



**Faculty of Computer Science and Information Technology**

**Compartmental Model for the Epidemiology of Infectious Diseases with Fear and  
Vaccination Consideration**

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Compartmental Model for the Epidemiology of Infectious Diseases with Fear and  
Vaccination Consideration

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## **ABSTRACT**

This thesis focuses on the integration of fearfulness on infectious diseases and vaccination behaviour in the population. This integration is incorporated in the conventional Susceptible-Infected-Recovered (SIR) model to describe the transmission dynamics of the vaccine-preventable infectious diseases so that the effect of the human behavioural changes on the spread of those diseases can be comprehended in a deeper level.

There are two modelling approaches used in this study, namely equation-based modelling and individual-based modelling. Before these two models are implemented, a compartmental model is constructed to describe the processes of the transmission of infectious diseases with the integration of fearfulness and vaccination behaviour. In equation-based model, a set of ordinary differential equations is constructed based on the compartmental model. On the other hand, a set of commands are assigned to the agents in the individual-based model. In both models, the vaccination behaviour is modelled as an imitation dynamics via game theory.

To examine the impact of the human behavioural changes in epidemiology, the simulation result from the equation-based model is compared with the literature on SIR model. In addition, the simulation results from both of equation-based model and individual-based model are compared to the actual incidences retrieved from Sarawak Weekly EpidNews, Sarawak State Health Department. Root mean square error (RMSE) is used as a measurement metric to compare the simulation results from equation-based model and individual-based model with the actual incidences. It is found that the results from individual-based model has lower RMSE (which means more fitted to the actual incidences) compared to equation-based model. This is due to the ability of individual-based model to capture the heterogeneous characteristic of the population.

# ***Model Compartmental untuk Epidemiologi Penyakit Berjangkit dengan Pertimbangan atas Ketakutan dan Vaksinasi***

## **ABSTRAK**

*Tesis ini menumpu kepada integrasi ketakutan mengenai penyakit jangkitan dengan tingkah laku vaksinasi dalam populasi. Integrasi ini dimasukkan dalam model biasa “Susceptible-Infected-Recovered” (SIR) untuk menerangkan dinamik penyebaran penyakit jangkitan yang dapat dicegah oleh vaksin supaya kesan perubahan tingkah laku manusia terhadap penularan penyakit-penyakit tersebut dapat difahami lebih mendalam.*

*Terdapat dua kaedah pemodelan digunakan dalam kajian ini, iaitu pemodelan “equation-based” dan pemodelan “individual-based”. Sebelum kedua-dua model ini dilaksanakan, satu model konseptual dibina untuk menggambarkan proses penghantaran penyakit jangkitan dengan integrasi ketakutan dan tingkah laku vaksinasi. Dalam model “equation-based”, satu set persamaan pembezaan biasa dibina berdasarkan model konseptual. Di samping itu, satu set peraturan telah diberikan kepada ejen-ejen dalam model “individual-based” tersebut. Dalam kedua-dua model tersebut, tingkah laku vaksinasi dimodelkan sebagai dinamik tiruan melalui teori permainan.*

*Untuk mengkaji kesan perubahan tingkah laku manusia dalam epidemiologi, hasil simulasi dari model “equation-based” itu dibanding dengan sastera model SIR. Selain itu, hasil simulasi dari kedua-dua model “equation-based” dan model “individual-based” dibandingkan dengan kes-kes sah yang didapatkan dari Sarawak Weekly EpidNews, Jabatan Kesihatan Negeri Sarawak. “Root mean square error” (RMSE) digunakan untuk mengira perbezaan antara*

*keputusan simulasi dan kes-kes sah. Ia didapati bahawa hasil daripada model “individual-based” mempunyai RMSE yang lebih rendah (lebih menyesuaikan dengan kes-kes benar) berbanding dengan model “equation-based”. Ini adalah disebabkan oleh keupayaan model “individual-based” untuk menyatakan ciri heterogen penduduk.*

# CHAPTER 1

## INTRODUCTION

### 1.0 Introduction

The study of disease modelling is started since decades ago. In year 1927, Kermack-McKendrick model marked the beginning of the mathematical disease modelling (Li and Zou, 2009). The conventional models, such as Susceptible-Infected-Recovered (SIR) model, consists of a set of ordinary differential equations (ODEs) where the parameters are mainly based on the disease transmission rate and recovery rate. Another example of disease model is Time-series SIR model which considered the stochastic characteristics in the model (Bjørnstad et al., 2002). Disease modelling plays a key role in predicting the disease dynamics in the future as it allows the extrapolation of the current information about the diseases (Keeling and Danon, 2009). It helps to study the “what-if” scenarios as well to allow the policy makers to have appropriate control measures on the diseases. This thesis will be focused on the infectious diseases instead of non-communicable diseases.

Infectious diseases are the illness caused by the pathogenic microorganisms such as protozoa and viruses (WHO, 2014). There are several factors that affect the spread of the infectious diseases, for instance, geographical, environmental or vector (Altizer et al., 2013). The relationship of the imperfect immunity and demographical factors is believed to affect the dynamics of the spread of the infectious diseases (Morris et al., 2015). To control the spread of the infectious diseases, the individuals are encouraged to take the precautions recommended by the public health organizations. Some of the infectious diseases are vaccine-preventable, for

instance, Rubella, Tuberculosis, and Measles. There is one third of the world population infected by Tuberculosis and in year 2012, 1.3 million deaths are reported due to Tuberculosis (World Health Organization [WHO], 2014). In order to control the spread of diseases, there are several precautions suggested by the public health organizations such as self-isolation and intensified hygienic care. Vaccination program is one of the precautions recommended to build the immunization of the population and it helps to reduce the morbidity and mortality caused by the diseases. For instance, smallpox has been eliminated after the vaccine is introduced to the public. In Malaysia, the new born children are compulsory to engage in the Bacille Calmette-Guérin (BCG) vaccination program where BCG is the vaccine for Tuberculosis. However, the BCG vaccine is only effective for 10 -15 years. After the duration of effective, the adults have to take another booster to protect themselves from the disease.

The decision of the individuals to take the precautions is mainly depends on their behavioural changes. In other words, human behaviour is affecting the spread of the infectious diseases. Thus, human behaviour plays an important role in epidemiology as well. The disease outbreak also brings impact on how human behave in such situation. This is because human are tend to modify their behaviour spontaneously according to the situation in order to protect themselves from the disease (disease avoidance) (Neuberg et al., 2011). During the outbreak of Severe Acute Respiratory Syndrome (SARS) back in year 2003, the travel and social contacts are reduced in both Hong Kong and Singapore (Ferguson, 2007). In this example, the individuals are protecting themselves from the disease by avoiding the interactions in the high risk country. In recent years, the importance of human behaviour in the study of disease modelling has been noticeable. As human behaviour is a social parameter that affects the spread of the disease, it is

necessary to capture human behaviour in response to the disease outbreak and its impacts on the interactions among individuals (Sahneh et al., 2012).

The conventional SIR model is considered as an equation-based model (EBM) and it assumes the population to be well-mixed. The EBM aggregated the individuals of a whole large population into a few homogenous subpopulations (Epstein, 2002). In real world, the individuals in the population will behave differently from each other and this caused the population to be heterogeneous. When human behaviour is introduced in the disease modelling, it is important for us to consider the characteristic of heterogeneity in a population.

### **1.1 Research Problem**

The researchers started to introduce human behaviour in disease modelling and they considered fear and the behaviour of taking precautions separately. In fact, the fearfulness of the disease affects the willingness of the individuals to take the precautions. Hence, it will indirectly influence the effectiveness of the precautions in controlling the spread of disease. Thus, there is a need to model the integration of fear on diseases and the decision of the individuals to take the precautions. The integration of human behaviour involves a heterogeneous population as the individuals are behaving different from one another in the population. EBM has a limitation in capturing the heterogeneity of a population.

### **1.2 Research Hypothesis**

To overcome the limitation of EBM, there are a few researches in epidemiology started to move to individual-based modelling (IBM) (Rahmandad and Sterman, 2008; Khalil et al., 2010). IBM helps to capture the individuals' interactions and behaviour in the population. Thus, in this study, IBM will be constructed as well to incorporate human behaviour. During the disease outbreak,

the individuals are allowed to move and interact with each other according to their respective behaviour. Besides, the individuals can be divided into two groups, one receives full or complete information about the diseases while another receives less or incomplete information. The level of fearfulness of these groups is hypothesized to be different and it is believed to induce different results in the spread of the disease. The difference of the fearfulness in both groups can be modelled by IBM approach.

### **1.3 Objectives**

The objectives of the research are as follows:

- To incorporate human behaviour factor as fear of infectious diseases and vaccination consideration in classical epidemic compartmental model.
- To construct a compartmental model which can be implemented as EBM and IBM that integrates fear of infectious diseases and vaccination consideration.
- To analyse the integration of fear of infectious diseases and vaccination consideration using graph visualisation and numerical solution.

### **1.4 Methodology**

From the research problem, we hypothesized there is a need to model the integration of fear on the diseases and the decision of individuals to take the precautions (specifically in vaccination) to prevent infection. On the other hand, as mentioned in research hypothesis, IBM will be another approach in disease modelling besides EBM in order to incorporate human behaviour. Therefore, there are two approaches in this study, which are EBM and IBM.

There are several stages of the methodology in this study. Stage 1 will be characterizing the problem. In this stage, the first step is to set the assumptions appropriately to characterize the

problem in a more comprehensible way before the formulation of the models. Then, the concept of the SIR model is deployed in the study. Instead of just three compartments (Susceptible, Infected, and Recovered), the compartments of “Fear” and “Vaccinated” are introduced in the model. The population is divided according to their compartments. A compartmental diagram is drawn to describe the processes of each compartment in the study. Here, related parameters and variables are identified. The vaccination decision making process is modelled as an imitation process where game theory is applied. A flow diagram is drawn to illustrate the decision making process in this study.

The second stage in the methodology is to formulate the model mathematically. EBM, which is governed by a set of ODEs, is formulated based on the parameters and variables determined in previous stage. This model is formulated to describe the flow of each compartment. The governing equations assist in understanding the transmission of the disease and the fearfulness of the individuals and its consequence impact. EBM is solved numerically as it is formulated by non-linear equations. In order to simulate the system numerically, the parameters and initial conditions are set accordingly. Sensitivity analysis of the parameters is carried out to determine the effect of each parameter on the dynamics of the spread of the disease.

The following stage of the methodology in this study will be the formulation of IBM. As discussed in the research hypothesis, IBM helps to capture the heterogeneity in a population. Thus, IBM is constructed to study the same problem in this research. Similar to EBM, the population is divided into five compartments, which are Susceptible, Infected, Feared, Vaccinated, and Recovered. A flow diagram is drawn to explain the commands to be assign to each compartment. The commands assigned to the individuals in each compartment allow them to behave accordingly and interact with one another. Besides, there are two environment setups in

our IBM, one for the groups who receive all or complete information about the diseases and another one for the groups who receive less or incomplete information. There are two random numbers to be assigned to each of the individuals to represent their health state and mindset respectively. The health state and mindset are dynamics according to the information they received. For instance, if the individual receives less information, his/her mindset will be lowered and it affects his/her incentive to take precautions and thus the health state will be lowered as well. This shows the difference among the individuals in the population.

The fourth stage is to compare and analyse the results from both EBM and IBM. Both models are simulated by the parameters from the same sources. The results are gathered and the data produced by the simulations are compared. Besides, the results from both models are compared to the actual incidences respectively. The actual incidences of one of the vaccine-preventable diseases in Malaysia are collected from the Ministry of Health, Sarawak. The related parameters and initial conditions are identified from the real data collected. The models are simulated with these values of parameters and initial conditions. The data from the simulations are then compared to the actual incidences. In this stage, root-mean-square error (RMSE) is used to measure the error between the simulations and the actual incidences.

## **1.5 Scope**

In this study, human behaviour is introduced as fear of infectious disease into the conventional basic SIR model. The type and source of the information gained by the individuals are not included in this study. In other words, these factors are kept as constant variables. The feared individuals in the population have the opportunity to make decision whether or not to vaccinate. Game theory is applied to aid the modelling of vaccination decision making process. The decision

making process is modelled as an imitation process where game theory takes place. The other factors that influencing the decision making such as cognitive factor are not included in this study. There are two approaches in this study, namely EBM and IBM. Both of the models are used to study the same research problem and comparison of both of the models will be carried out in the end of the study.

## **1.6 Thesis Outline**

This thesis is structured as follows. The overview of vaccine-preventable diseases and literature review of vaccination behaviour, fearfulness of infectious diseases and IBM are described in Chapter 2. Chapter 3 describes the model formulation of the equation-based Disease-Behaviour model. In addition, the review of the different platforms for IBM and the formulation of the IBM are discussed in this chapter as well. In Chapter 4, the implementations of both equation-based and individual-based models are presented. Chapter 5 discusses the results and analysis of both models. The validation of the models with actual incidences is presented in this chapter as well. Chapter 6 summarises the findings of this study, the limitations of the models, and also the future work for further study of human behaviour in epidemiology.

## **CHAPTER 2**

### **LITERATURE REVIEW**

#### **2.0 Introduction**

Disease outbreak occurs when the pathogen attack human immune system and this induces the disease spread in the population (WHO, 2015). Disease modelling is used to study the dynamics of the disease and it provides the prediction from the data gathered which can help in policy making. From the study of disease modelling, one of the factors influencing the spread of the diseases is the number of susceptible individuals in the population (Real and Biek, 2007). In other words, the spread of the diseases will be reduced if the number of susceptible is reduced. In order to reduce the number of susceptible in a population, vaccination programs are introduced by the health organizations. The overview of the vaccination preventable diseases will be presented in Section 2.1.

Vaccination decision is depending on the behaviour of each individual in the population. Each individual has different incentive to engage in the vaccination program. In the study of vaccination decision in disease modelling, the vaccination program is modelled as a game and the process of making the vaccination decision is modelled by game theory. The literatures of vaccination decision modelling are presented in Section 2.2.

As the vaccination decision is made depends on the individual's incentive, the factor that affecting the incentives is studied as well. Fearfulness of the diseases is one of the factors that influence the individuals' incentives to take the precautions to prevent the infections. The information spread during the disease outbreak induces the spread of the fearfulness of the diseases. Fearfulness is modelled as a contagious process in disease modelling as it can be spread

from a feared individual to the neighbour (family, close friends, or colleagues). The literatures of this study are reviewed in Section 2.3.

As discussed in previous chapter, IBM is used to capture the heterogeneity in the population. Thus, with the introduction of human behaviour in disease modelling, it is essential to construct IBM. The motivation of constructing IBM is presented in Section 2.4. A short discussion is presented at the end of this chapter.

## 2.1 Overview of Vaccine-preventable Diseases

Infectious diseases spread widely and threatened the health of the world population. To protect the individuals from getting infected by the viruses, researchers have recommended vaccines. Vaccine-preventable diseases are referred to the infectious diseases where there is existence of the vaccines. Table 2.1 shows a list of some of the vaccine-preventable diseases (Centers for Disease Control and Prevention [CDC], 2014):

**Table 2.1 List of some vaccine-preventable diseases.**

| <b>Diseases</b>           | <b>Existing Vaccine</b>  |
|---------------------------|--|
| Hepatitis B               | Recombivax HB ; Twinrix  |
| Influenza                 | Trivalent flu vaccine  |
| Measles                   | Measles, mumps, and rubella (MMR) vaccine                          |
| Pertussis                 | DTaP (childhood vaccination); Tdap (adolescent and adults booster) |
| Smallpox                  | Live vaccinia virus  |
| Tuberculosis              | Bacille Calmette-Guérin (BCG)                                      |
| Varicella<br>(Chickenpox) | Weakened varicella virus   |

According to WHO, vaccine is a biological preparation to stimulate the immune system of the individuals to improve the immunity against the particular disease. Vaccination programs are recommended by the public health organizations with the purpose of reducing the morbidity and

hence eliminate the infectious disease. For instance, a worldwide vaccination program to against smallpox has successfully eradicated smallpox infection. The last case of smallpox in United States was found in year 1949 and the last case in the world was found in Somalia in year 1977 (CDC, 2014). After the disease is eradicated, the routine vaccination program is stopped.

However, the vaccine is not always providing a perfect protection to the individuals. There are some terms that always in the context of the vaccination program, which are the efficacy, effectiveness and associated risk of the vaccine. The vaccine efficacy is defined as the reduction of the disease incidence in the vaccinated population compared to the unvaccinated population where the vaccine effectiveness is the evaluation whether or not the vaccine is effective in protecting the individuals from the disease (Weinberg and Szilagyi, 2010). On the other hand, the associated risk of the vaccine is defined as the probability that the vaccine brings adverse events and harm to the vaccinated individuals (WHO, 2014). In the field of biomedical sciences and public health, the vaccine efficacy is the main concern, whereas, the vaccine effectiveness and the associated risk are always discussed in public. The risks, efficacy and effectiveness of vaccine are considered by the individuals when they have to make the vaccination decision.

For instance, the vaccine for Tuberculosis, BCG, has the estimated protective efficacy ranged from 0% to 80% for the children; however, the protection will drop after 10-15 years (CDC, 1996). Another issue that always discussed by the public is the associated risk of the vaccine. BCG is recognized as a safe vaccine where the estimations for the risk of complications (e.g. ulceration and abscess formation) are less than 0.4 per 1000 vaccines under age of 1 year and less than 0.03 per 1000 vaccines under age between 1 to 20 years (Teo and Singadia, 2006).

Thus, in order to boost up the immunity, the adolescents and adults have to decide whether or not to vaccinate and at the same time consider about the associated risk of the vaccine itself.

Human behaviour is involved in the spread of the vaccine-preventable diseases as the individuals make their own decision on whether or not to vaccinate. In other words, the response of the individuals towards the vaccination program is depends on their behaviour. In the review of the introduction of human behaviour in disease modelling, the behavioural changes have been noticeable during the outbreak of Swine Flu H1N1 back in the year 2009 (Funk et al., 2010). The following sections discussed the fear of disease of the individuals and the vaccination behaviour in disease modelling.

## **2.2 Vaccination Decision in Disease Modelling**

One of the ways to prevent infectious diseases to be spread is through vaccination. Vaccination decisions of the individuals are mainly depend on their behaviour. The decision making process of the individuals can be modelled via game theory. There are many studies incorporated game theory in vaccination behaviour (Bauch and Earn, 2004; Bauch, 2005; Wu et al., 2011). In this study, game theory is applied as an imitation process in the population to make the vaccination decision.

Initially, game theory is applied in the field of economic. However, as it evolves throughout the years, it has been applied in many areas such as sciences and politics. Game theory plays a role as a tool to state the decision outcome of the individuals who take part in the particular situation. The individuals who participate in the particular situation are known as the players. The particular situation faced by the players is known as game. The game in the context of game theory is not a kind of entertaining activities or sport plays. The decision made by the

players is not only based on how the individuals opt for the strategies but also involved the interaction among the individuals in the community and the strategies of their neighbours (Slantchev, 2010). In other words, the decision of the neighbours is influencing the option of the strategies of the players. This condition is described as imitation process. The players are imitating their neighbours to make their own decision. There are many real world problems that can be modelled by game theory. For instance, an auction bid can be modelled by game theory (Miekisz, 2008). The players place the bid based on each other's decision and the result of the auction is based on how the players placed their bids.

In game theory, the individuals are interested to optimize their payoffs based on the strategies available in the game (Slantchev, 2010). The players make their decision to select the strategy depends on their rationality provided with the belief on which strategy the opponents will select (Bicchieri, 1993). There are three basic categories of game in game theory, namely social dilemma, cooperative, and anti-coordination (Easley and Kleinberg, 2010a). Social dilemma is a game where the dominant strategy only provides the suboptimal payoffs to the players. The players may obtain a better payoff or higher benefit if they select the non-dominant strategies. Dominant strategy refers to the strategy that can always provide a better payoff than other strategy does, regardless the strategy selected by the opponents (Turocy & Stengel, 2001). In cooperative game, the players have to cooperate with each other in order to gain a better payoff. On the other hand, the anti-coordination game has the opposite view with cooperative game. In anti-coordination game, the players have to select a different strategy from their opponents in order to gain a better payoff. In game theory, the information provided in the games can either be perfect or imperfect. In the game with perfect information, the players know their opponents' actions and these actions may influence the players' selections of the strategies. A game with

perfect information is the simplest game in the modelling of game theory. In this study, the individuals involved in the vaccination game will receive perfect information about the diseases and the vaccination programs.

In modelling the voluntary vaccination program, game theory is suitable to be applied. Vaccination is considered as a social dilemma game as it is related to the behavioural changes of the individuals (Perisic and Bauch, 2009; Wu et al., 2010). When the risk of the infection is lower than the risk of the vaccination, the individuals tend to choose to not vaccinate even though the vaccine can help to build up the immunization. They do not always select the dominant strategy as the individuals make their decision based on the risks which are changing with respect to time. Bauch (2005) modelled the vaccination behaviour by applying game theory. The vaccination behaviour is modelled as an imitation process. “Free rider” phenomenon always exists in a voluntary vaccination program. The unvaccinated individuals always take the advantages as the immunity of the population is increased when a certain number of vaccinated individuals has achieved.

**Table 2.2 List of the reviews on vaccination behaviour**

| <b>Year</b> | <b>Author</b>  | <b>Title</b>   | <b>Remarks</b>   |
|-------------|----------------|--|--|
| 2004        | Bauch and Earn | Vaccination and the theory of games  | Classical game theory is applied to model the vaccination behaviour in disease modelling.  |
| 2004        | Xia et al.     | Measles metapopulation dynamics: a gravity model for epidemiological coupling and dynamics | A gravity model is implemented to study the metapopulation dynamics and to capture the spatial temporal properties of Measles before vaccination behaviour |

|      |                       |  |  |
|------|-----------------------|--|--|
|      |                       |  | is introduced.   |
| 2005 | Bauch                 | Imitation dynamics predict vaccinating behaviour   | Vaccination decision of the individuals is modelled as an imitation process with the aid of game theory.               |
| 2005 | Van der Goot et al.   | Quantification of the effect of vaccination on transmission of avian influenza (H7N7) in chickens. | Statistical analysis on the effect of the vaccination on the transmission of H7N7 in chickens.                         |
| 2009 | Perisic and Bauch     | Social contact networks and disease eradicability under voluntary vaccination                      | Vaccination is modelled as a game of social dilemma.   |
| 2011 | Wu et al.             | Imperfect vaccine aggravates the long-standing dilemma of voluntary vaccination                    | Vaccination is a social dilemma. The efficacy of vaccination in certain level is sufficient to eradicate the diseases. |
| 2011 | Cornforth et al.      | Erratic flu vaccination emerges from short-sighted behaviour in contact networks                   | Contact networks are added into game theory in disease modelling to model the vaccination behaviour.                   |
| 2012 | Liu et al.            | Epidemiological game theory dynamics of chickenpox vaccination in the USA and Israel               | Vaccination decision is not only self-interest but also based on group-optimal coverage in the population.             |
| 2012 | Bauch and Bhattachary | Evolutionary game theory and social learning can determine how vaccine scares unfold               | Evolutionary game theory is applied in the disease modelling.  |
| 2013 | Schumm et al.         | Impact of preventive responses to epidemics in rural regions                                       | Vaccination behaviour in rural areas is  |

|  |  |  |                                       |
|--|--|--|---------------------------------------|
|  |  |  | modelled with<br>stochastics process. |
|--|--|--|---------------------------------------|

Table 2.2 shows the researches related to the incorporation of vaccination behaviour in disease modelling. In recent years, vaccination program has been included in the disease modelling. Bauch (2004) has introduced game theory to study vaccination behaviour to control the spread of infectious disease. Not only vaccination in human, the statistical analysis is carried out to study the effect of vaccination on the transmission of the avian influenza type H7N7 in chickens (Van der Goot et al., 2005). As time progresses, vaccination game is classified as social dilemma (Perisic and Bauch, 2009; Wu et al., 2011). Besides, the idea of contact network is applied in the vaccination decision modelling as well. In 2011, it is found that vaccination decision made by an individual is not only based on self-interest, but also based on the optimal strategy chosen by a group of individuals in the population (Liu et al., 2011). In short, vaccination decision of an individual can be modelled by game theory and it is considered as a social dilemma. The individual vaccination decision (local vaccination decision) will affect the population vaccination decision (global vaccination decision). This can be modelled as an imitation dynamics process or social learning process. The global decision to vaccinate will contribute to the eradication of the diseases as the immunization of the population is sufficient to combat the diseases viruses. As the fearfulness of an individual affects his/her vaccination decision, thus, the fearfulness of disease will be reviewed in the following section.

### **2.3 Review of Fear of Disease**

Human behaviour can be categorized as protective and preventive and it is influenced by several factors such as education, belief system and even close friends or family (Kollmuss and Agyeman,

2002; Funk et al., 2010). Due to these factors, the individuals behave uniquely from one another. The behaviour of the individuals is modified spontaneously during the disease outbreak (Ferguson, 2007). This is to allow the individuals to take some preventive actions in order to protect themselves. During the outbreak of a disease, the information about this disease is spread throughout the population. This created awareness to the individuals and some of them are feared. The fearfulness that is discussed in this context is about fear of the disease.

Fear is a social anxiety contagious process (Epstein et al., 2008) where the fearfulness can be spread to another individual in the community through the interaction among the individuals. The family, friends or neighbours are influenced by a feared individual and hence they then become feared as well. The advanced technologies nowadays have aided the spread of the fearfulness of the diseases. Beside of face-to-face interaction, the fearfulness can be spread by internet as well, especially social networks such as Twitter and Facebook. According to Lamb et al. (2013), Twitter has become digital surveillance of the spread of fear during an outbreak of disease. During the disease outbreak, the feared individuals will write some posts about their feeling towards the disease, for instance, "I am feared of the disease". Such tweets are shared in their social circle and hence the fear is spread in the circle.

Due to the fundamental purpose of human behaviour, the individuals are tend to protect themselves from the infection of the disease (disease avoidance) when they are aware of the health threat (Neuberg et al., 2011). Thus, there are higher incentives for the feared individuals to take the preventive actions, for instance, involve in the vaccination program, self-isolation, and intense daily hygienic care (Perra et al., 2011). The fear of the disease brings impact to these preventive actions suggested by the public health organizations. For instance, when the individuals are feared of the disease and they are aware on the vaccination program at the same

time, the probability of the individuals to decide to vaccinate is higher. When there are more individuals decided to vaccinate, the vaccine coverage in the population is increased and it affects the efforts to eradicate the disease (Xia and Liu, 2014). In other words, the vaccination decision of each individual is depends on the behaviour.

On the other hand, the feared individuals who decided not to vaccinate will take some preventive actions. These preventive actions taken by the feared individuals will reduce the probability of getting infection of the disease. As the feared individuals take the self-initiate preventive actions such as self-isolation, the probability of disease transmission will be reduced (Perra et al., 2011). However, the disease in the population will not be eliminated through these self-initiate preventive actions. The individuals still have the chances to be infected by the disease viruses.

**Table 2.3 List of the reviews on human behaviour (fear) in disease modelling**

| <b>Year</b> | <b>Author</b>  | <b>Title</b>  | <b>Remarks</b>   |
|-------------|----------------|---|--|
| 2007        | Ferguson       | Capturing Human Behaviour   | Human behaviour can be modified spontaneously according to the situation.                      |
| 2008        | Epstein et al. | Coupled Contagion Dynamics of Fear and Disease: Mathematical and Computational Explorations | Fear is introduced as an extension of SIR model and self-isolation is considered in the model. |
| 2010        | Funk et al.    | Modelling the influence of human behaviour on the spread of infectious disease: a review    | A review of the incorporation of human behaviour in disease modelling is presented.            |
| 2011        | Neuberg et al. | Human Treatment Management Systems: Self-Protection and Disease Avoidance.                  | Human are tend to protect themselves   |

|      |               |  |   |
|------|---------------|--|---|
|      |               |  | from infections.  |
| 2011 | Perra et al.  | Towards a characterization of behaviour-disease models.  | Individuals in fear have higher incentives to take preventive actions such as self-isolation.                                     |
| 2012 | Sahneh et al. | On the existence of a threshold for preventive behavioural responses to suppress epidemic spreading                    | Alert is introduced in disease modelling. The alerted individuals during disease outbreak tend to take the preventive strategies. |
| 2013 | Lamb et al.   | Separating Fact from Fear: Tracking Flu Infections on Twitter.   | Social media can be digital surveillance of the spread of fear during disease outbreak.   |
| 2014 | Xia and Liu   | A belief-based model for characterizing the spread of awareness and its impacts on individuals' vaccination decisions. | Awareness of individuals affected their vaccination decision.   |

Table 2.3 shows the literatures of human behaviour in disease modelling. Back in 2007, human behaviour has been emphasized as an element that should be captured in the disease modelling. In 2008, fear of the infectious disease is introduced as a contagious process in the disease modelling (Epstein et al., 2008). The individuals' fearfulness is included in SIR model. Along the time progresses, the researchers have emphasized on the human behavioural changes during disease outbreak (Funk et al., 2010; Neuberg et al., 2011). Human tend to protect themselves during this period by modifying their behaviour and take precautions. In 2011, Perra et al. pointed that feared individuals have higher incentives to take precautions to prevent the infections. The fearfulness of the individuals can be tracked from the internet which is act as

digital surveillance. This is due to the fearfulness of the individuals can be spread through social networks (Lamb et al., 2013). From the study of Xia and Liu (2014), it is believed that the awareness of the individuals affects their vaccination decision.

Based on these reviews, it is believed that the fearfulness affects the individuals' decision to take the preventive actions and thus affected the impact of these actions in preventing the spread of the diseases. Most of the preventive actions such as self-isolation provided protection to the individuals from the infections. However, these actions could not help to eradicate the diseases. To eradicate the diseases from the population, vaccine is introduced. Vaccination can build up the immunization of the population and hence the diseases will be eradicated. Therefore, both fearfulness and vaccination decision will be integrated in this study. As human behaviour is related in this study, the characteristic of heterogeneity in a population becomes a concern. The following section discusses on the individual-based modelling which is used to model the heterogeneity in a population.

## **2.4 Review on Individual-based Modelling**

The study of disease modelling starts with equation-based modelling (EBM) where the work of Kermack and McKendrick marked the beginning of this study (Keeling and Danon, 2009). For instance, the conventional Susceptible-Infected-Recovered (SIR) model which does not adapt human behaviour in disease modelling is constructed based on ordinary differential equations (ODEs). SIR model considers both the rate of disease transmission and the rate of recovery.

EBM assumed the population to be well-mixed. However, in real world, the population has the characteristic of heterogeneity. The individuals in the population behave differently from one another. As mentioned in Section 2.3, the behaviour of each individual is affected by a few

factors such as attitude, knowledge or demographic (Kollmuss and Agyeman, 2002). The heterogeneity can be captured by cellular automata (CA)-based or individual-based modelling (IBM). IBM is also known as agent-based modelling (ABM). In this thesis, the term individual-based modelling (IBM) will be used. CA-based models are characterized by the discrete time and space in the modelling environment (Fu and Milne, 2003). This helps to capture the non-homogenous and spatial factors. Although CA-based models are able to capture heterogeneity, however, it does not take into account the social behaviour and the interaction dynamics between individuals (Khalil et al., 2010). Due to the concern of these two attributes, IBM has been widely used by the modellers to describe the problem involving individuals' interaction.

Both of EBM and IBM shared a common characteristic, which is on expressing a relationship between two entities (or two compartments) (Parunak et al., 1998). However, the way to express this relationship is different for EBM and IBM. A set of equations is used in the EBM to state the relationship between two entities. Parunak et al. (1998) also mentioned that the equations used in the EBM do not present the relationship of the individuals in these entities explicitly as EBM present the solution for the relationship of the compartments instead of individuals. On the other hand, the IBM does not start the expression of the relationship with equations. Instead, the modellers describe the individuals' behaviour by assigning the commands for each individual (Macal and North, 2010). Through the commands that describe the behaviour of the individuals, they are allowed to interact with each other to form the relationship. This is how a relationship is expressed between two entities in the IBM.

In IBM, the agents are used to represent the individuals in the real world population. Each agent will have two characteristics: state and function. As mentioned earlier, the commands are assigned to each agent to allow them to behave in the model environment. Not only in behaving

or interacting, the commands may assist the agent to make their decision as well (Macal and North, 2007). The commands are acting as the function for the agents. The decision taken by each agent may cause its state to vary at the next time step. IBM has been applied in many fields such as economic (LeBaron, 1999; Hommes, 2005), disease modelling (Rahmandad and Sterman, 2008; Perez and Dragicevic, 2009; Nianogo and Arah, 2015), and social science (Epstein, 2002; Smith and Conrey, 2007). Epstein et al. (2008) have suggested taking into account of human behaviour in the disease modelling and the dynamics of the disease spread will be affected by the interaction of individuals.

**Table 2.4 List of reviews on IBM in disease modelling**

| <b>Year</b> | <b>Author</b>        | <b>Title</b>  | <b>Remarks</b>  |
|-------------|----------------------|---|---|
| 2009        | Callahan             | Agent based model of disease spreading coupled with fear                    | Spatial information and possible responses of individuals during disease outbreak are incorporated in the epidemic model by IBM approach.   |
| 2009        | Perez and Dragicevic | An agent-based approach for modelling dynamics of contagious disease spread | Geographic information system (GIS) is introduced in the epidemic model in urban environment.   |
| 2010        | Khalil et al.        | An agent-based modelling for pandemic influenza in Egypt                    | A few approaches (EBM, CA modelling, and IBM) in epidemic modelling are discussed. IBM is selected to model the pandemic influenza as it can capture the individuals' heterogeneous |

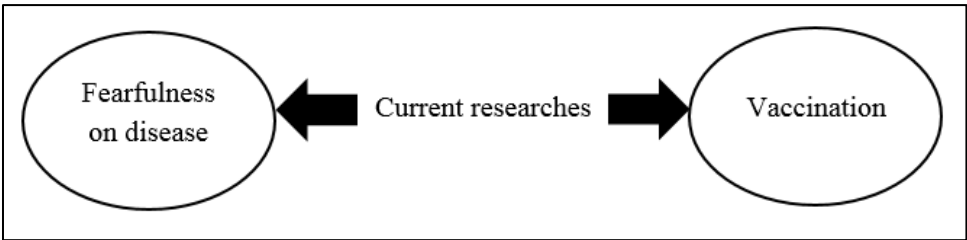
|      |                       |   |  |
|------|-----------------------|---|--|
|      |                       |   | attributes.  |
| 2011 | Frias-Martinez et al. | Agent-based modelling of epidemic spreading using social networks and human mobility patterns | IBM approach is used to include inherent information of the individuals in the epidemics models. Human mobility and social networks of the individuals are taken into account as the behaviour of the individuals. |

Table 2.4 listed the reviews on IBM in disease modelling. Back in the year of 2009, Callahan stated the responses of each individual during disease outbreak should be captured in the epidemic model. The heterogeneous information in the population can be included in IBM. IBM approach takes into account of the individuals' attributes to allow the agents in the model to communicate or interact. The communication or interaction among the agents affects the dynamics of the spreading of the infectious diseases.

## 2.5 Justification to Integrate Fear and Vaccination Decision

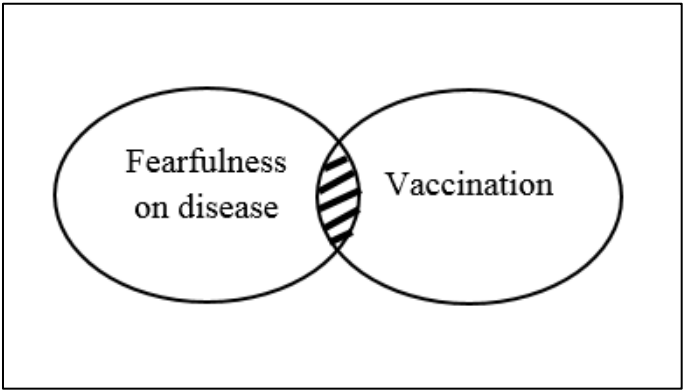
The previous sections discussed about the reviews on vaccination decision in disease modelling, fear of the infectious diseases and IBM. Section 2.2 mainly discussed on how to model vaccination decision in disease modelling where Section 2.3 focused on the introduction of fear of disease as a contagious process in disease modelling. From the reviews of Section 2.2 and 2.3, there is no integration between vaccination decision and fear of disease. In fact, the fearfulness influences the individuals in making their vaccination decision (Xia and Liu, 2014). As human have incentive to protect them, especially in a critical time, thus, the individuals have higher

incentive to engage in vaccination if they are fear of the disease during the disease outbreak. Most of the young adults are found to be feared in engaging vaccine as they fear of the risk of the vaccine (Nir et al., 2003). The public health organizations are encouraging healthcare workers to take the influenza vaccine, however, the decision of vaccination is based on the workers' behaviour (Hofmann et al., 2006). Figure 2.1 illustrates the current researches' trend. Most of the current researches study the fearfulness and the vaccination decision separately.



**Figure 2.1 Illustration of current researches**

Due to the fact of fearfulness affects vaccination decision, there should be an integration of these two elements (Figure 2.2). The shaded region in Figure 2.2 illustrates the integration of the fearfulness on disease and vaccination decision of each individual.



**Figure 2.2 Illustration of the integration of fearfulness and vaccination**

In the research hypothesis discussed in Chapter 1, the fearfulness of the individuals is assumed to be different from each other due to the information received by the individuals. Some of the individuals will receive full or complete information about the diseases but some of them will only receive less or incomplete information. This leads the research to consider the heterogeneity of the population. IBM approach can be applied in solving this problem. The fearfulness of the individuals can be quantified in several areas in Malaysia. This attribute can be included in the model of IBM approach and hence create the heterogeneous population in the model. Besides, the commands are assigned to the agents in the model based on this attribute. This is to allow the agents to communicate and interact with each other and hence to produce the dynamics of the disease spreading. Unlike IBM, EBM are used in the research to observe the global solution to the homogenous population. In the following chapters, the formulation of both IBM and EBM model will be discussed.

## **CHAPTER 3**

### **MODEL FORMULATION**

#### **3.0 Introduction**

In this chapter, a model integrated the fearfulness of diseases and vaccination behaviour will be formulated. Henceforth, this model will be known as Disease-Behaviour model. There are two approaches to be formulated in this chapter, namely EBM and IBM. The problem is first characterized where the assumptions are discussed. The formulation started with compartmentalizing the problem. Compartmental modelling is the conventional way of formulating the epidemiology problems. From the compartmental diagram, a set of non-linear ordinary differential equations is formulated and a set of commands to be assigned for the agents is formed for EBM and IBM respectively. Lastly, the discussion is done based on the models.

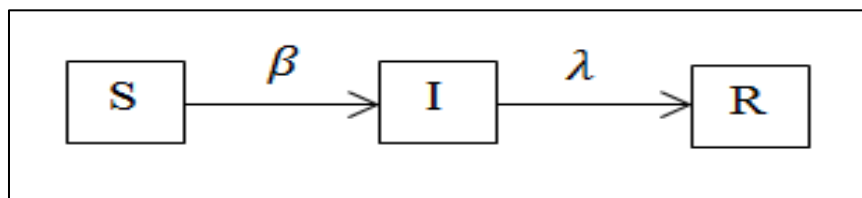
#### **3.1 Problem Characterization**

In order to assist in the understanding of the integration of fearfulness and vaccination decision in disease modelling, assumptions are set up in the beginning stage of the modelling process. The assumptions are set up based on some of the irrelevant details. If the assumptions are not set up appropriately, the problem may not be solved accordingly as there is distortion upon the nature of the problem (Seino, 2005). Thus, before the problem is being formulated, the assumptions are made to characterize the model. The following assumptions are set up to describe the basis of the Disease-Behaviour model:

- i. The interaction among the individuals in the population is random.
- ii. Total population is constant, i.e. growth rate is omitted.

- iii. The individuals who recovered from the infections are considered as immune to the disease.
- iv. The information about the disease is spread throughout the population via mass media and neighbourhood.
- v. Each individual in Fear compartment has to make decision whether or not to vaccinate.
- vi. The feared individuals who have decided to vaccinate are not allowed to reverse their vaccination of decision.

As mentioned in Chapter 2, there were many epidemiological models that are produced to study the transmission of the infectious diseases. The conventional SIR model (Figure 3.1) is used as the basis for our problem. The parameters,  $\beta$  and  $\lambda$  indicate the disease transmission rate and recovery rate respectively whereas  $S$ ,  $I$ , and  $R$  represent Susceptible, Infected, and Recovered subpopulations. The individuals are assumed as susceptible initially. During a disease outbreak, there are some random selected individuals who are infected. The disease will be spread at the transmission rate of  $\beta$  as the time progresses. In the meantime, the infected individuals will recover after a period of  $1/\lambda$ .

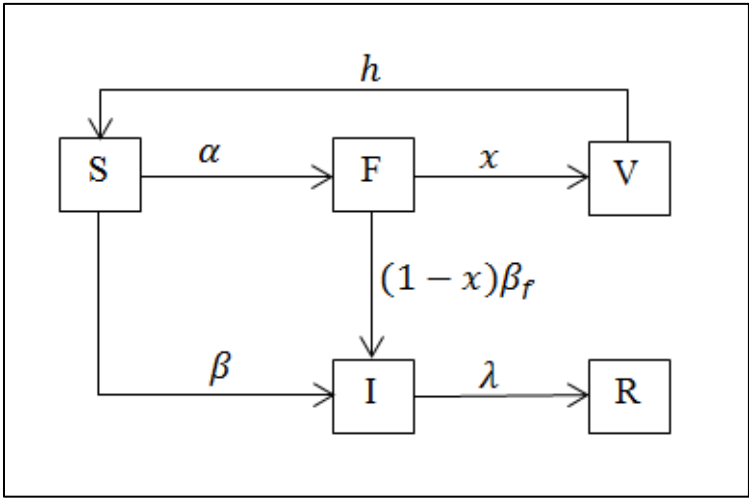


**Figure 3.1 The conventional basic SIR model.**

To integrate the fearfulness on the disease and the individuals' vaccination decisions, two new compartments are introduced into the conventional basic SIR model. This new model from henceforth is called the Disease-Behaviour model. There are five compartments in Disease-Behaviour model, namely Susceptible, Infected, Feared, Vaccinated, and Recovered. The two new compartments in the Disease-Behaviour model are “Feared” and “Vaccinated” as depicted in Figure 3.2. Similarly as the basic SIR model,  $\beta$  and  $\lambda$  indicate the disease transmission rate and recovery rate. There are some newly introduced parameters which are listed in Table 3.1.

**Table 3.1 List of newly introduced parameters.**

| Parameter | Description   |
|-----------|---|
| $\alpha$  | Probability of an individual to acquire fear  |
| $\beta_f$ | Reduced disease transmission rate   |
| $x$       | Frequency of vaccinators  |
| $(1 - x)$ | Frequency of non-vaccinators  |
| $h$       | Rate of vaccinator to be susceptible again after duration of effectiveness of vaccine |



**Figure 3.2 The compartmental diagram of the Disease-Behaviour model with the introduction of “Feared” and “Vaccinated” compartments.**

In the initial state of the Disease-Behaviour model, there are some feared and vaccinated individuals in the population. They are considered as the individuals who aware of the diseases and have taken precautions. A small number of infected individuals are modelled as the initial patients during a disease outbreak. As mentioned in the assumptions, the information about the disease is spread during the disease outbreak. During the disease outbreak, the susceptible individuals are getting infected at the disease transmission rate,  $\beta$  if they are in contact with the patients. On the other hand, the susceptible individuals may acquire fear at the given probability  $\alpha$  if they interact with the feared individuals. Each feared individual is provided with the opportunity to make their vaccination decision. If they opt to vaccinate, they will be moved to the Vaccinated compartment. Otherwise, they still stay in the Feared compartment and have a lower chance to get infected (reduced disease transmission rate,  $\beta_f$ ) when they interact with the patients. This is due to the precaution actions they have taken. For instance, they reduce the social contact and intensify the hygienic care. The reduced disease transmission rate is controlled by a parameter of  $r_\beta$  where  $0 < r_\beta < 1$  and  $\beta_f < \beta$  (Perra et al., 2011). As the vaccines studied in this research do not provide lifelong protection, there exists the duration of effectiveness of the vaccines. The duration of effectiveness of the vaccines is denoted as  $T$  unit time where  $h = 1/T$ . The vaccinators will be susceptible again at the rate of  $h$ . After a period of time ( $D$  unit time), the patients will be recovered and moved to the compartment of Recovered. Therefore, the recovery rate for the patients is denoted as  $\lambda$  where  $\lambda = 1/D$ .

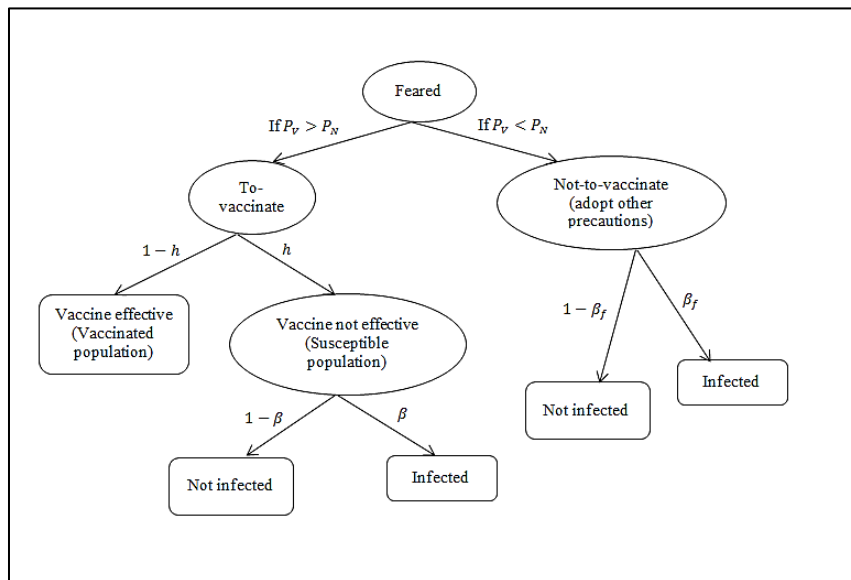
As mentioned before, the feared individuals are provided with the opportunity to make their vaccination decision. The vaccination decision making process is modelled as an imitation dynamics process with the aid of game theory. In imitation dynamics, there is a learning process

among the feared individuals in the population where they learn the strategy from their neighbours. The feared individuals learn both of the risks of infection and vaccination, the vaccine cost, and vaccine availability. All of these factors reflected to the payoff of to-vaccinate and not-to-vaccinate strategies. Figure 3.3 shows the vaccination decision making process for each individual. The payoff of the strategy of to-vaccinate is denoted as  $P_V$  where it considered of the risk of vaccination. On the other hand,  $P_N$  represented the payoff of the strategy of not-to-vaccinate where the risk of infection is taken into account. The formulation of these payoffs is as below (adopted from Bauch, 2005):

$$P_V = -r_V \tag{3.1}$$

$$P_N = -r_I m I(t) \tag{3.2}$$

The risk of vaccination and infection are indicated by  $r_V$  and  $r_I$  respectively in Eq.(3.1) and Eq.(3.2). In Eq. (3.2), the sensitivity of individuals' behavioural changes during prevalence is denoted as  $m$  where  $I(t)$  represents the current number of patients at time  $t$ .



**Figure 3.3 Visualisation of decision making process.**

The feared individuals will engage in vaccination if the payoff for the strategy of to-vaccinate,  $P_V$  is greater than the payoff for the strategy of not to-vaccinate,  $P_N$ . For the individuals opt for the strategy of to-vaccinate, they will be susceptible again after the duration of effectiveness of vaccine at the rate of  $h$ . On the other hand, the feared individuals who select the not vaccinate strategy will adopt other precautions to protect themselves from infection. This will reduce their probability of getting infected which denoted as  $\beta_f$ .

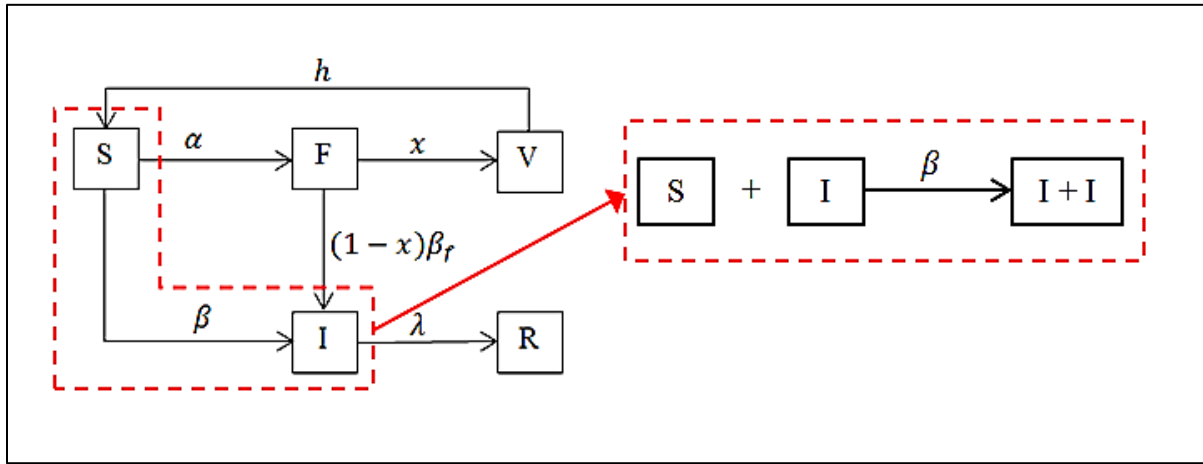
### 3.2 Equation-based Model

In Section 3.1, the compartmental model of this problem has been presented. The population is subdivided into five compartments. In addition, the assumptions are set up in the beginning before the compartmental model is constructed. Based on the compartmental model, a set of governing ordinary differential equations is formulated mathematically to describe the compartmental diagram in Figure 3.2. This formed the equation-based Disease-Behaviour model. In EBM, a supplemental assumption is included, which is the population is assumed to be homogenous in the model. Under this assumption, the individuals in the population are mixed uniformly and they are assumed to hold identical parameters values in the model. This characteristic of EBM makes the analysis tractable (Bansal et al., 2007).

