Mangalayatan Journal of
Scientific and Industrial Research

Man. J. Sci. Ind. Res.
Volume 2 (1) (2025), 25201
ISSN: 3049-2815

Article

Dynamic Reduction Factors in SEIR Models: Enhancing Disease Dynamics Prediction

Santosh C J[1] and Dr. Anurag Shakya[2]

[1]*Institute Of Business Management & Commerce, Mangalayatan University, Aligarh, Uttar Pradesh, India*
[2]*Institute Of Business Management & Commerce, Mangalayatan University, Aligarh, Uttar Pradesh, India*
**Corresponding author: 20201006_santosh@mangalayatan.edu.in*
Anurag.Shakya@mangalayatan.edu.in

Abstract

The SEIR model is a foundational framework in epidemiology used to analyze the transmission of infectious diseases. However, traditional models often treat susceptibility as static, neglecting the real-time effects of interventions such as vaccination campaigns and increased exposure awareness. This research introduces dynamic susceptibility reduction factors into the SEIR model to better reflect evolving disease dynamics. By modifying the compartmental equations, we account for changes in the susceptible population over time, influenced by exposure rates and immunization efforts. Using hypothetical data and standard epidemiological parameters, we demonstrate the enhanced model's behaviour over a 10-day simulation. Results indicate that dynamic reduction factors significantly slow the spread of disease and provide a more realistic depiction of outbreak progression. This improvement enhances the model's predictive power and supports more effective public health decision-making. Incorporating real-time factors into disease modelling is essential for accurate forecasting and for guiding timely interventions during epidemic or pandemic events.

Keywords: Pandemic, Ordinary differential calculus, Susceptibility, SEIR, Infectious disease

1. INTRODUCTION

The SEIR model is an essential tool in epidemiological research for simulating disease spread [1]. It segments the population into four categories: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R), effectively illustrating the transmission dynamics of diseases [2]. However, conventional SEIR models frequently neglect the influence of dynamic reduction factors, like rising exposure and vaccination rates, which can substantially modify disease dynamics. We hypothesize that adding dynamic reduction factors will improve the model's ability to reflect actual disease spread. This research aims to integrate dynamic susceptibility reduction factors into the SEIR model and analyze their effects on disease spread. Infectious diseases pose a significant threat to public health, and accurate

Received: 23 April, 2025; Accepted: 17 May. 2025

modelling of their spread is crucial for effective intervention and control [3]. By incorporating an exposed compartment, the SEIR model builds upon the basic SIR structure to offer a more nuanced understanding of disease progression [4]. As factors like increased exposure and vaccination rates influence the number of susceptible individuals, accounting for these dynamics becomes essential. Including dynamic reduction factors in the SEIR model strengthens its predictive capacity and offers more valuable insights for shaping public health strategies. This study seeks to address limitations in conventional SEIR frameworks by embedding dynamic susceptibility adjustments and analyzing their influence on disease progression. Through this approach, we aim to deliver a more accurate depiction of transmission patterns and support the development of more effective intervention strategies.

2. BACKGROUND

Infectious disease modeling plays a vital role in forecasting outbreaks and supporting the development of effective public health strategies. The SEIR model enhances the traditional SIR approach by introducing an exposed compartment, allowing for a more detailed depiction of disease transmission and progression [5]. While this framework improves analytical depth, it is important to consider that variables such as rising exposure levels and vaccination coverage can alter the size of the susceptible population, which must be accounted for to maintain model accuracy. To improve reliability, this study incorporates dynamic reduction elements into the SEIR structure. These elements include changing behaviours, immunization trends, and intervention measures that collectively influence susceptibility and disease transmission. The SEIR framework classifies individuals into four groups [6]: those at risk of infection (Susceptible) [7], those who have been exposed but are not yet infectious (Exposed) [8], those currently capable of spreading the disease (Infectious) [9], and those who have recovered and acquired immunity (Recovered) [10].

Incorporating dynamic reduction components into the SEIR framework enables the model to more accurately reflect real-world epidemic patterns and evaluate the effects of public health interventions. These components include factors such as increased exposure, vaccination efforts, behavioural changes, and policy measures—all of which contribute to lowering the number of susceptible individuals and influencing overall transmission trends. This study focuses on advancing the SEIR model by integrating dynamic susceptibility reduction factors and examining their role in shaping disease dynamics. Our goal is to deliver a more precise depiction of disease spread while offering insights that support the development of effective public health strategies. The upcoming sections outline the methodology, theoretical basis, and mathematical derivations used to construct the enhanced SEIR model, followed by an analysis of the results and their implications.

