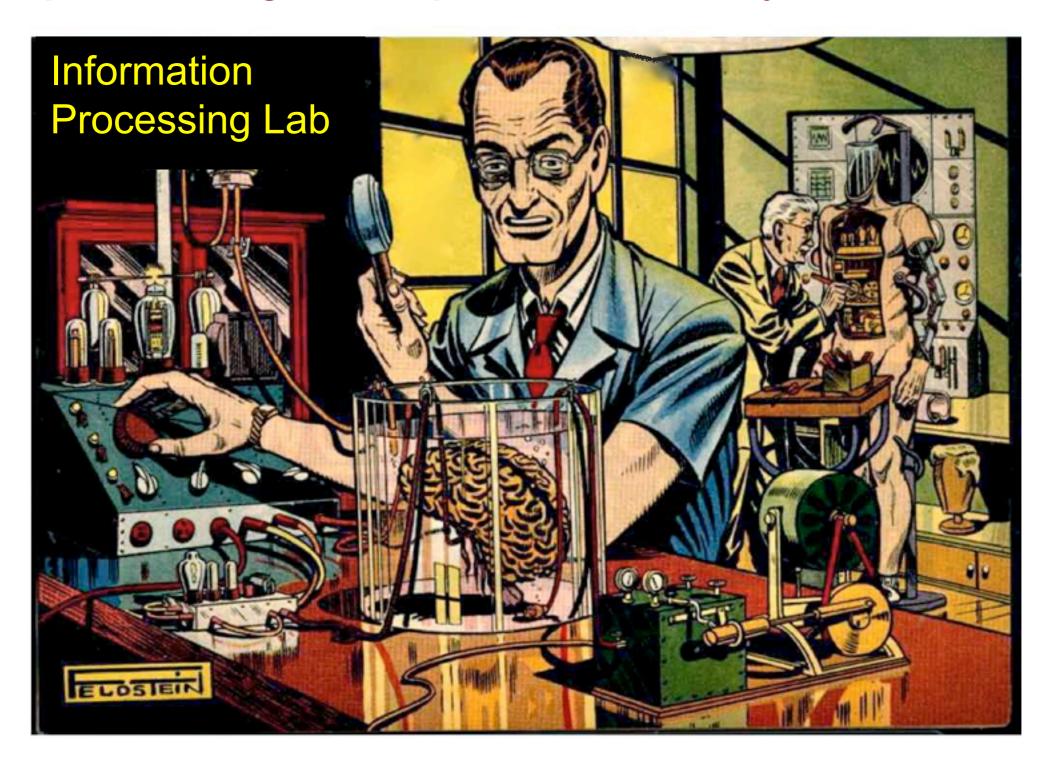
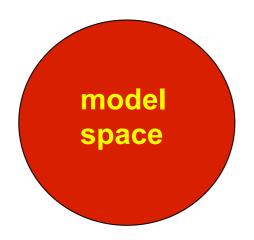
Sequential Analysis in High-Dimensional Multiple Testing and Sparse Recovery

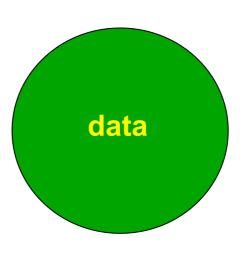


 \mathcal{Y} : possible measurements/experiments

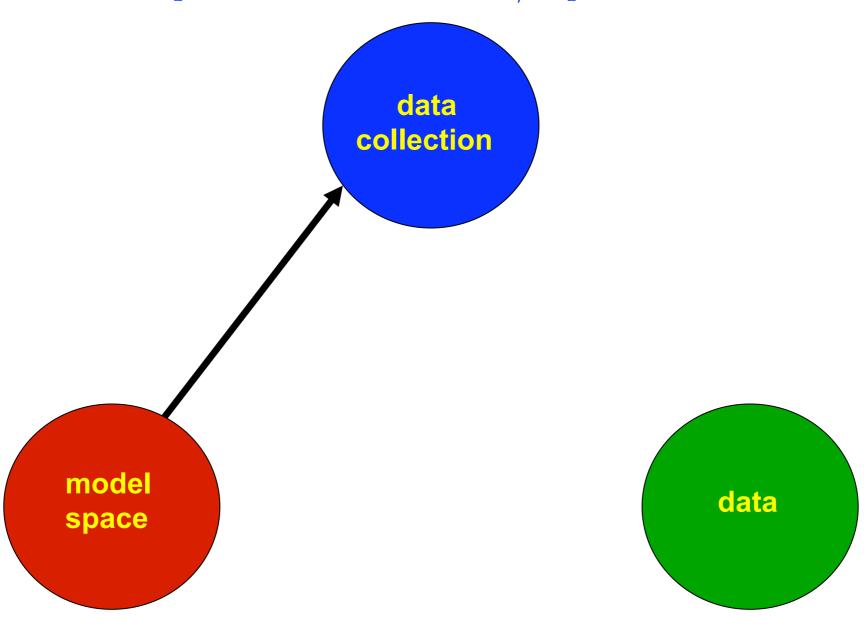




 \mathcal{X} : models/hypotheses under consideration

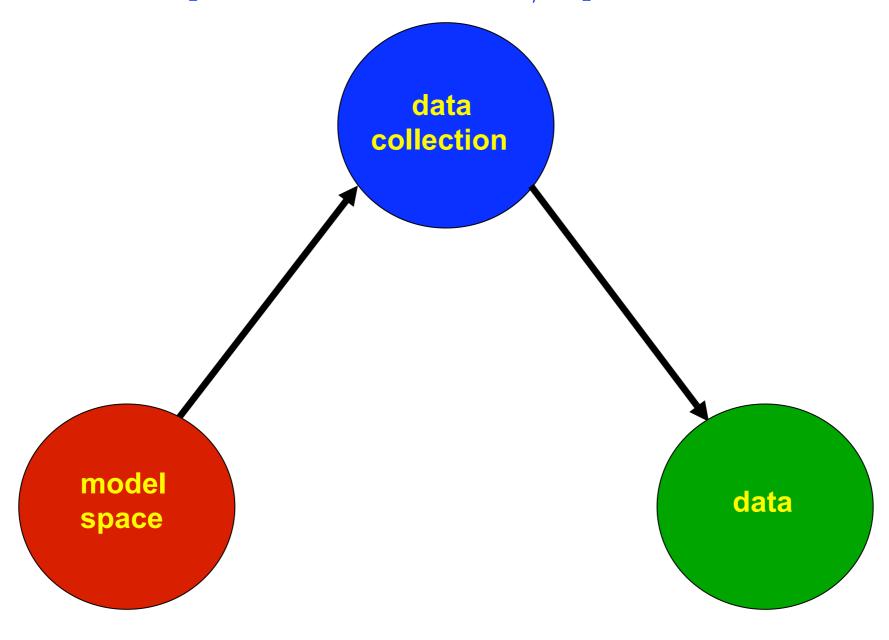


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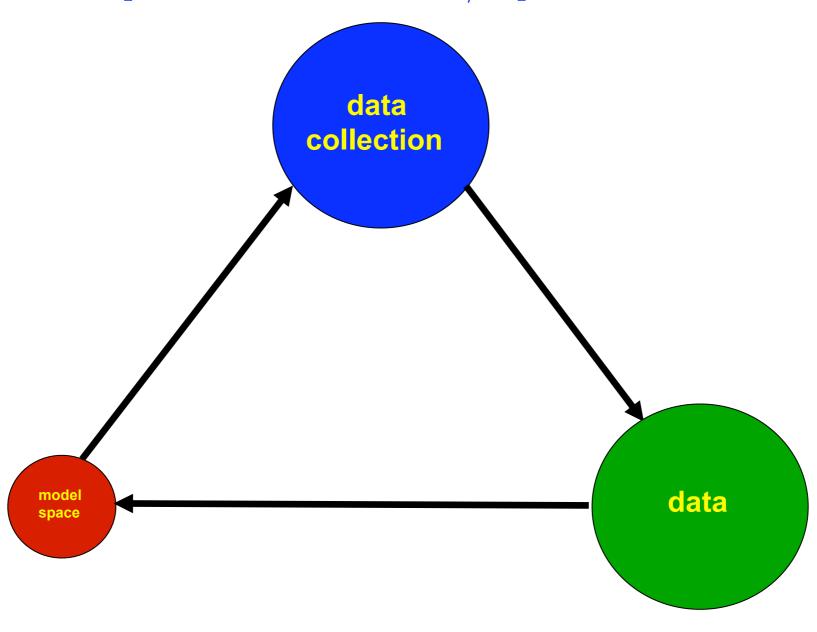
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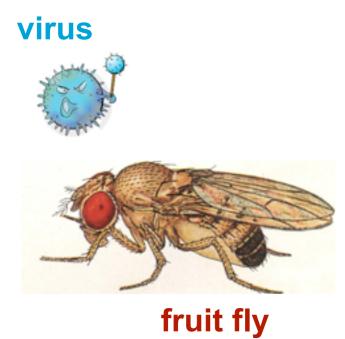
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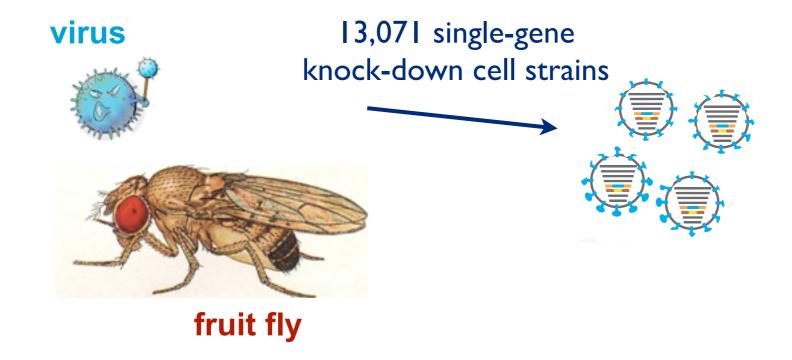


Paul Alhquist (Molecular Virology)



