

Outline

- •What is group testing?
- Homogeneous
 Population
- Heterogeneous
 Population
- Matrix Pooling

binGroup: A Package for Group Testing

Christopher R. Bilder¹ Boan Zhang¹ Frank Schaarschmidt² Joshua M. Tebbs³

¹University of Nebraska-Lincoln ²Leibniz Universität Hannover, Germany ³University of South Carolina

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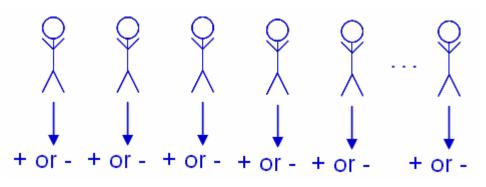


What is group testing?

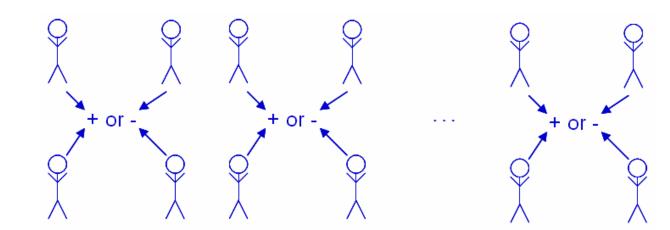
<u>Outline</u>

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- Testing a person for a disease
- Individual testing



- Problem: Cost and Time
- Group testing





What is group testing?

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- •What is group testing?
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- Group testing (continued)
 - Save time and resources
 - Applications in screening blood donations, drug discovery experiments, veterinary and public health studies
 - Estimation
 - Probability of disease
 - Identification
 - Which individuals are positive



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Notation

- Individual responses
 - *Y_{ik}* are independent Bernoulli(*p*) random variables for item *i* in group *k* (*i* = 1, ..., *I_k*, *k* = 1, ..., *K*)
 - Need to estimate $p = P(Y_{ik} = 1)$
 - *p* is the "prevalence in a population"
 - Y_{ik} are unobserved
- Group responses
 - Z_k are independent Bernoulli(θ_k) random variables
 - $\theta_k = P(Z_k = 1)$
 - $\theta_k = 1 (1 p)^{I_k}$



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Estimate p

Likelihood function

$$L(p) = \prod_{k=1}^{K} \theta_{k}^{z_{k}} (1 - \theta_{k})^{1-z_{k}} = \prod_{k=1}^{K} \left[1 - (1 - p)^{I_{k}} \right]^{z_{k}} (1 - p)^{I_{k}(1-z_{k})}$$

- Common group size *I*
 - MLE for $p: \hat{p} = 1 (1 \sum_{k=1}^{K} z_k / K)^{1/2}$
- Unequal group sizes
 - Iterative numerical methods needed



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bgtCI()

- Calculates point estimate and confidence interval for *p*
 - Common group size
- Different types of confidence intervals
- Example (Ornaghi et al., 1999)
 - The purpose is to estimate the probability that female planthopper transfer the MRC virus to maize crops



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• Example (continued)

- 24 plants with 7 planthoppers on each
- 3 plants test positive for the virus
 - > bgtCI(n=24, y=3, s=7, conf.level=0.95,
 - + alternative="two.sided", method="Score")

The 95 percent Score confidence interval is: [0.006325 0.05164] point estimator = 0.0189



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– Find the optimal group size

– Example

estDesign()

> estDesign(n = 24, smax = 100, p.tr = 0.0189)

group size s with minimal mse(p) = 43
\$varp [1] 3.239869e-05
\$mse [1] 3.2808e-05
\$bias [1] 0.0006397784
\$exp [1] 0.01953978

- Other functions include:
 - bgtvs(), bgtTest(), bgtPower(), nDesign(), sDesign()



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 - Need to estimate $p_{ik} = P(Y_{ik} = 1)$
 - Y_{ik} are unobserved
- Group responses
 - Z_k are independent Bernoulli(θ_k) random variables
 - $\theta_k = P(Z_k = 1)$ for group k
 - $\theta_k = 1 \prod_{i=1}^{I_k} (1 p_{ik})$



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- Notation (continued)
 - Covariates
 - $x_{ik1}, x_{ik2}, \dots, x_{ikp}$ for the i^{th} item in the k^{th} group
 - Incorporate factors which influence disease status
- Model: $logit(p_{ik}) = \beta_0 + \beta_1 x_{ik1} + \dots + \beta_p x_{ikp}$
- Estimation of $\beta_0, \beta_1, \beta_2, ..., \beta_p$
 - Note that Y_{ik} are not directly observed
 - Vansteelandt et al. (Biometrics, 2000)
 - Likelihood function is written in terms of the Z_k $L = \prod_{k=1}^{K} \theta_k^{z_k} (1 - \theta_k)^{1 - z_k}$ $= \prod_{k=1}^{K} \left[1 - \prod_{i=1}^{I_k} (1 - p_{ik}) \right]^{z_k} \left[\prod_{i=1}^{I_k} (1 - p_{ik}) \right]^{1 - z_k}$

