



Original Research Article

Modeling dengue data from Semarang, Indonesia



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ABSTRACT

Dengue fever is a viral mosquito-borne infection which in recent years has become a major international public health concern, a leading cause of illness and death in tropical and subtropical regions. Models from mathematical epidemiology, like the classical SIR-model and its variants, are used to describe the spread of dengue in a given population. Based on data of hospitalized dengue cases for the city of Semarang, Northern Java, Indonesia, we identify certain parameters in a simplified IR-model. In a second step, we connect those model parameters to available meteorological data, like precipitation.

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1. Introduction

Dengue fever is a viral mosquito-borne infection which in recent years has become a major international public health concern, a leading cause of illness and death in the tropics and subtropics. It is estimated that every year, there are about 390 million dengue infections with more than 12,000 deaths per year, cf. [World Health Organization \(2016a\)](#). The *Aedes aegypti* mosquito is the primary vector of dengue. The virus is transmitted to humans through the bites of infected female mosquitoes. After virus incubation for 4–10 days, an infected mosquito is capable of transmitting the virus for the rest of its life. Infected symptomatic or asymptomatic humans are the main carriers and multipliers of the virus, serving as a source of the virus for uninfected mosquitoes. At present, there is no specific treatment for dengue fever. Recently, a first vaccine has been developed and is now at an early stage of clinical trials. Hence, the main method to control and prevent the spread of the dengue virus is to combat vector mosquitoes through several measures including insecticides and

preventing mosquitoes from accessing egg-laying habitats like in- and outdoor containers with stagnant water.

The *Aedes* mosquito vector of dengue is also highly sensitive to climate conditions, and studies suggest that climate change is likely to continue to increase exposure to dengue, cf. [World Health Organization \(2016b\)](#).

In the recent years, mathematical modeling has become an important tool for the understanding of infectious diseases epidemiology and dynamics. A series of deterministic and nowadays also stochastic models have been proposed to describe the host and vector population, see e.g. [Wijaya et al. \(2015\)](#), [Rocha et al. \(2013\)](#), [Altmeier \(2016\)](#) and references therein. Dengue fever dynamic is well known to be particularly complex with large fluctuations of disease incidences. The integration of climatic factors into mathematical models for vector-borne diseases is a rather new development. In this article, we introduce a model for dengue dynamics including the effect of the precipitation amount on the infection rate. Since the vector mosquitoes breed in an aquatic environment, rainfall leads to an increase of the mosquito population and hence to an increased infection rate. Using available data of both, recorded dengue infections and local precipitation from the city of Semarang at the northern coast of Java island, Indonesia, we propose a disease model with an infection rate depending on the rainfall.

The paper is organized as follows: In Section 2 we reduce the classical SIR-UV to a simplified two-dimensional IR-system with variable infection rate. The available dengue data for the Semarang

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region in Indonesia is displayed in Section 3 and an optimal control approach to identify the infection rate is presented in Section 4. In Section 5 we combine the IR-model with meteorological data and present a surrogate model based on a infection rate, that depends on the precipitation. Simulation results indicate the validity of the model.

2. Classical SIR-UV- and reduced IR-model

To describe the dynamics of dengue within host and vector populations, we recall the classical SIR-UV model introduced by Kermack and McKendrick (1927)

$$S' = \mu(N-S) - \frac{\beta}{M}SV, \tag{1a}$$

$$I' = \frac{\beta}{M}SV - (\gamma + \mu)I, \tag{1b}$$

$$R' = \gamma I - \mu R, \tag{1c}$$

$$U' = \psi - \frac{\theta}{N}UI - \rho U, \tag{1d}$$

$$V' = \frac{\theta}{N}UI - \rho V, \tag{1e}$$

where S, I and R denote the susceptible, infected and recovered hosts and U and V denote the virus-free and virus-carrying vectors. The parameters β and θ denote the rates for vector-to-host or host-to-vector infection and γ equals to the recovery rate. By μ we denote the reproduction and mortality rate of the host; for the sake of simplicity we assume a constant host population $N = S + I + R$. The vectors reproduce at a constant rate ψ and drop out with mortality rate ρ . Assuming $\psi = \rho M$, the total vector population $M = U + V$ will remain constant.

This five-dimensional dynamical system $x' = f(t, x)$ for the state variable $x = (S, I, R, U, V)$ has to be supplemented by a suitable initial value $x(0) \in \mathbb{R}_+^5$.

