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Numerical Analysis of the SIR-SI Differential Equations with Application to Dengue Disease Mapping in Kuala Lumpur, Malaysia

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***Abstract*—**The main aim of this study is to describe and introduce a method of numerical analysis in obtaining approximate solutions for the SIR-SI differential equations (susceptible-infective-recovered for human populations; susceptible-infective for vector populations) that represent a model for dengue disease transmission. Firstly, we describe the ordinary differential equations for the SIR-SI disease transmission models. Then, we introduce the numerical analysis of solutions of this continuous time, discrete space SIR-SI model by simplifying the continuous time scale to a densely populated, discrete time scale. This is followed by the application of this numerical analysis of solutions of the SIR-SI differential equations to the estimation of relative risk using continuous time, discrete space dengue data of Kuala Lumpur, Malaysia. Finally, we present the results of the analysis, comparing and displaying the results in graphs, table and maps. Results of the numerical analysis of solutions that we implemented offers a useful and potentially superior model for estimating relative risks based on continuous time, discrete space data for vector borne infectious diseases specifically for dengue disease.

***Keywords*—**Dengue disease, disease mapping, numerical analysis, SIR-SI differential equations.

I. Introduction

THIS paper discusses and explains about the development of continuous time and discrete space stochastic SIR-SI models for dengue disease transmission. First, we describe relevant forms of ordinary differential equations, which are commonly used in the analysis of variables that change continuously with respect to time. Here, we present ordinary differential equations that specifically apply to infectious disease modeling, again in the particular context of dengue disease, based on the compartmental SIR-SI model presented in Fig. 1.

This is followed by methods of numerical analysis to obtain approximate solutions of these differential equations that represent a SIR-SI model of dengue disease transmission. These involve approximating the continuous time scale as discrete for these differential equations in order to calculate numerical solutions. The results of the numerical analysis provide us with useful information about the Susceptible, Infective and Recovered human populations, and the Susceptible and Infective vector populations. We demonstrate these results using dengue data from Malaysia.

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II. Differential Equations for SIR-SI Model of Dengue Disease Transmission

In the study of dengue disease transmission model, the most common compartmental model used is as displayed in the following Fig. 1. This model is adapted from [1] and [2] by [3].

In this study, for $i = 1,2,\ldots,M$ study regions, and $j = 1,2,\ldots,T$ time periods, each notation showed in Fig. 1 is defined as follows.

$S_{i,j}^{(h)}$: total number of susceptible humans at time j

$I_{i,j}^{(h)}$: total number of infective humans at time j

$R_{i,j}^{(h)}$: total number of recovered humans at time j

$S_{i,j}^{(v)}$: total number of susceptible mosquitoes at time j

$I_{i,j}^{(v)}$: total number of infective mosquitoes at time j

$\mu^{(h)}$: birth and death rates of humans per day (assumed equal)

$\mu^{(v)}$: birth and death rates of mosquitoes per day (assumed equal)

$\gamma^{(h)}$: rate at which humans recover per day

b : biting rate per day

m : number of alternative hosts available as the blood source

A : constant recruitment rate for the mosquito vector

$\beta^{(h)}$: the transmission probability from mosquitoes to humans

$\beta^{(v)}$: the transmission probability from humans to mosquitoes

$N_i^{(h)}$: the human population size for the study region i

$N_i^{(v)}$: the mosquito population size for the study region i

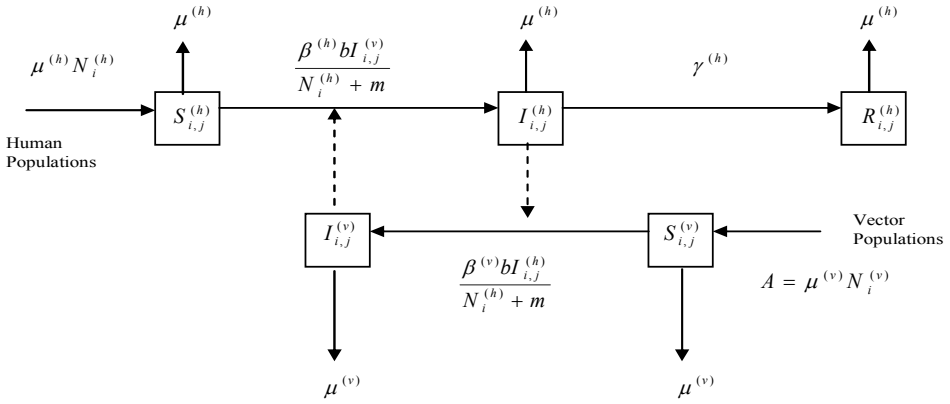

Fig. 1 Compartmental SIR-SI model for dengue disease transmission

For intervals over the continuous time scale indexed by *t*, the compartmental SIR-SI model for dengue disease transmission shown in Fig. 1 can also be written mathematically as a system of ordinary differential equations, as time is the only independent variable in this context.

