# Categorical Data Analysis I: Associations with nominal and ordinal data

#### Contents

- 1. Nominal-nominal association
  - 1.1. Estimating a population proportion based on a single sample
  - 1.2. Comparing two proportions—independent samples
    - 1.2.1. Confidence intervals
    - 1.2.2. Hypothesis tests
  - 1.3. Chi-squared test
    - 1.3.1. 2x2 tables
    - 1.3.2. More than two rows or columns
- 1.4. Measures of association
- 2. Nominal-ordinal association
  - 2.1. Comparing groups-independent samples
  - 2.2. Measures of association
- 3. Ordinal-ordinal association
- 4. Comparing dependent proportions

#### 1. Nominal/nominal association

A randomized clinical trial was conducted to estimate incidence of HPV and assess the effectiveness of the HPV 16 vaccine. 414 subjects aged 15-25 were assigned to receive the vaccine, while a control group of 385 did not receive the vaccine. The table below indicates the number in each group that acquired HPV infection during the study period.

Group	Infection		
	No	Yes	
Control	366	19	
Vaccine	413	1	

Question 1: What is the incidence of HPV in each group? Question 2: Is the incidence of HPV lower in the vaccine group?

#### **1.1. Estimating a population proportion based on a single sample.**

**Binomial experiment:** 

- Series of identical, independent "trials" (Observe subject throughout the study period)
- Each trial results in one of two possible outcomes (Acquires HPV or does not)
- Count the number of "successes" (number that acquire HPV)
- Interest is in the proportion of successes (proportion that acquire HPV)

95% Confidence interval for population proportion

Basic form of the interval: sample estimate +/- margin of error

Wald interval ("textbook" interval)

Sample estimate:  $\hat{p} = \frac{\# \ successes}{n}$ ; margin of error:  $1.96 * \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$ Works "OK" for large samples population proportion not close to 0 or 1 suffers from bias and undercoverage otherwise bias: systematically lower or higher than population proportion undercoverage: Actual confidence level less than 95% (intervals tend to be too narrow) Agresti-Coull interval (new and improved "textbook" interval)

Helps to "fix" problems with the Wald interval-add 2 successes and 2 failures

Sample estimate: 
$$\tilde{p} = \frac{\# \ successes + 2}{n+4}$$
; margin of error:  $1.96 * \sqrt{\frac{\tilde{p}(1-\tilde{p})}{n}}$ 

Works better for smaller samples, population proportions close to 0 or 1

Score interval ("Ideal" interval, but more complicated-doesn't appear in most textbooks)

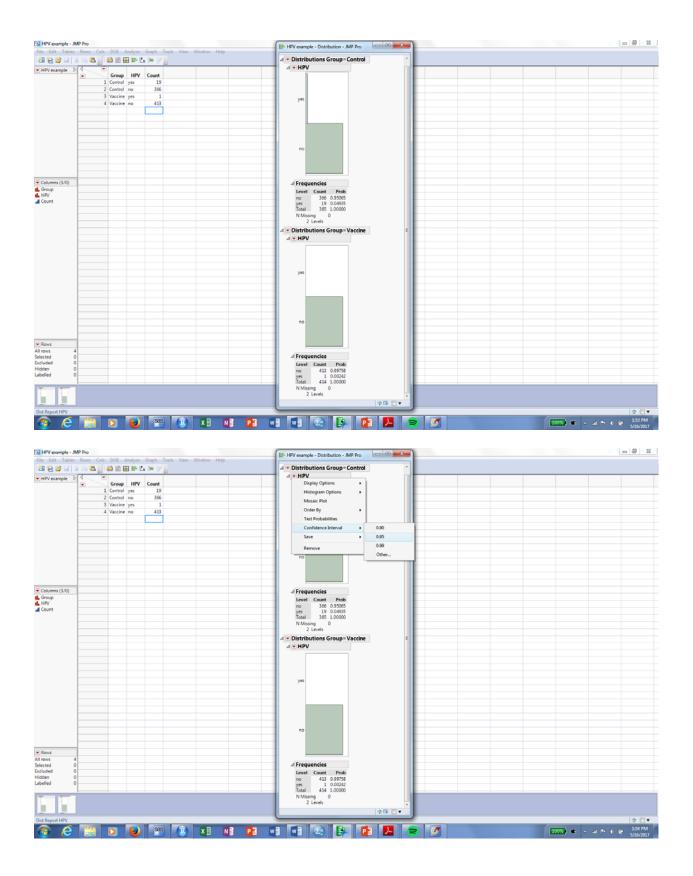
HPV example

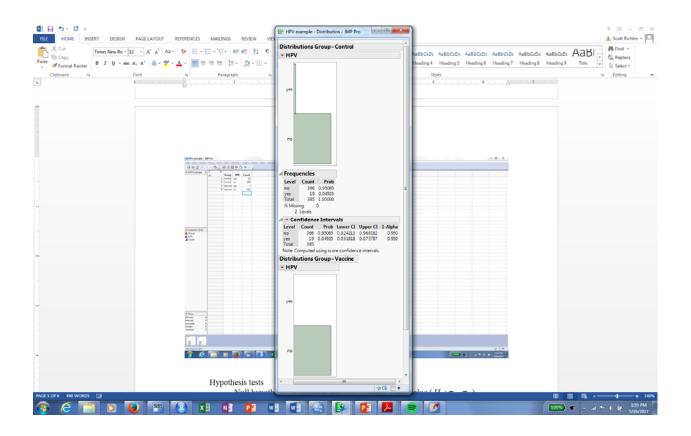
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	Agresti-Coull	0.0315	0.0764
	Score	0.0318	0.0757
Vaccine	Wald	-0.0023	0.00714
	Agresti-Coull	-0.0009	0.01526
	Score	0.0004	0.01355

