Mathematical Methods in the Applied Sciences

WILEY

RESEARCH ARTICLE OPEN ACCESS

Incidence and Time Until Disease Detection in a Stochastic Model With Vaccination and General Transmission

Mariajesus Lopez-Herrero[1] | Verdiana Mustaro[2] | Diana Taipe[1]

[1]Faculty of Statistical Studies, Complutense University of Madrid, Madrid, Spain | [2]Department of Mathematics, Università degli Study di Salerno, Fisciano, Italy

Correspondence: Mariajesus Lopez-Herrero (lherrero@ucm.es) | Verdiana Mustaro (vmustaro@unisa.it)

Received: 9 May 2025 | **Revised:** 12 September 2025 | **Accepted:** 25 October 2025

Funding: This work has been partially supported by the Ministry of Science and Innovation (Government of Spain) through project PID2021-125871NB-I00. The authors also acknowledge the support from the "European Union — NextGenerationEU" through MUR-PRIN 2022, project 2022XZSAFN "Anomalous Phenomena on Regular and Irregular Domains: Approximating Complexity for the Applied Sciences," and MUR-PRIN 2022 PNRR, project P2022XSF5H "Stochastic Models in Biomathematics and Applications" and INdAM–GNCS project, code CUP_E53C24001950001. The third author also acknowledges the support of Banco Santander and the Complutense University of Madrid, Predoctoral Researcher Contract CT63/19-CT64/19.

Keywords:detection of the disease | imperfect vaccine | Markov chain | stochastic epidemic model

ABSTRACT

In this study, we focus on the detection of a vaccine-preventable communicable disease using a stochastic SIR compartmental model, which includes an additional compartment for individuals protected by vaccination. Although the vaccine is administered as a preventive measure before the onset of the disease, its efficacy diminishes with time, which requires booster doses for susceptible individuals. Using a continuous-time Markov chain, we examine the time required for disease detection (i.e., full confirmation of the disease) and analyze the incidence rates before detection, both within the vaccinated group and throughout the population. To illustrate the usefulness of our theoretical derivations and algorithmic schemes, we will present a numerical study involving the above descriptors for outbreaks of foot-and-mouth disease (FMD) in cattle.

MSC2020 Classification: 92D30, 60J28, 60J22

1 | Introduction

Mathematical models in epidemiology are essential tools for understanding and predicting the dynamics of infectious diseases within a population. These models enable the evaluation of various control and prevention strategies, such as vaccination.

https://doi.org/10.1002/mma.70306

Vaccination, a widely used method, involves the introduction of attenuated or inactivated pathogens into an organism to confer immunity against a specific disease. However, vaccination is not always perfect; there can be failures in administration, variability in individual immune responses, and other factors that affect its efficacy. As a result, vaccinated individuals can still become infected. Moreover, studies suggest that immunity induced by a vaccine can wane over time, leading to an increase in the number of infections in previously vaccinated individuals [1, 2].

Incorporating imperfect vaccination into the mathematical formulation is crucial for understanding how vaccine failure and waning immunity impact disease spread and for designing more effective control strategies [3, 4]. These models often extend classical frameworks such as the susceptible–infected–recovered (SIR) and susceptible–exposed–infected–recovered (SEIR) models to include parameters that represent vaccine efficacy and vaccination characteristics [5–9]. In addition to vaccine characteristics, recent studies (see, e.g., [10–15]) include control measures such as treatment, quarantine, isolation, and boosting to discuss their effect in disease transmission.

To characterize epidemiological events, epidemic modeling often involves intervals representing the elapsed times for an infected individual to pass the infection on to others, such as the incubation period or other transmission patterns (see [16–19] and the references therein). However, there is not much literature that focuses on the detection period. As recent examples, we mention [20–22] for practical guidance and [23, 24] for mathematical modeling.

Many infectious diseases are difficult to diagnose because of the variability of presentation and the limitations of diagnostic testing. Many signs and symptoms are common to many different infections, regardless of the pathogen. Hence, different infections may initially present with a similar clinical picture. The time lag to disease detection (or the time between the onset of symptoms and the confirmed diagnosis) is a critical period during which the pathogen is free to spread in the population while a decision on infected individuals is made. Understanding how the disease spreads during this critical period is therefore essential to take effective action to control it.

In this paper, we are concerned with a stochastic model that employs a continuous-time Markov chain (CTMC) to model the spread of an epidemic process through a population. Infection is transmitted individual to individual through a general nonlinear infection force, but not only from within a community, as an external source of infection is considered [25–27]. The disease involved can be prevented by vaccination, but the administered vaccine may not protect an individual for several reasons, and the protection conferred wanes with time after vaccination [12, 28, 29]. To counteract the waning effect and maintain the level of protection in the population, the vaccine is administered to susceptible individuals according to a revaccination schedule. We assume that we are able to recognize symptoms in infected individuals as soon as the infection occurs and that, immediately, the suspicious individual is tested to identify the pathogen. Once identified, infectious individuals are isolated and treated appropriately.

To focus on the period until the disease is definitively confirmed by clinical tests, we start from a stochastic model of the SIR type where the R compartment, normally reserved for the removed individuals, will contain the detected diseased individuals.

The above-mentioned recent works [23, 24] explore the dynamics of deterministic epidemic models to understand the effects of diagnosis and delay in treatment on disease burden. The deterministic approach is flexible enough to represent the spread of a disease in large populations where the homogeneity of individuals is a natural assumption. In contrast, our stochastic approach models disease transmission as a sequence of stochastic stages and incorporates randomness and variability into the disease dynamics. As a consequence, they are especially helpful in dealing with populations of moderate size, where the variety of potential outcomes plays a crucial role in disease transmission.

The key contribution of this paper is the stochastic analysis of the disease detection period, which is based on two important random descriptors: the length of the detection period and the incidence of infection in the meantime. First, we derive the moments of the random distribution of the lag-time period. Second, we perform an exhaustive analysis of the random incidence of infection prior to identification of the disease, both in the entire population and among the vaccinated pool.

By exploiting the special transition structure of this model, which is directly related to the block tridiagonal form of the infinitesimal generator of our CTMC, we get stable recursive schemes for computing probabilities and moments. In the paper, we propose straightforward recursive algorithms that circumvent the need for subtractions or the use of mathematical expressions involving matrix powers and products that can lead to computational challenges as the population size increases.

The remainder of the paper is organized as follows. In Section 2, we introduce the model formulation and the CTMC that represents the progress of the disease. Section 3 deals with the detection of disease. Firstly, in Section 3.1, we study the time required to confirm the disease, and in Sections 3.2 and 3.3, we analyze the incidence of infection prior to disease detection, both in the whole population and within the vaccine-protected compartment. Regarding foot-and-mouth disease (FMD) outbreaks, Section 4 collects numerical results that show the applicability of theoretical results and algorithmic schemes presented in previous sections. Finally, Section 5 presents an additional discussion and future extensions of this work.

2 | Model Description

We consider a finite and homogeneous population of N individuals affected by a contagious viral disease that can be prevented by administering an available vaccine. We assume that this vaccine is not fully effective in protecting individuals and that it loses effectiveness over time. As a result, some people may become infected despite having been vaccinated. Vaccination of susceptible individuals is carried out before and during the outbreak to mitigate the effects of waning immunity. The virus is transmitted by direct contact with an infected person. We assume that we will be able to detect symptoms in all infected individuals. Therefore, our assumption is that all infected individuals will be tested for the presence of the pathogen.

To model the spread of the disease, we consider a stochastic susceptible–vaccinated–infected–removed (SVIR) model, where the removed class is interpreted as an infection-detected class, consisting of those individuals for whom the disease has been unequivocally confirmed and who are no longer participating in the spread of the epidemic, perhaps due to isolation or other control measures. Thus, at any time t, we shall define the following nonnegative, time-dependent variables:

- $S(t)$, representing the number of susceptible individuals, that is, unvaccinated elements of the populations who might become infected at time t;
- $V(t)$, the number of vaccine-protected individuals;
- $I(t)$, indicating the number of currently infected individuals at time t;
- $R(t)$, representing the number of removed (or confirmed infected) individuals at time t.

According to the constant finite size hypothesis, it is clear that the following relationship is fulfilled at any time:

$$S(t) + V(t) + I(t) + R(t) = N,$$

allowing us to represent the dynamic of the disease in terms of a three-dimensional CTMC, recording infectious, susceptible, and vaccinated individuals at any time $t > 0$. Thus, we introduce the Markov chain:

$$\chi = \{(I(t), S(t), V(t)) : t > 0\}, \tag{1}$$

with state space $\mathcal{S} = \{(i, s, v) : 0 \leq i + s + v \leq N\}$ containing $\binom{N+2}{3}$ states.

As it is shown in Figure 1, the possible events that cause a change in the state of χ are the following: E_1, which records transitions due to vaccination of a susceptible individual; E_2, which corresponds to a transition due to loss of vaccine-induced immunity; E_3, that is associated with infection of a susceptible individual; E_4, which is associated with infections of vaccinated individuals due to vaccine failure; and E_5, which identifies transitions due to the removal of an infectious individual after being confirmed as a case of infection with the disease.

We assume that the events described above are independent and that transition times between states are exponentially distributed, with parameter depending on the initial state $(i, s, v) \in \mathcal{S}$. Specifically, each susceptible individual is required to be vaccinated at time intervals of mean length ρ^{-1}. As mentioned, vaccine protection against the disease wanes and the immune response lasts for an exponential interval, where θ^{-1} identifies the expected duration of protection.

Infection transmission in the susceptible compartment is represented by the function $\beta(i, s) = sg(i)$, where the function $g(i)$ satisfies $g(0) \geq 0$ to cover the possibility of contacts with nonresident infectious individuals occurring at a rate ξ. However, the spread of the virus in the vaccinated group depends on the efficacy of the vaccine and is represented by a

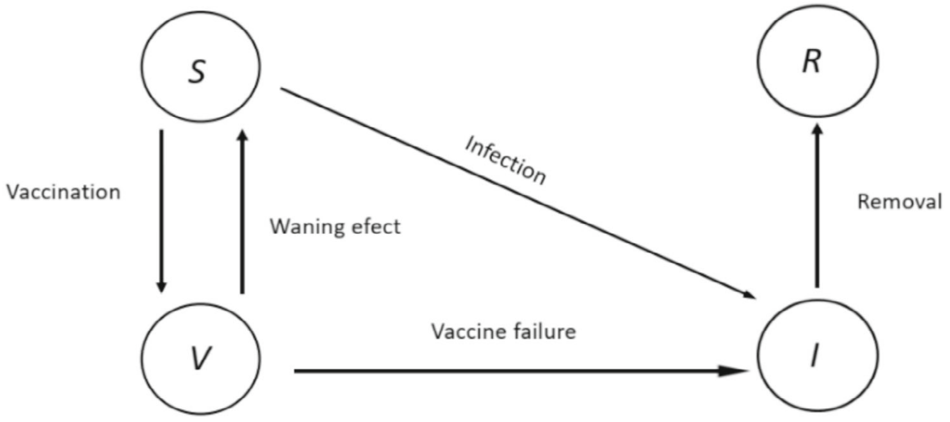

FIGURE 1 | Effective events and transitions between compartments in the SVIR model.