Therefore, the differential equations for dengue disease transmission in human populations based on Fig. 1 are as follows:

$$S'^{(h)}(t)=\mu^{(h)}N^{(h)}-\mu^{(h)}S^{(h)}(t)-\left((\beta^{(h)}b)/(N^{(h)}+m)\right)I^{(v)}(t)S^{(h)}(t) \quad (1)$$

$$I'^{(h)}(t)=\left((\beta^{(h)}b)/(N^{(h)}+m)\right)I^{(v)}(t)S^{(h)}(t)-\mu^{(h)}I^{(h)}(t)-\gamma^{(h)}I^{(h)}(t) \quad (2)$$

$$R'^{(h)}(t)=\gamma^{(h)}I^{(h)}(t)-\mu^{(h)}R^{(h)}(t) \quad (3)$$

Similarly, the differential equations for dengue disease transmission in vector populations are as follows:

$$S'^{(v)}(t)=\mu^{(v)}N^{(v)}-\mu^{(v)}S^{(v)}(t)-\left((\beta^{(v)}b)/(N^{(h)}+m)\right)I^{(h)}(t)S^{(v)}(t) \quad (4)$$

$$I'^{(v)}(t)=\left((\beta^{(v)}b)/(N^{(h)}+m)\right)I^{(h)}(t)S^{(v)}(t)-\mu^{(v)}I^{(v)}(t) \quad (5)$$

It is clear, because of the existence of products of functions, that this system of differential equations is nonlinear. As it involves five such equations, this system is very difficult to solve analytically, whereas analytic solution of a system of linear ordinary differential equations would be relatively straightforward. Many references point out that nonlinear system such as this can usually be solved only by performing numerical analysis with computer programming or by studying the asymptotic behavior of solutions as approximations to the actual solutions (for example as explained in [4]). The next section discusses how to solve these equations using numerical analysis with the help of computer software.

III. Numerical Analysis of Solutions of the SIR-SI Differential Equations

In this study, we develop computer programming to perform numerical analysis as a means of determining solutions of complicated systems of nonlinear ordinary differential equations such as those in (1) to (5). Many researchers have used various types of computer software to help them with the numerical analysis of differential equations in the context of disease modeling. For instance, [5] used Maple software to solve the system of differential equations in her study on vector-host models for epidemics, whilst others have used Mathematica software to solve similar complicated differential equations. For the purpose of this research, we choose to use WinBUGS software for the analysis because it has a natural iterative logic and readily enables us to include prior distributions for Bayesian analysis. WinBUGS software is a package designed to carry out Markov chain Monte Carlo (MCMC) computations for a wide variety of Bayesian models. Details explanation about this free software is discussed in [6]. While, a discussion and application of Bayesian analysis of disease mapping using this software can be found in [7].

In this section, we consider methods of numerical analysis for calculating solutions to our continuous time, discrete space SIR-SI model. In particular, we simplify the continuous time scale to a densely populated, discrete time scale. Although fundamentally different in nature and scale, this approach effectively reduces our continuous time, discrete space model to a similar form as the discrete time, discrete space SIR-SI models as introduced by [3]. We now adopt this approach to solve the system of nonlinear differential equations explained previously.

Therefore, for $i=1,2,\ldots,M$ study regions, and $j=1,2,\ldots,T$ time periods, the deterministic continuous time, discrete space SIR-SI model for dengue disease transmission in human populations reduces to this set of difference equations:

$$S_{i,j}^{(h)}=\mu^{(h)}N_i^{(h)}+\left\{1-\mu^{(h)}-\left((\beta^{(h)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(v)}\right\}S_{i,j-1}^{(h)} \quad (6)$$

$$I_{i,j}^{(h)} = (1-\mu^{(h)}-\gamma^{(h)})I_{i,j-1}^{(h)} + \left((\beta^{(h)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(v)}S_{i,j-1}^{(h)} \quad (7)$$

$$R_{i,j}^{(h)} = (1-\mu^{(h)})R_{i,j-1}^{(h)} + \gamma^{(h)}I_{i,j-1}^{(h)} \quad (8)$$

Similarly, the deterministic model for dengue disease transmission in vector populations reduces to this set of difference equations:

$$S_{i,j}^{(v)} = \mu^{(v)}N_i^{(v)} + \left\{1-\mu^{(v)}-\left((\beta^{(v)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(h)}\right\}S_{i,j-1}^{(v)} \quad (9)$$

$$I_{i,j}^{(v)} = (1-\mu^{(v)})I_{i,j-1}^{(v)} + \left((\beta^{(v)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(h)}S_{i,j-1}^{(v)} \quad (10)$$

All these five difference equations are given as (1) to (5) in [3].

Following on from the above deterministic model, our continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission in human populations reduces to this set of stochastic difference equations:

$$S_{i,j}^{(h)} = \mu^{(h)}N_i^{(h)} + (1-\mu^{(h)})S_{i,j-1}^{(h)} - \Im_{i,j}^{(h)} \quad (11)$$

$$\Im_{i,j}^{(h)} \sim Poisson\left(\lambda_{i,j}^{(h)}\right) \quad (12)$$

$$\lambda_{i,j}^{(h)} = \exp\left(\beta_0^{(h)} + c_i^{(h)}\right)\left((\beta^{(h)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(v)}S_{i,j-1}^{(h)} \quad (13)$$

$$I_{i,j}^{(h)} = (1-\mu^{(h)})I_{i,j-1}^{(h)} + \Im_{i,j}^{(h)} - \Re_{i,j}^{(h)} \quad (14)$$

$$R_{i,j}^{(h)} = (1-\mu^{(h)})R_{i,j-1}^{(h)} + \Re_{i,j}^{(h)} \quad (15)$$

$$\Re_{i,j}^{(h)} = \gamma I_{i,j-1}^{(h)} \quad (16)$$

However, the continuous time, discrete space SIR-SI model for dengue disease transmission in vector populations is assumed to be non-stochastic:

$$S_{i,j}^{(v)} = \mu^{(v)}N_i^{(v)} + (1-\mu^{(v)})S_{i,j-1}^{(v)} - \Im_{i,j}^{(v)} \quad (17)$$

$$\Im_{i,j}^{(v)} = \left((\beta^{(v)}b)/(N_i^{(h)}+m)\right)I_{i,j-1}^{(h)}S_{i,j-1}^{(v)} \quad (18)$$

$$I_{i,j}^{(v)} = (1-\mu^{(v)})I_{i,j-1}^{(v)} + \Im_{i,j}^{(v)} \quad (19)$$

The stochastic difference equations above are given as (6) to (14) in [3].