### JMP

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# R

Control group:

```
#Wald
19/385-1.96*sqrt(19/385*366/414/414)
## [1] 0.02922997
19/385+1.96*sqrt(19/385*366/414/414)
## [1] 0.06947133
#AC
21/389-1.96*sqrt(21/389*368/389/389)
## [1] 0.03152688
21/389+1.96*sqrt(21/389*368/389/389)
## [1] 0.07644227
#Score
```

```
prop.test(19,385,correct=F)
```

```
##
## 1-sample proportions test without continuity correction
##
## data: 19 out of 385, null probability 0.5
## X-squared = 312.75, df = 1, p-value < 2.2e-16
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
## 0.03181847 0.07578697
## sample estimates:
## p
## 0.04935065</pre>
```

Vaccine group

```
#Vaccine
#Wald
1/414-1.96*sqrt(1/414*412/414/414)
```

## [1] -0.002307391

1/414+1.96\*sqrt(1/414\*412/414/414)

## [1] 0.007138309

#AC 3/418-1.96\*sqrt(3/418\*414/418/418)

## [1] -0.0009055918

3/418+1.96\*sqrt(3/418\*414/418/418)

## [1] 0.01525966

#Score
prop.test(1,414,correct=F)

```
##
## 1-sample proportions test without continuity correction
##
## data: 1 out of 414, null probability 0.5
## X-squared = 410.01, df = 1, p-value < 2.2e-16
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
## 0.0004265151 0.0135535692
## sample estimates:
## p
## 0.002415459</pre>
```

SAS

```
data gibbs;
input Group$ HPV$ count @@;
datalines;
Control Yes 19 Control No 366
Vaccine Yes 1 Vaccine No 413
;
proc freq data=gibbs;
weight count;
tables HPV /
binomial (level='Yes' CL=all) /*Request confidence
intervals for proportion 'Yes'*/;
by Group;
run;
```

Group=Control

HPV	Frequency	Percent	Cumulative Frequency	Cumulative Percent
No	366	95.06	366	95.06
Yes	19	4.94	385	100.00

<b>Binomial Proportion</b>								
0.0494								
0.0110								

Туре	95% Confid	lence Limits
Wald	0.0277	0.0710
Wilson	0.0318	0.0758
Agresti-Coull	0.0314	0.0762

#### Group=Vaccine

HPV	Frequency	Percent	Cumulative Frequency	Cumulative Percent
No	413	99.76	413	99.76
Yes	1	0.24	414	100.00

Binomial Pr	<b>Binomial Proportion</b>							
HPV = Yes								
Proportion	0.0024							
ASE	0.0024							

Type Wald	95% Confid	lence Limits
Wald	0.0000	0.0071
Wilson	0.0004	0.0136
Agresti-Coull	0.0000	0.0150

# **1.2 Comparing two proportions—independent samples**

Proportion difference—interpretation depends on incidence rates

Risk ratio (relative risk)—may not be valid for retrospective studies

Odds ratio-most obscure for practitioners

# HPV example

Comparison	Estimate	Interpretation			
ControlVaccine	19 1 0.04025 0.00242 0.047	Incidence of HPV			
	$\frac{19}{385} - \frac{1}{414} = 0.04935 - 0.00242 = 0.047$	higher in Control			
		group by 4.7%			
Incidence(HPV) [Control]	$\frac{19}{10} / \frac{1}{10} = \frac{0.04935}{20.4} = 20.4$	Incidence of HPV in			
Incidence(HPV)[Vaccine]	$\left \frac{385}{385}\right  \frac{114}{414} = 1000000000000000000000000000000000000$	Control group 20.4			
incluence(III v)[vaceine]		times higher			
Odds(HPV) [Control]	$\frac{19}{1} / \frac{1}{1} = \frac{0.04935}{21.4} = 21.4$	Odds of HPV in			
Odds(HPV)[Vaccine]	$\left \frac{1}{366}\right  \frac{1}{413} = \frac{1}{0.00242} = 21.4$	Control group 21.4			
		times higher			

#### 1.2.1 Confidence intervals

#### Proportion difference

Wald interval Sample estimate:  $\hat{p}_1 - \hat{p}_2$ ; margin of error:  $1.96*\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$ Similar issues as in the one-sample case

Agresti-Caffo interval

Add 1 success and 1 failure to each group

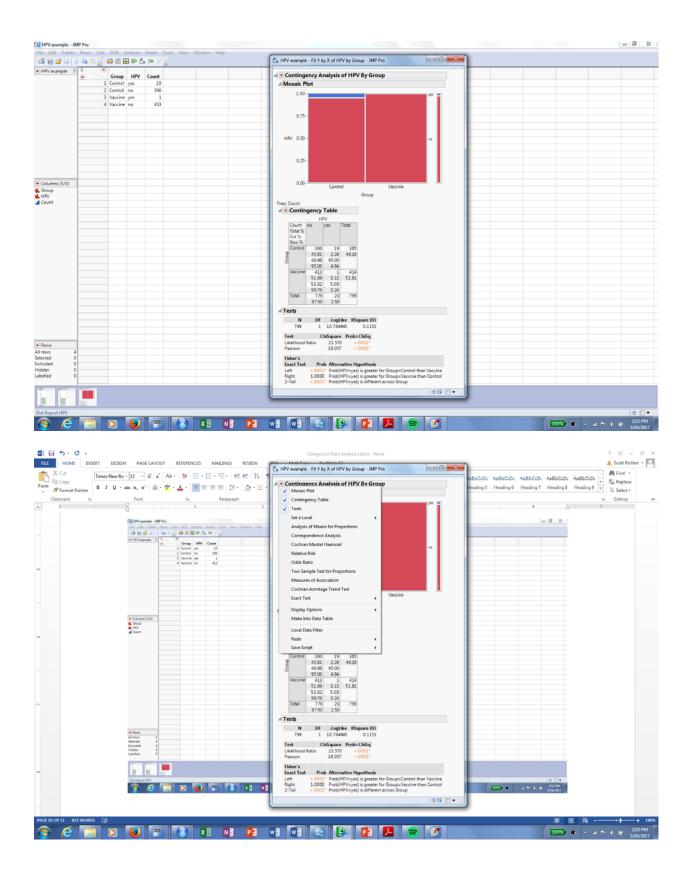
Use 
$$\tilde{p}_i = \frac{\# \ successes + 1}{n+2}$$
 instead of  $\hat{p}_i$ 

