

# Analysis of Categorical Data

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Science

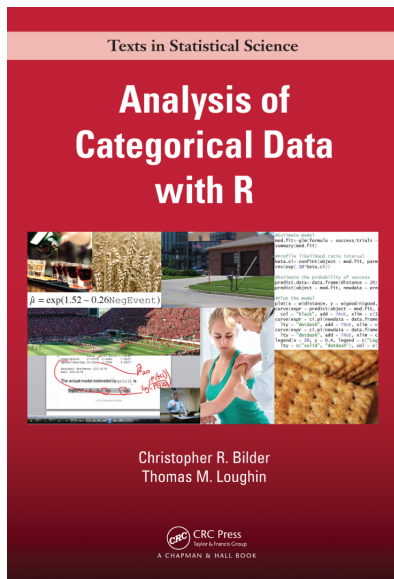
[www.chrisbilder.com/categorical](http://www.chrisbilder.com/categorical)

- Apply appropriate methods to analyze data in a contingency table
- State, interpret, and fit logistic, baseline-category, proportional odds, and Poisson regression models
- Use appropriate variable-selection methods
- Evaluate the fit of categorical regression models
- Identify and solve overdispersion problems
- Be comfortable with using R to analyze categorical data

- 1 Introduction
  - Objectives
  - Table of contents
  - Textbook
  - Additional items
- 2 Analyzing a binary response,  $2 \times 2$  tables
  - Binomial distribution
  - Estimation of  $\pi$
  - Inference for  $\pi$
  - Inference for  $\pi_1 - \pi_2$
  - Relative risks
  - Odds ratios
- 3 Conclusion
  - Objectives
  - Additional material

Section/subsection given at the top of each slide

- Bilder and Loughin (2014) published by CRC Press
- Provides more depth and additional material
- [www.chrisbilder.com/categorical](http://www.chrisbilder.com/categorical)
- All R programs available on the website



- 8:30AM – 5:00PM: Course in session
- When are the breaks?
  - 10:15AM – 10:30AM: Break!
  - 12:30PM – 2:00PM: Lunch!
  - 3:15PM – 3:30PM: Break!
- Recording
  - Computer screen, including annotations made on it
  - Live-action video of us
  - Post to [www.chrisbilder.com/JSM](http://www.chrisbilder.com/JSM) within one week from today; available for 1 month
- R Index
- Blue text – Added after handouts printed
- This is not a workshop

- 1 Introduction
- 2 Analyzing a binary response,  $2 \times 2$  tables
  - Binomial distribution
  - Estimation of  $\pi$
  - Inference for  $\pi$
  - Inference for  $\pi_1 - \pi_2$
  - Relative risks
  - Odds ratios
- 3 Conclusion

- Binary responses likely the most common type of categorical response
  - Define  $Y = 1$  as a “success” with probability  $\pi$
  - Define  $Y = 0$  as a “failure” with probability  $1 - \pi$
- Bernoulli distribution

$$P(Y = y) = \pi^y(1 - \pi)^{1-y}$$

for  $y = 0$  or  $1$

- $E(Y) = \pi$  and  $Var(Y) = \pi(1 - \pi)$
- Binomial distribution
  - Observe multiple Bernoulli random variables, say  $Y_1, \dots, Y_n$ , through repeated sampling or trials in identical settings
  - If all trials are identical and independent,  $W = \sum_{i=1}^n Y_i$  has a binomial distribution:

$$P(W = w) = \binom{n}{w} \pi^w(1 - \pi)^{n-w}$$

for  $w = 0, \dots, n$

- $E(W) = n\pi$  and  $Var(W) = n\pi(1 - \pi)$
- Goal: Estimate  $\pi$

- Given observed data, what is the most plausible value of  $\pi$ ?
- Maximum likelihood estimation
  - Likelihood function measures the plausibility of different values of  $\pi$
  - Bernoulli setting

$$\begin{aligned}L(\pi|y_1, \dots, y_n) &= P(Y_1 = y_1) \times \dots \times P(Y_n = y_n) \\&= \prod_{i=1}^n \pi^{y_i} (1 - \pi)^{1-y_i} \\&= \pi^w (1 - \pi)^{n-w}\end{aligned}$$

