A particle system model for dengue transmission

Mona Zevika[1], Edy Soewono[1]* and Oliver Tse[2]

[1]Department of Mathematics, Institut Teknologi Bandung, Indonesia

[2]Department of Mathematics and Computer Science, Technische Universiteit Eindhoven, the Netherlands

* Email: esoewono@math.itb.ac.id

Abstract

Dengue disease has been known for decades as a vector-borne disease which is rapidly spreading in many tropical and subtropical countries. The disease is transmitted mostly by female *Aedes aegypty* mosquitoes. Although detailed biological properties of the infection process are already known, in the field applications the disease transmission of dengue is still far from being successfully controlled. The complexity surrounding the transmission is contributed by various factors such as climate, mobility and human-mosquito behavior. Many deterministic models have been developed to investigate the spread of dengue. However, in a deterministic model, spatial heterogeneity factor is not considered. In fact, distances between people and mosquitoes greatly influence the spread of dengue. This paper discusses a microscopic model of the spread of dengue based on spatial heterogeneity. In this microscopic model, every human and mosquito is regarded as a particle and the corresponding human and mosquito populations with their health status are considered as a system of particles. Three important dynamical factors and processes are constructed for each particle, i.e., position and health status of each particle, natural birth and death, infection and transition processes. An estimate of the corresponding basic reproductive ratio is introduced to accommodate the variation of health status and spatial spread of particles

Keywords: Dengue hemorrhagic fever (DHF), particle model, particle systems.

1. INTRODUCTION

Dengue disease has been a global threat and rapidly spreading in tropical and subtropical countries for several decades and becomes a huge burden for the government in affecting countries. Various programs are recommended by WHO [18] to combat the disease with the focus mainly on prevention and control. Recent large outbreaks in several countries indicate that the control programs are still far from successful. The complexity of the transmission is related to the occurrence of secondary infection by the different strain of virus DEN-1, DEN-2, DEN-3, and DEN-4 which are identified in the phenomena of cross-reactive antibodies. This phenomenon is known as the antibody-dependent enhancement (ADE) which is considered as the main risk factor for DHF and DSS [6]. With all complicated factors affecting the infection process, mathematical modelers are forced to focus mostly on specific cases to allow the selection of proper assumptions to fit the reality in the fields.

Transmission models for diseases in the deterministic setting are in general constructed in a homogeneous and macroscopic environment in which each individual has the same chance to have contact with or get contact from other individuals, while disregarding the position and degree of infection of the individuals. In this construction, the basic reproductive ratio representing the endemic threshold of the disease transmission may be obtained [4]. In the case of dengue, several models have been developed, for example in [5], [16]. In these models, under the homogeneity assumption, the biological parameters such as biting rate, natural death rate, and recovery rate are usually known and are obtained as the average rates from the corresponding uniform distributions. On the other hand, the infection rate which comes from the successful contact between susceptible human with infected mosquito and between susceptible mosquito with an infected human is unobservable and is not known. In the field application, estimation of the infection rate may be obtained via graph fitting techniques for given daily incidence data (see for example in [7]).

2. DETERMINISTIC MODEL OF DENGUE TRANSMISSION

A deterministic model for dengue transmission in its simplest form was first formulated in a Susceptible-Infectious-Recovered-Susceptible-Infectious (SIR-SI) dynamical system representing the interaction of three human compartments (SIR) and two mosquito compartments (SI) [1], [5]. In this model, the human status of infection is characterized by three states (SIR) and the corresponding mosquito status by two states (SI). Within each compartment, the health status of an individual is considered as uniform. For such discrete state systems, the basic reproductive ratio (see for example the definition in [4], [17], [9]) may be obtained analytically. The status of infection may be refined, for example, by introducing an expose compartment E (incubation state) as an additional transition regime before entering the infectious compartment I [13], [16].

We begin by recalling a deterministic model for dengue transmission [5], [13] with additional mosquito intervention. Let $S_h(t)$, $E_h(t)$, $I_h(t)$ and $R_h(t)$ be the number of susceptible, exposed, infectious and recovered individuals of host at time t, respectively. Further, let $S_v(t)$, $E_v(t)$ and $I_v(t)$ be the number of susceptible, exposed and infectious vectors at time t, respectively. The total population size of host and vector are kept constant in time and are given by $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ and $N_v(t) = S_v(t) + E_v(t) + I_v(t)$, respectively. The deterministic model is then formulated as follows:

$$
\begin{aligned}
\dot{S}_h(t) &= A_h - \mu_h S_h(t) - \frac{\beta_h S_h I_v}{N_h}, \\
\dot{E}_h(t) &= \frac{\beta_h S_h I_v}{N_h} - \varphi_h E_h - \mu_h E_h, \\
\dot{I}_h(t) &= \varphi_h E_h - \gamma_h I_h - \mu_h I_h, \\
\dot{R}_h(t) &= \gamma_h I_h - \mu_h R_h, \\
\dot{S}_v(t) &= A_v - \frac{\beta_v S_v I_h}{N_h} - \mu_v S_v - \theta_v S_v, \\
\dot{E}_v(t) &= \frac{\beta_v S_v I_h}{N_h} - \varphi_v E_v - \mu_v E_v - \theta_v E_v, \\
\dot{I}_v(t) &= \varphi_v E_v - \mu_v I_v - \theta_v I_v.
\end{aligned}
\tag{1}
$$

The parameters A_h and A_v represent recruitment rates of host and vector population, whereas the parameters μ_h and μ_v represent the rates of natural death of host and vector, respectively. The parameters φ_h, γ_h and φ_v are the transition rates related to the infection process (incubation and recovery). The parameters β_h and β_v are considered as unobservable parameters, which in reality could depend on various non-biological factors such as variations in position. The control parameter θ_v represents the death rate of mosquitoes due to fogging. Host and vector populations in this model are kept constant with $N_h = A_h/\mu_h$ and $N_v = A_v/(\mu_v + \theta_v)$. In this particular case, the basic reproduction number which is derived from the spectral radius of the next generation matrix has the form

$$
R_0 = \left(\frac{\rho \beta_v \beta_h \varphi_v \varphi_h}{(\mu_v + \theta_v)(\gamma_h + \mu_h)(\varphi_h + \mu_h)(\theta_v + \mu_v + \varphi_v)} \right)^{\frac{1}{4}},
\tag{2}
$$

where ρ is the ratio between mosquito and human population. This is the main biological endemic indicator measuring the number of secondary infections which are generated from a single infectious individual in a fully susceptible environment during the respective infection periods (see the definition in [4], [17]). With no mosquito intervention ($\theta_v = 0$), the basic reproductive ratio (2) reduces to the same formulation in ([13]). Further reduction, with no exposed compartments, we have the standard form of R_0 in [5] in the form

$$
R_0 = \left(\frac{\rho \beta_h \beta_v}{\mu_v (\mu_h + \gamma_h)} \right)^{1/2}.
\tag{3}
$$