Risk ratio (relative risk) and odds ratio

Inference usually based on ln(*ratio*) and using Wald interval

### JMP

HPV example - JM	MP Pro																			- 0 <b>- X</b>
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HPV example 🕴			Contingency Table	
	Group HPV		HPV	
	1 Control yes	19	Count no yes Total	
	2 Control no	366	Total %	
	3 Vaccine yes	1	Col %	
	4 Vaccine no	413	g Row %	
			§ 46.98 95.00	
			95.06 4.94	
			Vaccine 413 1 414	
			51.60 0.13 51.81 53.02 5.00	
			9.76 0.24	
			Total 779 20 799	
			97.50 2.50	
			d Tests	
			N DF LogLike RSquare (U)	
Columns (3/0)			799 1 10.784945 0.1153	
Group			Test ChiSquare Prob>ChiSq	
HPV			Likelihood Ratio 21.570 <0001*	
Count			Pearson 18.007 <.0001*	
			Fisher's	
			Exact Test Prob Alternative Hypothesis	
			Left <.0001* Prob(HPV=yes) is greater for Group=Control than Vaccine	
			Right 1.000 Prob(HPV=ves) is greater for Group=Vaccine than Control	
			2-Tail <0001* Prob(HPV/syet) is different across Group	
	-		a Two Sample Test for Proportions	
			Propertion	
			Description Difference Lower 95% Upper 95%	
			P(no)Control)-P(no)Vaccine) -0.04694 -0.06991 -0.02384	
			Adjusted Wald Test Prob	
			P(na)Control)-P(na)Vaccine) ≤ 0 1.0000	
			P(no)Control)-P(no)Vaccine) 2.0 < 0001"	
			P(nojControl)-P(nojVeccine) = 0 <.0001"	
			Response HPV category of interest	
			@ no	
			© yes	
			d Relative Risk	
			Description Relative Risk Lower 95% Upper 95%	
			P(no)Control)/P(no)Vaccine) 0.952951 0.931053 0.975364 P(no)Vaccine)/P(no)Control) 1.049372 1.025258 1.074053	
Rows			P(na)Vaccine/P(na)Cantrol 1049/2 102528 10/4054 P(yes)Cantrol/P(yes)Vaccine 20.4317 2.748279 151.8888	
rows 4			Pyyet/Vaccine)/Pyyet/Control) 0.048945 0.006954 0.363864	
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iudea D den 0			Odds Ratio Lower 93% Upper 95%	
elled 0			0.046642 0.006233 0.350328	
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t Report HPV				1

# SAS

proc freq data=gibbs; weight count; tables Group\*HPV / riskdiff (Column=2 CL=Wald CL=AC)/\*Estimate difference between proportions\*/ relrisk /\*Estimate relative risk and odds ratio\*/; run;

Column 2 I	Column 2 Risk Estimates												
	Risk	ASE		(Exact) 95% Confidence Limits									
Row 1	0.0494	0.0110	0.0277		0.0300	0.0760							
Row 2	0.0024	0.0024	0.0000	0.0071	0.0001	0.0134							
Total	0.0250	0.0055	0.0142	0.0359	0.0154	0.0384							
<b>Difference</b>	<mark>0.0469</mark>	0.0113	0.0248	0.0691									
Difference	<mark>is (Row</mark>	<mark>/ 1 - Ro</mark> v	<mark>v 2)</mark>										

	Confidence Limits for the Proportion (Risk) Difference									
Column 2 (HPV = Yes)										
Proportion Diffe	Proportion Difference $= 0.0469$									
Туре	Type95% Confidence Limits									
Agresti-Caffo	Agresti-Caffo 0.0238 0.0699									
Wald	<mark>0.0248</mark>	<mark>0.0691</mark>								

Estimates of the Relative Risk (Row1/Row2)												
Type of Study	Value	95% Conf	idence Limits									
Case-Control (Odds Ratio)	<mark>0.0466</mark>	<mark>0.0062</mark>	<mark>0.3501</mark>									
Cohort (Col1 Risk)	0.9530	0.9311	0.9754									
Cohort ( <mark>Col2 Risk</mark> )	<mark>20.4312</mark>	<mark>2.7483</mark>	<mark>151.8888</mark>									

#### R

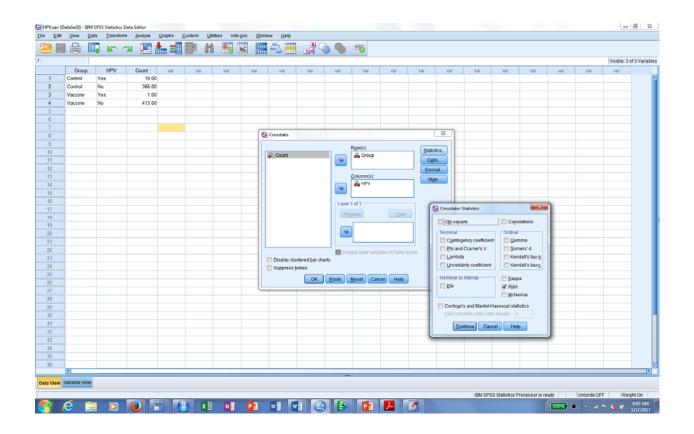
Confidence interval for proportion difference

```
prop.test(x=c(19,1),n=c(385,414),correct=F)
```

```
##
   2-sample test for equality of proportions without continuity
##
##
   correction
##
## data: c(19, 1) out of c(385, 414)
## X-squared = 18.007, df = 1, p-value = 2.201e-05
## alternative hypothesis: two.sided
## 95 percent confidence interval:
## 0.02478865 0.06908174
## sample estimates:
       prop 1
##
                   prop 2
## 0.049350649 0.002415459
```

