GROUP TESTING DURING THE COVID-19 PANDEMIC:
OPTIMAL GROUP SIZE SELECTION AND PREVALENCE CONTROL

ABSTRACT

Group testing pools multiple samples together and performs tests on these pooled samples to discern the infected samples. It greatly reduces the number of tests, however, with a sacrifice of increasing false negative rates due to the dilution of the viral load in pooled samples. Therefore, it is important to balance the trade-off between number of tests and false negative rate. We explore two popular group testing methods, namely linear array (a.k.a. Dorfman’s procedure) and square array methods, and analyze the optimal group size of a pooled sample that minimizes the group false negative number under a constraint of testing capacity. Our analysis shows that when there is reasonably large testing capacity, the linear array method yields smaller false negative number and hence is preferred. When the testing capacity is small, square array method is more feasible and preferred. In addition, we consider testing a closed community in a period of time and determine the optimal testing cycle that minimizes the final prevalence rate of infection at the end of the time period. Finally, we provide a testing protocol for practitioners to use these group testing methods in the COVID-19 pandemic.

1 Introduction

Group testing refers to the idea of pooling multiple samples together and performing tests on certain subsets of these samples to discern the infected samples. Due to the resource and time it takes to run the RT-qPCR test for COVID-19, it is nearly impossible to conduct individual test of everyone in a relatively large population. Instead, group testing provides a promising way to save the testing budget while detecting the infected samples out of a large population. Dating back to [1], many different group testing methods have been developed and analysed over the years, such as those based on compressed sensing (see [2], [3]), and information theory (see [4], [5]). The COVID-19 pandemic reignites a great interest in group testing, both from academic research (e.g. [6], [7], [8], [9], [10], [11], [12], [13], and [14]) and from the public (e.g. [15] and [16]).

To illustrate group testing, let’s first take a look at a simple group testing method, called binary search. Suppose there are eight people to test and only one person is infected (unknown to us). Since we don’t know there is only one infected person, we have to test them all in individual testing. In binary search, we first divide people into two groups of four. For the first four people, we pool their samples together and carry out one test. Suppose the result for the second group of four people is positive, we further divide these four people into two halves, and repeat the above
procedure. Here we use only six tests in binary search, which saves 25% number of tests compared with individual testing.

There are two paradigms of group testing, as illustrated in [17]. Combinatorial group testing (CGT) assumes a known number of infected people among the tested population. Probabilistic group testing (PGT) assumes that people test positive independently with probability \( p \). From the perspective of sequences of testing, group testing can be classified as adaptive testing and non-adaptive testing. In adaptive testing, first a group is chosen randomly and tested, and the outcome of this test determines the next group to test and so on. In non-adaptive testing, a fixed number of tests are always performed irrespective of the number of infected samples present in the pool, so all the tests can run in parallel. In particular, [18] formulate it as a two-stage process. At the first stage, all individuals are arranged into several groups and each group gets tested. At the second stage, positive/negative result for each individual is deduced.

However, the aforementioned work usually assumes that testing result is accurate. In other words, when samples are pooled together and tested, if there is at least one infected sample, then the test result is always positive. Under this assumption, naturally the main goal for developing different group testing methods is to minimize the total number of tests. [7] gives a scheme for comparing several different group testing methods, and shows that the prevalence rate is the major factor that determines the number of tests of a group testing method. In other words, performance of group testing varies when the prevalence rate changes. [19], [20] discuss the relationship between these quantities. However, when individual samples are pooled together, the viral load in the infected samples gets diluted and hence leads to false negative detection (i.e., infected samples test negative). We take this dilution effect into consideration, and consider how to optimize the group size to balance the trade-off between number of tests and false negative rate. On the one hand, the bigger the group size is, the less number of tests needed. On the other hand, a bigger group size also causes a larger false negative rate. When the group size is too large, the false negative rate will be so large that renders the group testing method useless. Therefore, we aim to choose the optimal pool size that minimizes the false negative number under a constraint of test capacity.

In addition, we consider testing everyone in a large population in a testing cycle of multiple days to help control the prevalence rate. To model the dynamics of the system, we proposed a testing-quarantine-infection model, where group testing is conducted at the very beginning of each day and people who test positive get quarantined, while the infection keeps spreading. This model requires the testing can be conducted in a short period of time, so we mainly consider non-adaptive group testing methods that can run in parallel. Specifically, we consider linear array and square array group testing methods that are easy to understand and implement in practice.

In summary, the contribution of this paper is two-fold:

- We take into consideration the dilution effect caused by pooling, balance the trade-off between the number of tests and the false negative number, and derive the optimal group size under a stochastic optimization formulation.
- We design a testing protocol such that we can test everyone in a testing cycle under a limited testing capacity and keep the prevalence rate low in the population.

The remainder of the paper is organized as follows: Section 2 briefly introduces the dilution effect in group testing. Section 3 studies the linear array and square array methods, and derives the optimal group size that minimizes the false negative number under a constraint of daily testing capacity. Section 4 proposes a testing-quarantine-infection model for group testing, and determines the optimal testing cycle length through simulation. Sensitivity analysis is also conducted in this section with regard to different parameters. Section 5 concludes the paper with the complete testing protocol for practitioners.

2 Dilution effect in Group Testing

Even though group testing is efficient in detecting the infected people using as few number of tests as possible, it is at the sacrifice of decreased sensitivity. In group testing, the false negative rate, defined as the probability of infected people being tested negative, comes from two sources.

- **Swabbing.** The swab used to take samples might not contain enough amount of the virus from an infected person.
- **Pooling.** When pooling many samples into one sample, those infected samples are pooled with uninfected samples, which will dilute the viral load in the pooled sample and hence decrease the sensitivity of the test.

We focus on the second source of pooling dilution. The impact of pooling dilution has been studied in [21], [22], [23] etc.. To the best of our knowledge, pooling dilution particularly for SARS-CoV-2 has been studied in [17] and [10], till
the time of completion of this manuscript. More specifically, [17] utilizes a dilution effect model derived for testing HIV, and argues that it is applicable to other viral testings including SARS-CoV-2. Most recently, based on the mechanism of the RT-qPCR test and the clinical data for SARS-CoV-2 virus, [10] proposes a new statistical model for determining the false negative rate induced by pooling. The basic idea is to measure the false negative rate as the probability that the amount of virus contained in the pooling sample exceeds the detection limit of RT-qPCR test. Assume exactly one infected individual is pooled with \( N - 1 \) uninfected individuals to form a group of size \( N \), the false negative rate caused by pooling is estimated as

\[
\gamma = 1 - \sum_{k=1}^{3} \pi_k F_{\mu_k, \sigma_k}(d_{\text{cens}} - \log_2 N) \frac{F_{\mu_k, \sigma_k}(d_{\text{cens}})}{F_{\mu_k, \sigma_k}(d_{\text{cens}})},
\]

where \( F_{\mu_k, \sigma_k}(\cdot) \), \( k = 1, 2, 3 \) is the cumulative distribution function (CDF) of normal distribution \( N(\mu_k, \sigma_k) \), \( k = 1, 2, 3 \), \( d_{\text{cens}} \) is the parameter called detection limit. For more details, such as mathematical deductions, parameters settings, etc., we refer the readers to Appendix D and [10]. Figure 1 shows the relationship between pooling size \( N \) and the false negative rate \( \gamma \). Note that in this so-called “uncensored model” in [10], the false negative rate from the first source of swabbing is neglected.

\[\text{Remark 1. The results throughout the paper are based on the uncensored model in [10]. If more precise models for the pooling dilution effect become available, they can be used to replace the current model in our approach proposed in this paper.}\]

3 Linear Array and Square Array Group Testing

Among the various group testing methods, we choose to focus on two methods: the linear array method and the square array method. These two methods are non-adaptive, easy to understand and implement in practice, and parallelable. We first introduce these two methods, and then evaluate and compare their performance. Specifically, we will compare the number of tests needed and the false negative number under different parameter regimes of testing capacity and initial prevalence rate.

In the linear array group testing, suppose the total number of people to test is \( N \) and the desired group size is \( n \) (\( n < N \)). Note that the corresponding pool size is also \( n \). We will form \( \left\lfloor \frac{N}{n} \right\rfloor \) linear array groups and perform group testing on each group. Figure 2 shows a linear array of size \( n = 5 \). Note that if \( N \) is not divisible by \( n \), \( \left\lfloor \frac{N}{n} \right\rfloor \) of the groups are of size \( n \) and the last group is of size \( N - \left\lfloor \frac{N}{n} \right\rfloor n \). If a group tests positive, we will test each one in the group individually. Without the follow-up diagnostic tests, the non-infected samples in the positive group will be deemed as infected, resulting in false positive detection. Notice that in the linear array method, we need two samples from each person. If only one sample is collected, it will be split into two sub-samples, of which one is used for group testing and the other for possible follow-up diagnostic test.

Another group testing method is square array group test used by [12]. Note that this method is almost the same as double pooling proposed by [9]. In the square array group testing, suppose the total number of people to test is \( N \) and we consider the square array of size \( n \times n \). Pools of size \( n \) are created from each row and each column. We will form \( \left\lfloor \frac{N}{n^2} \right\rfloor \) square arrays of size \( n \times n \). A sample is deemed as suspicious if both its row and its column pools test positive.
Figure 2: Placement of samples in a linear array of size 25.