As in our previous analysis in [3], a stochastic element is assigned to the deterministic number of new infective humans $\Im^{(h)}$. The main stochastic element is the spatial random effect $c_i^{(h)}$, which has a spatial prior distribution to allow for dependency between adjacent regions. This is because spatial random variation is an important element in any analysis involving geographical regions.

The continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission that we analyzed here is next used in Section IV for our development of a method to estimate relative risks. This subsequently enables us to achieve our main purpose of mapping indirect diseases such as dengue.

IV. Relative Risk Estimation of Dengue Disease Mapping

The relative risk estimation method used in this study is based on method proposed by [3]. In general, for $i = 1,2,\ldots,M$ study regions and $j = 1,2,\ldots,T$ time periods, the posterior expected relative risk can be approximated using an unbiased sample mean

$$\widetilde{\theta}_{ij}^{(h)} = \frac{\widetilde{\lambda}_{ij}^{(h)}}{e_{ij}^{(h)}} \quad (20)$$

Here, $\widetilde{\lambda}_{ij}^{(h)}$ represents posterior expected mean number of infective, and $e_{ij}^{(h)}$ represents expected number of new infective cases. This relative risk equation is given as (17) in study by [3].

In this analysis, relative risk is defined to be the conditional probability that a person within the region contracts the disease divided by the conditional probability that a person in the population contracts the disease. In this context, we condition upon no infection thus far.

A value for the relative risk close to 1 means that there is no real difference between the conditional probability that a person within the specific region contracts the disease compared to the conditional probability that a person in the general population contracts the disease. In other words, there is no real difference in terms of the likelihoods that people become infected by dengue virus within a region and within the whole population. If the value of relative risk increases above 1, then this indicates that people within the region are more likely to contract the disease compared with people in the population. Conversely, a value of relative risk below 1 shows a decrease in likelihood of contracting the disease, which means that people within the region are less likely to contract the disease compared with people in the population.

This formulation is utilized in the estimation of relative risk for disease mapping, based on the continuous time, discrete space, stochastic SIR-SI model as discussed in Section III using data for all tracts under consideration.

V. Application of Numerical Analysis of Solutions for the SIR-SI Model to Dengue Disease Mapping

This section demonstrates and discusses our extension of the SIR-SI model of dengue disease transmission that is applicable for the analysis of continuous time, discrete space data and the subsequent estimation of relative risk. In this analysis, we focus on dengue disease for illustration and the application of

the numerical analysis as the approximate method of solving the systems of ordinary differential equations.

In this application, the analysis of daily dengue data is based on a numerical analysis of the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission.

A. The Data Set

A different set of data was available for this analysis, specifically relating to case-event data for infective dengue cases in the human population, and was provided by the Department of Health, Kuala Lumpur. Other data used in this analysis were provided by the Ministry of Health, the Institute for Medical Research and the Department of Statistics, all in Malaysia.

In this analysis, dengue data refer to observed new infective dengue cases of humans, which were observed continuously every day from 1st January 2009 to 31st December 2009 within six health administration zones in Kuala Lumpur, Malaysia. These health administration zones specified by the Ministry of Health are City Centre, Kepong, Setapak, Cheras, Klang Lama and Damansara.

For the SIR-SI model of dengue disease transmission, the values for $\beta^{(h)}$ and $\beta^{(v)}$ are 0.50 and 0.75, respectively. Whilst, the number of alternative hosts available as the blood source m is assumed zero and the recruitment rate of the mosquito population, A, is assumed to be 5,000 per day, as suggested by [1] and [3]. The daily rates used in this analysis are

$$\mu_D^{(h)} = 0.0000391,\ \mu_D^{(v)} = 0.071,\ \gamma_D^{(h)} = 0.2 \text{ and } b_D = 0.33$$

Furthermore, based on the Malaysian Census 2000, the human population size, $N^{(h)}$, for the state of Kuala Lumpur is 1,379,310. However, data for human population sizes in individual health administrative zones are not available. According to the Department of Health, there are several types of division in the state of Kuala Lumpur and most of them divide the city differently, such as divisions based on parliamentary constituencies and council administration.

Parliamentary constituencies division includes 11 areas, which are Bandar Tun Razak, Batu, Bukit Bintang, Cheras, Kepong, Lembah Pantai, Segambut, Seputih, Setiawangsa, Titiwangsa and Wangsa Maju. However, council administration uses what is known as the Dewan Bandaraya Kuala Lumpur (DBKL) division and splits Kuala Lumpur into 9 areas, which are Damansara, Seputeh, Segambut, Kepong, Wangsa Maju, City Centre, Setiawangsa, Bandar Tun Razak and Sungai Besi. Moreover, according to [8], there are no clear boundary limits within the urban area of Kuala Lumpur. Most of the boundaries shown in maps are approximate, though some divisions use major highways as boundaries.

As a result, data for the human population size for each area are difficult to identify since there might be overlapping regions in terms of total human populations between adjacent areas or divisions. For simplicity and in order to demonstrate our models and analyses in practice, all divisions or zones in this section are assumed to have equal human population size. Therefore, $N_1^{(h)} = N_2^{(h)} = \ldots = N_6^{(h)} = 229{,}885$.