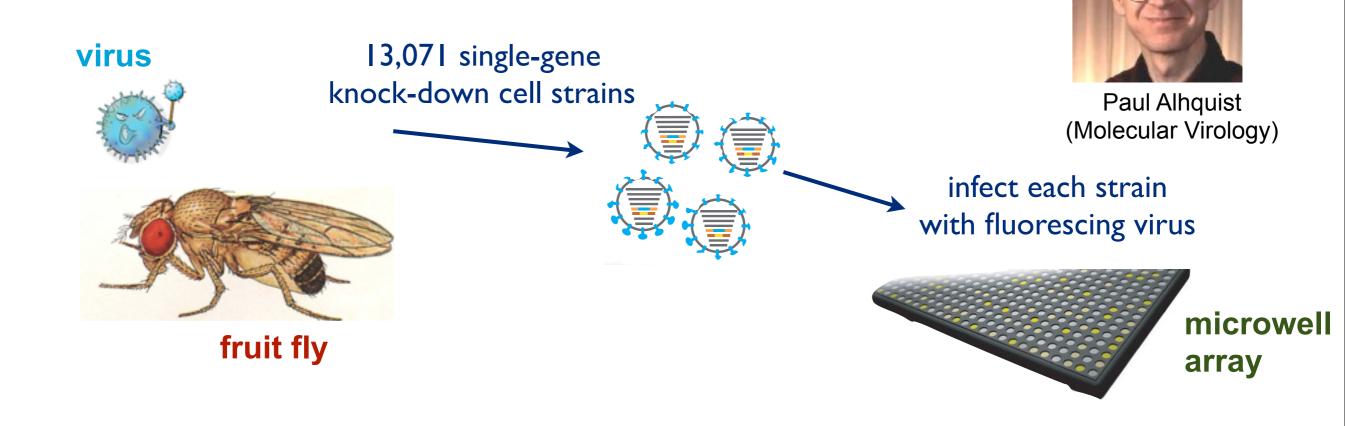


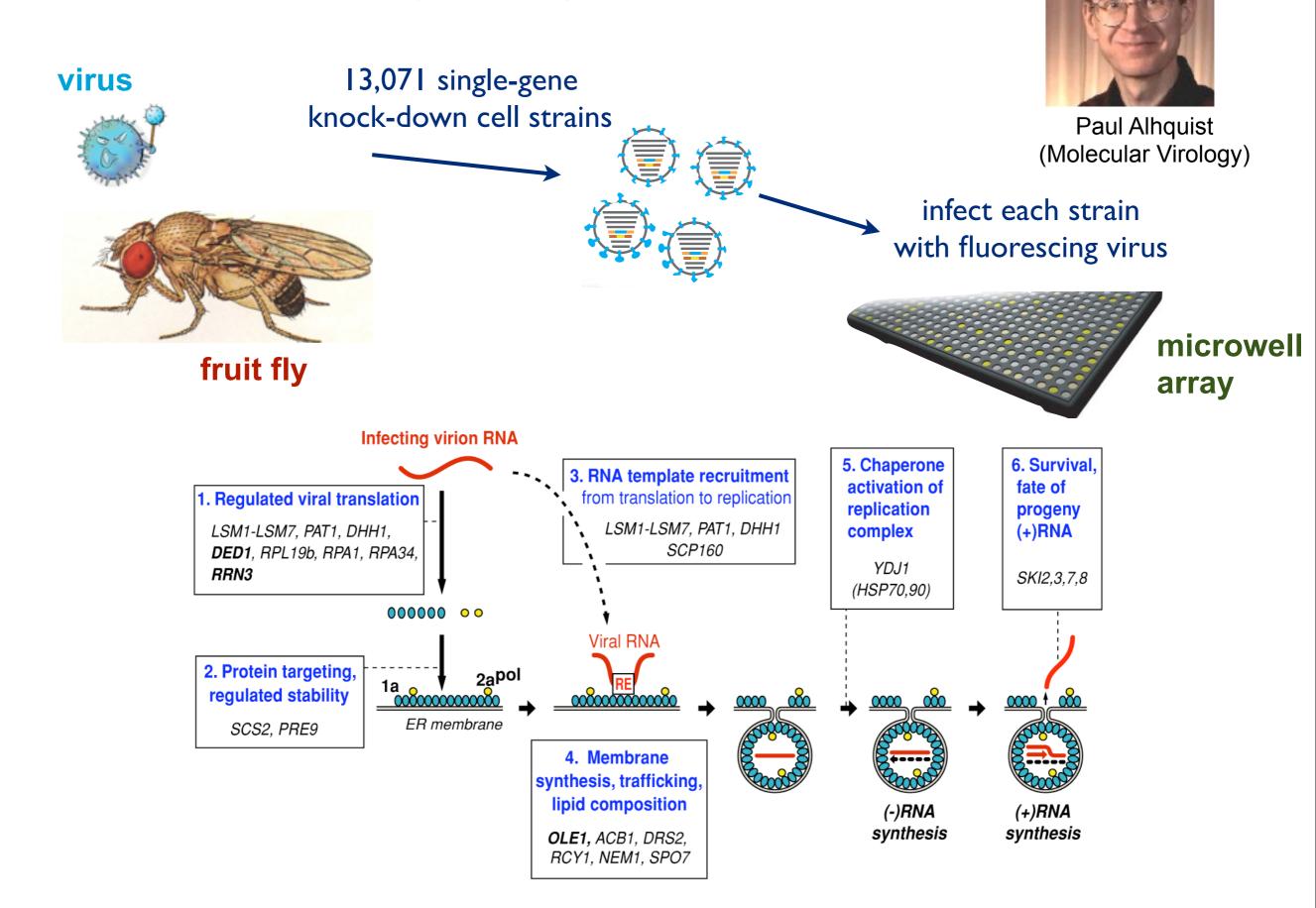
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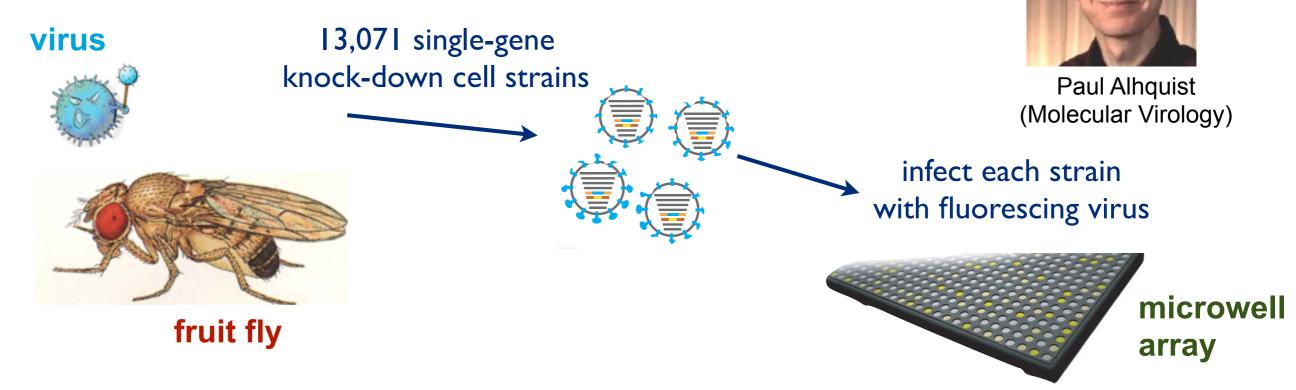




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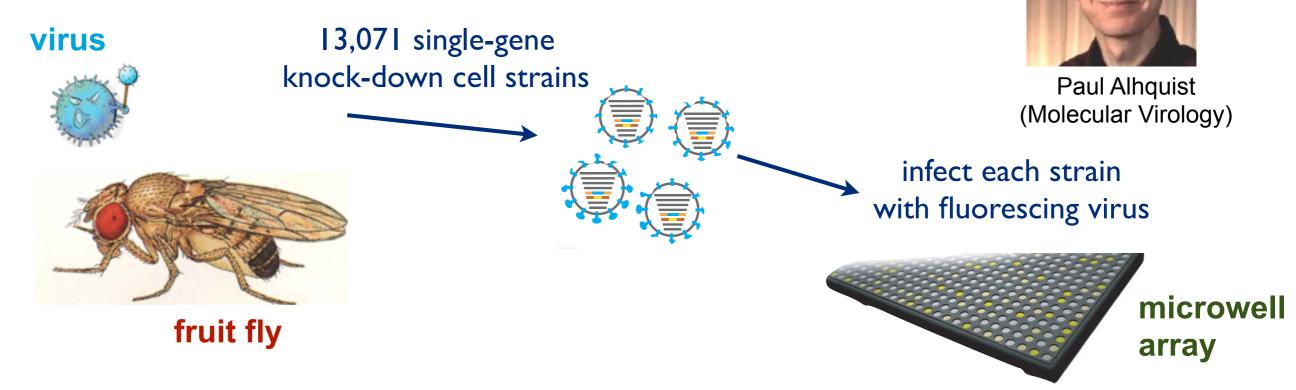






First question: Who are the players in the network?

"Drosophila RNAi screen identifies host genes important for influenza virus replication," Nature 2008. How do they confidently determine the ~100 out of 13K genes hijacked for virus replication from extremely noisy data?



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"Drosophila RNAi screen identifies host genes important for influenza virus replication," Nature 2008. How do they confidently determine the ~100 out of 13K genes hijacked for virus replication from extremely noisy data?

Sequential Experimental Design:

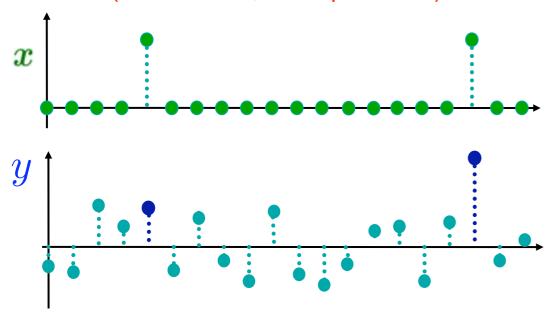
Stage 1: assay all 13K strains, twice; keep all with significant fluorescence in one or both assays for 2nd stage $(13K \rightarrow 1K)$

Stage 2: assay remaining 1K strains, 6-12 times; retain only those with statistically significant fluorescence (1K \rightarrow 100)

vastly more efficient that replicating all 13K experiments many times

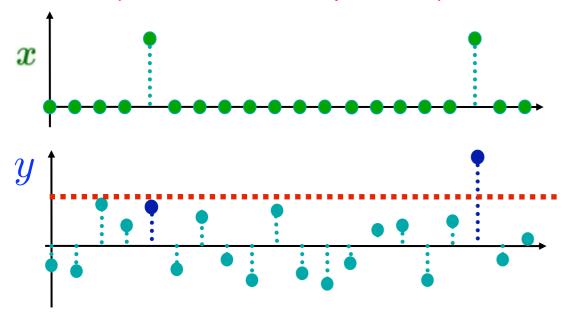
non-sequential design

(n cell strains, 3 samples each)



non-sequential design

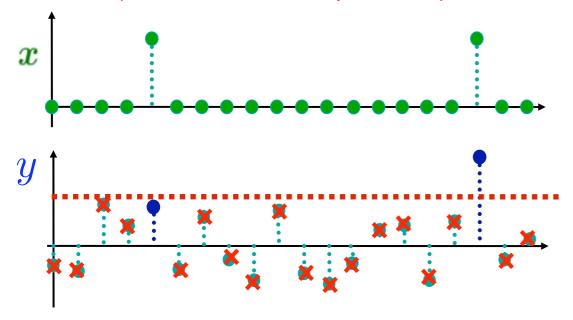
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measure each cell strain with equal precision/SNR, then threshold to control false-positive error

non-sequential design

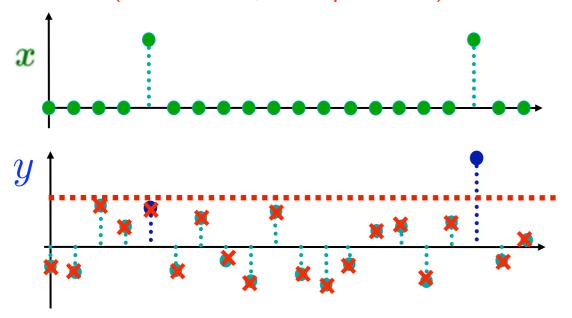
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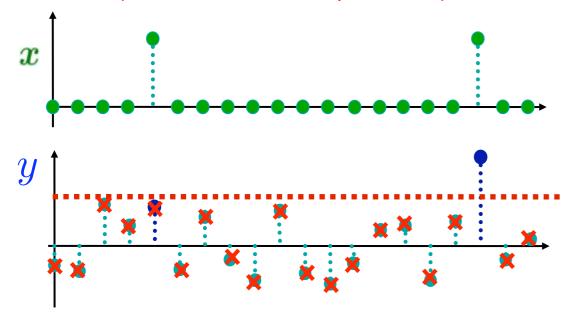


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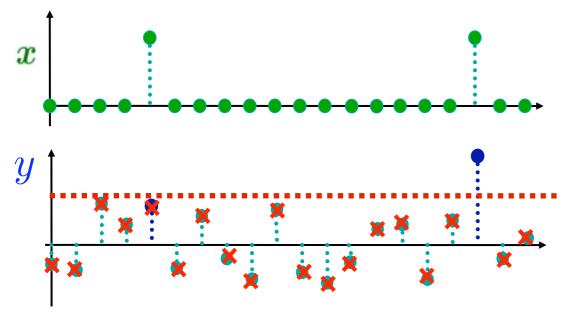
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two-stage design