A simple biological interpretation of the threshold number (3) can be viewed as follows. An infected human gets $\rho \beta_v$ successful mosquito bites during the human infection period $\frac{1}{\mu_h + \gamma_h}$, and then each infected mosquito successfully infects β_h humans during the mosquito infection period $\frac{d}{\mu_v}$. The square root operator represents the geometric mean of the two infectious processes (see similar interpretation in[10]). It is known that if

$R_0 < 1$ the disease free equilibrium is stable, and is becoming unstable when $R_0 > 1$, along with the appearance of a stable endemic state. This later statement can be shown analytically for low dimensional dynamics (see for example in [5], [11], [20]). Figure 1 depicts the level set of R_0 in (2) with respect to the parameters θ_v and $p = \beta_h \beta_v$, and indicates that variations in the nonlinear term $\beta_h \beta_v$ significantly affects the basic reproductive ratio.
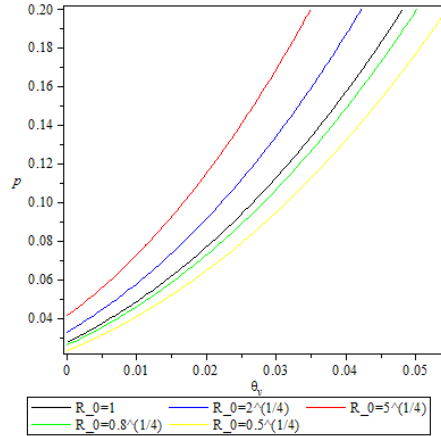

Fig. 1: Level set of R_0

3. PARTICLE (MICROSCOPIC) MODEL

Construction of particle system dynamic for disease transmission is important to view the dynamic at the micro level since the infection process occurs and varies at the micro level. The dynamic is then represented as interacting particles in which micro behavior of the disease transmission can be accommodated. Several applications of particle dynamics have been done in the form of agent-based models. The flexibility of the model is mainly facilitated with the ability to accommodate detail geographical information system [21] and to simulate the variety of complex system in biology, transportation, and network [15], socio-economic and many others [2]. This approach is very well adapted to various disease transmission problems (see for example in [12]) involving a large number of particles and consequently with a huge computational burden.

3.1. System of Particle of disease transmission

Simulation of disease transmission with agent-based simulator platform has been done, see for example in [8], [19]. In this system, individual-based activities in space and time incorporating infection process are constructed and simulated. In most simulations, input data is limited for estimating the involving parameters. Here in particle model, an analytical construction of the model is shown, in which each individual in the population is treated as a particle with a fixed position in the domain $\Omega \subset \mathbb{R}^2$, for which every particle has a unique health status at any time $t \geq 0$. This model is developed from the SIR particle model in [14], [3]. In the case of dengue, we consider two interacting populations, the human population as host and mosquito population as the vector.

We define the domain of the health state for the human population to be $\mathcal{I}^h = [-1, 1]$, which is composed of the susceptible state $\mathcal{I}_1^h = [-1, s_1^h)$, the exposed state $\mathcal{I}_2^h = [s_1^h, s_2^h)$, the infectious state $\mathcal{I}_3^h = [s_2^h, s_3^h)$, and the recovered state $\mathcal{I}_4^h = [s_3^h, 1]$ (see Figure 2).

Similarly, we define the domain of the health state for the mosquito population to be $\mathcal{I}^v = [-1, 1]$, which is composed of the susceptible state $\mathcal{I}_1^v = [-1, s_1^v)$, the exposed state $\mathcal{I}_2^v = [s_1^v, s_2^v)$, and the infectious state $\mathcal{I}_3^v = [s_2^v, 1]$ (see Figure 3).

Let $h_i^t \in \mathcal{I}^h$ and $v_j^t \in \mathcal{I}^v$ be the health status of the i-th human and the health status of the j-th mosquito at time $t \geq 0$, respectively. In this model, the following assumptions hold:
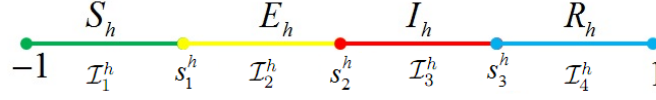
Fig. 2: Interval of human health status compartments

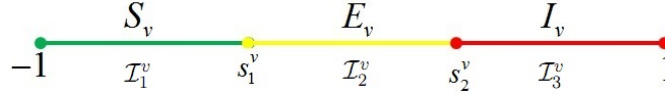

Fig. 3: Interval of mosquito health status compartments

1) Susceptible humans (mosquitoes) in $\mathcal{I}_1^h$ ($\mathcal{I}_1^v$) with no chance of contact with infectious mosquitoes (humans) will remain in $\mathcal{I}_1^h$ ($\mathcal{I}_1^v$) for the rest their life.
2) Infected humans (mosquitoes) in $\mathcal{I}_2^h \cup \mathcal{I}_3^h \cup \mathcal{I}_4^h$ ($\mathcal{I}_2^v \cup \mathcal{I}_3^v$) will increase their status as they undergo the incubation, infectious and recovery processes. In this status, contact with other individuals will have no additional effect.

We denote the position of the i-th human and the j-th mosquito at time $t \geq 0$ by x_i^t and y_j^t, respectively, where x_i^t and $y_j^t \in \Omega \subset \mathbb{R}^2$. Let N_h^t and N_v^t be human and mosquito population at time $t \geq 0$, respectively. Therefore, the interacting particle system may be written as $\aleph^t = \{(h_i^t, x_i^t) \mid i \in N_h^t\} \times \{(v_j^t, y_j^t) \mid j \in N_v^t\}$, where by an abuse of notation, $i \in N_h^t$ means $i \in \{1, \ldots, N_h^t\}$.

