# AMS 572 Data Analysis I Inference on two sample proportions

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## Inference on two proportions

- ► Small sample sizes
  - ► Fisher's exact test
- ► Large sample sizes
  - normal approximation to the binomial
  - $\rightarrow \chi^2 \text{ test}$

## Inference on two proportions

- $ightharpoonup X \sim \operatorname{Binomial}(n_1, p_1), Y \sim \operatorname{Binomial}(n_2, p_2)$
- ▶ Put data in 2 x 2 table

	Success	Failure	
Sample 1	$n_{11} = x$	$n_{12} = n_1 - x$	$n_1$
Sample 2	$n_{21} = y$	$n_{22} = n_2 - y$	$n_2$
	m = x + y	n-m	$\overline{n}$

Hypotheses

$$H_0: p_1 = p_2$$

versus

$$H_a: p_1 > p_2 \text{ or } H_a: p_1 < p_2 \text{ or } H_a: p_1 \neq p_2$$

## Fisher's Exact Test

- Assume margins  $m, n m, n_1, n_2$  fixed
- ▶ Then once we know  $n_{11} = x$ , the other values  $n_{12}$ ,  $n_{21}$ , and  $n_{22}$  are immediately determined
- ▶ Under  $H_0$ , can show

$$\Pr[X = k | X + Y = m] = \frac{\binom{n_1}{k} \binom{n_2}{m-k}}{\binom{n}{m}}$$

### Fisher's Exact Test

- ➤ To compute p-values, consider all 2 x 2 tables possible given the observed margins
- ▶ One tailed p-value: sum the probabilities of the observed table and all tables more extreme than the observed table in the direction of  $H_a$
- ➤ Two tailed p-value: sum the probabilities of tables that are more extreme in both directions than the observed table, given the fixed margins

### Fisher's Exact Test

1. One tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 > p_2$ 

p-value = 
$$p_U = P(X \ge x | X + Y = m) = \sum_{k=x}^{\min(m,n_1)} \frac{\binom{n_1}{k}\binom{n_2}{m-k}}{\binom{n}{m}}$$

2. One tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 < p_2$ 

p-value = 
$$p_L = P(X \le x | X + Y = m) = \sum_{k=\max(0,m-n_2)}^{x} \frac{\binom{n_1}{k}\binom{n_2}{m-k}}{\binom{n}{m}}$$

3. Two tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 \neq p_2$ 

$$p
-value = 2 \min(p_L, p_U)$$

is the formula presented in your textbook. A pitfall of this approach is that the value can exceed 1. Alternative approaches of defining two-sided p-value can be found in page 92 of Categorical Data Analysis (Agresti) (See the next Example).

Example: The result of a randomized clinical trial for comparing Prednisone and Prednisone+VCR drugs, is summarized below. Test if the success and failure probabilities are the same for the two drugs.

Drug	Success	Failure	Row total
Pred	14	7	$n_1 = 21$
PVCR	38	4	$n_2 = 42$
	m = 52	n-m=11	n = 63

Solution:

$$\begin{cases} H_0: p_1 = p_2 \\ H_a: p_1 \neq p_2 \end{cases}$$

$$p_L = \sum_{k=\max(0,52-42)}^{14} \frac{\binom{21}{k}\binom{42}{52-k}}{\binom{63}{52}} = \sum_{k=10}^{14} \frac{\binom{21}{k}\binom{42}{52-k}}{\binom{63}{52}} \approx 0.02537$$

Note: This is example 9.8 of your textbook. The p-value given in your textbook value is incorrect.

If we define two-sided p-value as= 2(0.02537) = 0.05074, we do not reject  $H_0$ . This p-value is different from the p-value SAS/R output. We will present the method of obtaining exact two sided p-value in the following slides.