non-sequential design

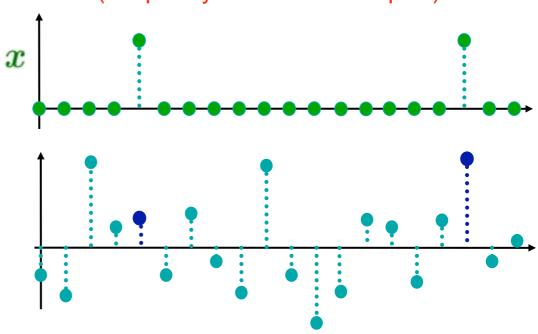
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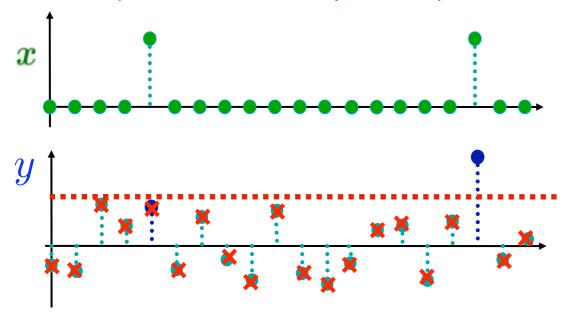
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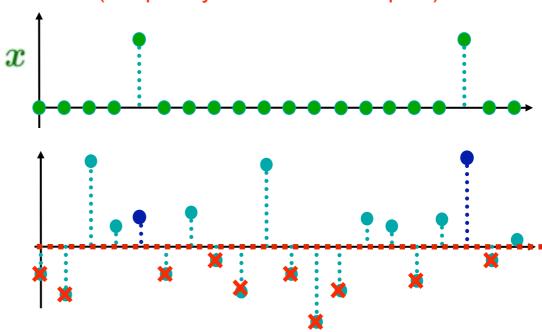
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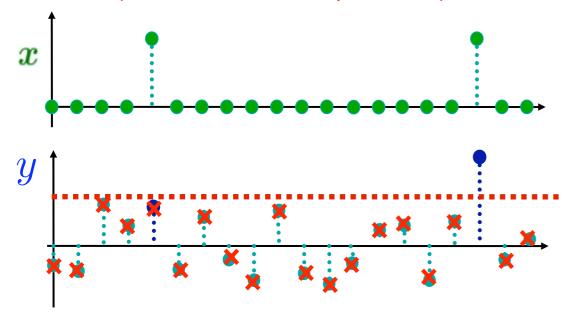
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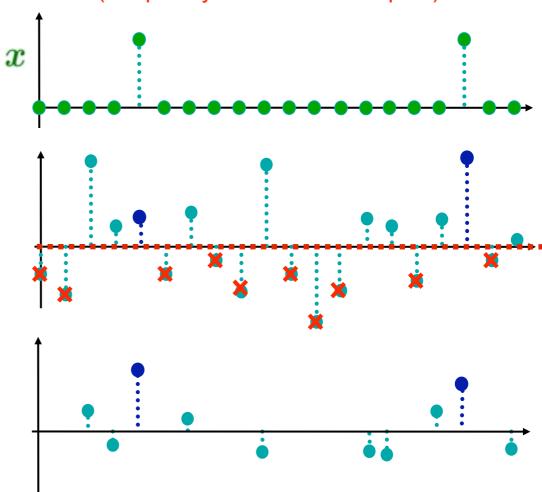
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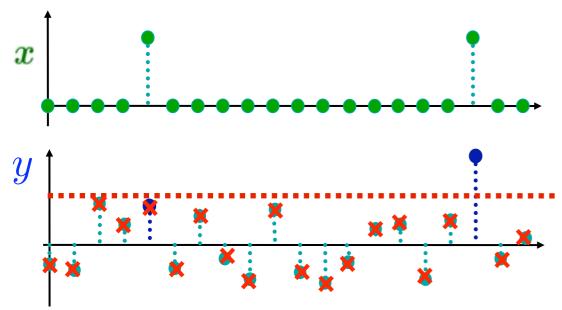
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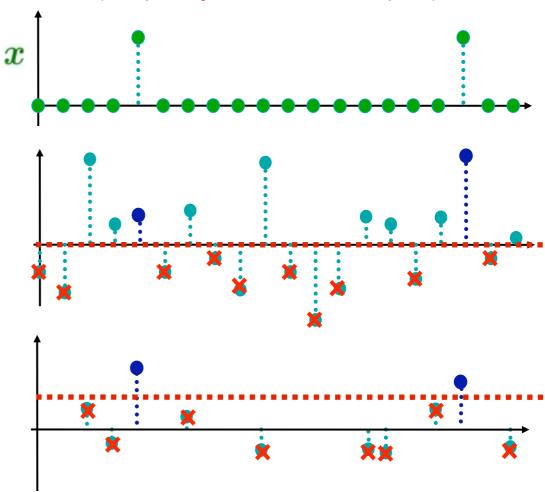


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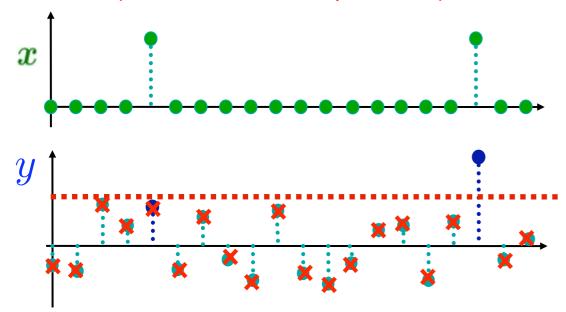
(adaptively allocate 3n samples)



first stage has large false-positive rate, but low false-negative. larger SNR in second stage makes it easier to separate signals from noise.

non-sequential design

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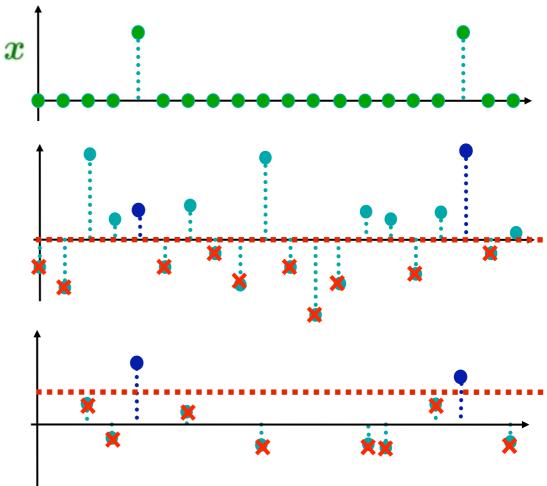


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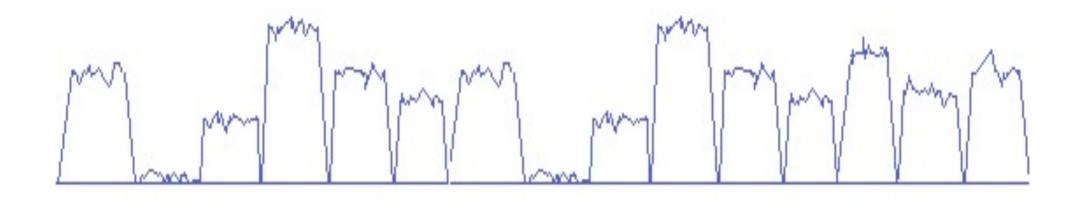




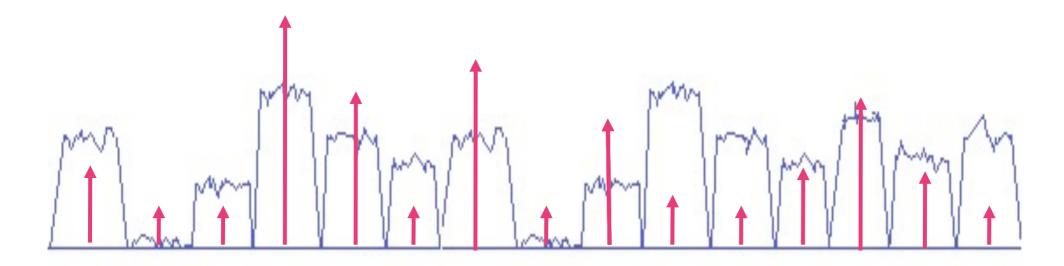
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Under a fixed sensing/experimental budget, does this two-stage design (or some other sequential design) provide better error control than non-sequential design?

"primary" users have preference over "secondary" users

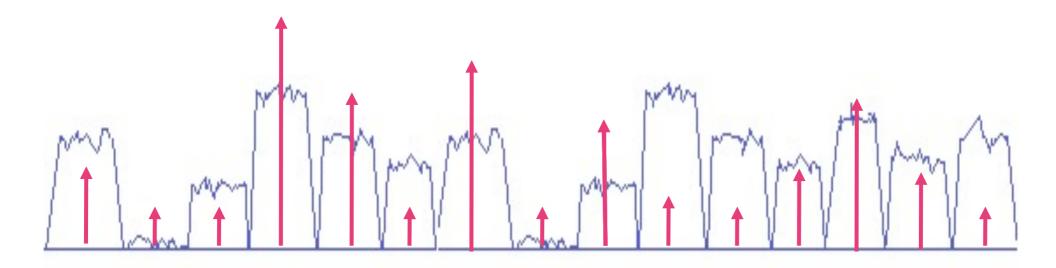


"primary" users have preference over "secondary" users



most channels occupied by primary users, but they come and go in unpredictable manner. Secondary users "sense" spectrum to find an unoccupied channel

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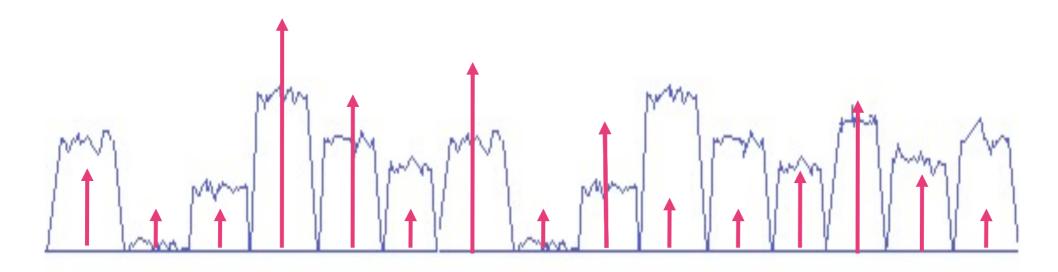


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Goal: Find open channel(s) as quickly as possible. Two approaches:

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- 2) listen to each channel for a data-adaptive amount of time to make decisions as quickly as possible

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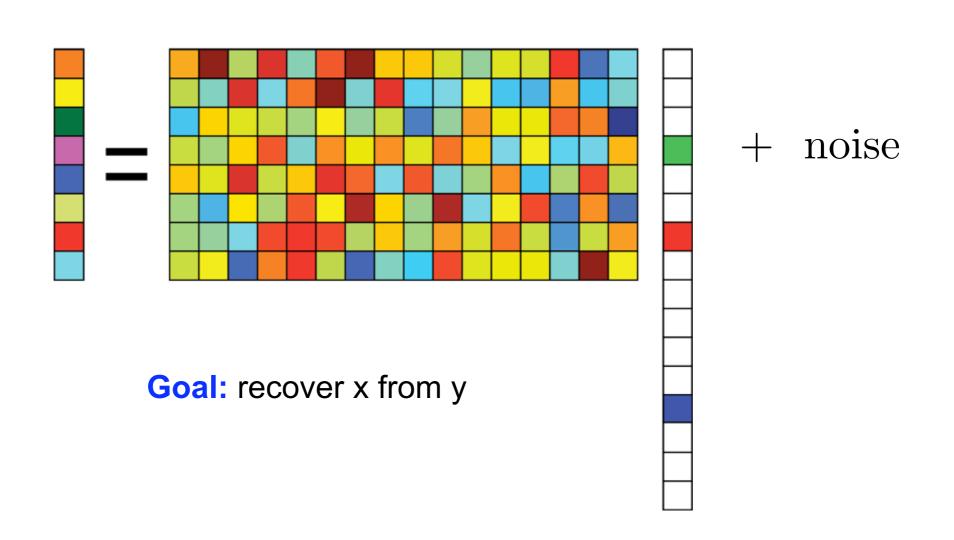
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adaptive spectrum sensing can be significantly more time-efficient than fixed sensing

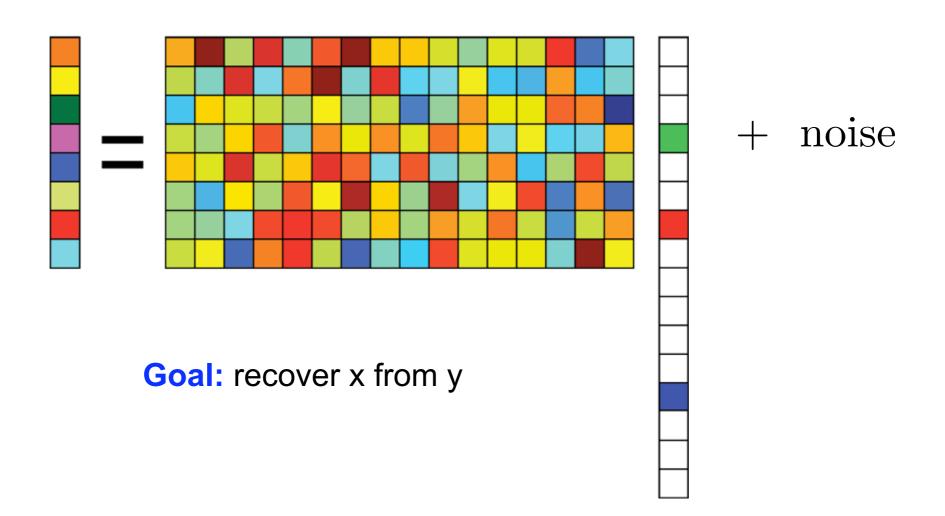
Sparse Recovery (image reconstruction, compressed sensing, inverse problems)

$$y = Ax + w$$
, with $A \in \mathbb{R}^{m \times n}$, $x \in \mathbb{R}^n$ (but sparse), $w \sim \mathcal{N}(0, I)$



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Is sequentially designing (rows of) A advantageous?

