Group Testing with a Dynamic Infection Spread

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***Abstract*—We study a dynamic infection spread model, inspired by the discrete time SIR model, where infections are spread via non-isolated infected individuals. While infection keeps spreading over time, a limited capacity testing is performed at each time instance as well. In contrast to the classical, static, group testing problem, the objective in our setup is not to find the minimum number of required tests to identify the infection status of every individual in the population, but to *control the infection spread by detecting and isolating the infections over time by using the given, limited number of tests*. To analyze the performance of the proposed algorithms, we focus on the mean-sense analysis of the number of individuals that remain non-infected throughout the process of controlling the infection. We propose two dynamic algorithms that both use given limited number of tests to identify and isolate the infections over time, while the infection spreads. While the first algorithm is a dynamic randomized individual testing algorithm, in the second algorithm we employ the group testing approach similar to the original work of Dorfman. By considering weak versions of our algorithms, we obtain lower bounds for the performance of our algorithms. Finally, we implement our algorithms and run simulations to gather numerical results and compare our algorithms and theoretical approximation results under different sets of system parameters.**

I. Introduction

The group testing idea, introduced by Dorfman in his seminal work [1], is an efficient approach to the detection of the prevalence of a certain infection in the test samples of a group of individuals. The group testing approach is based on the idea of dividing the individuals into groups, mixing the collected test samples within each group and testing those mixed samples. This way, a negative test result implies that every test sample included in that mixed sample is negative, while a positive test result implies that there is at least one positive sample in the mixed sample.

Dorfman's original algorithm divides the population into disjoint groups and performs group tests by mixing the samples within each group. Subsequently, depending on the test results, positive groups are further tested individually to identify the status of every individual in the population. After Dorfman's work in [1], various adaptive (tests performed in multiple steps) and non-adaptive (tests performed in a single step) group testing algorithms have been proposed, capacity of the group testing problem has been studied for a variety of system models and family of algorithms, and extended analyses have been conducted for different regimes for the total number of infections in the population [2]–[23].

In the classical system models, it is proven that the advantage of group testing over individual testing is considerable mostly in the scenarios where the infection prevalence rate in the population is not high [5], [15], [16]. Recently, there has been an increasing focus on modified system models, where practical considerations on the system models have significantly improved the performance of the group testing systems [24]–[31]. Although these extended system models resemble real-life scenarios, in reality, the testing and infection identification processes are dynamic, especially for contagious diseases. Instead of a static, single-shot identification, testing and identification need to be done over a long time period while the infection keeps spreading and the infection status of the individuals are dynamically changing. Moreover, rather than minimizing the number of tests for complete identification, in most practical scenarios, the limit on the testing capacity might be fixed and the objective might be to identify as many infections as possible with the limited testing capacity. In this context, [32] considers a limited identification scenario in a classical setting, and [33]–[36] consider dynamic infection spread and testing models based on the SIR model [37].

In this paper, we consider dynamic testing algorithms over discrete time for a dynamic infection spread model with fixed, limited testing capacity at each time instance, where a full identification is not possible. In our system, test results are available immediately, and thus, the disease spread is not due to the delay between applying tests and receiving test results, but rather due to the limited testing capacity at each time instance. We follow a dynamic infection spread model which is inspired by the well-known SIR model where the individuals are divided into three groups: susceptible individuals (S), non-isolated infections (I) and isolated infections (R). We do not assume a community structure in our system. We initialize our system by introducing the initial infections, and then, at each time instance, infection is spread by infected non-isolated individuals to the susceptible individuals. Meanwhile, at each time instance, after the infection spread phase, the testing phase is performed, where a limited number of T tests are performed to detect a number of infections in the system. In our system, the objective is not to minimize the number of required tests to identify everyone at each time instance, but to control the infection spread either as soon as possible or with minimum number of people that got infected throughout the process, by using the limited testing capacity T.

In this paper, we analyze the mean-sense performance of our system, i.e., the expected values of the number of susceptible individuals, non-isolated and isolated infections over time, which are random processes. For *symmetric and converging*

algorithms, we state a general analytical result for the expected number of susceptible individuals in the system when the infection is brought under control, which is the time when there is no non-isolated infection left in the system. We present two dynamic algorithms: dynamic individual testing and dynamic Dorfman type group testing algorithm. We provide weak versions of these two algorithms and use our general result to obtain a lower bound on the expected number of susceptible individuals when the infection is under control. Finally, we run simulations to get numerical results of our proposed algorithms for different sets of parameters. For the proofs of the lemmas and theorems in this paper, and for more details and additional numerical results, see [38].

