

Exploring the Impact of Jump Perturbations on Stochastic SIRS Dynamics

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Abstract: This study develops a comprehensive stochastic framework to examine the impact of Lévy perturbations on the dynamics of the SIRS (Susceptible-Infectious-Recovered-Susceptible) model. Initially, we established the existence and uniqueness of the solution, ensuring a solid foundation for our analysis. We identified the critical conditions for disease persistence, which are essential for evaluating the applicability of the model in real-world scenarios. Additionally, we determined the criteria for disease extinction. To support our theoretical findings, we conducted extensive computer simulations.

Keywords: Stochastic SIRS model, Lévy jumps, Persistence, Extinction, Lyapunov Function, Threshold.

1 Introduction

During the early 20th century, epidemiology underwent a significant transformation, driven by the groundbreaking contributions of eminent scientists such as Anderson Gray McKendrick and Janet Leigh. Their pioneering work introduced the concept of mathematical modeling, which has since evolved into an indispensable tool in the field. This mathematical modeling has profoundly impacted the management of outbreaks and epidemics, playing a pivotal role in guiding evidence-based public health interventions. Epidemiology has evolved significantly, owing to notable physicians such as Quinto Tiberio Angelerio, who demonstrated remarkable proficiency in managing the plague outbreak in Alghero, Sardinia, in 1582. However, the actual emergence of modern epidemiology as a formal scientific discipline occurred during the 19th century. Often referred to as the "father of modern epidemiology," John Snow made a meaningful breakthrough when he meticulously traced a devastating cholera outbreak in London to water contamination from the Broad Street pump. This groundbreaking investigation is the pivotal moment that laid the cornerstone for contemporary epidemiology, shaping it into the scientific field we recognize today. Epidemiology is a scientific discipline investigating epidemics, diseases, and various health-related conditions, including those unrelated to diseases. Its roots can be traced to ancient Greece, notably

through the influential work of Hippocrates of Kos, a renowned physician who made notable contributions by distinguishing between epidemic and endemic diseases. Epidemiology, in its broader scope, also encompasses the study of diseases affecting plants, domestic animals, and livestock. An epidemic is characterized by a significant and abnormal surge in the occurrence of a specific disease within a population, typically manifesting rapidly. Many factors influence the intricate disease transmission process [1–5], encompassing the infectious agent's characteristics and the host population's complex dynamics. Regarding the infectious agent, its inherent characteristics, such as its mode of transmission (e.g., respiratory droplets, direct contact), the duration of infectivity, and its responsiveness to medical interventions like treatments and vaccines, are crucial factors that determine its ability to spread among individuals. Equally important are the host population elements that influence the dynamics of an epidemic. Factors such as social interactions, demographics (e.g., age, gender), cultural practices, geographic distribution, and economic conditions are pivotal in determining a population's susceptibility and resilience in the face of the disease. Across the pages of recorded history, human civilization has wrestled with recurrent epidemics and pandemics. These outbreaks of infectious diseases have inflicted significant human suffering, societal upheaval, and economic turbulence. Given the formidable nature of

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these challenges, the precise prediction of outbreak progression becomes paramount to effectively mitigating their adverse impacts. Epidemiologic modeling is at the heart of this pursuit, a fundamental tool for comprehending the intricacies of disease transmission dynamics and formulating informed strategies for containment and prevention. Infectious diseases continue to exert substantial effects on communities worldwide, notwithstanding the era of modern medicine and advancements in medical science. These impacts extend to various facets, including public health, healthcare infrastructure, the economy, education, population dynamics, and international cooperation. The investigation of epidemic models holds considerable importance across multiple domains due to its numerous advantages. These benefits encompass enhanced comprehension and forecasting of epidemics, optimization of public health resource allocation, more effective planning of emergency responses, advancement of public health research, heightened public awareness, and the development of training programs in public health. This, in turn, facilitates informed public health decision-making, enhances epidemic readiness, and ultimately contributes to saving lives. This curious problem has attracted mathematicians since the 18th century. Kermack and McKendrick established the classical deterministic SIR model in 1927 [6], serving as a fundamental framework for analyzing epidemic dynamics within a closed population, categorizing individuals into three compartments: The SIR model, delineating individuals into susceptible S , infected I , and recovered R compartments, does not account for individuals who lose immunity post-recovery. To address this deficiency, an extended version known as the SIRS model has been introduced [7–12]. In the SIRS model, individuals who have previously recovered from an infection are susceptible to becoming infected again. Mathematically, this phenomenon is expressed as follows:

$$\begin{cases} \frac{dS_t}{dt} = [\rho(1 - S_t) + \eta R_t - \alpha S_t I_t], \\ \frac{dI_t}{dt} = [\alpha S_t I_t - (\rho + \lambda) I_t], \\ \frac{dR_t}{dt} = [\lambda I_t - (\rho + \eta) R_t]. \end{cases} \quad (1.1)$$