# SPSS

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	Control	No	366.0																		
	Vaccine	Yes	1.0																		
_	Vaccine	No	413.0	0																	
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#### **Risk Estimate**

		95% Confid Interval	lence
	Value	Lower	Upper
Odds Ratio for Group (Control / Vaccine)	.047	.006	.350
For cohort HPV = No	.953	.931	.975
For cohort HPV = Yes N of Valid Cases	20.431 799	2.748	151.889

#### 1.2.2 Hypothesis tests

HPV example. Suppose the research hypothesis is that the vaccine reduces the incidence rate. Then we wish to test one of three sets of equivalent hypotheses:

1. 
$$H_{0}: \pi_{v} = \pi_{c \text{ vs.}} H_{A}: \pi_{v} < \pi_{c},$$

$$H_{0}: \frac{\pi_{v}}{\pi_{c}} = 1 \qquad H_{A}: \frac{\pi_{v}}{\pi_{c}} < 1$$
2. 
$$H_{0}: \frac{\partial dds(HPV)_{v}}{\partial dds(HPV)_{c}} = 1 \qquad \text{, or}$$

$$H_{0}: \frac{\partial dds(HPV)_{v}}{\partial dds(HPV)_{c}} = 1 \qquad \text{, s.}$$

$$H_{A}: \frac{\partial dds(HPV)_{v}}{\partial dds(HPV)_{c}} < 1$$
Test statistic  $1-Z = \frac{\hat{\pi}_{v} - \hat{\pi}_{c}}{SE(\hat{\pi}_{v} - \hat{\pi}_{c})}, SE(\hat{\pi}_{v} - \hat{\pi}_{c}) = \sqrt{\frac{\pi(1-\pi)}{n_{1}} + \frac{\pi(1-\pi)}{n_{2}}}. \pi \text{ is the common true}$ 
incidence rate under the null hypothesis and is estimated by computing the combined sample incidence rate over both groups,  $\hat{\pi} = \frac{\text{total number of } HPV \text{ cases}}{n_{1} + n_{2}} = \frac{19+1}{385+414} = 0.025.$  Then
$$\frac{1}{414} - \frac{19}{285}$$

the test statistic value is  $Z = \frac{414 \quad 385}{\sqrt{\frac{0.025(0.975)}{414} + \frac{0.025(0.975)}{385}}} = -4.243$ , with corresponding p-

value less than 0.0001.

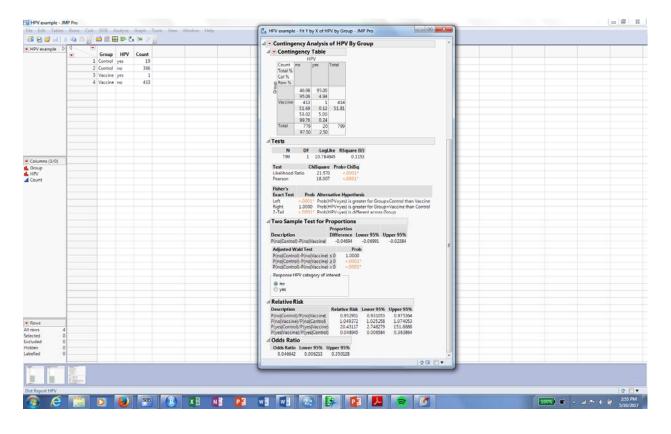
R is the only software that produced a test statistic (X-squared =  $Z^2$ ) and p-value, although JMP also showed the p-value. However, as we will see, the p-value can be calculated by all software using a chi-squared test.

p-value for proportion difference
prop.test(x=c(19,1),n=c(385,414),correct=F, alternative="greater")
##
## 2-sample test for equality of proportions without continuity
## correction
##

R

```
## data: c(19, 1) out of c(385, 414)
## X-squared = 18.007, df = 1, p-value = 1.101e-05
## alternative hypothesis: greater
## 95 percent confidence interval:
## 0.02834922 1.00000000
## sample estimates:
## prop 1 prop 2
## 0.049350649 0.002415459
```

#### JMP



#### **1.3.** Chi-squared test

Generalizes the Z-test to

- 1. 2 or more groups,
- 2. outcomes with 2 or more categories

#### 1.3.1. 2x2 table

Compares the observed table with what would be expected if the probabilities were the same:

Observed table:

Group	Infection	Infection						
	No	Yes	Total					
Control	366	19	385					
Vaccine	413	1	414					
Total	779	20	799					

#### Expected table:

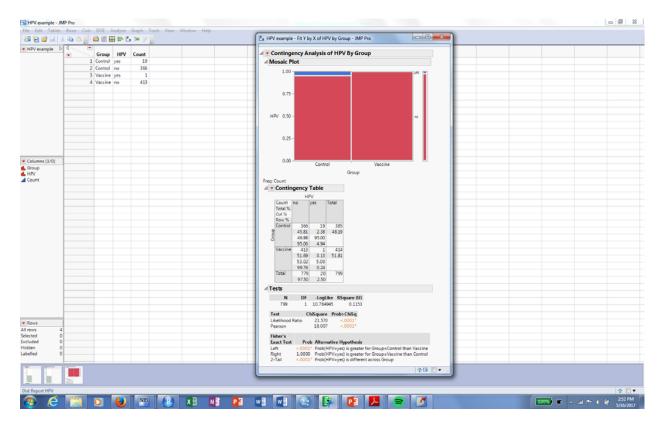
Group	Infection	
	No	Yes
Control	385*779/799 = 375.36	385*20/799 = 9.64
Vaccine	414*779/799 = 403.64	414*20/799 = 10.36

(Pearson) chi-squared test statistic is the sum across all cells in the table, of

 $\frac{(\text{observed} - \text{expected})^2}{\text{expected}}$ . For the HPV example, the value of the test statistic is  $X^2 = 18.007$ 

(this was the value given by the R output above). The p-value is usually based on the chi-squared distribution. All software packages will compute this statistic and corresponding p-value.

