Journal of Mathematics and Computing Science, 2023,
Volume 9, No 2, 109 - 122

Prediction of Tuberculosis Disease Using SIR Model with Implementation of Runge-Kutta Method in Malaysia

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Received 29 October 2023; Received in revised 18 November 2023; Accepted 1 December 2023
Available online 21 December 2023

Abstract: The purpose of this paper is to anticipate the rate of tuberculosis disease transmission by contrasting two scenarios: one with and one without demography. This paper involved the application of Susceptible-Infected-Recovered (SIR) mathematical model, SIR model with implementation of Fourth Order Runge-Kutta method in order to analyse the number of individuals in three compartments: susceptible, infected and recovered. Furthermore, this paper examined tuberculosis disease prediction by comparing two SIR models and percentage of error by comparing to actual data. The least percentage error model will be chosen to proceed with the prediction of tuberculosis incidence rate for each 100,000 people in Malaysia for 2022. Next, the value of parameters for transmission rate, β and recovery rate, γ, are varied in order to see the effect on incidence rate value. As a result, it was found that SIR model with demography was more accurate and applicable to use as a prediction model for tuberculosis disease. It was also shown that the number of people reported at the peak of the graph decreases with the decrease in transmission rate. Meanwhile, at the end of the year, the incidence rate per 100,000 individuals increased with a reduced transmission rate and a higher incidence rate per 100,000 individuals regardless of recovery rate. Thus, it can be concluded that these variables give significant impact in determining the incidence rate of tuberculosis.

Keywords: Runge-Kutta, SIR model, Tuberculosis

1 Introduction

Mathematical modelling serves as a valuable instrument for investigating the dynamics of intricate systems across various domains such as biology, physics, economics, and social sciences. According to the work of Yan and Cao [1], despite each disease possessing unique biological characteristics, adapting models to specific cases is essential for addressing real-world complexities. In epidemiology, one prevalent mathematical model is the compartmental model, dividing the population into distinct compartments based on their disease status. The SIR model, for example, assumes that individuals can be classified into one of three compartments: susceptible, infected, and recovered. Bahari et al [2] employed the SIR model to look up the tuberculosis epidemic in Kudus Regency. Meanwhile, the SEIR model, which includes an additional compartment for exposed individuals, is particularly useful for modelling diseases with a latency period between exposure and infectiousness. Li et al. [3] highlighted in their SEIR model analysis that infectious diseases involve parameters like exponential normal birth and death rates, as well as deaths due to the disease, impacting population size over time. Mathematical models can be used to make predictions about the future course of an epidemic, such as the total number of cases, the duration of the epidemic, and the impact of different interventions. It can also be used to evaluate the effectiveness of different control strategies, such as vaccination, social distancing, and contact tracing. Some researchers have examined these issues and Side et al. [4] wrote about the mathematical modelling of SIR and SEIR on the transmission of dengue fever and TB by using

Lyapunov function method. While mathematical models are powerful tools, they are only as good as the assumptions and data used to build them. Meanwhile, Ma and Ma [5] studied SEIRS models with seasonal fluctuations. It means that it is important to identify whether the disease shows seasonal behaviour or not before deciding what models to be used. With accurate and up-to-date models, public health officials can make informed decisions about how best to control the spread of infectious diseases and protect public health.

Tuberculosis (TB) poses a significant challenge to global public health and is resurging as an infectious disease. As per the World Health Organization (WHO) [6], approximately one-third of the world's population carries TB infections. Annually, nearly 9 million individuals contracted TB, resulting in approximately 2 million deaths. In underdeveloped nations, TB stands as the primary cause of death from a single infectious agent among adults. Moreover, TB surpasses other infectious diseases, including HIV and malaria, in annual mortality rates, underscoring its gravity as a global health concern (WHO) [7]. TB is communicable and can be transmitted through various means. Direct physical contact, such as touching or kissing an infected person, serves as one mode of transmission. Additionally, the infectious microbes can spread through the air when an infected individual sneezes or coughs. Persistent coughing lasting more than three weeks, along with symptoms like fever, coughing up blood, chest pain, fatigue, weight loss, exhaustion, and night sweats, indicate active tuberculosis [8, 9].

Runge-Kutta (RK) is a family of numerical methods used to approximate solutions to differential equations. These methods are widely used in scientific computing to solve differential equations that cannot be solved analytically. RK methods are particularly useful for solving ordinary differential equations (ODEs) because they are simple to implement and can approximate the solution with high accuracy. Kanwal et al [10], wrote about three numerical techniques, non-standard finite difference, forward Euler and RK of fourth-order (RK-4) in order to analyse the TB model. The RK-4 which is a member of RK family, is a widely-used numerical technique for solving ODEs. It is a higher-order method, which means it provides a relatively accurate approximation of the solution compared to simpler methods like Euler's method. RK-4 calculates the solution at each step by evaluating the function at four different points within the step and combining these evaluations to estimate the change in the solution. Besides that, RK-4 is particularly useful for solving ODEs that is used to describe dynamic systems, such as those encountered in physics, engineering, and various scientific fields.

