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THE IMPACT OF LÉVY JUMPS AND WHITE NOISE ON THE DYNAMICS OF A COVID-19 EPIDEMIC MODEL: A CASE STUDY OF THE KINGDOM OF SAUDI ARABIA

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Abstract. Recently, the pandemic of Covid-19 attacked many countries, and many public establishments were closed because of this pandemic. As well, the Covid-19 pandemic hurt the economy and various activities of countries around the world. Mathematical Modeling and numerical analysis can help governments to find solutions for controlling the propagation of the Covid-19 pandemic. In the present paper, we consider a stochastic Lévy jumps epidemic model that models the propagation of Covid-19 in a population divided into six groups of individuals. We investigate the extinction and persistence of our stochastic systems with and without Lévy jumps. Furthermore, we give a detailed numerical comparison of disease for the stochastic and deterministic systems.

Keywords: Covid-19 epidemic; randomness; Lévy jumps; numerical scheme.

2010 AMS Subject Classification: 92D30, 47H05.

1. INTRODUCTION

The first positive case infected by the Covid-19 epidemic was initially detected in December 2019 in China, precisely in Wuhan. Then, the case of infections has been fast-growing since

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the onset of the epidemic. As of 2 November, 2021, (WHO, [20]) situation report shows there are 246, 594, 191 and 4, 998, 784 official reported cases and deaths, respectively. According to this situation report, the Covid-19 situation has been worse in some nations like the United States, Italy, India. More than 40 case reports and deaths have occurred from these countries. Although China was the first zone to be hit by COVID-19, it is now well placed in tackling the disease. The cumulative case report of China (126,078) is about 362 times less than the USA report (45,635,708), 272 times less than the India report (34,285,814), 173 times less than the Brazil report (21,804,094).

WHO considers safe and effective vaccines can represent tools to control the propagation of Covid-19 epidemic (for more detail, see, [21]). For this reason, several research teams jumped to the challenge and created vaccinations that protect against SARS-CoV-2 in less than a 5 year after the epidemic began. As of June 3, 2021, AstraZeneca/Oxford vaccine, Johnson and Johnson, Moderna, Pfizer/BionTech, Sinopharm, and Sinovac are vaccinations against COVID-19 and have met the WHO's safety and efficacy standards (see, [21]). However, making these vaccines available to people around the world remains a challenge for the globe. Limited access to vaccines in low and middle-income nations, particularly in Africa, where HIV is most prevalent, can be regarded as an indicator for the challenge in vaccine distribution.

With all efforts made by the policymakers to control the impact of COVID-19 disease transmission. Human behavior represents the principal point to fight the epidemic of Covid-19 via compliance with health measures and wearing masks. WHO (Organization et al., [23]) recognizes the value of human behavior in managing pandemics. Margraf et al. [22] and Lin & Chen [24] recommend that to considerably reduce the disease's impact, governments should engage in behavior modification at the societal, community, and individual levels.

COVID-19 disease propagation rules and predictions necessitate theoretical, quantitative, and simulation investigation. The investigation is inextricably linked to a mathematical model developed for infectious diseases. Mathematical models have been very beneficial in providing various reasons for the dynamics of disease and designing practical controlling strategies. Many mathematical models have been proposed according to the specificity of each region. Hence, the different mathematical approaches are used to propose models that describe more realistically the propagation of Covid-19. For example, Arfan et al. in [1], to describe the effect of memory on the propagation of Covid-19 in Pakistan, proposed an epidemic model that divided the population into six classes and under the Atangana-Baleanu Caputo derivative [3]. Atangana and Araz [2], presented an epidemic model of Covid-19 for South Africa and Turkey. They showed a detailed analysis of the proposed model with the application to real data of South Africa and Turkey Covid-19. In [4], the authors formulated an epidemic SEIQR model of COVID-19 and proved a numerical investigation with the real data of the propagation Covid-19 in Pakistan. Gu et al. [5], modeled the propagation of the Covid-19 epidemic with a model of ordinary differential equations with six groups of the population including the isolation individuals. They proved a theoretical and numerical analysis of their proposed model. Also, they studied the sensitivity of model parameters. Other authors have used the stochastic approach to express the effect of environmental fluctuation on the transmission of Covid-19 in the population. We cite, for example, the work of Zhang [6] in which the authors affected a direct perturbation on the transmission rate of disease to study the effect of white noise on the transmission of Covid-19 in a population composed of four classes (Susceptible-Infected-Recovered). Rihan et al. [7], presented a stochastic epidemic model with general perturbation proportional to the variables, including a retard parameter that describes the incubation period of the viral infection (For more detail, see, [8]). The remains of this paper are organized as follows. In Section 2, we present a deterministic model of Covid-19 epidemic and its parameters. Our stochastic model is studied numerically and presented in Section 3. We close the paper by conclusion and future recherche direction in Section 4.

2. DETERMINISTIC MODEL

In the following, we consider a mathematic deterministic epidemic model that describes the transmission of the Covid-19 pandemic proposed by Li et al. in [9] and divide the population into six groups, namely, Susceptible individuals (S), Exposed individuals (E), Symptomatic individuals (I), Asymptomatic individuals (A), super-spreader individuals (P), Recovered individuals (R). $N(t)$ is the total population number such as

$$N(t) \quad = \quad S(t)+I(t)+E(t)+A(t)+P(t)+R(t).$$

The model is presented by the differential equations system follow:

$$(1) \qquad \begin{cases} \frac{dS(t)}{dt} = \Lambda - \beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} - \beta_2 \frac{P(t)S(t)}{N(t)} - \mu S(t), \\ \\ \frac{dE(t)}{dt} = \beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} + \beta_2 \frac{P(t)S(t)}{N(t)} - (\theta+\mu)E(t), \\ \\ \frac{dI(t)}{dt} = \theta\omega_1 E(t) - (\tau_1+\mu+\zeta_1)I(t), \\ \\ \frac{dP(t)}{dt} = \theta\omega_2 E(t) - (\tau_2+\mu+\zeta_2)P(t), \\ \\ \frac{dA(t)}{dt} = \theta(1-\omega_1-\omega_2)E(t) - (\tau_3+\mu)A(t), \\ \\ \frac{dR(t)}{dt} = \tau_3 A(t) + \tau_2 P(t) - \tau_1 I(t) - \mu R(t), \end{cases}$$

with:

$$S(0) = S_0 \geq 0, I(0) = I_0 \geq 0, E(0) = E_0 \geq 0, A(0) = A_0 \geq 0,$$
$$P(0) = P_0 \geq 0, R(0) = R_0 \geq 0,$$

where $S(t)$, $E(t)$, $I(t)$, $P(t)$, $A(t)$, $R(t)$ represent the density of Susceptible individuals, Exposed individuals, Symptomatic individuals Super-spreader individuals, Asymptomatic individuals and Recovered individuals from the disease at time t, respectively. The parameter of model (1) are all positive and have the following meanings:

- Λ is the recruitment rate.
- μ represents the natural mortality rate for all groups of population.
- β_1 denotes the disease transmission rates of symptomatic and asymptomatic COVID-19 individuals.
- β_2 is the disease transmission rate of super-spreader individuals

- Ψ_1 represents the proximate infectiousness rate corresponding $A(t)$.
- The parameter θ represent the incubation period.
- A fraction ω_1 of exposed individuals develop the disease signs(or symptoms) and thus join symptomatic compartment and a fractional ω_2 (with or without disease signs) join the superspreader class while the remaining with no or mild disease signs move to the asymptomatic class $A(t)$ [9].
- The parameters τ_1, τ_2 and τ_3 are the recovery rates for the class of symptomatic, super-spreader, and asymptomatic infected individuals, respectively.
- ζ_1 is the mortality rate due to Covid-19 in the symptomatic individuals.
- ζ_2 is the mortality rate due to Covid-19 in the super-spreader individuals.

The theoretical results of (1) are discussed in [9] by the following details. The region (or the biologically feasible region)

$$\Delta = \left\{(S(t),E(t),I(t),P(t),A(t),R(t)) \in \mathbb{R}^6_+ : S(t)+E(t)+I(t)+P(t)+A(t)+R(t) \le \frac{\Lambda}{\mu}\right\}.$$

is positive invariant set for model (1). The basic reproduction number of system (1) is defined by

$$\mathscr{R}_0 = \frac{\theta\left[\omega_1(\tau_3+\mu)+\psi_1(\tau_1+\mu+\zeta_1)(1-\omega_1-\omega_2)\right]\beta_1}{(\theta+\mu)(\tau_1+\mu+\zeta_1)(\tau_3+\mu)} + \frac{\theta\omega_2\beta_2}{(\theta+\mu)(\tau_2+\mu+\zeta_2)}$$

They are obtained by the use of the next generation matrix approach [25], namely, the basic reproduction number is provided by the largest eigenvalue of FV^{-1} with F and V are the required Jacobian matrices obtained from (1) as follows

$$F = \begin{pmatrix} 0 & \beta_1 & \beta_2 & \psi_1\beta_1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \theta+\mu & 0 & 0 & 0 \\ -\theta\omega_1 & \tau_1+\mu+\zeta_1 & 0 & 0 \\ -\theta\omega_2 & 0 & \tau_2+\mu+\zeta_2 & 0 \\ -\theta(1-\omega_1-\omega_2) & 0 & 0 & \tau_3+\mu \end{pmatrix}$$

In epidemiology, the basic reproduction number is very significant for a deterministic system because it makes it possible to determine the comportment of the system ie if $\mathscr{R}_0$ is less than one the disease disappears from the population if not if $\mathscr{R}_0$ is greater than one the disease prevails in population.

3. STOCHASTIC MODELS AND NUMERICAL INVESTIGATION

3.1. Stochastic models. In reality, biological systems are usually perturbed by environmental noises (see, [10–15]). El Koufi et al. in [10] have affirmed that environment fluctuation conduct to the system to fluctuate around a means value, and they expressed the stochastic effect by the direct perturbation of the disease transmission coefficient by the white noise. Hence, many woks have studied the effect of the stochastic perturbation on deterministic models to know how the power of environmental fluctuation on the dynamics of biologic systems. In this paper, we firstly suppose that the stochastic perturbation is proportional to the variables $S(t)$, $E(t)$, $I(t)$, $P(t)$, $A(t)$ and $R(t)$. And it's of the white noise type. Then, the stochastic Covid-19 epidemic model corresponding to the deterministic one (1) is presented by the following stochastic differential equations system

$$(2)\quad \begin{cases} dS(t) = \left[\Lambda - \beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} - \beta_2 \frac{P(t)S(t)}{N(t)} - \mu S(t)\right] dt + \sigma_1 S(t) d\mathscr{B}_1(t), \\ dE(t) = \left[\beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} + \beta_2 \frac{P(t)S(t)}{N(t)} - (\theta+\mu)E(t)\right] dt + \sigma_2 E(t) d\mathscr{B}_2(t), \\ dI(t) = [\theta\omega_1 E(t) - (\tau_1+\mu+\zeta_1)I(t)]\, dt + \sigma_3 I(t) d\mathscr{B}_3(t), \\ dP(t) = [\theta\omega_2 E(t) - (\tau_2+\mu+\zeta_2)P(t)]\, dt + \sigma_4 P(t) d\mathscr{B}_4(t), \\ dA(t) = [\theta(1-\omega_1-\omega_2)E(t) - (\tau_3+\mu)A(t)]\, dt + \sigma_5 A(t) d\mathscr{B}_5(t), \\ dR(t) = [\tau_3 A(t) + \tau_2 P(t) - \tau_1 I(t) - \mu R(t)]\, dt + \sigma_6 R(t) d\mathscr{B}_6(t), \end{cases}$$