II. System Model

We consider a population of n individuals whose infection status change over time. The time dimension t is discrete in our system. Similar to the classical discrete SIR model, the population consists of three distinct subgroups: susceptible individuals who are not infected but can get infected by infected individuals (S), infected individuals who can infect the susceptible individuals (I), and isolated individuals who were infected, have been detected via performed tests and isolated indefinitely (R)[1]. Let $U_i(t)$ denote the infection status of individual i at time t, where 1 represents being infected, 0 represents not being infected and 2 represents being isolated. At the beginning ($t = 0$), we introduce the initial infections in the system, independently with probability p, where $U_i(0)$ is a Bernoulli random variable with parameter p. Random variables $U_i(0)$ are mutually independent for $i \in [n]$. Let $\alpha(t)$ denote the number of susceptible individuals at time t, $\lambda(t)$ denote the number of non-isolated infected individuals at time t and $\gamma(t)$ denote the number of isolated individuals at time t. Starting from $t = 1$, each time instance consists of two phases: infection spread and testing, in the respective order.

Infected individuals spread the infection to the susceptible individuals at each time instance, starting from $t = 1$, independently: Each infected individual can infect each susceptible individual with probability q, independent across both infected individuals and susceptible individuals. Isolated individuals cannot infect others and their infection status cannot change after they are isolated. Thus, probability of the event that individual i gets infected by another individual j at time $t \geq 1$ is equal to $qP\left(U_j(t-1) = 1, U_i(t-1) = 0\right)$ for $i, j \in [n]$.

At each time instance starting from $t = 1$, T tests can be performed to the individuals. Note that the testing capacity T is a given parameter and thus, in contrast to the classical group testing systems, we do not seek to minimize the number of performed tests for full identification of the infection status of the population but aim to efficiently perform T tests at each time instance to identify and isolate as many infections as possible to control the infection spread. Here, performed tests can be group tests, and we define the $T \times n$ binary test matrices, $\boldsymbol{X}(t)$, which specify the pooling scheme for the tests at each time t. For each time instance $t \geq 1$, we have the test result vectors $y(t)$, which are equal to

$$y_i(t) = \bigvee_{j \in [n]} \boldsymbol{X}_{ij}(t) \mathbb{1}_{\{U_j(t)=1\}}, \quad i \in [T] \tag{1}$$

where $y_i(t)$ denotes the ith test result at time t, $\boldsymbol{X}_{ij}(t)$ denotes the ith row, jth column of the test matrix $\boldsymbol{X}(t)$.

Note that, since the previous test matrices and test results are available while designing these test matrices, $\boldsymbol{X}(t)$ can depend on the previous test results. We assume that when tests are performed at some time instance t', the test results $y(t')$ will be available before the infection spread phase at time $t' + 1$. Thus, after the test results are available, detected infections are isolated immediately, i.e., if the ith individual is detected to be infected during the testing phase at time t', then $U_i(t') = 2$. Recall that, after an infected individual is isolated at some time t', they cannot infect others at times greater than t' and their infection status cannot change.

A testing policy π is an algorithm that specifies how to allocate the given testing capacity T for each time instance, until the infection is under control. We define $\bar{t}$ to be the time when $U_i(\bar{t}) \neq 1$ for all individuals $i \in [n]$ for the first time and we say that the infection is under control at $\bar{t}$. Note that, after $\bar{t}$, infection status of the individuals cannot change and the steady state is achieved: They are either isolated ($U_i(t) = 2$) or non-infected ($U_i(t) = 0$). Since we do not consider re-entries of recoveries to the population, the infection spread is under control when all infections in the system are isolated. Otherwise, infection may keep spreading to the susceptible individuals by the non-detected infections.

The main objective is to bring the infection spread under control by detecting and isolating each infected individual by performing at most T tests at each time instance. Note that, meanwhile, infection keeps spreading and thus, detecting the infection status of an individual to be negative does not imply that they are identified for the rest of the process; they can get infected in the later time instances. There are two metrics to measure the performance of a testing policy π: The time $\bar{t}$ when the infection is brought under control and the total number of isolated individuals when the infection is under control. While comparing the performances of the testing policies, earlier infection control time $\bar{t}$ and less number of total infections at the time of infection control $\gamma(\bar{t})$ are favored. Proposed algorithms may not simultaneously improve both metrics: One policy may bring the infection spread under control fast (i.e., low $\bar{t}$) but may result in high number of total infections (i.e., high $\gamma(\bar{t})$) while another policy may bring the infection spread under control with high $\bar{t}$ and low $\gamma(\bar{t})$.

