EPJ Web of Conferences **369**, 02012 (2026) https://doi.org/10.1051/epjconf/202636902012
JIAMA'26

Stochastic Epidemic Models with Vaccination and Hybrid Perturbations: A Survey

***Saad* Doukkani**[1*], ***Younes* Abouelhanoune**[2], ***Ahmed* Moussaid**[1], **and *Hayat* Routaib**[3]

[1]FST Mohammedia, Hassan II University Casablanca, Morocco
[2]DMS, ENSA Al-Hoceima, Abdelmalek Essaadi University Tetouan, Morocco
[3]LSA, ENSA Al-Hoceima, Abdelmalek Essaadi University Tetouan, Morocco

Abstract. The objective of this work is to analyze some of the sophisticated stochastic epidemiology models that have emerged recently which go beyond the conventional deterministic modeling by including stochasticity, non-linear transmissions, and vaccination effects. This article discusses how the elements of randomness in terms of environment change, behavioral modification, imperfect vaccines, and reduced immunity are included in modern day models. Moreover, this paper also discusses some of the sophisticated hybrid models including diffusion dynamics, levy jumps, and Markovian switching representing the occurrence of sudden shock in the form of epidemiological events as well as the environmental changes. Some comparison among diffusion dynamics, vaccination model, and hybrid stochastic models was made in relation to extinction and persistence conditions, stochastic threshold theories, stability analysis, and the existence of fixed measures influencing them. However, it was found that even with advancements, there is a lack of consistency in the research being done today.

Keywords: Stochastic Epidemic Models, Non-Linear Incidence, Vaccination Dynamics, Lévy Jumps, Regime Switching, Hybrid Stochastic Systems.

1 Introduction

Mathematical modeling is crucial for gaining insight into the propagation of infectious diseases, predicting outbreak patterns, and making informed decisions regarding public health, and modern deterministic compartmental models were pioneered by the groundbreaking work of Kermack & McKendrick [1] that proposed the famous SIR model and established fundamental theories like epidemic threshold, endemicity, and herd immunity, among others.

Despite this fact, real epidemics do not always demonstrate predictable patterns of behavior. The models with deterministic parameters cannot properly consider the impact of randomness on multiple levels, influencing disease transmission process. Randomness will be influenced by various environmental factors, as well as the changes in the population and virus itself, such as mutations and super spreader cases, policy changes, and other factors. Thus, to model real epidemics, stochastic epidemiological models have been developed, in which randomness affects disease transmission. One of the stochastic methods for modeling disease spread with continuous noise was stochastic differential equations with the influence of Brownian motion. The application of these stochastic approaches has led to the emergence of some notable results in terms of random threshold conditions and criteria of extinction, as well as high-probability stability. However, even in this case, diffusion models could not

---

* Corresponding author: saad.doukkani11@gmail.com

provide proper explanation for any sudden changes, which happen during real epidemic outbreaks. Mutations, sudden behavioral changes, or rapid policy decision may lead to drastic changes. Jump processes, and particularly Levy noise, are considered the most appropriate tool for modeling them. Moreover, they pose quite a few problems from a mathematical point of view, and there are still many improvements to be made compared to the classic diffusion equations. The use of nonlinear incidences is certainly an improvement in the study of epidemics. In cases where the population size is very large, the assumption of bilinear incidence would not necessarily hold true since it assumes perfect mixing and infinite contact rates among individuals. Saturated incidences are thus a much better choice since they account for behavioral changes and contact rate restrictions.

However, vaccination complicates the scenario further. Modern mathematical models must consider parameters like vaccination of newborns, vaccination of risk groups, reduced immunity, and poor vaccine efficiency apart from the minimum vaccination levels required to confer herd immunity. There have been several fundamental contributions made through deterministic vaccination models in this field; nonetheless, stochastic vaccination models with the inclusion of environmental noise are yet to be adequately explored.

Some research gaps have been addressed in more recent literature. One research paper from the year 2025 about a stochastic SIS vaccination model with saturated incidence in random environments analyzed not only extinction and persistence but also stationary distribution conditions [36]. Prior to that, M. El Idrissi [31] contributed considerably to the analysis of stochastic epidemic models driven by diffusion-type noises, where the topics of positivity, stability, and thresholds were considered. Recently, El Bakkaoui [30] enriched the field of study with hybrid stochastic models involving such factors as Lévy jumps and Markovian switching, thus making the system able to exhibit both continuous changes and structural jumps.

However, even with all these advancements, there remain some challenges. For instance, there is yet no comprehensive model that integrates vaccination dynamics, non-linear incidence, jumps, and regime switching in one single framework. Moreover, some essential parameters like spatial heterogeneity, transmission on networks, multiscale dynamics, and parameter estimation based on data are often treated separately from the theoretical foundation of analysis. The challenge remains open to explore how these hybrid stochastic elements interact with control measures, particularly for formulating effective vaccination strategies under uncertain environments.

