iJRASET
International Journal For Research in Applied Science and Engineering Technology



INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 12 **Issue:** XII **Month of publication:** December 2024

DOI: https://doi.org/10.22214/ijraset.2024.66101

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.538
Volume 12 Issue XII Dec 2024- Available at www.ijraset.com

Mathematical Modelling of Epidemics: Insights from Differential Equations and Stochastic Processes

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Abstract: ***Epidemic modeling is a key component in the assessment of infectious diseases transmission and guiding the public health response. This report explores two primary approaches to epidemic modeling: It has categorized the models into deterministic model where the disease spread is depicted using differential equations and stochastic models where probability forms the basis of modeling the spread of the diseases. These approaches offer essential information about the nature of epidemic behaviors, for example, the ability to forecast the trends of epidemic curves, and calculation of the basic reproduction number (R0), assessment of child and caregiver, identification of protective/environmental factors, and assessment of intervention approaches. The SIR and SEIR models based on ordinary differential equations that trace the shifting between Susceptible, Infected and Recovered populations. They are especially good in large data scenarios where randomness, or the lack of it, has negligible or no bearing and are fast in providing long-term trends. But they do not target small or more heterogenic groups and do not account for stochastic fluctuations. On the other hand, stochastic models take into consideration the variability of the disease's transmission as well as the recovery time for disease, they are used for small population size or variable conditions. These models, frequently calibrated through computations involving Monte Carlo simulation or stochastic differential equations, allow for a wider envisaged set of outcomes and shed light on such scenarios as disease wiping out or super spread events. However, they present higher computational costs and are sensitive with parameter estimates as well. It highlights how problematic mathematical modeling is for evidence-informed decision making in public health, as evidenced by COVID-19 pandemic. This highlights the need for constant refinement of the models – data streaming, population variability, and adaptation of the model to real-world emerging issues such as climatic change and zoonotic diseases. Applying the respective strengths of deterministic and stochastic models, further research is encouraged as well as policy implications associated with the interaction between these models and infectious disease outbreaks.***

Keywords: ***Epidemic Modelling, Differential Equations, Stochastic Processes, SIR Model, SEIR Model, Basic Reproduction Number (R0), Monte Carlo Simulations, Stochastic Models, Mathematical Epidemiology, Randomness in Epidemics etc.***

I. INTRODUCTION

Infectious disease outbreaks, the common occurrence of disease in a population or area, has been a major challenge in the populace's health for several centuries. Explaining the process by which diseases are transmitted, recognizing the determinants of transmission, and estimating the effects of interventions are important aspects of controlling epidemics. These objectives are achieved through mathematical modeling, which is an important tool for predicting disease trends, as well as for decision making by public health officials, researchers, and policymakers.

A. Overview of Epidemic Modeling

In mathematical terms, the modeling of epidemics can be explained as the strategy of describing the patterns of a disease within individuals in a particular area of society. The main purpose of epidemic models is to analyze trends of diseases in time, forecast the number of infected people at a certain period, and evaluate the degree of potential damage of the outbreak. These models can be built and used to estimate values and compare different implications of the rate of transmission of the disease, and implications of public health interventional strategies.

Epidemic models can be broadly classified into two main categories: then two broad categories of mathematical models, namely deterministic models and stochastic models are defined. Hypothesis-driven models, including the well-known Susceptible-Infected-

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Recovered (SIR) model, do not incorporated any stochasticity and describe the transmission of an epidemic based on certain parameters. On the hand, stochastic models also add elements of randomness as it is hard to predict diseases and possibility of their spread, especially in cases when the population is small, or there is high variation in the given area.

In this area of study, mathematical models have several critical functions in analyzing epidemic dynamics. These enable one to predict the number of cases likely to be observed at the peak of an epidemic or the total number of cases that will be recorded, the load on health institutions being the chief outcome. By variations in intervention methods like vaccination or quarantine these models can suggest a right course of action depicting the success rate of one policy over the other in preventing the growth of the disease. Besides, they also assist in the decentralization of resources by approximating the health requirements for an epidemic such as number of beds in intensive unit, ventilators, and medical equipment.