In conclusion, the SIR model, when applied to TB prediction, enables the study of disease dynamics and the evaluation of control strategies. However, solving the ODEs of the SIR model requires numerical integration techniques of RK method to obtain accurate and reliable results.

2 Methodology

In this section, we present the susceptible-infected-recovered model, considering scenarios with and without demographic factors, and propose solutions utilizing the RK method. Furthermore, we introduced the formulation of the incidence rate and success rate within this context.

A Susceptible-infected-recovered model without demography

In the context of the SIR model without considering demography, it was assumed that the population remains constant throughout the designated investigation period. This assumption entails disregarding factors such as migration, mortality, and birth rates during the specified timeframe. By neglecting these demographic influences, the model focuses exclusively on the dynamics of susceptible, infected, and recovered individuals without the additional complexity introduced by population changes through migration, births, or deaths. Figure 1 depicts the compartments of the SIR model without demography.

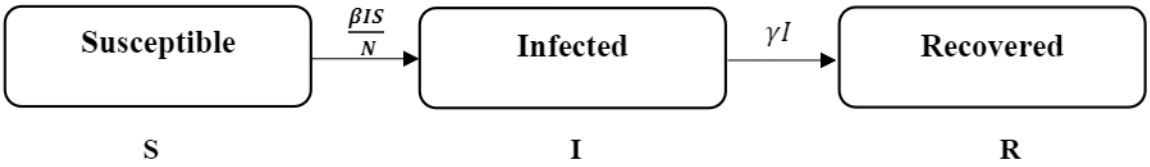

Figure 1: The SIR model compartments without demography

As illustrated in Figure 1, the term $\frac{\beta IS}{N}$ denotes the count of infected individuals reduced by the susceptible individuals in close contact with TB patients. This term reflects the transmission rate of the disease, contributing to an increase in the population of the infected group and a decrease in the population of those who recovered. Additionally, the term γI represents the recovery rate for each individual, leading to an increase in the recovered group. It is important to note that other elements have no impact on this recovery rate. Consequently, the ODEs governing the SIR model without demography, as proposed by Kousar et al. [11], are presented below.

$$\frac{dS}{dt} = \frac{-\beta SI}{N} \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

The initial conditions are S(0) = S_0, I(0) = I_0, R(0) = R_0. The variables S, I, and R denote the susceptible, infected, and recovered populations, respectively. Conversely, β and γ indicate the rates at which transmission and recovery occur, respectively.

Next, the SIR model was solved numerically using the Runge-Kutta method [12]. First, we let the equations (1) – (3) with:

$$k_1 = f(t_i, I_i, S_i) = \frac{-\beta S_i I_i}{N}$$

$$f_I(t, I, S) = \frac{dI}{dT} = \frac{\beta SI}{N} - \gamma I$$

$$f_R(t, I) = \gamma I$$

Subsequently, the coefficient for each iteration i needs to be computed, as detailed in [4]. Therefore, the numerical solution of the SIR model without demography is provided by:

$$S_{i+1} = S_i + \frac{h(k_1 + 2k_2 + 2k_3 + k_4)}{6}$$

$$I_{i+1} = I_i + \frac{h(l_1 + 2l + 2l_3 + l_4)}{6}$$

$$R_{i+1} = R_i + \frac{h(m_1 + 2m_2 + 2m_3 + m_4)}{6}$$

with

$$k_1 = f_s(t_i, I_i, S_i) = \frac{-\beta S_i I_i}{N}$$

$$k_2 = f_S\left(t_i + \frac{h}{2}, I_i + \frac{hl_1}{2}, S_i + \frac{hk_1}{2}\right) = \frac{-\beta(S_i + \frac{hk_1}{2})(I_i + \frac{hl_1}{2})}{N}$$

$$k_3 = f_S\left(t_i + \frac{h}{2}, I_i + \frac{hl_2}{2}, S_i + \frac{hk_2}{2}\right) = \frac{-\beta(S_i + \frac{hk_2}{2})(I_i + \frac{hl_2}{2})}{N}$$

$$k_4 = f_S(t_i + h, I_i + hl_3, S_i + hk_3) = \frac{-\beta(S_i + hk_3)(I_i + hl_3)}{N}.$$

B Susceptible-infected-recovered model with demography

In this section, we explore the SIR model with demography, incorporating birth and death rates while excluding any potential minor migration effects. To maintain a constant population size over time, the birth rate must equal the death rate, as highlighted by Widyaningsih et al. [13]. Figure 2 illustrates the compartments of the SIR model with demography as proposed by Side et al. [14], emphasizing the inclusion of demographic factors such as birth and death rates in the model dynamics.

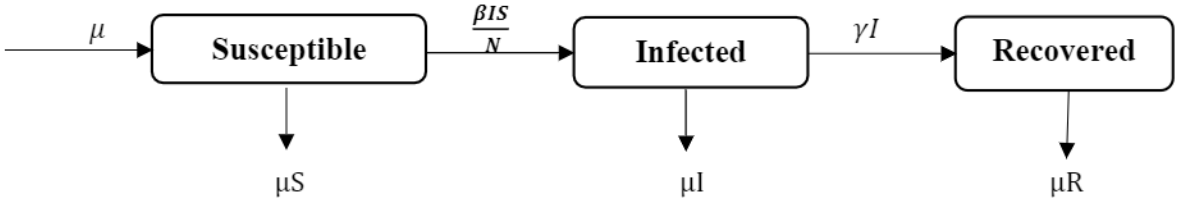

Figure 2: The SIR model compartments with demography

In this model, a parameter denoted as μ, encompassing both birth and death rates, was introduced. The susceptible population was assumed to undergo a balance between births (μ) and deaths (μS). In contrast, the infected and recovered populations were subjected to distinct death rate parameters, denoted as μI and μR, respectively. Consequently, the formulation of the SIR model in the presence of demography can be expressed as follows, considering these demographic considerations:

$$\frac{dS}{dt} = \mu - \frac{\beta SI}{N} - \mu S \tag{4}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I - \mu I \tag{5}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{6}$$

with initial conditions of S(0) = S_0, I(0) = I_0, R(0) = R_0.

Next, the SIR model with demography was solved numerically using the RK method. To do this, we let the equations (4) – (6) with:

$$f_s(t, I, S) = \frac{dS}{dt} = \mu - \frac{\beta SI}{N} - \mu S$$

$$f_I(t,I,S) = \frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I - \mu I$$

$$f_R(t,I,S) = \frac{dR}{dt} = \gamma I - \mu R$$

Subsequently, the coefficient for each iteration i was computed. Thus, the following is the numerical solution for the SIR model in the presence of demography:

$$S_{i+1} = S_i + \frac{h(k_1 + 2k_2 + 2k_3 + k_4)}{6}$$

$$I_{i+1} = I_i + \frac{h(l_1 + 2l + 2l_3 + l_4)}{6}$$

$$R_{i+1} = R_i + \frac{h(m_1 + 2m_2 + 2m_3 + m_4)}{6}$$

with

$$k_1 = f_s(t_i, I_i, S_i) = \mu - \frac{\beta S_i I_i}{N} - \mu S_i$$

$$k_2 = f_s\left(t_i + \frac{h}{2}, I_i + \frac{hl_1}{2}, S_i + \frac{hk_1}{2}\right) = \mu - \frac{\beta\left(S_i + \frac{hk_1}{2}\right)\left(I_i + \frac{hl_1}{2}\right)}{N} - \mu\left(S_i + \frac{hk_1}{2}\right)$$

$$k_3 = f_s\left(t_i + \frac{h}{2}, I_i + \frac{hl_2}{2}, S_i + \frac{hk_2}{2}\right) = \mu - \frac{\beta\left(S_i + \frac{hk_2}{2}\right)\left(I_i + \frac{hl_2}{2}\right)}{N} - \mu\left(S_i + \frac{hk_2}{2}\right)$$

$$k_4 = f_s(t_i + h, I_i + hI_3, S_i + hk_3) = \mu - \frac{\beta(S_i + hk_3)(I_i + hI_3)}{N} - \mu(S_i + hk_3).$$

C Incidence rate

The frequency of TB cases, known as the incidence rate, reflects the number of newly identified cases in a specific population over a defined time period. This calculation involves dividing the recently reported cases by the total population at risk during the specified timeframe. To standardize the data, the resulting figure was multiplied by a constant factor of 100,000. This standardized incidence rate serves as a metric per 100,000 population, enabling a meaningful assessment and comparison of the occurrence of new TB cases among diverse populations and regions.

$$Incidence\ rate\ _i = \frac{No\ of\ new\ TB\ cases\ reported\ in\ the\ period}{Total\ population\ at\ risk\ in\ period} \times 100{,}000$$

D Success rate

The term "success rate" serves as a metric to gauge the effectiveness of a given treatment. In the context of TB, data on the success rate was extracted from the Ministry of Health Malaysia's 2021 annual reports. The success rate of TB was calculated using the formula:

$$Success\ rate, rate_{\ i} = \frac{No\ of\ recovered\ in\ the\ period}{Total\ number\ of\ infected\ individuals\ in\ the\ period} \times 100$$

This mathematical expression enables the measurement of the percentage of people who have effectively overcome tuberculosis within a specified timeframe. In the assessment of the efficiency and relevance of the SIR model, both in the absence and presence of demographic variables, the aim is to predict the course of tuberculosis transmission in Malaysia for the year 2022. The reports from the Ministry of Health Malaysia in 2021 reveal a treatment success rate of 87% for tuberculosis in 2019. By employing the formula for the success rate, it is calculated that 22,927 individuals recovered from tuberculosis in 2019. Following this, relevant information on susceptible and infected individuals is gathered to construct the SIR model, facilitating a thorough examination of the dynamics of disease transmission in Malaysia. This information is summarized as in Table 1 below.