In this paper, we perform an intensive analysis of stochastic epidemic models which consider non-linear incidence rates, vaccination strategies, and hybrid perturbations. There are three aims behind this work:

1. To give a well-organized analysis of deterministic models, diffusive models, models considering vaccination, and hybrid models combining diffusion and jump-diffusion phenomena.
2. For carrying out an analysis of the existing approaches through the identification of differences in their methods, mathematical techniques, and conclusions obtained from them.
3. To identify lacunae in the present research, unsolved problems, and directions for further research.

This review is intended to help create a unified theoretical basis for studying hybrid stochastic epidemics by reviewing recent advances and encouraging research at the intersection of probability theory, non-linear dynamical systems, and epidemic modeling.

2 Related Work

2.1 Deterministic Compartmental Foundations

The theory of mathematical modeling of disease dynamics originated from the classical compartmental approach proposed by William O. Kermack [1] and Anderson G. McKendrick [2]. It is a deterministic model dividing the population into epidemiological compartments such as susceptible (S), infected (I) and recovered (R), while describing the process using nonlinear ordinary differential equations (ODE).

Further development led to the formulation of SIS, SIRS, SEIR, and vaccination models. Thanks to these developments, temporary immunity, incubation period, and demographic turnover could be incorporated in the model. In this regard, the reproduction number R0 has become an important threshold parameter determining extinction or survival of the species. Deterministic models based on next generation matrix and Lyapunov function approach impose stringent conditions on global stability of disease free and endemic equilibria.

Deterministic approaches, however, consider uniform mixing of the components, pre-set parameters, and lack of randomness. Consequently, such models are unable to incorporate variations in the environment, stochasticity in demographic processes, and sudden epidemics. Such limitations have been a driving force in adopting stochastic models in epidemic studies.

2.2 Diffusion-Driven Stochastic Epidemic Models

To integrate environmental randomness, deterministic epidemic systems were transformed into Stochastic Differential Equations (SDEs) influenced by Brownian motion. The equations indicate the temporal evolution of a system characterized by both deterministic drift $\beta(X_t)dt$ and random diffusion $\sigma(X_t)dW_t$, effectively modeling systems with noise intensity σ. Typically written as:

$$dX_t = \beta(X_t)dt + \sigma(X_t)dW_t \tag{1}$$

Typically, the transmission rate β is perturbed as:

$$\beta(X_t)dt \to \beta(X_t)dt + \sigma(X_t)dW_t \tag{2}$$

Diffusion processes have led to various ideas, such as almost sure extinction conditions, stochastic persistence, the existence of invariant measures, stochastic thresholds related to R0, stability in probability, and moment stability. The study of stochastic epidemic models driven by diffusion involves the use of Itô calculus that provides important tools for handling stochastic integrals and stochastic differential equations. Stochastic Lyapunov functions are often employed in order to investigate stability as well as longtime dynamics of stochastic systems and to obtain sufficient conditions for extinction or persistence of diseases in probability settings.

The work performed by [3][4] contributed systematically and rigorously to the study of diffusion-based stochastic epidemic processes. Specifically, his study dealt with the existence and uniqueness of positive global solutions, which validated the biological plausibility of the modeled population. Global stability under stochastic perturbations, exact criteria for extinction and stochastic permanence, as well as threshold-type results, extending the concept of classic deterministic reproduction number into a diffusion epidemic process were obtained.

Nevertheless, while diffusion processes can offer analytical and mathematical elegance to epidemic models, it is inherently unable to model instantaneous jumps, rare events, or regime shifts. Brownian processes assume that the changes experienced by an entity follow a Gaussian distribution, thus being unable to describe any sudden outbreak due to mutation, policy change, or super-spreader cases. For that reason, jump-diffusion and hybrid stochastic modeling is required.

2.3 Nonlinear and Saturated Incidence Rates

The classical epidemic models, including the Susceptible–Infectious–Recovered (SIR) model initially proposed by Kermack and McKendrick [1] and its more complex version – the SEIR model employ the simple bilinear incidence function formulated based on the mass action principle. As stated by Hethcote et. al., this function βSI, with β being the transmission coefficient, S standing for the susceptible individuals, and I representing the infected ones describes the infection process. According to this function, contacts between susceptibles and infectives depend only on their densities and therefore are assumed to be homogeneously distributed among all contacts possible in a population.

The bilinear incidence is commonly applied in models because of its biological meaning and ease of calculation [5]. It is especially suited for modeling the epidemics caused by pathogens with a direct route of transmission, for example, influenza-type infections in the case of homogeneous mixing of population members. However, the bilinear incidence formula is based on very specific assumptions, which do not always hold true when considering real epidemic situations. First of all, the number of contacts increases unlimitedly as population size rises, creating unrealistic conditions for pathogen transmission [3].