III. Proposed Algorithms and Analysis

We propose two algorithms and analyze their performances. First algorithm does not utilize the group testing approach and it is based on the idea of dynamically and individually testing the population. Second algorithm consists of a group testing approach at each time instance, similar to the original

[1]They are called recovered (R) in the SIR model; we call them isolated individuals. As they are isolated indefinitely, they are recovered eventually.

idea of Dorfman [1] in a dynamic setting. Before stating these two algorithms and further analyzing their performances individually, we first state general results.

In our analysis, we focus on *symmetric and converging dynamic testing algorithms*, which satisfy the *symmetry* criterion for each $t \geq 0$, for every $i, j \in [n]$ pair,

$$P(U_i(t) = k) = P(U_j(t) = k), \quad k \in \{0, 1, 2\} \tag{2}$$

and the *convergence* criterion,

$$\lim_{t\to\infty} P(U_i(t) = 1) = o(1/n), \quad i \in [n] \tag{3}$$

Furthermore, we assume that the probability of an individual not being identified in the tests at time t, denoted by $p'(t)$, only depends on the testing capacity T, $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$. Note that, $\alpha(t) + \lambda(t) + \gamma(t) = n$ for all time instances t.

We assume $q = o(1/n)$ for the infection spread probability. It is practical since q is the probability of the event of infection spread that is realized independently for every element of the set product of the infected individuals and susceptible individuals, at each time instance. We analyze the long term behavior of the system in the mean sense, i.e., we focus on the terms $E[\alpha(t)]$, $E[\lambda(t)]$ and $E[\gamma(t)]$ when t is large enough.

Lemma 1 *When a symmetric and converging dynamic testing algorithm is implemented,* $\lim_{t\to\infty} E[\lambda(t)] = o(1)$ *and thus, the system approaches the steady state, in the mean sense.*

Note that, when the system reaches a state where $\lambda(t) = 0$, there will be no further change in the infection status of the individuals, i.e., the infection will be under control. The following lemma is useful for the justification of the mean sense analysis of our system.

Lemma 2 *When a symmetric and converging dynamic testing algorithm is implemented, we have* $\lim_{t\to\infty} P(\lambda(t) > \epsilon) = o(1)$ *for arbitrarily small, constant,* $\epsilon \in \mathbb{R}$.

The focus of our analysis is to give a lower bound for the number of susceptible individuals (who have never gotten infected throughout the process) when the infection is brought under control, in the mean sense. To analyze the long term behavior of $E[\alpha(t)]$, we have to analyze the long term behavior of $P(U_i(t) = 0)$. A direct calculation of this probability is not analytically tractable, however, by conditioning on $\lambda(t-1)$, we give a recursive asymptotic calculation.

Lemma 3 *For* $q = o(1/n)$ *and for all* $t \geq 0$*, we have*

$$cov\left(P(U_i(t) = 0|\lambda(t)), (1-q)^{\lambda(t)}\right) \approx 0 \tag{4}$$

Lemma 4 *When a symmetric and converging dynamic testing algorithm is implemented, we have*

$$P(U_i(t) = 0) \approx (1-p)(1-q)^{n\sum_{j=0}^{t-1} P(U_1(j)=1)} \tag{5}$$

To complete our analysis and give a lower bound for the expected number of susceptible individuals when the infection is under control, we further need to focus on $P(U_i(t) = 1)$. Similar to the case of $P(U_i(t) = 0)$, a direct calculation is not analytically tractable, however, we have a recursive relation when conditioned on $\lambda(t-1)$.

Lemma 5 *When a symmetric and converging dynamic testing algorithm is implemented, we have*

$$P(U_i(t) = 1) \approx p((1 + nq(1-p)))^t \prod_{j=1}^{t} p'(j) \tag{6}$$

where the conditional probability of an individual not being identified in the tests at time t *given* $\lambda(t-1)$ *is denoted by* $p'_{\lambda(t-1)}$ *and when cov* $\left(P(U_i(t) = 0|\lambda(t)), p'_{\lambda(t)}(t+1)\right)$ *and cov* $\left(P(U_i(t) = 1|\lambda(t)), p'_{\lambda(t)}(t+1)\right)$ *are arbitrarily small for all* $t \geq 0$.

Combining the results of Lemma 4 and Lemma 5, we have the following approximation result.