Table 1: The number of populations in 2019

Susceptible population	Infected populations	Recovered populations
177,121	26,352	22,927

To analyze and predict the transmission of TB in Malaysia, it is crucial to establish specific parameter values, specifically for factors such as the transmission rate, recovery rate, and birth rate. The information provided furnishes the subsequent parameter values:

- Transmission rate, β: A person with TB disease can infect approximately 20.6 people through close contact. [12]

  $\beta = \frac{1}{20.6} = 0.04857$

- Recovery rate, γ: It takes around 140 days for a patient to recover from TB with the help of medication. [12]

  $\gamma = \frac{1}{140} = 0.007143$

- Birth rate /Mortality rate, μ: In 2019, there were 6.88 deaths from TB per 100,000 people [15].

- Total population at risk period 2020: The total population is 33.2 million people.

By employing these criteria, a thorough examination of the pattern of Tuberculosis (TB) spread in Malaysia during the year 2020 were carried out.

3 Results and Discussion

A Prediction of SIR model for 2020

In this section, we utilized the SIR model for predicting TB occurrences in 2020 by examining scenarios with and without demographic factors. The simulations were conducted through the implementation of Python software. A comprehensive presentation of the input variables crucial for predictive analyses, including all parameter values and initial conditions for both models, is provided in Table 2.

Table 2: Parameter values and initial conditions used in the models

Parameter	Value
S(0)	177,121
I(0)	26,352
R(0)	22,926

β	0.04857
γ	0.007143
μ	0.000068

i. Predicting TB transmission in 2020 using the SIR model without demography

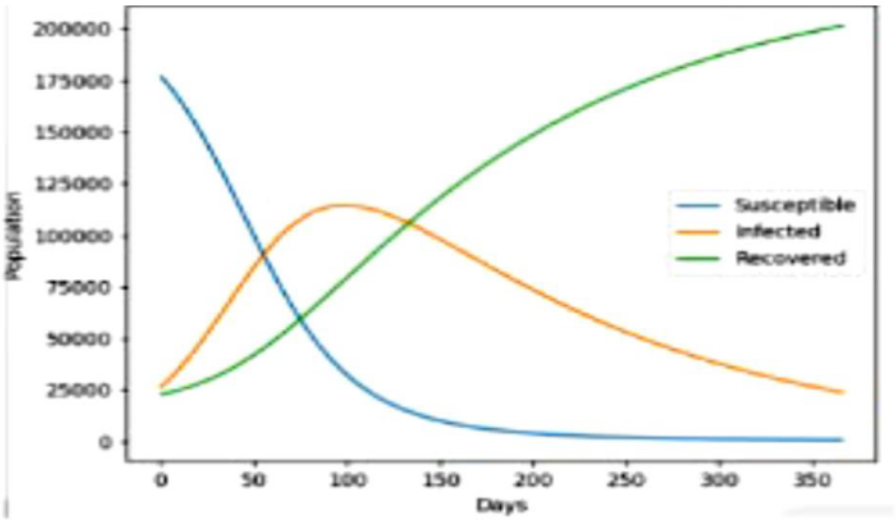

Figure 3: Graph of SIR Model without demography for 2020

Figure 3 illustrates the time series graph of the SIR model, excluding demographic factors. The initial data on the first day indicates that there were 177,121 susceptible individuals, 26,352 infected individuals, and 22,926 recovered individuals. The graph displays a peak in infections on the 99th day, with 114,524 individuals classified as infected. Subsequently, after day 99, the number of infections started to decrease until the end of the year 2020. Concurrently, the count of susceptible individuals initially reached its highest point and gradually decreases, while the number of recovered individuals steadily rose, reaching its maximum by the conclusion of 2020. It is assumed that the population remained constant throughout the entire period. Notably, at the end of 2020, the number of infected individuals was recorded at 24,092 people.

ii. Predicting TB transmission in 2020 using the SIR model with demography

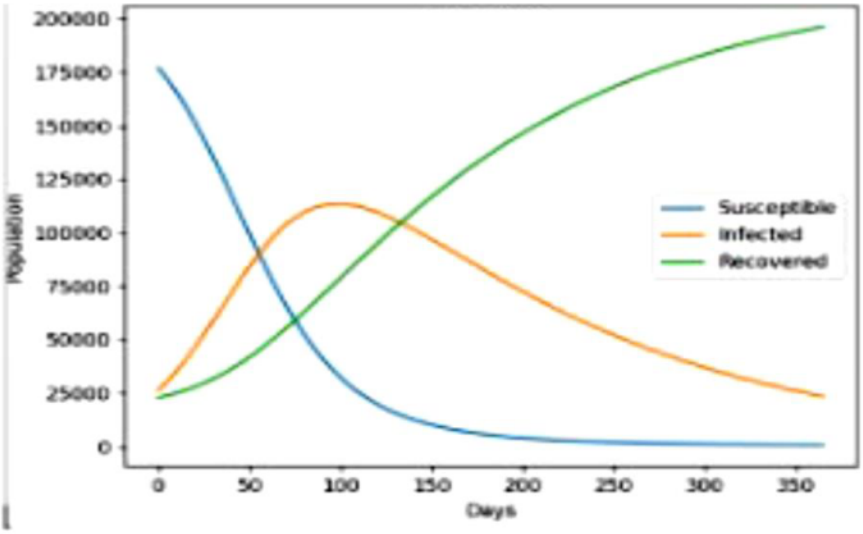

Figure 4: Graph of SIR Model with demography for 2020

Figure 4 presents a time series plot forecasting the transmission of TB in relation to demographic factors. In this scenario, a surge in the number of infections was observed on day 98, reaching 113,523 individuals in the infected category. After day 98, the incidence of infections progressively declined until the conclusion of the year 2020. Similarly, the count of susceptible individuals initially reached its peak and gradually diminished over time, while the number of recovered individuals steadily rose, reaching its highest point by the end of 2020. This examination considered demographic variables such as birth and death rates which reflects population dynamics.

iii. Comparison with the Actual Data

The actual number of infections and the incidence of TB per 100,000 people in 2020 are displayed in Table 3.

Table 3: Number of Susceptible, Infected and Recovered in 2020

Number of infected people	Incidence rate of the disease
23,644	71.21

Table 4: The Predicted and Actual Incidence Rate

Type of SIR Mode	Predicted Incidence Rate for TB	Actual Incidence Rate for TB	Error (%)
Without Demography	72.56	71.21	1.89
With Demography	70.91	71.21	0.42

Table 4 illustrates the predictions of TB incidence rates, with small errors of 1.89% and 0.42%. This indicates the effectiveness of employing the SIR model, particularly when utilizing the Runge-Kutta 4th order (RK4) method. Notably, the SIR model incorporating demography exhibits higher efficiency, as reflected in its lower error rate.

The simplification of the model, by excluding demographic factors, assumed a consistent population over time. When demographic variables were introduced, there seemed to be an impact on the trajectory of TB transmission, leading to a slightly decreased number of infections by the end of the year. Therefore, integrating demography into the SIR model for TB transmission prediction offers several benefits. Considering factors like birth and death rates enhances the model's resemblance to real-world situations, acknowledging the dynamics of the population. This increased realism enables a more precise depiction of disease transmission dynamics, especially in areas where demographic shifts have a notable influence. Henceforth, in the following section, our focus will be on utilizing the SIR model with demographic to analyze population dynamics across different parameters.

B Analyzing the population dynamics when the parameter β is varied

In this section, we explored the population dynamics in response to variations in the transmission rate. We specifically investigated four distinct transmission rate values: $\beta = 0.1, 0.05, 0.04857$, and 0.03333. These values were chosen because we want to see what is the trend in the number of infected individuals. The simulations incorporated all parameters outlined in Table 2. Figures 5 - 8 depict the corresponding simulated graphs illustrating the impact of these different transmission rate values on the population dynamics.

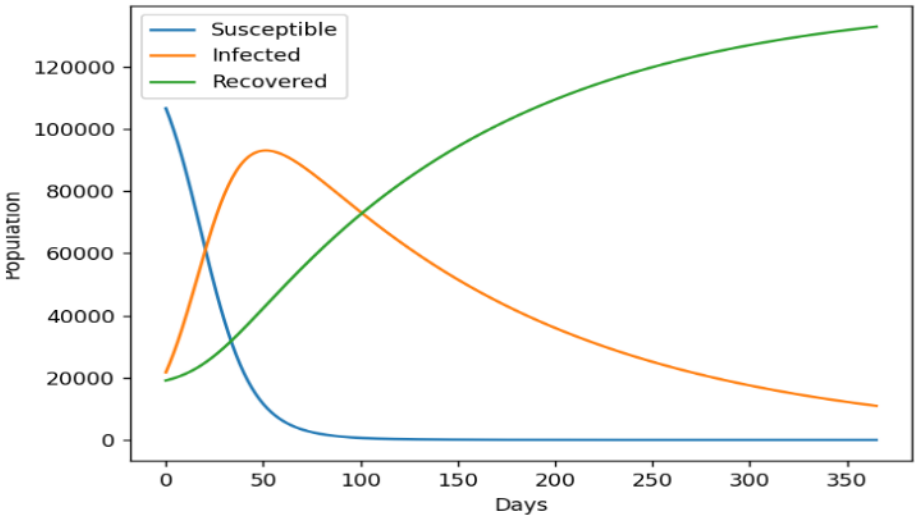

Figure 5: Graph when $\beta = 0.1$

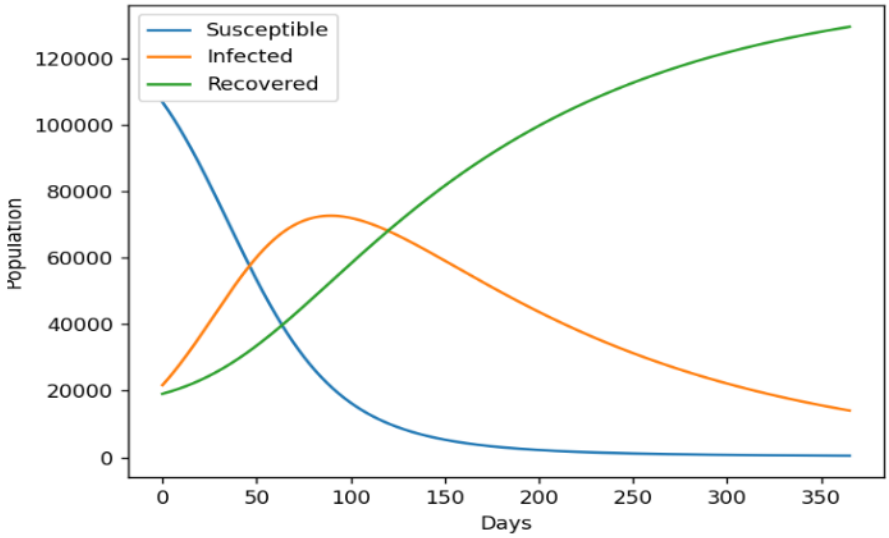

Figure 6: Graph when $\beta = 0.05$

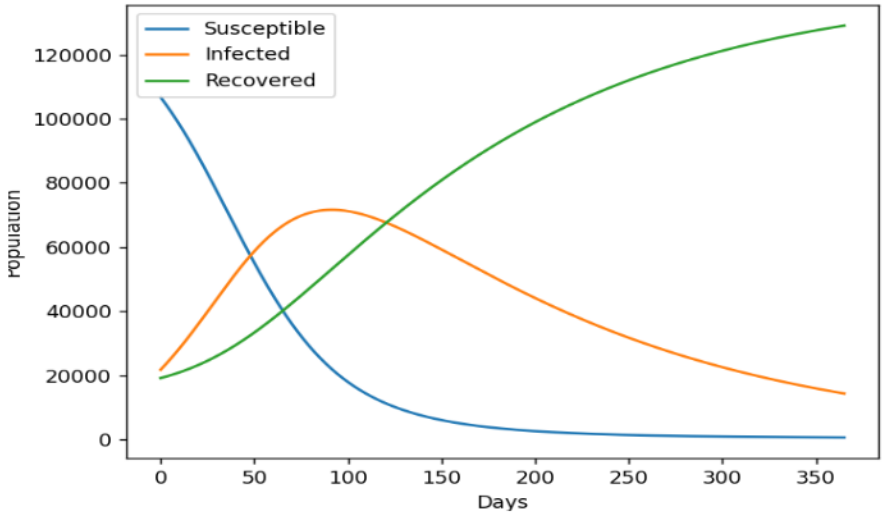

Figure 7: Graph when $\beta = 0.04857$

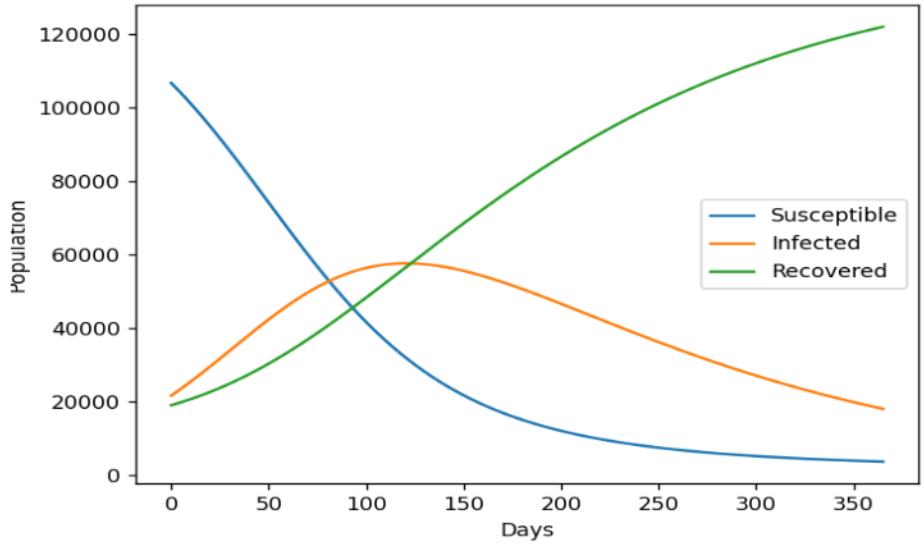

Figure 8: Graph when β = 0.03333

Table 5: Number of infected individuals recorded at peak day for different β

β	Number of infected individuals at peak	Peak Day
0.1	93,119	51
0.05	72,603	89
0.04857	71,598	91
0.03333	57,694	120

The results displayed in Table 5 reveal that when the transmission rate (β) decreases, there was a corresponding decrease in the number of infected individuals observed at the graph's peak. This reduction was linked to a slower spread of the disease within the population. Importantly, alterations in the transmission rate affect the time needed to reach the peak in the graph, underscoring the significance of β in determining the pace and intensity of disease transmission.

