

EFFECT OF IMMIGRATION ON DISEASE SPREAD: A SEI MODEL

Amar Qamariezman Kamaron Zaman¹, Nur Ferzana Johangir² and Nadhirah Abdul Halim^{3*}

Department of Mathematics, Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA, 40450, Shah Alam, Malaysia

¹2019883826@student.uitm.edu.my, ²2019218378@student.uitm.edu.my,

^{3*}nadhirahhalim@uitm.edu.my

ABSTRACT

An SEI model with constant immigration and standard incidence function is investigated. In this age, immigration is a common activity that happens due to various reasons. Unfortunately, immigration can become one of a reason for infectious diseases to spread globally. In order to investigate the impact of immigration on the disease spread, the SEI model is applied. Using the TB disease as an example, the model is solved numerically using the Runge-Kutta method of order 4 (RK4). The results are presented graphically and in tabular form. The effect of immigration does not seem crucial initially on the TB disease spread but will have an impact on the population that is noticeable as time goes by. Compared to the immigration parameter, another parameter has a bigger impact on our model. It is discovered that a higher contact rate with infectious people will outweigh the effect of immigration. An action plan has been presented where we have to determine who is highly potential to spread the disease and isolate them to control the disease from entering the country through immigration

Keywords: Immigration, RK4, SEI.

Received for review: 26-08-2022; Accepted: 09-09-2022; Published: 01-11-2022

1. Introduction

Immigration is a procedure that requires people to relocate permanently from their home nation to another for a variety of reasons. This activity has been going on for a long time since it can provide a lot of benefits, whether socially, economically, or culturally. People who are employed are the ones who use immigration the most. Some people are forced to move to another country to work because their superiors have assigned them to do so, while others immigrate to find work because it is easier to find than in their home country. Despite the fact that the process is not as straightforward as it appears, some people are willing to go through it just to survive and provide for their families. In some countries, immigration is required. Immigration, according to Orrenius (2016), stimulates the economy. This is because when they invest in human resources, economic productivity rises, resulting in an increase in the gross domestic product (GDP). Immigration is one of the most effective strategies to improve people's lives and the economies of some countries. Even though it is great, the process must be carried out with caution and precision.

A disease is a form of challenge that humanity has been dealing with since the beginning of time. It is an endless concern that continues to evolve with the advancement of human technology as time passes. Infectious diseases, specifically airborne diseases, are the most dangerous because germs and viruses can spread from one person to another by tiny

respiratory droplets. SARS, Covid-19, and tuberculosis (TB) are just a few examples. Today, it is becoming more and more common to travel and immigrate around the world due to the advancement of means of transport. With a significant increase in the numbers of travellers and immigrants in and out of a country, it is unavoidable that some of them may be carrying an infectious disease during the time of arrival.

Understanding how diseases move across countries is critical to preventing large epidemic outbreaks. Mathematical modelling has been a highly useful tool for analyzing disease progression and comprehending transmission mechanisms, among other things. The earliest account of mathematical modelling of the spread of disease was an inoculation against smallpox by Daniell Bernoulli in 1760. In order to create a mathematical model for the transmission of a communicable disease, it is necessary to make some assumptions about the means of spreading infection. In the study of compartmental disease transmission models, the population under study is divided into compartments, namely susceptible (S), exposed (E), infected (I), and recovered (R), and assumptions are made about the nature and time rate of transfer from one compartment to another. Kermack and McKendrick introduce the basic compartmental models for describing the spread of infectious illnesses in 1927 (Brauer, 2017). Since then, there has been a great deal of work on compartmental diseases transmission models such as SI, SIR, SEI, SIS, SEIR, SEIZ, and many others, with generalizations in many directions.