Theorem 1 *When a symmetric and converging dynamic testing algorithm is implemented and vanishing covariance constraints in Lemma 5 are satisfied for all* $t \geq 0$*, we have*

$$E[\alpha(t)] \approx n(1-p)(1-q)^{np\sum_{i=0}^{t-1}\left((1+nq(1-p))^i \prod_{j=1}^{i} p'(j)\right)} \tag{7}$$

Theorem 1 is a general result and holds for the symmetric and converging dynamic testing algorithms which satisfy the vanishing covariance conditions that we state in Lemma 5.

A. Dynamic Individual Testing Algorithm

In *dynamic individual testing algorithm*, we do not utilize the group testing approach, and uniformly randomly select T individuals to individually test at each time instance $t \geq 1$, from the non-isolated individuals. To analyze the performance of our dynamic individual testing algorithm, we show that it satisfies the symmetry and convergence criteria in (2) and (3), and we use the general result of Theorem 1.

Lemma 6 *For constant* T *and* n*, dynamic individual testing algorithm satisfies the convergence criterion*

$$\lim_{t\to\infty} P(U_i(t) = 1) = 0, \quad i \in [n] \tag{8}$$

Next, we consider a weak version of our algorithm, where at each time instance, during the testing phase, instead of selecting T individuals to test from $n - \gamma(t)$ non-isolated individuals, we select T individuals from n individuals, including the isolated ones, whose test results will be negative. For the weak dynamic individual testing algorithm, we have $1 - p'(t) = \frac{T}{n}$, which is the identification probability of an individual at time $t > 0$. Moreover, since it is an upper bound for the identification probability of an individual for the original dynamic individual testing algorithm, we have

$$\lim_{t\to\infty} E[\alpha_{orig}(t)] \geq \lim_{t\to\infty} E[\alpha_{weak}(t)] \tag{9}$$

Since the weak dynamic individual testing algorithm is a symmetric and converging algorithm and due to the fact that $p'(t)$ is constant in the weak dynamic individual testing algorithm, we can directly use the result of Lemma 5, due to the fact that the vanishing covariance criteria are already satisfied. Now, using Theorem 1, we have the following result for the weak dynamic individual testing algorithm.

Theorem 2 *When weak dynamic individual testing algorithm is used and* $(1-\frac{T}{n})(1+nq(1-p)) < 1$*, we have*

$$\lim_{t\to\infty} E[\alpha_{weak}(t)] \approx n(1-p)(1-q)^{\frac{np}{1-(1-\frac{T}{n})(1+nq(1-p))}} \quad (10)$$

which is a lower bound for $\lim_{t\to\infty} E[\alpha_{orig}(t)]$*, i.e., the limit of the expected number of susceptible individuals for the dynamic individual testing algorithm.*

B. Dynamic Dorfman Type Group Testing Algorithm

In *dynamic Dorfman type group testing algorithm*, we utilize the group testing idea while designing the test matrices. At each time instance, dynamic Dorfman type group testing algorithm uniformly randomly partitions the set of all non-isolated individuals to equal sized $T/2$ disjoint sets (with possible 1 unequal sized set). Then, test samples of the individuals are mixed with others in the same group: $T/2$ group tests are performed, and positive and negative groups are determined. Then, among the positive groups, one group (or multiple groups if the sizes of the groups are less than $T/2$) is uniformly randomly selected to be individually tested. $T/2$ individuals from the selected group are uniformly randomly selected and individually tested; here depending on the parameters, some individuals from the selected group may not be tested, as well as individuals from multiple positive groups may be selected. Detected infections are isolated and at the next time instance, the whole process is repeated with uniform random selections. We show that dynamic Dorfman type group testing algorithm is a symmetric and converging algorithm.

Lemma 7 *For constant T and n, dynamic Dorfman testing algorithm satisfies the convergence criterion*

$$\lim_{t\to\infty} P(U_i(t)=1) = 0, \quad i \in [n] \quad (11)$$

Similar to the dynamic individual testing case, we focus on a weak version of the dynamic Dorfman type group testing algorithm to provide a lower bound for the expected number of susceptible individuals in the system at the steady state.

In the weak version of the dynamic Dorfman type group testing algorithm, the results from the $T/2$ group tests are discarded and it is equivalent to the uniformly random individual testing of $T/2$ individuals. Furthermore, the isolated individuals are also included in the testing procedure. The probability of identification at time t for the weak dynamic Dorfman type group testing algorithm, given by $1-p'(t)$, is always less than the original dynamic Dorfman type group testing algorithm, due to the discarded $T/2$ group tests and included isolated individuals to the tests. Note that the weak dynamic Dorfman type group testing algorithm is also symmetric and satisfies the convergent criterion (3). Moreover, since the weak algorithm has constant value for $p'_{\lambda(t-1)}(t)$, it satisfies the vanishing covariance constraints given in the statement of Lemma 5. Using Theorem 1, we have the following result.

