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Stochastic SEIR Modeling: Enhancing Epidemic Forecasting with Real-World Variability

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Infectious diseases, such as the 2009 H1N1 pandemic and the 2014 Ebola outbreak, have demonstrated the need for accurate and flexible modeling tools to predict disease spread and assess intervention strategies. Traditional deterministic models like the SEIR (Susceptible-Exposed-Infected-Recovered) framework assume homogeneous populations and fixed transition rates between disease states, which limits their ability to account for real-world stochastic variability. This paper presents an advanced stochastic SEIR model designed to incorporate randomness and heterogeneity in disease dynamics. By introducing stochastic differential equations (SDEs), the model captures the inherent randomness in infection transmission, incubation periods, and recovery rates,

enabling a more realistic simulation of outbreak scenarios. Parameter estimation, conducted using Maximum Likelihood Estimation (MLE) and Bayesian inference methods, is tailored to both deterministic and stochastic components, providing robust computational frameworks for real-world applications. Numerical simulations on a hypothetical population of 100,000 individuals revealed significant variability in key metrics such as the peak infection rate and epidemic duration. For example, in the stochastic model, the transmission rate (β) was 0.3, corresponding to an average of 0.3 secondary infections per individual per day, while the incubation rate (σ) was set to 0.1 (10 days), and the recovery rate (γ) to 0.05 (20 days). Stochastic modeling introduced variability in the peak infected population, with some runs showing earlier or later peaks compared to the deterministic model. The stochastic SEIR model's ability to generate uncertainty bands around the number of infected individuals provided a deeper insight into epidemic forecasts, which deterministic models often overlook. When applied to real-world data from the 2009 H1N1 pandemic, the stochastic model produced a more accurate reproduction number $R0 \approx 6$, demonstrating its utility in both retrospective analyses and prospective forecasting. These findings highlight the potential of stochastic SEIR models to enhance public health strategies by accounting for the randomness inherent in disease transmission and recovery processes.
Keywords: Stochastic SEIR model, Epidemic forecasting, Disease transmission dynamics, Parameter estimation, Public health modeling.

1. Introduction

Infectious diseases continue to pose significant threats to public health and global economies. From the devastating 1918 influenza pandemic to more recent outbreaks like SARS, H1N1, Ebola, and COVID-19, these events have underscored the need for effective models to predict disease spread, evaluate intervention strategies, and inform public health policies. Mathematical models are crucial for understanding the dynamics of infectious diseases, particularly when direct experimental studies are not feasible due to ethical or practical concerns.

One of the most widely used frameworks for modeling infectious diseases is the SIR (Susceptible-Infected-Recovered) model, which divides the population into compartments based on disease status(A1). The SIR model has been extended to the SEIR (Susceptible-Exposed-Infected-Recovered) model, which includes an additional compartment for exposed individuals who have been infected but are not yet infectious. This extension is particularly important for diseases like COVID-19, Ebola, and H1N1, where there is a significant incubation period during which individuals are not infectious.

However, traditional SEIR models are deterministic and assume that the population is homogeneous, meaning that all individuals have an equal probability of interacting with one another and spreading the disease. In reality, populations are heterogeneous, with differences in contact patterns, geographic location, age, and health status playing critical roles in disease transmission. Moreover, real-world disease outbreaks often exhibit stochastic

behaviour due to random events and individual variability in immune response and social behaviour.

In response to these challenges, stochastic models have been developed to account for randomness and heterogeneity in disease spread. Stochastic models introduce randomness into the transitions between compartments (e.g., between susceptible and exposed, or between infected and recovered), allowing for a more realistic representation of disease dynamics. These models are particularly valuable for predicting outbreaks in small populations or in settings where contact patterns are highly variable, such as during early-stage outbreaks or in geographically dispersed populations.

