Modelling dengue epidemic spreading with human mobility

D.H. Barmak, C.O. Dorso, M. Otero *

Departamento de Física, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires 1428, Argentina
IFIBA, CONICET, Ciudad Universitaria, Buenos Aires 1428, Argentina

HIGHLIGHTS

- The effect of human mobility on the spatio-temporal dynamics of Dengue is explored.
- Human mobility strongly affects the spread of infection.
- Because of human mobility, multiple foci appear throughout the evolution of the outbreaks.
- The coalescence of these foci with the main one generates a fast spreading of the outbreaks.
- This effect increases the propagation of the outbreak before arrival of the winter season.

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ABSTRACT

We explored the effect of human mobility on the spatio-temporal dynamics of Dengue with a stochastic model that takes into account the epidemiological dynamics of the infected mosquitoes and humans, with different mobility patterns of the human population. We observed that human mobility strongly affects the spread of infection by increasing the final size and by changing the morphology of the epidemic outbreaks. When the spreading of the disease is driven only by mosquito dispersal (flight), a main central focus expands diffusively. On the contrary, when human mobility is taken into account, multiple foci appear throughout the evolution of the outbreaks. These secondary foci generated throughout the outbreaks could be of little importance according to their mass or size compared with the largest main focus. However, the coalescence of these foci with the main one generates an effect, through which the latter develops a size greater than the one obtained in the case driven only by mosquito dispersal. This increase in growth rate due to human mobility and the coalescence of the foci are particularly relevant in temperate cities such as the city of Buenos Aires, since they give more possibilities to the outbreak to grow before the arrival of the low-temperature season. The findings of this work indicate that human mobility could be the main driving force in the dynamics of vector epidemics.

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1. Introduction

Dengue fever is a vector-borne disease caused by a virus of the family *flaviviridae* [1] and transmitted mainly by the mosquitoes *Aedes aegypti* and *Aedes albopictus*.

Newton and Reiter [2] introduced the first SEIR model for dengue in the form of a system of Ordinary Differential Equations (ODE), in which the mosquito population was not modelled. Other ODE models have been developed with

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* Corresponding author at: Departamento de Física, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires 1428, Argentina.
  E-mail address: mjotero@df.uba.ar (M. Otero).

different considerations and assumptions: variability of vector population [3], human population [4], effect of vertical transmission of Dengue in vectors [5], seasonality [6], age structure [7], incomplete gamma distributions for the incubation and infectious times [8] and spatial heterogeneity as well [9].

Focks et al. [10,11] began describing mosquitoes populations by using a Dynamic Table Models, where later the human population and the disease were introduced [12].

Otero and Solari developed a spatially explicit stochastic dengue model [13] which includes the evolution of the mosquitoes population [14,15] but in which humans are considered as a spatially fixed population, i.e. the spatial spreading of the disease is possible only due to mosquito dispersal. Two later models [16,17] modelled the human population as an individual based model and studied the effect of different human mobility patterns on the final size, probability and duration of the epidemic outbreaks.

Recent studies [18–21] suggest that the spatial spreading of a dengue outbreak occurs not only in a diffusive way, but also because of many other secondary foci that appear at spatial scales not compatible with a spatial dynamics driven only by mosquito dispersal. Therefore, it is really important to evaluate the contribution of human mobility to the evolution of the epidemic outbreaks, i.e. the dynamics of the main focus and secondary foci along the dengue outbreaks.

Several works tackle the issue of the correct description of the human beings mobility, relaying on different methods and databases [22–29]. Databases from cellular phone networks, credit cards, hotel reservations, flight reservation databases, etc. are currently used to model human mobility and to study disease spreading. Nevertheless, they could introduce an intrinsic bias on the obtained results because human behaviour can change or adapt in presence of a disease [30–35].

Several studies consider human mobility in human–human transmitted diseases [36,34,37,35,33,38,32,31,39,40], but only a few consider human mobility in vector borne diseases [41–43,17].

In this work we review some details of the model [17] regarding human mobility (Section 2), we present the results of our numerical investigations related to the spatial distribution of recovered individuals, the foci dynamics according to different mobility patterns, the evolution of the main focus of recovered individuals, and an analysis of the contribution of short-range human movements to the evolution of dengue epidemic outbreaks (Section 3). Finally conclusions are drawn in Section 4.

2. Theory and calculations

The epidemiological model used in this work has already been published [17]. There are four key processes involved in the dengue contagion and spatial spreading: the epidemiological dynamics of the infected mosquitoes, the epidemiological dynamics of the infected humans, the mobility pattern of the individuals and the mosquito dispersal by flight. From an epidemiological point of view we divided the adult female vector population in three compartments representing the disease status: susceptible (S), exposed (E) and infectious (I), i.e. a *SEI* compartmental model. Humans are considered at the individual level, i.e., with an Individual Based Model (IBM) [16], and follow a susceptible (S), exposed (E), infectious (I) and recovered (R) (SEIR) sequence. In this section we are going to review only some aspects of the model regarding human mobility, for more details about the model and its implementation, we refer to Ref. [17].

The simulation of the evolution of dengue fever is performed in a schematic city (square grid) whose basic unit is the city block (a square of 100 m × 100 m), in which a human population of 100 individuals is placed. We worked with grids of different sizes: $L = 20, 50, 100$ and 150, being L the side length of the square grid, with L measured in city block units i.e. a grid with $L = 150$ corresponds to a square grid of 150×150 city blocks. The spatial scale simulated goes from small towns ($L = 20$) to a big city ($L = 150$). Mosquito populations were simulated using climatic data tuned to Buenos Aires city, Argentina, and a breeding site density of 400 BS/ha [15,17]. An exposed human (index case) is placed in the centre of the grid, on January 1st, considered as the beginning of the epidemic outbreak $t = 0$.

In order to describe the mobility patterns of the human population we have adopted the same schematic model already presented in Ref. [17]: 50 individuals of each block are randomly selected to be mobile, while the other 50 individuals stay in their original block (Home) during the simulation. Each mobile individual spends 2/3 of the day in its original block (Home), while the other 1/3 of the day the mobile individual stays in a randomly assigned block (Work) according to a particular distribution, which is assigned to each of the mobile individuals. The mobile individuals go to this destination everyday, and at the end of the day they return back to their original block. This random assignment is performed according to certain rules that characterize the human mobility pattern. Following recent works on human mobility (referred in Ref. [17]) the distribution of the displacement lengths of the individuals follow a truncated Levy distribution [23] given by Eq. (1):

$$P(r) \propto (r + r_0)^{-\beta} \exp(-r/\kappa). \tag{1}$$

being $P(r)$ the probability that an individual reaches a distance r, where r_0, β and κ are parameters that characterize the distribution.

In this work we have used the parameters shown in Table 1.

The implementation is as follows. One of these distributions is chosen and then each mobile human randomly selects (from this distribution) the distance 'r to the "Work" block, with a cut-off equal to $L/2$. This means that the distances are drawn from distributions with a displacement up to half of the city length for all individuals. Once the distance r is chosen the next steps are followed: