

STATISTICS 536B, Lecture #3

March 3, 2015

General options for binary Y , binary X , confounders $C = (C_1, \dots, C_p)$

- Build a logistic regression model for Y in terms of X and C
 - Think of the data “carved up” into a bunch of 2×2 (Y, X) mini data tables, one for each distinct value of C manifested in the data.
- For today’s lecture, will write m as the index to keep track of these mini-tables.

Demo: Generating and analyzing unmatched case-control data

```
### set up a population

t <- 100000

set.seed(17)

m.pop <- sample(0:6, size=t, prob=rep(1/7, 7), replace=T)

x.pop <- rbinom(t, size=1, prob=expit(2 - (4/6)*m.pop))

y.pop <- rbinom(t, size=1, prob=expit(-3 + (4/9)*(m.pop-3)^2 + 0.5*x.pop))
```

Misspecified model messes up the controlling for confounders

```
### do a (balanced, unmatched) case-control study
n <- 2000
set.seed(133)
cs <- sample((1:t)[y.pop==1], size=n)
cn <- sample((1:t)[y.pop==0], size=n)
```

```
y <- c(y.pop[cs], y.pop[cn])
x <- c(x.pop[cs], x.pop[cn])
m <- c(m.pop[cs], m.pop[cn])
```

```
### adjustment using main effect of m
ft <- glm(y~x+m, family=binomial)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.07383	0.08813	-0.838	0.402178	
x	0.26231	0.07781	3.371	0.000749	***
m	-0.02001	0.01792	-1.117	0.264118	

Aside: what about no control, proper control

```
glm(formula = y ~ x, family = binomial)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.15838	0.04516	-3.508	0.000452	***
x	0.31269	0.06344	4.929	8.28e-07	***

```
glm(formula = y ~ x + m + I(m^2), family = "binomial")
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	1.84813	0.13277	13.920	< 2e-16	***
x	0.49335	0.10175	4.849	1.24e-06	***
m	-2.81596	0.08521	-33.046	< 2e-16	***
I(m^2)	0.46643	0.01356	34.397	< 2e-16	***

Adjust for confounding without modelling?

```
dat.strfd <- table(y,x,m)
```

```
> dat.strfd
```

```
, , m = 0
```

```
  x
```

```
y      0      1
```

```
0     12     60
```

```
1     86    615
```

```
, , m = 1
```

```
  x
```

```
y      0      1
```

```
0     62    227
```

```
1     44    230
```

```
...
```

```
, , m = 6
```

```
  x
```

```
y      0      1
```

```
0    108      5
```

```
1    535     77
```

So have stratum-specific log-OR and SE

```
### function to get log-OR and SE from 2 by 2 table
myfun.lor <- function(dattbl) {
  est <- log(dattbl[1,1])+log(dattbl[2,2])-log(dattbl[1,2])-log(dattbl[2,1])
  se <- sqrt(sum(1/as.vector(dattbl)))
  c(est,se)
}
```

```
inf.strfd <- apply(dat.strfd, 3, myfun.lor)
```

	m						
	0	1	2	3	4	5	6
[1,]	0.358	0.356	0.563	0.713	0.661	0.328	1.134
[2,]	0.337	0.218	0.291	0.323	0.276	0.212	0.473

General statistical strategy for combining multiple estimators of the same target

```
ests <- inf.strfd[1,]  
vars <- inf.strfd[2,]^2  
whts <- (1/vars)/sum(1/vars)  
  
est.cmbd <- sum(whts*ests)  
se.cmbd <- sqrt(sum(whts^2*vars))  
  
c(est.cmbd, se.cmbd)  
[1] 0.496 0.105
```


Homogeneity of (X,Y) odds-ratio across strata?

We've *assumed* this. Empirically testable?

```
> sum( (ests-est.cmbd)^2/vars )  
[1] 3.891315
```

Or find a package...

```
> library(epicalc)
> mhor(mhtable=dat.strfd)
```

Stratified analysis by m

	OR	lower lim.	upper lim.	P value
m 0	1.43	0.672	2.82	2.68e-01
m 1	1.43	0.912	2.25	1.07e-01
m 2	1.75	0.968	3.30	5.98e-02
m 3	2.04	1.045	4.11	3.08e-02
m 4	1.93	1.086	3.45	2.20e-02
m 5	1.39	0.896	2.15	1.35e-01
m 6	3.11	1.232	10.07	9.33e-03
M-H combined	1.67	1.362	2.05	8.22e-07

M-H Chi2(1) = 24.3 , P value = 0

Homogeneity test, chi-squared 6 d.f. = 3.91 , P value = 0.689

Is the Odds-Ratio also a **collapsible** measure of association?

Example. Say the joint distribution of (C, X, Y) is characterized by:

- X and C are independent and identically distributed as Bernoulli(0.5)
- $Pr(Y = 1|X = 0, C = 0) = 0.2$ and $Pr(Y = 1|X = 0, C = 1) = 0.5$
- The stratified odds-ratios are $OR(Y, X|C = c) = 4$, for both $c = 0$ and $c = 1$.

Is C a confounder?

What is the crude odds-ratio $OR(Y, X)$?

