

# Interactive application for epidemic simulation using the SEIRD model

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## ABSTRACT

This work describes the implementation of a SEIRD (Susceptible, Exposed, Infected, Recovered, and Deceased) model for epidemic simulation, with a focus on high-impact diseases such as COVID-19 and its variants. The methodological approach is based on using the Python programming language and the Streamlit framework for developing an interactive web application. The objective is to provide an accessible tool for visualizing and analyzing the dynamics of disease spread, allowing for the exploration of different scenarios and epidemiological parameters.

## Introduction

This interactive and accessible tool aims to provide an understanding of the dynamics of high-impact epidemics, such as COVID-19 and measles, through the implementation of a SEIRD model. The web application, developed in Python and Streamlit, allows users to adjust epidemiological parameters and visualize the evolution of the disease on an intuitive dashboard. This dashboard includes line graphs that show the number of individuals in each state (Susceptible, Exposed, Infected, Recovered, Deceased) over time, as well as other relevant graphs for analyzing the simulated scenario.

The main objective of this work is to implement the SEIRD model to simulate the dynamics of epidemics. To achieve this objective, the following points will be developed: development of an interactive web application, definition of model parameters, execution of simulations, visualization of results on an intuitive dashboard, and facilitating data analysis and comprehension.

## Theoretical Framework

### Fundamental Concepts in Epidemiology and Epidemic Modeling

For the implementation of an epidemic simulation model, it is fundamental to understand the concepts that support it, from the basics of mathematical modeling to the parameters that describe the dynamics of the disease.

#### *Compartmental Models in Epidemiology*

Compartmental models represent a widely used approach in mathematical epidemiology to describe the dynamics of infectious diseases. They work by dividing the population into mutually exclusive groups, or "compartments," based on each individual's state regarding the disease. In an epidemiological context, these compartments can represent the states of susceptibility, exposure, infection, and recovery. The main characteristic of these models is the representation of the flow of individuals from one compartment to another over time, which is governed by a set of differential equations. This approach is the theoretical basis for the construction of the SEIRD model.

#### *SEIR Model*

The SEIR model (Susceptible, Exposed, Infected, Recovered) is an extension of the classic SIR model and is particularly relevant for diseases with a significant incubation period. It divides the population into four compartments and, through differential equations, simulates the evolution of individuals between these groups over time. The compartments are: Susceptible (S), who can contract the disease; Exposed (E), who have been infected but are not yet contagious; Infected (I), who are sick and can transmit the virus; and Recovered (R), who have healed and acquired immunity.

#### *SEIRD Model*

The SEIRD model is a variation of the SEIR model that includes an additional compartment for deceased individuals (D). This modification is essential for simulating epidemics with a notable mortality rate, such as COVID-19. The inclusion of the D compartment allows the tool to separate individuals who recover with immunity from those who have died as a result of the disease, providing a more complete and accurate analysis of the epidemic's impact on the population.

## Epidemiological Parameters

Epidemiological parameters are the coefficients that govern the model's differential equations, determining the speed and intensity of the flow of individuals between the compartments. In the context of the SEIRD model, the main parameters are: contact rate ( $\beta$ ), incubation period ( $\sigma$ ), recovery rate ( $\gamma$ ), and mortality rate ( $\mu$ ).

## Basic Reproduction Number ( $R_0$ )

The Basic Reproduction Number ( $R_0$ ) is a crucial metric in epidemiology. It represents the average number of new infections caused by a single infected individual in a completely susceptible population. If  $R_0 > 1$ , the disease tends to spread; if  $R_0 < 1$ , it tends to disappear. The  $R_0$  can be calculated from the SEIRD model parameters, serving as a way to evaluate and communicate the transmissibility of the disease.

## Related Works

The implementation of the SEIRD model in Python was developed based on the guidelines and methodologies presented in the article by Tannenbaum. This work served as a fundamental pillar, guiding each step of the process. The article details the calculation of the differential equations that govern population dynamics (susceptible, exposed, infectious, recovered, and deceased), the precise definition of the epidemiological parameters that influence disease spread, the execution of the SEIRD model in a computational environment, and the creation of an interactive graph for a clear and intuitive visualization of the obtained results.

## Method

In this section, we detail the methodological approach adopted for implementing the interactive epidemic simulation application. We present the materials and development tools, the model architecture, and the process of creating the graphical interface.

## Modeling and Simulation of Epidemic Dynamics

For the simulation of epidemic dynamics, we used the SEIRD model (Susceptible, Exposed, Infected, Recovered, and Deceased). This compartmental model was implemented through a system of ordinary differential equations (ODEs) that describe the flow of individuals between compartments, using the NumPy library for numerical operations and the SciPy library for solving the ODEs.

The model's equations are described as follows:

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta SI}{N} \\ \frac{dE}{dt} &= \frac{\beta SI}{N} - \sigma E \\ \frac{dI}{dt} &= \sigma E - \gamma I \\ \frac{dR}{dt} &= \gamma I \\ N &= S + E + I + R + D\end{aligned}$$

Where S, E, I, R, and D represent the number of individuals in each compartment, and N is the total population ( $N = S + E + I + R + D$ ). The parameters  $\beta$ ,  $\sigma$ ,  $\gamma$ , and  $\mu$  are the rates of transmission, incubation, recovery, and mortality, respectively.

