Available online at http://scik.org
J. Math. Comput. Sci. 11 (2021), No. 6, 7754-7772
https://doi.org/10.28919/jmcs/6331
ISSN: 1927-5307

A STOCHASTIC MODEL FOR COVID-19 WITH A HIGHLY EFFECTIVE VACCINE

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Abstract. We propose a stochastic model for the population dynamics of COVID-19 with vaccine. The model allows for waning immunity. We start off with a deterministic model in terms of ordinary differential equations (ODEs), which afterwards are stochastically perturbed to form a system of stochastic differential equations (SDEs). The ODE system and the SDE system have global positive solutions. We discuss the equilibrium points of the ODE system. For the SDE model we obtain a stability result in terms of almost sure exponential stability theorem for the disease-free equilibrium of the stochastic model. Our theoretical results are illustrated by numerical simulations.

Keywords: basic reproduction number; stochastic model; extinction; COVID-19 vaccine.

2010 AMS Subject Classification: 92D30, 34K20.

1. INTRODUCTION

COVID-19 has caused serious damage in public health sectors and economies of many countries. By January 2021, there have been more than 85 million cases and 1.8 million deaths reported worldwide [5]. As also for HIV, South Africa has become the epicenter for COVID-19 over the African continent with an estimated 1.56 millions cases and 53 498 related death cases [22] by April 2021. This crisis has led to a variety of urgent interventions across the world, such

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Received June 15, 2021

as lock-down, limited travel or travel ban and online work and schooling. These strategies well-planned have succeeded in suppressing the spread of the viral infection over populations. One way to mitigate the COVID-19 outbreak is to develop vaccine and supply it in big volumes for all the countries. A vaccine could prevent a susceptible person from being infected at least for a time period or even for life. Recently, several candidate vaccines has been developed around the globe [16]. Such long-term solutions of vaccines that protect against COVID-19 infection remain urgently needed [3]. The benefits of a highly effective vaccine for individuals and their communities have resulted in widespread demand. Therefore it is critical that decision-making on vaccine distribution is well motivated, particularly in the initial phases when vaccine availability is limited [6]. Currently, due to a large demand of vaccines worldwide, policy-makers and researchers have been seriously challenged to consider the best scenario of vaccination for suppressing the mortality and morbidity of COVID-19 in the long run.

Mathematical models can provide valuable insights into the population dynamics of COVID-19. These models provide essential information for the public health sector for decision-making and to formulate policies. Already at this stage, a number of research papers on COVID-19 models with vaccine can be found in the literature. The paper [1], for instance, proposes a vaccination model and derives threshold conditions for preventing the spread of infection in the case of imperfect vaccines. In [11], the authors studied fair allocation of COVID-19 vaccines using an optimization-based strategy for case study in Mexico. They considered different scenarios of the availability of potential COVID-19 vaccines in order to identify fair solutions. Quantifying early COVID-19 outbreak transmission in South Africa and exploring vaccine efficacy scenarios has been studied in [9]. The paper estimates the percentage reduction in effective contacts due to the social distancing measures implemented in South Africa. In [4] is presented a model for the transmission dynamics of the COVID-19 Pandemic in South Africa with emphasis on the importance of surveillance testing and contact tracing in curtailing the disease in South Africa.

In this research, we propose an *SEIRS* compartmental model with vaccination. Immunity may wane with time, and some variants may be able to evade the protection provided by COVID-19 vaccine. In the current model, the vaccination is only introduced to vulnerable susceptible individuals who are exposed to the virus. In real life, epidemic models experiences environmental

disturbance. In order to capture the effect of such disturbances it is advantageous to introduce stochastic perturbations into the deterministic model. Therefore from the deterministic model we shall build a stochastic model for novel COVID-19. There are SDE models in the literature, such as [2] for instance. One of the differences between the model of [2] and ours, is that the current model includes vaccination.