- Binomial setting:  $L(\pi|w) = P(W = w) = \binom{n}{w} \pi^w (1 - \pi)^{n-w}$
- The value of  $\pi$  which maximizes the likelihood function is considered to be the most plausible
  - Maximum likelihood estimate (MLE)
  - Derive MLE to be  $\hat{\pi} = w/n$
  - For more complicated likelihood functions, will need to use numerical iterative methods



- Maximum likelihood estimators have a normal distribution for a large sample
  - Suppose  $\hat{\theta}$  is MLE of  $\theta$
  - Mean is  $\theta$
  - $\text{Var}(\hat{\theta})$  is estimated by

$$-E \left( \frac{\partial^2}{\partial \theta^2} \log[L(\theta|W)] \right)^{-1} \Big|_{\theta=\hat{\theta}}$$

where  $\log(\cdot)$  is the natural log function

- Bernoulli/binomial:
  - $\hat{\pi} = w/n$  is MLE
  - Mean is  $\pi$
  - Estimated variance is

$$\begin{aligned} \widehat{\text{Var}}(\hat{\pi}) &= -E \left\{ \frac{\partial^2 \log [L(\pi|W)]}{\partial \pi^2} \right\}^{-1} \Big|_{\pi=\hat{\pi}} = -E \left\{ -\frac{W}{\pi^2} + \frac{n-W}{(1-\pi)^2} \right\}^{-1} \Big|_{\pi=\hat{\pi}} \\ &= \left[ \frac{n}{\pi} - \frac{n}{1-\pi} \right]^{-1} \Big|_{\pi=\hat{\pi}} = \frac{\hat{\pi}(1-\hat{\pi})}{n} \end{aligned}$$

- See Casella and Berger (2002) for more details about maximum likelihood estimation

- Wald interval

- Use large-sample normality of maximum likelihood estimator
- $(1 - \alpha)100\%$  confidence interval for  $\pi$

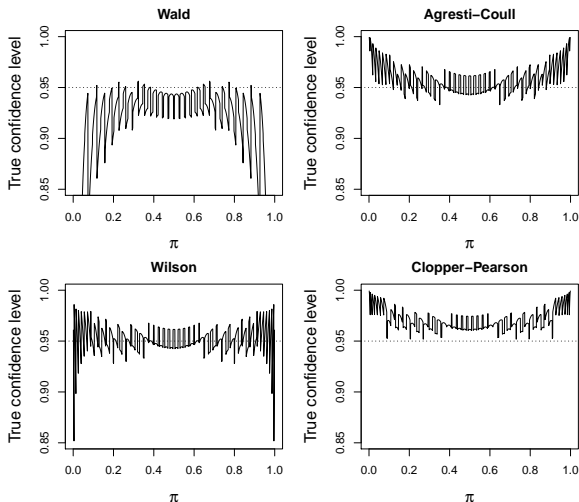
$$\hat{\pi} \pm Z_{1-\alpha/2} \sqrt{\hat{\pi}(1 - \hat{\pi})/n}$$

where  $Z_a$  is the  $a^{th}$  quantile from a standard normal distribution (e.g.,  $Z_{0.975} = 1.96$ )

- Problems:
  - Limits may be less than 0 or greater than 1
  - When  $w = 0$  or  $n$ ,  $\sqrt{\hat{\pi}(1 - \hat{\pi})/n} = 0$ , leading to an interval of (0,0) or (1,1)
  - True confidence level (coverage) is very often less than  $(1 - \alpha)100\%$

Example: True confidence levels, interval for  $\pi$  (ConfLevel4Intervals.R)

- $n = 40$  and  $\alpha = 0.05$
- When  $\pi = 0.157$ , true confidence level is 0.8759 for Wald interval
- Plots for  $0 < \pi < 1$ :



- Wilson (score) interval

- $H_0 : \pi = \pi_0$  vs.  $H_a : \pi \neq \pi_0$
- Score statistic

$$Z_0 = \frac{\hat{\pi} - \pi_0}{\sqrt{\pi_0(1 - \pi_0)/n}}$$

- Approximate with a **standard** normal distribution and use  $\pm Z_{1-\alpha/2}$  as critical values
- Invert the test to find interval
  - Find all possible values for  $\pi_0$  that lead to a “do not reject” of  $H_0$
  - Results in

$$\tilde{\pi} \pm \frac{Z_{1-\alpha/2}\sqrt{n}}{n + Z_{1-\alpha/2}^2} \sqrt{\hat{\pi}(1 - \hat{\pi}) + \frac{Z_{1-\alpha/2}^2}{4n}}$$

where

$$\tilde{\pi} = \frac{w + Z_{1-\alpha/2}^2/2}{n + Z_{1-\alpha/2}^2}$$

- Benefits:
  - Limits always between 0 and 1
  - Decent true confidence level properties

