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THE DEVELOPMENT OF STOCHASTIC SIR AND S(I^mI^f)R MODELS FOR HETEROSEXUAL HIV AND AIDS DISEASE MAPPING IN MALAYSIA

SUFI HAFAWATI BINTI IDERIS

05-4506832 pustaka.upsi.edu.my Perpustakaan Tuanku Bainun Kampus Sultan Abdul Jalil Shah PustakaTBainun ptbupsi

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ABSTRACT

The purpose of this research is to develop an alternative method of relative risk estimation based on stochastic discrete time-space model. There are two main methods proposed which are stochastic discrete time-space SIR (Susceptible-Infected-Removed) model and $S(I^mI^f)R$ (Susceptible-[Infected male]-[infected female]-Removed) according to gender for HIV and AIDS. Firstly, the deterministic compartmental SIR model that is suitable for the transmission of HIV and AIDS is discussed. This model then is adapted to develop corresponding discrete time-space stochastic SIR model. This is followed by the discussion of the alternative method of relative risk estimation based on the stochastic SIR model. Furthermore, applications of the common methods such as SMR and Poisson-gamma using HIV and AIDS data from Malaysia is also discussed in this thesis and the results are compared in tables, graphs and maps. Subsequently, discussion on modelling of $S(I^mI^f)R$ model based on gender is discussed in the same regulation of discussion based on SIR in order to identify risk for male and female respectively. Finally, the results of analysis showed that the alternative relative risk estimation method based on the discrete time-space stochastic SIR model and $S(I^mI^f)R$ according to gender have small number of range for estimating relative risk which has been examined by using goodness-of-fit method compared to the other common approaches. As conclusion, the proposed models are better than to the common methods in estimating of relative risk. However, the SIR model can be used for the analysis of HIV and AIDS generally while $S(I^mI^f)R$ model is used to analyse relative risk specifically for gender. Besides that, the proposed model also takes into account the transmission process of the disease while allowing spatial adjustment between risks in adjacent areas. The disease risk map in this study can be used as a tool to identify states that need more attention and further action by authorities at the same time to give awareness to society about the risks in the area where they live. Furthermore, this improvement of disease mapping is able to be used as a medical or inquiry tool in any corresponding HIV and AIDS research and development study.

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PEMBANGUNAN MODEL STOKASTIK SIR DAN S(I^mI^f)R BAGI PEMETAAN PENYAKIT HETEROSEKSUAL HIV DAN AIDS DI MALAYSIA

ABSTRAK

Kajian ini bertujuan membangunkan kaedah alternatif bagi penganggaran risiko relatif berdasarkan model masa-ruang diskrit stokastik. Terdapat dua kaedah utama yang diperkenalkan iaitu model masa-ruang diskrit stokastik SIR (*susceptible-Infected-Removed*) dan S(I^mI^f)R *(Susceptible-[Infected male]-[infected female]-Removed)* mengikut jantina bagi HIV dan AIDS. Pertama, suatu model kompartmen SIR bagi HIV dan AIDS dibina berdasarkan biologi jangkitan penyakit. Model ini kemudiannya disesuaikan bagi membina model diskrit masa-ruang stokastik SIR di mana bilangan jangkitan baharu bagi HIV dan AIDS adalah stokastik. Kemudian, kaedah alternatif penganggaran risiko relatif berdasarkan model SIR baharu diperkenalkan. Tambahan lagi, aplikasi kaedah biasa seperti SMR dan Poisson-gamma menggunakan HIV dan AIDS data dari Malaysia juga dibincangkan dalam kajian ini dan keputusannya dibandingkan di dalam jadual, graf dan peta. Seterusnya, model S(I^mI^f)R berdasarkan jantina turut diambilkira mengikut aturan perbincangan yang sama seperti SIR bagi mengenal pasti risiko HIV dan AIDS untuk lelaki dan perempuan. Akhir sekali, hasil analisis menunjukkan alternatif baru anggaran risiko relatif berdasarkan diskrit masa-ruang stokastik SIR model and S(I^mI^f)R mengikut jantina yang diperkenalkan mempunyai nilai julat g*oodness-of-fit* yang lebih kecil berbanding kaedah biasa. Kesimpulannya, model yang diperkenalkan adalah lebih sesuai bagi menganggar relatif risiko penyakit berbanding kaedah biasa. Walau bagaimanapun, model SIR adalah digunakan bagi analisis HIV dan AIDS secara amnya, sementara model S(I^mI^f)R pula digunakan untuk menganalisis risiko relatif HIV dan AIDS spesifikasi bagi jantina. Selain itu, model baru yang diperkenalkan juga mengambilkira akan proses jangkitan penyakit sementara membenarkan pengiraan kovariasi dan kawalan ruang di antara risiko kawasan sempadan. Peta risiko penyakit yang dihasilkan dalam kajian ini dapat digunakan sebagai alat untuk mengenal pasti negeri-negeri yang memerlukan tumpuan dan tindakan yang selanjutnya oleh pihak berkuasa pada masa yang sama memberi kesedaran kepada masyarakat mengenai risiko di kawasan yang didiami. Tambahan lagi, penambahbaikan ini juga dapat digunakan sebagai medium perubatan atau penyelidikan dan pembangunan kajian HIV dan AIDS yang berkaitan.

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LIST OF ABBREVIATIONS

AIDS	Acquired Immune Deficiency Syndrome
ART	Antiretroviral Theraphy
ARV	Antiretroviral Drugs
CAR	Conditional Autoregresive
CDC	Centre of Disease Control and Prevention (US)
DNA	Deoxyribonucleic Acid
GOF	Goodness-Of-Fit
HIV	Human Immunodefiency Virus
IDU	Injected Drug User(s)
MCMC	Markov Chain Morte Carlo
MOH	Ministry of Health
NSEP	Needle and Syringe Exchange Programme
OST	Opiate Substituition Theraphy
PLHIV	People Living With HIV
RNA	Ribonucleic Acid
SEIR	Susceptible-Expeosed-Infected-Recovered
SEIRS	Susceptible-Expeosed-Infected-Recovered-Susceptible
SI	Susceptible-Infected
$S(I^mI^f)R$	Susceptible-(Infected male)-(Infected female)-Removed
SIR	Susceptible-Infected-Removed

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SIS	Susceptible-Infected-Suscebtible
SMR	Standardized Morbidity Ratio
UNAIDS	United Programme on HIV
UNICEF	United Nations International Children's Emergency Fund
WHO	World Health Organization

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CHAPTER 1

INTRODUCTION

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1.1 Research Background

Disease mapping is a prevalent method used for more than two decades to display the geographical distribution of disease occurrence (Sasivimol et al., 2004). Mapping can be defined as a collection of spatial defined objects. It is simply a display of the spatial properties of a set of objects on a map. This mapping method could be a fundamental tool to show the areas affected by the epidemic using the interpretation

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of coloured maps. Disease mapping is also used to group the information in the data for all region in the study area into several group so that the region in the group has a similar risk (Nuzlinda and Abdul Aziz, 2007).

Disease mapping has two prevalent uses which are thing away noise to draw maps and as a method to assess specific hypotheses concerning incidence. Based on Olaf (2004), disease mapping, disease clustering, and geographical correlation analysis are the types of study focus that are featured in spatial epidemiology studies.

In disease mapping, the method is aimed to estimate the risk areas throughout the region where the disease map is used to highlight the areas of high or low disease occurrence. In spatial statistics, the terms of disease mapping refers to the spatial representation of morbidity and mortality rates across a region (Silva and Dean, 2012).

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Meanwhile, the ecological analysis focuses on the analysis of the geographical distribution of a disease and measure the explanatory factors. This distribution is also carried out at an aggregated spatial level. Another study focus for spatial distribution is disease clustering. Cluster means a group of things of the same kind that are very close together. This spatial distribution concerns the analysis of grouping the health-related events that are temporarily related and in the proximity area.

This study will focus more on the disease mapping to estimate and present the summary in measuring the epidemiology of HIV and AIDS by showing the areas of high and low risk of the disease in Malaysia. In disease mapping, the fundamental topic to be discussed and applied is the relative risk estimation. Therefore, this research aims to introduce the alternative method of relative risk estimations based on

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stochastic SIR (Susceptible-Infected-Removed), and S(I^mI^f)R (Susceptible-[Infected male]-[infected female]-Removed) for the transmission of HIV and AIDS respectively.

Firstly, the deterministic compartmental SIR models for HIV and AIDS are discussed and represented mathematically by a system of difference equations. These models are then adapted to develop a corresponding discrete time-space stochastic SIR model where the number of newly infective HIV and AIDS are stochastic and assumed to follow a Poisson distribution. Then, an alternative method of relative risk estimation which is based on this stochastic SIR model is discussed. Furthermore, the applications of common methods such as SMR and Poisson-gamma using the data of Malaysia's HIV and AIDS are also discussed in this thesis and the results are compared in tables, graphs, and maps.

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Besides, the discussion on the modelling of S(I^mI^f)R model based on gender is also considered in this thesis. Next, the deterministic compartmental and stochastic S(I^mI^f)R model for HIV and AIDS are discussed as the previous SIR transmission model but it focuses more on the gender whether they are male or female so it can be related to heterosexual analyses of HIV and AIDS. By performing a detailed analyses according to the gender, we could identify and estimate the relative risk for male and female respectively.

Finally, by using range as method for goodness-of-fit (GOF) these alternative relative risk estimation methods proposed which are based on the discrete time and discrete space stochastic SIR and S(I^mI^f)R models could offer a better model for estimating the relative risk of HIV and AIDS. This is because the approach models have small number of range compared to other common approaches. These proposed

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method also consider the disease transmissions as well as the spatial correlations between the neighbouring study regions.

In this analysis, discrete time-space stochastic $S(I^mI^f)R$ model according to gender is an extension for discrete time-space stochastic SIR model. Where the SIR model can be used for the analysis of HIV and AIDS generally while $S(I^mI^f)R$ model is used to analyse relative risk specifically for gender.

1.2 Problem Statement

In Malaysia, the relative risk estimation methods that are used to represent high and low risks are still based on the total number of cases based on behaviour of the population such as injected drug users, sex workers, men who have sex with men, and transgender. These are categorized as the population with the highest risk (Global AIDS Response Progress, 2014) instead of the total numbers of the disease occurrence across the study regions. High risk of disease occurrence is represented by the large number of cases reported without considering the geographical or spatial area of the population as well as the size or other factors that could possibly affect the disease occurrence.

For HIV and AIDS cases, most of the studies discussed on the basic reproduction number (Roxana, 2006; Basavarajaiah et al. 2012). It is very scarce to find analysis of HIV and AIDS based on the relative risk of discrete-time deterministic, discrete space deterministic, and stochastic model. Therefore, this study

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would examine the relative risk estimation using discrete-time deterministic, discrete-space deterministic, and stochastic models as the new approach for HIV and AIDS cases in order to estimate the high and low risk areas for HIV and AIDS diseases in Malaysia.

1.3 Objectives of the Research

The objectives of this research are as follows:

1) To develop and propose a new discrete time-space stochastic model based on the difference equations in the form of SIR and $S(I^mI^f)R$ models of heterosexual infectious disease transmission for HIV and AIDS cases.

2) To propose an alternative method of relative risk estimation for heterosexual cases of HIV and AIDS based on SIR and $S(I^mI^f)R$ disease transmission models.

3) To compare the results of the relative risk estimation for HIV and AIDS based on the proposed discrete time-space stochastic SIR and $S(I^mI^f)R$ models with the SMR method and Poisson-gamma model.

4) To propose disease risk maps for HIV and AIDS in Malaysia.

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1.4 Significant of Study

The following are the significances of the disease mapping study specifically for HIV and AIDS in Malaysia.

1. It will facilitate the authorities to identify the states that need more attention and further action to reduce the incidence of cases.

2. This risk maps could be used as a tool for public health centre in order to reveal the affected zones by the epidemic.

3. It will contribute knowledge or ideas in the research and development field as well as in the medical study of HIV and AIDS.

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1.5 Organization of the Report

This report is divided into five chapters. Chapter 1 provides the background of the study and the problem statement. This is followed by the study objectives and the significance of the research.

Chapter 2 introduces the explanation of HIV and AIDS including the transmission phase from early stage of HIV until AIDS, biological aspects of HIV and AIDS, the diseases timeline, the signs and symptoms of the diseases, the situation of HIV and AIDS in Malaysia, and the prevention and control of the diseases. Moreover,

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this topic will discuss the spatial spread of HIV and AIDS, the previous modelling disease transmission, and the analysis of disease mapping which considers the track-count data analysis. The analysis of disease mapping includes the explanation of the existing models such as Standardized Morbidity Ratios (SMR) method and Poisson-gamma model.

Next, Chapter 3 explains the methodology of the research. It begins with the discussion of the common and existing compartmental models of the diseases and followed by the compartmental and deterministic SIR model for both HIV and AIDS transmission, the stochastic SIR models for new infective HIV and AIDS, and continued with the compartmental $S(I^mI^f)R$ models for the transmission of HIV and AIDS according to gender, the stochastic $S(I^mI^f)R$ models of HIV and AIDS transmission for new infective male and female, and the last section will discuss in details about the relative risk estimation method based on the proposed stochastic models.

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Chapter 4 initially presents and demonstrates the results of the relative risk estimation for disease mapping by applying the existing methods and followed by the analysis using the proposed models which are discrete time-space stochastic SIR and $S(I^mI^f)R$ models. All analyses are based on the observation of heterosexual cases of HIV and AIDS discrete-time and discrete space data in Malaysia. Furthermore, the related findings are presented and compared in tables, graphs, and maps.

Finally, Chapter 5 summarizes the findings of the thesis and discusses the conclusions, contributions, and some recommendations for future work.

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CHAPTER 2

LITERATURE REVIEW

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2.1 Research Background

This chapter discusses the literature related to the statistical analysis of HIV and AIDS. The first section discusses the immunology of HIV and AIDS. This is followed by the explanation of the spatial spread of the disease. Moreover, the current situation of HIV and AIDS in Malaysia and the prevention and control of the disease are

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briefly presented. Finally, the modelling and the analyses of the diseases transmission and disease mapping are discussed.

2.2 Human Immunodeficiency Virus (HIV) and Acquired Immune Deficiency Syndrome (AIDS)

Certainly, AIDS is a disease caused by HIV. HIV is a kind of retrovirus that infects the human immune system. It makes people more vulnerable to the infection and diseases by destroying or impairing the CD4 positive T cells and macrophages which function as the key components of the cellular immune system. This virus has the potential to deplete the progression of the human immune system and cause immune deficiency. Based on Holand (2013), each day, millions of CD4 positive T cells will be produced and act as the body defenses to help fight the invading viruses and germs inside the body. CD4 positive T cell is a type of lymphocyte cell that has glycoprotein called CD4 on its surface which is very crucial for human immune system and immune response. Immune deficiency happens when the human immune system could no longer fight the infection and diseases. As a result, some of the HIV positive will develop into AIDS. Typically, the development of AIDS symptoms would finally lead to death. Until today, there is no known cure for HIV and AIDS (Ram Naresh, 2008). A person who is infected with HIV will go through various phases towards AIDS and death (Herbert and James, 1992).

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HIV and AIDS are a direct transmitted diseases which are the most common form of any virus or diseases to be transmitted. Unlike indirect disease transmission, HIV and AIDS in Malaysia could transmit the virus via four major situations which are blood-to-blood or fluid, prenatal, injected drug use, and sexual contact. Direct transmitted disease occurs when there is a physical contact between a person who is infected with HIV or a person with positive HIV and a susceptible person. Figure 2.1 depicts the transmitted HIV cases reported in Malaysia since 1986 until 2012 according to mode of transmission.

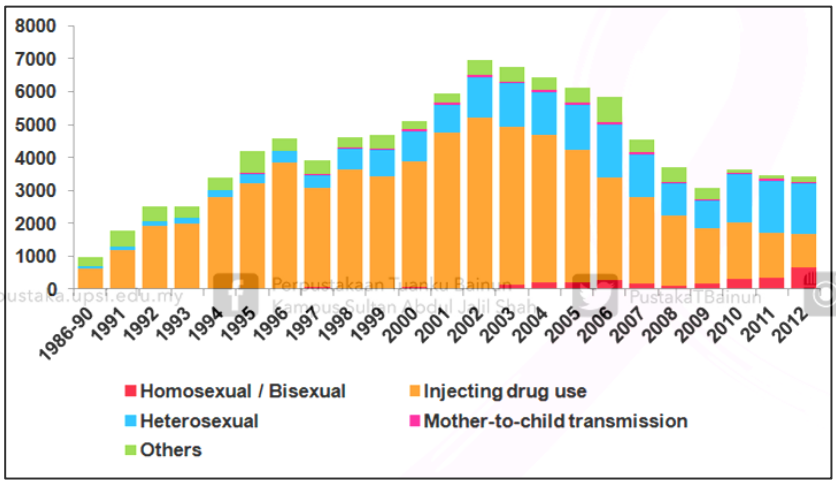


Figure 2.1. HIV Cases by Mode of Transmission (1986-2012). From Ministry of Health, 2014

As of the end of 2013, HIV in Malaysia is predominantly people with injected drug users as that case were the driven factor in the earlier phase of the HIV and AIDS spreading. However, the trend of infection has changed with increasingly number of infection caused by sex over the injected drug use cases started from year 2009 until 2012 as shown in Figure 2.1.

The transmission rate of HIV via sexual transmission happens when having unprotected sex including vaginal, oral or anal sex, and also by sharing sex toys which

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have been used by a person who is infected with HIV. Basically, sexual transmissions can be categorized into homosexual, bisexual, and heterosexual. Based on Global AIDS Response Progress (2014), heterosexual has the highest percentage of transmission in 2013 as shown in Table 2.1. Therefore, this analysis will be discussed on heterosexual as the main transmission.

Table 2.1

Percentage of New HIV Cases by Sexual Transmission

Sexual Transmission	**1990**	**2000**	**2010**	**2013**
Heterosexual	38 (4.9%)	902 (17.7%)	1,472 (40.3%)	1,743 (51.4%)
Homosexual/ Bisexual	3 (0.4%)	62 (1.2%)	301 (8.2%)	755 (22.3%)

Note. Adapted from "Malaysia GARPR 2014," Reported by Ministry of Health, 2014, p. 23.

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The third transmission of HIV is prenatal transmission where the infected mothers pass the infection to their child during childbirth, pregnancy or while breastfeeding their baby. A HIV-positive mother who is not being treated for HIV during pregnancy, labor or delivery, has a 25% chance of passing the virus to her baby (Centres for Disease Control and Prevention, 2013).

Next transmission with low transmission rate is through blood diffusion. As of today, HIV transmission through blood transfusion is extremely low due to the advanced technology. Since 1985 all blood in U.S. is screened for HIV antibodies, with positive units being discarded. Meanwhile, in South Africa, the blood donated

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for transfusions or blood products are screened and any contaminated blood is discarded. The probability of HIV transmission via blood transfusion in Malaysia is very low which is only 0.05 as shown in Figure 2.2 (Rozdiah, 2006).

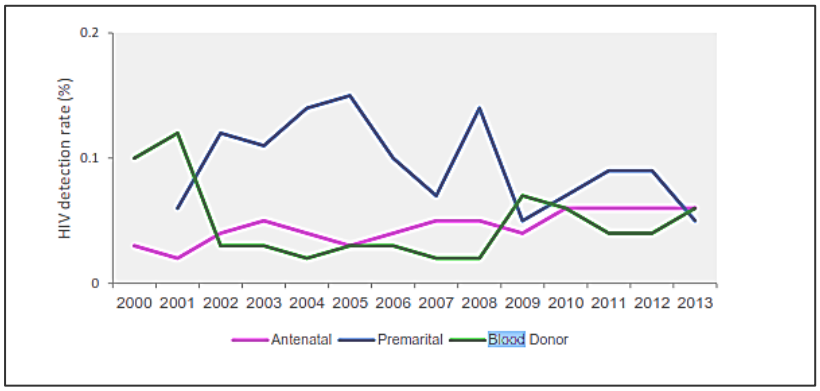


Figure 2.2. HIV Prevalence of Selected Screening Programmes, Malaysia 2000-2013. From Ministry of Health, 2014

In addition, this direct transmitted disease could spread the infections when the virus is passed from an infected person to a healthy person or known as susceptible person through direct physical contact or body fluids such as blood, semen (cum), pre-seminal fluid (pre-cum), vaginal fluid, and breast milk. HIV could enter the body via lining the anus or rectum, lining the vagina or cervix, opening to the penis, mouth that has sores or bleeding gums, cuts and sores and needles (syringes).

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2.3 The Immunology of HIV

2.3.1 Biological Aspects of HIV Infection

HIV is a virus which is also known as a retrovirus. It could infect multiple cells in the body and the major target is CD4 positive cells as the first phase. In this stage, HIV binds with CD4 positive cells and fuses within the cells to release its genetic material. The next phase is the reverse transcription. A special enzyme called reverse transcriptase changes the genetic material of the virus, so it can be integrated into the host's DNA. It then replicates itself, producing more infected cells. This retrovirus contains ribonucleic acid or called RNA. Replication occurs when an enzyme called reverse transcriptase is used to convert its RNA into deoxyribonucleic acid (DNA) and starts to duplicate itself using the cell's machinery. Figures 2.3 and 2.4 show the time course of the HIV infection for an infected adult, normal T cells, and infected T cells in human body respectively.

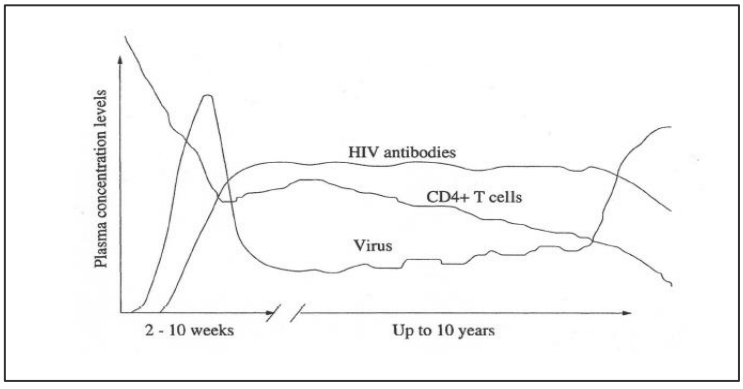


Figure 2.3. Time Course of HIV Infection for Infected Adult. From Matthias and Nafiu, 2010

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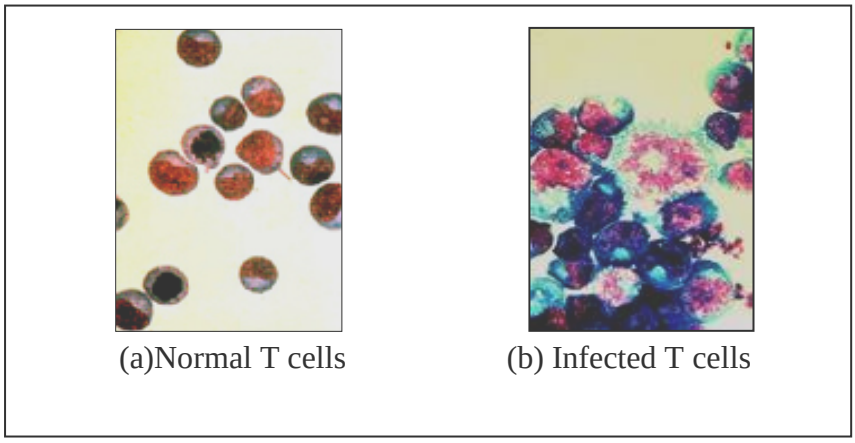


Figure 2.4. Normal T Cells (a) and Infected T Cells (b). From National Institutes of Health, 2013

HIV is a type of virus belongs to a subgroup of virus called lentiviruses. These viruses caused the infected persons to be unaware of their HIV infection. During this time, the CD4 positive cells are eventually killed by the HIV and the cells will gradually decrease. As a result, the infected person will be less able to fight the infections and eventually resulted in the development of AIDS.

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2.3.2 The Signs and Symptoms

Based on the fact by Herbert and James (1992), HIV infection has its own specific progression rule. Without any treatments, a person would certainly develop AIDS within a short period of time, depending on the individual. In the early stages of HIV, within two to four weeks after the HIV infection, most people will develop flu-like symptoms. This stage is called acute retroviral syndrome at an acute infection stage where the body will undergo natural responds towards the infection.

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The symptoms at this stage include fever, swollen glands, sore throat, rash, fatigue, muscle and joint aches, and headache. All these symptoms could last a few days to several weeks depend on the individual. During this period, virus is rapidly produced by using the CD4 positive cells to replicate itself and at the same time destroys the CD4 positive cells which eventually deplete the amount of CD4 positive cells in the body.

Next is, the clinical latency stage. During this stage, HIV virus continues to reproduce at a low level and develops in the infected person's body without showing any symptoms. This stage is also called as 'asymptomatic HIV infection'. Though the symptoms do not appear, the infected persons would be able to transmit the disease to others. After being asymptomatic for an average of five years, the patient will develop symptoms like oral candidiosis, hairy leukoplakia, herpes zoster, weight loss, diarrhea, persistent generalized lymphadenopathy, neurologic disease, and tuberculosis. At this stage, the infected person would probably die of these diseases. However, most people get one or more of the opportunistic infections or neoplasms which characterize AIDS.

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AIDS is the last stage of infections. At this stage, the immune system of the infected person is seriously damaged where the number of CD4 positive cells drop severely below 200 cells per cubic millimetre in the blood. Basically, without any treatments, people infected with AIDS would survive three years in average.

The symptoms that are commonly faced by patients while in this phase are caused by a lot of virus. Cytomegalovirus infection is a virus that usually lies dormant or inactive in the body of an infected person but it can be reactivated as the reactivation occurs when the immune system is weakened. Pneumocystis Carinii

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pneumonia is an infection that can cause lungs inflammation and toxoplasmosis of the brain.

Meanwhile, Kaposi's sarcoma is caused by cancer and it will develop from the blood vessels and appears as red or purple tumours or spots on the skin (CDC, 2013). Other symptoms are diarrhea that lasts for more than a week, mouth sores, anus, or genitals, red, brown, pink, or purplish blotches on or under the skin or inside the mouth, nose, or eyelids, memory loss, depression, and other neurologic disorders.

The average time for an individual to reach each stage are varied depend on many factors. Normally, an infected HIV person will head faster to the next stage due to his or her age, the HIV subtype (pre-antibody, asymptomatic and symptomatic), co-infection with other viruses, poor nutrition, severe stress, and genetic background.

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However, the factors that can slow down the process towards AIDS are by taking consistent therapy called antiretroviral therapy, keep on staying with HIV care, and closely obeying doctor's advice.

Figure 2.5 shows three basic stages for HIV infection which are acute infection as the first stage followed by clinical latency stage and last is AIDS stage where patient could survive at most two to three years before death caused by AIDS. Meanwhile Figure 2.6 shows timeline for HIV and AIDS together with the symptoms for every stage of infections.

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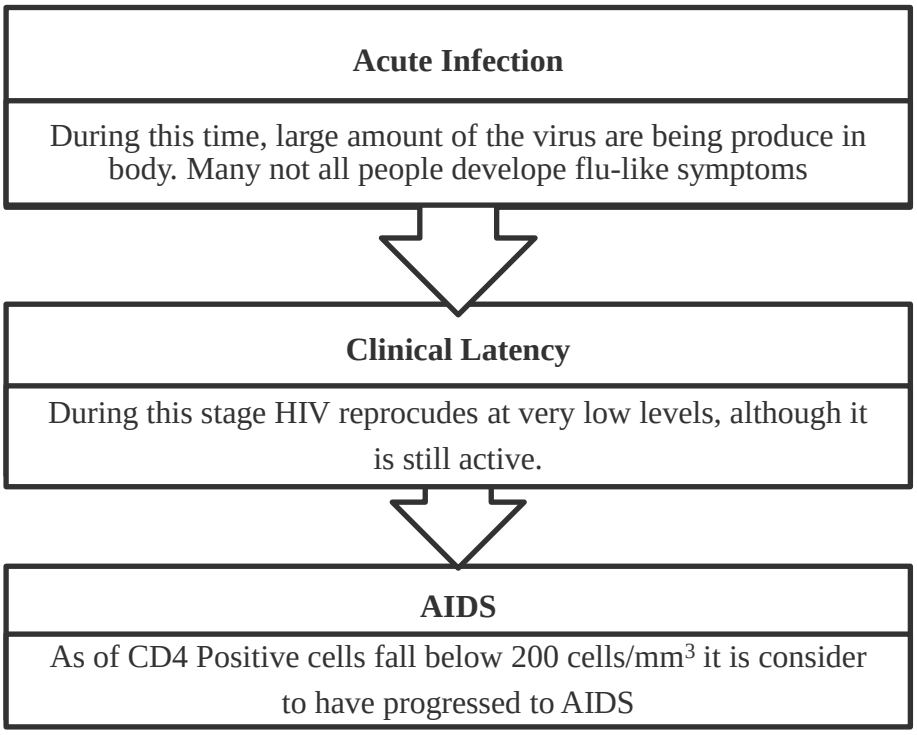


Figure 2.5. Stages of HIV Infections

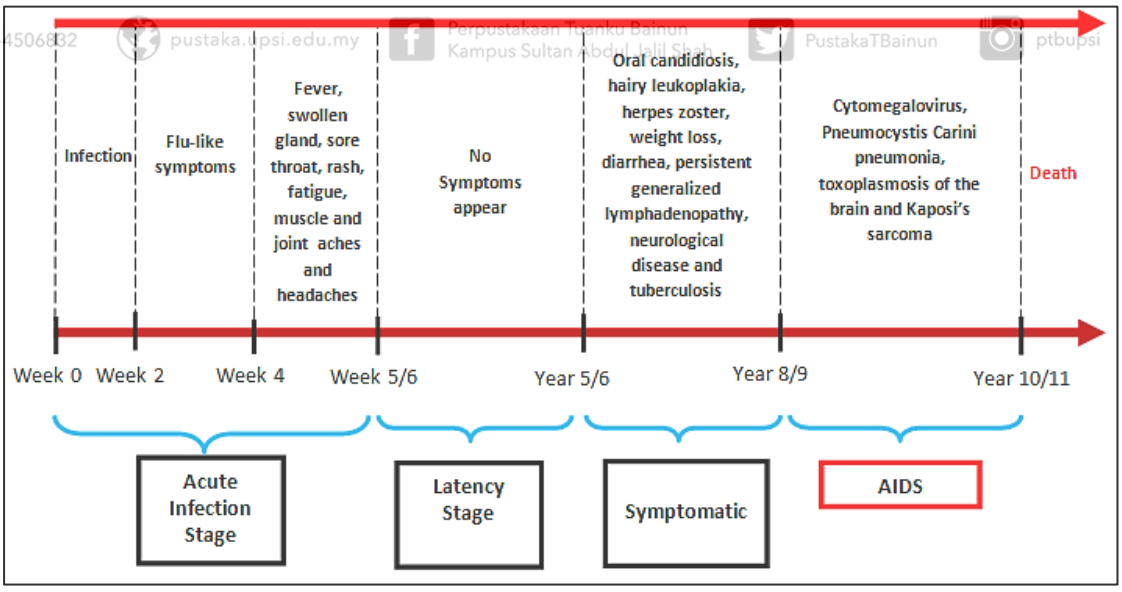


Figure 2.6. Timeline of HIV and AIDS Stages with Symptoms

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2.4 HIV Timeline

In 1981, one type of rare cancer among gay men in New York and California was reported which was referred as Kaposi's sarcoma (Herbert and James, 1992). At the same time, in New York City, youth men begin to have a kind of rash illness and symptoms such as fever, colds, flu-like symptoms, and pneumonia.

A few years later, The Centre for Disease Control and Prevention stated that it was a kind of disease associated with blood. In the first year, more cases were reported where there were over 1600 cases diagnosed with this kind of disease and almost 700 death cases.

Since the number of death increased drastically, medical experts worked hard to figure out the cause and cure. In 1984, the HIV virus was discovered by Institute Pasteur of France and after that, U.S. scientist stated that HIV is the cause of AIDS. Several years later, various efforts have been made to find the suitable vaccine to treat the disease. In 1987, more AIDS cases were reported. There were 71000 cases with 40 000 death cases. This showed that the epidemic continued to increase dramatically.

Based on United Nations program on HIV/Acquired Immune Deficiency Syndrome (UNAIDS) 2010, at the end of 2009, there were 33.3 million people lived with HIV compared to 1999 which were 27% higher. Figure 2.7 shows the global prevalence of HIV in 2009.

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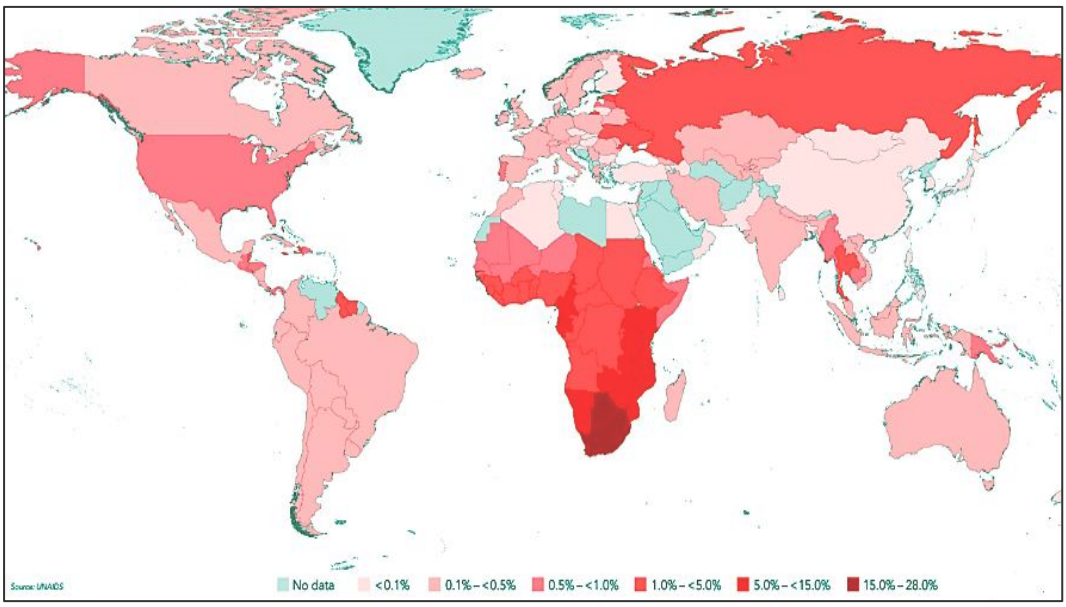


Figure 2.7. Global Prevalence of HIV in 2009. From UNAIDS, 2010

Table 2.2

Global Summary of the AIDS Epidemic

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Global Summary of the AIDS Epidemic (December 2008)

Number of people living with HIV	Total 33.4 million [31.1 million – 35.8 million] Adults 31.3 million [29.2 million – 33.7 million] Women 15.7 million [14.2 million – 17.2 million] Children under 15 years 2.1 million [1.2 million – 2.9 million]
People newly infected with HIV	Total 2.7 million [2.4 million – 3.0 million] Adults 2.3 million [2.0 million – 2.5 million] Children under 15 years 430 000 [240 000 – 610 000]

(Continue)

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Table 2.2 (Continued)

Global Summary of The AIDS Epidemic (December 2008)	
AIDS-related deaths	Total 2.0 million [1.7 million – 2.3 million] Adults 1.7 million [1.4 million – 2.1 million] Children under 15 years 280 000 [150 000 – 410 000]

Note. Adapted from Matthias and Nafiu, 2010.

In Malaysia, the first three cases of HIV were detected in 1986. Based on UNAIDS (2012), there were 1.7 million numbers of death caused by AIDS. While 2.5 million cases of newly infected, 34 million of the infected cases and 14.8 million people are eligible for HIV treatment, but only 8 million took the HIV treatment as shown in Table 2.2.

2.5 Spatial Spread of HIV

Based on Nafiu and Matthias (2010), HIV is categorized as an infectious disease which can be spread easily into communities and its distributions change in space as well as time which are affected by the mobility factor of the disease transmission. In addition, HIV transmission has strong relation with spatial distribution of the groups that have a high risk of HIV and AIDS.

