A Multi-Actor Spatio-Temporal Interaction Model used to Geosimulate the Zoonosis Propagation

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Abstract

Several approaches and models have been proposed to simulate the spread of infectious diseases such as West Nile virus (WNV) or Lyme disease. However, these models such as mathematical models have some weaknesses when trying to simulate the influence of geographic features on the disease spread. In this context, we developed a new theoretical model called MASTIM to remedy some shortcomings of current methods. Our model is used to specify the spatio-temporal interactions of various kinds of actors (e.g. mosquitoes, ticks, birds, mammals, etc.) involved in the zoonosis propagation. We applied our model to the case of WNV and the case of Lyme disease in order to illustrate its genericity. Besides, we are currently using our model to develop Zoonosis-MAGS, a generic geosimulation tool for zoonoses. This tool aims at helping health policy makers to better understand the spread of zoonoses and the consequences of their interventions.

1. INTRODUCTION

Infectious diseases are the leading cause of death on the planet, especially after their proliferation due to global warming. Thus, we are interested in using modelling and computer simulation to help public health policy makers to better understand the spread of infectious diseases. These diseases are the result of the transmission of a pathogen (e.g. virus, bacteria) from an infected individual (“host”, human or animal) to a healthy individual. Moreover, the expansion of some zoonoses (diseases transmitted from animal to human) such as the WNV or the Lyme disease led public health authorities to develop monitoring systems [1]. While these monitoring activities were undertaken to better understand the epidemiology of the disease and the level of risk it can represent for human populations, they cannot be used to forecast the probable propagation of zoonosis on the territory. Such a forecast, if it proved to be reliable, would allow public health authorities to initiate preventive actions at appropriate time and places. Besides, several approaches have been proposed to model and simulate the spread of zoonoses. However, these approaches such as mathematical modelling, cellular automata and traditional multi-agent systems have some weaknesses when trying to model and simulate the influence of geographic and climatic features on the disease spread and the spatio-temporal interactions of various kinds of actors (e.g. mosquitoes, ticks, birds, mammals, etc.). Indeed, the simulation based on mathematical models that generally uses compartment models and differential equations [2] does not take into consideration the geographical space in which populations operate, except in certain cases such as patchy models [3]. This last type of models uses an aggregated space that is not based on data from Geographic Information Systems (GIS). In spite of the fact that a simulation based on cellular automata models the evolution of the spatial characteristics of a geographic area involved in the disease, it does not represent individuals and their mobility [4]. On the other hand, traditional agent-based simulations of epidemics represent the disease vectors (e.g. animals) as agents, but usually do not take advantage of data provided by GIS in order to properly locate the agents in the geographic space [5].

In this context, we suggest to use a multi-agent geosimulation (MAGS) approach [6] to remedy the shortcomings of current methods. Indeed, such approaches enable a user to study in space and time one or several phenomena and to simulate the behaviours of the actors taking part in these phenomena, as well as their interactions in a geo-referenced virtual environment. Using such an approach we developed WNV-MAGS [7], a tool allowing public health decision policy makers to assess several intervention scenarios in order to understand and estimate the magnitude of the evolution of the WNV in a large territory. Furthermore, we are currently developing a generic solution (Zoonosis-MAGS) to be applied to other zoonoses such as Lyme disease. In Section 2 we present the model that we use to develop the Zoonosis-MAGS system. In Section 3 we apply this model to two different cases of infectious diseases in order to illustrate its genericity. Finally, we conclude this paper by evoking some future work.

2. PRESENTATION OF OUR MODEL: MASTIM

We developed a new theoretical model (called MASTIM: Multi-Actor Spatio-Temporal Interaction Model) to simulate the interactions of various types of actors, including those representing populations containing a large number of individuals. Indeed, the large number of individuals of some populations involved in the spread of infectious diseases is a major modelling problem. Existing approaches such as traditional agent-based systems [5] are not able to simulate this kind of populations. Given the limitations of computational resources of computers and the lack of data, we cannot represent each individual by an agent, especially if we have to simulate a population composed of millions or even billions of individuals. This is the case of the mosquitoes populations involved in the transmission of the WNV and ticks populations involved in the transmission of the Lyme disease. In this context, we propose our MASTIM model which can be used to simulate huge populations. We were inspired by the compartmental models to specify the evolution of the populations involved in the zoonosis propagation. So, we start by briefly presenting the compartmental models and then we present our own formalism.