- 1. The two sided p-value is defined as the sum of probabilities for those tables having a test statistic greater than or equal to the value of the observed test statistic.
- 2. For the Prednisone example, list all possible tables with fixed margins  $n_1 = 21, n_2 = 42, m = 52, n m = 11$ . There are 12 possible tables corresponding to possible values of x = 10, 11, ..., 21. Note that our observed x = 14. Compute P(X = x | X + Y = 52) for each possible x values.
- 3. The two sided p-value can be obtained by adding all probabilities  $\leq P(X=14|X+Y=52)$

```
The two sided p-value is given by \sum_{x \in C} P(X = x | X + Y = 52)
where C = \{10, 11, 12, 13, 14, 21\} which is equal to 0.0323.
> prob <- function(x){</pre>
choose(21,x)*choose(42,52-x)/choose(63,52)
}
> ### list all the possible values of x for fixed margin ###
> tab <- cbind(10:21,prob(10:21))</pre>
> colnames(tab) < c('x','p(X=x|X+Y=52)')
> tab
       x p(X=x|X+Y=52)
 [1,] 10 5.727859e-07
 [2,] 11 2.405701e-05
 [3,] 12 4.109739e-04
 [4,] 13 3.793605e-03
 [5,] 14 2.113580e-02
 [6,] 15 7.496164e-02
 [7,] 16 1.733488e-01
 [8,] 17 2.622083e-01
 [9,] 18 2.549247e-01
[10,] 19 1.520603e-01
[11,] 20 5.017991e-02
[12,] 21 6.951330e-03
```

AMS 572

```
Data trial;
input drug $ outcome$ count;
datalines;
pred S 14
pred F 7
PVCR S 38
PVCR F 4
run;
proc freq data=trial;
tables drug*outcome/chisq;
weight count;
run;
```

# SAS Output

#### The FREQ Procedure

#### Table of drug by outcome

drug	outcome		
Frequency Percent Row Pct Col Pct	F	S	Total
PVCR	4 6.35 9.52 36.36	38 60.32 90.48 73.08	42 66.67
pred	7 11.11 33.33 63.64	14 22.22 66.67 26.92	21 33.33
Total	11 17.46	52 82.54	63 100.00

12

# SAS Output

Statistics for Table of drug by outcome

Statistic	DF	Value	Prob
Chi-Square Likelihood Ratio Chi-Square Continuity Adj. Chi-Square Mantel-Haenszel Chi-Square Phi Coefficient Contingency Coefficient Cramer's V	1 1 1 1	5.5070 5.2010 3.9788 5.4196 -0.2957 0.2835 -0.2957	0.0189 0.0226 0.0461 0.0199

WARNING: 25% of the cells have expected counts less than 5. Chi-Square may not be a valid test.

#### Fisher's Exact Test

Cell (1,1) Frequency (F)	4
Left-sided Pr <= F	0.0254
Right-sided Pr >= F	0.9958
Table Probability (P)	0.0211
Two-sided Pr <= P	0.0323

Sample Size = 63

```
> obs \leftarrow matrix(c(14,7,38,4),nrow=2,byrow=T)
> fisher.test(obs)
Fisher's Exact Test for Count Data
data:
     obs
p-value = 0.03232
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.03998108 1.00410538
sample estimates:
odds ratio
0.2166817
```

## Inference on two proportions, large samples

- $\triangleright$  If X and Y are large, we can use the normal distribution
- Let X and Y be the number of successes in sample 1 and sample 2, respectively.
- Point estimators  $\hat{p}_1 = X/n_1$ ,  $\hat{p}_2 = Y/n_2$ ,  $\hat{p}_1 \hat{p}_2 = X/n_1 Y/n_2$
- ▶ The CLT shows that if  $n_i$  is large

$$\hat{p}_i \sim N\left(p_i, \frac{p_i(1-p_i)}{n_i}\right)$$

## Inference on two proportions, large samples

▶ If samples are independent and  $p_i$  known for i = 1, 2, it follows

$$\frac{\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)}{\sqrt{\frac{p_1(1 - p_1)}{n_1} + \frac{p_2(1 - p_2)}{n_2}}} \sim N(0, 1)$$

