Accelerating COVID-19 testing: An experimental approach

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The COVID-19 pandemic, ever since its global outbreak in 2020, has continued to wreak havoc. Governments across the world were compelled to enforce strict nation-wide lockdowns, while emphasising on social distancing and quarantining suspected people in order to slow down the spread of the virus. During this time, there was a massive increase in demand for COVID-19 test kits. However, given the limited supply, countries were finding it hard to test enough people. This study proposes an approach called Encoded Blending (EB) to increase the number of tests drastically, without increasing the number of test kits. EB modifies the pooled testing method; this has been followed by countries like Germany, Israel and South Korea for mass testing their citizens. EB has the potential to reduce test kits requirement by up to 85% and 80% in a population with 5% and 10% affected cases, respectively.

KEYWORDS
COVID-19, experiment, India, pandemic control, pooled testing, test kits

1 INTRODUCTION

On 31 December 2019, the country office of World Health Organization (WHO) in China was informed of cases of pneumonia of unknown etiology (unknown cause) detected specifically in Wuhan city, in the Hubei Province. The Chinese authorities later (on 7 January 2020) identified this as a new type of Coronavirus (nCoV), which later came to be known as COVID-19. The clinical name for this disease is Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). People affected developed symptoms, including respiratory problems and fever.

The virus spreads quickly through respiratory droplets of infected people or through handshakes, among other possible ways. On 11 March 2020, WHO declared COVID-19 a global pandemic; and as of May 2022, there were more than 520 million confirmed cases across 220 countries with 6.27 million deaths (https://covid19.who.int/). Some of the worst affected nations included USA, Spain, Italy, Brazil, France, Russia, India and China. The phase of acute shortage of vaccines is over, however there is still a shortage of supply, and controlling the spread is vital to coping with the existing healthcare infrastructure. Specifically, in India, the government undertook various initiatives to curb the spread of the virus (Kaushal & Dogra, 2020). Still, there were more than 43 million confirmed cases, and about 524,000 deaths reported as of 19 May 2021 (https://www.mohfw.gov.in/). As per the Lancet’s COVID-19 Commission report of April 2021, the situation become much worse in the second wave, and by the start of June-2021, India was forecasted to witness over 2300 deaths per day.

Since the time that it was declared a pandemic, countries have been trying their best to find a cure. In the absence of which, the general modus operandi was containing the spread of the virus through complete nationwide lockdowns, social distancing, and personal hygiene (washing hands) (Tuncer, 2020). The economic cost of the lockdowns has been enormous, estimated to be 7.2 trillion USD in USA alone (Thunstrom et al., 2020). Soon enough there were vaccines that were available in record time, but there were plaguing issues in terms of their efficiency and availability, and the time needed to build antibodies, among others. Therefore, one of the most important aspects to reduce the spread of the virus was to test individuals, given the significant occurrence of asymptomatic but highly contagious individuals in the localities. Massive testing was necessary to provide medical treatment to COVID-19 patients (Manrai & Mandl, 2020). Furthermore, the governments decided that mass testing would allow virus-free people to work; the rationale behind the same was to restart the economy, while ensuring that there was no danger of bringing on a fourth or fifth wave of the virus. However, the number of test-kits needed fell woefully short; mass testing was becoming difficult both in developed and developing countries too (Gollier &
Each test-kit needed to be viewed as a valuable resource, and be used as efficiently as possible.

Given this backdrop, in this study, we propose a new approach of the pooled test called Encoded Blending (EB) as a solution to this problem. We believe that EB is an efficient way to test a large number of people with limited number of kits as compared to traditional testing. EB is a modified pooled testing that would optimise the number of tests, yielding either a negative or a positive outcome. A negative outcome would mean that nobody has a virus within a group of people, while a positive outcome would imply that at least one person within the group is possibly infected. In the process, this would save a number of test kits, along with testing time, and other vital resources (e.g., lab, number of the pathologist, and so on).