Model Selection

Challenge: huge number of possible models, each with a different pattern of sparsity

Model Selection

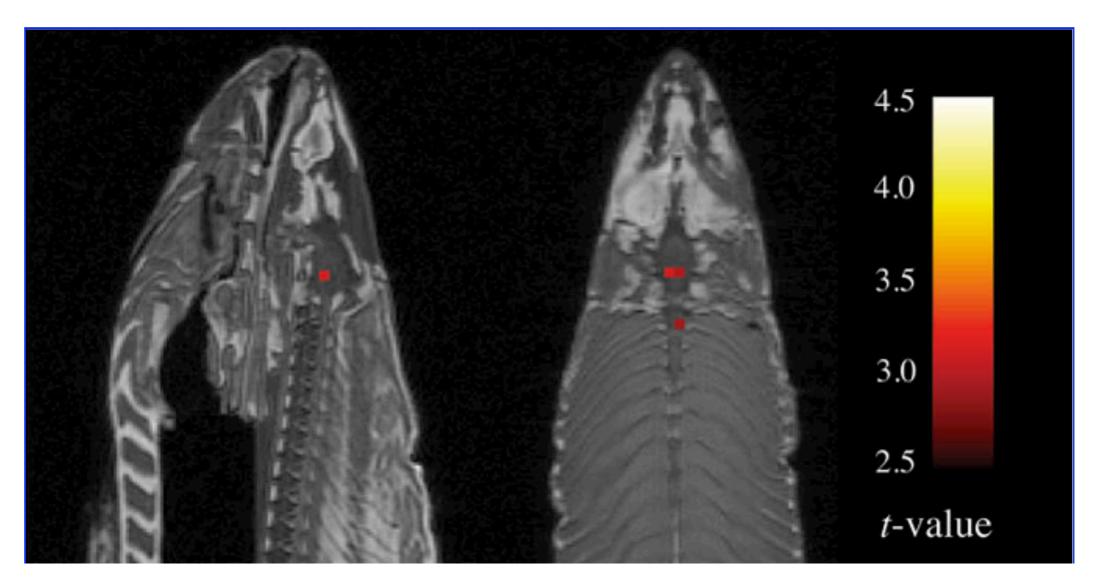
Wired Science
News for Your Neurons
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Challenge: huge number of possible models, each with a different pattern of sparsity

Scanning Dead Salmon in fMRI Machine Highlights Risk of Red Herrings

By Alexis Madrigal

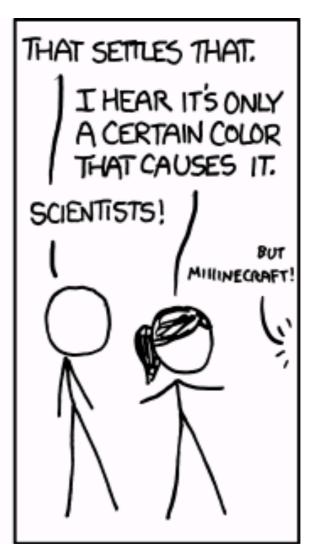
September 18, 2009 | 5:37 pm | Categories: Brains and Behavior



The Multiple Testing Problem







http://xkcd.com/882/

WE FOUND NO LINK BETVEEN PURPLE JELLY BEANS AND AONE (P > 0.05).



WE FOUND NO LINK BETWEEN BROWN JELLY BEANS AND ACNE (P>0.05),



WE FOUND NO LINK BETWEEN PINK JELLY BEANS AND ACNE (P>0.05).



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WE FOUND NO LINK BETWEEN CYAN JELLY BEANS AND ACNE (P>0.05).



WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE (P<0.05).



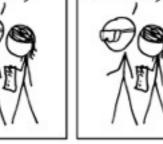
WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND AONE (P > 0.05).



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WE FOUND NO LINK BETWEEN MAGENTA JELLY BEANS AND AONE (P > 0.05).



WE FOUND NO LINK BETWEEN YELLOW JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN BEIGE JELLY BEANS AND ACNE (P > 0.05).



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SALMON JELLY

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LINK BETWEEN

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BEANS AND ACNE (P>0.05).

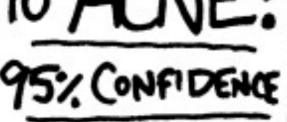


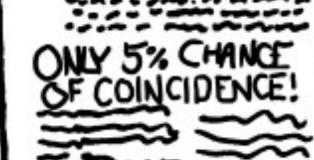
WE FOUND N LINK BETWEE TURQUOISE] BEANS AND A

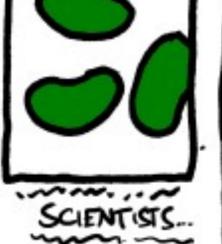


= NEWS = GREEN JEUY

BEANS LINKED







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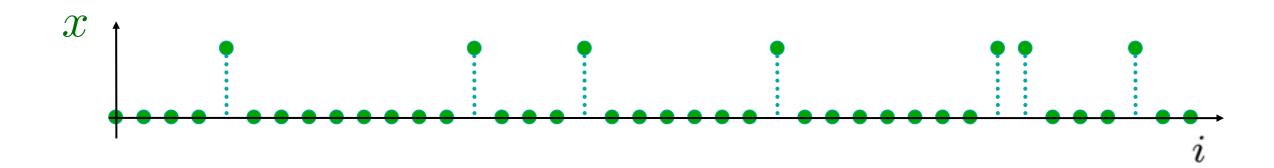
Single Experiment Model

$$y_i = x_i + z_i, i = 1, ..., n$$
 $z_i \overset{\text{iid}}{\sim} \mathcal{N}(0, 1)$
 $\mathbf{sparsity}: x_i = 0 \text{ except on a small subset } \mathcal{S} \subset \{1, ..., n\} \text{ where } x_i = \mu > 0$

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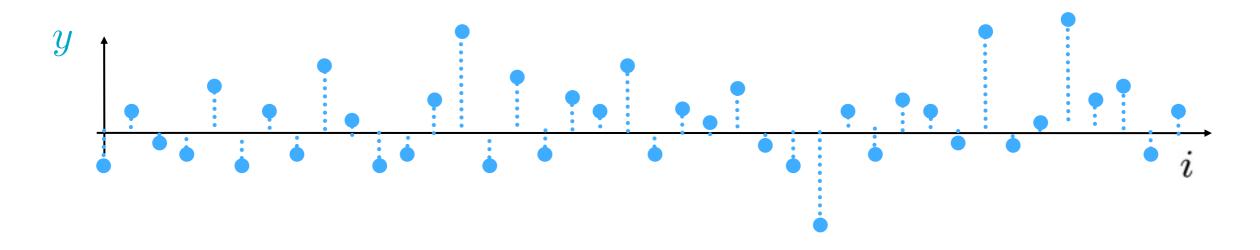
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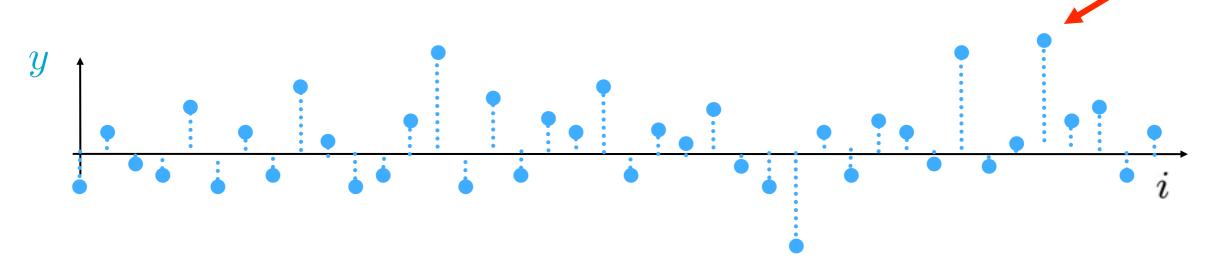
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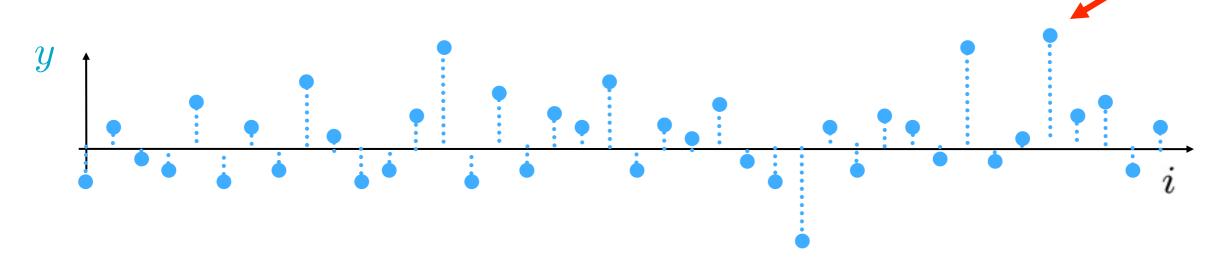


Suppose we want to locate just **one** signal component: $\hat{i} = \arg \max_i y_i$

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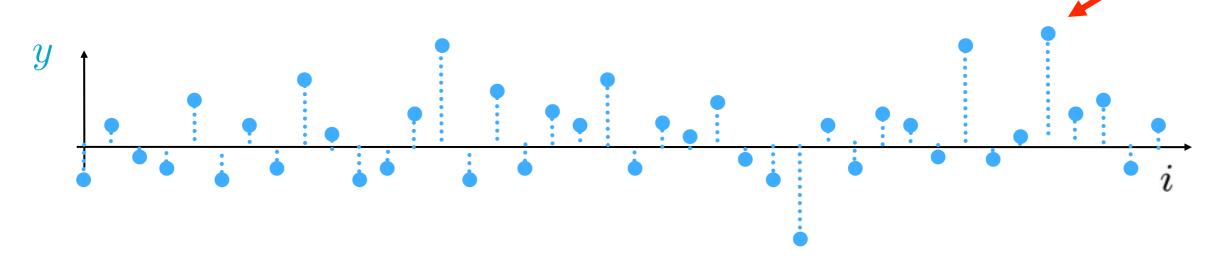
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It is *impossible* to reliably detect signal components if $\mu < \sqrt{2 \log n}$

An Alternative: Sequential Experimental Design

Instead of the usual non-adaptive observation model

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$$y_{i,j} = x_i + \gamma_{i,j}^{-1/2} z_{i,j}, \quad i = 1, \dots, n, \quad j = 1, \dots, k$$

where

j indexes the measurement steps

k denotes the total number of steps

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Total precision budget is constrained, but the choice of $\gamma_{i,j}$ can depend on past observations $\{y_{i,\ell}\}_{\ell < j}$.

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$$\sum_{j=1}^{k} \sum_{i=1}^{n} \gamma_{i,j} \leq n$$

For example, the usual non-adaptive, single measurement model corresponds to taking k = 1, and $\gamma_{i,1} = 1$, i = 1, ..., n. This baseline can be compared with adaptive procedures by allowing k > 1 and variable $\{\gamma_{i,j}\}$ satisfying budget.

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allocate precision sequentially and adaptively

Sequential Thresholding

```
initialize: S_0 = \{1, ..., n\}, \ \gamma_{i,j}^{-1} = 2
for j = 1, ..., k
```

- 1) measure: $y_{i,j} \sim \mathcal{N}(x_i, 2)$, $i \in \mathcal{S}_{j-1}$
- 2) threshold: $S_j = \{i : y_{i,j} \ge 0\}$

end

output: $S_k = \{i : y_{i,k} > 0\}$

$$\text{precision} = \begin{cases} \frac{1}{2} & \text{, if measured} \\ 0 & \text{, otherwise} \end{cases}$$

Sequential Thresholding

initialize:
$$S_0 = \{1, \dots, n\}, (\gamma_{i,j}^{-1} = 2)$$

for $j = 1, \dots, k$

- 1) measure: $y_{i,j} \sim \mathcal{N}(x_i, 2)$, $i \in \mathcal{S}_{j-1}$
- 2) threshold: $S_j = \{i : y_{i,j} \geq 0\}$

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output: $S_k = \{i : y_{i,k} > 0\}$

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total precision budget: $\mathbb{E}\left[\sum_{i,j} \gamma_{i,j}\right]$

$$= \frac{1}{2} \sum_{j=1}^{k} \mathbb{E} |\mathcal{S}_{j-1}|$$

$$\leq \frac{1}{2} \sum_{j=1}^{k} \left(\frac{n-s}{2^{j-1}} + s \right)$$

$$\leq n - s + ks \approx n$$

(when $n \gg s$)

