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A stochastic SVIR model with imperfect vaccine and external source of infection*

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Abstract. A stochastic SIR (Susceptible - Infected - Recovered) type model, with external source of infection, is considered for the spread of a disease in a finite population of constant size. Our interest is in studying this process in the situation where some individuals have been vaccinated prior to the start of the epidemic, but where the efficacy of the vaccine to prevent infection is not perfect. The evolution of the epidemic is represented by an absorbing three-dimensional continuous-time Markov chain. We focus on analysing the time for a threshold number of individuals to become infected, and carry out a global sensitivity analysis for the impact of varying model parameters on this summary statistic of interest.

Keywords: Stochastic epidemic model · Markov chain · Time to absorption · Imperfect vaccine

1 Introduction

Infectious diseases have been a serious threat to society throughout history. Plague, cholera and smallpox are examples of epidemics in the past that killed many people. This is a problem that we still suffer today, with emerging diseases such as Ebola, SARS and COVID-19 that continue to claim lives every day.

Understanding epidemic processes is vitally important to forecast the incidence of a disease and to establish mitigation strategies, and mathematical modelling has proven to be a robust tool in this area. Deterministic models have been widely used due to their mathematical tractability [1, 2], and are especially relevant when considering large populations or when stochastic effects can be neglected. On the other hand, when considering small populations or if extinction events play a relevant role, stochastic models need to be considered instead

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of classic ones due to the influence on the impact of the disease of random differences in infectiousness and susceptibility among individuals, while these random effects tend to cancel out each other as population size increases [3, 4].

The Kermack and McKendrick model [5] has probably been the most influential in representing the spread of an epidemic in the last decades. It is a compartmental deterministic model that classifies individuals according to their "state" with respect to the disease over time: susceptible (S), infected (I) and recovered (R). This SIR model is appropriate for describing a disease for which individuals develop permanent immunity after infection. The SIR model, and a number of different variations, has been widely analysed both for homogeneous [6, 7] and heterogeneous populations [8]. In these systems, of particular interest can be specific summary statistics that characterize an outbreak, such as the size of the outbreak [9], its length [10, 11] or the reproduction number [12].

Vaccination is an effective preventive measure to limit or avoid an outbreak, where the presence of a high percentage of vaccinated individuals in a given population can prevent transmission, reducing the size and impact of epidemic outbreaks, or the probability of these outbreaks happening at all. A number of mathematical models have considered vaccinated individuals as an extra compartment in the model [13], and some studies have added vaccination strategies into these mathematical models [14–17]. In some cases, vaccines do not provide permanent immunity, and boosters are required [18]. In other occasions, a vaccine might not be fully effective in preventing disease [19], and a proportion of vaccinated individuals might still be partially susceptible against infection. In this situation of an *imperfect* vaccine, the population runs the risk of losing or not achieving herd immunity [20].

In the literature we can find examples of studies assuming either fully protective [21] or imperfect [22, 23] vaccines. In [24, 25], authors quantify disease transmission in a stochastic SIS model with external source of infection and imperfect vaccine and study preventive measures surrounding vaccination. Under the assumption of imperfect vaccine, authors in [26] study the stationary distribution of the system for a closed population in a stochastic SVIR-type model. On the other hand, in [27] the time to extinction is studied for a non-linear incidence rate model.

In this paper, we consider a SVIR model with imperfect vaccine and external source of infection for a finite homogeneous population of fixed size. Our interest is in analysing the time until a threshold number of individuals get infected, as a way of quantifying the timescales for disease spread. We do this by representing the epidemic process in terms of a multidimensional continuous-time Markov chain (CTMC), and studying a time to absorption in this process. We show how a particular organization of states in this CTMC leads to the study of a level-dependent quasi birth-and-death process (LD-QBD) [28], and propose an efficient scheme to analyse the summary statistic of interest. Our methodology is based on the analysis of Laplace-Stieltjes transforms and the implementation of first-step arguments, adapting techniques in [24, 25].

