i Observational Study

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

i Risk Factor

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

8.2 Prospective vs. Retrospective Study

i 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

Risk Factor	Disease Status		Total at Risk
	Present	Absent	
Present	<i>a</i>	<i>b</i>	<i>a + b</i>
Absent	<i>c</i>	<i>d</i>	<i>c + d</i>
Total	<i>a + c</i>	<i>b + d</i>	<i>n</i>

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.