

# Stratified Contingency Tables

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## Session 8

Module 1 Probability & Statistical Inference

The Summer Institutes

DEPARTMENT OF BIostatISTICS

SCHOOL OF PUBLIC HEALTH

UNIVERSITY *of* WASHINGTON



# Overview

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## 1. 2 x 2 Tables

- Paired Binary Data

## 2. Stratified Tables

- Confounding
- Effect Modification

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# 2 x 2 Tables

## Epidemiological Applications: Matched Case Control Study

213 subjects with a history of acute myocardial infarction (AMI) were **matched** by age and sex with one of their siblings who did not have a history of AMI. The prevalence of a particular polymorphism was compared between the siblings.

**Question 1** Is there an association between the polymorphism prevalence and AMI?

**Question 2** If there is an association then what is the magnitude of the effect?

# 2 x 2 Tables

## Epidemiological Applications: Matched Case Control Study

**Q:** Can't we simply use Pearson's  $\chi^2$  Test to assess whether this is evidence for an increase in knowledge?

**A:** NO!!! Pearson's  $\chi^2$  test assumes that the columns are **independent** samples. In this design the 213 with AMI are genetically related to the 213 w/o AMI. This is an example of **paired binary data**.

		Disease Status		TOTAL
		AMI	no AMI	
Exposure Status	Carrier	96	87	183
	Noncarrier	117	126	243
TOTAL		213	213	426

# 2 x 2 Tables

## Epidemiological Applications: Paired Binary Data

For **paired binary data** we display the results as shown in the table.

This analysis explicitly recognizes the heterogeneity of subjects.

The **concordant pairs** (73 and 103) provide no information about the association between AMI and the polymorphism.

🔑 The information regarding the association is in the **discordant pairs**, 14 and 23.

		AMI		TOTAL
		carrier	non-carrier	
no AMI	carrier	73	14	87
	noncarrier	23	103	126
TOTAL		96	117	213

# 2 x 2 Tables

## Epidemiological Applications: Paired Binary Data

For **paired binary data** we display the results as shown in the table.


This analysis explicitly recognizes the heterogeneity of subjects.

$$p_1 = P(\text{carrier} \mid \text{AMI}) = p_{11} + p_{01}$$

$$p_0 = P(\text{carrier} \mid \text{No AMI}) = p_{10} + p_{00}$$

$$H_0 : p_1 = p_0$$

$$H_A : p_1 \neq p_0$$

 The information for testing these hypotheses is contained in the **discordant pairs** (0,1) and (1,0).

		AMI		TOTAL
		1	0	
no AMI	1	$n_{11}$	$n_{10}$	
	0	$n_{01}$	$n_{00}$	

TOTAL

$n_{11}/n =$ <b><math>p_{11}</math></b>	$n_{10}/n =$ <b><math>p_{10}</math></b>
$n_{01}/n =$ <b><math>p_{01}</math></b>	$n_{00}/n =$ <b><math>p_{00}</math></b>

n

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# 2 x 2 Tables

## Epidemiological Applications: McNemar's Test for Paired Binary Data

Under the null hypothesis we expect equal numbers of (0,1) pairs and (1,0) pairs. We can evaluate this hypothesis using or **McNemar's Test for Paired Binary Data**. The **McNemar's chi-squared statistic** is

$$X^2 = \frac{(|n_{10} - n_{01}| - 1)^2}{n_{10} + n_{01}} \sim \chi^2(1)$$

The **odds ratio** comparing the odds of carrier in those with AMI to odds of carrier in those w/o AMI is estimated by:

$$\widehat{OR} = \frac{n_{01}}{n_{10}}$$

Confidence intervals can be obtained as described in Breslow and Day (1981), section 5.2, or in Armitage and Berry (1987), chapter 16.

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# Break #1

**Pause the video,  
take a break, stretch,  
then review relevant exercises  
from worksheet.**

**Afterwards, continue on!**





# Effect Modification

## Stratified Tables

Often, a **third variable** influences the relationship between the two primary measures (e.g., disease and exposure).

### Example (right):

Effect of seat belt use on car accident fatality


		Seat Belt	
		Worn	Not Worn
Driver	Dead	10	20
	Alive	40	30
TOTAL		50	50
Fatality Rate		10/50 (20%)	20/50 (40%)

# Effect Modification

## Stratified Tables

But, suppose we also consider *impact speed*.

How does this affect your inference?

 This is an example of **effect modification** or **interaction**.

- Effects are different in subgroups of a third variable, and the overall effect is intermediate.

		< 40 mph Seat Belt		> 40 mph Seat Belt	
		Worn	Not Worn	Worn	Not Worn
Driver	Dead	3	2	7	18
	Alive	27	18	13	12
TOTAL		30	20	20	30
Fatality Rate		3/30 (10%)	2/20 (10%)	7/20 (35%)	18/30 (60%)

# Effect Modification

## Dependence on the effect measure used

 Effect modification depends on the effect measure used!