3. Methods

3.1. Study design and participants

The study involves a theoretical analysis of the SEIR model with dynamic reduction factors. No human participants are involved. The focus is on deriving the equations and demonstrating the model with hypothetical data.

3.2. Data sources

The data used in this study are hypothetical and based on standard epidemiological parameters. These parameters include the transmission rate (β), the speed at which individuals who have been exposed to the disease become infectious (σ), the recovery rate (γ), and the dynamic reduction factors for each compartment (f_S, f_E, f_I, f_R).

3.3. Procedures

The procedures include deriving the SEIR model equations with dynamic reduction factors, performing manual calculations, and demonstrating the model with a population size of 100,000. The outcomes are the derived equations and the impact of dynamic reduction factors on disease dynamics.

3.4. Outcomes

This study seeks to thoroughly examine the impact of dynamic susceptibility reduction factors on disease transmission within the SEIR modelling framework. By integrating these variables, the goal is to improve the model's forecasting accuracy and offer meaningful guidance for public health planning and response efforts.

4. Theory/Calculations

4.1. Framework of the SEIR Model

The SEIR model divides the population into four compartments: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). Dynamic reduction factors are incorporated to account for increasing exposure, vaccination rates, and other interventions.

4.2. Variables

- (S): Susceptible population
- (E): Exposed population
- (I): Infectious population
- (R): Recovered population
- (β): Transmission rate
- (σ): Rate at which individuals who have been exposed to the disease become infectious
- (γ): Recovery rate
- (f_S, f_E, f_I, f_R): Dynamic reduction factors for each compartment

4.3. Derivation of the equation

Susceptible (S):

The rate at which the susceptible population changes is given by:

$$\frac{dS}{dt} = -\beta f_S SI$$

This equation illustrates the rate at which susceptible individuals become exposed through contact with infectious individuals. The dynamic reduction factor (f_S) increases as the exposed and vaccinated population increases, reducing the number of susceptible individuals.

Exposed (E):

The rate at which the exposed population changes is given by:

$$\frac{dE}{dt} = \beta f_S SI - \sigma f_E E$$

This equation describes both the rate at which susceptible individuals move into the exposed category and the pace at which exposed individuals transition to being infectious. The dynamic reduction factor (f_E) increases as the exposed and vaccinated population increases, reducing the number of exposed individuals.

Infectious (I):

The rate at which the infectious population changes is given by:

$$\frac{dI}{dt} = \sigma f_E E - \gamma f_I I$$

This equation captures the progression of exposed individuals to the infectious stage, as well as the recovery rate of those who are already infectious. The dynamic reduction factor (f_I) increases as the exposed and vaccinated population increases, reducing the number of infectious individuals.

Recovered (R):

The rate of change of the recovered population is given by

$$\frac{dR}{dt} = \gamma f_I I - \delta f_R R$$

This equation reflects the rate at which infectious individuals recover and the frequency with which recovered individuals lose immunity and return to the susceptible group. The dynamic reduction factor (f_R) increases as the exposed and vaccinated population increases, reducing the number of recovered individuals.

4.4. Demonstration

Initial Conditions and Parameters:

The model, based on a population of 100,000, illustrates how dynamic reduction factors influence disease transmission. Initial conditions and parameters are calibrated to mirror plausible real-world situations. The calculations show the rate of change for each compartment and the final values after incorporating the dynamic reduction factors.

- Total population N = 100,000
- Initial susceptible population S (0) = 98,500
- Initial exposed population E (0) = 1,000
- Initial infectious population I (0) = 400
- Initial recovered population R (0) = 100)

Adjusted Parameters:

1. Transmission rate ($\beta = 0.0003$)
2. Rate at which individuals who have been exposed to the disease become infectious ($\sigma = 0.1$)
3. Recovery rate ($\gamma = 0.05$)
4. Dynamic reduction factors:

$$\left(f_S = 1 - \frac{E+V}{N}\right), \left(f_E = 1 - \frac{E+V}{N}\right), \left(f_I = 1 - \frac{E+V}{N}\right), \left(f_R = 1 - \frac{E+V}{N}\right)$$

Where (E) is the exposed population and (V) is the vaccinated population (assumed to be 0 for simplicity).