VI. Results

This section demonstrates and displays the results of a numerical analysis of continuous time, discrete space data to obtain solutions to the stochastic SIR-SI model of dengue disease transmission with application to relative risk estimation. This subsequently generates more accurate estimates of relative risk for dengue disease mapping. As previously mentioned, the continuous time, discrete space, stochastic SIR-SI model has the same form as the discrete time, discrete space, stochastic SIR-SI model except that is defined in terms of differential equations rather than difference equations. However, the need to use a discrete approximation to the continuous model to enable numerical analysis effectively results in the same formulation for both types of data. Nevertheless, the time periods involved differ substantially and so the continuous model formulation is able to retain much more information that is contained in the data, than is the discrete model formulation.

Furthermore, similar to our analysis of discrete time, discrete space data in [3], this analysis requires us to make the same four assumptions for imputed mosquito populations. This imputation is discussed next.

A. Estimation of Vector Mosquito Populations

Possible estimation of vector mosquito populations includes two simple methods, which are estimation based on seasonal averages reported in relevant journal publications written by [9] and [10], and estimation based on propagation of the discrete time, discrete space stochastic SIR-SI model for dengue disease transmission, where the starting values are set and the estimation propagates from the SIR-SI equations.

1. Estimation of Vector Mosquito Populations Based On Seasonal Averages

Figs. 2-4 display time series plots for imputed infective mosquitoes without seasonality (Assumption 1), with piecewise constant seasonality (Assumption 2) and with sinusoidal seasonality (Assumption 3), for six zones according to the health administrative division of Kuala Lumpur for the year 2009. Notice that all six traces are identical in each of these three graphs.

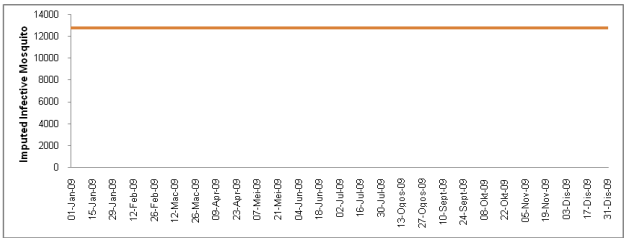

Fig. 2 Time series plot for imputed infective mosquitoes without seasonality for six zones in Kuala Lumpur

In this analysis, since we assumed that each zone has the same size of human population, then all six zones will have the same average number of imputed infective mosquitoes, which will then be used as an initial value in the estimation of infective mosquito population using four different assumptions. However, the pattern of the imputed infective mosquito population between time periods varies according to the three assumptions that are made.

In Assumption 1, the imputed infective mosquitoes are constant and equal for all six zones throughout all time periods, while in Assumption 2 the imputed infective mosquitoes are equal for all six zones but have a piecewise constant pattern throughout all time periods. In Assumption 3, the imputed infective mosquitoes are equal for all six zones but have a sinusoidal pattern throughout all time periods.

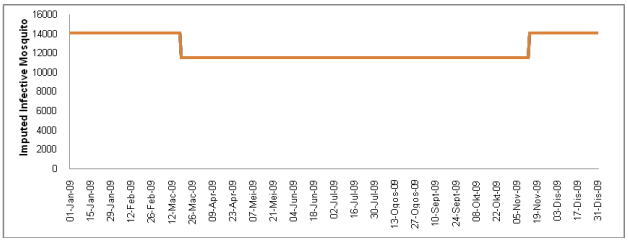

Fig. 3 Time series plot for imputed infective mosquitoes with piecewise constant seasonality for six zones in Kuala Lumpur

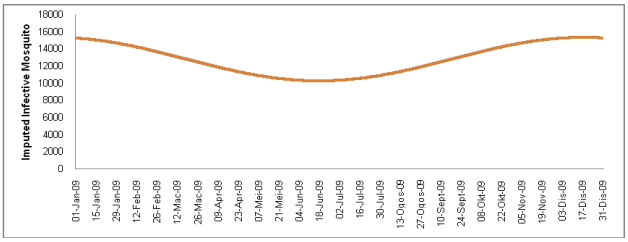

Fig. 4 Time series plot for imputed infective mosquitoes with sinusoidal seasonality for six zones in Kuala Lumpur

These three alternative assumptions for mosquito data are then imputed in the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission for all six zones of Kuala Lumpur. Subsequently, we can use this model to estimate the relative risks using posterior expectations, for dengue disease mapping in the state of Kuala Lumpur for the year 2009.

2. Estimation of Vector Mosquito Populations Based On Propagation

Fig. 5 depicts the time series plots for imputed infective mosquitoes based on propagation (Assumption 4) for six health administration zones of Kuala Lumpur during the year 2009.

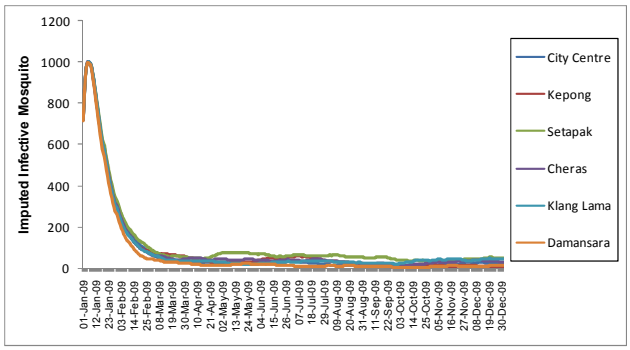

Fig. 5 Time series plot for imputed infective mosquitoes based on propagation for six health administration zones in Kuala Lumpur

From Fig. 5, it can be seen that the imputed numbers of infective mosquitoes using Assumption 4 vary slightly across all six health administrative zones based on daily time periods and are projected to decline rapidly. This is different from the pattern of imputed infective mosquitoes using Assumptions 1-3. The reason is probably because of; Assumption 4 did not assume seasonal patterns of dengue outbreak coincide with the rainy season compared to other assumptions. However, all zones have similar patterns of imputed infective mosquitoes across all daily time periods.

