Chikungunya Disease Mapping in Malaysia: an Analysis based on SMR Method, Poisson-gamma Model, SIR-SI Model 1 and SIR-SI Model 2

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Abstract. Disease mapping is a method that can be used to show the geographical distribution of disease occurrence. It presents the incidence of specified disease in areas of interest which involves the usage and interpretation of coloured or shaded maps. The focus of analysis in disease mapping study is to estimate the true relative risk. Better statistical method used to estimate the relative risk will subsequently give better appearance of risks on maps. Consequently, the maps might be used by the authorities to identify the area that deserves closer scrutiny or more attention, as well as for resources allocation. Therefore, the aim of this paper is to compare the estimated relative risks for chikungunya disease mapping using four different methods. These include the analysis of relative risk estimation based on Standardized Morbidity Ratio (SMR), Poisson-gamma model, discrete time-space stochastic SIR-SI model 1 and discrete time-space stochastic SIR-SI model 2 for vector-borne infectious disease transmission. SMR is the most common statistic used in disease mapping. However, the use of SMR in disease mapping has several disadvantages. Many other methods have been developed to overcome the drawbacks of the SMR, which include the earliest example of Bayesian disease mapping using Poisson-gamma model. However, covariate adjustment in this model is difficult and there is no possibility for allowing spatial correlation between risks in adjacent areas. Therefore, new approach in estimating relative risk based on discrete time-space stochastic SIR-SI model 1 is introduced and results of analysis shows that this new approach can overcome the problem of relative risk estimation based on SMR and Poisson-gamma model. However, this model only suitable for non-rare diseases as for rare diseases, the relative risk cannot be estimated due to the zero expected cases value. Therefore, improved method is proposed to estimate the relative risk based on discrete time-space stochastic SIR-SI model 2. Results of the analysis shows that this new method offers improved methodology for estimating the relative risk compared to the other three models. This is because this method offers a more detailed description of the biological process, which takes into account the transmission of the disease. This method also considers the total posterior mean infective in the denominator of the relative risk equation.

Key Words: Chikungunya disease, Disease mapping, Poisson-gamma model, Relative risk estimation, SIR-SI models, SMR method.

1.0 Introduction and Research Aim

Chikungunya is a mosquito-borne viral disease in which the virus is transmitted to humans by infected female mosquitoes. These mosquitoes are known as *Aedes aegypti* and *Aedes albopictus*, which can also transmit other mosquito-borne viruses which are DEN-1, DEN-2, DEN-3 and DEN-4 of dengue disease. However, chikungunya is rarely fatal. Since there is no cure for this disease, the treatment is focused on relieving the symptoms, while the prevention is based on mosquitos' surveillance and control measures. Disease map has been identified as an important tool to control the disease (see, for example, Rajabi et al., 2013; Nakapan et al. , 2012). The production of good risk map relies on the statistical models used to estimate the risk.

Hence, the main aim of this paper is to discuss and compare the relative risk estimation for chikungunya disease mapping based on four different methods. These involve the analysis for relative risk estimation based on the SMR method, Poisson-Gamma model, Stochastic SIR-SI Model 1 and Stochastic SIR-SI Model 2, and the application of these methods to observed chikungunya data from Malaysia.

2.0 Methodology

The most common statistics used in the study of disease mapping is the Standardized Morbidity Ratio (SMR) method. The SMR equation can be written as,

$$SMR_i = \frac{O_i}{e_i}. \qquad (1)$$

Here, the estimation for i regions is based on ratio estimator of observed cases, O_i, divided by the expected cases, e_i, which have several drawbacks. The most obvious drawback is that the SMR will be zero when there is no observed case in certain regions. The drawback of SMR method has led many researchers to explore other methods to estimate the relative risk of a disease (Lawson et al., 2003). This includes the use of Bayesian methods.

The Poisson-Gamma model is one of the earliest examples of Bayesian mapping. In this model, the numbers of new infective, y_i, are assumed to follow a Poisson distribution within a given period of time. This can be written as,

$$y_i \sim Poisson(e_i \theta_i). \qquad (2)$$

Many studies demonstrated that this Poisson-gamma model can overcome the problem of SMR when there is no observed case in a region. However, the

Poisson-Gamma model has a problem where covariate adjustment in this model is difficult in which there is no possibility for allowing spatial correlation between risks in adjacent areas.