TABLE 1 | Effective events that modify the state of the Markov chain χ defined in (1) and the corresponding transitions.

Event	Description	Transition
E1	Vaccination of a susceptible individual	$(i, s, v) \to (i, s-1, v+1)$
E2	Loss of vaccine-induced immunity	$(i, s, v) \to (i, s+1, v-1)$
E3	Infection of a susceptible individual	$(i, s, v) \to (i+1, s-1, v)$
E4	Infection of a vaccinated individual	$(i, s, v) \to (i+1, s, v-1)$
E5	Removal of an infectious individual	$(i, s, v) \to (i-1, s, v)$

TABLE 2 | Model parameters and their description.

Parameter	Description
$\beta(i, s) = sg(i)$	Transmission function among susceptible individuals
ξ	External infectious contact rate
ρ	Vaccination rate
θ	Waning rate of vaccine-induced immunity
h	Probability of vaccine failure
$\eta(i, v) = hvg(i)$	Transmission function among vaccinated individuals
γ	Removal rate

function analogous to viral transmission in the susceptible class. Specifically, the transmission function in the vaccinated group depends on the number of infected and vaccinated individuals and is defined as $\eta(i, v) = hvg(i)$, where h represents the probability of vaccine failure and the function $g(i)$ is the above mentioned for disease transmission in the susceptible compartment. Finally, clinical tests to confirm the disease are performed on each infectious individual independently, and an expected time of γ^{-1} units is required to have a conclusive result.

The events $\{E_1, \dots, E_5\}$ described previously, as well as the corresponding transitions between elements of χ, are summarized in Table 1. Furthermore, Table 2 shows a description of all the parameters that have been introduced for the model.

The infinitesimal generator, Q, of the Markov chain is a square $\binom{N+2}{3}$ matrix with nonnull entries:

$$q_{(i,s,v),(i^*,s^*,v^*)} = \begin{cases} \gamma i, & \text{if } \; i^* = i-1, s^* = s, v^* = v, \\ \rho s, & \text{if } \; i^* = i, s^* = s-1, v^* = v+1, \\ -q(i,s,v), & \text{if } \; i^* = i, s^* = s, v^* = v, \\ \theta v, & \text{if } \; i^* = i, s^* = s+1, v^* = v-1, \\ \beta(i,s), & \text{if } \; i^* = i+1, s^* = s-1, v^* = v, \\ \eta(i,v), & \text{if } \; i^* = i+1, s^* = s, v^* = v-1, \end{cases} \tag{2}$$

where $q(i,s,v) = \gamma i + \rho s + \theta v + \beta(i,s) + \eta(i,v)$ that corresponds to the sojourn rate at the state $(i,s,v) \in \mathcal{S}$.

The long-term behavior of the Markov chain depends on the action taken on the population once the presence of an infected individual is suspected. If the population is isolated, then $\xi = 0$ and subsequent infections can only occur through internal contacts. Otherwise, we set $\xi > 0$, and new infections can also occur through external contacts.

After isolation, the infectiousness of the virus between susceptible or vaccinated individuals is zero when $i = 0$. Thus, states in $\mathcal{S}$ with 0 infectious individuals belong to the absorbing set of states. Because the state space of the Markov chain contains a finite number of states, classical theoretical results guarantee that the Markov process will certainly be absorbed in one of the noncommunicating classes of absorbing states: $A_k = \{(0,s,k-s) \in \mathcal{S} : 0 \le s \le k\}$, for $0 \le k \le N-1$. Once the process enters into a communicating class A_k, it can move across these states, but it cannot leave the absorbing set.

When the population is not isolated (i.e., $\xi > 0$), the state space of the finite CTMC contains a single absorbing state given by $(0,0,0)$. Hence, the stationary distribution is concentrated in this single state. This means that occasionally the disease fades away (i.e., $I(t) = 0$) but is later reintroduced by an external contact.

3 | Detection of the Disease

In this section, we focus on the important issue of disease detection. As mentioned, we assume that the confirmation of the disease involves one or more diagnostic tests, in such a way that an exponential time of mean γ^{-1} units is required to diagnose the disease with certainty. Our challenge is twofold: First, to measure the time from the beginning of the epidemic until the disease is confirmed, and second, to measure disease incidence during this period.

Without loss of generality, we assume that at the beginning of the epidemic process, the population contains a single infected individual, s_0 susceptible individuals, and $v_0 = N - 1 - s_0$ individuals with active vaccine. That is, $(I(0), S(0), V(0)) = (1, s_0, v_0)$, with $s_0 + v_0 = N - 1$.

Let us introduce the random variables of interest. First, we introduce the time to confirmation of the disease, T_0, defined as the elapsed time between the onset of the epidemic and the definitive diagnosis of the disease. We note that this random variable is conditioned on the initial compartmental distribution of the population. Indeed,

$$T_0 = \min\{t \ge 0 : I(t) + S(t) + V(t) = N - 1 | (I(0), S(0), V(0)) = (1, s_0, N - 1 - s_0)\}.$$

Second, we focus on the incidence of the disease from the time the contact disease starts until it is fully confirmed. This is analyzed in terms of two random variables that count the total number of infections and the number of infections due to vaccine failure in the interval $[0, T_0]$.

In the following, for the sake of clarity of notation, we will avoid writing the initial state unless it will be necessary. Hence, in what follows, R_T will represent the variable that measures the total number of infections in the above period $[0, T_0]$, and R_T^v will record the number of infections due to vaccine failure that occur in the vaccinated pool prior to the confirmation of the disease. Both random variables are a particularization of the population transmission number that was introduced in [30] as a measure of disease spread and was studied by many other authors (see [27, 31–33]) for exponential and nonexponential distributional assumptions.

To study the random variables T_0, R_T, and R_T^v, we partition the state space $\mathcal{S}$ as $\mathcal{S} = A_N \cup \mathcal{S}_\mathcal{T} \cup \mathcal{S}_D$, where the set $A_N = \{(0, s, N-s) : 0 \le s \le N\}$ contains states representing the infection-free situations previous to the onset of the disease, $\mathcal{S}_\mathcal{T} = \{(i, s, v) \in \mathcal{S} : 1 \le i \le N, 0 \le s \le N-i, v = N-i-s\}$ contains states where the disease is detected but not yet confirmed, and the set $\mathcal{S}_D = \{(i, s, v) \in \mathcal{S} : 0 \le i+s+v \le N-1\}$ consists of the absorbing objective states.

Notice that $\mathcal{S}_D$ is a closed set accessible from the states of $\mathcal{S}_\mathcal{T}$, which is a set of transient states. Because we assume that $(I(0), S(0), V(0)) = (1, s_0, N-1-s_0)$, which is a state in $\mathcal{S}_\mathcal{T}$, the long-term behavior discussed at the end of Section 2 guarantees that the finite CTMC χ will be in a state in $\mathcal{S}_D$ of the form $(0, s, v)$, with $0 \le s+v \le N-1$, in an expected finite time. Therefore, $\lim_{t\to\infty} R(t) \ge 1$, meaning that the disease will be confirmed almost surely. Thus, the random variable T_0 has a proper distribution and $P\{T_0 < \infty\} = 1$.

Our aim is to investigate how the above variables behave, and for this purpose, we focus on their probabilistic distributions and moments.

3.1 | Time to the Confirmation of the Disease

We observe that T_0 is the conditional version of a random variable that can be seen as the first passage time of the CTMC χ into the set $\mathcal{S}_D$.

Well-known results for CTMCs [34, 35] provide that the distribution of the unconditional version of T_0 is given by a phase-type distribution depending on the submatrix of the infinitesimal generator Q corresponding to the set $\mathcal{S}_\mathcal{T}$ of transient states. Therefore, the computation of its distribution function and its moments requires dealing with powers and inverses of matrices with positive and negative entries, which makes the computations numerically unstable.

In this section, following a first step argument, we develop stable recursive schemes from which the computation of the moments of T_0 can be done at a low computational cost.

These recursive schemes involve a set of random variables describing the time to confirm the disease conditioned to the current state of the population. Obviously, for states $(i, s, v) \in \mathcal{S}_D$, the time until confirmation of the disease is 0. On the other hand, for states $(i, s, v) \in \mathcal{S}_\mathcal{T}$, we define

$$\tilde{T}_{(i,s,v)} = \min\{t \ge 0 : I(t) + S(t) + V(t) = N-1 | (I(0), S(0), V(0)) = (i, s, v)\}.$$

Because the states in $\mathcal{S}_\mathcal{T}$ are described as $(i, s, N-s-i)$, for $1 \le i \le N, 0 \le s \le N-i$, where the third component can be completely determined from the other two components, in what follows, the component representing the number of vaccinated individuals, v, will be removed from the notation when dealing with states in $\mathcal{S}_\mathcal{T}$.

Next, we split the set $\mathcal{S}_\mathcal{T}$ in levels according to the number of infectious individuals as $\mathcal{S}_\mathcal{T} = \cup_{i=1}^N S_i$, where each subset $S_i = \{(i, s, N-i-s) : 0 \le s \le N-i\}$ is finite and contains $N-i+1$ states, for $1 \le i \le N$.

To study the random variable T_0, we introduce some notation dealing with Laplace transforms and moments of the random variables $T_{(i,s)} \equiv \tilde{T}_{(i,s,N-i-s)}$, for $1 \le i \le N$ and $0 \le s \le N-i$ and notice that $T_0 = \tilde{T}_{(1,s_0,N-s_0-1)} = T_{(1,s_0)}$.

So, we define

$$\varphi_{(i,s)}(w) = E\left[e^{-wT_{(i,s)}}\right], \text{ for } \; Re(w) \ge 0,$$
$$M_{(i,s)}^k = E\left[T_{(i,s)}^k\right], \text{ for } \; k \ge 0,$$

and set the following notation to represent Laplace functions and kth-order moments in vector form, for each level $1 \le i \le N$:

$$\Phi_i(w) = \left(\varphi_{(i,0)}(w), \varphi_{(i,1)}(w), \dots, \varphi_{(i,N-i)}(w)\right)',$$
$$\mathbf{M}_i^k = \left(M_{(i,0)}^k, M_{(i,1)}^k, \dots, M_{(i,N-i)}^k\right)',$$

where the symbol $'$ stands for transpose.

In the following, $\mathbf{1}_a$ and $\mathbf{0}_a$ represent the all ones and all zeros vectors of dimension a, respectively; $\mathbf{e}_b(j)$ is a vector of dimension b with a single one at position j and zeros elsewhere; and empty products, appearing in theoretical derivations, are an identity matrix of the appropriate dimension.

The following theorem provides a result to derive the moments $\mathbf{M}_i^k$, for $1 \leq i \leq N$, in a recursive way from moments of one order less.

