

Optimization in the Race to a Liquid Biopsy

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A Little Biology

- Cancer is caused by DNA mutations
 - Tumors contain mutated DNA

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- Cancer is caused by DNA mutations
 - Tumors contain mutated DNA
- **Cell-free DNA:** blood contains tiny amounts of mutated DNA
 - Concentration of one in ten-thousand
 - Should hypothetically be a cancer signal

The Race is On

- Recent academic successes based on this idea:
 - [Cohen et al.] Detection and localization of surgically resectable cancers with a multi-analyte blood test. *Science* (2018).
 - [Liu et al.] Sensitive and specific multi-cancer detection and localization using methylation signatures in cell-free DNA. *Annals of Oncology* (2020).

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Forbes

Jan 18, 2018, 02:00pm EST

A New \$500 Blood Test Could Detect Cancer Before Symptoms Develop

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A New \$500 Blood Test Could Detect Cancer Before Symptoms Develop

- ...and biotech firms building on it:

GRAIL

 GUARDANT™

EXACT
SCIENCES

freenome

Nearing the Finish Line

- Grail's *Galleri* test

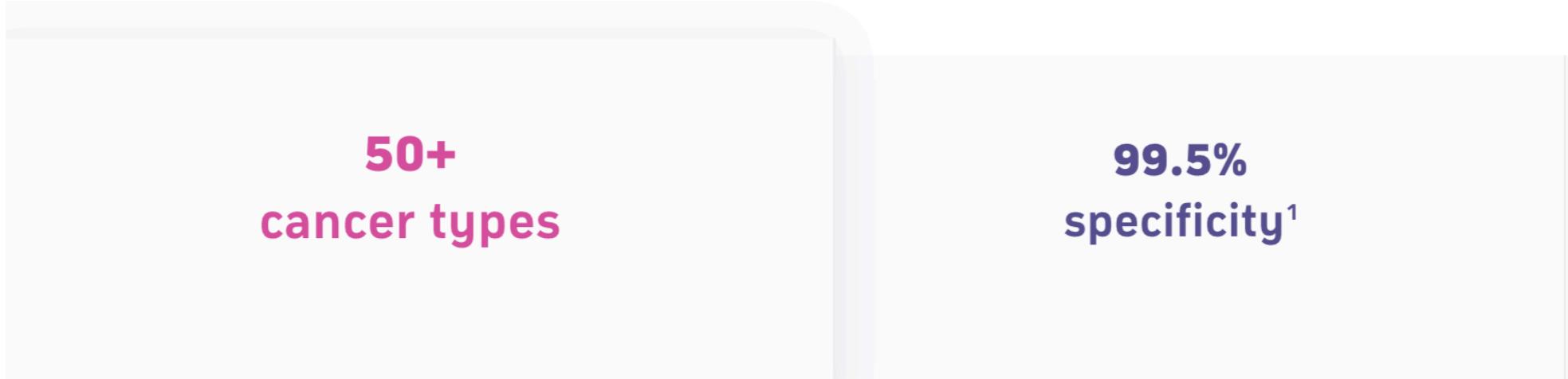
Nearing the Finish Line

- Grail's *Galleri* test
- \$949

The cost of the Galleri® test may vary depending on the healthcare practice or provider who orders the test. The list price for the Galleri test is \$949.

Nearing the Finish Line

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 - Detects 50+ cancer types
 - Specificity 99.5%



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cancer types

99.5%
specificity¹

Nearing the Finish Line

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 - Specificity 99.5%
 - Sensitivity 77%

Sensitivity

76.3% sensitivity in cancers that cause two-thirds of
cancer deaths in the US  ^{1,6,7}

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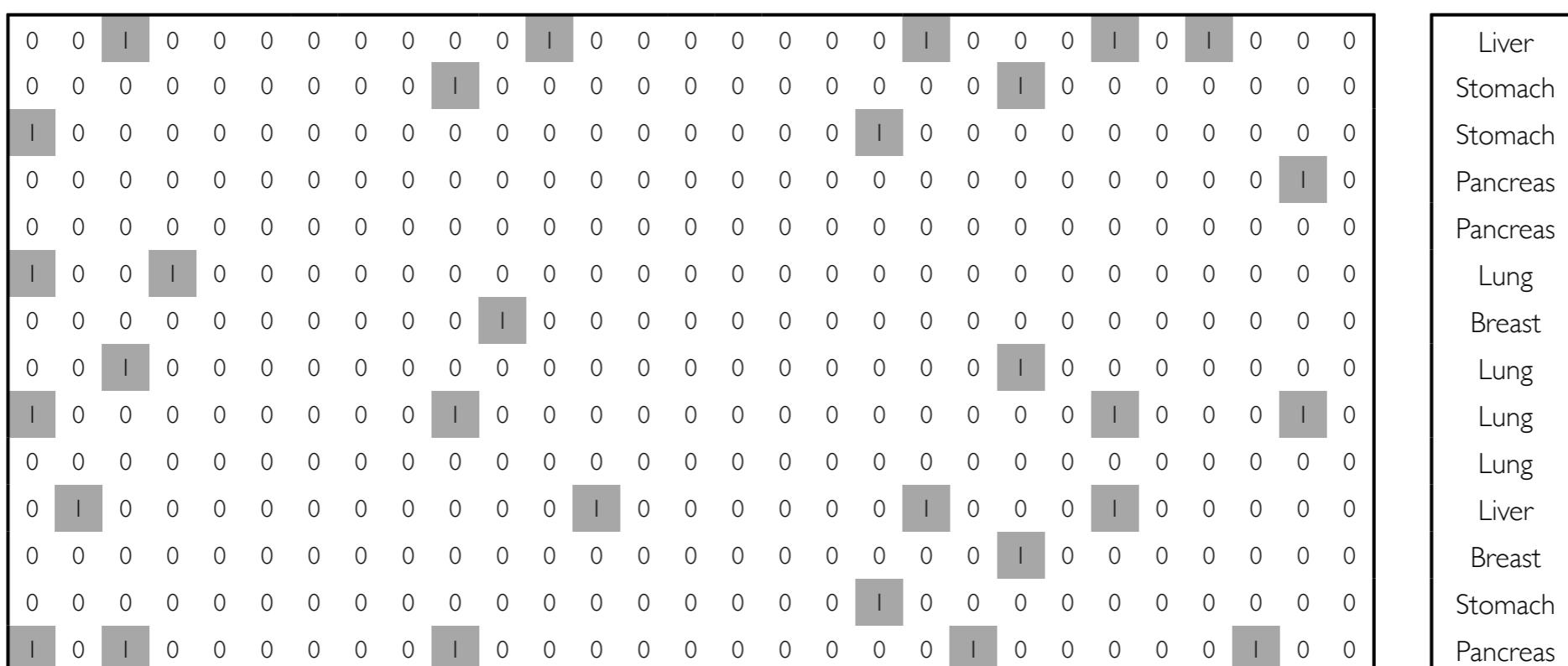
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- A back-of-the-envelope calculation:
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0	0	I	0	0	0	0	0	0	0	I	0	0	0	0	0	0	I	0	0	I	0	I	0	0	0
0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0	I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0
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0	I	0	0	0	0	0	0	0	0	I	0	0	0	0	0	I	0	0	I	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	I	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	I	0	0	0	0	0
I	0	I	0	0	0	0	0	0	I	0	0	0	0	0	I	0	I	0	I	0	0	I	0	I	0

