

Developing a Molecular Mathematical Model for the Dissemination of Dengue Fever Incorporating Human Mobility Variables

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ABSTRACT

In 2009, the World Health Organisation disclosed that Indonesia has the highest frequency of dengue fever in Southeast Asia. In 2014, the Ministry of Health of the Republic of Indonesia publicly disclosed that a substantial number of dengue fever cases were recorded across all regions of Indonesia. Spatial heterogeneity and human mobility are the principal variables that complicate dengue transmission. This work centres on developing a genetic model for dengue disease transmission, incorporating human movement between two distinct clusters. The molecular model addresses both human mobility and spatial heterogeneity. In this specific molecular model, each individual person and female *Aedes aegypti* mosquito is designated as a particle, but the collective population of humans and mosquitoes is termed a particle system. This molecular model consists of three different phases. Their coverage includes factors such as population growth dynamics, alterations in regional distribution, and fluctuations in infection status among humans and mosquitoes. The dynamics influence the interactions between humans and mosquitoes. Simulations have been carried out with a variety of contact radii and human motion patterns taken into consideration. The simulation results indicate that the intensity of dengue transmission escalates with heightened human mobility and an expanded interaction radius during disease propagation.

Keywords: Dengue fever, molecular mode, mathematical modelling, human mobility, spatial heterogeneity

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INTRODUCTION

Dengue fever is caused by the mosquito-borne dengue virus. DBD has developed extensively in recent decades. About half of the world's population is at risk of contracting dengue fever. Tropical and subtropical regions worldwide, especially urban and semi-urban areas, have dengue fever (Kularatne & Dalugama, 2022). This disease's complexity has always drawn scientists from other fields to develop new control measures (Yaacob et al., 2015). The vaccination and treatment options for dengue fever are currently unknown. Vaccine development and effectiveness analysis are underway (Shepard et al., 2004). Without medications or vaccinations, eliminating dengue-carrying mosquitoes is the only approach to prevent transmission (Achee et al., 2015; Ndi et al., 2020). Low mosquito control funds, especially in poor nations, have encouraged health officials to seek effective mosquito control techniques. Understanding disease spread and human and mosquito behaviour is essential for finding the best management methods (Yaacob et al., 2015).

Effective solutions require continuous mosquito control at the most productive *Aedes aegypti* breeding locations (Arias et al., 2015; Ligsay et al., 2022). Human mobility is key to dengue virus propagation (Maciel-de-Freitas et al., 2014). An *Aedes aegypti* mosquito only bites during the day. People who leave their homes throughout the day may encounter mosquitoes (Esler, 2009). Esteva and Vargas created the first host-vector dengue virus transmission model (Esteva & Vargas, 1998, 1999). Since then, researchers have improved the dengue virus model. The author (Nuraini et al., 2007) included Dengue Haemorrhagic Fever's severe infection consequences in the model. Most

hospitalised dengue cases are DHF (Yaacob et al., 2015). Research on DF and DHF groups at two textile companies in an endemic area in Bandung, where some workers were infected at work and some at home, showed that control programme problems affect human mobility (Porter et al., 2005). Human mobility must be included in control programmes.

Spatial heterogeneity affects dengue fever spread, according to Favier et al. (Favier et al., 2005). Deterministic models ignore spatial heterogeneity. Interactions between population members cannot be distinguished. In the deterministic dengue disease model, mosquitoes near and distant from humans have the same risk of infecting them. This study modelled dengue fever propagation using spatial heterogeneity and human mobility. This study distinguishes the impacts of distance and health on human-mosquito interactions. The molecular model in this study solely examines geographical heterogeneity and human mobility. Individuals are particles with a single position and health state in the molecular model (Zevika et al., 2017). Interactions between population members are particle interactions inside a particle system, where particle position and health state determine interaction probabilities.

In addition, this study aims to construct a molecular model of dengue fever disease spread with human mobility between two regions and interpret numerical simulation results. Since dengue fever was discovered, four serotypes have been identified: DEN-1, DEN-2, DEN-3, and DEN-4 (Kularatne & Dalugama, 2022). The female *Aedes aegypti* mosquito spreads dengue illness to humans. The effects of dengue virus infection on the body depend on the person's health and other circumstances. There are three types of dengue: those without warning signs, those with warning signals, and severe cases (Achee et al., 2015; Ndii et al., 2020). Nausea, vomiting, rash, discomfort and pains, a positive tourniquet test, and leukopenia are symptoms of dengue without warning. Abdominal pain, prolonged vomiting, fluid accumulation, mucosal bleeding, lethargy, weakness, liver enlargement > 2 cm, and a relatively rapid increase in haematocrit and platelet count are the same as in DHF without warning signs. Severe dengue cases are defined by plasma leakage, fluid accumulation, respiratory distress, bleeding, altered consciousness, liver dysfunction, and severe organ damage ($AST/ALT \geq 1000$) (Achee et al., 2015; Ndii et al., 2020). ALT is generated when liver cells are injured, while AST damages heart cells and liver cells.

Dengue fever is transferred by humans, called hosts, and female *Aedes aegypti* mosquitoes, called vectors. Therefore, a host-vector model can model dengue fever's spread. Infected mosquitoes spread dengue fever to humans, the host. Without contact with an infectious vector, a healthy host will stay healthy. The host usually incubates after 10 bites from a dengue virus vector (Aldila et al., 2013). The host incubates for 7–10 days (Yaacob et al., 2015). The virus grows in the host but cannot infect the vector during incubation. Dengue fever symptoms indicate that the virus is in the host's blood. The host suffers dengue fever for 7–14 days and can spread the virus to bite vectors. On the eighth day after symptoms develop, healing begins and lasts roughly a week. Dengue fever recovery confers protection against the virus that infected the host but makes the host more susceptible to other dengue viruses (Nuraini et al., 2007; Nuraini & Tasman, 2012). The host can be susceptible (S_h), exposed (E_h), infected (I_h), or recovered (R_h) based on its processes.

Healthy female *Aedes aegypti* mosquitoes bite hosts with viraemia or infected hosts to spread dengue. Vector incubation takes 4–7 days after biting an infected host (Yaacob et al., 2015). Incubation occurs when the vector grows the virus but cannot infect a host. The vector's body will fill with dengue virus until it reaches its maximum level. Mosquitoes live 1–2 months; therefore, the dengue virus can develop in them during their lives. Vectors are classified as susceptible (S_v), exposed (E_v), and infected (I_v) based on their processes.

Particle And Particle Systems

In dengue haemorrhagic fever, there are two populations involved, namely the human population and mosquitoes. Everyone that is in each population is called a particle. Zevika et al. (2017) modelled human and mosquito particles as in definition 1 and definition 2.

Definition 1

In $\Omega \subset \mathbb{R}^2$, each human particle has a single position $X_{h_t} \in \Omega$ and state of health $U_{h_t} \in [-1,1]$ that is the only one at the time $t \in [0, \infty)$.

Definition 2

In $\Omega \subset \mathbb{R}^2$, each mosquito particle has a single position $X_{v_t} \in \Omega$ and state of health $U_{v_t} \in [-1,1]$ that is the only one at the time $t \in [0, \infty)$.

N_{h1_t} , N_{h2_t} , N_{h_t} , N_{v1_t} , N_{v2_t} , and N_{v_t} consecutively as the sum of the human population in region 1, the sum of the human population in region 2, the sum of the human population, the sum of the mosquito population in region 1, the number of mosquito populations in region 2, and the number of mosquito populations alive at time t , then can be modelled in the particle system as in definition 3 and definition 4.