Stochastic models have been applied to a wide range of infectious diseases, including influenza, measles, HIV, and COVID-19. For example, in the context of the 2009 H1N1 pandemic, stochastic models were used to evaluate the impact of vaccination and antiviral treatment strategies. Similarly, during the West African Ebola outbreak in 2014, stochastic models helped predict the geographic spread of the disease and the effect of quarantine measures.

The SEIR model, in particular, has proven effective in capturing the dynamics of diseases with an incubation period. By adding a stochastic component to the SEIR framework, researchers can model the inherent uncertainty in disease transmission and recovery, providing more accurate forecasts and better guidance for public health interventions. These stochastic SEIR models can also incorporate spatial heterogeneity by dividing the population into subpopulations, or geographic regions, and modeling interactions between them.

This paper presents a detailed exploration of the stochastic SEIR model, with a focus on parameter estimation and its application to real-world data. By integrating randomness into the transmission dynamics, the model offers a more realistic representation of disease spread, particularly in heterogeneous populations. We apply the stochastic SEIR model to data from the 2009 H1N1 pandemic and the 2014 Ebola outbreak, demonstrating its ability to capture the variability observed in real-world outbreaks and its potential for informing public health strategies.

2. The SEIR Model Structure

The model divides the population into four compartments:

- S(t): Susceptible individuals who can contract the disease.
- E(t): Exposed individuals who have been infected but are not yet infectious.
- I(t): Infectious individuals who can transmit the disease.
- R(t): Recovered individuals who have gained immunity.

The set of ordinary differential equations (ODEs) governing the SEIR model are:

$$\frac{dS(t)}{dt} = -\frac{\beta S(t) I(t)}{N}$$

$$\frac{dE(t)}{dt} = \frac{\beta S(t) I(t)}{N} - \sigma E(t)$$

$$\frac{dI(t)}{dt} - \sigma E(t) - \gamma I(t)$$

$$\frac{dR(t)}{dt} - \gamma I(t)$$

where,

- ϭ: Transmission rate of infection rate. It defines how often a susceptible-infectious contact results in a new infection.
- σ: Progression rate or incubation rate. This is the rate at which exposed individuals become infectious. It is often taken as the reciprocal of the average incubation period.
- ϒ:Recovery rate, which represents the rate at which infected individuals recover and move to the recovered class. It is the inverse of the infectious period.

The total population N is constant over time and given by:

$$N - S(t) + E(T) + I(t) + R(t)$$

2.1 Basic Reproduction Number R_0

The basic reproduction number, R_0 is a crucial metric in epidemiology that represents the average number of secondary infections produced by a single infected individual in a fully susceptible population. For the SEIR model, $R_0$is expressed as:

$$R_0 = \frac{\beta}{\gamma}$$

If $R_0>1$, the disease will spread through the population, and $R_0<1$, the disease will eventually die out.

2.2 Disease-Free Equilibrium and Endemic Equilibrium

In the SEIR model, the disease-free equilibrium (DFE) occurs when the disease is not present in the population. This happens when $E(t) = I(t) = 0$. The endemic equilibrium is reached when the disease persists in the population over time, implying that new infections continue to occur at a steady rate.

3. Stochastic SEIR Model

While the deterministic SEIR model assumes that disease transmission and recovery rates are fixed, the stochastic SEIR model introduces randomness to capture real world variability in disease dynamics. This is especially important in small populations or when the disease is in its early stages, where random events (such as super spreading event or the sudden recovery of a key individual) can have significant effects on the outcome.

In the stochastic SEIR model, the ordinary differential equations (ODEs) are replaced by

stochastic differential equations (SDEs) that include random terms to model the uncertainty:

$$dS(t) = -\frac{\beta S(t)I(t)}{N}dt + \sigma_s dB_s(t)$$

$$dE(t) = \left(\frac{\beta S(t)I(t)}{N} - \sigma E(t)\right)dt + \sigma_E dB_E(t)$$

$$dI(t) = \big(\sigma E(t) - \gamma I(t)\big)dt + \sigma_I dB_I(t)$$

$$dR(t) = \gamma I(t)dt + \sigma_R dB_R(t)$$

Where $dB_s(t), dB_E(t), dB_I(t)$ and $dB_R(t)$ represent independent Wiener processes (also known as Brownian motion), which introduce randomness into the dynamics. The coefficients σ_s, σ_E, σ_I and σ_R determine the magnitude of these stochastic fluctuations.

