INVENTOPIA 2025

FBM-SEREMBAN INTERNATIONAL
INNOVATION COMPETITION (FBM-SIIC)

INNOVATION IN ACTION: TURNING IDEAS INTO REALITY

Chapter 2

GUI-Based Health Simulation Tool for Predicting Pandemic Spread Using the SEIR Model

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ABSTRACT

This project presents a user-friendly Graphical User Interface (GUI) simulation tool designed to support healthcare professionals and researchers in visualizing and predicting the spread of infectious diseases using the SEIR (Susceptible-Exposed-Infectious-Recovered) model. The tool incorporates a Multistep Block Method, a numerical technique that improves computational efficiency compared to traditional Runge-Kutta methods. By allowing users to input disease parameters such as infection rate, incubation period, and recovery rate, the tool dynamically generates graphs and numerical outputs that illustrate the potential trajectory of an outbreak. This innovation addresses the need for accessible, real-time decision support in public health, enabling users to model intervention strategies like quarantine, vaccination, or social distancing, and assess their projected impact. Unlike many modelling tools that require technical expertise, this GUI simplifies complex epidemiological concepts, making it suitable for medical personnel, public health officials, and students in health-related fields. Its intuitive design and low system requirements allow easy deployment on standard computers, making it ideal for use in clinics, universities, and resource-constrained settings. With further adaptation, the tool can be extended to simulate other communicable diseases, offering valuable insights for outbreak preparedness, training, and policy development.

Key Words: SEIR model, pandemic simulation, healthcare forecasting, medical decision support, GUI tool.

1. INTRODUCTION

Recently, the world has been alarmed by a new, fast-spreading variant of the coronavirus originating in Wuhan, China, known as SARS-CoV-2, which affects the respiratory system and other organs in the body (Jain, 2020). This disease, named COVID-19, has impacted not only thousands of individuals who have fallen ill or succumbed to the virus but has also disrupted daily life, businesses, global trade, and movement, all of which have significantly affected the global economy (Haleem et al., 2020). During this crisis, government decisions and interventions are essential to mitigate the virus's spread and estimate the number of susceptible, exposed, infected, and recovered individuals. These estimates support policymakers in making critical decisions on vaccination strategies, movement restrictions, social distancing, and other preventive actions. It is crucial that these estimates are generated rapidly to facilitate timely responses during this health crisis.

The SEIR model is a mathematical framework that simulates pandemic spread by categorizing individuals into four groups: those at risk of infection (susceptible), those who are infected but not yet contagious (exposed), those who can transmit the disease (infected), and those who have recovered. This model differs from the traditional SIR model by incorporating an incubation, or "exposed" period, representing the 2-3 days before an individual becomes infectious to others after contracting COVID-19.

Previously, researchers have explored various methods for solving the SEIR model. Rustan and Handayani (2020) applied the Euler method to a modified SEIR model for COVID-19 in Indonesia, while Aakash et al. (2023) used both the Euler and fourth-order Runge-Kutta methods to address the model's complexity. Recently, Palma et al. (2024) demonstrated that simulations using fourth- and fifth-order Runge-Kutta methods produced patterns consistent with MATLAB's ODE45 algorithm. Mungkasi (2021) introduced a multistage method, utilizing successive approximation and variational iteration methods to derive semi-analytical solutions for the SEIR model. The Mickens method, a non-standard finite difference approach, has also been applied, preserving the SEIR model's dynamic properties while simplifying implementation.

The SEIR pandemic model is a type of Ordinary Differential Equation (ODE), and selecting efficient numerical algorithms for solving these equations is crucial for reducing computational times. Recent research has focused on developing cost-effective computational methods, underscoring the importance of computational efficiency for solving ODEs (Cockayne et al., 2019). For instance, the Modified Euler method has shown considerable efficiency gains in simulating moderately stiff chemical kinetics in reactive-flow models on GPUs, outperforming traditional methods (Niemeyer et al., 2014). This highlights the impact of method selection on computational performance, particularly when handling large systems of independent ODEs.

In this paper, we present a multistep block approach that uses a block strategy to estimate two approximate solutions simultaneously and a multistep technique to reduce the number of functions calls in the algorithm. Together, these two features decrease the algorithm's computational time, making it particularly effective for models with numerous variables and parameters involving large populations. The accuracy of this approach is further enhanced through a predictor-corrector strategy, where the algorithm first predicts approximate solutions using a lower-order method, then corrects them using a higher-order method to improve precision.

Building on this new approach for solving the SEIR model, our next objective is to develop a Graphical User Interface (GUI) based on the proposed multistep block method to simulate pandemic spread. Such a GUI will be especially useful for policymakers, researchers, and health professionals who may lack expertise in mathematical modelling or programming (Mohd Jamil et al., 2022). This user-friendly interface will assist in forecasting disease transmission dynamics, providing essential data-driven recommendations to inform government policies and preventive measures across economic, social, and educational domains.