This paper is organized as follows. In Section 2 we introduce the SVIR stochastic model with imperfect vaccine and external source of infection. In Section 3 we define the summary statistic of interest, and provide an efficient algorithm to compute any of its moments. In Section 4 we illustrate our methodology by carrying out a global sensitivity analysis on model parameters. Finally, we present our conclusions in Section 5, and discuss possible future lines of research.

2 Model description

We model the spread of an infectious disease across a population of constant size N, where a percentage of individuals are vaccinated at time $t = 0$ as a prophylactic device to control disease spread. We assume that vaccine is not perfect so that vaccinated individuals can get the infection with probability $h \in (0, 1)$, which we refer to as the vaccine failure probability. Vaccine protection lasts for at least the length of an outbreak, hence further vaccination during the outbreak is not considered. We consider SIR-type dynamics, so that infected individuals become recovered after their infectious period, and denote the recovery rate by γ. Transmission can occur through direct contact, with rate β, or due to an external source of infection, with rate ξ.

We represent this epidemic process in terms of a three-dimensional continuous-time Markov chain (CTMC) $\mathcal{X} = \{(V(t), S(t), I(t)) : \ t \geq 0\}$, where $V(t)$, $S(t)$ and $I(t)$ represent the number of vaccinated, susceptible and infected individuals in the population at time $t \geq 0$. Given that the population size remains constant, it is clear that $R(t) = N - V(t) - S(t) - I(t)$ represents the number of recovered individual at time t. If one assumes that there are no recovered individuals at the beginning of the epidemic process, the initial state is given by $(V(0), S(0), I(0)) = (v_0, s_0, N - v_0 - s_0)$, for some $v_0, s_0 \geq 0$, with $v_0 + s_0 \leq N$. The state space of the Markov chain is then given by

$$\mathcal{S} = \{(v, s, i) : 0 \leq v \leq v_0, 0 \leq s \leq s_0, 0 \leq v + s + i \leq N\}, \tag{1}$$

which is finite and contains $(v_0 + 1)(s_0 + 1)(N + 1 - \frac{s_0+v_0}{2})$ states, with a unique absorbing state $(0, 0, 0)$.

We assume that recoveries and contacts between individuals happen independently of each other, with exponentially distributed inter-event times. The evolution of the epidemic process over time is represented by transitions between states in $\mathcal{S}$, where the possible events/transitions are outlined in Table 1. In particular, given the current state $(v, s, i) \in \mathcal{S}$, possible events are:

(E_1) A susceptible individual gets infected, which occurs with rate

$$\lambda_{s,i} = s\left(\frac{\beta i}{N} + \xi\right).$$

(E_2) Considering imperfect vaccination with vaccine failure probability h, a vaccinated individual can still become infected at rate

$$\eta_{v,i} = vh\left(\frac{\beta i}{N} + \xi\right).$$

(E_3) An infectious individual recovers with rate

$$\gamma_i = \gamma i.$$

Table 1. Possible events and their transition rates.

Effective Outgoing Event	Transition	Rate
Infection of susceptible individual	$(v, s, i) \to (v, s-1, i+1)$	$\lambda_{s,i}$
Infection of vaccinated individual	$(v, s, i) \to (v-1, s, i+1)$	$\eta_{v,i}$
Recovery	$(v, s, i) \to (v, s, i-1)$	γ_i

Times spent at each state $(v, s, i) \in \mathcal{S}$ are independent and exponentially distributed random variables, with rate $q_{v,s,i} = \lambda_{s,i} + \eta_{v,i} + \gamma_i$. The dynamics of $\mathcal{X}$ is determined by its infinitesimal generator, $\mathbf{Q}$, which one can efficiently construct by organising first the space of states $\mathcal{S}$ in terms of *levels* and *sub-levels*. In particular, for a particular initial state $(v_0, s_0, N - s_0 - v_0)$,

$$\begin{aligned} \mathcal{S} &= \cup_{v=0}^{v_0} l(v), \\ l(v) &= \cup_{s=0}^{s_0} l(v, s), \quad 0 \le v \le v_0, \\ l(v, s) &= \{(v, s, i) \in \mathcal{S} :\ 0 \le i \le N - v - s\}, \quad 0 \le s \le s_0,\ 0 \le v \le v_0. \end{aligned}$$

We note that the number of states in each sub-level is $\#l(v, s) = N - v - s + 1$, while the number of states in each level is $\#l(v) = (s_0+1)(N-v+1) - \frac{s_0(s_0+1)}{2}$.