For further illustration of the information provided by this analysis, we now present graphs of the estimated values of susceptible, infective and recovered human populations, and susceptible and infective mosquito populations, respectively, in the City Centre zone of Kuala Lumpur using Assumption 4. These time series plots are displayed in Fig. 6.

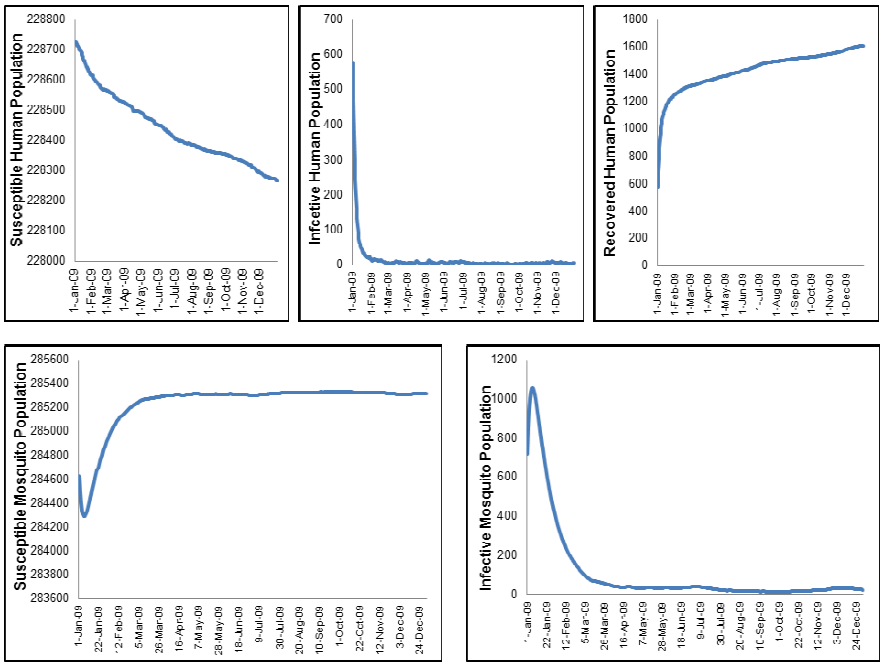

Fig. 6 Time series plots of fitted values of susceptible, infective and recovered human populations and susceptible and infective vector mosquito populations in the City Centre zone using Assumption 4

B. Comparison of Posterior Expected Relative Risks for Four Different Estimation Methods of the Vector Mosquito Population

The model in this analysis is posterior sampled and is run to convergence using WinBUGS software. Figs. 7-9 and 16 respectively illustrate time series plots for the posterior expected relative risk based on our continuous time, discrete space, stochastic SIR-SI model of dengue disease transmission from 1st January to 31st December 2009 across all six health administrative zones of Kuala Lumpur, using Assumptions 1-4.

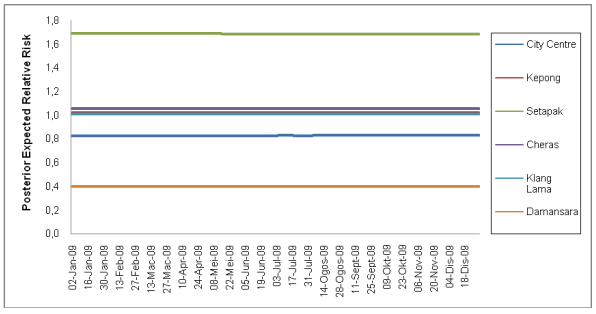

Fig. 7 Time series plots of posterior expected relative risk based on the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission using Assumption 1

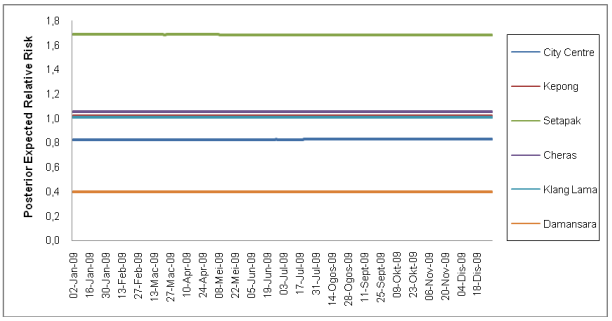

Fig. 8 Time series plots of posterior expected relative risk based on the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission using Assumption 2

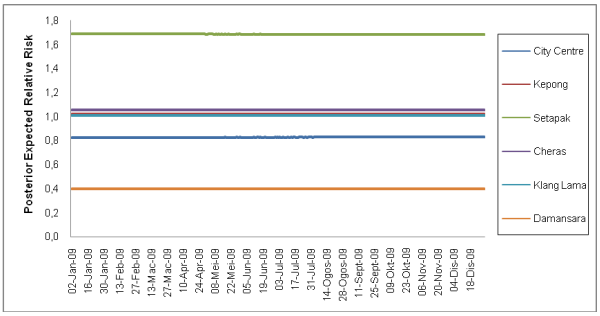

Fig. 9 Time series plots of posterior expected relative risk based on the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission using Assumption 3

Figs. 7-9 clearly indicate that the values for posterior expected relative risk using Assumptions 1-3 are almost

constant throughout the daily time periods for all zones. However, they are actually not exactly constant, but fluctuate among small ranges of values which cannot be seen when all six zones are presented in one graph. For example, Fig. 10 to 15 show more detail of the posterior expected relative risk for each zone separately using Assumption 2.