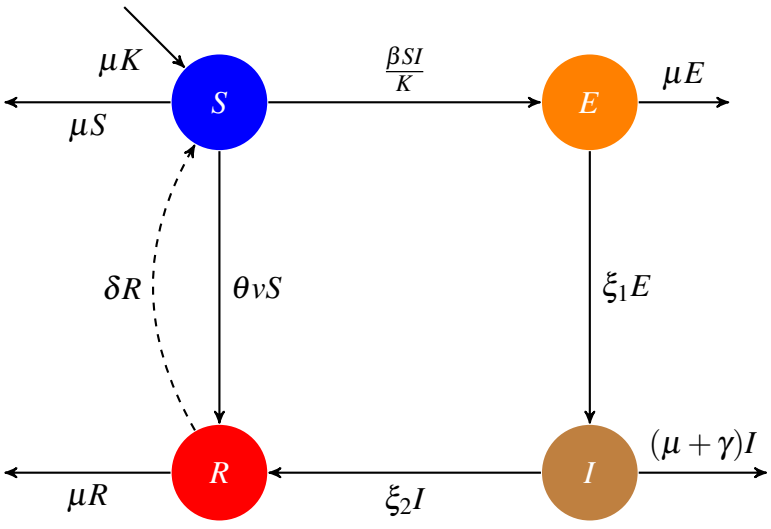
The remainder of this paper resumes as follows. In Section 2 we present the deterministic model and prove the existence of global positive solutions. We briefly study the equilibrium points in Section 3. In Section 4 we present the stochastic model for novel COVID-19, we show the existence of global positive solutions and we prove an extinction theorem. We provide numerical simulations to illustrate our theoretical results in Section 5. In Section 6 we present some concluding remarks.

2. Model Description

2.1. A deterministic model. We consider a population of size $N(t)$ at time t which is subdivided into the class of Susceptibles $S(t)$, the Exposed class $E(t)$, the Infectious class $I(t)$ and the Removed class $R(t)$. The population size $N(t)$ is given by

$$N(t) = S(t) + E(t) + I(t) + R(t).$$

Flow diagram of COVID-19 model



These assumptions give rise to the following mathematical model

$$
\begin{aligned}
\frac{dS}{dt} &= \mu K - \frac{\beta SI}{K} - (\mu + \theta v)S + \delta R, \\
\frac{dE}{dt} &= \frac{\beta SI}{K} - (\mu + \xi_1)E, \\
\frac{dI}{dt} &= \xi_1 E - (\mu + \xi_2 + \gamma)I, \\
\frac{dR}{dt} &= \theta v S + \xi_2 I - (\mu + \delta)R.
\end{aligned} \tag{1}
$$

$S(0) = S_0 > 0, E(0) = E_0 > 0, I(0) = I_0 > 0, R(0) = R_0 > 0.$

The parameter θ measures the ability of the vaccine to protect the vaccinee against the disease. However, new variants of the virus may evade the protection provided by a vaccine, and then vaccinated individuals may be exposed to the virus at the rate δ.

There are many models in the literature that are very close to the model above, for instance [10, 8] can be viewed as special cases of the model of (1).

2.2. Feasible solutions and invariant regions.

Let us introduce the set Ω,

$$
\Omega = \left\{ x \in \mathbb{R}^4 |\, x_i > 0,\ i = 1,2,3,4 \text{ and } x_1 + x_2 + x_3 + x_4 < K \right\}. \tag{2}
$$

Since model (1) describes a human population, all state variables and parameters of the model are assumed to be positive at all times $t > 0$. We deal with this positivity in the next two results, similarly as in [24] or [13] for instance.

Proposition 2.1. *Given any $t_0 > 0$, suppose that $X(t)$ is a local solution for which $X(t) \in \mathbb{R}^4_+$ for $0 < t < t_0$ and that $N(0) < K$. Then $N(t) < K$ for all $0 < t \leq t_0$.*

Proof. Given any local solution with $X(t) \in \mathbb{R}^4_+$ for all $0 < t \leq t_0$, we have

$$
\frac{d(N(t) - K)}{dt} = \mu K - \mu N(t) - \gamma I \leq -\mu \left[N(t) - K \right]. \tag{3}
$$

Therefore $N(0) < K$ implies that $N(t) < K$ for all $0 < t \leq t_0$. This completes the proof. □

Theorem 2.2. *For any point $X_0 \in \Omega$, there exists a unique solution $X(t)$ with $X(0) = X_0$ and $X(t) \in \Omega$ for each $t \in [0, \infty)$.*

Proof. Consider any point $y \in \Omega$. Then there exists a local solution $X(t)$ in Ω with initial value $X(0) = y$. Suppose that t_1 is the exit time. We shall show by contradiction that $t_1 = \infty$.

Let us define the following function for $0 \leq t \leq t_1$.

$$V_0(X) = V_0(S,E,I,R) = \ln\frac{K}{S} + \ln\frac{K}{E} + \ln\frac{K}{I} + \ln\frac{K}{R}. \tag{4}$$

Then each of the terms in $V_1(X)$ is a positive-valued function. In particular, we know that for a constant $K > 0$ if any of the $X_i(t)$ tends to 0 as $t \to t_1$, then $V_0(t) \to \infty$. We shall prove that this cannot happen if t_1 is finite.

