



MODELLING OF WEST NILE VIRUS: A SURVEY

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INTRODUCTION

West Nile Virus (WNV) is an arbovirus virus, first isolated from a feverish woman in 1937 [1] from the West Nile in Uganda. In the 1950s, the ecology of the virus and its symptoms were discovered. Outbreaks have since been found in various European countries [2]. In 1996, there was an epidemic in Bucharest, where WNV became a public health concern. In 1999, WNV appeared in New York [3]. In 2001, WNV reached southern Ontario, with the first human cases detected in August 2002.

The majority of people who become infected with WNV do not show any symptoms. Others who become ill with WNV show mild flu-like symptoms within two weeks of infection [4]. A few people will develop serious symptoms that can affect the central nervous system causing neurologic illnesses such as encephalitis or meningitis. There is no vaccine for humans yet, and the infection can result in death.

Mosquitoes, mainly the *Culex* genus, are the vectors of infection. Adult female mosquitoes take a blood meal from their hosts to obtain sufficient protein and iron to lay their eggs. During the mosquito life-cycle, eggs hatch into larvae, and then change into pupae that evolve into adult mosquitoes [5]. The adult may inherit the virus, although with a negligible transmission rate.

The main means of transmission and spread of WNV is through birds. An infectious mosquito can infect a healthy bird by feeding on it. An infectious bird can in turn infect a healthy mosquito that bites the bird. In this cycle, birds act as amplifying hosts since the virus is amplified in their bloodstream. There are also incidental or dead-end hosts. Dead-end hosts of WNV are various kinds of mammals.

Agent-based modelling (ABM) is a modelling system where many individual agents (e.g. people, mosquitoes, birds) play key roles. From micro-level inter-actions between agents within the system, the macro-level dynamics of the whole emerge [6]. A heterogeneous population of agents is inherently suitable to an ABM where each agent can have their own profile of movement and interaction. In WNV epidemiology, the main means of the virus transmission is the interaction cycles within different agent types. This makes ABMs an ideal tool to investigate the WNV epidemiology.

ABMS AND WNV MODELS

A. WNV non-ABM literature

Different approaches to model WNV transmission risk or spread can be categorized into classes of "risk factor analysis," "landscape epidemiology," and "transmission dynamic modelling" [7].

Risk factor analyses tries to identify various variables associated with WNV occurrence through observing the natural environment and making a connection between conditions and WNV prevalence. In these models, birds (in North America) and horses (in Europe and Middle East) have been used as infection markers to measure prevalence [7]. Variables such as climate, host competences and landscape characteristics are employed in statistical models to describe variations in WNV.

Landscape epidemiology is also known as spatial epidemiology can be used to produce risk maps over various landscapes. These approaches use Geographical Information System (GIS) software where spatial statistical tools may be used to model data based on covariates [7].

The third approach of transmission dynamic modelling includes integrative studies where spatio-temporal co-occurrence of vectors and hosts can be modeled [7]. There are difference or differential equation (DE) models of WNV transmission dynamics. Thomas and Urena formulated a difference equation for WNV in a mosquito–bird–human community with a focus on spraying pesticide [8]. Wonham et al. developed a single-season susceptible-infectious-removed (SIR) DE model for WNV transmission in a bird-mosquito population [9]. Bowman et al. propose a single-season DE model of WNV transmission dynamics in a mosquito–bird–human population [10]. Cruz-Pacheco et al. [11] formulate and analyse a DE model of WNV transmission with a focus on hosts and the competence of bird species.

B. Related ABMs

A wind and odor driven ABM for host-seeking behaviour of mosquitoes is proposed in [12]. They explicitly formulate their ABM based on the *Culex* mosquito feeding behaviour on roosting birds. The model generates movement trajectories for each mosquito as an individual agent. Using the Repast toolkit [13], an ABM is proposed to simulate population of *Aedes* mosquitoes, which are the primary vectors of dengue and chikungunya. Agents include mosquitoes, humans, dogs, and cats. An ABM for simulation of dengue transmission in Thailand with a focus on vaccination practices is proposed in [14]. This ABM includes aggregated mosquito (per building) and human agents who can be either at home or work. In [15], an ABM for Malaria transmission is proposed where different intervention strategies are explored. A number of different *Anopheles* mosquitoes and humans are among the agents. In this ABM, a probabilistic decision-tree defines the life-cycle and behaviour of mosquito agents. In [16], a temperature-driven ABM of *Anopheles gambiae* mosquitoes with an emphasize on its life-cycle is proposed. In [17], an ABM for the population dynamics of *Aedes Aegypti* mosquitoes is proposed where two control strategies for Zika virus are simulated.

There are other ABMs with focus on the impact of human behaviour, where an aggregation of mosquitoes is an agent. Typically, the dynamics of an aggregated

mosquito agent update is based on a DE model. In [18] an ABM is used to simulate spread of chikungunya where mosquitoes have a network-patch model. In a network-patch model [19], mosquitoes are divided into patches of high, medium, and low densities. Each patch can contain a number of location nodes (i.e. buildings in a town). Humans can move from one node to another within the network. A similar approach is used in [20] where each network node is associated with one patch. A framework for modelling mosquito-borne pathogens (e.g. malaria and dengue) transmission is proposed in [21]. An ABM for dengue transmission with houses arranged in 16 different mosquito patches is proposed in [22] where humans can visit these houses.

