

On Modeling of Interaction-Based Spread of Communicable Diseases

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Abstract. We use a queuing model to study the spread of an infection due to interaction among individuals in a public facility. We provide tractable results for the probability that a susceptible individual leaves the facility infected. This model is then applied to study infection spread in a closed system like a large campus, community, and model the interaction among individuals in the multiple public facilities found in such systems. These public facilities could be restaurants, shopping malls, public transportation, etc. We study the impact of relative timescales of the Close Contact Time (CCT) and the individuals' stay time in a facility on the spread of the virus. The key contribution is on using queuing theory to model time-spread of an infection in a closed population.

Keywords: M/M/∞ Queue · SEIR Model

1 Introduction

With the significant economic impact of the spread of COVID-19 in the recent times, there is a great emphasis on opening up of the various economic activities. We find an imperative need for study of dynamics of spread of such viruses in a closed facility where several individuals interact.

Several models to understand the dynamics of virus spread mechanisms exist in the literature, most of them having been derived from the SEIR models [3]. These models assume a transmission probability or a transmission rate of the infection. The determination of these transmission probabilities are usually based on empirical data available. The details of the models vary with the dominant mechanism underlying the transmission of the virus. For example, in the case of dengue fever, the models consider the mosquito bite rate [1].

In the case of COVID-19, the virus is known to spread by human-to-human contact, facilitated by droplet or aerosol transmission, leading to recommendation of social distancing norms along with mandates for wearing face masks. Models for the spread of the virus based on the dynamics of the droplets' motion

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in air exist [4,5]. A recent work [15] provides an interesting view of the probability of virus spread when individuals share a common physical queue, while incorporating the mechanical dynamics of aerosol (droplet) movement. The paper also provides insights into the impact of the waiting time of an individual in the queue on the transmission of the virus.

A generic abstraction of the above-mentioned key factors influencing the probability of transmission of the COVID-19 virus is the *Close Contact Time* (CCT) between an infected and a susceptible individual [2]. A representative figure used for the CCT for the COVID-19 virus spread is roughly 15 min. Such close contacts are achieved in several public facilities that one uses in daily life, for example, restaurants, shopping malls, public transportation systems, sports arena etc.

The CCT itself depends on the manner in which the individuals interact in the facility. For example, at the point of sale queues in a supermarket, the time that individuals spend in the queue depends on the extent of shopping done by the others ahead in the queue. Such systems lead to use of the single server models for the spread of the virus. Several studies exist in the literature that propose the use of such single server models to understand virus spread, not in the context of COVID-19 virus. However, for facilities such as restaurants, public transportation systems, sports arena etc., such dependency is not there, hence multi-server queuing models are also used in the literature.

Mathematical models using the queuing theory approach to capture the interaction among individuals have been considered in the case of other diseases as well. [9] uses the M/G/1 model to get the total cost of the epidemic. [10] uses the M/G/1 processor sharing queues to model an SIR (Susceptible infected Removed) epidemic with detection over time. [11] proposes an approach for SIS (Susceptible infected Susceptible) model extends to an SEIS (Susceptible Exposed infected Susceptible) model while using the M/G/N queue (multi-server) to model the system. [12] focused on Markovian queueing model as a birth-death process with emphasis on epidemiological analysis. [13] uses an M/M/1 model to study the dynamics of the Ebola virus disease. [14] provides a mix of Markovian (stochastic) and a deterministic dynamical system model for the evolution of Hepatitis C.

We use an infinite server queue to model the interaction among individuals in a public facility and provide tractable results assuming that the virus spread depends on the duration of contact between a susceptible individual and other infected individuals, thus incorporating the COVID-19-specific CCT considerations. This queuing model is then applied to study the infection spread in a closed system such as a large campus, community, to model the multiple public facilities found in such systems. We study the impact of relative timescales of the CCT and the individuals' stay time in a facility on the spread of the virus.

The paper is organized as follows: Sect. 2 describes the system model and provides the analytical expressions for probabilities of an individual getting infected in a public facility. Section 3 provides observation where an equivalent reduced load system can be identified to study the original system. Section 4 provides

an approach to apply the results of Sect. 2 to a finite-population closed system. Section 5 provides simulation-based validation of the models developed in the paper.

2 Queuing Model and Analysis

Consider a facility, like a common room for a Doctor's waiting room/Beauty Salon/Restaurant/Shopping Mall/Public Transportation/sports arena, etc. Individuals arrive to such a facility, obtain service (stay in the facility for some random amount of time), and depart. Individuals can be either Susceptible or Infected.