See Figure 3 for a toy example. Before we form each group, we need to swab three samples from the tested individual. If we only have one sample for each, it will be split into three sub-samples. One is used for row testing, one is used for column testing, and the remaining one is used for possible follow-up diagnostic test, when the person is deemed as suspicious in group testing phase. For the remaining \( N - \left\lfloor \frac{N}{n^2} \right\rfloor n^2 \) people, we will conduct individual tests. The follow-up diagnostic test is indispensable since the square array test may result in false positive number (defined as the number of not-infected samples that test positive). To illustrate, consider the case where only the sample labeled by ‘1’ and the sample labeled by ‘13’ are infected in the \( 5 \times 5 \) square array in Figure 3. It is very likely that there are four pools that will test positive, namely the first and the third row pools, and the first and the third column pools. If we do not perform the follow-up diagnostic tests, samples labeled by ‘3’ and ‘11’ will be deemed as infected, though none of them are infected actually.

Figure 3: Placement of samples in a \( 5 \times 5 \) square array.

We formally define the following notations:
• Total number of people to test: \( N \).
• Initial prevalence rate: \( p_0 \). It measures the probability that an individual is infected.
• Pool size in group testing: \( n \). It is the number of samples that are pooled together in one test.
• Maximum pool size: \( \bar{n} \). For the linear array test, \( \bar{n} = N \). For the square array test, \( \bar{n} = \lceil \sqrt{N} \rceil \).
• Optimal pool size: \( n^* \). \( n^* \leq \bar{n} \). The pool size which minimizes the expected total false negative number, subject to the constraint of the expected number of total tests.
• Number of pools: \( M_P(n) \). This is also the number of tests conducted in group testing phase. For the linear array test, the number of pools is \( \lceil \frac{N}{n} \rceil \). For the square array test, the number of pools is \( 2n \lceil \frac{N}{n} \rceil \).
• Group size in group testing: \( g(n) \). For the linear array test, \( g = n \). For the square array test, \( g = n \times n \).
• False negative rate caused by dilution effect: \( \gamma(n, d) \). It is a function of pool size \( n \) and number of infected \( d \) in a pooled sample.
• Testing capacity: \( C \). It is the maximum number of tests we can conduct.
• Randomness of the sample placements and pool positiveness: \( (\omega, \xi) \in (\mathbb{R}^N \times \mathbb{R}^m) \). Random variable \( \omega \) represents the placement of infected samples. \( \omega_i = 1 \) means the \( i^{th} \) sample is infected. Random variable \( \xi \) represents the positiveness of each pool, and hence \( \xi \) is dependent on \( \omega \). The reason we need the random variable \( \xi \) is that, given \( \omega \), we still cannot tell the test positiveness of a pool, because of the dilution effect. \( \xi_i = 1 \) means pool \( i \) tests positive, \( \xi_i = 0 \) means pool \( i \) tests negative.
• Number of tests conducted individually: \( M_I(n, (\omega, \xi)) \). Suppose we have a realization of random variables \( (\omega, \xi) \). For the linear array test, it tells us the numbering of pools that test positive. For the square array test, it tells us the numbering of samples at the intersection of positive rows and columns. Construct a suspect set \( S \) that contains the above numbers. For linear array test, \( M_I \) would be \( |S| \). For square array test, \( M_I \) would be \( |S| + (N - \lceil \frac{N}{n} \rceil n^2) \).
• Number of follow-up diagnostic tests followed by a single group test: \( m(n, (\omega, \xi)) \).
• Number of total tests: \( M(n, (\omega, \xi)) = M_P + M_I \).
• Number of people that test positive: \( I(n, (\omega, \xi)) \). Given the set \( S \) and \( \omega \), \( I = \sum_{i \in S} 1 \{ \omega_i = 1 \} \).
• Number of infected people: \( D \). \( D \) follows a binomial distribution with parameters \( N \) and \( p_0 \).
• False negative number: \( f(n, (\omega, \xi)) = D - I \).
• Value-at-Risk: \( \text{VaR}_q [\cdot] \). \( \text{VaR}_q [Z] := \inf \{ t : \mathbb{P}(Z \leq t) \geq q \} \), where \( 0 < q < 1 \).

In the following sections, we assume that the events that each individual gets infected are mutually independent. In addition, we suppress the randomness \( (\omega, \xi) \). We use superscripts ‘\( L \)’ for the linear array method, ‘\( S \)’ for the square array method, and ‘\( B \)’ for the benchmark of purely individual testing. For subscripts, ‘\( I \)’ stands for individual test, ‘\( G \)’ stands for group test. Finally, in order to find the optimal group size, we will first find the optimal pool size \( n^* \), and the optimal group size would be \( g(n^*) \). The following subsections will focus on finding the optimal pool size.

### 3.1 Linear Array Group Testing

In this subsection, we evaluate the expected number of tests and the expected total false negative number in the linear array group testing method. We leave the details of derivation for the following to Appendix A.

Denote by \( \mathbb{E} \left[ m^L(n) \right] \) the expected value of follow-up diagnostic tests for a single linear array group test of size \( n \).

\[
\mathbb{E} \left[ m^L(n) \right] = n \sum_{d=1}^{n} \left( 1 - \gamma(n, d) \right) \binom{n}{d} (1 - p_0)^{n-d} (p_0)^d
\]

Denote by \( \mathbb{E} \left[ M^L(n) \right] \) the total expected number of tests for the linear array method. Note \( \mathbb{E} \left[ M^L(n) \right] \) is lower bounded by \( \lceil \frac{N}{n} \rceil \), the total number of groups.

\[
\mathbb{E} \left[ M^L(n) \right] = \lceil \frac{N}{n} \rceil + \frac{N}{n} \mathbb{E} \left[ m^L(n) \right] + \mathbb{E} \left[ m^L(N - \lceil \frac{N}{n} \rceil n) \right]
\] (1)
Denote by $\mathbb{E} \left[ f_L^G(n) \right]$ the expected false negative number for a single linear array group test of size $n$.

$$
\mathbb{E} \left[ f_L^G(n) \right] = \sum_{d=1}^{n} d \gamma(n, d) \binom{n}{d} (1 - p_0)^{n-d} (p_0)^d
$$

For the follow-up diagnostic tests following a single linear array group test of size $n$, the expected false negative number is

$$
\mathbb{E} \left[ f_L^L(n) \right] = \gamma(1, 1) \sum_{d=1}^{n} d \left( 1 - \gamma(n, d) \right) \binom{n}{d} (1 - p_0)^{n-d} (p_0)^d
$$

The expected total false negative number, including all follow-up diagnostic tests due to $\left\lfloor \frac{N}{n} \right\rfloor$ arrays of size $n$ and one array of size $(N - \left\lfloor \frac{N}{n} \right\rfloor) n$, is

$$
\mathbb{E} \left[ f^L(n) \right] = \left( \frac{N}{n} \right) \left( \mathbb{E} \left[ f_L^L(n) \right] + \mathbb{E} \left[ f_L^G(n) \right] \right) + \left( \mathbb{E} \left[ f_L^L(n - \left\lfloor \frac{N}{n} \right\rfloor) n \right] + \mathbb{E} \left[ f_L^G(N - \left\lfloor \frac{N}{n} \right\rfloor n) \right] \right)
$$

The closed-form expressions above show the expected values of the total number of tests and false negative number. To see the variability of these quantities, we run simulations to plot the empirical distributions, as shown in Figure 4.

![Figure 4: Distribution of total number of tests and false negative number in linear array group testing, when $n = 25$, $N = 10000$, $p_0 = 0.001$, and $C = 600$. Simulations run 5000 times.](image)

**3.2 Square Array Group Testing**

In this subsection, we evaluate the expected number of tests and the expected total false negative number in the square array group testing method. We leave the details of derivation for the following to Appendix B.

Denote by $\mathbb{E} \left[ m^G(n) \right]$ the expected value of follow-up diagnostic tests for a single square array of size $n \times n$.

$$
\mathbb{E} \left[ m^{G}(n) \right] = n^2 \left( \sum_{d=0}^{n-1} \frac{(1 - \gamma(n, d + 1)) \binom{n-1}{d} (1 - p_0)^{n-1-d} (p_0)^d}{(1 - (1 - p_0)^{n-1} + (1 - p_0)^{2n-1})} \right) ^2
$$

As for the expected total number of tests, denote it by $\mathbb{E} \left[ M^G(n) \right]$. Note that $\mathbb{E} \left[ M^G(n) \right]$ is lower-bounded by $2n \left( \frac{N}{n^2} \right) + (N - \left( \frac{N}{n^2} \right) n^2)$, which is the number of tests for all row and column groups as well as all individual tests for the remaining samples outside arrays.

$$
\mathbb{E} \left[ M^G(n) \right] = \frac{N}{n^2} \left( \mathbb{E} \left[ m^G(n) \right] + 2n \right) + \left( N - \left( \frac{N}{n^2} \right) n^2 \right)
$$

(3)
Denote by $E[f_{S}(n)]$ the expected false negative number for a single square array of size $n \times n$. 

$$E[f_{S}(n)] = n^2 p_0 \left(1 - \left(\sum_{d=0}^{n-1} (1 - \gamma(n, d + 1))(n-1)(1 - p_0)^{n-1-d}(p_0)^d\right)^2\right)$$

Denote by $E[f_{SI}(n)]$ the expected false negative number for the follow-up diagnostic tests following a single square array of size $n \times n$. 

$$E[f_{SI}(n)] = n^2 p_0 \left(\sum_{d=0}^{n-1} (1 - \gamma(n, d + 1))(n-1)(1 - p_0)^{n-1-d}(p_0)^d\right)^2 \gamma(1, 1)$$

The expected total false negative number, including all tests due to the $\lfloor \frac{N}{n^2} \rfloor$ square arrays and the remaining ones outside the arrays, is:

$$E[f_{S}(n)] = \lfloor \frac{N}{n^2} \rfloor \left(E[f_{SG}(n)] + E[f_{SI}(n)]\right) + (N - \lfloor \frac{N}{n^2} \rfloor n^2) p_0 \gamma(1, 1) \quad (4)$$

Figure 5 shows the empirical distribution of the total number of tests and the distribution of the false negative number for the square array method. Notice that in all the group testing methods, the total expected number of tests and total expected false negative number depend on the pool size. For the purpose of comparing the methods, we will consider their total false negative number under the same testing capacity, in a stochastic programming formulation.