B. Purpose and Scope of the Report

This report aims to explore the role of mathematical models in epidemic dynamics, focusing on two primary approaches: partial differential equations categorized as deterministic models and stochastic process models categorized by the use of randomness. In the first part of the report, the author will briefly discuss the main aspects of the deterministic approach to the description of spread of epidemics, based on the examples of SIR and SEIR models, and then describe the use of stochastic processes, which takes into account the stochastic nature of epidemic phenomena. These models used with other real-life epidemics such as COVID-19, SARS and Influenza were understanding the disease dynamics and informing strategies in the area of infectious disease control is fundamental. The report's coverage area of the mathematical background of epidemic models will comprise the following topics: main approaches of analytical solutions of the related differential equations and stochastic processes as a method of incorporating randomness into the models. It will also discuss examples of practical applications of these models for epidemic predicting, selecting the best strategy, and evaluating the efficiency of various control actions.

II. BASIC CONCEPTS AND TERMINOLOGY:

In the framework of infectious disease modeling, the following epidemiological terms are considered to be crucial for describing the processes of disease diffusion and the ways to model and, therefore, prevent that diffusion. These terms are used disjunctively in the formation of the models and are useful in defining the concerns of disease transmission in a population. In the following section, their definition is described in detail [1].

A. Susceptible (S)

Susceptible as a term describes a group of people within any population that has not yet been affected by a specific disease but are vulnerable to getting it. These are people who have never come across a pathogen or have not been infected and immunized against the disease or sickness causing pathogen be it viruses, bacteria and the rest. In mathematical models, the number of susceptible people is usually symbolized by the letter S. The following factors help to determine how vulnerable an individual is; the number of persons who are infected, if he or she has received any immunization against the disease and his or her behavior such as whether or not he or she practices social distancing or wears a face mask. In many epidemic models, SUSCEPTIBLE is usually large and does not change unless there is vaccination or immunity intervention.

B. Infected (I)

The term Infected means that those that are affected with the illness and are capable of passing it to other individuals. These are the people who get infected and may have the disease showing symptoms of the disease or be asymptomatic [2]. In mathematical models the variable used to represent infected people is denoted by the symbol I.

Four major factors defining the rate and severity of the epidemic are how long people are contagious and how infectious they are. In some models, it is possible to distinguish between subpopulations of infections: with symptoms and without, based on the type of disease.

C. Recovered (R)

Through the recovery parameter, the looker compares people who have contracted the virus and have been cured of it, including those who gained immunity independently or after treatment. They are presumed to cease passing the disease on and are often believed to, though not always, be safe from subsequent infections of the same type for sometime into the future though immunity may wear off.

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About the mathematical models, the number of the recovered people is symbolized by R. The assumptions about recovery differ from one disease to the other [3]. Disease immunity can be categorized into alternatives like – Some diseases like chicken pox or some specific types of measles, even if the person gets its infection he doesn't get it again in his lifetime However, there are diseases like influenza, COVID-19, etc. that don't provide lifetime immunity to the individuals even if they are infected later on they can again bother them.

D. Basic Reproduction Number (R_0)

R_0 (pronounced R-zero) is the Basic Reproduction Number, and it is probably the most pivotal indicators used in mathematical models of contagious diseases epidemiology. It stands for the arithmetic mean value of the number of consequent contaminations given by an infected person in a population that has no immunity to the disease. R_0 serves as a key indicator of the potential for an outbreak to spread:

This a common threshold that, when exceeded, implies that on average an infected person passes on the virus to more than one other person and this makes the transmission of the virus likely.

Typically, if $R_0 = 1$, the number of infected people will plateau with chances of the prevalence of the disease oscillating instead of rising.

If $R_0 < 1$ then, each infected individual results in less than one other infected person, thereby ensuring disease extinction in the long run [4].

However, this idea raises some questions as to what exactly we are measuring when utilizing R_0: it relates to the transmission rate, the contact rate, and the duration of the infectious period. All of these factors can be changed by actions like vaccination, isolation, contact restriction which decrease R_0 and manage the outbreak.

