

---

---

# Tapestry Pooling

— IITB-InStem-NCBS-Wyss —

---

---

Asymptomatic super spreaders

Test → Ease Lockdown → Reboot Economy

Enhance PCR testing

More results per test

Faster

Conserve Effort

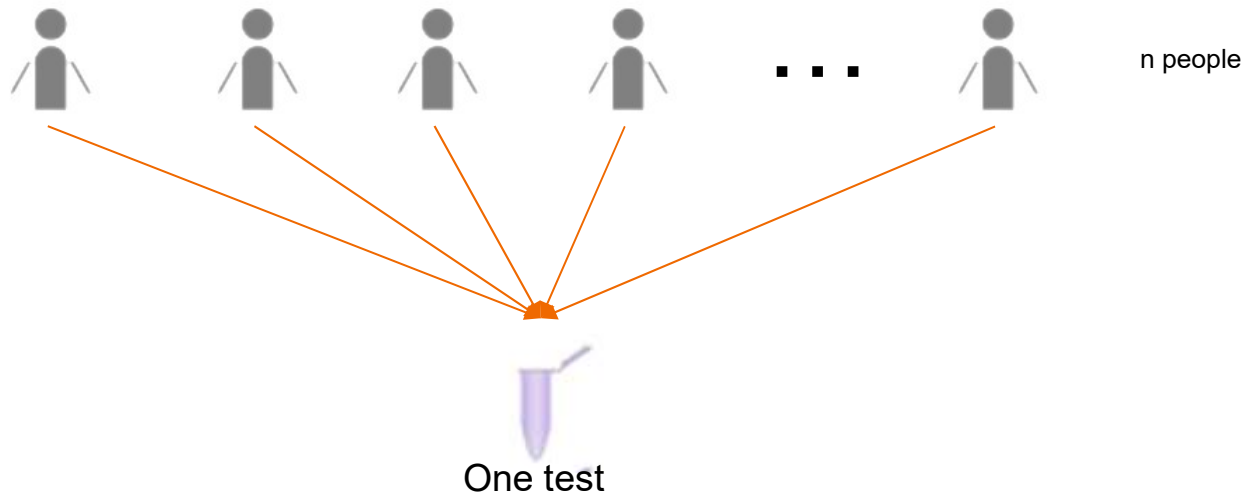
Conserve PPE, Kit, Reagents

High prevalence

Tapestry Pooling



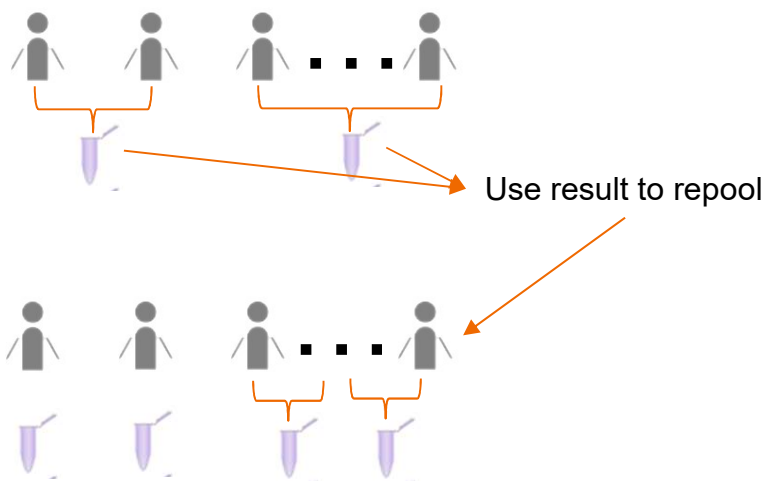
# Pooling



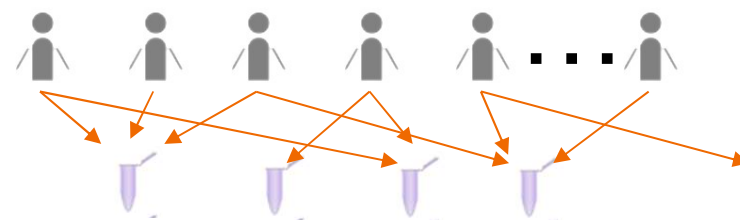
Positive result

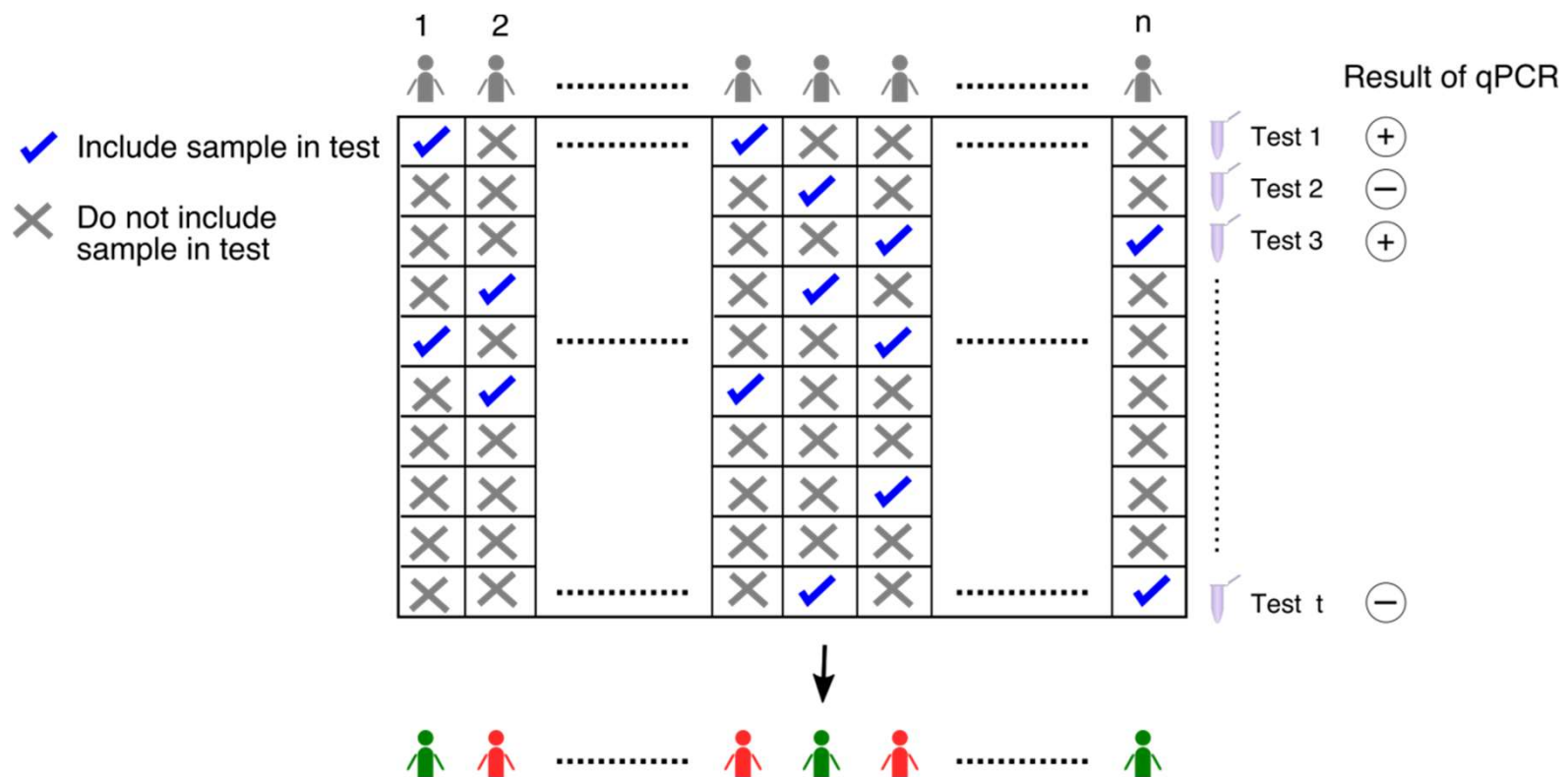
- Don't know which individual(s) are positive
- Do more tests or quarantine all

### Dorfman Pooling



### Tapestry Pooling





### Patient Samples

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	Ct Values					
T1		1											1	1				1																1	1				1							
T2		1			1						1						1								1			1								1										
T3					1			1	1			1												1				1			1		1											30.93		
T4	1		1		1										1							1				1				1			1													
T5					1					1				1			1					1								1							1									
T6			1									1						1		1					1													1	1							
T7								1		1															1		1													1	1	1				
T8										1		1								1				1	1													1						31.04		
T9	1															1							1					1			1	1								1				30.54		
T10	1			1					1													1					1					1								1						
T11			1							1							1	1								1									1	1				1						
T12		1							1						1	1						1			1																					
T13			1										1	1									1					1	1	1																
T14													1	1											1		1				1			1						1						
T15					1					1											1	1							1								1	1					1			30.67
T16			1			1	1			1													1								1					1						1				30.17

30.8

30.8

Each sample : 3 pools

Quantitative

Pool Ct values:  $y = (y_1, y_2, \dots, y_m)'$

Sample viral loads:  $x = (x_1, x_2, \dots, x_n)'$

