

Original Research

Dynamics of dengue disease with human and vector mobility

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ABSTRACT

Dengue is a vector borne disease transmitted to humans by *Aedes aegypti* mosquitoes carrying virus of different serotypes. Dengue exhibits complex spatial and temporal dynamics, influenced by various biological, human and environmental factors. In this work, we study the dengue spread for a single serotype (DENV-1) including statistical models of human mobility with exponential step length distribution, by using reaction–diffusion equations and Stochastic Cellular Automata (SCA) approach. We analyze the spatial and temporal spreading of the disease using parameters from field studies. We choose mosquito density data from Ahmedabad city as a proxy for climate data in our SCA model. We find an interesting result that although human mobility makes the infection spread faster, there is an apparent early suppression of the epidemic compared to immobile humans. The disease extinction time is lesser when human mobility is included.

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1. Introduction

Dengue fever (DF) is a vector borne disease widely prevalent in tropical and subtropical regions in about 100 countries worldwide. The World Health Organization (WHO) reports that over 3.9 billion people, in 128 countries, are at risk of infection with dengue viruses (Brady et al., 2012), and an estimated 390 million dengue infections occur per year (Bhatt et al., 2013; WHO, 2017a). Dengue is transmitted to humans mainly through *Ae. aegypti* female mosquito bites carrying dengue virus (Nishiura, 2006). Dengue fever (DF), dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) are different forms of dengue infection, caused by five serotypes of dengue virus, commonly known DENV:1–4 (WHO, 2017a) and the recently discovered DENV-5 (Mustafa et al., 2015). The people who recover from one serotype can become permanently immune to it, but may not be immune to

other serotypes. Dengue is becoming a major public health concern in various South Asian and Latin American countries. Many dengue infections may not produce severe symptoms, thereby evading early detection. Vaccine for dengue serotypes has been under development and clinical trials for some years. Recently live tetravalent dengue vaccine CYD-TDV has completed Phase III trials and registered for use in individuals with 9–45 years in some endemic areas (Guy et al., 2011), (WHO, 2017b). It is believed that any future dengue vaccination is imperfect (Bhamarapravati and Sutee, 2000), and may not offer protection against all serotypes. The most effective way to prevent dengue outbreak is to devise vector control strategies and minimize vector–human transmission. A sound understanding of the spatial and temporal dynamics of the dengue can help in devising strategies for containing the spread urban populations.

Numerous human, biological, social and environmental factors affect the transmission of dengue (de Freitas et al., 2011), (Adams and Boots, 2010; Kuno, 1995). Several mathematical models have been proposed (see Andraud et al., 2012; Derouich and Boutayeb, 2006; Nishiura, 2006 for reviews) for studying the dengue. Many of these are the

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compartmental ordinary differential equation (ODE) models (Anderson and May, 1991), (Bailey et al., 1975), which divide the human population into Susceptible, Exposed, Infected, and Recovered (SEIR) groups; and vectors into Susceptible, Exposed, Infected (SEI) groups (Newton and Reiter, 1992), and studying their temporal dynamics. These ODE models are essentially mean field models which neglect the spatial patterns of the spread of dengue, which makes it unsuitable for studying the mobility effects on the spread of diseases. Attempts at spatial modeling of dengue includes those based on spatial data mapping and statistical analysis (Bhandari et al., 2008; Bohra and Andrianasolo, 2001; Peterson et al., 2005; Rotela et al., 2007), reaction–diffusion partial differential equation (PDE) with vector or larval mobility (Maidana and Yang, 2008; Tran and Raffy, 2006), Individual Based Models (IBM) on a grid (Barmak et al., 2011; Bian, 2004; Karl et al., 2014; Otero et al., 2011; 2008) including Cellular Automata approach with vector mobility and models of human mobility (de Castro Medeiros et al., 2011; Santos et al., 2009).