Definition 3

A set of particles W_t , where $W_t \subset \mathbb{N}$, is called a human particle system measured N_{h_t} at time t . A set of particles W_{1_t} , where $W_{1_t} \subset \mathbb{N}$, called a human particle system that is in region 1 is measured N_{h1_t} at time t . A set of particles W_{2_t} , where $W_{2_t} \subset \mathbb{N}$, is called a human particle system that is in region 2 measured N_{h2_t} at time t . For $i \in W_t$, where $W_t = W_{1_t} + W_{2_t}$ and $W_{1_t} \cap W_{2_t} = \emptyset$, $X_{h_t}^i$ and $U_{h_t}^i$ as the position and health status of the i -th human at time t .

Definition 4

A set of particles V_t , where $V_t \subset \mathbb{N}$, is called a mosquito particle system measured N_{v_t} at time t . A set of particles V_{1_t} , where $V_{1_t} \subset \mathbb{N}$, called the mosquito particle system which is in region 1 is measured N_{v1_t} at time t . A set of particles V_{2_t} , where $V_{2_t} \subset \mathbb{N}$, is called a mosquito particle system that is in region 2 measured N_{v2_t} at time t . For $i \in V_t$, where $V_t = V_1 + V_2$ and $V_1 \cap V_2 = \emptyset$, $X_{v_t}^i$ and $U_{v_t}^i$ as the position and health status of the i -th mosquito at time t .

This study uses the nomenclature described in this section to develop a molecular model of dengue haemorrhagic fever dissemination with human movement across the two locations. Building a molecular model of dengue disease propagation with human mobility between these two locations involves three processes: population change, position change, and health status change.

Changes in the Number of Populations

Changes in the number of populations in humans and mosquitoes are only influenced by births and deaths in each population. Suppose $L_{h1_t}^i, M_{h1_t}^i, L_{h2_t}^i, M_{h2_t}^i, L_{v1_t}^i, M_{v1_t}^i, L_{v2_t}^i, M_{v2_t}^i$ consecutively is the birth of the i -th human at time t in region 1, the death of the i -th human at time t in region 1, the birth of the i -th human at time t in region 2, the death of the i -th human at time t in region 2, the birth of the i -th mosquito at time t in region 1, the i -th mosquito death at time t in region 1, the birth of the i -th mosquito at time t in region 2, and the death of the i -th mosquito at time t in region 2. Mortality in humans and mosquitoes is influenced by their respective lifetimes by being μ_h the chance of human death, and μ_v the chance of mosquito death. Natural births in human populations are assumed to depend on the number of populations at time t , i.e. equal to A_{h_t} . Births in mosquito populations for a very large number of populations are assumed to occur constantly by A_v . This is due to the limited availability of food and space for movement of mosquitoes so that the number of mosquitoes that can successfully live is constant.

Changes in the Number of Human Population

The changes in the number of human populations are modelled as follows:

$$dN_{h_t} = \left(\sum_{i \in W_t} L_{h1_t}^i + \sum_{i \in W_t} L_{h2_t}^i - \sum_{i \in W_t} M_{h1_t}^i - \sum_{i \in W_t} M_{h2_t}^i \right) dt$$

with

$$P(L_{h1_t}^i = 1) = \begin{cases} \frac{A_{h_t}}{N_{h_t}} & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases}, P(L_{h2_t}^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \frac{A_{h_t}}{N_{h_t}} & , i \in W_{2_t} \end{cases},$$

$$P(M_{h1_t}^i = 1) = \begin{cases} \mu_h & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases}, P(M_{h2_t}^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \mu_h & , i \in W_{2_t} \end{cases}.$$

$L_{h1_t}^i \in \{0,1\}$, which $L_{h1_t}^i = 1$ states that there is 1 individual born to the i -th human at time t in region 1. $L_{h1_t}^i = 0$ states that the i -th human does not give birth at time t in region 1. The odds of $L_{h1_t}^i = 0$ are $1 - P(L_{h1_t}^i = 1)$. $M_{h1_t}^i \in \{0,1\}$, where $M_{h1_t}^i = 1$ states that the i -th human dies at time t in region 1 with the chance of $P(M_{h1_t}^i = 1) = \mu_h = \frac{1}{\text{lifetime manusia}}$. $M_{h1_t}^i = 0$ states that the i -th human did not die at time t in region 1. The odds of $M_{h1_t}^i = 0$ are $1 - P(M_{h1_t}^i = 1)$. $L_{h2_t}^i \in \{0,1\}$, which $L_{h2_t}^i = 1$ states that there is 1 individual born to the first human at time t in region 2. $L_{h2_t}^i = 0$ states that the i -th human did not give birth at time t in region 2. The odds of $L_{h2_t}^i = 0$ are $1 - P(L_{h2_t}^i = 1)$. $M_{h2_t}^i \in \{0,1\}$, where $M_{h2_t}^i = 1$ states that the i -th human dies at time t in region 2 with the chance of $P(M_{h2_t}^i = 1) = \mu_h = \frac{1}{\text{lifetime manusia}}$. $M_{h2_t}^i = 0$ states that the i -th human being did not die at time t in region 2. The odds of $M_{h2_t}^i = 0$ are $1 - P(M_{h2_t}^i = 1)$. The changes in the number of human populations in region 1 are modelled as follows:

$$dN_{h1_t} = \left(\sum_{i \in W_t} L_{h1_t}^i - \sum_{i \in W_t} M_{h1_t}^i - \sum_{i \in W_t} G_t^i + \sum_{i \in W_t} C_t^i \right) dt$$

with

$$P(L_{h1_t}^i = 1) = \begin{cases} \frac{A_{h_t}}{N_{h_t}} & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases}, P(M_{h1_t}^i = 1) = \begin{cases} \mu_h & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases},$$

$$P(G_t^i = 1) = \begin{cases} \varphi(U_{h_t}^i) & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases}, P(C_t^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \varphi(U_{h_t}^i) & , i \in W_{2_t} \end{cases}$$

The changes in the number of human populations in region 2 are modelled as follows:

$$dN_{h2_t} = \left(\sum_{i \in W_t} L_{h2_t}^i - \sum_{i \in W_t} M_{h2_t}^i - \sum_{i \in W_t} G_t^i + \sum_{i \in W_t} C_t^i \right) dt$$

with

$$P(L_{h2_t}^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \frac{A_{h_t}}{N_{h_t}} & , i \in W_{2_t} \end{cases}, P(M_{h2_t}^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \mu_h & , i \in W_{2_t} \end{cases},$$

$$P(G_t^i = 1) = \begin{cases} \varphi(U_{h_t}^i) & , i \in W_{1_t} \\ 0 & , i \in W_{2_t} \end{cases}, P(C_t^i = 1) = \begin{cases} 0 & , i \in W_{1_t} \\ \varphi(U_{h_t}^i) & , i \in W_{2_t} \end{cases}.$$

$G_t^i \in \{0,1\}$, which $G_t^i = 1$ states that the i -th human being at time T moves from region 1 to region 2. $G_t^i = 0$ states that the i -th human at time t did not move from region 1 to region 2. The odds of $G_t^i = 0$ are $1 - P(G_t^i = 1)$. $C_t^i \in \{0,1\}$, which $C_t^i = 1$ states that the i -th human being at time t

moves from region 2 to region 1. $C_t^i = 0$ states that the i -th human at time t does not move from region 2 to region 1. The odds of $C_t^i = 0$ are $1 - P(C_t^i = 1)$.