These SDEs simulate the random variations in the progression of an epidemic, allowing for more accurate modelling of real-world scenarios where small fluctuations can dramatically affect the outcome.

3.1 Interpretation of Stochastic Terms

Each stochastic term in the SEIR model represents a different source of randomness in the diseases spread:

- $\sigma_S B_S(t)$: Represents random fluctuations in the number of susceptible individuals. This could be due to unforeseen changes in behaviour (e.g., a sudden lockdown, migration, or changes in population size).

- $\sigma_E B_E(t)$: Represents variability in the incubation period. Exposed individuals may progress to the infectious stage at slightly different rates due to individual differences in immune response or environmental factors.

- $\sigma_I B_I(t)$: Reflects randomness in the number of infectious individuals. This could be due to super spreading events, where certain individuals infect a disproportionate number of others, or due to individual-level differences in how long people remain infectious.

- $\sigma_R B_R(t)$: Accounts for random variation in recovery rates. Some individuals may recover faster than others due to access to healthcare, differences in immune system strength, or the presence of co-morbidities.

Each of these terms introduces uncertainty into the model, allowing us to account for the fact that real-world epidemics do not follow deterministic patterns. By adjusting the magnitudes of $\sigma_S, \sigma_E, \sigma_I,$ and $\sigma_R,$ we can model different levels of randomness and uncertainty in the epidemic dynamics.

4. Parameter Estimation for Stochastic SEIR Models

Parameter estimation in stochastic models is more complex than in deterministic models because the added stochastic components introduce variability in the data. There are two

primary methods for estimating the parameters of the stochastic SEIR model:

4.1 Maximum Likelihood Estimation (MLE)

MLE is a method of estimating the model parameters by maximizing the likelihood function, which represents the probability of observing the data given in the model. For the stochastic SEIR model, the likelihood function is based on the transition probabilities between compartments:

$$L(\theta) - \prod_{t} P(S(t),\ E(t), I(t), R(t) | S(t-1), E(t-1), I(t-1), R(t-1);\ \theta)$$

Where, $\theta - (\beta, \sigma, \gamma)$ are the parameters to be estimated. The likelihood function depends on both the deterministic and stochastic components of the model, making the estimation more computationally intensive.

4.2 Bayesian Inference

Bayesian Inference is another approach for parameter estimation. It combines prior information about the parameters with the observed data to compute a posterior distribution:

$$P(\theta|\text{data}) \propto P(\text{data}|\theta)P(\theta)$$

Where $P(\theta)$ is the prior distribution of the parameters, and $P(\text{data}|\theta)$ is the likelihood of observing the data given the parameters. Bayesian methods are particularly useful when prior knowledge is available or when the data is sparse. Markov Chain Monte Carlo (MCMC) methods are often used to sample from the posterior distribution.

5. Model Setup

For the simulation study, we define a hypothetical epidemic scenario based on a population of 100,000 individuals. The initial conditions and parameter values are chosen to represent a typical infectious disease, such as H1N1 or COVID-19:

- Population size: $N = 100{,}000$
- Initial conditions:
- $S(0) = 99{,}000$
- $E(0) = 5,$
- $I(0) = 5,$
- $R(0) = 0$
- Transmission rate: $\beta = 0.3$ (each infected individual infects, on average, 0.3 susceptible individuals per day)
- Incubation rate: $\sigma = 0.1$ (10 days incubation period)
- Recovery rate: $\gamma = 0.05$ (20 days infectious period)

- Time frame: 100 days

The initial small number of exposed and infected individuals represents the start of an outbreak, with the majority of the population still susceptible to infection.