3.2. Particle Model of Dengue Fever (SEIR-SEI)

In this microscopic model, we consider the dynamics of $\aleph^t$, in which no mobility takes place. In other words, the position of each particle remains fixed for all times $t \geq 0$. At an initial time, we distribute the particles randomly in the domain $\Omega \subset \mathbb{R}^2$. We emphasize that distance between human and mosquito determines the chance of interaction. To simplify notation, we set

$$d_{ij} = \|x_i - y_j\|, \qquad i \in N_h^t, \;\; j \in N_v^t.$$

In the following, we construct the potential functions which describe the transmission processes. For a single particle dynamics, we define the infection potential functions for human and mosquito as follow

$$dh_i^t = \mathcal{H}(h_i^t)dt, \qquad dv_j^t = \mathcal{V}(h_i^t)dt,$$

where $\mathcal{H}, \mathcal{V} : [-1, 1] \to [0, 1]$ with the boundary conditions
1) $\mathcal{H}(h_i) = 0$, if $h_i \in [-1, s_1^h) \cup \{1\}$
2) $\mathcal{H}(h_i) > 0$, if $h_i \in [s_1^h, 1)$, with
   a) $\int_{s_1^h}^{s_2^h} \frac{dh}{\mathcal{H}(h)} = \frac{1}{\varphi_h}$,
   b) $\int_{s_2^h}^{s_3^h} \frac{dh}{\mathcal{H}(h)} = \frac{1}{\gamma_h}$,

for a human, and
1) $\mathcal{V}(v_i) = 0$, if $v_i \in [-1, s_1^v) \cup \{1\}$,
2) $\mathcal{V}(v_i) > 0$, if $v_i \in [s_2^v, 1]$, with $\int_{s_1^v}^{s_2^v} \frac{dv}{\mathcal{V}(v)} = \frac{1}{\varphi_v}$

for a mosquito. An example of $\mathcal{H}$ and $\mathcal{V}$ may be seen in Figure 4 and possible dynamics for a single particle are depicted in Figure 5 for different initial states.

Next, we define the interaction potential that describes the changes in the health status due to contact between a susceptible human and infected mosquitoes, and between a susceptible mosquito with infected humans. The potential should depend on the distance d_{ij}, and the health status of the particles involved in the interaction. By construction, heterogeneity factors, which occur in reality, may be accommodated in the model. In comparison, spatial uniformity is always assumed in the deterministic model.
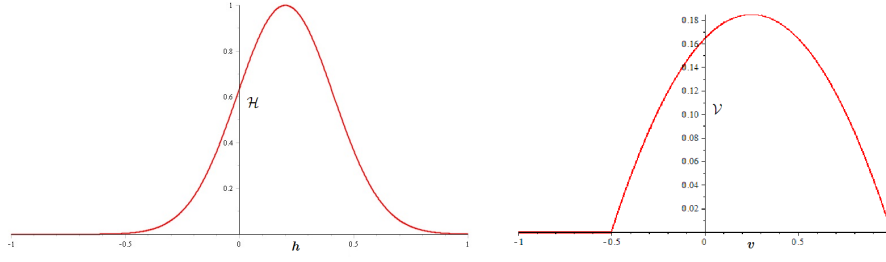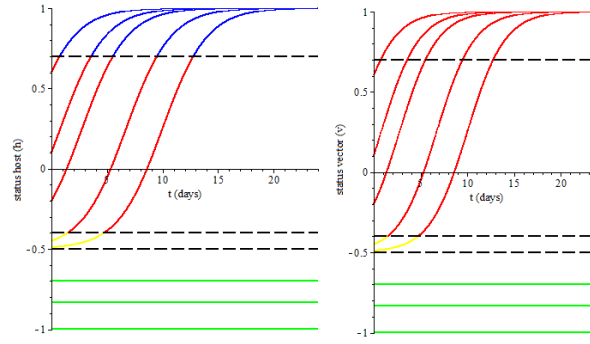
Fig. 4: Example of human and vector potential functions $\mathcal{H}$ and $\mathcal{V}$.

Fig. 5: The changes of health status of single particle

The interaction potential function for a human is given by

$$\mathcal{K}\colon \mathcal{I}^h \times \mathcal{I}^v \times [0, \infty) \to [0, 1]; \qquad \mathcal{K}(h_i, v_j, d_{ij}) = \xi(h_i)\eta(v_j)\lambda(d_{ij}),$$

where the functions ξ, η and λ are defined as follows:
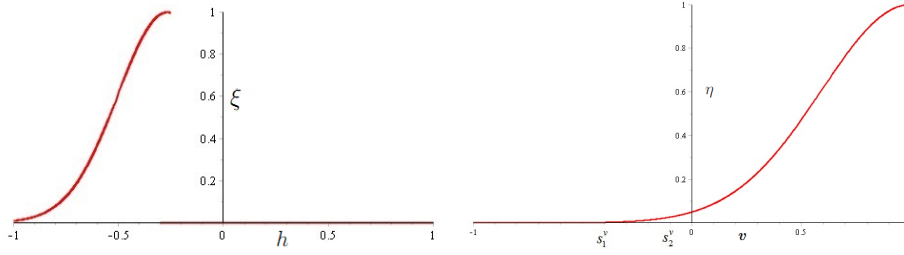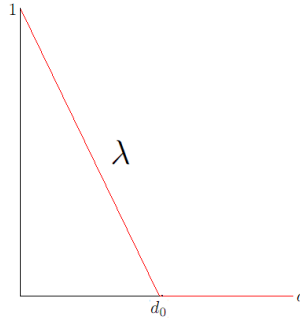
1) $\xi\colon \mathcal{I}^h \to [0, 1]$ represents the probability per unit time that a human with a susceptibility level h may be infected by an infectious mosquito, and satisfies
   a) $\xi(h) > 0$ for $h \in [-1, s_1^h)$,
   b) $\xi(h) = 0$ for $h \in [s_2^h, 1]$.
2) $\eta\colon \mathcal{I}^v \to [0, 1]$ represents the probability per unit time that an infectious mosquito with the infectivity level v may infect a susceptible human, and satisfies
   a) $\eta(v) = 0$ for $v \in [-1, s_2^v)$,
   b) $\eta(v) > 0$ for $v \in [s_2^v, 1]$.
3) $\lambda\colon [0, d_{\max}] \to [0, 1]$ measures the probability of successful transmission. This parameter, which depends on the distance d_{ij} of an interacting human and mosquito at the positions x_i and y_j respectively, is further assumed to be a monotonically decreasing function.