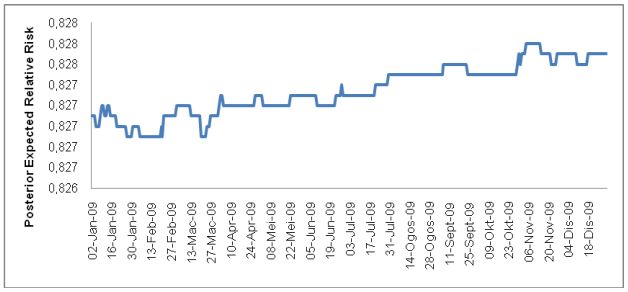

Fig. 10 Time series plot of posterior expected relative risk for City Centre

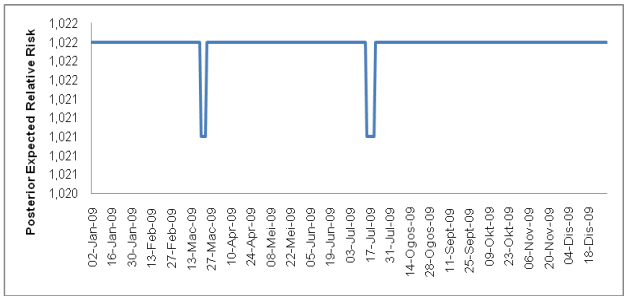

Fig. 11 Time series plot of posterior expected relative risk for Kepong

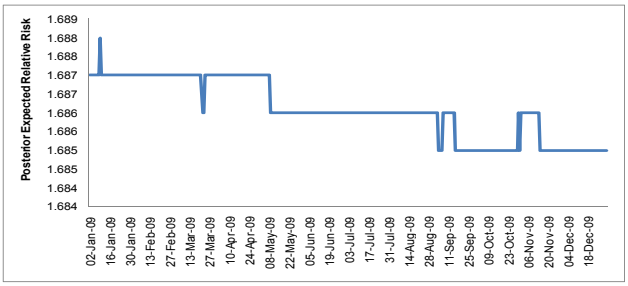

Fig. 12 Time series plot of posterior expected relative risk for Setapak

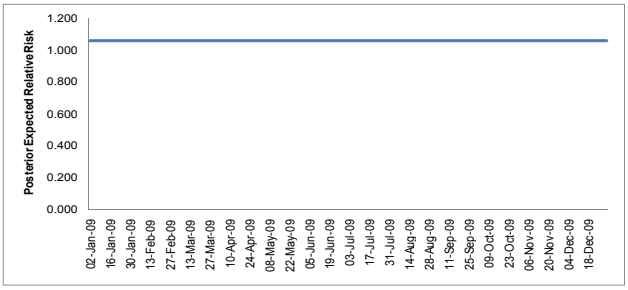

Fig. 13 Time series plot of posterior expected relative risk for Cheras

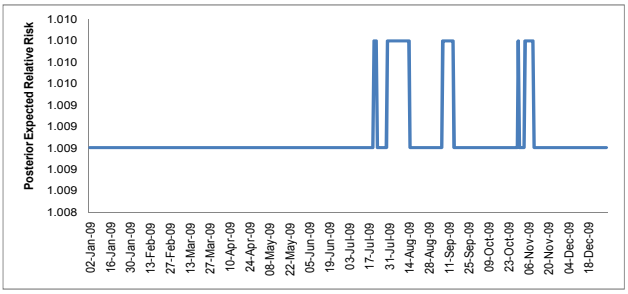

Fig. 14 Time series plot of posterior expected relative risk for Klang Lama

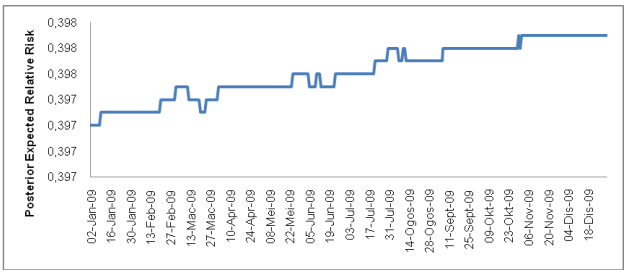

Fig. 15 Time series plot of posterior expected relative risk for Damansara

The time series plot of posterior expected relative risks for Cheras in Fig. 13 indicate constant values throughout all time periods. This is because we round off the results of our analysis to four significant figures, which conceals negligible variations over time. Another influential factor is that for the purposes of this demonstration, we made the reasonable assumption that each zone has the same size of human population due to unavailability of relevant data.

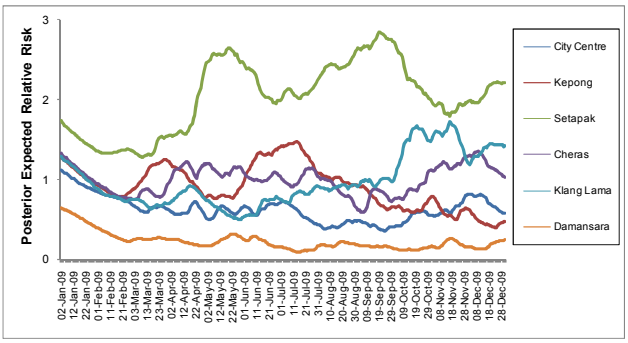

Fig. 16 Time series plots of posterior expected relative risk based on the continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission using Assumption 4

As our period of study for this analysis is only one year, it is entirely reasonable that the relative risks portrayed in Figs. 7-9 should remain almost constant over this period of time. However, unlike the posterior expected relative risks shown in those graphs, the posterior expected relative risks shown in the time series plots of Fig. 16 display considerable variability of values among zones and time periods under Assumption 4,

which corresponds to iterative propagation of mosquito population counts.