Changes in the Number of Mosquito Population

The changes in the number of mosquito population are modelled as follows:

$$dN_{vt} = \left(\sum_{i \in V_t} L_{v1t}^i + \sum_{i \in V_t} L_{v2t}^i - \sum_{i \in V_t} M_{v1t}^i - \sum_{i \in V_t} M_{v2t}^i \right) dt$$

with

$$P(L_{v1t}^i = 1) = \begin{cases} \frac{A_v}{N_{vt}} & , i \in V_{1t} \\ 0 & , i \in V_{2t} \end{cases}, P(L_{v2t}^i = 1) = \begin{cases} 0 & , i \in V_{1t} \\ \frac{A_v}{N_{vt}} & , i \in V_{2t} \end{cases},$$

$$P(M_{v1t}^i = 1) = \begin{cases} \mu_v & , i \in V_{1t} \\ 0 & , i \in V_{2t} \end{cases}, P(M_{v2t}^i = 1) = \begin{cases} 0 & , i \in V_{1t} \\ \mu_v & , i \in V_{2t} \end{cases}.$$

$L_{v1t}^i \in \{0,1\}$, which $L_{v1t}^i = 1$ states that there is 1 individual born from the i -th mosquito at time t in region 1. $L_{v1t}^i = 0$ states that the i -th mosquito does not give birth at time t in region 1. The odds of $L_{v1t}^i = 0$ are $1 - P(L_{v1t}^i = 1)$. $M_{v1t}^i \in \{0,1\}$, where $M_{v1t}^i = 1$ states that the i -th mosquito dies at time t in region 1 with a chance of $P(M_{v1t}^i = 1) = \mu_v = \frac{1}{\text{lifetime nyamuk}}$. $M_{v1t}^i = 0$ states that the i -th mosquito did not die at time t in region 1. The odds of $M_{v1t}^i = 0$ are $1 - P(M_{v1t}^i = 1)$. $L_{v2t}^i \in \{0,1\}$, which $L_{v2t}^i = 1$ states that there is 1 individual born from the i -th mosquito at time t in region 2. $L_{v2t}^i = 0$ states that the i -th mosquito does not give birth at time t in region 2. The odds of $L_{v2t}^i = 0$ are $1 - P(L_{v2t}^i = 1)$. $M_{v2t}^i \in \{0,1\}$, where $M_{v2t}^i = 1$ states that the i -th mosquito dies at time t in region 2 with the chance of $P(M_{v2t}^i = 1) = \mu_v = \frac{1}{\text{lifetime nyamuk}}$. $M_{v2t}^i = 0$ states that the i -th mosquito did not die at time t in region 2. The odds of $M_{v2t}^i = 0$ are $1 - P(M_{v2t}^i = 1)$.

The change in the number of mosquito populations in region 1 is modelled as follows:

$$dN_{v1t} = \left(\sum_{i \in V_t} L_{v1t}^i - \sum_{i \in V_t} M_{v1t}^i \right) dt$$

with

$$P(L_{v1t}^i = 1) = \begin{cases} \frac{A_v}{N_{vt}} & , i \in V_{1t} \\ 0 & , i \in V_{2t} \end{cases} \text{ and } P(M_{v1t}^i = 1) = \begin{cases} \mu_v & , i \in V_{1t} \\ 0 & , i \in V_{2t} \end{cases}.$$

The change in the number of mosquito populations in region 2 is modelled as follows:

$$dN_{v2t} = \left(\sum_{i \in V_t} L_{v2t}^i - \sum_{i \in V_t} M_{v2t}^i \right) dt$$

with

$$P(L_{v2t}^i = 1) = \begin{cases} 0 & , i \in V_{1t} \\ \frac{A_v}{N_{vt}} & , i \in V_{2t} \end{cases} \text{ and } P(M_{v2t}^i = 1) = \begin{cases} 0 & , i \in V_{1t} \\ \mu_v & , i \in V_{2t} \end{cases}.$$

Changes in Positions

In this model, the mosquitoes are assumed to move randomly within the region following Brown's random motion. Meanwhile, humans are assumed to move randomly within regions or move from region 1 to region 2 and vice versa. Changes in the positions of mosquitoes and humans are observed in the same unit of time, which is every minute. The speed of each population is different according to the average speed of movement of humans and mosquitoes.

Changes in Human Positions

Changes in human position are observed every minute. Suppose v_h is the average speed at which humans move every minute; then the change in the position of the i -th human at time t is modelled as

$$dX_{h_t}^i = \begin{cases} v_h dB_t^i, & \text{Brown's motion} \\ X_{p_t}^i dt, & \text{moving between regions} \end{cases} \quad \text{with } X_{p_t}^i \in \Omega.$$

The changes in the position of the i -th human at time t when moving randomly inside region 1 or region 2 are

$$dX_{h_t}^i = v_h dB_t^i.$$

The changes in the position of the i -th human at time t when moving between region 1 and region 2 are

$$dX_{h_t}^i = Y_t^i dt.$$

Changes in Mosquito Positions

Changes in the position of mosquitoes are observed every minute. Suppose v_v is the average speed at which the mosquito moves every minute; then the change in the position of the i -th mosquito at time t is modelled as

$$dX_{v_t}^i = v_v dB_t^i.$$

Changes in Health Status

Health status is defined as the state of an individual or particle that is related to the amount of dengue virus present in the particle's body. The health status of a human is denoted by U_h , where $U_h \in [-1,1]$. $U_h = -1$ declare the condition of man in the healthiest state. Meanwhile, $U_h = 1$ states the condition of humans who have been infected with dengue haemorrhagic fever and have recovered and become immune to the dengue virus, where there is no longer a dengue virus at all in the human body. Based on the SEIR model, the human health status in the interval $[-1,1]$ consists of 4 compartments, namely susceptible host (S_h), exposed host (E_h), infected host (I_h), and recovered host (R_h), divided as shown in Figure 1.

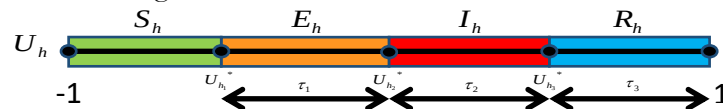


Figure 1. Distribution of human health status intervals

τ_1 , τ_2 , and τ_3 consecutively are the times it takes for a human to pass through the exposed host, infected host, and recovered host compartments. Suppose $\tau = \tau_1 + \tau_2 + \tau_3$ with τ being the total time it takes for a person, from the initial infection, through the incubation period, and experiencing the infection or illness, until they reach the highest level of immunity to the dengue virus. Meanwhile, the health status of mosquitoes is denoted by U_v , where $U_v \in [-1,1]$. $U_v = -1$ declaring the condition of mosquitoes that are clean from the dengue virus. Meanwhile, $U_v = 1$ states the condition of mosquitoes that contain the maximum number of dengue viruses in their bodies. Based on the SEI model, the health status of mosquitoes in the hose consists of 3 compartments, namely $[-1,1]$, susceptible vector (S_v), exposed vector (E_v), and infected vector (I_v) divided as shown in Figure 2.

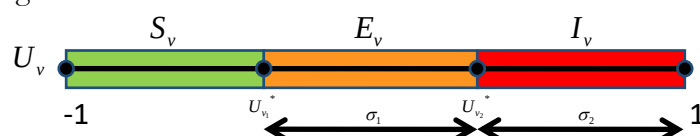


Figure 2. Distribution of mosquito health status intervals

σ_1 and σ_2 successively are the times it takes for a mosquito to pass through the exposed vector and infected vector compartments. Suppose $\sigma = \sigma_1 + \sigma_2$ with σ being the total time it takes for a mosquito to start being infected, experience an incubation period, and experience an infection period that can transmit the dengue virus to reach the maximum infective ability. Changes in the health status of particles (humans or mosquitoes) are influenced by internal factors and external factors. Internal factors that affect changes in the health status of particles are the number of dengue viruses in the body, which is modelled by the health status of the particles themselves without being influenced by interactions with the environment. Meanwhile, the external factor in question is the interaction between particles and their environment. Changes in particle health status without being influenced by the environment are modelled with potential functions, while changes in particle health status due to the influence of interaction with the environment are modelled by interaction functions. The interaction function is influenced by 3 functions, namely the function of the chance of success of the infected particle, the function of the chance of distance of the interaction, and the function of the chance of success of infecting by other particles.