For our simulation, we select ξ, η and λ as given in Table II (see Figures 6, 7).

In Figure 7, d_0 denotes the maximum distance between human and mosquito where biting takes place. From the discussion above, the interacting dynamics of the health status for the human population is now formulated as

$$dh_i^t = \mathcal{H}(h_i^t)dt + \frac{1}{N_v^t}\sum_{j=1}^{N_v^t}\mathcal{K}(h_i, v_j, d_{ij})dt, \qquad (4)$$

where $\mathcal{K}(h_i, v_j, d_{ij}) = \xi(h_i)\eta(v_j)\lambda(d_{ij})$.

Fig. 6: Example of ξ passive infected function and η active infected function

Fig. 7: Example of distance function, $\lambda(d) = \max\{0, 1 - d/d_0\}$

Similarly, the interaction potential function for mosquitoes is given by

$$\mathcal{L} \colon \mathcal{I}^h \times \mathcal{I}^v \times [0, \infty) \to [0, 1]; \qquad \mathcal{L}(v_i, h_j, d_{ji}) = \zeta(v_i)\psi(h_j)\lambda(d_{ji}),$$

where

1) $\zeta \colon \mathcal{I}^v \to [0, 1]$ represents the probability per unit time that a mosquito with a susceptibility level v may be infected by an infectious human, and satisfies
   a) $\zeta(v) > 0$ for $v \in [-1, s_1^v)$,
   b) $\zeta(v) = 0$ for $v \in [s_1^v, 1]$,
2) $\psi \colon \mathcal{I}^h \to [0, 1]$ represents the probability per unit time that an infectious human with the infectivity level h may infect a susceptible mosquito, and satisfies
   a) $\psi(h) = 0$ for $h \in [-1, s_2^h) \cup [s_3, 1]$,
   b) $\psi(h) > 0$ for $h \in [s_2^h, s_3^h)$.
3) $\lambda = \lambda(d_{ji})$ is a distance interaction function as in the case of humans.

For our simulation, we select ζ and ψ as given in Table II (see Figures 8).

Therefore, we describe the change of health status for the mosquito population by

$$dv_i^t = \mathcal{V}(v_i^t)dt + \frac{1}{N_h^t}\sum_{j=1}^{N_h^t}\mathcal{L}(v_i, h_j, d_{ji})dt. \tag{5}$$

Finally, we define the dynamic of human and mosquito populations, allowing the occurrence of natural birth and death, and mosquito control in the form of fumigation. The increase of human (mosquito) population is assumed only due to natural birth. The production $B(z)$ of individual z per unit time is defined as

$$B(z) = \begin{cases} 1, & \text{for } r \leq p(z); \\ 0, & \text{for } r > p(z), \end{cases} \tag{6}$$
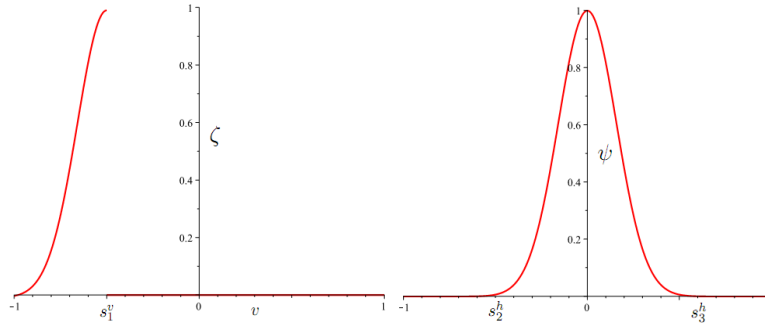
Fig. 8: Example of ζ passive infected function and ψ active infected function

where r is random number in the interval $[0, 1]$ and

$$p(z) = \begin{cases} \frac{A_h}{N_h^t}, & \text{for } z = h_i^t; \\ \frac{A_v}{N_v^t}, & \text{for } z = v_i^t, \end{cases} \tag{7}$$

with parameters A_h and A_v as given in Section 2. The reduction in the human (mosquito) population is assumed to be due to natural death. We define the removal $D(z)$ due to natural death of individual z per unit time as

$$D(z) = \begin{cases} 1, & \text{for } r \leq q(z); \\ 0, & \text{for } r > q(z), \end{cases} \tag{8}$$

where r is random number in interval $[0,1]$ and

$$q(z) = \begin{cases} \mu_h, & \text{for } z = h_i^t; \\ \mu_v, & \text{for } z = v_i^t. \end{cases} \tag{9}$$

with parameters μ_h and μ_v as given in Section 2. Intervention in the number of mosquitoes is also caused by fumigation control. For that we define the removal of mosquito $F(v_i^t)$ per unit time as

$$F(v_i^t) = \begin{cases} 1, & \text{for } r \leq \theta_v \\ 0, & \text{for } r > \theta_v. \end{cases} \tag{10}$$

To summarize, the dynamics of the human and mosquito population is described by

$$dN_h^t = \sum_{i=1}^{N_h^t} B(h_i) - \sum_{i=1}^{N_h^t} D(h_i) \tag{11}$$

$$dN_v^t = \sum_{i=1}^{N_v^t} B(v_i) - \sum_{i=1}^{N_v^t} D(v_i) - \sum_{i=1}^{N_v^t} F(v_i), \tag{12}$$

where $B(h_i)$ represents the number of new born from the i-th human, which depends on the recruitment rate of humans A_h; $D(h_i)$ represents probability of death of the i-th human and depends on μ_h. $B(v_j)$ represents the number of new born from the j-th mosquito, which depends on the recruitment rate of mosquitoes A_v; $D(v_j)$ and $F(v_j)$ represent the probability of natural death and due to intervention of the j-th mosquito, respectively.

3.3. Estimation of macroscopic Parameters

In this section we construct an estimation of the most important parameter in disease transmission for heterogeneous populations, i.e., the infection rates at the macroscopic level due to contact between susceptible and infected individuals. A susceptible human (mosquito) can only be infected by infected mosquitoes (humans) within an admissible radius to allow the occurrence of interaction. New infection takes place between susceptible human with the status h_i, $-1 < h_i < s_1^h$ and infected mosquito with the status v_j, $s_2^v < v_j < 1$. We denote by $\mathcal{B}_h^T$ the product of per-unit-time average human susceptible status, average mosquito infectious status and average distance between the human and mosquito population (computed at the end of simulation period T), and is defined as

$$\mathcal{B}_h^T = \left(\frac{1}{s_1^h + 1} \int_{-1}^{s_1^h} \xi(h)dh \right) \left(\frac{1}{1 - s_2^v} \int_{s_2^v}^{1} \eta(v)dv \right) C^T, \tag{13}$$

where the average contact C^T is defined as

$$C^T = \frac{1}{N_h^T N_v^T} \sum_{i=1}^{N_h^T} \sum_{j=1}^{N_v^T} \lambda(d_{ij}).$$

Similarly, we denote by $\mathcal{B}_v^T$ the product of per-unit-time average vector susceptible status, average human infectious status and average distance between human and vector (computed at the end of simulation period T) and is defined as

$$\mathcal{B}_v^T = \left(\frac{1}{s_1^v + 1} \int_{-1}^{s_1^v} \zeta(v)dv \right) \left(\frac{1}{s_3^h - s_2^h} \int_{s_2^h}^{s_3^h} \psi(h)dh \right) C^T. \tag{14}$$

We have now the estimate of the infection rates at the macro level related to deterministic model given in system (1),

$$\frac{\beta_h}{N_h^T} \approx E(\mathcal{B}_h^T), \qquad \frac{\beta_v}{N_v^T} \approx E(\mathcal{B}_v^T).$$

4. NUMERICAL SIMULATIONS

The parameter values for the numerical simulation of the deterministic model (1) and stochastic particle system are given in Table I. We use the baseline value of $\theta_v = \frac{1}{30}$ for the fogging-related death rate. The functions used for the numerical simulation of the particle model are given in Table II.

TABLE I: Model parameters related to dengue transmission.

Description	Parameter	Values
Host recruitment rate	A_h	$200\mu_h$
Host death rate	μ_h	$1/(365 \cdot 65)$
Host infection rate	β_h	$\mathcal{B}_h^T$
Host latent period	$1/\varphi_h$	7
Host recovery rate	γ_h	$1/14$
Vector recruitment rate	A_v	$100(\mu_v + \theta_v)$
Vector natural death rate	μ_v	$1/30$
Vector infection rate	β_v	$\mathcal{B}_v^T$
Vector latent period	$1/\varphi_v$	5
Fogging-related death rate	θ_v	$0 - 1/30$

The following numerical simulations are conducted for a period of 120 days, by varying the fumigation parameters θ_v listed in Table I. The proportion of infected areas with 5% infected humans and mosquitoes at the initial condition are shown in Table III. A comparison between estimated macroscopic dynamics and the average of five stochastic simulations for humans and mosquitoes are shown in Figures 9–14, with circle ($\circ$) and triangle ($\triangle$) respectively. In these simulations, humans and mosquitoes are uniformly distributed within the domain in Figure 9, 13, and randomly distributed in Figures 10–12, 14–16. Variation in the initial

TABLE II: Particle model functions related to dengue transmission.

Description	Function
Human potential function	$\mathcal{H}(h) = \begin{cases} a_h(2h+1)(h-1), & \text{for } h \in (h_e^*, 1); \\ 0, & \text{for } h = 1 \text{ or } h \in [-1, h_e^*]. \end{cases}$ with $a_h = 0.1466249977^*$
Passive function (susceptible human)	$\xi(h) = \begin{cases} -\frac{(h+1)(h-2h_e^*-1)}{(h_e^*)^2}, & \text{for } h \in [-1, h_e^*); \\ 0, & \text{for } h \in [h_e^*, 1]. \end{cases}$
Active function (infectious mosquito)	$\eta(v) = \begin{cases} -\frac{(v-v_i*)(v-2+v_i^*)}{(1-v_i^*)}, & \text{for } v \in [v_i^*, 1]; \\ 0, & \text{for } v \in [-1, v_i^*). \end{cases}$
Vector potential function	$\mathcal{V}(v) = \begin{cases} a_v(2v+1)(v-1), & \text{for } v \in (h_e^*, 1); \\ 0, & \text{for } v = 1 \text{ or } v \in [-1, v_e^*]. \end{cases}$ with $a_v = 0.1642199974$
Passive function (susceptible mosquito)	$\zeta(v) = \begin{cases} -\frac{(v+1)(v-2v_e^*-1)}{(v_e^*)^2}, & \text{for } v \in [-1, v_e^*); \\ 0, & \text{for } v \in [v_e^*, 1]. \end{cases}$
Active function (infectious human)	$\psi(h) = \begin{cases} -\frac{4(h-h_i^*)(h-h_r^*)}{(h_r^*-h_i^*)^2}, & \text{for } h \in [h_i^*, h_e^*); \\ 0, & \text{otherwise}. \end{cases}$
Distance interaction function	$\lambda(d) = \max(0, 1 - d/d_0), \quad d_0 = 20$

*we calculate a_h from integral of $\mathcal{H}(h)$.

distribution of infected humans and mosquitoes does not give significant effect to the macroscopic transmission behavior (Figures 9–16). This shows that the macroscopic dynamics does not significantly depend on the initial positions of infected individuals. In the next simulations, density of humans and mosquitoes are shown to give significant effect to the macroscopic behavior of the transmission.