Brauer and Driessche (2001) used the SIR model to calculate the spread of disease that depends on infected people's immigration and various sizes of the population. The model is also tested using mass action incidence that separates two different conditions in which the infected people end up dying or recover because of everlasting immunity, where both of the conditions have no differences in theoretical actions. Chen and Zou (2018) used the SIR model with shifting contagious immigrant population to investigate the restricting immigration of infectious people's effect on the contagious diseases spreading in a particular region. The optimum immigration of contagious people restriction can control the contagious population in a region at a particularly low level based on the analysis of global dynamical for the shifting method. Li et al. (2005) studied about SEIR model with the force of infectious in the period of exposed, infected, and recovered and the assumption of having unchanged rates of immigration for the susceptible and exposed persons. The endemic equilibrium global stability can be acquired using the theory of compound matrix and if the basic reproduction value is higher than 1, Bhunu et al. (2007) also use the SEIR model in their research to investigate the Tuberculosis model which includes the chemoprophylaxis and infection control measures. They found that the control measure is working better when the implementation was done in the first year out of a decade because treatment clears active TB right away, and chemoprophylaxis performs better at keeping the number of infectives under control after that since there is a slower transition to active TB. Arfan et al. (2020) have constructed a modified Susceptible and Infected (SI) population model to speculate the COVID-19 spread in Pakistan. They also apply the method of the next-generation matrix to obtain a value for local and global stability of various equilibrium point types. SIS type model was used by Saikh and Gazi (2021) in their study to find out about the infection force and the cure on the illness dynamics impacts, which exposed the contrast between infected immigrants and the ultimate capacity of cures has a considerable impact on the epidemic system's disease endemicity.

The SEI model with immigration is different compared to SEI without immigration in terms of the differential equation and the flow of the model. There have been a lot of examples to show how the SEI model with immigration was used. Sigdel and McCluskey (2014) have done research using the SEI disease spreading model with immigration to analyze the three groups which were susceptible, exposed, and infected. They apply a nonlinear variable to the infective value involving mass action and incidence of concentration as special samples. They acquired a globally asymptotically stable for their endemic equilibrium as a result. Abdelmalek and Bendoukha (2018), solved the SEI reaction-diffusion model of infectious disease using a

Lyapunov functional to investigate the local and global stability of solutions for a regionally spread SEI epidemic model with individual immigration. As a result, the unique steady state is proven to be globally stable in the presence of diffusion. In recent research by Khan et al. (2021), they explore the global dynamics of an SEI epidemic model with constant immigration and a general nonlinear incidence function. As an outcome for the type of model with immigration terms, it is proven that there is neither a disease-free equilibrium nor a basic reproduction number. Additionally, the presence of an exclusive endemic equilibrium is demonstrated. They establish the global stability of the positive equilibrium using the second Lyapunov approach.

In this research, we will be using the Susceptible-Exposed-Infected (SEI) model proposed by McCluskey & van den Driessche (2003) as the main reference to study how vital the immigration factor is in disease spread. We will be applying parameter values of an airborne infectious disease to investigate the problem numerically. Then, from the result and discussion, we will propose an action plan to control the spread of disease through immigration into the country. This knowledge can then be used in making a better plan for controlling a breakout of epidemic or pandemic level disease.

2. Methodology

2.1 SEI Formulation

A model is created for the spread of tuberculosis in a population that includes recent immigrants as well as those who are already affected. The population is separated into three classes based on epidemiological status: susceptible, exposed, and infective, with the proportion of each class designated by S , E , and I , respectively. The rate of new people entering the population is Λ , with fractions of $1 - p - q$, p , and q , entering the susceptible, exposed, and infective compartments respectively. μ is the rate constant of non-disease-related death and $1/\mu$ represents the average lifetime. Next, γ is the symbol for the rate constant for an exposed individual in becoming an infective individual, and $1/\gamma$ stands for an average latent period. The average number of contacts that an infective makes over time is c and β is transmission probability. Standard incidence is used to simulate transmission, so susceptible are infected and join the exposed class at a rate of $c\beta \frac{SI}{N}$, where the value of population size is depicted as $N = S + E + I$. The coefficients c , β , Λ , γ and μ are presumed to be positive and other non-negative coefficients with p , q , $p + q \in [0,1]$.