By ordering states within each sub-level as

$$(v, s, 0) \prec (v, s, 1) \prec \cdots \prec (v, s, N - v - s),$$

and ordering then states by sub-levels and levels, the infinitesimal generator of $\mathcal{X}$, $\mathbf{Q}$, is given by

$$\mathbf{Q} = \begin{pmatrix} \mathbf{Q}_{0,0} & & & & \\ \mathbf{Q}_{1,0} & \mathbf{Q}_{1,1} & & & \\ & \mathbf{Q}_{2,1} & \mathbf{Q}_{2,2} & & \\ & & \ddots & \ddots & \\ & & & \mathbf{Q}_{v_0,v_0-1} & \mathbf{Q}_{v_0,v_0} \end{pmatrix},$$

with $v_0, s_0 \ge 0$ and $v_0 + s_0 \le N$.

We note that sub-matrices $\mathbf{Q}_{v,v^*}$ are of dimensions $\#l(v) \times \#l(v^*)$. Sub-matrices $\mathbf{Q}_{v,v}$, for $0 \le v \le v_0$, contain rates corresponding to transitions between states within the level $l(v)$. These events, according to the definition of levels and Table 1, correspond to susceptible individuals becoming infected, or infected individuals recovering. On the other hand, sub-matrices $\mathbf{Q}_{v,v-1}$, for $1 \le v \le v_0$,

correspond to transitions from states in level $l(v)$ to states in level $l(v-1)$, which occur due to vaccinated individuals becoming infected. More specifically, sub-matrices $\mathbf{Q}_{v,v^*}$ are described as follows:

$$\mathbf{Q}_{v,v-1} = \begin{pmatrix} \mathbf{A}_{v,v-1}(0,0) & & & \\ & \mathbf{A}_{v,v-1}(1,1) & & \\ & & \ddots & \\ & & & \mathbf{A}_{v,v-1}(s_0,s_0) \end{pmatrix}, \quad 1 \le v \le v_0,$$

$$\mathbf{Q}_{v,v} = \begin{pmatrix} \mathbf{A}_{v,v}(0,0) & & & & \\ \mathbf{A}_{v,v}(1,0) & \mathbf{A}_{v,v}(1,1) & & & \\ & \mathbf{A}_{v,v}(2,1) & \mathbf{A}_{v,v}(2,2) & & \\ & & \ddots & \ddots & \\ & & & \mathbf{A}_{v,v}(s_0,s_0-1) & \mathbf{A}_{v,v}(s_0,s_0) \end{pmatrix}, \quad 0 \le v \le v_0.$$

Sub-matrices $\mathbf{A}_{v,v-1}(s,s)$, for $1 \le v \le v_0$, $0 \le s \le s_0$, have dimensions $(N-v-s+1) \times (N-v-s+2)$, and contain the transition rates from states in sub-level $l(v,s)$ to states in sub-level $l(v-1,s)$. These transitions represent infections of vaccinated individuals. Sub-matrices $\mathbf{A}_{v,v}(s,s)$ contain the transition rates from states in sub-level $l(v,s)$ to states within the same sub-level, and correspond to recoveries of infected individuals. Sub-matrices $\mathbf{A}_{v,v}(s,s-1)$ contain transition rates from states in sub-level $l(v,s)$ to states in sub-level $l(v,s-1)$, corresponding to infections of susceptible individuals. In particular, these sub-matrices are defined as follows:

- For $0 \le v \le v_0$, $0 \le s \le s_0$, $\mathbf{A}_{v,v}(s,s)$ is a matrix of dimensions $(N-v-s+1) \times (N-v-s+1)$, with

$$\mathbf{A}_{v,v}(s,s) = \begin{pmatrix} -q_{v,s,0} & & & & \\ \gamma & -q_{v,s,1} & & & \\ & 2\gamma & -q_{v,s,2} & & \\ & & \ddots & \ddots & \\ & & & (N-v-s)\gamma & -q_{v,s,N-v-s} \end{pmatrix}.$$