TABLE III: Simulation data

Simulation scenario	θ_v	Early-infected areas	Estimated R_0
1.a	0	100% (uniform)	1.9318
1.b	0	100%	1.8035
1.c	0	44.5%	1.8111
1.d	0	11.1%	2.1744
2.a	1/30	100% (uniform)	1.2459
2.b	1/30	100%	1.2179
2.c	1/30	44.5%	1.3162
2.d	1/30	11.1%	1.4559

TABLE IV: Simulation data

θ_v	$N_{h\mathfrak{a}}$	$N_{h\mathfrak{b}}$	$N_{v\mathfrak{a}}$	$N_{v\mathfrak{b}}$	$R_{0\mathfrak{a}}$	$R_{0\mathfrak{b}}$	R_0
	150	150	50	50	2.485194	2.485194	3.514595
	150	150	100	50	3.514595	2.485194	4.304482
$\frac{1}{3}$	150	150	200	50	4.970388	2.485194	5.557062
	150	150	225	50	5.271892	2.485194	5.828296
	150	150	250	50	5.557062	2.485194	6.087457

The distribution of humans and mosquitoes, as well as the distance function $\lambda(d_{ij}) = \max\{0, 1 - d_{ij}/d_0\}$ are critical in the estimation of the infection rate. The parameter d_0 is the maximum distance in which successful contact between a human and a mosquito may occur. As d_0 increases, the chance for successful contact also increases. Sensitivity analysis with varying the intensity parameter d_0 is shown in Figures 17. This analysis simulates a dengue transmission within two adjacent clusters with the same number of human population ($N_{h\mathfrak{a}} = N_{h\mathfrak{b}}$ at $t = 0$) (see Table IV). As the mosquitoes in cluster-$\mathfrak{a}$ increases, the ratio between mosquito and human population in cluster-$\mathfrak{a}$ becomes more dominant than in cluster-$\mathfrak{b}$. We see that the basic ratio in cluster-$\mathfrak{a}$ approaches the global basic reproductive ratio (see Table IV). At the same time if the
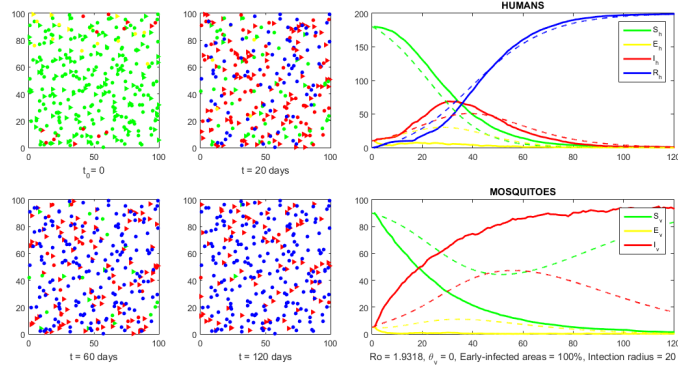
Fig. 9: Simulation of particle and ODE (dash) model scenario 1.a, $\theta_v = 0$, estimate $R_0 = 1.9318$, infected host and vector distribute 100% uniformly.
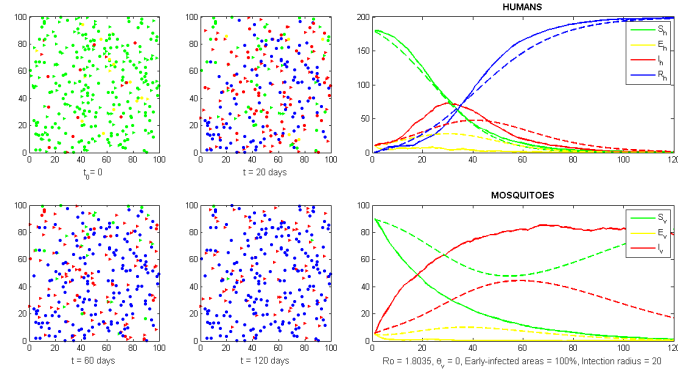

Fig. 10: Simulation of particle and ODE (dash) model scenario 1.b, $\theta_v = 0$, estimate $R_0 = 1.8035$, infected host and vector distribute 100% randomly.
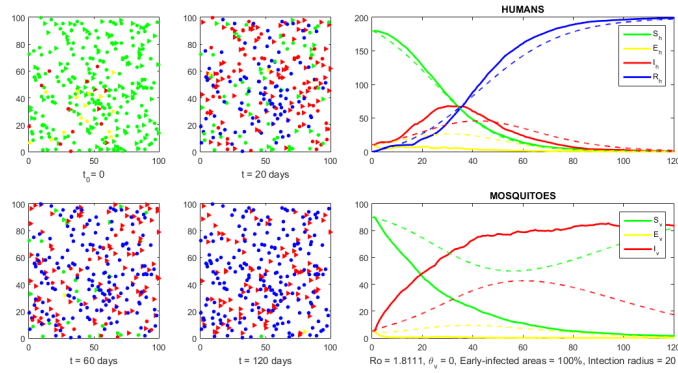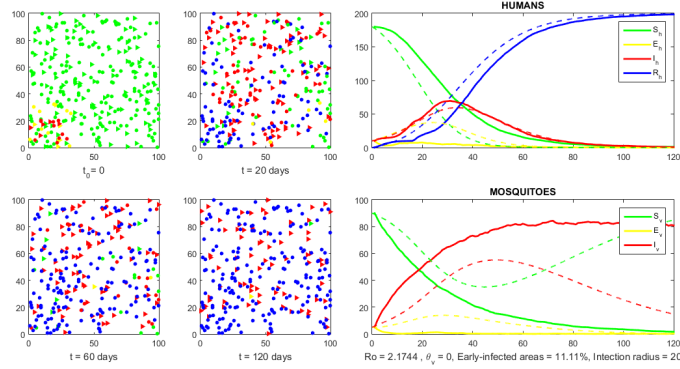

Fig. 11: Simulation of particle and ODE (dash) model scenario 1.c, $\theta_v = 0$, estimate $R_0 = 1.8111$, infected host and vector distribute 44.5% randomly.