To overcome these limitations, alternative incidence functions have been introduced. The standard incidence form, $\frac{\beta SI}{N}$, normalizes transmission by total population size N and is more appropriate when contact rates remain approximately constant as population size varies [2]. Additionally, saturated incidence functions of the form $\frac{\beta \mathrm{SI}}{1+\alpha \mathrm{I}}$, have been proposed to include behavioral responses, effects of crowding, and limited contact capacity [4]. These nonlinear incidence rates frequently produce more complex dynamic behaviors and more authentic epidemic trajectories. Mathematically, Lyapunov function techniques are often used to study epidemic models with bilinear incidence in order to show that equilibria are globally stable. Specifically, Volterra-type Lyapunov functions have been utilized to illustrate the global disease-free equilibrium is asymptotically stable when the basic reproduction number $R_0 < 1$, and the endemic equilibrium is stable when $R_0 > 1$ [6].

2.4 Vaccination Dynamics in Stochastic Environments

The concept of vaccination acts as an important element of current epidemic control programs, which has been widely applied to compartmental epidemic models. Within mathematical epidemiology, vaccination is considered within such approaches by means of incorporating new compartments (for example, vaccinated compartments) or using transitional rates that correspond to the key mechanisms of immunization. Such mechanisms include birth vaccination, vaccination of susceptible population, loss of immunity, and inefficiency of vaccines. The initial models demonstrated that the implementation of vaccination led to the reduction of the number of susceptible and changes in the reproductive number [2][6].

Vaccination deterministic models have shown that the effectiveness of vaccination influences the effective reproduction number Re, which is typically given by $Re = R0(1 - p)$, where p is the vaccine coverage, assuming optimal conditions. However, the complexity may be increased further if there is partial vaccine efficacy or waning immunity. Indeed, it was found that vaccination may lead to a backward bifurcation process, in which two equilibrium states exist simultaneously, one of which is the endemic equilibrium point, while the other is the disease-free equilibrium point. Such a situation may occur even when R0 < 1.

Although there are many studies on deterministic models of vaccination, there is relatively little development on stochastic models of vaccination. Stochastic models of epidemics, especially models that include environmental or demographic fluctuations, provide a more accurate depiction of the behavior of an epidemic in fluctuating environments [7]. There are some interesting problems in this area.

Firstly, it is necessary to determine reproduction thresholds for reproduction in random environments, since noise might affect the classical threshold value R0 = 1, leading to extinction even if the deterministic model predicts survival. Secondly, the calculation of extinction probabilities in partially immunized environments proves challenging, especially in finite populations or in the presence of environmental variability [8]. Thirdly, there is a need to establish whether invariant measures exist and are unique within the framework of stochastic models for vaccinated diseases, which requires careful analysis using stochastic Lyapunov functionals and ergodic theory. Finally, it is important to address the robustness of herd immunity to stochastic disturbances.

Most previous studies that deal with these issues focus on diffusion type of stochastic perturbation driven by Brownian motion (e.g., stochastic differential equations approach). It is noteworthy that hybrid stochastic processes that incorporate multiple types of stochasticity such as regime switching together with diffusion processes are virtually absent from the existing literature on vaccine dynamics.

2.5 Jump-Diffusion and Lévy-Driven Epidemic Models

Epidemic models show a clear example of a discontinuity due to phenomena like mutations of the virus, drastic policy changes (such as going into lockdown), changes in behavior, and super-spreading events. The Gaussian diffusion model is inadequate to capture the phenomenon since it only generates sample paths that are continuous. The use of Lévy processes, on the other hand, allows us to capture phenomena like these because they have jumps [13-14].

In jump-diffusion epidemic models, both the continuous and discontinuous effects in random environments are taken into consideration using the concept of jump process together with the concepts of Brownian motion. Even though jump diffusion has become common in modeling epidemics, it introduces significant analytical problems because of its nonlocal nature, complications related to the construction of appropriate Lyapunov functionals, and difficulties associated with discontinuous processes and interactions between different types of noise. In recent literature, results have been obtained regarding the extinction and persistence, as well as invariant measures for jump diffusion epidemic models. It is worth noting that other factors, such as vaccination and nonlinear incidence rates, are yet to be considered together in jump diffusion models [15-16].

2.6 Regime-Switching and Hybrid Stochastic Systems

The environmental changes and human-induced actions may cause structural changes leading to the shift from one epidemiological regime to another, for example, periods of high and low transmission. To model the process properly, one should use regime switching epidemic models where the switches occur according to finite-state Markov chains. That means that the model parameters like transmission rate, recovery rate, vaccination coverage, etc. depend on the state of some underlying continuous-time Markov chain. The result will be hybrid models that combine stochastic differential equations and Markovian switching with piecewise defined coefficients [17][18].

Mathematically, these types of models call for some special tools that can be used in hybrid systems theory and stochastic analysis. First, the generator of the process becomes intertwined in the sense that it now contains not only the diffusion part but also the generator of the Markov chain. Second, usually the stability problem will employ switching Lyapunov functions or modified common Lyapunov functions which are appropriate for analyzing Markov-modulated models. Third, ergodic theory related to Markov-modulated diffusions is important in terms of proving persistence, extinction criteria, and the existence of invariant measures [19].