In this context, the parameter ρ represents the rate of births and deaths in the population, α signifies the infection coefficient, λ represents the recovery rate of infected individuals, and η characterizes the rate at which recovered individuals lose their immunity, transitioning back to a susceptible state. Later, many studies used the stochastic approach to treat these models [13, 14]. Adding Lévy perturbations to the SIRS model can enrich epidemiological modeling by better capturing the complexity of real epidemic phenomena, including stochastic variations and rare events that significantly impact disease dynamics. This can provide valuable

information for public health decision-making and epidemic management. The reader can refer to [15–19]. In this study, we examine a system modeled as a stochastic SIRS (Susceptible-Infectious-Recovered-Susceptible) model incorporating a jump perturbation:

$$\begin{cases} dS_t = [\rho(1 - S_t) + \eta R_t - \alpha S_t I_t] dt \\ \quad - \int_{\mathbb{D}} \zeta_v S_{(t-)} I_{(t-)} \widetilde{\mathcal{N}}(dt, dv), \\ dI_t = [\alpha S_t I_t - (\rho + \lambda) I_t] dt \\ \quad + \int_{\mathbb{D}} \zeta_v S_{(t-)} I_{(t-)} \widetilde{\mathcal{N}}(dt, dv), \\ dR_t = [\lambda I_t - (\rho + \eta) R_t] dt, \end{cases} \quad (1.2)$$

where, dt is Lebesgue measure, and $\widetilde{\mathcal{N}}(dt, dv)$ is the compensated Poisson measure, such that

$$\widetilde{\mathcal{N}}(dt, dv) = \mathcal{N}(dt, dv) - \pi(dv)dt.$$

In this context, $\mathcal{N}(dt, dv)$ denotes a Poisson counting measure, while π represents a Lévy measure defined on $\mathbb{D} \subset \mathbb{R}^+$. Additionally, the continuously differentiable function $\zeta(\cdot)$ characterizes the impact of random jumps within the population. It is essential to ensure that $-1 < \zeta_v < 1$ for every $v \in \mathbb{D}$. Additionally, $S_{(s-)}$ and $I_{(s-)}$ represent the left-hand limits of the functions S_s and I_s , respectively. Henceforth, we will refer to these limits as S_s and I_s for practicality. This work stems from the need to enhance traditional epidemiological models by incorporating Lévy perturbations, which account for sudden, random changes in disease dynamics. The research aims to understand better disease persistence and extinction by developing a more realistic stochastic SIRS model, leading to improved strategies for managing infectious diseases in unpredictable environments. The manuscript is organized systematically, beginning with Section 2, which discusses the positivity and existence of solutions for the system described in equation (1.2). In Section 3, we derive the necessary conditions for disease persistence. Section 4 delves into a detailed analysis of disease Extinction. Next, Section 5 presents a series of computer simulations to confirm the accuracy of the analytical results. Section 6 thoroughly analyzes the results and outlines potential directions. Finally, the paper concludes in Section 7 with a thorough discussion of our findings and possible avenues for future research.

2 Positivity and Existence

This section will explore the global existence and positivity within the SDE system (1.2).

Definition 1(Meyer Angle Bracket). Let $(M_t)_{t \geq 0}$ be a continuous local martingale. The Meyer's Angle-Bracket, or the predictable quadratic variation of M , denoted by

$\langle M \rangle_t$, is a unique increasing predictable process such that $M_t^2 - \langle M \rangle_t$ is a local martingale.

Lemma 1. Let M_t be a local martingale that starts from zero at time 0. For $t \geq 0$, we define

$$\phi_{M_t} := \int_0^t (1+s)^{-2} d\langle M \rangle_s.$$

Here, $\langle M \rangle_t$ represents the Meyer angle bracket process. Then we have,

$$\mathbb{P}\left(\lim_{t \rightarrow \infty} \frac{M_t}{t} = 0\right) = 1,$$

if we establish

$$\mathbb{P}\left(\lim_{t \rightarrow \infty} \phi_{M_t} < \infty\right) = 1.$$

Proof. See for example [20].

First, we aim to ensure both the existence and uniqueness of the solution to our model within the set Δ , defined as follows:

$$\Delta = \{(x_1, x_2, x_3) \in (0, 1)^3; x_1 + x_2 + x_3 = 1\},$$

and $(\alpha, \eta, \lambda, \rho) \in (0, 1)^4$. Thus, we rely on the following theorem:

Theorem 1. Let $v \in \mathbb{D}$, $(S, I) \in (0, 1)^2$, and we define

$$\Psi(v, S, I) = [1 - \zeta_v I][1 + \zeta_v S],$$

if

$$\sup_{0 < S, I < 1} \int_{\mathbb{D}} \ln [\Psi^{-1}(v, S, I)] \pi(dv) < \infty. \quad (2.1)$$

So for each initial value $(S_0, I_0, R_0) \in \Delta$, we have unique solution $(S_t, I_t, R_t) \in \Delta$ for equation (1.2).

Proof. Define $N = S + I + R$ the total population, and we identify the values taken (the numbers) by S, I, R and N with their frequencies, and by the equation (1.2),

$$dN_t = dS_t + dI_t + dR_t = -\rho(N_t - 1)dt.$$

By integration for any $s \in [0, t]$, we obtain

$$N_s - 1 = [N_0 - 1] \exp(-\rho s) \text{ a.s.,}$$

from which for all $s \in [0, t]$,

$$(S_s, I_s, R_s) \in (0, 1)^3 \text{ and } N_s = 1 \text{ a.s..} \quad (2.2)$$

On the other hand, since the coefficients of the equations are locally Lipschitz continuous (see, e.g., [10, 21–25] for more information), it follows that there exists a unique local maximum solution (S_t, I_t, R_t) for $t \in [0, \tau_e)$, where τ_e denotes the timing of the explosion. Let $\varepsilon, \varepsilon_0 > 0$, for $\varepsilon \leq \varepsilon_0$, we define the stopping time:

$$\tau_\varepsilon = \inf\{t \in [0, \tau_e), (S_t \wedge I_t \wedge R_t) \leq \varepsilon\}. \quad (2.3)$$