▶ This approximation is good if  $n_i p_i (1 - p_i) \ge 10$  for i = 1, 2

# Inference on two proportions, large samples

▶ If samples are independent and  $p_i$  unknown for i = 1, 2, Slutsky/CLT imply

$$Z^* = \frac{\hat{p}_1 - \hat{p}_2 - (p_1 - p_2)}{\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}} \sim N(0,1)$$

for sufficiently large  $n_1$  and  $n_2$  (rule of thumb:  $n_i\hat{p}_i(1-\hat{p}_i)\geq 10$  for i=1,2)

# Confidence interval for $p_1 - p_2$ for large samples

$$\begin{aligned} 1-\alpha &= P\left(-z_{\frac{\alpha}{2}} \leq Z^* \leq z_{\frac{\alpha}{2}}\right) \\ &= P\left(\widehat{p}_1 - \widehat{p}_2 - z_{\alpha/2} \cdot s \leq p_1 - p_2 \leq \widehat{p}_1 - \widehat{p}_2 + z_{\alpha/2} \cdot s\right) \\ \text{where } s &= \sqrt{\frac{\widehat{p}_1(1-\widehat{p}_1)}{n_1} + \frac{\widehat{p}_2(1-\widehat{p}_2)}{n_2}} \end{aligned}$$

 $100(1-\alpha)\%$  large samples CI for  $p_1 - p_2$ :

$$\hat{p}_1 - \hat{p}_2 \pm z_{\alpha/2} \cdot s$$

## Hypothesis test on $p_1$ and $p_2$ for large samples

- Suppose  $H_0: p_1 p_2 = \Delta$
- ► Test statistic

$$Z_0 = \frac{\hat{p}_1 - \hat{p}_2 - \Delta}{\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}} \sim N(0,1) \text{ under } H_0$$

▶ For  $\Delta = 0$ , this reduces to  $H_0: p_1 = p_2$ . One may use the pooled proportion in the denominator

$$\hat{p} = \frac{n_1 \hat{p}_1 + n_2 \hat{p}_2}{n_1 + n_2} = \frac{X + Y}{n_1 + n_2}$$

and the test statistic

$$Z_0 = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}} \sim N(0,1) \text{ under } H_0$$

# Hypothesis test on $p_1$ and $p_2$ for large samples

- 1. One tailed  $H_0: p_1 p_2 = \Delta \text{ vs } H_1: p_1 p_2 > \Delta$ 
  - ▶ At significance level  $\alpha$ , reject  $H_0$  in favor of  $H_a$  if  $Z_0 \geq z_{\alpha}$
  - ► Alternatively, if p-value=  $P(Z_0 \ge z_0|H_0) \le \alpha$ , reject  $H_0$
- 2. One tailed  $H_0: p_1 p_2 = \Delta \text{ vs } H_1: p_1 p_2 < \Delta$ 
  - ▶ At significance level  $\alpha$ , reject  $H_0$  in favor of  $H_a$  if  $Z_0 \leq -z_\alpha$
  - ► Alternatively, if p-value=  $P(Z_0 \le z_0|H_0) \le \alpha$ , reject  $H_0$
- 3. Two tailed  $H_0: p_1-p_2=\Delta$  vs  $H_1: p_1-p_2\neq \Delta$ 
  - At significance level  $\alpha$ , reject  $H_0$  in favor of  $H_a$  if  $|Z_0| \geq z_{\alpha/2}$
  - Alternatively, if p-value=  $P(|Z_0| \ge |z_0||H_0) = 2P(Z_0 \ge |z_0||H_0) \le \alpha$ , reject  $H_0$

Example 1. A random sample of Democrats and a random sample of Republicans were polled on an issue. Of 200 Republicans, 90 would vote yes on the issue; of 100 democrats, 58 would vote yes. Let  $p_1$  and  $p_2$  denote respectively the proportions of all Democrats or all Republicans who would vote yes on this issue.

