

Sequential (Interactive) Testing in High Dimensions

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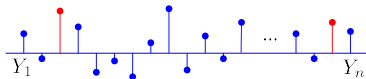
BIRS 2012 - Interactive Information Theory
Joint work with Rob Nowak



Problem Setup

- ▶ Consider a support set $\mathcal{S} \subset \{1, \dots, n\}$ with $|\mathcal{S}| = s \ll n$ and the random variables

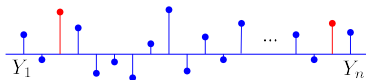
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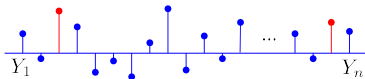
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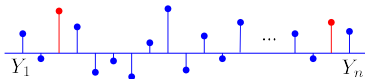
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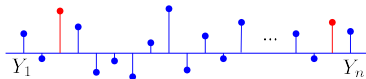
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- ▶ **Definition:** take on average m samples of each index:

$$m := \mathbb{E} \left[\sum_{i=1}^n J_i \right] / n$$

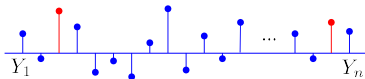
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- ▶ **This talk:** find relationship between (n, s, m) such that $\mathbb{P}(\hat{\mathcal{S}} = \mathcal{S}) \rightarrow 1$.



Related work



A. Wald and J. Wolfowitz

Optimum character of the sequential probability ratio test. 1948. [1-dimensional simple binary hypothesis test](#)



E. Posner

Optimal Search Procedures. 1963. [AWGN, \$s = 1\$, SPRT](#)



J. Haupt, R. Castro, and R. Nowak

Distilled Sensing: Adaptive Sampling for Sparse Detection and Estimation. 2010. [AWGN](#),

$$Y_{i,j} = x_j + \gamma_{i,j}^{-1/2} W_{i,j}, \text{ FDP/NDP}$$



L. Lai, H. Vincent Poor, Y. Xin, and G. Georgiadis

Quickest Search Over Multiple Sequences. Trans. on Info Theory. 2011. [Find one element in \$\mathcal{S}\$](#)



E. Bashan, G. Newstadt, and A. Hero

Two-Stage Multi-Scale Search for Sparse Targets. 2011. [AWGN, two stage procedure](#)



A. Tajer, R. Castro

Adaptive Spectrum Sensing for Agile Cognitive Radios. 2010.

[Spectrum Sensing](#)



Motivation – Gene knock-out studies in biology

fruit fly



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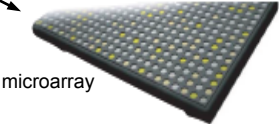
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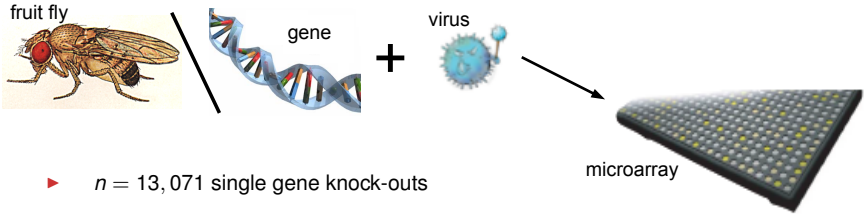
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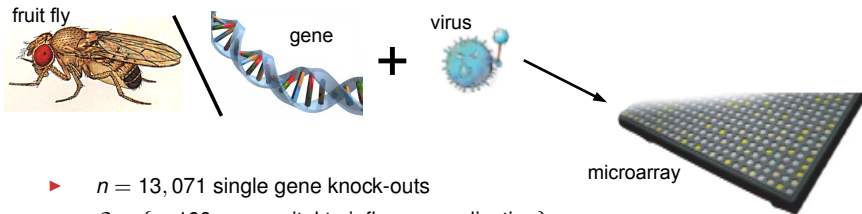
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- ▶ $n = 13,071$ single gene knock-outs



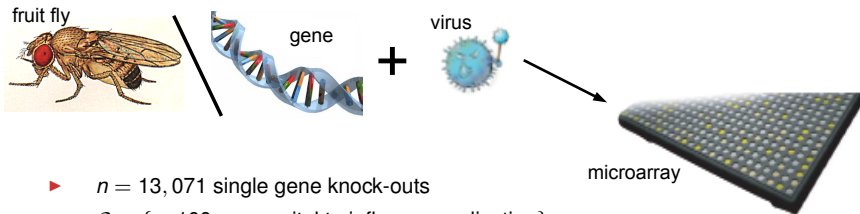
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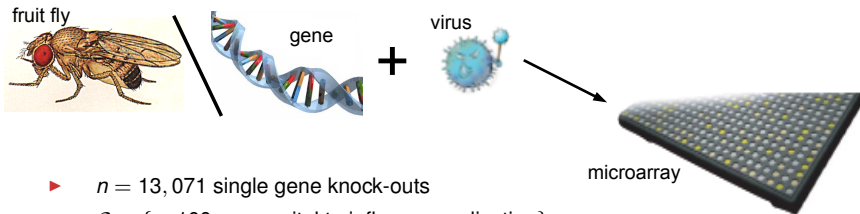
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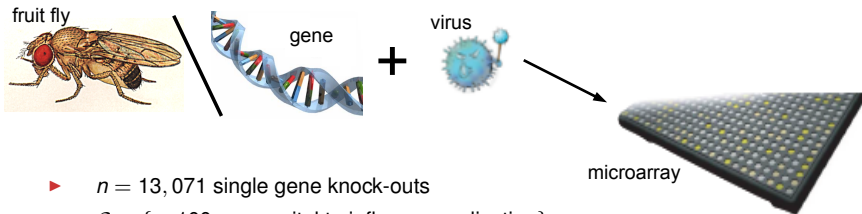