Arrival Dynamics: Individuals arrive to the facility according to a Poisson process of rate $\lambda + \omega$.
Infected Population Arrival: The infected population arrives to the facility at a rate λ.
Susceptible Population Arrival: The susceptible population arrives to the facility at a rate ω.
Service Requirements: Each individual, susceptible or infected, requires a service worth a random time that is distributed as $Exp(\mu)$.
Service Mechanism: The service imparted to the individuals by this facility, which controls the time that an individual stays in the facility, is assumed to be that of an infinite server queue. This means that an individual's stay time in the facility is equal to its service requirement, irrespective of the number of other individuals in the facility.
Infection Spread Dynamics: A susceptible individual, while in contact with at least one infected person, gets infected depending on an independent point process of rate ρ, without depending on the number of infected individuals in the facility (as long as there is at least one infected individual). Also, a susceptible individual that gets infected while in the facility cannot start spreading the infection immediately.

Consider the scenario depicted in Fig. 1 that shows a susceptible individual (lowest rectangular block) that sees two infected (red) and two susceptible individuals (green) in the facility on its arrival. This individual is shown to become infected after some time. Another susceptible individual also makes a similar transition to infected, but these transitions are independent across the susceptible individuals, i.e., one susceptible individual becoming infected has no impact on that of other susceptible individuals.

Now, since we have assumed that the infection rate is independent of the exact number of infected individuals as long as *at least* one such individual is present in the facility, we can define the following:

p_0 The probability that a susceptible individual arriving to the facility without any infected individuals leaves **un**infected.

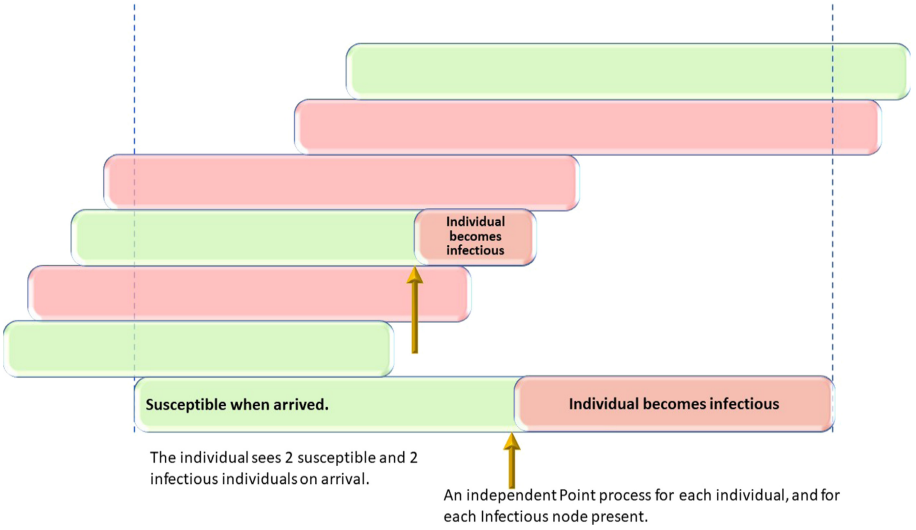

Fig. 1. The dynamics of evolution in the single facility system considered in the paper. (Color figure online)

p_1 The probability that a susceptible individual arriving to a system with exactly one infected individual leaves **un**infected.
p_{g1} The probability that a susceptible individual arriving to a system with more than one infected individuals leaves **un**infected.

We can observe that the dynamics of the infected individuals in the facility corresponds to the customers in an M/M/∞ queuing system, [8], with customer arrival rate λ and average service requirement of $\frac{1}{\mu}$. Let $B(\cdot)$ be the distribution of busy period length of such an M/M/∞ system. Recall that λ denotes the arrival rate of the infected individuals only, and does not include the susceptible individuals. Let $\tilde{B}(\cdot)$ denote the distribution of the *remaining* busy period length associated with $B(\cdot)$.

We can write the following equations:

Lemma 1.

$$p_{g1} = \int_{u=0}^{\infty} e^{-\rho u} p_0 e^{-\mu u} d\tilde{B}(u) + \int_{u=0}^{\infty} e^{-\rho u} \tilde{B}^c(u) \mu e^{-\mu u} du. \tag{1}$$

$$p_0 = \int_{u=0}^{\infty} \mu e^{-\mu u} e^{-\lambda u} du + \int_{u=0}^{\infty} p_1 e^{-\mu u} \lambda e^{-\lambda u} du. \tag{2}$$

$$p_1 = \int_{u=0}^{\infty} e^{-\rho u} p_0 e^{-\mu u} dB(u) + \int_{u=0}^{\infty} e^{-\rho u} B^c(u) \mu e^{-\mu u} du. \tag{3}$$