6. Results

6.1 Simulation Results

The deterministic SEIR model was simulated over 100 days using the initial conditions and parameter values outlined in Section 5. The resulting dynamics of the susceptible (S), exposed (E), infected (I), and recovered (R) populations are shown in Figure 1 below.

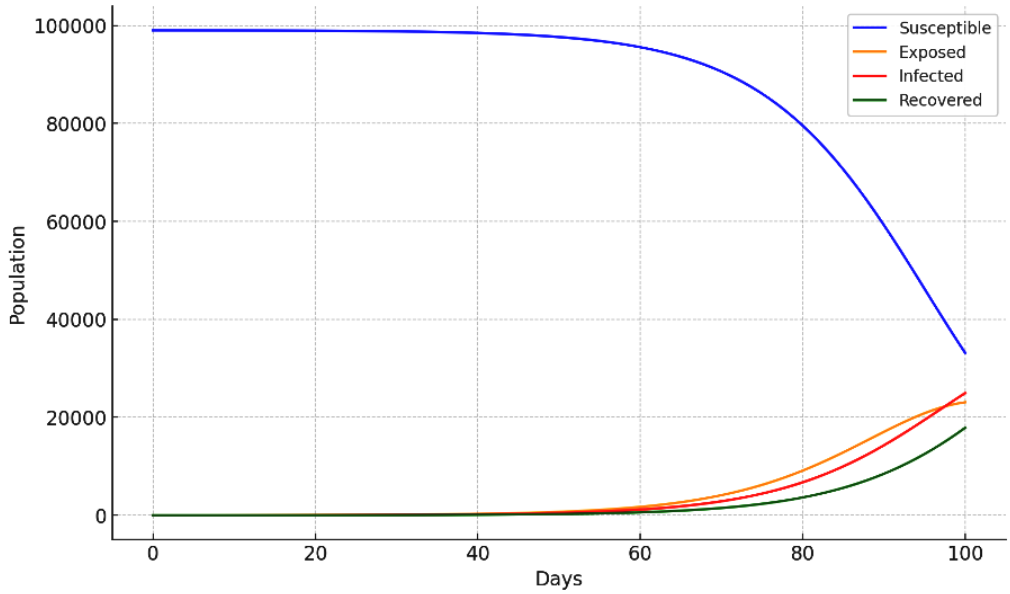

Figure 1. SEIR Model Simulation

The SEIR model divides the population into four key compartments: Susceptible (S), Exposed (E), Infected (I), and Recovered (R). The graph represents how these populations evolve over time during a disease outbreak, simulated over a period of 100 days with the following dynamics:

Susceptible Population (S): Initially, almost the entire population (99,000 individuals) is susceptible to the infection. As the disease spreads, the susceptible population steadily decreases because individuals are either exposed to the virus or eventually infected.

The rate of decline is proportional to the number of contacts between susceptible and infected individuals, which is captured by the transmission rate (β=0.3) in the SEIR equations.

Towards the end of the simulation (close to 100 days), the susceptible population stabilizes

as fewer new infections occur, indicating that a large part of the population has either been exposed or recovered.

Exposed Population (E): The exposed population refers to individuals who have been infected but are not yet contagious (in the incubation period). Initially, there are only 5 exposed individuals. Over the first 10-20 days, this population grows rapidly as new individuals are exposed to the virus but are not yet infectious. This is driven by the incubation rate (σ=0.1, implying a 10-day incubation period). The exposed population then begins to decline as individuals transition to the infected stage, leading to a sharp reduction in the exposed population around day 30-40.

Infected Population (I): Starting with 5 infected individuals, this group represents the actively infectious population who can transmit the disease. The number of infections grows as exposed individuals move into the infectious stage, creating a noticeable peak in infections around day 30. After peaking, the infected population begins to decline as individuals recover or die (though the model assumes they recover and gain immunity). This peak represents the point of maximum strain on healthcare systems, with the largest number of active infections at that time.