Theorem 3 *When weak dynamic Dorfman type group testing algorithm is used and* $(1-\frac{T}{2n})(1+nq(1-p)) < 1$*, we have*

$$\lim_{t\to\infty} E[\alpha_{weak}(t)] \approx n(1-p)(1-q)^{\frac{np}{1-(1-\frac{T}{2n})(1+nq(1-p))}} \quad (12)$$

which is a lower bound for $\lim_{t\to\infty} E[\alpha_{orig}(t)]$*, i.e., the expected number of susceptible individuals for the dynamic Dorfman type group testing algorithm.*

Note that, this result of weak dynamic Dorfman type group testing algorithm is a loose lower bound for the performance of the algorithm, which is only significant because it shows that, the weak dynamic Dorfman type group testing algorithm performs in a similar manner with weak dynamic individual testing algorithm, order-wise, which is a performance lower bound for the dynamic Dorfman type group testing algorithm.

C. Comparison of Dynamic Individual Testing and Dynamic Dorfman Type Group Testing Algorithms

To compare the average number of detected infections at a given time instance for the dynamic individual testing and dynamic Dorfman type group testing algorithms, we obtain the following results stated in the following lemmas.

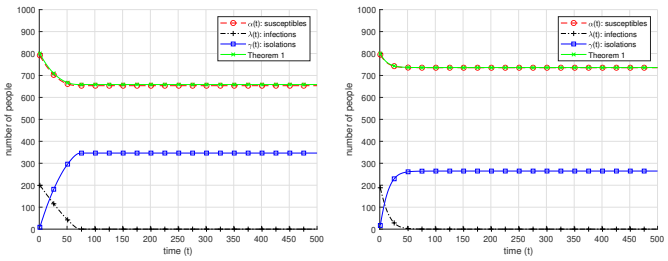
Lemma 8 *When there are $\tilde{\alpha}(t)$ susceptible and $\tilde{\lambda}(t)$ non-isolated infected individuals after the infection spread phase and just before the testing phase at time t, and dynamic individual testing algorithm is being used, on average, $\frac{T\tilde{\lambda}(t)}{\tilde{\alpha}(t)+\tilde{\lambda}(t)}$ infections are detected at time t.*

Lemma 9 *When there are $\tilde{\alpha}(t)$ susceptible and $\tilde{\lambda}(t)$ non-isolated infected individuals after the infection spread phase and just before the testing phase at time t, with $\tilde{\alpha}(t)+\tilde{\lambda}(t) \geq T^2/4$, and dynamic Dorfman type group testing algorithm is being used, if $\tilde{\alpha}(t) \geq 2(\tilde{\alpha}(t)+\tilde{\lambda}(t))/T$, on average,*

$$\frac{T\tilde{\lambda}(t)}{2(\tilde{\alpha}(t)+\tilde{\lambda}(t))}\left(1-\frac{\binom{\tilde{\alpha}(t)}{2(\tilde{\alpha}(t)+\tilde{\lambda}(t))/T}}{\binom{\tilde{\alpha}(t)+\tilde{\lambda}(t)}{2(\tilde{\alpha}(t)+\tilde{\lambda}(t))/T}}\right)^{-1} \quad (13)$$

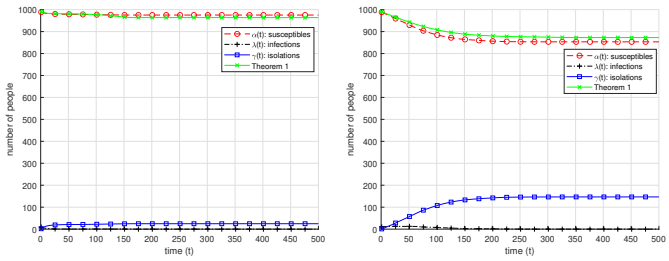
infections are detected and isolated at time t. If $\tilde{\alpha}(t) < 2(\tilde{\alpha}(t)+\tilde{\lambda}(t))/T$, then, on average, $\frac{T\tilde{\lambda}(t)}{2(\tilde{\alpha}(t)+\tilde{\lambda}(t))}$ infections are detected and isolated at time t. In the case of $\tilde{\alpha}(t)+\tilde{\lambda}(t) < T^2/4$, (13) is a lower bound for the average number of detected and isolated individuals at time t.