## Defining parameters for COVID-19 variants

The parameters used in the project to simulate COVID and its variants were inferred based on a series of scientific articles, including systematic reviews and meta-analyses, to obtain primary data for each variant, such as the incubation period, mortality rate, and basic reproduction number ( $R_0$ ). Missing data were obtained through estimates based on information published in the scientific literature that indicated higher transmissibility and lethality of that variant compared to the original. With this data in hand, the parameters were calculated: the incubation rate ( $\sigma$ ) was derived as the inverse of the incubation period, and the infection rate ( $\beta$ ) was calculated from the  $R_0$  and the mortality and recovery rates, ensuring the values were consistent with the observed epidemiological dynamics. This process allowed for the creation of a robust and scientifically-grounded set of parameters for each variant, which is essential for the accurate modeling of disease spread.

## Development of the Web Application and Interface

The web application was developed using the Python programming language and the Streamlit framework. Streamlit was chosen for its ability to quickly transform Python scripts into interactive interfaces without the need for advanced web development knowledge. The interface development followed the steps of input controls (using Streamlit's widget components like sliders and text boxes), data visualization with the 'plotly' library, and the organization of the dashboard.

## Results

The final result was a Streamlit application with a simple and intuitive interface. The home page presents the project and briefly explains the model and the parameters used. On the interface, the left column contains the disease preset selection and the fields for modifying the parameters, in addition to a button to run the simulation. The main part of the screen is occupied by the visualization of the results, including graphs showing the evolution of the compartments and key metrics such as the  $R_0$ , the peak number of infected individuals, and the percentage of deaths.

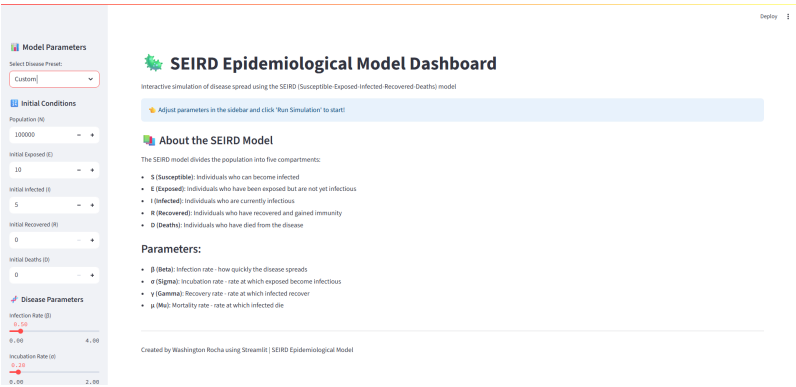


Figure 1. Application home page. 2025

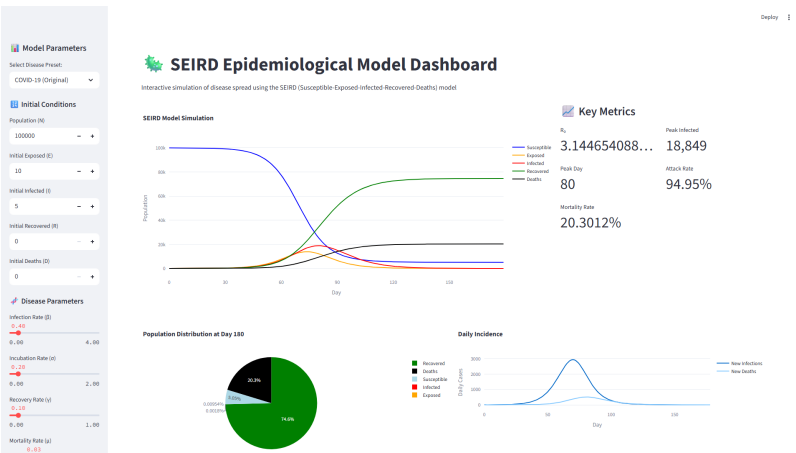
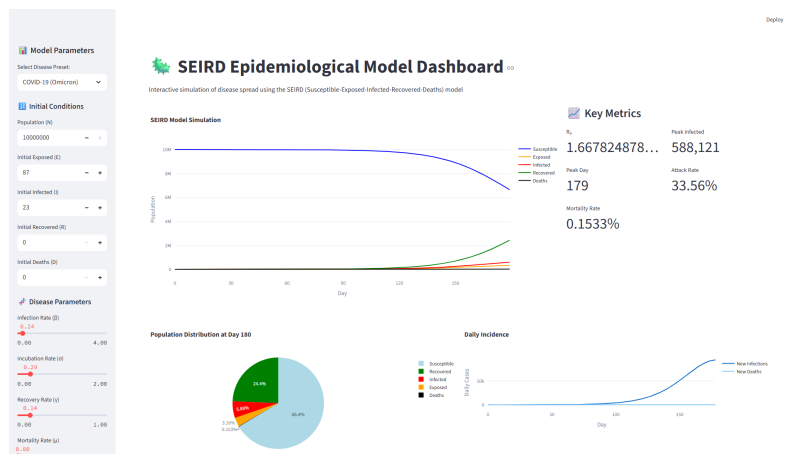


Figure 2. Simulation result of the original COVID-19. 2025



**Figure 3.** Simulation result of the Omicron variant. 2025

## Conclusion

This work's main objective was to build an epidemic simulator using the SEIRD epidemiological model to represent the propagation dynamics of COVID-19 and its variants. The main technical challenge faced was the model's parameterization, which required the collection and adaptation of complex data on infection, incubation, recovery, and mortality rates. The results achieved demonstrate that the simulation, while an approximation of reality based on available data, is functional and validated. We conclude that the model's greatest strength lies in its flexibility: parameters can be adjusted with a more precise dataset to reflect different epidemiological scenarios with greater accuracy. Thus, the developed platform is not limited to COVID-19 and is projected as an adaptable tool to simulate the spread of other diseases that fit the SEIRD model pattern, paving the way for future work focused on the analysis of intervention strategies in epidemics.

## Acknowledgements

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