- For $1 \le v \le v_0$, $0 \le s \le s_0$, $\mathbf{A}_{v,v-1}(s,s)$ is a matrix of dimensions $(N-v-s+1) \times (N-v-s+2)$, with

$$\mathbf{A}_{v,v-1}(s,s) = \begin{pmatrix} 0 & \eta_{v,0} & & \\ & 0 & \eta_{v,1} & \\ & & \ddots & \ddots \\ & & & 0 & \eta_{v,N-v-s} \end{pmatrix}.$$

- For $0 \leq v \leq v_0$, $1 \leq s \leq s_0$, $\mathbf{A}_{v,v}(s, s-1)$ is a matrix of dimensions $(N-v-s+1) \times (N-v-s+2)$, with

$$\mathbf{A}_{v,v}(s,s-1) = \begin{pmatrix} 0 & \lambda_{s,0} & & & \\ & 0 & \lambda_{s,1} & & \\ & & \ddots & \ddots & \\ & & & 0 & \lambda_{s,N-v-s} \end{pmatrix}.$$

3 Time until M individuals get infected

In this section, we analyse the speed of transmission by focusing on the time that it takes for a threshold number M of individuals to get infected, $W(M)$. $W(M)$ is a non-negative continuous random variable that denotes the time elapsed until a total of M individuals become infected. In order to analyse this summary statistic, we redefine the CTMC as $\mathcal{X}^* = \{(J(t), S(t), I(t)) : \ t \geq 0\}$ where $S(t)$ and $I(t)$ denote the number of susceptible and infected individuals respectively at time t, and $J(t) = S(t)+V(t)$ represents the sum of vaccinated and susceptible individuals at time t. For an initial state (j_0, s_0, i_0) and a threshold value M of interest, with $1 \leq M \leq N$, $W(M)$ can be defined as

$$W_{j_0,s_0,i_0}(M) = inf\{t \geq 0 : \ J(t) = N - M \mid (J(0), S(0), I(0)) = (j_0, s_0, i_0)\}.$$

To analyse this random variable, one can study the evolution of the Markov chain $\mathcal{X}^*$ in the set of states $\mathcal{S}^* = \{(j, s, i) : N-M \leq j \leq j_0, max(0, j+s_0-j_0) \leq s \leq s_0, max(0, N-M-j+1) \leq i \leq N-j\}$, and where trivially $W_{j_0,s_0,i_0}(M) \equiv 0$ if $M \leq N - j_0$. Then, the variable $W_{j_0,s_0,i_0}(M)$ can be studied as first-passage time to the set of absorbing states $S^*_M = \{(N-M, s, i) \in \mathcal{S}^*\}$ of the Markov chain $\mathcal{X}^*$.

For any initial state (j_0, s_0, i_0), and threshold value of interest $1 \leq M \leq N$, it is clear that $\mathbb{P}(W_{j_0,s_0,i_0}(M) < +\infty) = 1$, since the external source of infection ensures that all individuals will eventually become infected. On the other hand, the definition of $W_{j_0,s_0,i_0}(M)$ for the initial state of interest (j_0, s_0, i_0) can be extended to any other state $(j, s, i) \in \mathcal{S}^*$, and the random variable of interest $W_{j_0,s_0,i_0}(M)$ can be studied by analysing as well the auxiliary ones $W_{j,s,i}(M)$, $(j, s, i) \in \mathcal{S}^*$. In particular, we can introduce the Laplace-Stieltjes transforms for any $(j, s, i) \in \mathcal{S}^*$ as $\phi_{j,s,i}(z) = E\left[e^{-zW_{j,s,i}}\right]$, $z \in \mathbb{C}$, with $Re(z) \geq 0$, and where we omit M from notation from now on.