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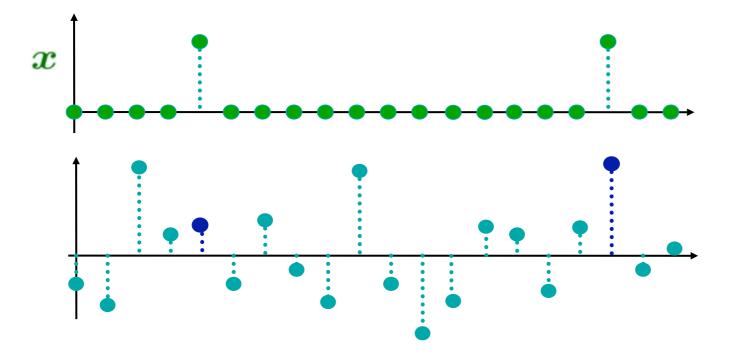
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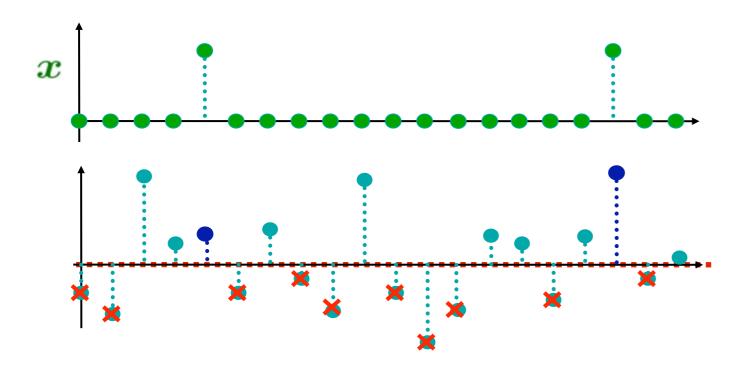
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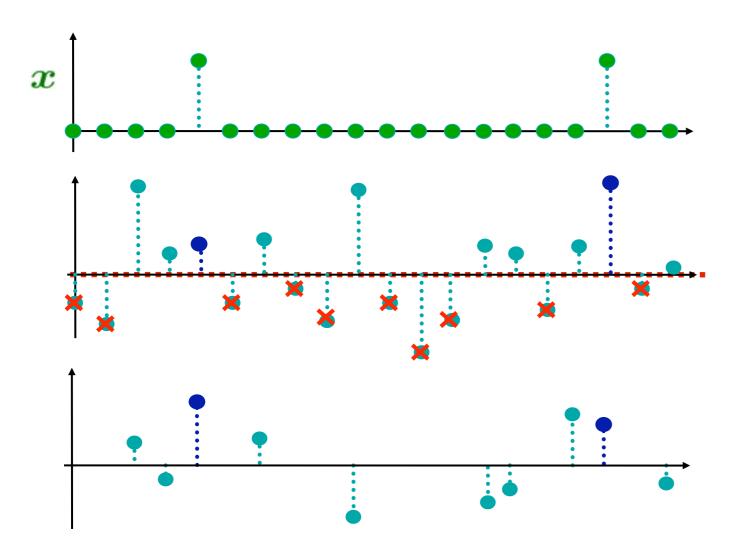
probability of error: $\mathbb{P}(\mathcal{S}_k \neq \mathcal{S}) = \mathbb{P}(\{\mathcal{S}^c \cap \mathcal{S}_k \neq \emptyset\} \cup \{\mathcal{S} \cap \mathcal{S}_k^c \neq \emptyset\})$ $\leq \mathbb{P}(\mathcal{S}^c \cap \mathcal{S}_k \neq \emptyset) + \mathbb{P}(\mathcal{S} \cap \mathcal{S}_k^c \neq \emptyset)$



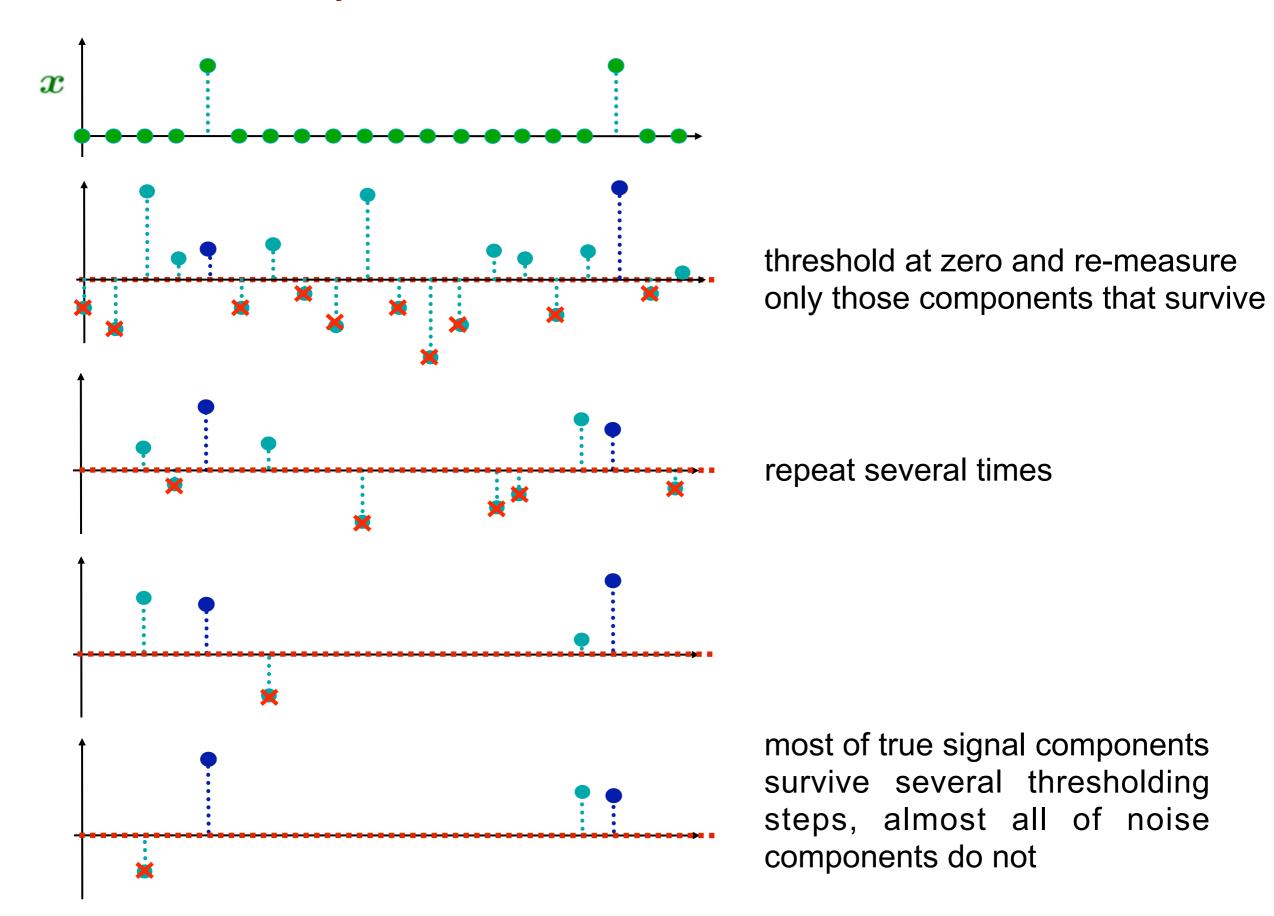


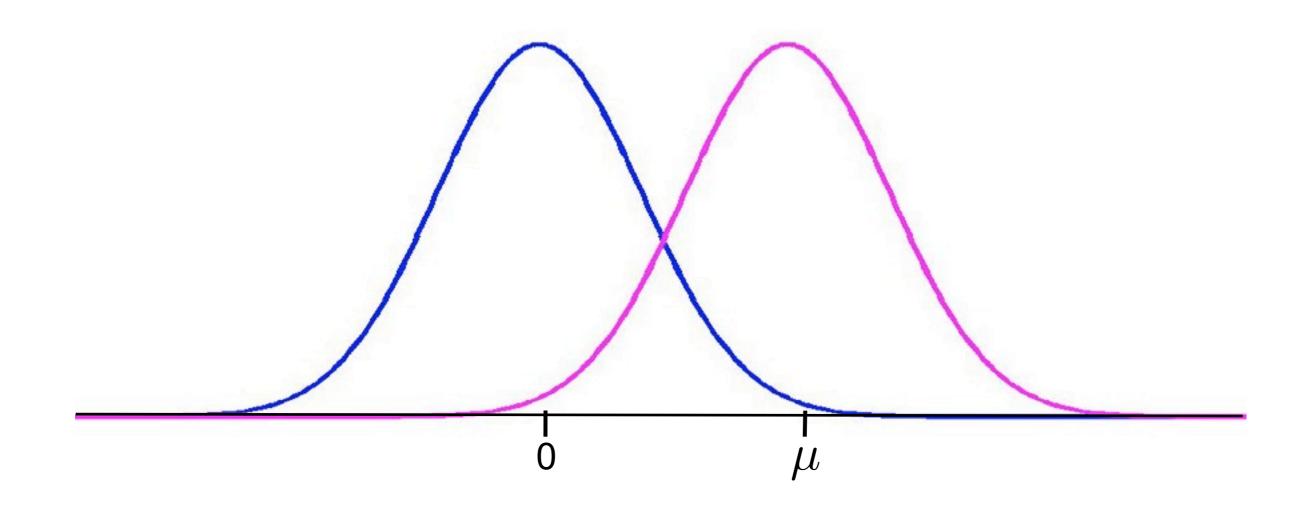


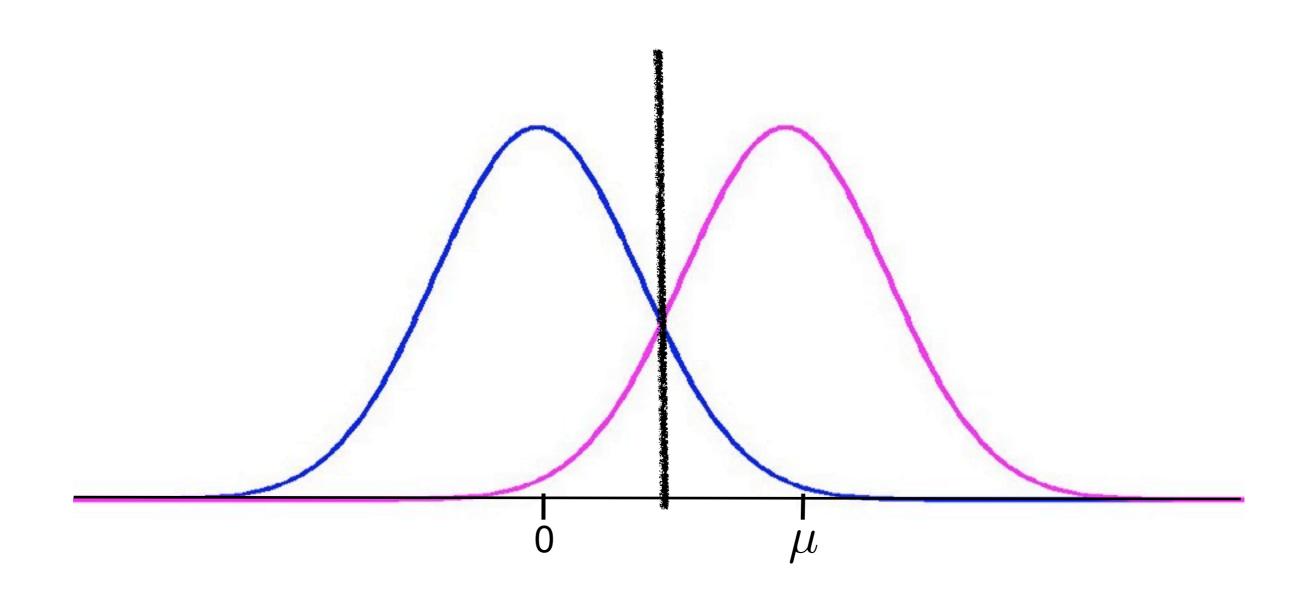
threshold at zero and re-measure only those components that survive