#### JMP



#### SAS

proc freq data=gibbs;	
veight count;	
ables Group*HPV /	
chisq /*chi-squared test*/;	
un;	

Statistic	DF	Value	Prob
Chi-Square	1	<mark>18.0068</mark>	<.0001
Likelihood Ratio Chi-Square	1	21.5699	<.0001
Continuity Adj. Chi-Square	1	16.1350	<.0001
Mantel-Haenszel Chi-Square	1	17.9843	<.0001
Phi Coefficient		-0.1501	
Contingency Coefficient		0.1485	
Cramer's V		-0.1501	

#### SPSS

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#### **Chi-Square Tests**

	Value		U	Exact Sig. (2- sided)	Exact Sig. (1- sided)
Pearson Chi-Square	18.007 <sup>a</sup>	1	.000		
Continuity Correction <sup>b</sup>	16.135	1	.000		
Likelihood Ratio	21.570	1	.000		
Fisher's Exact Test N of Valid Cases	799			.000	.000

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 9.64.

b. Computed only for a 2x2 table

#### 1.3.2. More than 2 rows/columns

Example: Alsunni et. al (2014) studied the relationship between patient misconceptions about diabetes with several sociodemographic variables. One such variable was age group, and they obtained the following data:

Age Group	Misconcept	Misconception score						
	Low	Moderate	High	Total				
<20	16	14	2	32				
21-40	32	28	2	62				
41-60	56	24	1	81				
>60	11	11	3	25				
Total	115	77	8	200				

2 Types of tests-

- 1. "homogeneity"—"ANOVA-type" hypothesis, where one variable represents a factor and the other a response,
- 2. "independence"—"correlation-type" hypothesis, where a single sample is measured on two variables

Computation is exactly the same, however.

Misconception score example.

1. Hypotheses:  $H_0$ : Misconception score is not associated with age

 $H_A$ : Misconception score is associated with age

2. Test statistic:  $X^2 = 12.228$ ; p-value (based on chi-squared distribution with 6 df) = 0.057.

#### SAS

#### Statistics for Table of age by score

Statistic	DF	Value	Prob
Chi-Square	<mark>6</mark>	<mark>12.2285</mark>	<mark>0.0571</mark>
Likelihood Ratio Chi-Square	6	11.4164	0.0763
Mantel-Haenszel Chi-Square	1	0.3005	0.5836
Phi Coefficient		0.2473	

Statistic	DF	Value	Prob			
Contingency Coefficient		0.2400				
Cramer's V		0.1748				
WARNING: 33% of the cells have expected counts less than 5						
(Asymptotic) Chi-Square may not be a valid test.						

P-value will be approximately correct if sample size is large, or more precisely if expected cell frequencies are not too small.

- 1. Cochran (1952): "if any expected frequency is less than 1 or if more than 20% are less than 5, the approximation may be poor"
- 2. Conover (1999): "if any expected frequency is less than 0.5 or if most are less than 1, the approximation may be poor".

#### Alternatives?

1. Combine columns/rows

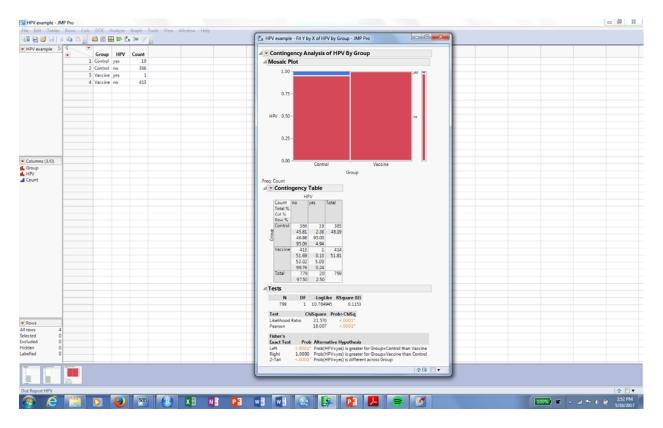
Misconception example. Combine Moderate and High categories.

Age Group	Misconcep	Misconception score			
	Low	Low Moderate/High			
<20	16	16	32		
21-40	32	30	62		
41-60	56	25	81		
>60	11	14	25		
Total	115	77	200		

Changes interpretation

- 2. Exact test
  - a. 2×2 table--Fisher's Exact test (usually output by default)
  - b.  $R \times C$  table—Permutation test

#### HPV example--JMP



Misconception example--SAS

```
data alsunni_age;

input age score count @@;

datalines;

1 1 16 1 2 14 1 3 2

2 1 32 2 2 28 2 3 2

3 1 56 3 2 24 3 3 1

4 1 11 4 2 11 4 3 3

;

proc freq data=alsunni_age;

weight count;

exact chisq;

tables age*score / chisq;

run;
```

Pearson Chi-Square Test					
Chi-Square	12.2285				
DF	6				
Asymptotic Pr > ChiSq	0.0571				
Exact Pr >= ChiSq	<mark>0.0547</mark>				

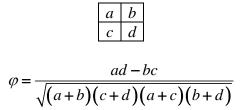
Notice that even though software printed a warning, the approximate p-value is very close to the exact p-value.