The Laplace-Stieltjes transforms $\phi_{j,s,i}(z)$ satisfy a set of linear equations, which is obtained via first-step arguments by conditioning on the possible transitions out of state $(j, s, i) \in \mathcal{S}^*$. In particular,

$$\begin{aligned} \phi_{j,s,i}(z) = (1-\delta_{i,0})\frac{\gamma_i}{z+q_{j-s,s,i}}\phi_{j,s,i-1}(z) \\ +(1-\delta_{j,0})(1-\delta_{s,0})\frac{\lambda_{s,i}}{z+q_{j-s,s,i}}\phi_{j-1,s-1,i+1}(z) \\ +(1-\delta_{j,0})\frac{\eta_{j-s,i}}{z+q_{j-s,s,i}}\phi_{j-1,s,i+1}(z), \end{aligned} \tag{2}$$

where $\delta_{i,j}$ represents the Kronecker's delta function, defined as 1 when $i = j$, and 0 otherwise. This system of equations has boundary conditions $\phi_{N-M,s,i}(z) = 1$ for those states at which the number M of infections is reached. We can also note that, by definition, $\phi_{j,s,i}(0) = 1$, for any $(j, s, i) \in \mathcal{S}^*$.

These Laplace-Stieltjes transforms could be computed, at any point $z \in \mathbb{C}$, by solving system (2). Furthermore, with the help of numerical methods for Laplace transforms inversion, it is possible to calculate the probability distribution function of $W(M)$ [29, 30]. Although the numerical inversion is indeed possible, it is many times computationally not feasible. However, our interest instead here is in computing different order moments of these variables. In particular, moments can be computed from direct differentiation of the transform, as

$$m^k_{j,s,i} = E\left[W^k_{j,s,i}\right] \;=\; (-1)^k \frac{d^k \phi_{j,s,i}(z)}{dz^k}\bigg|_{z=0}, \quad k \geq 1. \tag{3}$$

Thus, by differentiating Eq (2) with respect to z k times ($k \geq 1$) and evaluating at $z = 1$, we obtain the equations involving the moments as

$$q_{j,s,i} m^k_{j,s,i} = k m^{k-1}_{j,s,i} + \lambda_{s,i} m^k_{j-1,s-1,i+1} + \eta_{j-s,i} m^k_{j-1,s,i+1} + \gamma_i m^k_{j,s,i-1}, \tag{4}$$

with boundary conditions $m^0_{j,s,i} = 1$, $m^k_{N-M,s,i} = 0$ for any $k \geq 1$.

The loop-free structure of the transition rates of the CMTC $\mathcal{X}^*$ allows one to compute moments in a recursive way from the system above, for increasing values of $k \geq 1$ and taking into account that moments of order 0 are trivially equal to 1. Algorithm 1 outlines how to carry out this computation in an efficient and ordered way, which is based on Theorem 1 below. Proof of Theorem 1 is omitted here for the sake of brevity, since it consists of a recursive solution scheme directly based on Eq (4).

Algorithm 1 Computation of the k^{th}-order moments of the random variable $W_{j_0,s_0,i_0}(M)$, for $1 \leq k \leq k_{max}$ for some maximum desired order k_{max}