Changes in Health Status of Human

A single-particle condition is defined as a condition in which there is no interaction between humans and mosquitoes. In the single-particle condition, the change in the health status of 1 human is only affected by the health status of oneself, which is modelled with a potential function $\mathcal{H}_h$, where

$$\mathcal{H}_h: [-1, 1] \rightarrow \mathbb{R}_{\geq 0}$$

$U_h(t) = U_{h_t}$ is the solution of $\frac{dU_h}{dt} = \mathcal{H}_h(U_h)$ with $U_h(0) = U_{h_0}$.

The definition of the potential functions $\mathcal{H}_h$ is as follows:

1. $\mathcal{H}_h(U_{h_0}) = 0, \forall U_{h_0} \in [-1, U_{h_1}^*) \cup \{1\}$
2. $\mathcal{H}_h(U_{h_0}) > 0$ with $\int_{U_{h_0}}^{U_{h_t}} \frac{dU_h}{\mathcal{H}_h(U_h)} = t \forall U_{h_0} \in [U_{h_1}^*, 1)$
 - i. $\int_{U_{h_1}^*}^{U_{h_2}^*} \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau_1$
 - ii. $\int_{U_{h_2}^*}^{U_{h_3}^*} \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau_2$
 - iii. $\int_{U_{h_3}^*}^1 \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau_3$

From the definition of the potential functions $\mathcal{H}_h$ above, properties are obtained:

1. If $U_{h_0} \in [-1, U_{h_1}^*) \cup \{1\}$ then $U_{h_t} = U_{h_0}$.

Proof

Based on definition 1, it is obtained $\mathcal{H}_h(U_{h_0}) = 0$ so that $\frac{dU_h}{dt} = U_{h_{t+1}} - U_{h_t} = 0 \Leftrightarrow U_{h_{t+1}} = U_{h_t}$. Consequently $U_{h_t} = U_{h_0}$. ■

2. If $U_{h_0} = U_{h_1}^*$ and $U_{h_t} = 1$ then $\int_{U_{h_0}}^{U_{h_t}} \frac{dU_h}{\mathcal{H}_h(U_h)} = \int_{U_{h_1}^*}^1 \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau$.

Proof

Because $U_{h_0} = U_{h_1}^*$ then $1 - U_{h_0} = 1 - U_{h_1}^* \Leftrightarrow U_{h_t} - U_{h_0} = 1 - U_{h_1}^*$. Thus, $\int_{U_{h_0}}^{U_{h_t}} \frac{dU_h}{\mathcal{H}_h(U_h)} = \int_{U_{h_1}^*}^1 \frac{dU_h}{\mathcal{H}_h(U_h)} = \int_{U_{h_1}^*}^{U_{h_2}^*} \frac{dU_h}{\mathcal{H}_h(U_h)} + \int_{U_{h_2}^*}^{U_{h_3}^*} \frac{dU_h}{\mathcal{H}_h(U_h)} + \int_{U_{h_3}^*}^1 \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau_1 + \tau_2 + \tau_3 = \tau$. ■

3. If $U_{h_1}^* < U_{h_0} < 1$ and $\int_{U_{h_0}}^{U_{h_t}} \frac{dU_h}{\mathcal{H}_h(U_h)} = \tau^*$ then $\tau^* < \tau$

Proof

Because $U_{h_1}^* < U_{h_0}$ then $1 - U_{h_1}^* > 1 - U_{h_0}$. Based on the definition 2, property 2, and U_h continuous and $\mathcal{H}_h(U_h)$ positive, then $\int_{U_{h_1}^*}^1 \frac{dU_h}{\mathcal{H}_h(U_h)} > \int_{U_{h_0}}^1 \frac{dU_h}{\mathcal{H}_h(U_h)}$. Consequently $\tau > \tau^*$. ■

Based on the definition of the function $\mathcal{H}_h$ by selecting $U_{h_1}^* > -0.8$, one example of a function that can be selected is

$$\mathcal{H}_h(U_h) = \begin{cases} a(4 + U_h - 5U_h^2) & \text{for } U_{h_0} \in [U_{h_1}^*, 1), a > 0 \\ 0 & \text{for } U_{h_0} \in [-1, U_{h_1}^*) \cup \{1\} \end{cases}$$

Proof

- (a) For $U_{h_0} \in [-1, U_{h_1}^*) \cup \{1\}$, the selected function $\mathcal{H}_h(U_h)$ clearly meets definition 1.
(b) For $U_{h_0} \in [U_{h_1}^*, 1)$, it will be further proven that the function $\mathcal{H}_h(U_h)$ meets definition 2.

Based on the selected function $\mathcal{H}_h(U_h)$, it is obtained:

$$\mathcal{H}_h'(U_h) = a(1 - 10U_h)$$

$$\mathcal{H}_h''(U_h) = -10a$$

$$\mathcal{H}_h(-0.8) = 0 = \mathcal{H}_h(1)$$

From $\mathcal{H}_h'(U_h)$, $\mathcal{H}_h$ have 1 stationary point, for example, on U_h^* . Because $\mathcal{H}_h''(U_h) < 0$ for each one U_h , $\mathcal{H}_h$ is always concave downwards so that U_h^* is the maximum point. Consequently $0 < \mathcal{H}_h(U_h) \leq \mathcal{H}_h(U_h^*)$.

Look at the similarities.

$$\frac{dU_h}{dt} = \mathcal{H}_h(U_h) \neq 0 \Rightarrow \int_{U_{h_0}}^{U_{h_t}} \frac{dU_h}{\mathcal{H}_h(U_h)} = \int_0^t dt \Leftrightarrow \frac{1}{9a} \ln \left[\frac{4 + 5U_h}{1 - U_h} \right]_{U_{h_0}}^{U_{h_t}} = t$$

so that it is obtained $U_{h_t} = \frac{Ke^{9at} - 4}{Ke^{9at} + 5}$ with $K = \frac{4 + 5U_{h_0}}{1 - U_{h_0}}$ and $a = \frac{1}{9t} \ln \frac{(4 + 5U_{h_t})(1 - U_{h_0})}{(1 - U_{h_t})(4 + 5U_{h_0})}$, where t is given according to the time period of dengue disease. For $\tau_1 = \tau_2 = \tau_3 = 7.24.60$ minutes, select $U_{h_1}^* = -0.799$ then for $U_{h_t} \rightarrow 1$ gives $K = 0.0027793$ and $a = 0.000055078$. Thus, obtained $U_{h_2}^* = -0.663$ and $U_{h_3}^* = 0.863$. Graph of the function $\mathcal{H}_h(U_h)$ against U_h as shown in Figure 3.

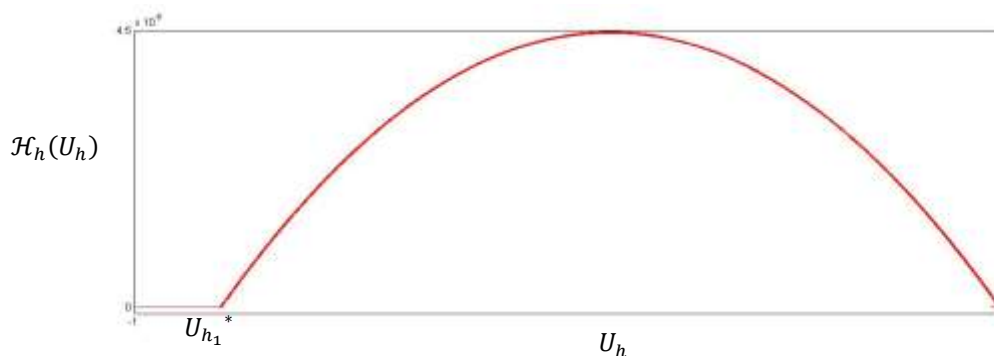


Figure 3. Graph of potential functions $\mathcal{H}_h$

Changes in the health status of 1 human by using the selected function $\mathcal{H}_h(U_h)$ with $K = 0.0027793$ and $a = 0.000055078$ as shown in Figure 4.