Theorem 1. *Given $k \geq 0$, the moments of order k of the random variables $T_{(i,s)}$, for $1 \leq i \leq N$ and $0 \leq s \leq N-i$, are obtained from the following equations:*

$$\mathbf{M}_i^0 = \mathbf{1}_{N-i+1}, \text{ for } \; 1 \leq i \leq N. \tag{3}$$

For $k \geq 1$,

$$\mathbf{M}_N^k = \frac{k!}{(\gamma N)^k}, \tag{4}$$

$$\mathbf{M}_i^k = -(\mathbf{C}_i)^{-1}\left(k\mathbf{M}_i^{k-1} + \mathbf{B}_i\mathbf{M}_{i+1}^k\right), \text{ for } \; 1 \leq i \leq N-1, \tag{5}$$

where $\mathbf{C}_i$ is an $(N-i+1)$ -dimensional square matrix and $\mathbf{B}_i$ is a matrix of dimension $(N-i+1) \times (N-i)$ of the form

$$\mathbf{C}_i = \begin{pmatrix} -q(i,0,N-i) & (N-i)\theta & 0 & \dots & 0 \\ \rho & -q(i,1,N-i-1) & (N-i-1)\theta & \dots & 0 \\ & \ddots & \ddots & \ddots & \vdots \\ & & (N-i-1)\rho & -q(i,N-i-1,1) & \theta \\ & & & (N-i)\rho & -q(i,N-i,0) \end{pmatrix},$$

and

$$\mathbf{B}_i = \begin{pmatrix} \eta(i,N-i) & 0 & \dots & 0 \\ \beta(i,1) & \eta(i,N-i-1) & \dots & 0 \\ \ddots & & \ddots & \\ & \beta(i,N-i+1) & & \eta(i,1) \\ 0 \quad \dots & 0 & & \beta(i,N-i) \end{pmatrix}.$$

Proof. Let us assume that the current state of the CTMC χ, which describes the compartmental situation of the population, is $(i,s,N-i-s) \in \mathcal{S}_T$. To lighten notation, the sojourn rate of the state will be written simply $q_{(i,s)}$, that is, $q_{(i,s)} \equiv q(1,s,N-i-s)$.

Using a first step argument, conditioning on the next outgoing effective event (i.e., disease confirmation, vaccination of a susceptible, loss of vaccine protection, new infection of a susceptible, and new infection due to vaccine failure) gives that Laplace transforms $\{\varphi_{(i,s)}(w), 1 \leq i \leq N, 0 \leq s \leq N-i\}$ satisfy the following equations:

$$\begin{aligned} \varphi_{(i,s)}(w) &= \frac{\gamma i}{w+q_{(i,s)}} + \frac{\rho s}{w+q_{(i,s)}}\varphi_{(i,s-1)}(w) + \frac{\theta(N-i-s)}{w+q_{(i,s)}}\varphi_{(i,s+1)}(w) \\ &\quad + \frac{\beta(i,s)}{w+q_{(i,s)}}\varphi_{(i+1,s-1)}(w) + \frac{\eta(i,N-i-s)}{w+q_{(i,s)}}\varphi_{(i+1,s)}(w), \text{ for } \; 1 \leq i \leq N-1, \\ \varphi_{(N,0)}(w) &= \frac{\gamma N}{w+q_{(N,0)}}, \end{aligned}$$

which are equivalent to

$$\begin{aligned} &-\rho s\varphi_{(i,s-1)}(w) + (w+q_{(i,s)})\varphi_{(i,s)}(w) - \theta(N-i-s)\varphi_{(i,s+1)}(w) \\ &\qquad = \gamma i + \beta(i,s)\varphi_{(i+1,s-1)}(w) + \eta(i,N-i-s)\varphi_{(i+1,s)}(w), \end{aligned} \tag{6}$$

for $1 \le i \le N-1$, and

$$(w + q_{(N,0)})\varphi_{(N,0)}(w) = \gamma N. \tag{7}$$

Equations (6) and (7) are the basis to get the moments of the distribution of $T_{(i,s)}$ and, more specifically, the moments of the random variable of interest, T_0.

First, we notice that the same arguments used in proving that the random variable T_0 has a proper distribution can be also applied to show that any random variable $T_{(i,s)}$, for states in $\mathcal{S}_T$, has a proper distribution and satisfies $P\{T_{(i,s)} < \infty\} = 1$. Consequently, we get that $M^0_{(i,s)} = \varphi_{(i,s)}(0) = 1$, which gives the result appearing in Equation (3) in the statement of the theorem.

To derive expressions involving the kth-order moment of $T_{(i,s)}$, we take derivatives, k-times, on Equations (6) and (7) with regard to w, and after evaluation at $w = 0$, we get

$$-\rho s M^k_{(i,s-1)} + q_{(i,s)} M^k_{(i,s)} - k M^{k-1}_{(i,s)} - \theta(N-i-s) M^k_{(i,s+1)} \tag{8}$$

$$\begin{aligned} &= \beta(i,s) M^k_{(i+1,s-1)} + \eta(i, N-i-s) M^k_{(i+1,s)}, \text{ for } \; 1 \le i \le N-1, \\ &q_{(N,0)} M^k_{(N,0)} - k M^{k-1}_{(N,0)} = 0. \end{aligned} \tag{9}$$

With the help of the matrices $\mathbf{C}_i$ and $\mathbf{B}_i$, for $1 \le i \le N$, appearing in the statement of the Theorem 1, we can express Equations (8) and (9) in matrix form as follows:

$$-k\mathbf{M}^{k-1}_i - \mathbf{C}_i \mathbf{M}^k_i = \mathbf{B}_i \mathbf{M}^k_{i+1}, \text{ for } \; 1 \le i \le N-1, \tag{10}$$

$$-k\mathbf{M}^{k-1}_N - \gamma N \mathbf{M}^k_N = 0. \tag{11}$$

The iteration of Equation (11) and the explicit result appearing in (3) for $i = N$ gives the result shown in Equation (4).

Finally, by making use of Equation (10), we can obtain the general matrix expression for moments of $T_{(i,s)}$ given in Equation (5). □

Given integers k and s_0, the moments of T_0 are recursively determined according to the algorithmic scheme appearing in Algorithm 1.

```
Algorithm 1 $T_0$ moments
For $k \ge 1$ and $0 \le s_0 \le N-1$, moments $\mathbf{M}^k_i$, for $1 \le i \le N$ are computed as follows
Step 1. Set $j = 0$
    Step 1a. For $1 \le i \le N-1$, set $\mathbf{M}^0_i = \mathbf{1}_{N-i+1}$.
Step 2. Set $j = 1$
    Step 2a. Set $i = N$, and $\mathbf{M}^j_N = (\gamma N)^{-1}$.
    Step 2b. Set $i = i - 1$. If $i = 0$, go to Step 3.
    Step 2c. Compute $\mathbf{M}^j_i = -(\mathbf{C}_i)^{-1}\left(j\mathbf{M}^{j-1}_i + \mathbf{B}_i\mathbf{M}^j_{i+1}\right)$, go to 2b.
Step 3. Set $j = j + 1$. If $j \le k$, go to Step 2a.
Step 4. Compute $E[T^k_0] = \mathbf{e}'_N(s_0 + 1)\mathbf{M}^k_1$.
```

3.2 | Disease Incidence Prior Detection

In this section, we analyze the incidence of the infection before the disease is confirmed. We introduce the random variable R_T defined as the number of cases of infection during the interval $[0, T_0]$ that can be seen as a measure of contact tracing forward from the index case to its offspring. This random variable counts the number of infections arising from the first infectious individual and its offspring until the disease is definitively diagnosed. Therefore, as in the precedent section, we assume that the initial state of the CTMC χ is $(I(0), S(0), V(0)) = (1, s_0, N-1-s_0)$, where $0 \le s_0 \le N-1$.

We have that, because the population is finite, the support of the R_T is also finite and is given by the set of integers $\{0, \dots, N-1\}$. So, we state that $P\{R_T < \infty\} = 1$.

To study, in detail, the probabilistic behavior of this random variable, we introduce the set of auxiliary variables $\{z_{(i,s)} : (i, s, N-i-s) \in \mathcal{S}_T\}$, which record the number of new cases of infection before the disease confirmation, given that the current state of the population is represented by $(i, s, N-i-s)$. In particular, using this notation, the random variable can be written as $R_T = z_{(1,s_0)}$.

Some notation for mass probability and generating functions and factorial moments of the auxiliary variables is required, and it is given by:

$$z^j_{(i,s)} = P\{z_{(i,s)} = j\}, \text{ for } \ 0 \le j \le N-1,$$

$$\phi_{(i,s)}(w) = E[w^{z_{(i,s)}}] = \sum_{j=0}^{N-i} w^j z^j_{(i,s)}, \text{ for } \ |w| \le 1,$$

$$m^k_{(i,s)} = E[(z_{(i,s)})_k] = \begin{cases} P\{z_{(i,s)} < \infty\}, & \text{for } \ k = 0, \\ E\left[\prod_{n=0}^{k-1}(z_{(i,s)} - n)\right], & \text{for } \ k \ge 1. \end{cases}$$

The following theorem provides the mass distribution function of R_T.

Theorem 2. *Given s_0, such that $0 \le s_0 \le N-1$, $R_T \in \{0, \dots, N-1\}$.*

For any integer j, $0 \le j \le N-1$, we have

$$P\{R_T = j\} = \gamma(j+1)\mathbf{e}'_N(s_0+1)\left(\prod_{n=1}^{j}(-\mathbf{C}_n)^{-1}\mathbf{B}_n\right)(-\mathbf{C}_{j+1})^{-1}\mathbf{1}_{N-j}, \tag{12}$$

where the matrices $\mathbf{C_n}$ and $\mathbf{B}_n$, for $1 \le n \le N-1$, are the ones appearing in Theorem 1, and $\mathbf{C}_N = -\gamma N$.

Proof. First, we notice that when the current situation is $(N, 0, 0)$, all the individuals in the population are unconfirmed infectious cases; then, the unique possible transition for the CTMC is the disease confirmation. Therefore, for any integer $j \ge 0$, we have

$$z^j_{(N,0)} = \delta_{0,j}, \tag{13}$$

where $\delta_{i,j}$ represents Kronecker's delta function defined as 1 when $i = j$ and as 0 otherwise.