From all four of these time series plots, we conclude that people in the zone of Setapak had the highest risk in contracting dengue, while people in the zone of Damansara had the lowest risk in contracting dengue, during the year 2009. People in the zones of City Centre, Kepong, Cheras and Klang Lama were indicated to have approximately medium risk with posterior expected relative risk close to one.

The seasonality and non-seasonality assumptions corresponding to Figs. 2-5 provide a reasonable variety of models for the sizes of mosquito populations, which subsequently affect the values of our posterior expected relative risks in the different zones as shown in Figs. 7-9 and 16. The assumption of constancy provides a reference model for comparisons, whereas the seasonal models are more biologically plausible. This is because many studies show that the transmission of dengue virus by *Aedes* mosquitoes is sensitive to changes of rainfall and temperature, and such climatic seasonality is notable throughout Malaysia.

The following Fig. 17 shows the time series plots of relative risk based on Standardized Morbidity Ratio for six zones of Kuala Lumpur. These plots show that the relative risk is equal to zero for certain days, which is the drawback of the SMR method. In contrast, Figs. 7-9 and 16 did not show any zero value of relative risk as the estimation based on our proposed continuous time discrete space stochastic SIR-SI model for dengue disease transmission can overcome the problem of SMR when there is no observed count in certain regions. In addition, it can be seen that the range of values of relative risk are reduced by more than 50% when using our proposed model compared to the SMR method.

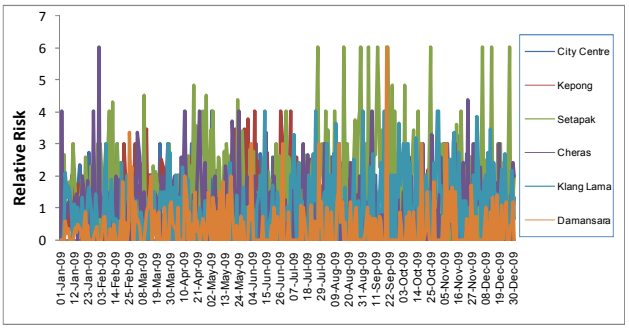

Fig. 17 Time series plots of relative risk based on Standardized Morbidity Ratio

Table I presents the deviance information criterion (DIC) values for posterior new infective humans in the six health administrative zones of Kuala Lumpur during the year 2009 under Assumptions 1-4. In this analysis, the DIC is used as a goodness-of-fit measure to help find the best fitting model empirically, among our four different assumptions for imputing the unknown mosquito population.

TABLE I
DEVIANCE INFORMATION CRITERION FOR RELATIVE RISK ESTIMATION BASED ON THE CONTINUOUS TIME, DISCRETE SPACE, STOCHASTIC SIR-SI MODEL USING FOUR ASSUMPTIONS FOR IMPUTING THE MOSQUITO POPULATION

	Assumption 1	Assumption 2	Assumption 3	Assumption 4
DIC	7498.09	**7425.07**	7526.8	10554.7

From the DIC values in Table I, we deduce that the model with Assumption 2 fits best empirically, as it gives the smallest DIC compared with the other models. This leads to the conclusion that the continuous time, discrete space, stochastic SIR-SI model, which assumes that the data for infective mosquitoes follow a cyclical seasonal pattern with piecewise constant seasonality, is the best model to be used in our analysis aimed at estimating the relative risk for dengue disease mapping using daily data for the six zones of Kuala Lumpur during the year 2009.

C. Maps of the Relative Risk Estimates for Dengue Disease Mapping in the Six Zones of Kuala Lumpur

Fig. 18 depicts a disease map for the posterior expected relative risks based on our continuous time, discrete space, stochastic SIR-SI model for dengue disease transmission using Assumption 2 in the six health administrative zones of Kuala Lumpur on one representative day during the year 2009. Similar maps can be generated to represent the posterior expected relative risks for each day from 1st January 2009 until 31st December 2009, though they are almost identical as noted in the previous section. By propagating through the system of differential equations, approximated by difference equations for computational convenience, it is also possible to construct disease maps that can be used for short-term forecasting. The disease map in Fig. 18 is classified into three levels of relative risk, corresponding low, medium and high risks, with corresponding intervals [0.0,0.8), [0.8,1.2) and [1.2,∞) respectively.

Fig. 18 illustrates that people in the zone of Setapak have a high risk of contracting dengue, while people in the zone of Damansara have a low risk of contracting dengue. People in the other four zones, Kepong, City Centre, Cheras and Klang, are portrayed to have a medium risk of contracting dengue. By definition, these categories of risk are relative to the corresponding risk in the general population of Kuala Lumpur.