According to the compartmental diagram drawn previously, the compartmental model is translated into mathematical equations. A set of ordinary differential equations is used to formulate the model. The equations are formulated based on balance law (Dym, 2004) where:

$$\{Rate\ of\ change\} = \{Rate\ in\} - \{Rate\ out\}. \quad (3.3)$$

The entrance and exit of the individuals to and from each compartment have to be formulated according to the balance law. Since the Disease-Behaviour model in this study is a temporal model,  $t$  is used to indicate time. For instance,  $S(t)$  indicates the number of susceptible individuals at time,  $t$ . The continuous Disease-Behaviour model will be governed by differential equations with respect to  $t$ .



**Figure 3.4 Dashed box highlights the process of susceptible individuals to get infected at a given disease transmission rate,  $\beta$ .**

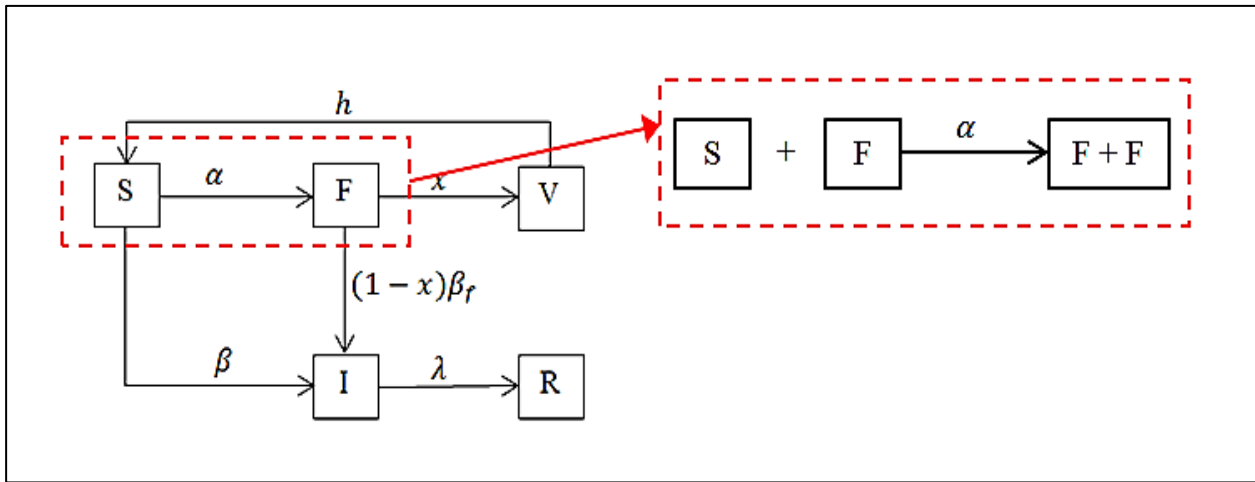
The first process to formulate is when susceptible individuals interact with infected individuals. At the given disease transmission rate,  $\beta$ , the susceptible individuals get infected by the disease viruses. The process of interaction and be infected is illustrated as in Figure 3.4. This process can be translated into the equation as below:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \quad (3.4)$$

The product of  $S$  and  $I$  implies the interaction between susceptible individuals and the patients. This lead the susceptible to be infected at the disease transmission rate,  $\beta$ . The negative sign in

the equation indicates the exit of individuals from that particular compartment. According to the balance law, the exit of individuals from a compartment has to be the entrance of another compartment. Therefore, the individuals exit from Susceptible compartment will enter to Infected compartment as below:

$$\frac{dI(t)}{dt} = \beta S(t)I(t) \quad (3.5)$$



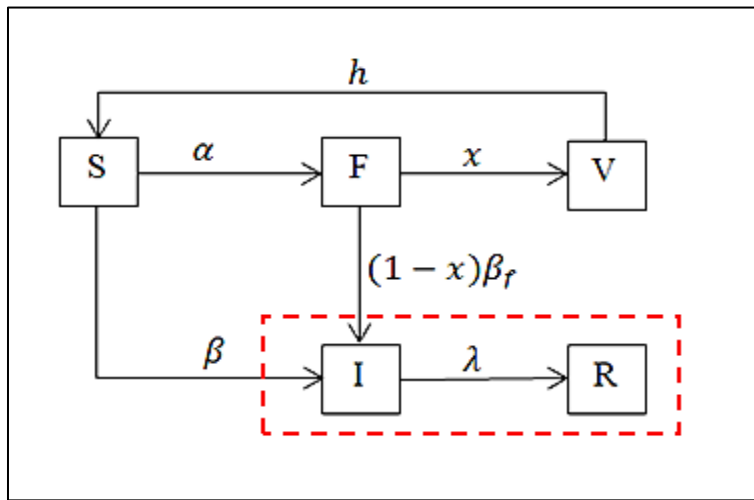
**Figure 3.5 Dashed box highlights the process of susceptible individuals to get feared with a given probability,  $\alpha$ .**

Next, the process of susceptible individuals interact with feared individuals and acquire fearfulness is formulated. Apart from the interaction with feared individuals, the susceptible individuals will receive the information about the disease during the outbreak. Through the interaction and the information gathered, they might acquire fearfulness at the fear transmission rate,  $\alpha$ , as shown in Figure 3.5. The mathematical equations for the Susceptible compartment and Feared compartment that modelled this process are shown in Eq. (3.6) and Eq. (3.7) respectively.

$$\frac{dS(t)}{dt} = -\alpha S(t)F(t) \quad (3.6)$$

$$\frac{dF(t)}{dt} = \alpha S(t)F(t) \quad (3.7)$$

Similar as previous discussion on the process of the infectious, fearfulness can be transmitted to the susceptible individuals. It is modelled as a contagious process. The product of  $S$  and  $F$  represents the interaction of susceptible individuals and feared individuals and this lead the fearfulness to be transmitted with the probability  $\alpha$ .



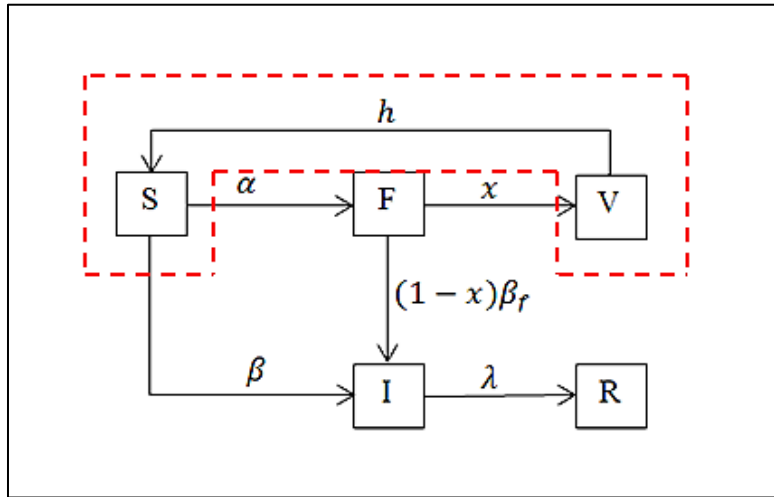
**Figure 3.6 Dashed box highlights the process of recovery of the infected individuals at recovery rate,  $\lambda$ .**

The patients will be recovered after a period of time,  $D$  unit time. The recovery rate is expressed as  $\lambda = 1/D$  unit time<sup>-1</sup>. This process is formulated as shown in Eq. (3.8) and Eq. (3.9).

$$\frac{dI(t)}{dt} = -\lambda I(t) \quad (3.8)$$

$$\frac{dR(t)}{dt} = \lambda I(t) \quad (3.9)$$

The number of individuals recovered from the disease is depending on the infectious subpopulation. Therefore, the recovered population is the multiplication of the recovery rate and infectious population as shown in Eq. (3.9).



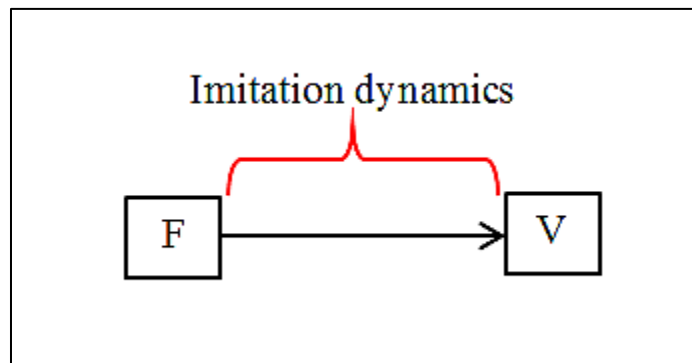
**Figure 3.7 Dashed box highlights the process of vaccinators turning susceptible again after the duration of vaccines' effectiveness.**

The vaccines that studied in this research are not provided with lifelong protection. There is duration of effectiveness for the vaccines,  $T$  unit time. After the vaccines' effectiveness duration, the vaccinators will be susceptible again and they will be moved out from the Vaccinated compartment at rate  $h$ , where  $h = 1/T$  unit time<sup>-1</sup>. The equations below help to model this situation:

$$\frac{dV(t)}{dt} = -hV(t) \quad (3.10)$$

$$\frac{dS(t)}{dt} = hV(t) \quad (3.11)$$

Similar as the recovery process, the number of individuals turning to susceptible again is depending on the subpopulation of vaccinated. Thus, the product of the rate of turning vaccinator to susceptible and subpopulation of vaccinated provides the total number of individuals entering Susceptible compartment from Vaccinated compartment.



**Figure 3.8 Decision making process of feared individuals which modelled as an imitation dynamics.**

The next process to be modelled is the process of decision making of the feared individuals. This process is modelled as an imitation dynamics (Figure 3.8). As mentioned before, the feared individuals will be provided the opportunity to select their preferable strategy (either to-vaccinate or not to-vaccinate) in the vaccination game. The individuals who decide not to-vaccinate at current time,  $t$ , will leave the possibility for them to make decision again at time  $(t + 1)$ . In other words, the feared individuals who decide to vaccinate cannot reverse their decision unlike those who select the strategy of not to-vaccinate. In the vaccination games, the feared

individuals are known as players. They are sampled randomly during the game. The rate of sampling is a constant,  $\sigma$ . The frequency of the vaccinators in the population is denoted as  $x$  where the frequency of the non-vaccinators is denoted as  $(1 - x)$ .  $x$  fall in the range of  $0 < x < 1$ . Thus,  $\sigma x$  indicates the rate of a feared individual samples a vaccinator. The payoffs for each strategy are referred in Eq. (3.1) and Eq. (3.2). The steps to formulate the imitation dynamics equation based on the sampling rate and the payoffs for both strategies are shown as follows:

- Let  $\delta P = P_V - P_N$  be the benefit gained if a feared individual switches his/ her decision to vaccinate.
- Let  $\rho * \delta P$  be the probability of a feared individual switches his/ her decision to vaccinate where  $\rho$  is proportionally constant.
- Thus, the imitation dynamics can be written as below:

$$\frac{dx}{dt} = \sigma x(1 - x)\rho\delta P . \quad (3.12)$$

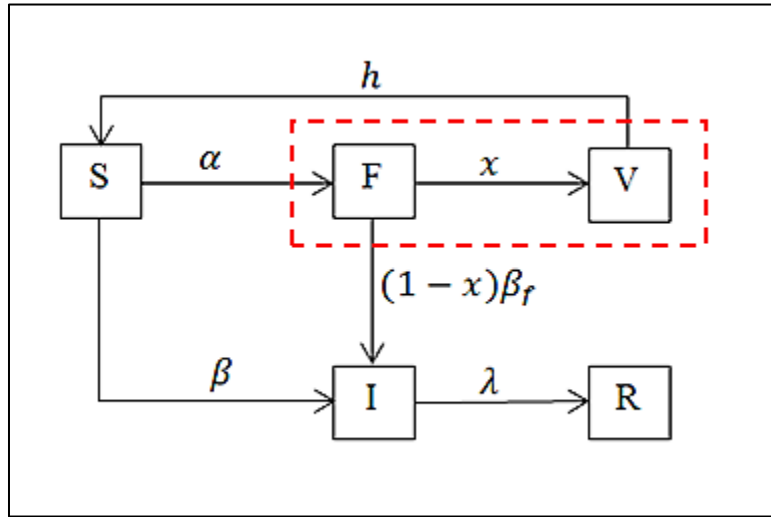
- Eq. (3.12) can be written in terms of payoffs which shown in Eq. (3.1) and Eq. (3.2):

$$\frac{dx}{dt} = \sigma x(1 - x)\rho(-r_V + r_I m I(t)) . \quad (3.13)$$

- Eq. (3.13) can be simplified with  $\kappa \equiv \sigma\rho r_V$  and  $\omega \equiv m \frac{r_I}{r_V}$ :

$$\frac{dx}{dt} = \kappa x(1 - x)(-1 + \omega I(t)) . \quad (3.14)$$

Eq. (3.14) is the final simplified imitation dynamics equation adopted from Bauch (2005) which will be used in the EBM in this study.  $\kappa \equiv \sigma\rho r_V$  is the imitation rate considered the risk of vaccines where  $\omega \equiv m \frac{r_I}{r_V}$  is the sensitivity of the individuals' behavioural changes after considering the proportion of the risks of both infectious and vaccines.



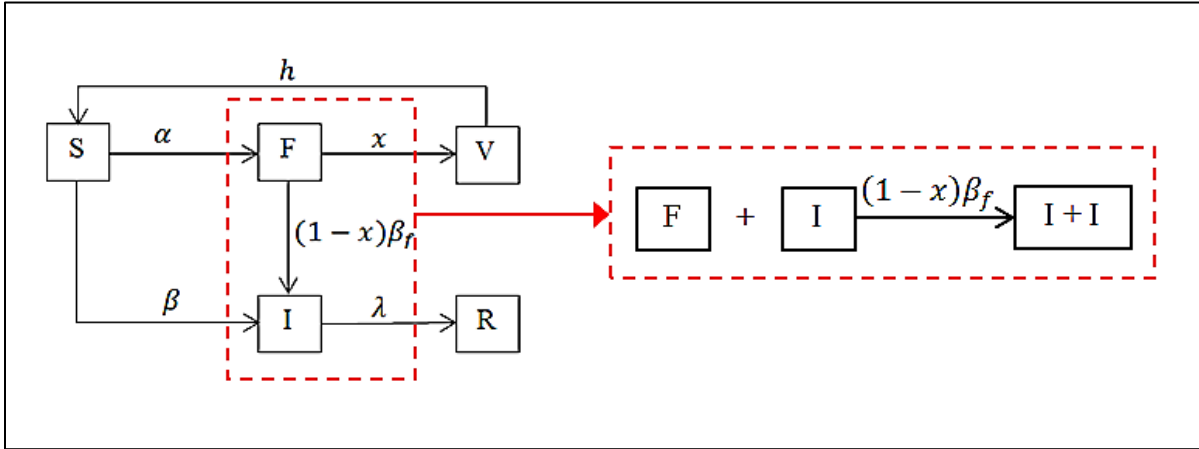
**Figure 3.9** The process of feared individuals decide to engage in vaccination program after sampling.

The coupled equations to formulate the process of feared individuals who decide to engage in the vaccination program after the sampling with imitation dynamics are shown as follows:

$$\frac{dF(t)}{dt} = -xF(t)V(t) \tag{3.15}$$

$$\frac{dV(t)}{dt} = xF(t)V(t) \tag{3.16}$$

Since the vaccination decision is an imitation dynamics, thus the interactions of feared subpopulation and vaccinator subpopulation are taken into account during the equations formulation. The interactions are represented by the product of both subpopulations.



**Figure 3.10** The process of feared individuals who do not decide to vaccinate and get infected at reduced rate of transmission,  $\beta_f$ .

If the feared individuals do not decide to vaccinate (represented by  $(1 - x)$ ), they will take other precaution actions such as intensified hygienic care. However, if they come into interaction with the patients, they might get infected as well.  $\beta_f$  indicates the reduced rate of disease transmission.  $\beta_f$  can be extended as  $r_\beta * \beta$  where  $r_\beta$  is the reducing rate which adopted from Perra et al. (2011).  $r_\beta$  has a value in the range of  $0 \leq r_\beta < 1$ . With the precaution actions the feared individuals taken, they will have a lower chance to get infected. This situation can be modelled by the following coupled equations.

$$\frac{dF(t)}{dt} = -(1 - x)\beta_f F(t)I(t) \quad (3.17)$$

$$\frac{dI(t)}{dt} = (1 - x)\beta_f F(t)I(t) \quad (3.18)$$

Similar to the previous processes, the interactions of both subpopulations are modelled with the production of both subpopulation feared and infected.

All the equations describing the processes of each compartment can be compiled as follows to form the governing equations for the Disease-Behaviour model:

$$\frac{dS(t)}{dt} = -\alpha S(t)F(t) - \beta S(t)I(t) + hV(t) \quad (3.19)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) + (1-x)\beta_f F(t)I(t) - \lambda I(t) \quad (3.20)$$

$$\frac{dF(t)}{dt} = \alpha S(t)F(t) - (1-x)\beta_f F(t)I(t) - xF(t)V(t) \quad (3.21)$$

$$\frac{dV(t)}{dt} = xF(t)V(t) - hV(t) \quad (3.22)$$

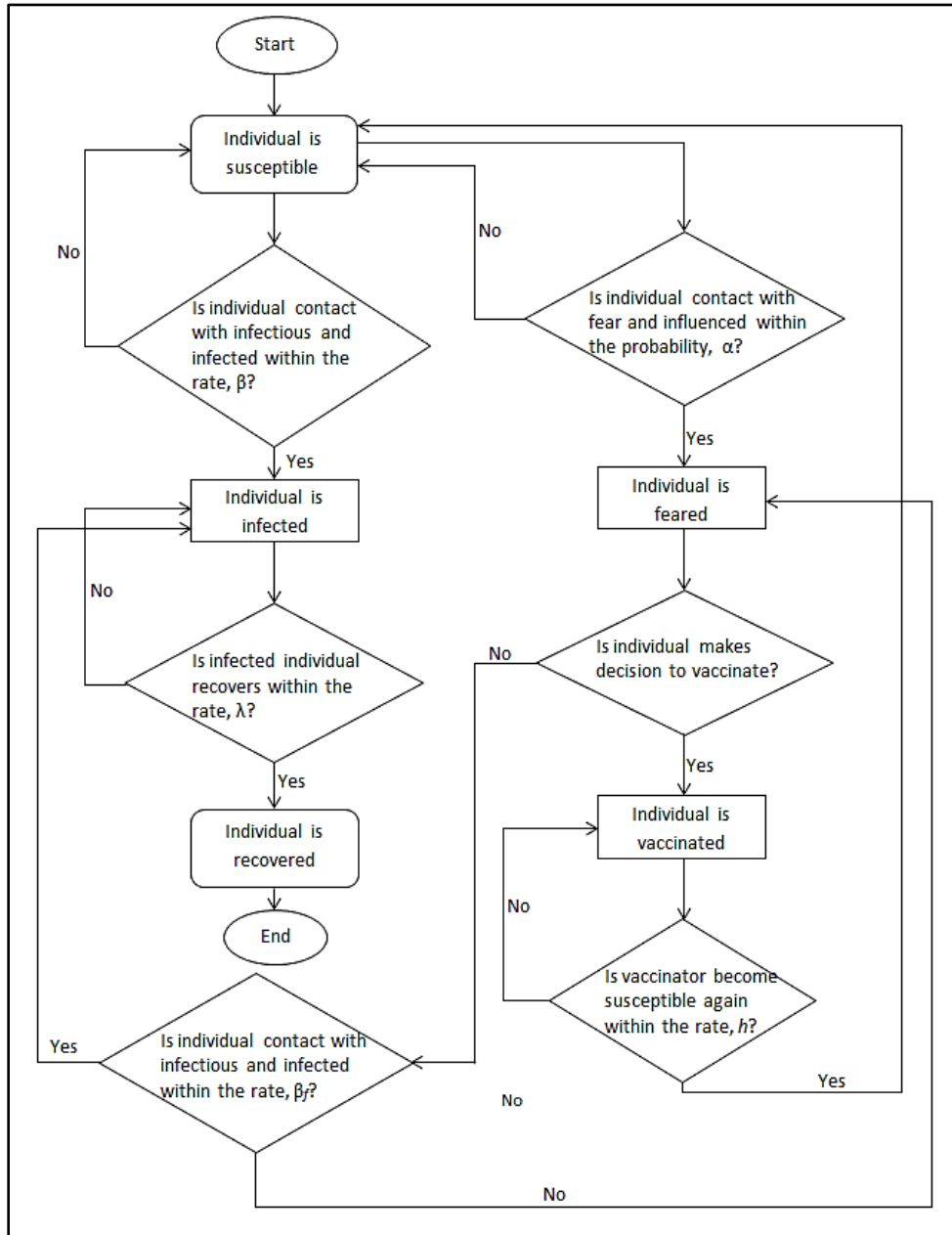
$$\frac{dR(t)}{dt} = \lambda I(t) \quad (3.23)$$

The subpopulations of each compartment are assumed to be non-negative at any time during the model simulation. All parameters values are assumed to be positive.

### 3.3 Individual-based Model

The mathematical formulation of the model is presented in Section 3.2. The EBM assumed the population is well-mixed. However, the population consists of individuals with unique behaviour. The unique behaviour of each individual created the heterogeneous characteristic in the population. To incorporate human behaviour in disease modelling, the heterogeneity of a population has to be taken into account. Thus, individual-based approach is used to describe the heterogeneity of a population. As mentioned in Chapter 2, a set of commands is set by the modellers to be assigned to the agents in IBM. The commands assigned to the agents allow them to move and interact with each other accordingly. To construct an IBM, a flow diagram (refer to

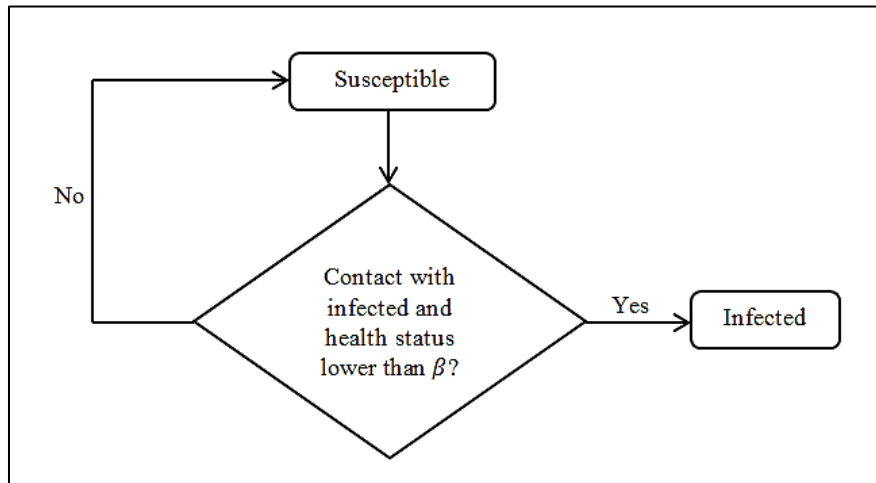
Figure 3.11) is prepared beforehand to describe the processes in the compartmental model. The commands are set up according to the flow diagram.



**Figure 3.11 Flow diagram that characterize the individual-based model.**

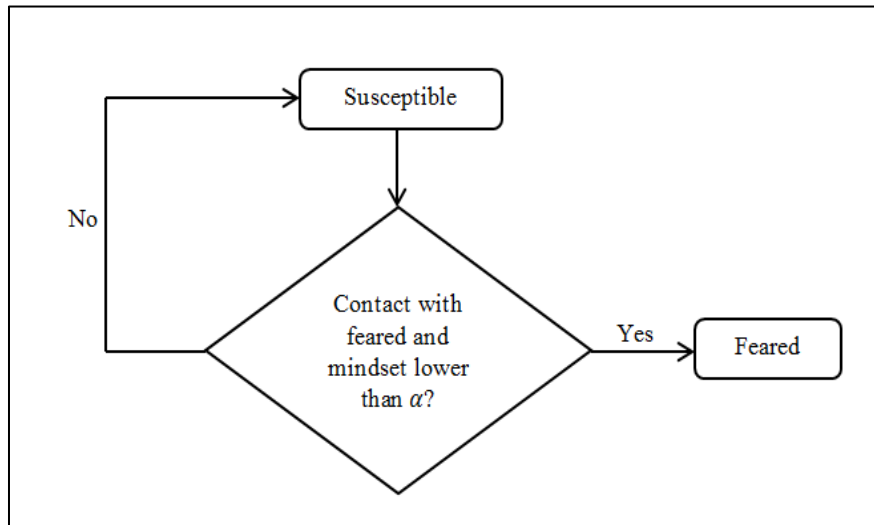
According to the compartmental model (Figure 3.2), the individuals in the population are assumed to be susceptible initially during disease outbreak. There are some infected, feared, and vaccinated individuals in the population. Each individual is assigned with two random numbers which are to represent their own health state and mindset. These random numbers are generated by uniform distribution. The random numbers will be updated at each time step as the health state and mindset of human will not be constant. In addition, the individuals are allowed to move randomly in the environment of the model. They are allowed to interact with whoever they meet in the environment.