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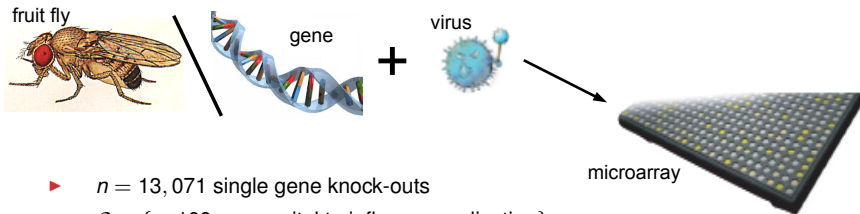
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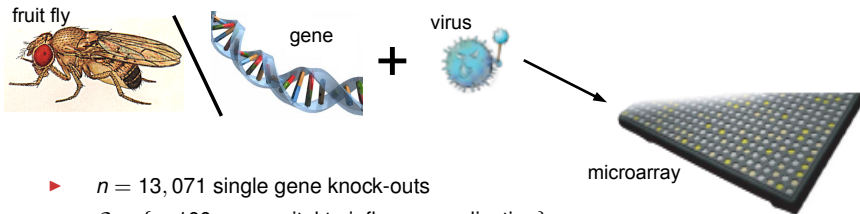
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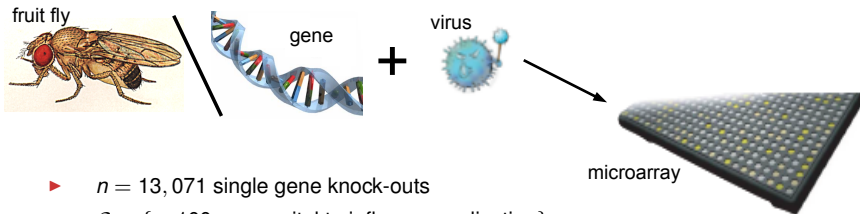
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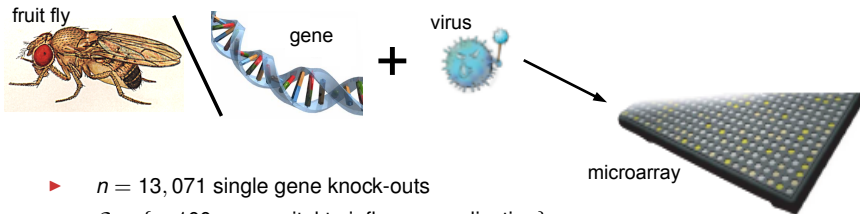
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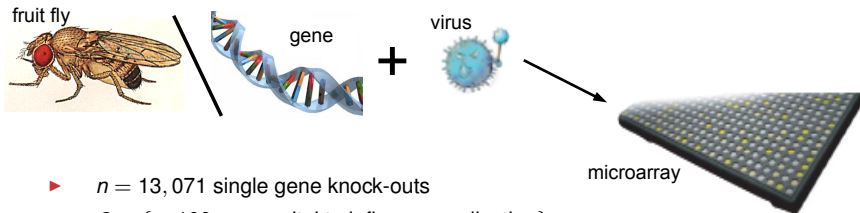
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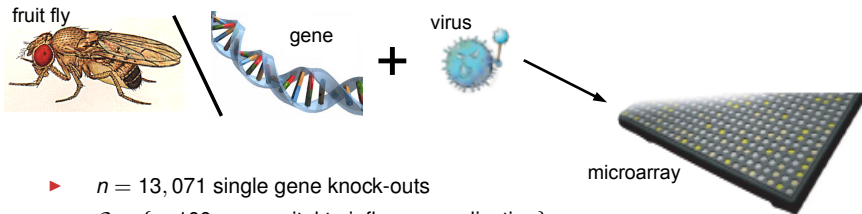
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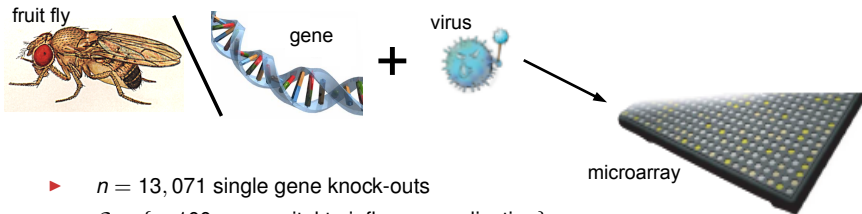
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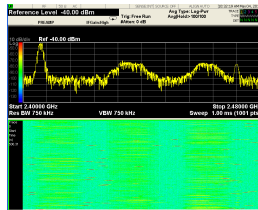
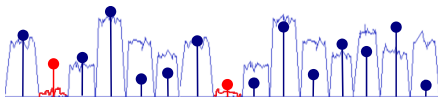
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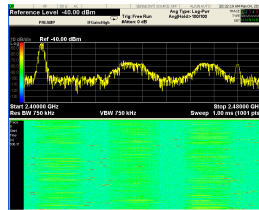
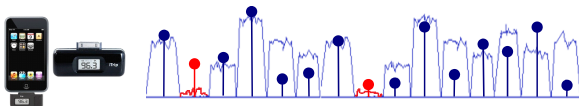
What can we do with limited knowledge of distributions?



Motivation – Spectrum Sensing



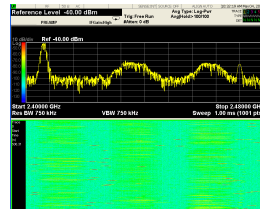
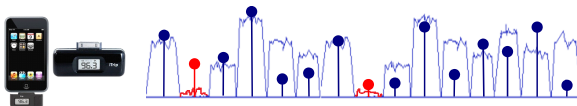
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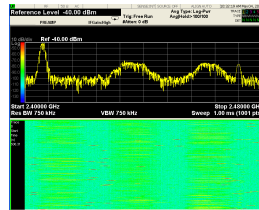
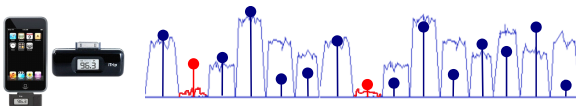
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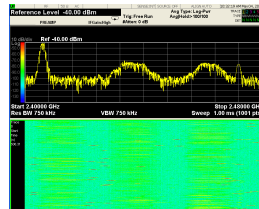
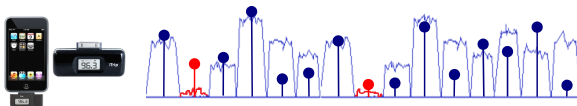
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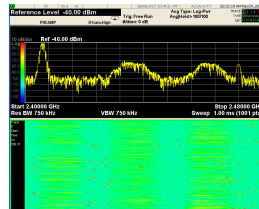
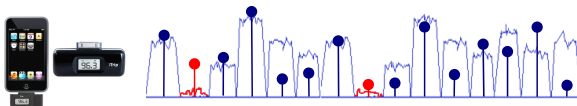