For any level i, $1 \le i \le N-1$, the following result is trivially true because the population is finite:

$$z^j_{(i,s)} = 0, \text{ for } \ j > N-i. \tag{14}$$

For the rest of cases, a first step argument conditioning on the first transition out of the initial state gives the following relationship:

$$\begin{aligned} z^j_{(i,s)} &= \delta_{0,j}\frac{\gamma i}{q_{(i,s)}} + \frac{\rho s}{q_{(i,s)}} z^j_{(i,s-1)} + \frac{\theta(N-i-s)}{q_{(i,s)}} z^j_{(i,s+1)} \\ &\quad + (1-\delta_{0,j})\left(\frac{\beta(i,s)}{q_{(i,s)}} z^{j-1}_{(i+1,s-1)} + \frac{\eta(i, N-i-s)}{q_{(i,s)}} z^{j-1}_{(i+1,s)}\right). \end{aligned} \tag{15}$$

Multiplying both sides of Equation (15) by $q_{(i,s)}$ and rearranging terms, we get an equivalent expression

$$\begin{aligned} &-\rho s z^j_{(i,s-1)} + q_{(i,s)} z^j_{(i,s)} - \theta(N-i-s) z^j_{(i,s+1)} \\ &\qquad = \delta_{0,j}\gamma i + (1-\delta_{0,j})\left(\beta(i,s) z^{j-1}_{(i+1,s-1)} + \eta(i, N-i-s) z^{j-1}_{(i+1,s)}\right). \end{aligned} \tag{16}$$

Next, we introduce an $(N-i+1)$-dimensional vector collecting the probabilities of having j new cases of infection given that at present, we record i infectious but unconfirmed cases.

$$\mathbf{z}^j_i = (z^j_{(i,0)}, \dots, z^j_{(i,N-i)})'.$$

With the help of vectors $\mathbf{z}_i^j$ and matrices $\mathbf{C}_i, \mathbf{B}_i$, for $1 \leq i \leq N-1$, we can write Equation (16) in matrix form as follows:

$$-\mathbf{C}_i \mathbf{z}_i^j = \delta_{0,j} \gamma i \mathbf{1}_{N-i+1} + (1-\delta_{0,j}) \mathbf{B}_i \mathbf{z}_{i+1}^{j-1}, \tag{17}$$

for $1 \leq i \leq N-1$ and $0 \leq j \leq N-i$.

Now, defining $\mathbf{C}_N = -\gamma N$, from Equation (13) and the explicit solution of Equation (17) for $j = 0$ and $0 \leq i \leq N-1$, we can state that

$$\mathbf{z}_i^0 = \gamma i (-\mathbf{C}_i)^{-1} \mathbf{1}_{N-i+1}, \text{ for } \ 1 \leq i \leq N.$$

For $1 \leq j \leq N-i$, iterating the result in Equation (17), we got that

$$\mathbf{z}_i^j = \gamma (i+j) \left(\prod_{n=1}^{i+j-1} (-\mathbf{C}_n)^{-1} \mathbf{B}_n \right) (-\mathbf{C}_{i+j})^{-1} \mathbf{1}_{N-(i+j)+1}.$$

Finally, because $R_T = z_{(1,s_0)}$, the mass function of the number of cases of infection taking place before disease confirmation is determined from $\mathbf{z}_1^j$, for $0 \leq j \leq N-1$, as $P\{R_T = j\} = \mathbf{e}'_N(s_0+1)\mathbf{z}_1^j$. □

The finiteness of the support of R_T may encourage the direct use of Equation (12) to derive the moments of R_T as $E[R_T^k] = \sum_{j=0}^{N-1} j^k P\{R_T = j\}$. However, using mathematical expressions involving powers and products of matrices depending on the size of the population can cause computational difficulties as the size of the population increases. Therefore, in the following lemma, we present a direct derivation of the factorial moments of the auxiliary variables, $z_{(i,s)}$, which provides an efficient recursive algorithm for deriving the moments of the random variable R_T.

For any integers $k \geq 0$ and $1 \leq i \leq N-1$, we introduce the $(N-i+1)$-dimensional vector whose components represent the factorial moment of order k of the number of new infections observed until the disease is confirmed, given that we currently have i unconfirmed infectious cases:

$$\mathbf{m}_i^k = (m_{(i,0)}^k, \ldots, m_{(i,N-i)}^k)'.$$

Lemma 1. *Given $k \geq 0$ and $1 \leq i \leq N$, the factorial moment of the auxiliary variables are determined from the following results:*

$$\mathbf{m}_i^0 = \mathbf{1}_{N-i+1}, \text{ for } \ 1 \leq i \leq N, \tag{18}$$

$$\mathbf{m}_i^k = \mathbf{0}_{N-i+1}, \text{ for } \ 1 \leq i \leq N \text{ and } \ k > N-i. \tag{19}$$

$$\mathbf{m}_i^k = -(\mathbf{C}_i)^{-1} \mathbf{B}_i \left(k \mathbf{m}_{i+1}^{k-1} + \mathbf{m}_{i+1}^k \right), \text{ for } \ 1 \leq i \leq N \text{ and } \ 1 \leq k \leq N-i, \tag{20}$$

where $\mathbf{C}_i$ and $\mathbf{B}_i$ are the matrices defined on Theorem 1.

Proof. First, we call the result shown in Equation (14) and state that the support of any auxiliary variable $z_{(i,s)}$ is given by the set $\{0, \ldots, N-i\}$, for $1 \leq i \leq N$ and $0 \leq s \leq N-i$. Therefore, $P\{z_{(i,s)} < \infty\} = 1$ and $E\left[\prod_{n=0}^{k-1} (z_{(i,s)} - n)\right] = 0$, for $k > N-i$, and results in Equations (18) and (19) are fulfilled.

To prove the result in Equation (20), we will deal with the generating functions $\phi_{(i,s)}(w)$, introduced before the statement of Theorem 2.

By multiplying Equation (16) by w^j and adding in j from 0 to $N-i$, after rearranging terms, we get the following relationship involving generating functions

$$\begin{aligned} &-\rho s \phi_{(i,s-1)}(w) + q_{(i,s)} \phi_{(i,s)}(w) - \theta(N-i-s) \phi_{(i,s+1)}(w) \\ &\quad = \gamma i + \beta(i,s) w \phi_{(i+1,s-1)}(w) + \eta(i, N-i-s) w \phi_{(i+1,s)}(w). \end{aligned} \tag{21}$$

We notice that $m_{(i,s)}^k = \frac{d^k}{dw^k}(\phi_{(i,s)}(w))|_{w=1}$. Hence, differentiating (21) k-times regarding w and evaluating at $w = 1$, we obtain

$$\begin{aligned} & -\rho s m_{(i,s-1)}^k + q_{(i,s)} m_{(i,s)}^k - \theta(N-i-s) m_{(i,s+1)}^k \\ & \qquad = \beta(i,s)(m_{(i+1,s-1)}^k + k m_{(i+1,s-1)}^{k-1}) + \eta(i, N-i-s)(k m_{(i+1,s)}^{k-1} + m_{(i+1,s)}^k), \end{aligned} \tag{22}$$

that, appealing to vectors $\mathbf{m}_i^k$ and to matrices $\mathbf{C}_i$ and $\mathbf{B}_i$ in Theorem 1, can be written in matrix form as

$$-\mathbf{C}_i \mathbf{m}_i^k = \mathbf{B}_i (k \mathbf{m}_{i+1}^{k-1} + \mathbf{m}_{i+1}^k), \tag{23}$$

for $k \geq 1$ and $1 \leq i \leq N-1$. □

By noticing that $R_T = z_{(1,s_0)}$, we can state the following result for the factorial moments of the number of infectious cases arising from the first infectious individual until the disease is fully confirmed.

Theorem 3. *Given s_0, $0 \leq s_0 \leq N-1$, for any integer $k \geq 0$, the factorial moment of order k of the random variable R_T is determined as follows:*

$$E\left[(R_T)_k\right] = \mathbf{e}'_N(s_0+1)\mathbf{m}_1^k. \tag{24}$$

Algorithm 2 R_T factorial moments

```
For $k \geq 1$ and $0 \leq s_0 \leq N-1$, the factorial moment of order $k$, $E\left[(R_T)_k\right]$, is computed as follows
Step 1. Set $j = 0$,
    Step 1a. For $1 \leq i \leq N-1$, set $\mathbf{m}_i^0 = \mathbf{1}_{N-i+1}$.
Step 2. Set $j = j+1$.
    Step 2a. Set $i = N$, and $\mathbf{m}_N^j = 0$.
    Step 2b. Set $i = i-1$. If $i = 0$, go to Step 2.
    Step 2c. If $i > N-j$, set $\mathbf{m}_i^j = \mathbf{0}_{N-i+1}$ and go to Step 2a.
    Step 2d. Compute $\mathbf{m}_i^j = -(\mathbf{C}_i)^{-1}\mathbf{B}_i\left(j\mathbf{m}_i^{j-1} + \mathbf{m}_{i+1}^j\right)$.
    Step 2e. If $j < k$, go to Step 2a.
Step 3. Compute $E\left[(R_T)_k\right] = \mathbf{e}'_N(s_0+1)\mathbf{m}_1^k$.
```

3.3 | Disease Incidence in the Vaccinated Pool Prior Detection

In this section, we derive results on the mass function and moments of the random variable R_T^v, which counts the number of cases of infection due to vaccine failure before the disease is confirmed. The random variable is tied to the random interval $(0, T_0]$, and without loss of generality, we assume that at the onset of the epidemic process, there is a single infectious individual in the population. Hence, the initial state of the Markov chain is again $(I(0), S(0), V(0)) = (1, s_0, N-1-s_0)$, for $0 \leq s_0 \leq N-1$.

As we stated for R_T, the support of the random variable R_T^v is finite and consequently $P\{R_T^v < \infty\} = 1$.

To derive the distribution of R_T^v and its moments, we will follow a parallel scheme to the one used in Section 3.2. Therefore, we introduce a new set of conditional random variables $\{y_{(i,s)} : (i, s, N-i-s) \in \mathcal{S}_\mathcal{T}\}$, which, for each state $(i, s, N-i-s) \in \mathcal{S}_\mathcal{T}$, count the number of cases of infection due to vaccine failure, observed before the confirmation of the disease, conditioned on the current state $(i, s, N-i-s)$. Because the population is finite, the support of the conditional random variables, given i infectious cases, is also finite and is given by the set $\{0, 1, \ldots, N-i\}$.