Although many studies on regime-switching epidemic models driven by diffusion processes have been well conducted, especially in seasonal variation and environmental disturbance, their combination with Lévy jump processes is still poorly investigated. Combining all the mentioned elements in one model, Markovian switching, Lévy process, the vaccination strategy, which includes partial vaccination and lost immunity, as well as nonlinear incidence rate, constitutes a major research question yet to be explored.

2.7 Stationary Distributions and Long-Term Stochastic Behavior

The asymptotics of stochastic epidemic models are usually studied using invariant probability measures and stationary distributions. As opposed to deterministic systems where asymptotics are described by equilibrium points, the qualitative asymptotics of stochastic processes is determined by the existence and uniqueness of invariant measures. In addition, periodicity plays a crucial role in the investigation of stochastic processes. These characteristics allow describing stochastic notions such as persistence, extinction in distribution, and average prevalence of disease. For epidemics with diffusion-induced dynamics, the existence of invariant measures usually follows from stochastic Lyapunov function techniques along with Foster–Lyapunov drift criteria. Under suitable assumptions concerning dissipativity and nondegeneracy, one can prove that there exists an invariant density function and a rate of exponential convergence to the invariant measure. In some recent diffusion-based models for stochastic vaccination, the process was shown to converge to the invariant measures if the stochastic reproduction threshold is greater than one [22][10].

Nevertheless, the mathematical complexity is increased drastically when diffusion, Lévy jumps, and Markovian regimes are involved together. The generator is composed of both local parts (for diffusion) and nonlocal terms (for jumps), together with regime-dependent parameters that follow a discrete-valued Markov chain. All these factors make checking irreducibility, strong Feller condition, and the drift condition difficult, which are important for ergodicity. Moreover, regime-switching might change stability behavior from one regime to another, and nonlocal jumps induce discontinuities that prevent the application of compactness results used in diffusion-based problems.

Therefore, investigating the existence, uniqueness, and ergodicity of stationary solutions for vaccine-induced SIS-type epidemic models in a hybrid jump-diffusion Markov regime becomes a difficult mathematical task [23][24]. More precisely, obtaining threshold criteria for ensuring positive recurrence and stochastic permanence within this framework appears to be a challenging problem within current stochastic epidemic models.

2.8 Synthesis and Current Limitations

It is evident from the evolution of modeling epidemics that there has been a gradual improvement in mathematical rigor, analytical accuracy, and realism. The deterministic approach laid down by Kermack et al. [1] served as the foundation for ODE modeling and was considered the core of mathematical epidemiology. The basic models in this category were based on the assumptions of homogeneous mixing and bilinear incidence rate. It offered a clear-cut criterion for threshold behavior using R0.

Later developments involved the addition of stochastic perturbation in order to account for environmental and demographic randomness; thus, stochastic differential equations (SDEs) became popular in mathematical modeling, leading to diffusion-induced extinction and persistence criteria [34][25].

Other improvements attempted to address the inadequacies in bilinear transmission by incorporating non-linear and saturated forms for incidence rates in order to account for behavioral changes and overcrowding [35][26]. At the same time, dynamics of vaccine use, taking into account their partial effectiveness and loss of immunity, have been included in deterministic and stochastic formulations, leading to interesting discoveries like backward bifurcations and stochastic thresholds [32][33][27].

In more recent times, hybrid stochastic models have been developed, as shown in Table 1, using both diffusion perturbation and Lévy jumps to describe occasional high impact disturbances [28], along with Markov regime switching to depict switching behavior due to environmental/policy changes [29]. Hybrid models demonstrate piecewise stochastic dynamics based on infinitesimal generators.

Table 1. Evolution of Epidemic Modeling Frameworks and Open Challenges.

Modeling Stage	**Mathematical Structure**	**Key Contributions**	**Main Limitations**	**Open Problems**
Deterministic ODE models	Nonlinear ODE systems (mass-action incidence)	Explicit R_0, equilibrium and bifurcation analysis	Homogeneous mixing, absence of randomness	Incorporation of environmental and demographic uncertainty
Diffusion-driven SDE models	Brownian stochastic differential equations	Stochastic extinction, invariant measures, probabilistic thresholds	Continuous sample paths only	Inclusion of discontinuous shocks
Nonlinear / Saturated incidence models	Rational or non-linear transmission functions	Behavioral response and crowding effects	Mostly deterministic formulations	Stochastic threshold characterization under nonlinear incidence
Vaccination-based models	Additional compartments and transition rates	Herd immunity analysis, backward bifurcation	Limited hybrid stochastic treatment	Vaccination dynamics under jumps and switching
Jump–diffusion systems	SDEs with Lévy jump processes	Modeling rare, high-impact shocks	Analytical complexity due to nonlocal operators	Unified stability and ergodicity theory
Regime-switching models	Markov-modulated stochastic systems	Structural environ-mental and policy transitions	Rare integration with jumps and vaccination	Hybrid threshold conditions
Spatial and network models	PDE systems or graph-based dynamics	Spatial heterogeneity and contact topology	Limited combination with hybrid stochasticity	Integrated multiscale stochastic frameworks
Data-driven models	Statistical inference coupled with dynamical systems	Parameter calibration and forecasting	Often decoupled from theoretical analysis	Theory–data integration in hybrid systems

