

## 16. Multiple 2x2 Contingency Tables

In the last chapter, we examined the relationship between 2 categorical variables (factors). Here, we continue to examine such relationships, but now focus on the relationship between 2 factors in the presence of a third factor. For example, we might be interested in the relationship between smoking and lung cancer, and how this relationship may change (if at all) with gender (a third factor). We will see that the apparent relationship between 2 factors may switch direction or change magnitude depending on whether we examine the relationship separately for each level of the third factor or whether we examine it after we aggregate over the levels of the third factor. Such a change is due to the first 2 factors being dependent on the third. We will test for such a dependency, and, if we don't seem to find one, we will analyze the aggregated data; if we do find such a dependency, then it is appropriate to examine the relationship of the 2 factors of interest separately for each of the levels of the third factor (don't aggregate). We will focus on 2 factors each with 2 levels, including a third factor with possibly several ( $g$ ) levels; thus we will be working with multiple 2x2 contingency tables.

### 16.1. Simpson's Paradox

Simpson's paradox occurs when the relationship between 2 factors of interest changes direction or magnitude depending on whether we aggregate the data over the levels of a third factor or whether we look at the relationship separately for each of the levels of the third factor. The third factor is often called a **lurking variable**.

E.g. Making an informed decision about your health care: do patients' chances of survival depend on which hospital a patient chooses?

	Hospital A	Hospital B
Died	63	16
Survived	2037	784
Total	2100	800

Odds ratio of dying for Hospital A relative to Hospital B:

OR:

Interpretation?

But...

Good Condition		
	Hospital A	Hospital B
Died	6	8
Survived	594	592
Total	600	600

Poor Condition		
	Hospital A	Hospital B
Died	57	8
Survived	1443	192
Total	1500	200

OR(good)

OR(poor)

Interpretations?

The relationship between survival and hospital seems to change depending on whether we aggregate or not. Patient condition seems to be influencing the relationship between survival and hospital. This apparent result may just be due to sampling variability; so we should perform a test to see if the result may be reasonably attributable to chance or not.

## 16.2. The Mantel-Haenszel Method

The first part of the Mantel-Haenszel method is to **test for homogeneity of a relationship between 2 factors across the levels of a third factor** (i.e., Is the relationship the same across levels of the third factor?). The null hypothesis is that there is no relationship. Not surprisingly, we will use a p-value to help us decide whether to reject the null and analyze the 2 factors separately for each of the levels of the third factor, or to not

reject and to analyze the 2 factors after aggregating over the levels of the third factor.

E.g., [Smoking, coffee drinking, and heart attacks](#) (POB page 376).

Smokers		
H. Attack	Coffee Yes	Coffee No
Yes	1011	81
No	390	77
Total	1401	158

Nonsmokers		
H. Attack	Coffee Yes	Coffee No
Yes	383	66
No	365	123
Total	748	189

Aggregated Over Smoke/Nonsmoke		
H. Attack	Coffee Yes	Coffee No
Yes	1394	147
No	755	200
Total	2149	347

Odds Ratio of having a heart attack for coffee drinkers (“exposed”) verses those who do not drink coffee (“unexposed”):

$OR_S$

$OR_{NS}$

## OR (overall)

Interpretations?

Is the relationship between heart attack and coffee drinking the same whether you smoke or not? In other words, is the (joint) distribution of probability amongst the levels coffee consumption and heart attack (yes/yes yes/no no/yes no/no) homogeneous across the levels of the smoking factor?

Before we proceed to the second step of the M-H method to combine information across tables, we first check for homogeneity across tables.

### Test for Homogeneity

$$H_0: OR_S = OR_{NS}$$

- $\chi^2 = \sum_{i=1}^g w_i (y_i - \gamma)^2$  is approximately a chi-square random variable with  $(g-1)$  df, where  $g$  is the number of levels of the third factor and
- $y_i = \log(OR)$  for level (table)  $i$

- $w_i = 1/(\text{Var}[\log(\text{OR})])$
  
- $Y = \text{weighted average of } \log(\text{OR})$

$\chi^2 =$

p-value =

Do we proceed with the M-H method for combining information in tables?

If we do not reject the test for homogeneity, we would like to calculate an overall measure of association between 2 factors (e.g., coffee drinking and heart attack) regardless of the level of the third factor (e.g., smoking). **Note: Check expected count**

rule of thumb to see if the chi-square approximation is “good” (see page 382 POB).

- Use weighted average of OR among the tables and the normal approximation to  $\ln(\text{OR})$  to construct point estimates and CI for  $\ln(\text{OR})$  or OR.

- Or, use the chi-square approximation to the Mantel-Haenszel statistic ([Test for Association](#))

$H_0: \text{OR} = 1$

(This refers to the overall odds ratio of heart attack for coffee drinkers relative to those not drinking coffee, regardless of smoking status)

# M-H statistic $X^2$

## S-Plus Says

Without the original “raw” responses we need to go to the command line in S-Plus and enter the data summarized as an array of counts in each category of the 2x2x2 cross-classification. I do not expect you to know what the command line coding means, I just want you now that S-Plus does perform a “Mantel-Haenszel” test. Note: This tests for association between 2 factors assuming homogeneity. In practice, you should first test for homogeneity as we did above (in Splus?).

```
> mh.array<-array(c(1011, 390, 81, 77, 383, 365, 66, 123), dim=c(2,2,2))
> dimnames(mh.array)<-list(c("mi.yes", "mi.no"), c("cof.yes", "cof.no"),
c("smok.yes", "smok.no"))
> mh.array
```

```
, , smok.yes
      cof.yes cof.no
mi.yes  1011    81
mi.no   390    77
```

```
, , smok.no
      cof.yes cof.no
mi.yes   383    66
mi.no   365   123
```

```
> mh.test<-mantelhaen.test(mh.array, correct=F)
> mh.test.cor<-mantelhaen.test(mh.array, correct=T)
> mh.test
```

Mantel-Haenszel chi-square test without continuity correction

```
data: mh.array
Mantel-Haenszel chi-square = 43.5778, df = 1, p-value = 0
```

```
> mh.test.cor
```

Mantel-Haenszel chi-square test with continuity correction

```
data: mh.array
Mantel-Haenszel chi-square = 42.778, df = 1, p-value = 0
```

```
>
```