2 | COMBATTING COVID-19

The COVID-19 pandemic has put significant pressure on governments and healthcare systems alike. By May 2022, the case load recorded was about 3.7 million every day on a seven-day average globally (https://covid19.who.int). It may be noted herein that the rate at which a population becomes infected, effectively determines whether there are enough hospital beds (and doctors and resources) to treat the sick. In epidemiology, the idea of slowing down a virus’ spread so that fewer people are required to seek treatment at any given time is known as ‘flattening the curve’. The curve refers to the number of people affected at a given time. The idea is better depicted in Figure 1.

A steep curve is reflective of the virus spreading exponentially, whereby the cases skyrocket, and the local healthcare system gets overloaded beyond its capacity to treat people. A flatter curve, on the other hand, assumes the same number of people ultimately get infected, but over a more extended period. This phenomenon means a less stressed healthcare system.

While countries adopted stringent lockdowns, followed by other COVID-19 protocols (e.g., social distancing, wearing masks, sanitization, vaccination etc.) to ‘slow down the virus spread’, the question that many asked was ‘were these efforts enough to flatten the curve?’

On 16 March 2020, Tedros Adhanom, Director-General, WHO, said:

Social distancing measures can help to reduce transmission and enable health systems to cope. Handwashing and coughing into your elbow can reduce the risk for yourself and others. However, on their own, they are not enough to extinguish this pandemic. It is the combination that makes the difference. The most effective way to prevent infections and save lives is by breaking the chains of transmission. Moreover, to do that, you must test and isolate. You cannot fight a fire blindfolded. Moreover, we cannot stop this pandemic if we do not know who is infected. We have a simple message for all countries: test, test, test.

3 | COVID-19 TESTING BY COUNTRIES

Interestingly, some countries were able to ‘flatten the curve’ through aggressive testing. For instance, South Korea ramped up its testing capacity, and embraced ‘testing and treating early’ as the cornerstone of its policy response to the COIVD-19 outbreak. According to the Korean Centre for Disease Control and Prevention, the country had tested 503,051 people (around 9812 people per million population). Herein, the first COVID case was detected on 19 February 2020; and as of 10 April 2021, there were 108,945 confirmed cases, 208 deaths, and less than 100 new cases every day, since the start of April. This is the reason why South Korea had one of the lowest mortality rates due to COVID-19.

As on 10 April 2020 Italy witnessed the highest number of deaths (i.e., 18,279)—due to its delayed reaction to the pandemic. Interestingly, within the country, one could see contrasting efforts and results.

FIGURE 1  Flattening the curve. Source: The U.S. Centers for Disease Control and Prevention (CDC)-2020
between regions with similar socioeconomic profiles (Pisano et al., 2020). For example, let us consider two regions: Lombardy and Veneto. Lombardy was disproportionately hit with 791,000 CoV cases, and more than 32,000 deaths in a population of 10 million. Veneto, by contrast, faced 406,000 cases and little more than 11,000 deaths in a population of 5 million, despite experiencing sustained community spread early on (as on 22 April 2021). While Lombardy and Veneto had similar approaches to social distancing and retail closures, Veneto took a much more proactive step towards the containment of the virus. The critical difference with Veneto was as follows:

- Extensive testing of symptomatic and asymptomatic cases early on.
- Proactive tracking of potential positives. If someone tested positive, everyone in that patient’s home, as well as their neighbors, were tested.

These countries have shown the world that effective testing did allow the governments and health authorities to understand how prevalent the disease was, and how it has been evolving. Tracking positive test results helped authorities make evidence-based decisions to try and slow its spread. However, not every country was able to do conduct tests at scale, especially countries as densely populated as India. Figure 2 is a snapshot of the number of tests performed by most impacted countries worldwide (data compiled as of 24 April 2021).

On the other hand, countries like Germany, Israel and South Korea were able to contain the virus spread through aggressive mass testing (Jeffay, 2020). An important question in this scenario would be: how were these countries able to test a large number of their populous while others were not?