Human mobility, especially of the infected individuals can create multiple dengue waves resulting in substantial deviation from mean field results. However, the current approaches to study dengue spreading with human mobility have been restricted to simple methods such as movement with fixed step size, introducing a global field altering transition probabilities (de Castro Medeiros et al., 2011; Santos et al., 2009) and meta-population models (Adams and Kapan, 2009; Colizza and Vespignani, 2007; 2008; Stolerman et al., 2015). It has been studied at multiple scales (Balcan et al., 2009) such as house to house mobility (Stoddard et al., 2013), time of the day dependent mobility parameters (Karl et al., 2014), rural–urban daily commuters (Mpolya et al., 2014), dengue transmission and social ties dependent mobility (Reiner et al., 2014), and dengue spread across countries (Wichmann and Jelinek, 2004). In this work, we first report the results of SEIR–SEI reaction–diffusion PDE model with diffusive human mobility as a reference, and then include realistic models of human mobility patterns using *Stochastic Cellular Automata* (SCA) approach (closely following de Castro Medeiros et al., 2011). Mobility patterns are derived from statistical studies of human movements observed through the circulation of currency notes, tracking of phone calls through cellular towers, and location based social networks such as Foursquare. These works have shown varied patterns such as Lévy flight (Brockmann and Hufnagel, 2007; Brockmann et al., 2006), truncated Lévy flight (González et al., 2008), exponential distribution in intra urban movements (Liang et al., 2013 and Noulas et al., 2012). The differences arise possibly due to the difference in scale and resolution of study (large distance, intra city movements, mobile tower coverage etc.) and the methodology used. Dengue is endemic in densely populated tropical regions, typically in urban areas (Pongsumpun et al., 2008), although recently many studies on dengue in rural areas can also be found (Pérez-Castro et al., 2016; Reller et al., 2016). Here we focus on the dengue spread within an urban area and use exponential tail (Liang et al., 2013) distribution for studying human mobility affects on spread of dengue.

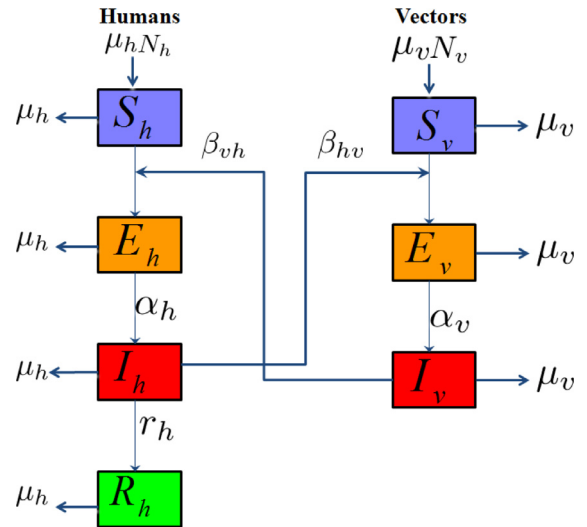


Fig. 1. SEIR–SEI compartmental model of human–vector interactions. Here μ_h , μ_v represent the human and vector mortality, β_{hv} (β_{vh}) represent the human (vector) to vector (human) transmission rate, α_h (α_v) is the exposed to infection rate, r_h is the recovery rate in humans, and N_h (N_v) is the total number of humans (vectors) involved in the dengue dynamics.

2. Model formulation

In this study, we use the standard compartmental model to divide the humans into SEIR and vector population into SEI groups (see Andraud et al., 2012; Nishiura, 2006 for review). Only infected vectors and infected humans can transmit the dengue virus to susceptible population (See Fig. 1 for illustration). Exposed population is infected with the virus but are *not infectious* (i.e. they cannot transmit the dengue virus). In Fig. 1, we show the flow diagram of SEIR–SEI model. The temporal evolution of the corresponding ordinary differential equations, their stationary states and stability conditions have been investigated and reported in many works (see for eg: Nishiura, 2006; Pongsumpun et al., 2008). In the next section, we focus on the spatial approaches to modeling dengue based on reaction diffusion equations.

2.1. Reaction–diffusion approach

In vector borne diseases, spatial spreading is possible only when there is mobility of vectors, humans or both. Vectors, especially *Ae. aegypti* rarely fly long distances by itself, and hence their mobility can be modeled a diffusion process (Maidana and Yang, 2008; Tran and Raffy, 2006). Their long distance mobility requires external drivers such as wind, vehicles, ships (Otero et al., 2008) and will not be considered here. Human mobility is more complex to analyze as multiple factors like population density, transportation networks, distribution of economic centers, urbanization pattern etc. However, these complex patterns can be summarized through statistical means by studying distributions like step length (Brockmann et al., 2006). A detailed discussions will be provided in Section 2.2.2.

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