Table 6: The number of infected individuals and number of recovered individuals at the end of 2022 for different β

β	Number of infected individuals	Number of recovered individuals
0.1	10,968	13,2970
0.05	14,072	12,9363
0.04857	14,302	12,9041
0.03333	18,149	12,1998

The results obtained from Table 6 highlight a significant relationship between the transmission rate (β) and the number of infected individuals at the conclusion of the year 2022. A lower transmission rate corresponded to a higher final count of infected individuals. This pattern emerged because a reduced transmission rate implies a slower spread of the disease, resulting in the graph reaching its peak later and allowing more time for individuals to become infected. In contrast, a higher transmission rate accelerated the spread of the disease, causing the graph to reach its peak earlier in the year and limiting the time available for individuals to recover. Consequently, the final count of infected individuals tended to be lower under higher transmission rates. Considering Malaysia's population of 33.57 million, the calculated incidence rate of TB per 100,000 people, as presented in Table 7, provides a standardized measure that accounts for population size. This enables a more meaningful comparison of TB incidence across different scenarios, helping to inform public health strategies and interventions based on varying transmission rates.

Table 7: Incidence rates of TB for different transmission rates per 100,000 population

β	Incidence Rate as per 100,000 people
0.1	32.67
0.05	41.91
0.04857	42.60
0.03333	54.06

C Analyzing the population dynamics when the parameter γ varied

In this section, we examined the changes in population dynamics by varying the recovery rate. For this purpose, we chose three distinct recovery rate values: $\gamma = 0.01$, 0.007143, and 0.005556 in order to observe what will happen to the number of infected individuals. The simulated graphs illustrating these variations are depicted in Figures 9 to 11.