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I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0	I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	I	0	0	0	0	0
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- A back-of-the-envelope calculation:
 - Test must cost at most \$ 10^2
 - Sequencing an address **ten-thousand times** costs \$ 10^{-2}
 - Thus, can only use a **panel** of $\sim 10^4$ addresses

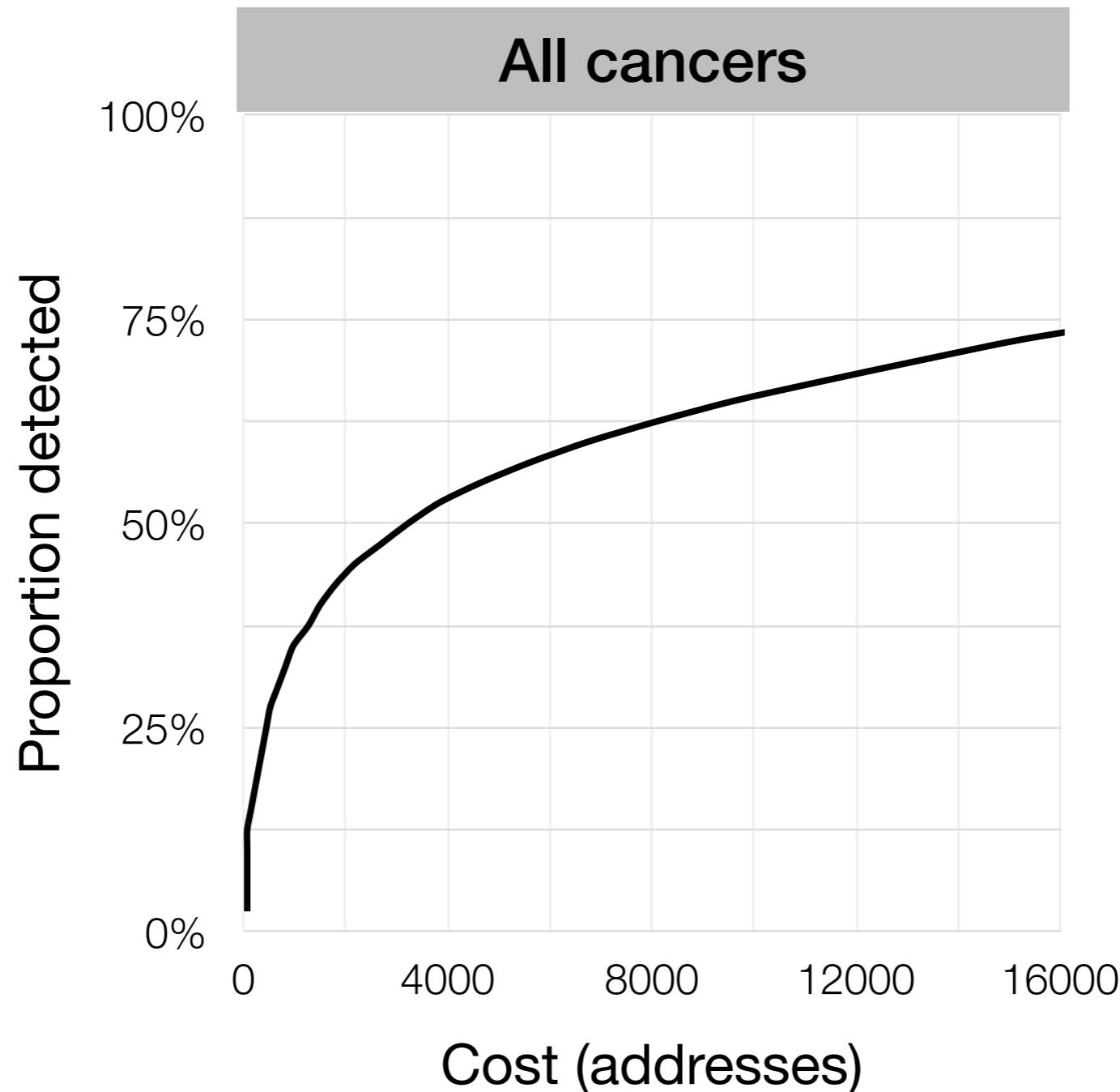
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0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I
0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I
I	0	0	I	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	I
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0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	I	I	0	0	I	0	0	0	0	I
0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	I	I	0	0	I	0	0	0	0	I
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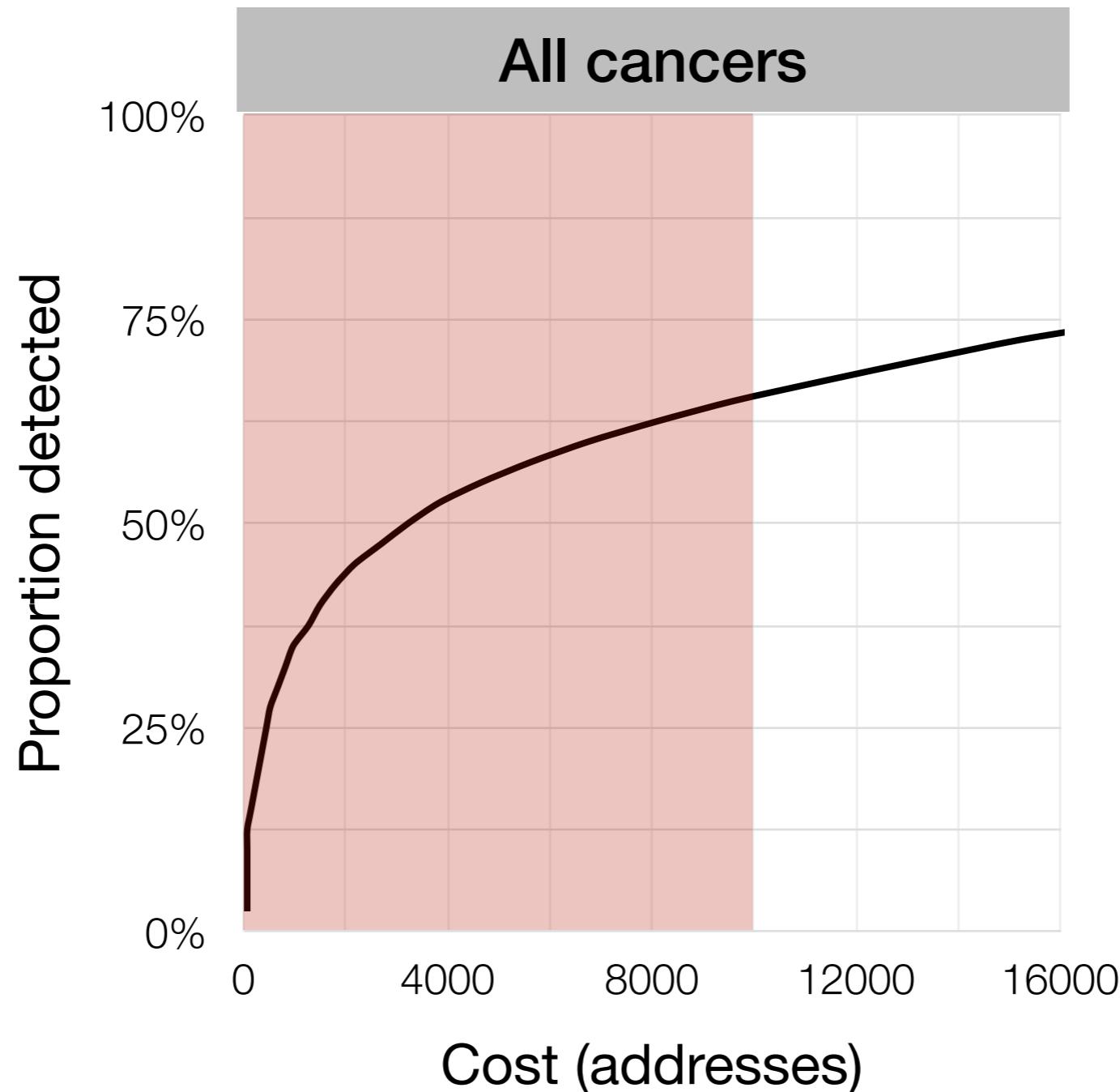
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I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	0	0	0	0	0	0			
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	I	0	0	I	0	0	0	0	I	0	
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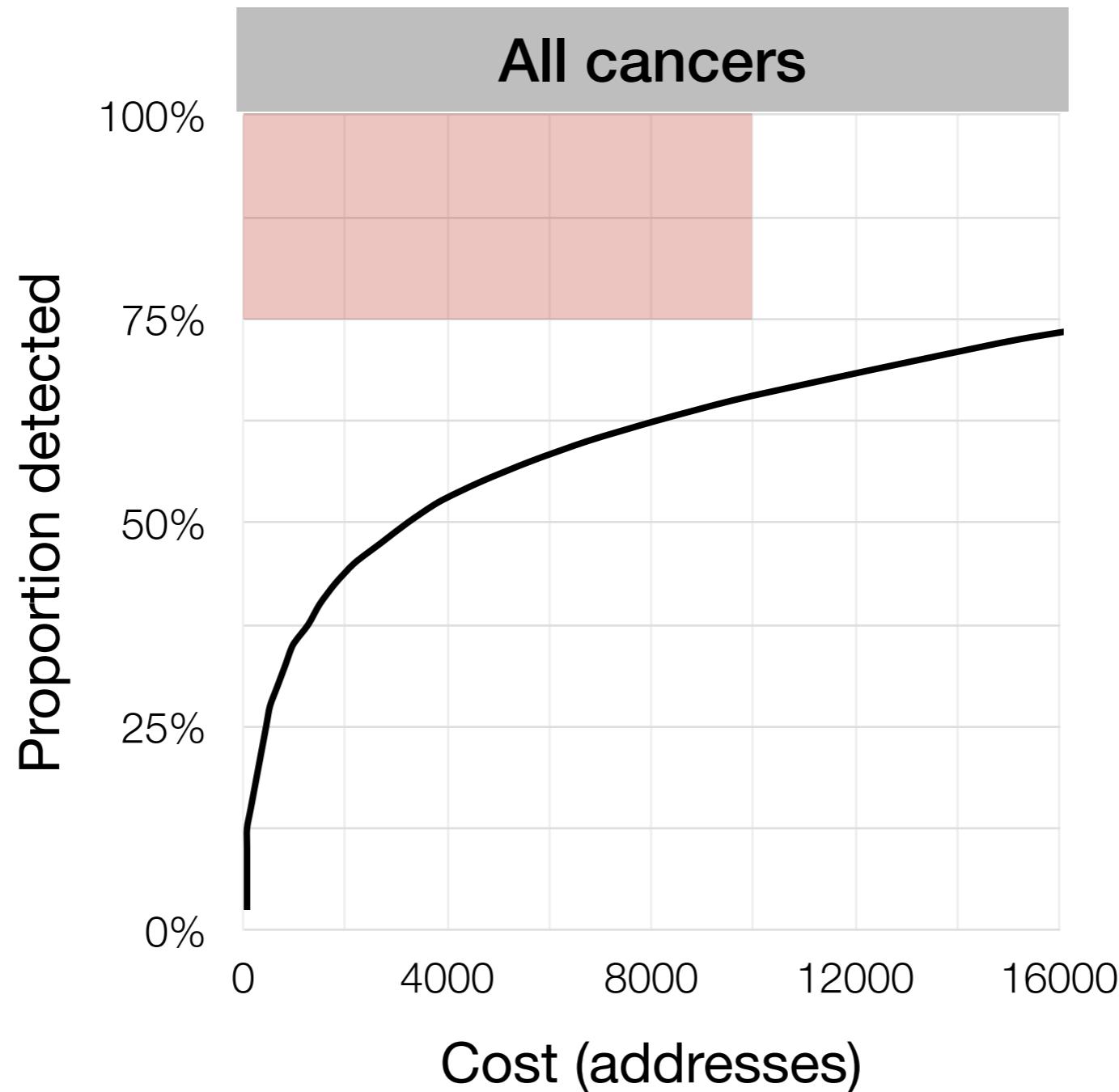
DNA Panels from [Cohen et al.]