2.1. Compartmental Models

Compartment models are the basis of mathematical modelling in epidemiology. For example, the two-compartment model (SI) considers only the susceptible and infected individuals. This is the simplest model, but there are other more complex models involving several parameters such as the SIS, SEI, SEIS, SEIR and SEIRS model. The compartment “E” represents exposed individuals which are not contagious because the pathogen needs an incubation period. Moreover, the compartment “R” represents recovered individuals which, in some instances, become immune to the infection [8]. We used a compartment model to compute the dynamics of populations involved in the propagation of WNV. This model is based on 8 differential equations which can compute over time the evolution of the different types of individuals: susceptible, infected, recovered and dead birds, the larvae of mosquitoes and the susceptible, exposed and infected adult mosquitoes [7].

2.2. Formalism of MASTIM

Epidemiologists and mathematicians create compartmental models to represent the evolution of interacting populations involved in the spread of infectious diseases as a set of differential equations. Most of these models do not integrate the spatial characteristics of the studied phenomenon and cannot take into account the influence of the environmental and geographical characteristics on the populations’ interactions and the disease spread. Moreover, these models usually involve a set of parameters and equations that health policy makers have difficulties to understand. To overcome these difficulties we propose an approach that aims at modelling the phenomena from a global point of view (‘the ecological system’) and emphasizing the spatial dimension of the populations’ interactions. Indeed, to rigorously specify our model we provide in this paper formulae and notations for each important aspect of an ecological system (denoted Σ) consisting of populations of organisms living in a definite space and time. The system is used to model phenomena that happen inside an ecological
system such as the evolution and interactions of populations involved in the spread of zoonoses. An ecological system may be associated with typical properties called system attributes (a, for example the duration of a simulation time step). The geographic environment in which a system is located is spatially divided into cells (usually of irregular shapes that conform to the spatial characteristics of the phenomena). The cells can be aggregated at different levels of detail in other cells at higher hierarchical levels that are useful for decision making. Time is divided in discrete steps of a selected duration. Living organisms are categorized in species which are the focus of the model that we discuss in this paper. Each species has its own evolution dynamics represented by a model similar to a compartmental model.

2.2.1. Cells
A cell represents a given region of space, the borders of which are well defined using GIS data that may pre-processed to reflect spatial characteristics that are important for the observation and analysis of natural phenomena. Basic cells can be aggregated into higher level cells into what is called a hierarchical level. A hierarchical level \( H_i \) contains \( n \) cells which are aggregates of a number of cells defined at the hierarchical level \( H_i \).

The set of cells of a system \( \Sigma \) with \( m \) hierarchical levels is written:

\[
C^\Sigma = \bigcup_{i=1}^{m} \{ C_{i}^H, C_{2}^H, \ldots, C_{n}^H \} \quad \text{where the lower index is a unique identifier of the cell in the hierarchical level} \quad H_i.
\]

2.2.2. Species
Each cell in a selected hierarchical level \( H_i \) can host a varying number of individuals of different species. Species are not constrained to any specific type and could represent any organism such as mammals, insects, birds, fishes, viruses and bacteria. The species’ dynamics and evolution in this cell is modelled using an extended form of compartment model. This model is unique for the species, but it is instantiated for each cell where individuals of the species can live, in order to keep track of the species population in each of these cells. The set of \( n \) species defined for an ecological system \( \Sigma \) is written:

\[
S^\Sigma = \{ S_1, S_2, \ldots, S_p \} \quad \text{where the lower index is a unique identifier for the species in the system}.
\]