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In Asia, HIV prevalence changes every certain year as discussed in UNAIDS report in 2010. As the year 1990 until 2009, most of the country in asia have less than 0.5 percent except Thailand which is the only country in this region with prevalence is close to 1 percent. Based on discussion by Global AIDS Epidemic report, an estimated 4.9 million people were living with HIV in 2009. An epidemic in the late 1990, up to 60 000 people were becoming newly infected annually has since receded. Most of national HIV epidemics appear to have stabilized for the next 1996 to 2009 . This can be attributed to the movement of patients from one area to another. The next section will discuss the history of HIV and AIDS and its situation in Malaysia.

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2.6 HIV and AIDS in Malaysia

In 1986, the first HIV case was detected in Malaysia. During that year, only three cases of HIV were detected in which one case of AIDS and one case of death were reported. Then after a couple of years, the cases of HIV, AIDS, and deaths increased dramatically.

Based on United Nations Children's Fund (UNICEF) Malaysia Communications (2009), since the first case was reported, a total of 11 234 people have died due to AIDS until 2008. In 2008, an average of 10 cases of HIV were reported each day and there were 10 new cases of HIV reported each day with a ratio of 2 females for every 8 males.

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In December 2010, over 80 922 people were living with HIV and at the end of 2010 the cumulative figure reported for HIV cases, AIDS cases and deaths were 91 362, 16 352 and 14 298 respectively. Thus, the reported people living with HIV (PLHIV) was 77 064 (Ministry of Health, 2011).

Figure 2.8 represents HIV and AIDS-related deaths reported in Malaysia between 1986 and 2011. It indicates the fluctuation in number of the cases reported and the notification rate for each 100 000 population in Malaysia. In this case, notifications are defined as the number of cases notified and it is expressed per 100 000 population for easy comparison among countries with different population sizes.

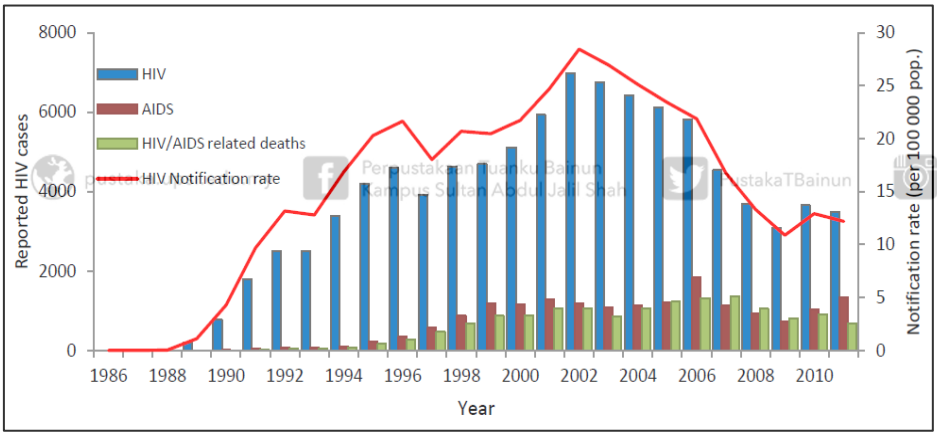


Figure 2.8. Reported HIV and AIDS-Related Deaths in Malaysia (1986 – 2011). From Global AIDS Response Progress Report, 2012

Based on the Figure 2.9, it can be clearly seen that there is a difference in the percentage of HIV cases between individual drug users (IDU) and sexual transmission from 1986 to 2011.

Based on Consensus Global AIDS Response Progress Report (2012), Malaysia is a country that recorded concentrated HIV epidemic with high infection rates of over 5% among most-at-risk populations especially injection drug users (IDU), sex workers, and transgender population.

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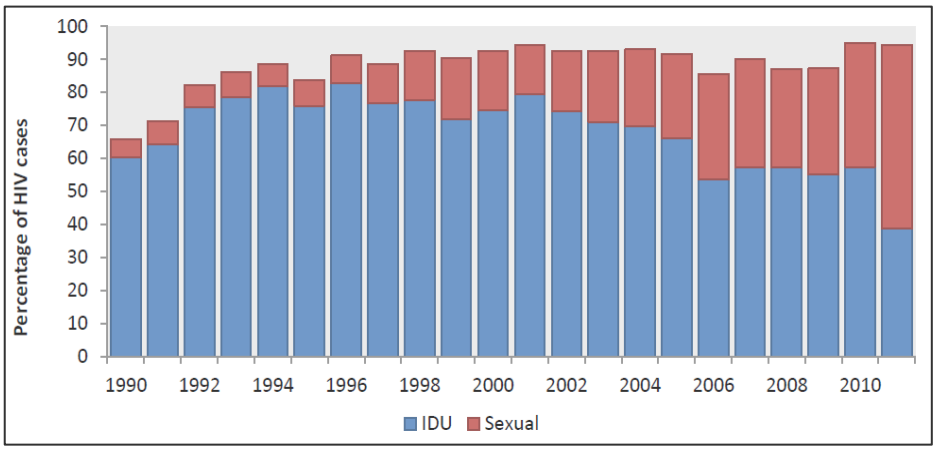


Figure 2.9. Reported HIV Cases Attributed to IDU and Sexual Transmission in Malaysia of the Year 1986 until 2011. From Global AIDS Response Progress Report, 2012

Furthermore, based on the collected data, there is a gap between the total number of males and females. The number of HIV prevalence for men is always greater than the number of females in each year. Figure 2.10 shows the gender-specific HIV prevalence in Malaysia from 1986 to 2011.

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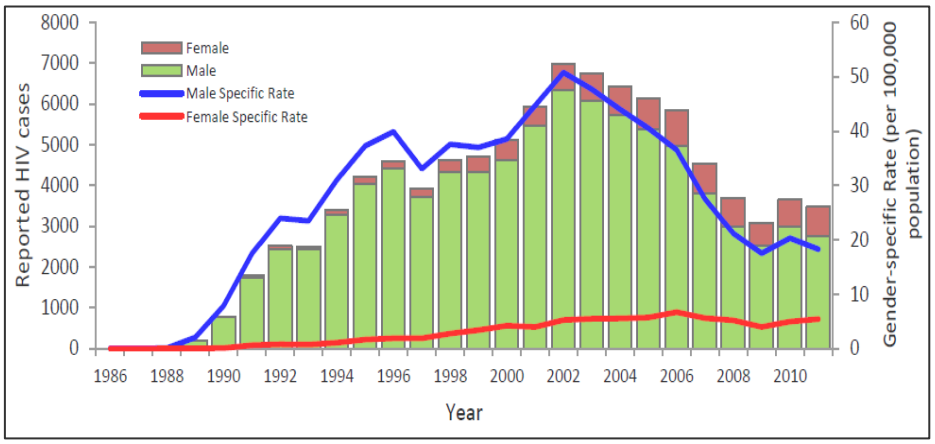


Figure 2.10. Gender-Specific HIV Prevalence in Malaysia (1986 – 2011). From Global AIDS Response Progress Report, 2012

Figure 2.11 shows percentage of four risk factors for HIV in Malaysia which are injected drug user (IDU), sexual transmission, vertical and indeterminate over the states in Malaysia. Here, vertical means mother-to-child transmission during pregnancy and breastfeeding from a mother to her child. Meanwhile, indeterminate

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case means cases by risk factor that are still under investigations and unidentified yet by Ministry of Health (MOH, 2014).

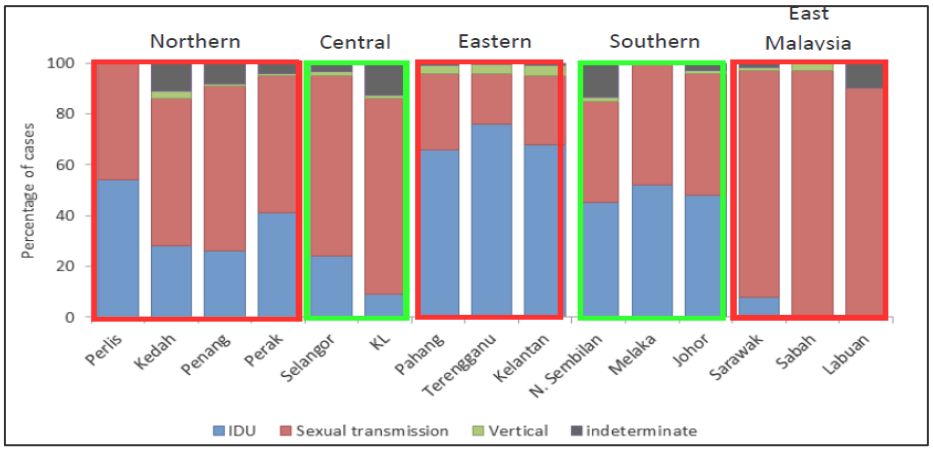


Figure 2.11. Newly Reported HIV by States in Malaysia in 2011. From Global AIDS Response Progress Report, 2012

With respect to geographical distribution in Figure 2.11, the total number of IDU and sexual transmission accounted a very high percentage for each state in Malaysia. It appears that some states especially in the states of Pahang, Terengganu and Kelantan are still driven by IDU whereas some states in northern which are Perlis, Kedah, Penang and Perak as well as southern region such as Negeri Sembilan, Melaka and Johor have shifted to more of sexual driven.

Meanwhile the state of Selangor and Federal Territory of Kuala Lumpur had used to be IDU driven but has turned to sexually driven. The states of east Malaysia which are Sarawak, Sabah and Federal Territory of Labuan have been predominantly sexually driven fron the beginning of the epidemic.

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2.7 Prevention and Control

After more than 20 years, HIV and AIDS have infected as many as 33 million people in the world (U.S. Department of Health & Human Services). The Ministry of Health Malaysia (2008) has implemented a wide range of prevention, treatment, and control of HIV and AIDS to ensure that the disease does not spread to uninfected people and reduce the morbidity for those who are infected with HIV. Changes in risk behaviour needs to be stopped or some action should be taken to prevent people from being infected with HIV and here are the prior steps to control the HIV infection (Ministry of Health Malaysia, 2008);

i. Not sharing needles and syringes for injecting drug users.

ii. Use condoms during sex for sexual partners of unknown HIV status or sexual partner with positive HIV.

iii. Perform voluntary HIV screening in health clinics if there is a need for doing risky behaviour especially people with HIV carrier.

There is no cure or vaccine yet to be found for HIV and AIDS. Nevertheless, there is a treatment called antiretroviral therapy (ART) that can slow down the growth of HIV in a patient's body. Nowadays, ART would be the best option for long-lasting viral suppression and subsequently, for the reduction of mortality rate (Matthias, 2010). Generally, ART uses different kinds of medication to slow down the HIV from growing and multiplying inside the body of an infected person. This therapy could help the infected person to live longer. Besides, it is also able to reduce the chances of an infected person to get non-HIV related illness and reduces the chances of transmitting the HIV to others.

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Medication alone is not enough, as patient should also live a healthy lifestyle. Those who are infected with HIV should undergo regular treatment in the medical profession. In addition, patients also need to practice regular exercises, avoid any alcohol, drugs or tobacco, and eat well-balanced and nutritious diet.

Malaysia already provides affordable access to clinical care through the public health system and will continue to do so. Two significant achievements have been accomplished: first, the availability and provision of first line ARV treatment at no cost for those who need it and second, the availability of ARV treatment for incarcerated populations, specifically for the prisoners with HIV as well as inmates in drug rehabilitation centres (Country Progress Report UNGASS, 2012)

In addition, Malaysia has started introducing HIV screening since 1985. All public health facilities provide free HIV screening facilities and the Anonymous HIV Voluntary Screening Programme was piloted in 2001 and later has been expanded nationwide in 2003. Since 2011, 19 804 people have accessed this facility to obtain their HIV status in which 57% were males and 65% of them were between the age of 20 and 39 (UNAIDS Global Report, 2012).

The Harm Reduction Programme which comprised of the Needle Syringe Exchange Programme (NSEP) and the Opiate Substitution Therapy (OST), remain the cornerstone of the Malaysian Government's HIV prevention strategy (Global AIDS Response Progress Report, 2012).

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2.8 Disease Transmission Model and Disease Mapping

In this section, the modelling for disease transmission and disease mapping are discussed. This includes the discussion on SMR method and Poisson-gamma model. This is followed by the discussion on the analysis of disease mapping which includes the common methods used in the relative risk estimation.

2.8.1 Modelling Disease Transmission Model

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Basically, there are two types of disease transmissions which are direct disease transmission and indirect diseases transmission. Both types of transmission are related to contact transmissions which are direct contact transmission and indirect contact transmission. Direct contact transmission involves physical contact between the infected person and susceptible person. Physical contact can be categorized as any contact by blood and body fluids of an infected HIV respondent to the susceptible person. In example, sexual contact, touching, and contact with body lesions.

While indirect disease transmission is not directly human-to-human touch, it involves vector for the disease transmission. The examples of diseases with indirect transmission are influenza, common cold, chicken pox, flu, and more. It could be easily spread through sneezing and coughing through air as the vector of transmission.

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Normally, in the study of infectious disease modelling, the transmissions could be constructed using SI model, SIS model, SIR model, SEIR model, as well as SEIRS model depends on the appropriateness of the diseases (Trottier and Philippe, 2000). These types of model can be categorized into direct disease transmission, where *S* indicates the susceptible, *I* indicates the infective, *E* is exposed, and *R* refers to removed or recovered. For direct disease transmission, the models usually refer to human population.

Moreover, direct and indirect disease transmissions can be written into two types of models which are deterministic model and stochastic model. Both types of models are very useful in the study of diseases infectiousness in the population (Trottier & Philippe, 2000). Compared to deterministic models, stochastic model depends on the individual possibilities of variation in risk of disease exposure studied. It is also used in study of disease mapping because in stochastic models the volatility coincidence or known heterogeneity is important for diversity in small or isolated populations. In this analysis, stochastic models for disease transmission is developed from deterministic models with difference equations.

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There are several steps to build a deterministic model. Firstly, it is important to have a realistic and a complete picture of the biology of the diseases studied. Secondly, the data collection are based on the demographic, epidemiologic, and biologic characteristics of the infection and the population. Lastly, selecting a suitable model. The epidemic process is deterministic where the behaviour of people in the study region is determined by the history as well as the rules which describe the deterministic model (Freud, 2012).

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To write the deterministic model, populations will be divided into subgroups which is also known as the compartments where it contains the assumptions about the nature and the rate of time for transferring from one compartment to another compartments (Freud, 2012). Compartmental model can be analyzed using either difference equations or differential equations. Difference equations in deterministic model describe the transitions between different disease compartments using discrete-time steps while differential equations consider the transitions for continuous rather than discrete-time intervals (Trottier & Philippe, 2000).

After making a deterministic formula either by difference or differential equation based on the deterministic or compartmental model, the next step would be calculating the stochastic mean population. Stochastic is a random probability. There are some probabilities at each time moving from one epidemiology class to another (Herbert & James, 1992). Stochastic models basically rely on among the individual chance variation in risk of exposure, disease and other factors (Trottier & Philippe, 2000).

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2.8.2 Disease Mapping

Disease mapping is a method commonly used by epidemiologist to understand the geographical distribution of a disease. Disease mapping aims to obtain the estimation of relative risk for each area across a region (Wakefield, 2006). In addition, disease mapping is also used to classify all states into different components in a map by using

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shading in order to demonstrate area with high or low level of risk (Nuzlinda and Abdul Aziz, 2013).

There are some common models used to estimate relative risk which are Standardized Morbidity Ratio (SMR), Poisson-gamma model, log-normal model, mixture model and so on. Traditionally, the ratio of observe to expected counts within tracts is called a standardized morbidity ratio (SMR) where the status of relative risk of an area respect to disease is the ratio of observed to expected counts. The other common method is Poisson-gamma model which is one of the earliest examples of Bayesian models used in the analysis of disease mapping. In Bayes method, the relative risk estimation is based on the posterior distribution which is defined as product of the likelihood functions and the prior distributions.

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Beside Poisson-gamma model and SMR method, log-normal model is a method used in estimating the relative risk which is assumed to follow Poisson distribution. A log-normal model for relative risk is more flexible where there is possibility for allowing spatial correlation between risks in nearby area compared to Poisson-gamma model. The log-normal model for relative risk is written as follows:

$$y_i \sim Poisson(e_i\theta_i)$$

$$\log\theta_i = \alpha + v_i$$

$$v_i \sim N(0, \tau_v^2)$$

Based on the equation of log normal, the number of newly infectives follow Poisson distribution as prior distribution where the relative risk is θ_i which comprises

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of α and v_i as heterogeneity random effects. The prior distribution for random effects v_i will follow normal distribution with mean zero and τ_v as the hyperparameter which follows gamma distribution as hyperprior distribution. A major drawback of gamma prior is this method is does not take into account the geographical location of the region where the model does not cope the spatial correlation (Mieke, 2014).

Next common method of relative risk estimation is mixture model which consider the risk at any area consists of contributions from a set discrete underlying risk components. The mixture model is assumed that the log-relative can be decomposed into three additive components which are one fixed component (v) and two mixing components (u, φ). Fixed component representing the unstructured heterogeneity which measures the overdispersion in an individual region. Meanwhile, the two mixing components are representing aspects of spatial correlation. The mixture model is formulated as follows;

$$\log \theta_i = \alpha + v_i + p_i u_i + (1 - p_i)\varphi_i$$

Where the priors used for the other components in this mixture models for all region *i* are specified as follows.

$$v_i \sim N(0, \tau_v^2)$$

$$p_i \sim Beta(0.5,0.5)$$

However, in this study the focus is on the relative risk estimation methods that are based on the common method which is Standardized Morbidity Ratio (SMR),

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followed by the Poisson-gamma model. These two methods are chosen for comparison purposes due to the characteristics of the model in which, the SMR is the traditional disease mapping method, while the Poisson-gamma model is the earliest example of Bayesian mapping. We are interested to investigate how the characteristics of our proposed model can offer a better method of relative risk estimation compared these two existing methods as well as to proposed a smoother map with less extreme values in relative risk estimation. These methods will be discussed further in the next chapter.

Basically in the study of disease mapping, there are two types of spatial data that are available for investigator, which are case-event data analysis and tract-count data analysis. Case event data are expressed as point locations such as residential or street addresses, post code, and the times of infections. This means that the case event data basically correspond to the data of disease occurrence which represents the detail of locations on a particular point at a time. This might also be referred as continuous data. When a small spatial scale become the interest, this kind of data would be very crucial.

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In spite of this, case event data is difficult to obtain due to certain factors that are hard to obtain with accurate details and maybe because of the confidential data need to be obtained primarily from the medical centre. Moreover, the case event data can be depicted as a map of the point of event location for the assessment of the differences in local disease risk and it is appropriate to convert these locations into a continuous surface and spatial model that use the case event data which describes long-range trend in risk (Lawson, 2005).

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Conversely, count data is the most common format data used in the study of spatial epidemiology. Basically, count data arise from the aggregation of case event (Lawson, 2005). A count is the number of study events or cases that occur in a given period where it involves only non-negative number (Bryan et al., 2008). For this type of data information of disease case is often presented in spatial aggregated form. In this study, the proposed surveillance method would be based on the tract count spatial data for a given time period and it is a discrete data with discrete space and time analysis.

In this study, we are interested on discrete time-space stochastic SIR and $S(I^mI^f)R$ models in which to overcome the shortcoming of SMR method and Poisson-gamma model. In addition, these proposed methods also consider the disease transmissions and spatial correlations between the neighbouring study regions.

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CHAPTER 3

METHODOLOGY

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3.1 Introduction

In this research, estimation of relative risk is used to demonstrate a map with the area of high and low risk of HIV and AIDS in Malaysia according to states. To estimate the relative risk of HIV and AIDS, this chapter introduces the common methods used in estimating of relative risk for disease mapping which are SMR method and Poisson-gamma model. This is followed by the common compartmental model for

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HIV and AIDS. Next, this topic will discuss about the compartmental model and stochastic SIR and S(I^mI^f)R models of disease transmission. These models will be fully described as approach tools to calculate the relative risk estimations. The last section will describe the method for the relative risk estimation based on stochastic SIR and S(I^mI^f)R models.

3.2 Traditional Approaches of Relative Risk Estimation of Disease Mapping

This section describes the SMR method and Poisson-gamma model in detail the methodology of relative risk estimation in disease mapping. These two methods are the most common methods used to produce disease maps and the latter represents one of the earliest application of Bayesian methodology in this context.

3.2.1 Standardized Morbidity ratio

SMR stands for standardized mortality or morbidity ratio where morbidity indicates the incidence and mortality indicates death. The SMR is a common measure of relative risk (Jane, 2002). SMR is used in disease mapping to estimate the relative risk estimation of a particular region in epidemiology. In many studies, the representation of disease mapping using relative risk is often implemented without considering the

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population size for the relevant areas (Samat and Percy, 2008). Therefore, in this study, the classical method of relative risk estimation is known as Standardized Morbidity Ratio (SMR) is used where the analysis will take into account the number of population size.

However, SMR has several drawbacks that make the interpretation of SMR become difficult. The SMR is a reliable measure of relative risk for large geographical regions such as countries or states, but may be unreliable for small areas such as counties (Jane, 2002). Moreover, the SMR is large in regions when there is a small population in size and vice versa. This is because the SMR depends on the expected value and the expected value depends on the total number of population (Lawson et al., 2000).

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Besides, the SMR would be zero for any region when no cases is observed. In this case, the zero value of relative risk indicates that there is no risk for the people in study regions infected by the disease though everybody has the chance to catch with the disease. These disadvantages of SMR is discussed in Lawson *et* al. (2003).

In this study of HIV and AIDS, Standardized Morbidity Ratio is defined as $\hat{\theta}_i = \frac{o_i}{e_i}$ where o_i is the observed number of HIV and AIDS cases and e_i is the expected number of HIV and AIDS cases for region *i*. It is used to estimate the relative risk where the probability of a person within a particular region contracts the disease is divided with the probability of a person in the population contracts the disease. The area of the disease map is divided into *M* mutually exclusive regions where $i = 1, 2, ..., M$ and each region is assumed to be homogenous with the own

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number observed. The expected cases which are being used to calculate the relative risk for region *i* are defined as follows:

$$e_i = N_i \frac{\sum o_j}{\sum N_j}$$

The observed number of disease cases could be find from health indicator from Ministry of Health Malaysia which is under the disease control department while the relative risk value could be counted using a particular formula as below for the study regions.

$$r_i = \frac{o_i}{N_i \frac{\sum o_j}{\sum N_j}}$$

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$$= o_i \times \frac{\sum N_j}{N_i \sum o_j}$$

$$= \frac{o_i}{N_i} \times \frac{\sum N_j}{\sum o_j}$$

$$= \frac{\left(\frac{o_i}{N_i}\right)}{\left(\frac{\sum o_j}{\sum N_j}\right)}$$

Thus, the relative risk can be calculate using the following formula:

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$$r_i = \hat{\theta}_i = \frac{\left(\frac{o_i}{N_i}\right)}{\left(\frac{\sum o_j}{\sum N_j}\right)}$$

Based on the formula of SMR above, N_i represents the population of region *i* and the summation of time *j* = 1, 2,…, *M*. As discussed earlier in Section 2.8.2.1, SMR has flaws that need to be addressed so that small districts could fit in the disease mapping and the SMR value will not be zero when there is no observed cases for a certain area or region. In order to overcome the drawbacks of SMR, many researchers have sought an alternative solution by introducing other better alternative methods for relative risk estimation in disease mapping, such as the Poisson-gamma model (Kismianti, 2009). Therefore, the analysis using Poisson-gamma model will be discussed in the next section.

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3.2.2 Poisson-Gamma Model

Based on Nurmalasari (2010), when the disease is rare, the numbers of diseases in each area are assumed to be mutually independent and follow Poisson distribution. Poisson distribution is a discrete probability distribution for the counts of event that occur randomly in a given time. When counts are assumed exchangeable, gamma distributions model is often chosen.

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In the study of relative risk, the Poisson-gamma used is basically based on the approach of Bayesian modeling and it is assumed to follow a distribution known as a prior distribution (Mieke, 2010). Basically in Bayes method, the prior distribution is used which is estimated from the data. A Poisson process is a counting process where the time interval of successive events or interarrival interval (X_i), has an exponential distribution function with random variables for some real $\lambda > 0$, each X_i has density $f(x) = \lambda \exp(-\lambda x)$ for $x \geq 0$. With this density, $P\{X_i \geq 0\} = 1$ where X_i can be regarded as a positive random variable. Furthermore Poisson gamma is also assumed to be independent.

In this model, y_{ij} is the number of new infective cases for county *i* at time *j* for $i = 1, 2, \ldots, M$ study region and $j = 1,2,\ldots,T$ time period, while e_{ij} is the expected number of new infective cases, and θ_{ij} is the relative risk parameter in the *i*th region where $e_{ij}\theta_{ij}$ is the mean of expectation of the Poisson distribution. y_{ij} is assumes to follow a Poisson distribution as below:

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$$y_{ij} \mid e_{ij}, \theta_{ij} \sim Poisson(e_{ij}\theta_{ij})$$

θ_{ij} is assumed to have a gamma distribution. A gamma prior distribution for the relative risk combines with the Poisson likelihood to give a gamma posterior distribution. In this case, the prior gamma is:

$$\theta_{ij} \sim Gamma(\alpha, \beta)$$

Based on Lawson (2003), hyperparameters α and β in prior gamma distribution are fixed otherwise the posterior distribution becomes more complex. The

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relative risk parameter, θ_{ij} has the following posterior distribution conditionally on y_{ij} as follows;

$$\theta_{ij} \sim Gamma(\alpha + y_{ij}, \beta + e_{ij})$$

And the posterior expectation of θ_{ij} is;

$$\frac{y_{ij} + \alpha}{e_{ij} + \beta}$$

Under the gamma distribution, the mean is $\frac{\alpha}{\beta}$ and the variance is $\frac{\alpha}{\beta^2}$. The hyperparameter are based on assumption that α and β had uniform hyperprior distribution as the hyperprameters are fixed. In this analysis, exponential distributions with mean 0.1 are applied on both hyperparameters as recommended by Lawson (2003). However, sensitivity analysis using different values of α and β (for example of number means used in sensitivity analysis are 0.3, 0.5 and 0.7) does not effect on the output of posterior expected relative risk for all study regions and for all time periods based on Poisson-gamma model. This means that the results of relative risk by using different value of means will give similar output as 0.1 mean as recommended by Lawson (2003).

In statistical analysis, smoothing method is a statistical technique for removal of short term irregularities in a time-series data. When data collected over time displays random variation, smoothing method can be applied to reduce or cancel the effect of these variations as well as can reveal more clearly the underlying trend, seasonal and cyclic components. In the study of relative risk based on Poisson-gamma

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model, the maps are more smoother with less extreme values for relative risk estimates compared to SMR method.

However, a major drawback of gamma prior is, there is no possibility of allowing spatial correlation between risk in nearby areas and the covariate adjustment is also difficult (Mieke, 2014). Therefore, many other methods have been introduced to overcome the drawbacks of prior gamma method (see, for example, Lawson, 2003; Samat and Percy, 2008).

3.3 Common Compartmental Model for HIV and AIDS

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This section introduces a common compartmental model used for HIV and AIDS diseases. HIV transmission usually occurs after a person is exposed to the first phase of HIV which is pre-antibody. It will then proceed to the next phase until the AIDS phase. This infectivity will persist throughout life. As of today, no cure for HIV has yet to be found. There is no vaccine that could prevent HIV infection. Nevertheless, there is a therapy called antiretroviral therapy (ART) to slow down the process of infection by preventing the virus from multiplying and destroying the immune system. However, even though ART could slow it down, the virus still remains in the body and infect the body of the infected person.

Based on the literature (Herbert and James, 1992 and Roxana, 2006), most HIV modelling divides the population according to its cohort. Individuals with the

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same cohort are supposed to have the same characteristics that are utilized in the model of HIV which is normally determined according to the disease stage; susceptible, infected, and removed.

This research will follow the Lawson (2006) theory by which used the SIR model for HIV and AIDS in which at any given time, there is a number of infective, a number of susceptible, and a number of removed humans from population. Lawson used the term susceptible-infective-removed for the SIR model of direct disease transmission. The susceptible represents the 'at-risk' population, infective represents the disease morbidity or case incidence, while removed represents the disease mortality. As discussed previously in Section 2.8.1, the SIR model can be in the form of susceptible, infected, and recovered. However, in this case, there is no recovered case. Instead, the process will end at the removed compartment.

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Basically, in common HIV and AIDS compartmental models, the compartments involved are susceptible, infected, and removed (see for example Herbert and James, 1992; Roxana, 2006; Basavarajaiah *et* al, 2012 and Leigh, 2004). A study by Herbert and James (1992) considered two level of activities in the analysis which are very active and active homosexual man.Where six compartments were included which were susceptible, pre-antibody, asymptomatic, symptomatic, AIDS, and death.

In another study by Trottier and Philippe (2000), the SEIR for deterministic model considered represents susceptible-exposed-infected-recovered. Figure 3.1 shows the common models used for infectious diseases.

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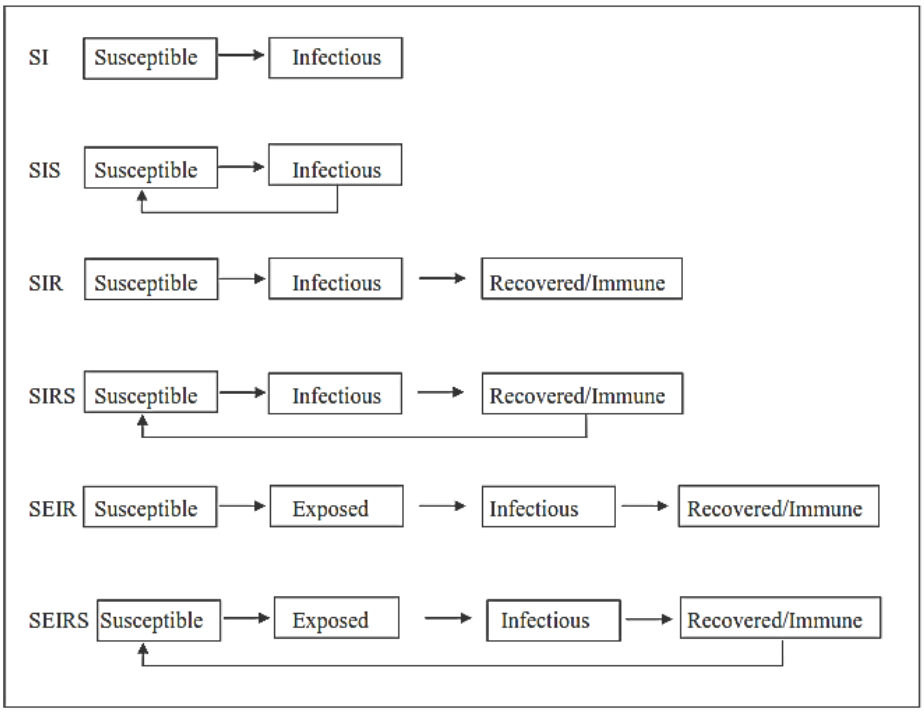


Figure 3.1. Common Models for Infectious Diseases. Adapted from Trottier and Philippe, 2000

Based on a study by Leigh (2004), active sexual population could be considered in two groups which are susceptible individuals and infected individuals. Figure 3.1 indicates the SI basic model of HIV transmission. In this model, it only uses the compartments of 'S' and 'I' to describe the transmission process without considering the removed cases for HIV and AIDS.

The arrow from susceptible to infected represents the rate of new infections occurred. Therefore, the analyses of HIV and AIDS in this research will discuss the transmission of the diseases based on SIR disease transmission according to Lawson (2006).

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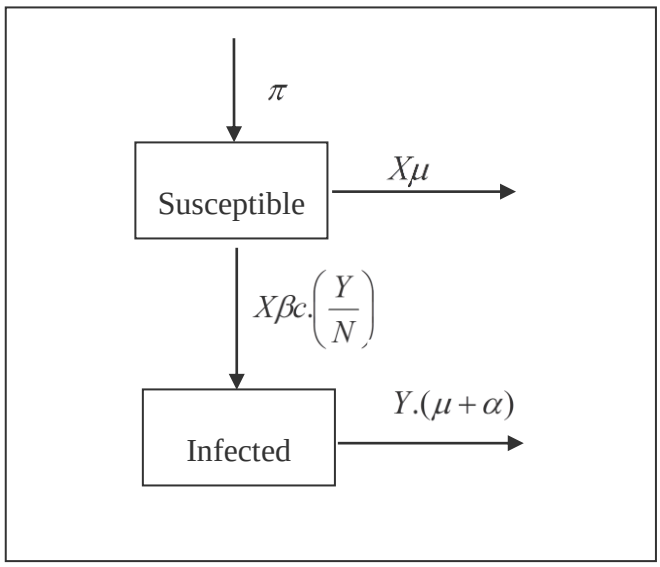


Figure 3.2. Model for HIV Transmission. Adapted from Leigh, 2004

Figure 3.3 shows the compartmental SIR model for direct disease transmission proposed by Lawson (2006).

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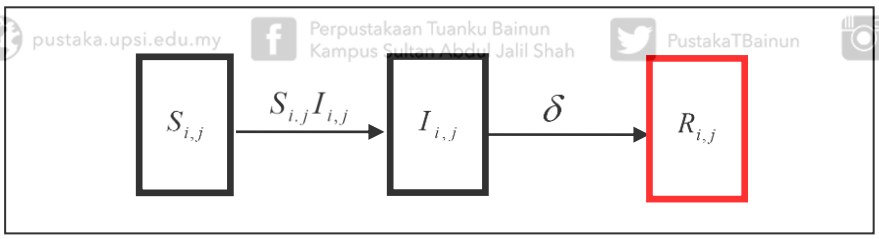


Figure 3.3. Compartmental SIR Model for Direct Disease Transmission based on Lawson, 2006. Adapted from Lawson, 2006

Based on Lawson (2006, pages 271 and 276), for i = 1, 2,…, M study regions and j = 1, 2,…, T time periods, the compartment for $S_{i,j}$ stands for susceptible population in region i at the beginning of the time period j, $I_{i,j}$ is referred as the infected cases in region i for time period j and $R_{i,j}$ presents the removed cases in region i during the time period j while δ represents the hazard for an infectious person's being removed.

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3.4 Compartmental Models for HIV and AIDS

Basically, compartment is a framework or progression of endemic model stands with common phases of compartments such as susceptible, infection and immune. One compartment will transport to the next compartment, known as the progression. This combination of the compartments commonly called as deterministic model. Meanwhile, stochastic model is a method to facilitate problem solving and analysis in applied probability. Stochastic is known as random process. It has random probability distribution which is analyzed statistically.

For HIV cases, a susceptible person could be infected with HIV and as the next phase, they might be infected with AIDS and eventually die. In this case, HIV and AIDS cases are separated where both cases have an individual SIR compartmental model. This is because, as discussed in section 2.2, a person infected with HIV will undergo all those symptoms related to immune deficiency that will definitely develop to AIDS and finally lead to death. However, some of the HIV-infected persons could die because of the symptoms of the HIV itself. Based on Herbert and James (1992), the HIV-infected person may die of HIV symptomatic symptoms such as candidiasis, hairy leukopia, herpes zoster, weight loss, diarrhoea, and so on as discussed in Section 2.3.2.

Besides, HIV and AIDS are long-term infected cases which could last about ten years. To analyze the data, ones need to have a long period of time to study and follow up the HIV-infected people from the beginning of HIV infection until the patients develop AIDS and perish or die because of HIV. This is known as the clinical test. However, the unavailability of data has been adapted with the proposed model

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HIV and AIDS which are congruent with the data provided by MOH. Therefore, in this analysis the compartment model of disease has been saperated into two compartments of HIV and AIDS respectively. In the next section, new compartmental and deterministic SIR models for both HIV and AIDS transmissions will be discussed thoroughly.

3.5 SIR Model of Direct Disease Transmission for HIV and AIDS

3.5.1 Compartmental and Deterministic SIR Model for HIV and AIDS

Biologically, the people who are confirmed to be HIV positive will undergo the infections process from one phase to another phase. It includes pre-antibody, asymptomatic, symptomatic, and lastly, AIDS. The compartmental model showed below will incorporate all phases of infections to be a single compartment of HIV which is the infection compartment. Figures 3.4 and 3.5 represent the compartmental SIR model for HIV and AIDS respectively.

