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An Analytical and Numerical Study of Disease Spread via the SIR Model

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ABSTRACT

Mathematical models are essential tools for understanding the transmission dynamics of infectious diseases and for evaluating effective control strategies. This paper investigates a classical **SIR (Susceptible–Infected–Recovered)** epidemiological model formulated as a system of ordinary differential equations for a closed population. The model behavior is analyzed using analytical methods and numerical simulations to examine the influence of key parameters, including transmission and recovery rates, on disease progression. The results illustrate the conditions under which an epidemic emerges, reaches a peak, and eventually declines. The study highlights the significance of parameter variation in controlling disease spread and demonstrates the applicability of differential equation–based models in supporting public health planning and decision-making.

KEYWORDS: *Epidemiological modeling, SIR model, infectious diseases, differential equations, epidemic dynamics, numerical simulation, disease transmission, mathematical modeling.*

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1. INTRODUCTION

Infectious diseases continue to pose significant challenges to public health worldwide. Understanding how diseases spread through populations is crucial for planning effective prevention and control strategies. Mathematical epidemiology uses quantitative tools to model disease transmission and forecast epidemic behavior, helping health authorities make informed decisions. Among various approaches, compartmental models formulated with differential equations have been particularly influential. One of the earliest and simplest models is the **SIR model**, introduced by Kermack and McKendrick in 1927, which divides a closed population into susceptible, infected, and recovered groups.

The SIR model, despite its simplicity, provides valuable insights into epidemic thresholds and intervention impacts. Extensions and generalizations of the basic SIR framework continue to appear in modern research, including adaptations with births, deaths, nonlinear incidence, and stochastic effects.

2. Model Formulation

2.1. Compartmental Structure

The SIR model classifies individuals according to their disease status:

- **Susceptible (S):** individuals who can contract the disease.
- **Infected (I):** individuals currently carrying and able to transmit the disease.
- **Recovered (R):** individuals who have recovered and gained immunity (or are removed from the possibility of further infection).

Assuming a closed population with no births, deaths (other than from disease), or migration, the total population NNN at time ttt satisfies:

$$S(t) + I(t) + R(t) = N.$$

2.2. Differential Equations System

The dynamics of the SIR model are described by the following ordinary differential equations:

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

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} - \gamma I$$

where:

- β\betaβ is the **transmission rate** (probability of disease spread per contact),
- γ\gammaγ is the **recovery rate**.

3. Analytical Insights

3.1. Basic Reproduction Number

A key metric in epidemiological modeling is the **basic reproduction number** (R_0), which indicates the expected number of cases directly generated by one infected individual in a fully susceptible population:

$$R_0 = \beta / \gamma$$

If $R_O > 1$, the infection is likely to spread through the population; if $R_0 < 1$, the outbreak will likely die out.

3.2. Epidemic Threshold

The threshold determined by R_0 helps identify whether an epidemic will occur. When I $R_O > 1$, the infection grows until a significant portion of the population moves into the recovered class, after which the number of infected declines.