![Histogram of total number of tests and false negative number in square array group testing](image)

Figure 5: Distribution of total number of tests and false negative number in square array group testing, when $n = 50$, $N = 10000$, $p_0 = 0.001$, and $C = 600$. Simulations run 5000 times.

### 3.3 Comparison of Group Testing Methods

In this subsection, we will measure the performance of group testing methods (linear array and square array) with respect to the total false negative number. The objective is to minimize the expected total false negative number, subject to the expected total number of tests not exceeding a given testing capacity. Recall that in Section 3, the total number of tests is $M(n)$, the false negative number is $f(n)$. With the same notations, we formulate the problem of selecting the optimal pool size as follows:

$$\begin{align*}
\text{minimize} & \quad n \in \{1, 2, \ldots, \lfloor \sqrt[3]{\frac{N}{C}} \rfloor\} \quad E[f(n)] \\
\text{subject to} & \quad E[M(n)] \leq C
\end{align*} \quad (5)$$

To solve (5), we make use of the closed-form expression for the expected total number of tests (i.e., (1), (3)) and find the feasible region of decision variable $n$, and evaluate the objective function using the closed-form expression for the expected total false negative number (i.e., (2), (4)).

Under the above formulation, we compare the aforementioned two group testing methods against the benchmark individual testing. Fix the population size to be $N = 10000$. Under different values of the initial prevalence rate $p_0$ and...
testing capacity $C$, we find the optimal pool size for each method and the corresponding total false negative number. Since the expected total infected samples is the same for both group testing methods, higher expected false negative number also means higher false negative rate. As a benchmark, we randomly select $C$ samples from the total $N$ samples to conduct the individual testing, ignoring the rest. The expected false negative number of benchmark individual testing can be approximated by $E[f_B] \approx (N - C)p_0$. We say a group test method is in its infeasible region if there is no pool size $n$ such that the expected number of tests required is less than $C$. Figure 6 shows the expected false negative number under optimal pool size for all three methods, leaving the infeasible region blank. In summary, both methods perform better than the benchmark individual testing. The square array group testing has larger feasible region than the linear array group testing does, since the former requires less number of tests on average. However, within its feasible region, the linear array group testing has uniformly less false negative number, and thus smaller false negative rate, than the square array group testing.

To see how the testing capacity $C$ affects the performance of both group testing methods, we fix $p_0 = 0.001$ and show more details of how the test capacity affects the performance of testing result for all methods. Figure 7 provides the relationship between the pool size and the total number of tests, as well as the total false negative number for the linear array method and the square array when $N = 10000$, $p_0 = 0.001$.

![Figure 6: Comparison of false negative number between linear array group testing, square array group testing, and benchmark individual testing. under different settings of $p_0$ and $C$.](image)

![Figure 7: The relationship between the pool size and the total number of tests, as well as the total false negative number for the linear array method and the square array when $N = 10000$, $p_0 = 0.001$.](image)
times, and obtain \( E[\cdot] \) (blue curves) by expressions (1) to (4). In the two graphs on the left side of Figure 7, the pool sizes corresponding to the test numbers below the testing capacity \( C \) (i.e., the horizontal lines) are feasible. In the two graphs on the right side of Figure 7, we find the minimal total false negative number for the feasible pool sizes. Take the square array method for example. Setting \( C = 300 \) gives optimal pool size \( n^* = 100 \) and minimal mean total false negative number \( f^* = 5.26 \).

| \( C \) | \( n^* \) | \( E[M^L(n^*)] \) | \( \text{VaR}_{0.95}[M^L(n^*)] \) | \( E[f^L(n^*)] \) | \( \text{VaR}_{0.95}[f^L(n^*)] \) |
|-------|-------|----------------|-----------------|----------------|----------------|
| 100   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 200   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 300   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 400   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 500   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 600   | 25.0 | 598.798 | 726.0 | 2.027 | 5.0 |
| 700   | 19.0 | 681.863 | 774.0 | 1.814 | 4.0 |
| 800   | 15.0 | 792.052 | 862.0 | 1.636 | 4.0 |
| 900   | 13.0 | 879.649 | 939.0 | 1.529 | 4.0 |
| 1000  | 12.0 | 935.955 | 1002.0 | 1.474 | 4.0 |

Table 1: Linear array method: the impact of test capacity on the performance of the test. \( p_0 = 0.001 \).

| \( C \) | \( n^* \) | \( E[M^S(n^*)] \) | \( \text{VaR}_{0.95}[M^S(n^*)] \) | \( E[f^S(n^*)] \) | \( \text{VaR}_{0.95}[f^S(n^*)] \) |
|-------|-------|----------------|-----------------|----------------|----------------|
| 100   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 200   | infeasible | infeasible | infeasible | infeasible | infeasible |
| 300   | 100.0 | 246.559 | 308.0 | 5.263 | 9.0 |
| 400   | 100.0 | 246.559 | 308.0 | 5.263 | 9.0 |
| 500   | 50.0 | 418.207 | 441.0 | 4.453 | 8.0 |
| 600   | 50.0 | 418.207 | 441.0 | 4.453 | 8.0 |
| 700   | 50.0 | 418.207 | 441.0 | 4.453 | 8.0 |
| 800   | 30.0 | 771.106 | 783.0 | 3.801 | 7.0 |
| 900   | 25.0 | 810.008 | 820.0 | 3.618 | 7.0 |
| 1000  | 25.0 | 810.008 | 820.0 | 3.618 | 7.0 |

Table 2: Square array method: the impact of test capacity on the performance of the test. \( p_0 = 0.001 \).

| \( C \) | \( E[f^B] \) | \( \text{VaR}_{0.95}[f^B] \) |
|-------|--------|----------------|
| 100   | 9.962  | 15 |
| 200   | 9.83   | 15 |
| 300   | 9.688  | 15 |
| 400   | 9.499  | 15 |
| 500   | 9.569  | 15 |
| 600   | 9.415  | 15 |
| 700   | 9.384  | 15 |
| 800   | 9.24   | 15 |
| 900   | 9.097  | 14 |
| 1000  | 9.003  | 14 |

Table 3: Benchmark individual testing. \( p_0 = 0.001 \)

Table 1 and Table 2 summarize more details of testing results for the linear array group test and the square array group test, respectively. In general, if we increase the testing capacity, we will have more feasible solutions, and smaller mean total false negative number. Again, we calculate the benchmark false negative number by randomly selecting \( C \) from the \( N \) samples for benchmark individual testing, ignoring the rest. Table 3 shows the benchmark result for comparison. Intuitively, given the same pool size for the two group testing methods, the square array method will have larger false negative number because each sample in the square array method will be tested in both the row pool and the column pool. Because of the dilution effect, the probability that infected sample will be tested negative in the square array group test is relatively larger. In conclusion, if we are given a relatively large test capacity, we should use the linear
array method. On the other hand, if we face the shortage of testing kits and only have a relatively small test capacity, we prefer using the square array group test.

**Remark 2.** We also notice a widely applied group testing method called general binary search (GBS). GBS is an adaptive group testing method which takes a long time to conduct, and the number of swab samples from each individual is large and uncertain. Therefore, we leave the details of GBS to Appendix C for those who are interested.

**Remark 3.** In case there are no closed-form expressions for the objective function and constraints, we can also apply sample average approximation (SAA) to both constraints and objective function, and solve the approximate deterministic problem in order to find the feasible region of decision variable \( n \) and evaluate the objective function to find the optimal pool size within the feasible region. We refer the readers to [24] and [25] for the application of SAA to stochastic programming.

**Remark 4.** We also consider some other performance metrics with regard to the total false negative number and the total number of test, from the risk-averse perspective. For example, the following two sets of performance metrics can be applied.

\[
\begin{align*}
\text{minimize} & \quad \mathbb{E} [f(n)] \\
\text{subject to} & \quad \text{VaR}_q [M(n)] \leq C, q \in (0, 1)
\end{align*}
\]

\[
\begin{align*}
\text{minimize} & \quad \text{VaR}_q [f(n)] \\
\text{subject to} & \quad \text{VaR}_q [M(n)] \leq C, q \in (0, 1)
\end{align*}
\]

4 Group Test Within A Testing Cycle

4.1 Testing-Quarantine-Infection Model

In this section, we consider testing a large population in a closed community such as college or nursing home. Due to limited daily testing capacity, we can only test the whole population in a testing cycle of multiple days. The daily model in Section 3 chooses the optimal group size to minimize the group false negative number in a day, and the group false negative number will affect the number of people quarantined, which further impacts the prevalence rate at the next day. The influence will propagate to eventually impact the final prevalence rate. Therefore, we propose a testing-quarantine-infection model for this scenario. Before we describe this model, we first make the following assumptions:

- Among untested population, people are randomly chosen to have the test.
- We use a simplified model for the infection process, where prevalence increases exponentially without intervention.
- We assume the tests are conducted in the morning, and results can be revealed immediately. Following test results, people who test positive are assumed to be quarantined, either by self-quarantine or hospitalization. Thus, those who test positive will be removed from the whole population in the morning right after the testing.
- We assume that people are within a closed community with no infections being imported. As a consequence, once all infected individuals are quarantined, the pandemic ends.
- We assume that there are no false positives.

We introduce more sets of notations. The first set of notations are the static quantities during the \( T \)-day testing:

- \( N_{\text{total}} \): total number of individuals in the closed community.
- \( T \): length of time period for group testing.
- \( l \): testing cycle length. Note that \( l \leq T \).
- \( \alpha \): daily growth rate of infection.
- \( p_0 \): initial prevalence rate at the beginning of the time period.
- \( C \): daily testing capacity.