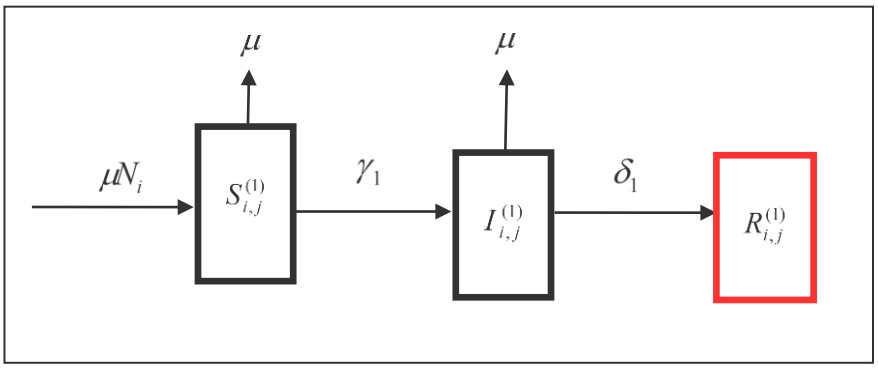


Figure 3.4. Compartmental SIR Model for HIV

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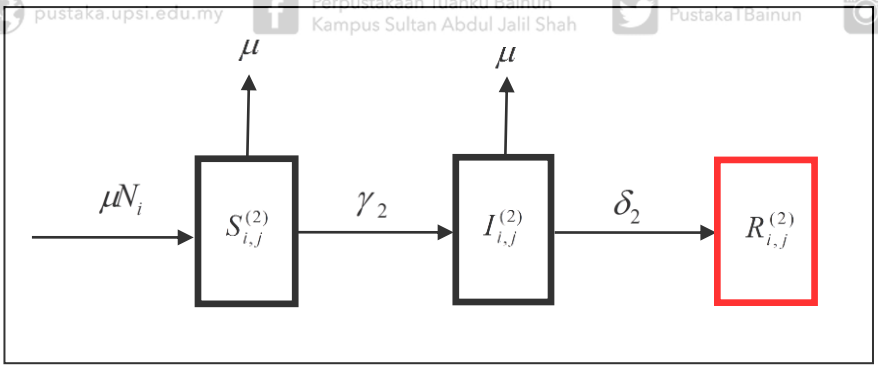


Figure 3.5. Compartmental SIR Model for AIDS

In this section, the SIR compartmental model for HIV and AIDS is described. In disease modelling, the compartmental model which stresses the population would be divided into different groups. In this population, let *'S'* be the susceptible, *'I'* is the infected and *'R'* is removed. In this study, for i=1, 2,…, M study regions and j=1, 2,…, T time periods, $S_{i,j}^{(1)}$ represents the total number of susceptible for HIV at time j, $S_{i,j}^{(2)}$ is the total number of susceptible for AIDS, $I_{i,j}^{(1)}$ represents the total number of person infected with HIV at time j, and $I_{i,j}^{(2)}$ represents the total number of person infected with AIDS at time j. In addition, $R_{i,j}^{(1)}$ and $R_{i,j}^{(2)}$ represents the total number of removed or death cases of HIV and AIDS at time j respectively.

Furthermore, μ represents the person who leaves the group because of natural death such as other illness like diabetic complications, myocardial infarct, malignancy, motor-vehicle accidents, and other factors. Next, γ_1 and γ_2 represent the incidence or rate by at which the infection occurs for HIV and AIDS respectively, and N_i denotes the total population. Next, δ_1 and δ_2 represent the mortality rate for those with HIV and AIDS respectively. The calculations for transmission probability of HIV and AIDS are the rate at which the new partnership occurs *(b)* multiply the

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probability of the infection if the partner is HIV-positive (β) and multiply with the probability that the partner is HIV-positive $\left(\frac{I}{N}\right)$. These can be written as

$$\gamma = \beta b\left(\frac{I}{N_i}\right)$$

Based on the compartmental in Figure 3.4 and Figure 3.5, the susceptible group represents the 'at-risk' population, the infective are the disease morbidity or case incidence while removed group represents HIV and AIDS mortality. For AIDS, susceptible people can become infective and then perish due to AIDS. Typically, the average time of a person living with AIDS is three years without treatment (CDC, 2013). This type of sexual and progression to AIDS in a population may depend on the age and the activity level of an individual, but currently there is no adequate data to analyze the incorporation of the parameters of age and sexual activity level (active and very active) into the model. These could be used as the extensions for further research.

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Next, the compartmental models for discrete-time intervals for HIV and AIDS in Figure 3.4 and Figure 3.5 are written mathematically in the system of difference equations as below.

For HIV, the deterministic models are,

$$S_{i,j}^{(1)} = \mu N_i + \left\{1 - \mu - \left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(1)}\right\} S_{i,j-1}^{(1)} \tag{3.1}$$

$$I_{i,j}^{(1)} = (1 - \mu - \delta_1) I_{i,j-1}^{(1)} + \left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(1)} S_{i,j-1}^{(1)} \tag{3.2}$$

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$$R_{i,j}^{(1)} = \delta_1 I_{i,j-1}^{(1)} \tag{3.3}$$

While for AIDS, the deterministic models are,

$$S_{i,j}^{(2)} = \mu N_i + \left\{1 - \mu - \left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(2)}\right\} S_{i,j-1}^{(2)} \tag{3.4}$$

$$I_{i,j}^{(2)} = (1 - \mu - \delta_2) I_{i,j-1}^{(2)} + \left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(2)} S_{i,j-1}^{(2)} \tag{3.5}$$

$$R_{i,j}^{(2)} = \delta_2 I_{i,j-1}^{(2)} \tag{3.6}$$

Here, N_i is assumed to be constant, where $N_i = S_i + I_i + R_i$. This formula can be used as the links to the stochastic mean population for the next section which is the determination of stochastic model.

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3.5.2 Stochastic SIR Model for New Infectives HIV and AIDS

Stochastic could be defined as randomly determined, and it is a technique used to facilitate problem-solving analysis. Stochastic yields quantities as the probability of occurrence of an epidemic and the mean time for the extinction of the disease. In a deterministic model, events are not subjected to chances or probability (Roxana, 2006). Conversely, stochastic models chance will always be taken into account. Stochastic models usually use the deterministic analysis in order to have a good mean

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approximation. Thus, the stochastic model will be discussed using the formulation of deterministic model to provide the approximation of mean stochastic.

This research includes new terms $\iota_{i,j}^{(1)}$ and $\iota_{i,j}^{(2)}$ to represent the number of newly infected HIV and AIDS respectively. The time interval utilized is Poisson stationary and independent increment properties which are $j-1$ and j while the study region is i. A stochastic process is a process which has a random likelihood with Poisson distribution that may be analyzed statistically but may not be predicted precisely. In this analysis, random Poisson distribution will be used to generate the probabilities outcomes of a system which is called Monte Carlo simulation and is explained in the last section of this chapter.

For $i = 1, 2,\ldots, M$ study regions and $j = 1, 2,\ldots T$ time periods, the proposed discrete-time and discrete space stochastic SIR model for HIV and AIDS transmission follow the deterministic equations, including a probability distribution to reflect the inherent randomness in the data are shown below.

For HIV,

$\iota_{i,j}^{(1)}$ = The total number of newly infected HIV

$$S_{i,j}^{(1)} = \mu N_i + S_{i,j-1}^{(1)} - \mu S_{i,j-1}^{(1)} - \iota_{i,j}^{(1)} \tag{3.7}$$

$$\iota_{i,j}^{(1)} \sim Poisson\left(\lambda_{ij}\right) \tag{3.8}$$

$$\lambda_{ij}^{(1)} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b}{N_i} I_{i,j-1}^{(1)} S_{i,j-1}^{(1)}\right) \tag{3.9}$$

$$I_{i,j}^{(1)} = \left(1-\mu-\delta_1\right) I_{i,j-1}^{(1)} + \iota_{i,j}^{(1)} \tag{3.10}$$

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$$R_{i,j}^{(1)} = \delta_1 I_{i,j-1}^{(1)} \tag{3.11}$$

While for AIDS,

$\iota_{i,j}^{(2)}$ = The total number of newly infected AIDS

$$S_{i,j}^{(2)} = \mu N_i + S_{i,j-1}^{(2)} - \mu S_{i,j-1}^{(2)} - \iota_{i,j}^{(2)} \tag{3.12}$$

$$\iota_{i,j}^{(2)} \sim Poisson\left(\lambda_{ij}\right) \tag{3.13}$$

$$\lambda_{ij}^{(2)} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b}{N_i} I_{i,j-1}^{(2)} S_{i,j-1}^{(2)}\right) \tag{3.14}$$

$$I_{i,j}^{(2)} = \left(1 - \mu - \delta_1\right) I_{i,j-1}^{(2)} + \iota_{i,j}^{(2)} \tag{3.15}$$

$$R_{i,j}^{(2)} = \delta_2 I_{i,j-1}^{(2)} \tag{3.16}$$

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From the equations, β_o represents the constant terms to describe the overall rates of the process and c_i represents the random effect that is designed to absorb the residual spatial variation for populations. According to Lucy (2014), for HIV and AIDS cases, the epidemiology is determined by the geographical structure. This is one of the characteristics for spatial correlated data where the outcomes are exposed to the influence transmission from neighbouring regions. Since the transmission of HIV is also affected by spatial data as discussed in Section 2.5, therefore the spatial terms is considered in the stochastic equation.

In this study, the intrinsic conditional autoregressive (CAR) priors are applied to fit the model for random effect c_i. The car.normal distribution is used as prior to

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allow for spatial dependence between the random effects c_i in nearby areas. These CAR prior is proposed by Besag *et al.*(1991), where the probability densities of values at any given location are conditional on the neighbouring areas. The CAR priors model used is as follow;

$$\left[c_i \mid c_j, i \neq j, \sigma_c^2\right] \sim N\left(\bar{c}_i, \sigma_i^2\right)$$

where the mean

$$\bar{c}_i = \frac{1}{\sum_j \kappa_{i,j}} \sum_j c_i \kappa_{i,j}$$

And variance

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$$\sigma_i^2 = \frac{\sigma_c^2}{\sum_j \kappa_{i,j}}$$

In this context, the $\kappa_{i,j}$ is equal to 1 if *i,j* are adjacent and 0 if they are not adjacent. For full Bayesian analysis, prior distributions have to be specified for this hyperparameter. Here, this analysis considers gamma distribution for parameter σ_i^2 that controls the variability of *c*.

In the next section, model of direct disease transmission for both HIV and AIDS and the compartmental as well as deterministic for $S(I^mI^f)R$ according to gender will be discussed in detail.

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3.6 S(I^mI^f)R Model of Direct Disease Transmission for HIV and AIDS based on Gender

According to the data provided by the Malaysia AIDS Council (AIDS/STI Unit, Ministry of Health Malaysia, 2010), about 91% of the people living with HIV in Malaysia are men. Furthermore, for every single year started from 1986 to 2010, the majority of people infected with HIV and AIDS were males. Therefore, this would be an important issue to discuss. A new model would be introduced based on the gender classification.

Besides that, according to the Health Ministry's Global Aids Response Country Progress Report 2012, more than half (55.5%) of last year's new infective of HIV cases were tranmitted through sex. This appears to be more prevelent among women, as 87% of them are ifected through heterosexual transmission compared to only 47% of men.

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3.6.1 Compartmental and Deterministic S(I^mI^f)R Model for HIV and AIDS

As previously mentioned, the number of infected male is always greater than the number of infected females. Subsequent from the introduced compartmental model in Section 3.3, new S(I^mI^f)R models for HIV and AIDS according to gender is introduced. These are shown in Figures 3.6 and 3.7.

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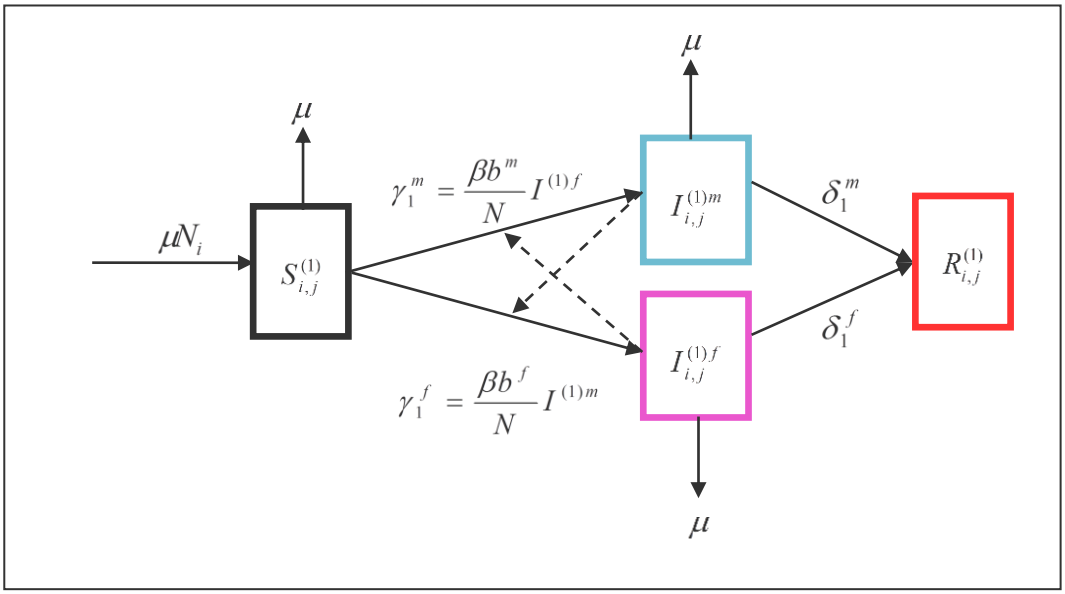


Figure 3.6. Compartmental S($I^m I^f$)R Model for HIV According to Gender

For i=1, 2,…, M study regions and j=1, 2,…, μ T time periods; $S_{i,j}^{(1)}$ and $S_{I,J}^{(2)}$ represent the total number of susceptible HIV and AIDS at time j respectively; $I_{I,J}^{(1)m}$ and $I_{i,j}^{(2)m}$ refer to the total number of infected HIV and AIDS for male at time j respectively; $I_{i,j}^{(1)f}$ and $I_{i,j}^{(2)f}$ represent the total number of infected HIV and AIDS for female at time j. Meanwhile, $R_{i,j}^{(1)}$ and $R_{i,j}^{(2)}$ indicate the number of removed HIV and AIDS respectively, and δ_1^m and δ_1^f are the mortality rate due to the HIV and AIDS for males and females. The features of this compartmental model for HIV and AIDS have been discussed in Section 3.3. For each compartment, there is a number of persons leaving the compartment because of natural death, μ. γ_1^m and γ_1^f are the infection rate at which the HIV occurs in male and female respectively whereas γ_2^m and γ_2^f are the infection rate at which AIDS occurs in male and female respectively. Furthermore, b^m is the partner acquisition rate for man while b^f is the partner acquisition rate for female.

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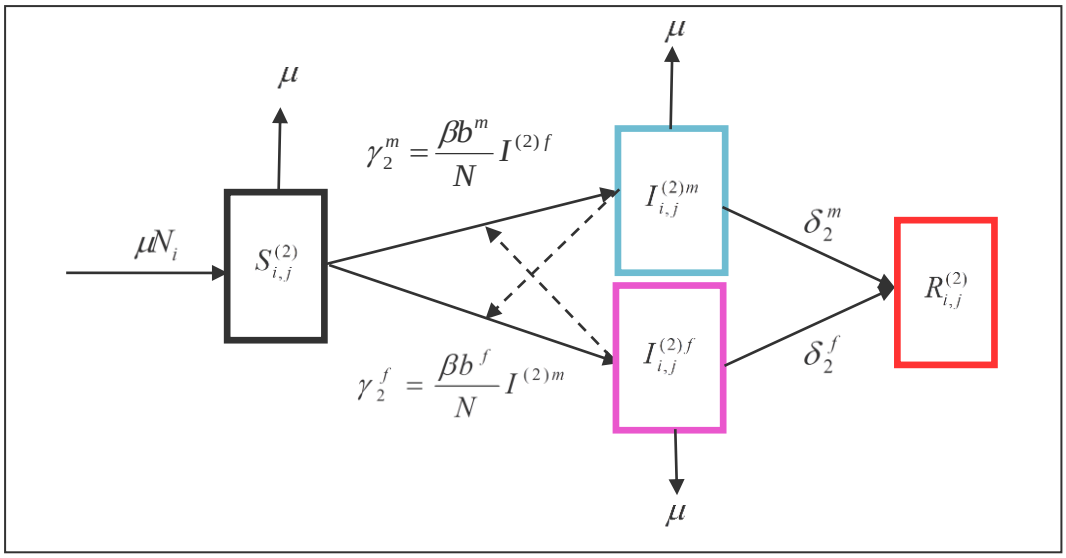


Figure 3.7. Compartmental S(I^mI^f)R Model for AIDS According to Gender

The compartmental S(I^mI^f)R model for HIV in Figure 3.6 can be written as deterministic equations as follows:

$$S_{i,j}^{(1)} = \mu N_i + \left(1 - \mu - \frac{\beta b^m}{N_i} I_{i,j-1}^{(1)f} - \frac{\beta b^f}{N_i} I_{i,j-1}^{(1)m}\right) S_{i,j-1}^{(1)} \tag{3.17}$$

$$I_{i,j}^{(1)m} = (1 - \delta_1^m - \mu) I_{i,j-1}^{(1)m} + \frac{\beta b^m}{N_i} I_{i,j-1}^{(1)f} S_{i,j-1}^{(1)} \tag{3.18}$$

$$I_{i,j}^{(1)f} = (1 - \delta_1^f - \mu) I_{i,j-1}^{(1)f} + \frac{\beta b^f}{N_i} I_{i,j-1}^{(1)m} S_{i,j-1}^{(1)} \tag{3.19}$$

$$R_{i,j}^{(1)} = (\delta_1^m + \delta_1^f) R_{i,j-1}^{(1)} \tag{3.20}$$

Meanwhile, the deterministic equations for compartmental S(I^mI^f)R model for AIDS in Figure 3.7 can be written as follows:

$$S_{i,j}^{(2)} = \mu N_i + \left(1 - \mu - \frac{\beta b^m}{N_i} I_{i,j-1}^{(2)f} - \frac{\beta b^f}{N_i} I_{i,j-1}^{(2)m}\right) S_{i,j-1}^{(2)} \tag{3.21}$$

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$$I_{i,j}^{(2)m} = (1-\delta_2^m - \mu)I_{i,j-1}^{(2)m} + \frac{\beta b^m}{N_i} I_{i,j-1}^{(2)f} S_{i,j-1}^{(2)} \tag{3.22}$$

$$I_{i,j}^{(2)f} = (1-\delta_2^f - \mu)I_{i,j-1}^{(2)f} + \frac{\beta b^f}{N_i} I_{i,j-1}^{(2)m} S_{i,j-1}^{(2)} \tag{3.23}$$

$$R_{i,j}^{(2)} = (\delta_2^m + \delta_2^f)R_{i,j-1}^{(2)} \tag{3.24}$$

These compartmental and deterministic models will be used to develop the stochastic models for HIV and AIDS transmission based on the system of difference equations. The development of stochastic models will be derived and explain in the next section.

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3.6.2 Stochastic S(I^mI^f)R Model for New Infectives HIV and AIDS

The stochastic S(I^mI^f)R model for HIV and AIDS for new infective HIV and AIDS in both males and females can be written as follows in which the discrete-time and discrete-space stochastic SIR models for both HIV and AIDS will be developed based on the SIR model proposed by Lawson (2003).

The stochastic S(I^mI^f)R model for HIV according to males and females can be written as follows:

$\iota_{i,j}^{(1)m}$ = The total number of newly infected males for HIV

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$$S_{i,j}^{(1)} = \mu N_i + S_{i,j-1}^{(1)} - \mu S_{i,j-1}^{(1)} - \iota_{i,j}^{(1)m} - \frac{\beta b^f}{N_i} I_{i,j-1}^{(1)m} S_{i,j-1}^{(1)} \tag{3.25}$$

$$\iota_{i,j}^{(1)m} \sim Poisson\left(\lambda_{ij}\right) \tag{3.26}$$

$$\lambda_{ij} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b^m}{N_i} I_{i,j-1}^{(1)f} S_{i,j-1}^{(1)m}\right) \tag{3.27}$$

$\iota_{i,j}^{(1)f}$ = The total number of newly infected females for HIV

$$S_{i,j}^{(1)} = \mu N_i + S_{i,j-1}^{(1)} - \mu S_{i,j-1}^{(1)} - \gamma_1^m S_{i,j-1}^{(1)} - \iota_{i,j}^{(1)f} \tag{3.28}$$

$$\iota_{i,j}^{(1)f} \sim Poisson\left(\lambda_{ij}\right) \tag{3.29}$$

$$\lambda_{ij} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b^f}{N_i} I_{i,j-1}^{(1)m} S_{i,j-1}^{(1)f}\right) \tag{3.30}$$

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This followed by the stochastic S(I^mI^f)R model for AIDS specified for males and females as follows:

$\iota_{i,j}^{(2)m}$ = The total number of newly infected males for AIDS

$$S_{i,j}^{(2)} = \mu N_i + S_{i,j-1}^{(2)} - \mu S_{i,j-1}^{(2)} - \iota_{i,j}^{(2)m} - \frac{\beta b^f}{N_i} I_{i,j-1}^{(2)m} S_{i,j-1}^{(2)} \tag{3.31}$$

$$\iota_{i,j}^{(2)m} \sim Poisson\left(\lambda_{ij}\right) \tag{3.32}$$

$$\lambda_{ij} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b^m}{N_i} I_{i,j-1}^{(2)f} S_{i,j-1}^{(2)m}\right) \tag{3.33}$$

$\iota_{i,j}^{(2)f}$ = The total number of newly infected females for AIDS

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$$S_{i,j}^{(2)} = \mu N_i + S_{i,j-1}^{(2)} - \mu S_{i,j-1}^{(2)} - \frac{\beta b^m}{N_i} I_{i,j-1}^{(1)f} S_{i,j-1}^{(2)} - \iota_{i,j}^{(2)f} \tag{3.34}$$

$$\iota_{i,j}^{(2)f} \sim Poisson\left(\lambda_{ij}\right) \tag{3.35}$$

$$\lambda_{ij} = \left[\exp\left(\beta_o + c_i\right)\right]\left(\frac{\beta b^f}{N_i} I_{i,j-1}^{(2)m} S_{i,j-1}^{(2)f}\right) \tag{3.36}$$

The discrete time-space stochastic SIR and S(I^mI^f)R models for HIV and AIDS and for HIV and AIDS according to males and females proposed here will be used in the estimation of relative risk for disease mapping as discussed in the next section.

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3.7 Relative Risk Estimation based on Stochastic SIR Model and S(I^mI^f)R for HIV and AIDS

In the previous section, we have highlighted some common approaches to relative risk estimation as well as the drawbacks of those common methods as the relative risk estimator. To overcome these drawbacks a variety of estimators have been proposed. One approach to improving the relative risk estimator is based on Bayesian modeling. Here, we introduce an alternative method of relative risk estimation of disease mapping based on the disease transmission model adapted specially for HIV and AIDS. The computational analysis is performed using WinBUGS software, which is a package design to carry out Markov chain Monte Carlo (MCMC) computations for a wide variety of Bayesian models (Spiegelhalter *et al*., 2003).

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In Bayesian analysis, posterior distribution is defined as product of the likelihood functions and the prior distributions. Likelihood is obtained from the observed data while prior distribution is based upon prior assumptions where both are functioning to produce posterior distribution as shown in simple proportional rule as below;

$$Posterior \propto Likelihood \times \Pr ior$$

In this context, the parameter of interest is $\lambda_{ij}^{(1)}$ and the data comprise the total number of newly infected, $\iota_{i,j}^{(1)}$ for all study regions *i* and time periods *j*. Denote the likelihood of data $\iota_{i,j}^{(1)}$ given the parameter $\lambda_{ij}^{(1)}$ as L($\lambda_{ij}^{(1)}$;*data*) and the $g(\lambda_{ij}^{(1)})$ is the joint prior distribution of the $\lambda_{ij}^{(1)}$ vector. Consequently, the product of these two components is called the posterior distribution which is defined as follows;

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$$f(\lambda_{ij}^{(1)} \mid data) \propto L(\lambda_{ij}^{(1)}; data) g\left(\lambda_{ij}^{(1)}\right)$$

The form of $g(\lambda_{ij}^{(1)})$ is the spatial CAR prior discussed in Section 3.5.2 and the constant of proportionality can be determined numerically. In this research, the posterior distribution of the mean number of infective HIV and AIDS are determined. Then, the information of posterior distribution will be used to find the posterior mean of relative risk which is explained in the next section. This estimation method is the applied to the SIR and S(I^mI^f)R models for HIV and AIDS.

In addition, in this study we used Markov chain Monte Carlo (MCMC) method, which is generally regarded as most suitable for complex models (Spiegelhalter *et al.*, 2003). MCMC method is a set of method which used iteration simulation of parameter values within a Markov chain. In this study, prior distribution

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for p components of $\lambda_{ij}^{(1)}$ are defined as $g_k(\lambda_{ijk}^{(1)})$ for $k = 1, 2,\ldots,p$. The posterior distribution of $\lambda_{ij}^{(1)}$ and data comprise the total number of newly infected, $\iota_{i,j}^{(1)}$ is then defined as:

$$P(\lambda_{ij}^{(1)} \mid data) \propto L(\lambda_{ij}^{(1)}; data) \prod_k g_{ijk}(\lambda_{ijk}^{(1)})$$

The aim is to generate a sample from $P(\lambda_{ij}^{(1)} \mid data)$. In spatial epidemiology, it is often the case of that $P(\lambda_{ij}^{(1)} \mid data)$ can be very difficult to sample from in complex models. Therefore, MCMC is useful to have a general method for such simulation.

The alternative method of relative risk estimation based on stochastic SIR and $S(I^mI^f)R$ models for both HIV and AIDS disease transmission will be introduced in the next sections which follow the computational analysis performed by using WinBUGS software, which is a package design to carry out MCMC simulation.

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3.7.1 Relative Risk Estimation based on Stochastic SIR Model for HIV and AIDS

Generally, for $i = 1, 2,\ldots,M$ study region and $j = 1, 2,\ldots T$ time periods, the observation sample used is the pseudo-random sample where λ_{ijk} for $k = 1, 2,\ldots,$ n is generated from a posterior distribution for the mean number of HIV and AIDS infective respectively. Pseudo-random is defined as the randomness by exhibiting a specific

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repeatable pattern. Below are the posterior expected mean number of infective $\lambda_{ij}^{(1)}$ and $\lambda_{ij}^{(2)}$ for HIV and AIDS respectively as defined in Section 3.3:

$$\lambda_{ij}^{(1)} = \exp\left(\beta_o + c_i\right)\left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(1)} S_{i,j-1} \tag{3.37}$$

$$\tilde{\lambda}_{ij}^{(1)} = \frac{1}{n}\sum_{k=1}^{n} \lambda_{ijk}^{(1)} \tag{3.38}$$

and

$$\lambda_{ij}^{(2)} = \exp\left(\beta_o + c_i\right)\left(\frac{\beta b}{N_i}\right) I_{i,j-1}^{(2)} S_{i,j-1} \tag{3.39}$$

$$\tilde{\lambda}_{ij}^{(2)} = \frac{1}{n}\sum_{k=1}^{n} \lambda_{ijk}^{(2)} \tag{3.40}$$

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Next, we need to determine the relative risk of HIV and AIDS which are θ_{ij}^{1} and θ_{ij}^{2} respectively. Meanwhile, e_{ij}^{1} is the expected number for the new infective HIV and e_{ij}^{2} is the expected number for the new infective AIDS. The relative risk equations are as follows:

$$\theta_{ij}^{(1)} = \frac{\lambda_{ij}^{(1)}}{e_{ij}^{(1)}} \tag{3.41}$$

and

$$\theta_{ij}^{(2)} = \frac{\lambda_{ik}^{(2)}}{e_{ij}^{(2)}} \tag{3.42}$$

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Based on the equation above, to approximate the posterior expected relative risk for HIV and AIDS, it could be written as:

$$\tilde{\theta}_{ij}^{(1)} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(1)} = \frac{\tilde{\lambda}_{ij}^{(1)}}{e_{ij}^{(1)}} \tag{3.43}$$

and

$$\tilde{\theta}_{ij}^{(2)} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(2)} = \frac{\tilde{\lambda}_{ij}^{(2)}}{e_{ij}^{(2)}} \tag{3.44}$$

The posterior expected relative risk for HIV, $\tilde{\theta}_{ij}^{(1)}$ is equal to the expected mean number of infective which is $\frac{1}{n}\sum_{k=1}^{n}\tilde{\lambda}_{ij}^{(1)}$ divided by the expected mean number of the new infective HIV which is denoted as $e_{ij}^{(1)}$ based on the population of the study regions. On the other hand, the posterior expected relative risk for AIDS, $\tilde{\theta}_{ij}^{(2)}$ is equal to the expected mean number of infective which is $\frac{1}{n}\sum_{k=1}^{n}\tilde{\lambda}_{ij}^{(2)}$ divided by the expected mean number of new infective AIDS denoted as $e_{ij}^{(2)}$ based on the population of the study regions.

In this study, the value of relative risk is defined based on a study done by Samat and Percy (2008). A value of relative risk that is equal to zero means people within the study region have no relative risk or infection risk for the disease compared to the people in the population. However, the value of relative risk not ought to be zero though everybody has the possibility or chance to catch with the disease. This is

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one of our major drawback of SMR method that we would like to overcome as discussed in Section 3.2.1.

Next, when the value of relative risk is close to 1 means that there is no significant difference between the conditional probability that a person in the study region contracts the disease and the conditional probability that a person in the general population contracts the disease.

On the other hand, if the value of relative risk is greater than 1, then it indicates that the people within the study region are more likely to contract the disease compared to the people in the population. Conversely, a value of relative risk below 1 indicates a decrease in likelihood of contracting the disease which means that the people in the study region are less likely to contract the disease compared to people in the population.

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3.7.2 Relative Risk Estimation Based on Stochastic S(I^mI^f)R Model for HIV and AIDS

The approximation of posterior expected mean for HIV and AIDS according to gender discussed in this section are similar to those SIR model discussed earlier. For HIV, the relative risk can be approximate using the following equations,

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$$\tilde{\theta}_{ij}^{(1)m} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(1)m} = \frac{\tilde{\lambda}_{ij}^{(1)m}}{e_{ij}^{(1)m}} \tag{3.45}$$

$$\tilde{\theta}_{ij}^{(1)f} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(1)f} = \frac{\tilde{\lambda}_{ij}^{(1)f}}{e_{ij}^{(1)f}} \tag{3.46}$$

While for AIDS, the relative risk equations are,

$$\tilde{\theta}_{ij}^{(2)m} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(2)m} = \frac{\tilde{\lambda}_{ij}^{(2)m}}{e_{ij}^{(2)m}} \tag{3.47}$$

$$\tilde{\theta}_{ij}^{(2)f} = \frac{1}{n}\sum_{k=1}^{n}\theta_{ijk}^{(2)f} = \frac{\tilde{\lambda}_{ij}^{(2)f}}{e_{ij}^{(2)f}} \tag{3.48}$$

The posterior expected relative risk for HIV, $\tilde{\theta}_{ij}^{(1)m}$, for male is equal to the expected mean number of infective male which is $\frac{1}{n}\sum_{k=1}^{n}\tilde{\lambda}^{(1)m}_{ij}$ divided by the expected mean number of the new infective HIV male which is denoted as $e_{ij}^{(1)m}$ based on the population of the study regions. On the other hand, the posterior expected relative risk for AIDS, $\tilde{\theta}_{ij}^{(2)m}$ is equal to the expected mean number of infective which is $\frac{1}{n}\sum_{k=1}^{n}\tilde{\lambda}_{ij}^{(2)m}$ divided by the expected mean number of new infective AIDS denoted as $e_{ij}^{(2)m}$ based on the population of the study regions. While for female cases the regulation of derivation posterior expected relative risks are the same as male cases for both HIV and AIDS.

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In this analysis of relative risk estimation based on $S(I^mI^f)R$ model for HIV and AIDS, the results are defined similar as discussed in Section 3.7.1 for both male and female cases of HIV and AIDS.

All the traditional and proposed methods discussed in this chapter will be applied by using WinBUGS software to HIV and AIDS data from Malaysia. The results are presented in tables, graphs and maps in order to compare which method has better relative risk estimation to produce a better map for the disease as discussed in Chapter 4.

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CHAPTER 4

APPLICATION TO RELATIVE RISK ESTIMATION FOR HETEROSEXUAL HIV AND AIDS

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4.1 Introduction

In this chapter, the applications are divided into four relative risk estimations which correspond to the models that are based on the analyses of HIV and AIDS. First and second applications are based on the common methods of disease mapping which are

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the SMR method and Poisson-gamma model. This is followed by the SIR model and finally the application of relative risk estimation based on the $S(I^mI^f)R$ model according to gender.

In this study, epidemiology of HIV and AIDS are referred as the distribution of health-related states of HIV and AIDS, and the application of this study to the control of diseases (WHO, 2013). Meanwhile, the epidemiology month refers as number or case for newly infected persons by HIV or AIDS over time period which is per calendar month such as January, February, March and so on until December. This period data usually displayed in time-series graph where the vertical or y-axis shows the observed case number and horizontal or x-axis shows the time period such as years, months or weeks (CDC, 2013).

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In the first application of relative risk estimation, the data used in the analysis are the monthly observed cases of infective HIV and AIDS in the form of count of cases for all 13 states and three federal territories in Malaysia. These states and federal territories are Perlis, Kedah, Penang, Perak, Selangor, Federal Territory of Kuala Lumpur, Federal Territory of Putrajaya, Negeri Sembilan, Malacca, Johor, Pahang, Terengganu, Kelantan, Sarawak, Sabah, and Federal Territory of Labuan. The data that are available for the analyses are from the epidemiology in January 2013 until the epidemiology in December 2014.

Firstly, the results of relative risk estimation based on the traditional method of disease mapping which are the SMR method and Poisson-gamma model are presented. This is followed by the results of relative risk from the proposed models which are the SIR model and $S(I^mI^f)R$ model according to gender for both HIV and AIDS.

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The two software used in this research are WinBUGS and ArcGIS. ArcGIS software is used to digitize the Malaysia map according to space (states) and time (epidemiology month), as well as to map the relative risks. Meanwhile, WinBUGS is an interactive program used in the Bayesian analysis of complex statistical method. This WinBUGS software is designed to carry out the Markov chain Monte Carlo (MCMC) computations for Bayesian models.

Next, these results of relative risk estimation for SMR method, Poisson-gamma model, SIR and $S(I^mI^f)R$ models are displayed and compared using tables, graphs, and maps to find the better model of relative risk estimation for HIV and AIDS mapping in Malaysia.

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4.2 HIV and AIDS Situation in Malaysia

The data used in these analyses were provided by the Disease Control Department from the Ministry of Health (MOH) Malaysia which involve all states and federal territories in Malaysia. The applications presented in this research are applied to HIV and AIDS data in the form of count of cases for all states in Malaysia for epidemiology month January 2013 to epidemiology month December 2014. Here, the observed counts of the new infective HIV and AIDS cases terms that are used for HIV and AIDS data are based on the time period $(j - 1, j]$ for $j = 1, 2,\ldots, 24$ epidemiology per calendar months.