where $\mathscr{B}_i(t)$, $(i = 1,2,3,4,5,6)$ are a standard Brownian motions (see definition) defined on a complete probability space $(\Omega, \mathscr{F}, \{\mathscr{F}_t\}_{t\geq 0}, \mathbb{P})$ with a filtration $\{\mathscr{F}_t\}_{t\geq 0}$ satisfying the usual conditions (i.e. it is increasing and right continuous while $\mathscr{F}_0$ contains all $\mathbb{P}$-null sets), σ_i, $(i = 1,2,3,4,5,6)$ are the noises intensities.

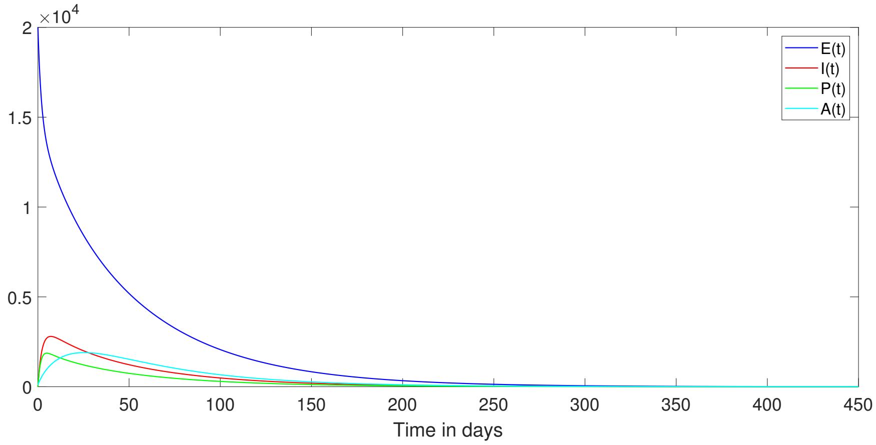

Figure 1. Paths of the deterministic systems (1).

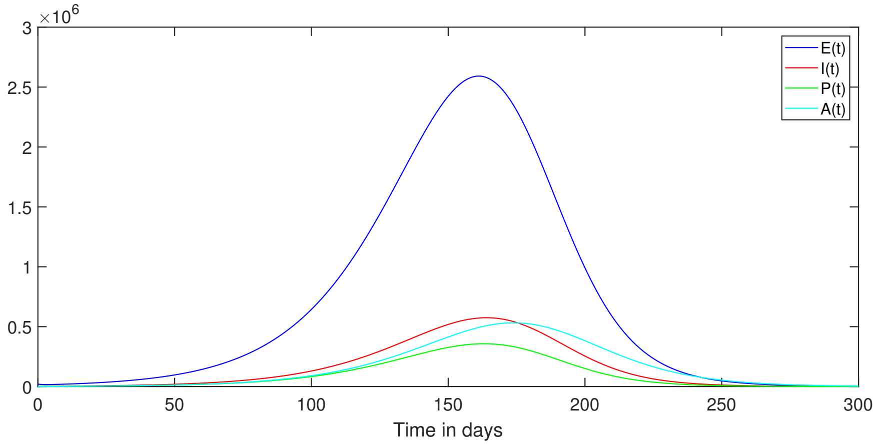

Figure 2. Paths of the deterministic systems (1).

Definition 3.1. *[16] The positive real-time numbers process $(\mathscr{B}(t))_{t\geq 0}$ is called the Wiener process if*

(1) $\mathscr{B}(0) = 0$, $\mathbb{P} - a.s.$

(2) $\forall\, 0 \leq s < t$, $\mathscr{B}(t) - \mathscr{B}(s)$ *are independent of* $\mathscr{F}_s$.

(3) $\forall\, 0 \leq s < t$, $\mathscr{B}(t) - \mathscr{B}(s) \backsim \mathscr{N}(0, t-s)$.

Brownian motion is a valuable tool for describing random motion for continuous systems. In addition, they have many good statistical properties, namely, the trajectory of the brownie motion is continuous, finite moments. Also, large theoretical literature that existent to use for solving the Brownian motion-related problems.