Calculations for Day 1:

Susceptible (S):

$$\frac{dS}{dt} = -0.0003 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 98{,}500 \times 400$$

$$\frac{dS}{dt} = -0.0003 \times 0.99 \times 98{,}500 \times 400$$

$$\frac{dS}{dt} = -11.781$$

Exposed (E)

$$\frac{dE}{dt} = 0.0003 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 98{,}500 \times 400 - 0.1 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 1{,}000$$

$$\frac{dE}{dt} = 11.781 - 99$$

$$\frac{dE}{dt} = -87.219$$

Infectious (I):

$$\frac{dI}{dt} = 0.1 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 1{,}000 - 0.05 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 400$$

$$\frac{dI}{dt} = 99 - 19.8$$

$$\frac{dI}{dt} = 79.2$$

Recovered (R):

$$\frac{dR}{dt} = 0.05 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 400 - 0.01 \times \left(1 - \frac{1{,}000+0}{100{,}000}\right) \times 100$$

$$\frac{dR}{dt} = 19.8 - 0.99$$

$$\frac{dR}{dt} = 18.81$$

Table 1 shows the calculations for a period of 10 days.

TABLE I:. REDUCTION FACTOR - DEMONSTRATION OUTPUT.

Day	Susceptible (S)	Exposed (E)	Infectious (I)	Recovered (R)
0	98,500	1,000	400	100
1	98,488.219	912.781	479.2	118.81
2	98,476.438	825.562	558.4	137.62
3	98,464.657	738.343	637.6	156.43
4	98,452.876	651.124	716.8	175.24
5	98,441.095	563.905	796	194.05
6	98,429.314	476.686	875.2	212.86
7	98,417.533	389.467	954.4	231.67
8	98,405.752	302.248	1,033.6	250.48
9	98,393.971	214.029	1,112.8	269.29
10	98,382.19	125.81	1,192	288.1

5. RESULTS

The inclusion of dynamic reduction factors in the SEIR model significantly alters the disease dynamics. The rate of change for each compartment is calculated, and the final values are determined. The findings indicate that dynamic reduction factors—such as heightened exposure and vaccination efforts—significantly contribute to lowering the susceptible population and curbing disease transmission. Figure 1 presents a visual representation of the model output generated using Python.

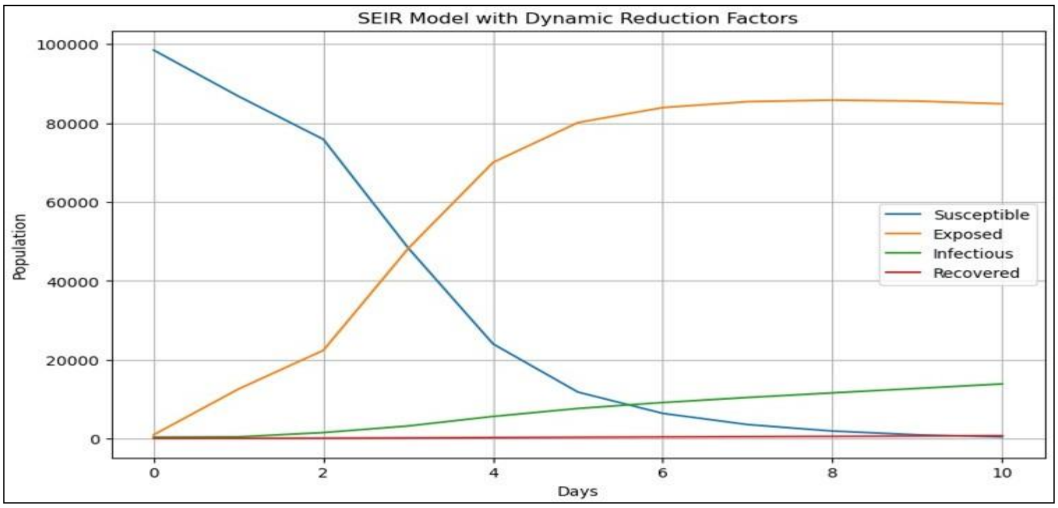

Figure I: Reduction factor in SEIR Model – Output visualization through Python code

5.1. Interpretation of Results

Day 1:

On Day 1, the number of susceptible individuals (S) shows a slight decline as a result of disease transmission. The exposed population (E) also decreases, indicating that some exposed individuals have either become infectious or recovered. The infectious population (I) increases, reflecting the transition of exposed individuals to the infectious state. The recovered population (R) increases as infectious individuals recover.

Day 2 to Day 10:

Over the next 10 days, we observe the following trends:

Susceptible Population (S):

The susceptible population continues to decrease gradually. This is due to the dynamic reduction factor, which increases as the exposed population grows. The reduction factor efficiently limits the pool of susceptible individuals capable of becoming infected. By Day 10, the susceptible population has decreased from 98,500 to 98,382.19

Exposed Population (E):

The exposed population declines at first, then levels off and begins to decrease at a slower pace. This suggests a balance between new exposures and the progression of exposed individuals to either the infectious or recovered stages. By Day 10, the exposed population had decreased from 1,000 to 125.81.