Note that the last two notations are the same as those defined in Section 3. The next set of notations are quantities measured before the testing stage of each day:
• $N_{test}^t$: number of people to test in day $t$. For a testing cycle of $l$ days for $N_{total}$ people, we have

$$N_{test}^t = \begin{cases} \lceil \frac{N_{total}}{l} \rceil, & j = 1, 2, \ldots, l - 1 \\ N_{total} - \lceil \frac{N_{total}}{l} \rceil (l - 1), & j = l \end{cases}$$

• $R_t^I$: infected ratio among those who haven’t been tested.

We consider testing $N_{total}$ people in $l$ days, and each day we test $N_{test}^t$ people. At the beginning of day $t$, we randomly choose $N_{test}^t$ people from those who have not been tested yet, and conduct group testing (linear array or square array methods) under a limited test capacity. After group testing, we mark those who already get tested, and quarantine those who test positive, and return the rest of the people back to the population. People who have been tested will not be tested again in this testing cycle. We divide one day into two stages, namely testing stage and infection stage. At the testing stage, people get tested and those who test positive will be quarantined accordingly. At the infection stage, people who are infected will continue to infect the susceptible people in the population.

The following set of notations are quantities measured before the testing stage of each day:

• $\gamma_t$: group false negative rate calculated in day $t$. It is calculated as the false negative number divided by the number of infected people in the tested population in day $t$.
• $y_{TI}^t$: increased number of individuals who are tested and infected at day $t$.
• $y_{TQ}^t$: increased number of individuals who are tested, infected and quarantined at day $t$.
• $y_{TNQ}^t$: increased number of individuals who are tested, infected but not quarantined at day $t$.
• $y_{TNI}^t$: increased number of individuals who are tested but not infected at day $t$.

The following set of notations are quantities measured after the testing stage of each day:

• $N_t$: remaining population size, i.e., number of individuals that have not been quarantined after the day $t$; Note $N_0 = N_{total}$.
• $Y_{TI}^t$: number of individuals who are infected and have been tested at day $t$.
• $Y_{TNI}^t$: number of individuals who are not infected and have been tested at day $t$.
• $Y_{NTI}^t$: number of individuals who are infected and have not been tested at day $t$.
• $Y_{NTNI}^t$: number of individuals who are not infected and not have been tested at day $t$.

The following set of notations are quantities measured before the infection stage of each day:

• $R_{NI}^t$: newly infected ratio among those who have not been tested till day $t$.
• $N_{NI}^t$: number of individuals who are newly infected at day $t$.
• $N_{NTNI}^t$: number of individuals who are newly infected from the untested population at day $t$.

The following set of notations are quantities measured after the infection stage of each day:

• $p_t$: prevalence rate at the end of day $t$.
• $X_{TI}^t$: number of individuals who are infected and have been tested till the end of day $t$.
• $X_{TNI}^t$: number of individuals who are not infected and have been tested at the end of day $t$.
• $X_{NTI}^t$: number of individuals who are infected and have not been tested at the end of day $t$.
• $X_{NTNI}^t$: number of individuals who are not infected and have not been tested at the end of day $t$.

Note that for the above notations with subscript $t$, a notation with $t = 0$ denotes the corresponding quantity at initial status, if applicable. The following algorithm shows the testing-quarantine-infection model, and outputs the optimal testing cycle length as well as the optimal pool size for each day within the cycle. Note that we use $B(N,p)$ to denote the binomial distribution with parameter $N$ and $p$. Details and analysis of the algorithm are presented in the following subsections.
Algorithm 1: Testing-quarantine-infection model.

**input**: total population \(N_{\text{total}}\), initial prevalence rate \(p_0\), infection rate \(\alpha\), testing capacity \(C\)

**output**: optimal testing cycle length \(l^*\), optimal pool size \(n_t^*\), \(t = 1, \cdots, l^*\)

for \(l \leftarrow 1\) to \(T\) do
  for replication \(\leftarrow 1\) to 100 do
    \(T = T\);  
    \(T \geq 0\) do
      initialization: set \(N_0 = N_{\text{total}}\), \(X_0^{TI} = X_0^{NTI} = 0\), \(X_0^{NTI} = B(N_{\text{total}}, p_0)\), \(X_0^{NTNI} = N_{\text{total}} - X_0^{NTI}\);
      for \(t \leftarrow 1\) to \(\min(l, \hat{T})\) do
        before the testing stage:
        solve (5) with input \(p_t\), \(N_t^{\text{test}}\), \(C\);
        find the optimal pool size \(n_t^*\) and the optimal false negative rate \(\gamma_t\);
        infected ratio among those not tested: \(R_t = \frac{X_t^{NTI}}{N_t^{NTI} + X_t^{NTI}}\);
        tested, infected: \(y_t^{TI} \sim B(N_t^{\text{test}}, R_t)\);
        tested, infected, and quarantined: \(y_t^{TI} = y_t^{TI} (1 - \gamma_t)\);
        tested, infected, but not quarantined: \(y_t^{TQ} = y_t^{TI} \gamma_t\);
        tested, not infected: \(y_t^{TNQ} = N_t^{\text{test}} - y_t^{TI}\);
        after the testing stage:
        tested, infected: \(Y_t^{TI} = X_t^{TI} + y_t^{TQ}\);
        not tested, infected: \(Y_t^{NTI} = X_t^{NTI} - (y_t^{TQ} + y_t^{TNQ})\);
        tested, not infected: \(Y_t^{TNI} = X_t^{TI} + y_t^{TQ}\);
        not tested, not infected: \(Y_t^{NTNI} = X_t^{NTI} - y_t^{TNQ}\);
        not quarantined: \(N_t = N_t^{NTI} - Y_t^{TQ}\);
        before the infection stage:
        newly infected: \(N_t^{NI} = (Y_t^{TI} + Y_t^{NTI}) \times (\alpha - 1)\);
        newly infected ratio among those not tested: \(R_t^{NI} = \frac{Y_t^{NTI}}{Y_t^{TI} + Y_t^{NTI}}\);
        newly infected from the population that have not been tested yet: \(N_t^{NTNI} = B(N_t^{NI}, R_t^{NI})\);
        after the infection stage:
        not tested, not infected: \(X_t^{NTNI} = Y_t^{NTNI} - N_t^{NTNI}\);
        tested, not infected: \(X_t^{TNI} = Y_t^{TNI} - (N_t^{NI} - N_t^{NTNI})\);
        tested, infected: \(X_t^{TI} = Y_t^{TI} + (N_t^{NI} - N_t^{NTNI})\);
        not tested, infected: \(X_t^{NTI} = Y_t^{NTI} + N_t^{NTNI}\);
        prevalence rate: \(p_t = \frac{X_t^{TI} + X_t^{NTI}}{N_t}\);
      end
      if \(t \leq \hat{T}\) then
        update the initial prevalence rate \(p_0\) with \(\frac{X_t^{TI} + X_t^{NTI}}{N_t}\);
        \(T = T - t\);
    end
  end
end
record the final prevalence rate at the end of the given time period;
compute the average final prevalence rate at the end of the given time period;
return the optimal testing cycle length \(l^*\) that yields the smallest average final prevalence rate;
return the optimal group size \(n_t^*\), \(t = 1, \cdots, l^*\) associated with the optimal testing cycle length;
4.2 Final Prevalence Rate: Analysis

Given all the pre-determined parameters, which are denoted precisely by the first set of notations in Section 4.1, we consider the factor that influences the prevalence rate. By the definition of $p_t$, we have

$$p_t = \frac{X_t^{TI} + X_t^{NTI}}{N_t}.$$  

With the testing-quarantine-infection model described in Section 4.1, we can analytically compute the final prevalence rate $p_T$ as follows:

$$p_T = \frac{\alpha^T \cdot \frac{N_{total}}{N_T} \cdot p_0}{1 - \gamma_t} \sum_{t=1}^{T} \frac{y_t^{TQ} \cdot t + 1}{N_T}.$$  

Eq(6) shows that an increase in the testing number is likely to increase $p_T$ for any $t = 1, 2, \cdots, T$ leads to a decrease in $N_T$. Hence, both the first and the second terms in Eq(6) will increase. However, it can be shown that an increase in $y_t^{TQ}$ will actually lead to a decrease in the final prevalence rate. To formalize this, let $\tilde{y}_t^{TQ} = y_t^{TQ} + k_t, t = 1, 2, \cdots, T$, where $k_t \in \mathbb{N}$ and $\tilde{p}_T$ denote the corresponding final prevalence rate. Then we have

$$\tilde{p}_T \leq p_T.$$  

We leave the details of the proofs for Eq(6) to Appendix E. Eq(7) implies that it suffices to focus on $y_t^{TQ}, t = 1, 2, \cdots, T$ when considering which factors affect final prevalence rate $p_T$. From the above argument, we know that the larger the number of quarantined, the lower the final prevalence rate will be. This result is consistent with the common sense in that the most effective approach for controlling the spread of virus is to quarantine the infected. Note that if testing cycle length $l$ becomes smaller, the daily test number will have to increase, but the false negative rate $1/\gamma_t$ will increase as well. An increase in the testing number is likely to increase $y_t^{TQ}$, but an increase in the false negative rate decreases $y_t^{TQ}$. Formally, in one testing cycle for $N_0$ people, the simulation is carried out in two stages for each $t$: during day $0$ to $t$ and during day $t$ to $t+1$.

$$E[y_t^{TQ}] = \frac{N_{total}}{l} \cdot p_{t-1} \cdot (1 - \gamma_t), t = t_0 + 1, t_0 + 2, \cdots, t_0 + l - 1$$

Due to this trade-off between the number of tests and the false negative rate, it is important to select the optimal cycle length $l$ to minimize the final prevalence rate. To this end, we compare different cycle lengths $l$ by simulating the above test-quarantine-infection model over a time period of $T$ days. The details and results are described in the next subsection.