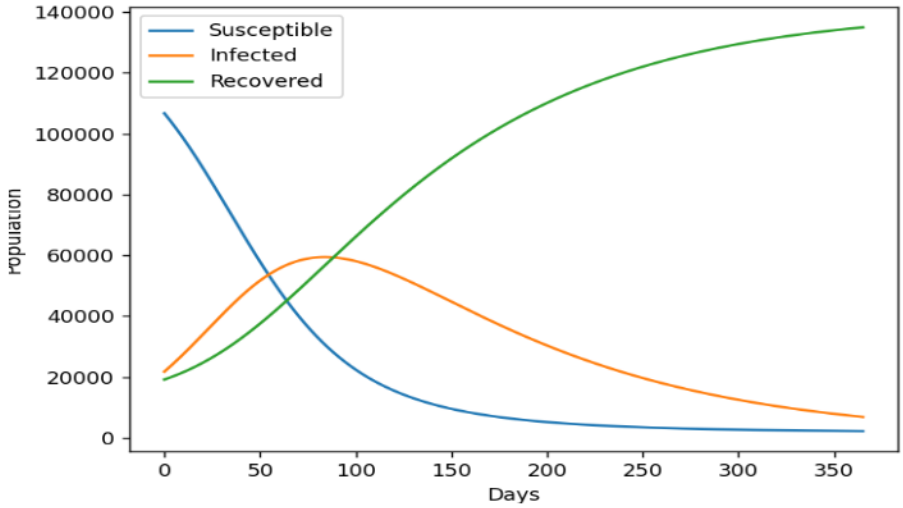

Figure 9: Graph when $\gamma = 0.01$

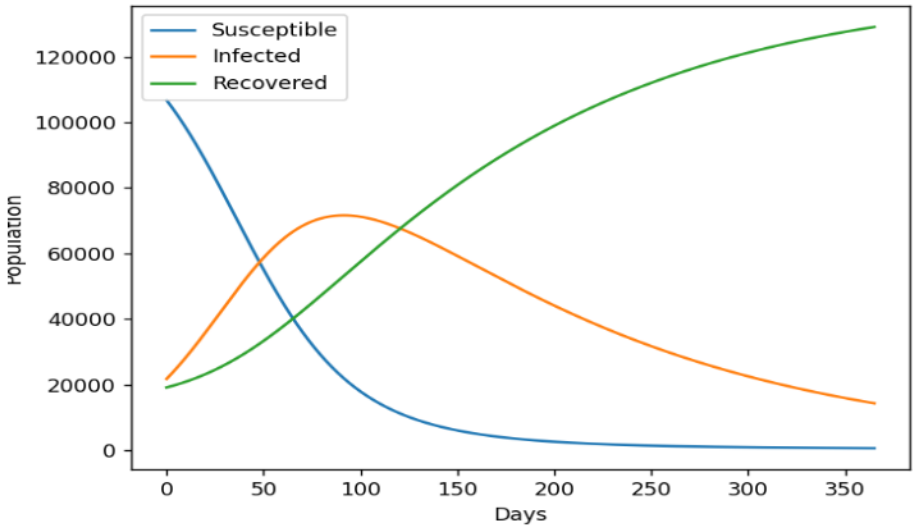

Figure 10: Graph when $\gamma = 0.007143$

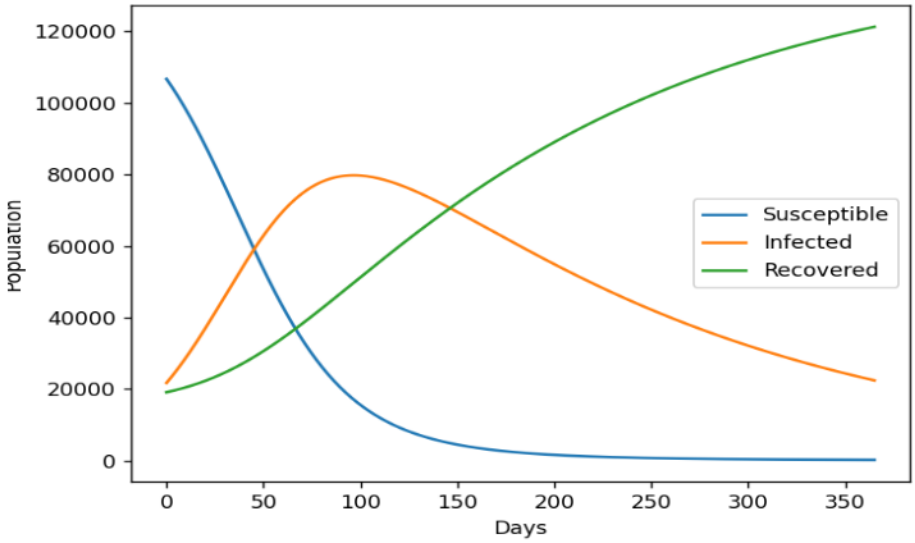

Figure 11: Graph when $\gamma = 0.005556$

Table 8: Number of Infected and Recovered Individuals in TB Transmission for different γ

γ	**Number of infected individuals**	**Number of recovered individuals**
0.01	67,97	135,015
0.007143	14,302	129,041
0.005556	22,432	121,289

The result presented in Table 8 demonstrates a significant correlation: a diminished recovery rate (γ) corresponded to an increased count of documented infected individuals by the close of the year 2022. This connection was attributable to the prolonged recovery time for infected individuals associated with a slower recovery rate. Within the framework of Malaysia's populace of 33.57 million, the subsequent Table 9 computes the prevalence of TB per 100,000 individuals. As a result, it becomes apparent that a reduced recovery rate was associated with a heightened TB incidence rate in Malaysia at the culmination of 2022.

Table 9: Incidence rates of TB for different recovery rates (γ) per 100,000 population.

γ	**Incidence Rate as per 100,000 people**
0.01	20.24
0.007143	42.60
0.005556	66.82

This observation highlights the pivotal role played by the recovery rate in shaping the overall impact of the disease. A swifter recovery rate facilitates a more effective reduction in the number of infected individuals, leading to a diminished incidence rate.

4 Conclusion and Recommendations

In this paper, the SIR models were employed to predict TB transmission in Malaysian population in 2022. The SIR model has been solved using the RK-4 method in Python. This project used Spyder and Jupyter notebook software to apply the Python language. The advantage of using these two models is, it is able to forecast the trajectory of the spread of the TB disease in the future. The SIR Model with demography was discovered and provided a more accurate forecast for TB epidemic's spread in 2022. This may be the result of several occurrences, including birth, death, immigration, etc. Furthermore, by

estimating the disease's incidence rate per 100,000 people, the pattern of TB transmission through the year 2022 was projected. It has also been thoroughly examined how parameters affect the transmission tendency. According to this research, the incidence rate for every 100,000 people increases when the value of the transmission rate decreases but it should be highlighted that the lower the transmission rate β, the lower the number of individuals recorded at the peak of the graph, due to the disease spreading less rapidly through the population and incidence rates increase as the value of the recovery rate decreases.

For recommendation, it is suggested to compare the SIR model with other epidemiological models, such as SEIR (Susceptible-Exposed-Infected-Recovered), SITR (Susceptible-Infected-Treatment-Recovered) or more complex agent-based models. Next, the SIR model can be extended for multiple strains of tuberculosis, including drug-resistant strains. This could provide insights into the interaction between different strains and the potential impact on disease transmission dynamics.

Acknowledgements

This research received no specific grant from any funding agency in the public, commercial, or private sectors.

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