Define for all $(S, I, R) \in \Delta$,

$$\Sigma_s = \Sigma_s(S_s, I_s, R_s) = -\ln(S_s I_s R_s).$$

By the Itô formula for every $t \geq 0$ and $s \in [0, t \wedge \tau_\varepsilon]$, we obtain

$$\begin{aligned} d\Sigma_s = & \left[3\rho + \lambda + \eta - \frac{\rho}{S_s} + \alpha I_s - \frac{\eta R_s}{S_s} - \alpha S_s - \frac{\lambda I_s}{R_s} \right] ds \\ & - \int_{\mathbb{D}} \{ \ln[(1 + \zeta_v S_s)(1 - \zeta_v I_s)] \\ & + (I_s - S_s)\zeta_v \} \pi(dv) ds \\ & - \int_{\mathbb{D}} \ln[(1 + \zeta_v S_s)(1 - \zeta_v I_s)] \widetilde{\mathcal{N}}(ds, dv). \end{aligned}$$

Using equations (2.1) and (2.2), one obtains

$$\begin{aligned} d\Sigma_s \leq & \left[3\rho + \lambda + \eta + \alpha + \pi(\mathbb{D}) \right. \\ & + \sup_{0 < S, I < 1} \int_{\mathbb{D}} \ln[\Psi^{-1}(v, S, I)] \pi(dv) \Big] ds \\ & - \int_{\mathbb{D}} \ln[(1 + \zeta_v S_s)(1 - \zeta_v I_s)] \widetilde{\mathcal{N}}(ds, dv). \end{aligned} \quad (2.4)$$

If we integrate (2.4) and the mathematical expectation property, this yields for each $t \geq 0$,

$$\begin{aligned} \mathbb{E}[\Sigma_t(S_{t \wedge \tau_\varepsilon}, I_{t \wedge \tau_\varepsilon}, R_{t \wedge \tau_\varepsilon})] & \leq \Sigma_t(S_0, I_0, R_0) + \kappa t, \\ & \leq \kappa t - 3 \ln(\varepsilon_0), \end{aligned} \quad (2.5)$$

where

$$\begin{aligned} \kappa = & 3\rho + \lambda + \eta + \alpha + \pi(\mathbb{D}) \\ & + \sup_{0 < S, I < 1} \int_{\mathbb{D}} \ln[\Psi^{-1}(v, S, I)] \pi(dv). \end{aligned}$$

Suppose $\tau_e < \infty$, so there is $t > 0$, where $\mathbb{P}(\{\tau_e < t\}) > 0$, implying $\mathbb{P}(\{\tau_e < t\}) > 0$. For $\omega \in \{\tau_e < t\}$ and equation (2.3), one obtains

$$-\ln(\varepsilon) \leq \Sigma_t[S_{t \wedge \tau_\varepsilon}(\omega), I_{t \wedge \tau_\varepsilon}(\omega), R_{t \wedge \tau_\varepsilon}(\omega)].$$

Hence

$$\begin{aligned} -\ln(\varepsilon) \mathbb{P}(\{\tau_e \leq t\}) & \leq \mathbb{E}[\Sigma_t(S_{\tau_e}, I_{\tau_e}, R_{\tau_e}) \mathbb{I}_{\{\tau_e \leq t\}}], \\ & \leq \mathbb{E}[\Sigma_t(S_{t \wedge \tau_\varepsilon}, I_{t \wedge \tau_\varepsilon}, R_{t \wedge \tau_\varepsilon})]. \end{aligned} \quad (2.6)$$

By using $\tau_e \leq \tau_e$, (2.5) and (2.6), we get

$$\begin{aligned} \mathbb{P}(\{\tau_e \leq t\}) & \leq \mathbb{P}(\{\tau_e \leq t\}), \\ & \leq \frac{3}{\ln(\varepsilon)} [\ln(\varepsilon_0) - \kappa t]. \end{aligned}$$

Letting $\varepsilon \rightarrow 0$, obtaining the contradiction $\mathbb{P}(\{\tau_e \leq t\}) = 0$, we conclude that $\tau_e = \infty$.

In the following section, we will examine the concept of disease persistence, focusing on determining the critical threshold conditions required for effective disease control and long-term management. This analysis will provide vital insights into the factors influencing the sustained presence of the disease within a population.