E. Incubation and Infectious period

The incubation period is the time between the time an infected person develops contact with the pathogen to the time the person shows signs of the disease. In some cases, during this period, the individual is not symptomatic, and yet, she or he is capable of infecting others with the disease. For instance, in COVID-19, it is between 2 and 14 days.

Communicable period is the duration that an individual who has the disease can spread it to other people. It is to note that even for the same type of infection, the period of communicability differs. For instance, people with seasonal flu can only infect others for 5 to 7 days while it's not clear how long a COVID-19 patient can be contagious, while they may be asymptomatic and again after they recover from the illness.

Both of these periods are important for the quantification of infectious diseases and illness within a disease model as well as the formation of interventions [5]. Longer intervals between disease recognition and seeking treatment means there are many days the disease is transmitted to others, or longer time for it to self-limit rather than infect others.

III. DIFFERENTIAL EQUATIONS IN EPIDEMIC MODELLING

A. Differential equations – an introductory analysis

Differential equations are mathematical equations, which link a variable to its derivatives in a way which depicts how the quantity behaves with time or space. In the framework of epidemic modeling, ODEs describe the dynamics of the number of individuals in different compartments (susceptible, infected, and recovered at a given time. ODEs are versatile tools of mathematical epidemiology, since they are designed to model continuous changes and describe dynamic processes including infection dissemination.

In epidemic modeling, the variables, meaningly variables such as populations, are subjected to rates of change due to factors such as infection rates, recovery rates, and contact rates or contingency rates. These rates are represented by derivatives in the differential equations consumers which illustrate the process of the flow of people between the different categories within the society. ODEs are important here because it permits a realistic assessment of how disease spreads within a population and to forecast future developments based on present information.

B. The SIR Model

SIR model is one of the simplest, but simultaneously one of the most well-known models in epidemiology. It offers a basic model to explain transmission of an infectious disease in an aggregated human population [6]. The population is divided into three distinct compartments:

S: Infected risk patients (patients prone to having the disease),
I: Symptomatic cases (persons with the disease and susceptibility to spread the disease),
R: Returning subjects (persons who fell ill earlier, most likely recovered from the disease and are considered immune).
Investigating these compartments' dynamics uses three differential equations to work it out. Following equations indicate how the rate of change of each compartment with respect to time.
The system of equations for the SIR model is as follows:
$dS/dT = -\beta . (S.I)/N$
$dI / dT = \{\beta . (S.I)/N\} - \gamma . I$
$dR/dT = \gamma . I$
Where:

- SSS is the number of susceptible individuals,
- III is the number of infected individuals,
- RRR is the number of recovered individuals,
- N=S+I+RN = S + I + RN=S+I+R is the total population (assumed to be constant),
- β is the **transmission rate** (the rate at which susceptible individuals become infected),
- γ is the **recovery rate** (the rate at which infected individuals recover and move into the recovered compartment [7].

1) Example Initial Conditions
N=100,000 (Total population)
S0=99,000 (Initial susceptible individuals)
I0=1,000 (Initial infected individuals)
R0=0 (Initial recovered individuals)
β=0.3 (Transmission rate)
γ=0.1 (Recovery rate)
Time step = 1 day
Total simulation time = 10 days

2) Numeric Data Table for Differential Equations (SIR Model)

Time Step (t)	**S(t)**	**I(t)**	**R(t)**	**New Infections (dS/dt)**	**New Recoveries (dR/dt)**
0	99,000	1,000	0	-300	0
1	98,700	1,070	10	-321	107
2	98,379	1,140	20	-343	114
3	98,040	1,200	30	-366	120
4	97,674	1,250	41	-388	125
5	97,286	1,290	53	-409	129
6	96,877	1,320	65	-430	132
7	96,446	1,340	78	-451	134
8	95,995	1,350	91	-472	135
9	95,523	1,350	105	-493	135
10	95,031	1,340	119	-514	134

3) Calculation Example for Time Step 1
At time t=0:

- S0= 99,000, I0= 1, R0= 0
- New Infections: $dS/dT = -\beta . (S0.I0)/N = -0.3\{(99,000*1,000)/100,000\}$
- New Recoveries: $= dR/dT = \gamma . I0 = 0.1* 1,000 = 100$