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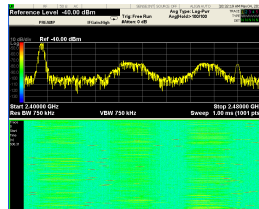
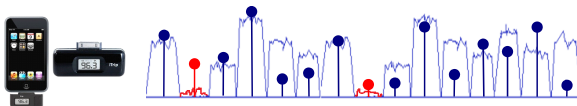
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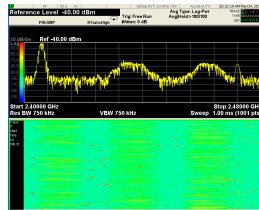
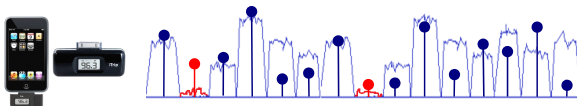
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2. *Sequential*

- ▶ sequential thresholding or coordinate-wise SPRT [A. Tajer 2010, W. Zhang 2010, M. Malloy 2011]



Limitations of non-sequential testing

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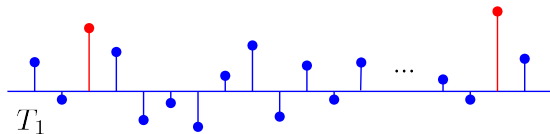
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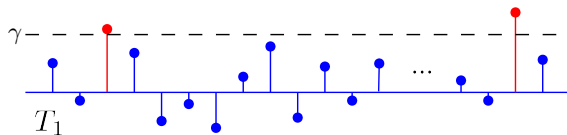
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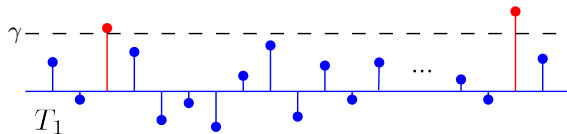
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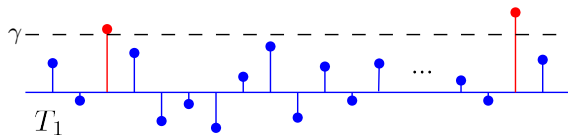


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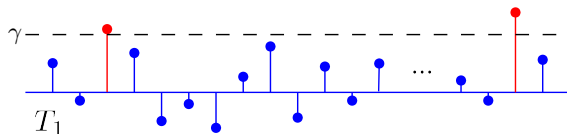


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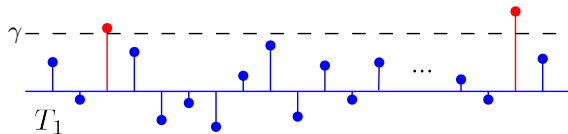
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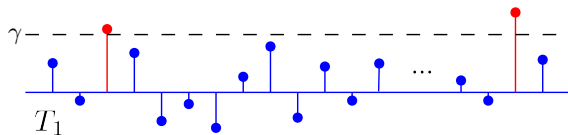
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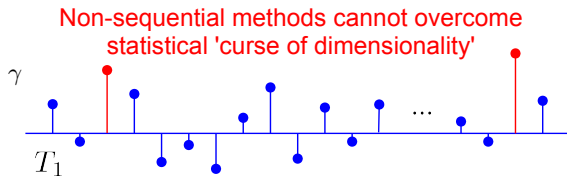
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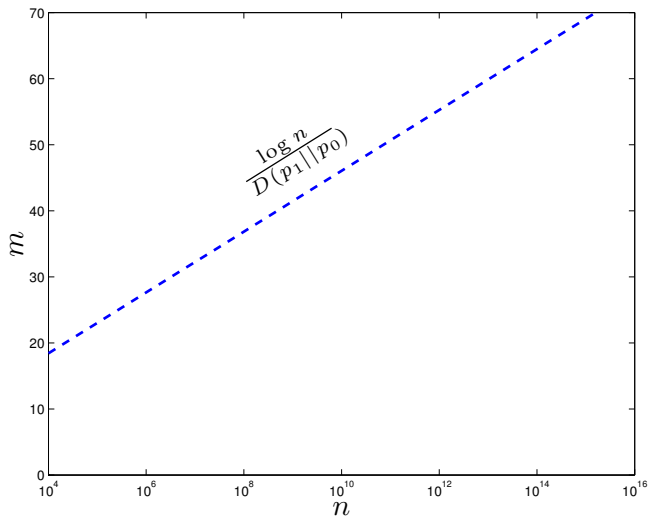
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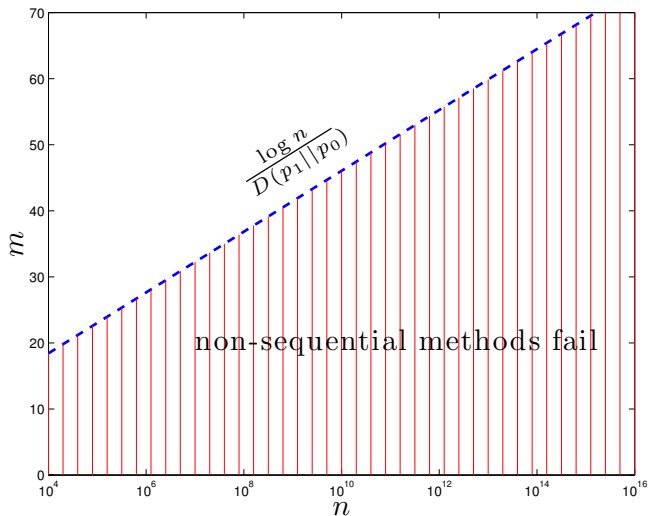
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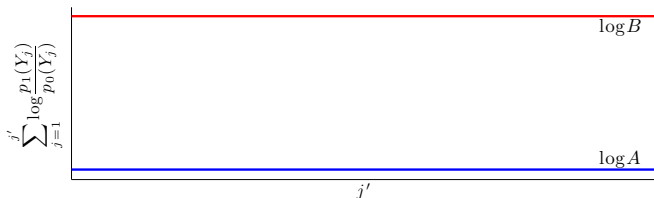