For a given state of the system at the time of the testing phase, using dynamic Dorfman type group testing algorithm



(a) (b)

Fig. 1: Average values of the random processes $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$, with obtained theoretical approximation given in Theorem 1 when $n = 1000$, $T = 80$, $q = 0.00003$, $p = 0.2$, for (a) dynamic Dorfman type group testing algorithm, (b) dynamic individual testing algorithm.



(a) (b)

Fig. 2: Average values of the random processes $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$, with obtained theoretical approximation given in Theorem 1 when $n = 1000$, $T = 80$, $q = 0.0001$, $p = 0.01$, for (a) dynamic Dorfman type group testing algorithm, (b) dynamic individual testing algorithm.

becomes advantageous with respect to the dynamic individual testing algorithm when $\tilde{\alpha}(t) \geq 2(\tilde{\alpha}(t) + \tilde{\lambda}(t))/T$ and

$$1/2 < \frac{\prod_{i=0}^{C} (\tilde{\alpha}(t) - i)}{\prod_{i=0}^{C} (\tilde{\alpha}(t) + \tilde{\lambda}(t) - i)} \tag{14}$$

where $C = 2(\tilde{\alpha}(t) + \tilde{\lambda}(t))/T$.

IV. Numerical Results

In our simulations, we implement the proposed algorithms. In all of our simulations, we start with n individuals with all of them susceptible. At time $t = 0$, we realize the initial infections in the system uniformly randomly with probability p. At each time instance that follows, for the infection spread phase, we simulate the random infection spread from the non-isolated infections to the susceptible individuals. For the testing phase, we simulate the random selection of individuals to be tested and perform the tests. Depending on the test results, we isolate the detected infections. We repeat these phases at each time instance until time $t = 500$, and obtain the sample paths of the random processes $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$. We iterate this whole process 1000 times to obtain 1000 sample paths of the random processes, and then we calculate the average of the sample paths to obtain the expected values of $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$, numerically. In Fig. 1 and Fig. 2, we plot these expected values of $\alpha(t)$, $\lambda(t)$ and $\gamma(t)$. We also consider the value of the theoretical approximation result that we obtained in Theorem 1. For each sample path, at each time instance, we numerically calculate the values of $p'(t)$ for both algorithms, and then use the expression that we obtained in Theorem 1 to calculate the $\alpha(t)$ approximation curve and plot the average of the sample paths of the approximation curve.

In Fig. 1, due to the relatively high number of initial infections in the system, we observe that the dynamic individual testing algorithm performs better than the dynamic Dorfman type group testing algorithm in terms of the average steady state $\alpha(t)$. In Fig. 2, relative to the first set of parameters, the number of initial infections is lower but the infection spread probability is higher. Because of the targeted individual testing to the positive groups in the dynamic Dorfman type group testing algorithm, it outperforms the dynamic individual testing algorithm for this set of parameters. In both sets of parameters, our approximation results in Theorem 1 match with the average $\alpha(t)$ curves in both dynamic Dorfman type group testing and dynamic individual testing algorithms.

V. Conclusions

In this paper, we considered a dynamic infection spread model over discrete time, inspired by the SIR model. Instead of recovered individuals in the system, we considered isolated infections, where infected individuals can be identified and isolated via testing. In our system model, infection status of the individuals are random processes, rather than random variables. We considered dynamic group testing algorithms: At each time instance, after the infection is spread by infected individuals to the susceptible individuals randomly, a given limited number of tests are performed to identify and isolate infected individuals. This dynamic system is more challenging than the classical group testing, as negative identifications are not finalized and can change over time while only the positive identifications are isolated. We analyzed the performance of the symmetric and converging algorithms by providing approximation results for the expected number of susceptible individuals when the infection is brought under control. We proposed two dynamic algorithms: *dynamic individual testing algorithm* and *dynamic Dorfman type group testing algorithm*. We considered the weak versions of these algorithms and used our general result to provide lower bounds on the expected number of susceptible individuals. We compared the average performance of these two algorithms by deriving conditions when one algorithm outperforms the other. In our simulations, we implemented the proposed algorithms and also simulated and compared the theoretical approximation that we derived. Our work is unique in that the disease spread in our dynamic system is due to limited testing capacity as opposed to delay in obtaining (unlimited) test results in the existing literature.

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