Proof: For a susceptible individual that arrives to the facility and sees more than 1 infected individuals, the remaining time till which at least one infected individual will continue to be in the facility has a distribution of $\tilde{B}(\cdot)$. Note that this is not the probability of all the *existing* infected individuals (that this susceptible individual saw on its arrival) leaving the system, but is the distribution of the first time instant, after the arrival of the susceptible individual, that the facility has no infected individuals left. Now, the expression follows by conditioning on the events where a) the susceptible customer is in the facility till the first time there is no infected individual in the facility, and b) the susceptible individual departs the facility before such the first time there is no infected individual in the facility. In case of event a), the susceptible person will see an empty system and due to the assumptions of Poisson arrivals for infected individuals and exponential stay time for the susceptible individual, the probability that this susceptible individual leaves the system uninfected is p_0. Similar reasoning leads to the other two expressions. □

Let $\hat{B}(s)$ be the Laplace-Stieltjes transform (LST) of the random variable corresponding to the distribution $B(\cdot)$. Then, the LST of $\tilde{B}(\cdot)$ is $\hat{\tilde{B}}(s) = \frac{1-\hat{B}(s)}{sE[B]}$. We thus get the following system of linear equations for p_{g1}, p_1, and p_0.

$$p_{g1} = p_0 \hat{\tilde{B}}(\rho+\mu) + \frac{\mu(1-\hat{\tilde{B}}(\rho+\mu))}{\rho+\mu}. \tag{4}$$

$$p_0 = \frac{\mu}{\lambda+\mu} + \frac{p_1\lambda}{\mu+\lambda}. \tag{5}$$

$$p_1 = p_0 \hat{B}(\rho+\mu) + \frac{\mu(1-\hat{B}(\rho+\mu))}{\rho+\mu}. \tag{6}$$

The LST of the busy period length is [8]

$$\hat{B}(s) = 1 + \frac{1}{\lambda}\left[s - \frac{1}{\int_0^\infty e^{-st-\lambda\int_0^t e^{-\mu u}du}dt}\right],$$

and

$$E[B] = \frac{e^{\frac{\lambda}{\mu}} - 1}{\lambda}.$$

Note the use of $\tilde{B}^c(u)$ in Eq. 3. The above set of linear equations can be solved and we get p_0 and p_{g1} in closed form. The probability that a randomly arriving susceptible individual then leaves the system **un**infected is

$$p_s(\lambda,\mu,\rho) = \pi_0 p_0 + \pi_{g1} p_{g1} \tag{7}$$

where π_0 is the probability that the corresponding M/M/∞ system is empty, and $\pi_{g1} = 1 - \pi_0$. A randomly arriving susceptible individual will see the facility having no infected individuals with probability π_0.

It is known that [6,8] the distribution of number of ongoing customers in the above M/M/∞ queue is Poisson with parameter $\frac{\lambda}{\mu}$. Thus,

$$\pi_0 = e^{-\frac{\lambda}{\mu}},$$

while noting that this probability is never 0, irrespective of how large (but finite) the value of λ or $\frac{1}{\mu}$ are.

It is also known that the departure process of the individuals from an M/G/∞ facility is Poisson [7]. The susceptible individuals also see the facility as an independent M/M/∞ queue. This property will help us in the upcoming sections where we consider multiple such interconnected queues.

3 A Reduced Load Approximation

Assume that the arrival rate of the susceptible individuals is ω, so that the overall arrival rate of individuals into the facility is $\lambda + \omega$. The facility can then be broken down into two independent M/M/∞ queues where the arrivals into one facility is only of susceptible individuals, while that into another facility is only of infected individuals. The effective arrival rates and average service requirements in these two facilities are provided in the below.

The independent facility that sees only infected individuals is M/M/∞ with an arrival rate of $\lambda + \omega(1 - p_s(\lambda, \mu, \rho))$ and average service requirement of $\frac{1}{\mu}$.

The independent facility that sees only susceptible individuals is M/G/∞ with arrival rate of ω and average service requirement as determined in the following.

The susceptible individuals see an alternating renewal process corresponding to the busy-idle periods of the M/M/∞ queue of the infected individuals. Define the following:

$\Psi(x,u)$ The probability that the total time spent in busy period is less than u units in the total interval of length x, conditioned on the event that the system was in idle period at time 0.

$\Gamma(x,u)$ The probability that the total time spent in busy period is less than u units in the total interval of length x, conditioned on the event that the system was in busy period at time 0.

$Q(x)$ The probability that a susceptible individual got a service of at least x without getting infected while getting this service.