We calculate the derivative:

$$\begin{aligned} \frac{dV_0}{dt} &= -\frac{1}{S}\left[\mu K - \frac{\beta SI}{K} - (\mu+\theta v)S + \delta R\right] - \frac{1}{E}\left[\frac{\beta SI}{K} - (\mu+\xi_1)E\right] \\ &\quad -\frac{1}{I}\left[\xi_1 E - (\mu+\xi_2+\gamma)I\right] - \frac{1}{R}\left[\theta v S + \xi_2 I - (\mu+\delta)R\right]. \end{aligned} \tag{5}$$

After cancellation of some terms which are obviously negative, we obtain an inequality $V_0'(t) \leq F_0$, with F_0 being the constant

$$F_0 = \beta + 4\mu + \theta v + \xi_1 + \xi_2 + \gamma + \delta. \tag{6}$$

Therefore, over the bounded interval $[0,t_1)$, $V_0(t)$ is bounded. We can conclude that $X(t)$ never exits the set Ω. □

3. Equilibrium and Stability

The model system (1) permits a disease-free equilibrium

$$E_0 = (S_v, 0, 0, R_v).$$

where

$$S_v = \frac{K(\mu+\delta)}{(\mu+\delta+\theta v)} \text{ and } R_v = \frac{K\theta v}{(\mu+\delta+\theta v)}.$$

We now follow the method illustrated in [19] to find the basic reproduction number for model (1), which represents the expected average number of new infections produced by a single infected individual when in contact with a completely susceptible population. Thus, we have

$$\mathscr{R} = \frac{\beta\xi_1(\mu+\delta)}{u_1u_2(\mu+\delta+\theta v)}$$

where

$$u_1 = (\mu+\xi_1) \text{ and } u_2 = (\gamma+\mu+\xi_2).$$

Theorem 3.1. *A unique endemic equilibrium point exists if and only if $\mathscr{R} > 1$. The coordinates are as follows:*

$$I^* = \frac{\mu K[\xi_1\beta(\mu+\delta) - u_1u_2(\mu+\delta+\theta v)]}{\beta[u_1u_2(\mu+\delta) - \xi_1\xi_2\delta]},$$

$$E^* = \frac{u_1}{\xi_1}I^*,\ S^* = \frac{u_1u_2K}{\xi_1\beta} \text{ and } R^* = \frac{u_1u_2K\theta v}{\xi_1\beta(\mu+\delta)} + \frac{\xi_2 I^*}{(\mu+\delta)}.$$

Proof. From the system (1), one can readily deduce the expressions appearing in the formulation of the theorem for S^*, E^* and R^* in terms of I^*. We substitute the S^*, E^* and R^* values into the first equation (at equilibrium) and after simplification we obtain the expression for I^*. Regarding the denominator, note that $u_1 > \xi_1$, $u_2 > \xi_2$, and so, $u_1u_2(\mu+\delta) > \xi_1\xi_2\delta$. Therefore the denominator is positive. The numerator is positive if and only if $\mathscr{R} > 1$. □

We shall now prove global stability of the disease-free equilibrium point. In the special case when we assume no transfer from the R-class back to the S-class, we can ignore the $R'(t)$-equation. The other compartments will still follow the same trajectories when we restrict to the resulting SEI-model. In this case, we can prove the following global stability theorem.

Theorem 3.2. *If $\delta = 0$ and $\mathscr{R} < 1$, the disease-free equilibrium of the resulting SEI model is globally asymptotically stable.*

Proof. Since $\mathscr{R} < 1$, the following inequality holds:

$$\beta\frac{S_v}{K} - \frac{u_1u_2}{\xi_1} < 0$$

with

$$S_v = \frac{\mu K}{(\mu + \theta v)}.$$

We can find $z > 0$ with $z < 1$, such that $\beta \frac{S_v}{K} - z\frac{u_1 u_2}{\xi_1} < 0$. Now let $a = z\frac{u_1}{\xi_1}$. We define a function

$$V_2(S(t), E(t), I(t)) = \left[S(t) - S_v - S_v \ln \frac{S_v}{S(t)}\right] + E(t) + aI(t).$$

Note that $V_2(t)$ is positive-definite at the equilibrium point $(S_v, 0, 0)$.

