COMPLEX ENVIRONMENT REPRESENTATION IN EPIDEMIOLOGY ABM: APPLICATION ON H5N1 PROPAGATION

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ABSTRACT

Agent-based models (ABM) are becoming standard tools to study complex systems especially in ecology and more recently in epidemiology. The developments of models in these domains have highlighted the need for more complex representations of the environment. In this paper, we present an individual-based epidemiological model that has the particularity to make heavy use of geographic data and complex spatial operations. From this example, we review several popular ABM simulation platforms. These platforms do not answer such model's requirements in a whole. In order to answer this problem, we propose a new approach to represent the environment in ABM. This approach along numerous spatial operations tools has been implemented in the GAMA simulation platform, which is described in this paper.

Keywords. agent-based model, environment representation, epidemiology, simulation.

1. INTRODUCTION

The H5N1 virus, which causes the avian influenza, is still a major threat for both economy and health. It has spread over Asia, Europe and some parts of Africa. Nowadays, the endemic appears to be circumscribed to South East Asia mainly. Nevertheless, the eradication of the virus is far from being achieved, and especially in Vietnam, where it is considered as endemic [1].

Many prophylactic measures such as improved hygiene, vaccination, monitoring and so on have been tested to eradicate the virus but none are really successful yet. Thus this eradication is one of the greatest challenges for modern epidemiology. According to epidemiologists, proposal of effective prophylactic measures need to rely on a good knowledge of the propagation and persistence mechanisms of the virus at a local scale. Concerning this propagation, epidemiologists have already proposed several hypotheses. However, testing them is impossible either on the field or in laboratory for practical and deontological reasons [2]. The only possible way is to use models.

However, designing a model adapted for this study is quite a challenging task. . The first reason is the major re-organization of the agricultural sector in Vietnam. It is accommodating a rapid expansion of the (semi-) industrial sector and a still omnipresent traditional sector. It is, then, impossible to have a relevant schematic view of the system. The second reason comes from the epidemiologists' hypotheses, which focus on the role of the environment. Consequently, an explicit representation of the environment has to be included in any model if it is to be useful. In

addition, the influence of the environment on the agro-production system, and its interactions with it, are not clearly understood by epidemiologists. Thus, building a model that would allow for the exploration of possible interactions or evolutions of the system is a major objective. The last reason is that the topologies and characteristics of the villages are suspected to have a strong influence on the dynamics of the disease. Thus, it is required to use real (geographic and demographic) data from the field.

For all these reasons, the most promising type of modeling techniques available today appears to be agent-based modeling (ABM), combined with an explicit representation of the environment stored in a Geographical Information System (GIS).

In this paper, we propose an agent-based model of the H5N1 propagation in North Vietnam. This model takes into account a complex representation of the environment. As we will show, the development of this model has required the use of advanced spatial features. In this context, we propose a new approach to represent and manage the environment in ABM.

In Section 2, we present the context of this work: the epidemiologic modeling. Section 3 is dedicated to the presentation of our agent-based model. In Section 4, we present several simulation platforms that may have been used to implement our model and introduce the GAMA simulation platform [3, 4], chosen for its high-level integration with environmental representations. Finally, we conclude and give some perspectives in Section 5.

2. EPIDEMIOLOGIC MODELING: AN EVER-EXPANDING CONTEXTUALIZATION

This section briefly presents the evolution of modeling in epidemiology through the questions it was appointed for by epidemiologists and the public. We will see that the early models did not take much of the context (environment, social context) into account, while the newest models tend to be fully aware of this context, up to very precise representations of the spatial environment.

2.1. Population-based models

In the early days of epidemiologic modeling, the first question that a model had to answer was "how long an epidemic would continue?". Kermack and McKendrick [**5**] proposed an analytical model (SIR) where the population is divided into three compartments: 'Susceptible' (not exposed to the virus yet), 'Infected' (having received the virus and transmitting it), 'Recovered' (immune or dead after infection). This model is based on ordinary differential equations (ODE) and allows forecast of the epidemic.

Many refinements have been made to this type of models, by adding compartments (e.g. the 'Exposed' compartment) or even adding a reference to the environment [**6**]. Nevertheless, these models still rely on global parameters, average behaviors of the population and do not allow to take into account local (i.e. non-macroscopic) dynamics.

