

Information theoretic and algorithmic aspects of binary and quantitative group testing in the sublinear regime

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Joint work with

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and

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Overview

Information-
theory and
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GT and QGT

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Basic setup

Binary group
testing

Quantitative
group testing

- 1 Basic setup
- 2 Binary group testing
- 3 Quantitative group testing

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- **Goal:** Are we able to identify the sick individuals?

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- **Goal:** Are we able to reduce the number of tests?

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- Binary: Is a sick individual contained?
- Quantitative: Number of sick individuals?

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- Options to choose the underlying testing procedure
 - 1 Number of stages
 - 2 Pooling procedure

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- Options to choose the underlying testing procedure
 - 1 Number of stages
 - 2 Pooling procedure
- **To Do:** Rigorous Analysis of the choice

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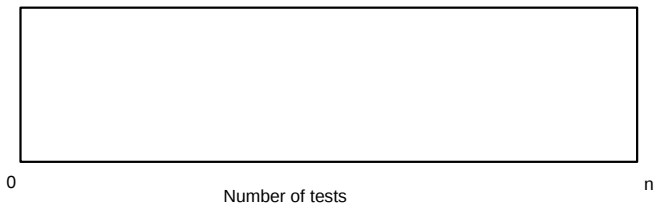
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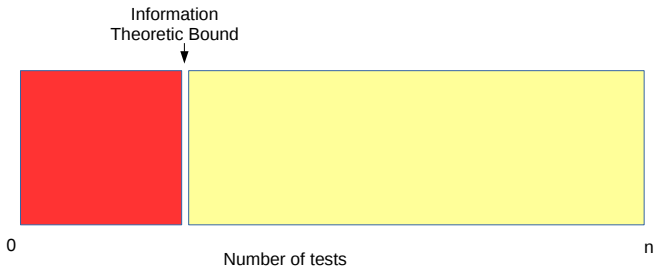
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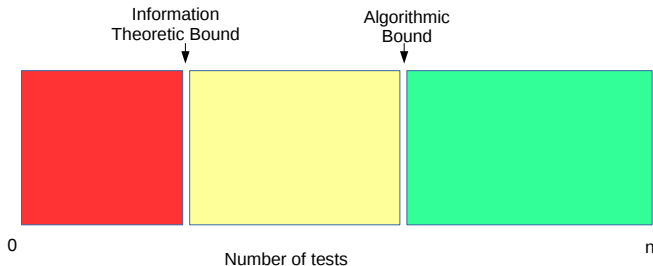
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**Binary group
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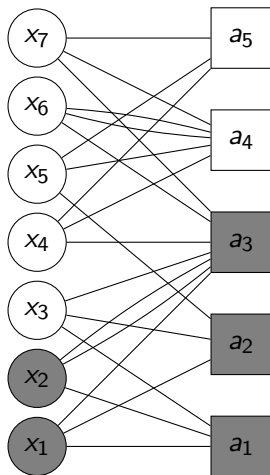
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- Counting Bound implies $m > k \cdot \log_2(n/k)$.

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- Counting Bound implies $m > k \cdot \log_2(n/k)$.
- Baldassini et al: Adaptive testing strategies achieve this bound.

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- Counting Bound implies $m > k \cdot \log_2(n/k)$.
- Baldassini et al: Adaptive testing strategies achieve this bound.
- **Question:** Is non-adaptive group testing able to achieve the bound as well?

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- Assume a constant weight testing scheme

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- Assume a constant weight testing scheme
- The underlying graph structure:

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- Assume a constant weight testing scheme
- The underlying graph structure:
 - Bipartite Factor Graph
 - Fixed variable node degree

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- Assume a constant weight testing scheme
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Theorem 1 [CGHL18]

$$\text{Let } m_{inf} = \frac{n^\theta \log(n)}{\min\{1, \frac{1-\theta}{\theta} \log(2)\} \log(2)}$$

- 1 $m < (1 - \epsilon)m_{inf}$: No algorithm exists to output the right configuration for the constant weight pooling
- 2 $m > (1 + \epsilon)m_{inf}$: There exist an algorithm, which outputs the right configuration w.h.p.