The time derivative of $V_2(t)$ is:

$$\begin{aligned} V_2'(t) &= -\frac{(\mu + v\theta)}{S(t)}(S_v - S(t))^2 - \frac{(S - S_v)}{K}\beta I \\ &\quad + E[(\mu + \xi_1) - a\xi_1] + I\big[\frac{\beta S}{K} - a(\mu + \xi_2 + \gamma)\big] \\ &= -\frac{(\mu + v\theta)}{S(t)}(S_v - S(t))^2 + Q_1 E(t) + Q_2 I(t) \end{aligned}$$

where

$$Q_1 = a\xi_1 - u_1 \text{ and } Q_2 = \beta\frac{S_v}{K} - au_2.$$

Then

$$Q_1 = z\frac{u_1}{\xi_1}\xi_1 - u_1 = u_1(z-1) < 0 \text{ since } z < 1. \tag{7}$$

Also, from the inequality (7) it follows that $Q_2 < 0$. Therefore, $V_2'(t)$ is negative-definite with respect to the disease-free equilibrium point. Thus, $V_2(t)$ is a Lyapunov function of SEI-model at disease-free equilibrium and this completes the proof. □

4. STOCHASTIC MODEL FOR COVID-19

Under this approach, we assume to have a complete probability space $(\Omega, \mathscr{F}, \mathbb{P})$ with a filtration, $\{\mathscr{F}_t\}_{t\geq 0}$, that is right continuous and with $\mathscr{F}_0$ containing all the subsets having measure zero. In this regard, we let $W(t) = (W_0(t), W_1(t), W_2(t), W_3(t))$ be a 4-dimensional Wiener process defined on this probability space. The components of W introduced in the stochastic model are assumed to be mutually independent and the non-negative constants $\sigma_0, \sigma_1, \sigma_2$ and σ_3 symbolize the intensities of the stochastic perturbations which we shall introduce into our stochastic model. We recall the formal multiplication rule below:

$$dtdt = 0, dW_i dt = 0, dW_i dW_i = dt \text{ and } dW_i dW_j = 0 \text{ if } i \neq j.$$

We now have the following model

$$\begin{aligned} dS &= [\mu K - \frac{\beta SI}{K} - (\mu + \theta v)S + \delta R]dt + \sigma_0 S dW_0(t), \\ dE &= [\frac{\beta SI}{K} - (\mu + \xi_1)E]dt + \sigma_1 E dW_1(t), \\ dI &= [\xi_1 E - (\mu + \xi_2 + \gamma)I]dt + \sigma_2 I dW_1(t) \\ dR &= [\theta v S + \xi_2 I - (\mu + \delta)R]dt + \sigma_3 R dW_1(t) \end{aligned} \tag{8}$$

Similar to the underlying deterministic model, we now prove that the solutions of (8) exist globally and are positive. This proof has been used popularly by many scholars, see for instance [7, 14, 15].

Let us denote by $\mathbb{R}^n_+$ (resp. $\mathbb{R}^n_{++}$) the set of points in $\mathbb{R}^n$ having only non-negative (resp. strictly positive) coordinates.

Theorem 4.1. *For model (8) and any initial value $(S(0), E(0), I(0), R(0)) \in \mathbb{R}^4_{++}$, there is a unique solution $(S(t), E(t), I(t), E(t))$ on $t \geq 0$ which remains in $\mathbb{R}^4_{++}$ with probability one.*

Proof. Note that the coefficients of the system (8) are locally Lipschitz continuous. Thus there exists a unique local solution on $t \in [0, \tau_e)$, where τ_e is the explosion time. We need to show that this solution is global almost surely (a.s) ; that is, $\tau_e = \infty$ a.s.

Let $m_0 > 0$ be sufficiently large so that $S(0), E(0), I(0)$, and $R(0)$ sits within the interval $[1/m_0, m_0]$. For each integer $m \geq m_0$, define a sequence of stopping times by

$$\begin{aligned} \tau_m = \inf \Big\{ t \in [0, \tau_e) : & \ S(t) \notin \left(\tfrac{1}{m}, m\right) \text{ or } E(t) \notin \left(\tfrac{1}{m}, m\right) \text{ or } I(t) \notin \left(\tfrac{1}{m}, m\right) \\ & \text{or } R(t) \notin \left(\tfrac{1}{m}, m\right) \Big\} \end{aligned}$$

where we set $\inf \emptyset = \infty$. Now since the sequence (τ_m) is non-decreasing, the following limit exists:

$$\tau_\infty = \lim_{m \to \infty} \tau_m,$$

and $\tau_\infty \leq \tau_e$ (a.s.). Now we need to show $\tau_\infty = \infty$ (a.s.). If this statement is violated, then there exist $T > 0$ and $\varepsilon \in (0,1)$ such that

$$\mathbb{P}\{\tau_\infty \leq T\} > \varepsilon.$$

Thus, there is an integer $m_1 \geq m_0$ such that

$$\mathbb{P}\{\tau_m \leq T\} \geq \varepsilon \quad \forall m \geq m_1.$$

Consider the function V_3 defined by

$$\begin{aligned} V_3(S,E,I,R) &= \Big(S - a_0 - a_0 \ln \frac{S}{a_0}\Big) + \Big(E - 1 - \ln E\Big) + \Big(I - 1 - \ln I\Big) \\ &\quad + \Big(R - 1 - \ln R\Big) \end{aligned} \tag{9}$$