During the disease outbreak, the information is spread throughout the whole population. Although the information is spread widely in the population, there are some individuals who do not expose to the complete information of the disease. This induced the population to be divided into two groups. One of these groups received more or complete information (named as  $M$ ) where another received less or incomplete information (named as  $L$ ). As group  $M$  received all information, they have higher level of awareness and fearfulness on the disease compared to group  $L$ . Therefore, in this study, groups  $M$  and  $L$  are modelled by altering the mindset where group  $M$  has higher value of mindset compared to group  $L$ .



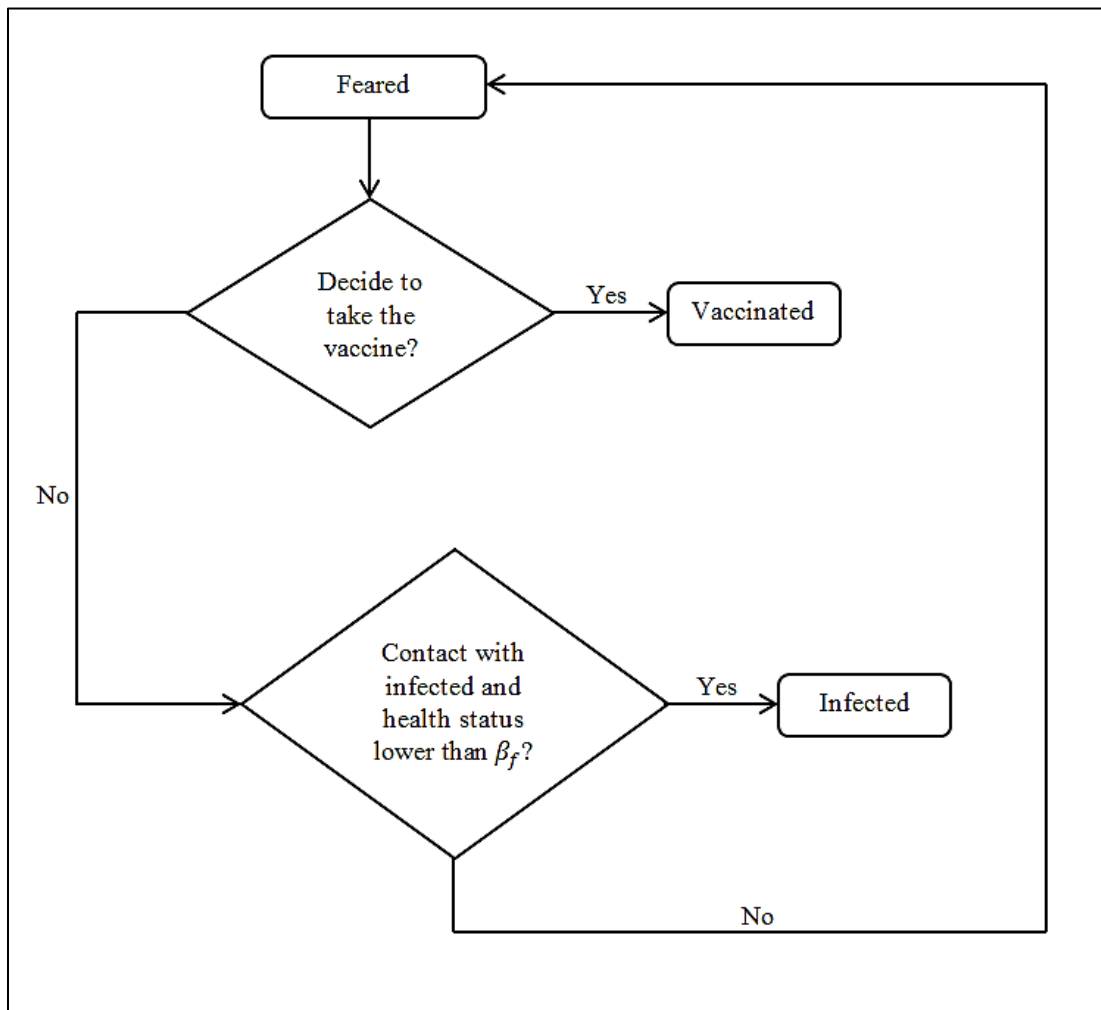
**Figure 3.12 Process during susceptible individuals interact with infected individuals.**

The individuals are holding their status according to the compartments they belong to. The interactions among the individuals will cause the change of their belonging compartment. Hence, the belonging compartment of the individuals will be updated at each time step. The processes in IBM are similar as what have discussed in the formulation of EBM (Section 3.2). The first process to be discussed is the interaction of susceptible and infected individuals (Figure 3.12). When a susceptible individual meet with an infected individual and they have some interaction, the viruses might transmit to the susceptible individual. Thus, during the interaction, the health state of the susceptible will be checked. If it is lower than the disease transmission rate per contact per unit time,  $\beta$ , the susceptible individual will get infected. Otherwise, the susceptible individual will remain as in the group of susceptible.



**Figure 3.13 Process during susceptible individuals interact with feared individuals.**

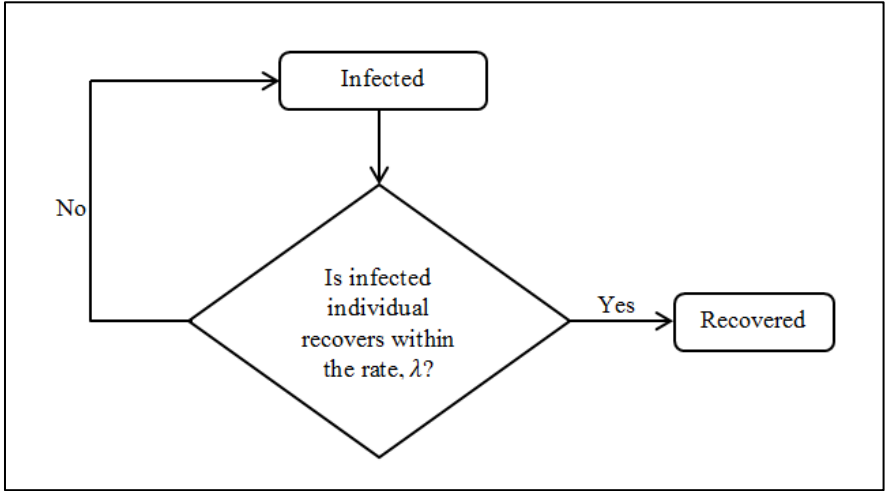
The second process (Figure 3.13) will be the interaction of the susceptible individuals with feared individuals. The susceptible will meet some of the feared people as well in the environment. Unlike the first process, during this interaction, the mindset of the susceptible individual will be checked. If it is lower than the probability of getting feared,  $\alpha$ , the susceptible individual will be influenced by the feared individual and acquires fear. Otherwise, he/she will remain in the group of susceptible.



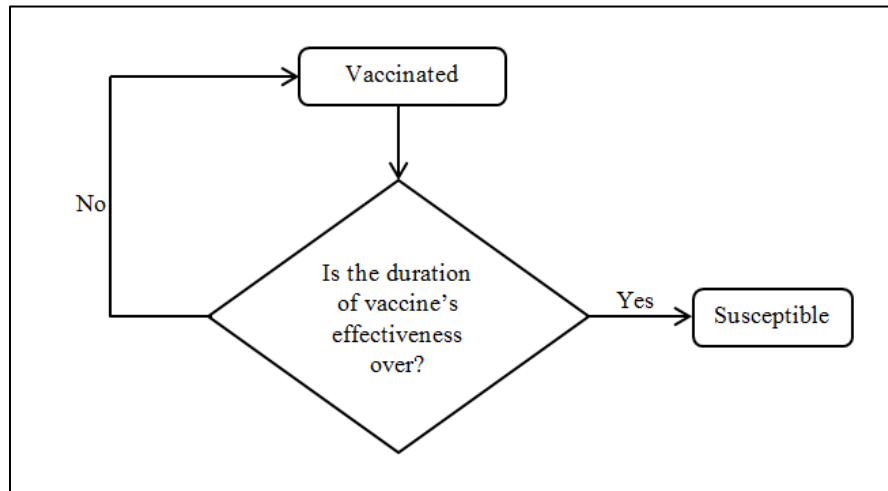
**Figure 3.14 Process during feared individuals interact with infected individuals.**

On the other hand, the feared individuals are given the opportunity to make their vaccination decision (Figure 3.14). Similarly as EBM, there are two strategies in the vaccination game, namely to-vaccinate and not-to-vaccinate. Each of the strategies consists of a payoff. The payoffs for to-vaccinate and not-to-vaccinate are depend on the risk of vaccination and risk of infection respectively. The feared individuals will make their vaccination decision based on their rationality to optimize the payoff which benefits them the most. The rationality of the individuals

is their mindset which assigned in the setup phase. If the feared individuals opt to vaccinate, they will be tagged in Vaccinated compartment. On the other hand, some of the feared individuals will take other precautions instead of vaccination to avoid the risk of vaccination. However, if they interact with the infected individuals, they may get infected as well. This is due to the fact of engaging in vaccination will build up the individuals' immune system. If the feared individuals take the other sorts of precautions, they will have lower chance to get infected as they do not have the immunity even they are preventing the disease infection. The disease transmission rate from infected individuals to feared individuals is reduced and it is denoted as  $\beta_f$ . If the unvaccinated feared individuals do not get infected, they will be given opportunity again to make their vaccination decision at next time step.



**Figure 3.15 The recovery process of infected individuals.**



**Figure 3.16** The process of vaccinated individual turn back to susceptible.

The infected individuals will be recovered after the disease duration,  $D$  unit time (Figure 3.15). The recovery rate is defined as  $\lambda = 1/D$  unit time. On the other hand, the vaccinated individuals will become susceptible again after the duration of the vaccine's effectiveness is over (Figure 3.16). In this model, the duration of the vaccine's effectiveness is denoted as  $T$  unit time. Thus, the vaccinated individuals will return to susceptible phase at the rate of  $h$ , where  $h = 1/T$ .

### 3.4 Discussion

In this chapter, the problem characterization is first presented. In this section, the compartmental model is constructed. The compartmental model assisted the understanding of the problem which defined in previous chapters. The compartmental model has contributed to the formulation of both EBM and IBM in this study. Both of the models have the same processes. EBM has a limitation of capturing the heterogeneity of a population. To overcome this limitation, IBM is constructed.

There are five compartments in the model, namely Susceptible, Infected, Feared, Vaccinated, and Recovered. The population is subdivided into these compartments accordingly. The susceptible individuals will either get infected by the viruses or get feared due to the spread of the fearfulness. The feared individuals are given opportunity to make their vaccination decision. Once they decided to vaccinate, they are not allowed to reverse the decision unlike those who do not want to vaccinate at the moment. The feared individuals who do not want to vaccinate are given a chance to make their decision again at next time step. They are assumed to take other sort of precautions at the moment and hence will reduce the disease transmissibility when they meet with infected individuals. The vaccination decision of the individuals is modelled as an imitation dynamics and it is aided by game theory. The vaccinated individuals will return to susceptible stage when the duration of vaccine's effectiveness is over. On the other hand, the infected individuals will be recovered after the infectious duration. Both of these processes are depending on the type of vaccines and diseases respectively.

In a nutshell, this chapter presented on how the model is formulated from the problem defined in previous chapters. The processes of each stage are presented. In the next chapter, the implementation of both models will be presented.

## **CHAPTER 4**

### **MODEL IMPLEMENTATION**

#### **4.0 Introduction**

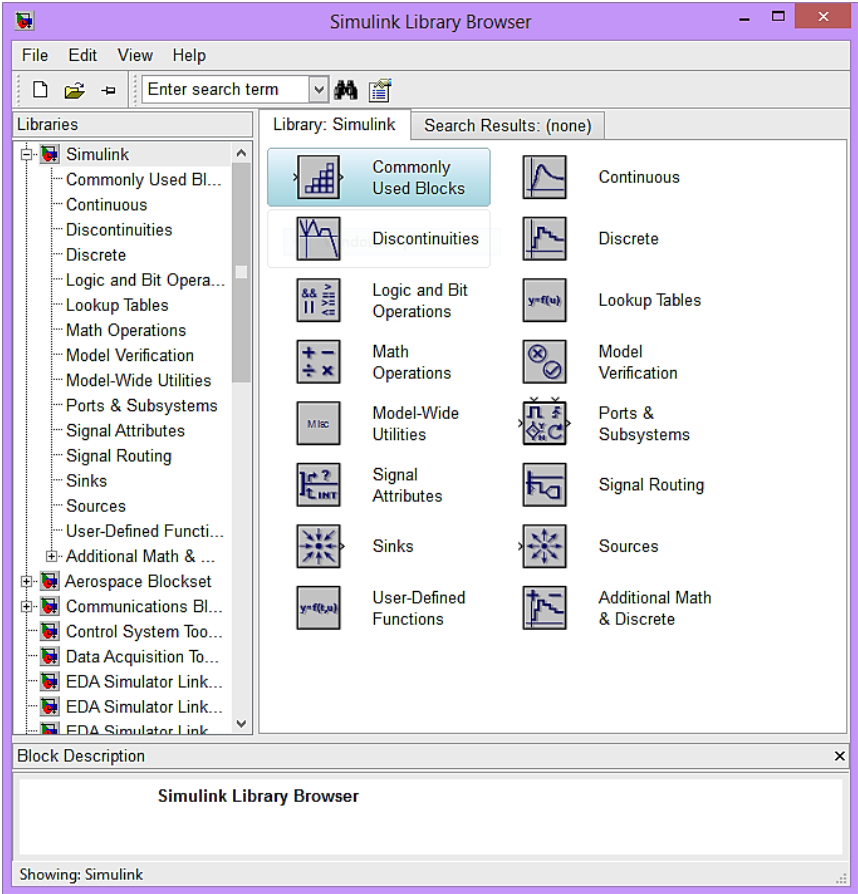
An EBM and an IBM are formulated to study the problem which discussed in previous chapters. The model formulation has been presented in the Chapter 3. The study is followed by the implementation of these models which will be discussed in this chapter. In this chapter, the implementation of the EBM in Simulink will be firstly presented. Section 4.2 discussed on the construction of IBM. This section is further divided into two parts. The first part (Section 4.2.1) will be reviewing different platforms of implementing IBM. The second part (Section 4.2.2) discussed on the implementation of IBM in this study. Lastly, the discussion and summary will be presented in Section 4.3.

#### **4.1 Equation-based Model in Simulink**

In Chapter 3, a set of governing equations is formulated for EBM in this study. This is a set of first order ordinary differential equations with the corresponding initial conditions. Thus, it is an initial value problem and therefore it will be solved accordingly. There are many numerical methods to solve initial value problems, for instance, Runge-Kutta and Euler method. These equations are non-linear and thus they cannot be solved analytically. The equations are converted into an executable simulation which is then simulated in Simulink. Simulink, which developed by MathWorks and integrated with MATLAB, provides an environment for modelling and simulating continuous system. The system simulation in Simulink provides numerical results to

the problem. The MATLAB's version that used to implement the EBM in this study is version R2007b.

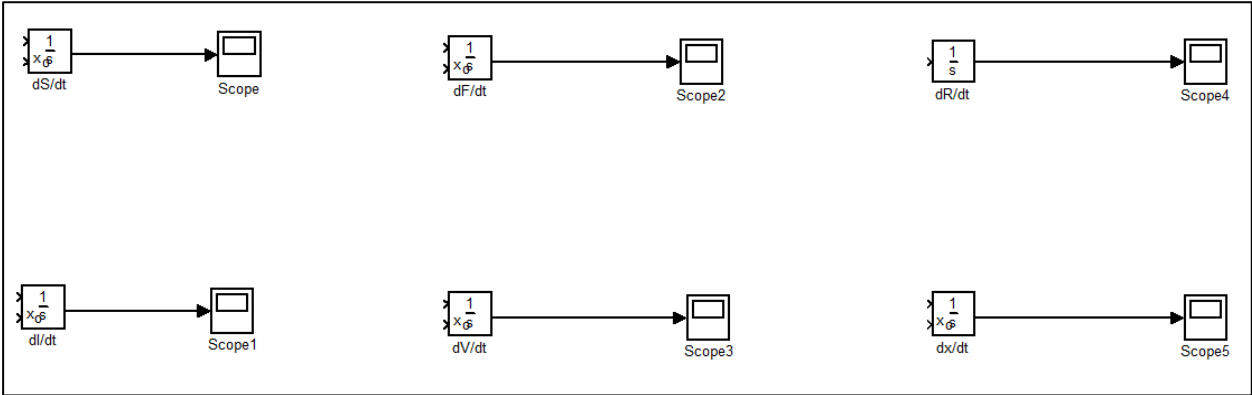
In Simulink, there are some predefined block libraries which allow the implementation of the model. Thus, the model constructed in the Simulink editor using block libraries is known as block diagram. The block libraries can be obtained through the Simulink library browser which is a built-in browser in MATLAB (Figure 4.1).



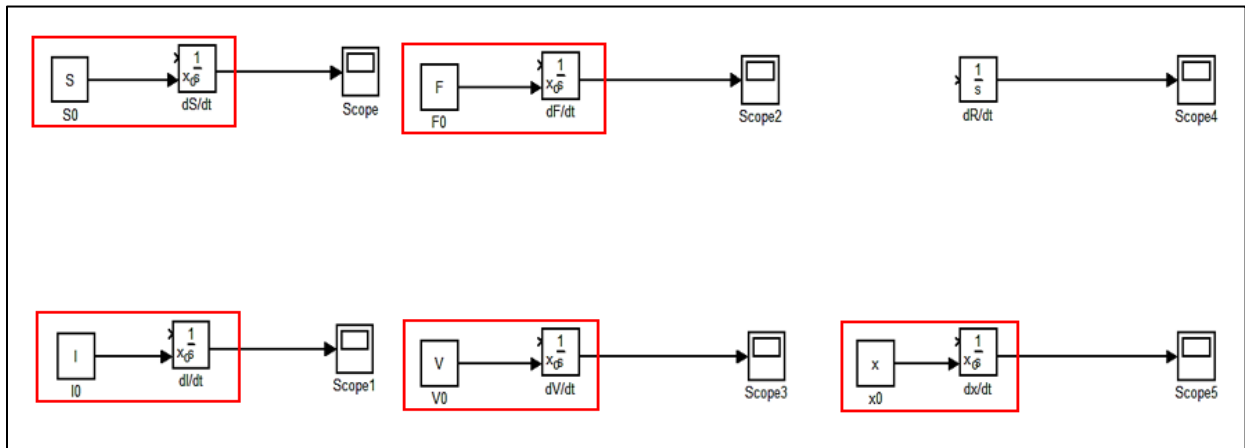
**Figure 4.1 Simulink library browser.**

To convert the governing equations to block diagrams, the definition and functions of the block libraries in Simulink have to be known by the modellers. Appendix B refers to the definition and functions of the block libraries used in the model of this study.

After determined the block libraries to be used in the model, the block libraries are dragged and dropped in Simulink editor according to the governing equations. Firstly, since there are five compartments in the model, thus five integrator blocks are dragged into the editor. An additional integrator block is included in order to carry out the operation of imitation dynamics equation. Each of the integrator blocks is paired up with a scope block. Therefore, there are six pairs of integrator and scope blocks in total (Figure 4.2). In the integrator block, the source of the initial value is set as external which accepts users' input from the command window in MATLAB (Figure 4.3). Since there is no recovery in the beginning of the disease outbreak, therefore the compartment of Recovered does not accept any initial value.



**Figure 4.2 Integrator-scope pairs in Simulink block diagram are initially arranged in the editor space.**



**Figure 4.3** The red boxes highlight the external source of initial value for each equation.

After the initial values are added into the block diagram, the next step is to add the respective operations for each equation in the editor. For instance, Eq. (4.1) is converted into block diagram which is shown in Figure 4.4. The values of the parameters such as  $\alpha$ ,  $\beta$ , and  $h$  receive the input from the command windows in MATLAB.

$$\frac{dS(t)}{dt} = -\alpha S(t)F(t) - \beta S(t)I(t) + hV(t) \quad (4.1)$$

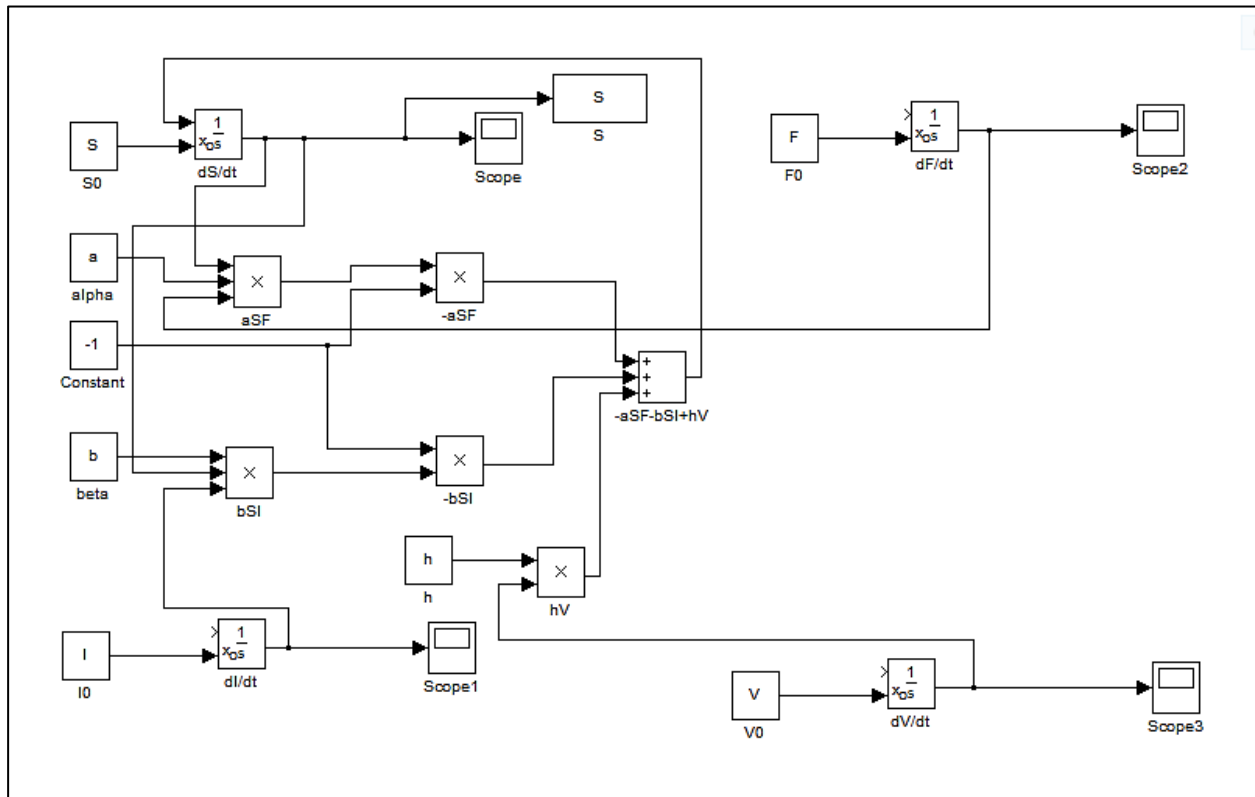


Figure 4.4 Part of the block diagram that describe equation  $\frac{dS}{dt}$ .

Similarly, the operations are added in the block diagram according to the equations stated in Chapter 3. The complete block diagram is attached in Appendix C. After constructing the block diagram based on the governing equations, the solver for the differential equations has to be determined. If the modellers do not specify the solver for the model, Simulink will assign ode45 as the solver by default. In this study, ode45, the built-in standard solver in MATLAB is used as the solver for the simulation. Ode45 is implemented by Runge-Kutta method to solve the differential equations with variable time step. The EBM is now completely implemented in Simulink and the parameters and initial values for the population can be assigned in the command window of MATLAB.