2.2. Micro-simulation and cellular automata

In order to take into account local dynamics, micro-simulation models were proposed later. These models propose, in addition to global parameters, to represent individuals, usually in a matrix where each vector is an individual of the population. Global functions are computed over the matrix to make each individual (and thus the population) evolve. A good example of such an epidemiologic model is detailed in Artzrouni et al. [7].

However, even though the attributes of individuals are accounted for, these models do not take into account their relationships, for instance the impact of neighboring relations.

Cellular automata (CA), another set of techniques introduced approximately at the same time, partly address this issue. They allow for an explicit representation of the neighboring relations between individuals. Thus, they allow to investigate these relations and to propose, for instance, new mitigation measures such as vaccination strategies, or to study, for example, the effect of immunity (clearly described in [8]).

Despite this better accounting of individuals and space in CA, a question still remains: what if the individuals have different behaviors?

2.3. Agent-based models

2.3.1. "Classic" Agent-Based Models

ABM is a possible answer. In these models, agents, representing individuals of the real system, can be given detailed and complex behaviors. Yorke et al. [**9**] has, for example, realized a basic yet easily extensible model of the epidemic of a generic disease transmitted by contact. Nevertheless, even in ABM, the question of the reciprocal influences between the environment and the individuals is still not addressed.

The first way to take into account the environment is to use a schematic representation whether it is a n-patches environment, a grid or a network of places. Muller et al. [**10**] evaluated such representations. Although they conclude that ABM has great potential for epidemiological modeling, they also point out that a more detailed representation of the environment has to be proposed.

2.3.2. ABM with explicit and detailed environmental representation

We claim in this paper that it is possible to represent the environment in an ABM in a much more precise way than by using grids or patches thanks to the recent development of GIS. This approach is developing since a few years. A good example is EpiSims [11], which integrates several sources of data and especially geo-referenced ones. This model allows exploring various scenarios about smallpox epidemics in a realistic virtual city with explicit representations of individuals. Another one, EpiSim [12], operates at the level of the districts of Portugal and takes into account social and environmental data with the same priority. Simulations of the model were able to reproduce the 1996 mump epidemic. The third and final example, SimPest [13], allows investigating the persistence of plague in rural areas of Madagascar. The objective of this model is to use real geographical data in order to correlate environment specificities and the plague endemic. Due to a difficult access to real data, the simulation were mainly conducted on prototypical data, though two real villages have been simulated with success.

2.4. Conclusion on evolution of epidemiologic modeling

We have seen that the evolution of research questions in epidemiology has an impact on the modeling techniques used: differential equations are well suited for a global point of view and the study of population-level dynamics; micro-simulations allow to focus on individual heterogeneity in terms of attributes; cellular automata add an explicit, albeit simple, representation of space; finally, agent-based models *discretize* individual's behavior and allow

for a more detailed representation of the environment through their coupling with GIS. This latter technique is the one we have developed and used in the GAMAVI model, presented below.

3. GAMAVI MODEL

In this section, we present the key elements of the model (GAMAVI) we have proposed for the study of H5N1 propagation in North Vietnam. To do so we use the ODD standard [14, 15].

3.1. Overview

The real system modeled here is the H5N1 endemics in the traditional and semi-industrial poultry production sector in the Red River Delta (North Vietnam). We limit the system represented to a village (several prototypes were determined using principal component analysis). Within this system, we focus on farms and poultry flocks (ducks or chicken). These flocks have different type of production: closed-building, with access to a pond, free-range (going to rice-fields at daytime) and backyard (roaming in the village at daytime). As implied by this description several natural environments are represented: buildings, inner-village ground, roads, rice-fields (flooded or dry) and ponds.

3.1.2. Purpose

Epidemiologists want to study the mechanisms of local spread and persistence of H5N1 in the context of semi-industrialized and traditional poultry sectors in North Vietnam. Their hypotheses focus on the agro-system, the social environment (village and culture) and their interactions. The purpose of GAMAVI is to investigate and evaluate the importance of various factors, including poultry production, environments (especially aquatic ones), topography, etc, on the persistence and spread of H5N1 within a village or a commune in the Red River delta. Specifically, the model is about investigating the relationships between environments (as virus reservoirs) and the traditional or semi-commercial poultry production systems.