The model used for this research is the simplified model proposed by McCluskey & van den Driessche (2003). The SEI model with immigration is separated into three different groups; susceptible (S), exposed (E), and infectious (I).

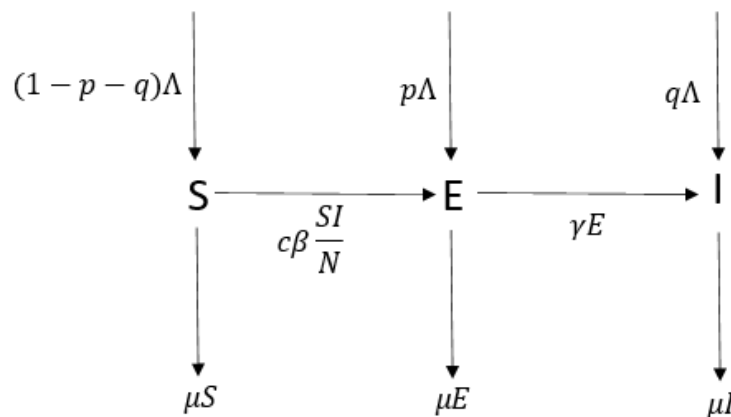


Figure 2. SEI model with immigration

Individuals move from the susceptible compartment to the exposed compartment at the rate of $c\beta \frac{SI}{N}$ and from the exposed compartment to the infected compartment at the γE .

The model's system of the differential equation is given by:

$$\begin{aligned}\frac{dS}{dt} &= (1 - p - q)\Lambda - c\beta \frac{SI}{N} - \mu S \\ \frac{dE}{dt} &= p\Lambda + c\beta \frac{SI}{N} - (\mu + \gamma)E \\ \frac{dI}{dt} &= q\Lambda + \gamma E - \mu I \\ N &= S + E + I\end{aligned}\tag{1}$$

where

- S : The number of people who are susceptible to disease infection and can be exposed to infectious people in a certain area
- E : The number of people in a certain area who are exposed to the virus and may get infected by infectious people
- I : The number of people infected and infectious in a certain area as a result of the virus's transmission
- Λ : The recruitment rate
- p : The fraction of people entering the exposed (E) class
- q : The fraction of people entering the infective (I) class
- c : The average number of contacts made by infectious individuals
- μ : The disease non-related death rate
- β : Transmission probability
- γ : The rate of exposed individuals in becoming infectious.

If $p = q = 0$, the model will then reduce to a model without immigration. Hence, it is always assumed that at least one of p and q is positive.

A SEI model of disease transmission with immigration into all three classes has no disease-free equilibrium and therefore no basic reproduction number. For all parameter values, the only equilibrium is an endemic equilibrium. A more detailed proof on the positive variant, uniqueness, and stability of the endemic equilibrium can be found in McCluskey and van den Driessche (2004).

The systems of equation (1) can be rewritten as an equivalent system in terms of N , $V = E + I$, and I .

$$\frac{dN}{dt} = \Lambda - \mu N\tag{2}$$

$$\frac{dV}{dt} = (p + q)\Lambda + c\beta \frac{(N - V)I}{N} - \mu V$$

$$\frac{dI}{dt} = q\Lambda + \gamma V - \mu I$$

Assuming that the equilibrium is given by $(N, V, I) = (N_*, V_*, I_*)$. In a state of equilibrium, $dN/dt = 0$, and so

$$N_* = \frac{\Lambda}{\mu} \quad (3)$$

Similarly, $dI/dt = 0$ implies

$$V_* = \frac{\gamma + \mu}{\gamma} I_* - \frac{q\Lambda}{\gamma} \quad (4)$$

When these formulas are substituted into the equation $dV/dt = 0$, we have

$$a_2 I_*^2 + a_1 I_* + a_0 = 0 \quad (5)$$

where

$$a_2 = -c\beta\mu(\gamma + \mu),$$

$$a_1 = \Lambda[c\beta(\gamma + q\mu) - (\gamma + \mu)(\mu)],$$

$$a_0 = \Lambda^2[(p + q)\gamma + q(\mu)].$$

2.2 Data Collection

In this study, we want to investigate the disease spread behaviour under the effects of immigration factor via numerical simulation. Important to note that McCluskey and van den Driessche's (2003) studies are concerned with the global stability of the model and hence, did not include any numerical solutions to their model. The data used in this study follows from Bhunu et al. (2007) where the parameter values (Table 1) correspond to Tuberculosis disease.

Table 1: Model parameters and their interpretations.

Definition	Symbol	Estimate (Range)	Source
Recruitment rate	Λ	0.03 yr ⁻¹	a*
Natural mortality rate	μ	0.013 yr ⁻¹	b*
Contact rate	c	80 yr ⁻¹	a*
Probability of being infected	β	0.35 (0.1 – 0.6) yr ⁻¹	a*
Natural rate of progression to active TB	γ	0.00013 (0.0001 – 0.0003) yr ⁻¹	a*

In Table 1, a* indicates parameter values from Bhunu et al. (2007), and b* indicates parameter values from Malaysia Life Expectancy 2022.

2.3 Numerical Analysis

The model is solved using the Runge-Kutta method of order 4 (RK4) which is formulated in Microsoft Excel. In this study, h is taken to be 0.01 and the initial conditions are $S(0) = 20000$, $E(0) = 5000$, and $I(0) = 500$. Note that the referred literature (McCluskey and van den Driessche, 2003) focused on the global stability of the model and does not provide any numerical analysis. To validate our results and calculations, we compare them with those obtained using MATLAB as shown in the Table 2 below. It can be seen that, the results obtained using Excel is as accurate as the results obtained using MATLAB.

Table 2. Comparison values of susceptible individuals (S) at selected time, t.

Susceptible (S)		
t (years)	EXCEL (RK4)	MATLAB (RK4)
0	20,000	20,000
10	63.30980	63.24653
20	0.17036	0.17025
30	0.02750	0.02756
40	0.02593	0.02593
50	0.02466	0.02466

Parameters c , p and q as well as the initial values of infected individuals $I(0)$ will be varied to study their impacts on disease spreading.

3. Results and Discussion

The numerical findings for the SEI model with immigration are shown in this section. The results of the investigation are presented in tabular and graphical forms. The calculation of the endemic equilibrium points (Eqn. 3 – 5) results in $N^* = 2.307692$, $V^* = 2.3020539$, $I^* = 0.251277$. From the values, it is expected that the population will keep decreasing and eventually almost dies out. Note that the value of $N^* \approx V^*$, which means there is no more susceptible individuals in the population.

Figure 4.1 depicts the trend of total population (N), susceptible (S), exposed (E), and infectious individuals (I) within a period of 50 years. The most notable feature is that the number of susceptible individuals increased rapidly at the start before steadily decreasing. As t increases, the whole population will eventually die out. This result satisfies the endemic equilibrium points calculated earlier.

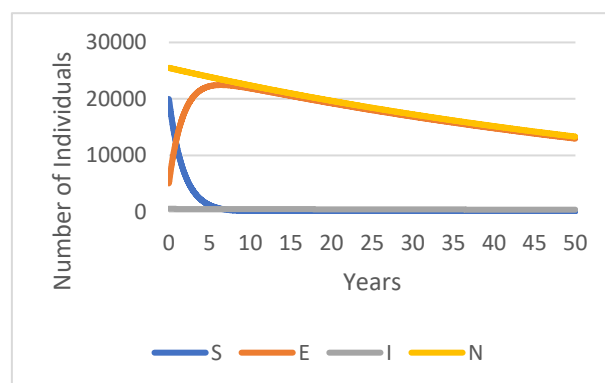


Figure 3. The trend of all classes in the model system is represented graphically

Impact of immigration on TB transmission is depicted in Table 5 (a - c). Immigration actually has no discernible effect on the spread of TB for our model with the chosen parameter values, as evidenced by the extremely little difference in values with or without immigration. However, realistically, this might not be true.