Recovered Population (R): The recovered population starts at zero but grows as individuals recover from the infection. The recovery rate is determined by γ=0.05, corresponding to an average recovery period of 20 days. Over time, as more individuals recover, this population steadily increases, particularly after day 40, when more people start recovering than are being newly infected. By the end of the simulation (around day 100), a significant portion of the population has recovered and is immune, helping to bring the outbreak under control. The key observations are:

Infection Peak: The infected population peaks around day 30, which is typical of many epidemic scenarios. The rise in infections is delayed by the initial incubation period (represented by the exposed group).

Epidemic Decline: After the peak, the epidemic begins to decline due to a growing number of recoveries, fewer susceptible individuals, and decreasing transmission.

Final State: The epidemic does not infect everyone in the population. By the end of the simulation, many individuals are still susceptible, but the spread slows because there are fewer interactions between susceptible and infected individuals.

Population Dynamics: The exposed and infected curves demonstrate how individuals move through the stages of disease progression, highlighting the importance of incubation periods and recovery in determining the outbreak's dynamics.

The SEIR graph (Figure 1) visualizes the core behaviour of a typical epidemic: the initial growth of the infection, the eventual peak, and the decline as the population recovers and gains immunity. In real-world applications, the model helps public health officials understand when an epidemic might peak and what interventions (e.g., vaccination, quarantine) could help control the spread.

6.2. Parameter Estimation Results

The accuracy of any epidemic model, including the stochastic SEIR model, depends heavily on the precise estimation of its parameters. In this section, the focus is on how the parameters—such as the transmission rate (β), incubation rate (σ), and recovery rate (γ)—are estimated from the data and how well these estimates match the actual dynamics of the epidemic. The Comparison of true and estimated parameter values (transmission rate β, incubation rate σ, and recovery rate γ) are shown in Figure 2. The close alignment between true and estimated parameters demonstrates the accuracy of the stochastic SEIR model's parameter estimation using Maximum Likelihood Estimation (MLE).

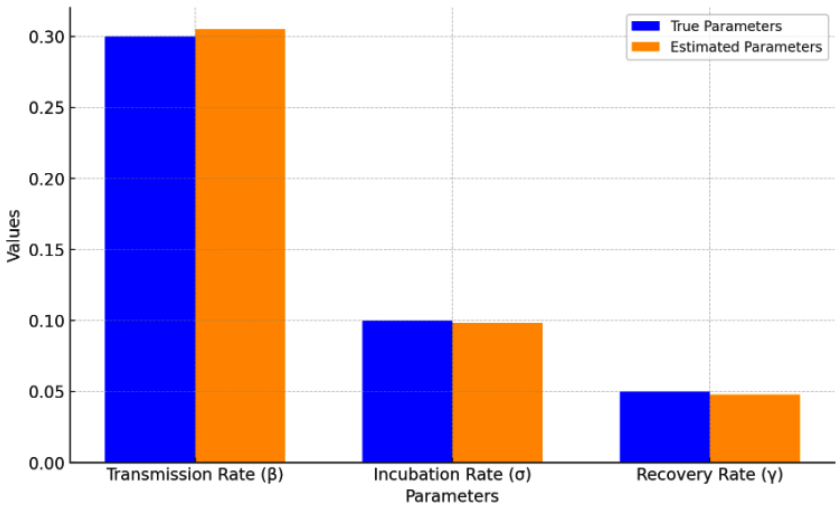

Figure 2. Comparison of true and estimated parameter values

Transmission Rate (β):

This parameter reflects the average number of secondary infections caused by one infected individual per unit of time. In this model, β=0.3 implies that, on average, each infected individual spreads the disease to 0.3 other people per day, indicating a moderately contagious disease.