We can then write the following equation

$$Q(x) = e^{-\mu x}\left[\pi_0 \int_{u=0}^{x} e^{-\rho u} d\Psi(x,u) + (1-\pi_0)\int_{u=0}^{x} e^{-\rho u} d\Gamma(x,u)\right]. \quad (8)$$

The distributions $\Gamma(x,u)$ and $\Psi(x,u)$ are provided in the Appendix using the results of [16].

Let $E[Q] = \int Q(x)dx$, the average service requirement of the customers in the independent queue for susceptible individuals. Then we must have the following work conservation equation satisfied

$$\frac{\lambda + \omega(1 - p_s(\lambda, \mu, \rho))}{\mu} + E[Q]\omega = \frac{\lambda + \omega}{\mu},$$

i.e., the total average work arrival rate in the original system is preserved in the new decoupled system.

4 Application to a Finite Population Model

Let there be N individuals in a system and let there be K such facilities in the system. Let the number of infected individuals at any point in time be $N_I(t)$ and the number of susceptible individuals is $N_s(t)$. Note that $N_I(t) + N_s(t) \leq N$ as there would be recovered or under-quarantine individuals at time t.

Let $\lambda_i(t)$ denote the arrival rate of infected individuals into facility i at time t, and let $\omega_i(t)$ be the rate of arrival of susceptible individuals into facility i at time t. Then, the rate of departure of susceptible individuals out of facility i is given by $\omega_i p_s(\lambda_i, \mu_i, \rho_i)$. We can see that

$$\omega_i = \sum_{j \neq i} \theta_{j,i} \omega_j p_s(\lambda_j, \mu_j, \rho_j).$$

$$\lambda_i = \sum_{j \neq i} \theta_{j,i} \left[(1 - \delta_j)\lambda_j + \omega_j (1 - p_s(\lambda_j, \mu_j, \rho_j)) \right].$$

where δ_j is the probability with which an infected individual is detected, hence quarantined, or recovered. Here $\theta_{j,i}$ is the probability that an individual coming out of facility j joins facility i.

It can be seen that

$$\delta_j = \frac{\zeta}{\mu_j + \zeta},$$

where ζ is the rate of the independent Poisson process that counts the event corresponding to detection or recovery of infection of an infected individual. Note that ζ is assumed to be independent of the facility number.

Figure 2 shows the system considered in this section. The location of a tagged individuals in the system is depicted as it moves across different facilities. The individual is initially susceptible and enters different facilities according to the routing probability $\theta_{i,j}$. While being in these facilities, the tagged individual may have come in contact with other infected individuals. The tagged individual turns infected at some point in time, but continues to visit facilities until it is detected to be infected. On detection, the tagged individual is moved to quarantine facility and comes out as a *removed* individual from such facility as it then no longer contributes to or is affected by virus spread.

Note the presence of *Private* facilities. These are the facilities where the individuals spend most of their time.

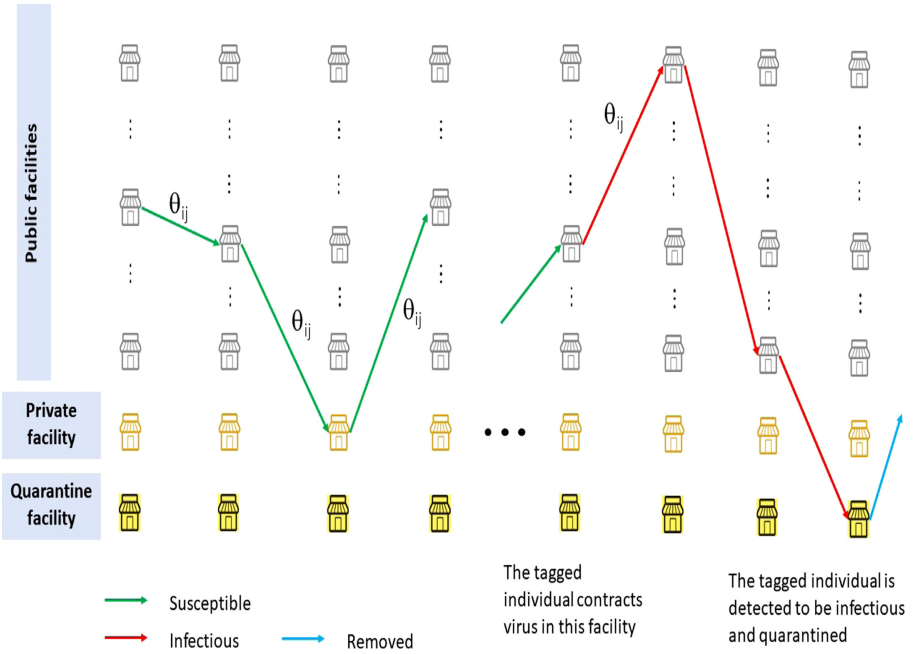

Fig. 2. Time evolution of the movement of the tagged individual across the different facilities in the multi-facility setup considered in the paper.