Input: $j_0, s_0, i_0, N, M, \beta, \xi, \gamma$ and $kmax$.
Step 1: Set $j = N - M$
  Step 1a: Set $s = max(0, j + s_0 - j_0)$
  Step 1b: Set $k = 0$ and set $m^0_{N-M,s,i} = 1$ for $max(0, N-M-j+1) \leq i \leq N-j$.
  Step 1c: Set $k = k+1$, set $m^k_{N-M,s,i} = 0$ for $max(0, N-M-j+1) \leq i \leq N-j$.
  Step 1d: If $k < kmax$, go to Step 1c.
  Step 1e: Set $s = s + 1$. If $s \leq s_0$, go to Step 1b.
Step 2: Set $j = N - M + 1$.
  Step 2a: Set $s = max(0, j + s_0 - j_0)$.
  Step 2b: Set $k = 0$ and set $m^0_{j,s,i} = 1$ for $max(0, N - M - j + 1) \leq i \leq N - j$.
  Step 2c: Set $k = 1$ and set $m^k_{j,s,i}$ for $max(0, N - M - j + 1) \leq i \leq N - j$, from (6).
  Step 2d: Set $k = k+1$ and compute $m^k_{j,s,i}$ for $max(0, N-M-j+1) \leq i \leq N-j$, from (7)-(8).
  Step 2e: If $k < k_{max}$, go to Step 2d.
  Step 2f: If $s < s_0$, set $s = s + 1$ and go to Step 2b.
Step 3: If $j = j_0$, stop.
Step 4: Set $j = j + 1$.
  Step 4a: Set $s = max(0, j + s_0 - j_0)$.
  Step 4b: Set $k = 0$ and set $m^0_{j,s,i} = 1$ from $max(0, N-M-j+1) \leq i \leq N-j$.
  Step 4c: Set $k = k+1$ and compute $m^k_{j,s,i}$ for $max(0, N-M-j+1) \leq i \leq N-j$, from (7)-(8).
  Step 4d: If $k < k_{max}$, go to Step 4c.
  Step 4e: If $s < s_0$, set $s = s + 1$ and go to Step 4b.
Step 5: If $j < j_0$, go to Step 4. If $j = j_0$, stop.
Output: $m^k_{j_0,s_0,i_0}$, *for* $0 \leq k \leq kmax$.

Theorem 1. *Given a number of initial vaccinated and susceptible individuals $v_0 \geq 0$ and $s_0 \geq 0$, with $0 \leq v_0 + s_0 \leq N$ and an integer k, $k \geq 0$, and $1 \leq M \leq N$, the central moments or order k of the variable $W_{j_0,s_0,i_0}(M)$, are obtained from the following expressions for all $(j, s, i) \in \mathcal{S}^*$:*

$$m^0_{j,s,i} = 1, \quad m^k_{N-M,s,i} = 0, \text{ for } k \geq 1, \tag{5}$$

$$m^1_{N-M+1,s,i} = \sum_{r=0}^{i} \frac{i! \frac{\gamma^{i-r}}{r!}}{\prod_{l=r}^{i} q_{N-M-s+1,s,l}}, \tag{6}$$

$$m^k_{j,s,i} = \sum_{r=0}^{i} \frac{i! \frac{\gamma^{i-r}}{r!} T^k_{j,s,r}}{\prod_{l=r}^{i} q_{j-s,s,l}} \text{ for } k \geq 1 \tag{7}$$

with

$$T^k_{j,s,i} = k m^{k-1}_{j,s,i} + (1 - \delta_{s,0}) \lambda_{s,i} m^k_{j-1,s-1,i+1} + (1 - \delta_{j,s}) \eta_{j-s,i} m^k_{j-1,s,i+1}. \tag{8}$$

4 Results

In this section, we illustrate our analysis in Section 3 by carrying out a global sensitivity analysis on model parameters for the summary statistic of interest. We set the recovery rate $\gamma = 1.0$ in all the numerical experiments, so that the time unit is taken as the expected time that an infected individual takes to recover. We consider a population of $N = 100$ individuals here, and assume that 50% of them are partially protected against the infection through the vaccine, so that the initial state is $(v_0, s_0, i_0) = (50, 49, 1)$.

