PART 1

Problem Statement

The Ministry of Health is tracking an infectious disease that is spreading through the population. It was initially thought that individuals who were infected and then recovered were immune to reinfection. As such, the Ministry was using the SIR model to track and predict the spread of the disease. However, recent data suggests that individuals who are infected and then recover can be reinfected. The Ministry has hired you, as a consultant, to modify the SIR model to a SIS model.

Introduction

The Ministry of Health is currently navigating the intricate landscape of an ongoing infectious disease outbreak that poses a critical public health concern. The situation is dynamic and managing it requires accurate and effective models for predicting disease spread. Initially, the Ministry relied on well-established Susceptible-Infected-Recovered (SIR) model. This model was predicated on the long-standing standing medical assumption that individuals who recover from the infection develop immunity, thereby moving from the "Infected" state to the "Recovered" state without the possibility of returning to the "Susceptible" state.

However, recent clinical studies and patient data have thrown a wrench into this assumption. New evidence suggests that recovered individuals can, in fact, be susceptible to reinfection. This revelation has far-reaching implications for disease control strategies, and renders the existing SIR model inadequate for the current crisis.

Acknowledging the urgency and complexity of the situation. The Ministry has engaged us as a consultant to undertake a significant adaptation of the existing model. Specifically, we have been tasked with transforming the SIR model into a Susceptible-Infected-Susceptible model, which accounts for the potential of reinfection.

Moreover, In epidemiological contexts, linear programming can be particularly effective for optimizing resource allocation and policy decisions. For instance, one could formulate a linear programming problem to determine the optimal way to allocate limited healthcare resources, such as vaccines or hospital beds, while simultaneously selecting the best set of public health policies

from a range of feasible options. The goal could be to minimize the number of infections or maximize the number of recovered individuals, subject to various constraints like budget, manpower, and public compliance. In such scenarios, both the objective function, which could be the rate of infection or recovery, and the constraints, such as resource limitations and policy options, would need to be linear or approximated as linear for the linear programming methodology to be applicable. While the SIS model itself is a dynamic system that describes how disease spreads and is not naturally an optimization problem, questions about resource allocation and policy effectiveness within the context of an SIS-type epidemic can be suitably addressed using linear programming.

This comprehensive report outlines the rigorous methodology employed in adapting the model, including the mathematical models and computational techniques used. It also presents the new SIS model, detailing how it differs from its SIR counterpart and what these differences mean. Finally, concluding with an evaluation of the model's effectiveness and offer recommendations for its practical application in the ongoing efforts to control the outbreak.

Methodology

In response to the evolving understanding of the infectious disease in question, the model transitioned from the Susceptible-Infected-Recovered (SIR) model to the Susceptible-Infected-Susceptible (SIS) model. The key distinction between these models lies in their interpretation of recovery: while the SIR model assumes post-recovery immunity, the SIS model acknowledges the potential for reinfection after recovery.

Model Modification

To simulate the spread of the disease, the Runge–Kutta method was implemented. Our simulation considered a population of one million individuals, initiating the transmission with a singular infected patient, often referred to as "patient zero".

Given the variables:

- S - Proportion of the population that is susceptible.
- I - Proportion of the population that is infected.
- β - Infectious contact rate between susceptible and infectious individuals.
- γ - Recovery rate.

The following assumptions are made:

1. The probability that a susceptible individual becomes infected upon contact with an infected individual is 50%.
2. An infected individual remains sick for a duration of 100 days.

Mathematical Representation of the SIS Model

The SIS model can be formulated using a system of ordinary differential equations (ODEs) as follows:

$$\frac{dS}{dt} = -\beta SI + \gamma I,$$
$$\frac{dI}{dt} = \beta SI - \gamma I.$$

Derivation of the Fourth-Order Runge-Kutta Method

Runge-Kutta methods serve as a family of iterative techniques employed for the numerical solution of ordinary differential equations (ODEs). Among these, the fourth-order Runge-Kutta method is especially noteworthy for its efficacy in solving first-order ODEs with a high degree of accuracy. This section provides an in-depth derivation of this method.

Mathematical Formulation of the Problem

To begin, consider a generic first-order ODE represented as:

$$\frac{dy}{dt} = f(t, y)$$

The aim is to approximate the function $y(t)$ for t in the interval $[t_0, T]$, given an initial condition $y(t_0) = y_0$.

The Core Principle of Runge-Kutta Methods

The essence of Runge-Kutta methods lies in approximating the function $y(t)$ by incrementing its current value through a weighted sum of several estimators. Each estimator is a derivative calculated at various points within the interval $[t_n, t_{n+1}]$, where $t_{n+1} = t_n + h$ and h is the chosen step size.