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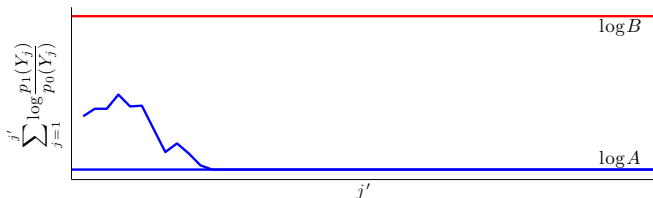


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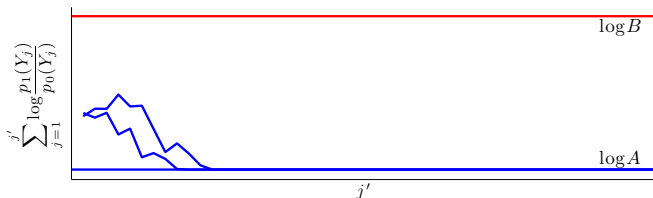


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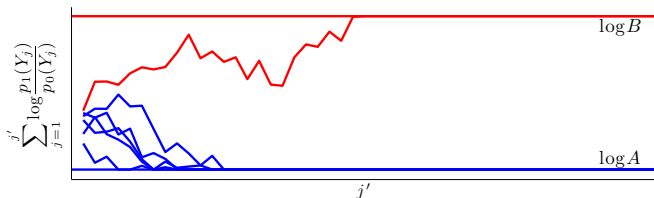


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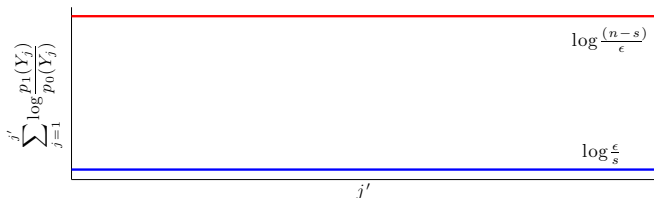


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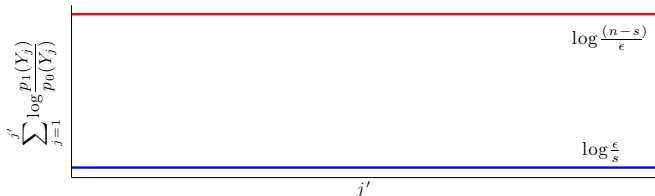


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Set $A = \frac{\epsilon}{2s}$, $B = \frac{2(n-s)}{\epsilon}$. The SPRT recovers S with probability

$$\mathbb{P}(\hat{S} = S) \geq 1 - \epsilon$$

and requires fewer than

$$m \leq (1 + \epsilon_0) \frac{\log s + \log \epsilon^{-1}}{D(P_0 || P_1)}$$

samples per dimension in expectation for any $\epsilon_0 > 0$, n sufficiently large.

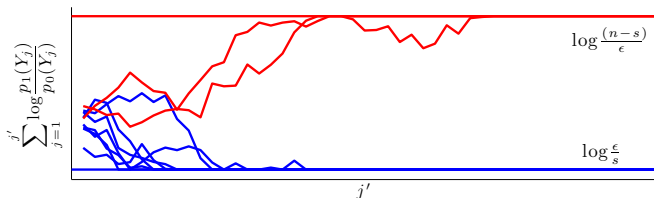


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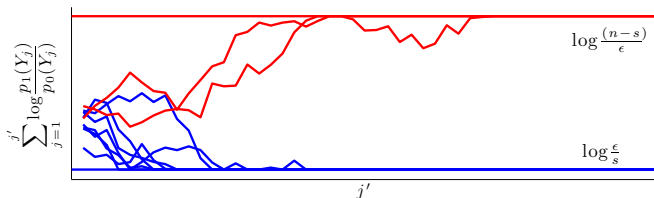


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There exist thresholds A and B such that the SPRT recovers \mathcal{S} exactly if