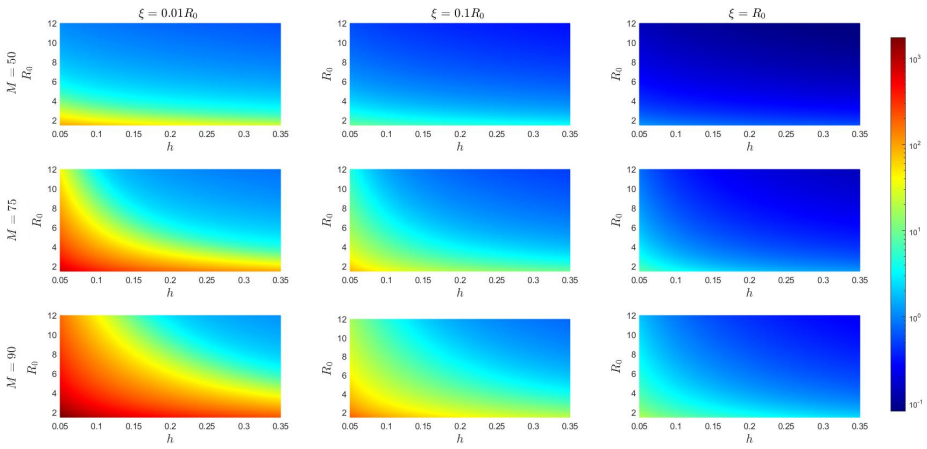

Fig. 1. Mean time $E[W(M)]$ until M individuals get infected, for different values of M, R_0, h and ξ. Initial state $(v_0, s_0, i_0) = (50, 49, 1)$.

In Figure 1, we plot $\overline{W}_M = E[W(M)]$ for different values of the Basic Reproduction Number, which for our model is taken as $R_0 = \beta/\gamma$, ξ, h and M. The average time to reach a total of M infections increases with increasing values of M, as one would expect. On the other hand, $\overline{W}_M$ decreases with the external source of infection rate, ξ, since these external infections can contribute towards reaching the threshold M. An interplay can be observed between the value of the reproduction number R_0 and the vaccine failure probability h, so that large values of $\overline{W}_M$ can be due to small transmission rates (small R_0) or small probability of vaccine failure, h. We note that the value of M, together with the proportion of individuals initially vaccinated, are directly relevant to understand the dynamics in Figure 1. The relevance of h is observed to be smaller for $M = 50$, since in this situation the outbreak can reach 50 infections just by those infections suffered by susceptible individuals in this system. On the other hand, increasing values of M require infections to happen among the vaccinated sub-population, and thus small values of the vaccine failure probability lead to significantly increased times $\overline{W}_M$ to reach M infections. We also

note that, for small values of ξ (e.g. $\xi = 0.01R_0$), the mean time $\overline{W}_M$ to reach M infections can span several orders of magnitude for different values of the parameters (M, R_0, h). This can be explained by the fact that, if the external source of infection is small and the outbreak were to finish without the level M of infections being reached, one would need to wait until a subsequent outbreak to occur in the remaining susceptible/vaccinated population, which would take long under small values of ξ. Larger values of ξ lead to "overlapping" outbreaks, where external infections can constantly occur, facilitating smaller values of the mean time $\overline{W}_M$.

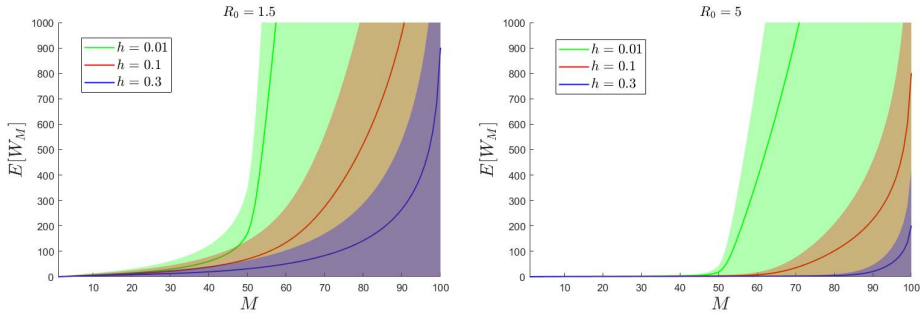

Fig. 2. Mean time $E[W(M)]$ (solid curves) plus and minus its standard deviation $\sigma[W(M)]$ (shaded area) versus M, for $\xi = 0.01R_0$, $N = 100$, $R_0 \in \{1.5, 5\}$ and $h \in \{0.01, 0.1, 0.3\}$. Initial state $(v_0, s_0, i_0) = (50, 49, 1)$.

