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A Spread Study for Dengue fever through SIR-SI compartmental model and fuzzy systems using cellular automata with stochastic approach

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Dengue fever is an endemic disease that continues to cause health problems in the world population. There are thousands of cases of dengue fever infections per year and for each detected case there are approximately five undetected. Methods used to deal with dengue fever includes cleaning and elimination of possible hatcheries for the vector (mosquito of the Aedes family) and the use of insecticides for fumigation to reduce vector population to an acceptable limit. Nonetheless, dengue fever resurfaces after a certain time. The aim of this work is to model dengue fever spread for the prediction of new cases. To this end, a SIR-SI model is used coupled to transition rules as part of a fuzzy system which includes probabilistic parameters for determining the changes in the agent status. This allows having an estimation of possible dengue cases in such a way that the health units can take necessary prevention actions and measure to corroborate the prediction.

To collect the data necessary to restrain the progress of dengue fever, the work methodology aims to use a compartmental SIR-SI model based on the simplest model of Nishiura [3], with six ordinary differential equations (ODE). The equations represent the behavior of susceptible, infected or recovered humans, the behavior of susceptible or infected vectors and the vector population. Transmission rate probabilities from vector to human and human to vector, recovery rate of humans, mortality rate per day of humans and vectors, alternative individuals available as blood source, bite rate of mosquito per day in addition to the intrinsic and extrinsic incubation period, viremia period, human mobility rate, the probability that human is out of house, the probabilities that a vector be infected and vice versa, a probability of target that vector may choice and a percentage control efficiency parameter will be used. There is also a value called basic reproduction number and it serves to indicate if there is an epidemic behavior.

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The ODE system will be solved using a Runge Kutta 4 method [2] for a time interval $[T_i, T_f]$, with T_i the initial time and T_f the final time of the simulation. Vectors are modeled as an agent moving on the cellular space. The functionalities for modeling based on agents and geographic information system (GIS) are provided by the TerraME toolkit. In addition to the ODE system, dengue fever spread on the cellular space must follow a fuzzy logic and probabilistic parameters as those cited in [1,4]. The region being analyzed consists in a neighborhood of the city of Asunción with active cases of dengue fever. Two cases are considered. The first case consists in using synthetic data created by specialists for obtaining possible dengue scenarios based on their practical knowledge. For the second case data were provided by local health agencies. The comparison of the dengue fever spread simulation gives useful information about the most critical regions to concentrate the efforts in prevention and for interrupting the spread of the illness. Preliminary studies show that the progression of the disease depends on the effectiveness of the methods used to limit the propagation of the disease and the velocity of the illness detection. In this undergraduate (ongoing) work, we used the tools in an *a posteriori* analysis for better understanding the current situation; future work includes new control methods, as well as, an *a priori* estimation of a future dengue spread dissemination.

References

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