## **4.2 Individual-based Model**

In the first section of this chapter, the implementation of the EBM in Simulink is presented. It is followed by the discussion on the implementation of IBM in this study. As mentioned in Chapter 3, a flow diagram is drawn to illustrate the processes modelled in the IBM. The flow diagram is important in constructing IBM as it will be converted into the commands given to the agents in the model. The commands are required to allow the agents to move and interact in the model's environment. The basic commands to be set in the IBM are discussed in Chapter 3 as well. In this section, the implementation of these commands will be presented.

Recent years, individual-based modelling approach arises in various disciplinary such as computer science and this caused numerous individual-based platforms were developed. For instance, GAMA, NetLogo, and Repast are individual-based platforms. The comparison of platforms GAMA, NetLogo, and Repast will be presented in Section 4.2.1. A basic SIR model is simulated in these platforms. The respective results are then compared to the literature. From the discussion of the comparisons, one of those platforms will be selected to implement the IBM in this study. The implementation of this model will be presented in Section 4.2.2.

### **4.2.1 Comparison of Individual-based Model on Different Platforms**

Previously, the processes of the interaction among the agents are discussed. The interaction may cause the infectious viruses and the fear on the disease to be transmitted. Besides, the agents will imitate the neighbours when they are given the opportunity to make their vaccination decision. These processes are served as the backbone of the IBM in this study. Thus, it is important to translate these processes to individual-based algorithm. There are several platforms providing individual-based modelling approach, for example, NetLogo, GAMA, and Repast. The concept of

constructing model on these platforms is similar. GAMA and Repast emphasize on Object Oriented Programming (OOP). Although NetLogo is not object oriented, however, the agents in this environment carry their own attributes and behaviours as well. In IBM, the agent is an object which has its own attributes and behaviours. The agents have different attributes and behaviours depending on the status whether susceptible, infected, feared, vaccinated, or recovered.

In this study, three open source platforms are taken into consideration in order to implement the IBM, namely GAMA (version 1.6.1), NetLogo (version 5.0.4), and Repast (version 2.1). Table 4.1 shows the different platforms of individual-based modelling and its respective characteristics.

**Table 4.1 List of different individual-based modelling platforms and the respective characteristics.**

| <b>Platform</b>                       | <b>Characteristics</b>   |
|---------------------------------------|--|
| GAMA<br>(Taillandier et al., 2012)    | <ul style="list-style-type: none"> <li>• An environment for modelling and simulating development specifically for constructing spatially explicit individual-based simulations.</li> <li>• It integrates with Geographical Information System (GIS) data in the IBMs.</li> <li>• An open source platform which can run in several operating systems such as Mac OS X, Windows, and Linux.</li> <li>• It is based on GAML modelling language and it is developed in Java.</li> </ul>  |
| NetLogo<br>(Tisue and Wilensky, 2004) | <ul style="list-style-type: none"> <li>• A well-established individual-based simulation platform with a ‘patches’ grid environment, which is programmable to simulate the natural and social phenomena.</li> <li>• The ease of use of the platform helps the beginners to get started in constructing IBMs.</li> <li>• It loads GIS data as well, however, it is limited to the simple GIS data.</li> <li>• An open source platform that provides user-friendly environments and can be run in any Java Virtual Machine (version 5 or later).</li> <li>• It is based on a simple modelling language, namely NetLogo language.</li> </ul> |
| Repast                                | <ul style="list-style-type: none"> <li>• A toolkit that provides individual-based modelling and simulation</li> </ul>  |

|                      |   |
|----------------------|---|
| (North et al., 2007) | <p>libraries which is widely used in social sciences.</p> <ul style="list-style-type: none"> <li>• It requires high level of programming skills in constructing the models.</li> <li>• GIS operations are limited in Repast.</li> <li>• An open source tool to be run in several operating systems, such as Mac OS X and Windows. It requires Java Runtime Environment to run the demonstration simulations.</li> <li>• It is developed in java environment and it supports multiple languages, for instance, Java (RepastS and RepastJ), Python (RepastPy), and Visual Basic, .Net, C++, C#, J# (Repast.net).</li> </ul> |
|----------------------|---|

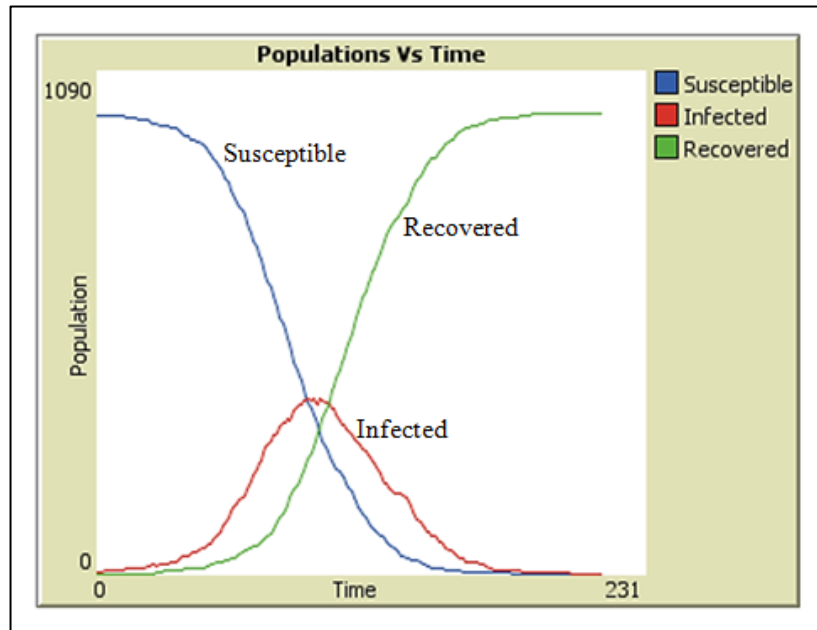
According to the review of the three open source individual-based modelling platforms in Table 4.1, an experiment is carried out in order to compare the result of the simple conventional Susceptible-Infected-Recovered (SIR) model. The simple conventional SIR model is constructed in the platforms reviewed in Table 4.1. The governing equations of SIR model are as below (Weiss, 2013):

$$\frac{dS(t)}{dt} = -\beta S(t)I(t), \tag{4.2}$$

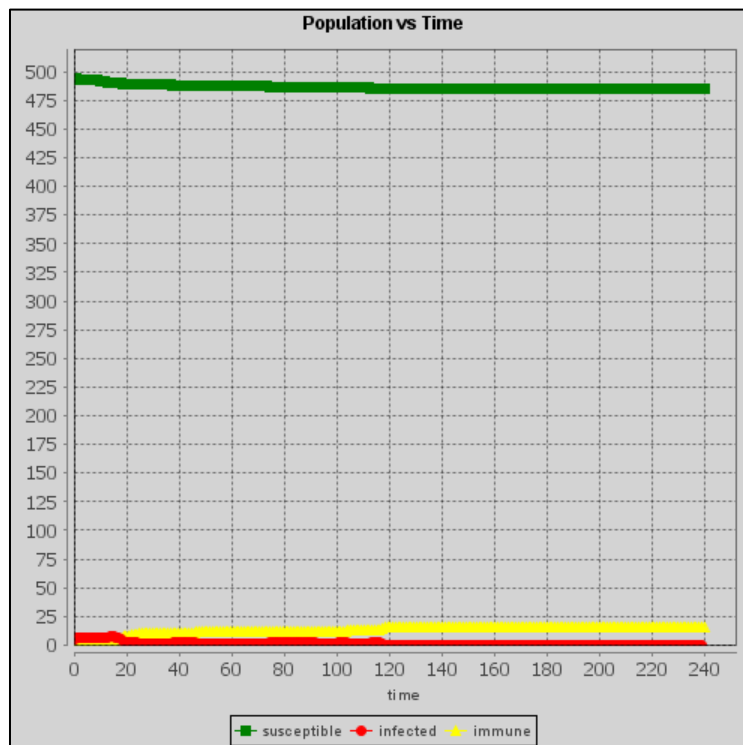
$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \lambda I(t), \tag{4.3}$$

$$\frac{dR(t)}{dt} = \lambda I(t). \tag{4.4}$$

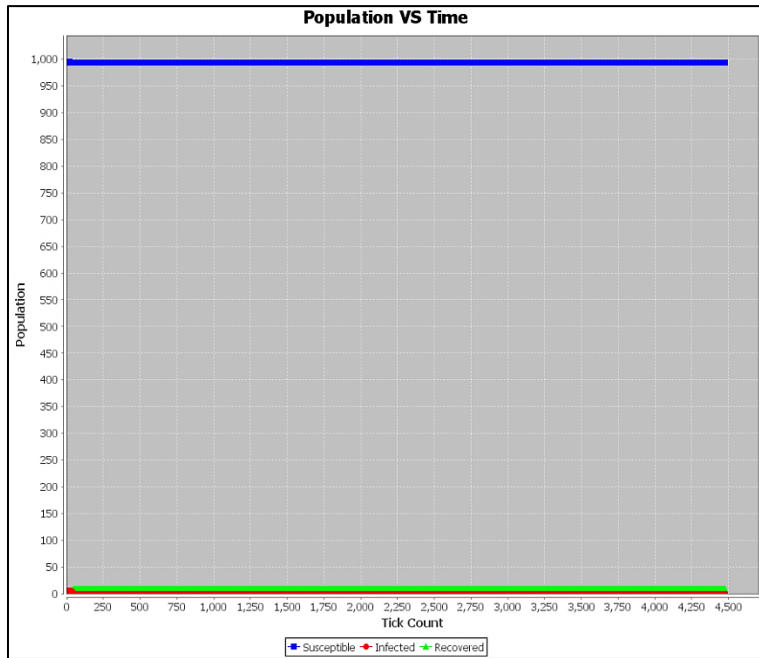
$\beta$  and  $\lambda$  represent the disease transmission rate and recovery rate respectively. This model is simulated in NetLogo, GAMA, and Repast. The results are shown in Figure 4.5, Figure 4.6, and Figure 4.7 respectively. The results are compared with the case study using EBM in Weiss (2013) (Figure 4.8).



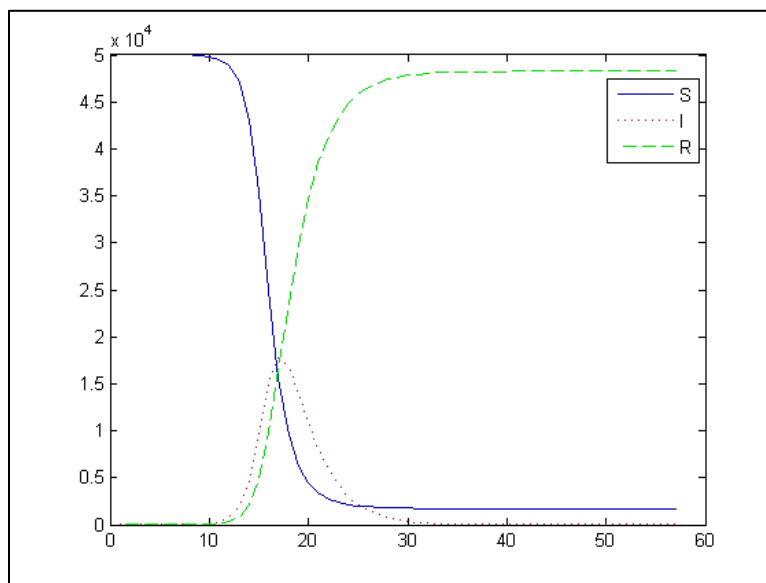
**Figure 4.5 SIR model results in NetLogo.**



**Figure 4.6 SIR model results in GAMA.**

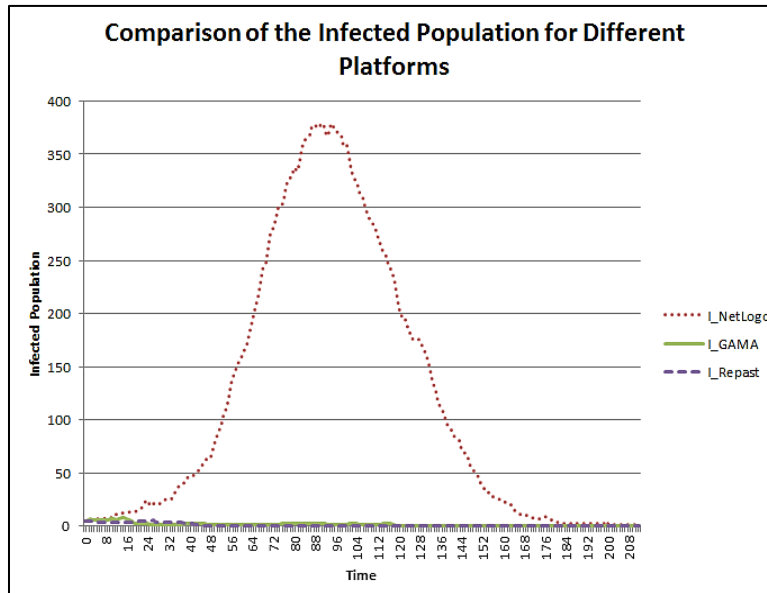


**Figure 4.7 SIR model results in Repast.**



**Figure 4.8 SIR model in EBM in Weiss (2013).**

The result in NetLogo consists of the same pattern of the curves as in EBM. The results are further compared among the infected curves from the three platforms. The comparison is shown in Figure 4.9. The perfect curve of Infected population is shown in the result of NetLogo.



**Figure 4.9 Comparison of Infected curves among three of the platforms.**

Based on the experiment carried out, NetLogo is the most suitable platform to be used in this study due to the ease-of-use of NetLogo and the accuracy of results compared to EBM. The friendly environment of NetLogo enhanced the progress of constructing the IBM. Unlike Repast and GAMA, NetLogo does not require high level programming skills. In this study, GIS data is not loaded in the IBM. Thus, NetLogo is sufficient in matching the purpose of constructing IBM in this study. On the other hand, GAMA and Repast are computationally costly in terms of performance. The time taken for GAMA and Repast to simulate the model is longer than that in

NetLogo due to the complexity of the processes in GAMA and Repast. Hence, NetLogo is chosen as the platform to implement IBM in this study.

#### 4.2.2 Implementation of Individual-based Model

As mentioned before, NetLogo has a user-friendly environment for modelling. The version of NetLogo in this study is version 5.0.4. In this study, the IBM consists of an interface which is subdivided into a few sections, namely input, operations, environment view, and results. In the section of input, the users are required to enter the parameter values such as the initial population of infected individuals, the location of the disease outbreak, type of the diseases, and the fear factor that allow the individuals to acquire fear during disease outbreak (Figure 4.10). The fear factor is the corresponding value of the awareness rising program that users taken. Dropdown list and text fields are used to construct this section.

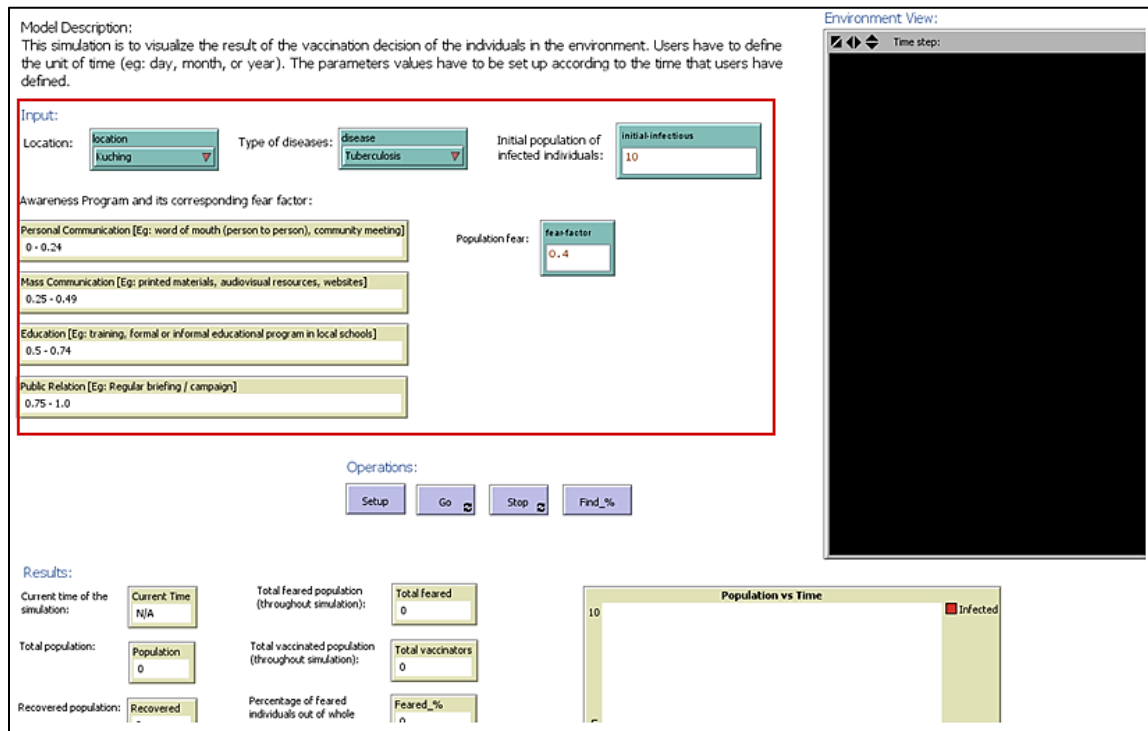
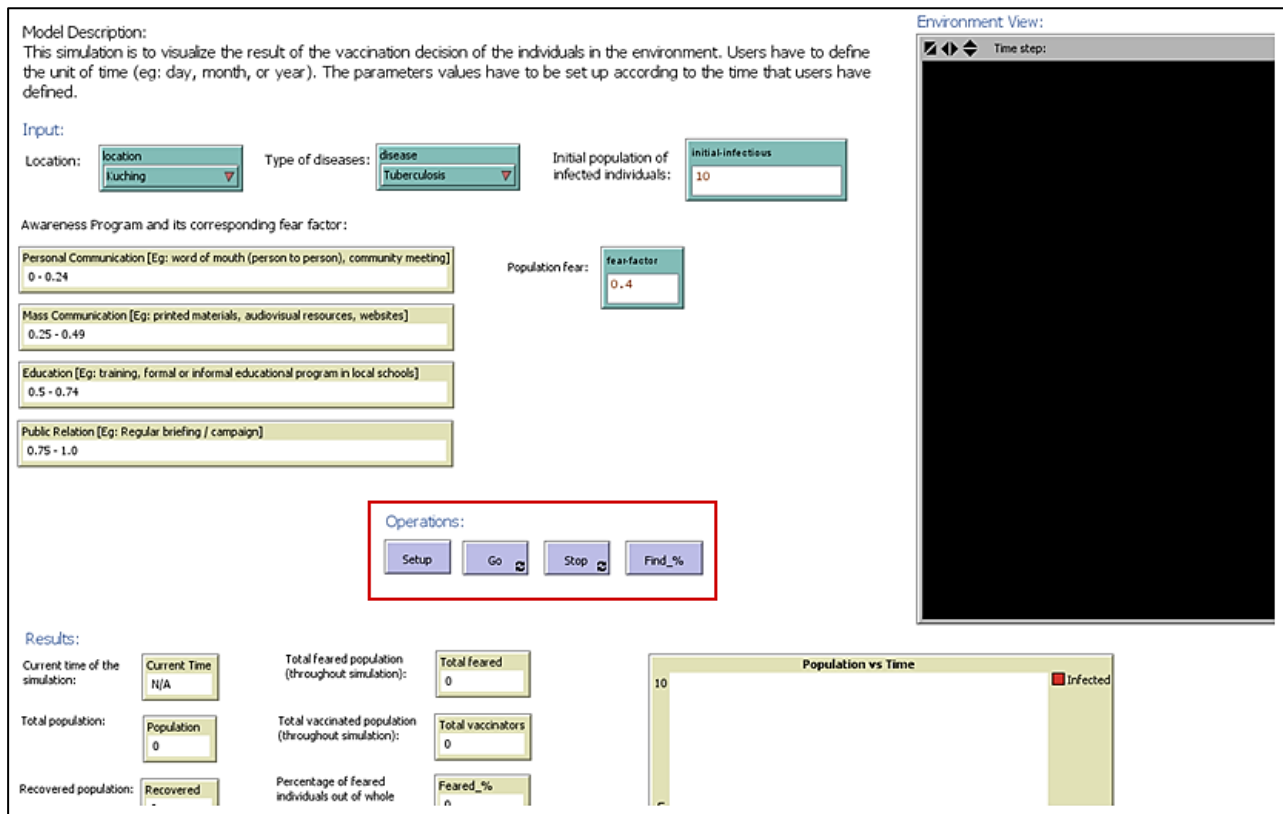
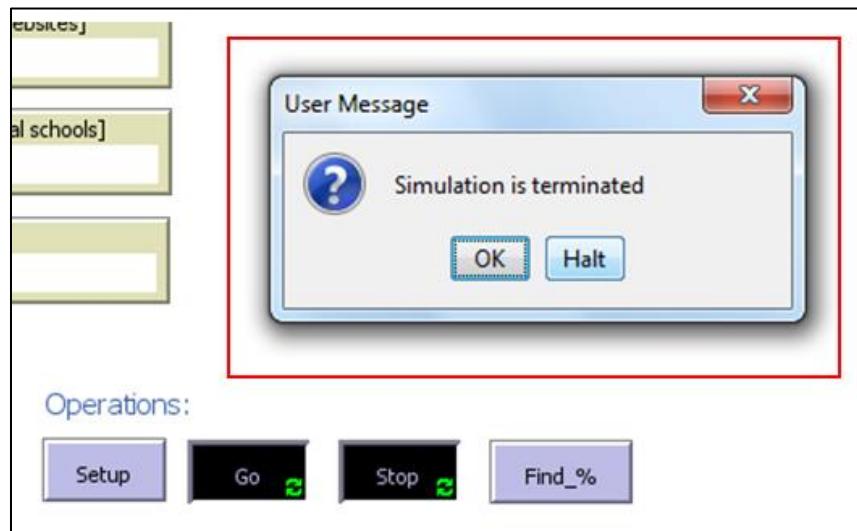


Figure 4.10 The red box highlights the section of input in the IBM in NetLogo.

The second section of the interface is about the operations that users would like to carry out in this model (Figure 4.11). Buttons are used to carry out the operations. The first operation is to setup the environment according to the parameters that users have entered. After the environment is set up, the operation of “Go” will be called to simulate the model. Users can stop the simulation by clicking the Stop button. A dialog box will be displayed when Stop button is clicked in order to confirm the simulation to be stopped (Figure 4.12). Users can click on “Halt” to stop the simulation if they wanted to. After the simulation is stopped, users can click on the button of “Find\_ %” to calculate the desired results from the simulation.

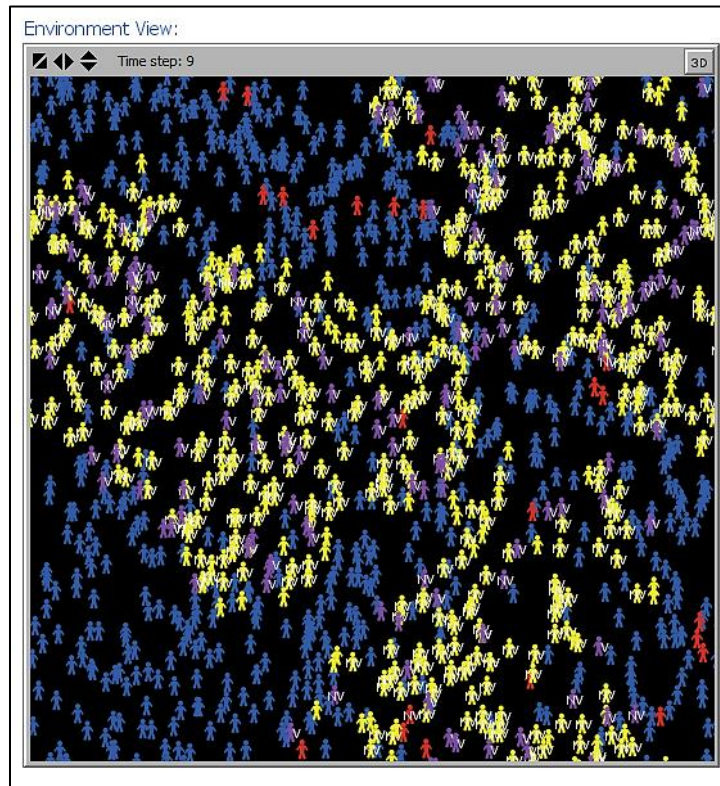


**Figure 4.11** The red box highlights the section of operations in the IBM in NetLogo.

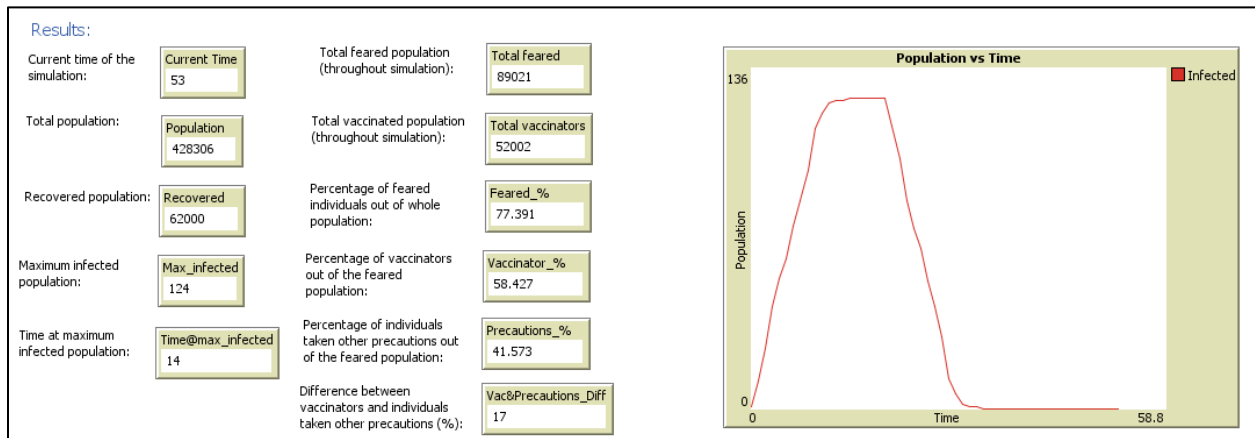


**Figure 4.12 A dialog box will be displayed after the Stop button is clicked.**

The third section of this model is the environment view (Figure 4.13). As NetLogo is a visualization tool, users can view the interaction of the agents in the environment. The last section of this model is the results of the simulation. It displays the desired results in figures and also in graph (Figure 4.14).