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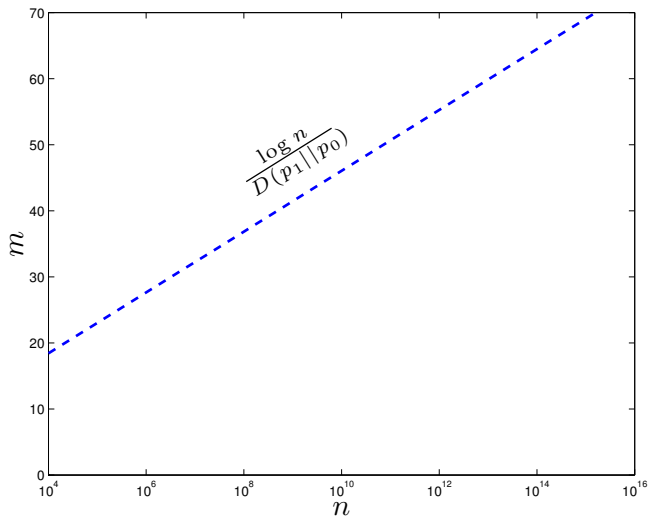
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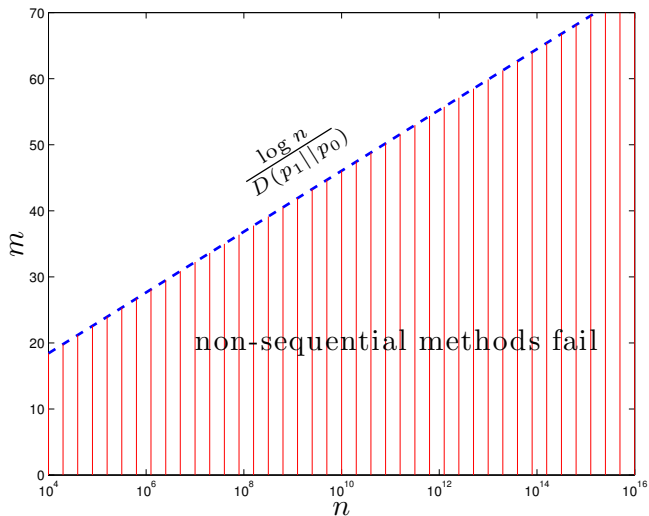
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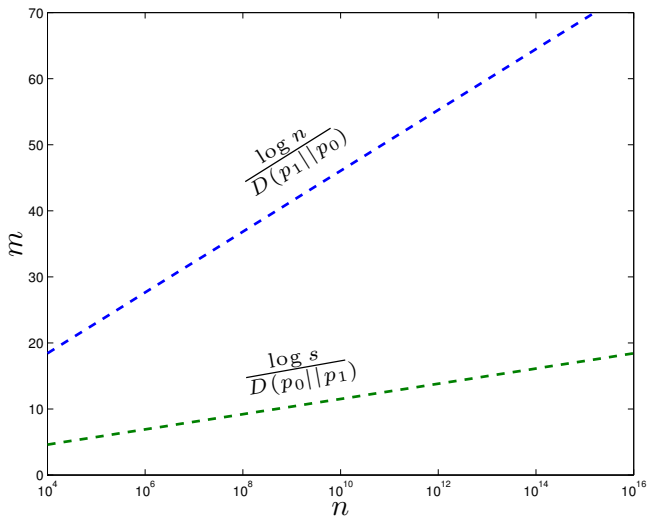
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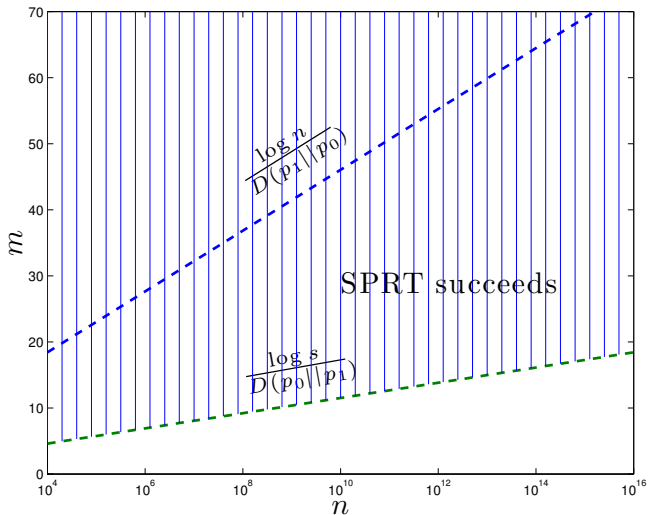
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Sketch of **coordinate-wise** lower bound



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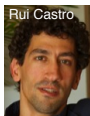
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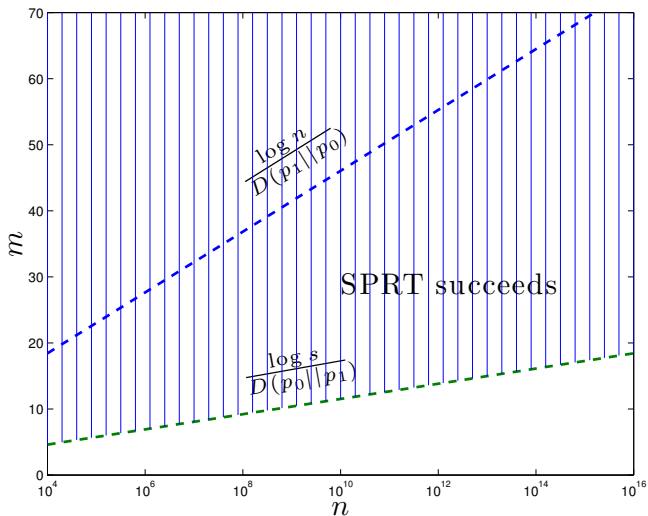
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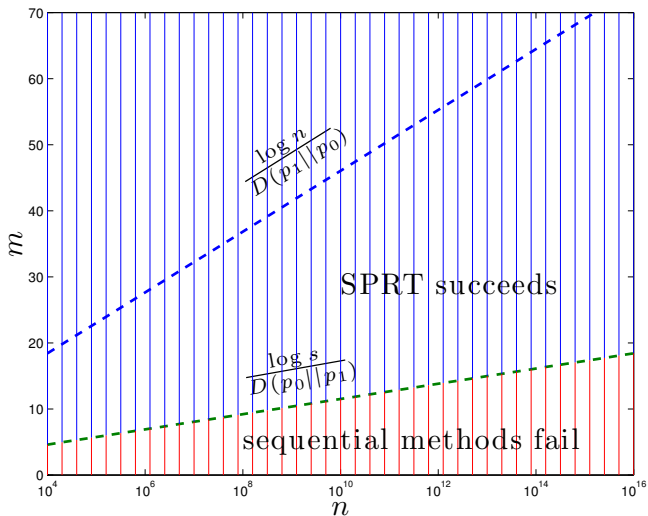
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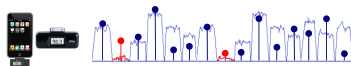
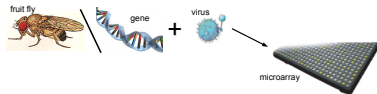
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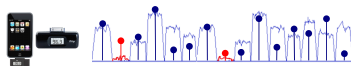
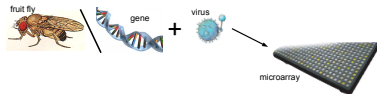
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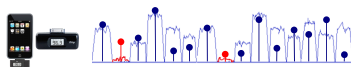
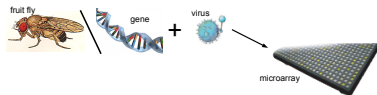
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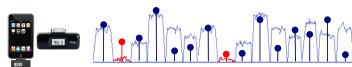
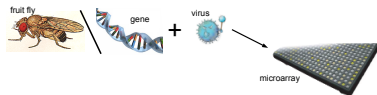
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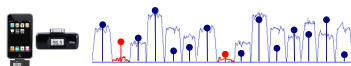
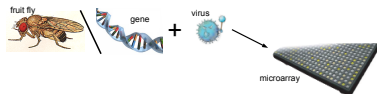
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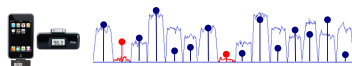
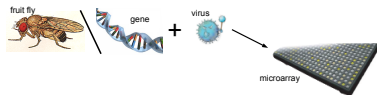
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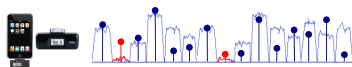
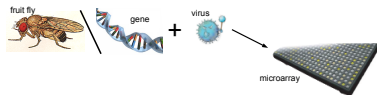
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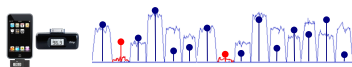
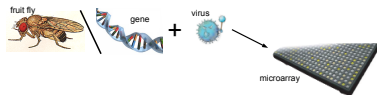
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Sequential Thresholding

