

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.