# Group testing with incomplete block designs and imperfect tests

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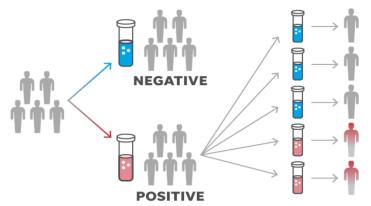
Research is supported by NIH grant R01 Al121351

Joint work with Christopher R. Bilder at University of Nebraska-Lincoln, Joshua M. Tebbs at University of South Carolina, and Christopher S. McMahan at Clemson University

June 10, 2024

# What is Group testing?

- Also known as "pooled testing"
- Screening for infectious diseases



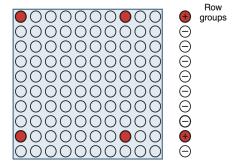
SOURCE USA TODAY research Karl Gelles/USA TODAY

### **Importance**

- Decrease number of tests
  - Increase in testing capacity
  - Works when disease prevalence is low
- A recent instance: COVID-19 pandemic
  - News media outlets: The New York Times, The Washington Post, ABC News, PBS NewsHour, USA Today, ...
  - Over 1 GB of papers published during the first 2 years of the pandemic!
    - Abdalhamid et al. (American Journal of Clinical Pathology, 2020)
    - Hogan et al. (Journal of the American Medical Association, 2020)
    - Lohse et al. (Lancet Infectious Diseases, 2020)
- Widely used elsewhere: Blood donation screening, computer network assessments, ...

### Algorithms

- Hierarchical algorithm
  - Dorfman testing (two stages)
  - Three stages and higher are possible
- Non-hierarchical algorithm
  - Array testing



# Algorithms

- Non-hierarchical algorithm (continued)
  - Incomplete block designs (IBDs)

	Treatments							
Blocks	1	2	3	4	5	6		
1	1	0	1	0	1	0		
2	0	1	0	1	1	0		
3	0	1	1	0	0	1		
4	1	0	0	1	0	1		

Group testing setting

	Specimens							
Groups	1	2	3	4	5	6		
1	1	0	1	0	1	0		
2	0	1	0	1	1	0		
3	0	1	1	0	0	1		
4	1	0	0	1	0	1		

#### Purpose

- Previous work using IBDs
  - Sudbury (Biometrics, 2010) and Eskridge et al. (Biotechnology Progress, 2018)
  - Did not incorporate false positive or false negative
- Our purpose
  - Examine IBDs when false positive or false negative possible
  - Compare with Dorfman testing and array testing
  - Use the expected number of tests as the performance measure

#### M matrix

• Matrix for specimen arrangements

		Specimens							
-	Groups	1	2	3	4	5	6		
M:	1	1	0	1	0	1	0		
	2	0	1	0	1	1	0		
	3	0	1	1	0	0	1		
	4	1	0	0	1	0	1		

• Referred as "M without immediate ambiguity"

#### M matrix

With immediate ambiguity

		Specimens						
	Groups	1	2	3	4	5	6	7
M:	1	1	0	1	0	1	0	1
	2	0	1	1	0	0	1	1
	3	0	1	0	1	1	0	0
	4	1	0	0	1	0	1	0

• Specimens 3 and 7 in same groups

### Comparisons

- Cases of M and other algorithms
  - IBD using restricted M (without ambiguity)
  - IBD using unrestricted M (with or without ambiguity)
  - Dorfman testing
  - Array testing
- Expected number of tests per individual
  - Let T be the number of tests for an initial set of I individuals
    - For Dorfman, stage 1 group size
    - For array, number of individuals in an array
    - For IBD, number of individuals represented by M
  - E(T)/I is the expected number of tests per individual
    - E(T)/I = 1 when testing each individual separately
    - Want E(T)/I < 1 for group testing
    - Example: E(T)/I = 0.25 ...
  - Closed form expressions exist for Dorfman and array testing (Kim et al., *Biometrics*, 2007)

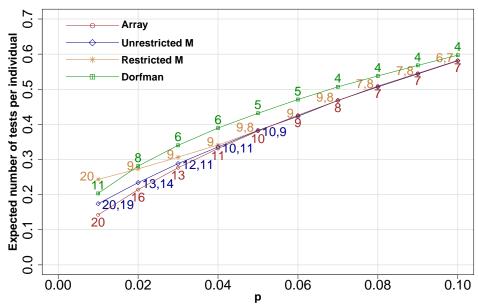
### Comparisons

- A closed form expression for E(T)/I does not exist currently for IBDs
  - Simulate the testing process for an M
  - Use Monte Carlo simulation
  - Repeat this process 10,000 times and observe number of tests each time
  - Estimate E(T)/I
- Best algorithm has the smallest E(T)/I

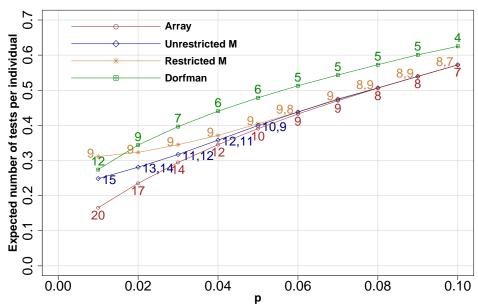
## Steps

- Find optimal testing configuration (OTC) for each algorithm at a prevalence (p)
  - p = 0.01, 0.02, ..., 0.10
  - Pr(False positive) = Pr(False negative) = 0.01, 0.10
  - IBD
    - Number of specimens: 5 60
    - Number of groups: 4 10
    - Number of groups a specimen can be in: 2 4
  - Dorfman testing
    - Group size: 2 100
  - Array testing:
    - Group size: 2 20
- Compare OTCs by expected number of tests per individual

Pr(False positive) = Pr(False negative) = 0.01



Pr(False positive) = Pr(False negative) = 0.10



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