Input:

- ▶ $K \approx \log n$ measurement passes
- ▶ threshold $\gamma : \mathbb{P}_0 (T^{(m/2)} \leq \gamma) = \frac{1}{2}$



Sequential Thresholding

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Sequential Thresholding

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- ▶ threshold $\gamma : \mathbb{P}_0 (T^{(m/2)} \leq \gamma) = \frac{1}{2}$ (depends only on P_0)

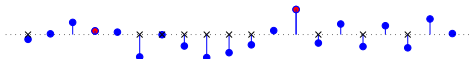


Sequential Thresholding

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- ▶ $K \approx \log n$ measurement passes
- ▶ threshold $\gamma : \mathbb{P}_0 (T^{(m/2)} \leq \gamma) = \frac{1}{2}$

$k = 1$



1) sample each index $\frac{m}{2}$ times

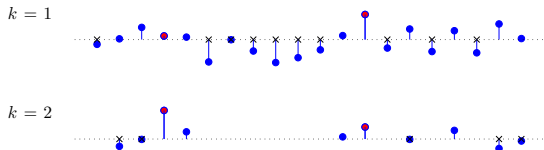
$$\mathbb{E} \left[\sum_{i=1}^n J_i \right] \approx \frac{mn}{2}$$



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1) sample each index $\frac{m}{2}$ times

2) re-measure only indices above threshold

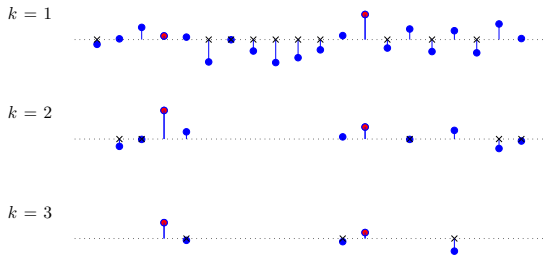
$$\mathbb{E} \left[\sum_{i=1}^n J_i \right] \approx \frac{mn}{2} + \frac{mn}{4}$$



Sequential Thresholding

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1) sample each index $\frac{m}{2}$ times

2) re-measure only indices above threshold

3) repeat

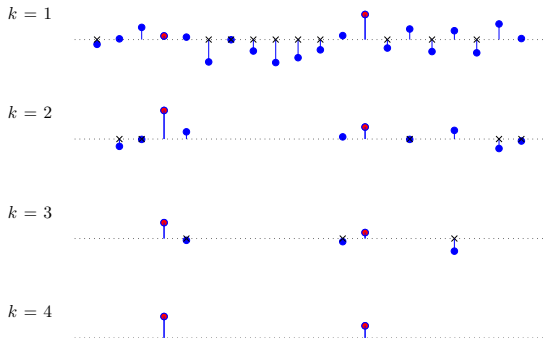
$$\mathbb{E} \left[\sum_{i=1}^n J_i \right] \approx \frac{mn}{2} + \frac{mn}{4} + \frac{mn}{8}$$



Sequential Thresholding

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1) sample each index $\frac{m}{2}$ times

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4) ...

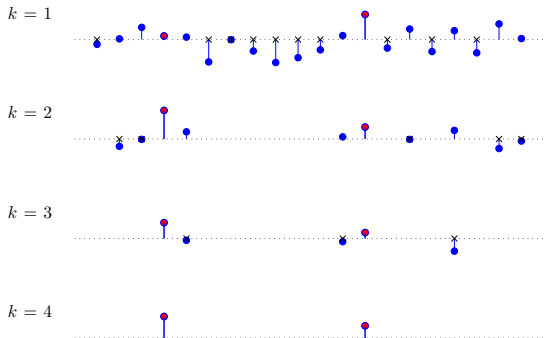
$$\mathbb{E} \left[\sum_{i=1}^n J_i \right] \approx \frac{mn}{2} + \frac{mn}{4} + \frac{mn}{8} + \dots$$



Sequential Thresholding

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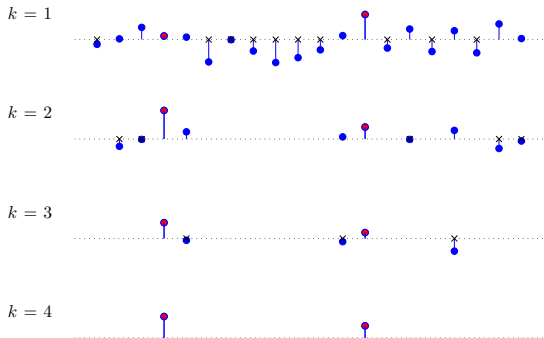
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Sequential Thresholding