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Estimation of β_0 , β_1 , β_2 , ..., β_p (continued): - Xie (*Statistics in Medicine*, 2001)

• Likelihood function is written in terms of the unobserved Y_{ik}

$$L = \prod_{k=1}^{K} \prod_{i=1}^{I_k} p_{ik}^{y_{ik}} (1 - p_{ik})^{1 - y_{ik}}$$

• EM algorithm used

$$E(Y_{ik} \mid Z_k = 1) = rac{p_{ik}}{1 - \prod\limits_{i=1}^{I_k} (1 - p_{ik})}$$
 $E(Y_{ik} \mid Z_k = 0) = 0$



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HIV surveillance (Verstraeten et al., *Tropical Medicine and International Health*, 1998)

AGE	EDUC.	groupres	gnum
21	4	0	1
16	2	0	1
17	1	0	1
17	2	0	1
18	1	0	1
			:
25	2	1	85
29	3	1	85
17	2	1	85
18	2	1	85
18	2	1	85



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Model HIV with two covariates: AGE and EDUC.

- Result is a list that contains a lot of information:

```
> class(fit1)
[1] "qt"
```

```
> names(fit1)
```

- [1] "coefficients"
- [4] "deviance"
- [7] "df.null"
- [10] "residuals"
- [13] "formula"
- [16] "terms"

"hessian" "df.residual" "aic" "z" "method" "fitted.group.values" "null.deviance" "counts" "call" "link"

- Summarize the results:
 - > summary(fit1)



Outline

```
(Continued)
•What is group
testing?
           Call:
Homogeneous
          gtreg(formula = groupres ~ AGE + EDUC., data = hivsurv, groupn
Population
              = qnum, linkf = "logit", method = "Vansteelandt")
Heterogeneous
Deviance Residuals:
Population
               Min 1Q Median 3Q Max
Matrix Pooling
           -1.1868 -0.9376 -0.8197 1.3223 1.6826
           Coefficients:
                         Estimate Std. Error z value Pr(>|z|)
            (Intercept) -2.78115 1.45576 -1.910 0.0561.
                   -0.04921 0.06224 -0.791 0.4292
           AGE
           EDUC. 0.67646 0.40087 1.687 0.0915.
           _ _ _
           Signif. codes: 0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 `' 1
                \hat{p} = \frac{\exp(-2.781 - 0.049age + 0.676educ)}{1 + \exp(-2.781 - 0.049age + 0.676educ)}
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```



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(Continued)

Null deviance: 112.1 on 428 degrees of freedom Residual deviance: 109.3 on 425 degrees of freedom AIC: 115.3

Number of iterations in optim(): 194

- summary.gt(), predict.gt(), residuals.gt()
 - Similar to those method functions for glm class
- sim.g()
 - Simulates data in group testing form

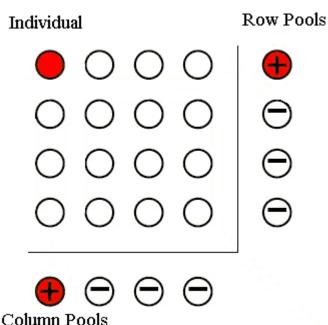


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Regression in the matrix pooling group testing scheme

- Put individual specimens in square arrays and test each row and column pool (Phatarfod and Sudbury, 1994)
- A simple example of 4×4 square array:



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- Regression in the matrix pooling group testing scheme (continued)
 - EM algorithm
 - $E(Y_{ij} | \text{Row and column responses})$ in the E-step cannot be explicitly expressed
 - Gibbs sampling in each E-step, suggested by Xie (*Statistics in Medicine*, 2001)



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- gtreg.mp()
 - Fit the group testing regression model in the matrix pooling setting
 - Individual retests can be included
- A set of method functions available
- Example

```
> head(sal)
```

x col.resp	rour roan	aaln	rour	$\gamma \kappa \kappa \gamma \tau \tau \tau$	ratat
A COLLESD	LOW.LESD	COTI	LOWII	arravii	LELESL

		-	-			-	
1	29.96059	0	0	1	1	1	NA
2	61.28205	0	1	1	2	1	NA
3	34.27341	0	1	1	3	1	NA
4	46.19001	0	0	1	4	1	NA
5	39.43801	0	1	1	5	1	NA
6	45.88038	1	0	2	1	1	NA

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Example (continued) > fit1 <- gtreg.mp(formula =</pre> cbind(col.resp, row.resp) ~ x, data = sa1, coln = coln, rown = rown, arrayn = arrayn, sens = 0.95, spec = 0.95, n.gibbs = 2000, trace = TRUE) beta is -6.4126 0.088847 diff is 0.091304 beta is -6.2670 0.086828 diff is 0.022727 beta is -6.2053 0.085777 diff is 0.012097 beta is -6.2486 0.086816 diff is 0.012102 beta is -6.2398 0.086598 diff is 0.0025023

Number of minutes runing: 1.43

$$\hat{p} = \frac{\exp(-6.2398 + 0.0866x)}{1 + \exp(-6.2398 + 0.0866x)}$$

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