The rate balance proposed in this section is pictorially depicted in Fig. 3 using the pictorial representation of Fig. 2.

In the limit, $\lambda_i = 0,\ \forall i$, while the behavior of ω_i is to converge to some value, positive or zero. Note that either all $\omega_i = 0$ in the limit, or all $\omega_i > 0$.

Theorem 1. *We can show the following:*

1. $\sum_i \lambda_i > 0 \Rightarrow \Pi_i \lambda_i > 0$
2. *In the limit, when* $\lambda_i = 0,\ \forall i$, ω_i *are given by the unique solution to the fixed point equation*

$$\omega_i = \sum_{j \neq i} \theta_{j,i} \omega_j,$$

irrespective of the value of ρ_j.

The second result in the above theorem is very important as it shows that the limiting value of ω_i does not depend on the values of ρ_j. This indicates that in a real closed system, the steady state rates will be a constant multiple of the solution of the system of linear equations above. The constant multiple will be dependent on the total number of individuals in the system.

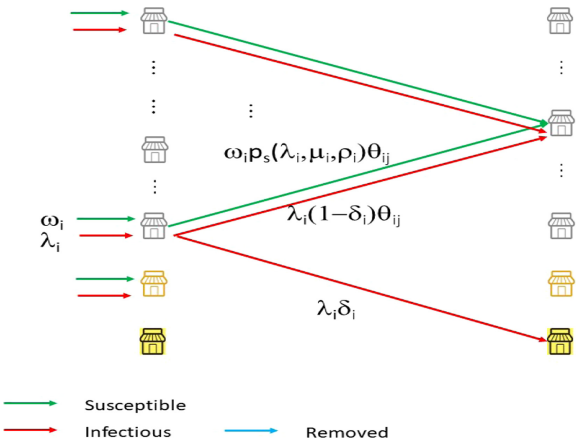

Fig. 3. The rate balance of flows into and out of various facilities.

We thus propose a discrete-time dynamical system model for the evolution of the arrival rates in the system as

$$\left.\begin{aligned}\omega_i(n+1) &= \sum_{j\neq i}\theta_{j,i}\omega_j(n)p_s(\lambda_j(n),\mu_j,\rho_j),\\ \lambda_i(n+1) &= \sum_{j\neq i}\theta_{j,i}\left[(1-\delta_j)\lambda_j(n)+\omega_j(n)(1-p_s(\lambda_j(n),\mu_j,\rho_j))\right].\end{aligned}\right\} \tag{9}$$

In this dynamical system model, the time difference between the successive updates is left unspecified.

5 Numerical Validation

5.1 Single Queue

To validate the results of the M/M/∞ queue, namely, Eq. 7, we have developed a slotted-time simulator for the M/M/∞ queue. A numerical computation of Eq. 7 is also implemented. Figure 4 provides the results for the value of $p_S(\lambda,\mu,\rho)$ as ρ is varied. It is seen from the figure that the mathematical model is accurate.

5.2 A Campus Scenario

Consider the scenario of a small closed campus or gated community. We have developed a simulator which follows the SIQR approach in order to validate the numerical results obtained from the dynamical system model of Eq. 9. It is a slot based time iterative model. In order to approximate this model to a continuous time based model and hence to a Poisson process, the slot length is set such that it is minuscule compared to the length of the smallest event in the system. The

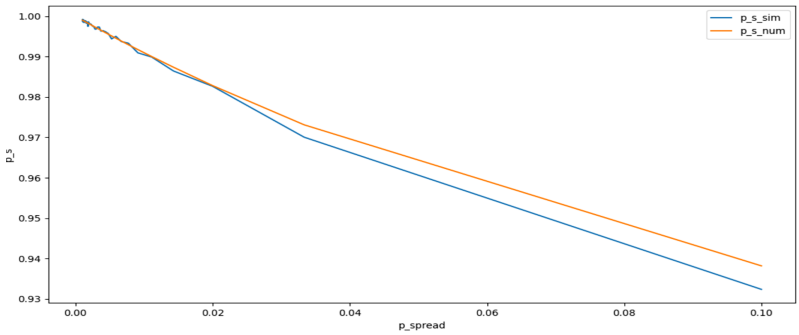

Fig. 4. Comparison of $p_S(\lambda, \mu, \rho)$ from simulation and analysis for different values of ρ.

purpose of this simulator is to simulate closed systems in which there is no inflow or outflow of individuals, rather, there is movement within the system among the various facilities. This system can be approximated to a college campus with facilities being lecture halls, stationery shops, health facilities etc. The simulator allows us to determine the scale of the simulation by allowing us to choose the population of the system. It then returns a graph which describes the time variation of the rates of arrival of susceptible and infected individuals into the public and private facilities.