Note that each of the four bracketed terms are non-negative while $(S(t),E(t),I(t),R(t)) \in \mathbb{R}^4_{++}$. We also note that,

$$\lim_{x\to 0^+}[x - 1 - \ln x] = \infty \text{ and } \lim_{x\to\infty}[x - 1 - \ln x] = \infty.$$

By applying Itô's formula we have,

$$\begin{aligned} dV_3(S,E,I,R) &= \mathscr{L}V_3 dt + (S-1)\sigma_0 dW_0(t) + (E-1)\sigma_1 dW_1(t) \\ &\quad + (I-1)\sigma_2 dW_2(t) + (R-1)\sigma_3 dW_3(t), \end{aligned}$$

where

$$\begin{aligned} \mathscr{L}V_3 &= \Big[\big(1 - a_0\frac{1}{S}\big)\big(\mu K - \frac{\beta SI}{K} - (\mu+\theta v)S + \delta R\big)\Big] + \Big[\big(1 - \frac{1}{E}\big)\big(\frac{\beta SI}{K} - (\mu+\xi_1)E\big)\Big] \\ &\quad + \Big[\big(1 - \frac{1}{I}\big)\big(\xi_1 E - (\mu+\xi_2+\gamma)I\big)\Big] \\ &\quad + \Big[\big(1 - \frac{1}{R}\big)\big(\theta v S + \xi_2 I - (\mu+\delta)R\big)\Big] + \frac{1}{2}(a_0\sigma_0^2 + \sigma_1^2 + \sigma_2^2 + \sigma_3^2) \\ &\leq \mu K + a_0\frac{\beta I}{K} - \mu I + 4\mu + \theta v + \xi_1 + \xi_2 + \delta + \gamma + \frac{1}{2}\left(a_0\sigma_0^2 + \sigma_1^2 + \sigma_2^2 + \sigma_3^2\right). \end{aligned}$$

We can choose $a_0 > 0$ sufficiently small such that

$$I[a_0\frac{\beta}{K} - \mu] < 0.$$

Therefore,

$$\mathscr{L}V_3 \leq F_3$$

where $F_3 = \mu K + 4\mu + \theta v + \xi_1 + \xi_2 + \delta + \gamma + \frac{1}{2}\left(a_0\sigma_0^2 + \sigma_1^2 + \sigma_2^2 + \sigma_3^2\right)$ is a constant.
The rest of the proof follows readily, similarly as in [7], [23] or [14], and we omit the details. We can conclude that the solution of model (8) is positive and will not explode in finite time, with probability one. □

Consider an equation of the form (10) below, for an k-dimensional Brownian motion $B(t)$ on Ω.

$$dx(t) = f(t,x)dt + g(t,x)dB(t) \ t \geq 0. \tag{10}$$

A solution with initial value $x(0) = x_0$ is denoted by $x(t,x_0)$. Assume that $f(t,0) = g(t,0) = 0$ for all $t \geq 0$, so as to have the origin point as an equilibrium of (10).
By $\mathscr{L}$ we denote the infinitesimal generator of an equation of the form (10), see [18] of Øksendal, defined for a function $V(t,x) \in C^{1,2}(\mathbb{R}_+ \times \mathbb{R}^k)$.

Definition 4.2. *(see* [7]*). The equilibrium $x = 0$ of the system (10) is said to be almost surely exponentially stable if for all $x_0 \in \mathbb{R}^n$,*

$$\limsup_{t\to\infty} \frac{1}{t} \ln|x(t,x_0)| < 0 \text{ a.s.}$$

Notation: For a stochastic process $\{x(t)\}_{t>0}$ we shall write:

$$\langle x\rangle_t = \frac{1}{t}\int_0^t x(s)ds.$$

In what follows we prove an extinction theorem for COVID-19 in an applicable population, and for this purpose we restrict ourselves to the case in which $\sigma_0 = \sigma_3 = 0$, and with $\delta = 0$. For this special case, we introduce the following stochastic processes, for a positive constant a.

$$U = S - S_v + S_v \ln(S_v/S) + E + aI. \tag{11}$$

and

$$V_4 = \ln U(t) \ \ (\text{where } \ U(t) > 0 \ \forall t > 0).$$

We note that S, E and I are positive (a.s.), and so V_4 is well-defined (a.s.). In particular here we are interested in

$$\Gamma := \limsup_{t\to\infty} \langle V_4 \rangle_t.$$

Let us also introduce the following notation.

$$\limsup \left\langle \frac{(S-S_v)^2}{SU} \right\rangle_t = q_0, \quad \limsup \left\langle \frac{E}{U} \right\rangle_t = q_1, \quad \limsup \left\langle \frac{I}{U} \right\rangle_t = q_2.$$

Proposition 4.3. *Consider the special case of model 8, when $\sigma_0 = \sigma_3 = \delta = 0$. The disease-free equilibrium of model system 8 is almost surely exponentially stable if*

$\lim_{t\to\infty} \sup \langle V_4(t) \rangle_t < 0 \ (a.s.)$.