## Example: Corn seed germination (Corn.R)

- My garden



- Planted 64 corn seeds of a particular variety in one  $4' \times 4'$  raised bed
- Followed seed packet directions
- After 21 days, 48 seeds had sprouted (7-14 days was period given on seed packet)

Example: Corn seed germination (Corn.R)

```

> w <- 48
> n <- 64
> alpha <- 0.05
> pi.hat <- w/n
> pi.hat
[1] 0.75
> pi.tilde <- (w + qnorm(p = 1 - alpha/2)^2/2)/(n + qnorm(p = 1 -
  alpha/2)^2)
> pi.tilde
[1] 0.735844
> wilson <- pi.tilde + qnorm(p = c(alpha/2, 1 - alpha/2)) * sqrt(n)/(n +
  qnorm(p = 1 - alpha/2)^2) * sqrt(pi.hat * (1 - pi.hat) +
  qnorm(p = 1 - alpha/2)^2/(4 * n))
> round(wilson, digits = 4)
[1] 0.6318 0.8399
> library(package = binom)
> binom.confint(x = w, n = n, conf.level = 1 - alpha, methods = "wilson")
  method x  n mean      lower      upper
1 wilson 48 64 0.75 0.6318372 0.8398507

```

- Compare to 95% Wald interval:  $0.6439 < \pi < 0.8561$

- Compare responses of two groups in a  $2 \times 2$  contingency table
- Larry Bird's free throws for two seasons (Wardrop, 1995)

		Second		Total
		Made	Missed	
First	Made	251	34	285
	Missed	48	5	53
Total		299	39	338



- HIV vaccine clinical trials (Rerks-Ngarm et al., 2009)



The Seattle Times

Nation &amp; World

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# Vaccine helps prevent HIV infection, new study shows

Originally published September 23, 2009 at 11:46 pm | Updated September 24, 2009 at 12:11 pm

**For the first time, an experimental vaccine has prevented infection with the AIDS virus, a watershed event in the deadly epidemic and a surprising result. Recent failures led many scientists to think such a vaccine might never be possible.**

By [Seattle Times news services](#)



For the first time, an experimental vaccine has prevented infection with the AIDS virus, a watershed event in the deadly epidemic and a surprising result. Recent failures led many scientists to think such a vaccine might never be possible.

The vaccine, known as RV 144, **cut the risk of becoming infected with HIV by more than 31 percent** in the world's largest AIDS vaccine trial of more than 16,000 volunteers in Thailand, researchers announced today.

		Response		
		HIV	No HIV	Total
Treatment	Vaccine	51	8,146	8,197
	Placebo	74	8,124	8,198
	Total	125	16,270	16,395



- Denote  $\pi_1$  and  $\pi_2$  as the probabilities of a success for the two groups
- $2 \times 2$  contingency tables

		Response		Total
		Success	Failure	
Group	1	$\pi_1$	$1 - \pi_1$	1
	2	$\pi_2$	$1 - \pi_2$	1

		Response		Total
		Success	Failure	
Group	1	$w_1$	$n_1 - w_1$	$n_1$
	2	$w_2$	$n_2 - w_2$	$n_2$