Subsequent from the drawback of the Poisson-gamma model, Samat and Percy (2012) has proposed an alternative method of the relative risk estimation. Their study considers the transmission of the disease as well as covariate adjustment between adjacent areas. The relative risk estimation method used in their study is based on the stochastic SIR-SI model. In this paper, we called it as a stochastic SIR-SI model 1. Here, the relative risk , r_{ij}, of the disease for i study regions and j time periods is equal to the posterior expected mean number of infective case, $\tilde{\lambda}_{ij}$, divided by the expected number of new infective disease, in which the denominator of the relative risk equation considers the total observed cases. These can be written as

$$r_{i,j}^{(h)} = \frac{\tilde{\lambda}_{i,j}^{(h)}}{e_{i,j}^{(h)}}. \qquad (3)$$

Furthermore, an improved method of relative risk estimation by Samat and Mohd Imam Ma'arof (2015) has been introduced. In this relative risk estimation method, the calculation of the denominator considers the total posterior expected new infective cases instead of total observed cases. This equation can be written as,

$$\tilde{r}_{i,j}^{(h)} = \frac{\tilde{\lambda}_{i,j}^{(h)}}{\tilde{e}_{i,j}^{(h)}}. \qquad (4)$$

Details explanation about the third and fourth models can be found in Samat and Percy (2012), and Samat and Mohd Imam Ma'arof (2015), respectively.

3.0 Application of the Relative Risk Estimation for Chikungunya Disease

This section displays the results of relative risk estimation based on the SMR method, Poisson-Gamma model, Stochastic SIR-SI Model 1 and Stochastic SIR-SI Model 2 using observed chikungunya data from Malaysia. All the data are analyzed using WinBUGS software, which is suitable to carry out wide variety of Bayesian models. Firstly, the data set used in this study is discusses. Then, the results of the relative risk estimation by using four different methods are presented in graph. Finally, the risk are displayed on maps to show the high and low risk areas of chikungunya disease occurrences.

In this study, relative risk above 1 means that the people within the region are more likely to contract with the disease compared to the people in the overall population. In contrast, relative risk below 1 show that the people within the region are less likely to contract with the disease compared to the people in the

overall population. While, if the relative risk close to 1, it means that there is no real differences in terms of the likelihood that people become infected with chikungunya virus within the state and within the whole population.

3.1 The Data Set

The data applied in this study are in the form of counts of chikungunya cases from epidemiology week 1 to epidemiology week 52 for the year 2013, for all sixteen states in Malaysia which include Perlis, Kedah, Pulau Pinang, Perak, Kelantan, Terengganu, Pahang, Selangor, Kuala Lumpur, Putrajaya, Negeri Sembilan, Melaka, Johor, Sarawak, Labuan and Sabah.

3.2 The Results

The outcomes of relative risk estimation based on the four different models in all 16 states of Malaysia are displayed in this section.

Figure 2(a) depicts the relative risk estimation for chikungunya cases based on the SMR method. The states of Perak, Selangor, Sabah and Sarawak show the relative risks above 2 for certain epidemiology weeks. From the analysis, it shows that people within the states have the high possibility to get infected with chikungunya disease compared to people in the whole population.

Figure 2(b) shows the relative risk estimation for chikungunya cases based on the Poisson-Gamma model. From the figure, the estimated relative risks are close to 1 for most of the epidemiology weeks. The highest relative risk is at Sabah with 1.3280. While, the lowest estimated relative risk is in the state of Selangor with 0.8908. Overall, the result from the analysis indicates that people in Malaysia are categorized to have low risk to contract with chikungunya disease since the estimated relative risk is close to one for most of the epidemiology weeks. There is no zero value of relative risk estimation when using the Poisson-Gamma model. Thus, it shows that this model can overcome the drawback of SMR method especially when there is no observed chikungunya case in certain regions.

For the relative risk estimation of chikungunya cases based on the stochastic SIR-SI model 1, the relative risk becomes difficult to estimate. This problem happens when there is no observed chikungunya case for all epidemiology weeks, which subsequently gives zero value of expected cases at the relative risk equation. Hence, when the denominator of relative risk equation is zero, the relative risk is difficult to estimate. Therefore, the improved method of the relative risk estimation based on the SIR-SI Model 2 is introduced.