Herein it may be noted that each country did have a different need for testing, depending on several factors, like the active number of cases, diversity of virus spread, infrastructure etc. However, for every country, it was imperative to be prepared to ramp up the current testing infrastructure if the virus continued to spread at the current rate. This was true especially for countries like India with 1.3 billion people, but with one of the least Tests/1 M population. This paper proposes an approach to increase the number of tests drastically without increasing the number of test kits required. This approach has the potential to reduce the number of test kits and the associated costs and time. The results show saving kits by up to 85% and 80% in a population with 5% and 10% positive cases.

4 | COVID-19 TESTING PROCESS

The most commonly used test has been RT-PCR test (Gollier & Gossner, 2020). It is a real-time reverse transcription-polymerase chain reaction (rRT-PCR) test for qualitative detection of nucleic acid from SARS-CoV-2 in upper and lower respiratory specimens (such as nasopharyngeal or oropharyngeal swabs, and sputum) collected from individuals suspected of COVID-19 by their healthcare provider. It usually takes around 5 h to deliver results. Figure 3 represents the pictorial representation of COVID-19 testing process.

5 | ACCELERATING COVID-19 TESTING

As discussed earlier, one of the major bottlenecks in the COVID-19 testing process was the limited supply of testing kits. With governments trying to partner with manufacturing firms to increase the testing capacity multifold, this paper suggests measures to increase the number of tests drastically without increasing the number of test kits. EB is not a technical breakthrough, but a logistical approach to
enhance the testing efficiency, and the numbers shown are indicative and experimental, and are subject to changes because of other technical constraints.

In this experiment, we consider a sample size of 140 people to be tested. When we follow conventional testing methodology, wherein we use a single test kit to test a single sample, the number of test kits we use end up being 140.

Some countries, therefore, went on to innovate the testing methodology and brought in a ‘pooled testing’ concept which happens in a phased manner (12, 18 and 24). Pooled testing is not a new idea; it was first adopted for detecting syphilis (Dorfman, 1943), hepatitis B (Fernandez et al., 2006), avian pneumovirus (Miller et al., 2009), and HIV (May et al., 2010; Weinberg, 2020). Pooled testing for COVID-19 has been employed in Israel and Nebraska, USA. Sunjaya and Sunjaya (2020) argued that for COVID-19, pooled testing has proven to be capable of detecting positive samples with adequate precision, and that it can be effectively implemented for population-wide screening, using existing equipment and staff. Cherif et al. (2020) stated that pool testing is a workable option, but the reliability of testing differs, depending on prevalence, test sensitivity and the size of the patient pool.

COVID-19 has been identified as ‘an ideal candidate for pooled testing’, because the viral load in persons increases quickly, plateaus for a while, and then drops quickly; consequently, the window of detection is relatively long. Because samples are diluted when pooled, proportionally less viral genetic material is available for detection, resulting in a greater likelihood of false negatives, which can vary by methods. However, a number of studies have indicated that a weak positive sample within the limit of detection of the assay may be identified in pooled studies. Currently, literature indicates that with a pool size of 32 for instance, sensitivity is 90% relative to that of a single analysis (10% false negative rate). Notably, ‘sensitivity here refers to sensitivity of the pool versus sensitivity of testing each of the individuals in the pool’ and pertains to one study and one model (Schulte et al., 2021).

To put it in layman terms, pooled testing means testing a combined sample (blend) of a pool of patients, say 14 in number. Now, there are 10 blends created for 140 patients, with each blend having 14 samples combined within them. In Phase 1, these 10 blends are tested using 10 test kits individually.

If the combined sample (blend) tests negative, it means that all 14 patients belonging to that blend are negative. On the other hand, if the combined sample tests positive in Phase-2 of the testing process, each of those 14 patients is then tested further individually. This testing works on a mass scale, as most of the times, the combined sample tests negative, saving thereby 13 potential tests. However, in rare cases, if it tests positive, it is just one extra test wasted.