- (a) Construct a 95% confidence interval for  $p_1 p_2$
- (b) Can we say that more Democrats than Republicans favor the issue at 1% level of significance? Report the p-value.

# Inference on two proportions: $\chi^2$ test

- Alternative test of  $H_0: p_1 = p_2$  is  $\chi^2$  test
- ► Recall 2 x 2 table

	Success	Failure	
Sample 1	$n_{11} = x$	$n_{12} = n_1 - x$	$n_1$
Sample 2	$n_{21} = y$	$n_{22} = n_2 - y$	$n_2$
	$m_1 = x + y$	$m_2 = n - m_1$	n

▶ It can be shown that under  $H_0$ , the statistic

$$X^{2} = \frac{n(n_{11}n_{22} - n_{12}n_{21})^{2}}{n_{1}n_{2}m_{1}m_{2}} \sim \chi_{1}^{2}$$

▶ Rejection region for  $H_a: p_1 \neq p_2$ 

$$C_{\alpha} = \{X^2 : X^2 \ge \chi^2_{1,\alpha,U}\}$$

# Inference on two proportions: $\chi^2$ test

- ▶ Aka "Pearson" chi-square statistic
- ► Equivalent form

$$X^{2} = \sum_{i=1}^{2} \sum_{j=1}^{2} \frac{(n_{ij} - En_{ij})^{2}}{En_{ij}}$$

where  $E(n_{ij}) = n_i m_j / n$ 

 $\blacktriangleright$  We will see this again for  $r \times c$  tables

# Inference on two proportions: Summary

- ► For small samples, use Fisher's Exact Test
- For large samples and two tailed test  $H_a: p_1 \neq p_2$ , use  $\chi^2$  or Z test, i.e., rejection region

$$C_{\alpha} = \{X^2 : X^2 > \chi^2_{1,\alpha,U}\} \text{ or } C_{\alpha} = \{z : |z| > z_{\alpha/2}\}$$

For large samples and one tailed test  $H_a: p_1 < p_2$  or  $H_a: p_1 > p_2$ , use Z test, i.e., rejection region

$$C_{\alpha} = \{z : z < -z_{\alpha}\} \text{ or } C_{\alpha} = \{z : z > z_{\alpha}\}$$

### Matched or Paired Observations

- ► In some studies, subjects occur naturally in pairs or matches; e.g., twins or response under two conditions
- ► If we want to compare binary responses in matched pairs, the assumption of independence is violated

### Matched or Paired Observations: McNemar's test

► The data are of the form

	Condition 2 response		
Condition 1 response	Yes	No	
Yes	a	b	
No	c	d	

▶ Let A, B, C, D be the random variables corresponding to the observed counts a, b, c, d

$$A + B + C + D = n$$
, and  $p_A + p_B + p_C + p_D = 1$ 

Then  $(A, B, C, D) \sim$ Multinomial

### Matched or Paired Observations: McNemar's test

- ▶ Response rate under condition 1 is  $p_1 = p_A + p_B$
- ▶ Response rate under condition 2 is  $p_2 = p_A + p_C$
- ▶ Consider  $H_0: p_1 = p_2$  (no difference between response rate between the two conditions)

$$p_1 = p_2 \Leftrightarrow p_B = p_C$$

▶ The test statistic for comparing  $p_1$  to  $p_2$  (or equivalently  $p_B$  to  $p_C$ ) can be derived using the conditional distribution of

$$B|B+C=m \sim B\left(m,p=\frac{p_B}{p_B+p_C}\right)$$

Thus  $H_0: p_1 = p_2 \Leftrightarrow H_0: p = 1/2$ 

► This is the McNemar's test

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 27

### McNemar's Test

1. One tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 > p_2$ or  $H_0: p = 1/2 \text{ vs } H_a: p > 1/2$ 

p-value = 
$$p_U = P(B \ge b|B + C = m) = \sum_{i=b}^{m} {m \choose i} \left(\frac{1}{2}\right)^m$$