2.2.3. Compartments
The compartmental model of a given species has several compartments representing the evolution of different stages of the species’ individuals. The set of compartments of a given species \( S_k \) is denoted:

\[
O(S_k) = \{ O_{S_k}^1, O_{S_k}^2, \ldots, O_{S_k}^n \}.
\]

In addition, a group of compartments for the same species is denoted as \( O_{i}^{S_k} \). Properties (also called attributes) can be associated with a compartment. A “stock” is a special attribute of a compartment whose value indicates the number of groups of individuals in a compartment. This stock value is modified through transitions (see Section 2.2.4). In a cell, stocks can be used to represent subdivisions of the compartment population representing cohorts from different origins. For instance, if one wants to keep track of individuals in a compartment that have different origins (e.g. migratory birds vs resident birds), a stock can be created for each relevant category of birds. The set of stocks of a compartment \( O^S_k \) is written as follows:

\[
R(O^S_k) = \{ R_{1}^{S_k}, R_{2}^{S_k}, \ldots, R_{m}^{S_k} \}.
\]

2.2.4. Transitions
We distinguish three kinds of transitions: (1) Evolutionary Transitions, (2) Mortality transitions and (3) Cells’ Transitions. Evolutionary transitions represent transitions between compartments, hence the transition of groups of individuals from one stage to another (located in the same cell). A species is associated with a set of evolutionary transitions:

\[
ET(S_k) = \{ ET_{i}^{S_k}, ET_{p}^{S_k}, \ldots, ET_{s}^{S_k} \}. \quad \text{An evolutionary transition} \quad ET_{s}^{S_k} \text{ allows individuals to pass from the compartment} \quad O_{s}^{S_k} \text{ to the compartment} \quad O_{d}^{S_k} \text{ where} \quad s, d, n, \text{being the number of possible and relevant compartments for the species} \quad S_k.
\]

Indeed, \( ET(S_k) \) is a subset of a transition matrix presented in Table 1.

We consider that a transition can be triggered by one or several events and/or one or several conditions (see Section 2.2.5). When a transition is triggered, one or several actions (or activities) take place and make individuals move from one compartment to another. Technically, an event or condition is specified by an expression that returns true or false.

Conditions are associated with events and are used to specify combinations of factors (property values) which must be verified to trigger some change or action, after or before the event occurs.

Table 1. Transition matrix for the compartments of the species \( S_k \).

<table>
<thead>
<tr>
<th>Source Compartment</th>
<th>( O_{1}^{S_k} )</th>
<th>( O_{2}^{S_k} )</th>
<th>\ldots</th>
<th>( O_{n}^{S_k} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( O_{1}^{S_k} )</td>
<td>( ET_{1}^{S_k} )</td>
<td>( ET_{2}^{S_k} )</td>
<td>\ldots</td>
<td>( ET_{n}^{S_k} )</td>
</tr>
<tr>
<td>( O_{2}^{S_k} )</td>
<td>( ET_{2}^{S_k} )</td>
<td>( ET_{3}^{S_k} )</td>
<td>\ldots</td>
<td>( ET_{n}^{S_k} )</td>
</tr>
<tr>
<td>\ldots</td>
<td>\ldots</td>
<td>\ldots</td>
<td>\ldots</td>
<td>\ldots</td>
</tr>
<tr>
<td>( O_{n}^{S_k} )</td>
<td>( ET_{n}^{S_k} )</td>
<td>( ET_{n+1}^{S_k} )</td>
<td>\ldots</td>
<td>( ET_{n}^{S_k} )</td>
</tr>
</tbody>
</table>