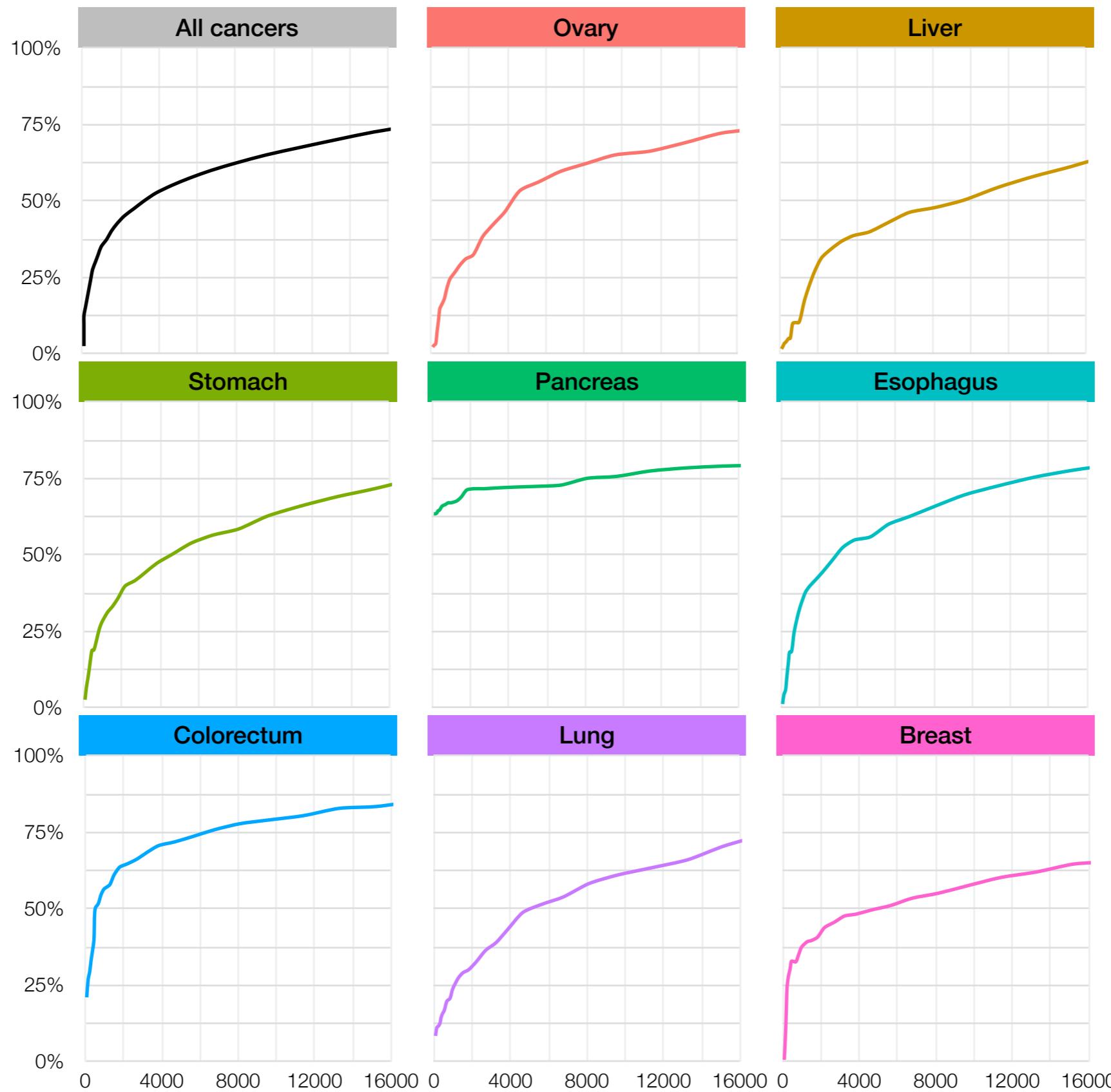
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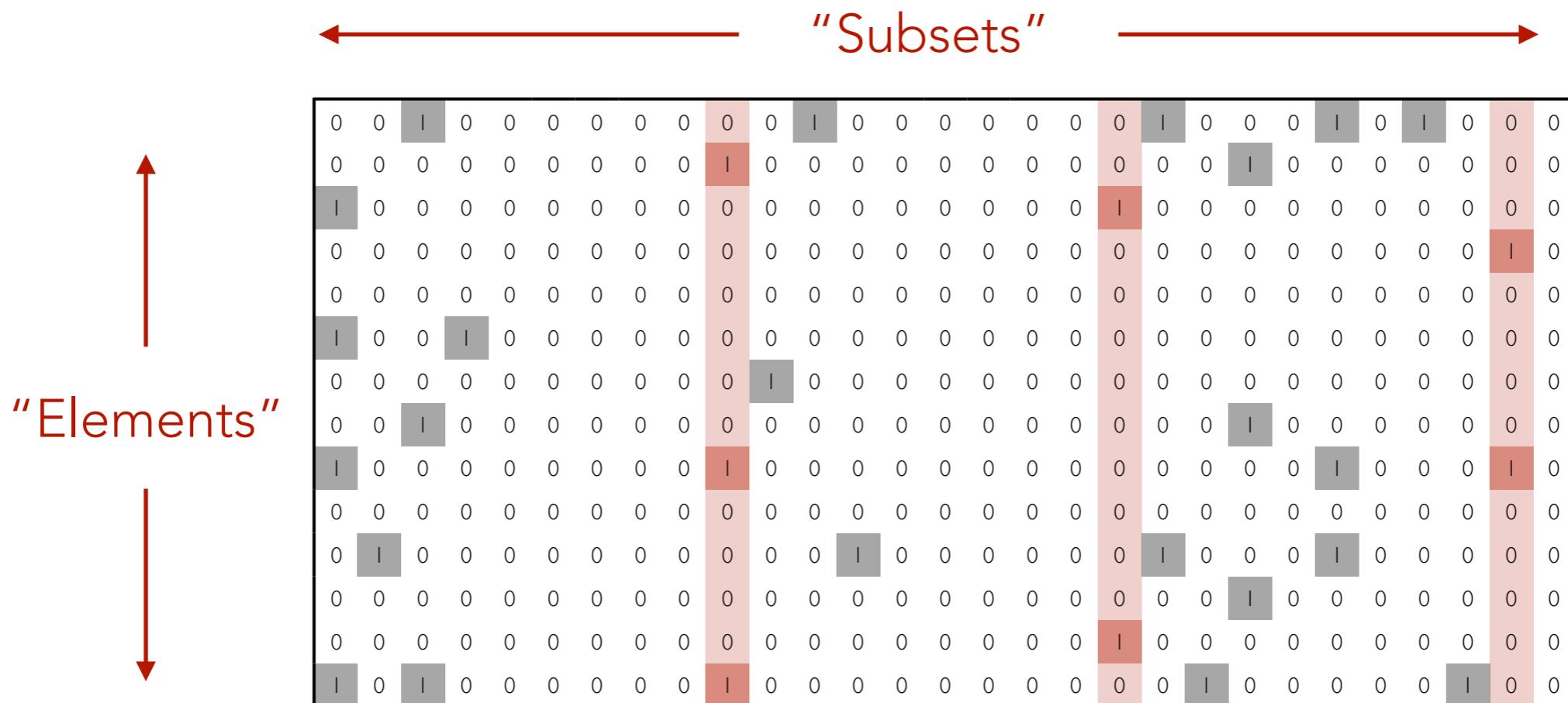