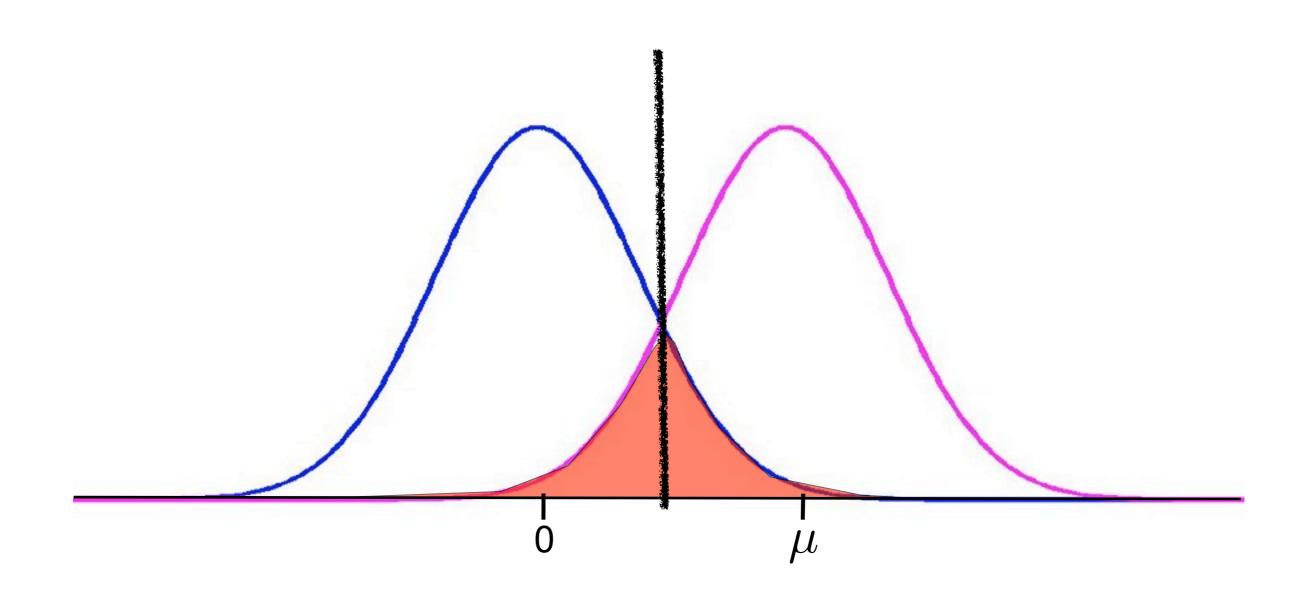


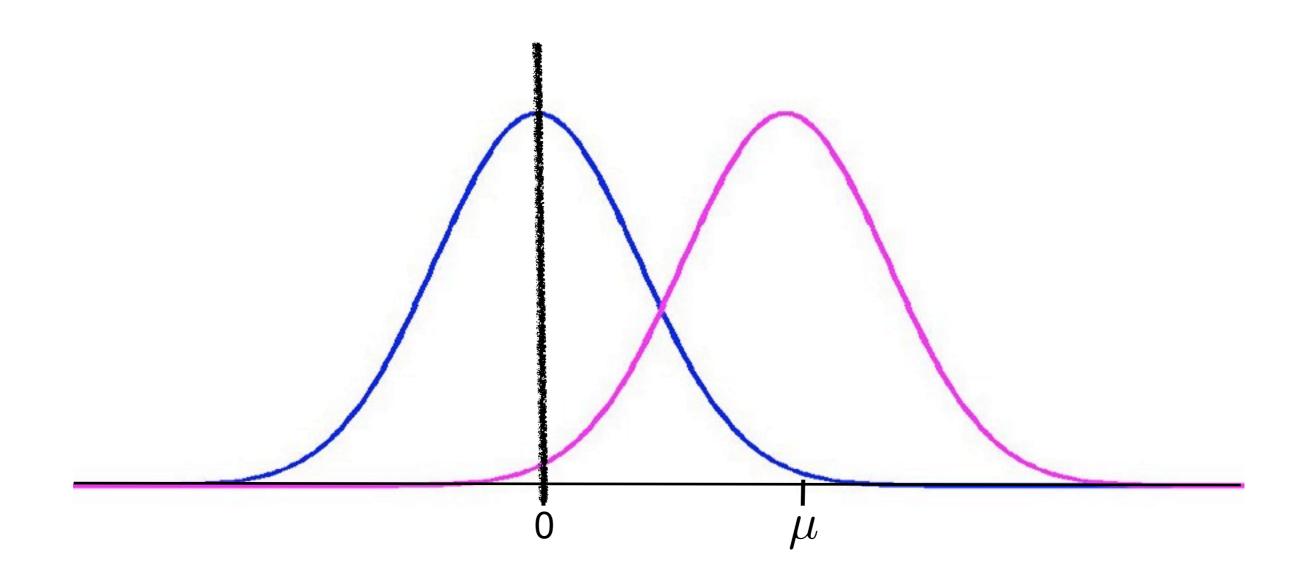
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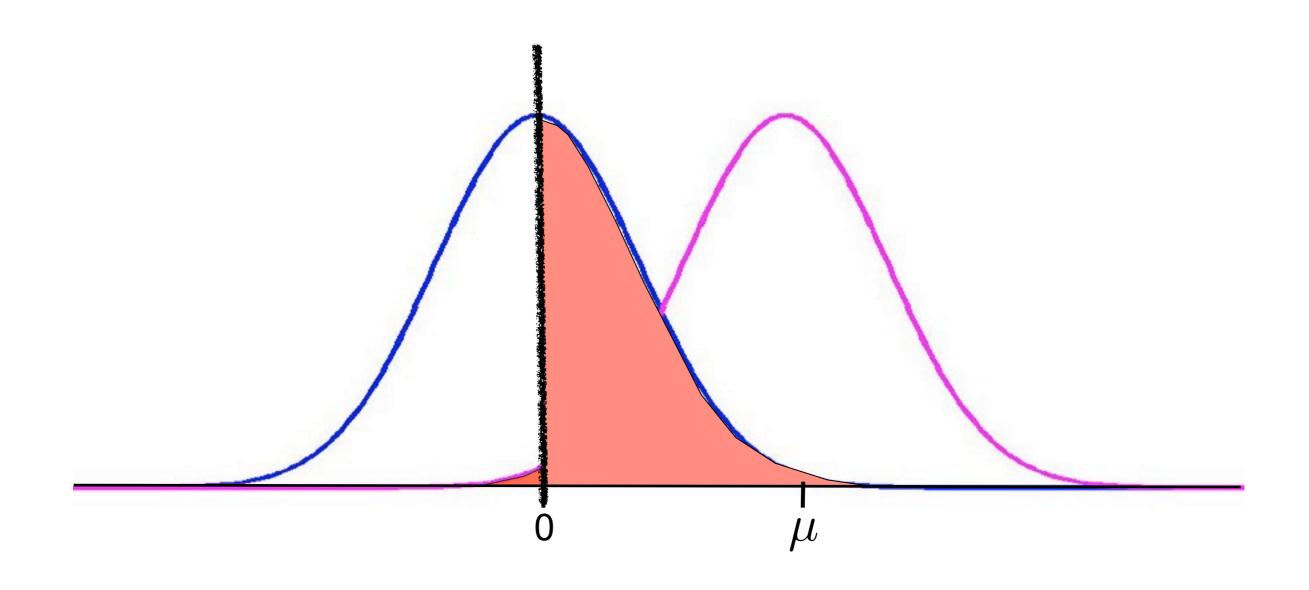




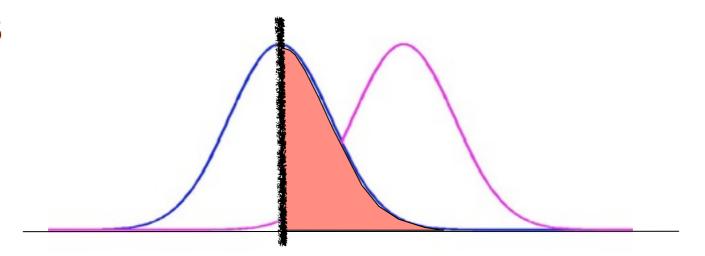






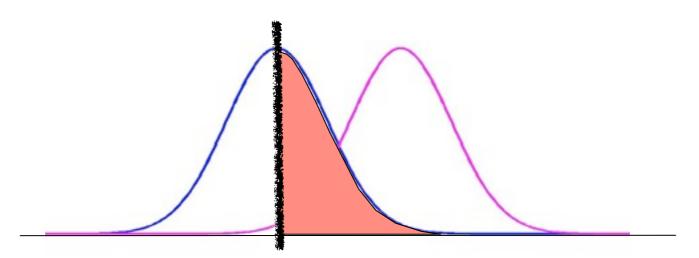


False Positives



$$\mathbb{P}(\mathcal{S}_k \neq \mathcal{S}) \leq \mathbb{P}\left(\mathcal{S}^c \cap \mathcal{S}_k \neq \emptyset\right) + \mathbb{P}\left(\mathcal{S} \cap \mathcal{S}_k^c \neq \emptyset\right)$$

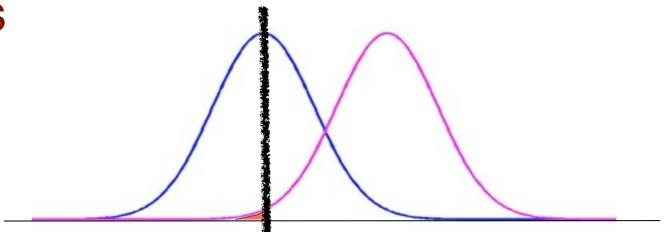
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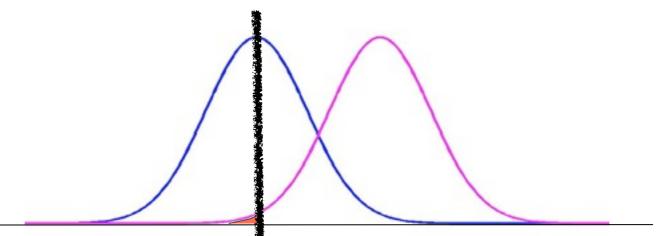
$$\mathbb{P}\left(\mathcal{S}^{c} \cap \mathcal{S}_{k} \neq \emptyset\right) = \mathbb{P}\left(\bigcup_{i \notin \mathcal{S}} \bigcap_{j=1}^{k} y_{i,j} > 0\right) \\
\leq \sum_{i \notin \mathcal{S}} \mathbb{P}\left(\bigcap_{j=1}^{k} y_{i,j} > 0\right) \\
= \sum_{i \notin \mathcal{S}} 2^{-k} = \frac{n-s}{2^{k}}$$

False Negatives



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$$\leq \frac{ks}{2} \exp\left(-\frac{\mu^{2}}{4}\right)$$

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Second term tends to zero if

$$\mu \ge \sqrt{c \log(s \log_2 n)}$$
, for any $c > 4$

Gains of Sequential Design







Rui Castro (Eindhoven)

(Minnesota)

Jarvis Haupt Matt Malloy (Madison)

non-sequential:
$$\mu > \sqrt{2 \log n}$$
 (necessary)

sequential thresholding: (sufficient)

$$\mu > \sqrt{4(\log s + \log \log_2 n)}$$

with a bit more work we can show

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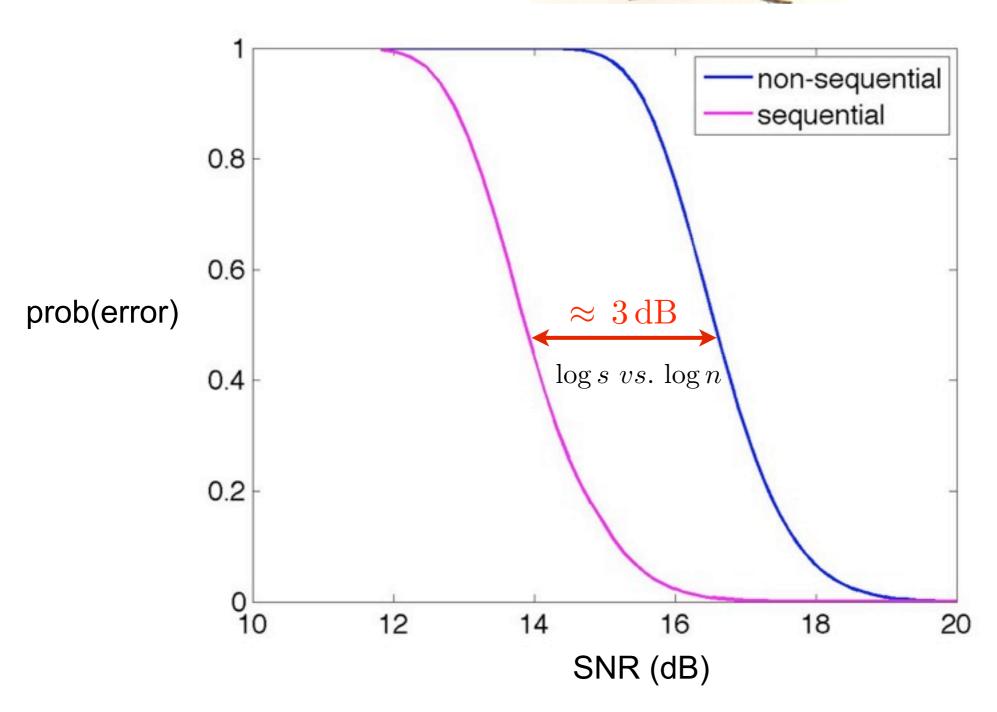
significant gains when $s \ll n$

greater sensitivity for same precision budget or lower experimental requirements for equivalent sensitivity