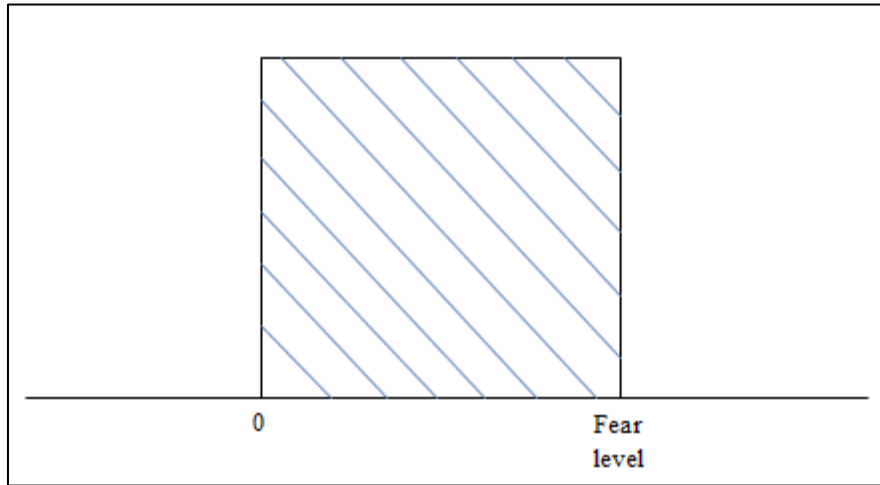


**Figure 4.13** The visualization of the model in NetLogo.

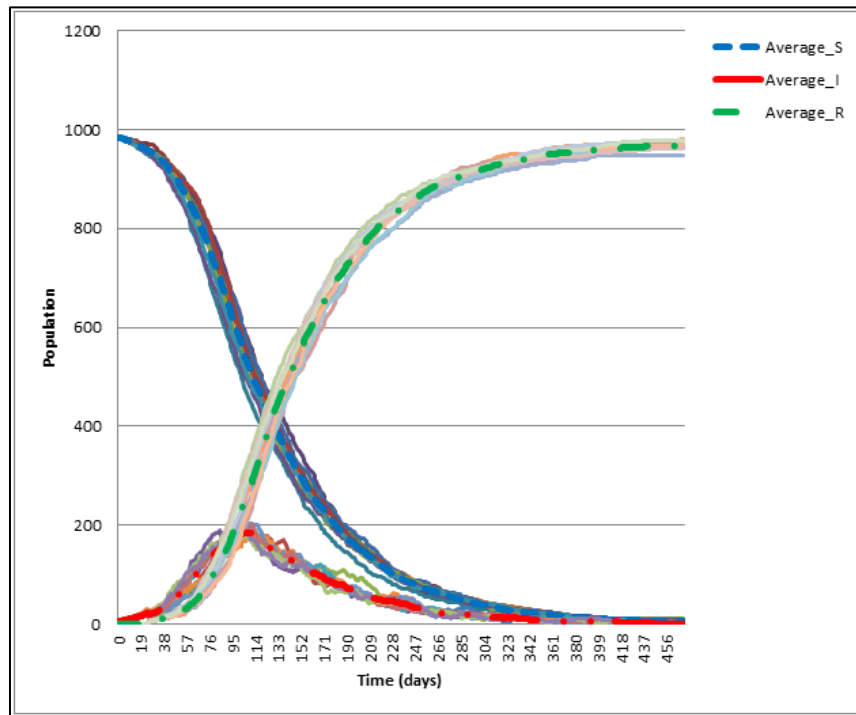


**Figure 4.14** The results shown in the model in NetLogo.

In order to implement the IBM, the first step is to determine the total subpopulation in the model. In this study, there are five compartments, meaning there are five subpopulations in the IBM. The subpopulations are initiated in the model by giving them the unique names and the initial number of individuals for the particular subpopulations. As discussed in the flow diagram in Chapter 3, each individual in the model is assigned by a set of random numbers to represent their own health state and mindset. There are several types of random number generator, for instance, Poisson, exponential, and uniform distributions. Both Poisson and exponential distributions are generating number based on the frequency of the event occurrences in a given duration. However, in this study, the model does not consider the frequency of an individual to change the health state and mindset. In fact, their health state and mindset will be updated at every time step. Thus, the built-in function of NetLogo which provides uniformly distributed random number to the individuals will be used as the generator in this study. The random number generator in NetLogo would be started by a “seed” value. In this study, the “seed” values will be indicated by the fear level and the health status of the population respectively. For instance, Figure 4.15 illustrates the distribution for the individuals’ mindset in the study. In NetLogo, the random number will be distributed uniformly in the shaded region in Figure 4.15 at every time step. Therefore, the individuals will receive the random numbers for their mindset and health state respectively based on this distribution. To examine the suitability of this generator in the study, an experiment is carried out. A series of simulations is run and there is no extreme outlier throughout these simulations (Figure 4.16). The similar patterns are obtained in this experiment. Thus, the uniform distribution is suitable to be used in generating the random numbers to represent the individuals’ health state and mindset.



**Figure 4.15 Illustration of random number distribution based on fear level in the study.**



**Figure 4.16 Average of 10 simulations of the model to examine the suitability of uniform distribution.**

The health state and mindset of the individuals help to decide whether or not the individuals are infected by the disease viruses and are acquired fear. The health state will be compared with the disease transmission rate when a susceptible is interacting with one of the infected individuals. If the health state is lower than the disease transmission rate, the susceptible will be infected. Otherwise, the susceptible remains in the same subpopulation. On the other hand, the mindset will be compared with the fear transmission rate when a susceptible is interacting with one of the feared individuals. If the mindset of the susceptible is lower than the fear transmission rate, the susceptible will be acquired fear; else, the susceptible will remain his/her susceptibility. The health state and mindset will be updated every time step.

The feared individuals are given opportunities to make their vaccination decision. They will compare the payoffs of both strategies (to-vaccinate or not-to-vaccinate). They will also imitate their neighbours to make decision. If most of their neighbours taken vaccine, they will tend to vaccinate as well. Since NetLogo provides a “patches” grid environment, the individuals in the surrounding 8 patches grid are considered as the neighbours. The feared individuals who decide to vaccinate will be labelled as “Vaccinated” and move into the subpopulation of vaccinated. On the other hand, those feared individuals who do not want to vaccinate at this moment are given another chance to make decision at the next time step. The unvaccinated feared individuals have a lower chance to get infected due to the precautions they have taken. Thus, their health state will be compared with the reduced disease transmission rate when they interact with the infected individuals. If the health state is lower than the reduced disease transmission rate, similarly, they will be infected by the viruses.

Since the vaccines considered in this study do not provide lifelong immunization, the vaccinated individuals will be susceptible again after the duration of the vaccine’s effectiveness.

Similar to the infected individuals, they will be recovered after the disease duration. Therefore, this model is able to keep track of the time count when the individuals engaged in the vaccination and when the individuals infected by the viruses.

### **4.3 Discussion**

In this chapter, the implementations of both EBM and IBM are presented. Firstly, the EBM is implemented based on the governing equations which have been discussed in the previous chapter. This model is constructed in Simulink, a simulation environment developed by MathWorks and it is integrated with MATLAB. The version of MATLAB in this study is version R2007b. A block diagram is built in Simulink to allow the simulation of the model. The block libraries used to construct the EBM in this study is discussed in Appendix B. The “Integrator” blocks are paired with “Scope” blocks to represent each governing equation. The results are stored as an array in the workspace which can be obtained from MATLAB workspace. The operations of the governing equations are implemented by using the Math Operations block libraries and “Constant” block. The standard solver in MATLAB, ode45, is used as the differential equations solver in this model.

On the other hand, there are several platforms to implement IBMs. In this study, three of the platforms are reviewed. The characteristics of each platform are listed in Table 4.1. Based on the review, NetLogo is chosen to implement the IBM in this study and the version of NetLogo in this study is version 5.0.4. NetLogo is a user-friendly environment and it is based on a simple programming language named NetLogo unlike GAMA and Repast which both require high level of programming skill and consume of high computational cost. Although both GAMA and Repast allow users to integrate with complex GIS data, however, GIS data is not loaded in this study. In

addition, an experiment is carried out to examine the suitability of the platforms. NetLogo provides the most accurate result compared to the others. Thus, NetLogo is suitable to be used as individual-based modelling tool in this study.

NetLogo provides visualization and interface to the users as well. In the interface of the IBM of this study, there are four sections, namely input, operations, environment view, and results. In the section of input, users are required to enter the parameters such as the location of the disease outbreak (eg. Kuching), type of the disease (eg: Tuberculosis), initial infected population, and fear factor which is sufficient to acquire fear in the population. There is a scale showing the awareness rising programs and the corresponding values in the interface as well. Users can enter the corresponding value of the awareness rising program organized as the fear factor. Each individual in the model will be assigned with a set of random numbers to represent own health state and mindset. These random numbers are generated by using uniform distribution. A series of simulations is carried out to examine the suitability of uniform distribution to be used as random generator in the model. There is no outlier found throughout the series of simulations. Moreover, the other distributions such as Poisson and exponential distributions are not suitable for this model as both of these distributions considered the frequency of the event occurrences in a given duration. However, in this study, the frequency of an individual to change his/her health state and mindset is not taken into account. In fact, the health state and mindset will be updated at every time step. In this chapter, the processes taken parts in the model are discussed. The flow diagram shown in Chapter 3 is transferred into the programming language of NetLogo.

In short, the EBM and IBM that discussed in Chapter 3 are implemented in Simulink and NetLogo respectively. In the next chapter, the simulation results and analysis will be discussed.

## **CHAPTER 5**

### **RESULT AND ANALYSIS**

#### **5.0 Introduction**

The formulations and implementations of both EBM and IBM are presented in the previous chapter. In this chapter, the output and results will be observed and analysed accordingly. A conventional SIR model is reproduced to verify the Disease-Behaviour model in this study. EBM is compared to the conventional SIR model and the result of the comparison is presented in Section 5.1. In the following section, the simulation results of both EBM and IBM are presented. The results will be analysed. The result of EBM will be compared with that of IBM. RMSE is calculated from the comparison of these results. In Section 5.3, the simulation results of EBM and IBM are validated through the actual incidences of Tuberculosis in Kuching, Sarawak, Malaysia. RMSE in between the simulations and the actual incidences is calculated as well. Next, sensitivity analysis of the Disease-Behaviour models will be carried out. The sensitivities of parameters  $\beta_f$  and  $\alpha$  are tested respectively. Section 5.5 will be the further analysis if the effect of heterogeneity of the population. IBM is used in this analysis. Lastly, there will be a short discussion to conclude this chapter.

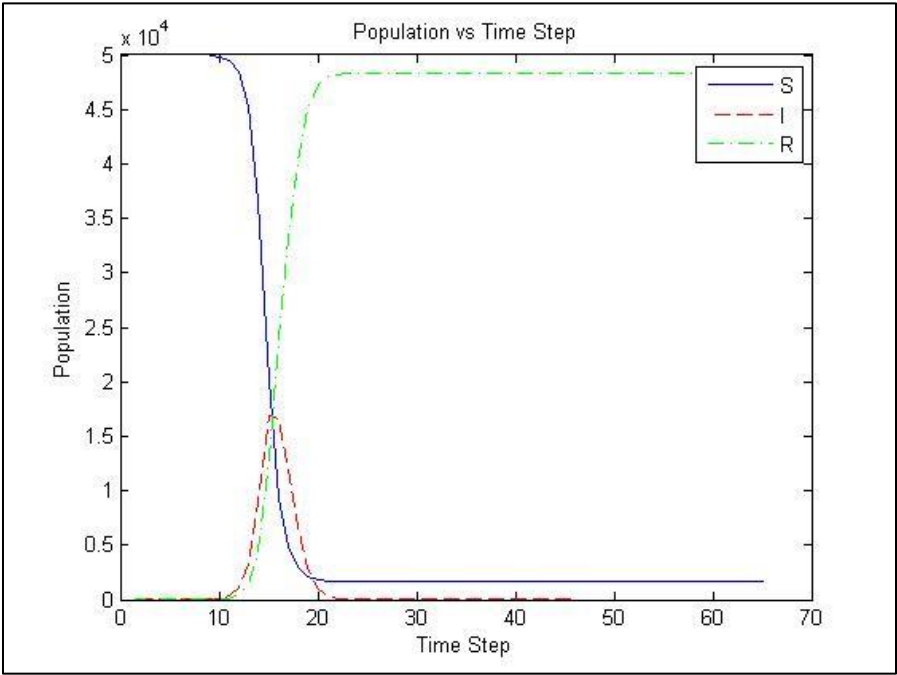
#### **5.1 Model Verification**

As mentioned in the previous chapter, EBM in this study consists of a set of first order ODEs which are implemented in Simulink and ode45 is chosen as the solver for this model. The conventional SIR model which was formulated by Weiss (2013) (Eq. (4.2) to Eq. (4.4)) is

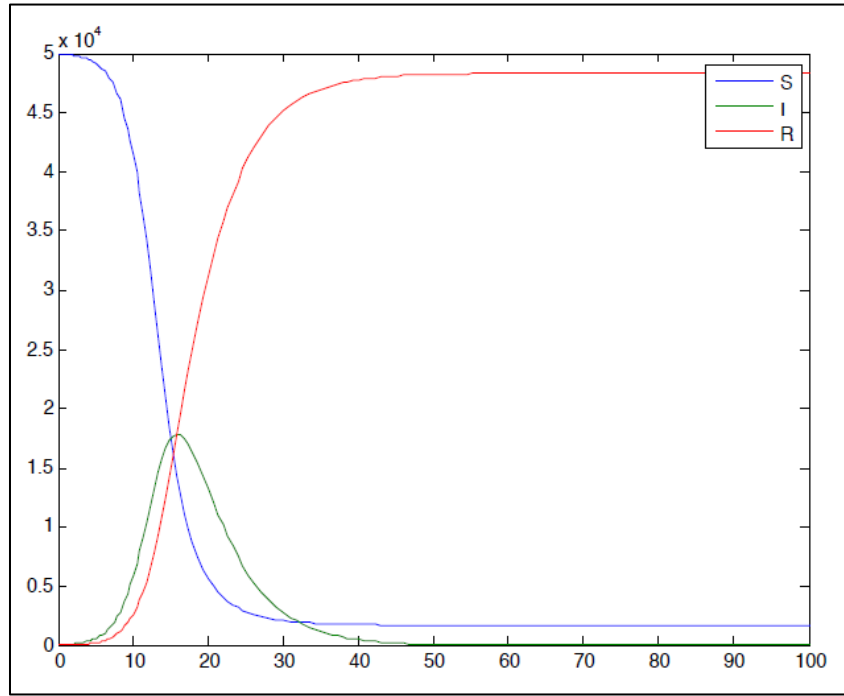
reproduced by Simulink to examine the effectiveness of Simulink in implementing the models. The result is shown in Figure 5.1.

The initial conditions of SIR model are denoted as  $S_0$ ,  $I_0$ , and  $R_0$  which represent the initial population of susceptible, infected, and recovered respectively. The unit of time for this experiment is per day. Therefore, all of the parameter values are measured in the same unit of time. Based on a flu epidemic in a small town with population of 50,000 people, the SIR model is simulated with the parameters  $\beta = 0.7/50000$  and  $\gamma = 1/5$ , and the initial population for each compartment in this case is  $S(0) = 49995$ ,  $I(0) = 5$ , and  $R(0) = 0$  (Weiss, 2013).

The simulation is reproduced in this study by Simulink. The screenshot of the simulation result based on the case study retrieved from Weiss (2013) is shown in Figure 5.2. Both Figure 5.1 and Figure 5.2 show similar pattern for all curves ( $S$ ,  $I$ , and  $R$ ).



**Figure 5.1 Flu epidemic simulation by SIR model reproduced from Weiss (2013) by Simulink.**



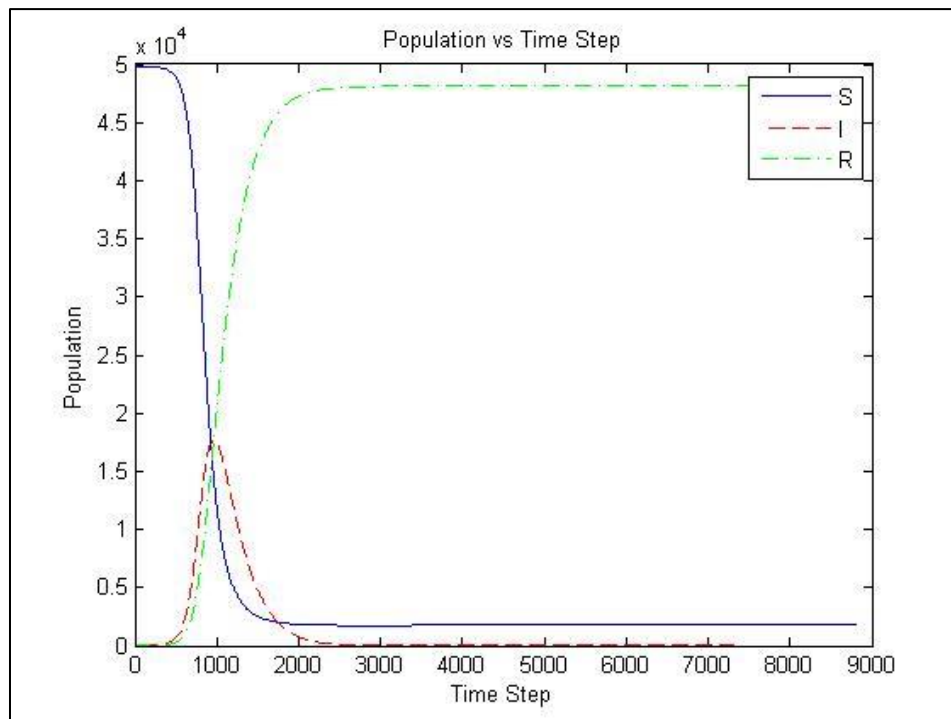
**Figure 5.2** Screen shot of the simulation result from Weiss (2013) [Source: Weiss, H. (2013). "The SIR Model and Foundation of Public Health." *MATerials Mathematics*, Vol 2013, pp. 5.

To examine the effect of the integration of fearfulness on diseases and vaccination decision in disease modelling, the model in this study is compared to the conventional SIR model in Weiss (2013). The experiment is carried out by simulating Disease-Behaviour model with the same epidemic case. The initial conditions of the disease-behaviour model are denoted as  $S_0$ ,  $I_0$ ,  $F_0$ ,  $V_0$ ,  $R_0$  and  $t_0$  which represent the initial population of susceptible, infected, feared, vaccinated, recovered and initial time respectively. Here, additional parameters are added according to the disease-behaviour model. The additional parameters are set as below:

**Table 5.1** List of additional parameters in disease-behaviour model.

| Parameter   | Value (per day)     | Source  |
|---|---------------------|---|
| Probability of an individual to acquire fear, $\alpha$        | 0.001               | Epstein et al. (2008)                         |
| Reduced disease transmission rate, $\beta_f = r_\beta(\beta)$ | $(0.7)*(0.7/50000)$ | $r_\beta$ is adopted from Perra et al. (2011) |

|  |                                       |                                 |
|--|---------------------------------------|---------------------------------|
| Rate of vaccinator to be susceptible again after duration of effectiveness of vaccine, $h$                           | 1/180                                 | Centre of Disease Control (CDC) |
| $\kappa$ and $\omega$ which contribute to the imitation dynamics equation, $\frac{dx}{dt}$ (discussed in Chapter 3). | $\kappa = 0.001$ ;<br>$\omega = 5000$ | Bauch (2005)                    |



**Figure 5.3 Flu epidemic simulation by disease-behaviour model using Simulink.**

The initial population for each compartment is set as  $S(0) = 49985$ ,  $I(0) = 5$ ,  $F(0) = 5$ ,  $V(0) = 5$ , and  $R(0) = 0$ . The values of  $S_0$ ,  $I_0$ , and  $R_0$  are adopted from Weiss (2013) where the initial values of the two new compartments,  $F_0$  and  $V_0$ , are set to be similar as  $I_0$  which is 5 respectively. Figure 5.3 shows the simulation result produced by the disease-behaviour model. Unlike Figure 5.1, the result produced by disease-behaviour model has a delay in time for the

infectious peak. Due to the behaviour that has been introduced in disease modelling, the population starts to engage some precautions include self-isolation and vaccination. Therefore, the population will gain immunization towards the disease through these precautions and there are lesser patients. After a duration, the infection will attack the population again when the population less aware of the disease. This explains why the infectious peak is delayed. Based on the comparison of the conventional SIR model and our disease-behaviour model, it shows the delay of the infectious peak to occur in the population and this lead to our further analysis on disease-behaviour model.

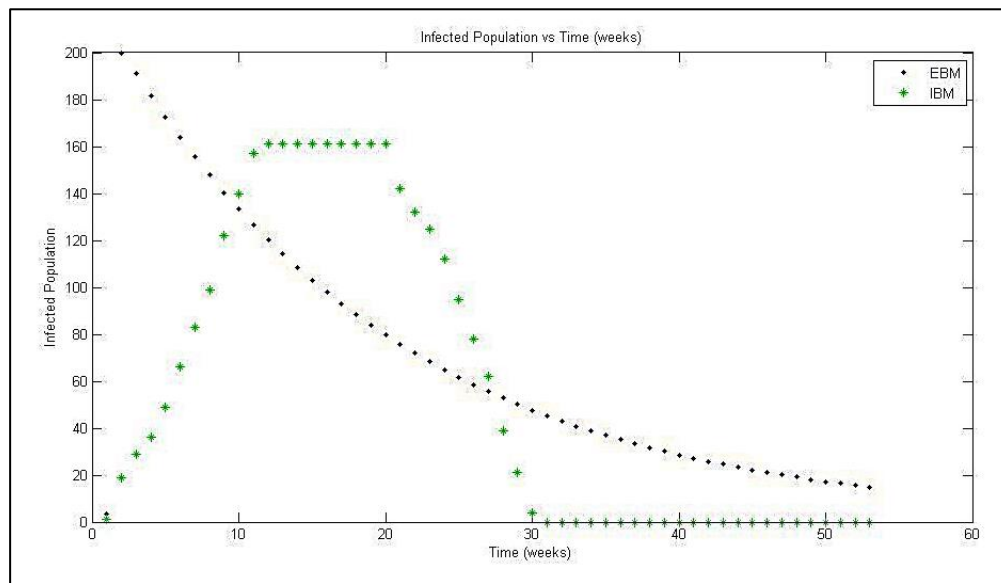
## **5.2 Simulations of Disease-Behaviour Models**

In this study, we have retrieved the actual incidences of Tuberculosis in Kuching from Sarawak Weekly EpidNews, Sarawak State Health Department. The data involved in this study is collected from the 44<sup>th</sup> week of the year 2012 to the 21<sup>st</sup> week of the year 2013, which is 30 weeks in total. The initial infected population,  $I(0)$ , is identified as 1 at the 44<sup>th</sup> week of year 2012. According to the Sarawak Facts and Figures 2012, the total population in Sarawak and Kuching are estimated as 2545800 and 616190 respectively. This leads the proportion of population in Kuching to the total population in Sarawak as 0.242. Based on the same source, the population of adults in Sarawak is estimated to be 1615200. By this information, the population of adults in Kuching is estimated as 390946. Since there is no data on feared individuals and vaccinated individuals, it is to be assumed that 10% of the population will be feared on the disease and 10% of these feared individuals have taken the vaccine. The rest of the population is assumed to be susceptible. The values of the parameters are listed in Table 5.2. These parameters values are used in the simulations of both EBM and IBM. The infected curves simulated from both EBM and IBM is

shown in Figure 5.4. In this figure, the error between EBM and IBM is observed and the RMSE between both models is calculated. The RMSE is found to be 0.8207.