Derivation of Fourth-Order Runge-Kutta Increments

For the fourth-order Runge-Kutta method, four such increments are computed at different locations within the interval. Mathematically, these increments are defined as follows:

1. $k_1 = hf(t_n, y_n)$
2. $k_2 = hf\left(t_n + \frac{h}{2}, y_n + \frac{k_1}{2}\right)$
3. $k_3 = hf\left(t_n + \frac{h}{2}, y_n + \frac{k_2}{2}\right)$
4. $k_4 = hf(t_n + h, y_n + k_3)$

Update Equation for y

With these four increments, the value of y for the next time step t_{n+1} can be computed through a weighted sum:

$$y_{\text{new}} = y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

This equation reflects an optimized weighted average of the four increments k_1, k_2, k_3, and k_4, designed to minimize the local truncation error and hence improve the solution's accuracy.

The fourth-order Runge-Kutta method thus provides a robust and accurate tool for the numerical solution of first-order ODEs. It achieves a compromise between computational efficiency and accuracy, making it one of the most widely-used methods for solving differential equations in scientific computing.

Implementation of Ordinary Differential Equations in Numerical Simulations

In this study, the implementation of Ordinary Differential Equations (ODEs) is central to simulating the dynamics of the SIS epidemiological model. The differential equations representing the rates of change for the susceptible and infected compartments are solved numerically to generate time-series data for these variables. By employing the Runge-Kutta 4th order method, a widely-used numerical technique for approximating solutions to ODEs, to ensure a high degree of accuracy in our simulations. The initial conditions and model parameters are carefully chosen based on empirical data and scientific literature to reflect biologically plausible scenarios. As a part of the workflow, to also calibrate the model by comparing the simulation outcomes with real-world epidemiological data, adjusting parameters as necessary to achieve a good fit. This numerical approach allows us to explore a variety of scenarios, including different public health interventions and initial infection levels, thereby providing a robust framework for understanding the potential evolution of the disease under various conditions.

Runge-Kutta Implementation

For implementing the Runge-Kutta method, it set up a loop to iterate through time steps, starting from an initial time t_0 up to a final time T. At each time step, was calculated k_1, k_2, k_3, and k_4 according to the previously mentioned equations. These were then used to update the value of y for the next time step. This process was repeated until it reached the final time T, thus obtaining a numerical approximation of the solution over the specified time range.

Sensitivity Analysis

In the study, sensitivity analysis is crucial for validating the robustness and reliability of the outcomes derived from the SIS model, formulated as a set of ordinary differential equations (ODEs). The approach involves slightly modifying the initial conditions and key parameters of the ODEs within a biologically plausible range to assess their impact on the system's dynamics, specifically the rates of infection and recovery over time. Furthermore, to extend the analysis to scenarios where multiple parameters are altered simultaneously, thereby offering a more comprehensive view of the system's sensitivity to a combination of uncertainties. This multi-parameter sensitivity analysis allows identification of critical variables that have a significant influence on the system's behavior and could, therefore, be targeted for more effective public health interventions and resource allocation. The insights gained from the sensitivity analysis are invaluable for understanding the model's vulnerability to changes in key variables and conditions, and they play a pivotal role in assessing the model's applicability to real-world epidemiological scenarios.

Results

Investigate how the spread of the disease changes as β varies from 0.1 to 1

For this investigation, we kept the step size at 1 day and varied β from 0.1 to 1. The values used were $\beta = 0.1, 0.3, 0.5, 0.7, 1$.

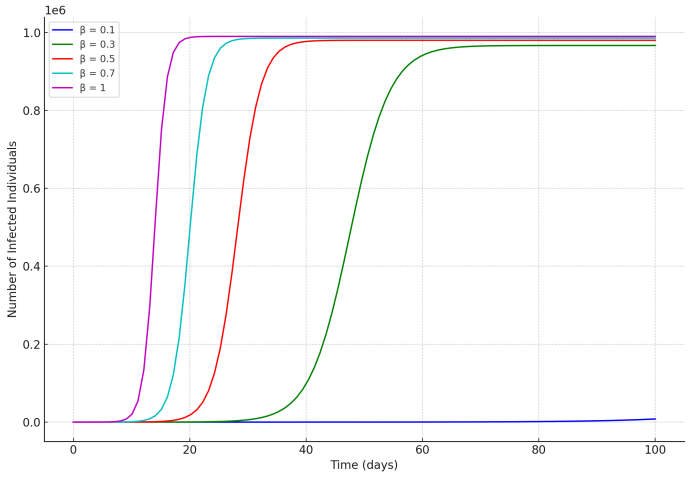

Figure 1: Effect of varying β on the SIS model (Runge-Kutta 4th-Order Method)

The relationship between β values and the dynamics of disease spread is evident in the plotted results. Higher β values correspond to a notably elevated peak of infection, accompanied by a swifter propagation of the disease throughout the population. This observation underscores the pivotal role that the infectious contact rate (β) plays in shaping the speed and intensity of disease transmission. The increase in β leads to a more rapid accumulation of infected individuals, highlighting the urgency of controlling and managing the infectious contact rate as a critical factor in mitigating disease outbreaks.