#### 1.3. Measures of association

In the previous section a larger chi-squared statistic implied a stronger association, provided the degrees of freedom remains the same. In the Alsunni et. al (2014) example, the chi-squared statistic, with 6 df, was  $X^2 = 12.23$ , which corresponded to an exact p-value of 0.055. However, for a 3x3 table with 4 df, a chi-squared value of  $X^2 = 12.23$  would correspond to a p-value of 0.016. Thus, it is clear that  $X^2$  cannot easily be used as a measure of the degree of association across tables of different sizes. However, several measures have been proposed to do this.

Phi coefficient

For 2x2 tables, phi ranges between -1 and 1 and thus can measure "direction" of the association. For the 2x2 table



A positive value suggests higher proportions of responses on the diagonal (cells a and d), while a negative value suggests higher proportion on the off-diagonal. Perfect positive association occurs when b and c are both 0, while perfect negative when a and d are both 0

*Cramer's contingency coefficient* Cramer's coefficient is defined as

$$C = \sqrt{\frac{X^2}{n(q-1)}},$$

where q is the smaller of the number of rows and the number of columns. The value n(q-1) is the maximum possible value of  $X^2$  for a given set of fixed row and column totals.

HPV example

Group	Infection		
	No	Yes	Total
Control	366	<mark>19</mark>	385
Vaccine	<mark>413</mark>	1	414
Total	779	20	799

$$\varphi = \frac{366*1 - 19*413}{\sqrt{(385)(414)(779)(20)}} = -0.15$$

The negative coefficient results from the fact that a higher proportion of control patients had infections while a higher proportion in the vaccine group did not.

$$C = \sqrt{\frac{18.0068}{799(1)}} = 0.15$$

proc freq data=gibbs; weight count; tables Group\*HPV / chisq /\*chi-squared test\*/; run;

Statistic	DF	Value	Prob
Chi-Square	1	18.0068	<.0001
Likelihood Ratio Chi-Square	1	21.5699	<.0001
Continuity Adj. Chi-Square	1	16.1350	<.0001
Mantel-Haenszel Chi-Square	1	17.9843	<.0001
Phi Coefficient		<mark>-0.1501</mark>	
Contingency Coefficient		<mark>0.1485</mark>	
Cramer's V		-0.1501	

Alsunni et. al (2014) example.

#### Statistics for Table of age by score

Statistic	DF	Value	Prob				
Chi-Square	6	12.2285	0.0571				
Likelihood Ratio Chi-Square	6	11.4164	0.0763				
Mantel-Haenszel Chi-Square	1	0.3005	0.5836				
Phi Coefficient		<mark>0.2473</mark>					
Contingency Coefficient		<mark>0.2400</mark>					
Cramer's V 0.1748							
WARNING: 33% of the cells have expected counts less than 5. (Asymptotic) Chi-Square may not be a valid test.							

#### 2. Nominal/ordinal association

#### 2.1 Comparing groups on an ordinal variable—independent samples

Rank tests for comparing groups can be used Wilcoxon rank-sum/Mann-Whitney test (2 groups) Kruskal-Wallis test (3 or more groups)

Misconception score example.

Hypotheses:	$H_0$ : Misconception score is not associated with age
	$H_A$ : Misconception score is associated with age

Since there are 4 age groups, Kruskal-Wallis test is performed:

Test statistic: KW = 9.0896; p-value = 0.0271 (exact)/ 0.0281 (based on chi-squared distribution with 3 df).

Stronger evidence of association than chi-squared test (p-value = 0.0571)

#### SAS

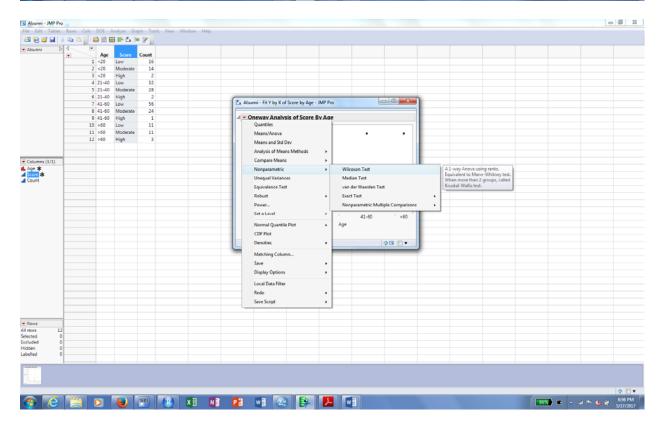
	Wilcoxon Scores (Rank Sums) for Variable score Classified by Variable age									
age	N		Expected Under H0		Mean Score					
1	32	3477.00	3216.00	260.357883	108.656250					
2	62	6561.00	6231.00	328.455463	105.822581					
3	81	7140.50	8140.50	348.623847	88.154321					
4	25	2921.50	2512.50	234.871396	116.860000					
Ave	Average scores were used for ties.									

Kruskal-Wallis Test	
Chi-Square	<mark>9.0896</mark>
DF	<mark>3</mark>
Asymptotic Pr > Chi-Square	<mark>0.0281</mark>
Exact Pr >= Chi-Square	0.0271

JMP Note: Response (Y) variable must by identified as continuous, Explanatory (X) as Nominal.