3 Persistence

It is essential in epidemiological studies of the disease to focus on cases where it persists and does not disappear spontaneously, as these cases can provide valuable information on its long-term impact and management. In what follows, we will demonstrate the persistence of the disease [26–28]. Let us define

$$\begin{cases} H(S) = -(\rho + \lambda) + \alpha S - \left[\frac{1}{4} \int_{\mathbb{D}} \zeta_v^2 \pi(dv) \right] S^2, \\ \mathcal{T}^1 = \alpha \left[\rho + \lambda + \frac{1}{4} \int_{\mathbb{D}} \zeta_v^2 \pi(dv) \right]^{-1}, \\ \Pi(S) = -(\rho + \lambda) + \alpha S - \left[\frac{1}{2} \int_{\mathbb{D}} \zeta_v^2 \pi(dv) \right] S^2, \\ \mathcal{T}^2 = \alpha \left[\rho + \lambda + \frac{1}{2} \int_{\mathbb{D}} \zeta_v^2 \pi(dv) \right]^{-1}. \end{cases} \quad (3.1)$$

Theorem 2. Let (2.1) and

$$\sup_{0 < y < 1} \int_{\mathbb{D}} \ln^2 [1 + \zeta_v y] \pi(dv) < \infty, \quad (3.2)$$

hold. For $(S_0, I_0, R_0) \in \Delta$, if $\mathcal{T}^1 > 1$, $\mathcal{T}^2 > 1$ and $|\zeta_v| < 1$ for each $v \in \mathbb{D}$, then

- (i) $\limsup_{t \rightarrow \infty} S_t \geq \rho$, a.s.,
- (ii) $\liminf_{t \rightarrow \infty} I_t \leq (\rho + \eta)(\rho + \eta + \lambda)^{-1}(1 - \rho)$, a.s.,
- (iii) $\liminf_{t \rightarrow \infty} R_t \leq \lambda(\rho + \eta + \lambda)^{-1}(1 - \rho)$, a.s.,
- (iv) $\liminf_{t \rightarrow \infty} S_t \leq \rho'$, a.s.,
- (v) $\limsup_{t \rightarrow \infty} I_t \geq (\rho + \eta)(\rho + \eta + \lambda)^{-1}(1 - \rho')$, a.s.,
- (vi) $\limsup_{t \rightarrow \infty} R_t \geq \lambda(\rho + \eta + \lambda)^{-1}(1 - \rho')$, a.s.,

where, ρ and ρ' denote the positive roots on the interval $(0, 1)$ of equations $H(S) = 0$ and $\Pi(S) = 0$, respectively.

Remark. Since $-1 < \zeta_v < 1$ for all $v \in \mathbb{D}$, as a result, for all $S \in (0, 1)$, $\Pi(S) < H(S)$, therefore, $\rho < \rho'$.

Proof. (i) From (1.2), and using Itô formula, one obtains

$$\begin{aligned} \ln(I_t) &= \ln(I_0) - \int_0^t [(\rho + \lambda) - \alpha S_s] ds \\ &\quad + \int_0^t \int_{\mathbb{D}} [\ln(1 + \zeta_v S_s) - \zeta_v S_s] \pi(dv) \\ &\quad + \int_0^t \int_{\mathbb{D}} \ln[1 + \zeta_v S_s] \widetilde{\mathcal{N}}(ds, dv). \end{aligned} \quad (3.3)$$

Applying the following inequality:

$$\ln(1+x) - x < -\frac{x^2}{4}, \quad -1 < x \leq 1. \quad (3.4)$$

Hence

$$\begin{aligned} \ln(I_t) &\leq \ln(I_0) + \int_0^t H(S_s) ds \\ &\quad + \int_0^t \int_{\mathbb{D}} \ln[1 + \zeta_v S_s] \widetilde{\mathcal{N}}(ds, dv). \end{aligned} \quad (3.5)$$

As $H(0) = -(\rho + \lambda) < 0$, when $\mathcal{T}^1 > 1$ it follows that $H(1) > 0$. Consequently, the equation $H(S) = 0$ possesses a unique root $\rho \in (0, 1)$, because if $\mathcal{T}^1 > 1$, we will have $H'(S_0) = 0$ for a $S_0 > 1$. Therefore, H exhibits a monotonic increase on the interval $(0, 1)$ in particular $(0, \rho)$. For any sufficiently small $\varepsilon > 0$, when $0 < S \leq \rho - \varepsilon$, we get

$$H(S) \leq H(\rho - \varepsilon) < 0. \quad (3.6)$$

Now, we begin the proof of assertion (i). Assume the contrary, implying that there exists a sufficiently small strictly positive ε , where

$$\mathbb{P} \left[\limsup_{t \rightarrow \infty} S_t \leq \rho - 2\varepsilon \right] > 0.$$

Consider

$$\Omega_1 = \left\{ \limsup_{t \rightarrow \infty} S_t \leq \rho - 2\varepsilon \right\}.$$

For every $\omega \in \Omega_1$, there exists $\tau(\omega) > 0$, such that

$$S_t \leq \rho - \varepsilon < 1, \quad \text{for each } t \geq \tau(\omega). \quad (3.7)$$

By (3.6) and (3.7), we get for each $s \geq \tau(\omega)$,

$$H(S_s) \leq H(\rho - \varepsilon) < 0. \quad (3.8)$$

By equation (3.2) and Lemma (1), we can easily prove the existence of a set $\Omega_2 \subset \Omega$, with $\mathbb{P}(\Omega_2) = 1$, where for each $\omega \in \Omega_2$, one has

$$\lim_{t \rightarrow \infty} \int_0^t \int_{\mathbb{D}} \frac{\ln[1 + \zeta_v S_s]}{t} \widetilde{\mathcal{N}}(ds, dv) = 0. \quad (3.9)$$