We first describe the mechanism of movement. The simulator itself divides the facilities into three sets, namely Public Facilities set (ϕ), Private Facilities set (χ) and a Quarantine Facility set(ψ). Initially, ϕ and χ have a uniform distribution of people and a random array of individuals are infected. Movement of individuals between ϕ and χ is determined by a routing probability matrix and a service probability characteristic of each facility representing the average time spent by individuals in the facility. Once the service time for an individual is over, they are moved to another facility. It is assumed that the facility visited by an individual at any given time is independent of the previous facilities they have been in however the absolute probability of going to a facility may be different from that of another facility. In order to reach a steady state, we first run the simulator for 20% of the total time. During this period, there is no infected individual.

Now, we define the mechanism of transmission. Infection can only spread in ϕ. It is assumed that a susceptible individual, if there is at least one infected individual in that facility, is infected according to the next event happening in an independent Poisson process. The rate of Poisson process is the same across all facilities and isn't dependent on the number of infected individuals in a facility as long as there is at least one infected individual in that facility. Once an individual is infected, they can either recover without being detected or be detected and be sent to ψ where they spend a fixed amount of time after which it is assumed that they have recovered. Once recovered, a person can no longer contract the disease.

At the end of the simulation, a graph is returned which gives us the arrival rates of susceptible and infected individuals into ϕ and χ. As all facilities in ϕ have the same properties, it is sufficient to plot the arrival rates for any one of these facilities. By default, the simulation plots the arrival rates into the first element of ϕ. The graph so obtained is then compared with the graph obtained by the dynamical system.

Table 1. The parameters used in simulation.

Parameter	Value
Simulation time	30 days
Number of Public Facilities	20
Number of Private Facilities	1
Spread Close Contact time	15 min
Average recovery time	14 days
Average detection time	50 days
Quarantine period	14 days
Average time spent in a public facility	varied
Average time spent in a private facility	5 h

Routing matrix Θ is applicable to all the individuals, and its (i, j)-th element is given by

$$\Theta_{i,j} = \begin{cases} \theta & i \in \phi, j \in \chi, \\ \frac{1-\theta}{|\phi|-1} & i, j \in \phi, j \neq i, \\ \frac{1}{|\phi|} & i \in \chi, j \in \phi. \end{cases}$$

The slotted simulation has two phases

Settling Phase. In this phase, the system is initialized randomly, i.e., no particular consideration is given to the location of the individuals. Further, all the individuals are marked as susceptible in this phase so that there is no virus spread. The simulator is then allowed to freely run for some time so that the steady state of the arrival rates in the system is achieved.
Infection Phase. Soon after the settling phase is over, the susceptible individuals are marked as infected according to the probability set for the initial infection penetration.

The dynamical system is initialized in the following manner: starting with the number of individuals (N_{init}) in the corresponding slotted simulator, it is assumed that all the individuals are in the private facility. This then indicates that the rate of departure of individuals from the private facility is N_{init} times

the service completion rate in this facility. This value is then distributed among the other facilities as per the routing matrix. The dynamical system is then allowed to freely run for some iterations so that these rates ω_i converge. Now the required percentage infection is introduced by reducing ω_i by the desired fraction (say, p_{inf}), i.e., $\omega_i \to (1 - p_{inf})\omega_i$ and letting $\lambda_i = p_{inf}\omega_i$.

Given the many parameters involved in the system, we have provided results that capture the impact of average service requirement of individuals in the system when compared with the CCT. All the numerical apparatus developed for the presented work are available online at https://github.com/Arzad-iitbh-projects/COVID-19-ICCSA.

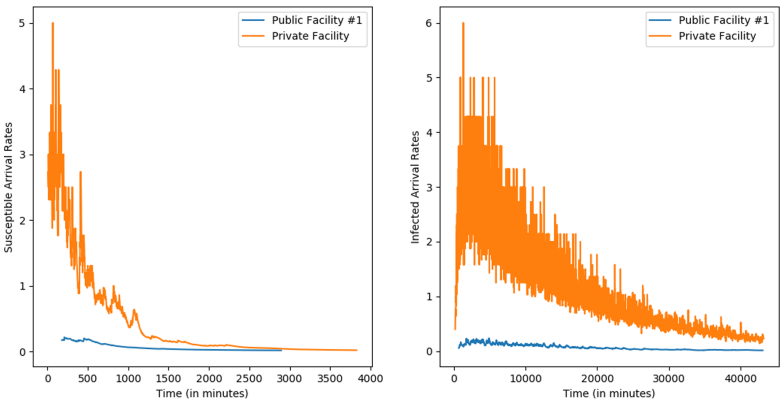

Fig. 5. The arrival rates of susceptible and infected individuals over time from the simulations for an average service time of 15 min.