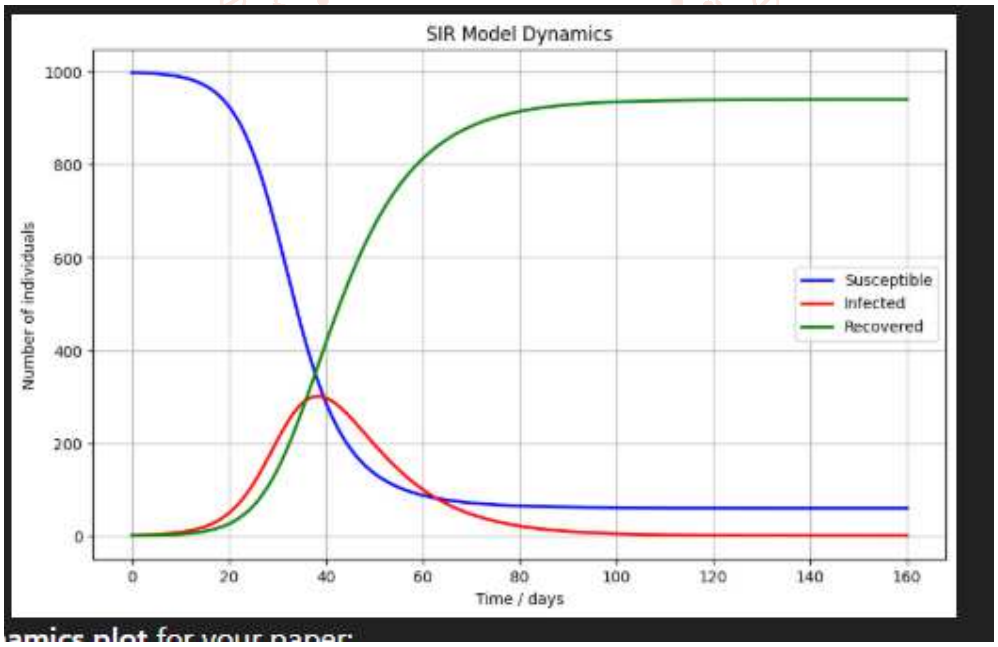
4. Numerical Analysis

The SIR model described in Section 2 was simulated numerically to examine the progression of an epidemic over time. The model parameters were chosen as follows: total population N=1000, initial infected I(0)=1, initial recovered R(0)=0, transmission rate β=0.3 and recovery rate γ=0.1The system of differential equations was solved using the Runge–Kutta method implemented in Python.

Figure 1 illustrates the time evolution of the three compartments: susceptible (S), infected (I), and recovered (R) individuals. The susceptible population gradually decreases as the infection spreads through the population, while the infected population rises to a peak before declining due to recovery. The recovered population steadily increases over time as individuals gain immunity.

This simulation highlights the impact of the transmission and recovery rates on the epidemic's peak and duration. Such numerical analysis provides valuable insight into epidemic dynamics and can aid in planning effective intervention strategies.

Figure 1. Dynamics of Susceptible, Infected, and Recovered populations over time in the SIR model.



- **Blue curve:** Susceptible individuals
- **Red curve:** Infected individuals
- **Green curve:** Recovered individuals

It clearly shows how the infection rises to a peak and then declines, while recovered individuals increase over time.

5. Discussion

The numerical simulation presented in **Figure 1** demonstrates key characteristics of epidemic spread within a closed population. The peak of the infected population occurs when a significant portion of the susceptible individuals has been exposed to the infection. Increasing the transmission rate (β) results in a higher and earlier peak of infections, while

increasing the recovery rate (γ) reduces the peak and shortens the epidemic duration.

The results also emphasize the importance of the **basic reproduction number** $R_0 = \beta/\gamma$ in determining whether an epidemic will occur. When $R_0>1$, the infection spreads rapidly, while $R_0<1$ indicates that the disease will gradually die out. These insights are crucial for planning effective public health interventions, such as vaccination programs, social distancing measures, or treatment strategies.

Although the classical SIR model provides valuable understanding, it assumes homogeneous mixing and ignores demographic factors such as births, deaths, or migration. More advanced models, such as SEIR or stochastic models, can incorporate these factors for increased realism. Nonetheless, the simplicity of the SIR model allows for clear interpretation of disease dynamics and serves as a foundation for more complex epidemiological studies.

6. Conclusion

This paper presented an analytical and numerical study of the classical SIR epidemiological model using ordinary differential equations. The model effectively captures the dynamics of infectious disease spread in a closed population, highlighting the interplay between susceptible, infected, and recovered individuals over time.

The simulation results, illustrated in **Figure 1**, demonstrate how variations in transmission and recovery rates affect epidemic progression, including the peak of infections and overall epidemic duration. Such modeling provides valuable insights for public health planning and decision-making, helping authorities implement timely interventions to control disease spread.

Future work may include extensions to more complex compartmental models (e.g., SEIR, SIRD), incorporation of stochastic effects, or real-world data calibration to improve predictive accuracy and applicability to current epidemics.

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