6 ENCODED BLENDING

For this study, we have slightly altered the pooled testing methodology to increase testing efficiency. This technique involves combining (or blending) multiple samples into one, like the pooled testing method. However, it differs from pooled testing in the way the test results of these blended samples are interpreted. The method involves basic binary arithmetic-based encoding-decoding mechanism to identify the unique set of individual samples in the pool that might be COVID positive.

In this method, the number of kits required for testing is much less than the conventional methods of testing and pooled testing. Additionally, in this approach, the tests take place in a phased manner, with Phase-1 being the same as in pooled testing methodology explained earlier. However, for Phase-2 of testing, the approach differs.

Let us consider 14 patients (numbered 1–14) to be tested for COVID-19. We use label encoding to encode the patients into a four-digit binary format; thus, the codes for the patients range from (0000) to (1110). The encoding schema is shown in Table 1.

Now, we consider four test blends/pools for the four digits of encoding (Blend 1, Blend 2, Blend 3 and Blend 4). For each of the
blends/pools, samples with patients having encoding as 1 for that digit are blended and tested. We also have four test kits—K1, K2, K3, and K4—to these blends, respectively.

Thus, we see that the first patient’s sample is blended into the fourth blend, while patient number 14 is blended into the first, second and third blend, and so on. The blend schedule is created based on simple binary arithmetic where every patient ID is converted into a four-bit binary number.

Now, each of the blends (Blend 1 to Blend 4) is tested individually, using the corresponding test kits (K1–K4).

### 6.1 Encoded blending mechanism

Then, we encode the test results using elementary binary logic. Let us record each test result in the following format: results from test kit K1, K2, K3 and K4. Note that number 1 is to be used in case a particular blend tests positive and number 0 is to be used if it tests negative. For example, if Blends 1 and 3 test positive, while Blends 2 and 4 do not, then the overall result is to be recorded as 1010. Similarly, if Blend 4 alone tests positive while all others test negative, the result is to be recorded as 0001, and so on.

Now, the encoded test results are decoded and converted to decimal numbers using binary arithmetic logic. This decimal number then points to the patient ID that could be positive. For example, if the first blend tests positive, while all others test negative, the encoded value is 1000. This unique result is possible only when patient 8’s sample tests positive, while others test negative. The easiest way to identify the patient ID is to find the decimal equivalent of encoded value (1000), which is 8. However, the decoding approach changes in case more than one blend tests positive.

Overall, there are four results possible:

1. Exactly one blend tests positive
2. Exactly two blends test positive
3. Exactly three blends test positive
4. All blends test positive

#### Case 1. Exactly One Blend Tests Positive.

Here, we can quickly identify the positive sample based on which, the blend turned out to be positive. Patient number 8 was the only sample, which was blended into only Blend 1; and hence, if only Blend 1 tested positive, it means that patient number 8 is positive. (Note: Write the binary code for test results of Blend 1, Blend 2, Blend 3 and Blend 4 as 1000 [positive, negative, negative, negative] in this case. The decimal equivalent of 1000 is 8. Similarly, if only blend two tests positive, the binary code is 0100, and the decimal equivalent is four, and so on.) Thus, we would require only four tests for 14 patients to identify positive cases. In the process, we could save 10 test kits as compared to regular testing.

#### Case 2. Exactly Two Blends Test Positive.

In this case, it is not possible to identify the positive patient directly. This is because, for example, if Blends 1 and 2 test positive, then it translates to a binary code of 1100, and a decimal equivalent of 12. Therefore, patient number 12 can be positive; alternatively, both patient number 4 and 8 can be positive ($4 + 8 = 12$); or all three can be positive. In either of these cases, we get the same binary code: 1100. Hence, we need to test these three patients individually. Thus, we would require 7 ($4 + 3$) tests to identify positive cases from a sample size of 14. Overall, in this case, we could save seven test kits as compared to regular testing.