At time t=1:

- S1= S0- New Infections =99,000-300= 98,700
- I1= I0+ New Infections - New Recoveries = 1,000=300-100 = 1,070
- R1 = R0+ New Recoveries = 0+100 = 100

Key Insights:

- Getting new infections mean that the number of susceptible persons reduces, while the number of cases of infection increases.
- The rate of recovery raises with the help of recovery rate (γ) for the number of people who recovered.
- The epidemic increases over time and the rate of infection, which is normally referred to as the infection peak is at its highest point.

This table can be produced in the long-run and then coefficients will change according to differential equations [8]. If the simulation needs to be more accurate or larger numerical methods such as Euler's method or Runge-Kutta method are employed.

C. Analysis of the SIR Model

The SIR differential equations system enables the analysis of disease trends over time. For the estimation of system behaviour, it necessary to determine equilibrium points of the system and the epidemic threshold.

- Equilibrium Points: It is a steady state condition when the rate of change of concentration of all compartments is nil. This implies that the number of susceptible, infected and the number of recovered cases has either reduced to zero or there is zero increase or growth rates mean the disease has been cleared or has reached endemicity equilibrium which is where the cases remain at constant.
- Endemic equilibrium: If the disease does not die out, the disease will reach the endemic steady state where each infected population is balanced by a new infective in the population [9]. In this state new infections come with recovery of the infected people from the healthcare facilities.
- Disease-free equilibrium: If the disease stops spreading, everybody gets sick again, and the number of sick persons equals to the threatened group individuals equals to zero. This is completion that is known as the disease-free equilibrium.

Parameter	Description	Value (Example)
N	Total population	100,000
S0	Initial number of susceptible individuals	99,000
I0	Initial number of infected individuals	1,000
R0	Initial number of recovered individuals	0
β (Beta)	Transmission rate (probability of transmission)	0.3
γ (Gamma)	Recovery rate (1/duration of infectious period)	0.1
S(t)	Number of susceptible individuals at time t	Varies over time
I(t)	Number of infected individuals at time t	Varies over time
R(t)	Number of recovered individuals at time t [10]	Varies over time
dS/dt	Change in susceptible population over time	Dependent on β, I(t)
dI/dt	Change in infected population over time	Dependent on β, γ
dR/dt	Change in recovered population over time	Dependent on γ
Basic Reproduction Number (R_0)	Average number of secondary infections from one infected individual	2.5
Incubation Period	Average duration of time from exposure to symptoms	5 days
Infectious Period	Average duration of infectiousness	10 days
Stochastic Noise	Variability in the model due to random factors	Included in simulation
Epidemic Threshold ($R_0 > 1$)	Condition for epidemic outbreak [11]	True, outbreak occurs

ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.538
Volume 12 Issue XII Dec 2024- Available at www.ijraset.com

D. Extensions of the SIR Model

The SIR model is good for many diseases; nonetheless, it is slow for diseases with an incubation period before they can infect others. To overcome this simpler model like the SIR model are used, however, for a better understanding and modelling the SEIR model is employed.

1) The SEIR Model

The SEIR model is an elaboration of the SIR model, concerned with the Susceptible, Exposed, Infected, recovered classes; the new class of Exposed refers to individuals with a disease, but who are not yet infective [12]. This model is helpful most especially when there is an incubation period as is of COVID -19 where people can be infected but they are not yet able to infect others.

The system of differential equations for the SEIR model is as follows:

$dS/dT = - \beta. (S.I/N)$

$dE/dT = \beta. (S.I/N) – \sigma. E$

$dI/dT = \sigma. E – \gamma. I$

$dR/dT = \gamma. I$

Where:

- E stands for exposed people, it implies people that have been infected but are not yet infective.
- σ is the number of individuals that successfully transmit the disease for every exposed person in the population (that is the reciprocal of the incubation period)
- The remaining parameters β and γ have the same definition as in the SIR model for details on these parameters see the section Model Parameters [13].