An evolutionary transition is denoted by:

\[
ET_{s,d}^{S_k} = \{ O_{s}^{S_k}, O_{d}^{S_k}, E, N, FR^{ET_{s,d}^{S_k}} \}. \quad O_{s}^{S_k} \text{ and} \quad O_{d}^{S_k} \text{ respectively represent the source and destination compartments.} \quad E \text{ represents a set of events and can contain zero or several events.} \quad N \text{ represents a set of conditions. This set can be empty if such a transition can be triggered when an event occurred and there is no condition to evaluate.}
\]

\[
FR^{ET_{s,d}^{S_k}} \text{ represents flow rates of absorption and production between stocks belonging to the two compartments involved in the evolutionary transition.} \quad \text{Indeed, the execution of a transition affects its source stocks (in its source compartment) and its destination stocks (in its destination compartment). The transition absorbs a number of individuals in the source stocks according to the computation of what we call an absorption procedure. It then produces a number of individuals to be added to the destination stocks as computed by a production procedure which takes as parameters the number of individuals that have been absorbed from the source stocks. Absorption and production are represented by flow rates, which are defined in Table 2. Flow rates of a transition} \quad ET_{s,d}^{S_k} \text{ are denoted as follows:}
\]

\[
FR^{ET_{s,d}^{S_k}} = \{ FR^{ET_{s,d}^{S_k}}^{R_{1}^{S_k}}, FR^{ET_{s,d}^{S_k}}^{R_{2}^{S_k}}, \ldots, FR^{ET_{s,d}^{S_k}}^{R_{n}^{S_k}} \}.
\]

The function representing the absorption of individuals from a source stock and the function representing the production of individuals into the destination stock are denoted as follows:

\[
FR^{ET_{s,d}^{S_k}}^{R_{i}^{S_k}} = \{ Absorption(R_{i}^{S_k}, \alpha_1, \beta_1, \ldots, \omega_1),\}
\]

\[
Production(R_{i}^{S_k}, \alpha_2, \beta_2, \ldots, \omega_2)\}
\]
The parameters $\alpha_i, \beta_j, \ldots, \omega_z$ represent different rates of absorption and production.

### Table 2. Flow rates of absorption and production between stocks.

<table>
<thead>
<tr>
<th>Stocks of source compartment</th>
<th>$R_k^{c_1}$</th>
<th>$R_k^{c_2}$</th>
<th>$\ldots$</th>
<th>$R_k^{c_{2n}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stocks of destination compartment</td>
<td>$R_i^{c_1}$</td>
<td>$R_i^{c_2}$</td>
<td>$\ldots$</td>
<td>$R_i^{c_{2n}}$</td>
</tr>
</tbody>
</table>

| Flow rates | $FR_k^{R_k}$ | $FR_i^{R_i}$ | $\ldots$ | $FR_k^{R_k}$ |

Moreover, we consider mortality to be a kind of transition that reduces the number of individuals in a compartment. It is denoted as follows:

$$\lambda T^{MT}_{S_h} = (O_k^{S_h}, \{E_i\}, \{N_j\}, FR^{MT}_{O_i})$$

This type of transition is defined similarly to an evolutionary transition; the only difference being the absence of a destination compartment.

The third kind of transition is called cells’ transition (‘transition between cells’). It allows individuals to move from one compartment of a species $S_k$ located in a cell $C_{1}^{H_j}$ to a similar compartment (with the same types of compartment and species) located in another cell $C_{1}^{H_i}$. A cell’s transition is defined like an evolutionary transition. The only difference lies in the characteristics of the compartments involved in the transition. Indeed, they are of the same type, but belonging to two different cells. Cells’ transition is written as follows:

$$\lambda T^{CT}_{S_{h}, d} = (O_k^{S_h}, \{E_i\}, \{N_j\}, FR^{CT}_{O_i})$$

#### 2.2.5. Events, Conditions and Attributes

We distinguish two kinds of events: (1) change events and (2) interactions (see Section 2.2.6). A change event may be a biological event or a temporal event. A change event can be repetitive (occurring several times during a certain duration). It is generated by the satisfaction (i.e. becoming ‘true’) of a boolean expression representing a condition on certain attribute values. Therefore, one or several conditions may need to be satisfied in order to trigger an event. For example, a change event may occur during the simulation when changing a system state (modifications of some system attributes). A change event has no duration, but rather a time when it occurs. An event is denoted:

$$E_i = \{Id_{E_i}, D_i, \{N_k\}, \{D_f, \text{Periodicity}\}\}$$

$Id_{E_i}$ is the name and/or the identifier of the event. $D_i$ is the start date of the event. $\{N_k\}$ is the set of conditions that ensure that the event is triggered. $D_f$ is optional and represents the end date for recurring events. Periodicity is optional and represents the number of days between two occurrences of a periodic event.