Now, fix any $\omega \in \Omega_1 \cap \Omega_2$. Hence, by (3.5) and (3.8), for $t \geq \tau(\omega)$, we obtain

$$\begin{aligned} \ln(I_t) - \ln(I_0) &\leq \int_0^{\tau(\omega)} H(S_s) ds + \int_{\tau(\omega)}^t H(\rho - \varepsilon) ds \\ &\quad + \int_0^t \int_{\mathbb{D}} \ln[1 + \zeta_v S_s] \widetilde{\mathcal{N}}(ds, dv). \end{aligned} \quad (3.10)$$

Based on (3.9) and (3.10), we deduce

$$\begin{aligned} \limsup_{t \rightarrow \infty} \frac{\ln(I_t)}{t} &\leq H(\rho - \varepsilon), \\ &< 0. \end{aligned} \quad (3.11)$$

Whence,

$$\lim_{t \rightarrow \infty} I_t = 0. \quad (3.12)$$

By integrating the last equation of (1.2), one obtains

$$\begin{aligned} R_t &= R_0 \exp\{-(\rho + \eta)t\} \\ &\quad + \lambda \int_0^t I_{(t-s)} \exp\{-(\rho + \eta)s\} ds. \end{aligned} \quad (3.13)$$

Using (3.13) and the Fatou lemma, we deduce

$$\limsup_{t \rightarrow \infty} R_t \leq \lambda(\rho + \eta)^{-1} \limsup_{t \rightarrow \infty} I_t. \quad (3.14)$$

Furthermore, in conjunction with (3.12), this implies $\lim_{t \rightarrow \infty} R_t = 0$ and thus $\lim_{t \rightarrow \infty} S_t = 1$. However, this contradicts (3.7).

(iv) In the same way, based on Itô formula as in (3.3) and applying

$$-\frac{x^2}{2} \leq \ln(1+x) - x, \text{ for each } x \geq 0.$$

Thus

$$\begin{aligned} \ln(I_t) &\geq \ln(I_0) + \int_0^t \Pi(S_s) ds \\ &\quad + \int_0^t \int_{\mathbb{D}} \ln[1 + \varsigma_v S_s] \tilde{\mathcal{N}}(ds, dv). \end{aligned} \quad (3.15)$$

Suppose (iv) is contradicted, implying the existence of a sufficiently small $\varepsilon' > 0$ with $\mathbb{P}(\Omega_3) > 0$, where

$$\Omega_3 = \left\{ \liminf_{t \rightarrow \infty} S_t \geq \rho' + 2\varepsilon' \right\}.$$

So, for each $\omega \in \Omega_3$, there exist $\tau'(\omega) > 0$ such that

$$S_t \geq \rho' + \varepsilon', \text{ for each } t \geq \tau'(\omega). \quad (3.16)$$

Similar (3.8), it is straightforward to confirm, by selecting $\varepsilon' > 0$ adequately small, that

$$\Pi(S_s) \geq \Pi(\rho' + \varepsilon') > 0, \text{ for } s \geq \tau'(\omega). \quad (3.17)$$

Using (3.9), (3.15), (3.17), and following a similar reasoning as in (3.10), we obtain

$$\limsup_{t \rightarrow \infty} \frac{\ln(I_t)}{t} \geq H(\rho' + \varepsilon') > 0.$$

Thus,

$$\lim_{t \rightarrow \infty} I_t = \infty.$$

This contradicts the condition $I < 1$.

(ii) By (i) and (2.2), one has

$$\liminf_{t \rightarrow \infty} I_t + \liminf_{t \rightarrow \infty} R_t \leq 1 - \rho, \text{ a.s..} \quad (3.18)$$

Using (3.13) and Fatou lemma, yields

$$\liminf_{t \rightarrow \infty} I_t \leq \lambda^{-1}(\rho + \eta) \liminf_{t \rightarrow \infty} R_t. \quad (3.19)$$

By combining equations (3.18) and (3.19), we establish the necessary assertion (ii).

(v) Similar to (ii), the conclusion follows from equations (3.14), (iv), and (2.2).

(iii)-(vi) These outcomes stem directly from equations (2.2), (i), (iv), (ii), and (v).

In the next section, we will analyze the extinction of the stochastic differential equation (SDE) (1.2) to determine the critical threshold necessary for achieving disease control or complete eradication.

4 Extinction

This section will examine the extinction phenomenon in the SDE system (1.2).

Theorem 3. Let $(S_0, I_0, R_0) \in \Delta$ and (2.1) holds. Assume that

$$\sup_{0 < y < 1} \int_{\mathbb{D}} \ln^2[1 + \varsigma_v y] \pi(dv) < \infty. \quad (4.1)$$

We define the new threshold

$$\mathcal{T}^3 = \alpha \left[\rho + \frac{1}{4} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv) \right]^{-1}, \quad (4.2)$$

and

$$\mathcal{T}^4 = \frac{1}{2} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv). \quad (4.3)$$

If $\mathcal{T}^3 < 1$ and $\alpha \geq \mathcal{T}^4$, then the system governed by (1.2) exhibits extinction with an exponential decay rate.