Alsunni - JMP Pr	0										
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	Age		Count								
		Low	16								
	2 <20	Moderate									
	3 <20	High	2								
	4 21-40	Low	32	_							
	5 21-40	Moderate	28	Score - JMP Pro							
	6 21-40	High	2					ОК			
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	-					**					
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- Count				optional item			e Value Labels is checked,	the			
						layed wherever the co	lumn data are displayed.				
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					2 = Moderat 3 = High		Change				
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	2 <2	0	Moderate	14					
	3 <2		High	2					
				32					
		-40							
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	7 41			56		Modeling types determine analysis.			
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								Age							
					⊿ Wilcoxon /	Kruskal-\		(Rank Sur	ns)						
							Expected								
					Level Count <20 32			Score Mean 108.656		1.001					
					21-40 62			105.823		1.003					
					41.60 81	7140.5	0 8140.50	88.154		-2.867					
					>60 25		0 251250	116.860		1.739					
					⊿ 1-Way Te			ximation							
					ChiSquare	DF Pr	ob>ChiSq								
					9.0896	3									
					Small sample si			is for tests, rat	ther than						
					large-sample a	oproximation	15.								
					Freq Count										
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The WRS/MW/KW tests are usually thought of in the same way as T/ANOVA tests as for testing for group differences, rather than testing for association. However, the distinction only affects interpretation of test results. However, as with the  $X^2$  statistic, it is difficult to use these tests statistics to compare degree of association between different data sets.

# 3. Ordinal-ordinal association

Several rank-based methods

- 1. Spearman correlation—Pearson correlation on rank scores
- Kendall's tau—measure of "concordance (Called the Jonckheere Terpstra test if testing for group differences)

Both are measures of either increasing or decreasing (monotonic) association, range between -1 and 1, and yield similar p-values.

Misconception example.

Spearman and Kendall coefficients are -0.060 and -0.056, respectively, with large sample p-values 0.399 and 0.387, respectively. Thus, there is not evidence of monotonic association between age and misconception score. That is, there is not statistical evidence that misconception score tends to increase or decrease with age.

SAS

proc corr data=alsunni\_age spearman kendall; var age score; freq count; run; proc freq data=alsunni\_age; weight count; exact measures jt; tables age\*score / measures jt; run;

Spearman Correlation Coefficients, $N = 200$ Prob > $ r $ under H0: Rho=0					
	age	score			
age	1.00000	<mark>-0.05993</mark>			
		<mark>0.3992</mark>			
score	-0.05993	1.00000			
	0.3992				

	Kendall Tau b Correlation Coefficients, $N = 200$ Prob >  tau  under H0: Tau=0					
	age	score				
age	1.00000	-0.05577				
		<mark>0.3871</mark>				
score	-0.05577	1.00000				
	0.3871					

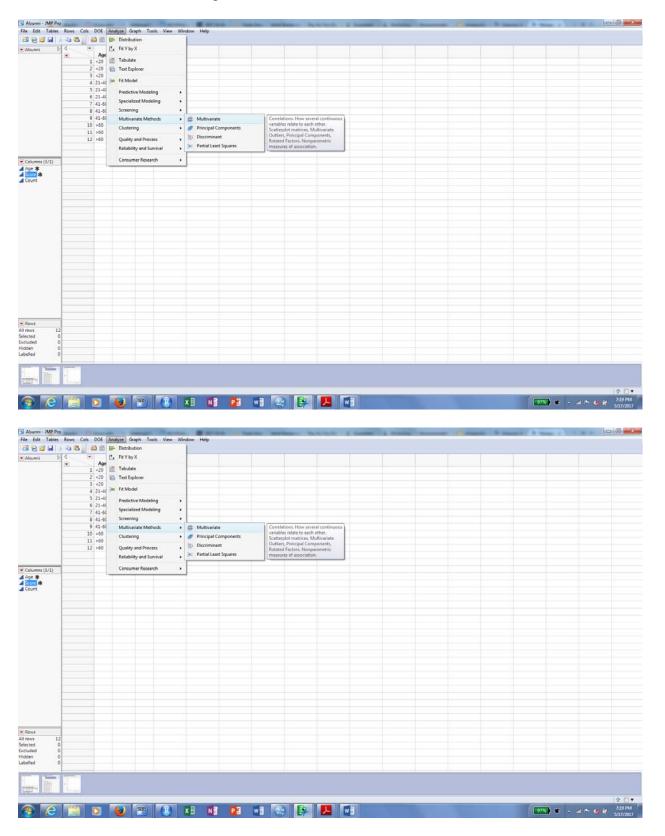
Spearman Correlation	on Coefficient
Correlation (r)	<mark>-0.0599</mark>
ASE	0.0749

Spearman Correlation Coefficient95% Lower Conf Limit-0.206795% Upper Conf Limit0.0868

Test of H0: Correlation $= 0$					
ASE under H0	0.0748				
Z	-0.8012				
One-sided Pr < Z	0.2115				
Two-sided $Pr >  Z $	0.4230				
Exact Test					
One-sided Pr <= r	<mark>0.1994</mark>				
Two-sided $Pr \ge  r $	<mark>0.3988</mark>				

Jonckheere-Terpstra Test	
Statistic (JT)	<mark>6650.5000</mark>
Ζ	-0.8649
Asymptotic Test	
One-sided Pr < Z	0.1936
Two-sided $Pr >  Z $	0.3871
Exact Test	
One-sided Pr <= JT	<mark>0.1941</mark>
Two-sided Pr >=  JT - Mean	<mark>0.3883</mark>