Typical parameter values are listed in Table 1, where we have chosen days as the scale for measuring time.

2.1. A reduced IR-system

Concerning the vector population we do not have any reliable data at our disposal, neither for the individual compartments U and V nor for the total vector population M . Moreover, the dynamics of the vectors occurs on a faster time scale compared to the host dynamics, cf. Rocha et al. (2013). Therefore, we consider the vector population to be in its coexistence equilibrium

$$U^* = M \frac{vN}{I + vN} \quad \text{and} \quad V^* = M \frac{I}{I + vN}, \tag{2}$$

where $v = \rho/\theta = 1/2$. Plugging the equilibrium value V^* for the virus-carrying vectors into the host equation (1b) and making use of the fact, that $S = N - I - R$, we obtain the reduced two-dimensional dynamical system

$$I' = \beta(N - I - R) \frac{I}{I + vN} - (\gamma + \mu)I, \tag{3a}$$

$$R' = \gamma I - \mu R. \tag{3b}$$

In the following subsection 2.2 we shortly analyze the equilibria of the above reduced IR-system in case of constant coefficients, i.e. for β, γ, μ and v independent of time.

However, to obtain a more realistic description and to capture seasonal effects in the dengue dynamics, we afterwards consider models based on time-dependent infection rates $\beta(t)$. The

Table 1

Parameter values used in the simulations; time measured in days. The recovery periods used here are quite long. In future research extensions we will analyze the influence of parameter changes on the results.

Parameter	μ	γ	ρ	θ	β	N
Value	$1/(65 \times 365)$	$1/30$	$1/10$	2ρ	see below	1.5×10^6

remaining parameters γ, μ and v are nevertheless assumed to be constant throughout the considered time interval.

2.2. Analysis of the IR-system

Consider the model parameters β, γ, μ and v to be constant and positive. The reduced IR-system (3) allows, besides the trivial equilibrium $y^0 = (I, R) = (0, 0)$ for a non-trivial equilibrium $y^* = (I^*, R^*)$ at

$$I^* := N\mu \frac{\beta - v(\mu + \gamma)}{(\beta + \mu)(\gamma + \mu)} \quad \text{and} \quad R^* := \frac{\gamma}{\mu} I^*. \tag{4}$$

The Jacobian at the non-trivial equilibrium is given by

$$J = \begin{pmatrix} \frac{\eta + \delta + 1}{\delta} b & b \\ \eta & -1 \end{pmatrix},$$

where $\delta = \frac{\gamma}{\mu}, \eta = \frac{\beta}{\mu}$ and $b = \frac{v(\delta+1)-\eta}{v(\delta+1)+1}$. Hence, the characteristic polynomial reads as

$$\chi(t) = t^2 + \left(1 - \frac{\eta + \delta + 1}{\eta} b\right) t - b \left(\delta + \frac{\eta + \delta + 1}{\eta}\right).$$

To determine the stability properties of the non-trivial equilibrium, we have to consider the real parts of the eigenvalues of J . Due to the Hurwitz-criterion, the eigenvalues have negative real parts, if the coefficients of the characteristic polynomial are non-negative. Hence the conditions for asymptotic stability are

$$1 - \frac{\eta + \delta + 1}{\eta} b \geq 0 \quad -b \left(\delta + \frac{\eta + \delta + 1}{\eta}\right) \geq 0.$$

Since $\eta, \delta \geq 0$, we obtain $b \leq 0$ or equivalently

$$\beta \geq v(\gamma + \mu)$$

since the denominator of b is always non-negative. Based on the parameter values given in Table 1, the non-trivial equilibrium will be asymptotically stable, provided the infection rate β satisfies the condition $\beta \geq 0.167$.

3. Dengue data from Semarang

The city of Semarang is located at the northern coast of the island of Java, Indonesia. It has a total population of about $N = 1.5$ millions, see Wikipedia contributors (2016). Semarang features a typical tropical climate with almost constant temperatures throughout the year and a pronounced wet season; the months of December to March receive most precipitation.

For the city of Semarang, the total number of hospitalized dengue cases has been recorded and is available to us for the period January 1, 2010 to April 30, 2015 resulting in a time series $I^{\text{data}} \in \mathbb{R}^n$ of $n = 1945$ days Dinas (Kesehatan). The total number of hospitalized cases has to be understood as the sum of dengue fever (DF), dengue hemorrhagic fever (DHF) and dengue shock

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