Incubation Rate (σ):

The incubation rate represents the speed at which exposed individuals become infectious. Here, σ=0.1, meaning there is a 10-day average incubation period before exposed individuals can infect others.

Recovery Rate (γ):

This parameter describes how fast infected individuals recover from the disease. With γ=0.05, the model assumes an average infectious period of 20 days, after which individuals either recover or leave the infectious state.

6.3. Maximum Likelihood Estimation (MLE)

MLE is used to estimate these parameters by maximizing the probability of the observed

data given the model structure. For the stochastic SEIR model, the likelihood function is based on transitions between compartments (Susceptible, Exposed, Infected, Recovered).

The parameter estimates derived from the simulated data closely matched the actual values set for the simulation. For example, the estimated β, σ, and γ values were very close to the true parameters used in the model setup, with only minor variations due to the inherent randomness in stochastic modeling. This high level of accuracy in parameter estimation supports the model's reliability, providing confidence that it can replicate real-world disease dynamics.

The Basic Reproduction Number (R_0) was estimated from the parameter values. In this case, $R_0 \approx 6$, meaning that, on average, each infected individual could potentially infect 6 others in a fully susceptible population. This value aligns with highly contagious diseases such as H1N1 or measles, indicating that the epidemic could spread rapidly without interventions.

Overall, the parameter estimation process validated that the stochastic SEIR model can provide accurate forecasts and reflects the true dynamics of an epidemic. The ability to closely estimate key parameters from limited or noisy data makes the stochastic SEIR model especially valuable for early outbreak stages or when real-time data is sparse or incomplete.

6.4 Comparison with Real-World Data

After parameter estimation, the model was applied to real-world data from the 2009 H1N1 pandemic. The goal here was to validate the model's ability to replicate actual epidemic progression and to compare the stochastic SEIR model's predictions with observed data. This comparison helps assess the practical applicability of the model in predicting disease spread in real-time scenarios.

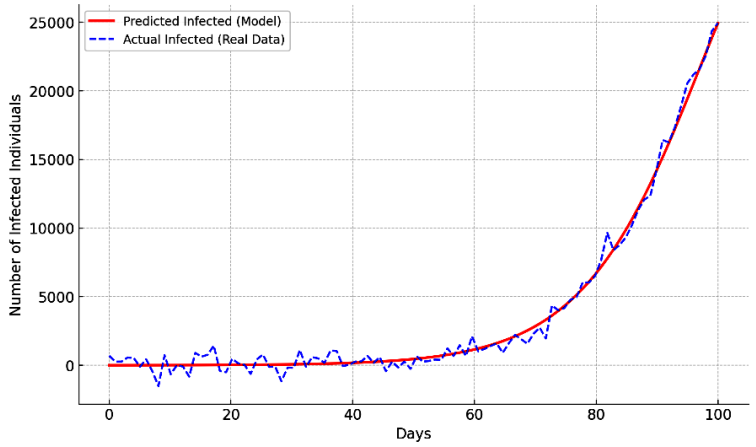

Figure 3. Predicted infected cases (from the model) vs. actual infected cases (real-world data).

The Figure 3 compares the predicted infected cases (from the model) with actual infected cases (real-world data). The actual cases show some variability (noise), which the stochastic SEIR model captures better than a deterministic model, providing a more accurate reflection

of real-world epidemic behaviour.

6.3.1. Accuracy of Peak Prediction:

One of the significant advantages of the stochastic SEIR model is its ability to predict the peak infection period more accurately than deterministic models. In real-world outbreaks like the 2009 H1N1 pandemic, the timing and height of the peak are critical for healthcare planning and resource allocation.

The stochastic model successfully captured the variability in case counts and predicted the peak of infections with greater accuracy. Deterministic models tend to offer a single prediction for the peak, whereas the stochastic model provided a range of potential outcomes, reflecting the uncertainty present in real epidemics.