Moreover, we note that $R_T^v = y_{(1,s_0)}$, and in what follows, we present results regarding the conditional random variables from which we derive those for the mass distribution and moments of the disease incidence in the vaccinated pool. Let us begin by introducing some notation for probabilities, generating function and factorial moments of the conditional variables.

$$y^j_{(i,s)} = P\{y_{(i,s)} = j\}, \text{ for } \ 0 \le j \le N-i,$$

$$\psi_{(i,s)}(w) = E[w^{y_{(i,s)}}] = \sum_{j=0}^{N-i} w^j y^j_{(i,s)}, \text{ for } \ |w| \le 1,$$

$$\hat{m}^k_{(i,s)} = E[(y_{(i,s)})_k] = \begin{cases} P\{y_{(i,s)} < \infty\}, & \text{for } \ k=0, \\ E\left[\prod_{n=0}^{k-1}(y_{(i,s)} - n)\right], & \text{for } \ k \ge 1. \end{cases}$$

Furthermore, given i, for $1 \le i \le N$, for any integers j and k, we define the $(N-i+1)$-dimensional column vectors

$$\mathbf{y}^j_i = (y^j_{(i,0)}, \dots, y^j_{(i,N-i)})', \text{ for } \ 0 \le j \le N-i,$$
$$\hat{\mathbf{m}}^k_i = (\hat{y}^k_{(i,0)}, \dots, \hat{m}^k_{(i,N-i)})', \text{ for } \ k \ge 0,$$

containing probabilities and factorial moments of the conditional variables, and the $(N-i+1) \times (N-i)$ matrices $\hat{\mathbf{B}}_i$ and $\tilde{\mathbf{B}}_i$ resulting from the matrix $\mathbf{B}_i$ (in Theorem 1), by splitting new infections according to their previous health status, that is, susceptible or vaccine-protected individuals. In more detail, for $1 \le i \le N-1$, we set

$$\hat{\mathbf{B}}_i = \begin{pmatrix} 0 & & 0 & \dots & 0 \\ \beta(i,1) & & 0 & \dots & 0 \\ & \ddots & & \ddots & \\ & & \beta(i,N-i+1) & & 0 \\ 0 & \dots & 0 & & \beta(i,N-i) \end{pmatrix},$$

and

$$\tilde{\mathbf{B}}_i = \begin{pmatrix} \eta(i,N-i) & & 0 & \dots & 0 \\ 0 & & \eta(i,N-i-1) & \dots & 0 \\ & \ddots & & \ddots & \\ & & 0 & & \eta(i,1) \\ 0 & \dots & 0 & & 0 \end{pmatrix}.$$

The following lemma shows the iterative equations that yield conditional probabilities.

Lemma 2. *Given i, $1 \le i \le N$ and an integer j, $0 \le j \le N-i$, the conditional probabilities are determined from the following equations:*

$$\mathbf{y}^j_N = \delta_{0,j}, \tag{25}$$

$$\mathbf{y}^0_i = -(\mathbf{C}_i)^{-1}\left(i\gamma \mathbf{1}_{N-i+1} + \hat{\mathbf{B}}_i \mathbf{y}^0_{i+1}\right), \text{ for } \ 1 \le i \le N-1, \tag{26}$$

$$\mathbf{y}^j_i = -(\mathbf{C}_i)^{-1}\left(\tilde{\mathbf{B}}_i \mathbf{y}^{j-1}_{i+1} + \hat{\mathbf{B}}_i \mathbf{y}^j_{i+1}\right), \text{ for } \ 1 \le i \le N-1. \tag{27}$$

Proof. If the population is completely infected, no additional infectious cases can occur. Then, the result in Equation (25) is trivially true.

The proof of Equations (26) and (27) follows by a first step argument. By conditioning on the first transition out of the state $(i, s, N-i-s) \in \mathcal{S}_{\mathcal{T}}$, we get the recursive equation

$$\begin{aligned} y^j_{(i,s)} = {} & \delta_{0,j}\frac{\gamma i}{q_{(i,s)}} + \frac{\rho s}{q_{(i,s)}} y^j_{(i,s-1)} + \frac{\theta(N-i-s)}{q_{(i,s)}} y^j_{(i,s+1)} \\ & + \frac{\beta(i,s)}{q_{(i,s)}} y^j_{(i+1,s-1)} + (1-\delta_{0,j})\left(\frac{\eta(i,N-i-s)}{q_{(i,s)}} y^{j-1}_{(i+1,s)}\right), \end{aligned} \tag{28}$$

which is equivalent to

$$\begin{aligned}\rho s y^{j}_{(i,s-1)} - q_{(i,s)} y^{j}_{(i,s)} + \theta(N-i-s) y^{j}_{(i,s+1)} + \beta(i,s) y^{j}_{(i+1,s-1)} \\ = -\delta_{0,j}\gamma i - (1-\delta_{0,j})\eta(i,N-i-s) y^{j-1}_{(i+1,s)},\end{aligned} \tag{29}$$

for $1 \le i \le N,\ 0 \le s \le N-i$, and $0 \le j \le N-i$. Finally, expressing (29) in matrix form, we obtain

$$\begin{aligned}\mathbf{C}_i \mathbf{y}^0_i + \hat{\mathbf{B}}_i \mathbf{y}^0_{i+1} &= -i\gamma \mathbf{1}_{N-i+1}, \text{ for } \ 1 \le i \le N-1, \\ \mathbf{C}_i \mathbf{y}^j_i + \hat{\mathbf{B}}_i \mathbf{y}^j_{i+1} &= -\tilde{\mathbf{B}}_i \mathbf{y}^{j-1}_{i+1}, \text{ for } \ 1 \le i \le N-1 \text{ and } \ 1 \le j \le N-i.\end{aligned}$$

□

The mass function of the number of vaccine-protected individuals that become infected prior disease confirmation follows by noticing that $R^v_T = y_{(1,s_0)}$.

Theorem 4. *Given s_0, such that $0 \le s_0 \le N-1$, the support of the random variable R^v_T is $\{0, \dots, N-1\}$, and its probability distribution is*

$$P\left\{R^v_T = j\right\} = \mathbf{e}'_N(s_0+1)\mathbf{y}^j_1, \text{ for } \ 0 \le j \le N-1. \tag{30}$$

Algorithm 3 R^v_T mass function

```
For $0 \le s_0 \le N-1$, the mass function of $R^v_T$ is computed by the following pseudo code:
Step 1. Set $j = 0$.
    Step 1a. Set $i = N$ and $\mathbf{y}^0_N = 1$.
    Step 1b. Set $i = i - 1$. If $i = 0$, go to Step 2.
    Step 1c. Compute $\mathbf{y}^0_i = -(\mathbf{C}_i)^{-1}\left(i\gamma\mathbf{1}_{N-i+1} + \widehat{\mathbf{B}}_i\mathbf{y}^0_{i+1}\right)$ and go to Step 1b.
Step 2. Set $j = j + 1$. If $j = N$, Stop.
    Step 2a. Set $i = N - j + 1$ and $\mathbf{y}^j_i = \mathbf{0}_{N-i+1}$.
    Step 2b. Set $i = i - 1$. If $i = 0$, go to Step 3.
    Step 2c. Compute $\mathbf{y}^j_i = -(\mathbf{C}_i)^{-1}\left(\widetilde{\mathbf{B}}_i\mathbf{y}^{j-1}_{i+1} + \widehat{\mathbf{B}}_i\mathbf{y}^j_{i+1}\right)$ and go to Step 2b.
Step 3. Compute $P\{R^v_T = j\} = \mathbf{e}'_N(s_0+1)\mathbf{y}^j_1$ and go to Step 2.
```

Finally, we present the recursive results that drive to the factorial moments of the random variable R^v_T.

Lemma 3. *Given $k \ge 0$ and $1 \le i \le N$, the factorial moment of the conditioned variables are determined from the following results:*

$$\hat{\mathbf{m}}^0_i = \mathbf{1}_{N-i+1}, \text{ for } \ 1 \le i \le N, \tag{31}$$

$$\hat{\mathbf{m}}^k_i = \mathbf{0}_{N-i+1}, \text{ for } \ 1 \le i \le N \text{ and } \ k \ge N-i+1, \tag{32}$$

$$\hat{\mathbf{m}}^k_i = -(\mathbf{C}_i)^{-1}\left(k\tilde{\mathbf{B}}_i\hat{\mathbf{m}}^{k-1}_{i+1} + \mathbf{B}_i\tilde{\mathbf{m}}^k_{i+1}\right), \text{ for } \ 1 \le i \le N-1 \text{ and } \ 1 \le k \le N-i. \tag{33}$$

Proof. The result in Equation (31) follows by observing that $\hat{m}^0_{(i,s)} = P\{y_{(i,s)} < \infty\} = 1$, for (i,s) such that $(i, s, N-i-s) \in \mathcal{S}_{\mathcal{T}}$. Moreover, because the support of the conditional random variable $y_{(i,s)}$ is the set of integers $\{0, 1, \cdots, N-i\}$, then $\hat{m}^k_{(i,s)} = E[(y_{(i,s)})_k] = 0$, which is the result appearing in Equation (32).

To prove the result in (33), we start with Equation (28). First, we multiply all terms by w^j and by adding in j, for $0 \le j \le N-i$, we get the generating functions relation:

$$\begin{aligned}\psi_{(i,s)}(w) = \frac{\gamma i}{q_{(i,s)}} + \frac{\rho s}{q_{(i,s)}}\psi_{(i,s-1)}(w) + \frac{\theta(N-i-s)}{q_{(i,s)}}\psi_{(i,s+1)}(w) \\ + \frac{\beta(i,s)}{q_{(i,s)}}\psi_{(i+1,s-1)}(w) + \frac{\eta(i,N-i-s)}{q_{(i,s)}} w\psi_{(i+1,s)}(w).\end{aligned} \tag{34}$$

For $k \geq 1$, we recall the relationship linking factorial moments and generating functions of any random variable X: $E[(X)_k] = \frac{d^k}{dw^k}\phi_X(w)|_{w=1}$.

Multiplying both sides of Equation (34) by $q_{(i,s)}$, taking k derivatives with respect to w and evaluating at $w = 1$, we get

$$\begin{aligned} &\rho s \hat{m}^k_{(i,s-1)} - q_{(i,s)}\hat{m}^k_{(i,s)} + \theta(N-i-s)\tilde{m}^k_{(i,s+1)} \\ &\quad = -\beta(i,s)\tilde{m}^k_{(i+1,s-1)} - \eta(i, N-i-s)\left(k\tilde{m}^{k-1}_{(i+1,s)} + \tilde{m}^k_{(i+1,s)}\right), \end{aligned} \tag{35}$$

for $k \geq 1,\ 1 \leq i \leq N-1$, and $0 \leq s \leq N-i$.

Finally, we observe that Equation (33) comes from the matrix form expression of Equation (35). □

The result for deriving factorial moments of R^v_T is presented in the following theorem.

Theorem 5. *Given $s_0,\ 0 \leq s_0 \leq N-1$, for any integer $k \geq 0$, the factorial moment of order k of the random variable R^v_T is determined as follows:*

$$E\left[(R^v_T)_k\right] = \mathbf{e}'_N(s_0+1)\hat{\mathbf{m}}^k_1. \tag{36}$$

Given an integer $k \geq 0$, a recursive scheme, implementing Lemma 3 and Theorem 5, allows the computation of the factorial moment of order k for R^v_T. The corresponding algorithm presents the same structure of Algorithm 2 just by substituting R_T for R^v_T, $\hat{\mathbf{m}}^j_i$ for $\mathbf{m}^j_i$, and the expression in Step 2d for $\hat{\mathbf{m}}^j_i = -(\mathbf{C}_i)^{-1}\left(k\tilde{\mathbf{B}}_i\hat{\mathbf{m}}^{j-1}_{i+1} + \mathbf{B}_i\tilde{\mathbf{m}}^j_{i+1}\right)$.