2. METHODOLOGY: GUI PROGRAM

Next, we will implement our multistep block method in the GUI program created by using C programming with GTK widget toolkit under macOS operating system. A GUI is a type of computer human interface on a computer, where people and computers communicate with each other (Jansen, 1998). A GUI allows users to interact with software by handling events like mouse clicks, selections, and text input. It responds to these inputs by updating the visible elements (widgets) on the screen (Banerjee et al., 2013). This user-friendly interface benefits users from various backgrounds who may not be familiar with mathematics or programming. By simply inputting parameter values, users can view visual and numerical data of the spread simulation, helping them analyse and recommend suitable intervention solutions.

The GUI program involve the process of developing and running a simulation for the SEIR (Susceptible-Exposed-Infectious-Recovered) model using a C programming interface with GTK widgets. The process begins with designing a user-friendly interface, where users can input various parameters, total population, and step sizes, essential for configuring the simulation. These inputs are then processed through a multistep block method algorithm to solve the SEIR model equations, which simulate the spread of a disease over time. The simulation generates both graphical projections of pandemic trends and numerical values for each population category (S, E, I, R). The simulation continues iteratively, allowing users to analyse changes until they choose to end it. This process provides insights into how different parameters affect pandemic dynamics.

3. RESULTS AND DISCUSSION

After entering the input parameters, users can monitor the model's behaviour. By pressing the 'Run SEIR Model' button, a projection graph (as shown in Figure 1) and numerical values (as shown in Table 1) for the S, E, I, and R groups will be displayed.

The Figure 1 shows the dynamics of the SEIR (Susceptible-Exposed-Infected-Recovered) model over a period of 20 days. Initially, the Susceptible population (purple line) starts high and steadily decreases as individuals move into the Exposed (blue line) and subsequently the Infected (green line) categories. The Exposed group rises gradually as more susceptible individuals are exposed to the infection, eventually levelling off as these individuals transition to the Infected category. The Infected population grows as exposed individuals become actively infectious, peaking and eventually declining as they recover. The Recovered population (orange line) increases as infected individuals recover, reflecting the cumulative number of recoveries over time.

Similarly, Table 1 illustrates the dynamics of disease spread in the SEIR model in terms of numerical values. The susceptible population declines as individuals transition through the exposed and infected phases, with a corresponding rise in the recovered category. This pattern is typical of infectious disease progression, where susceptible individuals are gradually replaced by exposed, infected, and eventually recovered individuals over time.

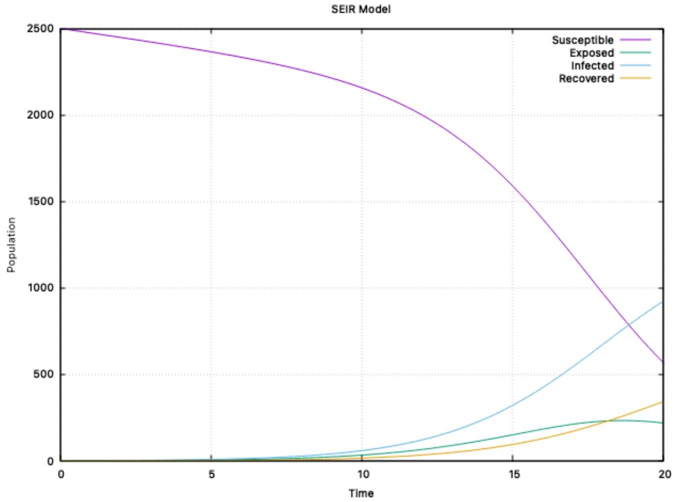

Figure 1: The projection graph of SEIR individuals.

Table 1: The numerical values of SEIR individuals.

t	S approximate	E approximate	I approximate	R approximate
0	2500	1	1	0
2	2448.29599	1.658886	2.624919	0.415349
4	2394.13718	3.61357	5.900195	1.306114
6	2333.79245	7.819432	13.004974	3.254551
8	2259.55187	16.559746	28.155796	7.451931
10	2156.62101	33.985648	59.585725	16.290092
12	1999.53412	66.311176	122.028125	34.269446
14	1753.76283	118.717339	237.33836	68.864603
16	1397.00463	184.13965	425.261704	129.680506
18	965.570782	230.138906	675.578949	223.048155
20	566.538128	219.047677	924.053643	343.778783

Given that a new method is being introduced, it is important to compare its performance with previously established methods to assess and analyse its effectiveness. For this purpose, comparisons will be conducted with the Runge-Kutta order 4 (RK4) method.

Table 3: The comparison of computational time

	RK4	Multistep
Total function calls	1280	652
Total step of iterations	80	42
Time taken (seconds)	0.000202	0.000190

4. CONCLUSION

The SEIR model effectively captures disease progression dynamics, showing a decline in the susceptible population as individuals transition through exposure, infection, and recovery stages. When compared with RK4, the proposed multistep method improves computational efficiency by reducing iteration steps and function calls, offering a faster alternative ideal for large-scale simulations, thus supporting cost-effective and timely analysis in fields requiring extensive computational resources.

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