Despite significant advancements, the literature remains structurally fragmented. Most studies examine diffusion noise, jump processes, vaccination mechanisms, nonlinear incidence, spatial effects, or network topology in isolation, rather than within a cohesive analytical framework. Specifically, comprehensive models that simultaneously integrate the following components are lacking:

1. Vaccination dynamics with imperfect coverage and waning immunity,
2. Saturated or nonlinear incidence structures,
3. Lévy jump perturbations representing discontinuous shocks,
4. Markovian regime switching to account for environmental or policy variability,
5. Spatial heterogeneity and meta-population diffusion,
6. Network-based contact topology,
7. Data-driven parameter inference and statistical calibration.

Past studies have largely modeled the various elements in epidemic modeling independently or partially together, with rather strict assumptions regarding their structure, thereby impeding the formulation of a consistent theory of threshold, stability, and persistence properties of hybrid stochastic processes. This calls for a holistic approach integrating stochastic processes, hybrid systems, spatial and network structure, and inference techniques to tackle interacting sources of uncertainty and model the behavior of epidemics.

3 Comparative Analysis of Existing Frameworks

The recent stochastic epidemic models may be broadly categorized under three distinct streams, namely, the diffusion approach models, for example, El Idrissi [31]; vaccination models with nonlinear incidence, for example, probabilistic SIS model for 2025 [36]; and advanced models of hybrid jump-regime switching proposed by El Bakkaoui [30]. Though based on identical mathematical principles, there exist fundamental differences in structure, as presented in Figure 1. All models include the Brownian motion process as environmental fluctuations. However, while Idrissi et al. [31] present a simplified model using the diffusion-vaccination process with a focus on stability and extinction, the 2025 model [36] introduces the saturated incidence rate with vaccination.

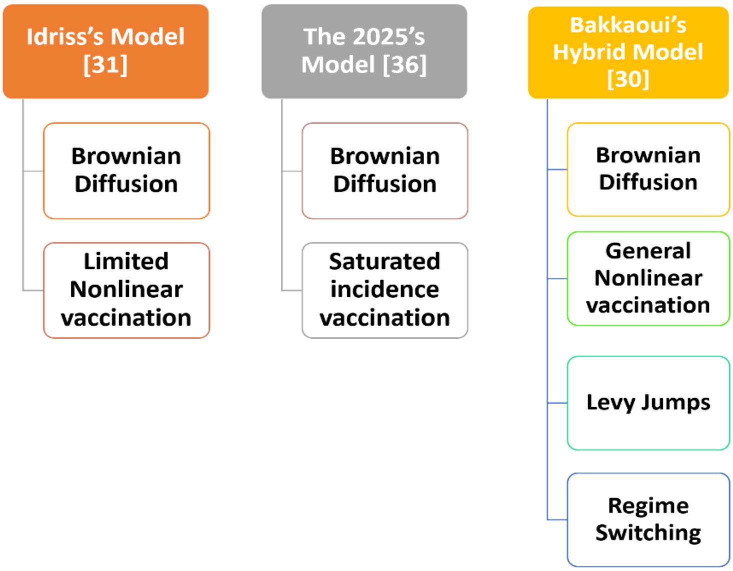

Fig. 1. Comparative Framework of Stochastic Epidemic Models.

Moreover, the chart illustrates the development of threshold and stability analysis methods, which began with the development of partial criteria [31] and then progressed to sufficient conditions [36] before reaching necessary and sufficient conditions in a hybrid stochastic setting [30]. As far as computational methods are concerned, the chart highlights the progression to increasingly complex computations methods, which have advanced from basic simulation to discontinuity- and switching-aware methods. Finally, the diagram shows the distinct tradeoff between analytical tractability and modeling realism with respect to growing stochastic elements.