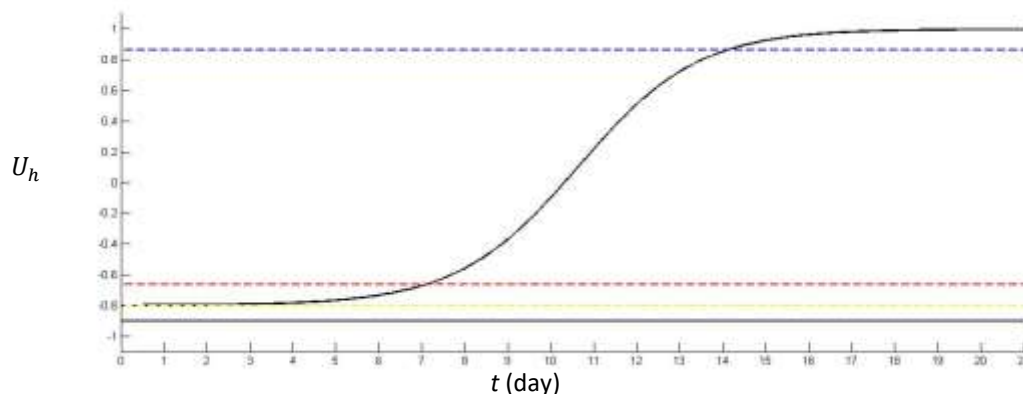


Figure 4. Human health status affected by potential function $\mathcal{H}_h$

Furthermore, the interaction function that affects human health status is modelled. The function of human interaction is a function that affects changes in human health status caused by human interaction with a number of mosquitoes. Suppose the interaction function that affects the health status of the human is the function $\mathcal{K}_h$. Write $\mathcal{K}_h$ as

$$\mathcal{K}_h(\|X_{h_t}^i - X_{v_t}^j\|, U_{h_t}^i, U_{v_t}^j) = \phi_h(\|X_{h_t}^i - X_{v_t}^j\|) \cdot \chi_h(U_{h_t}^i) \cdot \psi_h(U_{v_t}^j).$$

The function states the chance of interaction seen from the distance between humans and mosquitoes. Interaction can occur if mosquitoes are in the R radius $\phi_h(\|X_{h_t}^i - X_{v_t}^j\|)$ of humans. Mosquitoes that are within the R radius of humans can interact with humans. Based on the illustration above, define the function $\phi_h(\|X_{h_t}^i - X_{v_t}^j\|)$ as follows:

$$\phi_h: \mathbb{R}_{\geq 0} \rightarrow [0,1]$$

1. $\phi_h(\|X_{h_t}^i - X_{v_t}^j\|) \geq 0$ and inversely proportional to $\|X_{h_t}^i - X_{v_t}^j\|$, for $\|X_{h_t}^i - X_{v_t}^j\| \leq R$.
2. $\phi_h(\|X_{h_t}^i - X_{v_t}^j\|) = 0$ for $\|X_{h_t}^i - X_{v_t}^j\| \geq R$.

An example of a function $\phi_h(\|X_{h_t}^i - X_{v_t}^j\|)$ is

$$\phi_h(\|X_{h_t}^i - X_{v_t}^j\|) = \max\left\{0, 1 - \frac{\|X_{h_t}^i - X_{v_t}^j\|}{R}\right\}.$$

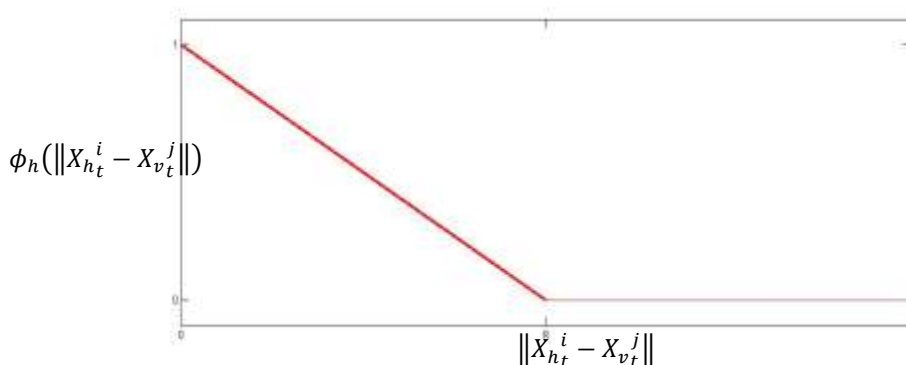


Figure 5. Function graph ϕ_h

Function $\chi_h(U_{h_t}^i)$ is a function of the chance of success in being infected in humans. Humans who will be affected by interaction with the infected vector are only susceptible hosts. Based on assumptions, define the function $\chi_h(U_{h_t}^i)$ as follows:

$$\chi_h: [-1,1] \rightarrow [0,1]$$

1. $\chi_h(U_{h_t}^i) > 0$ and monotony rises, for $U_{h_t}^i \in [-1, U_{h_1}^*)$;
2. $\chi_h(U_{h_t}^i) = 0$ for $U_{h_t}^i \in [U_{h_1}^*, 1]$.

An example of a function $\chi_h(U_{h_t}^i)$ is

$$\chi_h(U_{h_t}^i) = \begin{cases} -\frac{1}{2} \left(\frac{U_{h_t}^i - U_{h_1}^*}{1 + U_{h_1}^*} \right)^2 + 1 & ; \quad U_{h_t}^i \in [-1, U_{h_1}^*) \\ 0 & ; \quad U_{h_t}^i \in [U_{h_1}^*, 1] \end{cases}.$$

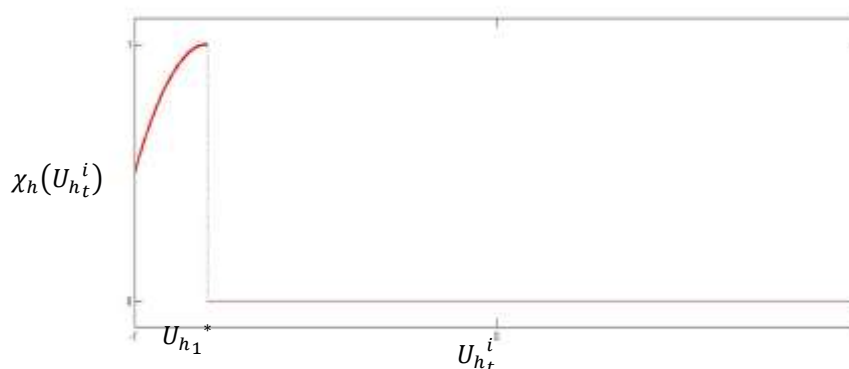


Figure 6. Function graph χ_h

Function $\psi_h(U_{v_t}^j)$ is a function of the chance that mosquitoes will succeed in infecting humans. Mosquitoes that can transmit the dengue virus are infected vectors. Based on assumptions, define the function $\psi_h(U_{v_t}^j)$ as follows:

- $$\psi_h: [-1, 1] \rightarrow [0, 1]$$
1. $\psi_h(U_{v_t}^j) > 0$ and monotony rises, for $U_{v_t}^j \in [U_{v_2}^*, 1]$;
 2. $\psi_h(U_{v_t}^j) = 0$ for $U_{v_t}^j \in [-1, U_{v_2}^*)$.