Proof. Let

$$\Sigma_t(Z_t) = \ln(Z_t),$$

where, $Z_t = I_t + R_t$. Using the Itô formula, one obtains

$$\begin{aligned} d\Sigma_t &= \frac{1}{Z_t} [-\rho I_t - (\rho + \eta) R_t + \alpha S_t I_t] dt \\ &\quad + \int_{\mathbb{D}} \left[\ln \left(1 + \varsigma_v \frac{S_t I_t}{Z_t} \right) - \varsigma_v \frac{S_t I_t}{Z_t} \right] \pi(dv) dt \\ &\quad + \int_{\mathbb{D}} \ln \left(1 + \varsigma_v \frac{S_t I_t}{Z_t} \right) \tilde{\mathcal{N}}(dt, dv). \end{aligned} \quad (4.4)$$

Using (3.4) and the following inequalities:

$$-1 < \varsigma_v < 1, \quad \frac{SI}{Z} \leq 1, \quad (4.5)$$

and

$$\frac{1}{Z} [-\rho I - (\rho + \eta) R] \leq -\rho.$$

Thus

$$\begin{aligned} d\Sigma_t &\leq \left[-\rho + \alpha \frac{S_t I_t}{Z_t} - \frac{1}{4} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv) \left(\frac{S_t I_t}{Z_t} \right)^2 \right] dt \\ &\quad + \int_{\mathbb{D}} \ln \left(1 + \varsigma_v \frac{S_t I_t}{Z_t} \right) \tilde{\mathcal{N}}(dt, dv), \\ &\leq \sup_{0 < \delta \leq 1} \Phi(\delta) dt + \int_{\mathbb{D}} \ln \left(1 + \varsigma_v \frac{S_t I_t}{Z_t} \right) \tilde{\mathcal{N}}(dt, dv), \end{aligned} \quad (4.6)$$

where

$$\Phi(\delta) = -\rho + \alpha \delta - \frac{1}{4} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv) \delta^2.$$

If $\alpha \geq \frac{1}{2} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv)$, then Φ is increasing on $(0, 1)$. By integration, we get

$$\begin{aligned} \Sigma_t &\leq \Sigma_0 + \int_0^t \left(-\rho + \alpha - \frac{1}{4} \int_{\mathbb{D}} \varsigma_v^2 \pi(dv) \right) ds \\ &\quad + M_t, \end{aligned} \quad (4.7)$$

where, M_t is a real-valued local martingale such that

$$M_t = \int_{\mathbb{D}} \int_0^t \ln \left(1 + \zeta_v \frac{S_s I_s}{Z_s} \right) \tilde{\mathcal{N}}(ds, dv).$$

Or

$$\begin{aligned} \langle M \rangle_t &= \int_{\mathbb{D}} \int_0^t \ln^2 \left(1 + \zeta_v \frac{S_s I_s}{Z_s} \right) \pi(dv) ds, \\ &\leq \left[\sup_{0 < y < 1} \int_{\mathbb{D}} \ln^2(1 + \zeta_v y) \pi(dv) \right] t < \infty. \end{aligned}$$

From (4.1) and (1), we get

$$\limsup_{t \rightarrow \infty} \frac{M_t}{t} = 0 \text{ a.s..} \quad (4.8)$$

The assertion is validated with (4.7) and (4.8).

Next, we will examine the SDE (1.2) computer simulations to validate and reinforce our theoretical findings.

5 Computer Simulations

In this section, we propose a few examples of numerical computer simulations to illustrate the theoretical results of Theorem 2 for persistence and Theorem 3, which prove the extinction of the disease by using the Maruyama Euler method (see, e.g., [29] for further information and the references cited therein).

5.1 Graphical representations in case of persistence theorem 2

The graphical representation plots the proportions of susceptible, infected, and recovered individuals over time. Each case specified in the cases list corresponds to a set of parameter values defining the transmission rate ρ , infection rate α , recovery rate λ , reintroduction rate η , and volatility parameter ζ . For each case, the model is simulated, and the results are plotted on separate graphs, with the time on the **x-axis** and the proportion of individuals on the **y-axis**. The plots provide insights into how different parameter combinations affect the disease dynamics, allowing for comparative analysis.

5.2 Analysis, comparison and interpretation in case of persistence theorem 2

The variations in the dynamics of susceptible, infected, and recovered populations are analyzed concerning the values of $\mathcal{T}^1$ and $\mathcal{T}^2$, particularly when $\mathcal{T}^1 > 1$ and $\mathcal{T}^2 > 1$, see figures 1 and 4, as well as in the case of the negation of these conditions, see figures 2 and 3. The parameters $\mathcal{T}^1$ and $\mathcal{T}^2$ are derived from the model's equations and represent critical thresholds related to

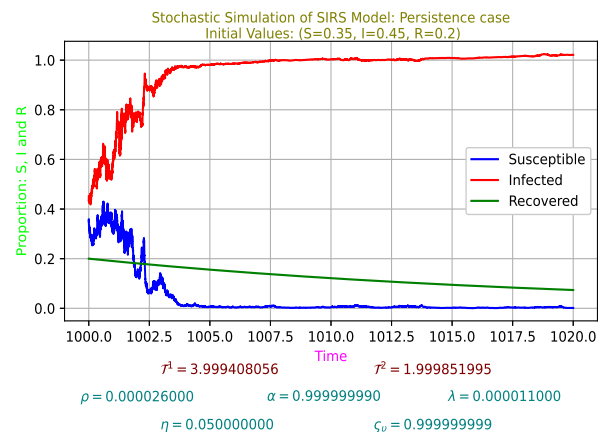


fig. 1. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 2.