#### Case 3. Exactly Three Blends Test Positive.

This case is like case 2 but with more possibilities. For example, let us assume that Blends 2, 3 and 4 test positive. This translates to a binary code of 0111. This has multiple possibilities—patient number 7 can be positive, patient number 1 and 6 can be positive, patient number 3 and 4 can be positive, patient number 2 and 5 can be positive, or all the above. Hence, we need to test these seven patients individually. Thus, we would require 11 ($4 + 7$) tests to identify the positive from a sample size of 14. In this case, we could save seven test kits as compared to regular testing.

#### Case 4. All Blends Test Positive.

This covers the entire spectrum of possibilities (patient number 13 and 14 are positive or patient number 7 and 14 are positive, or patient number 1 and 14 are positive or patient number 2 and 13 are positive, and so on), and it becomes complicated as to who is a suspect. Thus, we need to perform individual tests on all 14 patients. This pushes the number of tests required to 18 (see Figure 4). In this case, we need four more test kits as compared to regular testing.

### Table 1

| Patient ID | Blend 1 | Blend 2 | Blend 3 | Blend 4 |
|------------|---------|---------|---------|---------|
| 1          | 0       | 0       | 0       | 1       |
| 2          | 0       | 0       | 1       | 0       |
| 3          | 0       | 0       | 1       | 1       |
| 4          | 0       | 1       | 0       | 0       |
| 5          | 0       | 1       | 0       | 1       |
| 6          | 0       | 1       | 1       | 0       |
| 7          | 0       | 1       | 1       | 1       |
| 8          | 1       | 0       | 0       | 0       |
| 9          | 1       | 0       | 0       | 1       |
| 10         | 1       | 0       | 1       | 0       |
| 11         | 1       | 1       | 0       | 1       |
| 12         | 1       | 1       | 0       | 0       |
| 13         | 1       | 1       | 0       | 1       |
| 14         | 1       | 1       | 1       | 0       |

Source: Developed by authors.
Table 2 shows a scenario analysis of the difference between conventional and pooled testing at various levels of percentage of positive cases per sample of 140.

For each of the scenarios, the number in conventional tests remains the same.

**Scenario 1:** 5.00% of sample size test positive (7 patients)
- **Pooled Testing**
  - The number of tests range from 24 to 108 (see Figure 5)
- **Encoded Blending**
  - The number of tests range from 21 to 87

**Scenario 2:** 7.50% of sample size test positive (11 patients)
- **Pooled Testing**
  - The number of tests range from 24 to 150 (see Figure 7)
- **Encoded Blending**
  - The number of tests range from 28 to 148

**Scenario 3:** 10.00% of sample size test positive (14 patients)
- **Pooled Testing**
  - The number of tests range from 24 to 150 (see Figure 9)

**Encoded Blending**
- The number of tests range from 28 to 148 (see Figure 10)

From Table 2, at both 5% and 7.5%, EB yields better results than conventional testing or Pooled Testing, even in the worst case.

However, at 10.00%, in the worst-case scenario, EB’s results are worse compared to conventional testing (i.e., 148 as compared to the traditional number of 140). However, while comparing these tests, it is the range that should be investigated between the best and worst cases rather than the number itself. The range comparison between EB approach and Pooled Testing approach indicates significant savings in the number of test kits. The comparison with conventional tests is described here.

From Figure 10, we see that EB approach when applied at 10% positivity rate might require anywhere between 28 tests, which is the best case, and 148 tests, which is the worst scenario. Assuming a uniform distribution of these scenarios (ranging between 28 and 148), about 92.5% of the times, the EB approach would require lesser tests than the conventional approach, which requires 140 tests. Thus, we would be requiring more test kits only in 7.5% of all the scenarios.
### FIGURE 5
Tests required in pooled testing for a 5% positive population: Best case versus worst case. Source: Developed by Authors