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- Lower Bound: Derive the value m^* , below which infected/uninfected individuals occur that may swap status without harming the test result

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- Lower Bound: Derive the value m^* , below which infected/uninfected individuals occur that may swap status without harming the test result
- Upper Bound: Derive the value m^{**} above which no satisfying assignment beside the original one exists

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- Lower Bound: Derive the value m^* , below which infected/uninfected individuals occur that may swap status without harming the test result
- Upper Bound: Derive the value m^{**} above which no satisfying assignment beside the original one exists
 - 1 Small overlap argument: Analyse probability that configuration with certain overlap fulfills the test result
 - 2 Large overlap argument: Analyse probability that positive (negative) tests stay positive (negative)

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- Lower Bound: Derive the value m^* , below which infected/uninfected individuals occur that may swap status without harming the test result
- Upper Bound: Derive the value m^{**} above which no satisfying assignment beside the original one exists
 - 1 Small overlap argument: Analyse probability that configuration with certain overlap fulfills the test result
 - 2 Large overlap argument: Analyse probability that positive (negative) tests stay positive (negative)
- m^* , m^{**} set conditions to derive the $m_{inf}(n, \theta)$ as stated

Binary group testing: Algorithmic Aspect

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- Allemann: multi-stage algorithm at the predicted lower bound

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- Allemann: multi-stage algorithm at the predicted lower bound
- Aldridge, Scarlett et. al.: Sub-optimal non-adaptive strategies available

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- Allemann: multi-stage algorithm at the predicted lower bound
- Aldridge, Scarlett et. al.: Sub-optimal non-adaptive strategies available
- Most promising algorithms: SCOMP, Definite Defective

Binary group testing: Algorithmic Aspect

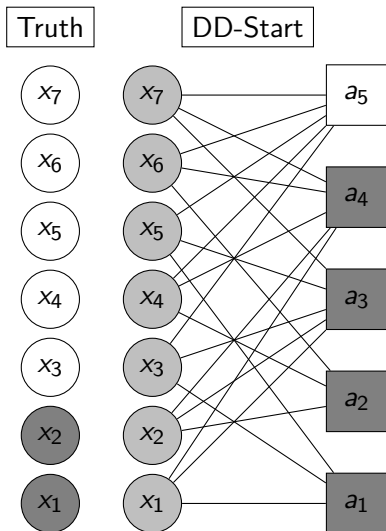
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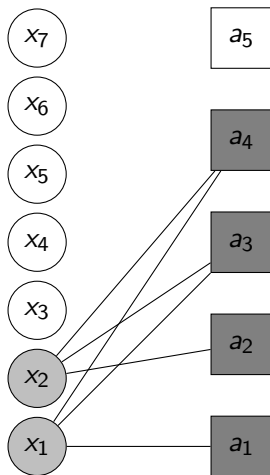
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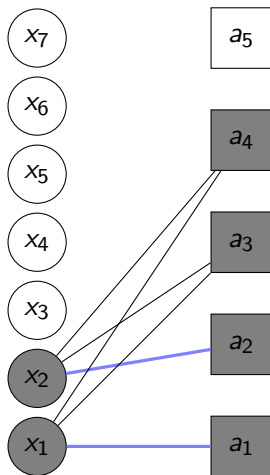
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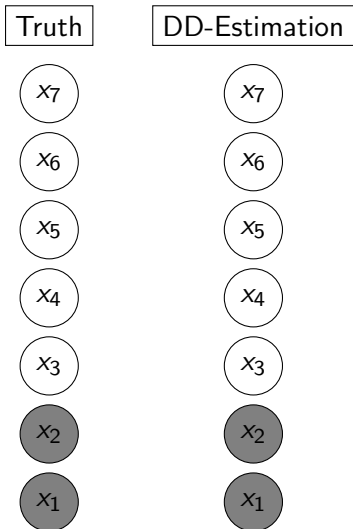
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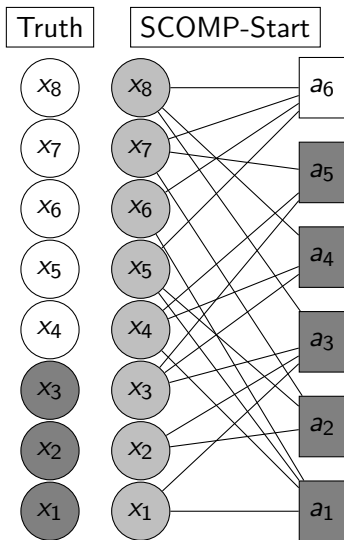
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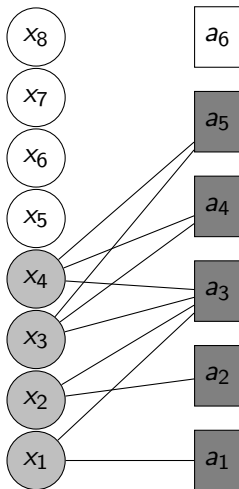
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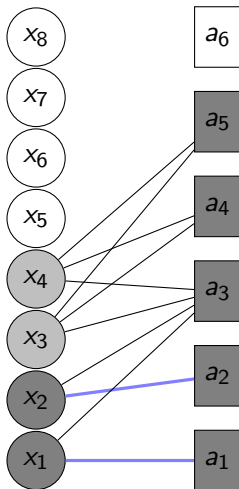
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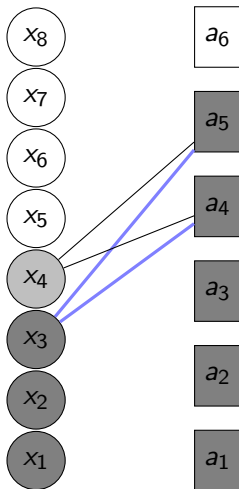
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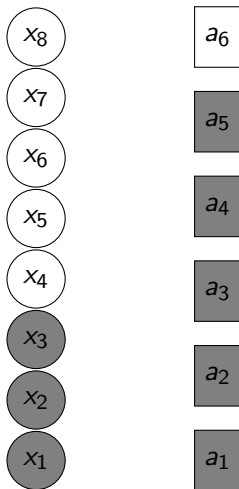
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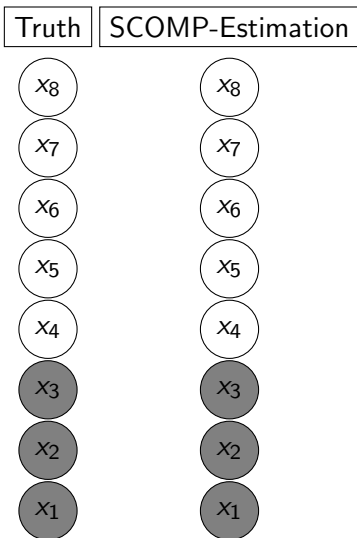
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- **Conjecture:** SCOMP outperforms the Definite Defective