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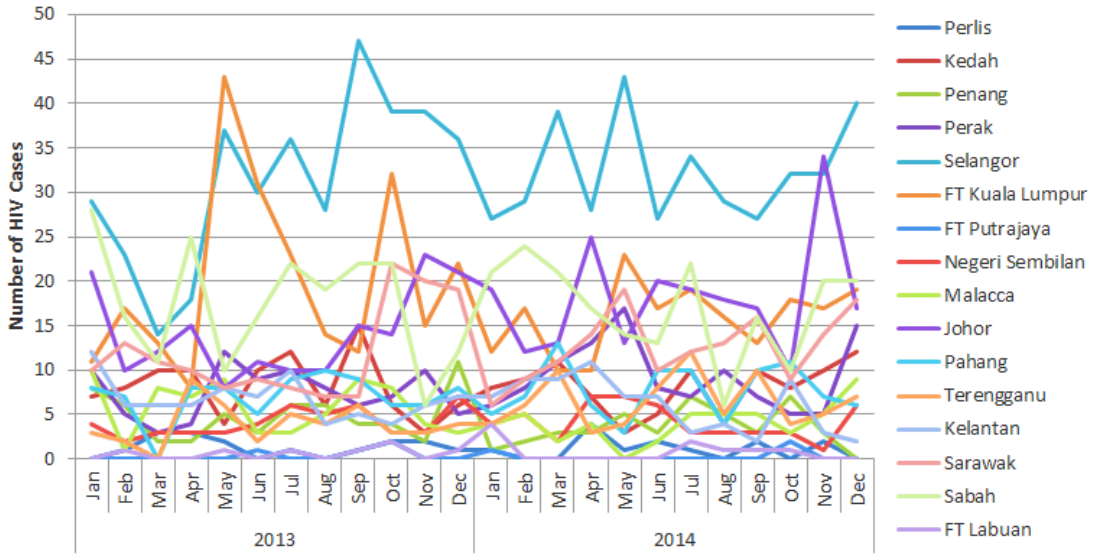


Figure 4.1. Time Series Plot of HIV Cases in Malaysia from Epidemiology Month January 2013 until Epidemiology Month December 2014

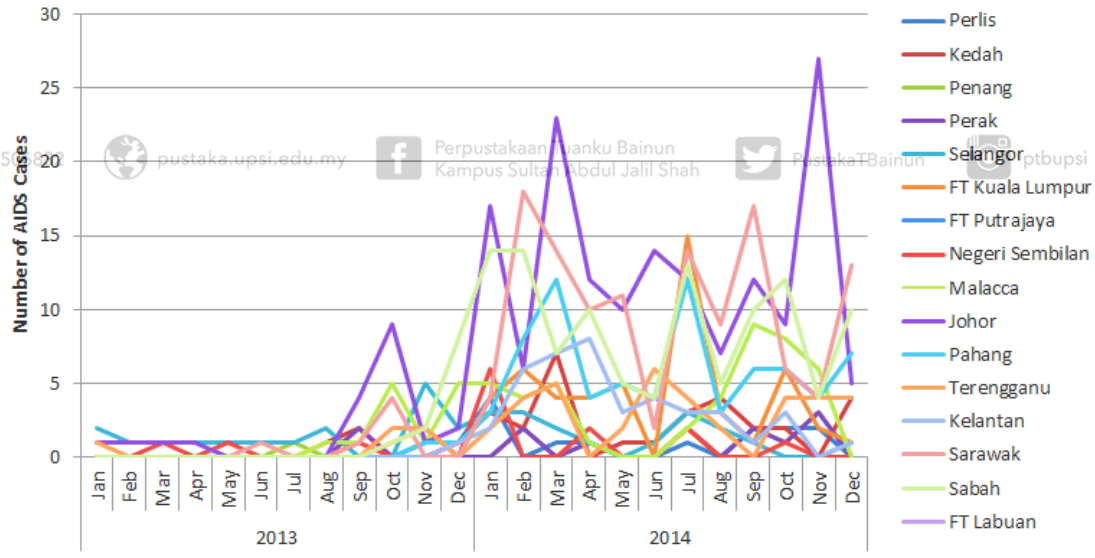


Figure 4.2. Time Series Plot of AIDS Cases in Malaysia from Epidemiology Month January 2013 until Epidemiology Month December 2014

Figures 4.1 and 4.2 depict the time series graphs of HIV and AIDS cases reported for every state in Malaysia from January 2013 until December 2014. Based on Figure 4.1, it can be seen that the frequency of cases is assembled about 0 to 10 number of HIV cases except for Selangor and federal territory of Kuala Lumpur. This is followed by Sarawak, Sabah and Johor where the number of cases for all

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epidemiology months in 2013 and 2014 were about 10 to 50 number of cases reported whereas federal territories of Labuan and Putrajaya have the lowest number of HIV cases recorded. Figure 4.2 shows that the distribution number of cases is between zero to 3 at the beginning of epidemiology from January to August on 2013 and increase abruptly started from the end of August until December 2014. The depletion number of cases is assumed due to the high rate number of death caused by AIDS.

4.3 Estimation of Relative Risk for HIV and AIDS Mapping based on Standardized Morbidity Ratio and Poisson-Gamma Model

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This section demonstrates the results of relative risk estimation based on traditional methods which are the SMR method and the earliest application of Bayesian mapping called Poisson-gamma model. This section is extended with the demonstration results of relative risk estimation based on proposed discrete-time and discrete-space of stochastic SIR model and $S(I^mI^f)R$ model according to gender for HIV and AIDS transmission.

The methodology of the relative risk estimation based on these two methods were explained in Section 3.21 and Section 3.2.2. Here, the results of relative risk estimation based on the SMR method and Poisson-Gamma model are presented in graphs and tables for both cases of HIV and AIDS.

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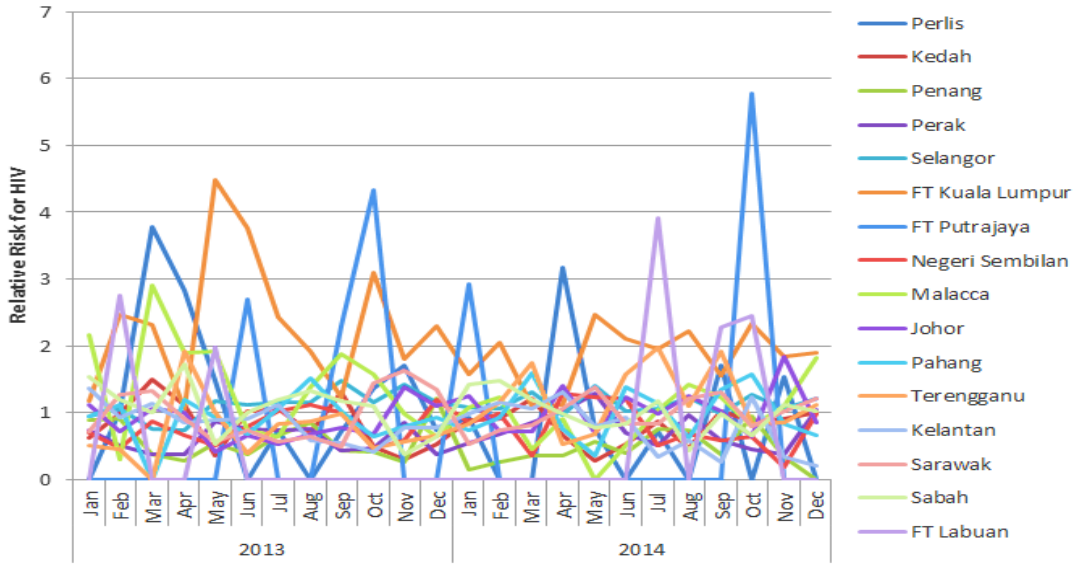


Figure 4.3. Time Series Plots of the Estimated Relative Risk based on the SMR Method for HIV Cases

With respect to time series graphs in Figures 4.3 and 4.4, the graphs plotted are meant to demonstrate the pattern of relative risk value for each state for all epidemiology months which is not touch the zero line when there is no zero relative risk value for number of observe cases as well as to show the range of relarive risk value at y-axis.

Based on both graphs in Figures 4.3 and 4.4, it can be seen that Kuala Lumpur has relative risk greater than one for most of the epidemiology months, which means that susceptible people within this area are more likely to contract HIV compared to the people in overall population. While Penang has a relative risk less than one for most of the epidemiology months which mean that susceptible people within this area are less likely to contract HIV compared to the people in overall population.

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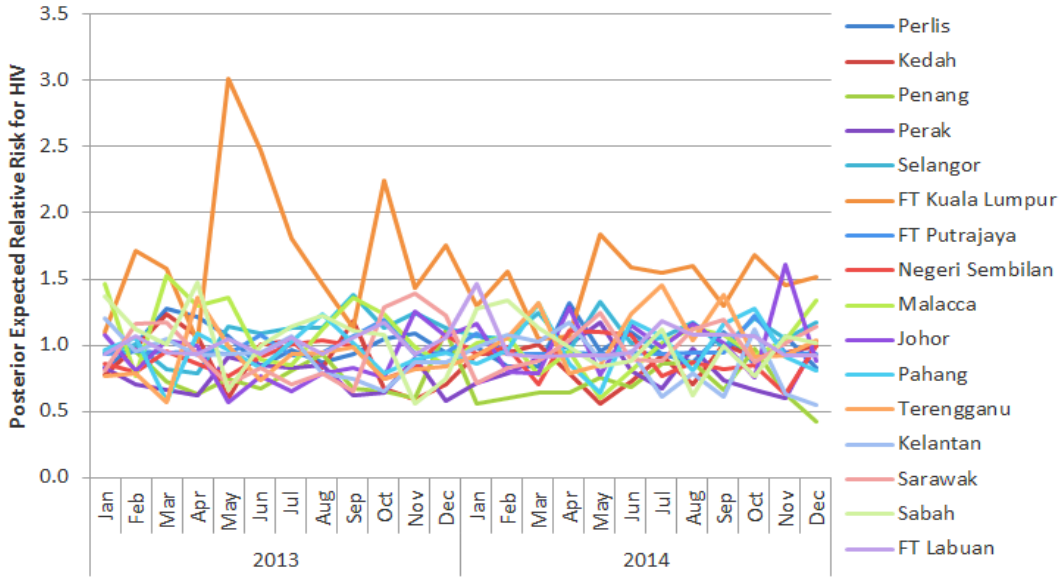


Figure 4.4. Time Series Plots of the Estimated Relative Risk based on the Poisson-gamma Model for HIV Cases

The high level of risk in Kuala Lumpur is likely due to many rehabilitation and treatment centres in the area. This is supported by an article published by World Health Organization (2014) which states that the rate of risk increase in Kuala Lumpur is caused by the medical treatment and support facilities in Kuala Lumpur where the patients in rural areas will normally be referred to and treated at the urban centre. In addition, the University of Malaya Medical Centre is the premier infectious disease unit for HIV and AIDS cases which is located in Kuala Lumpur.

For the case of AIDS, the time series plot are presented in Figures 4.5 and 4.6. From both figures, Malacca has the relative risk greater than one for most epidemiology months. This means that susceptible people within Malacca have a high risk to catch HIV compared to the people in the overall population. Increasing risk of AIDS in Malacca is likely due to the high number of illegal prostitution centre in the middle of the city state and it is also probably caused by the high number of foreign people in that state since Malacca is attraction tourist as historical city in this country (Sofi Wahab, 2009).

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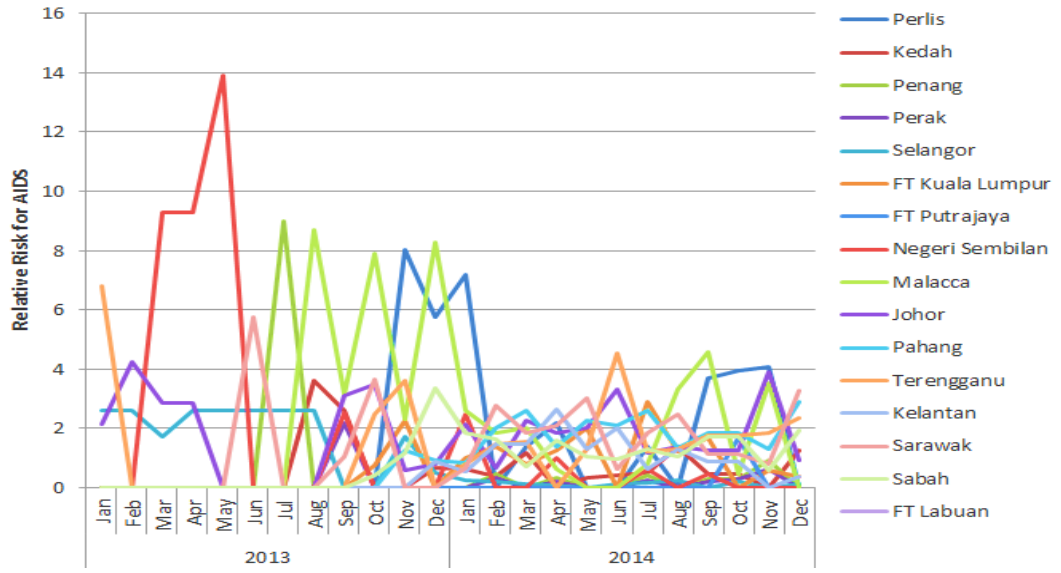


Figure 4.5. Time Series Plots of the Estimated Relative Risk based on the SMR Method for AIDS Cases

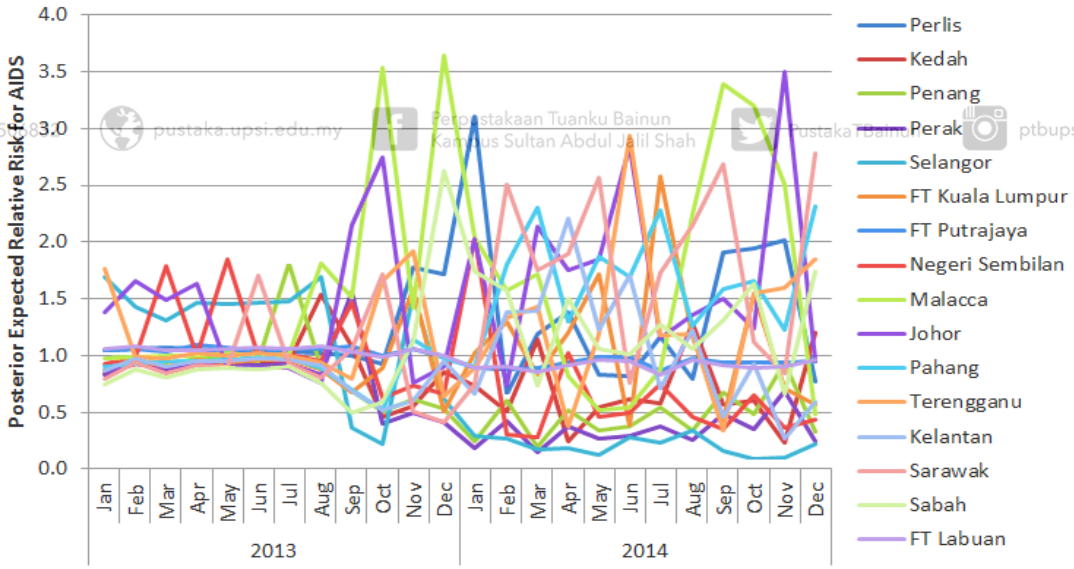


Figure 4.6. Time Series Plots of the Estimated Relative Risk based on the Poisson-gamma Model for AIDS Cases

By using the Poisson-gamma model, it leads to the same conclusion as SMR method that the susceptible people in Kuala Lumpur have the highest risk of contracting HIV and the susceptible people in the state of Malacca have the high risk to catch AIDS. It can be seen that, when using the SMR method, the relative risk

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estimation for certain states become exactly zero when there is no cases observed. Conversely, by using the Poisson-gamma model, it generates positive relative risk estimation for any states that have no value of cases observed.

Tables 4.1 and 4.2 present the numerical values for the relative risk based on the SMR method and Poisson-gamma model for the epidemiology month April 2014 for both HIV and AIDS, in which the month is chosen because in that particular month contains zero value of relative risks in order to demonstrate the drawbacks of SMR method as discussed in Section 3.2.1 for estimate relative risk of HIV and AIDS in Malaysia.

Analysis based on SMR method presented in Table 4.1 showed that Perlis has the highest relative risk of HIV with approximately 3.176 while Federal Territories of Putrajaya and Labuan have zero relative risk. This means that people in Perlis have the highest risk of contracting HIV compared to the overall population. Meanwhile, people in the Federal Territories of Putrajaya and Labuan have no risk to contract with HIV compared to the overall population.

However, the risk not ought to be zero though everybody has the possibility or chance to catch with the disease. This is one of our major drawback of SMR method that we would like to overcome by proposing new models in estimating relative risk as discussed in Section 3.5. and Section 3.6.

The high relative risk for the state of Perlis is possibly because of the geographical state which is situated near to southern Thailand and the transmission occurs usually among unfortunates especially poor community with less quality of life (Tan and Indra, 2007).

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Table 4.1

Relative Risk Estimation for HIV based on the SMR Method and Poisson-gamma Model for Epidemiology Month April 2014

State	SMR	Poisson-gamma Model
Perlis	3.1761	1.3170
Kedah	0.6632	0.7876
Penang	0.3547	0.6436
Perak	1.0239	1.0120
Selangor	0.9593	0.9680
FT Kuala Lumpur	1.1236	1.0680
FT Putrajaya	0	0.9400
Negeri Sembilan	1.2827	1.1150
Malacca	0.9153	0.9580
Johor	1.402	1.2890
Pahang	0.7491	0.8613
Terengganu	0.5364	0.7855
Kelantan	1.3168	1.1700
Sarawak	1.0623	1.0400
Sabah	0.9837	0.9839
FT Labuan	0	0.9288

Note, FT = Federal Territory.

Similarly, by using Poisson-gamma model, Perlis has the highest relative risk of HIV for the epidemiology in April 2014. Meanwhile, Penang has the lowest relative risk which is 0.6436.

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According to Table 4.2, by using the SMR method, Kelantan has the highest risk of contracting AIDS while Terengganu, Kedah and Federal Territory of Putrajaya has relative risk 2.6446. Meanwhile, Federal Territory Labuan has the lowest risk of contracting AIDS compared to the overall population which is 0 relative risk for the epidemiology month April 2014. This shows that people in the Federal Territory of Putrajaya has no risk to contract with AIDS compared to the overall population but this risk not supposed to be zero as discuss before in Section 3.7.1.

Meanwhile, by using Poisson-gamma model, Kelantan has relative risk 2.2110 followed by Kedah which is 0.2427, Terengganu is 0.3763 and federal territories of Putrajaya and Labuan are0.9350 and 0.9288. Based on Hasanah *et.,* al (2010), the state of Kelantan is situated in the north east part of peninsular Malaysia, bordering southern Thailand. The increasing of risk is possibly due to the lack of HIV and AIDS knowledge, unsafe sex, more prostitution activities influenced by the neighbouring country and a poorer quality of life value in social domain where the patients had possibly anxiety or depression and psychological disturbances.

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These results of relative risk demonstrated that the Poisson-gamma model could overcome the problem of SMR when the value of observed HIV case is zero. In addition, Poisson-gamma model also can help to reduce the noise in the map with smoothing away the value of relative risk estimation.

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Table 4.2

Relative Risk Estimation for AIDS based on the SMR Method and Poisson-gamma Model for Epidemiology Month April 2014

State	SMR	Poisson-gamma Model
Perlis	2.1944	1.3810
Kedah	0	0.2427
Penang	0.3267	0.5219
Perak	0.2177	0.3802
Selangor	0.0947	0.1889
FT Kuala Lumpur	1.2421	1.2020
FT Putrajaya	0	0.9350
Negeri Sembilan	1.0129	1.0240
Malacca	0.6324	0.8234
Johor	1.8599	1.7500
Pahang	1.3801	1.2980
Terengganu	0	0.3763
Kelantan	2.6446	2.2110
Sarawak	2.097	1.8910
Sabah	1.5992	1.5050
FT Labuan	0	0.9288

Note, FT = Federal Territory.

However, the major drawbacks of gamma prior are, there is no possibility of allowing spatial correlation between risk in neighbouring regions as well as difficult to do covariate adjustment for the model of relative risk.

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Therefore, in order to overcome these drawbacks of SMR method and Poisson-gamma model, new methods which are discrete time-space stochastic SIR model and S(I^mI^f)R model according to gender for HIV and AIDS are introduced in this study.

4.3.1 WinBUGS Code for Relative Risk Estimation based on the Poisson-gamma Model

Figure 4.7 shows the WinBUGS code which represents the relative risk estimation of HIV and AIDS based on Poisson-gamma model. This code is written by Lawson et al. (2003) in his study on disease mapping.

The model used in Figure 4.7 is based on the Bayesian modeling which intends to overcome the shortcomings of SMR and also smoothing the methods for relative risk as discussed in Section 3.2.2. In Bayesian analysis, the inference must be based on a posterior distribution which incorporates both the likelihood and prior distributions (Lawson, 2006).

Based on Figure 4.7, *M* represents the states in Malaysia, *T* is epidemiology month *i,* and *y* [i,j] is the number of infective HIV or AIDS using the Poisson distribution model with *mu* [i,j] is denoted as the mean number of infective HIV or AIDS.

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The product of *e* [i,j] and *theta* [i,j] gives the posterior distribution of the mean number of infective HIV or AIDS where *e* [i,j] represents the number of expected value for HIV or AIDS cases while *theta* [i,j] is the relative risk of prior distribution with parameter α and β. In this analysis, hyperprior distributions with a mean of 0.1 is considered for both parameters as suggested by Lawson (2003) as discussed in Section 3.2.

```
Model{



for (i in 1:M){
for (j in 1:T){
                #Poisson likelihood for observed counts
                y[i,j]~dpois(mu[i,j])
                mu[i,j]<-e[i,j]*theta[i,j]
                #Relative Risk
                Theta[i,j]~dgamma(a,b)
}
}
#Prior distribution for "population" parameter
a~dexp(0.1)
b~dexp(0.1)

#Population Mean and Population variance
mean<-a/b
var<-a/pow(b,2)

}
```

Figure 4.7. Poisson-Gamma Model in WinBUGS

Table 4.3 represents the example of statistical output for the relative risk estimation based on the Poisson-gamma model using the WinBUGS software for the state of Perlis from epidemiology month of February until November 2013 which is chosen arbitrarily for the demonstration of the WinBUGS output of the mean relative risk estimation results for HIV.

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Table 4.3

Example of WinBUGS Output for Expected Relative Risks of HIV in the State of Perlis for Epidemiology Month February to November 2013 based on Poisson-gamma Model.

Node	Mean	Sd	MC error	2.5%	Median	97.5 %	Start	Sample
theta[1,2]	1.003	0.352	0.00477	0.426	0.9613	1.80	1000	4001
theta[1,3]	1.273	0.408	0.00757	0.623	1.222	2.22	1000	4001
theta[1,4]	1.219	0.388	0.00654	0.592	1.174	2.10	1000	4001
theta[1,5]	1.067	0.360	0.00463	0.498	1.022	1.89	1000	4001
theta[1,6]	0.844	0.315	0.00556	0.347	0.8028	1.56	1000	4001
theta[1,7]	0.963	0.340	0.00530	0.411	0.9248	1.73	1000	4001
theta[1,8]	0.875	0.331	0.00504	0.357	0.8349	1.64	1000	4001
theta[1,9]	0.937	0.329	0.00483	0.399	0.9002	1.66	1000	4001
theta[1,10]	1.053	0.351	0.00524	0.494	1.011	1.86	1000	4001
theta[1,11]	1.085	0.365	0.00538	0.497	1.046	1.91	1000	4001

From Table 4.3, the output of WinBUGS for estimated relative risk based on Poisson-gamma for both HIV and AIDS are presented in table that comprise of nine columns of default display which are labelled as ‘node’, ‘mean’, ‘sd’, ‘MC error’, ‘2.5 %’, ‘median’, ‘97.5%’, ‘start’, and ‘sample’.

Node represents the name of the unknown quantity which is the centre of interest in a study and is predefined in sample monitor tool during computing the posterior distribution in the WinBUGS software. The term ‘node’ refers as the

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unknown name of an interest. This study concerns about the relative risk. Based on Table 4.3, *theta*[1,2] represents the relative risk for the first state which is Perlis for the second epidemiology month which is February 2013, followed by *theta*[1,3] which represents Perlis for the epidemiology in March 2013 and so on.

The 'start' column represents the initial value of simulation. In this study, the value of 1000 is chosen in order to have a stable starting block of iterations for the simulations. Hence the cut-off point is 1000. Next, the 'mean' in the second column describes the average of the simulations which is the approximation mean of the posterior distribution for the relative risk quantity. On the other hand, 'sd' means the approximation of standard deviation of posterior distribution and 'MC error' identifies the estimation of Monte Carlo standard error of the mean. This error can be made as small as desired by increasing the number of simulations.

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Subsequently, the '2.5%' column describes the 2.5th percentile of the simulations which is an approximation of the lower endpoint of the 95% credible interval. The 'median' column shows the median or the 50^{th} percentile of the simulations while '97.5%' shows the 97.5^{th} percentile of the simulations as an approximation of the upper endpoint of the 95% credible interval.

It can be seen from Table 4.3 that the mean of the posterior distribution is close to the value of median which indicates that the density of the posterior distribution is reasonably symmetric. Figure 4.8 displays an example of the WinBUGS results of the posterior densities of the relative risk estimation based on the Poisson-gamma model from epidemiology month February to November 2013 for the state of Perlis which the month and state are chosen arbitrarily for demonstration purposes.

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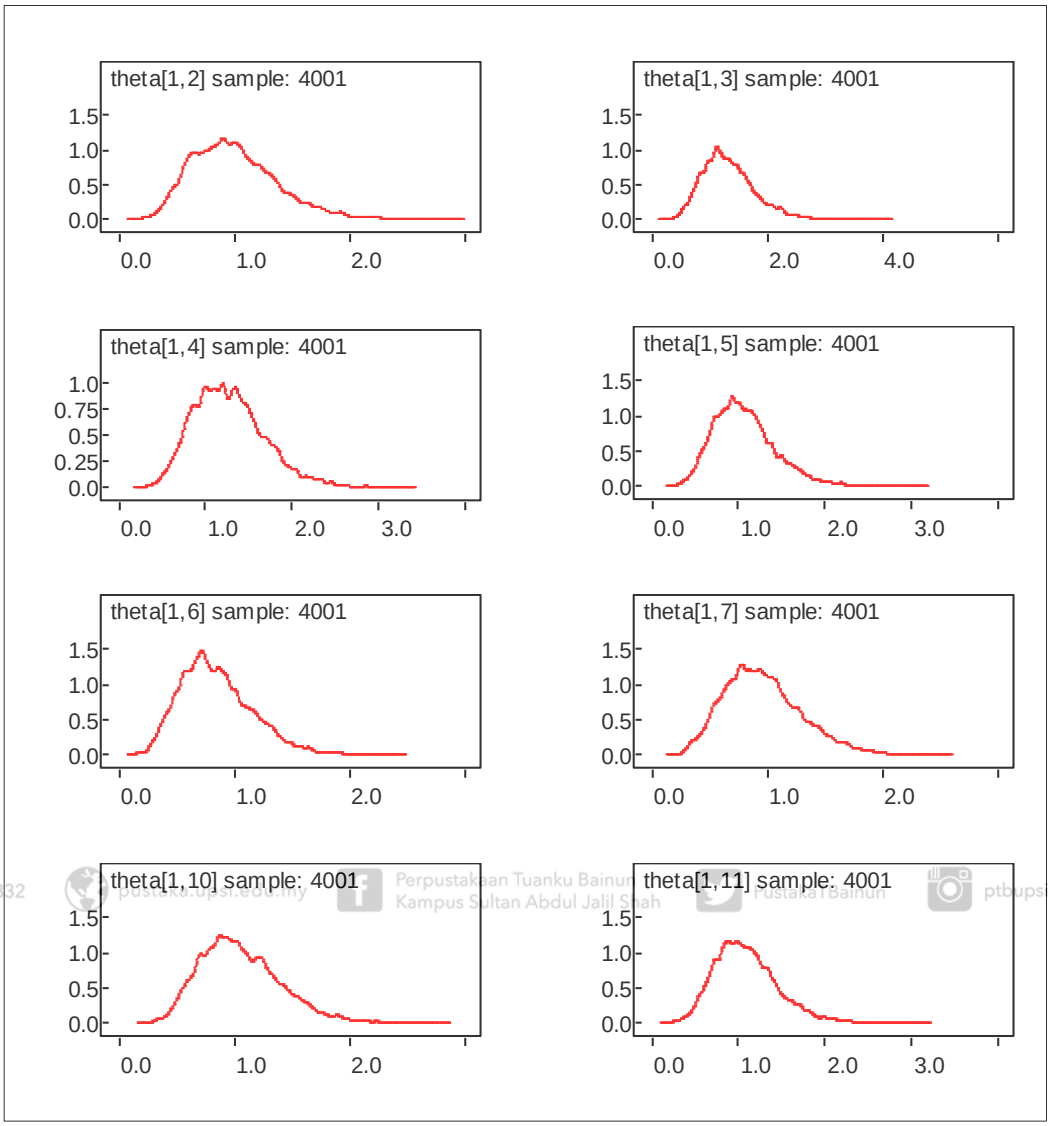


Figure 4.8. Example of WinBUGS Results of the Posterior Densities

The last column is 'sample' with the value of 4001 which refers to the sample taken from the simulation. This value is also utilized to find the convergence of the MCMC method which can be done by examining the 'history' plot of the sample at each iteration and look for random scatter. This convergence is functioning to view the stability of the iteration of simulation for the random scatter. Figure 4.9 shows the 'history' plot of this analysis.

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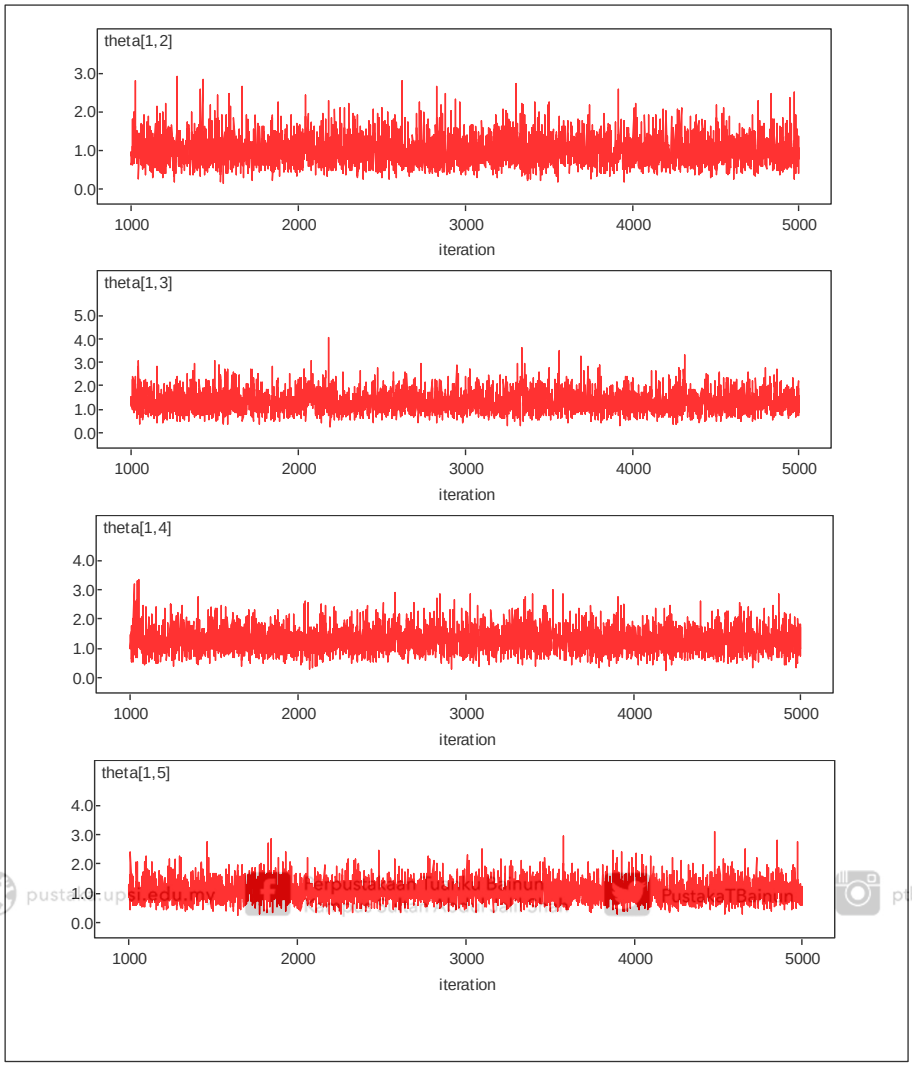


Figure 4.9. Example of WinBUGS Results for the 'History' Plot for Convergence

In the application of Bayesian statistics, WinBUGS software is also used in determining whether the Markov Chain has reach or converged to its stationary distribution. If the Markov Chain is still progressing toward its stationary distribution at a given point in the run without having reached it, the current and all previous iteration from the computational must be omitted as burn-in iterations. Thus, one diagnostic to consider is a plot of moving average of the quantiles and mean of the distribution as shown in Figure 4.10. Based on the plotted graphs, if the posterior distribution has been reached, the mean should be relatively stable over various subsets of Markov Chain.

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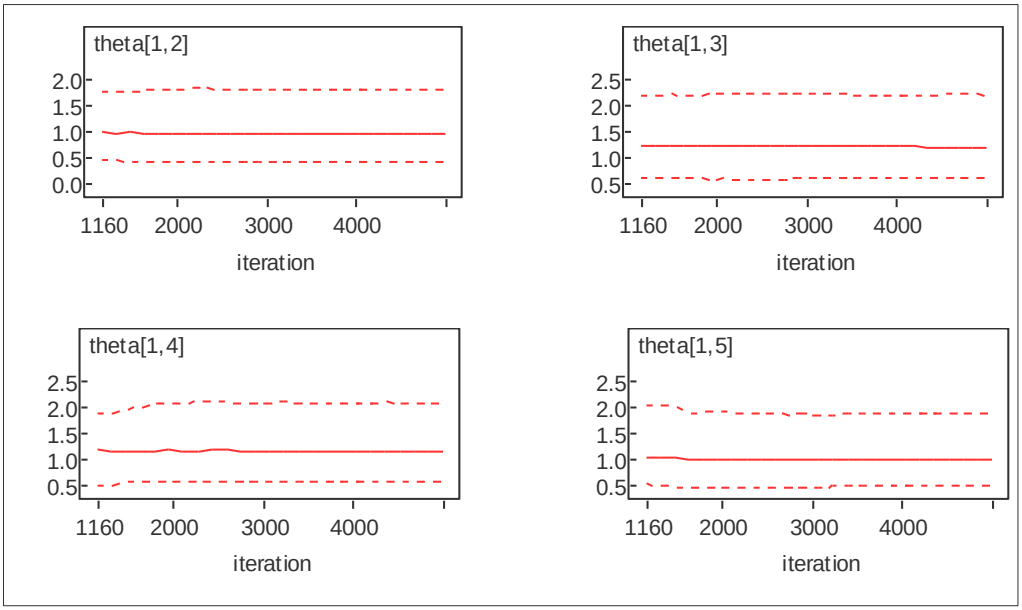


Figure 4.10 Example of WinBUGS Results for the Posterior Densities

Similarly, the estimates of the quantiles should be stable over various subsets of the Markov Chain. Hence, plotting moving average of the mean and quantiles of the distribution should show relatively little movement over course of the run if the chain has converged.

If the chain has not converged, a moving average of the mean and quantiles should be drifting forward the stationary distribution over the course of the run.Form Figure 4.10, it can be seen that the running mean and quantiles are plotted correspond with the iteration number on the x-axis and WinBUGS is taking 160 iteration moving average of the quantiles plotted.

Therefore, the moving average of the mean and 95% credible interval for theta in this analysis will appears stable over the course of the run. Next section will discuss on both estimation for relative risk HIV and AIDS based on the proposed discrete time-space stochastic SIR model.

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4.4 Estimation of Relative Risk for HIV and AIDS Mapping Based on The Discrete Time, Discrete Space Stochastic SIR Model

In this section, firstly, some parameters used in the analysis of relative risk estimation is discussed. Then this is followed by the WinBUGS code which is used for the relative risk estimation based on discrete time-space stochastic SIR for both HIV and AIDS cases.

Next, the result of relative risk estimation based on the SIR model is demonstrated in a graph of time series and a table of numerical values for the relative risk based on the model for both HIV and AIDS.

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4.4.1 The Parameter Estimation of HIV and AIDS Infection for SIR Model

In this analysis, the monthly rate parameters μ, δ_1 and δ_2 were 0.000391, 0.00000575 and 0.0000182 respectively. These parameters were converted from annual rates to monthly rates which will be discussed in the following section.

Furthermore, the probability of infection if the partner is HIV-positive, β is based on Jan (1999) which discussed the analysis of stochastic migration on the SIR Model for the transmission of HIV. According to that research, the parameter value for relative infection rate was 0.15 per partner. This rate is assumed to be equal to the

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probability of infection rate of HIV in Malaysia. This is because the probability of the HIV infection for humankind could be considered similar.

In addition, since there is no available data for the rate of new partnership that occurs in Malaysia, we impute suitable values of parameter *b* based on the literature (see, for example Tothill *et al.*, 2013; and 2005 Durex Global Sex Survey) which will be explained in the next section.