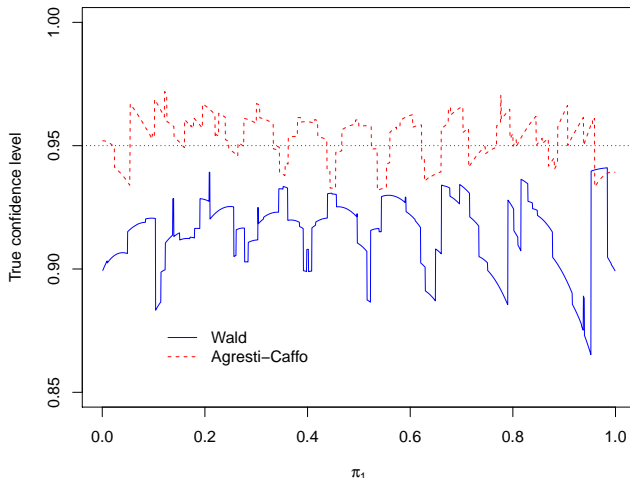
- $W_j \sim \text{Binomial}(n_j, \pi_j)$  for  $j = 1, 2$ 
  - MLE for  $\pi_j$ :  $\hat{\pi}_j = w_j/n_j$
  - $\hat{\pi}_j \sim N(\pi_j, \widehat{\text{Var}}(\hat{\pi}_j))$  for large  $n_j$ , where  $\widehat{\text{Var}}(\hat{\pi}_j) = \hat{\pi}_j(1 - \hat{\pi}_j)/n_j$
- $(1 - \alpha)100\%$  Wald interval

$$\hat{\pi}_1 - \hat{\pi}_2 \pm Z_{1-\alpha/2} \sqrt{\frac{\hat{\pi}_1(1 - \hat{\pi}_1)}{n_1} + \frac{\hat{\pi}_2(1 - \hat{\pi}_2)}{n_2}}$$

- Problems with Wald interval:
  - Limits may be less than -1 or greater than 1
  - When  $w_j = 0$  or  $n_j$ , the  $\hat{\pi}_j(1 - \hat{\pi}_j)/n_j$  part of the variance becomes 0
  - True confidence level (coverage) is very often less than  $(1 - \alpha)100\%$

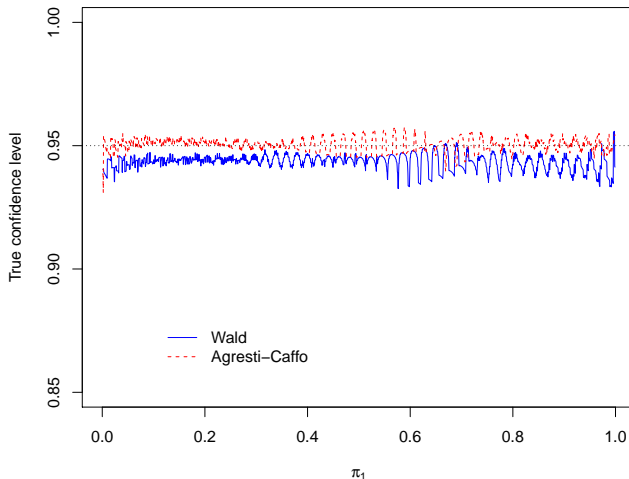
Example: True confidence levels, interval for  $\pi_1 - \pi_2$   
(ConfLevelTwoProb.R)

- $n_1 = n_2 = 10$ ,  $\pi_2 = 0.4$ , and  $\alpha = 0.05$



Example: True confidence levels, interval for  $\pi_1 - \pi_2$   
(ConfLevelTwoProb.R)

- $n_1 = n_2 = 50$ ,  $\pi_2 = 0.4$ , and  $\alpha = 0.05$



- $(1 - \alpha)100\%$  Agresti-Caffo interval

$$\tilde{\pi}_1 - \tilde{\pi}_2 \pm Z_{1-\alpha/2} \sqrt{\frac{\tilde{\pi}_1(1 - \tilde{\pi}_1)}{n_1 + 2} + \frac{\tilde{\pi}_2(1 - \tilde{\pi}_2)}{n_2 + 2}}$$

where

$$\tilde{\pi}_1 = \frac{w_1 + 1}{n_1 + 2} \text{ and } \tilde{\pi}_2 = \frac{w_2 + 1}{n_2 + 2}$$

- Benefit: True confidence level is much closer to  $(1 - \alpha)100\%$  than Wald
- Score interval
  - $H_0 : \pi_1 - \pi_2 = d$  vs.  $H_a : \pi_1 - \pi_2 \neq d$
  - Invert test
  - Performs similarly to Agresti-Caffo interval
  - No closed form expression
  - See p. 57 of Bilder and Loughin (2014)

Example: Larry Bird free throws (Bird.R)

```
> c.table <- array(data = c(251, 48, 34, 5), dim = c(2, 2),
  dimnames = list(First = c("made", "missed"), Second = c("made",
    "missed")))
> c.table
```