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- **Conjecture:** SCOMP outperforms the Definite Defective
- We refute the conjecture by showing that the algorithms fail at the same point

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- **Conjecture:** SCOMP outperforms the Definite Defective
- We refute the conjecture by showing that the algorithms fail at the same point

Theorem 2 [CGHL18]

Let $m_{\text{alg}}(n, \theta) = \frac{k \log(n/k)}{\min\{1, \frac{1-\theta}{\theta} \log^2 2\}}$, $0 < \theta < 1$ and $\epsilon > 0$:

For $m < (1 - \epsilon)m_{\text{alg}}(n, \theta)$, both SCOMP and DD fail to output σ w.h.p.

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- DD work iff every infected individual is in at least one test with only uninfected individuals that are themselves in at least one test with only other uninfected individuals
- Additional SCOMP step is a Greedy Vertex Cover
- Show w.h.p.: Local structure of infected/ uninfected individuals in remaining graph look the same
- SCOMP fails in first step w.h.p.

⇒ SCOMP and DD have the same algorithmic threshold

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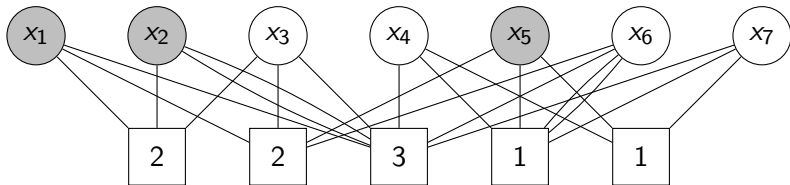
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- Counting bound: $(k + 1)^m \geq \binom{n}{k}$.

