A Cellular Automaton Approach to Dengue Transmission Simulation

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ABSTRACT

Dengue fever is a mosquito-borne viral disease that poses a major global health challenge, particularly in tropical and subtropical regions. The complexity of its transmission dynamics arises from interactions between human hosts, *Aedes aegypti* mosquitoes, and environmental factors such as temperature, humidity, and urban infrastructure. This paper presents a cellular automaton (CA)-based simulation for modeling the spread of dengue within a simplified population, providing a computationally efficient and conceptually transparent tool for exploring outbreak patterns. The model captures local interactions between infected and susceptible individuals mediated by mosquito vectors, incorporating probabilistic rules to represent the stochastic nature of disease transmission. Implemented in Python and visualized through Matplotlib, this adaptable framework allows for the integration of real-world parameters such as mosquito density, vector control interventions, and seasonal variations, offering valuable insights for public health planning.

Introduction

Dengue affects hundreds of millions of people annually, causing significant public health and socioeconomic burdens. Its transmission cycle involves a complex interplay between *Aedes aegypti* mosquitoes, which act as vectors, and human hosts, in which the virus replicates. Unlike directly transmitted diseases, dengue propagation requires the presence of both vector and host populations in close proximity, making spatial and environmental factors crucial to outbreak dynamics.

Traditional epidemiological models often rely on differential equations that, while powerful, can be computationally expensive and less intuitive when dealing with heterogeneous spatial distributions of hosts and vectors. Cellular automata provide an alternative modeling approach that operates through simple, local rules applied on a discrete grid, yet can capture emergent, complex behaviors.

In this work, we present a CA model that simulates the spread of dengue across an urban-like grid, accounting for mosquito movement, human–mosquito interactions, and recovery dynamics. The model is designed for flexibility, allowing users to adjust transmission probabilities, vector densities, and control measures, enabling exploration of outbreak scenarios under varying conditions.

Results

Simulation results demonstrate that the CA model effectively reproduces key epidemiological patterns of dengue spread. By varying the mosquito density and transmission probability, distinct outbreak profiles emerge:

- High vector density combined with high transmission probability produces rapid, widespread infection waves.

- Lower densities or reduced probabilities result in slower, more localized outbreaks. The model also highlights the importance of spatial clustering—densely packed susceptible populations experience more intense transmission, whereas urban layouts with physical barriers (such as green spaces) can slow vector–host contact rates.
  Figure 1 illustrates a frame from one simulation, showing infected individuals (red), susceptible individuals (green), and infected mosquitoes (yellow). The progression of infection visibly follows patterns consistent with field observations, including hotspots of sustained transmission and eventual stabilization as the susceptible pool decreases.
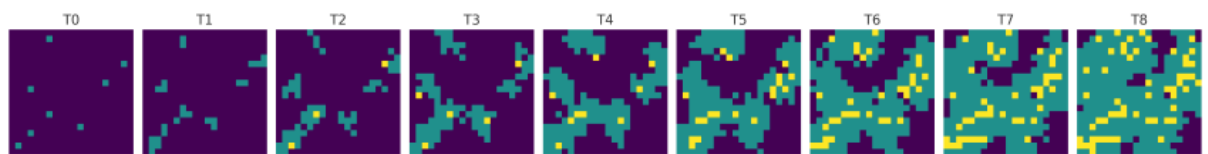
The CA-based dengue transmission model offers an accessible yet powerful framework for exploring vector-borne disease dynamics. While it abstracts many biological details, it captures essential aspects of dengue spread, including vector-mediated transmission and the influence of spatial heterogeneity.

One limitation is that the current model does not directly account for environmental drivers such as temperature-dependent mosquito breeding or rainfall patterns that influence larval habitat availability. These could be incorporated in future iterations to improve realism.

Another promising extension would be integrating vector control interventions—such as insecticide spraying or release of *Wolbachia*-infected mosquitoes—into the model, enabling the assessment of intervention timing and spatial targeting strategies. By doing so, the CA framework could serve as a decision-support tool for municipal health agencies during dengue season.

Methods

The simulation is built on a two-dimensional grid where each cell can represent one of several states:

1. Susceptible human (S)
2. Infected human (I)
3. Susceptible mosquito (M)
4. Infected mosquito (IM)

5. Empty space (E)

The simulation begins with a small number of infected humans and/or infected mosquitoes placed randomly on the grid. Transmission occurs when a mosquito and a human occupy neighboring cells:

- If a susceptible mosquito is adjacent to an infected human, it may become infected with probability p_{mh}.

- If a susceptible human is adjacent to an infected mosquito, they may become infected with probability p_{hm}.
  Infected humans recover after a fixed recovery period, transitioning to a recovered state (R), which confers immunity. Infected mosquitoes remain infectious until they die after a defined lifespan.
  The model progresses in discrete time steps, updating all cells simultaneously. Probabilities, recovery time, and mosquito lifespan are adjustable parameters. Python is used for implementation, with NumPy for efficient array operations and Matplotlib for graphical visualization of simulation states.

Conclusion

The cellular automaton model described here provides a flexible and interpretable method for simulating dengue transmission dynamics. Despite its simplicity, it can replicate spatial patterns and outbreak dynamics observed in real-world settings, offering a useful foundation for more detailed modeling efforts. Future work should focus on integrating climate-driven vector population changes, real-world spatial layouts, and intervention strategies to enhance applicability. Such advancements could support proactive dengue prevention and control measures, ultimately reducing the burden of this persistent global health challenge.

References

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