Table 5 (a). Number of susceptible individuals with and without immigration factor

Time (Years)	With Immigration	No Immigration
	Susceptible (S)	
10	63.3098	63.3411
20	0.1704	0.1897
30	0.0276	0.0458
40	0.0259	0.0432
50	0.0247	0.0411

Table 5 (b). Number of exposed individuals with and without immigration factor

Time (Years)	With Immigration	No Immigration
	Exposed (E)	
10	21864.9210	21864.9178
20	19230.1589	19230.1924
30	16864.3522	16864.4084
40	14789.5233	14789.5995
50	12969.9924	12970.0860

Table 5 (c). Number of infectious individuals with and without immigration factor

Time (Years)	With Immigration	No Immigration
	Infectious (I)	
10	463.4840	463.4559
20	432.0145	431.9617
30	401.3158	401.2414
40	371.6604	371.5670
50	343.2533	343.1432

The same pattern can be observed when the value of p and q are varies (Table 6). This shows that for our model, other parameter has a more significant impact compared to the immigration parameter. Although the differences between each value of p and q are very small, we can see that when p and q increases, the number of infected and exposed individuals will also increase.

Table 6: Number of infected and exposed individuals when p and q are varies

Time (years)	I			E		
	$q = 0.1$	$q = 0.3$	$q = 0.5$	$p = 0.1$	$p = 0.3$	$p = 0.5$
10	463.4840	463.5404	463.5967	21864.9108	21864.9210	21864.9311

20	432.0145	432.1202	432.2258	19230.1493	19230.1589	19230.1685
30	401.3158	401.4647	401.6136	16864.3431	16864.3522	16864.3612
40	371.6604	371.8472	372.0340	14789.5147	14789.5233	14789.5319
50	343.2533	343.4733	343.6934	12969.9842	12969.9924	12970.0005

Figure 4.2 shows the trend of each class over a 50-year period when subjected to various contact rates while maintaining all other parameters constant. In Fig. 4.2(a), as the value of contact rates rises, the susceptible class decreases more rapidly while the exposed class increases sharply in Figure 4.2(b). Due to TB's very low infection rate, the infected class graph in Figure 4.2(c) does not show significant differences, but it does show that the number of infectious people is higher when the contact rate is high. This means that the contact rate plays a significant role in the disease spreading trend. With high contact rates, more individuals are getting exposed to the disease. By putting the infected individuals in quarantine, we can reduce the contact rate thus controlling the disease spread.