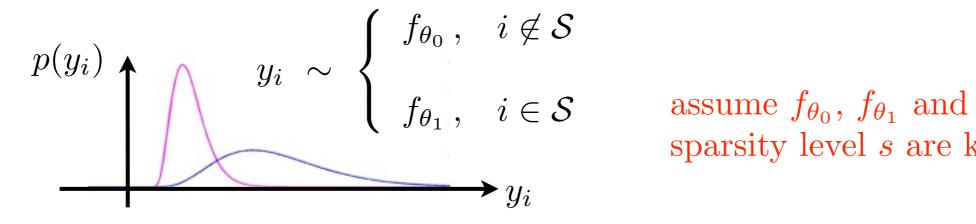
Biology Example



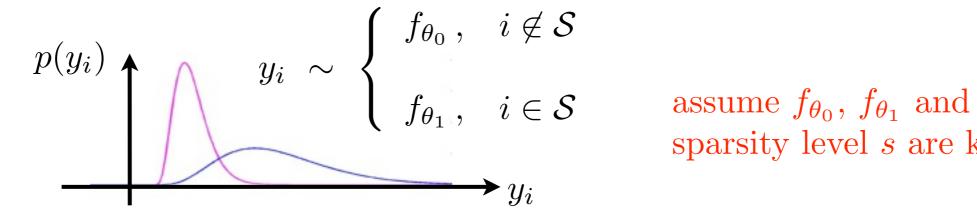
13,071 single-gene knock-down cell strains



sequential thresholding is about twice as sensitive (for equal experimental budget) or requires half the number experiments (for same sensitivity)



sparsity level s are known

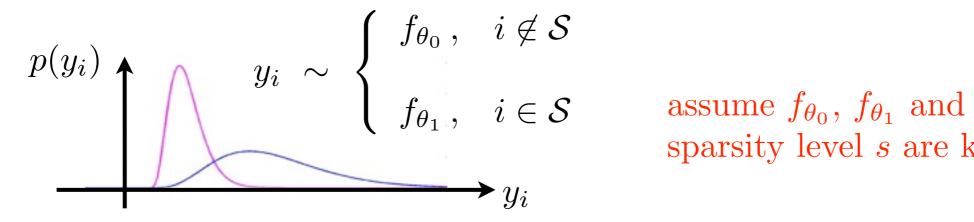


sparsity level s are known

specify error rates (per-test):

false-positive probability: $\alpha = \epsilon/(n-s)$

false-negative probability: $\beta = \epsilon/s$



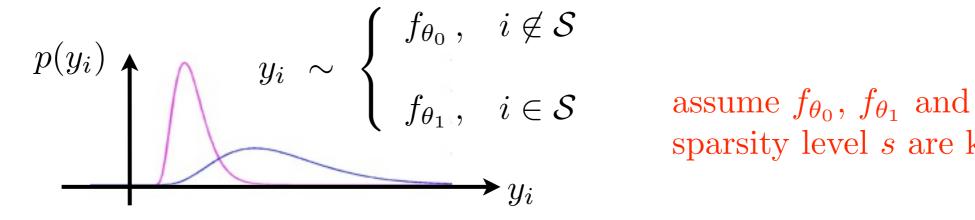
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expected number samples (precision per-test): for α , $\beta \approx 0$

$$\mathbb{E}_0[M] \gtrsim D_0^{-1} \log \frac{1}{\beta} = D_0^{-1} \log \frac{s}{\epsilon}$$

$$\mathbb{E}_1[M] \gtrsim D_1^{-1} \log \frac{1}{\alpha} = D_1^{-1} \log \frac{n-s}{\epsilon}$$

where D_0 , D_1 are KL divergences $D_0 := D(f_{\theta_0} || f_{\theta_1})$ and $D_1 := D(f_{\theta_1} || f_{\theta_0})$

expected total sampling/precision:

$$\mathbb{E}[N] = (n-s)\mathbb{E}_0[M] + s\mathbb{E}_1[M] \gtrsim \frac{n}{D_0}\log\frac{s}{\epsilon}$$
, when $s \ll n$

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minimum requirement for any testing scheme with expected sample/precision budget m

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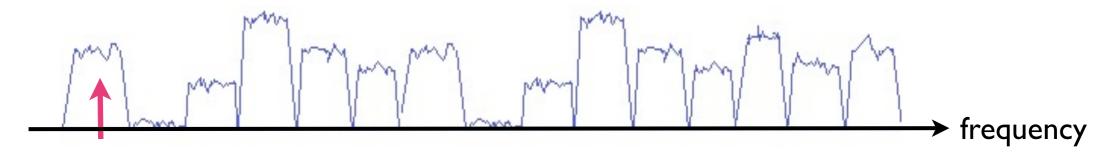
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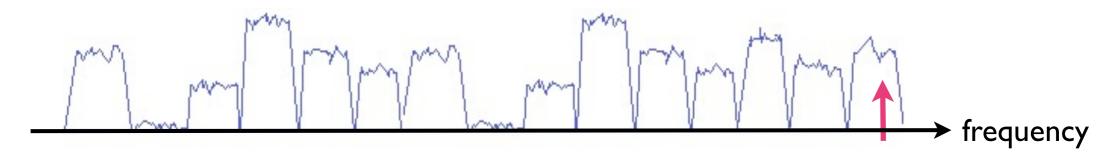
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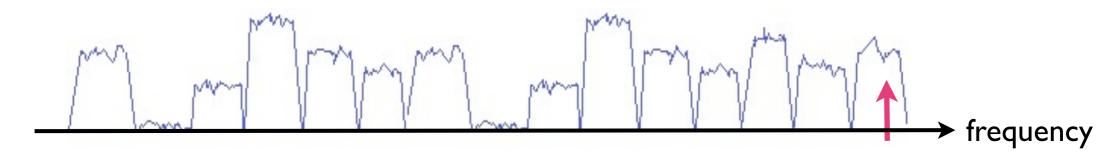
Gaussian case:
$$N(0,1)$$
 vs. $N(\mu,1) \Rightarrow D_0 = \mu^2/2$ and so prob(error) $\leq \epsilon$ iff $\mu > \sqrt{2\log s/\epsilon}$

sequential thresholding:
$$\mu > \sqrt{2(\log s + \log \log_2 \log n)}$$

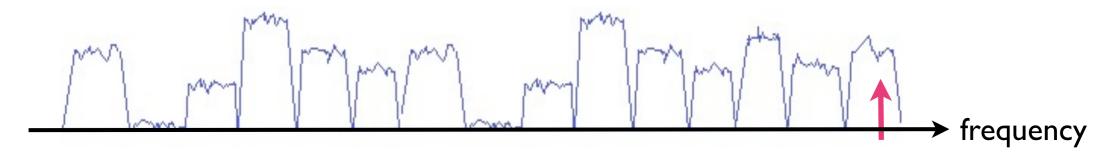
and is adaptive to sparsity level





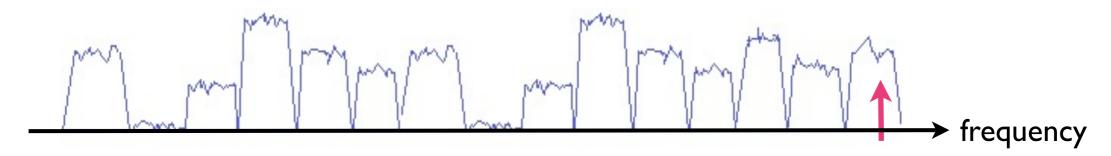


channel samples:
$$y_{i,j} \stackrel{\text{iid}}{\sim} \mathcal{CN}(0,\theta)$$
, $\theta_0 > \theta_1 = 1$



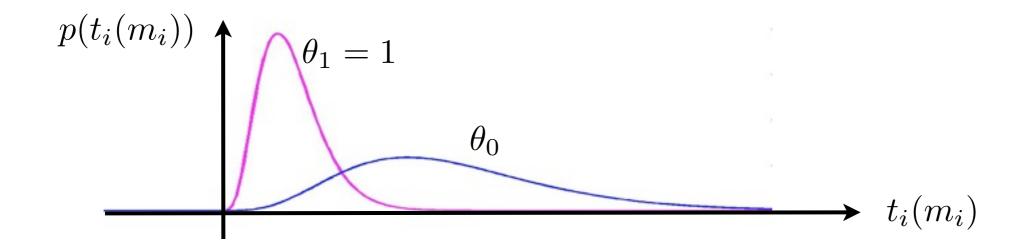
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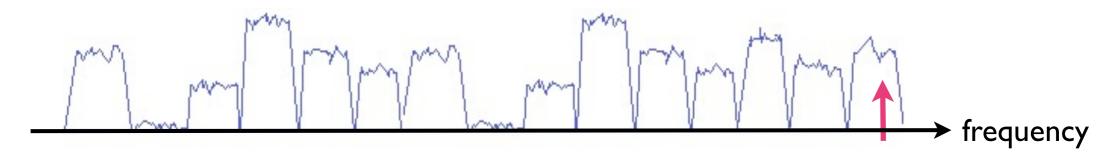
test statistic:
$$t_i(m_i) = \sum_{j=1}^{m_i} |y_{i,j}|^2 \sim \begin{cases} \Gamma(m_i, \theta_0), & i \notin \mathcal{S} \\ \Gamma(m_i, 1), & i \in \mathcal{S} \end{cases}$$



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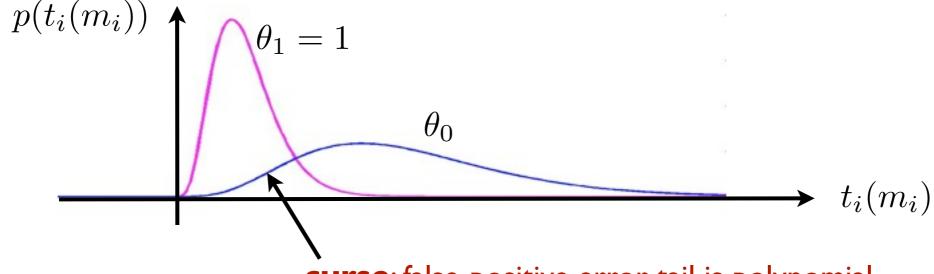




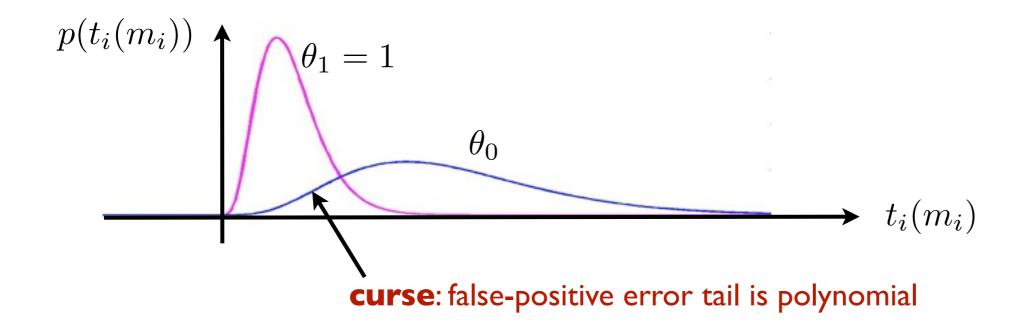
goal: scan to find open channel(s) as quickly as possible

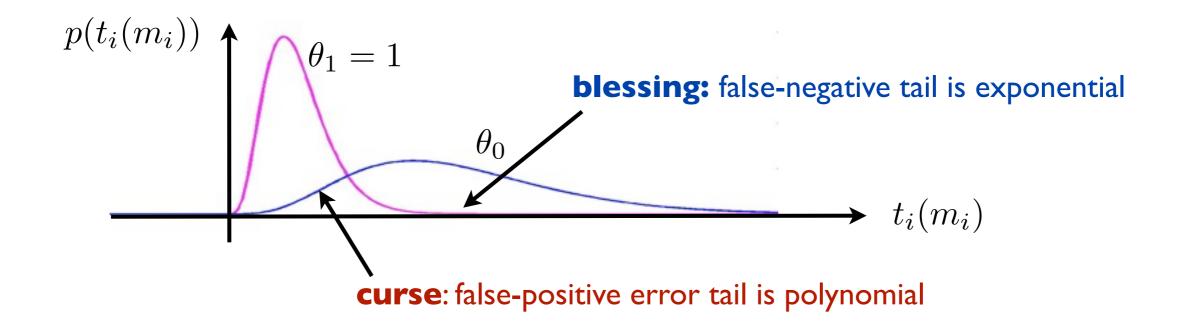
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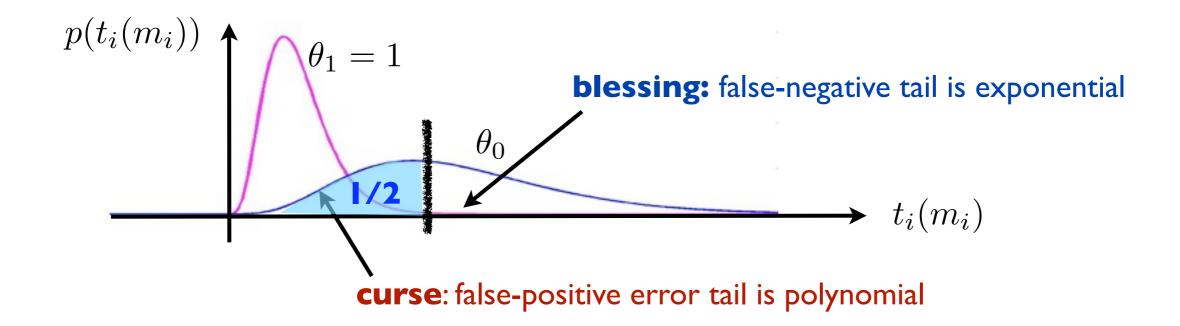
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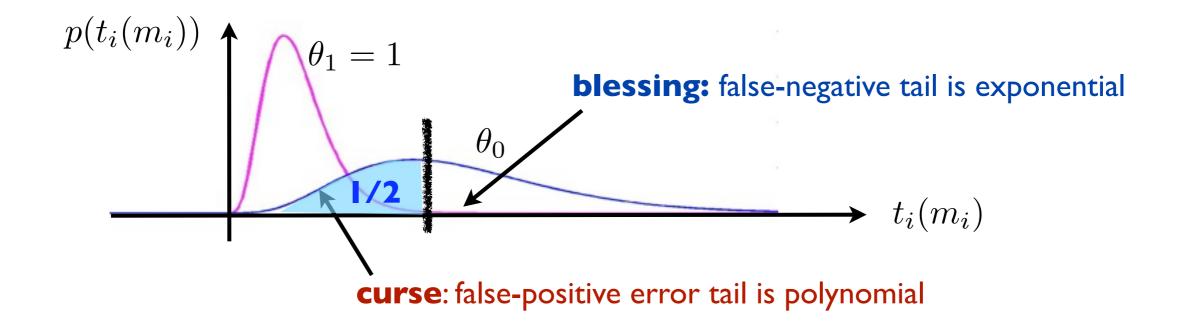