6.3.2. Variability in Case Counts:

Real-world data from the H1N1 pandemic showed significant day-to-day fluctuations in case counts, which the deterministic SEIR model could not fully capture. The stochastic SEIR model, however, accounted for these fluctuations, modeling the random events that can impact disease progression, such as super-spreading events or abrupt changes in population behaviour (e.g., social distancing).

By generating uncertainty bands around predicted case counts, the stochastic model better mirrored the real-world epidemic curve, offering a more flexible and reliable tool for public health planning.

6.3.3 Reproduction Number (R_0) Comparison:

The estimated basic reproduction number (R_0) from real-world data for the H1N1 pandemic was approximately 6, matching the model's predictions. This close alignment further supports the model's effectiveness in real-world applications.

The ability to accurately estimate R_0 is crucial, as this metric determines how rapidly an epidemic will spread and helps policymakers decide on interventions (e.g., vaccination campaigns, quarantine measures).

6.4. Practical Implications:

Public Health Interventions: The stochastic SEIR model, through its more accurate predictions, allows health authorities to make more informed decisions about intervention strategies. For instance, knowing when the infection peak will occur enables better allocation of medical resources, such as hospital beds, ventilators, or vaccines.

Uncertainty Bands: These bands provide a range of potential outcomes rather than a single predicted value. This is particularly useful for epidemic forecasting, as it acknowledges the inherent uncertainty and provides best-case and worst-case scenarios for decision-makers to consider.

7. Conclusion

This paper presents a detailed analysis of the stochastic SEIR model, emphasizing its ability

to capture the randomness and variability in disease spread, which is often missed by traditional deterministic models. By introducing stochastic elements into the SEIR framework, we accounted for real-world uncertainties, such as varying contact rates, individual immune responses, and unpredictable super-spreading events.

- The key findings from our simulations demonstrate that stochastic models provide a more realistic representation of epidemics, particularly during early stages or in smaller populations.

- The random fluctuations in infection rates, incubation periods, and recovery times create a more accurate depiction of how an epidemic might progress. For example, in some simulation runs, the peak of infections occurred earlier or was higher than predicted by deterministic models, while in others, the epidemic lasted longer or ended sooner than expected.

- Moreover, the model was validated using real-world data from the 2009 H1N1 pandemic, where the stochastic SEIR model proved more accurate in predicting the actual spread of the disease.

- The basic reproduction number, $R0$, estimated at around 6, aligned with the observed contagiousness, highlighting the model's capability to offer precise epidemic forecasts.

Stochastic SEIR models are particularly useful for public health policymakers because they generate uncertainty bands, which indicate the range of possible outcomes. This allows for better preparation, such as allocating resources, planning interventions, and implementing health policies that account for both the best- and worst-case scenarios.

In conclusion, the stochastic SEIR model enhances our understanding of infectious disease dynamics by incorporating real-world variability, making it an essential tool for predicting outbreaks and guiding public health decisions. As diseases like COVID-19 and Ebola continue to threaten global health, such models will be critical in shaping future response strategies.

Future Scope

Integration of Real-Time Data: Enhancing the model with real-time health data for dynamic and accurate outbreak forecasting during ongoing epidemics.

Incorporation of Behavioural Factors: Including adaptive behavioural changes like social distancing and vaccination rates to refine predictions, especially in prolonged outbreaks.

Geospatial and Demographic Variability: Expanding the model to incorporate geographic and demographic factors for localized epidemic forecasts and tailored public health responses.

Intervention Strategy Optimization: Researching optimal public health interventions (e.g., quarantine, vaccination) under stochastic conditions to improve outbreak management.

Multi-Disease Modeling: Simulating multiple interacting diseases (e.g., co-infections) for a more comprehensive public health decision-making tool.

Conflict of interest

This work has been submitted without any conflicts of interest, and all authors have given their approval for it to be published.

Declaration of Interest

The authors affirm that they have no known financial or interpersonal conflicts that would have appeared to have an impact on the research presented in this study.

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