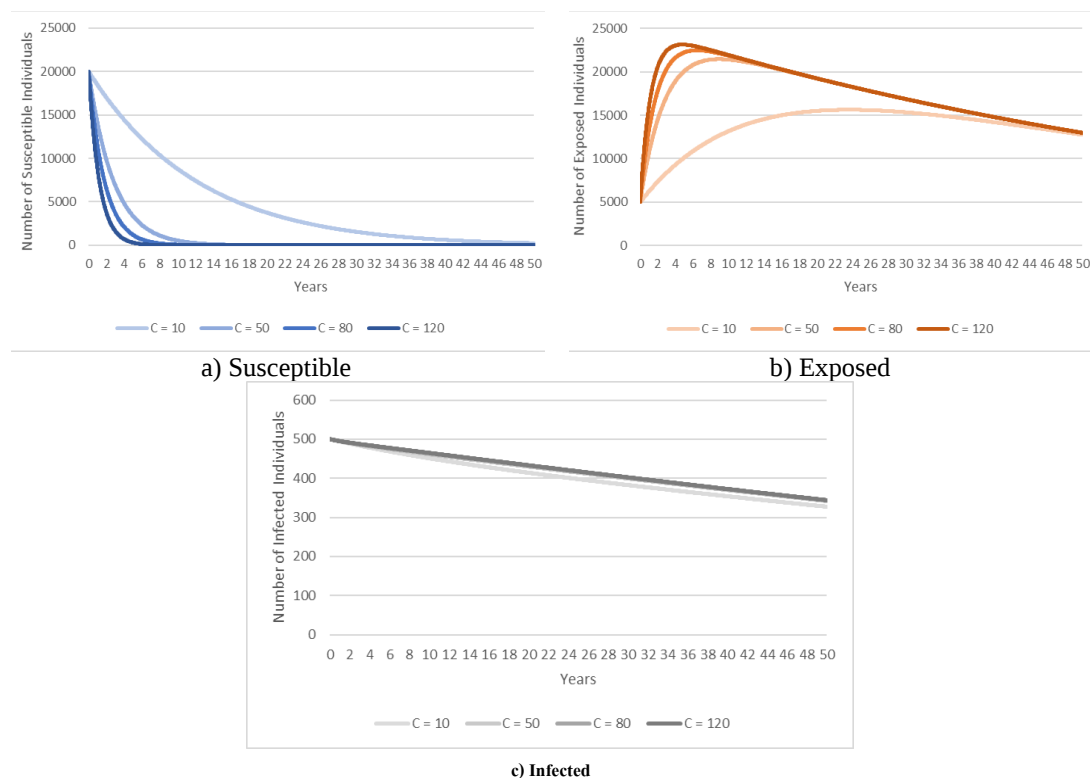


Figure 4.2. The model system when contract rates changes while the other parameters are still the same

Figure 4.3 shows the exposed and infected class when initial values of infected class are varies. When $I(0) = 0$, it means there are no infected individuals in the population at the beginning. The infected are introduced only through immigration. From Figure 4.3(b) it can be seen the number of infected individuals remain very small due to the low infection rate of TB. Indirectly, this affects the number of exposed individuals that remains relatively low for years before it slowly increases (Figure 4.3 (a)). From this result, we can see the impact of immigration on the TB disease spread. Although the effect may not seem significant in the beginning, as years pass, it will leave a notable effect towards the population. As the initial value $I(0)$ increases, both the exposed and infected individuals will increase accordingly. This shows that controlling the number of infected at the early stage can influence the pattern of disease spreading.

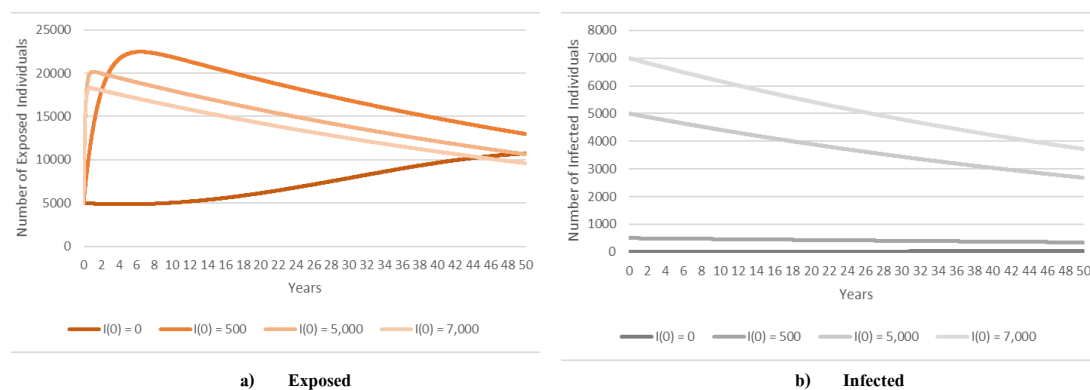


Figure 4.3 The model system with various initial values for the Infected class with the constant total population

4. Conclusions and Recommendations

A SEI mathematical model with immigration has been investigated to simulate the dynamics of tuberculosis transmission under various conditions and to find the important elements that contributes to the spreading of the disease. The model has been solved using Runge-Kutta method and the results shows that:

- I. The immigration had no noticeable impact towards disease spreading as there is little difference in the data for population with and without immigration.
- II. Changes in contact rates has a more significant impact compared to the immigration parameter.
- III. Controlling the number of infectious individuals at the initial stage plays a very important role in determining the severity of the disease spread in the long run.