	Second	
First	made	missed
made	251	34
missed	48	5

```
> c.table[1, 2]  #Row 1, column 2 count
[1] 34
> pi.tilde1 <- (c.table[1, 1] + 1)/(sum(c.table[1, ]) + 2)
> pi.tilde2 <- (c.table[2, 1] + 1)/(sum(c.table[2, ]) + 2)
> var.AC <- pi.tilde1 * (1 - pi.tilde1)/(sum(c.table[1, ]) +
  2) + pi.tilde2 * (1 - pi.tilde2)/(sum(c.table[2, ]) +
  2)
> alpha <- 0.05
> pi.tilde1 - pi.tilde2 + qnorm(p = c(alpha/2, 1 - alpha/2)) *
  sqrt(var.AC)
[1] -0.10353254  0.07781192
```

Example: Larry Bird free throws (Bird.R)

```
> library(PropCIs)
> wald2ci(x1 = c.table[1, 1], n1 = sum(c.table[1, ]), x2 = c.table[2,
  1], n2 = sum(c.table[2, ]), conf.level = 0.95, adjust = "AC")
```

data:

95 percent confidence interval:

-0.10353254 0.07781192

sample estimates:

[1] -0.01286031

- With 95% confidence, the difference in the probability of success on the second attempt is between  $-0.1035$  and  $0.07781$  when the first free throw is made vs. when the first free throw is missed
- Wald:  $-0.1122 < \pi_1 - \pi_2 < 0.0623$ ; use `adjust = "Wald"` with `wald2ci()`
- Could enter values of  $w_1, n_1, w_2, n_2$  directly into R rather than use contingency table structure

Example: Larry Bird free throws (Bird.R)

- What if the data was not already summarized in a contingency table format?

Observation	First	Second
1	Made	Made
2	Missed	Made
3	Made	Made
$\vdots$	$\vdots$	$\vdots$
338	Made	Missed

- Suppose `all.data2` contains this form of the data

```
> bird.table2 <- xtabs(formula = ~first + second, data = all.data2)
> bird.table2
```

```
      second
first  made missed
made   251     34
missed  48      5
```

```
> # table(all.data2$first, all.data2$second) #This also works
```

- Proceed with using `bird.table2` object in place of `c.table`

- Meaning of  $\pi_1 - \pi_2$  changes depending on the sizes of these probabilities
  - Two examples:
    - ①  $\pi_1 = 0.51$  and  $\pi_2 = 0.50$
    - ②  $\pi_1 = 0.011$  and  $\pi_2 = 0.001$
  - Both have  $\pi_1 - \pi_2 = 0.01$ , but
    - ① Difference is small relative to size of probabilities
    - ② Difference is large relative to size of probabilities
- Relative risk
  - $RR = \pi_1 / \pi_2$ 
    - ①  $RR = 0.51 / 0.50 = 1.02$  — ~~Group 1 is 1.02 times as likely as group 2~~
    - ②  $RR = 0.011 / 0.001 = 11.0$  — ~~Group 1 is 11 times as likely as group 2~~
  - Interpretation for 2.:
    - A success is 11 times **as** likely for group 1 than for group 2
    - A success is 10 times **more** likely for group 1 than for group 2
- What if  $RR = 1$ ?



- MLE:  $\widehat{RR} = \hat{\pi}_1 / \hat{\pi}_2$
- Wald confidence interval
  - Normal approximation is better for  $\log(\hat{\pi}_1 / \hat{\pi}_2)$  than for  $\hat{\pi}_1 / \hat{\pi}_2$
  - Estimated variance

$$\widehat{Var}(\log(\hat{\pi}_1 / \hat{\pi}_2)) = \frac{1}{w_1} - \frac{1}{n_1} + \frac{1}{w_2} - \frac{1}{n_2}$$

- Interval for  $\log(RR)$

$$\log(\hat{\pi}_1 / \hat{\pi}_2) \pm Z_{1-\alpha/2} \sqrt{\frac{1}{w_1} - \frac{1}{n_1} + \frac{1}{w_2} - \frac{1}{n_2}}$$

- Interval for  $RR$

$$\exp \left[ \log(\hat{\pi}_1 / \hat{\pi}_2) \pm Z_{1-\alpha/2} \sqrt{\frac{1}{w_1} - \frac{1}{n_1} + \frac{1}{w_2} - \frac{1}{n_2}} \right]$$