Moreover, a conservation is a boolean expression that consists of a set of expressions linked by logical operators (AND, OR). Each expression is composed of operands and comparison operators ($<, >, \geq, \leq$). Each operand consists of parameters (attributes) and arithmetic operators. We used a BNF grammar in order to specify various kinds of conditions. For example, the condition $value(A_{ij}) > 5 \text{ min}$ may be used to trigger a time event, 5 minutes after the beginning of the simulation. $A_{ij}$ represents a system attribute that corresponds to global parameter of the simulated system (i.e. the time of the simulation). Different other kinds of attributes can characterize the system at a given simulation step as for example the attributes of a cell (denoted $A^{c_{ij}}_j$), the attributes of a species (denoted $A^{s_{ij}}_j$), and the attributes of a compartment (denoted $A^{p_{ij}}_j$).

#### 2.2.6. Interactions

Spatio-temporal interactions between species are commonplace in nature. In our formalism we consider that a species $S_k$ located in the same cell as another species $S_j$ may influence one or several transitions of $S_j$, taking into account a probability of interaction. Species interactions are an important aspect of transitions since very often the transition from one species’ stage to another depends on the probability of finding hosts. However, not every transition requires an interaction. In our case, we consider the interactions between two species that depend on each other. Indeed, we are interested in a host species that allow another species to evolve by taking for example a blood meal (such as in the case of mosquitoes and ticks). Besides, we distinguish two kinds of interactions, considering their possible consequences: (1) instantaneous interactions and (2) sustainable interactions. Instantaneous interaction may result in some evolutionary transitions. For example, individuals of a species may lay eggs after a blood meal (e.g. when mosquitoes bite birds) and thus become infected if the host species is a reservoir of the pathogen. In contrast, sustainable interactions may result in some cells’ transitions. These interactions can potentially lead to the clinging of some individuals to individuals of a host species (e.g. when ticks cling to deers), allowing the transfer of these individuals from one cell to another as a consequence of the individuals’ movements. The list of relevant interactions between the different compartments of two species is written as follows:

$$\text{Interaction}_{S_k, S_j} = \{I^{a_{ij}, a_{ij}}_1 \ldots I^{a_{ij}, a_{ij}}_{n_i} \ldots \}$$

This list is a subset of a two-dimensional matrix. The first dimension is the number of compartments of the species $S_k$ and the second dimension is the number of compartments of the species $S_j$ (see table 3).

### Table 3. Interaction matrix between the two species $S_k$ and $S_j$.

<table>
<thead>
<tr>
<th>Compartment of $S_k$</th>
<th>$O^{S_k}_1$</th>
<th>$O^{S_k}_2$</th>
<th>$\ldots$</th>
<th>$O^{S_k}_{n}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$O^{S_k}_1$</td>
<td>$I^{a_{ij}}_1$</td>
<td>$I^{a_{ij}}_2$</td>
<td>$\ldots$</td>
<td>$I^{a_{ij}}_{n_i}$</td>
</tr>
<tr>
<td>$O^{S_k}_2$</td>
<td>$I^{a_{ij}}_1$</td>
<td>$I^{a_{ij}}_2$</td>
<td>$\ldots$</td>
<td>$I^{a_{ij}}_{n_i}$</td>
</tr>
<tr>
<td>$O^{S_k}_{n}$</td>
<td>$I^{a_{ij}}_1$</td>
<td>$I^{a_{ij}}_2$</td>
<td>$\ldots$</td>
<td>$I^{a_{ij}}_{n_i}$</td>
</tr>
</tbody>
</table>