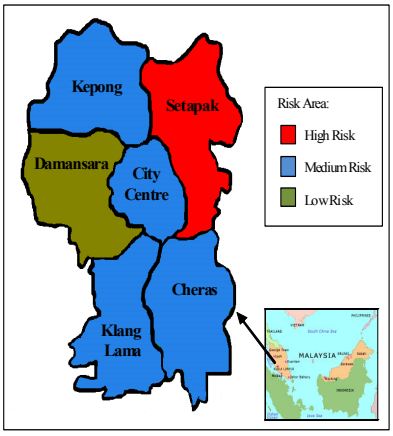

Fig. 18 Disease map of posterior expected relative risks based on the continuous time, discrete space stochastic SIR-SI model for one representative day during the year 2009

D. WinBUGS Code for Relative Risk Estimation Based On the Continuous Time, Discrete Space, Stochastic SIR-SI Model

```
model{
for (i in 1:M){
Sh[i,1]<-Nh[i]-Ih[i,1]-Rh[i,1]
Ih[i,1]<-0.00252*Nh[i]
Rh[i,1]<-0.00252*Nh[i]
}

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

#HUMAN POPULATIONS
Sh[i,j]<-(muH*Nh[i])+(1-muH)*Sh[i,j-1]-newIh[i,j]
newIh[i,j]~dpois(lambdanewH[i,j])
log(lambdanewH[i,j])<-betaH0+log((betaH*b)/(Nh[i]+m))+log(Iv[i,j-
1]+0.001)+log(Sh[i,j-1]+0.001)+Ch[i]
Ih[i,j]<-(1-muH-gamma)*Ih[i,j-1]+newIh[i,j]
Rh[i,j]<-(1-muH)*Rh[i,j-1]+newRh[i,j]
newRh[i,j]<-(gamma*Ih[i,j-1])

#RELATIVE RISK
RRH[i,j]<-lambdanewH[i,j]/eH[i,j]
}}

#CAR prior distribution for random effects Ch. The sum of Ch is always 0
Ch[1:6]~car.normal(adjH[], weightsH[], numH[], varCh)
for (k in 1:SumNumNeighH){
weightsH[k]<-1}

#Other priors
betaH0~dflat()                    #Flat prior for the intercept
varCh~dgamma(0.01,0.01)           #Prior on precision for spatial random effect Ch
gamma<-0.2
}
```

Fig. 19 Continuous time, discrete space, stochastic SIR-SI model for Assumptions 1-3 in WinBUGS

Fig. 19 displays the WinBUGS code that we developed for relative risk estimation based on our continuous time, discrete space, stochastic SIR-SI model using Assumptions 1-3 for imputing infective mosquito population counts. While, Fig. 20 displays the WinBUGS code that we developed for relative risk estimation using Assumption 4 for imputing infective mosquito population counts.

```
model{
for (i in 1:M){
Sh[i,1]<-Nh[i]-Ih[i,1]-Rh[i,1]
Ih[i,1]<-0.00252*Nh[i]
 Rh[i,1]<-0.00252*Nh[i]
Sv[i,1]<-Nv[i]-Iv[i,1]
Iv[i,1]<-0.00252*Nv[i]
}

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

#HUMAN POPULATIONS
Sh[i,j]<-(muH*Nh[i])+(1-muH)*Sh[i,j-1]-newIh[i,j]
newIh[i,j]~dpois(lambdanewH[i,j])
log(lambdanewH[i,j])<-betaH0+log((betaH*b)/(Nh[i]+m))+log(Iv[i,j-1]+0.001)+log(Sh[i,j-
1]+0.001)+Ch[i]
Ih[i,j]<-(1-muH-gamma)*Ih[i,j-1]+newIh[i,j]
Rh[i,j]<-(1-muH)*Rh[i,j-1]+newRh[i,j]
newRh[i,j]<-(gamma*Ih[i,j-1])

#MOSQUITO VECTOR POPULATIONS
Sv[i,j]<-(muV*Nv[i])+(1-muV-((betaV*b)/(Nh[i]+m))*Ih[i,j-1])*Sv[i,j-1]
newIv[i,j]<-((betaV*b)/(Nh[i]+m))*Ih[i,j-1]*Sv[i,j-1]
Iv[i,j]<-(1-muV)*Iv[i,j-1]+newIv[i,j]
#RELATIVE RISK
#RRH[i,j]<-lambdanewH[i,j]/eH[i,j]
}}

#CAR prior distribution for random effects Ch. The sum of Ch is always 0
Ch[1:6]~car.normal(adjH[], weightsH[], numH[], varCh)
for (k in 1:SumNumNeighH){
weightsH[k]<-1}

#Other priors
betaH0~dflat()                    #Flat prior for the intercept
varCh~dgamma(0.01,0.01)           #Prior on precision for spatial random effect Ch
gamma<-0.2
}
```

Fig. 20 Continuous time, discrete space, stochastic SIR-SI model for Assumption 4 in WinBUGS

VII. Conclusion

In this application, we apply numerical analysis in order to obtain finite-time solutions, with an algorithm that uses a discrete time approximation to solve the continuous time problem. This is because the SIR-SI system of nonlinear ordinary differential equations could not be solved analytically. Therefore, these equations are transformed into discrete relations, which effectively change the continuous time, discrete space, stochastic SIR-SI model into the same form as the discrete time, discrete space, stochastic SIR-SI model described previously in [3]. In other words, the continuous time model is solved using the discrete algorithm, and the continuous time model is reduced to the discrete time model for calculation purposes. Based on the results of the analysis, it can be concluded that the numerical analysis described above provide useful information about solution methods for the nonlinear system of ordinary differential equations representing the SIR-SI models. The numerical analysis of solutions gives information about the SIR and SI populations, which is subsequently used in the estimation of relative risk. This method of solution give a clear picture on how this nonlinear SIR-SI system can be applied, solved and interpreted for continuous time, discrete space, dengue data, and could be use for estimating relative risks based on continuous time, discrete space data specifically for dengue disease.

Extensions to this work include the predictions of dengue disease for future time period conditional upon the observed history such as suggested by [11]. These predictions could contribute to the development of prevention and control

strategies for dengue disease.

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