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|-----------------------------------------|----------|-----------------------------------------|
| 1B1      | 0/14                                    | 1B1      | 0/14                                    |
| 1B2      | 0/14                                    | 1B2      | 0/14                                    |
| 1B3      | 0/14                                    | 1B3      | 0/14                                    |
| 1B4      | 0/14                                    | 1B4      | 1/14                                    |
| 1B5      | 0/14                                    | 1B5      | 1/14                                    |
| 1B6      | 0/14                                    | 1B6      | 1/14                                    |
| 1B7      | 0/14                                    | 1B7      | 1/14                                    |
| 1B8      | 0/14                                    | 1B8      | 1/14                                    |
| 1B9      | 0/14                                    | 1B9      | 1/14                                    |
| 1B10     | 7/14                                    | 1B10     | 1/14                                    |

Individual tests on blend 1B10. Total tests are 24 (10+14).

### FIGURE 6
Tests required in encoded blending for a 5% positive population: Best case versus worst case. Source: Developed by Authors

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|-----------------------------------------|----------|-----------------------------------------|
| 1B1      | 0/14                                    | 1B1      | 0/14                                    |
| 1B2      | 0/14                                    | 1B2      | 0/14                                    |
| 1B3      | 0/14                                    | 1B3      | 0/14                                    |
| 1B4      | 0/14                                    | 1B4      | 1/14                                    |
| 1B5      | 0/14                                    | 1B5      | 1/14                                    |
| 1B6      | 0/14                                    | 1B6      | 1/14                                    |
| 1B7      | 0/14                                    | 1B7      | 1/14                                    |
| 1B8      | 0/14                                    | 1B8      | 1/14                                    |
| 1B9      | 0/14                                    | 1B9      | 1/14                                    |
| 1B10     | 7/14                                    | 1B10     | 1/14                                    |

These seven people might turn out to be encoded from (0001) to (0111) which are the binary equivalents of 1 and 7. Thus, 3 of the blends of Phase-2 might end up positive. This is as per case 2 of the Blended encoding approach explained above. Thus, the total tests in Phase-2 will be 77 (11 tests x 7 blends) in number, and the total tests across both phases are 87.

In Phase-2 testing, if each of the patients is coincidentally encoded between (0111) to (1110), which are the binary equivalent of 7 and 14. Therefore, 3 of the blends of Phase-2 might end up positive. This is as per case 2 of the Blended encoding approach explained above. Thus, the total tests in Phase-2 will be 77 (11 tests x 7 blends) in number, and the total tests across both phases are 87.
**FIGURE 7** Tests required in pooled testing for a 7.5% positive population: Best case versus worst case. Source: Developed by Authors

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|-----------------------------------------|----------|-----------------------------------------|
| 1B1      | 0/14                                    | 1B1      | 2/14                                    |
| 1B2      | 0/14                                    | 1B2      | 1/14                                    |
| 1B3      | 0/14                                    | 1B3      | 1/14                                    |
| 1B4      | 0/14                                    | 1B4      | 1/14                                    |
| 1B5      | 0/14                                    | 1B5      | 1/14                                    |
| 1B6      | 0/14                                    | 1B6      | 1/14                                    |
| 1B7      | 0/14                                    | 1B7      | 1/14                                    |
| 1B8      | 0/14                                    | 1B8      | 1/14                                    |
| 1B9      | 0/14                                    | 1B9      | 1/14                                    |
| 1B10     | 11/14                                   | 1B10     | 1/14                                    |

Individual tests on blend 1B10. Total tests are 24 (10+14).

Ten blends undergo individual tests. Total tests is 150 (14 *10 + 10).

**FIGURE 8** Tests required in encoded blending for a 7.5% positive population: Best case versus worst case. Source: Developed by Authors

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|-----------------------------------------|----------|-----------------------------------------|
| 1B1      | 0/14                                    | 1B1      | 2/14                                    |
| 1B2      | 0/14                                    | 1B2      | 1/14                                    |
| 1B3      | 0/14                                    | 1B3      | 1/14                                    |
| 1B4      | 0/14                                    | 1B4      | 1/14                                    |
| 1B5      | 0/14                                    | 1B5      | 1/14                                    |
| 1B6      | 0/14                                    | 1B6      | 1/14                                    |
| 1B7      | 0/14                                    | 1B7      | 1/14                                    |
| 1B8      | 0/14                                    | 1B8      | 1/14                                    |
| 1B9      | 0/14                                    | 1B9      | 1/14                                    |
| 1B10     | 11/14                                   | 1B10     | 1/14                                    |