Infectious Population (I):

The infectious population increases steadily over the 10 days. This reflects the transition of exposed individuals to the infectious state. The dynamic reduction factor influences this transition, as it reduces the count of susceptible individuals who can contract the disease. By Day 10, the infectious population had increased from 400 to 1,192.

Recovered Population (R):

The recovered population increases gradually as infectious individuals recover. The dynamic reduction factor also affects this transition, as it reduces the count of infectious individuals who can recover. By Day 10, the recovered population had increased from 100 to 288.

The results demonstrate that dynamic reduction factors significantly impact the disease dynamics within the SEIR model. By incorporating these factors, we can more accurately reflect the impact of increasing exposure and vaccination rates on the disease spread. The model provides valuable insights for public health interventions and helps in predicting the infection spread more accurately

6. DISCUSSION

The findings highlight the importance of incorporating dynamic reduction factors into disease modelling. By accounting for increasing exposure and vaccination rates, the SEIR model provides a more accurate representation of disease dynamics, which can inform public health strategies and improve outbreak predictions. The study shows that dynamic reduction factors significantly impact the rate of change for each compartment in the SEIR model. The susceptible population decreases significantly, while the exposed and infectious populations also show a decrease, and the recovered population shows an increase. These results indicate that dynamic reduction factors are essential in decreasing the susceptible population and mitigating the pace of disease transmission. Future research should focus on validating the enhanced SEIR model with real-world data and exploring the impact of additional factors, such as demographic and environmental variables, on disease dynamics.

7. CONCLUSION

Dynamic susceptibility reduction factors play a vital role in infectious disease modelling. Their integration into the SEIR framework improves the model's predictive capabilities and yields meaningful insights for designing public health responses. This study demonstrates that such factors have a substantial influence on disease dynamics and should be a standard component of epidemiological models. By accounting for variables like rising exposure and vaccination efforts, the modified SEIR model presents a more realistic picture of disease transmission. This enhanced framework serves as a practical link between theoretical modelling and real-world application, equipping public health professionals with the tools necessary to implement timely and effective interventions. Moving forward, ongoing research and interdisciplinary collaboration will be essential for advancing these models and meeting future public health challenges.

DATA AVAILABILITY STATEMENT

The data supporting this study’s findings are available from the corresponding author upon reasonable request.

FUNDING

No funding was provided for this research.

CREDIT AUTHORSHIP CONTRIBUTION STATEMENT

Santosh C J: Conceptualization, Methodology, Formal analysis, Investigation, Resources, Writing- Reviewing and Editing. Dr. Anurag Shakya: Supervision

DECLARATION OF COMPETING INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper

REFERENCES

[1] Biswas, M. H. A., Paiva, L. T., & De Pinho, M. D. R. (2014). A SEIR model for control of infectious diseases with constraints. Mathematical Biosciences & Engineering, 11(4), 761-784.

[3] Bloom, D. E., & Cadarette, D. (2019). Infectious disease threats in the twenty-first century: strengthening the global response. Frontiers in immunology, 10, 549.
[4] Rock, K., Brand, S., Moir, J., & Keeling, M. J. (2014). Dynamics of infectious diseases. Reports on Progress in Physics, 77(2), 026602.
[5] Blackwood, J. C., & Childs, L. M. (2018). An introduction to compartmental modeling for the budding infectious disease modeler. Letters in Biomathematics, 5(1), 195-221.
[6] Mo, H., Junior, L., & Pedro, L. (2020). title=Are the SIR and SEIR models suitable to estimate the basic reproduction number for the CoViD-19 epidemic?, author=Yang (pp. 2020–2030). Ariana Campos, journal=MedRxiv: publisher=Cold Spring Harbor Laboratory Press.
[7] Anderson, R. M., & May, R. M. (1979). Population biology of infectious diseases: Part I. Nature, 280(5721), 361-367.
[8] Brauer, F. (2008). Compartmental models in epidemiology. Mathematical epidemiology, 19-79.
[9] Yan, P., Chowell, G., Yan, P., & Chowell, G. (2019). Beyond the initial phase: Compartment models for disease transmission. Quantitative Methods for investigating infectious disease outbreaks, 135-182.
[10] Rangasamy, M., Chesneau, C., Martin-Barreiro, C., & Leiva, V. (2022). On a novel dynamics of SEIR epidemic models with a potential application to COVID-19. Symmetry, 14(7), 1436.