Fig. 12: Simulation of particle and ODE (dash) model scenario 1.d, $\theta_v = 0$, estimate $R_0 = 2.1744$, infected host and vector distribute 11.1% randomly
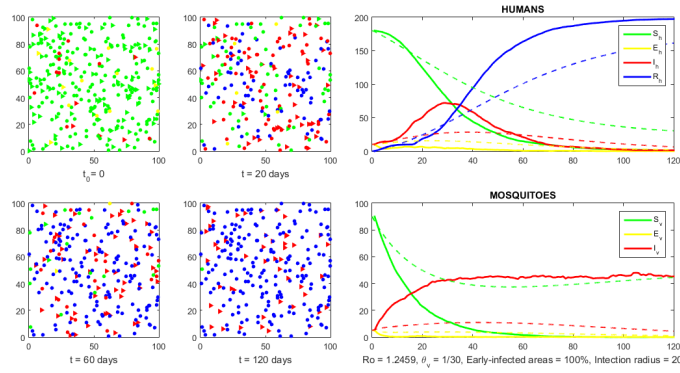

Fig. 13: Simulation of particle and ODE (dash) model scenario 2.a, $\theta_v = \frac{1}{30}$, estimate $R_0 = 1.2459$, infected host and vector distribute 100% uniformly.
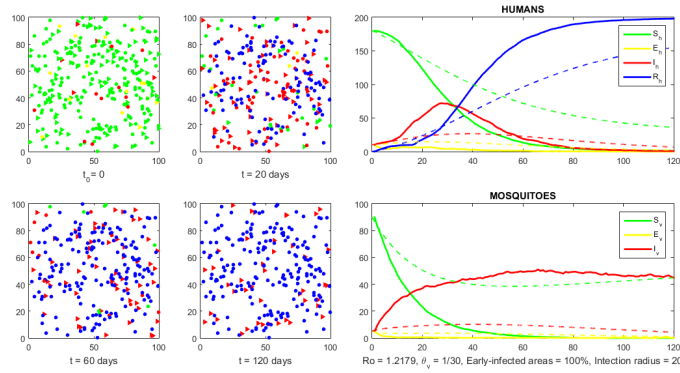

Fig. 14: Simulation of particle and ODE (dash) model scenario 2.b, $\theta_v = \frac{1}{30}$, estimate $R_0 = 1.2179$, infected host and vector distribute 100% randomly.
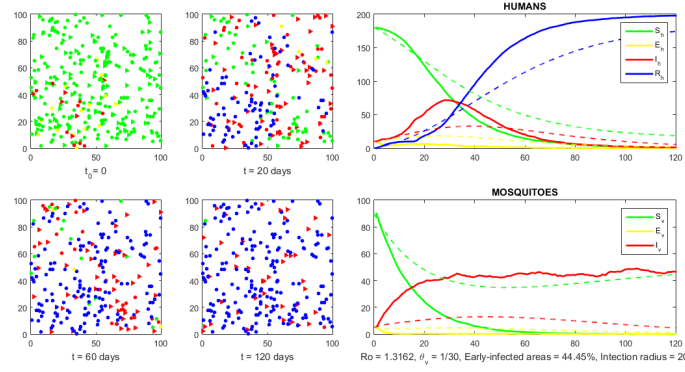
Fig. 15: Simulation of particle and ODE (dash) model scenario 2.c, $\theta_v = \frac{1}{30}$, estimate $R_0 = 1.3162$, infected host and vector distribute 44.5% randomly.
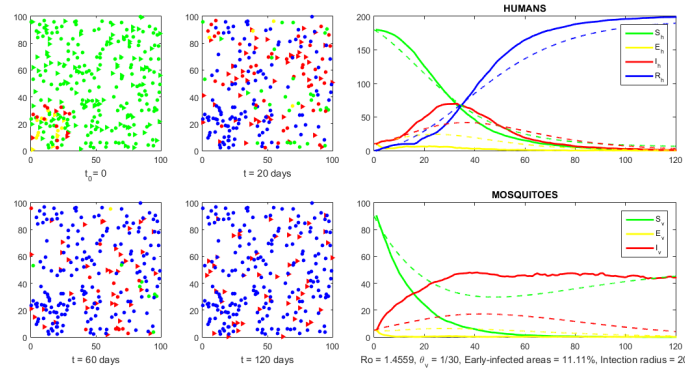

Fig. 16: Simulation of particle and ODE (dash) model scenario 2.d, $\theta_v = \frac{1}{30}$, estimate $R_0 = 1.4559$, infected host and vector distribute 11.1% randomly.
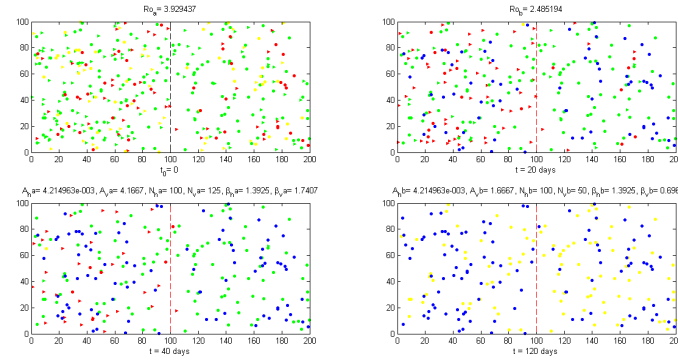

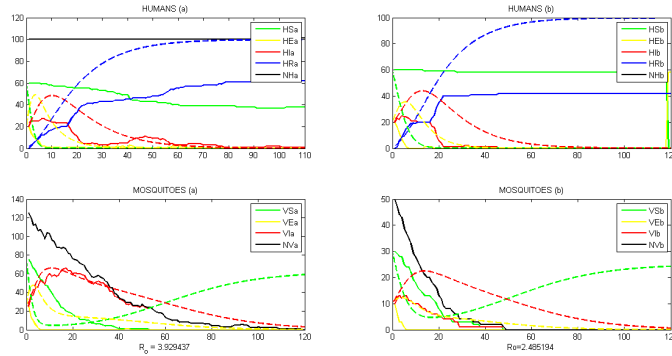Fig. 17: Position and status of particles in two population $\mathfrak{a}$ and $\mathfrak{b}$

