Analysis of a modified SEIRS compartmental model for infectious diseases

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Abstract

Mathematical representations of infectious diseases include compartment-based SEIR and SEIRS models. These models are represented using coupled differential equations that capture the flow of populations from one compartment to another. While these models have been used for several infectious diseases such as HIV/AIDS, tuberculosis, Dengue fever, and COVID-19, the models do not generally incorporate compartments for vaccinated populations, asymptomatic infections, and the possibility of reinfection.

In this paper, we present a modified SEIRS compartment model for infectious diseases. We incorporate compartments for exposed vaccinated and non-vaccinated populations, and those with symptomatic and asymptomatic infections. We represent this model with a set of coupled differential equations and derive the basic reproduction number R_0.

We show that this system has, among its fixed points, an endemic equilibrium. This is validated through attractor plots, which confirm the endemic fixed point, and show that the endemic fixed point is globally stable.

In future work, we will perform stability analysis on the system using Gersgorin and Lyapunov theorems.

1 Introduction and System Model

Modeling infectious diseases is a crucial step to control the spread of such infectious diseases.

Mathematical representations such as Susceptible - Infected - Recovered (SIR) and Susceptible - Exposed - Infected - Recovered (SEIR) [1, 2] have been used to model infectious diseases such as COVID-19 [3], Dengue fever [4], Tuberculosis [5], and HIV/AIDS [6, 7].

While these models provide a framework for modeling diseases, they are very simple and leave out significant aspects such as vaccinations, hospitalization, and quarantine. Recent research in this area has attempted to address this problem in various ways. For example, in [3], the authors include compartments for diagnosed and non-diagnosed individuals. The hybrid SEIQR model [8] was developed to include quarantine regulations. While this model was highly customizable, it did not provide the expected results because the effect of the viral variants and mortality rates were not factored into the model.

Another drawback of several existing models is the lack of possibility of reinfection, not accounting for vaccinations, and not considering asymptomatic infections. In this paper, we modify the SEIRS model [2] to include vaccinated and non-vaccinated cases, symptomatic and asymptomatic cases, and the possibility of reinfection.

In this paper, we present a modified SEIRS model (see Figure 1) that consists of six compartments: (1) Susceptible, S; (2) Exposed with vaccination, E_V; (3) Exposed with non-vaccination, E_{NV}; (4) Infected persons with symptoms, I_S; (5) Asymptomatic infected, I_{AS}; and (6) Recovered, R.

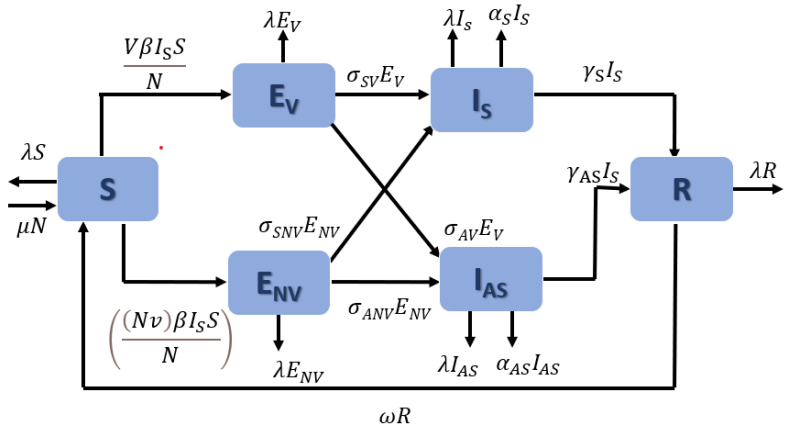


Figure 1: Transition diagram of modified six compartmental SEIRS model to predict the infections of disease spread.