3.1.3. Entities, state variables and scales

The model considers mainly three kinds of entities: poultry flocks, farms and virus reservoir in the general environment: rice-field and pond.

3.1.3.1. Entities

– *Poultry flock*

They are the main type of entities in our system. These groups hold homogeneous individuals (with respect to their species, age, behavior and location) so it is not mandatory to represent explicitly the individuals. Nevertheless, the infectious status of each individual can be different. It is held, within the flock, in an *infection matrix*. In general, production occurs all year long, flocks are kept indoors and the whole flock is renewed when needed.

In addition to this general type, the model includes two types of flocks called "free range duck" and "backyard". The first ones represent a seasonal production (warm season) because they go and graze in rice fields. A "backyard" flock (90% of households own one) is a mix of different species; (taken into account in the individual matrix), with a continuous renewal process (private consumption).

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Table 1. Flocks' state variables

Variable name	Brief description
Matrix of individual	Representing each individual's infection status (SIR) and elapsed time in this status. Species information is added in the backyard case
Location	Which environment it is in
Species	It can be backyard, chicken, duck, Muscovy duck
Number of individuals	Determined at creation and thus implies the matrix
Production type	Outlet (meat/egg), it determines length of production and seasonality
Housing	Whether the flock is kept indoors all the time or not
Within-flock infection probability	A daily probability for an infected individuals to infect each susceptible individuals
BID50*	Quantity of virus to ingest to get 0.5 probability of getting infected
Excretion rate*	Quantity of virus excreted per time step
Renewal transmission probability	If the flock is infected it might leave virus within the building after its renewable and thus infect the new flock (0 means there is a building quarantine procedure)

*: duck and Muscovy duck.

– *Farm*

They aggregate several flocks and are responsible of the production dynamic.

Table 2. Farms' state variables

Variable name	Brief description
Location	Coordinates
List flock types	Parameter to know which to create at first and at renewal
Renewal dates	List of list of dates at which each flock should renewed
Intra-farm infection probability	Daily probability for an infected flock of the farm to infect a susceptible one (compound with the number of infected individuals)
Inter-farm infection probability	Daily probability for an infected farm to infect a susceptible flock of another farm (compound with the number of infected individuals)

3.1.3.2. Environment

First, the environment allows spatialization of the entities (localization and movement). Second, it is a medium of transmission of the H5N1 virus. To do so we use vector GIS data

(corresponding to the inner village and its rice-field area surrounding) where entities are localized and moves.

A grid is added and used as a virus transmission medium. The grid's cells are responsible of the virus depletion rate (differentiated by the type of natural environment they represent). Finally, a grid with a lower resolution is used to represent rice-field lots as free-range ducks stay during daytime within one lot.

3.1.3.3. Scales

The whole represented system is the village that is a few kilometers side. The smallest elements are farm buildings, a dozens of meters side, while rice-fields are a few hundred square meters. As the model is about persistence of the virus in the village for more than a year, the simulated time can be up to two years. The smallest time step is set to one hour in order to represent the movements of flocks but a daily time-step is used for the production and infectious status related processes.

3.1.4. Process overview and scheduling

- *Flock*
- *Infection processes*

Flocks' main processes are related to infection and all are parameterised with species-dependent rates:

- Hourly excretion and virus collection
- Daily computation of direct transmission (within flock)
- Daily computation of environment mediated infection (ponds and watered rice-fields)
- Daily individuals' infectious status update (infectious to recovered)
- Daily natural death
- *Movement processes*
- Backyard flocks wander within the village (random movement), at night they go back to the farm by the shortest path.
- Free-range flocks go graze in the rice-fields with predefined schedule:

1. Selection of the rice-field: it must be free (not taken by another flock) within a defined range from the farm

2. Leaving the farm: shortest path to the nearest point of the village's outskirt to the selected rice-field

3. Grazing: stay in the rice-field (no movement)

4. Go back to farm following the reversed scheme

– *Farm*

Farms are responsible for production dynamics. Farms renew flocks according to a schedule (production type dependent). This renewal can be instantaneous or includes a building quarantine (a few days). Backyard flocks are handled specifically because of the continuous consumption. Regularly, one individual is "renewed" (or consumed).