Proof. The stochastic process $V_4(t)$ can be expressed as

$$V_4(t) = V_4(0) + \int_0^t \mathscr{L} V_4(s) ds + J_1(t) + J_2(t)$$

where

$$J_1(t) = \int_0^t \sigma_1 \frac{E(s)}{U(s)} dW_1(s),$$

and

$$J_2(t) = \int_0^t a\sigma_2 \frac{I(s)}{U(s)} dW_2(s).$$

Note that $\frac{E(t)}{U(t)} < 1$ and $a\frac{I(t)}{U(t)} < 1$ for all $t > 0$. Therefore, the assertion of the proposition follows by the strong law of large numbers for martingales

$$\lim_{t\to\infty} \sup \frac{1}{t} [(J_1(s) + J_2(s)] = 0 \ \text{(a.s)}.$$

Now we also note that

$$\limsup_{t\to\infty}\frac{V_4(0)}{t}=0.$$

This completes the proof. □

Now we compute $\mathscr{L}V_4$.

$$\begin{aligned}\mathscr{L}V_4 &= \frac{1}{U}\left(1-\frac{S_v}{S}\right)\left[\mu K-(\mu+v\theta)S-\frac{\beta SI}{K}\right]+\frac{1}{U}\left[\frac{\beta SI}{K}-(\mu+\xi_1)E\right]\\ &\quad+\frac{a}{U}\left[\xi_1E-(\mu+\xi_2+\gamma)I\right]-\frac{1}{2U^2}[(\sigma_1E)^2+(a\sigma_2I)^2]\\ &= -\frac{(\mu+v\theta)}{SU}(S-S_v)^2+\frac{1}{U}\left[\beta S_vI-(\mu+\xi_1)E+a(\xi_1E-(\mu+\xi_2+\gamma)I)\right]\\ &\quad-\frac{1}{2U^2}[(\sigma_1E)^2+(a\sigma_2I)^2]\\ &= -\frac{(\mu+v\theta)}{SU}(S-S_v)^2+Q_1\frac{E}{U}+Q_2\frac{I}{U}-\frac{1}{2U^2}[(\sigma_1E)^2+(a\sigma_2I)^2]\end{aligned}$$

with

$Q_1=a\xi_1-(\mu+\xi_1)$,

and

$Q_2=\beta S_v-a(\mu+\xi_2+\gamma)$.

In particular then

$$\mathscr{L}V_4\le-\frac{(\mu+v\theta)}{SU}(S-S_v)^2+Q_1\frac{E}{U}+Q_2\frac{I}{U}\ (a.s). \tag{12}$$

Proposition 4.4. *For K and S_v as in the model, let us define the following functions, all having the interval $(0,K)$ as domain. Let $F(x)=x(1-S_v/x)^2$, $G(x)=x-S_v+S_v\ln(S_v/x)$ and $H(x)=F(x)-G(x)$.*

Then $H(x)\ge 0$ for every $0<x<K$.

Proof. We note that $H'(x) = 0$ if and only if $x = S_v$. Next we observe that $H''(S_v) = 1/S_v > 0$. Therefore H has a local minimum at $x = S_v$. Further we note that for $0 < x < K$, H is differentiable. Therefore H has an absolute minimum at $x = S_v$. Consequently, $H(x) \geq 0$ for all $0 < x < K$. □

In particular we can deduce the following.