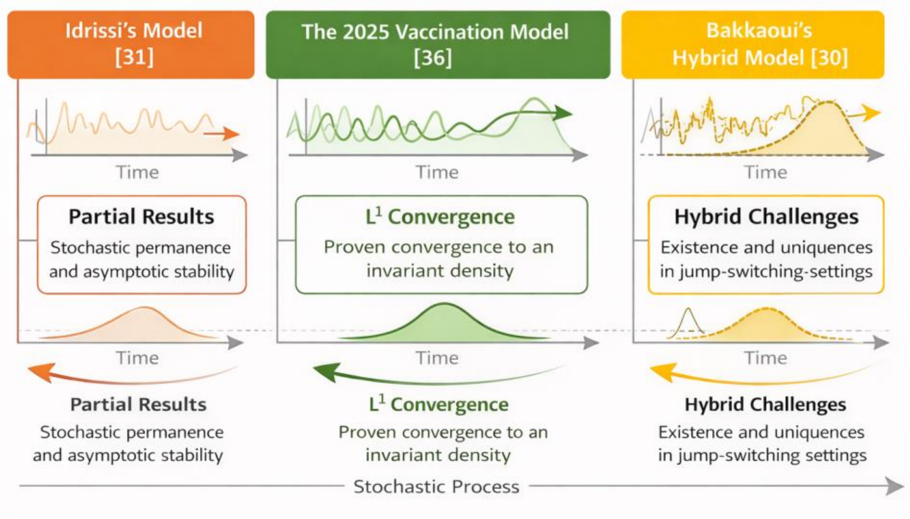

Fig. 2. Stationary Distributions & Long-Term Stochastic Behavior.

4 Critical Discussion

4.1 Global Strengths of the Existing Frameworks

There are various aspects about the existing body of work on diffusion models, vaccination models, and switch-jump epidemic models. To begin with, one such aspect is that the existing body of work employs mathematical to prove existence and uniqueness of positive solutions to systems using the concepts of stochastic methods including Itô Calculus, martingale theory, infinitesimal generators, and the Lyapunov method. Secondly, one key feature of this set of literature is the use of Lyapunov function methodology to explore the stochastic stability of model systems concerning extinction, permanence, and threshold behavior. Thirdly, another key feature of this line of research is stochastic thresholds, which can be regarded as an expansion of the basic reproductive number in stochastic environments.

4.2 Common Structural Limitations

Despite these strengths, several structural limitations are evident in the literature:
- **Lack of Structure in Network**: Existing models assume homogenous mixing. They fail to integrate features of heterogeneity in contacts, clustering in communities, and scale free networks. This is a major drawback because the existing stochastic model cannot simulate the impact of superspreaders and locality in disease transmission.

- **No Spatial Dimension**: The existing model has been formulated based on finite-dimensional SDE. They lack any dimension regarding spatial diffusion, movement, or geographical heterogeneity. There are no developments on transitioning from SDE systems to SPDE in the domain of hybrid stochastic epidemic models.
- **No Use of Machine Learning Methods**: Traditional stochastic models of epidemics are not well connected with current data-driven methods. Current machine learning techniques, such as neural differential equations and probabilistic networks, have not yet been effectively integrated with traditional stochastic methods.
- **Parameter Values Are Assumed to Be Known**: Parameters related to transmission rates, noise strengths, and vaccination are always assumed to be known parameters. These parameters are generally unknown and time-varying, and some are even unobservable.
- **No Optimal Control in a Stochastic Environment**: While the process of vaccination and transmission are included in models, their optimization in a stochastic environment is not adequately considered. Robust controls, stochastic optimal vaccination, and stochastic epidemic games need more consideration.
- **No Multi-Scale Models**: Most of the models are based on one specific level of time scales and structural scales. They do not consider the effects of both levels together, creating an inadequacy in the multi-scale approach to epidemiology.

Table 2. Comparative Overview of Stochastic Epidemic Modeling Frameworks

Dimension	El Idrissi [31]	2025 Vaccination SIS Model [36]	Bakkaoui [30]
Primary stochastic mechanism	Brownian diffusion	Brownian diffusion	Brownian diffusion and Lévy jumps
Incidence structure	Mostly bilinear / mildly nonlinear	Saturated nonlinear incidence	Extended nonlinear incidence
Vaccination modeling	Limited / simplified	Explicit vaccination compartments	Limited emphasis
Lévy jump perturbations	No	No	Yes
Markovian regime switching	No	No	Yes
Stationary distribution analysis	Partial (stochastic permanence)	Existence and L^1 convergence	Existence addressed in hybrid setting
Extinction and persistence criteria	Rigorous but partial	Sufficient conditions	Necessary and sufficient conditions
Threshold characterization	Diffusion-based stochastic threshold	Modified threshold under vaccination	Hybrid threshold under jumps and switching
Numerical methodology	Basic simulations	Limited computational focus	Adaptive schemes for hybrid systems
Modeling scope	Diffusion epidemic systems	Vaccination and nonlinear incidence	Hybrid stochastic epidemic systems
Structural complexity	Moderate	Moderate to high	High

5 Current Scientific Challenges

5.1 Stochastic Parameter Calibration

A key unresolved issue pertains to parameter estimation in stochastic epidemic systems.

✓**Estimation Under Multiplicative Noise:** In the case of noise influencing the transmission terms in a multiplicative way, conventional estimation procedures might lead to bias and inconsistency. Maximum likelihood estimation of the diffusion process involving nonlinear drift and diffusion functions is computationally difficult.

✓**Identification in Jump-Diffusion Systems:** The addition of Lévy jumps causes significant challenges in parameter estimation. It is necessary to distinguish whether the variance results from diffusion processes or arises from jumps, and this can be accomplished only with the aid of high-frequency data and complex statistical filtering methods.