*Table Rate of fractures over 5 years by age and calcium level in drinking water.*

- > There's evidence of effect modification on the risk ratio scale.
- > There's no evidence of effect modification on the risk difference scale.

		Age		Overall (pooled)
		20-35 yrs	55-80 yrs	
Calcium Level	High	1.1%	11.0%	7.8%
	Low	3.3%	13.2%	10.0%
Risk Ratio		0.33	0.83	0.78
Risk Difference		-2.2%	-2.2%	-2.2%

# Confounding

Suppose we are interested in the relationship between  
**lung cancer incidence**  
and  
**heavy drinking** (defined as  $\geq 2$  drinks per day)

We conduct a **prospective cohort study** where drinking status is determined at baseline and the cohort is followed for 10 years to determine cancer endpoints.

We also measure **smoking status** at baseline.

# Confounding

## 1) Pooled data, not controlling for smoking

		Heavy Drinker		TOTAL
		Yes	No	
Lung Cancer Status	Yes	33	27	60
	No	1667	2273	3940
TOTAL		1700	2300	4000

# Confounding

- A higher proportion of heavy drinkers are smokers (800/1700 vs 200/2300)
- A higher proportion of lung cancer cases are smokers (30/1000 vs 30/3000)
- The comparison of heavy drinkers to not-heavy drinkers is really a comparison of smokers to nonsmokers

## 2) Stratify by smoking status at baseline

### Smokers

		Heavy Drinker		TOTAL
		Yes	No	
Lung Cancer Status	Yes	24	6	30
	No	776	194	970
TOTAL		800	200	1000

OR = 1

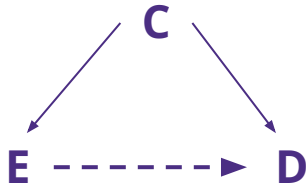
### Nonsmokers

		Heavy Drinker		TOTAL
		Yes	No	
Lung Cancer Status	Yes	9	21	30
	No	891	2079	2970
TOTAL		900	2100	3000

OR = 1

# Confounding

 A confounder is associated with both the disease and exposure and is not in the causal path between disease and exposure



An apparent association between E and D is completely explained by C.  
**C is a confounder.**

- The implicit assumption is that we want to know if E “causes” D
- A simple, common example from genetics is the linked gene: we discover a gene which appears to be associated with disease ... does it cause the disease or is it merely linked to the true causal gene?

# Break #2

Pause the video,  
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Afterwards, continue on!

Image Credit: indg0.com





# Adjusting the OR via Stratification

## Basic idea

- Compute separate OR for each stratum
- Assess homogeneity of OR's across strata  
*Is there EM?*
- Pool OR's: used weighted average  
*Adjust for confounding*
- Global test of pooled OR = 1  
*Is there association, after adjustment*
- Different methods of pooling, testing have been proposed.  
*We will focus on Mantel-Haenszel methods*
- 🖐 Same idea for RR and RD

# Rosner §13.5

## Mantel-Haenszel Methods

A 1985 study identified a group of **509 cancer cases and 489 controls** by mail questionnaire. The main purpose of the study was to look at the **effect of passive smoking on cancer risk**.

In the study **passive smoking** was defined as exposure to the cigarette smoke of a spouse who smoked at least one cigarette/day for at least 6 months.

One **potential confounding variable was smoking by the test subjects themselves** since personal smoking is related to both cancer risk and having a spouse that smokes.

**Therefore, it was important to control for personal smoking before looking at the relationship between passive smoking and cancer risk.**

# Rosner §13.5

## Mantel-Haenszel Methods

### 1) Pooled data, not controlling for personal smoking

#### 1) Pooled data, not controlling for *personal smoking*

		Passive Smoking		TOTAL
		Yes	No	
Cancer Status	Case	281	228	509
	Control	210	279	489
TOTAL		491	507	998

```
. cci 281 228 210 279
```

	Exposed	Unexposed	Total	Proportion Exposed
Cases	281	228	509	0.5521
Controls	210	279	489	0.4294
Total	491	507	998	0.4920

	Point estimate	[95% Conf. Interval]	
Odds ratio	1.637406	1.265013	2.119599
Attr. frac. ex.	.3892779	.2094943	.5282126
Attr. frac. pop	.2149059		

```
chi2(1) = 15.00 Pr>chi2 = 0.0001
```

For information on how to complete these calculations in R:

<https://a-little-book-of-r-for-biomedical-statistics.readthedocs.io/en/latest/src/biomedicalstats.html>