4.3 Optimal Testing Cycle Length to Control Final Prevalence Rate

In this subsection, we use the square array method, since it uses less number of tests and has a relatively higher accuracy, according to our findings in Section 3.3. We also assume that before the testing, people go through pre-screening, such that the initial prevalence rate $p_0$ would be kept low (for example 0.1%).

To find the optimal testing cycle length, we compare the final prevalence rates of different testing cycle lengths by simulating the test-quarantine-infection model till the end of $T$ days. When the testing cycle length $l$ is less than $T$, we run multiple cycles till $T$ days. For every cycle length $l$, we run 100 simulation replications and average the final prevalence rates over these replications. In an iteration of this $T$-day time period, if at some day the test capacity constraint can not be satisfied for all possible group sizes, then this iteration will not be recorded.

We set $T = 7, N_{total} = 10000, p_0 = 0.001, \alpha = 1.26, C = 300$. We consider testing cycle length $l$ ranges from 1 to 7 to make sure at least one complete testing cycle can be done, which means everyone in the population is tested at least once. Given values of parameters $N_{total}, \alpha, p_0, C$ and $l$, the simulation is carried out in two stages for each day as mentioned before: the testing stage and the infection stage. We initialize each simulation run as follows: $X_0^{TI} = X_0^{NTI} = 0, X_0^{NTQ} = N_{total} \times p_0, X_0^{NTNI} = N_{total} \times (1 - p_0), N_0 = N_{total}$. During day $t, 1 \leq t \leq 7$, we first randomly select $N_t^{test}$ individuals who have not been tested so far, then we apply square array tests on these $N_t^{test}$ individuals with different pool size to obtain the optimal pool size $n^*$, which minimizes the expected group false negative detection (as expressed in Eq(4) under the daily testing capacity $C$. The corresponding average number of total tests for pool size is calculated according to Eq(5). Based on the false negative rate, we obtain values of
In the infection stage, we sample newly infected individuals from those who have not been infected yet, based on the infection rate $\alpha$. Then we update $X_t^{TQ}, X_t^{TNQ}, X_t^{TNI}, X_t^{NTI}, Y_t^{TN1}, Y_t^{NT1}, Y_t^{NTN1}$ and $N_t$. As a benchmark, we also simulate using the individual testing method, which randomly select and test $C$ individuals each day from people who have not been tested so far.

We keep track of the prevalence rate each day within the 7-day time period. Figure 8 shows the prevalence rate under different cycle lengths $l$ and that of the individual testing. The cycle length $l = 1$ is not feasible due to the daily testing capacity, so it is not included in Figure 8. The estimated final prevalence rates, total number of quarantined individuals and total number of testing are listed in Table 4. The optimal pool size and the number of tests each day are shown in Figure 9.

Figure 8: Prevalence rates of the square array method with different testing cycle length $l$ and of the individual testing, $p_0 = 0.001, C = 300, N_{total} = 10000$.

| Test cycle length | Final prevalence rate | Total number of quarantined | Total number of tests |
|-------------------|-----------------------|-----------------------------|-----------------------|
| 1                 | NAN                   | NAN                         | NAN                   |
| 2                 | 0.00022               | 13.02                       | 1609                  |
| 3                 | 0.00048               | 12.97                       | 1885                  |
| 4                 | 0.00084               | 12.55                       | 1577                  |
| 5                 | 0.00098               | 12.35                       | 1875                  |
| 6                 | 0.00122               | 12.03                       | 1589                  |
| 7                 | 0.00132               | 11.9                        | 1937                  |
| individual        | 0.00328               | 4.27                        | 2100                  |

Table 4: The estimated final prevalence rate, total number of quarantined, and total number of tests for square array group testing with different cycle length $l$ and the benchmark individual testing.

Figure 9: (Left) Optimal pool size each day; (Right) Number of tests each day.
From Figure 9, we can see that the square array method leads to a much lower final prevalence rate than the individual testing. Group testing with cycle length \( l = 2 \) or 3 lowers the prevalence rate over time, while cycle length 4 – 7 keeps the prevalence rate almost steady. In contrast, the prevalence rate gets out of control when individual test is used. In the current parameter setting, the optimal testing cycle length is 2 days, leading to a final prevalence rate 0.00022 at the end of 7 days, which is about 80\% lower than the initial.

When \( l \) increases, the population get tested in each day \( N_{t}^{text} = N_{t}^{total} \) decreases. Therefore, the optimal pool size decreases as \( l \) increases, as the left of Figure 9 suggests. Compared with the individual testing, group testing uses much less number of tests each day. Table 4 shows that the number of tests is minimized when \( l = 4 \). We notice that there are sudden increases of number of tests at day 3 for \( l = 2 \), and at day 5 for \( l = 4 \). These two jumps are corresponding to the increase of the optimal pool size. The reason for this kind of jump is that when determining the optimal pool size \( n^{*} \) under a given test capacity, the feasible region for the pool size \( n \) contains discrete integers. Hence the optimal pool size may jump from one integer to another due to some tiny change of the prevalence rate from day to day.

![Figure 10: (Left) Number of the newly quarantined each day; (Right) False negative rate each day.](image)

In the left of Figure 10 and table 4, we see that the number of newly quarantined individuals each day decreases as the testing cycle length \( l \) increases. Recall that the final prevalence rate is also monotonically increasing with respect to \( l \), we confirm our analysis in Section 4.2 that an increase in the number of quarantined each day, \( y_{TQ}^{T} \), leads to a decrease in the final prevalence rate. Furthermore, it is interesting to observe that the optimal cycle length of 2 days initially has the largest false negative rate because of the large pool size, but the false negative rate drops quickly over time and becomes comparable with other cycle lengths. Under current parameter setting, it turns out that when \( l \) is small, the larger tested population offsets the disadvantage brought by higher false negative rate, leading to the result that more infected individuals get quarantined and hence less virus carrier in the population.

### 4.4 Sensitivity Analysis

![Figure 11: (Left)Prevalence rate when \( p_{0} = 0.0005 \); (Right) Prevalence rate when \( p_{0} = 0.0015 \).](image)

We conduct sensitivity analysis on the simulation output with respect to three key parameters \( p_{0}, \alpha, C \), and our decision, the optimal cycle length \( l \). We test for the cases \( p_{0} = 0.0005, 0.0015, \alpha = 1.16, 1.36, \) and \( C = 200, 400, \) respectively. The results for final prevalence rates are shown in Figure 11.
It turns out that small changes of $p_0$ and $\alpha$ bring significant changes to the final prevalence rate. In contrast, it seems that varying $C$ slightly only has a small impact on the prevalence rate. This is because there exist several ranges of values of $C$ such that we have the same optimal pool size within the range, as it is shown in Table 2.

From the above results, it is interesting to see that the optimal cycle length seems to be robust with respect to the parameters $p_0$, $\alpha$, $C$. In all scenarios that we simulate, it turns out that $l = 2$ is always the optimal cycle length for controlling the prevalence rate. Moreover, among all the feasible cycle lengths, a smaller optimal cycle length always have a better performance on controlling the virus than a bigger one. Based on these observations, we have two remarks for the robustness of the optimal pool size with respect to $p_0$, $\alpha$, $C$.

**Remark 5.** Though the false negative rate $\gamma_t$ is relatively high when $l = 2$, the testing population size $N_{\text{test}}$ each day is large. The large testing population size will dominate the number of quarantined each day. In Figure 14, although the number of newly quarantined when $l = 2$ is not always the largest, it is common that the number of newly quarantined in the first couple of days is the highest among all scenarios, and more quarantined individuals in the beginning will be helpful to control the spread of virus.

**Remark 6.** We note that even though the false negative rate is higher when $l = 2$, the infected individuals that are deemed to be negative have more opportunities to be correctly diagnosed later on. Specifically, if an infected individual tests negative in the first run, it will have the chance of getting retested for three times when $l = 2$. However, it will have at most two more tests when $l = 3$. In the worst case, it will no longer have opportunity to get more test when $l = 7$. Hence, with a smaller testing cycle length, the false negatives have a higher chance of being corrected in later runs of the testing procedure, which leads to more quarantined individuals, hence lower final prevalence rate.

## 5 Conclusion

We consider group testing for a relatively large community during the COVID-19 pandemic. In particular, two non-adaptive group testing methods are considered, namely linear array and square array methods. We take into consideration the dilution effect that will increase the false negative rate in the group testing, and derive the optimal

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1The difference of the optimal pool size $n^*$ between Table 2 and our simulation output in Section 4.3 is because in Table 2 we consider one-day testing with $N_{\text{total}} = 10000$ while in Section 4.3 we consider a $l$-day testing cycle for testing $N_{\text{total}} = 10000$ individuals.
pool size that minimizes the daily total false negative number, under a constraint of testing capacity. In addition, we incorporate the daily model into a testing cycle, propose a testing-quarantine-infection model, and compute the optimal testing cycle length that minimizes the final prevalence rate at the end of the given time period. We find that under certain parameter setting, the shorter the testing cycle length is, the more infected people will be quarantined, and it leads to a lower final prevalence rate in spite of the increased false negative number. The sensitivity analysis shows that the simulation output is sensitive to the infection rate and the initial prevalence rate, while less insensitive to the testing capacity within a certain range.

The testing protocol is summarized as follows.