(a) Converting Annual Rates into Monthly Rates

According to a report published by Health Facts (2014), the average annual number of death is 4.7 per 1,000 of the population in Malaysia in a year. Here, the annual rate is μ_Y and the monthly rate is μ. Therefore,

Annual rate, $\mu_Y = \frac{4.7}{1000} = 0.0047$

Converting this monthly rate:

Monthly rate, $\mu = (1+\mu_Y)^{\frac{1}{12}} - 1 = (1+0.0047)^{\frac{1}{12}} - 1 = 0.000391$

Thus, the monthly death rate, μ is 0.000391.

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(b) Estimating Partner Acquisition Rate

Since this analysis was applied using the data from Malaysia, the rate for partner acquisition must be appropriate and compatible for this country. The estimation of the rate are based on Tothil et al. (2013) and a report by 2005 Durex Global Survey. A report based on 2005 Durex Global Sex Survey point out that more than 30 countries have carried out a survey including Malaysia and Australia with 5.8 and 9.7 number of partners.

However, the number of reported partner do not have a specific time frame (year, month or week) in which the number of couples cannot be accounted for as the acquisition rate but can be used as a measure to estimate the ratio of acquisition rate in Malaysia. Nevertheless, Tothil et al. (2013) in his paper entitled Heterosexual Partner Acquisition Rates in the Australian Population has discovered the rate for partner acquisition amongst the population from Australian. According to Tothil et al. (2013), the partner acquisition rate is based on the age as follows;

Table 4.4

Partner Acquisition Rates in the Australian Population

Age	Rate per year
16 to 19	0.5
20 to 24	0.7
24 and above	0.2

Note. Adapted from Tothill et al. 2013.

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The rate will be computed on average for simplicity. Therefore, the average partner acquisition rate in the Australian population is 0.467 per year for all ages, starts from 16 years and above. Hence, one year is equal to 0.467 rate of partnership and 9.7 number or partners is equivalent to 20.771 years. Then, the time frame assumed in 2005 Durex Global Sex Survey is 20.771 years.

Based on the time frame computed, the number of partner for Malaysia is 5.8 partners within 20.771 years. Therefore, the number of partner in Malaysia is 0.28 per year which can be considered as the rate of partnership occurs in a year.

Next, the number of rate is converted from annual rate to monthly rate in which the rate is 0.0208 of partner acquisition per month. This rate is used as initial value for the rate of partner acquisition in Malaysia.

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In this study, sensitivity analysis has been done to check the effect on the relative risk estimation output by using WinBUGS software of different parameter values. This is because some analysis could change the value of the output when different value of parameter is used. A sensitivity analysis using different values of rate of acquisition, b and the probability of infection if the partner is HIV-positive, β instead of the value discussed in this section, do not effect on relative risk results for the study on all states.

According to Table 4.4, the values of acquisition rate per year are 0.5, 0.7 and 0.2 according to age. The rate acquisition 0.5 for age 16 to 19 is chosen arbitrarily among the other age for the partnership acquisition rate,b used in WinBUGs software to estimate the value of relative risk.

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Table 4.5

Example of WinBUGS Output for Expected Relative Risks of HIV in the State of Perlis for Epidemiology Month February to November 2013 based on SIR Model by Using Parameter b is Equal to 0.0208

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	sample
RR[1,2]	0.1645	0.01581	2.078E-4	0.1333	0.1641	0.1969	1000	9001
RR[1,3]	0.2991	0.02875	3.778E-4	0.2425	0.2983	0.3581	1000	9001
RR[1,4]	0.4216	0.04052	5.324E-4	0.3417	0.4204	0.5046	1000	9001
RR[1,5]	0.4915	0.04724	6.207E-4	0.3984	0.4901	0.5883	1000	9001
RR[1,6]	0.6979	0.06708	8.814E-4	0.5657	0.696	0.8354	1000	9001
RR[1,7]	0.644	0.06189	8.133E-4	0.522	0.6422	0.7709	1000	9001
RR[1,8]	0.9117	0.08762	0.001151	0.739	0.9092	1.091	1000	9001
RR[1,9]	0.6509	0.06256	8.221E-4	0.5276	0.6492	0.7792	1000	9001
RR[1,10]	0.6572	0.06316	8.3E-4	0.5327	0.6554	0.7867	1000	9001
RR[1,11]	0.9459	0.09091	0.001195	0.7667	0.9433	1.132	1000	9001

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Table 4.6

Example of WinBUGS Output for Expected Relative Risks of HIV in the State of Perlis for Epidemiology Month February to November 2013 based on SIR Model by Using Parameter b is Equal to 0.5

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,2]	0.1645	0.01581	2.078E-4	0.1333	0.1641	0.1969	1000	9001

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Table 4.6 (Continued)

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,3]	0.2991	0.02875	3.778E-4	0.2425	0.2983	0.3581	1000	9001
RR[1,4]	0.4216	0.04052	5.324E-4	0.3417	0.4204	0.5046	1000	9001
RR[1,5]	0.4915	0.04724	6.207E-4	0.3984	0.4901	0.5883	1000	9001
RR[1,6]	0.6979	0.06708	8.814E-4	0.5657	0.696	0.8354	1000	9001
RR[1,7]	0.644	0.06189	8.133E-4	0.522	0.6422	0.7709	1000	9001
RR[1,8]	0.9117	0.08762	0.001151	0.739	0.9092	1.091	1000	9001
RR[1,9]	0.6509	0.06256	8.221E-4	0.5276	0.6492	0.7792	1000	9001
RR[1,10]	0.6572	0.06316	8.3E-4	0.5327	0.6554	0.7867	1000	9001
RR[1,11]	0.9459	0.09091	0.001195	0.7667	0.9433	1.132	1000	9001

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Table 4.7

Example of WinBUGS Output for Expected Relative Risks of HIV in the State of Perlis for Epidemiology Month February to November 2013 based on SIR Model by Using Parameter β is Equal to 0.5

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,2]	0.1645	0.01581	2.078E-4	0.1333	0.1641	0.1969	1000	9001
RR[1,3]	0.2991	0.02875	3.778E-4	0.2425	0.2983	0.3581	1000	9001
RR[1,4]	0.4216	0.04052	5.324E-4	0.3417	0.4204	0.5046	1000	9001
RR[1,5]	0.4915	0.04724	6.207E-4	0.3984	0.4901	0.5883	1000	9001
RR[1,6]	0.6979	0.06708	8.814E-4	0.5657	0.696	0.8354	1000	9001
RR[1,7]	0.644	0.06189	8.133E-4	0.522	0.6422	0.7709	1000	9001

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Table 4.7 (Continued)

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,8]	0.9117	0.08762	0.001151	0.739	0.9092	1.091	1000	9001
RR[1,9]	0.6509	0.06256	8.221E-4	0.5276	0.6492	0.7792	1000	9001
RR[1,10]	0.6572	0.06316	8.3E-4	0.5327	0.6554	0.7867	1000	9001
RR[1,11]	0.9459	0.09091	0.001195	0.7667	0.9433	1.132	1000	9001

Results in Tables 4.5 and 4.6 show the relative risk estimation for the value of *b* is equal to 0.0208 (as discussed before) and the relative risk for the value of *b* is equal to 0.5. Meanwhile, Table 4.7 shows the result of relative risk by using the value of relative infection rate, β is equal to 0.5 per partner which is taken arbitrarily for demonstration .

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Based on the Tables 4.5 and 4.6 there is no effect on the value of relative risk when different value of parameter *b* is used. Similar for Tables 4.5 and 4.7 where there is no change on relative risk by using different value of β.

(c) Estimating the Rate of Death for HIV and AIDS

Based on Health Fact (2014) by Ministry of Health Malaysia, the mortality rate of HIV and AIDS in 2013 per 100 000 population is 0.58 and 1.82 respectively. Therefore, the mortality rate for HIV and AIDS is calculate as follows;

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Mortality rate for HIV, $\delta_1 = \frac{0.58}{100000} = 0.0000058$

Mortality rate for AIDS, $\delta_2 = \frac{1.82}{100000} = 0.0000182$

In this research, the WinBUGS code for relative risk estimation is based on the discrete-time and discrete-space of stochastic SIR models for both HIV and AIDS. Those codes are based on the discrete time SIR written by Lawson (2006) in his analysis of influenza seasons in 13 consecutive time periods in South Carolina for 2004 until 2005. Nevertheless, in this study, the notations and formulations used in that WinBUGS code are modified to suit the particular requirements and conveniences of this study.

The WinBUGS code for relative risk estimation based on the discrete-time and discrete-space of stochastic SIR models for HIV and AIDS look similar in terms of the code utilized, except for the values of parameters used. This is because some of parameters used are different for the cases of HIV and AIDS. The details of the WinBUGS code has been attached in appendix for reference.

Next section shows the result of relative risk estimation discrete time-space of stochastic SIR models for HIV and AIDS developed in this chapter.

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4.4.2 WinBUGS Code for Relative Risk Estimation based on the SIR Model

Tables 4.8 and 4.9 represent the example of statistical output for the relative risk estimation based on the discrete time-space stochastic SIR model using the WinBUGS software for the state of Perlis from epidemiology month of February until November 2013 which are chosen arbitrarily for the demonstration of the WinBUGS output of the mean relative risk estimation results for HIV and AIDS.

Table 4.8

Example of WinBUGS Output for Expected Relative Risks of HIV in the State of Perlis for Epidemiology Month February to November 2013 based on SIR Model

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,2]	0.1655	0.0159	2.089E-4	0.1342	0.1651	0.1981	1000	9001
RR[1,3]	0.3008	0.02889	3.797E-4	0.2438	0.3	0.36	1000	9001
RR[1,4]	0.4239	0.04071	5.35E-4	0.3436	0.4228	0.5074	1000	9001
RR[1,5]	0.494	0.04745	6.236E-4	0.4005	0.4927	0.5913	1000	9001
RR[1,6]	0.7012	0.06735	8.851E-4	0.5684	0.6993	0.8393	1000	9001
RR[1,7]	0.6465	0.06209	8.16E-4	0.5241	0.6448	0.7738	1000	9001
RR[1,8]	0.9147	0.08786	0.001155	0.7415	0.9123	1.095	1000	9001
RR[1,9]	0.6526	0.06268	8.237E-4	0.529	0.6509	0.7811	1000	9001
RR[1,10]	0.6586	0.06325	8.312E-4	0.5339	0.6568	0.7883	1000	9001
RR[1,11]	0.9477	0.09103	0.001196	0.7683	0.9452	1.134	1000	9001

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Based on the Tables 4.8 and 4.9, the first column represents node which is RR deputed as relative risk for HIV and AIDS respectively. The table shown comprises of nine columns of default display which are labelled as 'node', 'mean', 'sd', 'MC error', '2.5 %', 'median', '97.5%', 'start', and 'sample'. The details for these nine columns have been discussed in Section 4.3.1.

Table 4.9

Example of WinBUGS Output for Expected Relative Risks of AIDS in the State of Perlis for Epidemiology Month February to November 2013 based on SIR Model

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RR[1,2]	3.782	0.9048	0.01058	2.25	3.72	5.77	1000	9001
RR[1,3]	3.777	0.9037	0.01057	2.247	3.715	5.763	1000	9001
RR[1,4]	3.773	0.9026	0.01056	2.244	3.711	5.756	1000	9001
RR[1,5]	3.768	0.9015	0.01055	2.242	3.706	5.749	1000	9001
RR[1,6]	3.763	0.9004	0.01053	2.239	3.702	5.742	1000	9001
RR[1,7]	3.759	0.8993	0.01052	2.236	3.697	5.736	1000	9001
RR[1,8]	2.503	0.5988	0.007006	1.489	2.462	3.819	1000	9001
RR[1,9]	0.8333	0.1994	0.002332	0.4958	0.8196	1.271	1000	9001
RR[1,10]	0.4162	0.09957	0.001165	0.2476	0.4093	0.635	1000	9001
RR[1,11]	0.6235	0.1492	0.001745	0.3709	0.6132	0.9513	1000	9001

In statistics, the collection of data taken over time is some form of random variation. In order to smooth a data set is to create an approximating function that attempts to capture important patterns in the data, while leaving out noise. In smoothing, the data points are modified so individual points that probably because of noise are reduce. One of the most common algorithm in smoothing method is the

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moving average which is used to assess important trends in repeated statistical simulations. Moving average is a calculation to analyze data points by creating series of averages of different subsets of the full data set.

Based on the application of moving average in WinBUGS, when there is a series of numbers and a fix subset size, the first element of the moving average is obtained by taking the average of the initial fix subset where the subset is determined by WinBUGS software of the number series. Then the subset is modified by 'shifting forward' by excluding the first number of the series and including the next number following the original sub set in the series. This creates a new subset of numbers, which is averaged. This process is repeated over entire data series. The plot line connecting all the averages is the moving average.

Therefore, in WinBUGS output in Tables 4.8 and 4.9 shows the relative risk in the first column start from February instead January. The next section will discussed the results of relative risk which is represented in time-series graph and table based on SIR model for HIV and AIDS.

4.4.3 Results of Relative Risk Estimation based on Discrete Time-Space Stochastic SIR Model for HIV and AIDS

This section discusses the results of the relative risk estimation for HIV and AIDS in Malaysia according to discrete time-space stochastic SIR model. The model is

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posterior sampling using a software called WinBUGS. The relative risk results from the software for the epidemiology month from February 2013 until December 2014 for all states and federal territories in Malaysia are shown in Figures 4.11 and 4.12.

Based on the time series plots in Figures 4.11 and 4.12, the epidemiology months begin with February 2013 until December 2014. Here, the starting month of February is appear instead of January because of the moving average concept used in WinBUGS software as discussed in Section 4.4.2. In WinBUGS, a moving average is used for time series data to smooth out short-term fluctuation and highlight longer term trends or cycle.

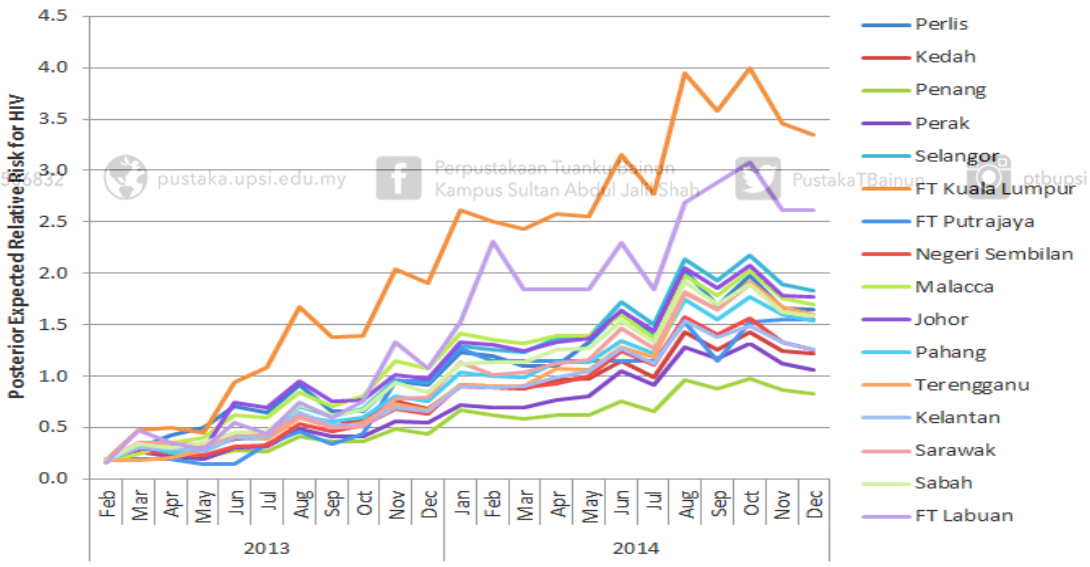


Figure 4.11. Time Series Plot of the Estimated Relative Risk based on SIR Model for HIV Cases

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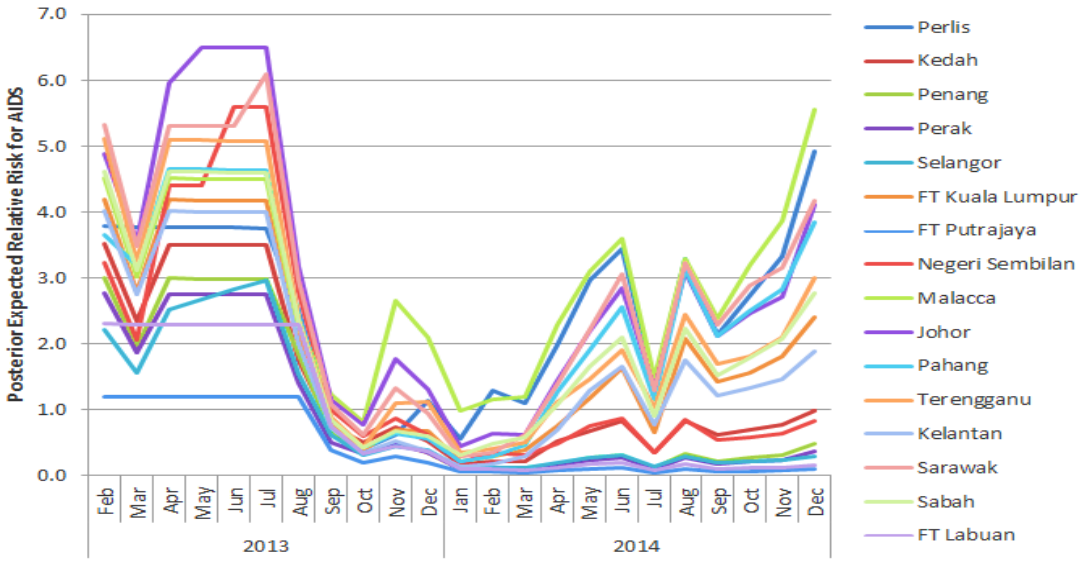


Figure 4.12. Time Series Plot of the Estimated Relative Risk based on SIR Model for AIDS Cases

Based on Figure 4.11, most of the states have relative risk less than 2.5 for all epidemiology months except for the Federal Territories of Kuala Lumpur and Labuan. This lead to a general conclusion that people in the area of Kuala Lumpur and Labuan are more likely to contract with HIV compared to all population in Malaysia. Besides, Figures 4.11 and 4.12 depict that there is no zero relative risk for all epidemiology months. This means that the proposed model can overcome the problems of SMR when there is no observed count in certain regions.

Furthermore, the time series plot in Figure 4.11 looks like there is an increasing pattern which begins from the epidemiology month February 2013 until December 2014. This is because of the mean number of infective λ_{ij}^{1} keeps increasing from month to month. The increasing value of λ_{ij}^{1} is caused by the increasing number of infective cases while the number of removed cases is less for HIV. Here, this

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analysis of SIR is assumed to be close to the population where N_i is a constant and $N_i = S_i + I_i + R_i$ as defined in Trottier and Philippe (2001).

Thus, the value of infective, I_i for HIV will keep increasing as the value of susceptible S_i decreases. While the value of R remains less as the rate of death for HIV is close to zero. Therefore, for any longitudinal infectious analysis with less rate of death for stochastic model will cause the graph of infectious to increase in time, *j*.

Next, in Figure 4.12, the time series plot for the risks estimations of AIDS are fluctuated across the epidemiology from February 2013 until December 2014. This can be assumed that the number of infective reported can determine the relative risk for AIDS. For example, the increasing of relative risk for AIDS in the epidemiology month April to July 2013 is caused by the increasing number of infective cases. Meanwhile, the small number of relative risk might be affected by the decreasing number of infective AIDS reported in time, *j*.

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Furthermore, Tables 4.10 and 4.11 show the comparison of the relative risk estimation for the epidemiology month April 2014 for HIV and AIDS, respectively, according to discrete time-space stochastic SIR model. The epidemiology month April is chosen arbitrarily to demonstrate the result of posterior expected relative risk for the proposed SIR model for heterosexual HIV and AIDS transmissions

According to Table 4.10, it can be seen that Kuala Lumpur has the highest number of relative risk of contracting HIV which is 2.578 while Penang has the lowest value of relative risk which is 0.6194. The highest number of risk for Kuala Lumpur is probably because of the high number of sex workers in some parts of

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Kuala Lumpur and also because of the large number of patients seek treatment in Kuala Lumpur as it has sufficient support facilities and complete availability of medical treatment as well (Kartikeyen *et.* al. 2007).

Table 4.10

Estimated Relative Risk in Epidemiology Month April 2014 based on Discrete Time-Space Stochastic SIR Models for HIV Transmission

States	Posterior Expected Relative Risk
Perlis	1.1000
Kedah	0.9675
Penang	0.6194
Perak	0.7672
Selangor	1.3650
FT Kuala Lumpur	2.578
FT Putrajaya	1.1490
Negeri Sembilan	0.9323
Malacca	1.3850
Johor	1.3290
Pahang	1.1350
Terengganu	1.0690
Kelantan	0.9836
Sarawak	1.1250
Sabah	1.2540
FT Labuan	1.8480

Note, FT = Federal Territory.

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Table 4.11

Estimated Relative Risk in Epidemiology Month April 2014 based on Discrete Time-Space Stochastic SIR Models for AIDS Transmission

States	Posterior Expected Relative Risk
Perlis	1.991
Kedah	0.5186
Penang	0.1827
Perak	0.1652
Selangor	0.2046
FT Kuala Lumpur	0.7533
FT Putrajaya	0.0846
Negeri Sembilan	0.4914
Malacca	2.296
Johor	1.441
Pahang	1.282
Terengganu	1.126
Kelantan	0.7076
Sarawak	1.4
Sabah	1.076
FT Labuan	0.1332

Note, FT = Federal Territory.

Based on Table 4.11, Malacca has the highest number of relative risk for the epidemiology month April 2014 which is 2.296. This is followed by Perlis with a relative risk of 1.991. This means that people in Malacca and Perlis are more likely to

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contract with AIDS compared to overall population in Malaysia. The high relative risk for the states of Malacca and Perlis have been discussed in Section 4.3.

In addition, Table 4.11 shows most of the states have a relative risk less than one. This can be concluded that people in these states are less likely to contract with AIDS compared to the people in overall population in Malaysia for the epidemiology month April 2014.

Generally, with respect to Tables 4.10 and 4.11, there is no zero expected relative risk observed for all states as we discussed before in Section 4.3 this proposed model is purposed to overcome the major drawback of SMR when there is zero relative risk estimation.

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4.5 Estimation of Relative Risk for HIV and AIDS Mapping based on the Discrete Time-Space Stochastic S(I^mI^f)R Model According to Gender

This section begins by the discussion and explanation on the parameters estimation for discrete time-space stochastic S(I^mI^f)R model based on gender. This is followed by the WinBUGS code of the relative risk estimation for HIV and AIDS according to the S(I^mI^f)R model and lastly is discussion on the relative risk results which are demonstrated in a graph of time series plot and tables for clarity.

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4.5.1 The Parameter Estimation of HIV and AIDS Infection for S(I^mI^f)R Model According to Gender

In this analysis of discrete time-space stochastic S(I^mI^f)R model, the analysis aims to estimate the relative risk according to gender. Thus, the subjects will be divided into male and female as described in Chapter 3. In order to estimate the relative risks, some parameters are required to compute relative risk for both male and female using the WinBUGS software.

The parameters used here are similar to the parameter used in the analysis of discrete time-space stochastic SIR model as discussed in Section 4.4.1 with some differences for the parameters acquisition rate, b and death rate, δ.

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(a) Estimation of Acquisition Rate for Male and Female

The estimation of parameter for the acquisition rate according to gender for both male and female are not provided by MOH as this specific analysis is scarce in Malaysia. In this study, the values for b^m and b^f were 0.016432 and 0.004368 respectively, for both HIV and AIDS case where the acquisition rate for male and female were based on the calculation ratio of male to female infected with HIV according to the data obtained from MOH as follows;

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Total infected cases for HIV male in the year 2013 and 2014 = 5369

Total infected cases for HIV female in 2013 and 2014 = 1462

The total case for male and female = 6831

Therefore, the percentage for male is = $\frac{5369}{6831} \times 100 = 78.6\% \approx 79\%$

While, the percentage for female is = $\frac{1462}{6831} \times 100 = 21.4\% \approx 21\%$

Thus, the ratio for male to female is 79:21. As we obtained the ratio, the acquisition rate is divided by the ratio as follows;

Acquisition rate for male = $0.0208 \times 0.79 = 0.016432$

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Acquisition rate for female = $0.0208 \times 0.21 = 4.368 \times 10^{-3} \approx 0.004368$

This calculation is based on the observed cases for HIV as we assumed the ratio for parameter new partnership occur, *b* must be taken at the early stage of infection such as HIV which is finally caused to AIDS.

(b) Estimation of Death Rate for Male and Female

Meanwhile, the values for δ_1^m and δ_1^f were chosen to be 0.00000458 and 0.00000122 for HIV male and female respectively. Meanwhile, δ_2^m and δ_2^f were 0.0000153 and 0.00000291 for AIDS male and female cases respectively. This value of parameter are

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also based on the ratio 79: 21 of male to female infected with HIV and ratio 84:16 of male to female for AIDS according to the data obtained from MOH as follows.

Mortality rate for HIV, $\delta_1 = 0.0000058$

Mortality rate for AIDS, $\delta_2 = 0.0000182$

Mortality rate for HIV male = $0.0000058 \times \frac{79}{100} = 4.582 \times 10^{-6} \approx 0.00000458$

Mortality rate for HIV female = $0.0000058 \times \frac{21}{100} = 1.218 \times 10^{-6} \approx 0.00000122$

Mortality rate for AIDS male = $0.0000182 \times \frac{84}{100} = 1.5288 \times 10^{-5} \approx 0.0000153$

Mortality rate for AIDS female = $0.0000182 \times \frac{16}{100} = 2.912 \times 10^{-6} \approx 0.00000291$

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Therefore, the mortality rate caused by HIV for male and female are 0.00000458 and 0.00000122 respectively. Meanwhile the rate of death caused by AIDS are 0.0000153 and 0.00000291 respectively for male and female.

However, a sensitivity analysis using different values of rate of acquisition, b and the rate of death, δ for both male and female instead of the value discussed in this section, do not effect on relative risk results for the study on all states as discussed in Section 4.4.1.

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4.5.2 WinBUGS Code for Relative Risk Estimation based on the S(I^mI^f)R Model

Based on the WinBUGS (see appendices), the term CAR is included in the code using the function car.normal of spatial distribution in WinBUGS for the random effects. The four arguments used for the distribution of car.normal in this analysis are '*adj* []', '*weights* []','*num* []' and '*var* []'. Here, '*adj* []' is a listing of a vector identification number of the adjacent areas for each area. For instance, Perlis is identified as 1 followed by Kedah as 2 and onwards. Therefore, '*adj* []' for Perlis is 2 which represents as Kedah. Meanwhile, '*weights* []' represents a vector that is the same length as '*adj* []' which gives the weights associated with the each pair of areas.

Here, '*weights* []' will be equivalent to one if *i* and *j* are neighbours and 0 otherwise. Further explanation of CAR model has been discussed in Section 3.5.2. Furthermore, '*num* []' is referring to the number of adjacent areas and '*var* []' is the scalar arguments related to the spatial random effects.

Tables 4.12 until 4.15 demonstrate the example of WinBUGS results for the relative risk estimation based on the discrete time-space stochastic S(I^mI^f)R model for HIV and AIDS according to male and female respectively, for the state of Perlis from the epidemiology month February until November 2013.

In this section, the state of Perlis is taken arbitrary to demonstrate the output for the expected relative risk while the epidemiology month begins with February is because of the moving average concept as discussed in Section 4.2.2.

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Table 4.12

Example of WinBUGS Output for the Expected Relative Risks of HIV Male in the State of Perlis for Epidemiology Month February to November 2013

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RRM[1,2]	0.1158	0.01353	1.607E-4	0.09042	0.1153	0.1445	1000	9001
RRM[1,3]	0.1388	0.01622	1.927E-4	0.1084	0.1382	0.1732	1000	9001
RRM[1,4]	0.3475	0.04061	4.823E-4	0.2713	0.346	0.4336	1000	9001
RRM[1,5]	0.4343	0.05075	6.028E-4	0.339	0.4324	0.5419	1000	9001
RRM[1,6]	0.6946	0.08117	9.64E-4	0.5422	0.6916	0.8667	1000	9001
RRM[1,7]	0.607	0.07094	8.425E-4	0.4739	0.6044	0.7574	1000	9001
RRM[1,8]	1.04	0.1216	0.001444	0.8122	1.036	1.298	1000	9001
RRM[1,9]	0.7793	0.09107	0.001082	0.6084	0.776	0.9724	1000	9001
RRM[1,10]	0.8466	0.09893	0.001175	0.6609	0.843	1.056	1000	9001
RRM[1,11]	1.087	0.127	0.001509	0.8487	1.083	1.356	1000	9001

Table 4.13

Example of WinBUGS Output for the Expected Relative Risks of HIV Female in the State of Perlis for Epidemiology Month February to November 2013

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RRF[1,2]	0.161	0.01882	2.235E-4	0.1257	0.1603	0.2009	1000	9001
RRF[1,3]	0.3407	0.03982	4.729E-4	0.266	0.3393	0.4252	1000	9001
RRF[1,4]	0.3558	0.04158	4.938E-4	0.2777	0.3543	0.4439	1000	9001
RRF[1,5]	0.4224	0.04937	5.863E-4	0.3298	0.4206	0.5271	1000	9001

(Continue)

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Table 4.13 (Continued)

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Start	Sample
RRF[1,6]	0.5821	0.06803	8.079E-4	0.4544	0.5796	0.7263	1000	9001
RRF[1,7]	0.5814	0.06794	8.069E-4	0.4539	0.5789	0.7255	1000	9001
RRF[1,8]	0.7259	0.08483	0.001007	0.5667	0.7228	0.9057	1000	9001
RRF[1,9]	0.4833	0.05648	6.708E-4	0.3773	0.4813	0.6031	1000	9001
RRF[1,10]	0.5793	0.0677	8.04E-4	0.4523	0.5769	0.7229	1000	9001
RRF[1,11]	0.9127	0.1067	0.001267	0.7126	0.9089	1.139	1000	9001
RRF[1,12]	0.8051	0.09409	0.001117	0.6285	0.8017	1.005	1000	

Table 4.14

Example of WinBUGS Output for the Expected Relative Risks of AIDS Male in the State of Perlis for Epidemiology Month February to November 2013

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Node	Mean	Sd	MC error	2.5%	Median	97.5%	Sample
RRM[1,2]	0.0409	0.0095	9.679E-5	0.02445	0.04014	0.062	9001
RRM[1,3]	0.04902	0.0114	1.16E-4	0.02931	0.04811	0.074	9001
RRM[1,4]	0.0408	0.0095	9.656E-5	0.0244	0.04005	0.062	9001
RRM[1,5]	0.03056	0.0071	7.233E-5	0.01828	0.03	0.046	9001
RRM[1,6]	0.03489	0.0081	8.257E-5	0.02086	0.03424	0.053	9001
RRM[1,7]	0.03049	0.0071	7.216E-5	0.01823	0.02993	0.046	9001
RRM[1,8]	0.04061	0.0095	9.61E-5	0.02428	0.03986	0.061	9001
RRM[1,9]	0.03042	0.0071	7.199E-5	0.01819	0.02986	0.046	9001
RRM[1,10]	0.02701	0.0063	6.392E-5	0.01615	0.02651	0.041	9001
RRM[1,11]	0.03468	0.0081	8.208E-5	0.02074	0.03404	0.052	9001

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Table 4.15

Example of WinBUGS Output for the Expected Relative Risks of AIDS Female in the State of Perlis for Epidemiology Month February to November 2013

Node	Mean	Sd	MC error	2.5%	Median	97.5%	Sample
RRF [1,2]	3.109	0.7289	0.00735	1.859	3.052	4.725	9001
RRF [1,3]	1.553	0.364	0.00367	0.9284	1.524	2.360	9001
RRF[1,4]	3.102	0.7272	0.00734	1.855	3.044	4.714	9001
RRF[1,5]	3.098	0.7263	0.00733	1.852	3.041	4.708	9001
RRF[1,6]	3.094	0.7254	0.00732	1.85	3.037	4.702	9001
RRF[1,7]	3.091	0.7246	0.00731	1.848	3.033	4.697	9001
RRF[1,8]	3.087	0.7237	0.00730	1.846	3.03	4.691	9001
RRF[1,9]	0.7928	0.1859	0.00187	0.4741	0.7782	1.205	9001
RRF[1,10]	0.5229	0.1226	0.00123	0.3127	0.5133	0.794	9001
RRF[1,11]	0.2854	0.06691	6.754E-	0.1706	0.2801	0.433	9001

Based on the Tables 4.12 until 4.15, the node RRM represents relative risk for male while RRF is relative risk for female for both heterosexual HIV and AIDS cases. In the following subsection, the results of relative risk estimation based on the discrete time-space stochastic $S(I^mI^f)R$ model according to gender are displayed in plot time series graph for all epidemiology months February 2013 until December 2014.

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4.5.3 Results of Relative Risk Estimation Based on Discrete Time-Space Stochastic S(I^mI^f)R Model According to Gender

The results of relative risk estimation based on the model of discrete time-space stochastic S(I^mI^f)R according to gender will be discussed in this section. The relative risks are demonstrated and represented in graphs and tables for both HIV and AIDS cases according to gender.

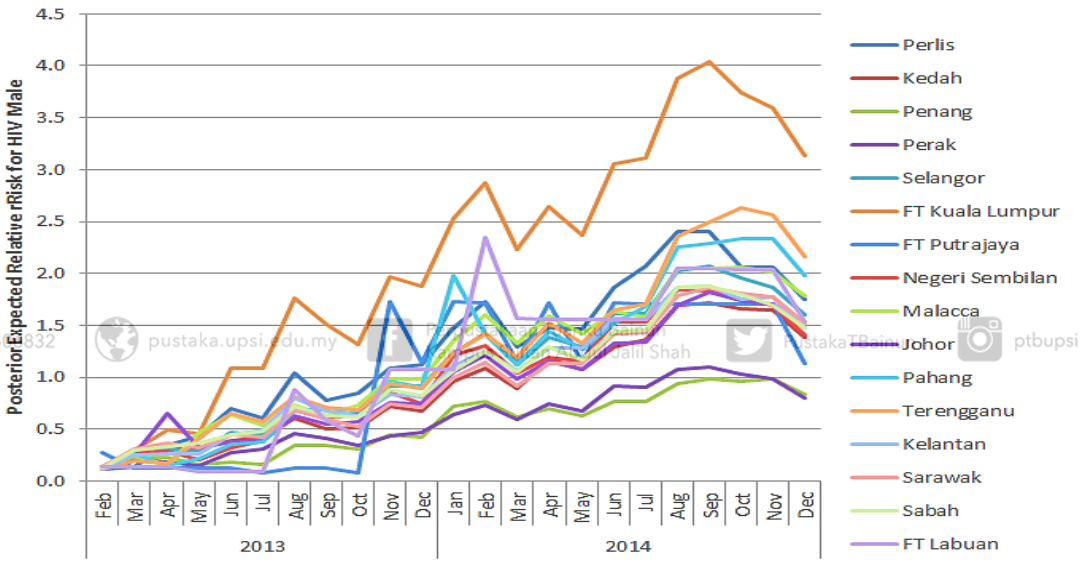


Figure 4.13. Time Series Plot of the Estimated Relative Risk based on the Discrete Time-space Stochastic S(I^mI^f)R for HIV Male Cases

Based on both graphs in Figures 4.13 and 4.14, Kuala Lumpur has higher relative risk compared to the other states. Meanwhile, Penang has lower relative risk for most of the epidemiology month. As discussed in Section 4.4.3, the pattern of the plotted graph seems increasing from epidemiology month February 2013 until December 2014 due to the value of posterior distribution for the mean number of infective $\lambda_{ij}^{(1)}$ that keeps increasing from month to month.