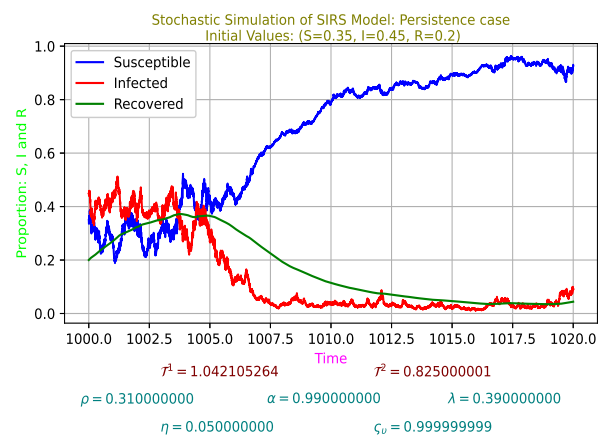


fig. 2. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 2.

transmission, infection, and recovery rates. By comparing the simulations under different parameter conditions, insights are gained into how parameter changes impact the disease spread, including the emergence of endemic or epidemic behaviors.

5.3 Graphical representations in case of theorem extinction 3

The graphical representation plots the proportions of susceptible, infectious, and recovered individuals over time for each simulated case. Each case corresponds to a different set of parameter values defining transmission

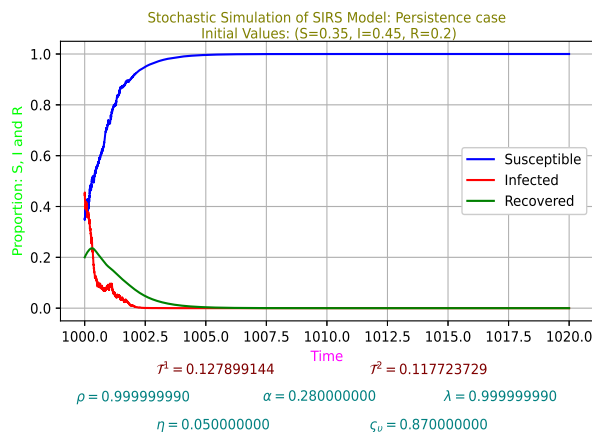


fig. 3. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 2.

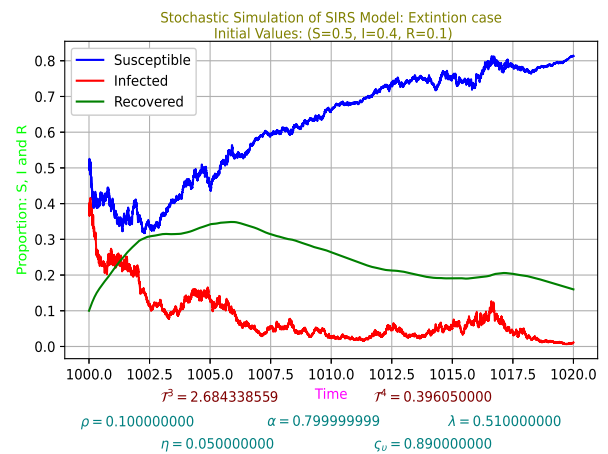


fig. 5. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 3.

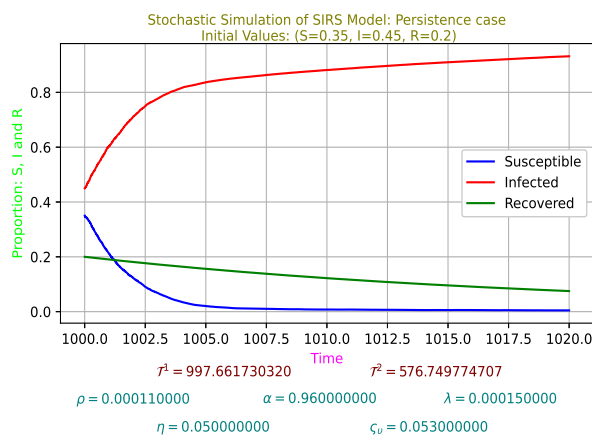


fig. 4. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 2.

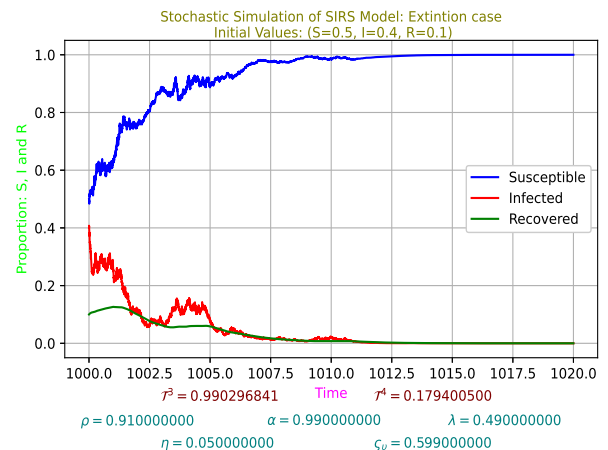


fig. 6. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 3.

rates ρ , infection α , recovery λ , reintroduction into the susceptible population η , and volatility ζ . The plots provide visual insights into how changes in these parameters affect the dynamics of the disease spread, allowing for comparative analysis across different scenarios.