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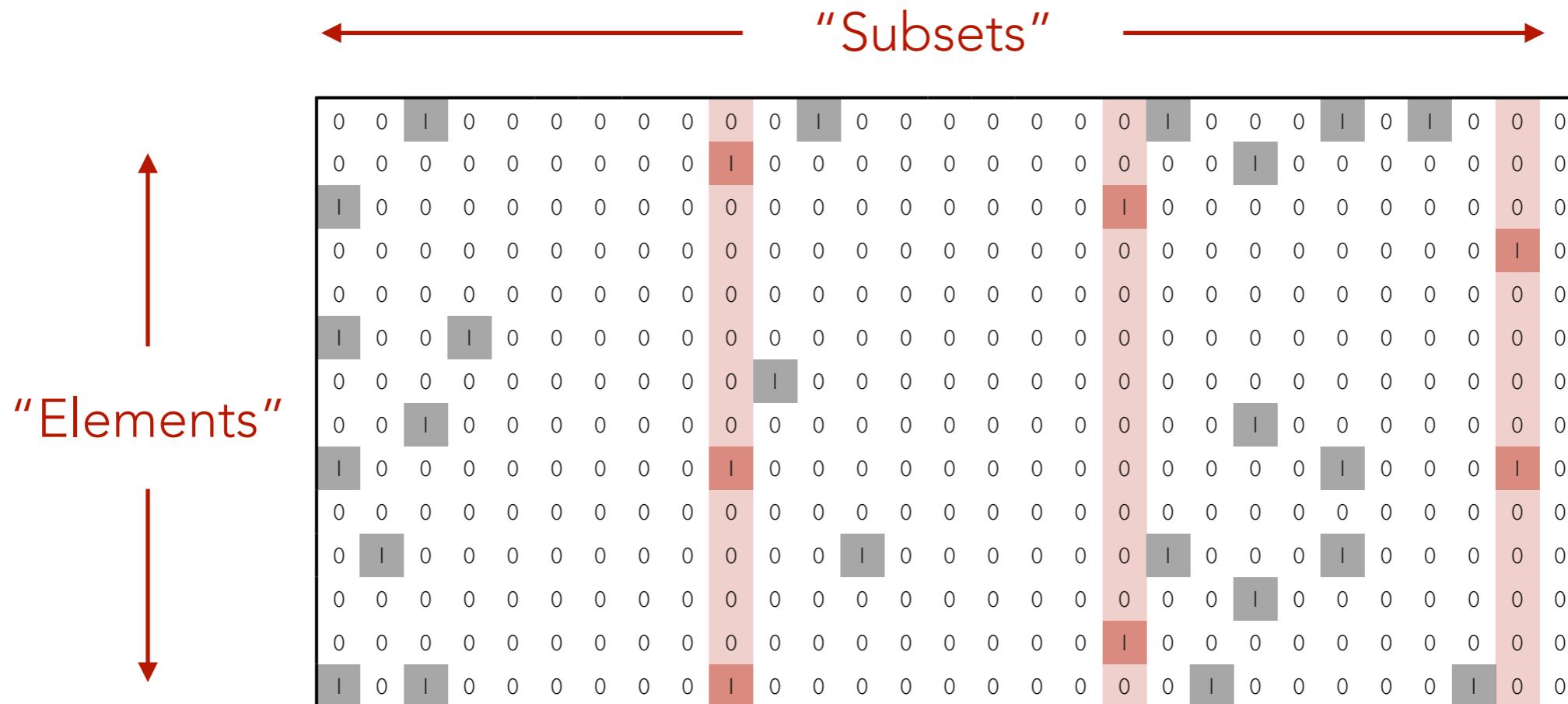
This is an optimization problem!