This means that 9 of these blends have one patient, and 1 of the blends has two patients. In Phase-2 testing of 9 blends having one patient in it, if each of the patients is coincidentally encoded between (0111) to (1110) the binary equivalent of 7 and 14. Therefore, 3 of the blends of Phase-2 might end up positive. This is as per case 2 of the Blended encoding approach explained above. Thus, the total tests in Phase-2 will be 99 (11 tests x 9 blends) in number. For the other blend where there is the presence of 2 patients if each of the patients is coincidentally encoded between (0111) to (1110) which are the binary equivalent of 7 and 14, at the worst case 4 of the blends of Phase-2 might end up positive which leads to a requirement of 18 tests for this blend as per our approach. The total tests across both phases sum up to be 127 (10 + 99 + 18).
In Phase-1, ten blended tests happen as explained in the approach.

### BEST CASE

Nine of these blended tests may return as negative, and all 10% of the total sample falls into the same blend.

### WORST CASE

All 14 of these patients might end up across all ten blends. Thus, all 10 of these blends test positive.

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|----------------------------------------|----------|----------------------------------------|
| 1B1      | 0/14                                   | 1B1      | 2/14                                   |
| 1B2      | 0/14                                   | 1B2      | 2/14                                   |
| 1B3      | 0/14                                   | 1B3      | 2/14                                   |
| 1B4      | 0/14                                   | 1B4      | 2/14                                   |
| 1B5      | 0/14                                   | 1B5      | 1/14                                   |
| 1B6      | 0/14                                   | 1B6      | 1/14                                   |
| 1B7      | 0/14                                   | 1B7      | 1/14                                   |
| 1B8      | 0/14                                   | 1B8      | 1/14                                   |
| 1B9      | 0/14                                   | 1B9      | 1/14                                   |
| 1B10     | 14/14                                  | 1B10     | 1/14                                   |

Individual tests on blend 1B10. Total tests are 24 (10 +14).

Ten blends undergo individual tests. Total tests are 150 (14 *10 +10).

**FIGURE 9** Tests required in pooled testing for a 10% positive population: Best case versus worst case. Source: Developed by Authors

In Phase-1, ten blended tests happen as explained in the approach.

### BEST CASE

Nine of these blended tests may return as negative, and all 10% of the total sample falls into the same blend.

### WORST CASE

All 7 of these patients might end up in different blends. Thus, 7 of these blends test positive, and the other three turn out to be negative.

| Blend ID | No. of positives out of total sample size | Blend ID | No. of positives out of total sample size |
|----------|----------------------------------------|----------|----------------------------------------|
| 1B1      | 0/14                                   | 1B1      | 2/14                                   |
| 1B2      | 0/14                                   | 1B2      | 2/14                                   |
| 1B3      | 0/14                                   | 1B3      | 2/14                                   |
| 1B4      | 0/14                                   | 1B4      | 2/14                                   |
| 1B5      | 0/14                                   | 1B5      | 1/14                                   |
| 1B6      | 0/14                                   | 1B6      | 1/14                                   |
| 1B7      | 0/14                                   | 1B7      | 1/14                                   |
| 1B8      | 0/14                                   | 1B8      | 1/14                                   |
| 1B9      | 0/14                                   | 1B9      | 1/14                                   |
| 1B10     | 14/14                                  | 1B10     | 1/14                                   |

We have already seen from the approach that when more than seven patients are present in Phase-2 of this process, all four blends turn out to be positive. This is as per case 4 of the Blended encoding approaches explained above. Thus, the total tests in Phase-2 will be 18 in number, and the total tests across both phases are 28.