For example, the interaction between the first two compartments of the two species $S_k$ and $S_j$ is denoted:

$$I^{a_{ij}, a_{ij}}_1 = \{Id_{i}^{a_{ij}, a_{ij}} \cdot \text{Probl}_{a_{ij}, a_{ij}} \cdot \{(T_{ij}^{S_k}, T_{ij}^{S_j}) \ldots (T_{ij}^{S_k}, T_{ij}^{S_j})\} \}$$

$Id_{i}^{a_{ij}, a_{ij}}$ is the name and/or the identifier of the interaction between the two compartments. $\text{Probl}_{a_{ij}, a_{ij}}$ represents the probability of interaction that can occur between individuals of the two compartments. The other two terms (between square brackets) are optional and represent the consequences of the interaction. The first term represents the consequences of an instantaneous interaction. The first consequences (noted $\{T_{ij}^{S_k}, T_{ij}^{S_j}\}$) can result in the activation of one or several
transitions that will make individuals move from the compartment $O^S_i$ to the other compartments of the same species $S_i$. These consequences are a subset of the matrix presented in Table 4a. The second consequences (notated $\{T_{1,1}^S, \ldots, T_{1,n}^S\}$) can result in the activation of one or several transitions that will make individuals move from the compartment $O^S_p$ to the other compartments of the same species $S_p$. These consequences are a subset of the matrix presented in Table 4b.

Table 4. Consequences of an instantaneous interaction.

<table>
<thead>
<tr>
<th>(a) From</th>
<th>To</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$O^S_i$</td>
<td>$T_{1,1}^S$</td>
<td>$T_{1,2}^S$</td>
<td>$T_{1,3}^S$</td>
<td>$T_{1,4}^S$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>(b) From</th>
<th>To</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
<th>$O^S_k$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$O^S_i$</td>
<td>$T_{1,5}^S$</td>
<td>$T_{1,6}^S$</td>
<td>$T_{1,7}^S$</td>
<td>$T_{1,8}^S$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Besides, the second optional term represents the consequences of a sustainable interaction. $Drop_{O^S_i, O^S_p}$ represents a dropping function and parameters such as the average time of the clinging between individuals of two compartments of the two species. $Transfer_{O^S_i, O^S_p}$ represents a function that denotes the transfer of individuals of carrier and hitchhiker species from one cell to another. This transfer may result in the activation of two cells’ transitions. The first one allows the passage of individuals from the compartment of the hitchhiker species to a compartment of the same type, but located in a different cell. The second one allows the passage of individuals from the compartment of the carrier species to a compartment of the same type, but located in a different cell.

3. APPLICATION OF THE MASTIM MODEL

We present in this Section the application of MATSIM to two different cases of infectious diseases in order to illustrate its genericity.

3.1. A Model for the West Nile Virus

WNV is a flavivirus which was isolated for the first time in 1937. Its name comes from the district of West Nile in Uganda. WNV was detected on the American continent in 1999 and more specifically in New York. In Canada, WNV reached southern Ontario in 2001, while the first human cases were detected in August 2002. WNV made its appearance in Quebec in July 2002 [1]. There are mainly two populations involved in the transmission of the WNV: the population of mosquitoes ($Culex sp.$) and the population of birds (we mainly consider the Corvidae family and more specifically crows which have been chosen by public health authorities as indicator birds for the WNV). The transmission of the WNV: the infectious diseases in order to illustrate its genericity.

For the $Culex$ populations, we use six compartments ($O^S_1$: $Culex$ eggs, $O^S_2$: $Culex$ larvae, $O^S_3$: susceptible adult $Culex$, $O^S_4$: exposed adult $Culex$, $O^S_5$: infected adult $Culex$, and $O^S_6$: adult $Culex$ in diapause). The transition matrix for these compartments is shown in Table 5. The grey transitions are relevant for our model while barred transitions are irrelevant.

For example, the transition $ET_{1,2}^S$ which represents the passage from eggs to larvae is relevant, but the transition $ET_{3,1}^S$ which represents the passage from larvae to eggs does not make sense.

