

Analyzing epidemic spread through differential equations : SEIR model with time-varying parameters and social structure

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Abstract

New Model of Public Health Value of Vaccination Integrating Social Network Structure and Time-Varying Parameters. We introduce a new mathematical model of public health

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value of vaccination that integrates social network structure and time-varying parameter into a traditional model, the SEIR model. Traditional epidemiological models tend to assume homogeneity of the population and constant parameters for all health-relevant measurements such as transmission rates and vaccine efficacy. However, in practical contexts, the contact rates between individual and population and the epidemiology of transmission of the disease vary extensively among different social groups and over time.

Subject Classification: 34A34.

Keywords: Herd immunity, SEIR model, Social networks, Vaccination strategies.

Introduction

Mathematical modelling is a great tool in understanding the spread of disease and the efficacy of interventions, such as vaccination. In educational contexts, integrating mathematical models into public health curriculum can promote students' greater acquisition of data literacy and critical thinking skills regarding complex epidemiological dynamics and decision-making processes. Previous models have used uniform contact rates and static parameters, which are often oversimplifications for real epidemics. Our model considers heterogeneity in individual interactions represented by their spatial location, such as schools, workplaces, homes—and allows significant variables such as disease transmission rate and vaccine efficacy to be shaped by time. Through simulations, our model provides both accurate predictions of the trend of infection trends and the thresholds of herd immunity. The model also serves as an excellent learning tool both for learners and researchers. This approach allows for 'what if' scenarios to be explored, how behavioural and policy changes impact infection trends and understand how interplays with mathematical theory and social behaviour play a role in public health planning.

Literature Review

Bardach et al. [1] finds that how mathematical models have been applied to evaluate the health burden caused by alcohol consumption and the cost-effectiveness of interventions targeting this issue. The authors reviewed studies published up to mid-2017 and selected 63 relevant works from over 4,000 initial records. This study was grouped into three main modelling approaches most commonly used. The review highlights that while various modelling strategies are employed, each comes with its strengths and data requirements. They argue the choice of model should

be guided by available local data and specific health policy goals. Overall, the study offers valuable insight for policymakers and researchers designing alcohol-related public health strategies, emphasizing the practical use of modelling to inform decisions on resource allocation and intervention planning.

Buonomo, Carbone, and D'Onofrio [2] expands previous models of voluntary vaccination behaviour by integrating seasonal variations in disease transmission and public health interventions within an SEIR framework. Unlike traditional economic approaches, the authors use a biologically grounded method to model individuals' changing willingness to vaccinate based on social imitation. A key insight of the paper is that the average transmission rate alone does not fully determine whether a disease can be eliminated. Instead, the shape and amplitude of seasonal fluctuations play a critical role. Notably, the research shows that strong seasonal dips in transmission—such as during school holidays—can enhance the effectiveness of public health strategies, potentially leading to disease eradication even when average transmission rates suggest otherwise. Through analytical techniques and simulations, the authors demonstrate how timing and intensity of interventions must be aligned with these seasonal patterns to achieve optimal results. The study contributes both methodologically and practically to the understanding of how behaviour and seasonality intersect in epidemic control.

Chumachenko [3] presents a timely and innovative agent-based modelling framework that explores how misinformation and vaccine hesitancy shape infectious disease dynamics. Tested through a COVID-like scenario, the simulations show that even low levels of vaccine skepticism can lead to higher death rates and prolonged outbreaks. Conversely, well-timed counter misinformation strategies can mitigate these effects by boosting vaccination rates. This work contributes meaningfully to public health planning by emphasizing the critical role of communication and behavioural dynamics in epidemic control. It offers a valuable tool for testing policy responses in the face of uncertainty and misinformation.

Alemneh et al. [4] says that previous studies have shown that mathematical models and optimal control strategies effectively reduce cholera transmission through vaccination, treatment, sanitation, hygiene, and awareness programs. However, most models considered only limited interventions. This study addresses that gap by integrating direct and indirect transmission with five combined control measures and cost-effectiveness analysis for improved cholera management.

Authors in [5, 6] has developed a mathematical model based on the Susceptible–Infectious–Recovered (SIR) framework using differential equations to analyse infectious disease transmission. Their study incorporated population density, vaccination strategies, and disease-specific parameters to better understand epidemic dynamics. Stability analysis, sensitivity analysis, and numerical simulations were performed to evaluate disease progression and intervention effectiveness. The findings highlighted the importance of the basic reproduction number (R_0) in outbreak prediction and demonstrated that mathematical modelling provides valuable support for public health planning and disease control strategies.