Fig. 18: Simulation of particle and ODE (dash) model in two population 𝖆 and 𝖇
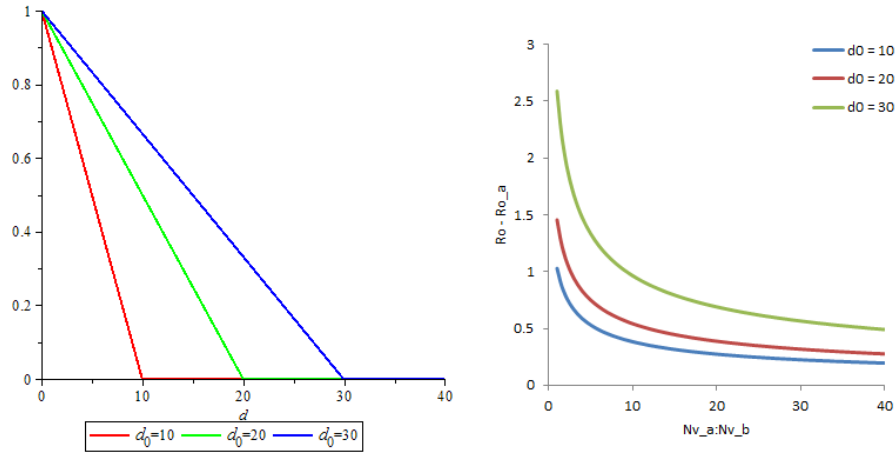
Fig. 19: $\lambda(d)$ (left) and the difference $R_0 - R_{0\mathfrak{a}}$ (right) plotted against the ratio $N_{v\mathfrak{a}}/N_{v\mathfrak{b}}$ for several values of d_0

intensity parameter d_0 decreases, the difference between the global R_0 and local basic ratio $R_{0\mathfrak{a}}$ ($R_0 - R_{0a}$) decreases and tends to zero. This indicates that high domination of the ratio ρ between mosquito and human population in one cluster is the main contribution to the global basic reproductive ratio.

5. CONCLUSION

A particle model for dengue transmission in a heterogeneous environment with natural birth and death is constructed, in which the health status for each human and mosquito changes in time. The dynamics of the "individual" status changes due to contact between human and mosquito, infection process, and recovery process. In comparison to the deterministic model, disease transmission in humans as well as in mosquitoes strongly depends on the distance between humans and mosquitoes involved in the interaction. Finally, the rate of infection at the macroscopic level is constructed by averaging all possible successful contact between humans and mosquitoes, thereby obtaining the basic reproductive ratio for a heterogeneous model.

ACKNOWLEDGEMENT

References

[1] N.T.J. Bailey, The Mathematical Theory of Infectious Diseases, Griffin, London, 1975

[2] S. Bandini, S. Manzoni, G. Vizzari, Agent based modeling and simulation: An informatics perspective, Journal of Artificial Societies and Social Simulation V12, 4, 2009

[3] W. Bock, T. Fattler, I. Rodiah, O. Tse, Numerical simulation of agent-based modeling of spatially inhomogeneous disease dynamics, AIP Conference Proceedings 1871, 020009 (2017); doi: 10.1063/1.4996519

[4] O Diekmann, J.A.P Heesterbeek, Mathematical Epidemiology of Infectious Diseases, John Wiley & Son., New York, 2000.

[5] L. Esteva, C. Vargas, Analysis of a dengue disease transmission model, Math. Biosc. 150 (1998) 131-151.

[6] N. Ferguson, R. Anderson, S. Gupta,The effect of antibody-dependent enhancement on the transmission dynamics and persistence of multiple-strain pathogens, Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 790794, January 1999, Population Biology

[7] T. Götz, T., N. Altmeier, W. Bock, Sutimin, K.P. Wijaya, Modeling dengue data from Semarang, Indonesia, Ecological Complexity,30, 2017, 57-62, DOI: 10.1016/j.ecocom.2016.12.010

[8] C. Isidoro, N. Fachada, F. Barata, A. Rosa, (2011) Agent-Based Model of Dengue Disease Transmission by Aedes aegypti Populations. In: Kampis G., Karsai I., Szathmry E. (eds) Advances in Artificial Life. Darwin Meets von Neumann. ECAL 2009. Lecture Notes in Computer Science, vol 5777. Springer, Berlin, Heidelberg

[9] C.-K. Li, H. Schneider, Applications of PerronFrobenius theory to population dynamics. J. Math. Biol., 2002, 44, 450462

[10] A.L. Nevai, E. Soewono, A mathematical model for the spatial transmission of dengue with daily movement between villages and a city, Mathematical Medicine and Biology 31 (2) 2014, dqt002,150-178

[11] N.Nuraini, E. Soewono, KA Sidarto, Mathematical Model Of Dengue Disease Transmission with Severe DHF Compartment, Bull.Malay. Math. Sci. Soc v. 30 No. 2, 2007,143-157

[12] L. Perez, S. Dragicevic, An agent-based approach for modeling dynamics of contagious disease spread, International Journal of Health Geographics 2009, 8:50, doi:10.1186/1476-072X-8-50

[13] S. T. R. Pinho, C. P. Ferreira, L. Esteva, F. R. Barreta, V. C. Morato E Silva, M. G. L. Teixeira, Modelling the dynamics of dengue real epidemics, Phil. Trans. R. Soc. A (2010) 368, 56795693, doi:10.1098/rsta.2010.0278

[14] M. Schmidtchen, On an Inhomogeneous Disease Spreading Model via Particle Systems, Bachelor Thesis, T.U. Kaiserslautern, 2014.

[15] C. Strickland, G. Dangelmayr, P. D. Shipman, S. Kumar, T.J. Stohlgren, Network spread of invasive species and infectious diseases, Ecological Modelling 309310 (2015), 19

[16] A.K. Supriatna, E. Soewono, S.A. van Gils, A two-age-classes dengue transmission model, Math. Biosciences 216, 2008, 114-121

[17] P. Van Den Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci., vol. 180, pp. 2948, 2002.

[18] WHO Fact Sheet Updated April 2017, Dengue and severe dengue, http://www.who.int/mediacentre/factsheets/fs117/en/

[19] Y. Yang, P. Atkinson, D. Ettema, Individual spacetime activity-based modelling of infectious disease transmission within a city, J. R. Soc. Interface (2008) 5, 759772, doi:10.1098/rsif.2007.1218

[20] H.M. Yang, D. Greenhalgh, Proof of conjecture in The basic reproduction number obtained from Jacobian and next generation matricesA case study of dengue transmission modelling, Applied Mathematics and Computation 265 (2015) 103107

[21] L. I. Zambrano, M. Sierra, B. Lara, I. Rodrguez-N?nez, M. T. Medina, C. O. Lozada-Riascos, A.J.Rodrguez-Morales, Estimating and mapping the incidence of dengue and chikungunya in Honduras during 2015 using Geographic Information Systems (GIS), J. Infect. Public Health, 2017, 10, 446-456.