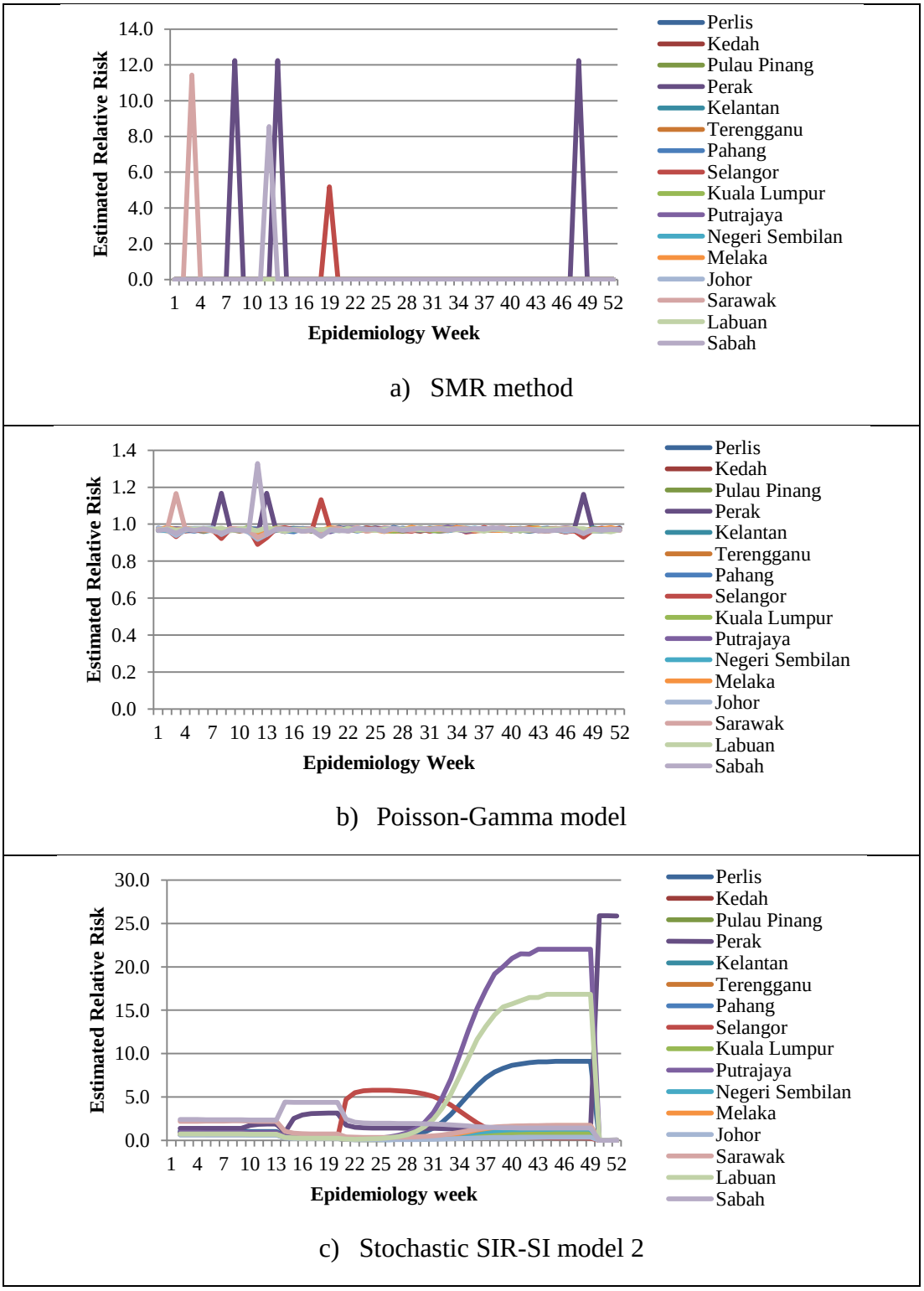

Figure 2: Relative Risk Estimation based on the SMR Method, Poisson-Gamma Model and the Stochastic SIR-SI Model 2

Figure 2(c) displays the relative risk estimation of chikungunya cases based on the stochastic SIR-SI model 2. From the figure, the highest estimated relative risk is at Perak during epidemiology week 50 with 25.860. While, there is a similar pattern at the end of the year at the states of Perlis, Labuan and Putrajaya. This could have happen due to the existence of chikungunya cases in the states with small populations compared to the whole population in Malaysia.

The overall comparison between Figures 2(a), 2(b) and 2(c) give a conclusion that different methods used to estimate the relative risk will subsequently give different appearance of disease risks on map. Therefore, it is very important to identify a better statistical method so that its depict the real situation.

Finally, the relative risks are displayed in maps to show the high and low risk area of chikungunya disease occurrences. In this study, ArcGIS software is used to create the map, and the disease risk map for epidemiology week 10 is chosen for example and demonstration purposes only.

Figure 3 represents the chikungunya risk maps at epidemiology week 10 based on different models that has been discussed. Unfortunately, there is no risk map for the stochastic SIR-SI model 1 because the relative risk is difficult to be estimated due to the zero value of the denominator. From Figure 3(a), the chikungunya risk map based on the SMR method depicts that people in all states are at very low risk to get infected with the chikungunya disease. Meanwhile, the chikungunya risk map based on the Poisson-Gamma model displayed in Figure 3(b) depicts that people in all states are at low risk to get infected with the chikungunya disease compared to the people in the whole population.