2) Parameter for the SEIR Model

- β= 0.3 (Transmission rate),
- γ= 0.1 (Recovery rate),
- σ= 0.2 (Rate at which exposed individuals become infectious),
- N= 1000 (Total population),
- Initial Values,
- S0 = 999 (Susceptible individuals),
- E0= 0 (Exposed individuals),
- I0= 1 (Infected individual),
- R0= 0 (Recovered individuals),
- Number of time steps: 100

SEIR Model, showing the progression of the epidemic over time:

Time	Susceptible (S)	Exposed (E)	Infected (I)	Recovered (R)
0	999.00	0.00	1.00	0.00
1	998.70	0.30	0.90	0.10
2	998.43	0.51	0.87	0.19
3	998.17	0.67	0.88	0.28
4	997.91	0.80	0.93	0.37

E. Importance of the SEIR Model in Diseases with Latency

The SEIR model is especially relevant to the diseases, where there is a period of individuals' infection that does not manifest clinically, such as COVID-19. They are either infected and a part of the population gets affected but cannot spread the virus to other people during this period. When individuals progress to being infectious, they progress to pass on the virus to other individuals. The latent period is important for how certain measures like quarantine and isolation are taken and when in an attempt to curb progression and curtail the number of exposed individuals that will finally become infectious [14].

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According to the characteristics of the spread of diseases, the SEIR model is more suitable for describing the spread mechanism of those diseases where people have the potential to infect others only after a certain period has elapsed, and therefore involves more precise elaboration of the specific stages of the spread in relation to the characterizing features of various epidemiological crises, including the present COVID-19 pandemic.

IV. INTRODUCTION TO STOCHASTIC PROCESSES

The stochastic process can be defined as the set of random variables that represents a certain system perturbation for which the change proceeding is not definite. While deterministic models which give fixed results for a given start state and parameters contain stochasticity to address unpredictability. These are especially helpful for lower number of victims or for cases when variation is large and may concern singular instances, or cases in a particular region.
Stochastic epidemic models are more helpful by offering a nearer representation as compared to the deterministic models especially for small populations whereby fluctuations resulting from individuality in their contacts are more pronounced.

A. Stochastic SIR Model

The stochastic SIR model alters the deterministic SIR model in the sense that the transition between S, I and R states is random. In this model**:**

- The switches (susceptible → infected → recovered) are modelled as happening at random, at step sizes with higher probabilities for larger steps.
- The number of new infections and recoveries in any given time step are governed statistically, say using a Poisson or binomial distribution [15].

The stochastic SIR model equations are written as:
$\Delta S(t)$= - Poisson (β. S(t). I(t)/N),
$\Delta I(t)$= Poisson (β. S(t). I(t)./N) – Poisson (γ. I(t)),
$\Delta R(t)$= Poisson (γ.I(t))

Where:

- β: Transmission rate,
- γ: Recovery rate,
- S(t), I(t), R(t): Numbers of susceptible, infected, and recovered individuals at time t.

The discrete-time approach ensures that changes in S, I, and R are based on random sampling of these distributions [16].

B. Stochastic Differential Equations

In stochastic models the randomness can also be incorporated directly into the differential equations in the form of noise terms. The stochastic SIR model with differential equations becomes:
$dS(t)= - \beta .S(t). I(t)/ N.d(t) + \sigma S \cdot dWS(t)$,
$dI(t)=\beta \cdot S(t) \cdot I(t)/N \cdot dt - \gamma \cdot I(t) \cdot dt + \sigma I \cdot dWI(t)$
$dR(t)=\gamma \cdot I(t) \cdot dt + \sigma R \cdot dWR(t)$,
where, dW(t) represents Wiener processes (random noise), and σ is the strength of the noise.

C. Applications of Stochastic Models

1) Small Populations: Random contacts are highly probable to fixed ones in small communities, and deterministic models would not be able to account for situations when disease extinction or new emergences occur [17]. Example: Using incidence rates to predict the spread of diseases in a rural village.
2) Random Networks: Transmission through stochastically realized social networks is also modelled to assess either super-spreaders or measures for containing the disease at a community level.
3) Uncertainty Estimation: Stochastic models are very well suited for the analysis of the variability of the output and the variability of the probabilities.