# Rosner §13.5

## Mantel-Haenszel Methods

### 2) Stratified by *personal smoking*

#### Personal Smoking: Smokers

		Passive Smoking		
		Yes	No	TOTAL
Cancer Status	Case	161	117	278
	Control	130	124	254
	TOTAL	291	241	532

**OR = 1.31**  
*p-value = 0.1192*

#### Personal Smoking: Nonsmokers

		Passive Smoker		
		Yes	No	TOTAL
Cancer Status	Case	120	111	231
	Control	80	155	235
	TOTAL	200	266	466

**OR = 2.09**  
*p-value = 0.0001*

For information on how to complete these calculations in R:

<https://a-little-book-of-r-for-biomedical-statistics.readthedocs.io/en/latest/src/biomedicalstats.html>

# Rosner §13.5

## Mantel-Haenszel Methods

### 2) Stratified by *personal smoking*

#### Personal Smoking: Smokers

```
. cci 161 117 130 124
```

Proportion	Exposed	Unexposed	Total	Exposed
Cases	161	117	278	0.5791
Controls	130	124	254	0.5118
Total	291	241	532	0.5470
	Point estimate		[95% Conf. Interval]	
Odds ratio	1.312558		.9184614	1.875813
Attr. frac. ex.	.2381286		-.0887774	.4668978
Attr. frac. pop	.137909			
-----				
	chi2(1) =	2.43	Pr>chi2 =	0.1192

#### Personal Smoking: Nonsmokers

```
. cci 120 111 80 155
```

	Exposed	Unexposed	Total	Proportion Exposed
Cases	120	111	231	0.5195
Controls	80	155	235	0.3404
Total	200	266	466	0.4292
	Point estimate		[95% Conf. Interval]	
Odds ratio	2.094595		1.41754	3.097165
Attr. frac. ex.	.5225806		.2945527	.6771241
Attr. frac. pop	.2714705			
-----				
	chi2(1) =	15.24	Pr>chi2 =	0.0001

For information on how to complete these calculations in R:

<https://a-little-book-of-r-for-biomedical-statistics.readthedocs.io/en/latest/src/biomedicalstats.html>

# Stratified Contingency Tables

## Mantel-Haenszel Methods

**Q:** How can we combine the information from both stratum-specific tables to obtain an overall test of significance that takes account of the stratification?

**A: Mantel-Haenszel Methods** – assesses association between disease and exposure after controlling for one or more confounding variables.

		Exposure		TOTAL
		yes	no	
Disease	yes	$a_i$	$b_i$	$a_i + b_i$
	no	$c_i$	$d_i$	$c_i + d_i$
TOTAL		$a_i + c_i$	$b_i + d_i$	$N_i$

where  $i = 1, 2, \dots, K$  is the number of strata.

# Stratified Contingency Tables

## Mantel-Haenszel Methods

**(1) Test of effect modification** (heterogeneity, interaction)

$$H_0: OR_1 = OR_2 = \dots = OR_K$$

$H_A$ : not all stratum-specific ORs are equal

**(2) Estimate the common odds ratio**

The Mantel-Haenszel estimate of the odds ratio assumes there is a common odds ratio:

$$OR_{\text{pool}} = OR_1 = OR_2 = \dots = OR_K$$

To estimate the common odds ratio we take a weighted average of the stratum-specific odds ratios:

$$\text{MH estimate: } \widehat{OR}_{\text{pool}} = \sum_{i=1}^K w_i \cdot \widehat{OR}_i$$

**(3) Test of common odds ratio**

$H_0$ : common odds ratio is 1.0

$H_A$ : common odds ratio  $\neq$  1.0

# Rosner §13.5

## Mantel-Haenszel Methods

	case	passive	number	smoke
1.	1	1	120	0
2.	1	0	111	0
3.	0	1	80	0
4.	0	0	155	0
5.	1	1	161	1
6.	1	0	117	1
7.	0	1	130	1
8.	0	0	124	1

Entering the  
stratum-specific data



```
. cc case passive [freq=number], by(smoke) bd
```

Calculating the pooled  
OR and testing whether  
it is different from 1



Personal Smoking	OR	[95% Conf. Interval]	M-H Weight
0	2.094595	1.41754 3.097165	19.05579 (exact)
1	1.312558	.9184614 1.875813	28.59023 (exact)
Crude	1.637406	1.265013 2.119599	(exact)
M-H combined	1.625329	1.263955 2.090024	

Test of homogeneity (M-H)	chi2(1) =	3.27	Pr>chi2 = 0.0706
Test of homogeneity (B-D)	chi2(1) =	3.27	Pr>chi2 = 0.0704

Test that combined OR = 1:			
Mantel-Haenszel	chi2(1) =	14.42	
	Pr>chi2 =	0.0001	



# Break #3

**Pause the video,  
take a break, stretch,  
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**Afterwards, continue on!**