**Table 5.2 List of parameters value used in the simulation for Tuberculosis in Malaysia.**

| Parameter  | Value (per week)                      | Source   |
|--|---------------------------------------|--|
| Disease transmission rate, $\beta$   | 0.0023/100                            | Calculated from Sarawak Weekly EpidNews          |
| Probability of an individual to acquire fear, $\alpha$   | 0.001                                 | Epstein et al. (2008)                            |
| Reduced disease transmission rate, $\beta_f = r_\beta(\beta)$  | (0.7)*(0.0023/100)                    | $r_\beta$ is adopted from Perra et al. (2011)    |
| Rate of vaccinator to be susceptible again after duration of effectiveness of vaccine, $h$                           | 1/700                                 | Centre of Disease Control (CDC) for Tuberculosis |
| Recovery rate, $\lambda$   | 1/19.2875                             | Centre of Disease Control (CDC) for Tuberculosis |
| $\kappa$ and $\omega$ which contribute to the imitation dynamics equation, $\frac{dx}{dt}$ (discussed in Chapter 3). | $\kappa = 0.001$ ;<br>$\omega = 5000$ | Bauch (2005)                                     |



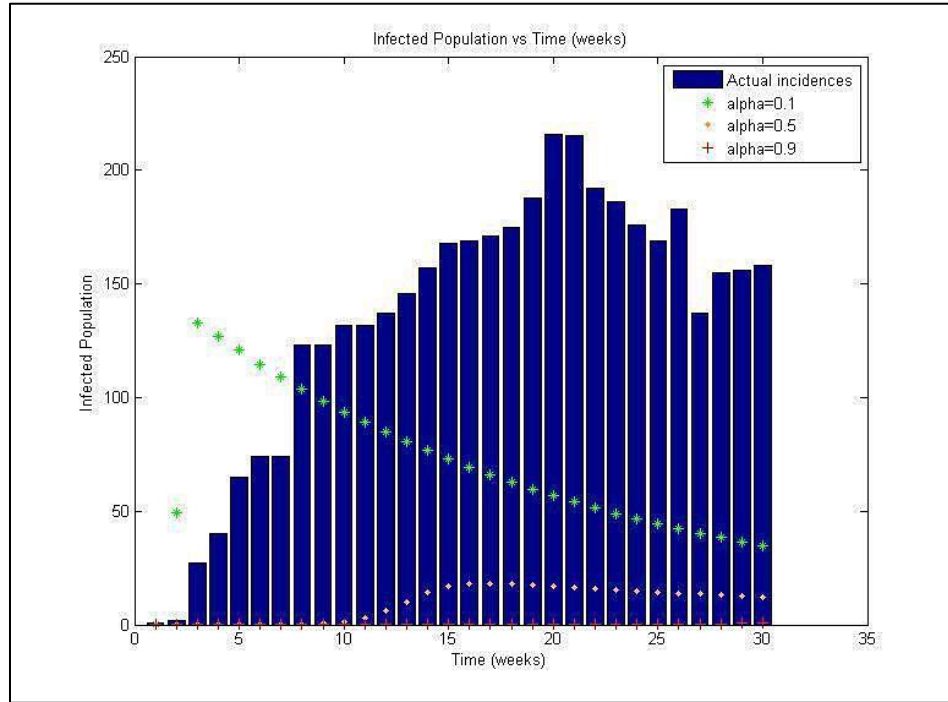
**Figure 5.4 Simulation results by EBM and IBM respectively when the value of  $\alpha$  is 0.001.**

The difference between EBM and IBM is caused by the heterogeneity created when the human behaviour is introduced into the model. When there is fearfulness or awareness introduced in the population, the individuals tend to behave uniquely as human behaviour is unpredictable. The individuals will have their own thoughts in making the decision to prevent themselves to be infected by the viruses. To examine the accuracy of the models, both EBM and IBM will be used to compare with the actual incidences in the next section.

### **5.3 Model Validation**

In the previous section, the simulations of both EBM and IBM are carried out and the RMSE found between these two simulations is 0.8207. In this section, the actual incidences retrieved from Sarawak Weekly EpidNews are compared to the simulations results to observe the effect of the probability of an individual to get feared during the disease outbreak,  $\alpha$ , in Sarawak. The parameters values for both EBM and IBM are set to be the same as in Table 5.2. The value of  $\alpha$  is predicted through a series of experiments in order to get the smallest error with the actual incidences. Figure 5.5 shows the comparison of the actual incidences and the simulation results with three different  $\alpha$ -values where  $\alpha = 0.1$ ,  $\alpha = 0.5$ , and  $\alpha = 0.9$ . Root mean square error (RMSE) is used to calculate the error between the simulation result and actual incidences. From the comparison shown in Figure 5.5, the fear of the disease is a factor that affects the spread of the disease. The infected cases will be reduced when there is more awareness and fearfulness of the disease in the population. The RMSE is found to be 4.4377 when  $\alpha = 0.1$  which is not a good result in the term of model fitting. For the case of  $\alpha = 0.9$ , the RMSE is 0.99 which implies the simulation result is not fit with the actual incidences. On the other hand, the RMSE is 0.94 when of  $\alpha = 0.5$  which the simulation results is more fitted with the actual incidences. The high RMSE

for both cases is due to the human behaviour introduced into the model which does not record in the actual incidences.

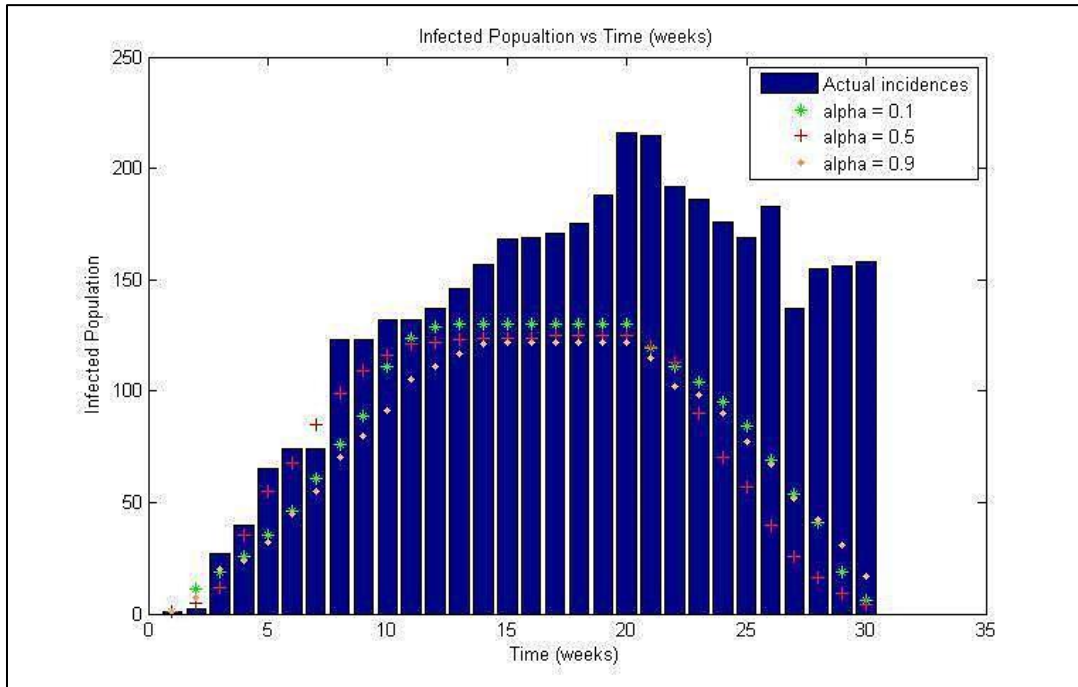


**Figure 5.5 Comparison of different  $\alpha$  values and the actual Tuberculosis incidences in Kuching, Sarawak.**

On the other hand, the simulation of IBM is carried out as well. Similar as the EBM, the simulation result of IBM is compared with the actual Tuberculosis incidences in Kuching, Sarawak. The values of the parameters are set to be the same as in EBM which presented in Table 5.2.

Figure 5.6 show the results of the comparisons of the actual Tuberculosis incidences in Kuching and the simulation results from IBM which constructed in NetLogo. The  $\alpha$ -values tested in this experiment are 0.1, 0.5, and 0.9 respectively. The RMSE for these cases are calculated as well. The RMSE for  $\alpha = 0.1$ ,  $\alpha = 0.5$ , and  $\alpha = 0.9$  are found to be 0.8552, 0.2902, and 0.4040

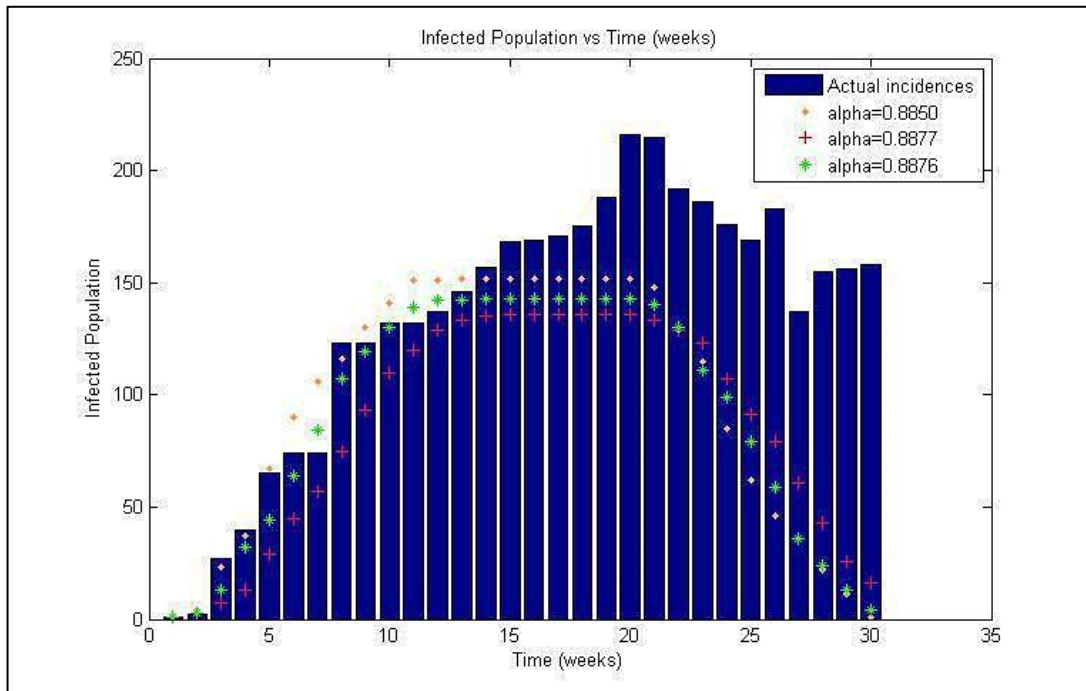
respectively. Based on the RMSE, we found that the simulation result is more fitted with the actual incidences when  $\alpha = 0.5$ . This shows the agreement with the comparison of EBM with the actual incidences. However, as mentioned before, the simulation results are not well fitted in the actual incidences due to the human behaviour which has introduced into the conventional model. The actual incidences do not record the variable of human behaviour. However, the infected incidences would be reduced if the awareness about the diseases is introduced into the population.



**Figure 5.6 Comparison of the actual Tuberculosis incidences and the simulation result from IBM with different values of  $\alpha$ .**

We further investigated the value of  $\alpha$  in the individual-based simulation. The values of  $\alpha$  are chosen between 0.5 and 0.9, which are 0.8850, 0.8877, and 0.8876. The RMSE for these values of  $\alpha$  are 0.2064, 0.1938, and 0.1793 respectively which are found to be more fitted to the

actual incidences (Figure 5.7). However, in order to get more fitted curve for the model, the value of  $\alpha$  has to be known. From the results, the range of the  $\alpha$ -value is fall in between 0.5 and 0.9.



**Figure 5.7 Comparison of the actual Tuberculosis incidences and the simulation result from IBM with further investigated values of  $\alpha$ .**

From this experiment, the RMSE between IBM and the actual incidences is lower than that between EBM and the actual incidences. For instance, when the value of  $\alpha$  is 0.5, the RMSE for IBM is 0.2902 while the RMSE for EBM is 0.9454. This means that IBM in this study is more fitted to the actual incidences compared to EBM. In IBM, there are two random numbers assigned to the individuals to represent the heterogeneous characteristic (health state and mindset) in the population. These random numbers are updated at every time step. The updates of these random numbers indicated the behavioural changes of the individuals at different time. This setup of the

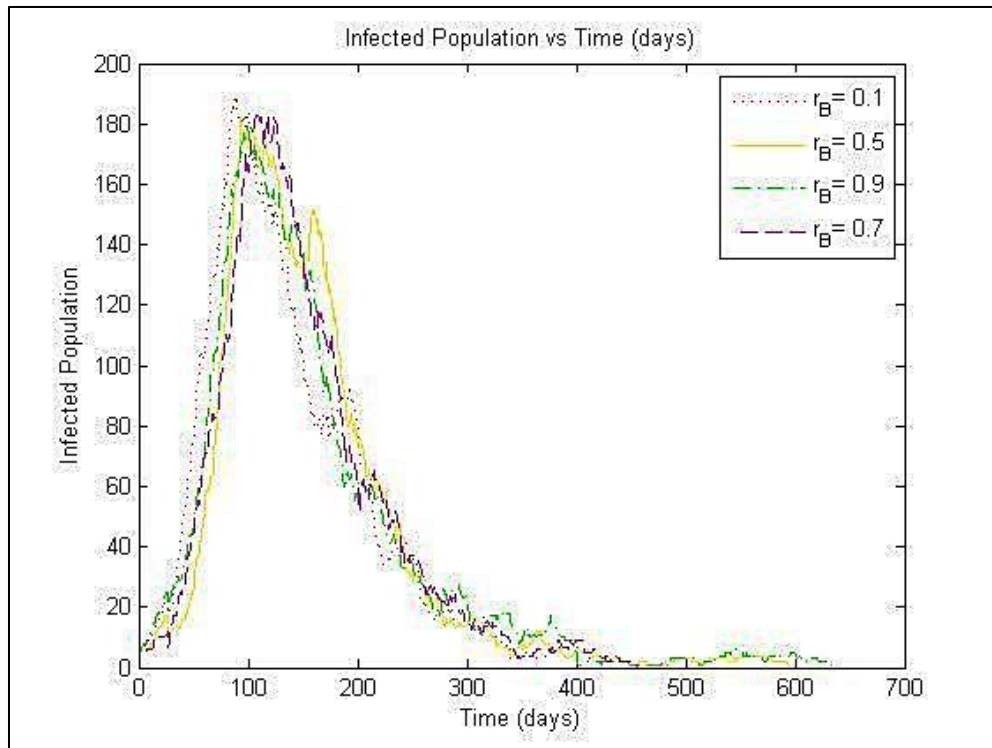
IBM is closer to the real world problem, thus, it has a smaller error when compared to the actual incidences. Unlike IBM, EBM does not consider the assignments of the heterogeneous value to the individuals. Instead, EBM only considered overall disease transmission rate and probability of an individual to acquire fear for the whole population. In EBM, the individuals get infected or feared depend on the proportion of the susceptible and infected individuals or the proportion of the susceptible and feared individuals. On the other hand, in IBM, the individuals hold their own unique health state and mindset. These unique values will determine whether or not they get infected or feared. Therefore, the individuals in the environment of IBM have different chance of getting infected by the viruses or feared.

However, the RMSE in this study is considered high. This is due to the assumption of the patients who recovered from the infection are considered as immune to the disease (Section 3.1). In other words, the recovered individuals will not be susceptible again in this model. This caused the infected population in the simulation result to be declined after week 21. Hence, it induced the big difference between simulation result and the actual incidences and the RMSE is high. For the following sections, IBM will be simulated to produce more analyses.

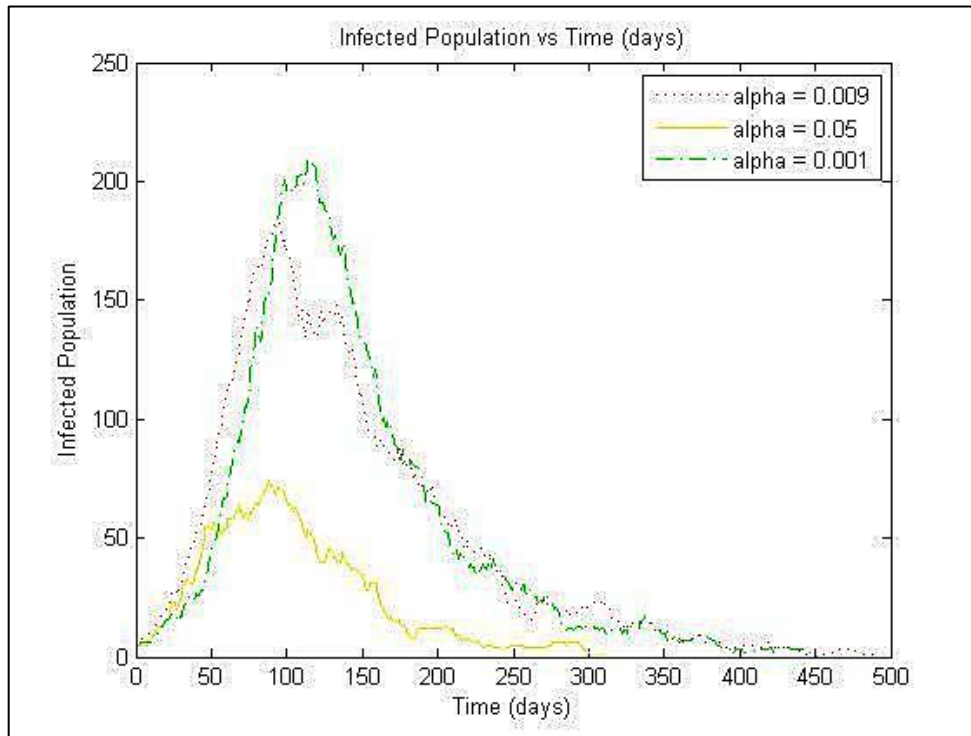
## **5.4 Sensitivity Analysis**

In this section, the sensitivity of the main parameters ( $\beta_f$  and  $\alpha$ ) in the Disease-Behaviour model will be examined. The parameter  $\beta$  which is the disease transmission rate is not examined here as this parameter is depending on the diseases. The values for the other parameters are kept the same as in Section 5.1. Firstly, the sensitivity of parameter  $\beta_f$  is tested by adjusting the coefficient  $r_\beta$ . The coefficient  $r_\beta$  is a reducing rate originally adopted from Perra et al. (2011) with a value of 0.7. As  $\beta_f$  is the reduced disease transmission rate, the main factor that impacting this parameter is the

coefficient  $r_\beta$ . Here, three values of  $r_\beta$  are examined and the results are shown in Figure 5.8. The second parameter tested in this section is  $\alpha$ , which is the probability of an individual acquire fear. The value of  $\alpha$  is set as 0.001 initially. In this experiment, the values used to test the sensitivity are 0.009 and 0.05. The results are shown in Figure 5.9.



**Figure 5.8 Results simulated by IBM with different values of coefficient  $r_\beta$ .**



**Figure 5.9 Results simulated by IBM with different  $\alpha$ -values.**

From the results simulated, there is a little or insignificant change on the infected population when  $r_\beta$  is altered. As  $\beta_f$  is the reduced disease transmission rate relating the feared individuals to get infected, therefore, the infected population is depending on the feared population. During the sensitivity analysis test, the value of  $\alpha$ , which is the probability of an individual getting feared is fixed. Thus, the feared population is fixed as well. Under this condition, the adjustment of the values of  $\beta_f$  will not bring a significant impact on the infected population.

Instead, when  $\alpha$  is altering in the simulation, there is more significant change in the infected population. With higher value of  $\alpha$ , the fearfulness will be spread to more individuals. If there are more feared individuals in the population, the tendency of the feared individuals to

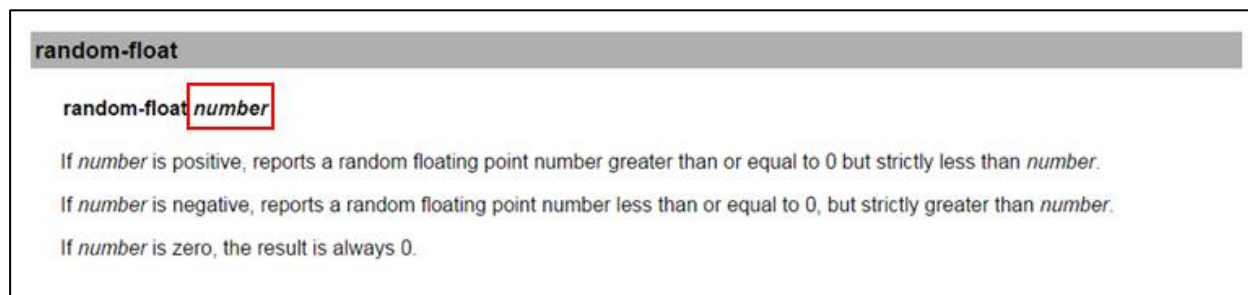
engage in vaccination program has increased. They also tend to engage in other precautions to prevent themselves from getting infected by the disease viruses. This will hence reduce the infected population. As there are some feared individuals who do not select the strategy to-vaccinate, they might get infected at the reduced rate of disease transmission,  $\beta_f$ . This is the reason of the peak of the infected curves in the results shown.

From the test upon two parameters,  $\beta_f$  and  $\alpha$ ,  $\alpha$  is found to be more sensitive in the model. The significant figure is very sensitive in the values of  $\alpha$ . A little increment in the value of  $\alpha$  will reduce the infected population. In other words, the total number of the feared individuals is a key in controlling the disease to be spread in population. Information of the diseases has to be spread to the individuals to acquire the fearfulness and awareness on the diseases. The further analysis on the information spread and the fearfulness induced in the population will be discussed in the next section.

## **5.5 Further Analysis of Individual-based Model**

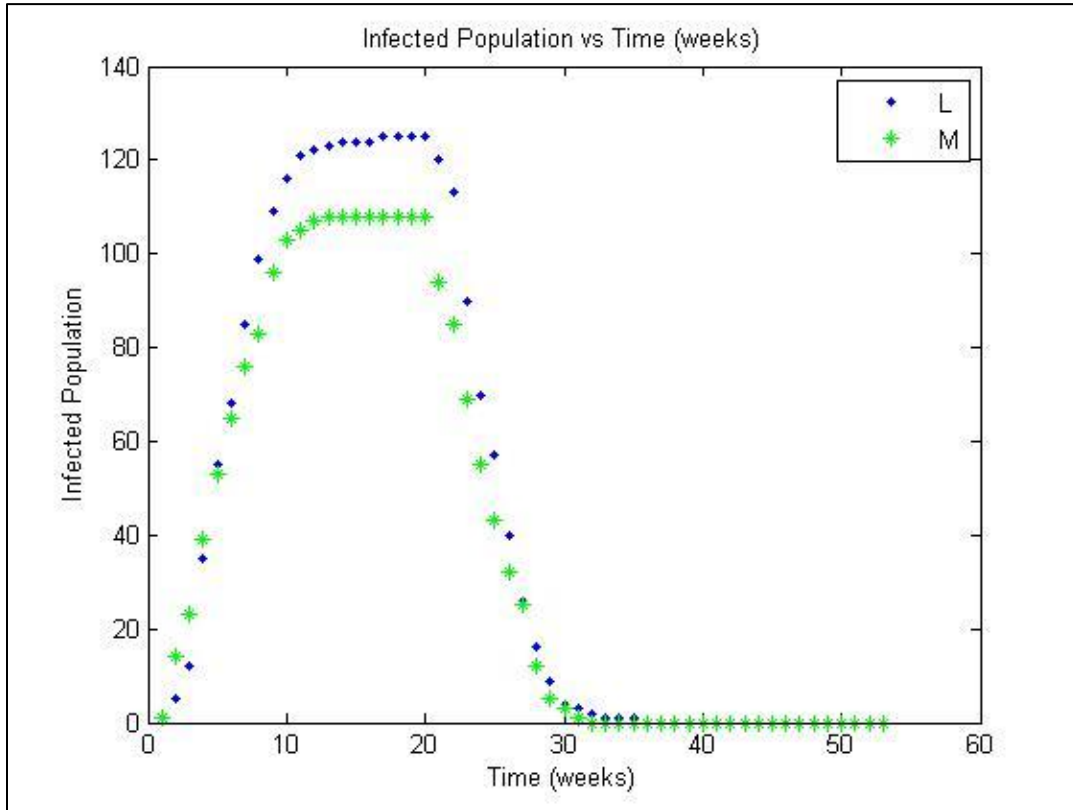
From previous discussion, we found that the environment of IBM is closer to the real world environment. The individuals in this model are determined to get infected or feared by their own health state and mindset which are unique to each of them. During the environment set up, the individuals in this model are assigned by two random numbers which represent their health state and mindset. These numbers served as the uniqueness to the individuals as the random number generator will generate the unique number for each of them at each time. Since these numbers are the main determinants of the transmission of the diseases and fearfulness, the effect of the different number assigned to the generator will be discussed in this section.