Figures 5, 6, 7 and 8 show the results from our simulator and the numerical evaluation of the dynamical system. The results are for different values of average time spent in public facilities, 15 min and 30 min. Other parameters are provided in Table 1. It is seen from these figures that the dynamical system models the behaviour of the original system to a satisfactory level, and that the infection spread reduces if the average service time in a facility reduces.

Figure 9 provides the average time to extinction of susceptible population as the average service requirement increases. The results are obtained from the dynamical system model, as well as the slotted time simulator. The vertical time axis has been normalized to provide a unified view for comparison. As noted earlier, the notion of time in the dynamical system model is not accurately mapped to the real system. Note the knee-shaped behavior of this dependency, with the knee point around 15 min, which is the configured CCT in this model.

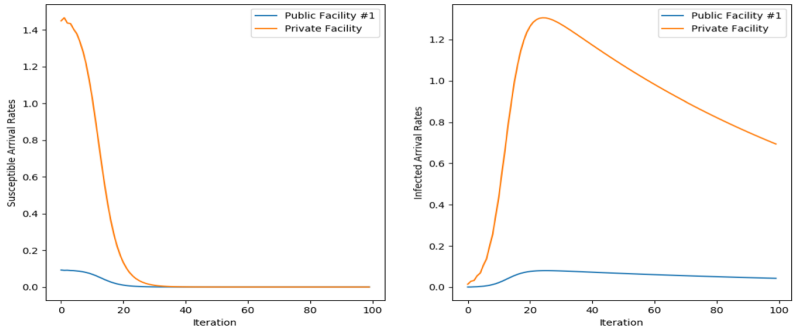

Fig. 6. The arrival rates of susceptible and infected individuals over time as per the dynamical model for an average service time of 15 min.

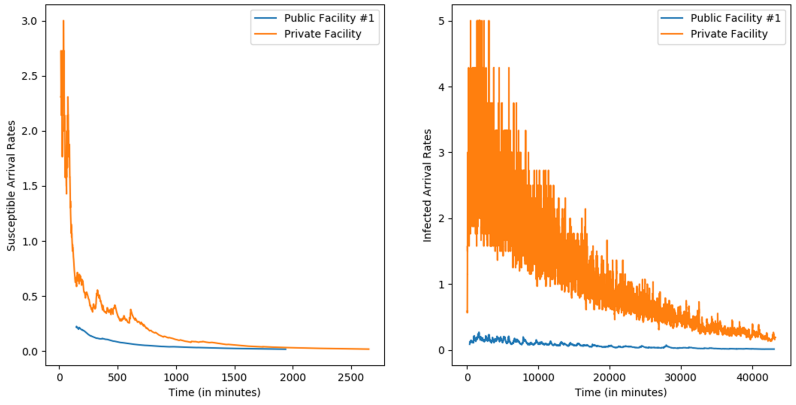

Fig. 7. The arrival rates of susceptible and infected individuals over time from the simulations for an average service time of 30 min.

The rapid decrease in the extinction time in the left-of-knee region is indicative of the very high sensitivity of $p_s(\lambda, \mu, \rho)$ when $\mu > \rho$. This indicates that keeping $\frac{1}{\mu} < \frac{1}{\rho} = CCT$ is not enough to contain the spread of a virus that spreads according to the dynamics studied in this paper. This figure also indicates that the dynamical system model is accurate in providing the qualitative analysis of the evolution of the system.

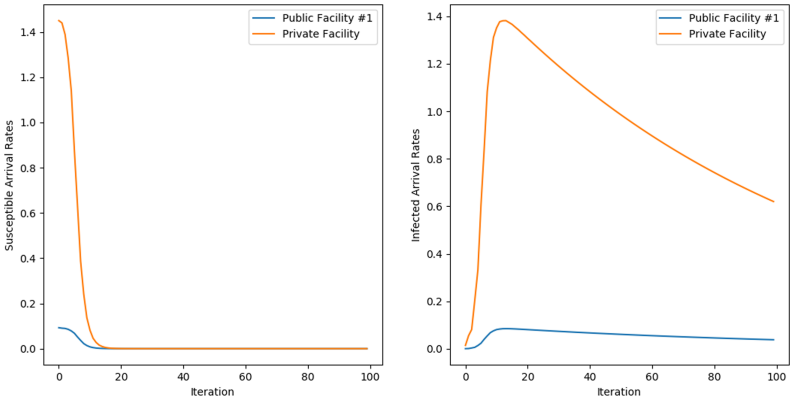

Fig. 8. The arrival rates of susceptible and infected individuals over time as per the dynamical model for an average service time of 30 min.