Research Method

Quantitative methodology is applied research that focuses on numerical data, measurements, and mathematical analysis to understand phenomena. It emphasizes objectivity, precision, and reproducibility by using numbers, formulas, and statistical or computational tools. The model uses a set of differential equations to describe how individuals move between these compartments over time, based on parameters like transmission rate, incubation rate, and recovery rate.

This is extended model of SEIR (Susceptible–Exposed–Infected Recovered) compartmental framework by adding social network structures and incorporating time-dependent functions for key parameters like - transmission rates and vaccine efficacy.

Traditional SEIR Model - four compartments:

- $S(t)$ means Susceptible individuals
- $E(t)$ means Exposed (infected but not yet infectious)
- $I(t)$ means Infectious individuals
- $R(t)$ means Recovered (and immune) individuals

The system of differential equations governing the dynamics is:

$$dS(t)/dt = -\beta S(t) I(t)$$

$$dE(t)/dt = \beta S(t) I(t) - \sigma$$

$$E(t) dI(t)/dt = \sigma E(t) - \gamma$$

$$I(t) dR(t)/dt = \gamma I(t)$$

where:

- β (Transmission rate): This represents how easily the infection spreads
- σ (Incubation rate): This refers to how quickly an infected person starts showing symptoms
- γ (Recovery rate): This indicates how fast an infected person recovers

Time-Varying Parameters

Dynamic Transmission Rate ($\beta(t)$)

The transmission rate β is not constant in real life. It changes due to interventions, behavior, and seasons.

Vaccine Efficacy ($\epsilon(t)$)

Vaccine protection wanes over time.

The New SEIR Model with Time-Varying Parameters

With these modifications, the final set of equations becomes:

$$dS/dt = -\beta(t) S I(t)$$

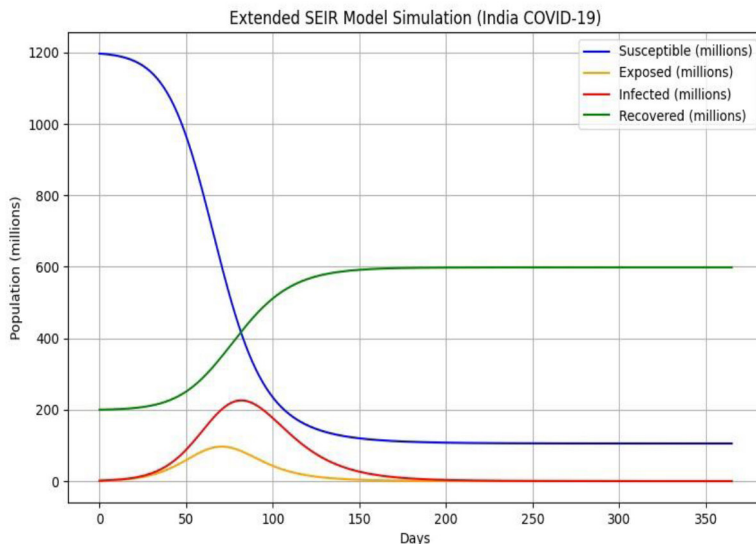


Figure 1
Extended SEIR Model Simulation

$$dE/dt = \beta(t) S I - \sigma E$$

$$dI/dt = \sigma E - \gamma I$$

$$dR/dt = \epsilon(t) \gamma I$$

The data sample of covid-19 is taken for reliability of this model and a graph Figure 1 is produced with the help of python programming.

Participants

This study utilizes a large-scale dataset representing a population of approximately 1.2 billion individuals to model the spread of COVID-19 using the extended SEIR framework. Population Size is approximately 1.2 billion individuals, representing the total population under study. Data Sources: Epidemiological data on COVID-19 infections, recoveries, and vaccination rates collected from national health databases and public health surveillance systems during the study period.

Results Discussion and Conclusions

This research builds upon the traditional SEIR model by integrating time dependent parameters and social network frameworks, which leads to more accurate representations of how diseases spread and the effectiveness of vaccinations. By factoring in diverse patterns of interactions and shifts in transmission and vaccination rates, the model offers better predictions regarding herd immunity levels and the overall impact on public health. The results from the simulations highlight the value of this approach in refining vaccination strategies and guiding policy choices. In conclusion, this study contributes to more flexible and data-oriented public health measures that ensure effective disease management and optimal resource allocation as epidemiological conditions change.

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