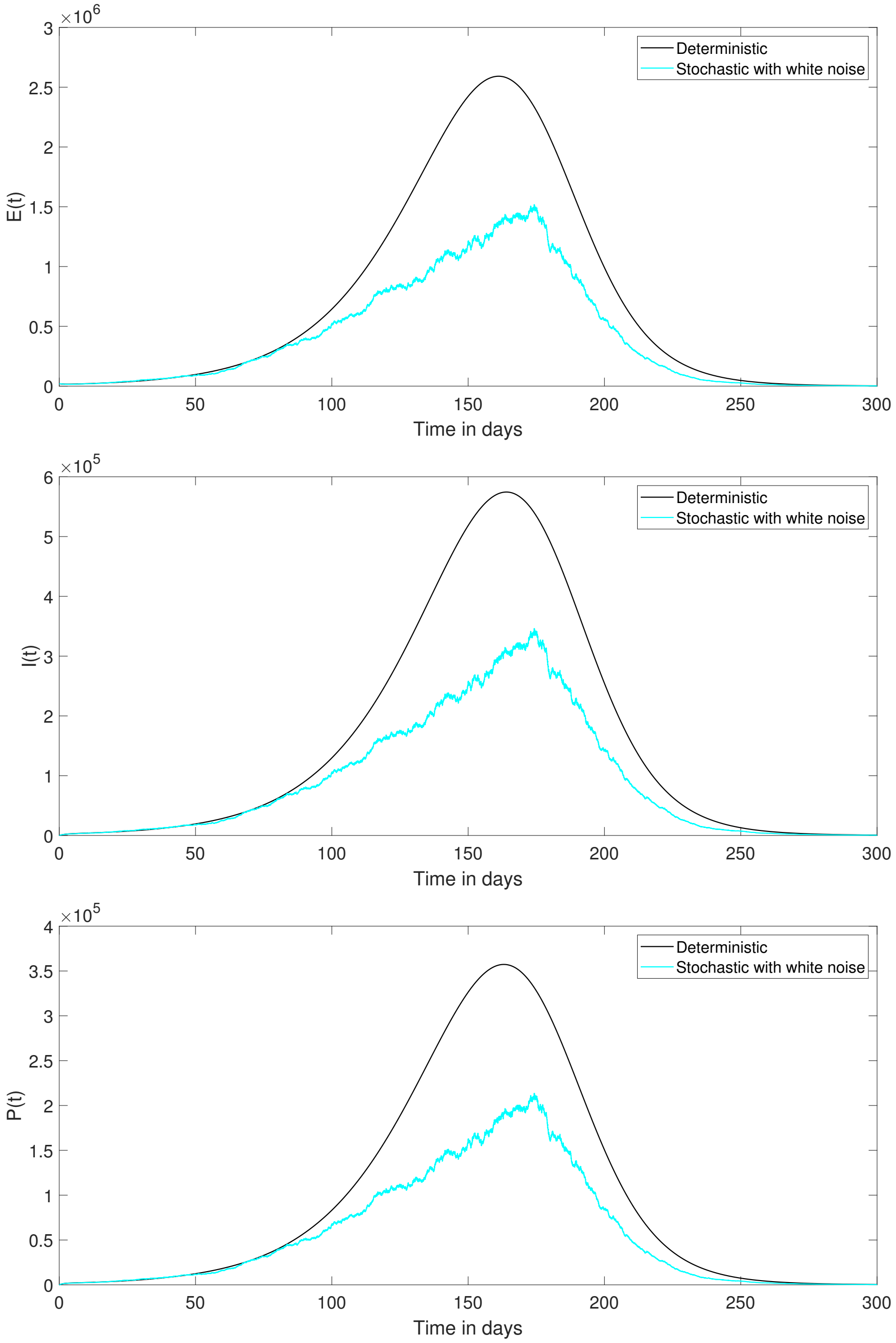

Figure 3. Comparison between the paths of stochastic (2) and deterministic (1) systems.

On the other hand, as you know, the solution of the stochastic system with white noise is continuous, though, in a biological environment, the populations are always subject to some massive and severe phenomena like volcanoes, tsunamis, earthquakes, and famines. These events can make break the continuity of the solution. Also, we use the stochastic differential equations with Lévy jumps to will describe these events. Thus, to express a stochastic system with Lévy jumps, we need to use the discontinuous Lévy jump process. A Lévy jump process represents a stochastic process with stationary and independent increments. Mathematically, it's divided into the sum of three terms [11] that are: linear drift process, Brownian motion, compensated Poisson process. Motivated by the above discussion in the present paper we propose the following stochastic model with Lévy jumps process for the Covid-19 epidemic:

$$
\begin{cases}
dS(t) = \left[\Lambda - \beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} - \beta_2 \frac{P(t)S(t)}{N(t)} - \mu S(t)\right] dt + \sigma_1 S(t) d\mathscr{B}_1(t) \\
\qquad + \int_{\mathbb{H}} \eta_1(k) S(t-) \tilde{N}(dt,dk), \\
dE(t) = \left[\beta_1 \frac{(I(t)+\Psi_1 A(t))S(t)}{N(t)} + \beta_2 \frac{P(t)S(t)}{N(t)} - (\theta+\mu)E(t)\right] dt + \sigma_2 E(t) d\mathscr{B}_2(t) \\
\qquad + \int_{\mathbb{H}} \eta_2(k) E(t-) \tilde{N}(dt,dk), \\
dI(t) = [\theta\omega_1 E(t) - (\tau_1+\mu+\zeta_1)I(t)] dt + \sigma_3 I(t) d\mathscr{B}_3(t) + \int_{\mathbb{H}} \eta_3(k) I(t-) \tilde{N}(dt,dk), \\
dP(t) = [\theta\omega_2 E(t) - (\tau_2+\mu+\zeta_2)P(t)] dt + \sigma_4 P(t) d\mathscr{B}_4(t) + \int_{\mathbb{H}} \eta_4(k) P(t-) \tilde{N}(dt,dk), \\
dA(t) = [\theta(1-\omega_1-\omega_2)E(t) - (\tau_3+\mu)A(t)] dt + \sigma_5 A(t) d\mathscr{B}_5(t) \\
\qquad + \int_{\mathbb{H}} \eta_5(k) A(t-) \tilde{N}(dt,dk), \\
dR(t) = [\tau_3 A(t) + \tau_2 P(t) - \tau_1 I(t) - \mu R(t)] dt + \sigma_6 R(t) d\mathscr{B}_6(t) + \int_{\mathbb{H}} \eta_6(k) R(t-) \tilde{N}(dt,dk),
\end{cases}
\tag{3}
$$

where $S(t-)$, $E(t-)$, $I(t-)$, $P(t-)$, $A(t-)$ and $R(t-)$ are the left limit of $S(t)$, $E(t)$, $I(t)$, $P(t)$, $A(t)$ and $R(t-)$, respectively. $\tilde{N}(dt,dk) = N(dt,dk) - \nu(k)dt$, N is a Poisson counting measure with characteristic measure ν on measurable subset $\mathbb{H}$ of $[0,\infty)$, with $\nu(\mathbb{H}) < \infty$, and

$\eta_i : \mathbb{H} \times \Omega \longrightarrow \mathbb{R}$ $(i = 1,2,3,4,5,6)$ represents the effects of random jumps it's bounded and continuous with respect to ν and $\mathfrak{B}(\mathbb{H}) \times \mathscr{F}_t$-measurable.