Corollary 4.5. *For any positive constant a, the following two inequalities hold:*

$$(a) \quad \frac{S(1-S_v/S)^2 + E + aI}{S - S_v + S_v \ln(S_v/S) + E + aI} \geq 1.$$

$$(b) \quad q_0 + q_1 + aq_2 \geq 1.$$

Theorem 4.6. *Consider the special case of model 8, when $\sigma_0 = \sigma_3 = \delta = 0$. If $\mathscr{R} < 1$, then the disease-free equilibrium is almost surely exponentially stable.*

Proof. Since $\mathscr{R} < 1$, it follows that

$$\beta S_v - \left(\frac{\mu + \xi_1}{\xi_1}\right)(\mu + \xi_2 + \gamma) < 0.$$

There exist $\varepsilon > 0$ such that

$$\beta S_v - \left(\frac{\mu + \xi_1 - \varepsilon}{\xi_1}\right)(\mu + \xi_2 + \gamma) < 0.$$

Now let $U(t)$ and $V(t)$ be the stochastic processes as in equation (11), with

$$a = \frac{\mu + \xi_1 - \varepsilon}{\xi_1}.$$

Then from equation (12) we obtain:

$$\Gamma \leq -(\mu + v\theta)q_0 + Q_1 q_1 + Q_2 q_2. \tag{13}$$

From inequality (13), the coefficient of q_2 is negative, and by the choice of a, the coefficient of q_1 is negative. From Corollary 4.5 we have

$$q_0 + q_1 + aq_2 \geq 1.$$

Therefore the limits q_i cannot all be zero. Since at least one of the q_i is non-zero, it follows that $\Gamma < 0$ and the theorem is proved. □

5. NUMERICAL SIMULATION

There is a rapidly increasing number of papers on compartmental modeling of population dynamics of COVID-19. Consequently, it is possible to obtain or deduce numerical values for most of the parameters in model (1) and model (8). At this relatively early stage with respect to vaccination, we can only experiment with different values of v and θ since there has not been the opportunity to collect population data on vaccine roll-out and its results, at least not in South Africa, where the vaccination process started relatively late. Otherwise, we shall deduce numerical values for the parameters of our model from the existing literature. This will enable us to present a number of explorative sample simulations. We list these numerical values and the sources in the Table (1) below. In the paper [4] the effective contact rate β is estimated as ranging between 0.002-0.75. Of course, β depends on human behaviour and living conditions, and therefore it varies from dramatically between populations. Even in a given population, β may vary over time, due to variation in lock-down conditions. In our simulations, we take the value of β a little bit higher. In South Africa, the first case of COVID-19 was confirmed in March 05 2020. Later in March 19 2020, the country had 150 COVID-19 confirmed cases [4]. In May 01 2021, South Africa has reached 1581210 cases of COVID-19, 54350 deaths and 1505620 recovered. This means that the number of active cases was just the difference, which is 21240. We take K to be 58.56 millions as the total population in South Africa [20].
The initial values for our simulations will be taken as:

$$I_0 = 0.02124 \text{ million } \ R_0 = 1.5 \text{ million}$$

Thus, we can technically search the initial values for S and E using a routine method which entails finding the equilibrium point of the model (1), and then to split the current total between these classes. This consideration leads us to assign initial values to S_0 and E_0, and thus our initial state for these two initial values are taken as:

$$S_0 = 51.36 \text{ million}, \ \ E_0 = 5.12 \text{ million} .$$

TABLE 1. Description of parameters and their estimate values

Parameter	Description	Numerical value	Reference/comment
μ	Birth and mortality rates by natural causes	$\frac{1}{365\times 64.6}$ per day	[20]
γ	COVID-19 induced mortality rate	0.09 per day	cf. [21]
K	Population size when disease-free	58.56 million	[20]
μK	Recruitment rate of the susceptibles	0.00248 million per day	[20]
ξ_1	Progression rate from E to I	0.000712 per day	Estimate
ξ_2	Progression rate from I to R	$0.08(0.01, 0.5)$ per day	[12]
θ	Vaccine efficacy	$\theta = 100\%, 80\%, 70\%$	Estimate
δ	Rate of transfer from R to S due to immunity loss	0.0001 per day	Estimate
v	Proportion of susceptible vaccinated	0.0005 per day	Estimate