In Phase-2 testing of the six blends having one patient in each, if each of the patients is coincidentally encoded between (0111) to (1110). This coding is the binary equivalent of 7 and 14, 3 of the blends of Phase-2 might end up positive. This is as per case 2 of the Blended encoding approach explained above. Thus, the total tests in Phase-2 will be 66 (11 tests x 6 blends) in number. For the other four blends where there is the presence of 2 patients, if each of the patients is coincidentally encoded between (0111) to (1110) which are the binary equivalent of 7 and 14, at the worst case 4 of the blends of Phase-2 might end up positive which leads to a requirement of 72 (18 tests x 4 blends) for this blend as per our approach. The total tests across both phases sum up to be 148 (10 + 66 + 72).

**FIGURE 10** Tests required in encoded blending for a 10% positive population: Best case versus worst case. Source: Developed by Authors
On the other hand, if we assume a normal distribution between the best and worst-case scenarios as per the calculation, we can see that the EB approach is worse off only 0.47% (as calculated from normal distribution curve) of the total occurrences. Thus, in both the probability distribution scenarios, we can see that the EB approach helps to save test kits, and hastens the testing process.

Given the increasing number of cases worldwide, and the shortage of resources at hand, achieving optimality in the processes is of utmost importance to provide support to the existing healthcare infrastructure. Though technically the tests done with and without blending are the same and require the same test kits of varying quantities, the logistic process differs slightly.

In the normal testing scenarios, the individual sample is collected with an entry made using the Social Security Number (SSN) or Unique Identification, based on the country. These samples are sent to the laboratories where the individual samples are tested to obtain the results.

In EB, the individual samples collected would have to be carefully blended by the biologist, while retaining a part of the sample for further phases. This involves significant training. Based on the results from Phase-1 of the testing, further blends/individual sample tests have to be done by the biologist again. Hence, the logistic process is more serial in nature, with steps of blending and testing in each phase.

8 | CONCLUSIONS, LIMITATIONS AND THE WAY AHEAD

This paper proposed a statistical method of acceleration of the testing process, keeping in view the limitations posed by the finite number of test kits at hand at any given point of time. We believe that this method would help, both from medical and economic perspectives, in fighting the current pandemic. The EB approach helps in reducing both cost and time associated with testing, as the number of test kits required tends to reduce drastically. Also, speeding up testing translates to faster identification of disease spread in geography, which enables governments to schedule and enforce lockdown measures effectively.

While the paper was inspired to solve the testing crisis in the COVID-19 pandemic situation, the philosophy of pooled testing can be extended to multiple applications beyond COVID-19. To start with, the methodology is applicable across testing for multiple other diseases (which allow pooling blood/urine samples in clinical environment). Some of the common diseases including HIV, Influenza, Gonorrhoea, Chlamydia allow pooled testing. As the concept is similar to parallel batch processing, this also finds application in quality control, where a large batch of products can be pooled and tested. This methodology can also be leveraged by multiple industries, including but not limited to FMCG, CPG, Automobile, Energy and Natural Gas. Apart from testing products for quality compliance, this methodology can also be used by the pharmaceutical companies in their research. For example, pooling multiple chemical samples together to check for quality/concentration, pooling samples from multiple rats/guinea pigs for testing and so on. COVID-19 is not the last pandemic faced by human beings, and there will be more outbreaks of viruses in the future; thus, pooled testing is a technique that would help policymakers to conduct testing both efficiently and economically.

The limitation of this method is that although pooled testing has been practiced before, the probabilities and possibilities of this approach should be verified by medical practitioners, because the paper projects a solution only through a statistical perspective. The results indeed pave the way ahead for future research. Furthermore, biologists have to attain expertise with the new process, and get adequate training. From the various scenarios described already, the other possible limitation is that an individual’s result might take more time to arrive in the EB process. However, this could possibly be traded off with a reduction in the testing kits that are going to be utilised. Also, the solution may not be optimal, and thus, could be further optimised, using contemporary softwares and techniques.

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