- What if  $w_1$  or  $w_2 = 0$ ? Possible ad-hoc solutions:
  - Add 0.5 to the count
  - Add 0.5 to all counts

Example: HIV vaccine (HIVvaccine.R)

```

> c.table <- array(data = c(51, 74, 8146, 8124), dim = c(2, 2),
  dimnames = list(Trt = c("vaccine", "placebo"), Response = c("HIV",
    "No HIV")))
> c.table

      Response
Trt    HIV No HIV
vaccine  51   8146
placebo  74   8124
> n1 <- sum(c.table[1, ])
> n2 <- sum(c.table[2, ])
> pi.hat1 <- c.table[1, 1]/n1
> pi.hat2 <- c.table[2, 1]/n2
> pi.hat1/pi.hat2
[1] 0.6892733

```

- Article said “cut the risk of becoming infected with HIV by more than 31 percent”

## Example: HIV vaccine (HIVvaccine.R)

```
> alpha <- 0.05
> var.log.RR <- 1/c.table[1, 1] - 1/n1 + 1/c.table[2, 1] - 1/n2
> RR.ci <- exp(log(pi.hat1/pi.hat2) + qnorm(p = c(alpha/2, 1 -
  alpha/2)) * sqrt(var.log.RR))
> round(RR.ci, 2)
[1] 0.48 0.98
> rev(round(1/RR.ci, 2))
[1] 1.02 2.07
```

- With 95% confidence,
  - HIV infection is between 0.48 and 0.98 times as likely for the vaccine group than for the placebo group
  - the probability of HIV infection is between 0.48 and 0.98 times as large for the vaccine group than for the placebo group
  - the vaccine reduces the probability of HIV infection by 2% to 52%
  - HIV infection is between 1.02 to 2.07 times as likely for the placebo group than for the vaccine group
  - HIV infection is between 0.02 to 1.07 times more likely for the placebo group than for the vaccine group
  - the probability of HIV infection is between 0.02 to 1.07 times larger for the placebo group than for the vaccine group

Example: HIV vaccine (HIVvaccine.R)

- The `twoby2()` function from the `Epi` package produces the same calculations

```
> library(package = Epi)
> twoby2(c.table, alpha = 0.05)
2 by 2 table analysis:
```

```
-----
Outcome      : HIV
Comparing    : vaccine vs. placebo
```

	HIV	No HIV	P(HIV)	95% conf. interval
vaccine	51	8146	0.0062	0.0047 0.0082
placebo	74	8124	0.0090	0.0072 0.0113

	95% conf. interval
Relative Risk: 0.6893	0.4831 0.9834
Sample Odds Ratio: 0.6873	0.4805 0.9832
Probability difference: -0.0028	-0.0055 -0.0001

```
Asymptotic P-value: 0.0401
-----
```

- Odds of a success

- Rescaling of the probability of a success
- (probability of a success)/(probability of a failure) =  $\pi/(1 - \pi)$
- If  $\pi = 0.1$ , then *odds* =  $0.1/(1 - 0.1) = 1/9$ 
  - “9-to-1 odds *against*” because the probability of failure is 9 times the probability of success
- Group 1:  $odds_1 = \pi_1/(1 - \pi_1)$
- Group 2:  $odds_2 = \pi_2/(1 - \pi_2)$

- Odds ratio

$$OR = \frac{odds_1}{odds_2} = \frac{\pi_1/(1 - \pi_1)}{\pi_2/(1 - \pi_2)} = \frac{\pi_1(1 - \pi_2)}{\pi_2(1 - \pi_1)}$$

- Interpretation

- The odds of a success are  $OR$  times as large for group 1 than for group 2
- The odds of a success are  $1/OR$  times as large for group 2 than for group 1

- Odds of a **failure**:  $(1 - \pi)/\pi$

- Odds ratio:

$$\frac{(1 - \pi_1)/\pi_1}{(1 - \pi_2)/\pi_2} = \frac{\pi_2(1 - \pi_1)}{\pi_1(1 - \pi_2)} = \frac{1}{OR}$$

- Interpretation:

- The odds of a failure are  $1/OR$  times as large for group 1 than for group 2
- The odds of a failure are  $OR$  times as large as for group 2 than for group 1

- What if  $OR = 1$ ?