**Algorithm 2:** Testing protocol.

**Input:** total population $N_{total}$, estimate of initial prevalence rate $p_0$, estimate of infection rate $\alpha$, testing capacity $C$;

**Run** the testing-quarantine-infection model (i.e., Algorithm 1);

**Output:** optimal testing cycle length $l^*$, optimal pool size $n^*_t$, $t = 1, \cdots, l^*$;

Test the total population in $l^*$ days, hence test $N_{total}$ in each day;

**while** $t \leq l^*$ **do**

- In day $t$, take three swabs from each individual;
- Form $\left\lfloor \frac{N_{total}}{l_t} \right\rfloor$ square array of size $n^*_t \times n^*_t$. Pools of size $n^*_t$ are created from each row and each column;
- Conduct RT-qPCR test for each pool;
- Conduct individual test for the remaining $N_{total} - \left\lfloor \frac{N_{total}}{l_t(n^*_t)^2} \right\rfloor (n^*_t)^2$ people;
- Conduct individual test for samples at the intersection of positive row and positive column;
- Quarantine people who test positive, and return people who test negative back to the community;
- Set $t = t + 1$.

**end**
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A Derivation for the Linear Array Group Test

A.1 Expected Number of Follow-up Diagnostic Tests

The average number of tests for a single group of size $n$ is $\mathbb{E}[m^L(n)]$.

$$\mathbb{E}[m^L(n)] = \mathbb{E} \left[ \text{number of individual test for one group} \right]$$

$$= n \mathbb{P}(\text{group test positive}) + 0 \mathbb{P}(\text{group test negative})$$

$$= n \mathbb{P}(\text{group test positive})$$

$$= n \sum_{d=0}^{n} \mathbb{P}(\text{group test positive, } d \text{ of the group contains virus})$$

$$= n \sum_{d=0}^{n} \mathbb{P}(\text{group test positive} | d \text{ of the group contains virus}) \mathbb{P}(d \text{ of the group contains virus})$$

$$= n \sum_{d=1}^{n} \mathbb{P}(\text{group test positive} | d \text{ of the group contains virus}) \mathbb{P}(d \text{ of the group contains virus})$$

$$= n \sum_{d=1}^{n} \left(1 - \gamma(n,d)\right) \binom{n}{d}(1 - p_0)^{n-d}(p_0)^d$$

The total expected number of tests for the linear array group test is:

$$\mathbb{E}[M^L(n)] = \lceil N/n \rceil + \lfloor N/n \rfloor \mathbb{E}[m^L(n)] + \mathbb{E} \left[ m^L(N - \lfloor N/n \rfloor n) \right]$$

A.2 Expected False Negative Number

The average number of false negatives for a single group test of size $n$ is $\mathbb{E}[f^L_G(n)]$.

$$\mathbb{E}[f^L_G(n)] = \sum_{d=0}^{n} d \mathbb{P}(\text{group test negative, } d \text{ of the group contains virus})$$

$$= \sum_{d=0}^{n} d \mathbb{P}(\text{group test negative} | d \text{ of the group contains virus}) \mathbb{P}(d \text{ of the group contains virus})$$

$$= \sum_{d=1}^{n} d \gamma(n,d) \binom{n}{d}(1 - p_0)^{n-d}(p_0)^d$$

The expected number of false negatives for the resulted individual tests by a single group test of size $n$ is:

$$\mathbb{E}[f^L_I(n)] = \gamma(1,1) \sum_{d=0}^{n} d \mathbb{P}(\text{group test positive, } d \text{ of the group contains virus})$$

$$= \gamma(1,1) \sum_{d=0}^{n} d \mathbb{P}(\text{group test positive} | d \text{ of the group contains virus}) \mathbb{P}(d \text{ of the group contains virus})$$

$$= \gamma(1,1) \sum_{d=1}^{n} d \left(1 - \gamma(n,d)\right) \binom{n}{d}(1 - p_0)^{n-d}(p_0)^d$$

The total expected number of false negatives for the linear array group test is:

$$\mathbb{E}[f^L_{\text{total}}(n)] = \lceil N/n \rceil \left( \mathbb{E}[f^L_I(n)] + \mathbb{E}[f^L_G(n)] \right) + \left( \mathbb{E}[f^L_I(N - \lceil N/n \rceil n)] + \mathbb{E}[f^L_G(N - \lceil N/n \rceil n)] \right)$$
B Derivation for the Square Array Group Test

B.1 Expected Number of Follow-up Diagnostic Tests

The average number of tests for a single group of size $n$ is $\mathbb{E}[m^S(n)]$.

$$\mathbb{E}[m^S(n)] = \mathbb{E}[\text{number of individual test}]$$

$$= \mathbb{E} \left[ \sum_{i=1}^{n} \sum_{j=1}^{n} 1_{\{i^{th} \text{ row and } j^{th} \text{ column test positive}\}} \right]$$

$$= \sum_{i=1}^{n} \sum_{j=1}^{n} \mathbb{E}[1_{\{i^{th} \text{ row and } j^{th} \text{ column test positive}\}}]$$

$$= \sum_{i=1}^{n} \sum_{j=1}^{n} P(i^{th} \text{ row and } j^{th} \text{ column test positive})$$

$$= n^2 P(i^{th} \text{ row and } j^{th} \text{ column test positive})$$

$$= n^2 P(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive})$$

$$= n^2 \{ P(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive}, A_{i,j} \text{ contains virus and } A_{i,:} \text{ contains virus})$$

$$+ P(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive}, A_{i,j} \text{ contains no virus or } A_{i,:} \text{ contains no virus}) \}$$

$$= n^2 \{ P(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive}, A_{i,j} \text{ contains virus and } A_{i,:} \text{ contains virus})$$

$$+ P(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive} | A_{i,j} \text{ contains virus and } A_{i,:} \text{ contains virus}) P(A_{i,j} \text{ contains virus and } A_{i,:} \text{ contains virus})$$

$$= n^2 \{ P(A_{i,j} \text{ contains virus and } A_{i,:} \text{ contains virus})$$

$$= n^2 \{ P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus}) P(A_{i,:) \text{ contains virus})$$

$$= n^2 \{ (1-\gamma(n,d+1)^{-1}(n-1-d)(1-p_0)^{n-1-d}(p_0)^d)^2 p_0$$

$$+ \left[ \sum_{d=0}^{n-1} (1-\gamma(n,d))^{-1}(n-1-d)(1-p_0)^{n-1-d}(p_0)^d \right]^2 (1-p_0) - 2(1-p_0)^n + (1-p_0)^{2n-1} \}$$

Where:

$$P(i^{th} \text{ row contains no virus}) = P(\text{individual contains no virus})^n = (1-p_0)^n$$

$$P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})$$

$$= P(A_{i,j} \text{ contains virus})/P(A_{i,:} \text{ contains virus})$$

$$= p_0/(1 - (1-p_0)^n)$$
\[
P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= P(A_{i,j} \text{ contains virus}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
+ P(A_{i,j} \text{ contains virus}, A_{i,j} \text{ contains no virus} | A_{i,:} \text{ contains virus})
\]
\[
= P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus}) + P(A_{i,j} \text{ contains no virus} | A_{i,:} \text{ contains virus})
\]
\[
P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains no virus})
= p_0/(1 - (1 - p_0)^n) + [1 - p_0/(1 - (1 - p_0)^n)](1 - (1 - p_0)^{n-1})
\]
\[
y = P(A_{i,j} \text{ tests positive} \text{ and } A_{i,:} \text{ tests positive} | A_{i,j} \text{ contains virus} \text{ and } A_{i,:} \text{ contains virus})
= P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ tests positive}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
+ P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus} AND A_{i,:} \text{ contains virus})
\]
\[
= P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ tests positive}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
+ P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus} AND A_{i,:} \text{ contains virus})
\]
\[
P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
+ P(A_{i,j} \text{ tests positive}, A_{i,j} \text{ containing no virus}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
P(A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
+ P(A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains no virus}, A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})
= ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
P(A_{i,j} \text{ contains virus} | A_{i,:} \text{ contains virus})^2
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
+ P(A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains no virus}, A_{i,j} \text{ contains virus})^2
= ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
P(A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains virus})^2
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
+ P(A_{i,j} \text{ tests positive} | A_{i,j} \text{ contains no virus}, A_{i,j} \text{ contains virus})^2
= ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
= \left( \sum_{d=0}^{n-1} P(A_{i,j} \text{ tests positive, } d \text{ of } A_{i,k\neq j} \text{ contains virus} | A_{i,j} \text{ contains virus}, A_{i,j} \text{ contains virus}) \right)^2
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[
+ \left( \sum_{d=1}^{n-1} P(A_{i,j} \text{ tests positive, } d \text{ of } A_{i,k\neq j} \text{ contains virus} | A_{i,j} \text{ contains no virus}, A_{i,j} \text{ contains virus}) \right)^2
= ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})
\]
\[\begin{align*}
\sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} \mid d \text{ of } A_{i,k\neq j} \text{ contain virus, } A_{i,j} \text{ contains virus, } A_{i,j} \text{ contains virus})
\end{align*}\]