4 | Numerical Results: an Application to FMD Virus

To illustrate the usefulness of our descriptors, we shall apply theoretical results to outbreaks of FMD in cattle. FMD is a highly contagious viral disease of cloven-hoofed (bipedal) animals. It causes painful sores and blisters on the animal's feet, mouth, and teats. The virus is transmitted by direct contact with infected animals and by indirect contact with a contaminated environment. FMD is rarely fatal, but infected animals display high fever, depression, loss of weight, and drop in milk production. Lastly, some animals who catch this illness may display permanent symptoms caused by FMD even after recovery, producing less good quality milk and meat. In general, a suspected case of FMD can be identified on the basis of clinical signs, but diagnosis on this basis is highly unreliable because many other diseases have similar symptoms. Therefore, confirmatory laboratory diagnosis of any suspicion of FMD is essential. Diagnostic procedures and laboratory test for determining evidence of infection can be found in [36, 37].

One preventive measure is the use of vaccines. In endemic areas, a prophylactic vaccine can protect animals from clinical signs, and in virus-free countries, vaccination is an emergency measure to reduce virus transmission during an outbreak. The vaccines routinely used are prophylactic and generally provide immunity for only 4–6 months. Therefore, animals protected by such vaccines are usually given one to three doses per year. On the other hand, a study conducted in a Cambodian province [38] revealed that more than half of cattle vaccinated with FMD vaccines became infected with the virus and showed clinical signs of the disease, indicating possible vaccine failure. Consequently, it may occur that the administered vaccine loses effectiveness over time and does not fully protect the animal.

In this section, we present numerical results to illustrate the influence of the incidence function, $\beta(i,s)$; the probability of vaccine failure, h; the detection rate, γ; and the basic reproductive number, R_0, for FMD transmission.

Numerical scenarios will share the population size, $N = 100$, the external contact rate $\xi = 2.1428 \times 10^{-5}$, the mean time between booster doses, $\rho^{-1} = 167$ days, and the expected duration of the vaccine protection, $\theta^{-1} = 90$ days.

We consider three different incidence functions, all of them depending on the bilinear transmission function: $\beta(i,s) = s(\frac{\beta i}{N} + \xi)$, where β is the infection rate parameter. The first one is $\beta_1(i,s) = \beta(i,s)/(1+i^2)$, a rescaled version of the incidence function appearing in [39, 40], where $1/(1+i^2)$ measures the inhibitory effect resulting from the change in behavior of the noninfectious individuals as the incidence of infection increases; the second is the bilinear transmission function $\beta_2(i,s) = \beta(i,s)$, which gives equal contribution of susceptible and infectious individuals in the transmission; and the reaction–diffusion force of infection $\beta_3(i,s) = \beta(i,s)(1+i)$ appearing in [41, 42] that was considered in [43] to represent

TABLE 3 | Expected value and standard deviation of T_0.

		$h = 0.11$				$h = 0.5$			
		$v_0 = 0.1\ N$		$v_0 = 0.8\ N$		$v_0 = 0.1\ N$		$v_0 = 0.8\ N$	
	$1/\gamma$	$E[T_0]$	$SD[T_0]$	$E[T_0]$	$SD[T_0]$	$E[T_0]$	$SD[T_0]$	$E[T_0]$	$SD[T_0]$
$\beta_1(i, s)$	8	5.4777	4.6224	6.6926	6.0560	5.4116	4.5378	5.9626	5.1679
	15	8.7100	6.9437	11.1535	9.4786	8.5772	6.7874	9.6250	7.8394
$\beta_2(i, s)$	8	3.9774	2.9435	5.7394	4.8177	3.8948	2.8532	4.6477	3.6182
	15	5.5344	3.6786	8.7731	6.6642	5.3903	3.5385	6.6854	4.6791
$\beta_3(i, s)$	8	2.2821	1.5058	4.3347	3.2810	2.2077	1.4440	2.9743	2.0623
	15	2.6855	1.6225	5.8050	3.9078	2.5843	1.5483	3.6372	2.2844

TABLE 4 | Expected value and standard deviation of R_T.

		$h = 0.11$				$h = 0.5$			
		$v_0 = 0.1\ N$		$v_0 = 0.8\ N$		$v_0 = 0.1\ N$		$v_0 = 0.8\ N$	
	$1/\gamma$	$E[R_T]$	$SD[R_T]$	$E[R_T]$	$SD[R_T]$	$E[R_T]$	$SD[R_T]$	$E[R_T]$	$SD[R_T]$
$\beta_1(i, s)$	8	0.7905	0.8473	0.3633	0.5899	0.8186	0.8630	0.6064	0.7503
	15	1.1767	1.0281	0.6178	0.7690	1.2168	1.0483	0.9449	0.9334
$\beta_2(i, s)$	8	2.4796	2.8424	0.8849	1.2982	2.6074	2.9748	1.7113	2.1256
	15	4.5110	4.7093	1.7165	2.1731	4.7588	4.9621	3.1870	3.5584
$\beta_3(i, s)$	8	23.2839	30.0501	3.9121	7.3687	25.5810	32.5541	14.0442	22.9858
	15	42.1729	37.9437	10.3286	15.8616	45.5587	40.1937	30.8636	35.2960

an imitative process for susceptible to become infectious. For any fixed number of susceptible individuals, the selected transmission functions present the same initial infection force, $\frac{\beta i}{N} + \xi$, and satisfy $\beta_1(i, s) \leq \beta_2(i, s) \leq \beta_3(i, s)$.

In a first set of experiments, we show the expected values and standard deviation of T_0 and R_T, for the transmission functions described above when fixing the infection rate $\beta = 0.3583$, as the parameters h, the initial coverage of the vaccine, v_0, and the expected time to confirm the disease $1/\gamma$ are varied as follows: $h \in \{0.11, 0.5\}$, $v_0 \in \{0.1\ N, 0.8\ N\}$, and $1/\gamma \in \{8, 15\}$ days.

The results in Table 3 correspond to expected value and standard deviation of T_0. We can observe that, once we fix the vaccine characteristics, the initial coverage and the expected time to get clinical results then, regarding the transmission function, the expected value and standard deviation of the time to confirm the disease satisfy the following relationship: $E[T_0|\beta_1] \geq E[T_0|\beta_2] \geq E[T_0|\beta_3]$ and $SD[T_0|\beta_1] \geq SD[T_0|\beta_2] \geq SD[T_0|\beta_3]$. For each choice on the transmission function, initial coverage level and vaccine failure probability, both the expected value and standard deviation of the time to confirm the disease increase with respect to the mean time to get clinical results $(1/\gamma)$. The same effect is observed when we increase the initial coverage, v_0, keeping the other parameters fixed. In general, less efficient vaccines (i.e., $h = 0.5$) imply shorter values for the mean and standard deviation of the time to confirm the disease. We note that for low vaccination coverage (i.e., $v_0 = 0.1\ N$), the influence of the probability of vaccine failure on $E[T_0]$ and $SD[T_0]$ is small.

Table 4 displays the expected value and standard deviation of R_T, the total incidence (i.e., the number of cases of infection until the disease is confirmed). Regarding the transmission function, when other parameters are fixed, we observe that $E[R_T|\beta_1] \leq E[R_T|\beta_2] \leq E[R_T|\beta_3]$ and $SD[R_T|\beta_1] \leq SD[R_T|\beta_2] \leq SD[R_T|\beta_3]$. For any single parameter, while the others are fixed, $E[R_T]$ and $SD[R_T]$ behave according to intuition. That is, both measures increase as the expected time to get clinical results increases or as the vaccine failure probability increases but decrease as the initial vaccine coverage increases. As mentioned for the T_0 measures, we observe small influence of h on $E[R_T]$ and $SD[R_T]$ for low vaccination coverage.

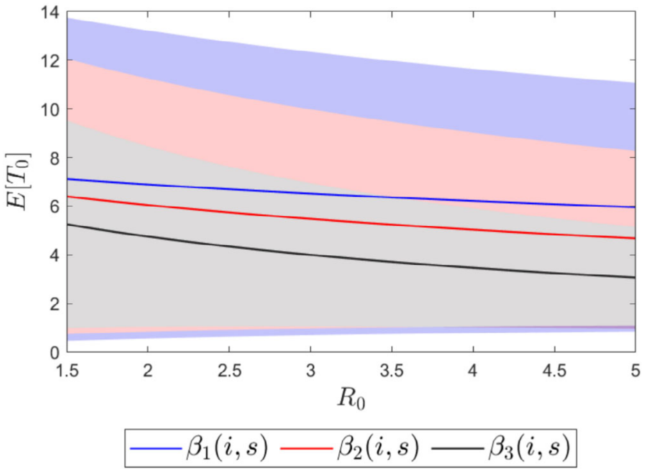

FIGURE 2 | $E[T_0]$ and $SD[T_0]$ as a function of R_0, when the initial state is $(i_0, s_0, v_0) = (1, 19, 80)$. [Colour figure can be viewed at wileyonlinelibrary.com]

In the second set of experiments, we study the influence of the transmissibility of the disease on T_0 and R_T by displaying the expected values and standard deviations as a function of R_0. In the literature (see, for instance, [36, 44, 45]), estimates of R_0 vary between 1.1 and 5.0, depending on geographical areas, cattle species, control measures, and other factors.

We use the simple expression for $R_0 = \beta\epsilon^{-1}$ in a Markovian SIR model [46], which involves the contact rate parameter, β, and the expected length of the infectious period, ϵ^{-1}. In this second set of experiments, following [47], we set $\epsilon^{-1} = 7$ days and determine the values of the contact rate for each transmission function considered. We also assume that the probability of vaccine failure is $h = 0.11$ and that the average time for confirmatory laboratory diagnosis is 8 days (i.e., $\gamma = 1/8$ days^{-1}).

Figure 2 plots the expected time to disease confirmation as a function of R_0 in combination with the transmission function. It is assumed that at $t = 0$, the population has one infected individual, 19 susceptible individuals, and 80 vaccine-protected individuals. Each curve corresponds to a choice on the transmission function $\beta_j(i, s)$, for $j = 1, 2, 3$. Shaded areas are obtained by representing $E[T_0] \pm SD[T_0]$.

The expected confirmation time $E[T_0]$ decreases with increasing values of R_0, regardless of the transmission function. Intuitively, as R_0 increases, so does the number of cases of infection. As a result, more laboratory tests are performed simultaneously, and the diagnosis is confirmed earlier. For a fixed R_0, we observe that $E[T_0|\beta_3] \leq E[T_0|\beta_2] \leq E[T_0|\beta_1]$. Thus, the inhibitory choice gives, on average, longer times to confirm the disease, while shorter times are observed when the reaction–diffusion force of infection is considered.

Using the same assumptions as for Figure 2, Figure 3 shows the expected incidence of infection up to the time of confirmation of the disease as a function of R_0. Similarly, the shaded areas correspond to $E[R_T] \pm SD[R_T]$.

An increase in R_0 indicates a greater ability of the disease to spread through a naive population. Therefore, the monotonically increasing behavior of the expected number of infections observed in the interval $(0, T_0]$, as a function of R_0, is intuitively consistent. Moreover, for a fixed R_0, we observe that $E[R_T|\beta_1] \leq E[R_T|\beta_2] \leq E[R_T|\beta_3]$. That is, the inhibitory choice gives, on average, shorter times to confirm the disease compared with those observed when the bilinear or the reaction–diffusion force of infection is considered.