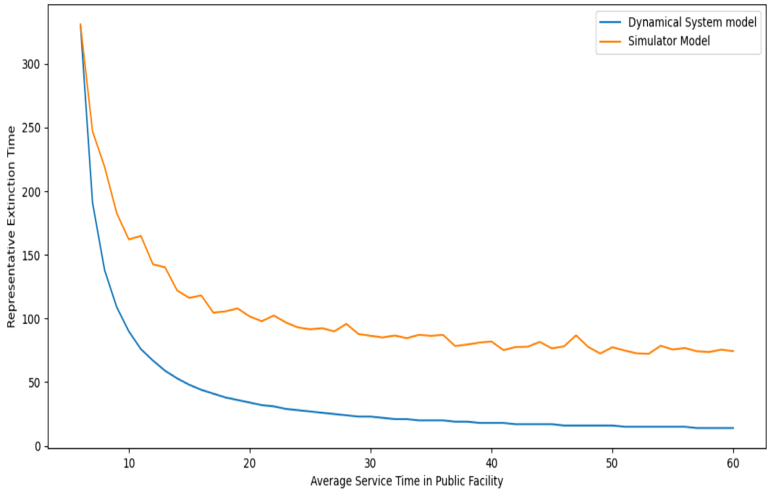

Fig. 9. Dependency of average time-to-extinction of susceptible individuals as a function of average service requirement.

6 Conclusion

This paper uses an M/M/∞ queue to model the interaction of infected and susceptible individuals at a public facility, and provides analytical derivation of the probability that a susceptible individual leaves the facility without infection. This analytical expression is validated against a slotted time M/M/∞ simulator built in-house.

We then use this model to approximate the interaction in a finite population system where the individuals interact at some of the public facilities. The interaction at these public facilities can lead to spread of the virus - this is modeled

as an independent Poisson process of a constant rate. A discrete time deterministic model for such a system is provided by assume fast averaging in the related individual queues. A slotted-time simulator is developed for this system.

There are several important directions that we plan to extend the current work to:

1. When moving from the stochastic model to the deterministic one, we currently do not have a direct way of mapping the time. We think that a approach like that of [14] would help us.
2. Extending the model to incorporate M/M/1-like facilities.
3. Extending the model to incorporate an infection spread rate that increases with the number of infected individuals in the facility.

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A Expressions for $\Psi(x,u)$ and $\Gamma(x,u)$ of Sect. 4

We will first find $\Psi(x,u)$. Since we are given that the system is Idle at time 0 and using the memoryless property of the exponential distribution, we can claim that the susceptible individual sees an alternating renewal process I_1, B_1, I_2, B_2, I_3, B_3, ... where I_i (resp. B_i is the random variable corresponding to the ith Idle period (resp. Busy period). I_i are independent and distributed as $Exp(\lambda)$, while B_i have distribution of busy period of M/M/∞ queue with arrival rate λ and service requirement $Exp(\mu)$. Let $\Psi_0(x,u) = P(\text{Total Idle Period length} > u|\text{Starting with idle period})$ so that $\Psi(x,u) = 1 - \Psi_0(x, x-u)$. Using [16, Theorem 2.1], we can show that

$$\Psi_0(x,u) = \sum_{n=0}^{\infty} (E^{(n)}(x-u) - E^{(n+1)}(x-u))B^{(n)}(u),$$

where $E^{(n)}(\cdot)$ (resp. $B^{(n)}(\cdot)$ is $n-$fold convolution of $Exp(\lambda)$ (resp., $B(\cdot)$).

The distribution $\Gamma(x,u)$ is obtained again using [16, Theorem 2.1]

$$1 - \Gamma(x,u) = \sum_{n=0}^{\infty} (C_n(u) - C_{n+1}(u))E^{(n)}(x-u),$$

where $C_n(\cdot) = \tilde{B} * B^{(n-1)}(\cdot)$ for $n \geq 1$, i.e., convolution of $\tilde{B}(\cdot)$ and $B^{(n-1)}(\cdot)$, with $C_0(u) = 1, \ \forall u$.

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