Some of the dynamics described above can be better understood by exploring Figure 2, that shows the expected time elapsed until M infections have been reached as a function of M, for a relatively small value of $\xi = 0.01R_0$ and for several values of h and two different values of R_0. Shaded areas are obtained by considering $E[W(M)] \pm \sigma[W(M)]$. As expected, increasing values of R_0 or smaller values of h lead to increasing times to reach M infections. On the other hand, vaccines with higher probability of failure lead to situations where less time is needed in order to reach M infections, and in consequence the expansion of the disease is faster. This behaviour reveals the importance of the vaccine effectiveness. Particularly interesting is the asymptotic behaviour of the curves, where the time to reach M infections can significantly increase when approaching particular values of M in some situations. This is directly related to the vaccine failure probability h, and the initial number of susceptible and vaccinated individuals $(s_0, v_0) = (49, 50)$. In particular, and when focusing for example on $R_0 = 1.5$ and $h = 0.01$, the small vaccine failure probability means that infections in order to reach the threshold value M are likely to occur among susceptible individuals, and unlikely to happen among vaccinated ones. Since 50% of the population is vaccinated, and we start with 1 infected individual, up to $M = 50$ individuals can become infected in relatively short periods of time (given that $R_0 = 1.5$)

by infections happening in the susceptible pool. However, as soon as M exceeds the value 50 infections among the vaccinated pool are required to happen for this threshold to be reached. These infections would be rare ($h = 0.01$), leading to significant increases in the expected time $E[W(M)]$. These behaviours nicely illustrate the protection that a nearly perfect vaccination confers to the pool of vaccinated individuals, where a relatively fast outbreak (due to $R_0 = 1.5 > 1$) would decelerate when approaching $M = s_0 + i_0$. For significantly small values of h (e.g. $h = 0.01$), the dynamics described above are relatively similar regardless of considering $R_0 = 5$ instead of $R_0 = 1.5$, although increasing values of R_0 facilitate an *overshoot* effect, as can be observed when comparing the two plots in Figure 2. For relatively larger vaccine failure probabilities (e.g. $h = 0.1$ or $h = 0.3$), these asymptotic behaviours can be partially compensated by increasing values of R_0, where some infections in the vaccinated pool can be achieved due to the large value of R_0, facilitating the attainment of the threshold number of infections M.

Numerical experiments show that the expected value of $W(M)$ presents an increasing behaviour, as a function of M. Moreover, when we increase the vaccination coverage v_0 and keep fixed the remaining model parameters, the mean time to achieve a number of M infections also increases. This is in accordance to intuition because when an outbreak starts with a big proportion of vaccine protected individuals, infections are becoming less likely and the time to infect M individuals is larger in comparison with outbreaks starting with a lesser number of vaccinated individuals.

Computational times are very high and complexity increases when considering populations larger than 1000 individuals. For instance, when $N = 1000$ individuals the state space $\mathcal{S}^*$ contains around 4.16×10^7 states, while for a population of 10000 individuals the number of states increases to 4.16×10^{10}. The elapsed time to compute $E[W(M)]$ takes around 4 minutes when $N = 1000$ and it lasts more than 5 hours when $N = 10000$, in a personal computer with 8 GB of RAM, M1 memory Chip with GPU of 7 Kernels.

5 Conclusions

In this paper, we have considered a stochastic SVIR model with imperfect vaccine and external source of infection. We have represented this in terms of a multidimensional continuous-time Markov chain, and have showed that by appropriately ordering its space of states in terms of levels and sub-levels, this leads to the study of a LD-QBD. Our interest was in analysing the speed at which the epidemic occurs, by studying the time to reach a threshold number M of infections in the population. By means of first-step arguments, we have obtained a system of linear equations which can be solved efficiently and recursively, as outlined in Algorithm 1. In our results in Section 4, we have illustrated our methodology by carrying out a wide sensitivity analysis on model parameters, where an interplay can be observed between the reproduction number R_0, the threshold of interest M, the vaccine failure probability h, the external source of

infection rate ξ, and the initial number of vaccinated individuals v_0. Our techniques can in principle be applied in order to study other summary statistics of potential interest in this system, such as the exact reproduction number [24, 31] or the time until the end of the outbreak [8]. This remains the aim of future work.

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