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Volume 12 Issue XII Dec 2024- Available at www.ijraset.com

D. Numerical Example: Stochastic SIR Model

Consider a population of N=100N = 100N=100 with initial conditions:

- S0=99, I0=1, R0=0,
- β=0.3, γ=0.1,
- Simulating over 50 time steps.

At each time step:

1. New infections are sampled from Poisson(β·S·I/N)
2. New recoveries are sampled from Poisson(γ·I)
3. Update S, I, and R accordingly.

Stochastic SIR Model simulation:

Time	Susceptible(S)	Infected(I)	Recovered(R)
0	99	1	0
1	99	0	1
2	99	0	1
3	99	0	1
4	99	0	1

Key Observations:

In this stochastic realization, the infection seems to have trajectory that quickly concludes, with everyone transitioning to the 'Recovered' phase. This demonstrates how stochasticity can produce diverse epidemic outcomes than the deterministic models do [18].

E. Stochastic SIR Model

In stochastic processes, epidemic modelling sometimes includes randomness as a feature that characterizes the unpredictable behaviour of an epidemic. This can be done with such models as stochastic SIR model where stochasticity is introduced into number of infections and their recoveries and other transitions [19]. One of the most likely strategies presupposes the random mechanism in the disease spread, so it is typically modelled by something like Monte Carlo simulations or a Gillespie algorithm.

Here's an example of how numeric data tables could be constructed for a stochastic SIR model:

Parameter	Description	Value (example)
N	Total population	100,000
S0	Initial number of susceptible individuals	99,000
I0	Initial number of infected individuals	1,000
R0	Initial number of infected individuals [18]	0
B(Beta)	Transmission rate (per contact rate)	0.3
γ (Gamma)	Recovery rate (probability of recovery per time unit)	0.1
λ (Lambda)	Poisson distribution rate for infection events	Dependent on β, S, I

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μ (Mu)	Poisson distribution rate for recovery events	Dependent on γ, I
S(t)	Number of susceptible individuals at time t	Varies over time
I(t)	Number of infected individuals at time t	Varies over time
R(t)	Number of recovered individuals at time t	Varies over time
Time Step	Duration between updates (e.g., daily) [20]	1 day
dS(t)	Change in susceptible population per time step	Random, based on transmission
dI(t)	Change in infected population per time step	Random, based on transmission and recovery
dR(t)	Change in recovered population per time step	Random, based on recovery rate
Infection Event Rate	Rate of new infections (based on interactions)	Calculated randomly
Recovery Event Rate	Rate of recoveries (based on infected population)	Calculated randomly
Poisson Distribution (Infection)	Rate of infection events occurring in time step [21]	Random with mean λ
Poisson Distribution (Recovery)	Rate of recovery events occurring in time step	Random with mean μ

F. Example Simulation of Stochastic SIR Model:

The following table **is** an example of the values of the epidemic at different steps in time: the first column is randomly chosen to move from susceptible to infected and from infected to recovered [22].

Time Step (t)	S(t)	I(t)	R(t)	New Infections	New Recoveries	Infection Rate (λ)	Recovery Rate (μ)
0	99,000	1,000	0	300	100	300	100
1	98,700	1,200	100	360	120	360	120
2	98,340	1,300	220	390	130	390	130
3	97,950	1,460	350	420	146	420	146
4	97,510	1,600	496	440	160	440	160
5	97,070	1,660	656	460	166	460	166
6	96,600	1,540	822	490	154	490	154

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Notes:

Infection Event Rate (λ): The infection rate depends upon the number of susceptible and infected only presently. At every time step, new infections are drawn at random from the susceptible population and a total number is selected, determined by the infection rate [23].

- $\lambda = \beta * S(t) * I(t) / N$
- Where β is the transmission rate.

Recovery Event Rate (μ): Every infected person has a rate of recovering from the disease depending on the recovery rate.