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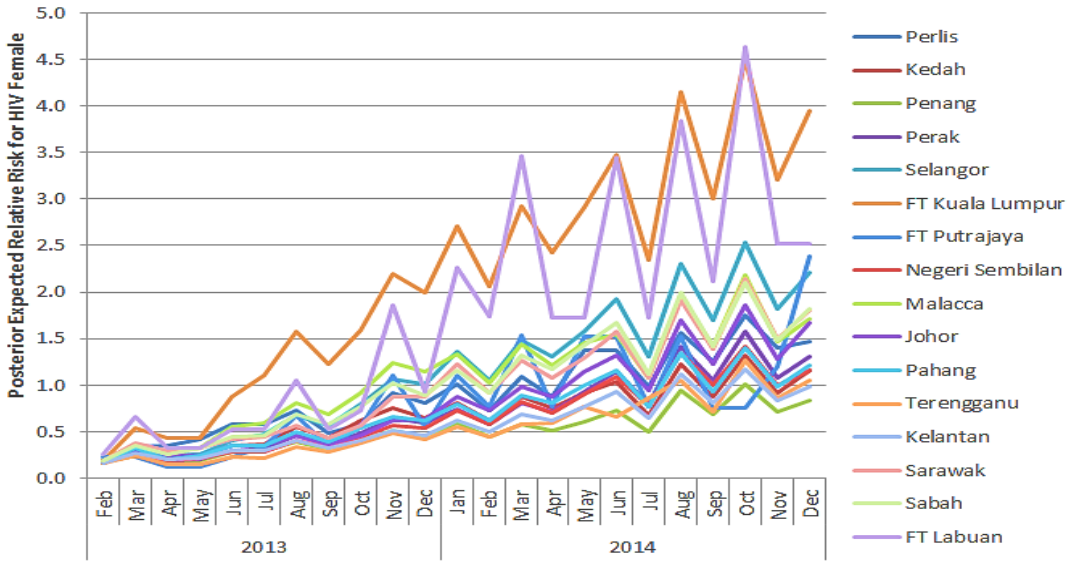


Figure 4.14. Time Series Plot of the Estimated Relative Risk based on the Discrete Time-space Stochastic S(I^mI^f)R for HIV Female Cases

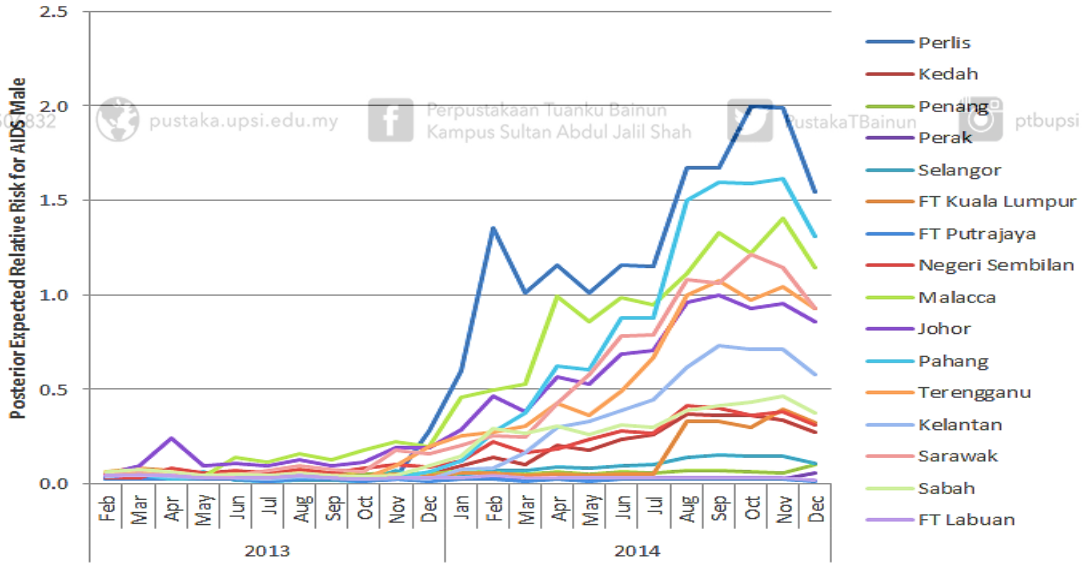


Figure 4.15. Time Series Plot of the Estimated Relative Risk based on the Discrete Time-space Stochastic S(I^mI^f)R for AIDS Male Cases

For AIDS cases, especially for male as shown in Figure 4.15, it shows that Perlis has highest number of risk for most of the epidemiology month and is followed by Malacca while Federal Territories of Labuan and Putrajaya have lowest number of risk.

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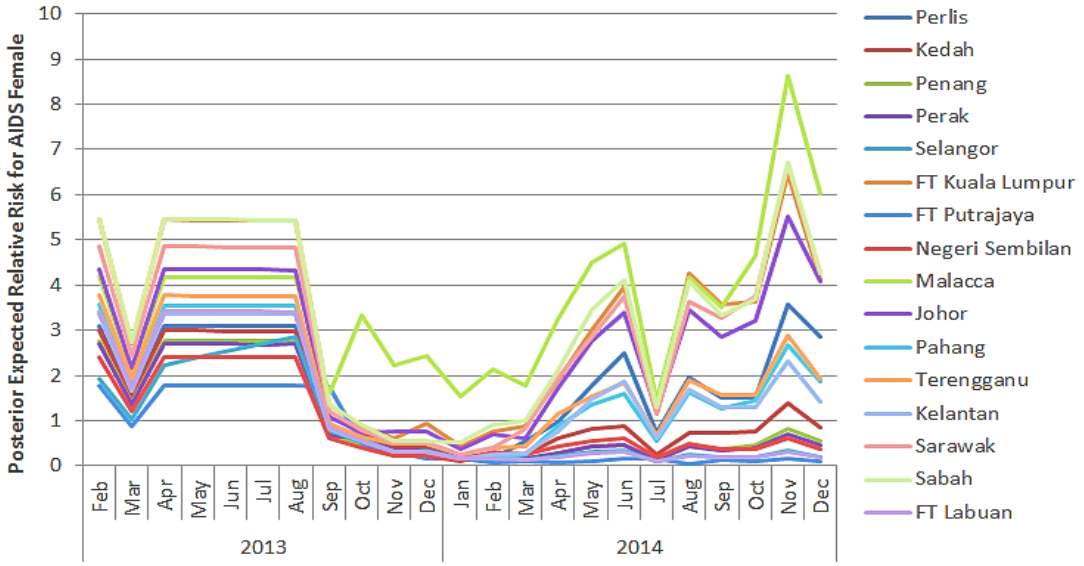


Figure 4.16. Time Series Plot of the Estimated Relative Risk based on the Discrete Time-space Stochastic $S(I^mI^f)R$ for AIDS Female Cases

According to Figure 4.16, it can be seen that the state of Malacca has that highest number of relative risk for AIDS in female cases, meanwhile the Federal Territories of Labuan and Putrajaya have the lowest risk of AIDS compared to the other states in Malaysia. The high number of relative risk for the states of Perlis and Malacca have been discussed in Section 4.3.

Tables 4.16 and 4.17 show the numerical value for the relative risks based on the discrete time-space stochastic $S(I^mI^f)R$ model according to male and female cases for the epidemiology month April 2014 for HIV and AIDS which is chosen arbitrarily to demonstrate posterior expected relative risks for both male and female.

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Table 4.16

Estimated Relative Risk in Epidemiology Month April 2014 According to Discrete Time-Space Stochastic S(I^mI^f)R Model for HIV Transmission According to Gender

States	Posterior Expected Relative Risk for Male	Posterior Expected Relative Risk for Female
Perlis	1.4770	0.8769
Kedah	1.1830	0.7484
Penang	0.7030	0.5142
Perak	0.7447	0.7173
Selangor	1.3820	1.3110
FT Kuala Lumpur	2.6440	2.4200
FT Putrajaya	1.7160	0.7649
Negeri Sembilan	1.1950	0.6989
Malacca	1.5880	1.2120
Johor	1.1560	0.8769
Pahang	1.4450	0.8045
Terengganu	1.5260	0.5970
Kelantan	1.2810	0.6241
Sarawak	1.1310	1.0750
Sabah	1.2900	1.1770
FT Labuan	1.5620	1.7280

Note, FT = Federal Territory.

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Table 4.17

Estimated Relative Risk in Epidemiology Month April 2014 According to Discrete Time-Space Stochastic S($I^m I^f$)R Model for AIDS Transmission According to Gender

States	Posterior Expected Relative Risk for Male	Posterior Expected Relative Risk for Female
Perlis	1.1580	0.9558
Kedah	0.2058	0.6117
Penang	0.0612	0.2698
Perak	0.0267	0.2943
Selangor	0.0916	0.2271
FT Kuala Lumpur	0.0512	1.8990
FT Putrajaya	0.0233	0.0672
Negeri Sembilan	0.1874	0.4190
Malacca	0.9894	3.2460
Johor	0.5675	1.7040
Pahang	0.6233	0.8944
Terengganu	0.4264	1.1630
Kelantan	0.3020	0.7507
Sarawak	0.4264	1.9710
Sabah	0.3079	2.1070
FT Labuan	0.0299	0.2065

Note, FT = Federal Territory.

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Based on Table 4.16, the general conclusion is similar with the relative risk estimation based on the discrete time-space stochastic SIR model discussed in Section 4.4.3, where the state with the highest relative risk for male and female HIV is Kuala Lumpur with 2.6444 for male and 2.4200 for female value of relative risks. This means that people either male or female in Kuala Lumpur are more likely to contract the disease compared to the overall population.

Meanwhile, the state of Penang has the lowest number of relative risk estimation which is 0.7030 and 0.5142 for male and female, respectively. Both relative risk values are less than 1 which show that the people in Penang which either male or female are less likely to contract HIV compared to the whole population.

Similar with the relative risk estimation based on discrete time-space stochastic SIR model as shown in Table 4.17, Perlis and Malacca have the highest number of relative risk, while Federal Territories of Labuan and Putrajaya have the lowest number of relative risk for male and female respectively.

The value of relative risk for AIDS male for Perlis is 1.1580 which is approximately close to 1. It can be concluded that there is no real difference in the probabilities of contracting HIV between people in the state of Perlis compared to people in overall population. Meanwhile, the value of relative risk of AIDS for female for the state of Malacca is 3.2460 which is greater than one. This means that female population within the area are easier to contract with the disease compared to people in overall population.

The next section will discuss the comparison for all methods of relative risk which are SMR method, Poisson-gamma model, discrete time-space stochastic SIR

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and $S(I^mI^f)R$ models according to the gender in order to find the better model to estimate relative risk for HIV and AIDS in Malaysia.

4.6 Comparison of Expected Relative Risk for HIV and AIDS based on SMR Method, Poisson-Gamma Model, Discrete Time-Space Stochastic SIR Model and Discrete Time-Space Stochastic $S(I^mI^f)R$ Model

Tables 4.18 and 4.19 demonstrate a comparison of the results for relative risk estimation for both HIV and AIDS based on the SMR method, the Poisson-gamma model, the discrete time-space stochastic SIR model and discrete time-space stochastic $S(I^mI^f)R$ model according to the gender. This comparison is carry out to demonstrate the drawback of existing method and how Bayesian method can overcome this problem of SMR method in order to find the better model of estimation relative risk for HIV and AIDS mapping in this country.

Basically, every month has its own pattern of relative risk observed. In this analysis of relative risk, we considered other months from January 2013 until December 2014. However, only one month is chosen for demonstration which is epidemiology month of September because that month has more than one zero value of SMR for certain states especially for AIDS cases.

According to Tables 4.18 and 4.19, it can be seen that the value of SMR equal to zero due to the zero observed case in certain states such as the states of

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Perlis, Penang, Selangor, Federal Territories of Kuala Lumpur and Putrajaya, Pahang, Terengganu, Kelantan, Sabah and Federal Territory of Labuan.

In this case, the value of relative risk not ought to be zero. This is because when the value of relative risk is zero it shows that there is no risk for the persons in study regions infected by the disease though everybody has the possibility or chance to catch with the disease. Thus, Bayesian methods is purposed to overcome this problem by producing value of relative risk for those states with zero observed case recorded for HIV and AIDS.

Basically, there is no goodness-of-fit (GOF) in WinBUGS could be used to test the best method between different model structure so far. DIC can only be used upon the models with the same structure. Therefore in this analysis, we used range as the GOF to measure the better model of relative risk compared where the smallest range indicates the better method applied. Based on the Tables 4.18 and 4.19, the results corresponding to the SIR and $S(I^mI^f)R$ models showed smallest range of expected relative risk. Therefore, the Bayesian model of the SIR and $S(I^mI^f)R$ models is better compared to SMR method and Poisson-gamma model of expected relative risk for HIV and AIDS.

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Table 4.18

Estimated Relative Risks in Epidemiology Month September 2013 for HIV Mapping using Four Different Methods

States	Relative Risk Estimation for HIV				
	SMR method	Poisson-Gamma model	SIR model	$S(I^mI^f)R$ model (Gender)	
				Male	Female
Perlis	0.7271	0.9378	0.6521	0.7793	0.5833
Kedah	1.3018	1.1870	0.5149	0.5089	0.5339
Penang	0.433	0.6746	0.4587	0.4034	0.4813
Perak	0.4327	0.6223	0.4820	0.4120	0.4697
Selangor	1.4745	1.3840	0.6029	0.6334	0.6607
FT Kuala Lumpur	1.2346	1.1340	1.0375	1.0050	1.2310
FT Putrajaya	2.2957	1.0700	0.4532	0.1261	0.4339
N. Sembilan	1.0067	0.9998	0.4653	0.6107	0.5460
Melaka	1.8857	1.3600	0.7076	0.6258	0.6833
Johor	0.7703	0.8260	0.7518	0.5550	0.4593
Pahang	1.0288	1.0210	0.5557	0.6878	0.4490
Terengganu	0.9824	0.9822	0.5039	0.7076	0.4865
Kelantan	0.5481	0.7445	0.5196	0.6716	0.4319
Sarawak	0.4864	0.6517	0.5033	0.5953	0.4355
Sabah	1.1657	1.1160	0.6202	0.6279	0.5754
FT. Labuan	0	1.0550	0.5978	0.5843	0.5276
RANGE	2.2957	0.7617	0.5788	0.6016	0.7497

Note, FT = Federal Territory.

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Table 4.19

Estimated Relative Risks in Epidemiology Month September2013 for AIDS Mapping using Four Different Methods

States	Relative Risk Estimation for AIDS				
	SMR method	Poisson-Gamma model	SIR model	$S(I^mI^f)R$ model (Gender)	
				Male	Female
Perlis	0	1.0010	0.8333	0.0304	0.7928
Kedah	2.6185	1.0870	0.7658	0.0551	0.7422
Penang	0	0.6915	0.6652	0.0571	0.6882
Perak	2.1765	1.5630	0.5064	0.0249	0.6709
Selangor	0	0.3689	0.6168	0.0163	0.7958
FT Kuala Lumpur	0	0.6723	0.7804	0.0480	1.1370
FT Putrajaya	0	1.0790	0.3982	0.0235	1.0760
N. Sembilan	2.5323	1.4710	1.0000	0.0600	0.6927
Melaka	3.1616	1.5190	1.2310	0.1257	1.0540
Johor	3.0998	2.1460	1.1540	0.0975	1.0790
Pahang	0	0.6967	0.8766	0.0291	0.8883
Terengganu	0	0.7896	0.8865	0.03272	0.9435
Kelantan	0	0.6911	0.7313	0.0292	0.8289
Sarawak	1.0485	1.0620	1.0890	0.0739	1.2060
Sabah	0	0.4987	0.8437	0.0453	1.0560
FT. Labuan	0	1.0330	0.7612	0.0301	0.8504
RANGE	3.1616	1.7771	0.8328	0.1094	0.5351

Note, FT = Federal Territory.

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For the analysis of SIR and S(I^mI^f)R models, the comparison are not purposed to define which model is better. This is because S(I^mI^f)R model is an extension for SIR model where SIR can be used for the analysis of HIV and AIDS generally while S(I^mI^f)R model is used to analyze relative risk specifically for gender in which researcher could estimate which gender are more risky toward HIV and AIDS for particular states. At the same time, we can estimate whether there is any different in relative risk between male and female toward HIV and AIDS for a particular region. Therefore, authority can have closer prevention and surveillance target especially for the states and gender.

Furthermore, discrete time-space stochastic SIR and S(I^mI^f)R models involve a more detailed description of the biological process and diseases transmission of HIV and AIDS and also allow covariate adjustment as well as the spatial correlation between neighbouring regions. Furthermore, the strong and robust model should include spatial correlation heterogeneity (Lawson, 2006).

Based on the above consideration of biological and mathematical factors, discrete time-space stochastic SIR and S(I^mI^f)R models according to gender would be the better method compared to SMR method and Poisson-gamma model in representing the process of the diseases.

The results of relative risks for all these methods can be displayed in a form of maps. The maps would demonstrate the model by showing high and low-risk areas of HIV and AIDS occurrence without considering the sexual behaviour of the population in the study states.

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4.7 Maps for Relative Risk of HIV and AIDS in Malaysia During Epidemiology Month April 2014

In this analysis, disease maps are utilized to indicate the high and low-risk region of HIV and AIDS for all states in Malaysia. Figures 4.17 to 4.26 represent the risk maps for HIV and AIDS based on the SMR method, Poisson-gamma model, discrete time-space stochastic SIR model, and discrete time-space stochastic $S(I^mI^f)R$ model according to gender respectively for epidemiology month April 2014.

Epidemiology month of April is chosen to demonstrate the disease risk maps because of the relative risk level or range are more obvious for every states in Malaysia compared to the other months of analysis. For the classification of risk maps, data has been grouped into different classes of interval. There are several ways to classify the dataset. The major methods of data classification are equal interval, mean-standard deviation, quantiles, maximum breaks, naturals breaks, and other (S.Boris *et.*,2011)

The method of equal interval and quantiles classification are appropriately used when the dataset are fairly distributed which include every single interval. In this case, most of the results of relative risks are accumulated in the range between 1.0 and 3.0 while some are too far from that range which is approximately 5.0 value of relative risk.

Therefore, in this research, to facilitate the classification of risk, the results of relative risks are divided into five different levels which are very low, low, medium, high and very high with the respective interval of (0,0.5), [0.5 – 1.0), [1.0 – 1.5), [1.5

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– 2.0), and $[2.0, \infty)$, respectively. For the maps, the darkest shaded region represents the area with highest risk while the lightest shaded region indicates the lowest risk area for HIV and AIDS.

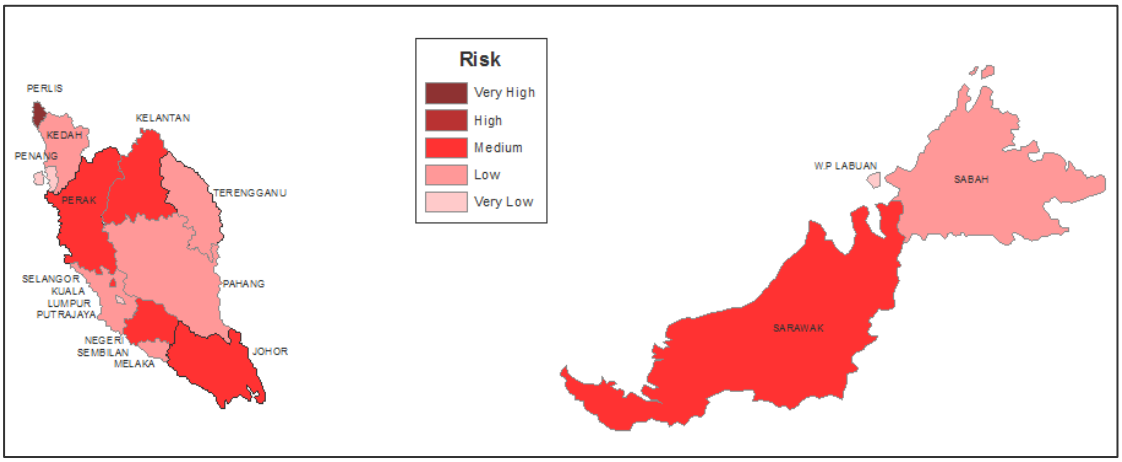


Figure 4.17. Disease Risk Map based on SMR for HIV during Epidemiology Month April 2014

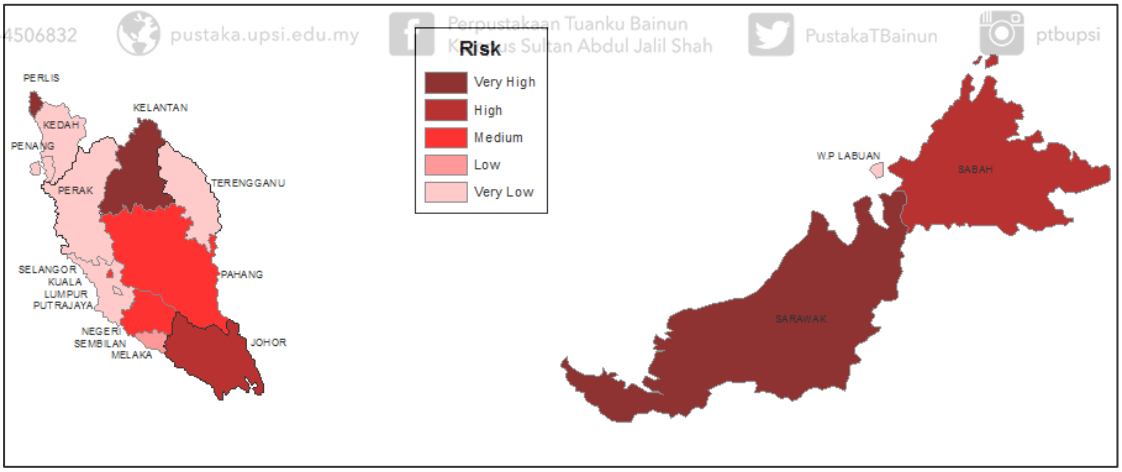


Figure 4.18. Disease Risk Map based on SMR for AIDS during Epidemiology Month April 2014

Furthermore, maps shaded in Figure 4.17 and Figure 4.18 demonstrate the relative risk estimation based on the SMR method for both HIV and AIDS. Figure 4.17 shows that the only state with a very high risk is Perlis. This is followed by Perak, Kelantan, Negeri Sembilan, Johor, and Sarawak with a medium risk while

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Federal Territory of Putrajaya has a very low risk, and the rest of the states have low risk.

For AIDS cases, in Figure 4.18, the states with very high risk includes Perlis, Kelantan, and Sarawak. The states with medium risk are Negeri Sembilan and Pahang, while other states are classified as very low risk.

The Poisson-gamma model map in Figures 4.19 shows that there is no state with very high and very low risks. The states with medium risk includes Perlis, Perak, Federal Territory of Kuala Lumpur, Negeri Sembilan, Johor, Kelantan, and Sarawak. Other states are categorized as low-risk areas.

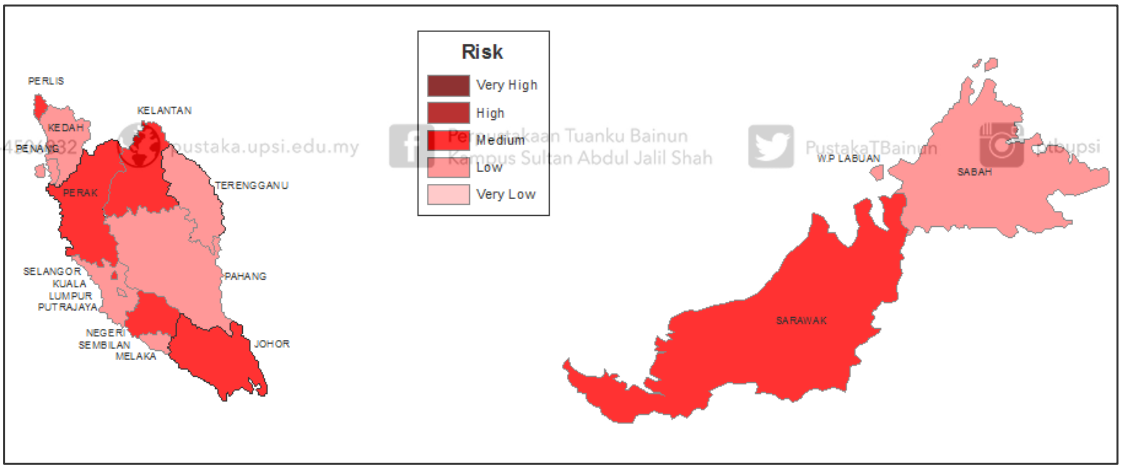


Figure 4.19. Disease Risk Map based on Poisson-gamma Model for HIV during Epidemiology Month April 2014

Meanwhile, for AIDS cases in Figure 4.20, Kelantan is the only state with very high risk. This is followed by Johor, Sarawak, and Sabah with high risk. Penang, Malacca and Federal Territories of Putrajaya and Labuan have low risk while the other four states are classified as very low risk.

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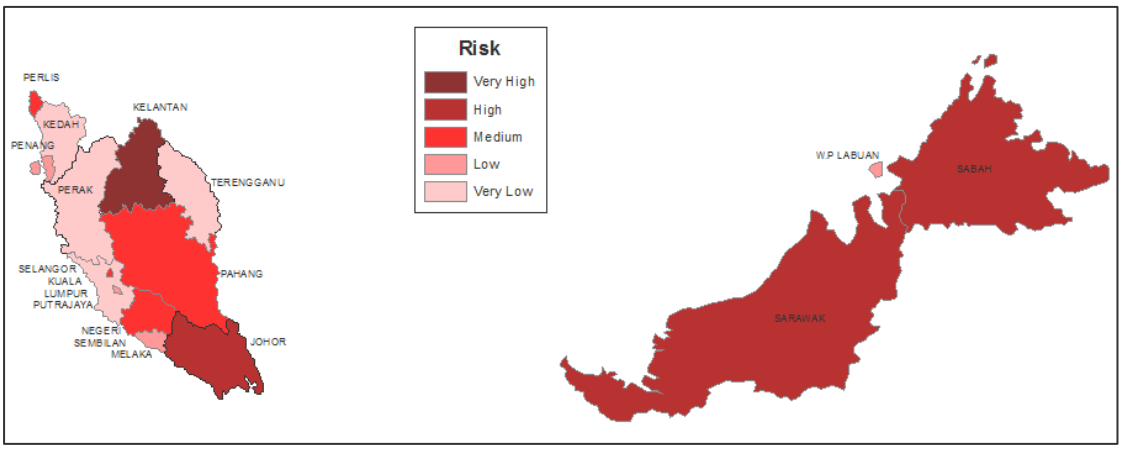


Figure 4.20. Disease Risk Map based on Poisson-gamma Model for AIDS during Epidemiology Month April 2014

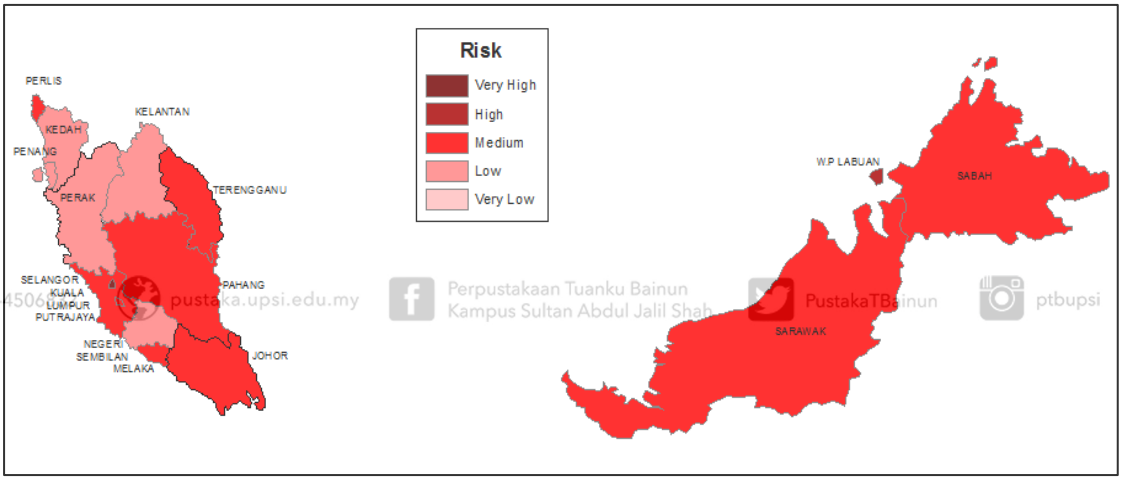


Figure 4.21. Disease Risk Map based on Discrete Time-space Stochastic SIR Model for HIV during Epidemiology Month April 2014

Figures 4.21 and 4.22 depict the maps for expected relative risk based on the discrete time-space stochastic SIR model for HIV and AIDS transmission, respectively. The risk map in Figure 4.21 demonstrates that the states with high risk includes Kuala Lumpur and Federal Territory Labuan. Most of the states have medium risk which are Perlis, Selangor, Federal Territory of Putrajaya, Malacca, Johor Pahang, Terengganu, Sarawak, and Sabah while the other five states are include as low risk.

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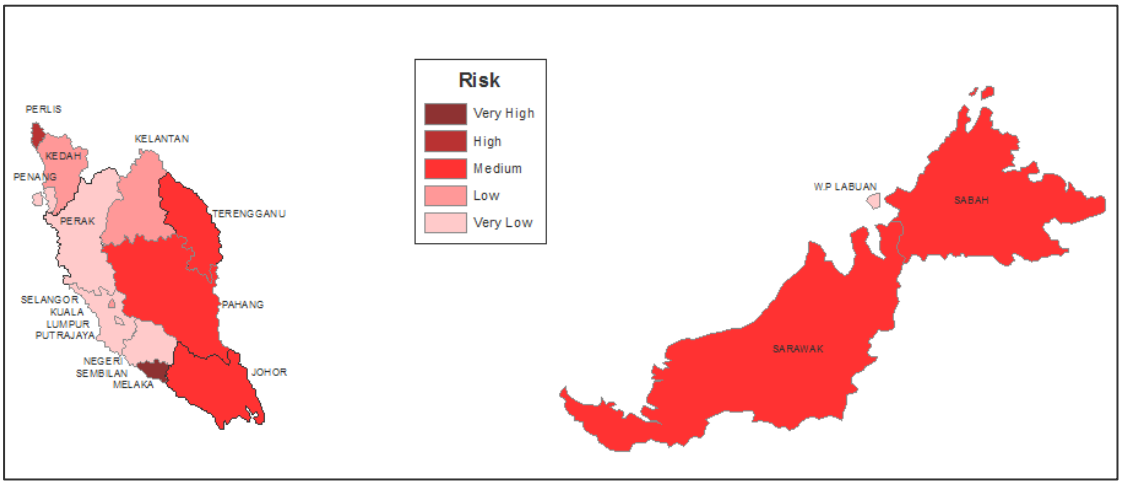


Figure 4.22. Disease Risk Map based on Discrete Time-space Stochastic SIR Model for AIDS during Epidemiology Month April 2014

For AIDS cases, in Figure 4.22, the only state with very high risk is Malacca followed by Perlis with high risk. The states of Johor, Pahang, Terengganu, Sarawak, and Sabah are classified as medium risk. The other states with low risk are Kedah, Kelantan, Kuala Lumpur and Federal Territory of Labuan while the other five states Penang, Perak, Selangor, Negeri Sembilan, and Federal Territory of Putrajaya are include as very low risk.

Figures 4.23 to 4.26 demonstrate the maps for relative risk estimation based on discrete time-space stochastic $S(I^mI^f)R$ model according to gender for both HIV and AIDS. Map in Figure 4.23 shows that the male population in Kuala Lumpur has very high risk for contracting HIV and this is followed by Malacca, Terengganu, and Federal Territory of Labuan with high risk. Most of the states have medium risk including Perlis, Kedah, Selangor, Negeri Sembilan, Johor, Pahang, and Kelantan. The only states with low risk are Penang and Perak.

Furthermore, Figure 4.24 shows that the female population in Kuala Lumpur has very high risk, followed by Federal Territory of Labuan with high risk.

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Meanwhile the female population in Selangor, Malacca, Sarawak, and Sabah have medium risk, and the rest of states are classified as low risk.

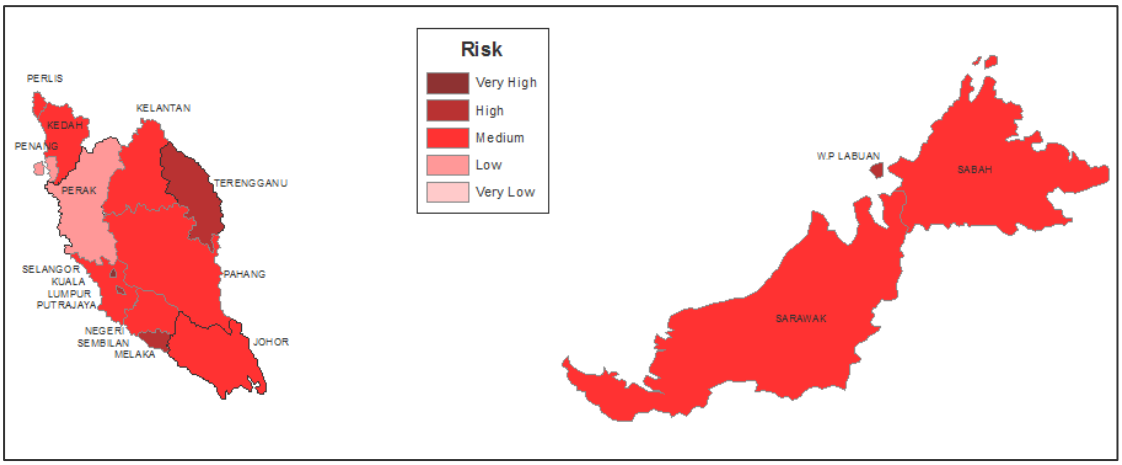


Figure 4.23. Disease Risk Map based on Discrete Time-space Stochastic $S(I^mI^f)R$ Model for HIV Male during Epidemiology Month April 2014

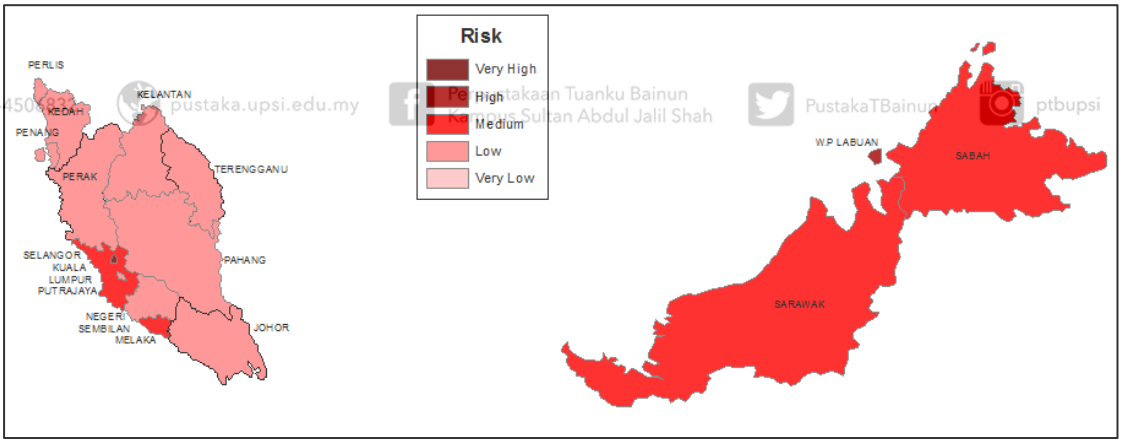


Figure 4.24. Disease Risk Map of Relative Risks based on Discrete Time-space Stochastic $S(I^mI^f)R$ Model for HIV Female during Epidemiology Month April 2014

The discrete time-space stochastic $S(I^mI^f)R$ model for male AIDS in Figure 4.25 shows that there is no state with very high and high risk. The only state with medium risk is Perlis. The other 15 states are classified as low and very low risks. Whereas, for the female population, Figure 4.26 shows that the state with very high risk are Malacca and Sabah. This is followed by Johor, Sarawak, and Kuala Lumpur

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as high risk. The only state with medium risk is Terengganu while the rest of the states are classified as low and very low risk.