An example of a function $\psi_h(U_{v_t}^j)$ is

$$\psi_h(U_{v_t}^j) = \begin{cases} \frac{(U_{v_2}^* - U_{v_t}^j)(U_{v_t}^j + U_{v_2}^* - 2)}{(U_{v_2}^* - 1)^2} & ; \quad U_{v_t}^j \in [U_{v_2}^*, 1] \\ 0 & ; \quad U_{v_t}^j \in [-1, U_{v_2}^*) \end{cases}$$

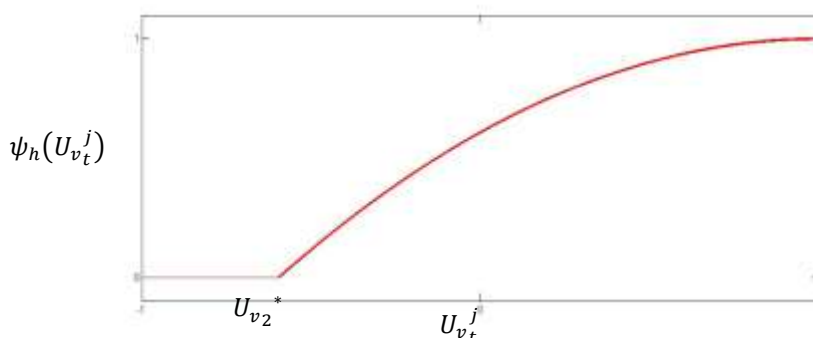


Figure 7. Function graph ψ_h

If there are N_{v_t} as many mosquitoes, then the value of possible interactions for 1 human is modelled as

$$\frac{1}{N_{v_t}} \sum_{j \in V_t} \mathcal{K}_h(\|X_{h_t}^i - X_{v_t}^j\|, U_{v_t}^j, U_{h_t}^i).$$

Thus, changes in human health status influenced by potential functions and interaction functions are modelled as

$$dU_{h_t}^i = \mathcal{H}_h(U_{h_t}^i) dt + \frac{1}{N_{v_t}} \sum_{j \in V_t} \mathcal{K}_h(\|X_{h_t}^i - X_{v_t}^j\|, U_{v_t}^j, U_{h_t}^i) dt \text{ for } i \in W_t.$$

The changes in human health status i at time t when in region 1 are modelled as

$$dU_{h_t}^i = \mathcal{H}_h(U_{h_t}^i) dt + \frac{1}{N_{v_{1t}}} \sum_{j \in V_{1t}} \mathcal{K}_{h1}(\|X_{h_t}^i - X_{v_t}^j\|, U_{v_t}^j, U_{h_t}^i) dt \text{ for } i \in W_{1t}.$$

The changes in i -th human health status at time t when in region 2 are modelled as

$$dU_{h_t}^i = \mathcal{H}_h(U_{h_t}^i) dt + \frac{1}{N_{v_{2t}}} \sum_{j \in V_{2t}} \mathcal{K}_{h2}(\|X_{h_t}^i - X_{v_t}^j\|, U_{v_t}^j, U_{h_t}^i) dt \text{ for } i \in W_{2t}.$$

Changes in Health Status of Mosquitoes

In the single-particle condition, the change in the health status of 1 mosquito that is only affected by the health status of the mosquito itself is modelled with the potential function $\mathcal{H}_v$ where

$$\mathcal{H}_v: [-1, 1] \rightarrow \mathbb{R}_{\geq 0}$$

so that $U_v(t) = U_{v_t}$ is the solution of $\frac{dU_v}{dt} = \mathcal{H}_v(U_v)$ with $U_v(0) = U_{v_0}$.

Define the potential function $\mathcal{H}_v$ as follows:

1. $\mathcal{H}_v(U_{v_0}) = 0, \forall U_{v_0} \in [-1, U_{v_1}^*) \cup \{1\}$;
2. $\mathcal{H}_v(U_{v_0}) > 0, \int_{U_{v_0}}^{U_{v_t}} \frac{dU_v}{\mathcal{H}_v(U_v)} = t, \forall U_{v_0} \in [U_{v_1}^*, 1)$ with
 - i. $\int_{U_{v_1}^*}^{U_{v_2}^*} \frac{dU_v}{\mathcal{H}_v(U_v)} = \sigma_1$;
 - ii. $\int_{U_{v_2}^*}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} = \sigma_2$.

From the definition of potential functions $\mathcal{H}_v$ above, properties are obtained:

1. If then $U_{v_0} \in [-1, U_{v_1}^*) \cup \{1\} U_{v_t} = U_{v_0}$

Proof

Based on definition 1, it is obtained $\mathcal{H}_v(U_{v_0}) = 0$ so that

$$\frac{dU_v}{dt} = U_{v_{t+1}} - U_{v_t} = 0 \Leftrightarrow U_{v_{t+1}} = U_{v_t}. \text{ Consequently } U_{v_t} = U_{v_0}. \blacksquare$$

2. If $U_{v_0} = U_{v_1}^*$ and then $U_{v_t} = 1 \int_{U_{v_0}}^{U_{v_t}} \frac{dU_v}{\mathcal{H}_v(U_v)} = \int_{U_{v_1}^*}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} = \sigma$.

Proof

Because $U_{v_0} = U_{v_1}^*$ then. Thus, $1 - U_{v_0} = 1 - U_{v_1}^* \Leftrightarrow U_{v_t} - U_{v_0} = 1 - U_{v_1}^*$

$$\int_{U_{v_0}}^{U_{v_t}} \frac{dU_v}{\mathcal{H}_v(U_v)} = \int_{U_{v_1}^*}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} = \int_{U_{v_1}^*}^{U_{v_2}^*} \frac{dU_v}{\mathcal{H}_v(U_v)} + \int_{U_{v_2}^*}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} = \sigma_1 + \sigma_2 = \sigma. \blacksquare$$

3. If and then $U_{v_1}^* < U_{v_0} < 1 \int_{U_{v_0}}^{U_{v_t}} \frac{dU_v}{\mathcal{H}_v(U_v)} = \sigma^* \sigma^* < \sigma$

Proof

Because then. Based on the definition of 2, nature 2, and continuous and positive, then .

$$\text{Consequently } U_{v_1}^* < U_{v_0} 1 - U_{v_1}^* > 1 - U_{v_0} U_v \mathcal{H}_v(U_v) \int_{U_{v_1}^*}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} > \int_{U_{v_0}}^1 \frac{dU_v}{\mathcal{H}_v(U_v)} \sigma < \sigma^*. \blacksquare$$

Based on the definition of the function by selecting, one example of a function that can be selected is $\mathcal{H}_v U_{v_1}^* > -0.8$

$$\mathcal{H}_v(U_v) = \begin{cases} b(4 + U_v - 5U_v^2) & \text{to } U_{v_0} \in [U_{v_1}^*, 1), b > 0 \\ 0 & \text{to } U_{v_0} \in [-1, U_{v_1}^*) \cup \{1\} \end{cases}$$

Proof

(a) For , the selected function clearly meets definition 1. $U_{v_0} \in [-1, U_{v_1}^*) \cup \{1\} \mathcal{H}_v(U_{v_0})$

(b) For , it will be further proven that the function meets definition 2. Based on the selected function, obtained $U_{v_0} \in [U_{v_1}^*, 1) \mathcal{H}_v(U_{v_0}) \mathcal{H}_v(U_v)$

$$\mathcal{H}_v'(U_v) = b(1 - 10U_v)$$

$$\mathcal{H}_v''(U_v) = -10b$$

$$\mathcal{H}_v(-0.8) = 0 = \mathcal{H}_v(1)$$

From $\mathcal{H}_v'(U_v)$, $\mathcal{H}_v$ have 1 stationary point, for example, on U_v^* . Because $\mathcal{H}_v''(U_v) < 0$ for each one U_v , $\mathcal{H}_v$ is always concave downwards so that U_v^* is the maximum point. Consequently $0 < \mathcal{H}_v(U_v) \leq \mathcal{H}_v(U_v^*)$.