Theorem 3.1. *[16] For any initial value* $(S(0),E(0),I(0),P(0),A(0),R(0)) \in \mathbb{R}^6_+$*, there is a unique solution* $(S(t),E(t),I(t),P(t),A(t),R(t))$ *to Equation* (2) *on* $t \geq 0$ *and the solution will remain in* $\mathbb{R}^6_+$ *with probability one, namely* $(S(t),E(t),I(t),P(t),A(t),R(t)) \in \mathbb{R}^6_+$ *for all* $t \geq 0$ *almost surely (briefly a.s.).*

We can prove the above theorem by the same method of Theorem 2.1. presented in [11]. In the following section, we will present numerical simulations for the models (1), (2) and (3) to demonstrate the effect of white and Lévy noises on the dynamics of the Covid-19 epidemic in the Kingdom of Saudi Arabia.

4. NUMERICAL INVESTIGATION

The stochastic models with white noise and Lévy jumps are used to analyze the cases infected by Covid-19 reported in the Kingdom of Saudi Arabia from the start of the pandemic. Then, to show the numerical simulation of systems (1), (2) and (3) we use the Euler scheme presented in [17]. The initial conditions are presented as follows: $S(0) = 34806870$, $E(0) = 20000$, $I(0) = 2$, $P(0) = 100$, $A(0) = R(0) = 0$. We consider the parameters registered in the Kingdom of Saudi Arabia (KSA) since the start of the pandemic of Covid-19. According to [9], the total population size is 35694557, and the value of the parameters Λ is 1254.9 per day under the hypothesis that the current total population of KSA is susceptible to infection. The average lifespan in years in the Kingdom of Saudi Arabia is 74.7, then, the natural mortality rate is reported by $\mu = (74.7 * 365)^{-1}$. Also, we present the rest of the parameters in Table 1.

Therefore, by simple computation, we can obtain that $\mathscr{R}_0 = 1.3965$, then the disease will persist in the population for the deterministic model (1) (see, Figure 2). If we arrive to decrease the rate of transmission of the disease β_1 and the transmission of disease rate β_2 due to (P), we find that the basic reproduction number will be less than one. For example, for $\beta_1 = 0.3030$ and $\beta_2 = 0.4242$ we find exactly $\mathscr{R}_0 = 0.8308 < 1$. Hence, the disease will die out in the population for the deterministic model (1) Figure 1. confirms this remark. In addition, we conclude that the coefficients β_1 and β_2 can likewise decrease if we reduce the contact between the infected individuals and the other groups of the population.

On the other hand, we keep the same parameter values grouped in Table 1 (the case where $\mathscr{R}_0 = 1.3965$), and to study the effect of environmental fluctuation on the dynamics of Covid-19, we choose the white noise values in model (2) as: $\sigma_1 = 0.03$, $\sigma_2 = 0.03$, $\sigma_3 = 0.03$, $\sigma_4 = 0.03$, $\sigma_5 = 0.03$ and $\sigma_6 = 0.03$. We note that the addition of the white noise terms to the systems (1) leads to reduce the cases of infected individuals, Figure 3 validate this result. Next, we compare the trajectory of the solution of systems (1) and (2) using different noises values such as:

Case 1.: $\sigma_1 = 0, \sigma_2 = 0, \sigma_3 = 0, \sigma_4 = 0, \sigma_5 = 0, \sigma_6 = 0.$

Case 2.: $\sigma_1 = 0.03, \sigma_2 = 0.03, \sigma_3 = 0.03, \sigma_4 = 0.03, \sigma_5 = 0.03, \sigma_6 = 0.03.$

Case 3.: $\sigma_1 = 0.05, \sigma_2 = 0.05, \sigma_3 = 0.05, \sigma_4 = 0.05, \sigma_5 = 0.05, \sigma_6 = 0.05.$

So, in the above cases, we observe in Figure 4 that when the value of white noise intensity increases, the number of infected individuals with Covid-19 decreases. Similarly, in the case where ($\mathscr{R}_0 = 0.8308 < 1$), we see that the disease tends more quickly to extinction in the stochastic system (2) (see, Figure 5) and when the noise value increases (see, Figure 6). Consequently, the large values of the white noise parameters lead to controlling the propagation of the epidemic.

Therefore, in order to compare the spread of the epidemic in the three system (deterministic (1), stochastic with white noise (2) and Stochastic with jumps (3), we keep the same parameter values grouped in Table 1, we choose $\mathbb{E} = (0,1)$, $\nu(k) = 0.5$, and the Lévy noise parameters $\eta_1 = 0.01$, $\eta_2 = 0.01$, $\eta_3 = 0.01$, $\eta_4 = 0.01$, $\eta_5 = 0.01$, $\eta_6 = 0.01$. So, the result of the computer running presented in Figure 7 shows that the environmental noises conduct to control the spread of diseases.

Table 1. Values of the parameters used in the simulation.