In NetLogo, a number is required to be set in order to get the generation of random number through uniform distribution. Figure 5.10 explains the random floating number generations in NetLogo.



**Figure 5.10** Screen captured from <http://ccl.northwestern.edu/netlogo/docs/dictionary.html> showing the random float number generations. The red box highlights the number which to be assigned to the generator as an indicator for the random floating number generation.

The number to be assigned in this study is depending on the disease transmission rate and the probability of an individual to acquire fear on the diseases. In this study, in order to test the heterogeneity of the population, we assumed there is a group of individuals who do not receive complete information about the infectious diseases. This group is named as  $L$  (less informative) as they receive less or incomplete information. On the other hand, there is another group of individuals who receive complete information about the infectious disease. Since they receive complete information, we named this group as  $M$  (more informative). These groups are distinguished by altering their health state and mindset. For group  $L$ , the health state and mindset are set to be lower compared to group  $A$ 's. When they received less or incomplete information, they will have less awareness or feeling less fear to the diseases and hence having less incentive to protect their health.



**Figure 5.11 The difference of the infected curve between group *M* and *L*.**

Figure 5.11 shows the difference of the infected curve for both of the group *M* and *L*. The values of the parameters are kept constant as in Table 5.2. The  $\alpha$  value is set as 0.5. Since the random floating numbers are depending on the disease transmission rate and the probability of an individual to acquire fear, the numbers to be assigned in the generator for group *M* are the values  $\beta$  and  $\alpha$  respectively. On the other hand, the numbers to be assigned in the generator for group *L* are reduced by 0.01. A slight reduction is carried out to differentiate the groups in a population. From this parameters setting, it is observed that there are more infected individuals in group *L* compared to group *M*. It is due to the lower awareness of the individuals in group *L* to take the

precautions to protect their health. As mentioned before, the individuals in group  $L$  has lower mindset on the infectious diseases and hence they have lower incentives to avoid the disease. This caused the health state to be lowered as well. Therefore, the disease viruses can easily invaded in their group. On the contrary, the individuals in group  $M$  have higher awareness and health state and this caused them to protect themselves from the disease viruses. Thus, there are lesser infected individuals in this group as shown in Figure 5.11.

## **5.6 Discussion**

In this chapter, the results from the Disease-Behaviour model are presented. The conventional SIR model adopted from Weiss (2013) is reproduced by Simulink in this study. The result is compared to the Disease-Behaviour model. From the comparison, it is found that the disease outbreak is delayed when fearfulness of the disease and vaccination decision are integrated in the model.

There are two model implemented in this study, EBM and IBM. The results simulated by these models are discussed in this chapter as well. RMSE is applied to calculate the error between these models and it is found to be 0.8207. Besides, both EBM and IBM are compared to the actual incidences of Tuberculosis in Kuching, Sarawak. RMSE is applied in this comparison as well. Overall, IBM gives a lower RMSE when comparing to the actual incidences. This is due to the heterogeneity that exists in the IBM. The environment set up in the IBM is closer to the real world. Therefore, the RMSE between the simulation in IBM and actual incidences will be lowered as compared to the simulation in EBM. The EBM has a limitation to capture the heterogeneity of the population. Instead, it assumes the population to be homogenous. However, the RMSE in both EBM and IBM are considered high as the assumptions of the compartmental

model in this study allow the growth rate to be omitted. Since the population is targeted on the adults, the assumption of growth rate is omitted during the first stage of the model formulation.

The sensitivity analysis is carried out in IBM with two parameters,  $\beta_f$  and  $\alpha$ . Based on the test, parameter  $\alpha$  provides a more significant impact on the simulation. As the  $\alpha$ -value determines the feared population and hence determines the vaccinated population, thus it has higher sensitivity in the Disease-Behaviour model compared to  $\beta_f$ .

In the IBM, the characteristic of the heterogeneous population can be included. In this study, the individuals in the model are assigned with a set of random numbers which represents their health state and mindset respectively. These numbers are unique to each of the individuals in the environment and the numbers will be updated at every time step. Thus, this created the heterogeneity in the population. Each of the individuals will have different chance to get infected by the disease viruses and get acquired the fearfulness to the diseases. Since the disease transmission and the probability of the individuals to get feared are depending on these random numbers, an experiment is carried out to examine the effect of these random numbers in the simulation. In this experiment, the individuals are divided into two groups, one receive less or incomplete information about the diseases (named as  $L$ ) and another receive all or complete information about the diseases (named as  $M$ ). Group  $L$  is assigned with lower value of health state and mindset as they receive less or incomplete information. Oppositely, group  $M$  is assigned with higher value of health state and mindset. From such assignments of health state and mindset, the result shows group  $L$  has higher infected cases compared to group  $M$ . The information about the diseases would affect the behavioural changes of the individuals in the population (Funk et al., 2010). Due to less or incomplete information received by the individuals in group  $L$ , they have

lower awareness and less fear to the diseases. Thus, they have lower incentive to take the precautions to avoid the diseases. On the other hand, group  $M$  will tend to take more precautions to protect themselves and their health will be improved.

In a nutshell, this study shows the behavioural changes of the individuals reduce the infected cases in the population. IBM produced the simulation results with lower RMSE than EBM when comparing both to actual incidences in Kuching. This is mainly caused by the heterogeneity which can be captured in IBM but not in EBM. The heterogeneity of a population can be the main reason for the disease transmission and fearfulness spread. For instance, the group of receiving less information will cause a lower awareness and health state and hence will increase the infected cases in the population. This explains why the IBM has a closer simulation result to actual incidences.

## **CHAPTER 6**

### **CONCLUSION**

#### **6.0 Introduction**

In this chapter, a summary for this study and the contributions of this study are presented. Apart from that, the limitations are discussed as well. Lastly, the potential future work to be extended from this study will be discussed.

#### **6.1 Summary**

In the beginning of this thesis, a short introduction of the conventional way to model infectious diseases has been presented. The infectious diseases, for example, Measles and Tuberculosis, have threatened the public health. These diseases are vaccine-preventable. Even though there are vaccination programs existed to encourage the vaccination engagement in the world, there are still many incidences of the vaccine-preventable infectious diseases. This drawn the interest to study human behavioural changes of the population in the spread of these infectious diseases. The spread of the infectious diseases can be modelled by EBMs (also known as mathematical models). For instance, the well-known conventional model to study the spread of infectious disease is Susceptible-Infected-Recovered (SIR) model. In this thesis, both of the fearfulness of the disease and vaccination decision are integrated in the model. In other words, the concept of the conventional SIR model is adopted with the integration of human behavioural changes where human behavioural changes refer to the fearfulness of the disease and the vaccination decision. Besides, an IBM is constructed to study the limitation of the EBMs.

According to the literatures, there is only a little attention in incorporating human behavioural changes in epidemiology. The literatures that have been reviewed in this study can be divided into three parts: the studies of vaccination decision in disease modelling, the fearfulness of the infectious diseases, and the individual-based modelling. The current literatures do not integrate fearfulness and vaccination decision in the study of disease modelling. In fact, the fearfulness on the diseases would be an influence to the vaccination behaviour. From the review of the fearfulness on the diseases, we know that fearfulness is an anxiety contagious process (Epstein et al., 2008) and it will cause the feared individuals to have higher incentive to avoid the health threat (Neuberg et al., 2011). Since the fearfulness is a contagious process, it can be spread to the neighbourhood. The family, friends and neighbours may get feared as well when a feared individual is introduced in the population. This will then increase the number of individuals who take precautions to protect themselves from the diseases. The precautions discussed in this study included intensified hygienic care, self-isolation, and vaccination. From the review of the vaccination decision in disease modelling, Bauch (2005) has introduced the way to study vaccination behaviour which is through game theory. In game theory, vaccination decision is modelled as a social dilemma and imitation dynamics can be applied to model the vaccination decision. However, there is no literature shows the integration between fearfulness and vaccination behaviour in the study of epidemics. In fact, the fearfulness would influence the individuals' decision to whether or not to vaccinate. Thus, in this thesis, the fearfulness and vaccination decision are integrated in the conventional SIR model. Besides, as human behaviour is involved in this study, the heterogeneity of the population becomes a concern. The EBMs have limitation in capturing the heterogeneity of the population, instead, the population is assumed as homogenous. In order to overcome this limitation, the review of the individual-based modelling

is done as well. Individual-based modelling is an approach to capture the heterogeneity of the population in the study. Hence, in this study, there are two modelling approaches been used, equation-based modelling and individual-based modelling.

In Chapter 3, the model formulation is discussed. As mentioned before, there are two modelling approaches in this study. In Chapter 3, the characterization of the problem is first presented. Assumptions are made as the basis of the compartmental Disease-Behaviour model. A compartmental diagram is drawn to visualize the interactions of the compartments in the Disease-Behaviour model. There are five compartments in the Disease-Behaviour model, namely Susceptible, Infected, Feared, Vaccinated, and Recovered. The susceptible individuals will either get infected by the disease viruses or acquire the fear on diseases or stay as susceptible in the population. The infected individuals will infect the others and they will be recovered after the duration of infectious. The feared individuals are given the opportunity to make their vaccination decision. If they decide to engage in vaccination program, they will be moved to the compartment of Vaccinated. Oppositely, if they do not want to vaccinate, they will be stayed as feared and take the other precautions. They may be infected by the disease viruses as well at a lowered disease transmission rate. On the other hand, the vaccinated individuals will become susceptible again after the duration of vaccine's effectiveness. Besides, a flow diagram is drawn to visualize the vaccination decision making process. From the compartmental model, a set of ordinary differential equations is formed to describe the model mathematically. Each of the processes is transformed to the equations. The formation of imitation dynamics equation also presented. For the individual-based modelling approach, a flow diagram is drawn to describe the processes in compartmental model. The flow diagram helped to set the commands to the agents in the IBM in order to allow the agents to move and behave.

Chapter 4 described the implementation of both EBM and IBM. Simulink which integrated with MATLAB is used as the platform to implement the EBM. To implement the EBM, a block diagram is constructed in Simulink and the solver used in this model is ode45 which is a standard solver for ordinary differential equations. On the other hand, the review on the different individual-based modelling platforms, GAMA, NetLogo, and Repast, is done in this study. NetLogo is selected as the platform in this study to construct the IBM. NetLogo is a user-friendly platform which provides visualization and interface to the users. Besides, NetLogo provides lower computational cost in comparison with GAMA and Repast. Besides, NetLogo cost lesser in term of the computational performance compared to GAMA and Repast due to the complexity of the processes in both GAMA and Repast. The interface of the IBM in this study consists of four sections, namely input (users are required to enter the parameters values), operations (buttons to carry out the operation of the model), results (shows the results of the simulation), and environment view (visualize the interactions of the individuals in the environment). In this model, the individuals are carrying two random numbers which represent their unique health state and mindset. These random numbers are generated by uniform distribution and they will be updated at every time step.

After the models are implemented, the results of the simulations are presented in Chapter 5. A delay of the peak in the infectious curve is occurred in the Disease-Behaviour model compared to the conventional SIR model. This delay happened when the fearfulness and vaccination decision are integrated in disease modelling. The results from both EBM and IBM are compared and the error between these models is calculated. RMSE is used to calculate the error and it is found to be 0.8207. The simulations results from both of the models are compared to the actual incidences retrieved from Sarawak Weekly EpidNews, Sarawak State Health Department.

From the results of the comparisons, we observed that the lowest RMSE is produced in both models when the value of the parameter  $\alpha$  (probability of an individual to acquire fear) is set as 0.5. However, the IBM produced a lower RMSE than EBM when it is compared to the actual incidences. This is due to the heterogeneity captured in the IBM. The heterogeneity of the population captured in the IBM caused it to be closer to the real world environment. Hence, it produced a more fitted result to the actual incidences. We further investigated the  $\alpha$ -value in the IBM and it is found that the  $\alpha$ -value is fall between the range of 0.5 to 0.9. The RMSE is found to be 0.1793 when  $\alpha$  is set to 0.8876. However, the value of RMSE in this study is still considered high. The model assumed the patients who recovered will gain immunity and they will not be susceptible again. This induced the infected population to be induced after week 22. This is opposite from the actual incidences. Hence, the RMSE is high in this study.

As mentioned before, there are two groups of individual, one receives more or complete information (named as  $M$ ) and another receives less or incomplete information (named as  $L$ ). The results shown group  $L$  has more infected cases compared to group  $M$ . This is due to the lower mindset and health state of the individuals getting less or incomplete information. As they have lower mindset and health state, they have lower incentive to take the precautions to avoid the diseases and hence easier to get infected.

## **6.2 Contributions**

In this thesis, human behavioural changes are incorporated in the conventional SIR model. The Disease-Behaviour model in this study consists of the integration of fearfulness on the diseases and the individuals' vaccination behaviour. This new integration describes how the vaccination decision influenced by the fearfulness. The incorporation of the fearfulness and vaccination

behaviour also shows the reduction of infected cases in comparison with the conventional SIR model. Besides, in this study, we implemented an IBM to capture the heterogeneity of the population where it helped to overcome the limitation of the EBM.

Apart from the contribution on the study of epidemics, the public health organizations can get benefits from the Disease-Behaviour model as well. From the model, the public health organizations can have an idea on how much awareness and fearfulness should be spread in the population in order to reduce the infected cases. They can organize the awareness program and vaccination program more effectively. With the Disease-Behaviour model, the numbers of the feared individuals and the vaccinators will be known. With these numbers, the public health organizations can set their target in the programs held.

### **6.3 Limitations**

In this thesis, the probability of an individual to acquire fear ( $\alpha$ ) could not be retrieved from Sarawak Weekly EpidNews, Sarawak State Health Department. Through the simulation in IBM, it is found that  $\alpha$  is in the range of 0.5 to 0.9. However, this range of value is yet to be validated. Besides, the vaccination programs in this study are targeted for the adults. The Disease-Behaviour model is implemented to study the infectious diseases where the adults can make their vaccination decision on their own. Childhood infectious diseases are not considered in this study. Although the IBM is able to capture the heterogeneity of the population, however, the environmental factors which cause the disease transmission are not included in this study. In addition, the model also did not take into account of demographic factors such as education background, birth rate and death rate. Instead, this study is focused on the mindset and health state of the adult population.

## 6.4 Future Work

This study incorporated human behavioural changes in the study of the spread of infectious diseases with the integration of fearfulness on the diseases and vaccination behaviour. However, some refinements can be carried out in the future to improve the current study discussed in this thesis.

As mentioned in Section 6.3, the  $\alpha$ -value is yet to be validated. As it gives a significant impact in the model, the validation of this parameter should be carried out. It can be validated through questionnaire or survey. The validation can be done through the cooperation with public health organizations.

In addition, the model can be modified to study childhood vaccine-preventable diseases such as chickenpox. In this case, the parents will be making the vaccination decision for their children. The children who take the vaccine once they are born will be moved to the Vaccinated compartment. Also, since IBMs can capture the heterogeneity of the population, the demographic factors and environmental factors can be studied.

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## APPENDICES

### Appendix A

Example of Prisoner's Dilemma (Miekisz, 2008):

After a bank robbery, there are two suspects been caught and interrogated by the police. The police are offering two strategies for the suspects which are defection (D) and cooperation (C).

The following deals have been offered to the suspects separately:

- i. If a suspect testifies against his partner which is a defection strategy (D), and the other does not choose the same strategy as him (C), his sentence will be reduced by five years.
- ii. If both suspects testify which is a strategy of defect (D), they will get a reduction of one year.
- iii. If both suspects are cooperate to each other and do not testify, they will get a reduction by three years because the police are lack of hard evidence.


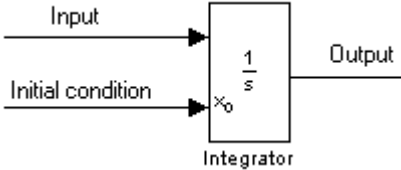


A payoff matrix is obtained:


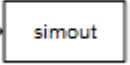
|     |   |   |   |
|-----|---|---|---|
|     |   | C | D |
| U = | C | 3 | 0 |
|     | D | 5 | 1 |

Strategy C is dominant strategy. As we can see that strategy C gives the lower payoff than strategy D gives, regardless of a strategy that other player chosen. Thus, strategy D is the only Nash equilibrium in this game. This is a typical social dilemma game because the players will choose a strategy which does not provided them with the best payoff.

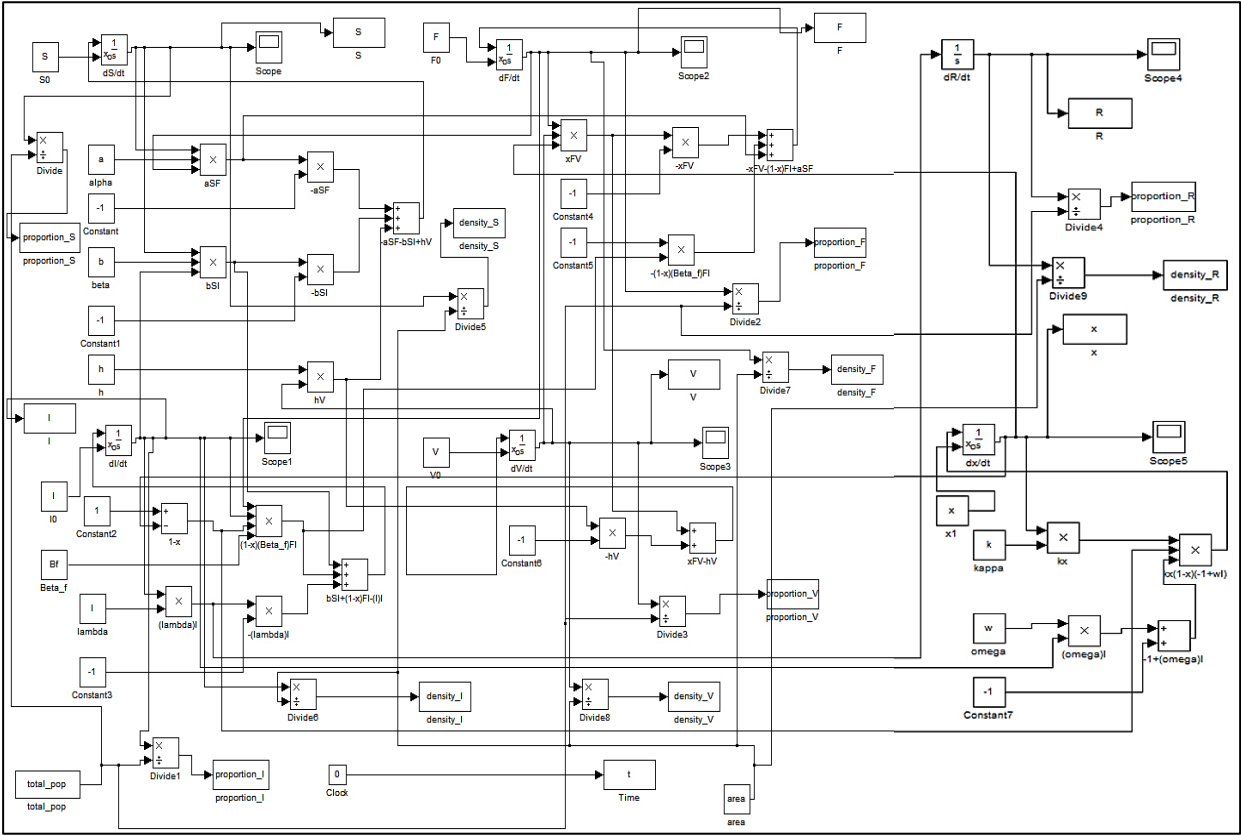
## Appendix B

### List of the definition and functions of the block libraries used in Simulink.

| Block library   | Definition and functions   |
|---|--|
|  <p>Integrator</p> | <ul style="list-style-type: none"> <li>• Integrator is classified in continuous system.</li> <li>• The input variable of integrator is with respect to time. In the case of this study, the governing equations served as the input of its respective integrator.</li> <li>• The output of this block is the value of the integral of its input.</li> <li>• In this study, the initial conditions have to be defined by the modelers. There are two ways to define the initial condition. First, the users can set the “initial condition source” as internal and input the initial value. Second, the users can specify the “initial condition source” as external and an external port will be appeared in the input port of the integrator block as shown in the figure below. Through this way, the initial condition can be changed easily by the users and it provides the initial condition for the governing equations.</li> </ul> <div style="text-align: center;">  </div> |
|  <p>Product</p>  | <ul style="list-style-type: none"> <li>• Product is classified in Math Operations.</li> <li>• There are many multiplication processes in the model in this study. Thus, the block of “Product” is widely used in constructing the model.</li> <li>• The inputs of this block can be varies in term of behaviour, for instance, scalar * scalar, scalar * non-scalar, and non-scalar * non-scalar. The behaviour of scalar * scalar is used in this study.</li> <li>• The number of inputs of this block can be controlled by the users. For example, for the term of <math>-aS(t)F(t)</math>, three inputs are required in order to carry out the multiplication.</li> </ul>   |
|  <p>Constant</p> | <ul style="list-style-type: none"> <li>• Constant is classified in Sources.</li> <li>• Constant is used to represent the coefficients of the equations. It can be used as a number or can be defined as a variable. For instance, <math>\alpha</math> served as a constant in the term of <math>-aS(t)F(t)</math>. In</li> </ul>   |

|  |   |
|--|---|
|  | <p>this case, <math>\alpha</math> is defined as a variable instead of a number. The value entered to this variable will be load to all variable named <math>\alpha</math> in the model. By assigning <math>\alpha</math> as a variable, users do not need to enter the value for multiple times. Thus, the performance will be improved.</p>  |
| <br>Scope     | <ul style="list-style-type: none"> <li>• Scope is classified in Sinks.</li> <li>• Scope displays the results after the simulation stop. The results will be displayed as a plot with respect to simulation time.</li> </ul>   |
| <br>Workspace | <ul style="list-style-type: none"> <li>• Similar as Scope, Workspace is classified in Sinks as well.</li> <li>• Workspace allows users to store the simulation data in several formats which are array, structure, and structure with time. These data stored in workspace in Simulink will be load into the main workspace of MATLAB after the simulation stopped.</li> <li>• In this study, the data stored in workspace will be used to plot the graphs and analysis will be carried out based on the graphs.</li> </ul> |

# Appendix C



The complete Simulink block diagram of the model in this study.

## Appendix D

Pusat Pengajian Siswazah  
Centre for Graduate Studies  
Dekan/ Dean Prof Dr Ernest Cyril De Run



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29 September 2014

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Sarawak

Tuan/ puan

**Permohonan Kebenaran Mendapatkan Maklumat-Maklumat Berkaitan  
Penyelidikan Ilmiah Untuk Calon Sarjana Sains - Teoh Shian Li  
(14020047)**

Dengan segala hormatnya perkara di atas adalah dirujuk.

Dimaklumkan bahawa penama di atas merupakan pelajar bagi program Sarjana Sains dalam bidang *Computer Science* di Fakulti Sains Komputer dan Teknologi Maklumat, Universiti Malaysia Sarawak. Beliau telah mendaftar pada 7 Oktober 2013 dan dijangka menamatkan pengajian pada 6 Oktober 2015. Beliau sedang menjalankan penyelidikan bertajuk:

***"A Computational Approach in Epidemiological Game Theory"***

Sehubungan itu, saya memohon kerjasama dari pihak tuan untuk memberi kebenaran dan bantuan kepada beliau bagi mendapatkan maklumat berkaitan penyelidikan tersebut di organisasi tuan. Sekiranya terdapat sebarang kemusykilan, mohon menghubungi penyelia beliau iaitu Prof Madya Dr Jane Labadin dari Fakulti Sains Komputer dan Teknologi di talian 082-583734.

Sekian, terima kasih.

Yang benar

A handwritten signature in black ink, appearing to read 'Hadijah Bt Hj. Morni'.

Hadijah Bt Hj. Morni  
Ketua Penolong Pendaftar

s.k. - Fail Pelajar



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**The approval letter from Centre for Graduate Studies, UNIMAS to get the data from Department of Statistics, Sarawak.**