\[\begin{align*}
&\mathbb{P}(d \text{ of } A_{i,k\neq j} \text{ contain virus} \mid A_{i,j} \text{ contains virus, } A_{i,j} \text{ contains virus})^2 \\
&\hskip 1em p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1}) \\
&\hskip 1em + \left[\sum_{d=1}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} \mid d \text{ of } A_{i,k\neq j} \text{ contain virus, } A_{i,j} \text{ contains no virus, } A_{i,j} \text{ contains virus}) \mathbb{P}(d \text{ of } A_{i,k\neq j} \text{ contain virus} \mid d \geq 1)^2\right. \\
&\hskip 2em ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1}) \\
&\hskip 1em \left. + \sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} \mid d + 1 \text{ of } A_{i,j} \text{ contain virus})^2\right] \\
&\hskip 1em p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1}) \\
&\hskip 1em + \left[\sum_{d=1}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} \mid d \text{ of } A_{i,j} \text{ contain virus}) (\binom{n-1}{d}(1 - p_0)^{n-1-d}p_0^d)^2\right. \\
&\hskip 2em ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1}) \\
&\hskip 1em \left. + \sum_{d=0}^{n-1} (1 - \gamma(n, d + 1)) (\binom{n-1}{d}(1 - p_0)^{n-1-d}p_0^d)^2 p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})\right. \\
&\hskip 2em \left. + \sum_{d=1}^{n-1} (1 - \gamma(n, d)) (\binom{n-1}{d}(1 - p_0)^{n-1-d}p_0^d)^2 ((1 - p_0) - 2(1 - p_0)^n + (1 - p_0)^{2n-1})/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1})\right]
\end{align*}\]

\[\begin{align*}
\mathbb{P}(A_{i,j} \text{ contains virus} \mid A_{i,j} \text{ contains virus and } A_{i,j} \text{ contains virus}) \\
= \mathbb{P}(A_{i,j} \text{ contains virus, } A_{i,j} \text{ contains virus and } A_{i,j} \text{ contains virus})/\mathbb{P}(A_{i,j} \text{ contains virus and } A_{i,j} \text{ contains virus}) \\
= \mathbb{P}(A_{i,j} \text{ contains virus})/\mathbb{P}(A_{i,j} \text{ contains virus and } A_{i,j} \text{ contains virus}) \\
= p_0/(1 - 2(1 - p_0)^n + (1 - p_0)^{2n-1}) \\
\mathbb{P}(A_{i,j} \text{ tests positive} \mid d \text{ of } A_{i,j} \text{ contain virus}) \\
= 1 - \gamma(n, d)
\end{align*}\]

For the total N subjects, we need \([N/n^2]\) array tests, and \((N - [N/n^2]n^2)\) individual tests. Therefore, the average total number of tests needed for the array test is:

\[\begin{align*}
\mathbb{E}[M^S(n)] = [N/n^2]\left(\mathbb{E}[m^S(n)] + 2n\right) + (N - [N/n^2]n^2)
\end{align*}\]
B.2 Expected False Negative Number

The average number of false negatives for a single group test of size \( n \) is

\[
\mathbb{E} \left[ f^G(n) \right] = \mathbb{E} \left[ \text{number of group test false negatives} \right]
\]

\[
= \mathbb{E} \left[ \sum_{i=1}^{n} \sum_{j=1}^{n} 1\{A_{i,j} \text{ contains virus and } A_{i,j} \text{ tests negative or } A_{i,:} \text{ tests negative} \} \right]
\]

\[
= \mathbb{E} \left[ \sum_{i=1}^{n} \sum_{j=1}^{n} 1\{A_{i,j} \text{ contains virus} \} - 1\{A_{i,j} \text{ contains virus and } A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive} \} \right]
\]

\[
= \sum_{i=1}^{n} \sum_{j=1}^{n} \mathbb{E} \left[ 1\{A_{i,j} \text{ contains virus} \} - 1\{A_{i,j} \text{ contains virus and } A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive} \} \right]
\]

\[
= \sum_{i=1}^{n} \sum_{j=1}^{n} \left[ \mathbb{P}(A_{i,j} \text{ contains virus}) - \mathbb{P}(A_{i,j} \text{ contains virus and } A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive}) \right]
\]

\[
= n^2 \left[ \mathbb{P}(A_{i,j} \text{ contains virus}) - \mathbb{P}(A_{i,j} \text{ contains virus and } A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive}) \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \mathbb{P}(A_{i,j} \text{ tests positive and } A_{i,:} \text{ tests positive} | A_{i,j} \text{ contains virus}) \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \left( \sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} | d, A_{k:j} \text{ contain virus}) | A_{i,j} \text{ contains virus} \right)^2 \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \left( \sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} | d+1, A_{i,j} \text{ contain virus}) \right)^2 \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \left( \sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} | d, A_{i:j} \text{ contain virus}) \right)^2 \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \left( \sum_{d=0}^{n-1} \mathbb{P}(A_{i,j} \text{ tests positive} | d+1, A_{i,j} \text{ contain virus}) \right)^2 \right]
\]

\[
= n^2 \mathbb{P}(A_{i,j} \text{ contains virus}) \left[ 1 - \left( \sum_{d=0}^{n-1} (1 - \gamma(n, d+1))(n_d^{-1})(1-p_0)^{n-1-d}(p_0)^d \right)^2 \right]
\]

\[
= n^2 p_0 \left[ 1 - \left( \sum_{d=0}^{n-1} (1 - \gamma(n, d+1))(n_d^{-1})(1-p_0)^{n-1-d}(p_0)^d \right)^2 \right]
\]
The average number of false negatives for the resulted individual tests by a single group test of size $n$ is:

$$E[f_I^S(n)] = E[\text{number of false negatives in the } m \text{ people for individual test}]$$

$$= E \left[ \sum_{i=1}^{n} \sum_{j=1}^{n} 1\{A_{i,j} \text{ tests negative and } A_{i,j} \text{ contains virus and } A_{i,:} \text{ tests positive} \} \right]$$

$$= \sum_{i=1}^{n} \sum_{j=1}^{n} E \left[ 1\{A_{i,j} \text{ tests negative and } A_{i,j} \text{ contains virus and } A_{i,:} \text{ tests positive} \} \right]$$

$$= \sum_{i=1}^{n} \sum_{j=1}^{n} P(A_{i,j} \text{ tests negative and } A_{i,j} \text{ contains virus and } A_{i,:} \text{ tests positive})$$

$$= n^2 P(A_{i,j} \text{ tests negative and } A_{i,j} \text{ contains virus and } A_{i,:} \text{ tests positive})$$

$$= \gamma(1, 1)n^2 P(A_{i,j} \text{ contains virus and } A_{i,:} \text{ tests positive})$$

$$= \gamma(1, 1)n^2 p_0 \left( \sum_{d=0}^{n-1} (1 - \gamma(n, d + 1))(n^{-1})^{(n-1-d)}(n^{-1})^{d} \right)^2$$

The total average number of false negatives for square array test is:

$$E[f_{total}^S(n)] = \left[ N/n^2 \right] \left( E[f_G^S(n)] + E[f_I^S(n)] \right) + (N - \left[ N/n^2 \right]n^2)p_0\gamma(1, 1)$$
General Binary Search

GBS is the generalization of the binary splitting procedure (BSP). BSP aims to identify exactly one of the infected people in total sample $N$. BSP algorithm can be found in Appendix C.1. GBS simply attempts to perform the BSP $\delta$ times to identify at most $\delta$ infected samples in a given population of size $N$. Note that $\delta$ plays the similar role as pool size $n$ in the square array test. With small $\delta$ we may underestimate the number of infected samples. In such case, GBS stops searching after finding $\delta$ infected samples, causing false negative in group test. We recommend to test the remaining group at the end of GBS. If we already find $\delta$ infected samples and the remaining group tests positive, we should conduct individual tests for the remaining group. If $\delta$ is too large, we would have small pool size in GBS test, which leads to inefficient binary searching but also small false negative rate in group test. Since the closed form solution for the expected total number of test needed for GBS is hard to derive, we resort to Monte Carlo simulation. The distribution of the total number of tests and the distribution of the false negative number are shown in the first two graphs of Figure 15. The relationship between $\delta$ and the total number of tests, as well as the total false negative number, is shown in the last two graphs of Figure 15. As $\delta$ increases, the total number of tests will increase and the false negative number will decrease, since the pool size will be smaller.

Figure 15: Distribution of total number of tests and false negative number in GBS under group size $\delta = 83$, $N = 10000$, $p_0 = 0.001$, $C = 600$. & The relationship between the pool size and the total number of tests, as well as the total false negative number for GBS. Simulations run 5000 times.

GBS performs badly in our setting, due to the high splitting dilution effect, since we need to split each sample into $C$ sub-samples (it is impossible to collect $C$ sample from the subject all at once). In addition, GBS is adaptive, and we have to wait until the previous test result is revealed to continue the whole procedure. The long time it takes to conduct GBS group test makes it hard to implement in practice.
C.1 BSP Algorithm

Algorithm 3: BSP

**Result:** location of the infected in the sample pool, number of tests conducted

Input: number of samples \( N \) and samples pool \( A = \{ A(1), A(2), ..., A(N) \} \);

Set testcount = 0, location = 0;

while \( N \geq 1 \) do

| Select \( N_1 = \lfloor N/2 \rfloor \);
| Test group \( G = \{ A(j) : j \leq N_1 \} \);
| Update testcount = testcount + 1;
| if test outcome is positive then
| | Update \( A = G \);
| | Update \( N = N_1 \);
| else
| | Update \( A = \{ A(j) : j > N_1 \} \);
| | Update \( N = N - N_1 \);
| | Update location = location + \( N_1 \);
| end

end

C.2 GBS Algorithm

Algorithm 4: GBS

Input: \( N, \delta \) and samples pool \( P = \{1, 2, ..., N\} \);

while \( N \geq 2\delta - 1 \) and \( \delta > 0 \) do

| Choose a group \( G \) of size \( 2^{\lfloor \log_2 \frac{N-\delta-1}{\delta} \rfloor} \);
| Test group \( G \subseteq P \);
| if test outcome is positive then
| | Identify an infected sample in \( G \) with BSP (Since the group tested positive, it must contain at least one infected sample);
| | Update \( N = N - 1 - g \) (where \( g \) is the number of uninfected items diagnosed from BSP, remove these from the pool);
| | Update \( \delta = \delta - 1 \) (remove the identified infected sample from the pool);
| else
| | Update \( N = N - |G| \) (\( |G| \) is the number of uninfected items in \( G \), remove these from the pool);
| end

end

if \( N > 0 \) and \( \delta > 0 \) then

| Test the \( N \) samples individually;

end
D Pooling Dilution Effect Model

In Section 2 we mentioned a new proposed model about the false negative induced by pooling proposed by [10]. Here we briefly introduce some detailed information about this model. First, they examine how the RT-qPCR test is conducted.