The farm renews its flocks according to 'renewal dates' (see input for details of how is generated this list). Each day the flock checks the 'renewal dates' if any flocks are to be renewed the current flock is deleted. A new one is created according to the 'renewal dates' list, immediately most of the time.

– *Viro-grid cells*

• Receiving virus from a flock: increases the virus concentration

• Decrease of the virus concentration according to temperature dependent equation [16].

• Change of season: rice-field type cells become watered in the warm (and dry during the cold one). It changes the depletion rate of the virus.

3.2. Details

3.2.1. Initialization

First, vector data are loaded in order to build the continuous environment which used by agents to move. Then the two grids (viro-grid and rice-fields grid) are instantiated from these data using geometrical operations. At initialization, the viro-grid cells are free for virus

Then, the date of beginning of simulation is defined in order to set which seasonal flocks are to be created. Flocks have an "age" randomly set because of the renewal process (if not renewal would be synchronized). Depending on the season, rice-fields will be watered or dry. Flocks are all located within the farms (we assume it is the beginning of the day 00am) and their individuals are all susceptible to be infected except some individuals in some flocks according to a parameter (initial infection).

3.2.2 Input

– *Environment*

We have vector data of nine different villages from Bac Giang and Ha Tay provinces, which can be used as nine different environmental inputs. They contain the localization of houses, inner-village grounds, rice-fields, road/street and ponds. Monthly temperatures are used for the computation of the virus reservoir's depletion rate (data from Bac Ninh station).

– *Poultry production system*

Table 3. Input data

Name	Brief description
Number of backyards	Usually 90% of households
Number of farms	

Distribution of flocks per farm	
Distribution of flocks per production type	X% free-range ducks, Y% short time chicken
Configuration of flocks per production type	Includes: size, duration, renewal pattern, seasonality
Seasonality	
Water consumption	Ducks only
Wandering time	Free-range & backyard flocks
Natural death rate	Per species

3.3. Features linked to the environment required in GAMAVI

In our model, the first requirement comes from the dual function of the environment: it is both a topological space and a medium of transmission. Consequently, we have GIS field data that are used to represent the village and its topology, while a grid is used to represent the virus dispersal and persistence.

Concerning localization in space, we need to be able to represent the different moving behaviors of poultry flocks: random movements and shortest path movements within the inner village, straight movements within the rice-field areas. We also need to represent a path between farms, the inner village area, the ponds and the rice-field area. Finally, as the free-range flocks stay in the same rice-field lot all day long we need to represent these lots in the rice-field area. To do so, another grid is used. The definition of this grid is parameterized with the average size of rice-field lots.

4. REPRESENTATION OF THE ENVIRONMENT IN EXISTING PLATFORMS

In this section, we briefly introduce some of the major agent-based simulation platforms that could have been used to implement our model. From the previously expressed requirements we will present for each platform the specific drawbacks that lead us to use the GAMA simulation platform.

4.1. Simulation platforms with minimal support for complex environments

Swarm [17] is a well-established simulation platform and an inspiration for many others. At first, the environment is not accounted for. However , several libraries have been implemented in order to offer classic grids. The support for GIS, is also offered by a tool like Kenge [18]. It loads raster data and creates a cellular-automata based environment.

Netlogo [19] is also a well-established simulation platform, largely used for educational purpose and also for research. Basically, the environment is made of a 'patches' grid though agents have their coordinates defined in a continuous space. Patches can have behaviors. Other services offered are: diffusion, distance, agents/patches within a radius, neighbors, etc. The GIS support has been added recently through an extension. It allows import and export of raster and vector data with or without projection. Vector data polygons attributes are made accessible as well as their geometric attributes (centroid, list of vertex, etc.). Some basic geometrical operations are also available (bounding rectangles, union of polygons, etc.). Unfortunately

Netlogo is not open source and other services that may be required by a model can not be added easily to the platform.

4.2. Simulation platform with limited support for complex environments

CORMAS [20] is a platform initially dedicated to the natural resources management issues but used in ecology related issues in general. It is developed in Smalltalk language in the Visual Works IDE. There are 2 environmental modes: a vector and a raster mode. They have the same organization that includes 3 classes called "spatial entity", "agent" and "object". This organization allows to have a standard protocol for movement but make it quite rigid. Within CORMAS, only basic services are provided (like localization, neighborhood, basic movement and perception). The modeler has to implement any other higher-level service.

In 2008, Urbani proposed the SMAG (portmanteau word from SMA-SIG) architecture and implemented it over CORMAS, calling it CORMGIS [21]. The author used only a "loose link" [21] between MAS and GIS (exchanging data), with the GIS (shared code). The GIS part is made of the use of ArcGIS only. Access to geo-referenced data is made only through a data connection (no access to GIS service) and in raster mode only. It is not a real integration of GIS services in an MAS simulation platform, just a bridge.

4.3. Simulation platform with advanced support for complex environments

Repast3 [22] is a modeling toolkit inspired by Swarm. It has three different "pure" implementations in Java (RepastJ), C# and python. We will focus on the first implementation. As a toolkit, RepastJ includes only basic services. Grids are implemented (hexagonal or rectangular cells, torus or not, Von Neumann or Moore neighboring) but agents are not (only an interface is given). The GIS support is done thanks to a link with the OpenMap library. OpenMap offers the basic services of any GIS: importing/exporting of shapefiles and raster data, geometrical operations, access to data attributes, etc. However, as RepastJ is a toolkit and provides only access to OpenMap, the modeler has to program almost everything when it comes to more complex operations. This requirement, especially when using GIS, is far from reach of non computer scientist modelers.

Repast Symphony (RepastS) [23] is an updated version of the Repast toolkit. It provides the same basic features as RepastJ, but offers additional GIS tools. In particular, RepastS allows to directly model a network of lines as a graph and to compute the shortest paths from one point to another. It allows as well visualizing and managing 3D data.

RepastS shares some of the limitations of RepastJ: it does not provide tools to directly synchronize several environmental representations (like grids and GIS data) and only provides basic GIS functions. For example, it provides no function of displacement inside a specific geometry.

5. ENVIRONMENT'S REPRESENTATION IN GAMA

5.1. The GAMA multi-agents based simulation platform

GAMA [4] is a recent simulation platform that has been developed by the research team MSI (part of the IRD International Research Unit UMMISCO) since 2007. It provides a complete modelling and simulation development environment for building spatially explicit multi-agent simulations. The main advantage of this platform is the simplicity to define a model

with it. Indeed, GAMA provides a rich XML-based modelling language, GAML, which can be easily extendable.

The idea of GAMA concerning the management of environment is to locate the agent in a continuous environment, which serves as a reference. In this environment, all of the agents are provided with a geometric representation. The geometry of an agent can be simple (a point, a polyline or a polygon) or complex (composed of several sub-geometries). When loading GIS data to describe agent geometries, they are automatically projected in the continuous environment.

All of the computations related to spatial relationships are made refer to the reference environment. Thus, the distance between two agents, the overlapping of geometries, etc., are directly computed from it. In addition, the role of the reference environment is to adapt all the situated actions of agents (movement, action, interaction) to all registered environments. Thus, for example, when an agent moves, the reference environment manages itself the movement of the agent on the potential grids. This operation is totally transparent for the modeler, who does not have to manage the synchronization of the different environments.

In GAMA, several spatial features have also been implemented to ease the work of the modeler:

• Computation of the geometry resulting from the union, intersection or difference of different agent geometries

• Computation of the distance between complex geometries

• Computation of an agent neighborhood (that takes its geometry into account).

• Computation of shortest paths inside any geometry (line networks or polygon) between two places located in the geometry.

Concerning this last point, our approach consists in modeling the geometry as a graph, and in computing from it the shortest path between the two places. In the context of a line network, the modeling as a graph is trivial. In the context of a polygon, it is based on a Delaunay triangulation of the geometry: each triangle resulting from the triangulation is modeled as a node and an edge represents the fact that two triangles are adjacent. Figure 1 shows an example of automatic triangulation of a complex polygon that contains holes.
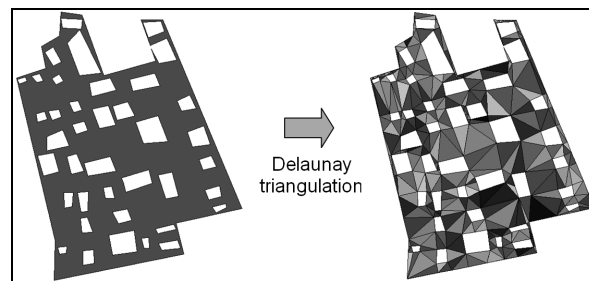
Figure 1. Delaunay triangulation of a complex polygon

5.2. Use of GAMA features in GAMAVI

The environment is based first on field data stored as shape-files (vector data). The village itself and its rice-field or surroundings are created from these shape-files.

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The environment used for localization is directly created from it. This environment is constituted of polygons. In order to connect ponds, farms, inner village area and rice-field area, a Delaunay triangulation is conducted on the inner-village. It defines a connectivity graph linking the different places together. It allows random movement within the inner village. On this graph, a *Floyd-Warshall* shortest path algorithm [24] is computed to allow directed shortest path movement of poultry flocks within all the previously stated places. Figure 2 shows this representation within the GAMA simulator interface. The vector environment shown (right end part) comprise: rice-field areas (green), the heart of the village with farms (beige), ponds (blue), flocks (fully susceptible are green, infected are red) and links from farm (beige) show where a flock (free-range or pond ducks) is going for the current day.

The collecting and depletion of the virus in the environment is done thanks to a fine-grained grid called the viro-grid. Basic geometrical comparisons are conducted between this grid and the vector data to define the natural environment type of the cells. Concerning the collection of the virus, the excreting flocks update an *excretion* variable of the cell; at the end of a time-step a behavior updates the current concentration according to this variable; finally a daily behavior is executed in order to compute the depletion of the virus level.

In order to simulate the rice-field lots we define another grid. Each cell of this grid represents a rice-field lot. Actually, when the grid is created, each cell checks if it is contained in the rice-field area, if not the cell is not active.

The two grids and the continuous environment are seamlessly and automatically synchronized thanks to the GAMA's environment management.
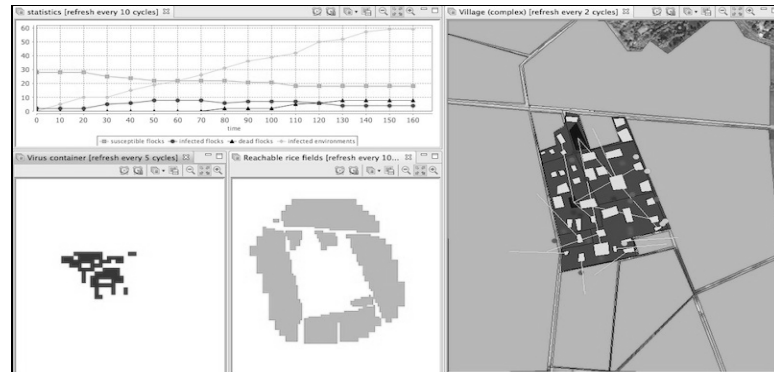

Figure 2. The simulated system with four panes: the epidemics evolution, the viro-grid, the rice-fields grid and the vector environment

5. CONCLUSION

In this paper, we highlighted the importance of having a rich representation of the environment to study epidemiologic problem. In this context, we presented a model dedicated to the study of the H5N1 propagation. The implementation of this model had required the synchronized use of a continuous environment and grids. It had also required the use of complex spatial operations. In this context, we have shown the limitations of the existing simulation platforms in terms of environment representation and management. In order to tackle this issue, we have proposed a new approach to represent the environment. In addition, we have proposed

to integrate in the simulation platform a set of advanced spatial features easing the modeling task. This workhave been implemented in the GAMA simulation platform [3].

We intend to represent a graph of infection, which is a common tool for epidemiologists, in order to ease the epidemiologists' understanding of simulation. , It will also allow to do centrality computation which possibly points out key farms in the epidemics process.

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