2. One tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 < p_2$ or  $H_0: p = 1/2 \text{ vs } H_a: p < 1/2$ 

p-value = 
$$p_L = P(B \le b|B+C=m) = \sum_{i=0}^{b} {m \choose i} \left(\frac{1}{2}\right)^m$$

3. Two tailed test:  $H_0: p_1 = p_2 \text{ vs } H_a: p_1 \neq p_2$ or  $H_0: p = 1/2 \text{ vs } H_a: p \neq 1/2$ 

$$p$$
-value =  $2 \min(p_L, p_U)$ 

is the formula presented in your textbook. A pitfall of this approach is that the value can exceed 1. Alternative approach is by summing all the probabilities  $\leq P(B=b|B+C=m)$  (Similar to two tailed exact binomial ©PF.Kuan

toat)

Example: A preference poll of a panel of 75 voters was conducted before and after a TV debate during the campaign for the 1980 presidential election between Jimmy Carter and Ronald Reagan. Test whether there was a significant shift from Carter as a result of the TV debate.

	Preference after		
Preference before	Carter	Reagan	
Carter	28	13	
Reagan	7	27	

```
Data election;
input before $ after $ count;
datalines;
Carter Carter 28
Carter Reagan 13
Reagan Reagan 27
Reagan Carter 7
run;
proc freq data=election;
exact agree;
tables before*after/agree;
weight count;
run;
```

30

# SAS Output

The FREQ Procedure

Table of before by after

before	after			
Frequenc	у			
Percent				
Row Pct				
Col Pct	Carter	Reagan	Total	
Carter	28	13	41	
	37.33	17.33	54.67	
	68.29	31.71		
	80.00	32.50		
Reagan	7	27	34	
0	9.33	36.00	45.33	
	20.59	79.41		
	20.00	67.50		
Total	35	5 40		75
	46.67	53.33	100.	00

31

## SAS Output

#### Statistics for Table of before by after

#### McNemar's Test

Statistic (S) 1.8000
DF 1
Asymptotic Pr > S 0.1797
Exact Pr >= S 0.2632

The SAS System
The FREQ Procedure

#### Statistics for Table of before by after

#### Simple Kappa Coefficient

Kappa (K) 0.4700 ASE 0.1003 95% Lower Conf Limit 0.2734 95% Upper Conf Limit 0.6666

### Test of H0: Kappa = 0

ASE under H0 0.1140 Z 4.1225 One-sided Pr > Z <.0001 Two-sided Pr > |Z| <.0001

Exact Test

One-sided Pr >= K <.0001 Two-sided Pr >= |K| <.0001

### R Code and Output

```
> obs < matrix(c(28,13,7,27),nrow=2,byrow=T)
> rownames(obs) = colnames(obs) <- c('Carter', 'Reagan')
> names(dimnames(obs)) <- c('Before', 'After')</pre>
> mcnemar.test(obs)
McNemar's Chi-squared test with continuity correction
data: obs
McNemar's chi-squared = 1.25, df = 1, p-value = 0.2636
> mcnemar.test(obs,correct=FALSE)
McNemar's Chi-squared test
data: obs
McNemar's chi-squared = 1.8, df = 1, p-value = 0.1797
```

```
> library(exact2x2)
> exact2x2(obs,paired=TRUE,alternative='greater')
Exact McNemar-type test
data:
     obs
b = 13, c = 7, p-value = 0.1316
alternative hypothesis: true odds ratio is greater than 1
95 percent confidence interval:
 0.7920039
                 Tnf
sample estimates:
odds ratio
  1.857143
```