- The sample is treated to transcribe the target RNA sequence into DNA sequence.
- The sample is placed in a PCR machine, which can measure the concentration by making the target DNA fluorescent.
- A reaction is made to approximately double the DNA sequence. This is called a cycle of amplification.
- A time series of the concentration of DNA over time is recorded and then a linear regression is applied on this data. The initial DNA concentration is the linear regression value at the origin.
- The return value of the test corresponds to \(- \log_{2} \) of the initial number of viral DNA in the sample.

Denote by \( C_t \) the \(- \log_{2} \) of \( C \), the number of virus DNA contained in a sample, which is interpreted as the number of amplification cycles needed to make the intensity reach a threshold. Besides, there is a parameter \( d_{\text{cens}} \), which is called the limit of detection, meaning that one positive sample will not be detected if its \( C_t \) value is no less than \( d_{\text{cens}} \). Compared with the single individual case, the intensity curve of the pooled case is pushed rightward. Consequently, the number of amplification cycles to reach the threshold becomes large, which is more likely to be overpass the limit of detection, and that is why pooling operations will increase the false negative rate from the perspective of methodology.

Next, \( C_t \) is modeled as a random variable \( X \). Based on the re-simulated data derived by the clinical data in [26], the distribution of \( X \) is established as follows, which is referred to as mixture model.

\[
f_X(x) = \sum_{k=1}^{3} \pi_k \frac{f_{\mu_k, \sigma_k}(x)}{F_{\mu_k, \sigma_k}(d_{\text{cens}})} 1\{x \leq d_{\text{cens}}\}
\]

where the parameters are estimated as \( d_{\text{cens}} = 37.2 \), \( \pi_1 = 0.33, \pi_2 = 0.54, \pi_3 = 0.13; \mu_1 = 20.13, \mu_2 = 29.41, \mu_3 = 34.81; \sigma_1 = 3.60, \sigma_2 = 3.02, \sigma_3 = 1.31 \). \( \{f_{\mu_k, \sigma_k}(x), k = 1, 2, 3\} \) are the probability density function (PDF) of Gaussian distribution \( N(\mu_k, \sigma_k^2) \), and \( \{F_{\mu_k, \sigma_k}(x), k = 1, 2, 3\} \) are the CDF of Gaussian distribution \( N(\mu_k, \sigma_k^2) \). Note that here \( d_{\text{cens}} = 37.2 \) is corresponding to the maximum of the re-simulated data of \( C_t \), meaning that the false negative rate caused by taking swab (i.e., the first source) is neglected.

With the model for random variable \( X \), the false negative rate induced by pooling with \( N \) individuals can be deduced. It is assumed that there is one infected individual who is pooled with other \( N - 1 \) negative individuals. The virus of that infected individual need to carry at least \( N2^{-d_{\text{cens}}} \) virus DNA to allow it to be detected even if it is diluted in a group with pool size \( N \). Denote by \( \gamma \) the false negative rate, it is estimated as

\[
\gamma = 1 - P(C \geq N2^{-d_{\text{cens}}}) \\
= 1 - P(- \log_{2} C \leq d_{\text{cens}} - \log_{2} N) \\
= 1 - P(C_t \leq d_{\text{cens}} - \log_{2} N) \\
= 1 - \int_{-\infty}^{d_{\text{cens}}-\log_{2} N} f_X(x)dx \\
= 1 - \sum_{k=1}^{3} \pi_k \frac{F_{\mu_k, \sigma_k}(d_{\text{cens}} - \log_{2} N)}{F_{\mu_k, \sigma_k}(d_{\text{cens}})}.
\]

For a given group test, if the number of infected individuals is greater than 1, we re-scale the pool size to treat it as if it has only one infected individual. For instance, if we have pool size \( N \) but with \( \delta \) infected individuals among them, then we treat the case as there is one infected individual in \( \frac{N}{\delta} \) individuals. The reason that we can apply re-scaling is, in RT-qPCR test, the total volume for the sample get tested is a pre-determined constant. In other words, no matter how large is the group size and how many infected individuals, the volume gets tested are unchanged. From the analysis above, we know that \( C_t \) is determined by the viral load in the tested sample. Therefore, different test pools will have the same number of viral load as long as the ratio of infected individuals to the pool size is the same.
E  Analysis for $p_T$ with respect to $y^{TQ}_t$

In Section 4.2 we establish the relationship between the initial prevalence rate $p_0$ and final prevalence rate $p_T$. Furthermore, we deduce that the increase of $y^{TQ}_t$ will reduce $p_T$. We leave the detailed proof here.

First we show the Eq[6]

$$p_T = \alpha^T \frac{N_{total} \cdot p_0}{N_T} - \sum_{t=1}^{T} \alpha^t y^{TQ}_{t-t+1} \frac{N_T}{N_T}$$

We have

$$p_t = \frac{X^T_t + X^{NTI}_t}{N_t}$$

and

$$X^T_t + X^{NTI}_t = Y^{NTI}_t + Y^T_t + N^{NI}_t$$

$$= Y^{NTI}_t + Y^T_t + (\alpha - 1)(Y^{NTI}_t + Y^T_t)$$

$$= \alpha(Y^{NTI}_t + Y^T_t)$$

$$= \alpha(X^T_{t-1} + y^{TQ}_t + X^{NTI}_t) - y^{TQ}_t - y^{TQ}_t + y^{TQ}_t$$

Therefore,

$$p_t = \frac{X^T_t + X^{NTI}_t}{N_t}$$

$$= \frac{\alpha(X^T_{t-1} + X^{NTI}_{t-1} - y^{TQ}_t)}{N_{t-1} - y^{TQ}_t}$$

$$= \frac{\alpha(\sum_{t=1}^{T} y^{TQ}_t)}{1 - y^{TQ}_t}$$

(9)

Let $q_t = \frac{y^{TQ}_t}{N_{t-1}}$ and apply Eq[9] we will obtain

$$p_t = \frac{\alpha(p_{t-1} - q_t)}{1 - q_t}$$

$$= \frac{\alpha(p_{t-2} - q_{t-1})}{1 - q_t} - q_t$$

$$= \alpha^2 \frac{p_{t-2} - q_{t-1}}{(1 - q_t)(1 - q_{t-1})} - \alpha \frac{q_t}{1 - q_t}$$

$$= \cdots$$

$$= \alpha^t \frac{p_0 - q_1}{(1 - q_t) \cdots (1 - q_1)} - \alpha^{t-1} \frac{q_2}{(1 - q_t) \cdots (1 - q_2)} - \cdots - \alpha q_t$$

Hence the final prevalence rate $p(T)$ can be expressed as

$$p_T = \alpha^T \frac{p_0 - q_1}{\prod_{j=1}^{T} (1 - q_j)} - \sum_{t=1}^{T-1} \frac{q_{T-t+1}}{\prod_{j=T-t+1}^{T} (1 - q_j)}$$

(10)

Notice that for $t = 1, 2, \cdots, T$, we have

$$\prod_{j=T-t+1}^{T} (1 - q_j) = \prod_{j=T-t+1}^{T} \frac{N_{j-1} - y^{TQ}_j}{N_{j-1}} = \prod_{j=T-t+1}^{T} \frac{N_{j-1}}{N_T} = \frac{N_T}{N_{Q_T-t}}$$

(11)
Bring Eq.11 into Eq.10 and we simplify Eq.10 into

\[ p_T = \alpha \frac{N_{\text{total}} \cdot p_0}{N_T} - \sum_{t=1}^{T} \alpha^t \frac{k_{T-t+1}}{N_T} \]

which is exactly Eq.6.

For the Eq.7, first we recall a lemma that if \( x = \frac{A}{B} \in (0, 1) \) and \( C \geq D \geq 0 \), then we have

\[ x' = \frac{A - C}{B - D} \leq \frac{A}{B} = x \]

if \( B - D > 0 \). In our case, notice that

\[
\tilde{p}_T = \alpha^T \frac{N_{\text{total}} \cdot p_0}{N_T - \sum_{t=1}^{T} k_{T-t+1}} - \sum_{t=1}^{T} \alpha^t \frac{y_{T-t+1}^{TQ}}{N_T - \sum_{t=1}^{T} k_{T-t+1}} \\
= \frac{\alpha^T \cdot N_{\text{total}} \cdot p_0 - \sum_{t=1}^{T} \alpha^t y_{T-t+1}^{TQ} - \sum_{t=1}^{T} \alpha^t k_{T-t+1}}{N_T - \sum_{t=1}^{T} k_{T-t+1}}
\]

Notice that

\[ p_T = \frac{\alpha^T \cdot N_{\text{total}} \cdot p_0 - \sum_{t=1}^{T} \alpha^t y_{T-t+1}^{TQ}}{N_T} < 1 \]

and since \( \alpha \geq 1 \),

\[ \sum_{t=1}^{T} \alpha^t k_{T-t+1} \geq \sum_{t=1}^{T} k_{T-t+1} \]

Also, \( N_T - \sum_{t=1}^{T} k_{T-t+1} > 0 \) holds as well since the sum of the increased number of quarantined individuals can not be greater than the number of non-quarantined individuals at the end of day \( T \) in the original case(without increase of \( y_{t}^{TQ} \)). Applying the above-mentioned lemma, we have

\[ \tilde{p}_T \leq p_T \]

which completes the proof of Eq.7.