The modified SEIRS model can be represented using a set of coupled differential equations:

$$\frac{dS}{dt} = \mu N + \omega R - \lambda S - \frac{(V\beta I_S S)}{N} - \frac{((NV)\beta I_S S)}{N}, \tag{1}$$

$$\frac{dE_V}{dt} = \frac{(V\beta I_S S)}{N} - (\lambda + \sigma_{SV} + \sigma_{AV})E_V, \tag{2}$$

$$\frac{dE_{NV}}{dt} = \frac{((NV)\beta I_S S)}{N} - (\lambda + \sigma_{SNV} + \sigma_{ANV})E_{NV}, \tag{3}$$

$$\frac{dI_S}{dt} = \sigma_{SV} E_V + \sigma_{SNV} E_{NV} - (\lambda + \alpha_S + \gamma_S)I_S, \tag{4}$$

$$\frac{dI_{AS}}{dt} = \sigma_{AV} E_V + \sigma_{ANV} E_{NV} - (\lambda + \alpha_{AS} + \gamma_{AS})I_{AS}, \tag{5}$$

$$\frac{dR}{dt} = \gamma_S I_S + \gamma_{AS} I_{AS} - (\lambda + \omega)R, \tag{6}$$

where λ is the natural death rate, μ is the natural birth rate, β is the contact rate, V is the fraction of the population vaccinated against the infectious disease, NV is the fraction without the vaccine so that V + NV = 1, α_S and α_{AS} are the death rates due to the infectious disease for symptomatic and asymptomatic infections, respectively, γ_S and γ_{AS} are the recovery rates for the symptomatic and asymptomatic individuals, respectively, σ_{SV}, σ_{SNV}, σ_{AV}, σ_{ANV} are the rates of transition from exposed to infected, and ω is the fraction of recovered persons who lose immunity and become susceptible to infection again.

2 Basic Reproduction Number

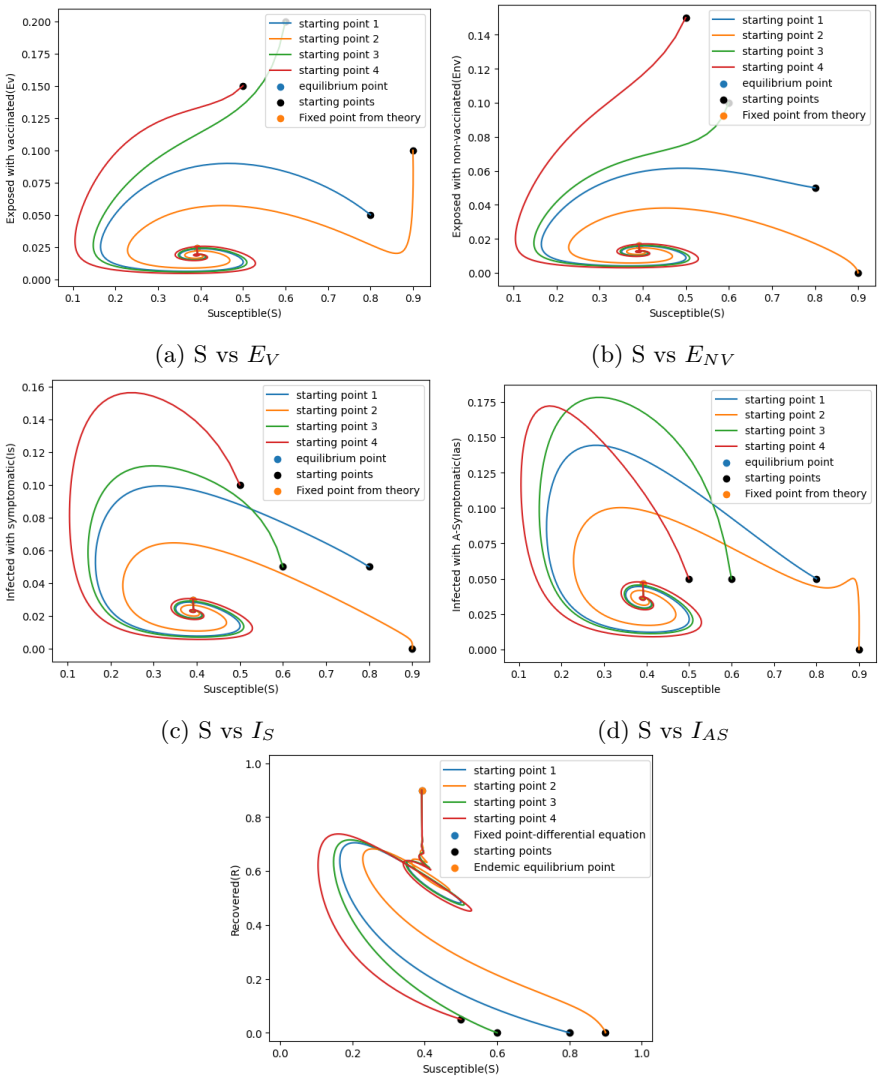
The basic reproduction number is a measure of how contagious an infectious disease is. It represents the average number of secondary infections that result from one infected person in a population of susceptible individuals. The R_0 value refers to how many people, on average, each infected person will transmit the virus to in a population where no one has immunity to the virus. R_0 is determined by considering the dominant eigenvalue of a next-generation matrix (NGM) [1].