Consider the equation

$$\frac{dU_v}{dt} = \mathcal{H}_v(U_v) \neq 0 \Rightarrow \int_{U_{v_0}}^{U_{v_t}} \frac{dU_v}{\mathcal{H}_v(U_v)} = \int_0^t dt \Leftrightarrow \frac{1}{9b} \ln \frac{4 + 5U_v}{1 - U_v} \Big|_{U_{v_0}}^{U_{v_t}} = t$$

so that it is obtained $U_{v_t} = \frac{Le^{9bt} - 4}{Le^{9bt} + 5}$ with $L = \frac{4 + 5U_{v_0}}{1 - U_{v_0}}$ and $b = \frac{1}{9t} \ln \frac{(4 + 5U_{v_t})(1 - U_{v_0})}{(1 - U_{v_t})(4 + 5U_{v_0})}$, where t is given according to the period when the dengue virus develops in the mosquito body.

For $\sigma_1 = 4.24.60$ and $\sigma_2 = 7.24.60$ minutes, select $U_{v_1}^* = -0.799$, giving $U_{v_t} \rightarrow 1$ to get $L = 0.0027793$ and $b = 0.000105149$. Thus, it obtains $U_{v_2}^* = -0.594$.

Graph of the function $\mathcal{H}_v(U_v)$ against U_v as shown in Figure IV.10.

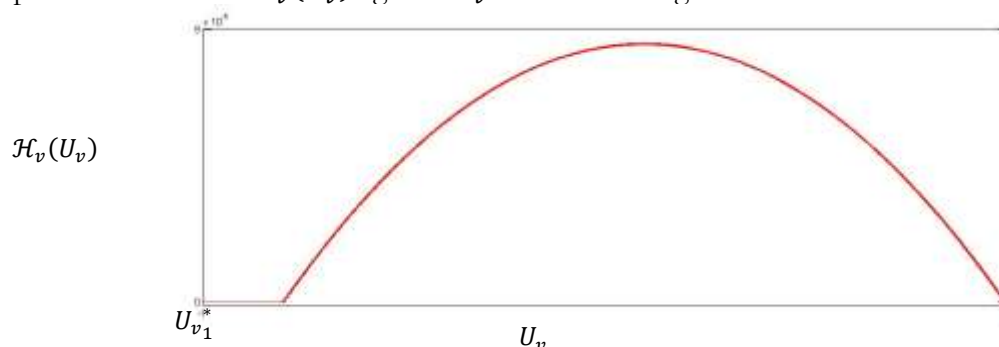


Figure 8. Graph of potential functions $\mathcal{H}_v$

Changes in the health status of 1 mosquito using the function selected $\mathcal{H}_v(U_v)$ with $L = 0.0027793$ and $b = 0.000105149$ as shown in Figure IV.11.

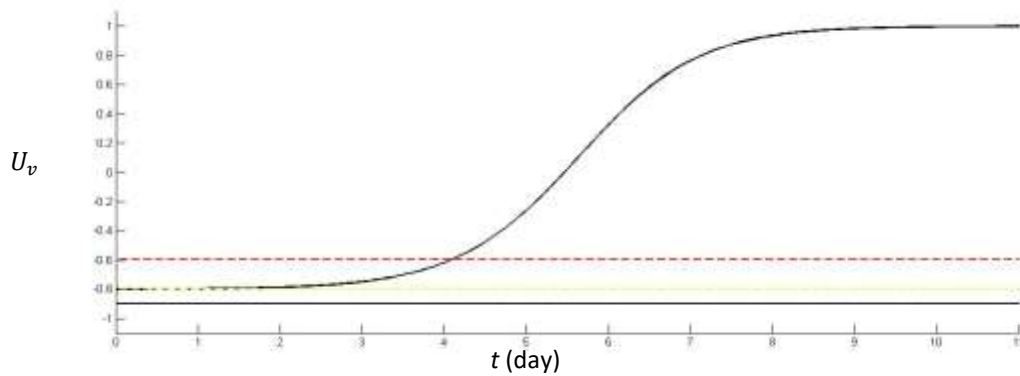


Figure 9. Health status of mosquitoes affected by potential function $\mathcal{H}_v$

Furthermore, the interaction function that affects the health status of mosquitoes is modelled. The function of mosquito interaction is a function that affects changes in the health status of mosquitoes caused by the interaction of the mosquito with several humans. Suppose the interaction function that affects the health status of the mosquito is the $\mathcal{K}_v$. Write $\mathcal{K}_v$ as

$$\mathcal{K}_v(\|X_{v_t}^i - X_{h_t}^j\|, U_{v_t}^i, U_{h_t}^j) = \phi_v(\|X_{v_t}^i - X_{h_t}^j\|) \cdot \chi_v(U_{v_t}^i) \cdot \psi_v(U_{h_t}^j).$$

The function $\phi_v(\|X_{v_t}^i - X_{h_t}^j\|)$ expresses the opportunity for interaction to occur from the distance between mosquitoes and humans. Interactions can occur if humans are at the R radius of mosquitoes. In Figure 3.11, humans who are within the R radius of mosquitoes can interact with mosquitoes. Based on the illustration above, define the function $\phi_v(\|X_{v_t}^i - X_{h_t}^j\|)$ as follows:

$$\phi_v: \mathbb{R}_{\geq 0} \rightarrow [0,1]$$

1. $\phi_v(\|X_{v_t}^i - X_{h_t}^j\|) \geq 0$ and inversely proportional to $\|X_{v_t}^i - X_{h_t}^j\|$, for $\|X_{v_t}^i - X_{h_t}^j\| \leq R$;
2. $\phi_v(\|X_{v_t}^i - X_{h_t}^j\|) = 0$ for $\|X_{v_t}^i - X_{h_t}^j\| \geq R$.

An example of a function $\phi_v(\|X_{v_t}^i - X_{h_t}^j\|)$ is

$$\phi_v(\|X_{v_t}^i - X_{h_t}^j\|) = \max\left\{0, 1 - \frac{\|X_{v_t}^i - X_{h_t}^j\|}{R}\right\}.$$

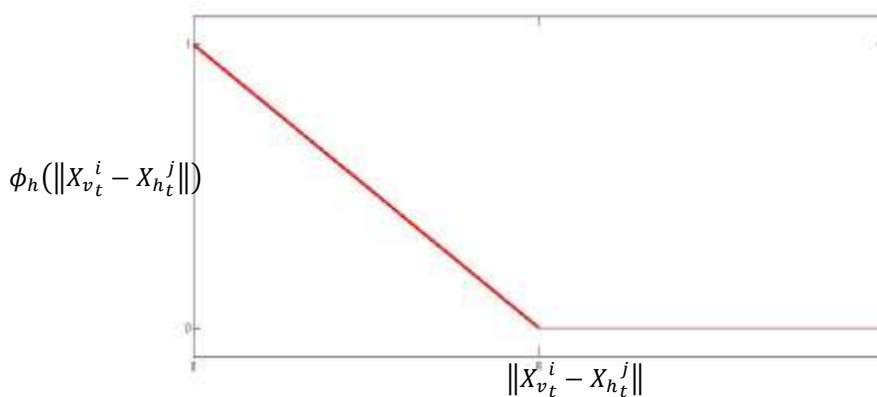


Figure 10. Graph of the function ϕ_v

Function $\chi_v(U_{v_t}^i)$ is a function of the chance of success in mosquitoes. Mosquitoes that will be affected by interaction with the infected host are only susceptible vectors. Based on assumptions, define the function $\chi_v(U_{v_t}^i)$ as follows:

$$\chi_v: [-1,1] \rightarrow [0,1]$$

1. $\chi_v(U_{v_t}^i) > 0$ and monotony rises, for $U_{v_t}^i \in [-1, U_{v_1}^*)$;
2. $\chi_v(U_{v_t}^i) = 0$ for $U_{v_t}^i \in [U_{v_1}^*, 1]$.