The model of infectious disease with immigration we utilized was insufficiently precise to capture the complexity of the real world. This might be a result of the linear form picked as well as the simplified model. Future studies might benefit from incorporating non-linear terms and incorporating other factors to model the problem more accurately.

Acknowledgment

The author would like to thank the Department of Mathematics, Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA for supporting this project.

References

Journal Article

- Abdelmalek, S., & Bendoukha, S. (2018). Global asymptotic stability for a SEI reaction-diffusion model of infectious disease with immigration. *International Journal of Biomathematics*, 11(3).
- Arfan, M., Shah, K., Abdeljawad, T., Mlaiki, N., & Ullah, A. (2020, September 6). A Caputo power law model predicting the spread of the COVID-19 outbreak in Pakistan. *Alexandria Engineering Journal*, 60(1), 447-456.

- Bhunu, C.P., Garira, W., Mukandavire, Z., & Zimba, M. (2007). Tuberculosis Transmission Model with Chemoprophylaxis and Treatment. *Bulletin of Mathematical Biology*, 70(1), 1163-1191.
- Brauer, F. (2017). Mathematical epidemiology: Past, present, and future. *Infectious Disease Modelling*, 2(2), 113-127.
- Brauer, F., & Driessche, P.V. (2001, March 7). Models for transmission of disease with immigration of infectives. *Mathematical Biosciences*, 171(2), 143-154.
- Butcher, J. C. (2016). *Numerical Methods for Ordinary Differential Equations (3rd ed.)*. John Wiley & Sons, Ltd.
- Chen, H., & Zou, L. (2018, July 13). How to control the immigration of infectious individuals for a region?. *Nonlinear Analysis: Real World Applications*, 45(1), 491-505.
- Kiser, M. (2019). The Bernoulli Principle: Epidemiological Models for Identity. *SailPoint*.
<https://www.google.com/amp/s/www.sailpoint.com/blog/the-bernoulli-principle/amp/>.
- Li, G., Wang, W., & Jin, Z. (2005, September 1). Global stability of an SEIR epidemic model with constant immigration. *Chaos, Solitons & Fractals*, 30(4), 1012-1019.
- Macrotrends. (n.d). Malaysia Life Expectancy 1950-2022. <https://www.macrotrends.net/countries/MYS/malaysia/life-expectancy>
- McCluskey, C.C., & van den Driessche, P. (2003, May 16). Global analysis of two tuberculosis models, *Journal of Dynamics and Differential Equations*, 16(1), 139-166.
- Orrenius, P. (2016, Spring). Benefits of Immigration Outweigh the costs. <https://www.bushcenter.org/catalyst/north-american-century/benefits-of-immigration-outweighcosts.html>
- Saikh, A., & Gazi, N.H. (2021, January 20). The effect of the force of infection and treatment on the disease dynamics of an SIS epidemic model with immigrants. *Result in Control and Optimization*, 2(1).
- Sigdel, R.P., & McCluskey, C.C. (2014). Global stability for an SEI model of infectious disease with immigration. *Applied Mathematics and Computation*, 243(1), 684-689.
- Khan, Z.A., Alaoui, A.L., Zeb, A., Tilioua, M., & Djilali, S. (2021). Global dynamics of a SEI epidemic model with immigration and generalized nonlinear incidence functional. *Result in Physics*, 27(1).