- *Max Cover*, to be specific



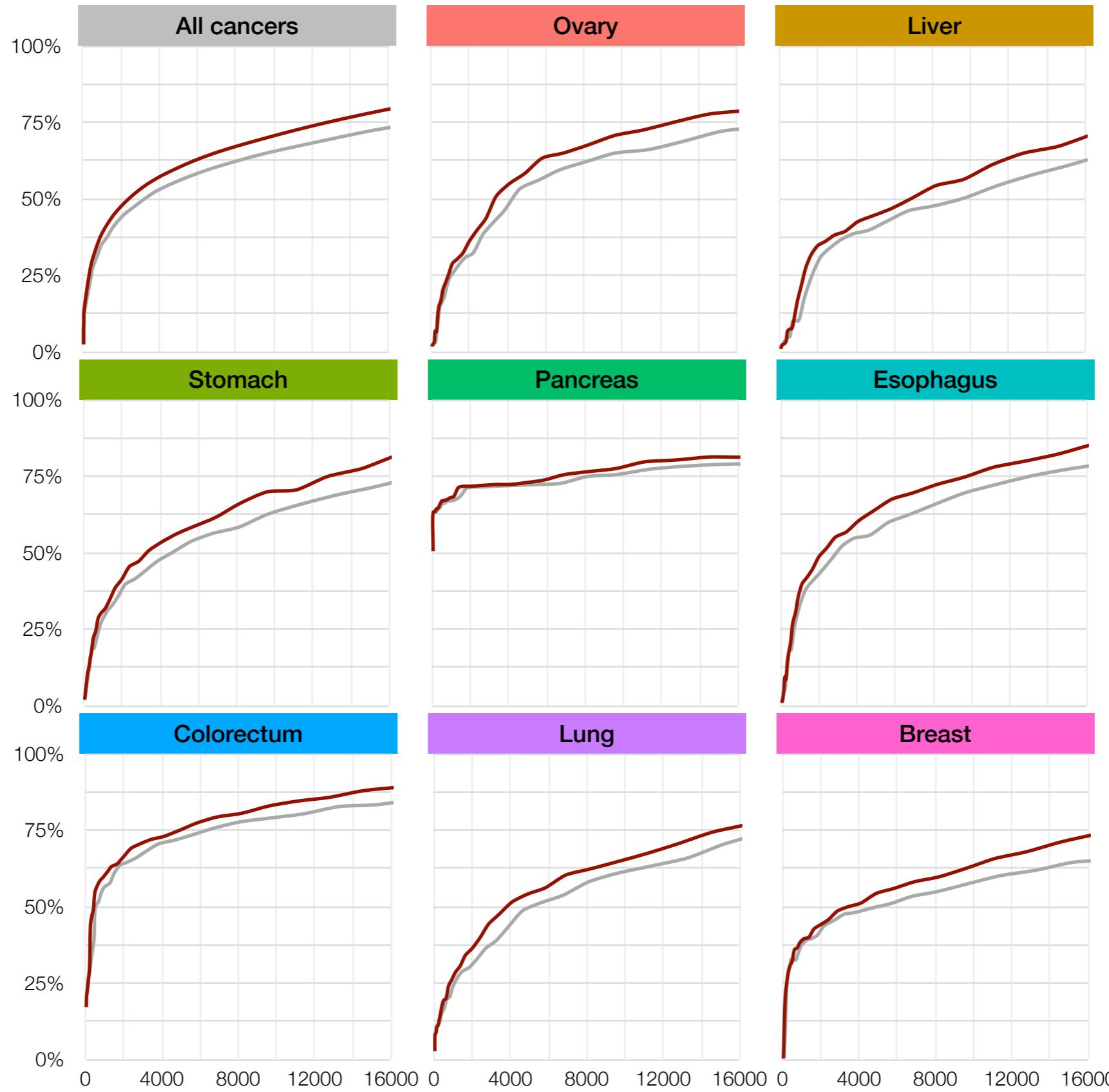
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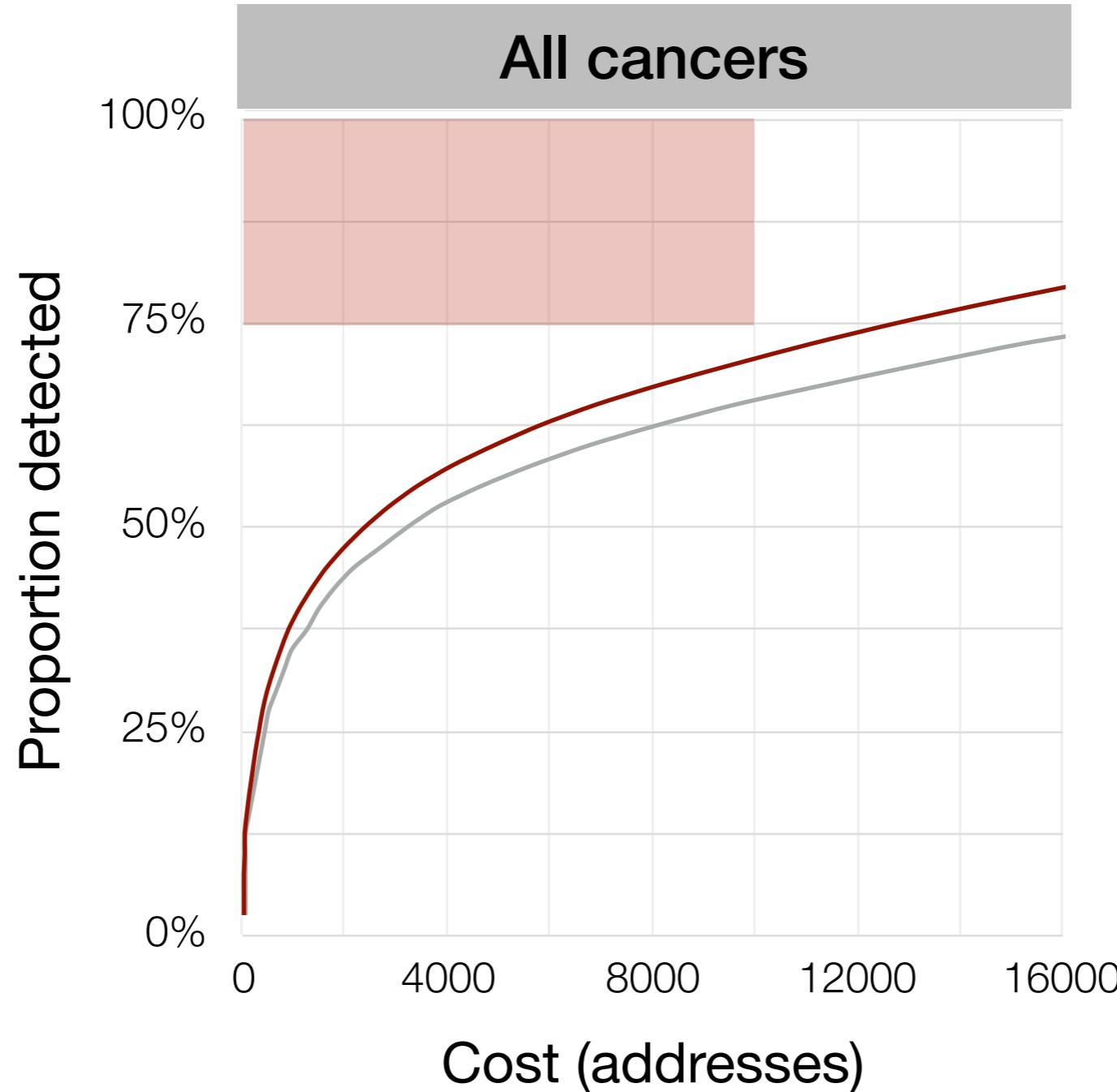