Investigate how the spread of the disease changes as γ varies from 0.01 to 0.1

For this part, the step size was kept at 1 day and γ was varied from 0.01 to 0.1. The values used were $\gamma = 0.01, 0.03, 0.05, 0.07, 0.1$.

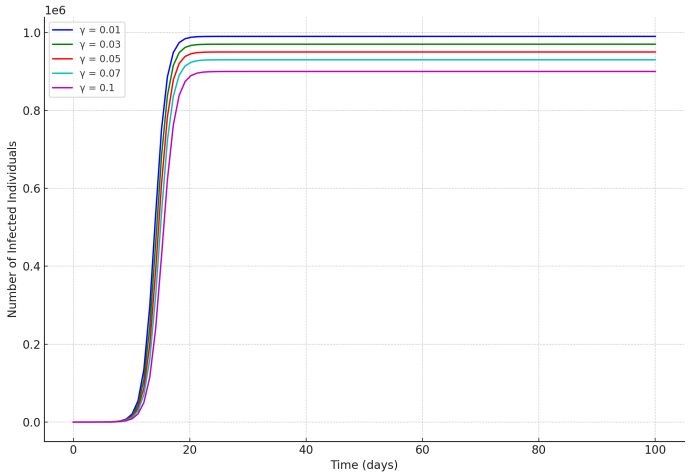

Figure 2: Effect of varying γ on the SIS model

An analysis of the simulations reveals a relationship between the recovery rate γ and the dynamics of the disease spread. Specifically, higher values of γ are associated with a more rapid decline in the number of infected individuals, leading to a lower peak in the infection curve. This suggests that an increase in γ effectively reduces the overall burden of the disease on the population. Moreover, higher γ values lead to a quicker attainment of a steady-state, where the number of new infections is roughly equal to the number of recoveries. This could potentially shorten the duration of outbreaks, allowing healthcare systems to recover more quickly and reduce long-term societal and economic impacts.

Investigate how the spread of the disease changes as I_0 varies from 1 to 100

For this investigation, the initial number of infected individuals I_0 was varied from 1 to 100. The values used were $I_0 = 1, 10, 25, 50, 100$.

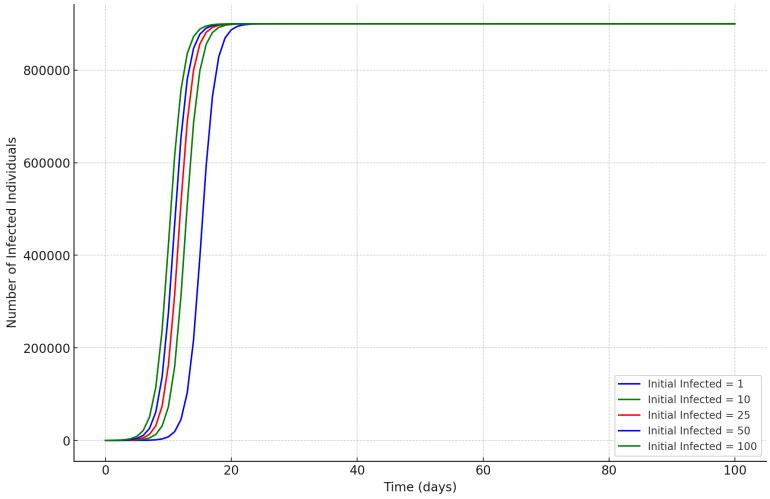

Figure 3: Effect of varying I_0 on the SIS model

The initial number of infected individuals (I_0) has a more pronounced impact on short-term dynamics. Higher I_0 values lead to a faster initial spread due to a larger pool of infected individuals. As the disease progresses and a significant portion of the population becomes infected, the rate of transmission declines. This results in the infection reaching similar prevalence levels over time, irrespective of the initial I_0 value. Ultimately, the long-term dynamics are influenced more by transmission and recovery rates than the initial I_0. This observation emphasizes the need for effective strategies to control transmission rates and optimize recovery efforts, as these factors play a pivotal role in managing the outbreak's impact on the population.

Analytic Methods to Find the Equilibrium Points and Their Stability

Equilibrium points occur where the system remains stable, i.e., where $\frac{dS}{dt} = 0$ and $\frac{dI}{dt} = 0$.