Next, we derive a numerical analysis for the ratio $E[R_T^v]/E[R_T]$, which compares the expected number of infections due to vaccine failure with the expected total number of infections up to disease confirmation. We plot this ratio as a function of the probability of vaccine failure h and the mean time to confirm the disease by laboratory tests $1/\gamma$, for the transmission function $\beta_j(i, s)$ for $j = 1, 2, 3$, where the contact rate β is set at $R_0 \in \{1.5, 2.5, 5.0\}$.

For Figure 4, we assume that the initial state in the population is $(i_0, s_0, v_0) = (1, 19, 80)$. We observe that the ratio of the expected values varies in $(0.25, 0.76)$, that is, for high vaccine coverage ($v_0 = 80$), the expected incidence among vaccinated is at most the 75% of the total incidence before disease confirmation. For fixed R_0 and incidence function,

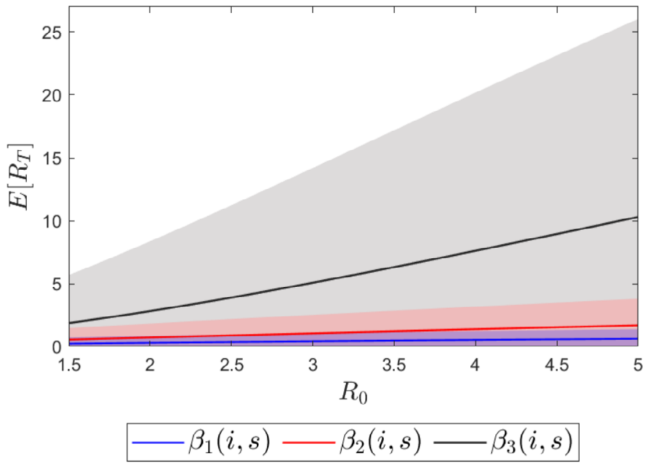

FIGURE 3 | $E[R_T]$ and $SD[R_T]$ as function of R_0, when the initial state is $(i_0, s_0, v_0) = (1, 19, 80)$. [Colour figure can be viewed at wileyonlinelibrary.com]

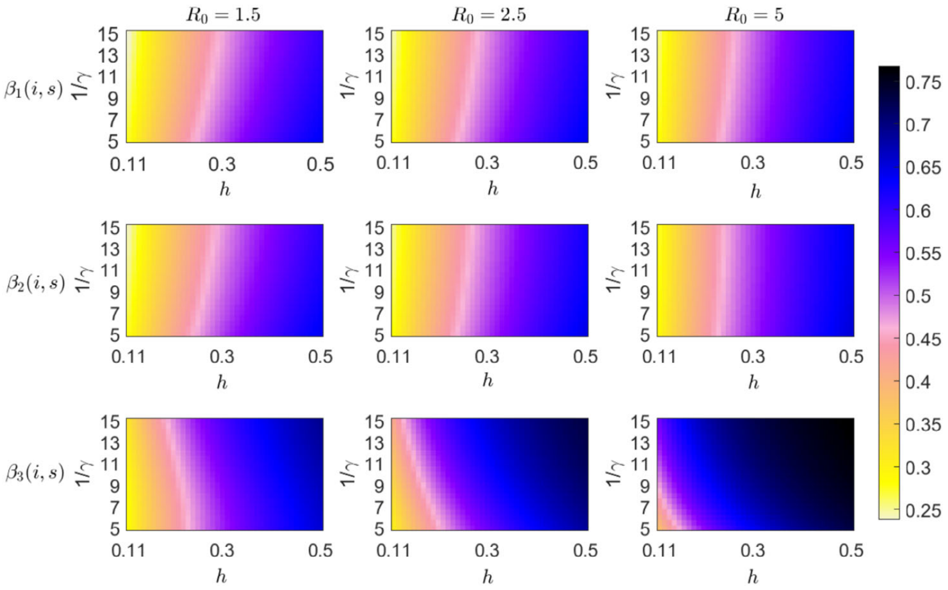

FIGURE 4 | $E[R_T^v]/E[R_T]$ as a function of h and $1/\gamma$, for values of $R_0 \in \{1.5, 2.5, 5.0\}$, $N = 100$, and an initial state $(i_0, s_0, v_0) = (1, 19, 80)$. [Colour figure can be viewed at wileyonlinelibrary.com]

the ratio increases as a function of the probability of vaccine failure, showing the importance of the vaccine as a control measure. When the average time to obtain clinical results varies between 5 and 15 days, we observe only small changes in this ratio, especially under inhibitory or bilinear choices for the incidence transmission function. Under the reaction–diffusion transmission, a longer time to obtain clinical results leads to an increase in the proportion of cases of infection in the vaccine-protected group compared with the expected total incidence. Changes in R_0 show little influence on $E[R_T^v]/E[R_T]$ when the incidence function is chosen as inhibitory or bilinear. For reaction–diffusion incidence, we observe an increase in the ratio of expectations as R_0 increases.

Additional experiments, not reported here, show a similar behavior to Figure 4 when considering a vaccine coverage v_0 lower than 80%.

5 | Conclusion

In this paper, we study the time lag to disease detection. With the help of a CTMC, we model changes in the state of a stochastic SIR-type process, that records the number of individuals who are susceptible, vaccinated, infected (i.e., showing symptoms), or clinically confirmed cases. To make the model more realistic, infection can be transmitted through internal and external contacts not only to susceptible individuals but also to vaccinated individuals, due to vaccine failure. The vaccine is used preventively in susceptible individuals but is also planned during the outbreak to mitigate the waning effects of the vaccine. In this paper, we assume that it is possible to detect symptoms of the disease in all infected individuals. However, this is a very restrictive assumption that can be relaxed by including an asymptomatic compartment in the model [10, 48, 49] with a subsequent increase in the size of the state space and computational times.

We introduce and analyze interesting random variables that measure the time to confirm the disease, T_0, and the incidence of cases of infection during $(0, T_0]$ in the whole population, R_T, and among vaccine-protected individuals, R_T^v. Results regarding moments and probabilities of these random variables, appearing in Section 4, come from applying the recursive algorithms included in Section 3 to outbreaks of FMD. The numerical results for the ratio $E[R_T^v]/E[R_T]$ are a first step towards understanding the relationship between $E[R_T^v/R_T]$ and vaccine efficacy. This requires a joint study of the two-dimensional random variable (R_T^v, R_T), as we have done in [27, 50], and could be applied to estimate the probability of vaccine failure, h, from real data sets.

The conclusions drawn from this study have important implications for decisions that influence farm profitability and the well-being of its animals. Once producers are confident that an active outbreak of FMD is present on a farm, our methodology provides probabilistic information on how long the infection may have been present and how many infected cases can be found at the time of detection. Both quantities are particularly helpful in enabling timely actions to be taken regarding isolation, culling, and/or other measures that will reduce the risk of a small outbreak turning into a larger one and the subsequent economic consequences.

Our research can be generalized; for example, we can consider environmental changes in the present model to represent not only behavioral changes [48] but also modifications in an ecosystem [51–53] or treatments that produce changes in parameters [32, 54, 55]. The introduction of population structures, such as households, and the inclusion of assumptions about epidemics with latent periods of infection or lifelong immunity after recovery would allow more sophisticated models to be treated.

Author Contributions

Mariajesus Lopez-Herrero: writing – review and editing, conceptualization, methodology, writing – original draft, formal analysis, supervision, validation. **Verdiana Mustaro:** writing – review and editing, writing – original draft, methodology, software. **Diana Taipe:** writing – review and editing, writing – original draft, methodology, software.

Acknowledgements

The authors thank anonymous reviewers for their insightful comments. This work has been partially supported by the Ministry of Science and Innovation (Government of Spain) through project PID2021-125871NB-I00. The authors also acknowledge the support from the “European Union—NextGenerationEU” through MUR-PRIN 2022, project 2022XZSAFN “Anomalous Phenomena on Regular and Irregular Domains: Approximating Complexity for the Applied Sciences,” and MUR-PRIN 2022 PNRR, project P2022XSF5H “Stochastic Models in Biomathematics and Applications” and INdAM–GNCS project, code CUP_E53C24001950001. The third author also acknowledges the support of Banco Santander and the Complutense University of Madrid, Predoctoral Researcher Contract CT63/19-CT64/19.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

No data involved.

References

1. A. Robert, A. M. Suffel, and A. J. Kucharski, “Long-Term Waning of Vaccine-Induced Immunity to Measles in England: A Mathematical Modelling Study,” *Lancet* 9 (2024): e766–e775.

2. T. V. Giannouchos, N. L. Hair, B. Olatosi, and X. Li, “Waning Effectiveness of mRNA COVID-19 Vaccines Against Inpatient and Emergency Department Encounters,” *PLoS ONE* 19 (2024): e0300198.

3. O. Forrest and M. Al-arydah, “Optimal Control Strategies for Infectious Diseases With Consideration of Behavioral Dynamics,” *Math Meth Appl Sci.* 48 (2025): 1362–1380.

4. G. Zaman, Y. H. Kang, G. Cho, and I. H. Jung, “Optimal Strategy of Vaccination and Treatment in an SIR Epidemic Model,” *Mathematics and Computers in Simulation* 136 (2017): 63–77.

5. M. Gamboa, M. López-García, and M. J. Lopez-Herrero, “A Stochastic SVIR Model With Imperfect Vaccine and External Source of Infection,” in *Performance Engineering and Stochastic Modeling. EPEW ASMTA 2021. Lecture Notes in Computer Science*, vol. 13104, eds. P. Ballarini, H. Castel, I. Dimitriou, M. Iacono, T. Phung-Duc, and J. Walraevens (Springer, 2021).

6. Y. Liu, S. Jian, and J. Gao, “Dynamics Analysis and Optimal Control of SIVR Epidemic Model With Incomplete Immunity,” *Advances in Continuous and Discrete Models* 2022 (2022): 51.

7. N. T. Hieu, D. H. Nguyen, N. N. Nguyen, and G. Yin, “Analyzing a Class of Stochastic SIRS Models Under Imperfect Vaccination,” *Journal of the Franklin Institute* 361 (2024): 1284–1302.

8. A. Nabti and B. Ghanbari, “Global Stability Analysis of a Fractional SVEIR Epidemic Model,” *Mathematical Methods in the Applied Sciences* 44 (2021): 8577–8597.

9. M. El Hajji and A. H. Albargi, “A Mathematical Investigation of an SVEIR Epidemic Model for the Measles Transmission,” *Mathematical Biosciences and Engineering* 19 (2022): 2853–2875.

10. M. Rabiu, R. Willie, and N. Parumasur, “Mathematical Analysis of a Disease-Resistant Model With Imperfect Vaccine, Quarantine and Treatment,” *Ricerche di Matematica* 69 (2020): 603–627.