An example of a function $\chi_v(U_{v_t}^i)$ is

$$\chi_v(U_{v_t}^i) = \begin{cases} -\frac{1}{2} \left(\frac{U_{v_t}^i - U_{v_1}^*}{1 + U_{v_1}^*} \right)^2 + 1 & ; \quad U_{v_t}^i \in [-1, U_{v_1}^*) \\ 0 & ; \quad U_{v_t}^i \in [U_{v_1}^*, 1] \end{cases}.$$

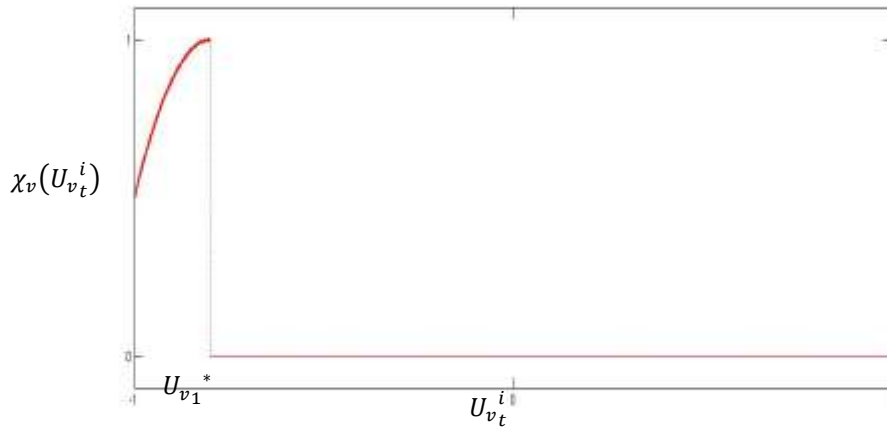


Figure 11. Function graph χ_v

Function $\psi_v(U_{h_t}^j)$ is a function of human chances of successfully infecting mosquitoes. Humans who can transmit the dengue virus are infected hosts. Based on assumptions, define the function $\psi_v(U_{h_t}^j)$ as follows:

1. $\psi_v(U_{h_t}^j) > 0$ for $U_{h_t}^j \in [U_{h_2}^*, U_{h_3}^*) \cup [U_{h_3}^*, 1]$;
2. There is $\widehat{U}_h \in [U_{h_2}^*, U_{h_3}^*)$ so $\widehat{U}_h = \arg \max_{U_{h_t}^j \in [U_{h_2}^*, U_{h_3}^*)} \psi_v(U_{h_t}^j)$;
3. $\psi_v(U_{h_t}^j) = 0$ for $U_{h_t}^j \in [-1, U_{h_2}^*)$.

An example of a function $\psi_v(U_{h_t}^j)$ is

$$\psi_v(U_{h_t}^j) = \begin{cases} \frac{4(U_{h_3}^* - U_{h_t}^j)(U_{h_t}^j - U_{h_2}^*)}{(U_{h_3}^* - U_{h_2}^*)^2} & ; \quad U_{h_t}^j \in [U_{h_2}^*, U_{h_3}^*) \\ 0 & ; \quad U_{h_t}^j \in [-1, U_{h_2}^*) \cup [U_{h_3}^*, 1] \end{cases}.$$

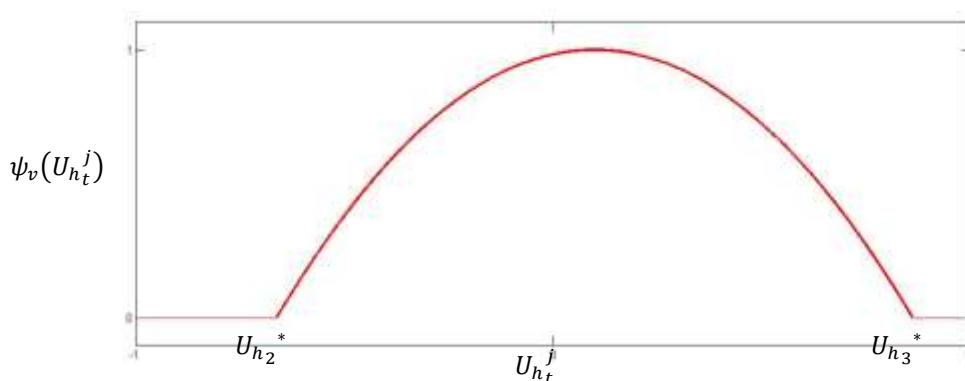


Figure 12. Function graph ψ_v

If there are N_{h_t} as many humans, then the value of the possible interaction for 1 mosquito is modelled as

$$\frac{1}{N_{h_t}} \sum_{j \in W_t} \mathcal{K}_v(\|X_{v_t}^i - X_{h_t}^j\|, U_{v_t}^i, U_{h_t}^j).$$

Thus, changes in mosquito health status influenced by potential functions and interaction functions are modelled as

$$dU_{v_t}^i = \mathcal{H}_v(U_{v_t}^i) dt + \frac{1}{N_{h_t}} \sum_{j \in W_t} \mathcal{K}_v(\|X_{v_t}^i - X_{h_t}^j\|, U_{v_t}^i, U_{h_t}^j) dt \text{ for } i \in V_t.$$

The changes in the health status of the i -th mosquitoes at time t that live in region 1 are modelled as $dU_{v_t}^i = \mathcal{H}_v(U_{v_t}^i) dt + \frac{1}{N_{h1t}} \sum_{j \in W_{1t}} \mathcal{K}_{v1}(\|X_{v_t}^i - X_{h_t}^j\|, U_{v_t}^i, U_{h_t}^j) dt$ for $i \in V_{1t}$.

The changes in the health status of the i -th mosquitoes at time t living in region 2 are modelled as $dU_{v_t}^i = \mathcal{H}_v(U_{v_t}^i) dt + \frac{1}{N_{h2t}} \sum_{j \in W_{2t}} \mathcal{K}_{v2}(\|X_{v_t}^i - X_{h_t}^j\|, U_{v_t}^i, U_{h_t}^j) dt$ for $i \in V_{2t}$.

CONCLUSIONS

Two conclusions are derived from the single-particle simulations. This simulation demonstrates that, under this molecular model, the health state of sensitive humans or mosquitoes remains unchanged in the absence of interaction between the two species. The simulation results indicate that a smaller disparity between an individual's health state and $U = 1$ correlates with a more rapid attainment of $U = 1$. Simulations of interaction functions between humans and mosquitoes indicate that increased human mobility accelerates the shift of both humans and insects from the vulnerable compartment to the exposed compartment. Moreover, an expanded region of interaction between humans and mosquitoes correlates with a deceleration in the transmission of dengue disease.

Two results are derived from the modelling of variations in population size within the molecular model. The simulations of population change indicated that the choice of maximum successful interaction distance influences the rate of dengue disease transmission. An increased maximum successful interaction distance correlates with a heightened likelihood of interaction, hence accelerating the transmission of dengue disease, and vice versa. A reduced maximum successful interaction distance diminishes the likelihood of interaction, hence decelerating the transmission of dengue illness. The simulations of population change demonstrated that the selection of human mobility parameter values between region 1 and region 2 influences the velocity of dengue disease transmission. Increased human mobility between region 1 and region 2 accelerates the transmission rate of dengue disease, and conversely. A reduction in human mobility between region 1 and region 2 correlates with a diminished rate of dengue disease transmission.

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