A: Pooling Matrix

Solve  $Ax = y$  for sparse  $x$

**Compressed Sensing (CS).**

---

Viable upto 20% prevalence

Quantitative reconstruction

Conserves kits

Single round: Fast Results, Less work, Save PPE

Prior information



# Tapestry Pooling by Numbers

Samples	Tests	Prevalence rate	Pool size
50	30	20%	5
72	36	12%	6
105	45	10%	7
70	21	5.71%	10
195	45	4.1%	13
399	63	2.5%	19
961	93	1%	31

---

# Experimental Validation

Synthetic COVID-19 RNA genome spiked into mock samples.

120 samples in 40 tests with 3 positives

- Correctly identified all 3

1140 samples in 90 tests with 11 positives

- 18 minutes pipetting with a liquid handling robot!
  - Correctly identified all 11 positives
  - Three false positives
-

# Clinical Trials with COVID19 samples (Ongoing)

105 samples in 45 tests with 7,8 positives

- Correctly identified all 210 samples

320 samples in 48 tests with 5 positives

- Correctly identified all 320 samples

500 samples in 60 tests with 10 positives

- No false negatives, 5 false positives
-

# Guarantees

## **Graceful failure**

Call each sample positive or negative

Unexpectedly many positives → few samples called undetermined

**Sparse:** Small pool sizes saves on pipetting

**Robust** to errors in pipetting, contamination

**Tested:** 2000 clinical samples\*

\*Clinical trials projected to finish by July 27

---

# Team

## At IIT Bombay

Manoj Gopalkrishnan, Ajit Rajwade, Sabyasachi Ghosh, others

Phone App: Aditya Gupta, Vidhya Appu, Raunak Ramakrishnan, others

## At NCBS-InStem

Dasaradhi P, Sandeep Krishna, Srikar Krishna, Anirudh, Sriram Varahan, Vinay Sagar, others

## At Wyss Institute - Harvard Medical School

Peng Yin, Nikhil Gopalkrishnan, Thomas Schauss

MG and AR thank WRCB and DST for funding