curse: false-positive error tail is polynomial

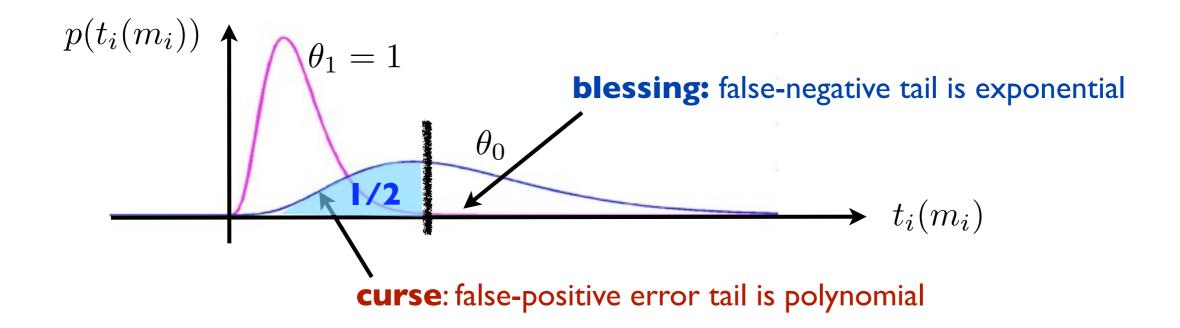








scanning budget: m = average number of samples per channel



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non-sequential:
$$\theta_0 > 2(m-1)(n-s)^{1/2m} \sim n^{1/2m}$$
 (necessary)

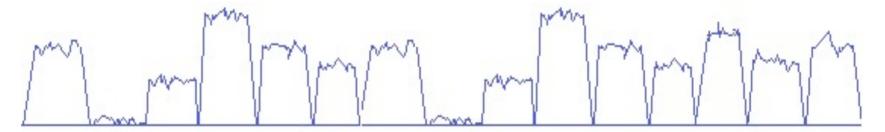
SPRT:
$$\theta_0 > \frac{1}{m} \log s$$
 minimum requirement for any testing scheme with average sample budget m

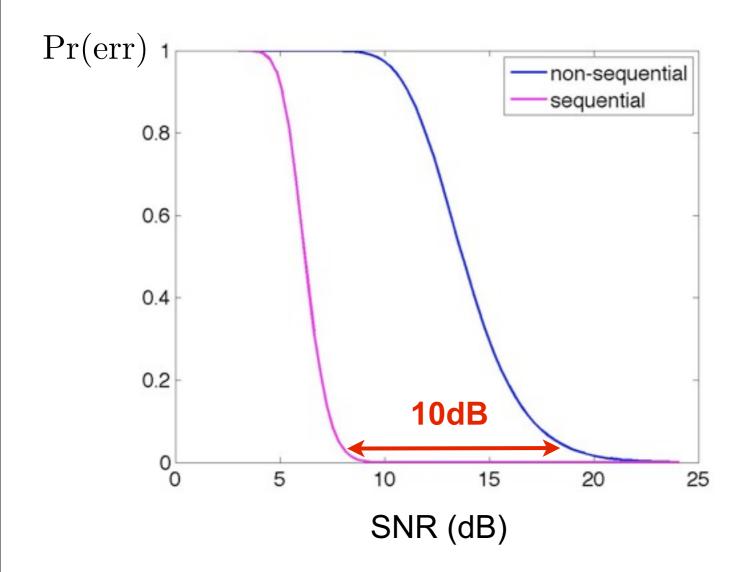
sequential thresholding:
$$\theta_0 > \frac{1}{m}(\log s + \log \log_2 n)$$
 (sufficient)

... and automatically adaptive to sparsity level

Performance

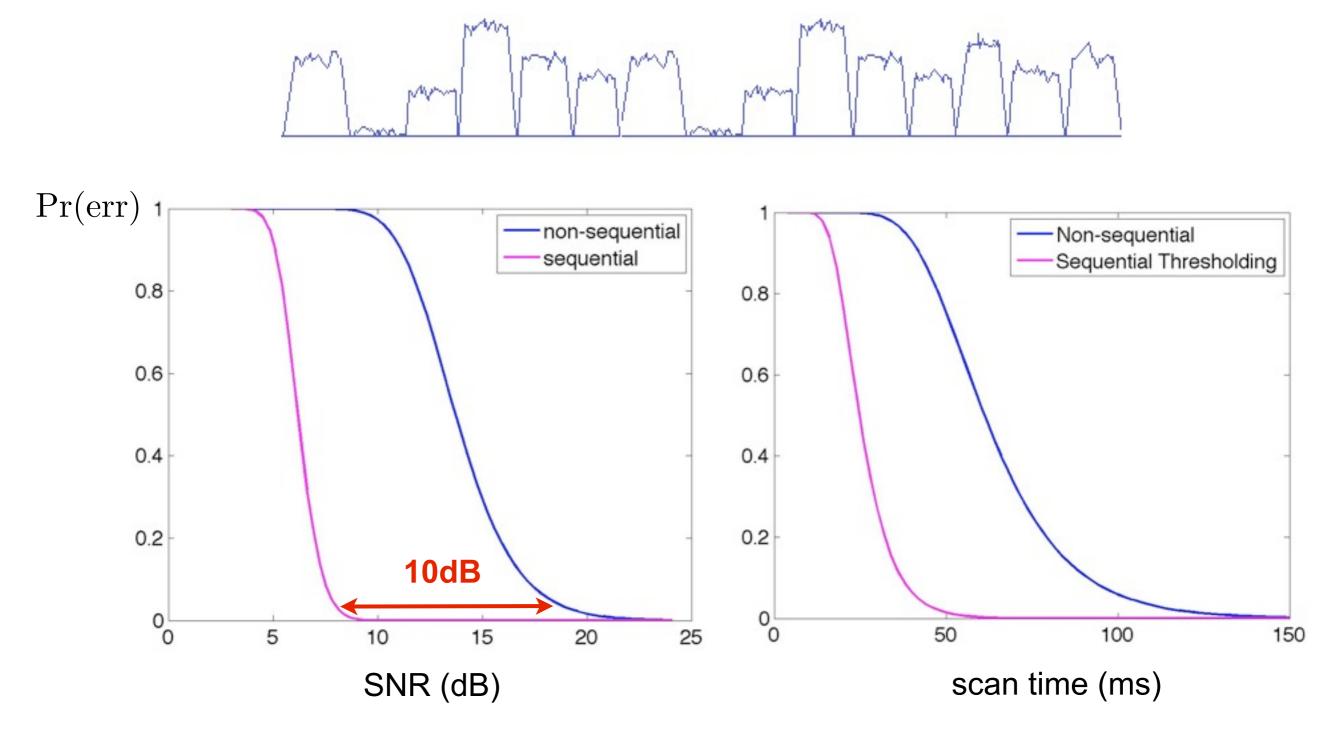
n=1000 channels, s=6 unoccupied

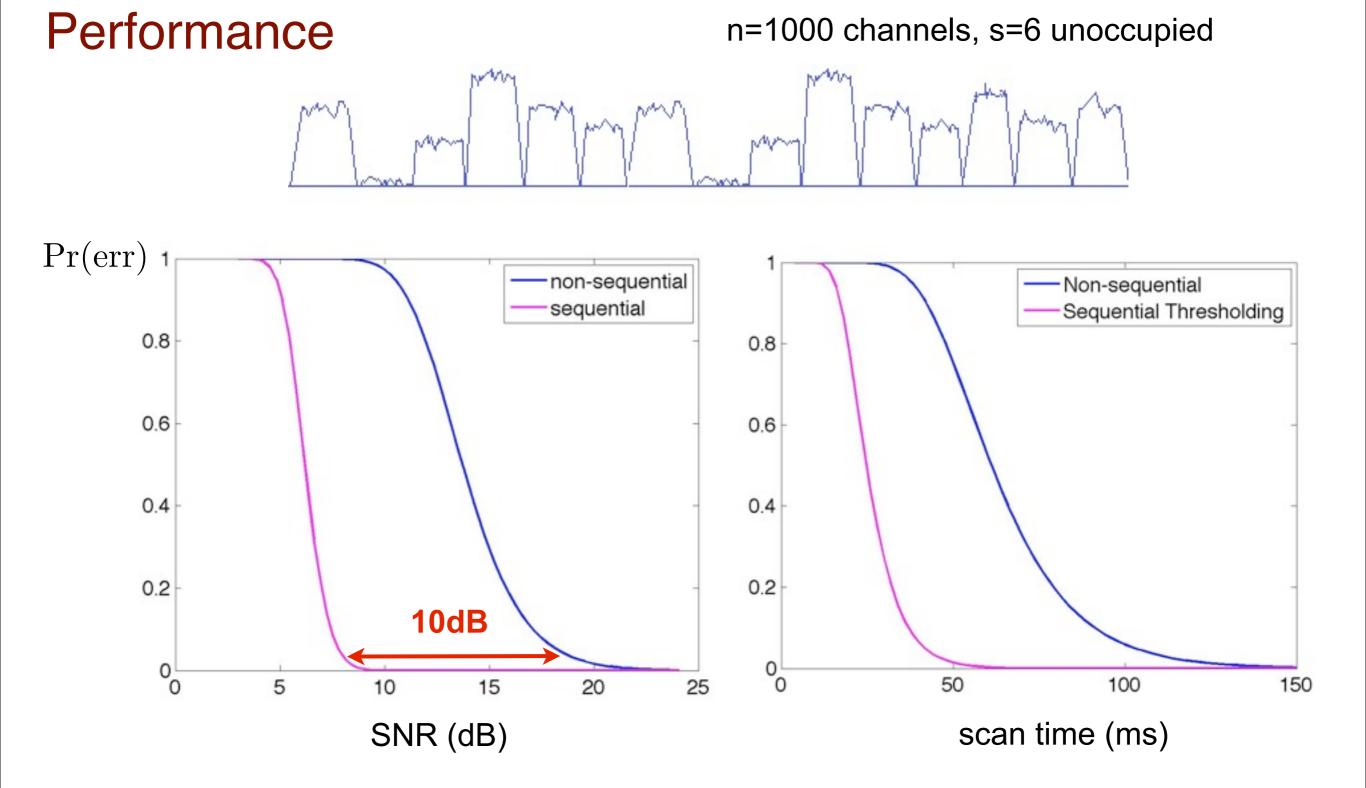






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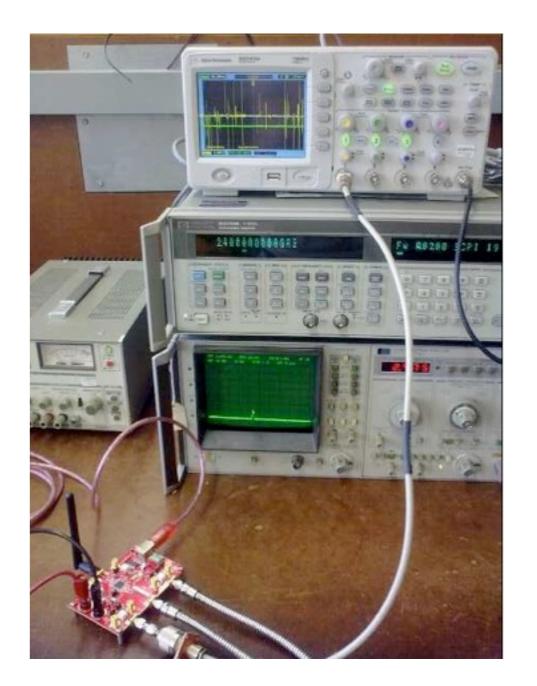




sequential thresholding is about 10 times more sensitive (for equal scan time) or scans 3 times faster (with same reliability)

Spectrum Sensing in the Lab





Matt Malloy in the lab

requirements for reliable sequential testing in high-dimensional sparse problems:

- I. SNR $\sim \max(\log(s), \log\log\log(n))$
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see Jarvis Haupt's poster

Conclusions

Sequential Experimental Designs for High-Dimensional Models

thresholds for recovery in high-dimensional limit:

```
non-sequential designs SNR \sim log(dimension) (or worse) sequential designs SNR \sim log(sparsity level) (or better)
```

Sequential Analysis High-Dimensional Multiple Testing and Sparse Recovery M. Malloy and RN, arXiv:1103.5991

Distilled Sensing: Adaptive Sampling for Sparse Detection and Estimation J. Haupt, R. Castro, and RN, arXiv:1001.5311v2