5.4 Analysis, comparison, and interpretation in case of theorem extinction 3

The variations in the susceptible, infectious, and recovered populations are analyzed concerning the values of $\mathcal{T}^3$ and $\mathcal{T}^4$, particularly when $\mathcal{T}^3 < 1$ and $\mathcal{T}^4 \leq \alpha$,

see figures 6, as well as in the case of the negation of these conditions, see figures 5, 7, and 8. The parameters $\mathcal{T}^3$ and $\mathcal{T}^4$ are derived from the model's equations and represent critical thresholds related to the rates of transmission and infection. By comparing the simulations under different parameter conditions, insights are gained into how changes in these parameters impact the disease dynamics, including the emergence of endemic or epidemic behaviors.

6 Perspective

In recent years, the study of stochastic dynamics in epidemiology has gained significant traction, particularly

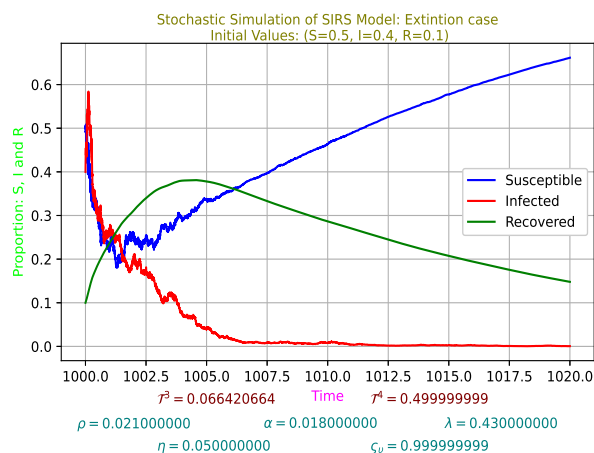


fig. 7. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 3.

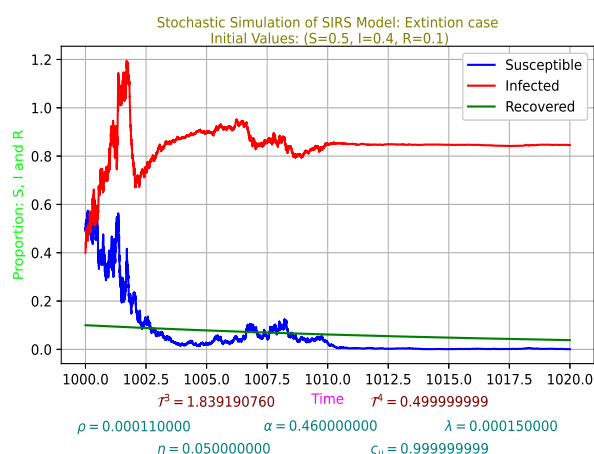


fig. 8. Trajectories of $S(t)$, $I(t)$, and $R(t)$ for system 1.2 with respect to Theorem 3.

in understanding the complexities of infectious disease transmission [38–62]. One such model, the stochastic model (SIRS), provides a valuable framework for investigating the dynamics of infectious diseases in populations where individuals move between susceptible, infectious, and recovered states. However, traditional SIRS models often assume continuous transitions between these states, overlooking the potential impact of sudden, large-scale perturbations or “jumps.” Exploring the effects of jump perturbations on stochastic SIRS dynamics presents a novel avenue for understanding the behavior of infectious diseases in real-world scenarios. Unlike gradual transitions, jump perturbations can arise from various factors, such as sudden changes in

environmental conditions, mass gatherings, or interventions like vaccination campaigns or policy changes. These perturbations can significantly alter disease transmission dynamics, leading to non-intuitive outcomes and challenging traditional modeling assumptions. From a scientific perspective, investigating jump perturbations in stochastic SIRS dynamics offers insights into the resilience and vulnerability of populations to abrupt changes in disease dynamics. Researchers can capture the inherent uncertainty and variability observed in real-world epidemiological data by incorporating stochasticity and jump processes into SIRS models. This allows for more accurate predictions of disease spread, improved assessment of intervention strategies, and a better understanding of the underlying mechanisms driving disease emergence and persistence. Professionally, this research has far-reaching implications for public health policy, infectious disease surveillance, and epidemic preparedness. Understanding how jump perturbations influence stochastic SIRS dynamics can inform the development of more effective disease control measures and response strategies. By identifying critical thresholds, tipping points, and high-risk scenarios, policymakers and public health officials can proactively mitigate the impact of sudden perturbations and minimize the risk of epidemic outbreaks or resurgence. In conclusion, exploring the impact of jump perturbations on stochastic SIRS dynamics represents a valuable interdisciplinary endeavor at the intersection of epidemiology, mathematics, and complex systems science [30–37]. Through rigorous scientific inquiry and collaboration, researchers can advance our understanding of infectious disease dynamics, enhance predictive capabilities, and ultimately contribute to more resilient and adaptive public health systems.

7 Conclusion

In conclusion, the stochastic SIRS model with jump perturbation provides a valuable framework for exploring and understanding the dynamics of infectious diseases with abrupt changes in transmission rates. This model offers insights into the potential impact of sporadic events or interventions on disease spread within a population. Its mathematical rigor and stochastic nature make it a valuable tool for researchers and policymakers in assessing and devising disease control and prevention strategies in dynamic and uncertain environments. Further research and refinement of this model may continue to contribute to our understanding of epidemiological processes and the development of effective public health measures.

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