Parameter	Value	Source
Λ	14	Estimated
μ	1/(74.87*365)	[18]
Ψ_1	0.1001	Fitted
β_1	0.5030	Fitted
β_2	0.7242	Fitted
θ	0.1600	Fitted
ω_1	0.4718	Fitted
ω_2	0.4430	Fitted
ζ_1	0.0124	Estimated
ζ_2	0.0100	Fitted
τ_1	0.3265	Fitted
τ_2	0.5030	Fitted
τ_3	0.0601	Fitted

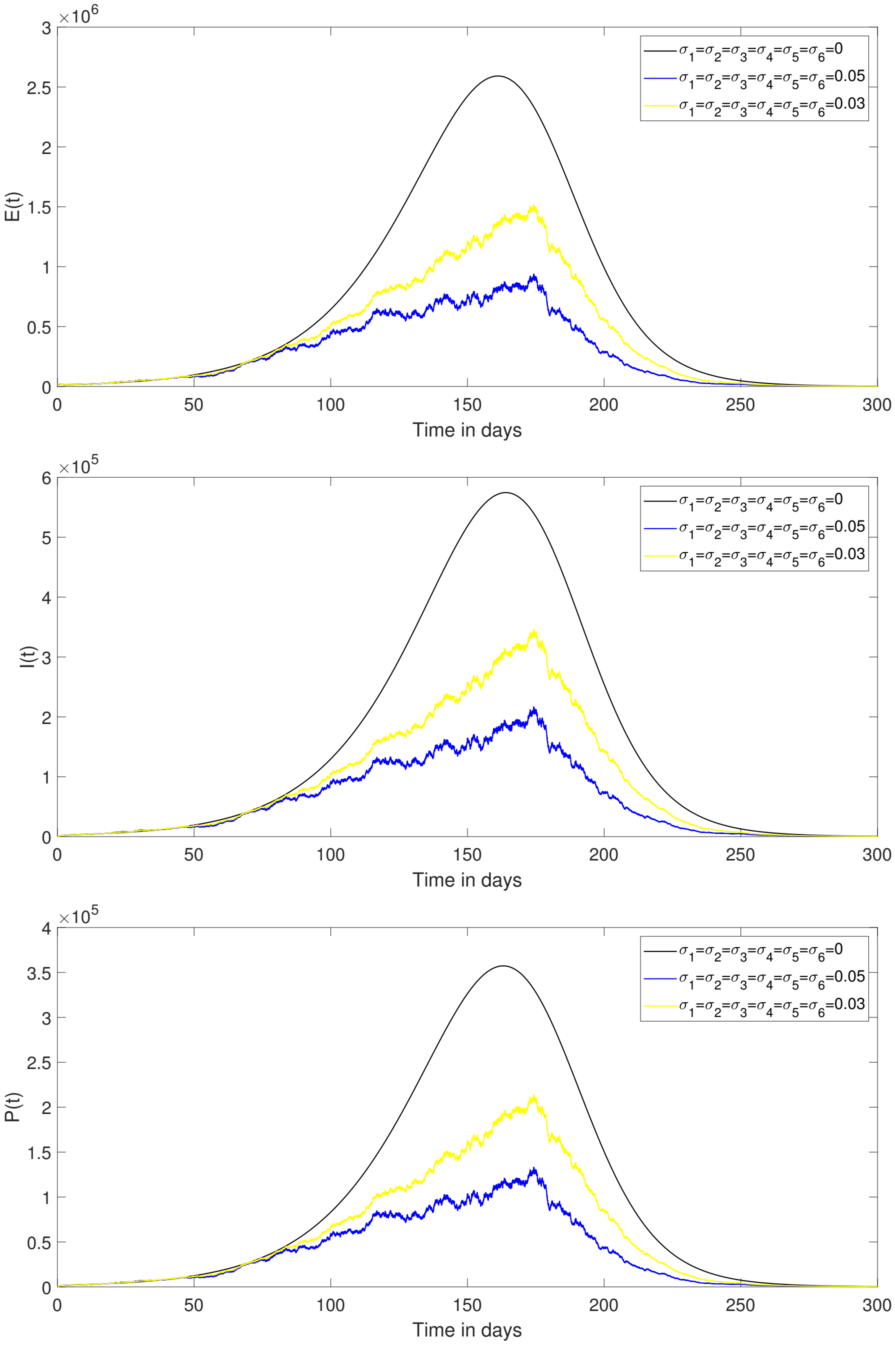

Figure 4. Comparison between the paths of stochastic (2) and deterministic (1) systems with different noise values.