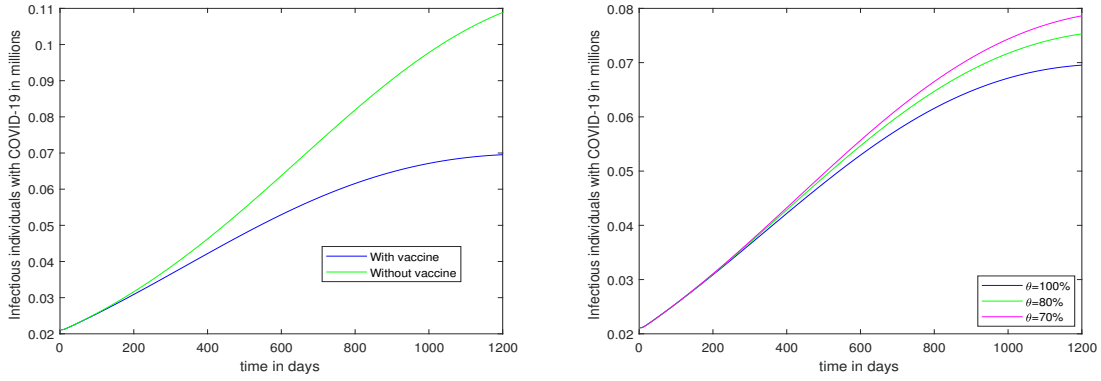


FIGURE 1. Trajectory of I-class for COVID-19 deterministic model

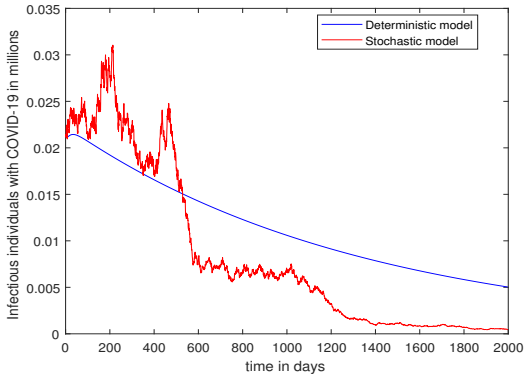


FIGURE 2. Exploring Theorem (4.6) with small values for σ_i. (a small value)

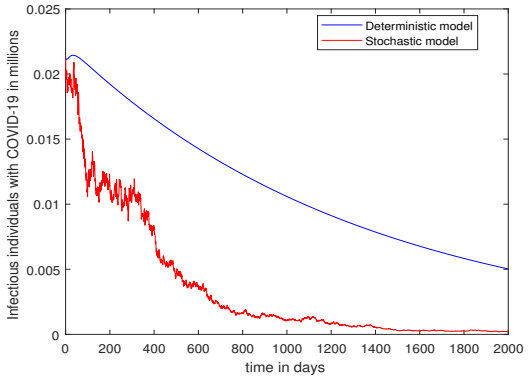


FIGURE 3. Exploring Theorem (4.6) with bigger values for the σ_i.

In Figure $1(a)$, we assume a highly effective vaccine, that is $\theta = 100\%$, $\beta = 0.8189$ and we plot the I-class with $v = 0.0005$ (the line in blue) and on the other when there is no vaccine at all (see the line in green). The basic reproduction number $\mathscr{R}$ is found to be $\mathscr{R} = 4.56$ for $v = 0$, and $\mathscr{R} = 1.0076$ for $v = 0.0005$. We observe in these simulations how a highly effective vaccine has the potential to reduce the number of infected cases.

In Figure 1 (b), we show a different case scenario of the force of vaccine coverage, for instance, 100%, 80% and 70%. In the following figures we extend the time period to investigate the long term behavior of the stochastic model. In Figure 2, we choose $v = 0.005$, $\sigma_0 = 0.01, \sigma_1 = 0.02, \sigma_2 = 0.01$ and $\sigma_3 = 0.01$. In this case, there does not seem to be a strong convergence of the stochastic model to the disease-free equilibrium. In Figure 3 for $\sigma_0 = 0.02, \sigma_1 = 0.03, \sigma_2 = 0.04, \sigma_3 = 0.02$. It is noticed that increasing stochastic perturbations leads to a strong convergence of the stochastic model to the disease-free equilibrium of the underlying deterministic model.

6. CONCLUSION

In this research we present a stochastic model for COVID-19 with a highly effective vaccine measured by θ. However, immunity wanes with time or some variants of COVID-19 may be able to evade the protection provided by a vaccine. Therefore vaccinated individuals may be exposed to some extent to the virus. Starting off with a deterministic compartmental model, we proved global stability of the disease-free equilibrium. In the stochastic version, we study almost exponential stability theorem. We use the Euler-Maruyama scheme to run our numeral simulations with data applicable to South Africa. Our results show that a highly effective vaccine has the potential to reduce the number of infected cases as observed in Figure $1(a)$ and (b). Thus, the number of new cases will continue to grow if a highly effective vaccine is not made available in the long run as observed in the simulations.

Theorem 4.6 discusses extinction of the disease in the stochastic model. Our simulations suggest that there might be extinction almost surely, even if $\mathscr{R}$ is increased slightly above unity. In other words, it may be possible to prove a slightly stronger extinction theorem, such as for instance in [23] and other articles cited therein.

The model can be extended to allow the direct inflow and outflow rates of COVID-19 cases into the system. Stochastic stability in the mean or other stability results, for the case of the endemic equilibrium, is another interesting theme for future investigation.

DISCLOSURE

This research did not require or request any funding, and no funding was received.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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