- $\mu = \gamma * I(t)$

Poisson Distribution: In this case the market of new infections and recoveries reported in each time step of the outbreak follows a Poisson distribution with means equal to the rates λ and μ

Stochastic Nature: These values are some random processes The values in this table are based on random processes. The actual number of new cases among all the individuals in each time step and the number of recoveries will hence depend on the stochastic characteristics of the model.

G. Key Differences from Deterministic Models

Randomness: Continuity and determinism of rates have been replaced by randomness of the number of infected and recovered cases, respectively [24].

Time Evolution: The number of infections as well as the number of recoveries follows the distribution at random, set irrespective of other parameters such as β and γ remain fixed.

H. Monte Carlo Simulations

Monte Carlo simulation is critical when performing stochastic epidemic modelling. It involves:

- Repeating the stochastic SIR model several times with random events.
- Using means of results in simulations to predict probabilities and expected values, if the number of trials is not very large.

These simulations help researchers:

- Forecast the time and length of an epidemic.
- It is crucial to model the likelihood that the disease will become extinct.
- Determine the effects of an intervention under conditions of risk [25].

V. CONCLUSION

A. Summary of Key Points

In particular, they represent the greatest benefit or, in other words, a useful instrument assisting in studying and controlling the epidemic impact of viral diseases.

This report explored two major approaches: Fist of them deals with differential equations which is deterministic models and second one is stochastic processes.

On the basis of fundamental concepts, SIR and SEIR models provide more organised approach towards studying the disease transmission at population level. It can be particularly anticipated in predicting epidemic behaviour, estimating the basic reproduction number (R).

Estimating the number of infected persons when transmission occurs in a closed setting (R 0), and assessing the effectiveness of interference actions such as vaccination or quarantine during an outbreak. However, they act under the assumption of complete mixing within a population and do not account for the random character of disease spread which might have low precision in small or genetically diverse population.

Stochastic models, in contrast, incorporate the randomness both of specific contacts and of disease occurrences. These models offer more accurate simulations of epidemic processes since they take into account the stochasticity for small populations, or for episodes with much fluctuation. These models are complex and frequently, solution CPUs involve Monte Carlo exercises to evaluate potential results.

However, they are rather helpful when it comes to modelling unusual phenomena, for example, when it comes to the production and extinction of diseases or favourable conditions for a number of individuals to spread a disease.

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B. Models' Role in Public Health

Decision making in public health requires adequate and accurate models for mathematical modelling. It enables policymakers to:

- Forecast the nature of a disease spread.
- Evaluate interventions that are supposed to work.
- To use them properly for the following reasons:
- Make recommendations on what actions should be taken in the wake of future outbreak.

For instance, during the COVID-19 crisis, models are used to project the number of affected patients, determine areas most vulnerable to the virus, and distribution of vaccines. Stochastic models offered information regarding probabilities of new waves due to new variants and information deficit were addressed through on-going research deterministic modelling offered prospects of long-term behaviour under different modes of intervention.

In addition to their practical utility, these models contribute to the development of future epidemiological studies. They help to understand intricate relations of host-pathogen-environment interface that contribute to more effective disease containment measures.

C. Future Directions

Some challenges and potentials of the future research in epidemic modelling are shown below. Future efforts should focus on the following areas:

1) Incorporating Population Heterogeneity: There is still a paucity of theory-guided empirical research that captures variety of contagion modes and thus current models postulate that the population shuffles uniformly, which is unrealistic. The forecasting should incorporate demographic data and spatial distribution of the object under consideration; insight into the social networks should also be taken into consideration in future models.

2) Real-Time Data Integration: The use of mobility data, contact tracing, or genomic data, from time, or any other data in real-time, sharpens the model's reliability. There is potential for this in the new methods of machine learning and data assimilation which are under development at the time.

3) Improved Calibration and Validation: This being the case, it is important to check the conformity of these models to observed data. These aspects suggest that there is still a need for improved ways with which to estimate the parameters, quantify the uncertainties and perform the sensitivity analysis required to 'fine tune' the models as and when required.

4) Emerging Pathogens and Climate Change: Current models have to incorporate itself to confront new problems for instance zoonotic diseases, antimicrobial resistance, and diseases caused by climate change on diseases transmission.