Using the methods described in [1], and from equations (1)-(6), the basic reproduction number, R_0, is calculated to be:

$$R_0 = \frac{[(\sigma_{SV}(V)\beta)(\lambda + \sigma_{SNV} + \sigma_{ANV})] + [(\sigma_{SNV}(NV)\beta(\lambda + \sigma_{SV} + \sigma_{AV})]}{(\lambda + \sigma_{SV} + \sigma_{AV})(\lambda + \sigma_{SNV} + \sigma_{ANV})(\lambda + \alpha SV + \gamma_{AV})}. \tag{7}$$

The basic reproduction number can be examined to provide one heuristic to determine the stability of the system [7]:

1. When $R_0 < 1$, disease spread decreases and it leads to disease-free equilibrium (DFE).
2. When $R_0 > 1$, disease spread increases and it leads to endemic equilibrium (EE).
3. When $R_0 = 1$, the system oscillates between the two stable equilibrium points, DFE and EE.



(a) S vs E_V

(b) S vs E_{NV}

(c) S vs I_S

(d) S vs I_{AS}

(e) S vs R

Figure 2: Attractor plots: Fig (a) to (e) show the long-term behavior of the model by varying the compartment values of E_v, E_{NV}, I_S, I_{AS} and I_R as a function of S. The contact rate, β, is fixed at 0.5. All the curves in the attractor plots, irrespective of initialization, converge at a single point, which is the endemic equilibrium point, demonstrating that the fixed point derived from the differential equations and the endemic equilibrium analysis are identical.

3 Long-term Behavior

Attractor plots are used to understand the evolution of stability of a complex system with a variety of initial points. They can also show the long-term behavior of the system and the endemic equilibrium point. Results show that the fixed point from the differential equations [1], the endemic equilibrium obtained [7], and the point of convergence from simulation results (see Figure 2) are all identical. Because attractor plots of a six-dimensional model would be hard to visualize, we present five simplified two-dimensional plots as shown in Figure 2. By fixing the susceptible(S) in the horizontal axis and varying the other five compartments such as Exposed with vaccinated (E_V), Exposed with non-vaccinated (E_{NV}), Infected persons with symptomatic, (I_S), Infected persons with Asymptomatic, (I_{AS}) and Recovered(R).

4 Conclusions and Future Work

In this paper, we present a modified SEIRS model for airborne infectious diseases. This compartmental SEIRS model was developed by incorporating vaccination status, symptomatic, and asymptomatic cases, and re-infection rates. We derived the equation for the basic reproduction number for our proposed model and performed a stability analysis. From attractor plots, we were able to show that our theoretical results and numerical results match and that we obtain a stable fixed point.

In future work, utilizing the Gersgorin and Lyapunov theorems, we will investigate the stability of the SEIRS model system [9].

5 Acknowledgments

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