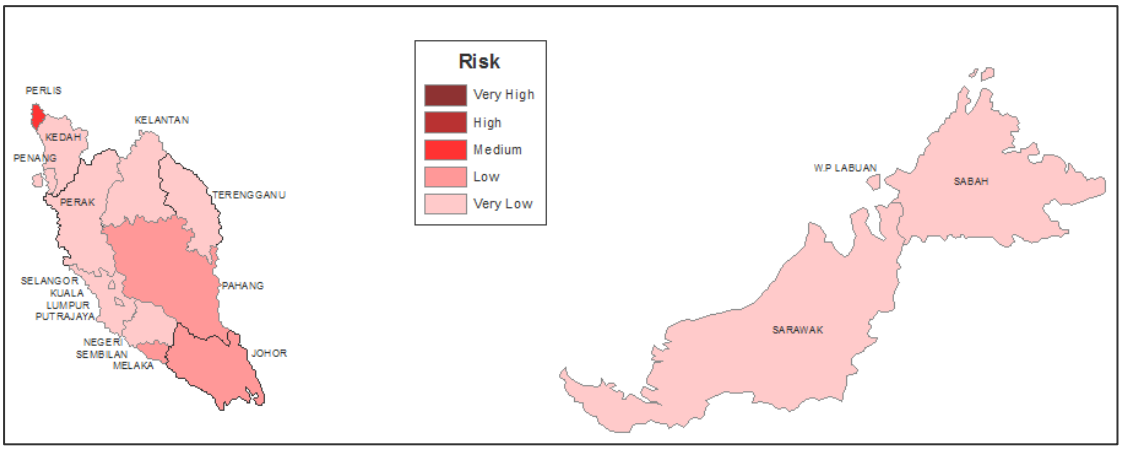


Figure 4.25. Disease Risk Map based on Discrete Time-space Stochastic $S(I^mI^f)R$ Model for AIDS Male during Epidemiology Month April 2014

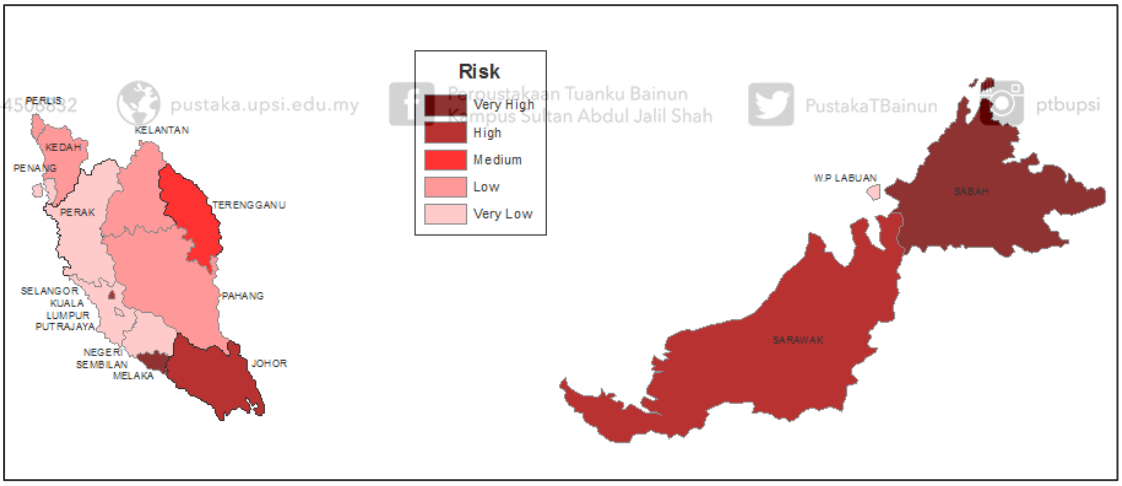


Figure 4.26. Disease Risk Map of Relative Risks based on Discrete Time-space Stochastic $S(I^mI^f)R$ Model for AIDS Female during Epidemiology Month April 2014

The activity presented in this section describes the application of the models in order to estimate the relative risk for the purpose of HIV and AIDS mapping in Malaysia. Here, the focused models are the discrete time-space stochastic SIR and discrete time-space stochastic $S(I^mI^f)R$ according to gender, which are most suitable for the analysis of heterosexual as well as the data which are specified for

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heterosexual cases of HIV and AIDS. These stochastic models include the random nature of the transmission for HIV and AIDS as well as the space-time factor. Even though in this study the analysis of the discrete time-space stochastic SIR and $S(I^mI^f)R$ model is based on heterosexual HIV and AIDS, all of these methods are able to apply more generally to other infectious diseases whether direct or indirect transmitted disease.

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CHAPTER 5

CONCLUSION, CONTRIBUTION AND RECOMMENDATION

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5.1 Conclusion

This thesis aimed to introduce alternative methods for the relative risks estimation of HIV and AIDS infectious disease. These methods would consider the transmission model of HIV and AIDS disease and improved the disease mapping. This idea was approached by reviewing the literature of relative risk estimation methods in disease

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mapping by Samat and Percy (2008) and relating these methods to HIV and AIDS infectious disease transmission methods. These new models of transmissions were motivated by the conventional and traditional models in the estimation of relative risk which were the SMR and Poisson-gamma model as discussed in Chapter 2.

Therefore, this research developed new models to overcome the problem of SMR and Poisson-gamma as discussed earlier in Section 2.8.2 which are SIR and $S(I^mI^f)R$ models. These models are sensitive when there is no observed count in certain regions. In addition, these models would facilitate the covariate adjustment where there is possibility for spatial correlation between risks in adjacent regions and the diseases.

Furthermore, based on the analysis of the literature by Samat and Percy (2012), relative risk estimation methods for disease mapping could be improved by considering other significant variables in the model. By applying this information, a new approach has been developed for relative risk estimation based on the stochastic HIV and AIDS infectious disease transmission models.

Specifically, the development of the models for relative risk estimation which was based on stochastic HIV and AIDS infectious disease transmission were consisted of modelling the discrete-time, discrete-space, stochastic SIR model, and discrete time, discrete space stochastic $S(I^mI^f)R$ model according to gender for HIV and AIDS infectious disease transmission, respectively. Then it was adapted into the relative risk estimation model. This new alternative models were developed based on the discrete time-space stochastic SIR model proposed by Lawson (2006) and Samat and Percy (2012). Here are some important conclusions based on this research;

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1. Disease mapping is a crucial tool in the prevention and control strategies for diseases. The selection of model used for relative risk estimation is important as a good model will subsequently produce a better disease risk map.
2. Relative risk estimations which is based on the new alternative proposed models for HIV and AIDS considered the number of population instead of the current method which is only based on the percentage of the number from reported cases of HIV and AIDS.
3. The stochastic terms in the SIR and $S(I^mI^f)R$ infectious diseases transmission models that have been developed for relative risk estimation allow us to assign distribution to variables and parameters that represent the random nature of the transmission of a disease as well as the time-space factor for HIV and AIDS cases.
4. In order to estimate the relative risk, the posterior expected new infective HIV and AIDS cases is determined by the fitted model, instead of just data as been used in the SMR method.
5. The application of relative risk estimation is based on the stochastic SIR and $S(I^mI^f)R$ disease transmission models of HIV and AIDS heterosexual data in Malaysia using 'discrete-time, discrete space' data. These models are better than the SMR method and Poisson-gamma model because the proposed models offer detailed description of the biological process, which take into account the transmission of the disease. Furthermore, these models also allow spatial correlation between the risks in neighbouring areas.
6. Even though the SIR and $S(I^mI^f)R$ models for HIV and AIDS diseases are the focus of this study, the methods also can be used for other infectious diseases transmission.

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Next section discusses the contributions of this study and is presented in a table form which describes the fields of reference, current methods and the contributions of this sudy.

5.2 Research Contribution

The contributions of this research are focus on advancing the knowledge of HIV and AIDS infectious diseases mapping and also for the purpose of estimating the relative risk of the diseases in Malaysia. Table 5.1 shows the list of approaches and the contributions of this research according to the fields of reference related to the estimation of relative risk for disease mapping in more concise form.

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Table 5.1

Contributions of this Research to the Knowledge of Relative Risk Estimation in Disease Mapping

Fields of Reference	Current Methods	Contributions of this Research
1. HIV and AIDS infectious disease transmissions model	• Many studies only consider the deterministic models in the analysis (for	• Introduced the stochastic disease transmission model: a) Model of SIR transmission for HIV and AIDS disease

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Table 5.1 (Continued)

Fields of Reference	Current Methods	Contributions of this Research
	example: Basavarajaiah et., al 2012, Chitnis, 2011, Herbert and James, 1992 and John et, al 1988) Most studies about HIV and AIDS transmission concern more on the model of differential equations (for example: Herbert and James 1992 and Basavarajaiah et., al 2012)	b) Model of $S(I^mI^f)R$ transmission for HIV and AIDS based on gender
2. Relative risk estimation method	• Currently, there is no published study based on the relative risk estimation related to HIV and AIDS.	• Proposed an alternative method for relative risk estimation based on stochastic difference equations for SIR of HIV and AIDS disease transmission models. • Proposed an alternative method for relative risk estimation based on stochastic difference equations for $S(I^mI^f)R$ of HIV and AIDS disease transmission model according to gender.

(Continue)

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Table 5.1 (Continued)

Fields of Reference	Current Methods	Contributions of this Research
3. Application of relative risk estimation disease mapping	• There is no HIV and AIDS infectious disease risk map for Malaysia. Current approaches for identifying the risk are based on the behavioural factors.	• Proposed a risk map for heterosexual HIV and AIDS in Malaysia

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5.3 Recommendations

All of the future works for this research are summarize as follows:

1. In this research, the discrete time-space stochastic $S(I^mI^f)R$ proposed was according to the gender; male and female. Therefore, a future study could consider other factors such as age, race, and occupation.
2. In this research, the relative risk estimation was based on stochastic SIR and $S(I^mI^f)R$ models for HIV and AIDS transmission using discrete-time and discrete space data. Future study might consider stochastic SIR and $S(I^mI^f)R$ models of HIV and AIDS transmission using continuous time and discrete-space data.

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3. Investigate the transmission of HIV and AIDS based on gender by using basic reproduction number.
4. Investigate the transmission model of the infection phases of HIV to AIDS based on basic reproduction number.
5. Introduce the prediction of HIV and AIDS infectious disease risk maps for Malaysia using the predictive relative risk estimation method based on the proposed stochastic model.

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APPENDICES

APPENDIX 1: KNOWLEDGE DISSEMINATION

Ideris, S.H and Samat, N.A (2014). "**Relative Risk Estimation for HIV and AIDS in Malaysia: Analysis based on Standardized Morbidity Ratio (SMR)**". International Postgraduate Conference on Science and Mathematic (IPCSM) 2014. Universiti Pendidikan Sultan Idris, 18-19 October.

Ideris, S.H and Samat, N.A (2015). "**HIV and AIDS Mapping: Relative Risk Estimation based on Discrete Time-Space Stochastic SIR Model for HIV and AIDS in Malaysia (Heterosexual)**". Seminar Kebangsaan Institut Statistik Malaysia ke-9, Universiti Kelbangsaan Malaysia (UKM), 30 Mac.

APPENDIX 2: PUBLICATION (Indexed Journal)

05-4506832 pustaka.upsi.edu.my Perpustakaan Tuanku Bainun Kampus Sultan Abdul Jalil Shah PustakaTBainun ptbupsi

Ideris, S.H and Samat, N.A (2015). "**Estimation of Relative Risk for HIV and AIDS in Malaysia based on Discrete Time-Space Stochastic SIR Model**". *Malaysia Journal of Science and Mathematics, UPM,* 1-10 (Submitted)

APPENDIX 3: PUBLICATION (Refereed Journal)

Ideris, S.H and Samat, N.A (2015). "**Comparison of HIV and AIDS Disease Mapping in Malaysia based on Standardized Morbidity Ratios and Poisson-Gamma Model".** *Journal of Science and Mathematics, Univeristi Pendidikan Sultan Idris.* (In press)

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APPENDIX 4: WINBUGS CODE

```
#NEW MODEL (for HIV)-Stochastic newI

model{

for (i in 1:M){
S[i,1]<-N[i]-I[i,1]-R[i,1]
I[i,1]<-0.0000091652*N[i]
R[i,1]<-0.000000409906*N[i]

}

for (i in 1:M){
for (j in 2:T){

#HUMAN POPULATIONS

S[i,j]<-(mu*N[i])+(1-mu)*S[i,j-1]-newI[i,j]
newI[i,j]~dpois(lambdanew[i,j])
log(lambdanew[i,j])<-betaH0+log((beta*b)/N[i])+log(I[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
I[i,j]<-(1-mu-gamma)*I[i,j-1]+newI[i,j]
R[i,j]<-R[i,j-1]+newR[i,j]
newR[i,j]<-(gamma*I[i,j-1])


#RELATIVE RISK

RR[i,j]<-lambdanew[i,j]/e[i,j]

}
}

#CAR prior distribution for random effects C. The sum of C is always 0

C[1:16]~car.normal(adj[], weights[], num[], varC)
for (k in 1:SumNumNeigh){
weights[k]<-1}

#Other priors

betaH0~dflat()                    #Flat prior for the intercept
varC~dgamma(0.01,0.01)            #Prior on precision for spatial random effect C
gamma<-0.00000575
}
```

Discrete Time-space Stochastic SIR Model for HIV

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```
#NEW MODEL (for AIDS)-Stochastic newI


model{

for (i in 1:M){
S[i,1]<-N[i]-I[i,1]-R[i,1]
I[i,1]<-0.00000261317*N[i]
R[i,1]<-0.000000971063*N[i]

}

for (i in 1:M){
for (j in 2:T){

#HUMAN POPULATIONS

S[i,j]<-(mu*N[i])+(1-mu)*S[i,j-1]-newI[i,j]
newI[i,j]~dpois(lambdanew[i,j])
log(lambdanew[i,j])<-betaH0+log((beta*b)/N[i])+log(I[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
I[i,j]<-(1-mu-gamma)*I[i,j-1]+newI[i,j]
R[i,j]<-R[i,j-1]+newR[i,j]
newR[i,j]<-(gamma*I[i,j-1])


#RELATIVE RISK

RR[i,j]<-lambdanew[i,j]/e[i,j]
}
}

#CAR prior distribution for random effects C. The sum of C is always 0

C[1:16]~car.normal(adj[], weights[], num[], varC)
for (k in 1:SumNumNeigh){
weights[k]<-1}

#Other priors

betaH0~dflat()                    #Flat prior for the intercept
varC~dgamma(0.01,0.01)            #Prior on precision for spatial random effect C
gamma<-0.0000172
}
```

Discrete time-space stochastic SIR model for AIDS

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```
#NEW MODEL (for AIDS According to Gender)-Stochastic newIM and newIF

model{

for (i in 1:M){
S[i,1]<-N[i]-IM[i,1]-IF[i,1]-R[i,1]
IM[i,1]<-0.00000708644*N[i]
IF[i,1]<-0.00000207872*N[i]
R[i,1]<-0.000000409906*N[i]
}
for (i in 1:M){
for (j in 2:T){

#HUMAN POPULATIONS

S[i,j]<-(mu*N[i])+(1-mu)*S[i,j-1]-newIM[i,j]-newIF[i,j]
newIM[i,j]~dpois(lambdanewM[i,j])
log(lambdanewM[i,j])<-betaH0+log((beta*bM)/N[i])+log(IF[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
IM[i,j]<-(1-mu-gammaM)*IM[i,j-1]+newIM[i,j]
newIF[i,j]~dpois(lambdanewF[i,j])
log(lambdanewF[i,j])<-betaH0+log((beta*bF)/N[i])+log(IM[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
IF[i,j]<-(1-mu-gammaF)*IF[i,j-1]+newIF[i,j]
R[i,j]<-R[i,j-1]+newRM[i,j]+newRF[i,j]
newRM[i,j]<-(gammaM*IM[i,j-1])
newRF[i,j]<-(gammaF*IF[i,j-1])

#RELATIVE RISK

RRM[i,j]<-lambdanewM[i,j]/eM[i,j]
RRF[i,j]<-lambdanewF[i,j]/eF[i,j]
}
}
#CAR prior distribution for random effects C. The sum of C is always 0

C[1:16]~car.normal(adj[], weights[], num[], varC)
for (k in 1:SumNumNeigh){
weights[k]<-1}

#Other priors
betaH0~dflat()                    #Flat prior for the intercept
varC~dgamma(0.01,0.01)            #Prior on precision for spatial random effect C
gammaM<-0.0000045195
gammaF<-0.0000012305

}
```

Discrete time-space stochastic $S(I^mI^f)R$ model for HIV in WinBUGS

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```
#NEW MODEL (for AIDS According to Gender)-Stochastic newIM and newIF

model{

for (i in 1:M){
S[i,1]<-N[i]-IM[i,1]-IF[i,1]-R[i,1]
IM[i,1]<-0.00000217*N[i]
IF[i,1]<-0.000000514908*N[i]
R[i,1]<-0.000000409906*N[i]

}

for (i in 1:M){
for (j in 2:T){

#HUMAN POPULATIONS

S[i,j]<-(mu*N[i])+(1-mu)*S[i,j-1]-newIM[i,j]-newIF[i,j]
newIM[i,j]~dpois(lambdanewM[i,j])
log(lambdanewM[i,j])<-betaH0+log((beta*bM)/N[i])+log(IF[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
IM[i,j]<-(1-mu-gammaM)*IM[i,j-1]+newIM[i,j]
newIF[i,j]~dpois(lambdanewF[i,j])
log(lambdanewF[i,j])<-betaH0+log((beta*bF)/N[i])+log(IM[i,j-1]+0.001)+log(S[i,j-1]+0.001)+C[i]
IF[i,j]<-(1-mu-gammaF)*IF[i,j-1]+newIF[i,j]
R[i,j]<-R[i,j-1]+newRM[i,j]+newRF[i,j]
newRM[i,j]<-(gammaM*IM[i,j-1])
newRF[i,j]<-(gammaF*IF[i,j-1])

#RELATIVE RISK

RRM[i,j]<-lambdanewM[i,j]/eM[i,j]
RRF[i,j]<-lambdanewF[i,j]/eF[i,j]

}
}

#CAR prior distribution for random effects C. The sum of C is always 0

C[1:16]~car.normal(adj[], weights[], num[], varC)
for (k in 1:SumNumNeigh){
weights[k]<-1}

#Other priors

betaH0~dflat()                    #Flat prior for the intercept
varC~dgamma(0.01,0.01)            #Prior on precision for spatial random effect C
gammaM<-0.0000135192
gammaF<-0.0000036808