- Huge instance (10^4 elements, 10^9 subsets)
- Still solves in Gurobi

Optimal Panels



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Adaptive Panels

- **Adaptivity:** perform the test in stages
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- Challenge: this problem is **hard** (theoretically) and **hard** (practically)

A Simple Model for DNA Mutations

- Cancer types $t = 1, \dots, T$

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- DNA addresses $a = 1, \dots, A$

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← Addresses →

↑
Types
↓

0.09	0.80	0.68	0.34	0.59	0.56	0.66	0.10	0.07	0.14	0.80	0.74	0.05	0.25	0.90	0.30	0.58	0.62	0.18	0.12	0.12	0.30	0.61	0.27	0.38	0.88	0.62
0.26	0.17	0.68	0.16	0.25	0.01	0.78	0.56	0.05	0.82	0.97	0.49	0.65	0.99	0.73	0.85	0.45	0.60	0.25	0.28	0.83	0.54	0.29	0.85	0.66	0.48	0.69
0.70	0.84	0.47	0.69	0.98	0.66	0.41	0.65	0.51	0.97	0.82	0.92	0.74	0.75	0.53	0.34	0.40	0.67	0.12	0.08	0.58	0.62	0.41	0.41	0.66	0.99	0.83
0.01	0.28	0.03	0.46	0.50	0.26	0.73	0.44	0.68	0.74	0.31	0.31	0.62	0.92	0.04	0.61	0.74	0.47	0.44	0.45	0.87	0.24	0.68	0.55	0.28	0.34	0.87
0.18	0.03	0.57	0.14	0.07	0.99	0.17	0.66	0.02	0.05	0.87	0.80	0.03	0.45	0.75	0.43	0.07	0.06	0.51	0.57	0.16	0.96	0.85	0.89	0.91	0.06	0.06
0.29	0.18	0.53	0.81	0.64	0.69	0.83	0.30	0.06	0.94	0.26	0.15	0.19	0.92	0.35	0.36	0.99	0.97	0.14	0.10	0.51	0.11	0.84	0.81	0.66	0.00	0.42
0.01	0.96	0.49	0.02	0.52	0.97	0.21	0.82	0.49	0.09	0.60	0.46	0.93	0.07	0.55	0.06	0.74	0.74	0.24	0.88	0.92	0.10	0.58	0.09	0.78	0.36	0.96
0.75	0.45	0.64	0.67	0.26	0.15	0.72	0.17	0.49	0.05	0.36	0.86	0.77	0.86	0.90	0.88	0.13	0.99	0.08	0.34	0.65	0.95	0.73	0.13	0.44	0.21	0.42
0.14	0.42	0.31	0.99	0.63	0.43	0.62	0.12	0.78	0.77	0.92	0.36	0.80	0.89	0.33	0.29	0.62	0.99	0.80	0.85	0.07	0.67	0.13	0.26	0.57	0.58	0.56
0.24	0.48	0.13	0.55	0.16	0.56	0.89	0.18	0.11	0.43	0.65	1.00	0.57	0.52	0.47	0.89	0.03	0.72	0.49	0.36	0.65	0.34	0.71	0.19	0.15	0.56	0.52