11. F. Wang, L. Cao, and X. Song, “Mathematical Modeling of Mutated COVID-19 Transmission With Quarantine, Isolation and Vaccination,” *Mathematical Biosciences and Engineering* 19 (2022): 8035–8056.

12. M. V. Barbarossa and G. Röst, “Mathematical Models for Vaccination, Waning Immunity and Immune System Boosting: A General Framework,” *Journal of Mathematical Biology* 71 (2015): 1737–1770.

13. R. Opoku-Sarkodie, F. A. Bartha, M. Polner, and G. Röst, “Dynamics of an SIRWS Model With Waning of Immunity and Varying Immune Boosting Period,” *Journal of Biological Dynamics* 16 (2022): 596–618.

14. C. Xu, Z. Liu, Y. Pang, and A. Akgl, “Stochastic Analysis of a COVID-19 Model With Effects of Vaccination and Different Transition Rates: Real Data Approach,” *Chaos, Solitons & Fractals* 170 (2023): 113395.

15. C. Xu, Y. Pang, Z. Liu, J. Shen, M. Liao, and P. Li, “Insights Into COVID-19 Stochastic Modelling With Effects of Various Transmission Rates: Simulations With Real Statistical Data From UK,” *Australia, Spain, and India, Phys Scr.* 99 (2024): 025218.

16. N. T. J. Bailey, *The Mathematical Theory of Epidemics* (Charles Griffin and Company Limited, 1957).

17. S. Dias, K. Queiroz, and A. Araujo, “Introduction to Group-Structured-Epidemic Model,” *Journal of Control, Automation and Electrical Systems* 33 (2022): 2337.

18. D. S. Burke, “Origins of the Problematic E in SEIR Epidemic Models,” *Infectious Disease Modelling* 9 (2024): 673–679.

19. P. Paraggio and S. Spina, “A Spreaders-Ignorants-Skeptics Model for the Spreading of Fake News a a Related Finite Birth-Death Process,” in *Computer Aided Systems Theory EUROCAST 2024. EUROCAST 2024. Lecture Notes in Computer Science*, vol. 15174, eds. A. Quesada-Arencibia, M. Affenzeller, and R. Moreno-Díaz (Springer, 2025), 213–227.

20. I. J. East, P. A. J. Martin, I. Langstaff, R. M. Iglesias, E. S. G. Sergeant, and M. G. Garner, “Assessing the Delay to Detection and the Size of the Outbreak at the Time of Detection of Incursions of Foot and Mouth Disease in Australia,” *Preventive Veterinary Medicine* 123 (2016): 1–11.

21. P. H. F. Hobbelen, A. R. W. Elbers, M. Werkman, et al., “Estimating the Introduction Time of Highly Pathogenic Avian Influenza Into Poultry Flocks,” *Scientific Reports* 10 (2020): 12388.

22. S. Gao, A. K. Chakraborty, R. Greiner, M. A. Lewis, and H. Wang, “Early Detection of Disease Outbreaks and non-outbreaks Using Incidence Data: A Framework Using Feature-Based Time Series Classification and Machine Learning,” *PLoS Computational Biology* 21 (2025): e1012782.

23. A. O. Egonmwan and D. Okuonghae, “Analysis of a Mathematical Model for Tuberculosis With Diagnosis,” *Journal of Applied Mathematics and Computing* 59 (2019): 129–162.

24. H. Dicko, A. Traor, and D. Ouedraogo, “Dynamics of a SVEIR Epidemic Model With a Delay in Diagnosis in a Changing Environment,” *Contemporary Mathematics* 5 (2024): 3762–3789.

25. P. Stone, H. Wilkinson-Herbots, and V. Isham, “A Stochastic Model for Head Lice Infections,” *Journal of Mathematical Biology* 56 (2008): 743–763.

26. K. P. Das and J. Chattopadhyay, “Role of Environmental Disturbance in an Ecoepidemiological Model With Disease From External Source,” *Mathematical Methods in the Applied Sciences* 35 (2012): 659–675.

27. M. Gamboa, M. López-García, and M. J. Lopez-Herrero, “On the Exact and Population bi-Dimensional Reproduction Numbers in a Stochastic SVIR Model With Imperfect Vaccine,” *Applied Mathematics and Computation* 468 (2024): 128526.

28. M. El Khalifi and T. Britton, “Extending Susceptible-Infectious-Recovered-Susceptible Epidemics to Allow for Gradual Waning of Immunity,” *Journal of the Royal Society Interface* 20 (2023): 20230042.

29. M. J. Lopez-Herrero and D. Taipe, “Disease Incidence in a Stochastic SVIRS Model With Waning Immunity,” in *Computer Aided Systems Theory EUROCAST 2024. EUROCAST 2024. Lecture Notes in Computer Science*, vol. 15174, eds. A. Quesada-Arencibia, M. Affenzeller, and R. Moreno-Díaz (Springer, 2025), 199–212.

30. J. R. Artalejo and M. J. Lopez-Herrero, “On the Exact Measure of Disease Spread in Stochastic Epidemic Models,” *Bulletin of Mathematical Biology* 75 (2013): 1031–1050.

31. M. J. Lopez-Herrero, “Epidemic Transmission on SEIR Stochastic Models With Nonlinear Incidence Rate,” *Mathematical Methods in the Applied Sciences* 40 (2017): 2532–2541.

32. E. Almaraz and A. Gómez-Corral, “On SIR-Models With Markov-Modulated Events: Length of an Outbreak, Total Size of the Epidemic and Number of Secondary Infections,” *Discrete Contin Dyn Syst.-B* 23 (2018): 2153–2176.

33. R. Fernández-Peralta and A. Gómez-Corral, “A Structured Markov Chain Model to Investigate the Effects of pre-Exposure Vaccines in Tuberculosis Control,” *Journal of Theoretical Biology* 509 (2021): 110490.

34. V. G. Kulkarni, *Modeling and Analysis of Stochastic Systems* (Chapman and Hall/CRC, 1995).

35. G. Latouche and V. Ramaswami, *Introduction to Matrix Analytic Methods in Stochastic Modeling* (ASA-SIAM, 1999).

36. K. Orsel, A. Dekker, A. Bouma, J. A. Stegeman, and M. C. M. de Jong, “Quantification of Foot and Mouth Disease Virus Excretion and Transmission Within Groups of Lambs With and Without Vaccination,” *Vaccine* 25 (2007): 2673–2679.

37. C. L. Wong, C. Y. Yong, H. K. Ong, K. L. Ho, and W. S. Tan, “Advances in the Diagnosis of Foot-and-Mouth Disease,” *Frontiers in Veterinary Science* 7 (2020): 477.

38. S. Sieng and J. Kerr, “Investigation of Vaccination Effectiveness in two Cambodian Villages Facing an Outbreak of Foot-and-Mouth Disease,” in *Cattle Health, Production and Trade in Cambodia*, vol. 138, eds. J. R. Young, L. Rast, S. Sothoeun, and P. A. Windsor (ACIAR Proceedings, 2013), 67–71.

39. W. M. Liu, S. A. Levin, and Y. Iwasa, “Influence of Nonlinear Incidence Rates Upon the Behavior of SIRS Epidemiological Models,” *Journal of Mathematical Biology* 23 (1986): 187–204.

40. S. Ruan and W. Wang, “Dynamical Behavior of an Epidemic Model With Nonlinear Incidence Rate,” *Journal of Difference Equations* 188 (2003): 135–163.

41. F. Capone, V. De Cataldis, and R. De Luca, “On the Nonlinear Stability of an Epidemic SEIR Reaction-Diffusion Model,” *Ricerche di Matematica* 62 (2013): 161–181.

42. S. Anita and V. Capasso, “Reaction-Diffusion Systems in Epidemiology,” *Annals of the Alexandru Ioan Cuza University-Mathematics* 66 (2020): 171–196.

43. J. Mushanyu, F. Nyabadza, G. Muchatibaya, and A. G. R. Stewart, “On the Role of Imitation on Adolescence Methamphetamine Abuse Dynamics,” *Acta Biotheoretica* 65 (2017): 3761.

44. L. Xue, Y. Ren, W. Sun, and T. Wang, “Modelling the Dynamics of Hand, Foot, and Mouth Disease Transmission Through Fomites and Immigration,” *Mathematical Methods in the Applied Sciences* 47 (2024): 9385–9408.

45. C. B. De Rueda, A. Dekker, P. L. Eblé, and M. C. M. De Jong, “Vaccination of Cattle Only Is Sufficient to Stop FMDV Transmission in Mixed Populations of Sheep and Cattle,” *Epidemiology and Infection* 143 (2015): 2279–2286.

46. H. Andersson and T. Britton, *Stochastic Epidemic Models and Their Statistical Analysis* (Springer Science & Business Media, 2012).

47. T. B. Gashirai, S. D. Musekwa-Hove, P. O. Lolika, and S. Mushayabasa, “Global Stability and Optimal Control Analysis of a Foot-and-Mouth Disease Model With Vaccine Failure and Environmental Transmission,” *Chaos, Solitons & Fractals* 132 (2020): 109568.

48. B. Buonomo, R. Della Marca, and S. S. Sharbayta, “A Behavioral Change Model to Assess Vaccination-Induced Relaxation of Social Distancing During an Epidemic,” *Journal of Biological Systems* 30 (2022): 1–25.

49. J. Arino and E. Milliken, “Bistability in Deterministic and Stochastic SLIAR-Type Models With Imperfect and Waning Vaccine Protection,” *Journal of Mathematical Biology* 84 (2022): 61.

50. A. Di Crescenzo, A. Gómez-Corral, and D. Taipe, “A Computational Approach to Extreme Values and Related Hitting Probabilities in Level-Dependent Quasi-Birthdeath Processes,” *Mathematics and Computers in Simulation* 228 (2025): 211–224.

51. C. Xu and M. Liao, “Dynamical Behavior for a Stochastic two-Species Competitive Model,” *Open Mathematics* 15 (2017): 1258–1266.

52. P. Li, R. Gao, C. Xu, Y. Li, A. Akgül, and D. Baleanu, “Dynamics Exploration for a Fractional-Order Delayed Zooplankton–Phytoplankton System,” *Chaos, Solitons & Fractals* 166 (2023): 112975.

53. M. Z. Baber, M. W. Yasin, C. Xu, N. Ahmed, and M. S. Iqbal, “Numerical and Analytical Study for the Stochastic Spatial Dependent Prey–Predator Dynamical System,” *Journal of Computational and Nonlinear Dynamics* 19 (2024): 101003.

54. A. Economou and M. J. Lopez-Herrero, “The Deterministic SIS Epidemic Model in a Markovian Environment,” *Journal of Mathematical Biology* 73 (2016): 91–121.

55. X. Zhang, T. Su, and D. Jiang, “Dynamics of a Stochastic SVEIR Epidemic Model Incorporating General Incidence Rate and OrnsteinUhlenbeck Process,” *Journal of Nonlinear Science* 33 (2023): 76.