In contrast, Figure 3(c) which is the chikungunya risk map based on the stochastic SIR-SI model 2 shows that the states of Sabah and Sarawak have darkest coloured regions in the map. This means that people within both states have very high risk to be infected with the chikungunya virus compared to people in the whole population of Malaysia. This is followed by the states of Perak and Perlis which have estimated relative risks more than one. This means that people in these states are at high risk and are categorized as more likely to get infected with the chikungunya disease compared to the people in overall population of Malaysia.

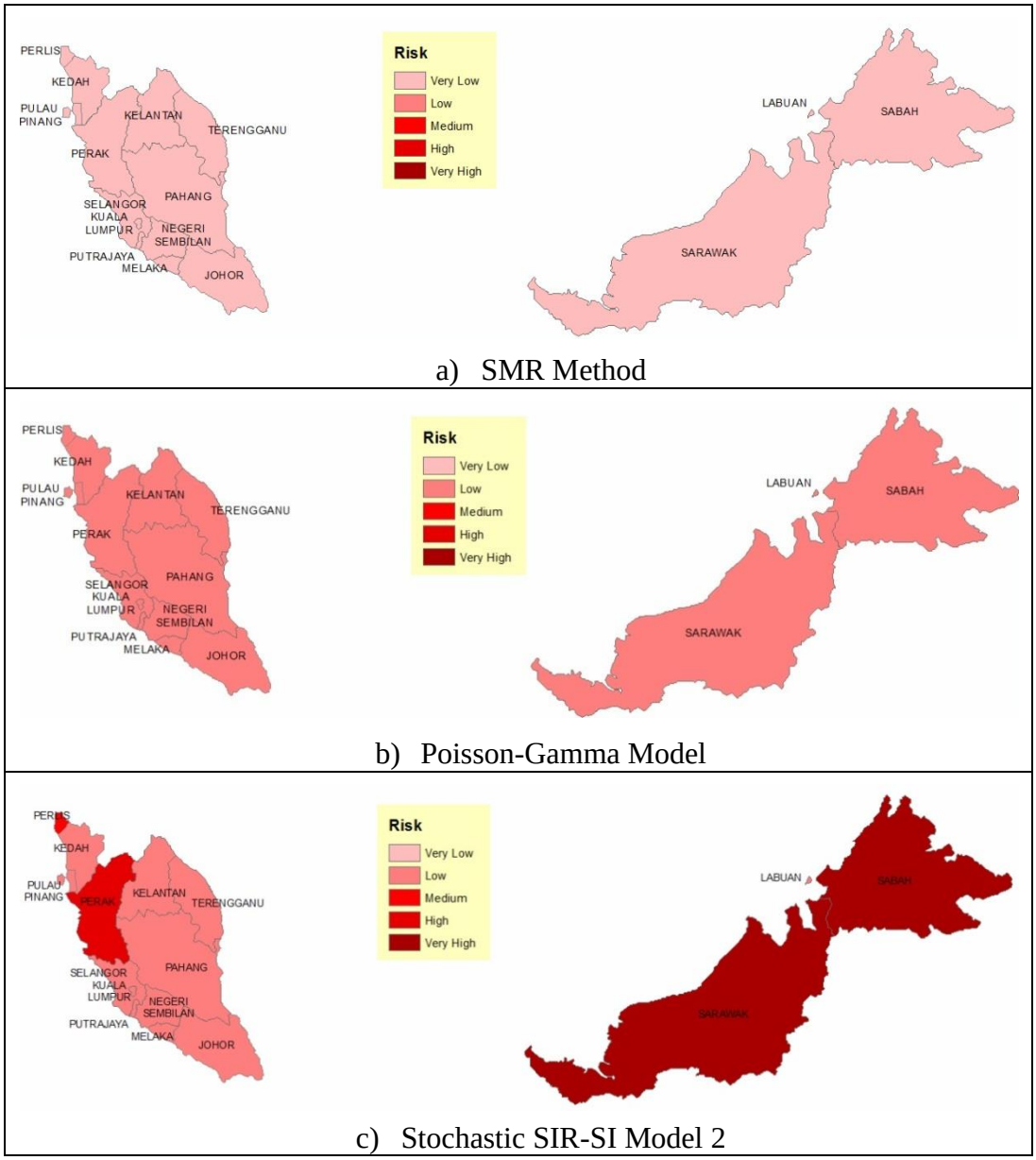

Figure 3: The Chikungunya Risk Maps

4.0 Conclusion

Results of the analysis show that the Stochastic SIR-SI Model 2 offers improved methodology for estimating the relative risk compared to the other three methods. This is because the improved model offers a more detailed description of the biological process, which takes into account the transmission of the disease while enables covariate adjustments and allows for spatial correlation between risks in adjacent areas. Furthermore, this new approach has been demonstrated is better and suitable for the case of rare disease like chikungunya.

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