From the first equation, setting $\frac{dS}{dt} = 0$:

$$-\beta SI + \gamma I = 0$$

$$\Rightarrow \beta SI = \gamma I$$

$$\Rightarrow \beta S = \gamma \quad \text{or} \quad I = 0.$$

From the second equation, setting $\frac{dI}{dt} = 0$:

$$\beta SI - \gamma I = 0$$
$$\Rightarrow \beta S = \gamma \quad \text{or} \quad I = 0.$$

Combining these, we get two equilibrium points:

1. $(S, I) = (1, 0)$ — Disease-free equilibrium.
2. $(S, I) = \left(\frac{\gamma}{\beta}, I\right)$ where $I \neq 0$ — Disease-Persistent equilibrium.

Stability Analysis

To determine the stability of these points, a linear stability analysis is performed by examining the Jacobian matrix J of the system to evaluate the how sensitive a system is to change in its variables.

$$J = \begin{pmatrix} -\beta I & \gamma - \beta S \\ \beta I & \beta S - \gamma \end{pmatrix}$$

Stability at Disease-free Equilibrium $(S, I) = (1, 0)$

Substituting into the Jacobian matrix:

$$J = \begin{pmatrix} 0 & \gamma \\ 0 & -\gamma \end{pmatrix}$$

The eigenvalues are $\lambda_1 = \gamma$ and $\lambda_2 = -\gamma$.

- $\lambda_1 = \gamma > 0$ — One eigenvalue is positive, so the disease-free equilibrium is unstable.

Stability at Disease-Persistent Equilibrium $(S, I) = \left(\frac{\gamma}{\beta}, I\right)$

Substituting into the Jacobian matrix:

$$J = \begin{pmatrix} -\beta I & 0 \\ \beta I & 0 \end{pmatrix}$$

The eigenvalues are $\lambda_1 = 0$ and $\lambda_2 = 0$.

- $\lambda_1 = \lambda_2 = 0$ — The eigenvalues are zero, so the system is neutrally stable at this point.

Conditions for an Epidemic

1. **Epidemic occurs**: An epidemic will occur if the disease-free equilibrium is unstable, which is the case here as one of its eigenvalues is positive ($\gamma > 0$).

2. **Disease does not reach epidemic proportions**: The disease-persistent equilibrium is neutrally stable, meaning that small perturbations will not cause it to move away from this point. Thus, in this particular SIS model, if the system reaches the disease-persistent equilibrium, it will stay there, and the disease will not reach epidemic proportions.

Cyclic Behavior Possibility

In the standard Susceptible-Infected-Susceptible (SIS) model, it is unlikely for periods of high disease prevalence to be followed by periods of low prevalence in a cyclical manner. The model is characterized by first-order ordinary differential equations (ODEs) that are linear in nature. Such systems typically do not exhibit complex behaviors like cycles or oscillations unless there are added non-linearities or external influences. The stability analysis of the SIS model reveals two types of equilibrium points: a Disease-Free Equilibrium at $(S, I) = (1, 0)$, which is unstable, and a Disease-Persistent Equilibrium at $(S, I) = \left(\frac{\gamma}{\beta}, I\right)$ where $I \neq 0$, which is neutrally stable. The eigenvalues for both of these are real numbers, not complex, indicating that the system does not inherently possess oscillatory behavior. Additionally, the basic SIS model does not incorporate elements like time delays, seasonal variations, or behavioral changes in the population, which are factors that could potentially introduce cycles in disease prevalence. Therefore, within the constraints of the basic SIS model, observing cycling behavior in disease prevalence is not possible.

Conclusion

The transition from the Susceptible-Infected-Recovered (SIR) model to the Susceptible-Infected-Susceptible (SIS) model was necessitated by new clinical evidence that challenged the long-standing assumption of immunity post-recovery. Through rigorous simulation, the study illuminated how varying key parameters like the infectious contact rate (β), the recovery rate (γ), and the initial number of infected individuals (I_0) could impact the spread of the disease. Notably, higher β values resulted in accelerated disease transmission, emphasizing the need for strategies to control this rate. Conversely, an increase in γ led to quicker recoveries and fewer peak infections, highlighting its role in effective public health strategies. The initial number of infected individuals (I_0) influenced short-term dynamics but had less impact on long-term outcomes.

Stability analysis further revealed that the disease-free equilibrium is inherently unstable, making an epidemic likely under the current conditions. On the other hand, the disease-persistent equilibrium was found to be neutrally stable,

suggesting that the disease, once established, is likely to persist within the population. These findings have significant implications for public health policy, emphasizing the importance of reducing infectious contact rates and optimizing recovery efforts. The study serves as a cornerstone for more complex models like SIRS or SEIR, which could capture cyclical patterns and additional complexities not accounted for in the basic SIS model. In summary, the adapted SIS model provides a robust framework for understanding the disease's potential evolution, thereby offering valuable guidance for devising effective containment and treatment strategies.