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- Counting bound: $(k + 1)^m \geq \binom{n}{k}$.
- Alaoui et. al.: For the linear case Information Theoretic phase transition and efficient algorithm at lower bound established

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- For sub-linear regime: Information Theory not entirely understood (Djackov) and only sub-optimal algorithms available (Karimi et. al.) .

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- Counting bound: $(k + 1)^m \geq \binom{n}{k}$.
- Alaoui et. al.: For the linear case Information Theoretic phase transition and efficient algorithm at lower bound established
- For sub-linear regime: Information Theory not entirely understood (Djackov) and only sub-optimal algorithms available (Karimi et. al.) .
- **Contribution:**
 - 1 Establish sharp phase transition in the sublinear regime (i.e. we show the achievability).
 - 2 Introduce a Greedy Algorithm that outperforms the best known one in certain sparsity levels

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Theorem 3 [GHKL19]

Suppose that $0 < \theta < 1$, $k = n^\theta$ and $\epsilon > 0$ and let

$$m_{inf} = 2 \frac{1 - \theta}{\theta} k$$

- 1 For $m < (1 - \epsilon) m_{inf}(n, \theta)$: No algorithm that outputs σ exists
- 2 For $m > (1 + \epsilon) m_{inf}(n, \theta)$: An algorithm exists that outputs σ with high probability

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- Derive a m^* s.t. for $m > m^*$ no second satisfying assignment exists

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- Derive a m^* s.t. for $m > m^*$ no second satisfying assignment exists
- Analyse it for small and high overlaps

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Basic setup

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- Derive a m^* s.t. for $m > m^*$ no second satisfying assignment exists
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 - 1 Large overlap: Analyse changes via Balls and Bins
 - 2 Small overlap: Analyse changes as returning random walk

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- Derive a m^* s.t. for $m > m^*$ no second satisfying assignment exists
- Analyse it for small and high overlaps
 - 1 Large overlap: Analyse changes via Balls and Bins
 - 2 Small overlap: Analyse changes as returning random walk
- Analysis establishes conditions for m_{inf}

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Maximum-Neighborhood Algorithm [GHKL19]

Input: \mathcal{G}, y, k

Output: Estimation $\tilde{\sigma}$ for $\vec{\sigma}$.

1. For every x_i for $i \in [n]$ calculate $\Psi_i = \sum_{j \in \partial x_i} y_j$
2. Set $\Psi'_i := \Psi_i \cdot \frac{m/2}{\Delta_i}$
3. Order the individuals i in decreasing order due to Ψ'_i
4. Declare the first k ordered individuals as infected, declare the other individuals as healthy

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3. Order the individuals i in decreasing order due to Ψ'_i
4. Declare the first k ordered individuals as infected, declare the other individuals as healthy

Theorem 4 [GHKL19]

Define $m_{MN}(n, \theta) = \frac{1+\sqrt{\theta}}{1-\sqrt{\theta}} k \log(n/k)$. The MN-Algorithm outputs the correct configuration w.h.p. if $m > m_{MN}$

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- Separate the distribution of Ψ_i for uninfected and infected individuals.

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- Separate the distribution of Ψ_i for uninfected and infected individuals.
- Union bound over all k infected and $n - k$ uninfected individuals.

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- Separate the distribution of Ψ_i for uninfected and infected individuals.
- Union bound over all k infected and $n - k$ uninfected individuals.
- Applying the Chernoff Bound and optimizing w.r.t. the separating-parameter gives the (sufficient) condition on m_{MN} .

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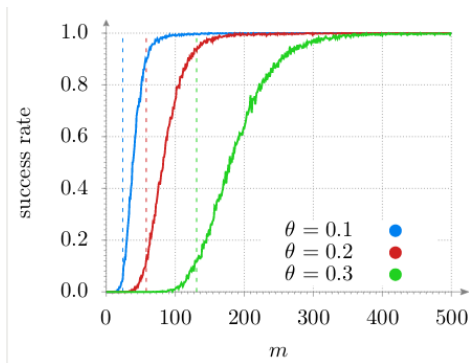
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Recovery success rate

- $n = 1000$ individuals.
- 1000 rounds of simulation.
- Dashed lines: Asymptotic prediction of the required number of tests.

Thank you for your attention