- Odds ratio written in terms of expected counts

- Expected number of successes:  $E(W_j) = n_j\pi_j$
- Expected number of failures:  $n_j - E(W_j) = n_j(1 - \pi_j)$
- Odds of a success:

$$\begin{aligned} odds_j &= \pi_j/(1 - \pi_j) \\ &= n_j\pi_j/[n_j(1 - \pi_j)] \\ &= E(W_j)/[n_j - E(W_j)] \end{aligned}$$

- Contingency table

		Response		
		1	2	Total
Group	1	$w_1$	$n_1 - w_1$	$n_1$
	2	$w_2$	$n_2 - w_2$	$n_2$

- MLE:

$$\widehat{OR} = \frac{\hat{\pi}_1(1 - \hat{\pi}_2)}{\hat{\pi}_2(1 - \hat{\pi}_1)} = \frac{(w_1/n_1)[(n_2 - w_2)/n_2]}{(w_2/n_2)[(n_1 - w_1)/n_1]} = \frac{w_1(n_2 - w_2)}{w_2(n_1 - w_1)}$$

- What if a cell count is 0? Possible ad-hoc solutions:

- Add 0.5 to the count
- Add 0.5 to all counts

- Wald confidence interval

- Normal approximation is better for  $\log(\widehat{OR})$  than for  $\widehat{OR}$
- Estimated variance

$$\widehat{Var}(\log(\widehat{OR})) = \frac{1}{w_1} + \frac{1}{n_1 - w_1} + \frac{1}{w_2} + \frac{1}{n_2 - w_2}$$

- Problems when a cell count is 0
- Interval for  $\log(OR)$

$$\log(\widehat{OR}) \pm Z_{1-\alpha/2} \sqrt{\frac{1}{w_1} + \frac{1}{n_1 - w_1} + \frac{1}{w_2} + \frac{1}{n_2 - w_2}}$$

- Interval for  $OR$

$$\exp \left[ \log(\widehat{OR}) \pm Z_{1-\alpha/2} \sqrt{\frac{1}{w_1} + \frac{1}{n_1 - w_1} + \frac{1}{w_2} + \frac{1}{n_2 - w_2}} \right]$$



## Example: HIV vaccine (HIVvaccine.R)

```
> OR.hat <- c.table[1, 1] * c.table[2, 2]/(c.table[2, 1] * c.table[1,
  2]) #  $w1*(n2-w2)/(w2*(n1-w1))$ 
> round(OR.hat, 2)
[1] 0.69
> alpha <- 0.05
> var.log.or <- 1/c.table[1, 1] + 1/c.table[1, 2] + 1/c.table[2,
  1] + 1/c.table[2, 2] #  $1/w1 + 1/(n1-w1) + 1/w2 + 1/(n2-w2)$ 
> OR.CI <- exp(log(OR.hat) + qnorm(p = c(alpha/2, 1 - alpha/2)) *
  sqrt(var.log.or))
> round(OR.CI, 2)
[1] 0.48 0.98
> rev(round(1/OR.CI, 2))
[1] 1.02 2.08
```

- With 95% confidence,

- the odds of contracting HIV are between 0.48 and 0.98 times as large for the vaccine group than for the placebo group
- the vaccine reduces the odds of HIV infection by 2% to 52%
- the odds of contracting HIV are between 1.02 and 2.08 times as large for the placebo group than for the vaccine group
- the odds of being HIV free are between 1.02 and 2.08 times as large for the vaccine group than for the placebo group

Example: HIV vaccine (HIVvaccine.R)

- The `twoby2()` function from the `Epi` package produces the same calculations
  - Similar values for the relative risk and odds ratio here
    - $OR = \frac{\pi_1(1-\pi_2)}{\pi_2(1-\pi_1)} = RR\left(\frac{1-\pi_2}{1-\pi_1}\right)$
    - May not occur for other  $2 \times 2$  tables

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- 3 **Conclusion**
  - Objectives
  - Additional material

- Apply appropriate methods to analyze data in a contingency table
- State, interpret, and fit logistic, baseline-category, proportional odds, and Poisson regression models
- Use appropriate variable-selection methods
- Evaluate the fit of categorical regression models
- Identify and solve overdispersion problems
- Be comfortable with using R to analyze categorical data

# Analysis of Categorical Data

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