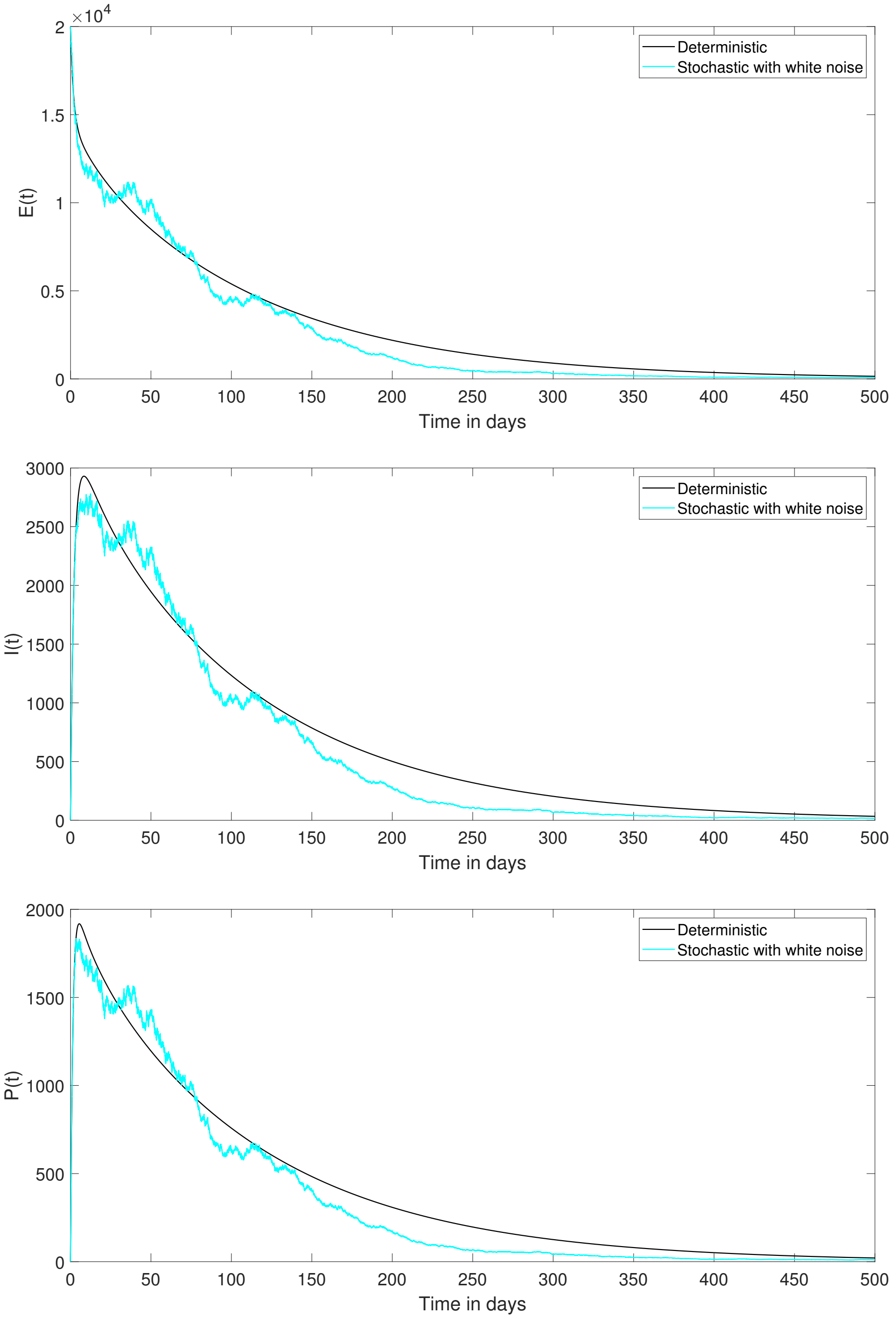

Figure 5. Comparison between the paths of stochastic (2) and deterministic (1) systems.

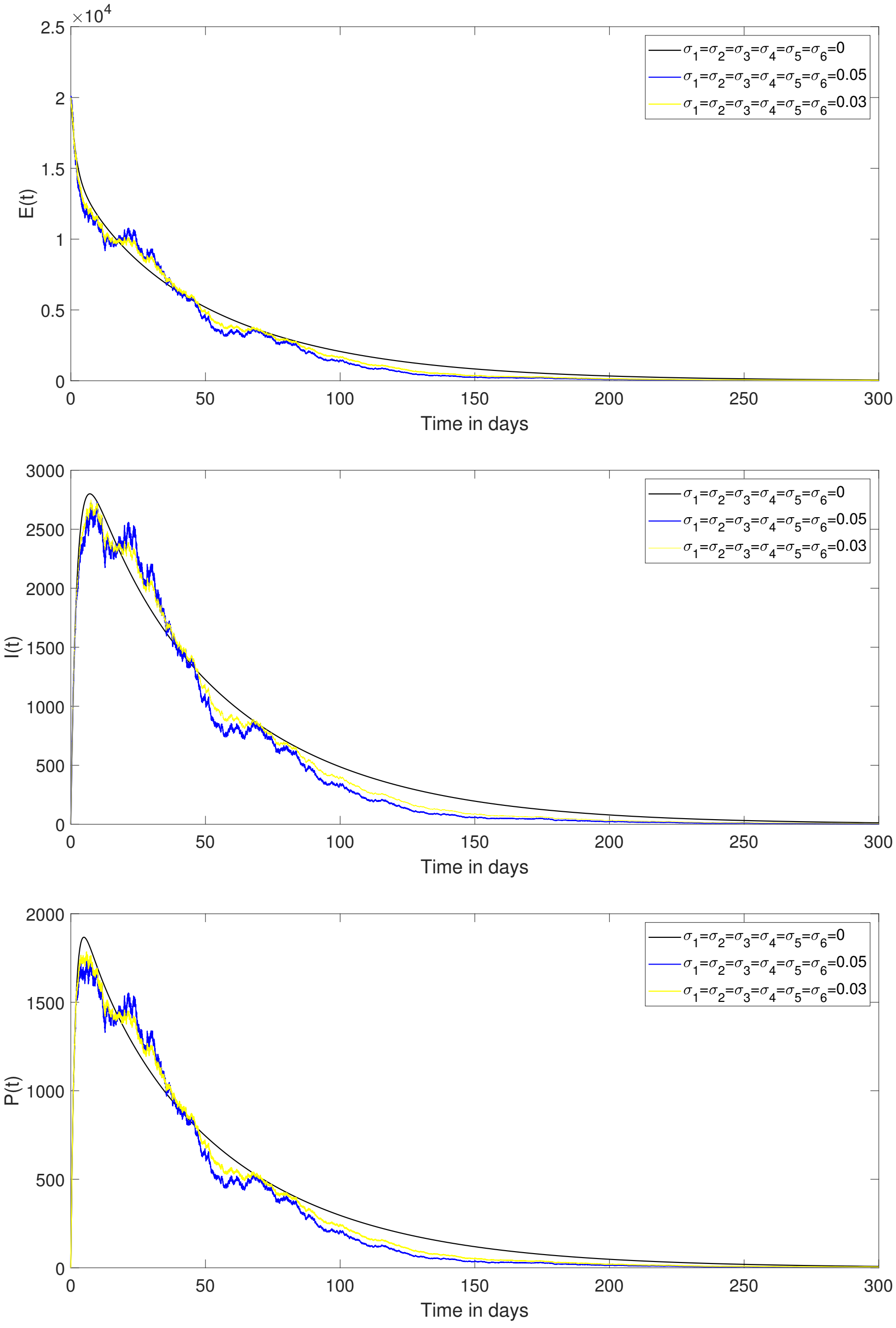

Figure 6. Comparison between the paths of stochastic (2) and deterministic (1) systems with different noise values..