For the $Crows$ populations we use four compartments ($O^S_1$: susceptible $Crows$, $O^S_2$: infected $Crows$, $O^S_3$: dead $Crows$, and $O^S_4$: recovered $Crows$). The transition matrix for these compartments is shown in Table 6. Based on the interaction matrix (Table 7), the list of relevant interactions between different compartments of $Culex$ and $Crows$ is denoted:

$Interaction_{S_i, S_j} = \{I_{O^S_i, O^S_j}, I_{O^S_i, O^S_j}, I_{O^S_i, O^S_j}, I_{O^S_i, O^S_j}, I_{O^S_i, O^S_j}\}$.

Table 5. Transition matrix for the compartments of $Culex$.

<table>
<thead>
<tr>
<th>From</th>
<th>To</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>$ET_{1,2}^S$</td>
<td>$ET_{2,1}^S$</td>
<td>$ET_{3,1}^S$</td>
<td>$ET_{4,1}^S$</td>
<td>$ET_{5,1}^S$</td>
</tr>
<tr>
<td>$O^S_1$</td>
<td>$O^S_2$</td>
<td>$O^S_3$</td>
<td>$O^S_4$</td>
<td>$O^S_5$</td>
<td>$O^S_6$</td>
<td></td>
</tr>
</tbody>
</table>

Table 6. Transition matrix for the compartments of $Crow$.

<table>
<thead>
<tr>
<th>From</th>
<th>To</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
<th>$O^S_i$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>$ET_{1,2}^S$</td>
<td>$ET_{2,1}^S$</td>
<td>$ET_{3,1}^S$</td>
<td>$ET_{4,1}^S$</td>
<td>$ET_{5,1}^S$</td>
</tr>
<tr>
<td>$O^S_1$</td>
<td>$O^S_2$</td>
<td>$O^S_3$</td>
<td>$O^S_4$</td>
<td>$O^S_5$</td>
<td>$O^S_6$</td>
<td></td>
</tr>
</tbody>
</table>

Table 7. Interaction matrix between $Culex$ and $Crow$.

<table>
<thead>
<tr>
<th>Compartment of $Crow$</th>
<th>$O^S_1$</th>
<th>$O^S_2$</th>
<th>$O^S_3$</th>
<th>$O^S_4$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$O^S_1$</td>
<td>$I_{O^S_1, O^S_1}$</td>
<td>$I_{O^S_1, O^S_1}$</td>
<td>$I_{O^S_1, O^S_1}$</td>
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In Figure 1, we present a graphical representation of the dynamics and interactions (conforming to tables 5 to 7) of the Culex and Crows species involved in the spread of WNV. The biological cycle of the Culex population includes the disease effects represented by 6 compartments and 9 transitions. Moreover, 4 compartments and 3 transitions are used to represent the biological cycle of the population of crows. Each rectangle represents a compartment and an arrow containing a small circle represents a transition between compartments. This circle acts as a container that can receive other arrows (shown with small dots) representing the consequences of the interactions. Moreover, we use others arrows (shown with interrupted lines) and other small circles (they are isolated and therefore are not like those attached to transitions) to precisely represent the interactions between the different compartments of Culex and crows. For example, $I_{O^1}^{S}$ (see bottom of Figure 1) is an interaction representing the bite of a group of susceptible crows by a group of infected Culex adults. As a result of this interaction, the susceptible crows may become infected crows (i.e. transition $ET_{2,3}^{1}$) and the infected Culex adults may lay eggs (i.e. transition $ET_{5,1}^{1}$). Besides, the mortality transition is plotted using an arrow started from a compartment and ending with a bar, which represents the fact that individuals have died and are resorbed by the system. Moreover, we use a rectangle with rounded corners to globally represent species other than crows (and denoted $S_{h,w,l,2}$) that may be bitten by Culex.

We found out that this addition is mandatory in order to avoid developing a too simplistic model in which crows are the only species bitten by mosquitoes (Figure 1).

3.2. A Model for the Lyme Disease

Lyme disease which is a borreliosis caused by a bacterium (Borrelia burgdorferi) is carried and transmitted to human by ticks (Ixodes scapularis). The first description of this disease has been made in the United States in 1977 in the town of Lyme, Connecticut. Ticks generally live in wooded areas or tall grass. Small rodents and certain types of birds (especially migratory species) are considered as the natural reservoirs of the bacterium. Moreover, White-tailed deer (Odocoileus virginianus) is the most common host for the adult stage of ticks [9].

We used Ogden’s model [9] in order to represent the different compartments involved in the biological cycle of ticks. We only present here the graphic representations since the principle of using matrices was well elucidated in the previous example (WNV). Indeed, Figure 2 only presents a graphical representation of the interactions between tick and rodent populations involved in the spread of Lyme disease. We created similar models for the interactions between ticks and other species involved in the propagation of the disease such as birds and deers, but we cannot present them here due to lack of space. For the population of ticks, we take account for the biological cycle as well as the infection by the bacterium. We use sub-compartments in order to properly represent the different stages of the ticks’ evolution. For example, the susceptible larvae compartment contains four sub-compartments: (1) hardening, (2) questing, (3) feeding, and (4) engorged larvae. A new aspect that is worth to mention is the use of transitions between compartments and sub-compartments. For example, the transition $ET_{2,1}^{3}$ represents the passage of individuals from the compartment eggs $O_{1}^{S}$ to the sub-compartment hardening $O_{2,1}^{S}$. For the population of rodents, we only use two compartments (susceptible and infected rodents) and one transition. In fact, we made a simplification by not taking into account the juvenile rodents (as Ogden et al. did) since we do not need to go at this level of detail in the present model. Moreover, Figure 2 shows six different interactions between ticks and rodents. For example, $I_{O_{2}^{S}O_{2}^{S}}^{S}$ is an interaction representing a clinging of a feeding infected nymph ($O_{2}^{S}$) on a susceptible rodent ($S_{1}^{S}$). Following this interaction, the susceptible rodent may become an infected rodent (i.e. transition $ET_{3,2}^{1}$) and the feeding infected nymph may become engorged (i.e. transition $ET_{5,2}^{1}$).
4. CONCLUSION AND FUTURE WORK

In this paper, we presented a new generic model used to simulate the propagation of an infectious disease, taking into account the spatio-temporal characteristics of this phenomenon. We applied this model to two different cases of zoonoses: WNV and Lyme disease. Our model provides several advantages if we compared it to the classical compartmental models which have been used to simulate the propagation of epidemics up to now [2,9]. Indeed, classical compartmental models do not take into consideration the characteristics of the geographical space in which populations operate. In contrast, our approach allows us to clearly specify all the interesting aspects of an ecological system to be simulated, and especially the spatio-temporal interactions between the different actors involved in the zoonosis propagation. In addition, our approach allows for the development of generic models that can be used not only to simulate the propagation of WNV or Lyme disease, but also that can be adapted to various other phenomena that do not necessarily relate directly to the spread of such zoonotic diseases. This innovative model opens the door to the study and control of other pandemic diseases (such as SARS). Moreover, simulation based on classical compartmental models can only give results at a very aggregated level (so called 'macro level') without taking into account details of the geographic space and its influence on the studied phenomena. Such models are useful to establish guidelines for actions at a strategic level (and support political decisions). In contrast, our approach can produce simulations at different levels (that’s why we used hierarchical levels $H_i$ of granularity (i.e., 'Macro', 'Meso' and/or 'Micro') that fit with the decision makers’ interests. It can help policymakers to establish guidelines for action at a strategic level, as well as help tactical or operational decision makers to develop plans for intervention at more detailed levels. For future works, we plan to refine our model and we are particularly interested in modelling processes such as the birds’ migrations that are the major import of ticks in Quebec from the US. We also plan to calibrate our model using the data collected in the field. Moreover, we are currently using MASTIM to develop our generic tool Zoonosis-MAGS. We have completed the architecture of our new system and we are currently implementing it.

5. REFERENCES

effects of climate on geographic range and seasonality of the tick Ixodes scapularis.” Int. J. Parasitol. 35, pp. 375-389.