}
```

Discrete time-space stochastic $S(I^mI^f)R$ model for AIDS in WinBUGS

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APPENDIX 5: EXAMPLE OF WINBUGS OUTPUT

(a) Poisson-gamma for HIV

node	mean	sd	MC error	2.5%	median	97.5%	start	sample
theta[1,1]	0.8345	0.3212	0.005024	0.3255	0.7957	1.562	1000	4001
theta[1,2]	1.003	0.352	0.004772	0.4267	0.9613	1.803	1000	4001
theta[1,3]	1.273	0.4081	0.007578	0.6231	1.222	2.22	1000	4001
theta[1,4]	1.219	0.388	0.006542	0.5928	1.174	2.107	1000	4001
theta[1,5]	1.067	0.3603	0.004639	0.4985	1.022	1.893	1000	4001
theta[1,6]	0.8442	0.3151	0.005563	0.3477	0.8028	1.564	1000	4001
theta[1,7]	0.9633	0.3407	0.005308	0.4113	0.9248	1.732	1000	4001
theta[1,8]	0.8758	0.3311	0.005045	0.3572	0.8349	1.643	1000	4001
theta[1,9]	0.9378	0.3294	0.004839	0.399	0.9002	1.663	1000	4001
theta[1,10]	1.053	0.3518	0.005241	0.4942	1.011	1.863	1000	4001
theta[1,11]	1.085	0.3652	0.005382	0.4977	1.046	1.913	1000	4001
theta[1,12]	0.9454	0.3333	0.005477	0.4005	0.908	1.687	1000	4001
theta[1,13]	0.9849	0.3476	0.005029	0.4309	0.9452	1.8	1000	4001
theta[1,14]	0.8403	0.3215	0.004687	0.3404	0.8036	1.581	1000	4001
theta[1,15]	0.837	0.314	0.005307	0.3562	0.7966	1.575	1000	4001
theta[1,16]	1.317	0.4054	0.007746	0.6587	1.276	2.226	1000	4001
theta[1,17]	0.9526	0.3328	0.00523	0.417	0.916	1.713	1000	4001
theta[1,18]	1.102	0.3782	0.005904	0.4913	1.054	1.967	1000	4001
theta[1,19]	0.9377	0.3352	0.005338	0.4054	0.8945	1.701	1000	4001
theta[1,20]	0.8708	0.3283	0.00567	0.3485	0.8345	1.621	1000	4001
theta[1,21]	1.096	0.3573	0.00535	0.5073	1.061	1.895	1000	4001
theta[1,22]	0.858	0.3285	0.005461	0.3528	0.8106	1.611	1000	4001
theta[1,23]	1.073	0.3528	0.006036	0.4997	1.038	1.864	1000	4001
theta[1,24]	0.8292	0.3094	0.005114	0.329	0.7922	1.518	1000	4001
theta[2,1]	0.7735	0.2038	0.003151	0.4161	0.7561	1.218	1000	4001
theta[2,2]	0.9846	0.2549	0.003631	0.5548	0.9672	1.551	1000	4001
theta[2,3]	1.231	0.3029	0.005188	0.7178	1.206	1.905	1000	4001
theta[2,4]	1.068	0.2586	0.003769	0.6302	1.049	1.628	1000	4001
theta[2,5]	0.5987	0.1823	0.003369	0.2963	0.5833	1.002	1000	4001
theta[2,6]	1.008	0.2455	0.003782	0.5821	0.9894	1.544	1000	4001
theta[2,7]	1.041	0.2404	0.003634	0.6311	1.028	1.573	1000	4001
theta[2,8]	0.8301	0.2346	0.00357	0.4403	0.8076	1.365	1000	4001
theta[2,9]	1.187	0.2455	0.004611	0.7594	1.169	1.711	1000	4001
theta[2,10]	0.6756	0.1912	0.003382	0.356	0.6548	1.098	1000	4001
theta[2,11]	0.5873	0.1865	0.002688	0.2779	0.5652	0.9996	1000	4001
theta[2,12]	0.7077	0.1949	0.003182	0.3783	0.6898	1.127	1000	4001
theta[2,13]	0.9323	0.2418	0.003916	0.5132	0.9152	1.458	1000	4001
theta[2,14]	0.9403	0.2327	0.003828	0.546	0.9203	1.446	1000	4001
theta[2,15]	1.01	0.2371	0.004372	0.5943	0.9893	1.533	1000	4001
theta[2,16]	0.7876	0.213	0.003726	0.4268	0.7631	1.269	1000	4001
theta[2,17]	0.5555	0.1793	0.003678	0.2603	0.5374	0.9675	1000	4001
theta[2,18]	0.721	0.2078	0.003105	0.3654	0.7046	1.181	1000	4001
theta[2,19]	0.9192	0.2232	0.003329	0.5325	0.9018	1.388	1000	4001
theta[2,20]	0.705	0.212	0.003318	0.3492	0.6873	1.173	1000	4001
theta[2,21]	1.004	0.246	0.003285	0.5776	0.9832	1.542	1000	4001
theta[2,22]	0.9171	0.236	0.003872	0.5184	0.8958	1.431	1000	4001
theta[2,23]	0.9425	0.2249	0.003379	0.5635	0.9252	1.433	1000	4001
theta[2,24]	1.0	0.2277	0.003701	0.6096	0.9811	1.496	1000	4001
theta[3,1]	0.9398	0.2436	0.003995	0.5265	0.9123	1.488	1000	4001
theta[3,2]	0.9558	0.2618	0.004105	0.5057	0.9343	1.548	1000	4001
theta[3,3]	0.7279	0.2456	0.003752	0.3309	0.6987	1.27	1000	4001
theta[3,4]	0.6334	0.2084	0.003536	0.2884	0.6111	1.087	1000	4001
theta[3,5]	0.7435	0.2192	0.004213	0.3837	0.7197	1.239	1000	4001
theta[3,6]	0.676	0.2101	0.003792	0.3236	0.6579	1.133	1000	4001
theta[3,7]	0.8131	0.2236	0.003653	0.442	0.7894	1.307	1000	4001
theta[3,8]	0.9331	0.2582	0.003582	0.4985	0.9113	1.501	1000	4001
theta[3,9]	0.6746	0.2038	0.003929	0.3356	0.6508	1.136	1000	4001
theta[3,10]	0.6501	0.1953	0.003656	0.3238	0.633	1.085	1000	4001
theta[3,11]	0.599	0.2023	0.00439	0.2707	0.5769	1.045	1000	4001
theta[3,12]	1.106	0.2624	0.003823	0.6614	1.085	1.673	1000	4001

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theta[3,13]	0.56	0.1989	0.004513	0.232	0.535	1.009	1000	4001
theta[3,14]	0.5995	0.1985	0.003686	0.274	0.5797	1.05	1000	4001
theta[3,15]	0.6404	0.2019	0.003877	0.3085	0.6209	1.094	1000	4001
theta[3,16]	0.6436	0.2008	0.003882	0.3137	0.6233	1.08	1000	4001
theta[3,17]	0.7522	0.22	0.004038	0.3786	0.7308	1.237	1000	4001
theta[3,18]	0.6817	0.216	0.004084	0.3294	0.6566	1.152	1000	4001
theta[3,19]	0.8605	0.2285	0.00363	0.4712	0.8378	1.366	1000	4001
theta[3,20]	0.8674	0.2502	0.003888	0.4477	0.8428	1.409	1000	4001
theta[3,21]	0.666	0.2122	0.003972	0.3193	0.6412	1.144	1000	4001
theta[3,22]	0.9758	0.2622	0.004204	0.5326	0.9524	1.547	1000	4001
theta[3,23]	0.6295	0.2004	0.003441	0.2991	0.6086	1.073	1000	4001
theta[3,24]	0.423	0.1602	0.004396	0.1663	0.4054	0.7836	1000	4001
theta[4,1]	0.8329	0.2015	0.003244	0.4951	0.8168	1.269	1000	4001
theta[4,2]	0.71	0.2027	0.003185	0.3617	0.6912	1.149	1000	4001
theta[4,3]	0.663	0.2086	0.003711	0.3178	0.6419	1.123	1000	4001
theta[4,4]	0.621	0.1882	0.003561	0.3067	0.6041	1.033	1000	4001
theta[4,5]	0.912	0.2089	0.00323	0.5546	0.8943	1.384	1000	4001
theta[4,6]	0.8475	0.2107	0.003261	0.4875	0.8292	1.309	1000	4001
theta[4,7]	0.8314	0.2	0.00307	0.4852	0.8119	1.263	1000	4001
theta[4,8]	0.8544	0.2191	0.003383	0.4688	0.8413	1.33	1000	4001
theta[4,9]	0.6223	0.1721	0.003195	0.3371	0.6044	1.004	1000	4001
theta[4,10]	0.6447	0.1723	0.002647	0.3503	0.632	1.015	1000	4001
theta[4,11]	0.899	0.2166	0.003261	0.5243	0.8845	1.354	1000	4001
theta[4,12]	0.5847	0.1684	0.003591	0.3012	0.5704	0.9466	1000	4001
theta[4,13]	0.7205	0.1986	0.003477	0.3874	0.7018	1.17	1000	4001
theta[4,14]	0.7913	0.2039	0.003478	0.4439	0.7757	1.243	1000	4001
theta[4,15]	0.9027	0.2132	0.003231	0.5288	0.8865	1.382	1000	4001
theta[4,16]	1.012	0.2296	0.003898	0.6257	0.9921	1.525	1000	4001
theta[4,17]	1.176	0.2362	0.003806	0.7673	1.156	1.689	1000	4001
theta[4,18]	0.8058	0.2076	0.003236	0.4456	0.7914	1.268	1000	4001
theta[4,19]	0.6714	0.1802	0.002949	0.3737	0.6496	1.076	1000	4001
theta[4,20]	0.9758	0.2406	0.0039	0.5679	0.9544	1.505	1000	4001
theta[4,21]	0.7414	0.1968	0.002968	0.4055	0.7261	1.17	1000	4001
theta[4,22]	0.6679	0.1937	0.003543	0.3456	0.6444	1.104	1000	4001
theta[4,23]	0.5913	0.171	0.002931	0.3018	0.5758	0.9602	1000	4001
theta[4,24]	1.025	0.2177	0.003426	0.6489	1.006	1.487	1000	4001
theta[5,1]	0.9451	0.1554	0.002497	0.6723	0.9371	1.281	1000	4001
theta[5,2]	1.009	0.1848	0.002993	0.6803	0.9974	1.399	1000	4001
theta[5,3]	0.824	0.1822	0.002957	0.51	0.81	1.224	1000	4001
theta[5,4]	0.791	0.1592	0.002769	0.5149	0.7807	1.139	1000	4001
theta[5,5]	1.138	0.1704	0.002333	0.8273	1.127	1.489	1000	4001
theta[5,6]	1.086	0.1797	0.002516	0.7571	1.08	1.462	1000	4001
theta[5,7]	1.127	0.1726	0.002412	0.8139	1.12	1.482	1000	4001
theta[5,8]	1.127	0.1918	0.003305	0.7801	1.116	1.543	1000	4001
theta[5,9]	1.384	0.1848	0.002899	1.034	1.376	1.758	1000	4001
theta[5,10]	1.128	0.1652	0.002808	0.8299	1.122	1.47	1000	4001
theta[5,11]	1.341	0.1983	0.003456	0.9844	1.331	1.747	1000	4001
theta[5,12]	1.127	0.1745	0.002719	0.8151	1.117	1.495	1000	4001
theta[5,13]	1.065	0.1802	0.002997	0.7468	1.051	1.454	1000	4001
theta[5,14]	1.047	0.1781	0.00279	0.7253	1.033	1.422	1000	4001
theta[5,15]	1.248	0.1845	0.00264	0.9144	1.242	1.635	1000	4001
theta[5,16]	0.968	0.1649	0.002962	0.6674	0.9638	1.313	1000	4001
theta[5,17]	1.331	0.1874	0.003504	0.9839	1.322	1.721	1000	4001
theta[5,18]	1.015	0.1725	0.002529	0.7045	1.007	1.39	1000	4001
theta[5,19]	1.056	0.1668	0.002417	0.7532	1.046	1.4	1000	4001
theta[5,20]	1.176	0.1933	0.003086	0.8359	1.169	1.581	1000	4001
theta[5,21]	0.9845	0.1688	0.002501	0.6787	0.9767	1.336	1000	4001
theta[5,22]	1.206	0.1921	0.003269	0.8594	1.194	1.615	1000	4001
theta[5,23]	1.045	0.1639	0.002706	0.7468	1.034	1.391	1000	4001
theta[5,24]	1.177	0.1703	0.002579	0.8664	1.166	1.529	1000	4001
theta[6,1]	1.098	0.2556	0.004499	0.6623	1.08	1.656	1000	4001
theta[6,2]	1.715	0.354	0.007823	1.111	1.686	2.466	1000	4001
theta[6,3]	1.577	0.3565	0.008152	0.9624	1.557	2.322	1000	4001
theta[6,4]	1.025	0.2671	0.004268	0.5827	0.998	1.611	1000	4001
theta[6,5]	3.012	0.4485	0.01367	2.203	2.993	3.957	1000	4001
theta[6,6]	2.471	0.4083	0.01093	1.74	2.445	3.324	1000	4001
theta[6,7]	1.803	0.3326	0.006904	1.216	1.78	2.516	1000	4001
theta[6,8]	1.463	0.323	0.006298	0.9004	1.438	2.172	1000	4001
theta[6,9]	1.134	0.256	0.003818	0.7031	1.106	1.688	1000	4001
theta[6,10]	2.243	0.3695	0.009281	1.561	2.233	3.013	1000	4001

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(b) Discrete time-space stochastic SIR model for HIV

node	mean	sd	MC error	2.5%	Median	97.5%	start	sample
RR[1,2]	0.1655	0.0159	2.089E-4	0.1342	0.1651	0.1981	1000	9001
RR[1,3]	0.3008	0.02889	3.797E-4	0.2438	0.3	0.36	1000	9001
RR[1,4]	0.4239	0.04071	5.35E-4	0.3436	0.4228	0.5074	1000	9001
RR[1,5]	0.494	0.04745	6.236E-4	0.4005	0.4927	0.5913	1000	9001
RR[1,6]	0.7012	0.06735	8.851E-4	0.5684	0.6993	0.8393	1000	9001
RR[1,7]	0.6465	0.06209	8.16E-4	0.5241	0.6448	0.7738	1000	9001
RR[1,8]	0.9147	0.08786	0.001155	0.7415	0.9123	1.095	1000	9001
RR[1,9]	0.6526	0.06268	8.237E-4	0.529	0.6509	0.7811	1000	9001
RR[1,10]	0.6586	0.06325	8.312E-4	0.5339	0.6568	0.7883	1000	9001
RR[1,11]	0.9477	0.09103	0.001196	0.7683	0.9452	1.134	1000	9001
RR[1,12]	0.919	0.08826	0.00116	0.745	0.9165	1.1	1000	9001
RR[1,13]	1.237	0.1188	0.001561	1.002	1.233	1.48	1000	9001
RR[1,14]	1.195	0.1148	0.001508	0.9687	1.192	1.43	1000	9001
RR[1,15]	1.102	0.1058	0.001391	0.8931	1.099	1.319	1000	9001
RR[1,16]	1.1	0.1057	0.001389	0.8921	1.097	1.317	1000	9001
RR[1,17]	1.331	0.1278	0.00168	1.079	1.327	1.593	1000	9001
RR[1,18]	1.639	0.1575	0.002069	1.329	1.635	1.962	1000	9001
RR[1,19]	1.394	0.1339	0.00176	1.13	1.39	1.669	1000	9001
RR[1,20]	2.025	0.1945	0.002556	1.641	2.019	2.423	1000	9001
RR[1,21]	1.685	0.1619	0.002127	1.366	1.681	2.017	1000	9001
RR[1,22]	1.973	0.1895	0.00249	1.6	1.968	2.362	1000	9001
RR[1,23]	1.668	0.1602	0.002105	1.352	1.663	1.996	1000	9001
RR[1,24]	1.654	0.1589	0.002088	1.341	1.65	1.98	1000	9001
RR[2,2]	0.1706	0.009139	1.338E-4	0.1529	0.1707	0.1886	1000	9001
RR[2,3]	0.2993	0.01603	2.347E-4	0.2682	0.2994	0.3308	1000	9001
RR[2,4]	0.3104	0.01663	2.434E-4	0.2782	0.3105	0.3431	1000	9001
RR[2,5]	0.3087	0.01654	2.42E-4	0.2767	0.3088	0.3412	1000	9001
RR[2,6]	0.3897	0.02087	3.055E-4	0.3492	0.3898	0.4308	1000	9001
RR[2,7]	0.4084	0.02188	3.202E-4	0.366	0.4085	0.4515	1000	9001
RR[2,8]	0.63	0.03374	4.939E-4	0.5646	0.6301	0.6963	1000	9001
RR[2,9]	0.5157	0.02762	4.043E-4	0.4621	0.5158	0.57	1000	9001
RR[2,10]	0.5789	0.03101	4.539E-4	0.5188	0.579	0.6399	1000	9001
RR[2,11]	0.7586	0.04063	5.948E-4	0.6798	0.7588	0.8385	1000	9001
RR[2,12]	0.684	0.03664	5.363E-4	0.613	0.6841	0.756	1000	9001
RR[2,13]	0.9085	0.04866	7.122E-4	0.8141	0.9086	1.004	1000	9001
RR[2,14]	0.8863	0.04747	6.949E-4	0.7942	0.8864	0.9796	1000	9001
RR[2,15]	0.8748	0.04685	6.858E-4	0.7839	0.8749	0.9669	1000	9001
RR[2,16]	0.9691	0.0519	7.597E-4	0.8684	0.9692	1.071	1000	9001
RR[2,17]	0.9811	0.05254	7.692E-4	0.8792	0.9812	1.084	1000	9001
RR[2,18]	1.147	0.06141	8.989E-4	1.027	1.147	1.267	1000	9001
RR[2,19]	0.989	0.05297	7.754E-4	0.8863	0.9892	1.093	1000	9001
RR[2,20]	1.426	0.07637	0.001118	1.278	1.426	1.576	1000	9001
RR[2,21]	1.253	0.06713	9.827E-4	1.123	1.254	1.385	1000	9001
RR[2,22]	1.43	0.07658	0.001121	1.281	1.43	1.58	1000	9001
RR[2,23]	1.25	0.06693	9.797E-4	1.12	1.25	1.381	1000	9001
RR[2,24]	1.218	0.06521	9.546E-4	1.091	1.218	1.346	1000	9001
RR[3,2]	0.1657	0.01058	1.62E-4	0.1438	0.166	0.1859	1000	9001
RR[3,3]	0.29	0.01852	2.835E-4	0.2517	0.2905	0.3253	1000	9001
RR[3,4]	0.2371	0.01514	2.318E-4	0.2058	0.2375	0.266	1000	9001
RR[3,5]	0.201	0.01284	1.965E-4	0.1745	0.2014	0.2256	1000	9001
RR[3,6]	0.2818	0.01799	2.754E-4	0.2446	0.2823	0.3161	1000	9001
RR[3,7]	0.2686	0.01715	2.626E-4	0.2332	0.2691	0.3014	1000	9001
RR[3,8]	0.4085	0.02608	3.993E-4	0.3546	0.4092	0.4583	1000	9001
RR[3,9]	0.3588	0.02291	3.507E-4	0.3114	0.3594	0.4025	1000	9001
RR[3,10]	0.3666	0.02341	3.584E-4	0.3183	0.3673	0.4113	1000	9001
RR[3,11]	0.4918	0.0314	4.807E-4	0.4269	0.4927	0.5517	1000	9001
RR[3,12]	0.4427	0.02827	4.327E-4	0.3843	0.4436	0.4967	1000	9001
RR[3,13]	0.6721	0.04291	6.57E-4	0.5834	0.6734	0.754	1000	9001
RR[3,14]	0.6212	0.03966	6.072E-4	0.5392	0.6224	0.6969	1000	9001
RR[3,15]	0.5872	0.03749	5.74E-4	0.5097	0.5883	0.6587	1000	9001
RR[3,16]	0.6195	0.03955	6.056E-4	0.5378	0.6207	0.695	1000	9001
RR[3,17]	0.6229	0.03977	6.089E-4	0.5408	0.6241	0.6989	1000	9001
RR[3,18]	0.7592	0.04847	7.421E-4	0.6591	0.7606	0.8517	1000	9001
RR[3,19]	0.6588	0.04206	6.44E-4	0.5719	0.6601	0.7391	1000	9001
RR[3,20]	0.9666	0.06171	9.448E-4	0.8391	0.9684	1.084	1000	9001

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RR[3,21]	0.8779	0.05605	8.581E-4	0.7621	0.8795	0.9849	1000	9001
RR[3,22]	0.9794	0.06253	9.573E-4	0.8502	0.9812	1.099	1000	9001
RR[3,23]	0.8704	0.05557	8.508E-4	0.7556	0.872	0.9765	1000	9001
RR[3,24]	0.8287	0.05291	8.1E-4	0.7194	0.8303	0.9297	1000	9001
RR[4,2]	0.1751	0.007378	9.582E-5	0.1609	0.175	0.1902	1000	9001
RR[4,3]	0.2653	0.01118	1.452E-4	0.2438	0.2652	0.2883	1000	9001
RR[4,4]	0.2201	0.009274	1.204E-4	0.2022	0.2199	0.2391	1000	9001
RR[4,5]	0.1945	0.008197	1.065E-4	0.1787	0.1944	0.2114	1000	9001
RR[4,6]	0.3052	0.01286	1.67E-4	0.2804	0.305	0.3316	1000	9001
RR[4,7]	0.3186	0.01343	1.743E-4	0.2927	0.3184	0.3461	1000	9001
RR[4,8]	0.4837	0.02038	2.647E-4	0.4443	0.4833	0.5255	1000	9001
RR[4,9]	0.41	0.01728	2.243E-4	0.3766	0.4097	0.4454	1000	9001
RR[4,10]	0.4191	0.01766	2.294E-4	0.385	0.4188	0.4554	1000	9001
RR[4,11]	0.5632	0.02373	3.082E-4	0.5174	0.5628	0.6118	1000	9001
RR[4,12]	0.5497	0.02316	3.008E-4	0.505	0.5493	0.5972	1000	9001
RR[4,13]	0.721	0.03038	3.945E-4	0.6623	0.7205	0.7833	1000	9001
RR[4,14]	0.699	0.02946	3.825E-4	0.6422	0.6986	0.7595	1000	9001
RR[4,15]	0.6926	0.02919	3.79E-4	0.6363	0.6921	0.7525	1000	9001
RR[4,16]	0.7705	0.03247	4.216E-4	0.7078	0.7699	0.8371	1000	9001
RR[4,17]	0.8113	0.03419	4.44E-4	0.7453	0.8108	0.8814	1000	9001
RR[4,18]	1.053	0.04436	5.761E-4	0.9672	1.052	1.144	1000	9001
RR[4,19]	0.9151	0.03856	5.007E-4	0.8406	0.9144	0.9942	1000	9001
RR[4,20]	1.287	0.05421	7.04E-4	1.182	1.286	1.398	1000	9001
RR[4,21]	1.178	0.04964	6.446E-4	1.082	1.177	1.28	1000	9001
RR[4,22]	1.323	0.05573	7.238E-4	1.215	1.322	1.437	1000	9001
RR[4,23]	1.131	0.04764	6.187E-4	1.039	1.13	1.228	1000	9001
RR[4,24]	1.07	0.04507	5.854E-4	0.9827	1.069	1.162	1000	9001
RR[5,2]	0.1839	0.005652	6.934E-5	0.1732	0.1837	0.1953	1000	9001
RR[5,3]	0.329	0.01011	1.241E-4	0.31	0.3288	0.3496	1000	9001
RR[5,4]	0.2925	0.00899	1.103E-4	0.2755	0.2922	0.3107	1000	9001
RR[5,5]	0.275	0.008452	1.037E-4	0.259	0.2748	0.2921	1000	9001
RR[5,6]	0.4311	0.01325	1.626E-4	0.4062	0.4308	0.458	1000	9001
RR[5,7]	0.4543	0.01396	1.713E-4	0.428	0.454	0.4827	1000	9001
RR[5,8]	0.708	0.02176	2.67E-4	0.667	0.7075	0.7522	1000	9001
RR[5,9]	0.6062	0.01863	2.286E-4	0.5711	0.6057	0.644	1000	9001
RR[5,10]	0.6854	0.02107	2.585E-4	0.6457	0.6849	0.7282	1000	9001
RR[5,11]	0.9647	0.02965	3.638E-4	0.9088	0.964	1.025	1000	9001
RR[5,12]	0.9456	0.02906	3.566E-4	0.8907	0.9448	1.005	1000	9001
RR[5,13]	1.297	0.03986	4.89E-4	1.221	1.296	1.378	1000	9001
RR[5,14]	1.267	0.03895	4.778E-4	1.194	1.266	1.346	1000	9001
RR[5,15]	1.239	0.03809	4.673E-4	1.167	1.238	1.316	1000	9001
RR[5,16]	1.373	0.04219	5.176E-4	1.293	1.372	1.458	1000	9001
RR[5,17]	1.388	0.04266	5.233E-4	1.307	1.387	1.474	1000	9001
RR[5,18]	1.728	0.05312	6.518E-4	1.628	1.727	1.836	1000	9001
RR[5,19]	1.503	0.04621	5.67E-4	1.416	1.502	1.597	1000	9001
RR[5,20]	2.148	0.06602	8.1E-4	2.023	2.146	2.282	1000	9001
RR[5,21]	1.941	0.05968	7.322E-4	1.829	1.94	2.063	1000	9001
RR[5,22]	2.18	0.06701	8.221E-4	2.054	2.178	2.316	1000	9001
RR[5,23]	1.905	0.05854	7.183E-4	1.794	1.903	2.023	1000	9001
RR[5,24]	1.837	0.05647	6.929E-4	1.731	1.836	1.952	1000	9001
RR[6,2]	0.1834	0.007946	7.731E-5	0.1681	0.1834	0.1993	1000	9001
RR[6,3]	0.4731	0.0205	1.994E-4	0.4335	0.473	0.5142	1000	9001
RR[6,4]	0.4941	0.02141	2.083E-4	0.4528	0.494	0.537	1000	9001
RR[6,5]	0.4535	0.01965	1.912E-4	0.4155	0.4534	0.4929	1000	9001
RR[6,6]	0.9461	0.04099	3.988E-4	0.8669	0.9459	1.028	1000	9001
RR[6,7]	1.092	0.04729	4.601E-4	1.0	1.091	1.186	1000	9001
RR[6,8]	1.676	0.07259	7.063E-4	1.535	1.675	1.821	1000	9001
RR[6,9]	1.377	0.05966	5.805E-4	1.262	1.377	1.497	1000	9001
RR[6,10]	1.39	0.06023	5.86E-4	1.274	1.39	1.511	1000	9001
RR[6,11]	2.037	0.08826	8.588E-4	1.867	2.037	2.214	1000	9001
RR[6,12]	1.907	0.0826	8.037E-4	1.747	1.906	2.072	1000	9001
RR[6,13]	2.616	0.1133	0.001103	2.397	2.616	2.843	1000	9001
RR[6,14]	2.511	0.1088	0.001058	2.3	2.51	2.729	1000	9001
RR[6,15]	2.439	0.1057	0.001028	2.235	2.439	2.651	1000	9001
RR[6,16]	2.583	0.1119	0.001089	2.366	2.582	2.807	1000	9001
RR[6,17]	2.556	0.1107	0.001078	2.342	2.556	2.778	1000	9001
RR[6,18]	3.163	0.137	0.001333	2.898	3.162	3.437	1000	9001
RR[6,19]	2.781	0.1205	0.001172	2.548	2.78	3.022	1000	9001
RR[6,20]	3.957	0.1714	0.001668	3.625	3.956	4.3	1000	9001
RR[6,21]	3.585	0.1553	0.001511	3.285	3.585	3.897	1000	9001

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(c) Discrete time-space stochastic $S(I^m I^f R)$ model for HIV male

node	mean	sd	MC error	2.5%	median	97.5%	start
RRM[1,2]	0.1158	0.01353	1.607E-4	0.09042	0.1153	0.1445	1000
RRM[1,3]	0.1388	0.01622	1.927E-4	0.1084	0.1382	0.1732	1000
RRM[1,4]	0.3475	0.04061	4.823E-4	0.2713	0.346	0.4336	1000
RRM[1,5]	0.4343	0.05075	6.028E-4	0.339	0.4324	0.5419	1000
RRM[1,6]	0.6946	0.08117	9.64E-4	0.5422	0.6916	0.8667	1000
RRM[1,7]	0.607	0.07094	8.425E-4	0.4739	0.6044	0.7574	1000
RRM[1,8]	1.04	0.1216	0.001444	0.8122	1.036	1.298	1000
RRM[1,9]	0.7793	0.09107	0.001082	0.6084	0.776	0.9724	1000
RRM[1,10]	0.8466	0.09893	0.001175	0.6609	0.843	1.056	1000
RRM[1,11]	1.087	0.127	0.001509	0.8487	1.083	1.356	1000
RRM[1,12]	1.124	0.1314	0.00156	0.8775	1.119	1.403	1000
RRM[1,13]	1.482	0.1732	0.002057	1.157	1.476	1.849	1000
RRM[1,14]	1.727	0.2018	0.002397	1.348	1.72	2.155	1000
RRM[1,15]	1.294	0.1512	0.001795	1.01	1.288	1.614	1000
RRM[1,16]	1.477	0.1726	0.002049	1.153	1.47	1.843	1000
RRM[1,17]	1.464	0.1711	0.002033	1.143	1.458	1.827	1000
RRM[1,18]	1.87	0.2186	0.002596	1.46	1.863	2.334	1000
RRM[1,19]	2.067	0.2416	0.002869	1.614	2.058	2.579	1000
RRM[1,20]	2.409	0.2815	0.003343	1.88	2.398	3.005	1000
RRM[1,21]	2.406	0.2811	0.003339	1.878	2.396	3.002	1000
RRM[1,22]	2.06	0.2407	0.002859	1.608	2.051	2.57	1000
RRM[1,23]	2.057	0.2404	0.002855	1.606	2.048	2.567	1000
RRM[1,24]	1.753	0.2048	0.002433	1.368	1.745	2.187	1000
RRM[2,2]	0.1233	0.007363	1.025E-4	0.1093	0.1232	0.1379	1000
RRM[2,3]	0.2479	0.0148	2.061E-4	0.2196	0.2476	0.2772	1000
RRM[2,4]	0.3366	0.0201	2.798E-4	0.2982	0.3362	0.3764	1000
RRM[2,5]	0.3204	0.01913	2.664E-4	0.2839	0.3201	0.3584	1000
RRM[2,6]	0.3875	0.02313	3.221E-4	0.3433	0.387	0.4333	1000
RRM[2,7]	0.4274	0.02552	3.554E-4	0.3787	0.4269	0.478	1000
RRM[2,8]	0.6019	0.03594	5.004E-4	0.5333	0.6013	0.6732	1000
RRM[2,9]	0.5089	0.03038	4.231E-4	0.4509	0.5083	0.5692	1000
RRM[2,10]	0.5143	0.0307	4.276E-4	0.4556	0.5137	0.5751	1000
RRM[2,11]	0.7197	0.04297	5.984E-4	0.6377	0.7189	0.8049	1000
RRM[2,12]	0.6778	0.04047	5.635E-4	0.6005	0.677	0.758	1000
RRM[2,13]	0.9596	0.05729	7.978E-4	0.8501	0.9585	1.073	1000
RRM[2,14]	1.093	0.06525	9.086E-4	0.9682	1.092	1.222	1000
RRM[2,15]	0.8947	0.05342	7.438E-4	0.7926	0.8936	1.001	1000
RRM[2,16]	1.183	0.07065	9.838E-4	1.048	1.182	1.323	1000
RRM[2,17]	1.077	0.06429	8.952E-4	0.954	1.076	1.204	1000
RRM[2,18]	1.293	0.07718	0.001075	1.145	1.291	1.446	1000
RRM[2,19]	1.363	0.08135	0.001133	1.207	1.361	1.524	1000
RRM[2,20]	1.693	0.1011	0.001407	1.5	1.691	1.893	1000
RRM[2,21]	1.712	0.1022	0.001423	1.516	1.71	1.914	1000
RRM[2,22]	1.661	0.0992	0.001381	1.472	1.66	1.858	1000
RRM[2,23]	1.644	0.09818	0.001367	1.457	1.642	1.839	1000
RRM[2,24]	1.384	0.08265	0.001151	1.226	1.383	1.548	1000
RRM[3,2]	0.12	0.008843	1.046E-4	0.1024	0.12	0.1378	1000
RRM[3,3]	0.2264	0.01668	1.973E-4	0.1932	0.2263	0.26	1000
RRM[3,4]	0.2332	0.01718	2.032E-4	0.1989	0.2331	0.2678	1000
RRM[3,5]	0.1639	0.01207	1.429E-4	0.1398	0.1638	0.1882	1000
RRM[3,6]	0.1881	0.01386	1.639E-4	0.1605	0.188	0.216	1000
RRM[3,7]	0.1577	0.01162	1.374E-4	0.1345	0.1576	0.1811	1000
RRM[3,8]	0.3432	0.02528	2.991E-4	0.2927	0.343	0.3941	1000
RRM[3,9]	0.3443	0.02536	3.0E-4	0.2937	0.3441	0.3953	1000
RRM[3,10]	0.312	0.02298	2.719E-4	0.2661	0.3119	0.3583	1000
RRM[3,11]	0.4459	0.03285	3.886E-4	0.3803	0.4457	0.512	1000
RRM[3,12]	0.423	0.03116	3.687E-4	0.3608	0.4228	0.4857	1000
RRM[3,13]	0.7216	0.05316	6.289E-4	0.6155	0.7213	0.8286	1000
RRM[3,14]	0.7722	0.05689	6.73E-4	0.6587	0.7719	0.8867	1000
RRM[3,15]	0.6174	0.04548	5.381E-4	0.5266	0.6171	0.709	1000
RRM[3,16]	0.703	0.05179	6.127E-4	0.5997	0.7027	0.8072	1000
RRM[3,17]	0.6294	0.04637	5.485E-4	0.5369	0.6291	0.7228	1000
RRM[3,18]	0.7727	0.05692	6.734E-4	0.6591	0.7723	0.8873	1000
RRM[3,19]	0.7689	0.05664	6.701E-4	0.6559	0.7686	0.8829	1000
RRM[3,20]	0.9434	0.06949	8.222E-4	0.8047	0.943	1.083	1000

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RRM[3,21]	0.9844	0.07252	8.579E-4	0.8397	0.984	1.13	1000
RRM[3,22]	0.9595	0.07068	8.363E-4	0.8185	0.9591	1.102	1000
RRM[3,23]	0.9843	0.07251	8.578E-4	0.8396	0.9839	1.13	1000
RRM[3,24]	0.8402	0.0619	7.323E-4	0.7167	0.8399	0.9648	1000
RRM[4,2]	0.1318	0.007085	8.967E-5	0.1195	0.1312	0.1474	1000
RRM[4,3]	0.2179	0.01172	1.483E-4	0.1976	0.2169	0.2437	1000
RRM[4,4]	0.1871	0.01006	1.273E-4	0.1696	0.1863	0.2093	1000
RRM[4,5]	0.1503	0.00808	1.023E-4	0.1363	0.1496	0.1681	1000
RRM[4,6]	0.2784	0.01497	1.894E-4	0.2524	0.2771	0.3114	1000
RRM[4,7]	0.3038	0.01634	2.067E-4	0.2755	0.3025	0.3399	1000
RRM[4,8]	0.4578	0.02461	3.114E-4	0.415	0.4557	0.512	1000
RRM[4,9]	0.412	0.02215	2.803E-4	0.3735	0.4101	0.4608	1000
RRM[4,10]	0.3436	0.01847	2.338E-4	0.3115	0.342	0.3843	1000
RRM[4,11]	0.4323	0.02324	2.941E-4	0.392	0.4304	0.4836	1000
RRM[4,12]	0.4696	0.02525	3.195E-4	0.4258	0.4675	0.5253	1000
RRM[4,13]	0.6448	0.03467	4.387E-4	0.5846	0.6419	0.7213	1000
RRM[4,14]	0.7319	0.03935	4.979E-4	0.6635	0.7286	0.8186	1000
RRM[4,15]	0.5902	0.03173	4.016E-4	0.5351	0.5875	0.6601	1000
RRM[4,16]	0.7447	0.04003	5.066E-4	0.6751	0.7413	0.8329	1000
RRM[4,17]	0.6761	0.03635	4.6E-4	0.613	0.6731	0.7563	1000
RRM[4,18]	0.9112	0.04898	6.199E-4	0.8261	0.907	1.019	1000
RRM[4,19]	0.9003	0.0484	6.125E-4	0.8162	0.8962	1.007	1000
RRM[4,20]	1.072	0.05764	7.295E-4	0.972	1.067	1.199	1000
RRM[4,21]	1.094	0.05881	7.443E-4	0.9918	1.089	1.224	1000
RRM[4,22]	1.029	0.05535	7.004E-4	0.9334	1.025	1.152	1000
RRM[4,23]	0.9819	0.05279	6.68E-4	0.8902	0.9774	1.098	1000
RRM[4,24]	0.7968	0.04284	5.421E-4	0.7224	0.7932	0.8912	1000
RRM[5,2]	0.133	0.004604	6.728E-5	0.1243	0.1329	0.1423	1000
RRM[5,3]	0.2805	0.009713	1.419E-4	0.2622	0.2804	0.3002	1000
RRM[5,4]	0.3097	0.01072	1.567E-4	0.2895	0.3095	0.3314	1000
RRM[5,5]	0.2865	0.00992	1.449E-4	0.2678	0.2864	0.3066	1000
RRM[5,6]	0.4661	0.01614	2.358E-4	0.4356	0.4658	0.4988	1000
RRM[5,7]	0.4455	0.01543	2.254E-4	0.4164	0.4453	0.4768	1000
RRM[5,8]	0.7186	0.02488	3.635E-4	0.6716	0.7183	0.769	1000
RRM[5,9]	0.6334	0.02193	3.204E-4	0.592	0.6331	0.6779	1000
RRM[5,10]	0.6375	0.02207	3.225E-4	0.5958	0.6372	0.6822	1000
RRM[5,11]	0.9202	0.03186	4.655E-4	0.86	0.9197	0.9847	1000
RRM[5,12]	0.9104	0.03152	4.606E-4	0.8509	0.91	0.9743	1000
RRM[5,13]	1.234	0.04272	6.242E-4	1.153	1.233	1.32	1000
RRM[5,14]	1.418	0.04911	7.175E-4	1.326	1.418	1.518	1000
RRM[5,15]	1.125	0.03895	5.691E-4	1.051	1.124	1.204	1000
RRM[5,16]	1.382	0.04784	6.99E-4	1.291	1.381	1.479	1000
RRM[5,17]	1.289	0.04462	6.52E-4	1.205	1.288	1.379	1000
RRM[5,18]	1.611	0.05578	8.15E-4	1.506	1.61	1.724	1000
RRM[5,19]	1.618	0.05602	8.185E-4	1.512	1.617	1.732	1000
RRM[5,20]	2.027	0.0702	0.001026	1.895	2.026	2.17	1000
RRM[5,21]	2.07	0.07169	0.001047	1.935	2.07	2.216	1000
RRM[5,22]	1.953	0.06761	9.878E-4	1.825	1.952	2.09	1000
RRM[5,23]	1.87	0.06473	9.458E-4	1.747	1.869	2.001	1000
RRM[5,24]	1.601	0.05544	8.1E-4	1.497	1.6	1.714	1000
RRM[6,2]	0.135	0.006178	7.279E-5	0.1229	0.1349	0.1473	1000
RRM[6,3]	0.2997	0.01372	1.616E-4	0.273	0.2996	0.327	1000
RRM[6,4]	0.4911	0.02248	2.648E-4	0.4473	0.4908	0.5358	1000
RRM[6,5]	0.4577	0.02095	2.468E-4	0.4169	0.4575	0.4994	1000
RRM[6,6]	1.088	0.0498	5.867E-4	0.991	1.087	1.187	1000
RRM[6,7]	1.093	0.05003	5.895E-4	0.9957	1.093	1.193	1000
RRM[6,8]	1.766	0.08084	9.524E-4	1.609	1.765	1.927	1000
RRM[6,9]	1.507	0.06899	8.128E-4	1.373	1.507	1.645	1000
RRM[6,10]	1.312	0.06006	7.076E-4	1.195	1.311	1.432	1000
RRM[6,11]	1.966	0.08999	0.00106	1.791	1.965	2.145	1000
RRM[6,12]	1.872	0.08567	0.001009	1.705	1.871	2.042	1000
RRM[6,13]	2.53	0.1158	0.001364	2.304	2.528	2.76	1000
RRM[6,14]	2.867	0.1312	0.001546	2.611	2.865	3.128	1000
RRM[6,15]	2.228	0.102	0.001201	2.029	2.227	2.431	1000
RRM[6,16]	2.644	0.121	0.001426	2.409	2.643	2.885	1000
RRM[6,17]	2.366	0.1083	0.001276	2.155	2.365	2.582	1000
RRM[6,18]	3.052	0.1397	0.001646	2.78	3.05	3.33	1000
RRM[6,19]	3.113	0.1425	0.001679	2.836	3.111	3.397	1000
RRM[6,20]	3.878	0.1775	0.002091	3.533	3.876	4.231	1000
RRM[6,21]	4.045	0.1851	0.002181	3.684	4.043	4.413	1000

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(d) Discrete time-space stochastic S($I^m I^f$R) model for HIV female

node	mean	sd	MC error	2.5%	median	97.5%	start
RRF[1,2]	0.161	0.01882	2.235E-4	0.1257	0.1603	0.2009	1000
RRF[1,3]	0.3407	0.03982	4.729E-4	0.266	0.3393	0.4252	1000
RRF[1,4]	0.3558	0.04158	4.938E-4	0.2777	0.3543	0.4439	1000
RRF[1,5]	0.4224	0.04937	5.863E-4	0.3298	0.4206	0.5271	1000
RRF[1,6]	0.5821	0.06803	8.079E-4	0.4544	0.5796	0.7263	1000
RRF[1,7]	0.5814	0.06794	8.069E-4	0.4539	0.5789	0.7255	1000
RRF[1,8]	0.7259	0.08483	0.001007	0.5667	0.7228	0.9057	1000
RRF[1,9]	0.4833	0.05648	6.708E-4	0.3773	0.4813	0.6031	1000
RRF[1,10]	0.5793	0.0677	8.04E-4	0.4523	0.5769	0.7229	1000
RRF[1,11]	0.9127	0.1067	0.001267	0.7126	0.9089	1.139	1000
RRF[1,12]	0.8051	0.09409	0.001117	0.6285	0.8017	1.005	1000
RRF[1,13]	1.005	0.1175	0.001395	0.7847	1.001	1.254	1000
RRF[1,14]	0.7325	0.0856	0.001017	0.5718	0.7293	0.9139	1000
RRF[1,15]	1.097	0.1282	0.001523	0.8567	1.093	1.369	1000
RRF[1,16]	0.8769	0.1025	0.001217	0.6845	0.8731	1.094	1000
RRF[1,17]	1.379	0.1611	0.001914	1.076	1.373	1.721	1000
RRF[1,18]	1.377	0.161	0.001912	1.075	1.371	1.719	1000
RRF[1,19]	0.9802	0.1146	0.00136	0.7652	0.9761	1.223	1000
RRF[1,20]	1.563	0.1827	0.00217	1.22	1.557	1.951	1000
RRF[1,21]	1.249	0.146	0.001734	0.9752	1.244	1.559	1000
RRF[1,22]	1.749	0.2044	0.002427	1.365	1.742	2.182	1000
RRF[1,23]	1.398	0.1633	0.00194	1.091	1.392	1.744	1000
RRF[1,24]	1.472	0.172	0.002042	1.149	1.465	1.836	1000
RRF[2,2]	0.1665	0.009939	1.384E-4	0.1475	0.1663	0.1862	1000
RRF[2,3]	0.2966	0.01771	2.466E-4	0.2628	0.2963	0.3317	1000
RRF[2,4]	0.2371	0.01416	1.971E-4	0.2101	0.2369	0.2652	1000
RRF[2,5]	0.2614	0.01561	2.173E-4	0.2316	0.2611	0.2924	1000
RRF[2,6]	0.3465	0.02069	2.881E-4	0.307	0.3461	0.3876	1000
RRF[2,7]	0.3678	0.02196	3.058E-4	0.3259	0.3674	0.4114	1000
RRF[2,8]	0.5517	0.03294	4.586E-4	0.4887	0.551	0.6169	1000
RRF[2,9]	0.4339	0.02591	3.608E-4	0.3844	0.4334	0.4853	1000
RRF[2,10]	0.6165	0.03681	5.126E-4	0.5462	0.6158	0.6895	1000
RRF[2,11]	0.7585	0.04529	6.306E-4	0.672	0.7576	0.8483	1000
RRF[2,12]	0.6536	0.03902	5.434E-4	0.579	0.6529	0.731	1000
RRF[2,13]	0.8147	0.04864	6.773E-4	0.7218	0.8138	0.9111	1000
RRF[2,14]	0.6257	0.03736	5.202E-4	0.5543	0.625	0.6997	1000
RRF[2,15]	0.8765	0.05233	7.287E-4	0.7765	0.8755	0.9802	1000
RRF[2,16]	0.7484	0.04468	6.222E-4	0.6631	0.7476	0.837	1000
RRF[2,17]	0.9105	0.05436	7.569E-4	0.8066	0.9094	1.018	1000
RRF[2,18]	1.043	0.06227	8.671E-4	0.924	1.042	1.166	1000
RRF[2,19]	0.6741	0.04024	5.604E-4	0.5972	0.6733	0.7538	1000
RRF[2,20]	1.222	0.07294	0.001016	1.082	1.22	1.366	1000
RRF[2,21]	0.8693	0.0519	7.227E-4	0.7701	0.8683	0.9721	1000
RRF[2,22]	1.322	0.07891	0.001099	1.171	1.32	1.478	1000
RRF[2,23]	0.9143	0.05459	7.602E-4	0.81	0.9133	1.023	1000
RRF[2,24]	1.153	0.06881	9.582E-4	1.021	1.151	1.289	1000
RRF[3,2]	0.1609	0.01185	1.402E-4	0.1372	0.1608	0.1848	1000
RRF[3,3]	0.2931	0.02159	2.554E-4	0.25	0.293	0.3366	1000
RRF[3,4]	0.189	0.01392	1.647E-4	0.1612	0.1889	0.217	1000
RRF[3,5]	0.1889	0.01392	1.646E-4	0.1611	0.1888	0.2169	1000
RRF[3,6]	0.2866	0.02111	2.498E-4	0.2445	0.2865	0.3291	1000
RRF[3,7]	0.3035	0.02236	2.645E-4	0.2589	0.3034	0.3485	1000
RRF[3,8]	0.3845	0.02832	3.351E-4	0.328	0.3843	0.4415	1000
RRF[3,9]	0.313	0.02306	2.728E-4	0.267	0.3129	0.3595	1000
RRF[3,10]	0.407	0.02998	3.547E-4	0.3471	0.4068	0.4673	1000
RRF[3,11]	0.51	0.03757	4.444E-4	0.435	0.5097	0.5856	1000
RRF[3,12]	0.4417	0.03253	3.849E-4	0.3767	0.4415	0.5072	1000
RRF[3,13]	0.5933	0.04371	5.171E-4	0.5061	0.5931	0.6813	1000
RRF[3,14]	0.4427	0.03261	3.859E-4	0.3777	0.4425	0.5084	1000
RRF[3,15]	0.5843	0.04305	5.093E-4	0.4984	0.5841	0.671	1000
RRF[3,16]	0.5142	0.03788	4.482E-4	0.4387	0.514	0.5905	1000
RRF[3,17]	0.6075	0.04475	5.294E-4	0.5182	0.6072	0.6976	1000
RRF[3,18]	0.7306	0.05382	6.367E-4	0.6232	0.7303	0.8389	1000
RRF[3,19]	0.4991	0.03677	4.35E-4	0.4257	0.4989	0.5731	1000
RRF[3,20]	0.9468	0.06975	8.252E-4	0.8076	0.9464	1.087	1000

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RRF[3,21]	0.6811	0.05017	5.936E-4	0.581	0.6808	0.7821	1000
RRF[3,22]	1.008	0.07425	8.784E-4	0.8598	1.008	1.157	1000
RRF[3,23]	0.7134	0.05256	6.218E-4	0.6086	0.7131	0.8193	1000
RRF[3,24]	0.8398	0.06186	7.319E-4	0.7164	0.8395	0.9644	1000
RRF[4,2]	0.1773	0.009534	1.207E-4	0.1608	0.1765	0.1984	1000
RRF[4,3]	0.2776	0.01492	1.889E-4	0.2517	0.2763	0.3105	1000
RRF[4,4]	0.1951	0.01049	1.328E-4	0.1769	0.1942	0.2182	1000
RRF[4,5]	0.1962	0.01055	1.335E-4	0.1779	0.1953	0.2195	1000
RRF[4,6]	0.2974	0.01599	2.023E-4	0.2696	0.296	0.3326	1000
RRF[4,7]	0.3211	0.01726	2.185E-4	0.2911	0.3196	0.3591	1000
RRF[4,8]	0.4641	0.02495	3.158E-4	0.4208	0.462	0.5191	1000
RRF[4,9]	0.3697	0.01988	2.516E-4	0.3352	0.3681	0.4136	1000
RRF[4,10]	0.4903	0.02636	3.336E-4	0.4445	0.4881	0.5484	1000
RRF[4,11]	0.6441	0.03463	4.382E-4	0.5839	0.6412	0.7204	1000
RRF[4,12]	0.5926	0.03186	4.032E-4	0.5373	0.5899	0.6629	1000
RRF[4,13]	0.7414	0.03986	5.044E-4	0.6721	0.738	0.8292	1000
RRF[4,14]	0.5792	0.03114	3.941E-4	0.5251	0.5766	0.6478	1000
RRF[4,15]	0.8124	0.04368	5.528E-4	0.7366	0.8087	0.9087	1000
RRF[4,16]	0.7173	0.03856	4.88E-4	0.6503	0.7141	0.8023	1000
RRF[4,17]	0.934	0.05021	6.355E-4	0.8468	0.9298	1.045	1000
RRF[4,18]	1.14	0.06129	7.757E-4	1.034	1.135	1.275	1000
RRF[4,19]	0.7942	0.0427	5.404E-4	0.72	0.7906	0.8883	1000
RRF[4,20]	1.413	0.07597	9.615E-4	1.281	1.407	1.581	1000
RRF[4,21]	1.049	0.05639	7.136E-4	0.9509	1.044	1.173	1000
RRF[4,22]	1.571	0.08444	0.001069	1.424	1.564	1.757	1000
RRF[4,23]	1.077	0.05788	7.325E-4	0.976	1.072	1.204	1000
RRF[4,24]	1.307	0.07028	8.895E-4	1.185	1.301	1.462	1000
RRF[5,2]	0.1986	0.006877	1.005E-4	0.1856	0.1985	0.2126	1000
RRF[5,3]	0.3546	0.01228	1.794E-4	0.3314	0.3544	0.3795	1000
RRF[5,4]	0.2489	0.00862	1.259E-4	0.2327	0.2488	0.2664	1000
RRF[5,5]	0.2561	0.008867	1.296E-4	0.2394	0.256	0.2741	1000
RRF[5,6]	0.4046	0.01401	2.047E-4	0.3781	0.4044	0.433	1000
RRF[5,7]	0.4714	0.01632	2.385E-4	0.4406	0.4711	0.5044	1000
RRF[5,8]	0.6793	0.02352	3.437E-4	0.6349	0.679	0.727	1000
RRF[5,9]	0.5607	0.01941	2.836E-4	0.524	0.5604	0.6	1000
RRF[5,10]	0.7887	0.02731	3.99E-4	0.7372	0.7884	0.8441	1000
RRF[5,11]	1.066	0.03692	5.395E-4	0.9968	1.066	1.141	1000
RRF[5,12]	1.006	0.03484	5.09E-4	0.9404	1.006	1.077	1000
RRF[5,13]	1.366	0.04728	6.909E-4	1.276	1.365	1.461	1000
RRF[5,14]	1.051	0.03639	5.317E-4	0.9824	1.051	1.125	1000
RRF[5,15]	1.476	0.0511	7.467E-4	1.38	1.475	1.58	1000
RRF[5,16]	1.311	0.04541	6.635E-4	1.226	1.311	1.403	1000
RRF[5,17]	1.58	0.05472	7.995E-4	1.477	1.58	1.691	1000
RRF[5,18]	1.921	0.06652	9.719E-4	1.796	1.92	2.056	1000
RRF[5,19]	1.302	0.04507	6.585E-4	1.217	1.301	1.393	1000
RRF[5,20]	2.309	0.07995	0.001168	2.158	2.308	2.471	1000
RRF[5,21]	1.703	0.05897	8.616E-4	1.592	1.702	1.823	1000
RRF[5,22]	2.528	0.08754	0.001279	2.363	2.527	2.706	1000
RRF[5,23]	1.816	0.06288	9.188E-4	1.698	1.815	1.944	1000
RRF[5,24]	2.206	0.07639	0.001116	2.062	2.205	2.361	1000
RRF[6,2]	0.1949	0.008918	1.051E-4	0.1775	0.1947	0.2126	1000
RRF[6,3]	0.5424	0.02482	2.925E-4	0.494	0.542	0.5917	1000
RRF[6,4]	0.4248	0.01944	2.291E-4	0.3869	0.4246	0.4635	1000
RRF[6,5]	0.4258	0.01949	2.296E-4	0.3878	0.4255	0.4645	1000
RRF[6,6]	0.8747	0.04003	4.716E-4	0.7967	0.8741	0.9543	1000
RRF[6,7]	1.106	0.05061	5.963E-4	1.007	1.105	1.206	1000
RRF[6,8]	1.576	0.07213	8.497E-4	1.435	1.575	1.719	1000
RRF[6,9]	1.231	0.05635	6.639E-4	1.121	1.23	1.343	1000
RRF[6,10]	1.586	0.07259	8.552E-4	1.445	1.585	1.73	1000
RRF[6,11]	2.196	0.1005	0.001184	2.0	2.194	2.396	1000
RRF[6,12]	1.994	0.09124	0.001075	1.816	1.992	2.175	1000
RRF[6,13]	2.709	0.124	0.001461	2.468	2.708	2.956	1000
RRF[6,14]	2.058	0.09418	0.00111	1.874	2.056	2.245	1000
RRF[6,15]	2.919	0.1336	0.001574	2.659	2.918	3.185	1000
RRF[6,16]	2.42	0.1108	0.001305	2.204	2.419	2.641	1000
RRF[6,17]	2.908	0.1331	0.001568	2.649	2.906	3.173	1000
RRF[6,18]	3.47	0.1588	0.001871	3.161	3.468	3.786	1000
RRF[6,19]	2.343	0.1072	0.001263	2.134	2.342	2.556	1000

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