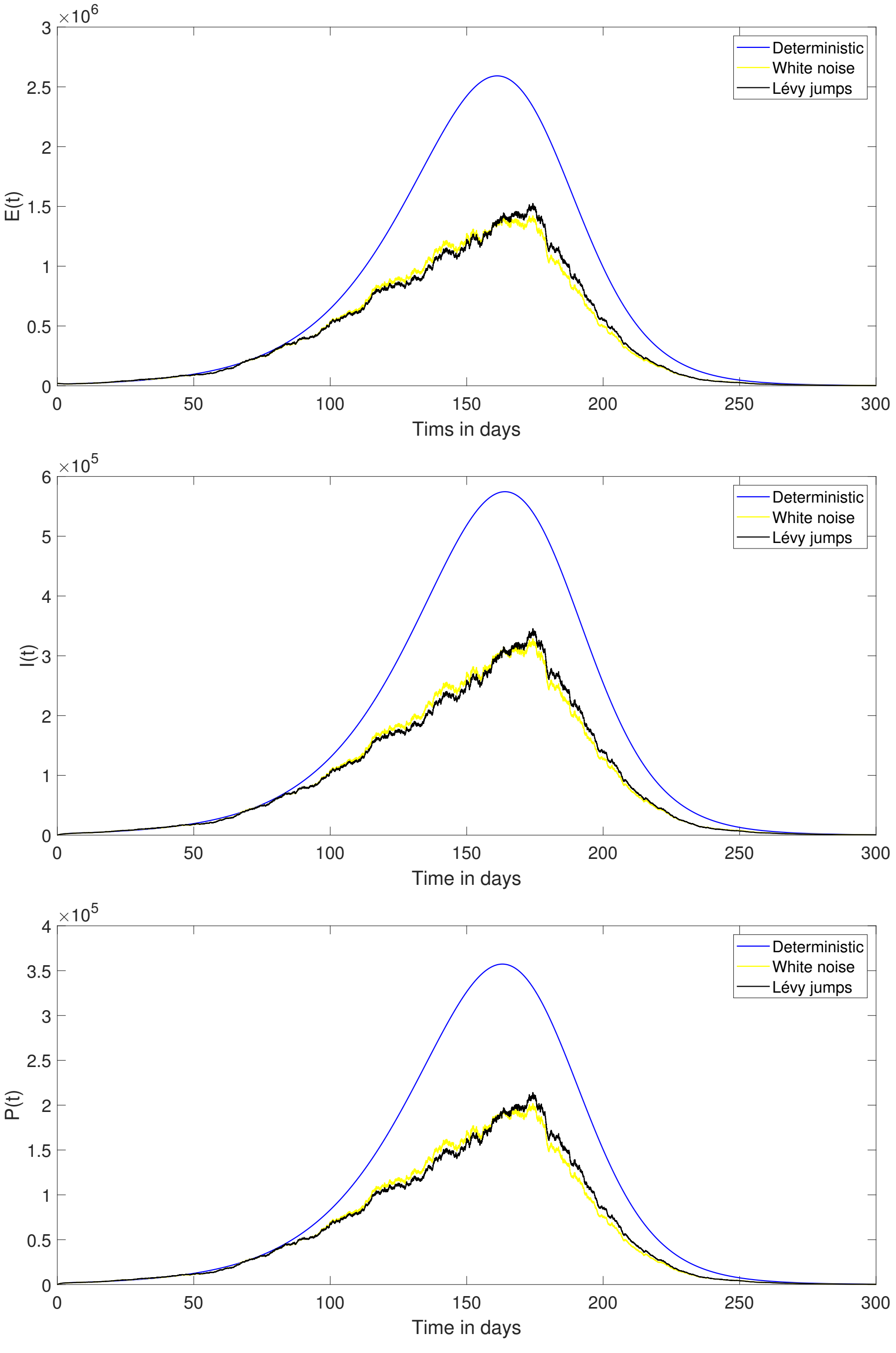

Figure 7. Comparison between the paths of stochastic with Lévy noise (3), stochastic with white noise (2) and deterministic (1) systems.

5. CONCLUSION

In this investigation, we proposed a stochastic differential equations system with and without Lévy jumps that models the dynamics of Covid-19, and we applied it to the Kingdom of Saudi Arabia case study. Our proposed model divides the population into six groups: susceptible, exposed, symptomatic individuals super-spreader, asymptomatic and recovered. We have impacted an environmental perturbation of white and Lévy noises types in the model (1) to examine the effect of environment fluctuation and the grave and massive events on the transmission of Covid-19. We have used the Euler scheme [17] to see the trajectory of the solution and give a comparison between the models (1), (2), and (3) in the function of noise value and the transmission rates. Then, we presented graphs (with, MATLAB 9.4) that show the power of randomness to reduce the number of infected individuals by the Covid-19 epidemic in the Kingdom of Saudi Arabia. In our future direction and to ameliorate the model (3), we will examine the effect of another environment noise named the Telegraphic or colored noise which represents the case where the transmission of Covid-19 in the population is affected by the diversity of environmental regimes.

CONFLICT OF INTERESTS

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

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