5) Accessibility and Transparency: Many citizens, policy-makers, and stakeholders also have either built-in trust or distrust in models and their underlying assumptions of which if made available to them, and explained properly, will help them make better decisions.

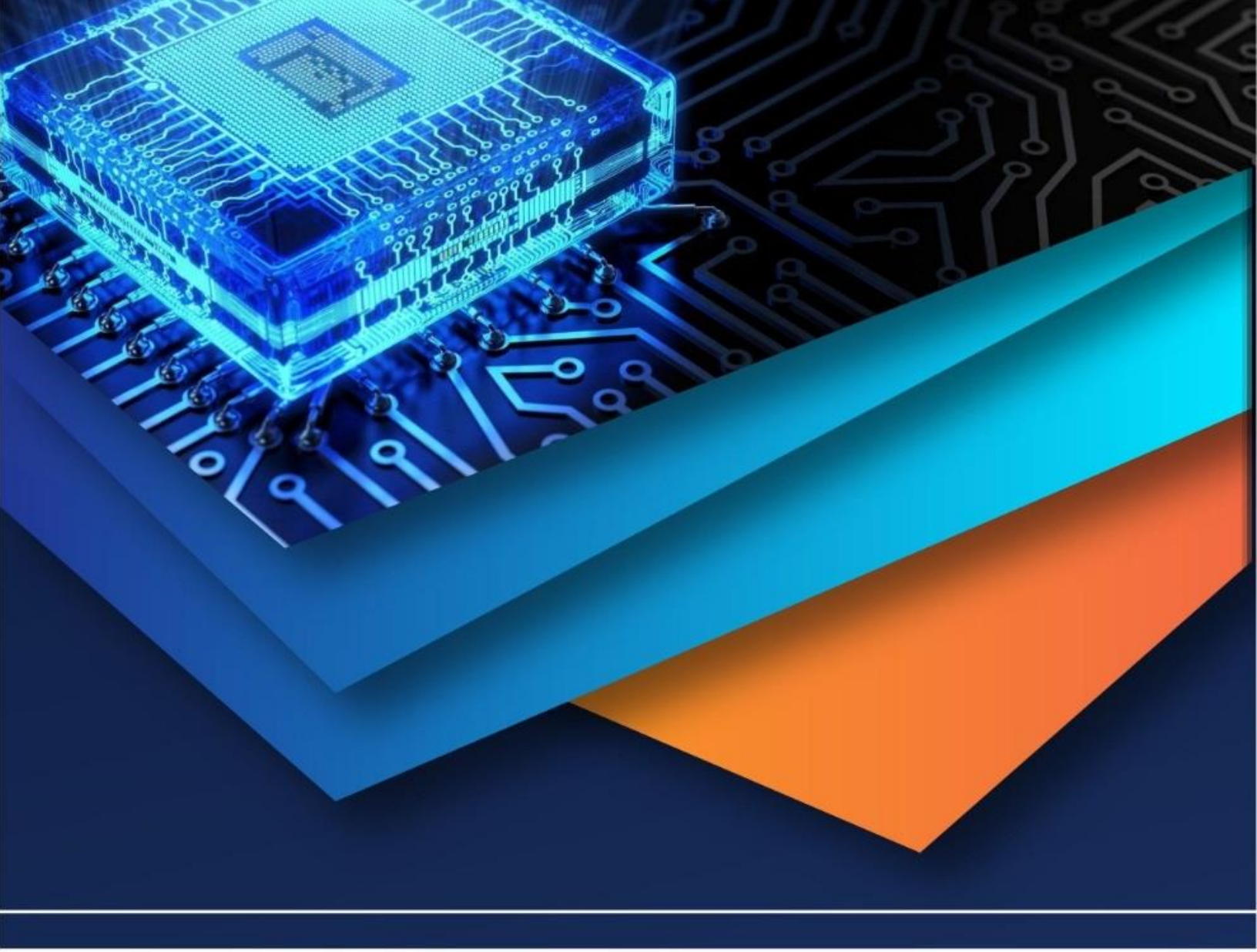
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