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1) sample each index $\frac{m}{2}$ times

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3) repeat

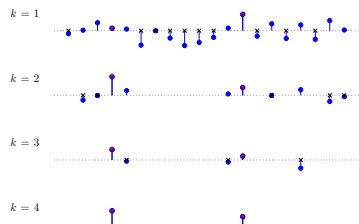
4) ...

$$\mathbb{E} \left[\sum_{i=1}^n J_i \right] \approx \frac{mn}{2} + \frac{mn}{4} + \frac{mn}{8} + \dots \leq mn$$

After $K \approx \log n$ passes, return remaining indices!

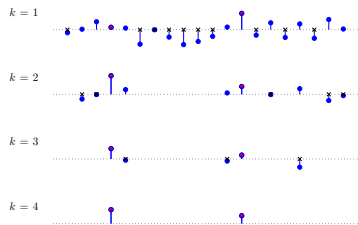


Controlling Family Wise Error Rates



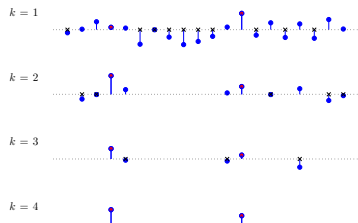
Controlling Family Wise Error Rates

$$\mathbb{P}(\hat{\mathcal{S}} \neq \mathcal{S}) = \mathbb{P}\left(\left\{\bigcup_{i \notin \mathcal{S}} \bigcap_{k=1}^K T_{i,k} \geq \gamma\right\} \cup \left\{\bigcup_{i \in \mathcal{S}} \bigcup_{k=1}^K T_{i,k} \leq \gamma\right\}\right)$$



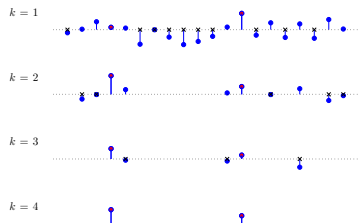
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Controlling Family Wise Error Rates

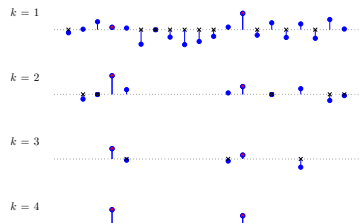
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Controlling Family Wise Error Rates

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provided ...

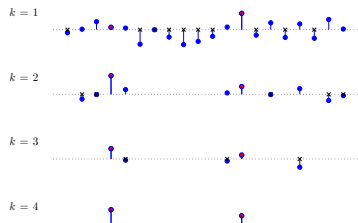


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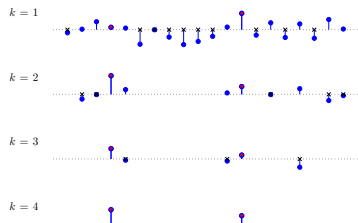


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2. $m > \frac{2 \log(sK)}{D(P_0 \| P_1)}$



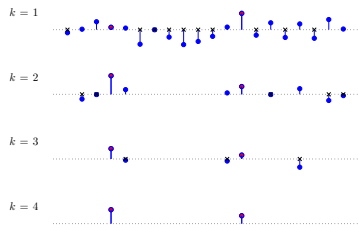
Controlling Family Wise Error Rates

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Controlling Family Wise Error Rates

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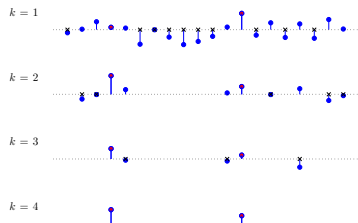
1. $K = (1 + \epsilon) \log n$
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Adjust definition of γ removes 2 . . .

Theorem

Sequential Thresholding succeeds in exactly recovery of \mathcal{S} if

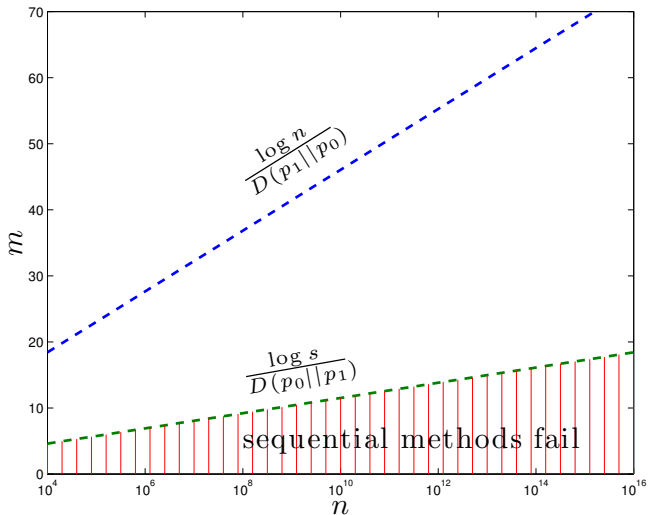
$$m > \frac{\log s}{D(P_0 \| P_1)} + \frac{\log \log n}{D(P_0 \| P_1)}$$