It is notable that humans in many mosquito-borne diseases act as amplifying hosts, in contrast to WNV. In addition, these models do not need to explicitly account for a third agent type i.e. birds. This makes WNV a more complex disease to model and even more appropriate for an ABM approach.

C. WNV-ABMs

In [23], a WNV-ABM is proposed. The scope of their model is an area of around 165 km² in Cook county, Illinois, US. This area is modeled as a raster map where each cell of the map represents one acre. Landscape is classified into 63 classes of land-use. Each cell of the raster map contains various land-use classes. Each cell is associated with a habitat quality index of one to three. The ABM models birds and humans as individual agents capable of flying or moving around the map as part of their daily activities. However, the population of mosquitoes and the transmission of the disease are controlled by a set of proposed differential equations. Their equations are controlled by weather-dependant parameters such as soil surface moisture.

Land-use parameters of each cell determine initial distribution/density of birds, mosquitoes and human, habitat quality (food abundance) for birds and the likelihood of human outdoor activities. Basically, birds fly into neighbour cells of higher habitat quality based on the parameters of cells and return to their home

cell at night. If humans are outdoor, and infectious mosquitoes are present at the same cell at the same time, the transmission of WNV may occur. The mathematical equation of transmission is based on a human infection rate, number of infected mosquitoes, and the total number of mosquitoes in the cell. There are heavily simplified assumptions throughout the paper. The equations for transmission of WNV between birds and mosquitoes are not reported. The mosquito model was too general to include any specific specie or to distinguish different stages of its life-cycle. Finally, there is no report on any kind of model validation.

A WNV-ABM with no human component is proposed by Bouden et al. [24]. The scope of their model is southern Quebec, Canada, with a daily time step and weekly assessments. GIS information is used in the calculation of the locations and initial population of birds and mosquitoes. The map is divided into municipalities for visualization and mosquito habitat. Weather data are used in mathematical equations to compute the dynamics of the mosquito population at each time step. BIOSIM software [25] is used to interpolate values for temperature and precipitations at certain locations on the map based on four neighboring weather stations and elevation data. Two bird-biting species of *Culex pipiens* and *Culex restuans* are considered. The mosquitoes are modeled as intelligent density maps which are defined by a set of parameters assigned to municipalities in the map. Two main stages of mosquito-life cycle, 'adult mosquitoes' and 'larvae' are separated in the equations. The dynamics of the population of the two stages and birds, as well as the transmission of disease are controlled by a DE model based on Wonham et al.'s mathematical model [9]. In the new proposed DE, different bird species are distinguished. Climate effects are included in this DE model based on Madder and colleagues' work [26]. Unfortunately, the new proposed DE model is not expanded upon.

Sumps along the roads are considered to be the main reservoirs of mosquitoes and larvae. Total length of roads for each municipality is computed. On average, for each 30 linear meters of road, a sump is considered, and 20% of sumps are assumed to contain larvae. Heavy rainfall and larvicide spraying flush sumps,

killing a large proportion of larvae. The parameters such as emerging number of adult mosquitoes from each sump are set according to expert opinion. The main bird species studied is the American crow. The birds are divided into two classes of crow and generic birds (i.e. other birds' species known to carry WNV). Changes in the population of crows are calibrated based on data of dead birds. Roost agents are used to represent a group of birds belonging to a roost. Location of roosts and the average number of crows per square kilometer for each region of the map are extracted from the data. Moving behaviour of a roost agent is modeled with a particle system proposed by Reeves [27]. The WNV propagation is simulated from July 1 until October 1. Many of parameters of the model can also be modified by the user. Due to lack of data, simulation for only a few municipalities are calibrated. Their most complete data was for Laval municipality in 2003 where the number of *Culex* mosquitoes in the simulation and field data had a similar trend. They conclude that an important limit of the system is the lack of field data. The lack of a human component is the main shortcoming of their ABM.

A more complete ABM developed by the author addressing some of these deficiencies will be presented at the conference.

SUMMARY

This paper reviewed the current state of ABMs for mosquito-borne diseases, and in particular WNV. These ABMs often capture one or more mosquito population dynamic, virus transmission cycle, weather or landscape (or mosquito-habitat) variation, different bird species movement patterns, and human behaviour, activities, as well as their mobility. Typically as the number of components of an ABM increases, the individual agents are merged together and modeled as an aggregate agent. ABMs with aggregate agents are often hybrid with some means of controlling the dynamics of the aggregate (e.g. a DE model). ABMs allow for a fine-scale accuracy in prediction as well as allowing less homogeneity. However, these ABMs are computationally extensive. Two other difficulties associated with ABMs are a robust validation procedure and

extraction of appropriate and sufficient data for the phenomenon of interest. Notwithstanding, ABMs in general offer remarkable potential for a detailed understanding of complex systems.

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