$P \in \mathbb{R}^{T \times A}$

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0.26	0.17	0.68	0.16	0.25	0.01	0.78	0.56	0.05	0.82	0.97	0.49	0.65	0.99	0.73	0.85	0.45	0.60	0.25	0.28	0.83	0.54	0.29	0.85	0.66	0.48	0.69
0.70	0.84	0.47	0.69	0.98	0.66	0.41	0.65	0.51	0.97	0.82	0.92	0.74	0.75	0.53	0.34	0.40	0.67	0.12	0.08	0.58	0.62	0.41	0.41	0.66	0.99	0.83
0.01	0.28	0.03	0.46	0.50	0.26	0.73	0.44	0.68	0.74	0.31	0.31	0.62	0.92	0.04	0.61	0.74	0.47	0.44	0.45	0.87	0.24	0.68	0.55	0.28	0.34	0.87
0.18	0.03	0.57	0.14	0.07	0.99	0.17	0.66	0.02	0.05	0.87	0.80	0.03	0.45	0.75	0.43	0.07	0.06	0.51	0.57	0.16	0.96	0.85	0.89	0.91	0.06	0.06
0.29	0.18	0.53	0.81	0.64	0.69	0.83	0.30	0.06	0.94	0.26	0.15	0.19	0.92	0.35	0.36	0.99	0.97	0.14	0.10	0.51	0.11	0.84	0.81	0.66	0.00	0.42
0.01	0.96	0.49	0.02	0.52	0.97	0.21	0.82	0.49	0.09	0.60	0.46	0.93	0.07	0.55	0.06	0.74	0.74	0.24	0.88	0.92	0.10	0.58	0.09	0.78	0.36	0.96
0.75	0.45	0.64	0.67	0.26	0.15	0.72	0.17	0.49	0.05	0.36	0.86	0.77	0.86	0.90	0.88	0.13	0.99	0.08	0.34	0.65	0.95	0.73	0.13	0.44	0.21	0.42
0.14	0.42	0.31	0.99	0.63	0.43	0.62	0.12	0.78	0.77	0.92	0.36	0.80	0.89	0.33	0.29	0.62	0.99	0.80	0.85	0.07	0.67	0.13	0.26	0.57	0.58	0.56
0.24	0.48	0.13	0.55	0.16	0.56	0.89	0.18	0.11	0.43	0.65	1.00	0.57	0.52	0.47	0.89	0.03	0.72	0.49	0.36	0.65	0.34	0.71	0.19	0.15	0.56	0.52

$P \in \mathbb{R}^{T \times A}$

- Sequencing address a on individual of type t :
- Yields observation $\sim \text{Ber}(P_{ta})$

Problem: Active Sequential Hypothesis Testing

- Unknown cancer type drawn according to (known) **prior**

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- **Partial Adaptivity:** select a **sequence** of addresses
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- Constraint: correctly identify type with probability at least $1 - \delta$
- Objective: minimize **expected cost** (number of addresses used)

Theoretical Guarantee

- Recall:
 - A = number of addresses (3 billion)
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Brute Force	A^L	OPT

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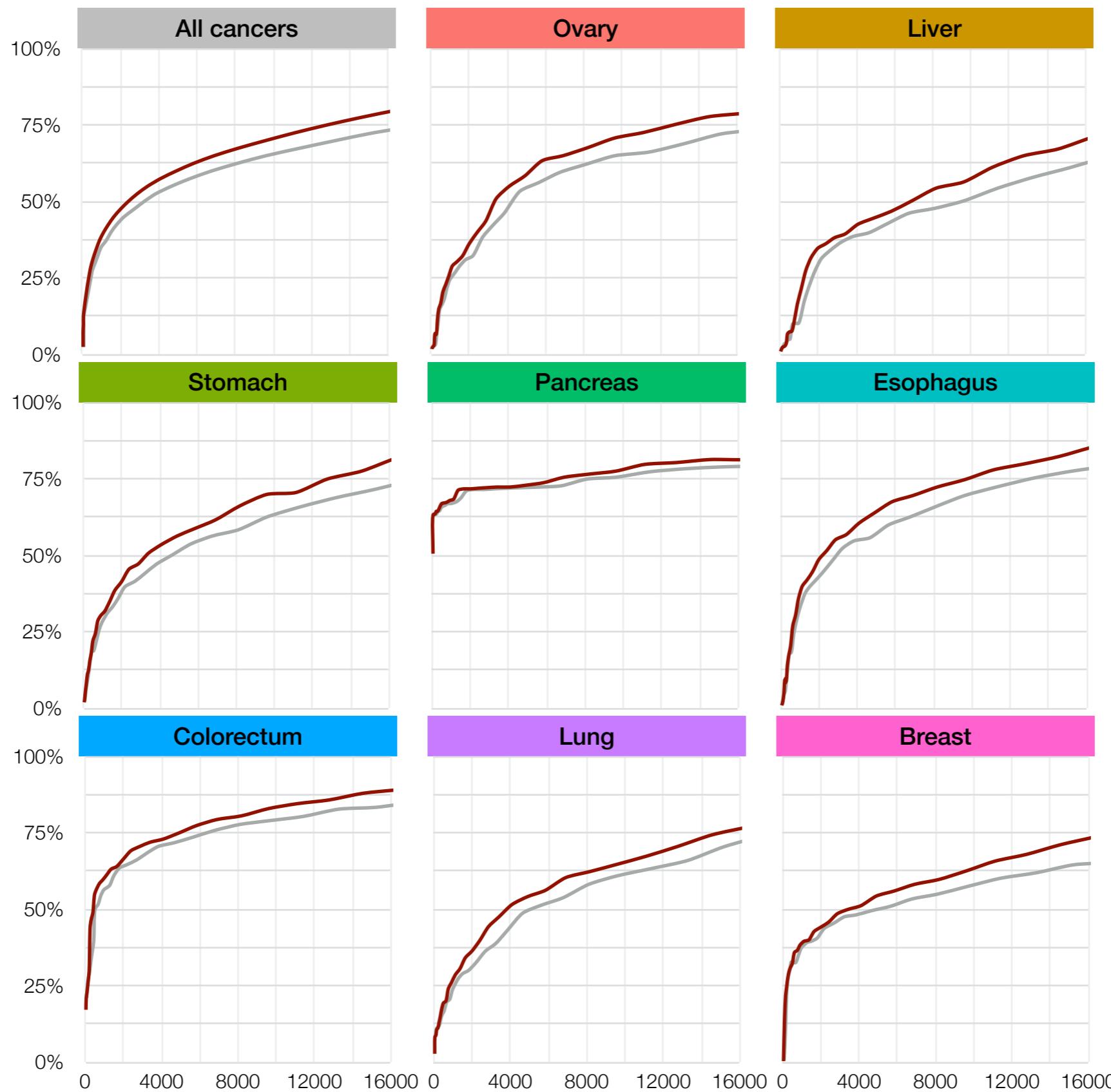
	Runtime	Cost Guarantee
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Theoretical Guarantee

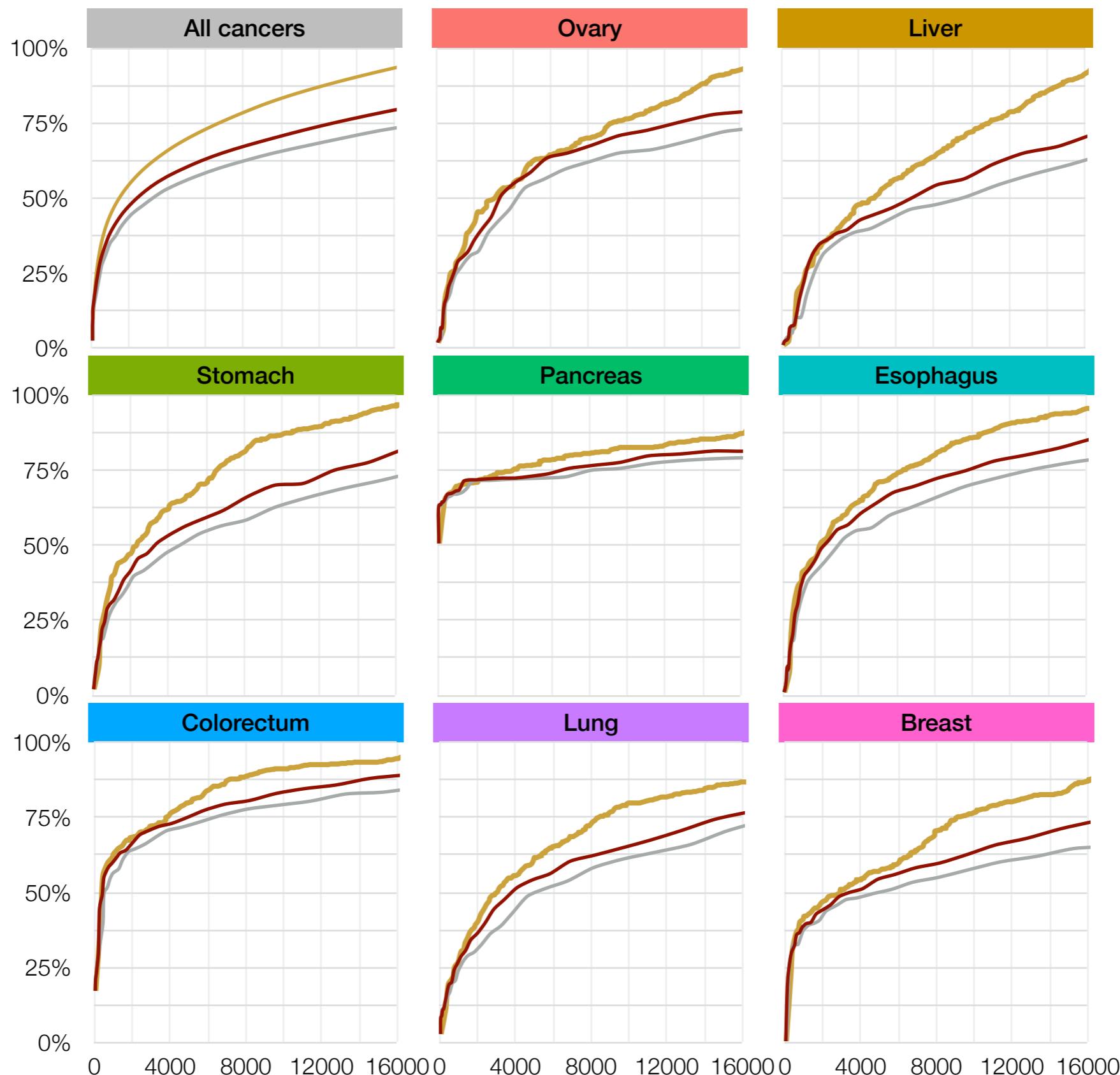
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	Runtime	Cost Guarantee
Brute Force	A^L	OPT
LP Heuristic [Naghshvar,Javidi'13]	$O(AT^2)$	None
Our Algorithm	$O(ATL)$	$O(\log T + \log \log \delta^{-1})$ OPT

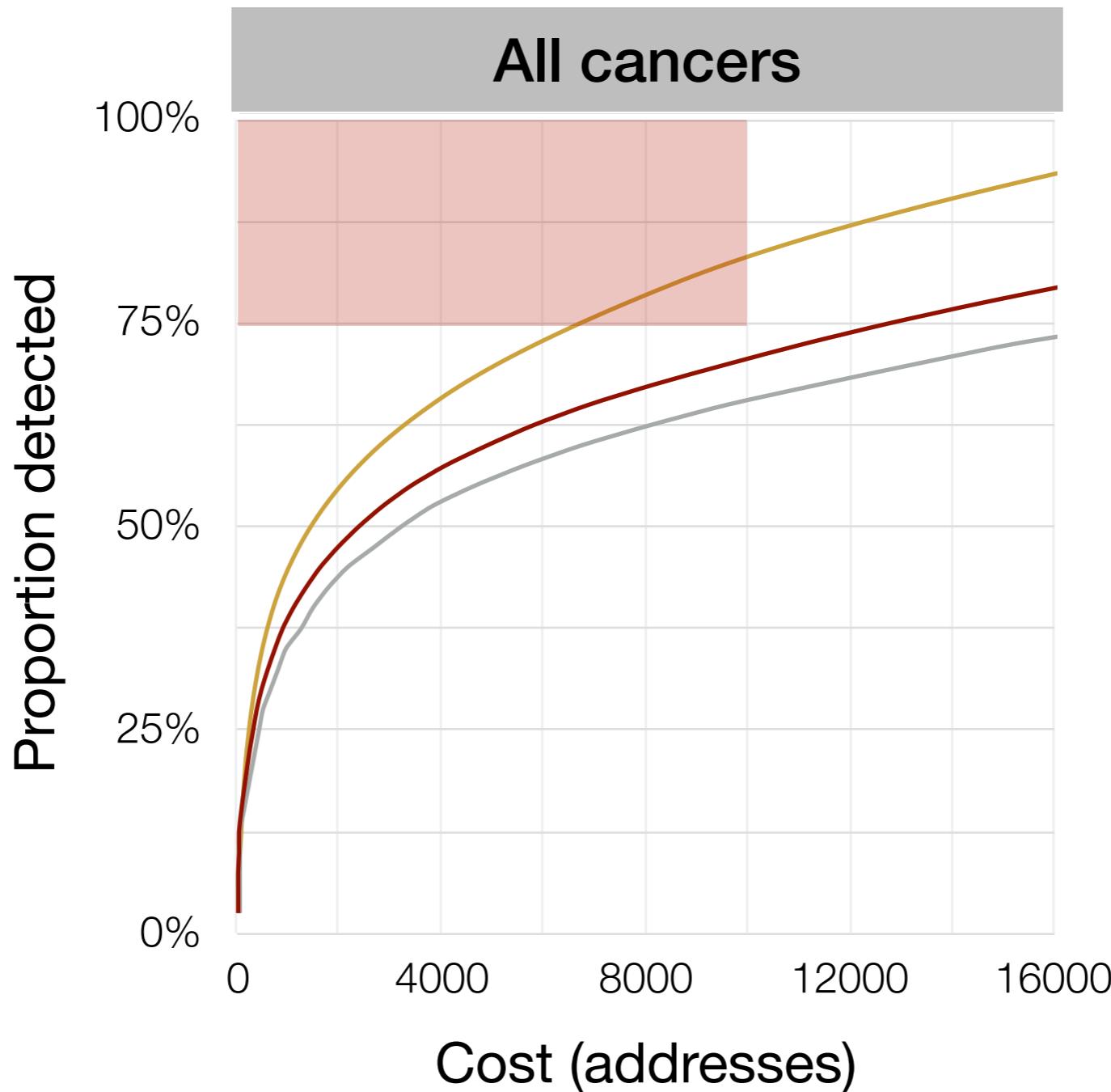
Optimal (Non-adaptive) Panels



(Sub-optimal) Adaptive Panels



(Sub-optimal) Adaptive Panels



Thanks!