Results

$$s = n^{\frac{1}{4}}$$

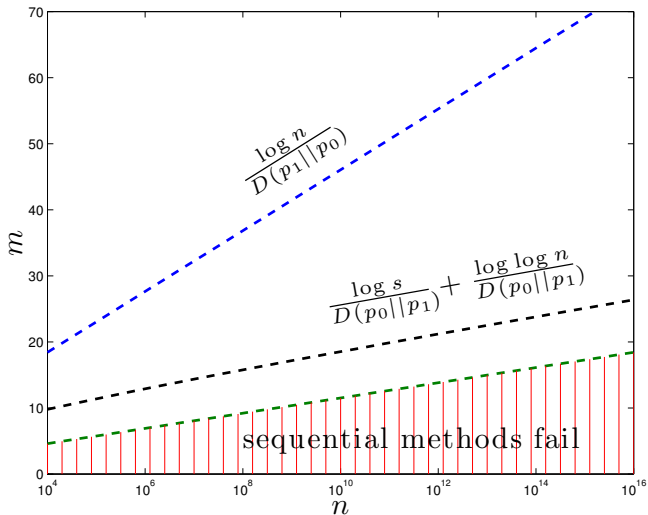
$$D(P_0||P_1) = \frac{1}{2}.$$



Results

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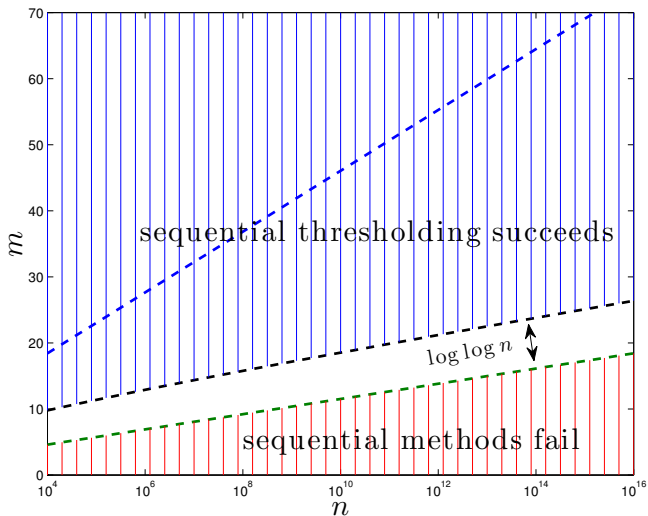
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Results

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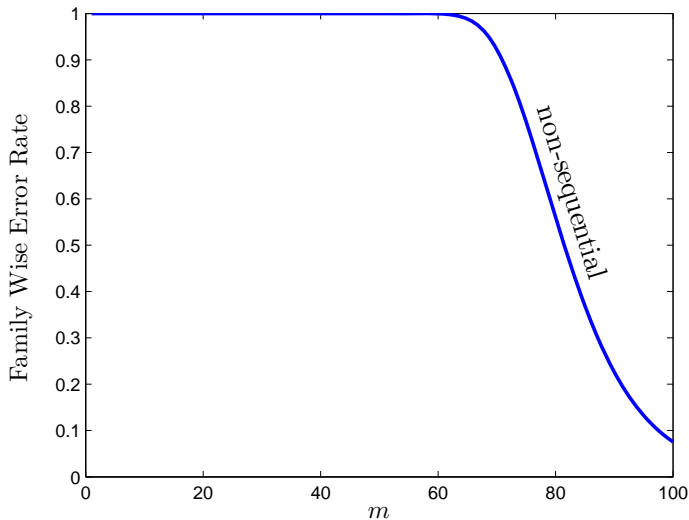


Results

$$n = 10^9$$

$$s = n^{\frac{1}{4}}$$

$$D(P_0 || P_1) = \frac{1}{2}.$$

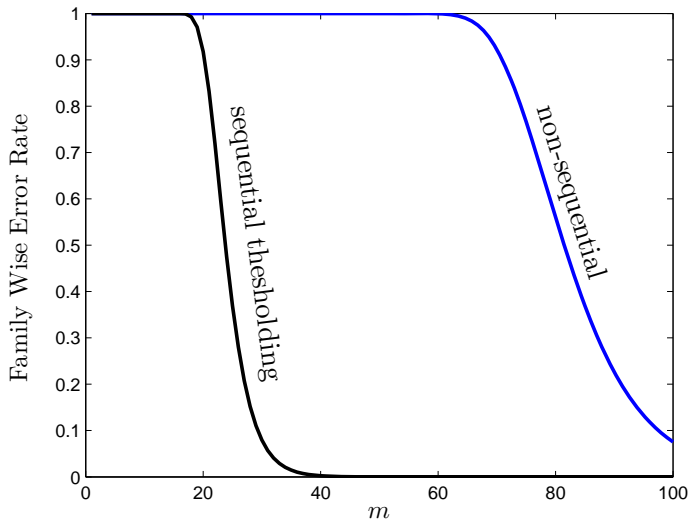


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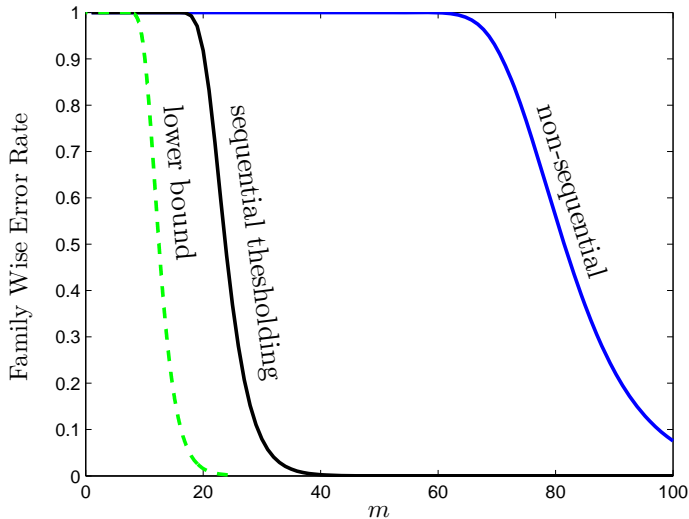


Results

$$n = 10^9$$

$$s = n^{\frac{1}{4}}$$

$$D(P_0 || P_1) = \frac{1}{2}.$$



Conclusion

Remaining questions: can procedures remove doubly logarithmic gap without full knowledge of distributions?

For further reading:



M. Malloy, R. Nowak

Sequential Analysis in High Dimensional Multiple Testing and Sparse Recovery.

ISIT 2011.



M. Malloy, R. Nowak

On the limits of Sequential Testing in High Dimensions.

Asilomar 2011.