5.2 Multi-Regime Numerical Simulation

Hybrid epidemic models involving diffusion, jumps, and switching regimes present substantial difficulties in computing.

- The numerical methods have to handle well the jumps' discontinuous effects.
- Switching calls for variable time-steps.
- Stability and convergence must be maintained for long periods.

The basic Euler-Maruyama approach is inadequate for the hybrid case, and the advanced adaptive approaches used in epidemiology have not been thoroughly investigated either.

5.3 Generalized Stochastic Threshold Definition

In models of diffusion-type processes, thresholds have been defined via the noise-dependent reproduction numbers. However, it is very difficult to define a general threshold in situations where there are several different stochastic factors that are incorporated in the system, such as continuous noise, jump disturbance, and regime switching.

A few important questions that arise here are as follows:

- Can a single scalar threshold capture the notion of persistence?
- Is it necessary that the thresholds depend on the distribution of the regimes?
- How do rare events affect extinction probabilities?

5.4 Coupling with Real Epidemiological Data

Even though there is considerable advancement in theory, the lack of empirical validation is significant. The hybrid approach of stochastic modeling does not often involve calibration using actual data on epidemics. The concepts of data assimilation, Bayesian filters, and real-time updates are not systematically used.

6 Research Gaps and Perspectives

Despite substantial developments made in the stochastic models for epidemics, there still exist certain limitations in terms of both the structural design of the models and the methods utilized to analyze the models in the literature.

First, there is a lack of hybrid modeling framework that could accommodate all possible sources of randomness. It is a general practice that current literature models focus on one source of stochasticity in epidemic models, including, for example, diffusion driven noise, nonlinear incidence with vaccination, or hybrid models with Lévy jumps and Markovian switching. Nonetheless, a more complex model that combines dynamics of vaccination, saturation incidence, jump perturbations, switching, contact structures on networks, and diffusion is not yet developed. In other words, although each aspect of randomness has been considered separately in the literature, the problem of combining all of these factors in one model is not solved yet.

The second gap refers to the inadequacy of the link between stochastic theories about epidemics and modern data-driven methods. Machine learning algorithms such as neural differential equations, physics-informed neural networks, and Bayesian deep learning have already proven themselves highly effective in identifying complex dynamics. However, the application of these techniques has been relatively weak in the context of stochastic epidemic modeling. To the best of our knowledge, no universal method exists that integrates stochastic differential equation modeling with the process of real-time data integration using neural networks or parameter estimation in a jump-diffusion setting via deep learning.

However, stochastic epidemic models suffer from several weaknesses, especially about uncertainty quantification, parameter inference, and structure incorporation. Although they give sufficient conditions for extinction and persistence, the consideration of sensitivity analysis or even rare-event risk assessment is neglected in most cases. Besides, some key parameters remain constant without considering their random nature and temporal dependency, while there is no common methodology yet for inference procedures. Lastly, heterogeneity in space and networks should be incorporated more thoroughly together with the hybridity and randomness of epidemic dynamics.

There are several promising ways in which the future research in stochastic epidemic modeling could progress, making it more realistic and predicting more accurately. This includes the formulation of spatial models using SPDEs and jump processes along with the process of vaccinations that account for spatial heterogeneity in an outbreak; including heterogeneous contact structures via the use of Lévy noise; and the use of hybrid AI approaches such as PINNs, Bayesian approaches, and neural SDEs. Designing optimal controls under uncertain settings and the use of rare-event simulations for extreme scenarios of the outbreak are also key steps in future research.

7 Conclusion

The current survey aims at exploring the history of stochastic epidemic models by paying attention to recent progress in moving from purely deterministic models to hybrid ones that include the nonlinear incidence rate, vaccination, and different types of stochastic factors. However, even with such advances, the area still lacks a unified approach that would incorporate such important components as vaccination, nonlinearity, jumps, and regime switching. This problem affects not only the theoretical aspects of studying epidemics but also reduces its potential practical value. Moreover, several issues still persist, such as the issues pertaining to the definition of the threshold, stability criteria, computation strategies, and data integration. For future studies, more focus needs to be paid on creating hybrid models which will be able to integrate the spatial and network structures, as well as use artificial intelligence techniques.