#### JMP Both variables need to be recognized as continuous.



514 - 🔍	i⊞⊫ Ľ. :	- 10		
	e Score			
1 <20				
			# Alsunni - Multivariate of Score, Age - JMP Pro	
			D Scatterplot Matrix	
			A Nonparametric: Spearman's p	
			Age Score -0.0599 0.3992	
12 >60	High	3		
			Variable by Variable Kendall x Prob>1x] -8 -6 -4 -2 0 -2 4 -6 -8	
			Age Score -0.0558 0.3871	
-				
2				
0				
0				
0				
0				
	1 <20 2 <20 3 <20 4 21- 5 21- 7 41- 9 41- 10 >60 11 >60 12 >60 12 >60 14 - 10 - 12	1 (20) Low 2 (20) Moderate 3 (20) Moderate 5 (21-40) Kow 5 (21-40) Kigh 7 (41-50) Low 8 (41-50) Moderate 10 (50) Low 10 (50) Low 11 (50) Low 11 (50) Low 12 (50) Moderate 12 (50) Moderate 14 (50) Mo	1 <20 Low 16 2 <20 Moderate 14 3 <20 High 2 4 22:40 Low 32 5 22:40 Moderate 28 6 22:40 High 2 7 42:60 Low 56 8 42:60 Moderate 24 9 42:60 Moderate 24 9 42:60 Moderate 11 10 >60 Low 11 11 >60 Moderate 13 22 >60 High 3 10 -70 Low 11 11 >0 -70 Low 11 12 >60 Low 11 13 -70 Low 11 14 -70 High 3 -70 Low 11 14 -70 High 3 -70 Low 11 15 -70 Low 11 16 -70 Low 11 17 -70 Low 11 17 -70 Low 11 18 -70 Low 11 19 -70 Low 11 10 -70 Low 11 11 -70 Low 11 -	1 - 20 km 15 3 - 20 km 14 3 - 20 km 15 5 21-40 km 12 5 21-40 km 15 6 21-40 km 15 6 21-40 km 15 6 21-40 km 15 1 - 10 km 12 1 - 10 km

We found good statistical evidence of an association using the Kruskal-Wallis test, and moderate evidence using the chi-squared test, but virtually no evidence using rank correlations.

In general,

- if one variable is ordinal and the other nominal, the WRS/MW/KW test will have more power to detect an association than the chi-squared test
- if both variables are ordinal,
  - the WRS/MW/KW tests will have more power to detect an association than the chi-squared test
  - the Spearman/Kendall/JT tests will have more power than the chi-squared test to detect an increasing or decreasing association, but may have less power otherwise.

# Hypothetical example

Age Group	Misconception	n score		
	Low	Moderate	High	Total
<20	2(6%)	14(44%)	16(50%)	32
21-40	6(10%)	24(39%)	32(52%)	62
41-60	50(62%)	25(31%)	6(7%)	81
>60	20(80%)	4(16%)	1(4%)	25
Total	78	67	55	200

Now the Spearman and Kendall coefficients are -0.607 and -0.534, respectively, with p-values less than 0.0001.

Spearman Correlation Coefficients, $N = 200$ Prob >  r  under H0: Rho=0					
	age	score			
age	1.00000	-0.60660			
		<.0001			
score	-0.60660	1.00000			
	<.0001				

Kendall Tau b Correlation Coefficients, N = 200 Prob >  tau  under H0: Tau=0					
	age	score			
age	1.00000	-0.53241			
		<.0001			
score	-0.53241	1.00000			
	<.0001				

# 4. Comparing proportions—dependent samples

#### Mc Nemar's Test

Example. Participants are asked their preferred candidate before and after a debate. Each subject gives a response before and after:

Subject	Before	After
1	Α	Α
2	Α	Α
3	A	A
4	A	В 🖌
5	A	B 🚩
6	A	В 🛩
7	A	В 🚩
8	A	B 🖌
9	A	B 🖌
10	A	В 🗲
11	Α	В 🛩
12	Α	B 🚩
13	В	A 🖌
14	В	A 🚩
15	В	В
16	В	В
17	В	В
18	В	В
19	В	В
20	В	В

Observed Table

Population Table

	Α	В	
Α	Χ	$X_{AB}$	$\begin{array}{c c} P_{AA} & P_{AB} \end{array} \qquad P_{A \bullet} = P_{AA} + P_{AB}$
	AA		$P_{BA}$ $P_{BB}$ $P(A \text{ is first response})$
В	$X_{BA}$	$X_{BB}$	
			$P_{A} = P_{AA} + P_{BA}$ $P(A \text{ is second response})$

If there is no effect of the debate, then A is equally likely to be chosen before and after, i.e.  $P_{A} = P_{A}$ .

$$H_0: P_{A} = P_{A}$$
, or  $P_{AA} + P_{AB} = P_{AA} + P_{BA}$  or  $P_{AB} = P_{BA}$ 

Test Statistic:  $T = X_{AB} = \#$  switched from A to B. We can consider just people who switched (The rest are "ties"). Then under  $H_0$  the switches to B are just as likely as to A. So, we can calculate a one-sided p-value as  $P(X \ge X_{AB} | n = X_{AB} + X_{BA}, p = .5)$ .

#### Example

9+2=11 people switched, and of those  $X_{AB} = 9$  switched to *B*.  $P(X \ge 9 \mid n = 11, p = .25) = .027 + .005 + .000 = .032$ Here the alternative is that more likely to switch to *B*, or  $H_a: P_A < P_A$ .

SAS

```
data ta5_8_1;
input before $ after $ count @@;
datalines;
A A 3 A B 9
B A 2 B B 6
;
proc freq data=ta5_8_1;
weight count;
exact mcnem; /* Requests McNemar test, exact p-value */
tables before*after;
run;
```

Statistics for Table of before by after

McNemar's Test			
Statistic (S)	4.4545		
DF	1		
Asymptotic Pr > S	0.0348		
Exact Pr >= S	0.0654		

R

```
table <- matrix(</pre>
c(3, 9,
2, 6),
nrow = 2, byrow = TRUE,
dimnames = list(
"First" = c("A", "B"),
"Second" = c("A", "B")
)
)
library(coin)
## Loading required package: survival
##
## Attaching package: 'survival'
## The following object is masked from 'package:epitools':
##
       ratetable
##
mh_test(as.table(table), distribution = "exact")
##
## Exact Marginal Homogeneity Test
##
## data: response by
     conditions (First, Second)
##
##
     stratified by block
## chi-squared = 4.4545, p-value = 0.06543
```

JMP