References

1. Kermack, W. O., & McKendrick, A. G. (1927). A contribution to the mathematical theory of epidemics. Proceedings of the Royal Society A, 115(772), 700–721.
2. Anderson, R. M., & May, R. M. (1991). Infectious Diseases of Humans: Dynamics and Control. Oxford University Press.
3. Brauer, F. (2008). Compartmental models in epidemiology. In F. Brauer, P. van den Driessche, & J. Wu (Eds.), Mathematical Epidemiology (Lecture Notes in Mathematics, Vol. 1945). Springer.
4. Capasso, V., & Serio, G. (1978). A generalization of the Kermack–McKendrick deterministic epidemic model. Mathematical Biosciences, 42(1–2), 43–61.
5. Hethcote, H. W. (2000). The mathematics of infectious diseases. SIAM Review, 42(4), 599–653.
6. Korobeinikov, A., & Wake, G. C. (2002). Lyapunov functions and global stability for SIR, SIRS, and SIS epidemiological models. Applied Mathematics Letters, 15(8), 955–960.
7. Allen, L. J. S. (2008). An introduction to stochastic epidemic models. In F. Brauer, P. van den Driessche, & J. Wu (Eds.), Mathematical Epidemiology (Lecture Notes in Mathematics, Vol. 1945). Springer.
8. Anderson, R. M., & May, R. M. (1991). Infectious Diseases of Humans: Dynamics and Control. Oxford University Press.
9. Gomes, M. G. M., White, L. J., & Medley, G. F. (2004). Infection, reinfection, and vaccination under suboptimal immune protection: Epidemiological perspectives. Journal of Theoretical Biology, 228(4), 539–549.
10. Gray, A., Greenhalgh, D., Hu, L., Mao, X., & Pan, J. (2011). A stochastic differential equation SIS epidemic model. SIAM Journal on Applied Mathematics, 71(3), 876–902.
11. Hethcote, H. W. (2000). The mathematics of infectious diseases. SIAM Review, 42(4), 599–653.
12. van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences, 180(1–2), 29–48.
13. Allen, L. J. S. (2008). An introduction to stochastic epidemic models. In F. Brauer, P. van den Driessche, & J. Wu (Eds.), Mathematical Epidemiology (Lecture Notes in Mathematics, Vol. 1945). Springer.
14. Applebaum, D. (2009). Lévy Processes and Stochastic Calculus (2nd ed.). Cambridge University Press.
15. Bao, J., Yuan, C., & Mao, X. (2011). Stability in distribution of stochastic differential equations with jumps. Stochastic Processes and their Applications, 121(11), 2409–2431.
16. Øksendal, B., & Sulem, A. (2007). Applied Stochastic Control of Jump Diffusions (2nd ed). Springer.
17. Wang, K., & Wang, W. (2012). Stochastic epidemic models with Lévy jumps. Applied Mathematics Letters, 25(3), 494–498.
18. Zhu, C., & Yin, G. (2009). On competitive Lotka–Volterra model in random environments. Journal of Mathematical Analysis and Applications, 357(1), 154–170.
19. Gray, A., Greenhalgh, D., Hu, L., Mao, X., & Pan, J. (2011). A stochastic differential equation SIS epidemic model. SIAM Journal on Applied Mathematics, 71(3), 876–902.
20. Mao, X., & Yuan, C. (2006). Stochastic Differential Equations with Markovian Switching. Imperial College Press.
21. Yin, G., & Zhu, C. (2010). Hybrid Switching Diffusions: Properties and Applications. Springer.
22. Zhu, C., & Yin, G. (2009). On competitive Lotka–Volterra model in random environments. Journal of Mathematical Analysis and Applications, 357(1), 154–170.
23. Applebaum, D. (2009). Lévy Processes and Stochastic Calculus (2nd ed.). Cambridge University Press.
24. Gray, A., Greenhalgh, D., Hu, L., Mao, X., & Pan, J. (2011). A stochastic differential equation SIS epidemic model. SIAM Journal on Applied Mathematics, 71(3), 876–902.

25. Has'minskii, R. Z. (1980). Stochastic Stability of Differential Equations. Sijthoff & Noordhoff.
26. Khasminskii, R. (2012). Stochastic Stability of Differential Equations (2nd ed.). Springer.
27. Mao, X. (2007). Stochastic Differential Equations and Applications (2nd ed.). Horwood Publishing.
28. Yin, G., & Zhu, C. (2010). Hybrid Switching Diffusions: Properties and Applications. Springer.
29. Allen, L. J. S. (2008). An introduction to stochastic epidemic models. In F. Brauer, P. van den Driessche, & J. Wu (Eds.), Mathematical Epidemiology. Springer.
30. El bakkaoui, K., Méthodes stochastiques innovantes dans l'étude des systèmes dynamiques. Thèse de doctorat en Mathématiques Appliquées, Faculté des Sciences et Techniques de Tanger, Université Abdelmalek Essaâdi, 2025.
31. El idrissi, M., Stochastic Modeling of Epidemiological Dynamics with White and Lévy Noises Doctoral dissertation, Faculty of Sciences and Technology of Tangier, Abdelmalek Essaâdi University, 2025.
32. Capasso, V., & Serio, G. (1978). A generalization of the Kermack–McKendrick deterministic epidemic model. Mathematical Biosciences, 42, 43–61.
33. Mao, X. (2007). Stochastic Differential Equations and Applications (2nd ed.). Horwood Publishing.
34. Van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences, 180, 29–48.
35. Yin, G., & Zhu, C. (2010). Hybrid Switching Diffusions: Properties and Applications. Springer.
36. Disease dynamics of a probabilistic model with vaccination and nonlinear incidence rate, 2025.